



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 06:03 AM UTC

PDB ID : 6IP8 / pdb_00006ip8
EMDB ID : EMD-9703
Title : Cryo-EM structure of the HCV IRES dependently initiated CMV-stalled 80S ribosome (Structure iv)
Authors : Yokoyama, T.; Shigematsu, H.; Shirouzu, M.; Imataka, H.; Ito, T.
Deposited on : 2018-11-02
Resolution : 3.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

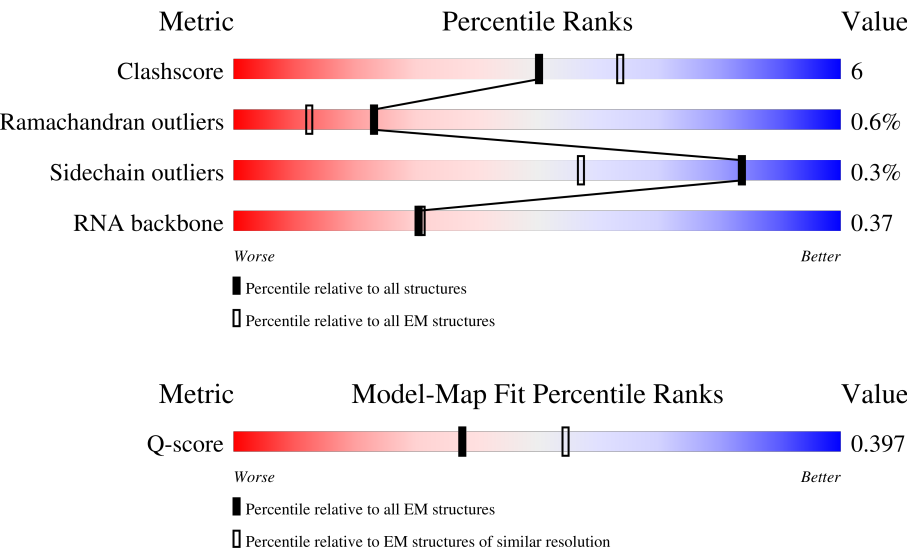
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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

Mol	Chain	Length	Quality of chain
1	1A	5070	
2	1B	121	
3	1C	157	

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Mol	Chain	Length	Quality of chain
4	1D	257	
5	1E	403	
6	1F	427	
7	1G	297	
8	1H	288	
9	2A	248	
10	2B	266	
11	2C	192	
12	2D	214	
13	2E	178	
14	2F	211	
15	2G	215	
16	2H	204	
17	2I	203	
18	2J	184	
19	2K	188	
20	2L	196	
21	2M	176	
22	2N	160	
23	2O	128	
24	2P	140	
25	2Q	157	
26	2R	156	
27	2S	145	
28	2T	136	

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Mol	Chain	Length	Quality of chain
29	2U	148	
30	2V	159	
31	2W	115	
32	2X	125	
33	2Y	135	
34	2Z	110	
35	2a	117	
36	2b	123	
37	2c	105	
38	2d	97	
39	2e	70	
40	2f	51	
41	2g	128	
42	2h	25	
43	2i	106	
44	2j	92	
45	2k	137	
46	2m	1869	
47	2n	295	
48	2o	264	
49	2p	243	
50	2q	263	
51	2r	204	
52	2s	194	
53	2t	208	

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Mol	Chain	Length	Quality of chain
54	2u	165	
55	2v	158	
56	2w	145	
57	2x	146	
58	2y	135	
59	2z	152	
60	20	145	
61	21	119	
62	3A	83	
63	3B	143	
64	3C	115	
65	3D	69	
66	3E	56	
67	3F	317	
68	3G	293	
69	3H	249	
70	3I	194	
71	3J	132	
72	3K	151	
73	3L	151	
74	3M	130	
75	3N	133	
76	3O	125	
77	3P	84	
78	3Q	59	

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Mol	Chain	Length	Quality of chain
79	3R	156	32% 35% 8% 57%
80	zV	12	17% 67% 17% 17%
81	zW	431	63% 85% 15%
82	zX	17	47% 76% 24%
83	zY	75	5% 64% 29% 7%
84	zZ	290	10% 22% 29% 5% 44%

2 Entry composition [i](#)

There are 84 unique types of molecules in this entry. The entry contains 222618 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	3667	Total	C	N	O	P	0	0
			78599	35000	14383	25550	3666		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1B	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1C	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1D	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1E	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1F	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1G	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1H	237	Total	C	N	O	S	0	0
			1913	1228	363	318	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	2A	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	2B	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	2C	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	2D	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	2E	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2F	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2G	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	2H	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	2I	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2J	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	2K	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2L	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	2M	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 22 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2N	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2O	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 24 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	2P	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	2Q	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	2R	119	Total	C	N	O	S	0	0
			976	625	184	166	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2S	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2T	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2U	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	2V	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	2W	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	2X	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	2Y	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2Z	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2a	113	Total	C	N	O	S	0	0
			895	560	183	146	6		

- Molecule 36 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	2b	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	2c	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2d	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	2e	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	2f	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	2g	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	2h	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	2i	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	2j	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2k	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2m	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 47 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	2n	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2o	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2p	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 50 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	2q	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 51 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	2r	187	Total	C	N	O	S	0	0
			1479	924	282	266	7		

- Molecule 52 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2s	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 53 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2t	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 54 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2u	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 55 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	2v	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 56 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	2w	97	Total	C	N	O	S	0	0
			804	505	155	138	6		

- Molecule 57 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	2x	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 58 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	2y	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 59 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	2z	150	Total	C	N	O	S	0	0
			1235	776	250	208	1		

- Molecule 60 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	20	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 61 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	21	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 62 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	3A	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 63 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	3B	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 64 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	3C	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 65 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	3D	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 66 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	3E	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 67 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	3F	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 68 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	3G	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 69 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	3H	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 70 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	3I	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 71 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	3J	122	Total	C	N	O	S	0	0
			952	596	169	179	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3J	52	GLN	LEU	conflict	UNP P25398
3J	69	LEU	CYS	conflict	UNP P25398
3J	99	ASN	LYS	conflict	UNP P25398

- Molecule 72 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	3K	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 73 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	3L	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 74 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	3M	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 75 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	3N	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 76 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	3O	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	3P	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	3Q	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	3R	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 80 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	zv	12	Total	C	N	O	P	0	0
			247	111	39	85	12		

- Molecule 81 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	zw	431	Total	C	N	O	S	0	0
			3410	2168	575	655	12		

- Molecule 82 is a protein called nascent peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	zx	17	Total	C	N	O	S	0	0
			129	86	20	22	1		

- Molecule 83 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	zy	75	Total	C	N	O	P	0	0
			1599	713	284	528	74		

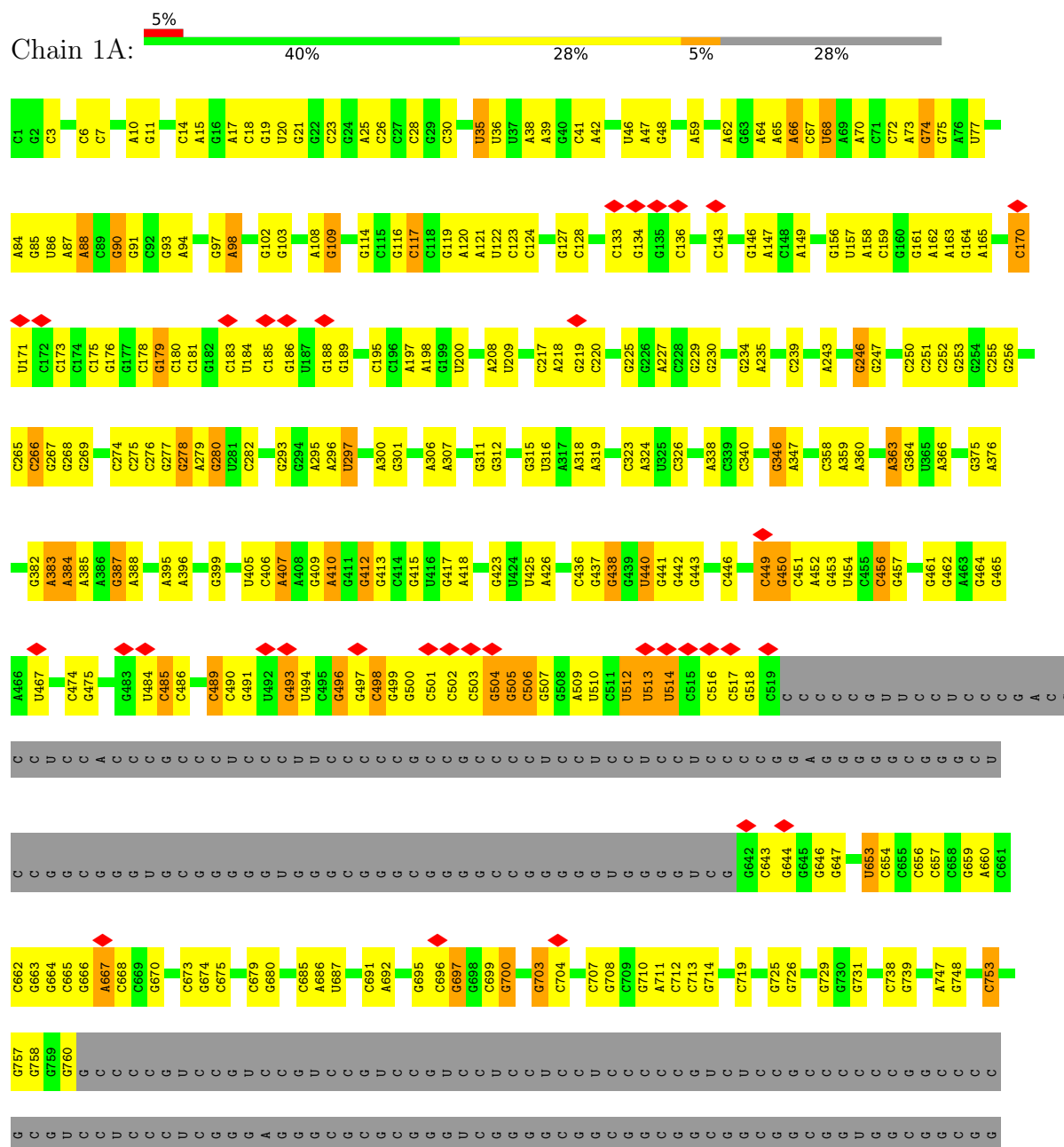
- Molecule 84 is a RNA chain called HCV-IRES RNA.

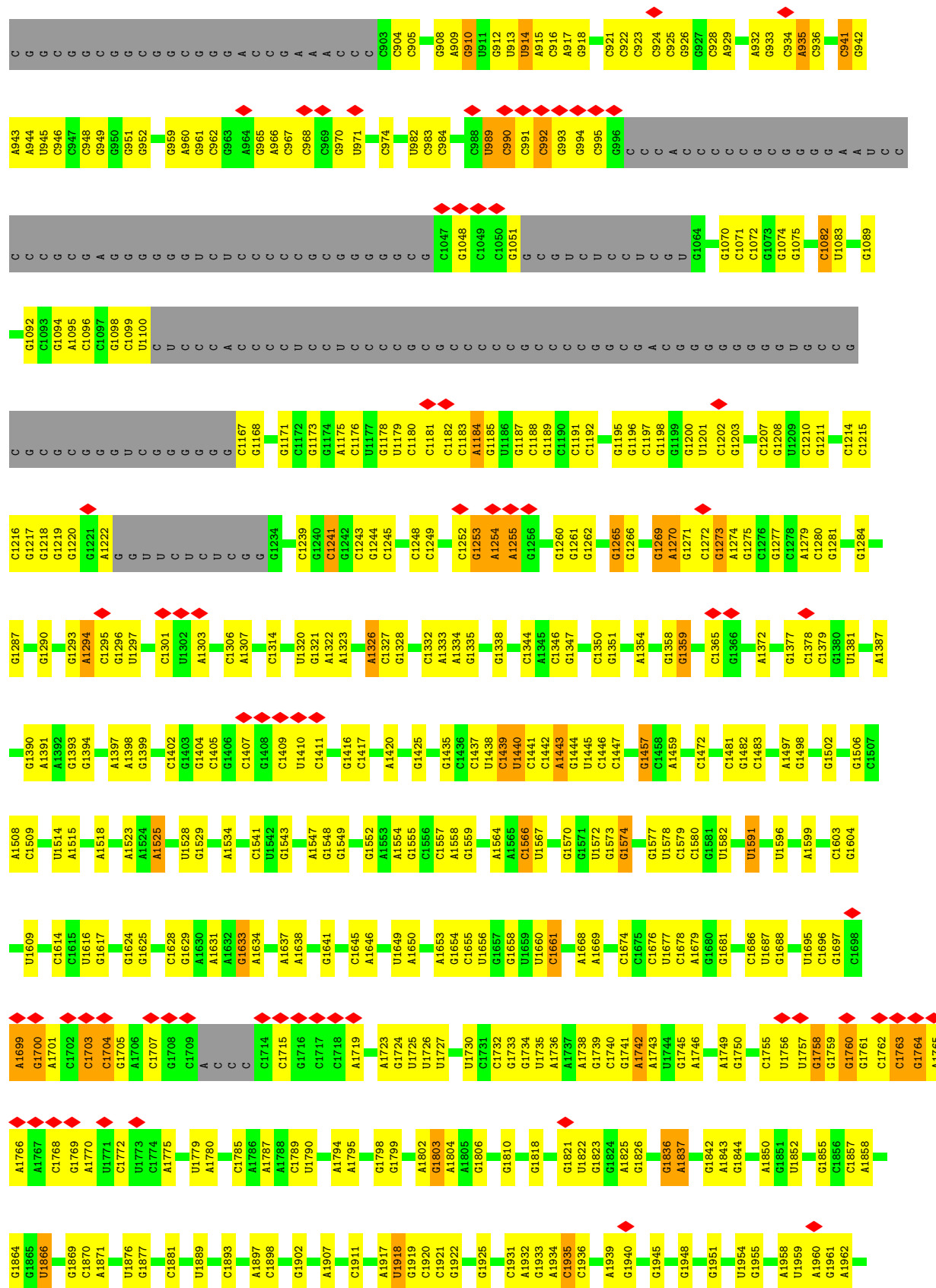
Mol	Chain	Residues	Atoms					AltConf	Trace
84	zz	163	Total	C	N	O	P	0	0
			3492	1553	627	1149	163		

3 Residue-property plots

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

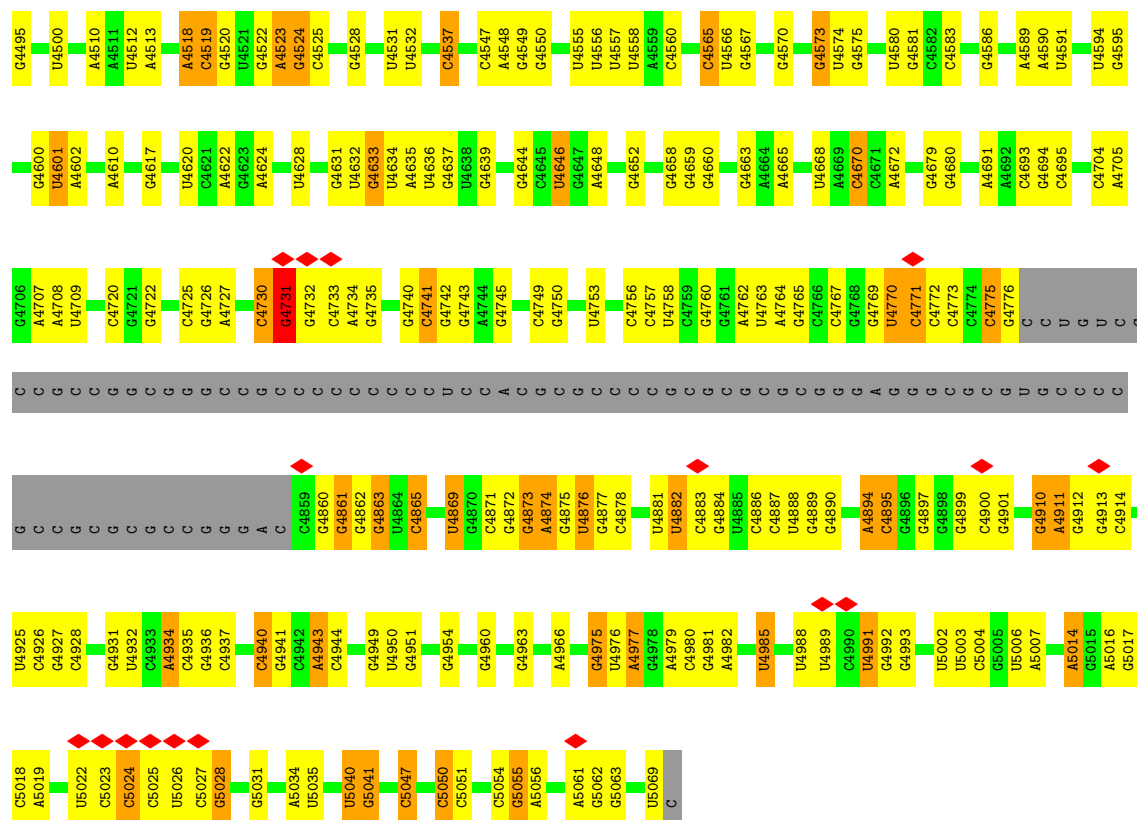
• Molecule 1: 28S ribosomal RNA



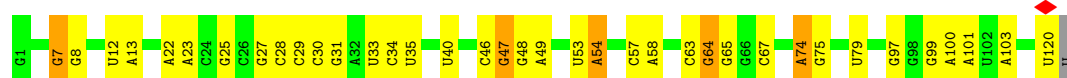


G1965	U2097	G2106	G	G2306	G2406	G2502	A2587	G2699	A2787	A2881	G	G
C1966	C2028	C2107	G	A2307	U2409	G2503	C2588	C2699	U2788	U2881	C	G
A1967	A2029	G2108	C	A2313	U2410	G2504	C2589	G2703	A2789	U2891	C	A
G1968	G2033	G2111	C	G2316	U2412	G2505	G2599	U2707	C2792	A2896	C	G
A1969	A2034	G2112	C	C2317	A2413	G2506	A2600	U2708	G2793	G2896	C	G
A1970	G2038	G2113	C	G2318	A2417	A2507	A2601	C2709	A2794	G2897	C	G
C1971	U2038	G	G	G2319	U2420	G2510	C2602	G2710	A2795	G2898	C	G
G1972	G2039	G	G	G2321	A2421	A2511	C2603	G2711	G2796	C2899	C	G
G1973	A2040	G	G	G2322	G2421	G2512	C2604	G2712	G2797	G2900	C	G
U1974	A2041	G	G	C2323	U2426	A2513	G2607	G2713	A2798	G2901	C	G
G1975	A2042	G	G	C2324	U2434	G2514	G2608	G2714	G2799	U2902	C	G
G1976	U2044	G	G	G2327	G2438	G2520	G2609	G2715	G2800	G2903	C	G
C1977	G2045	G	G	G2328	A2439	G2521	G2610	G2716	A2806	U2904	C	G
C1978	A2047	G	G	U2329	U2440	G2522	G2611	G2717	G2905	G2906	C	G
A1979	G2049	G	G	G2330	C2441	A2529	G2612	U2718	A2807	G2907	C	G
U1980	G2050	G	G	G2331	C2442	G2530	G2613	G2721	G2809	U2810	C	G
G1981	C2051	G	G	A2332	U2443	G2531	G2618	G2724	G2811	G2810	C	G
G1982	G2052	G	G	G2333	U2444	G2532	G2622	A2725	A2812	G2811	C	G
A1983	C2053	G	G	G2334	U2444	A2533	G2627	G2726	G2813	G2812	C	G
A1984	U2054	G	G	G2335	A2449	G2534	C2627	G2727	A2814	G2813	C	G
G1985	G2055	G	G	G2336	G2450	G2543	U2637	G2739	G2815	G2814	C	G
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C1987	A2057	G	G	G2339	G2463	U2545	G2640	U2741	C2820	G2816	C	G
G1988	G2062	G	G	G2345	U2463	G2546	G2641	G2742	A2825	G2817	C	G
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G1995	G2079	G	G	U2352	G2473	G2553	G2648	G2750	G2842	U2843	C	G
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G2001	G2088	G	G	G2376	C2482	G2559	U2666	G2756	G2850	G2850	C	G
A2002	U2090	G	G	A2377	G2483	G2560	C2669	G2757	G2851	G2851	C	G
G2003	C2091	G	G	G2378	U2484	G2561	C2670	U2761	G2852	G2852	C	G
U2004	G2092	G	G	G2379	U2485	A2565	G2671	G2762	G2853	G2853	C	G
G2005	G2093	G	G	G2380	U2486	G2566	G2672	U2763	G2854	G2854	C	G
U2006	A2093	G	G	A2381	G2487	G2567	G2673	A2764	G2855	G2855	C	G
G2007	G2094	G	G	G2390	G2488	G2568	G2674	A2765	C2860	C2860	C	G
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G2009	G2096	G	G	G2392	U2490	U2570	G2681	U2767	U2862	U2862	C	G
A2010	U2097	G	G	A2393	C2491	G2571	G2682	G2768	G2863	G2863	C	G
G2011	G2098	G	G	G2394	C2492	A2572	G2683	U2769	G2864	G2864	C	G
A2012	G2099	G	G	A2395	G2493	G2573	G2684	G2770	U2865	U2865	C	G
A2013	A2100	G	G	G2396	U2494	U2574	G2685	G2771	G2866	G2866	C	G
G2014	C2101	G	G	G2397	U2495	G2575	G2686	G2772	U2867	U2867	C	G
U2015	G2102	G	G	G2402	U2496	G2576	G2687	C2773	G2868	G2868	C	G
G2016	G2103	G	G	G	U2497	G2577	A2895	G2774	A2896	A2896	C	G
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C2018	G	G	G	G	C2499	G	G	G2776	G	G	C	G
C2019	G	G	G	G	G	G	G	G2777	G	G	C	G
U2020	G	G	G	G	G	G	G	G2778	G	G	C	G
G2021	G	G	G	G	G	G	G	G	G	G	C	G
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A2026	G	G	G	G	G	G	G	G	G	G	C	G

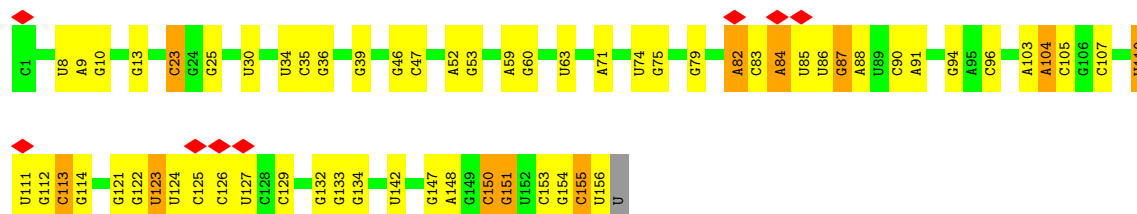




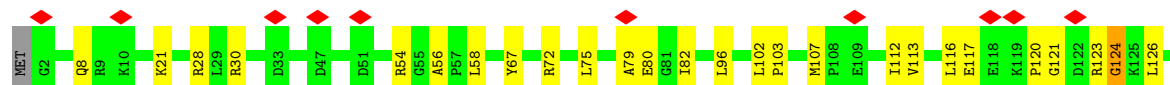
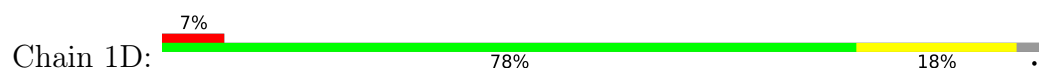
- Molecule 2: 5S ribosomal RNA

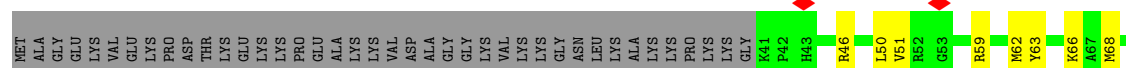


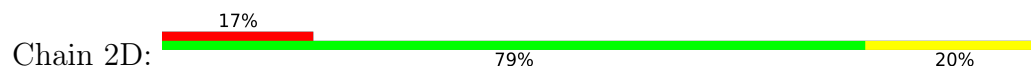
- Molecule 3: 5.8S ribosomal RNA

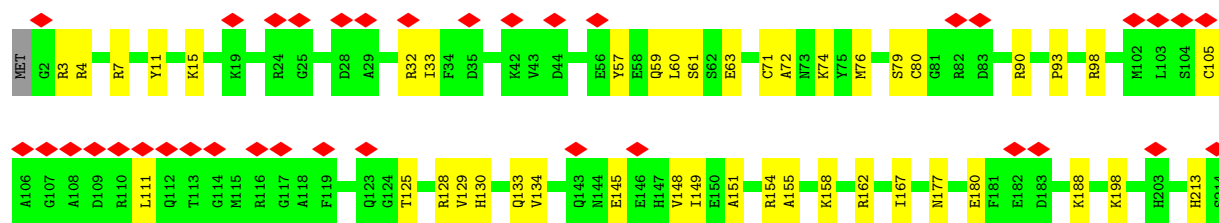


- Molecule 4: 60S ribosomal protein L8

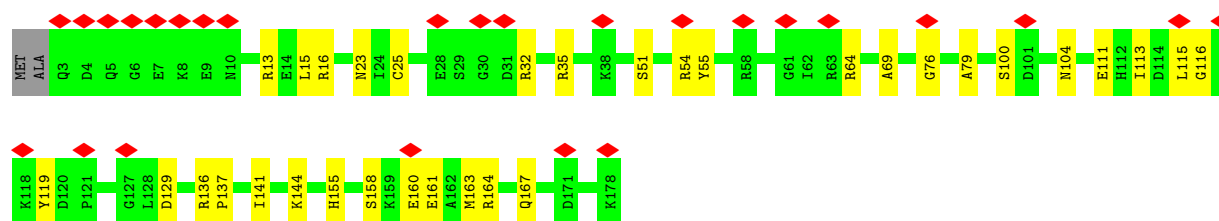
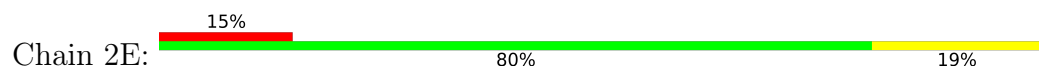




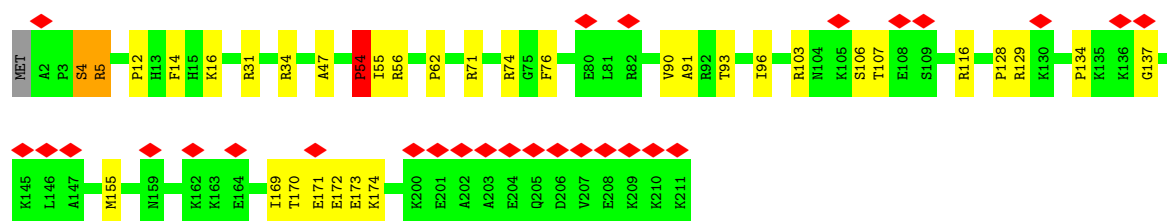
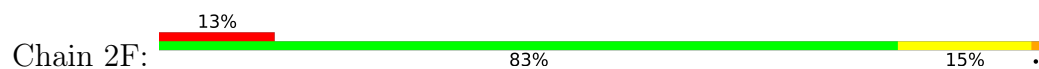




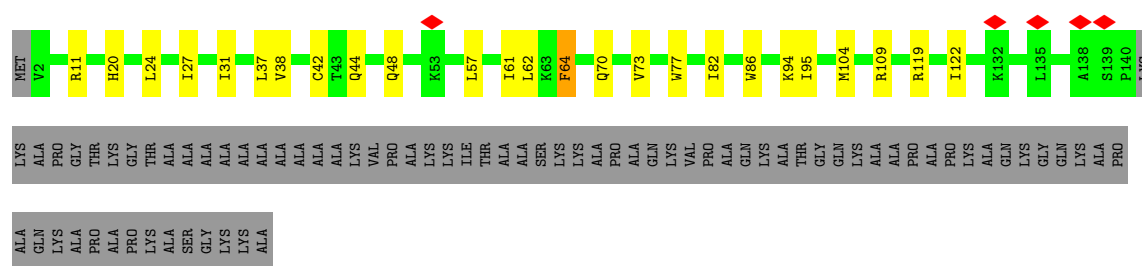
• Molecule 13: 60S ribosomal protein L11



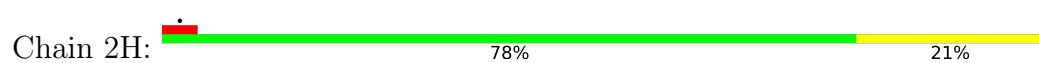
• Molecule 14: 60S ribosomal protein L13

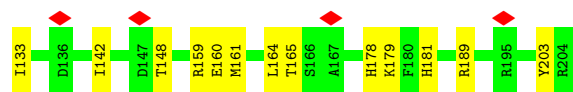


• Molecule 15: 60S ribosomal protein L14

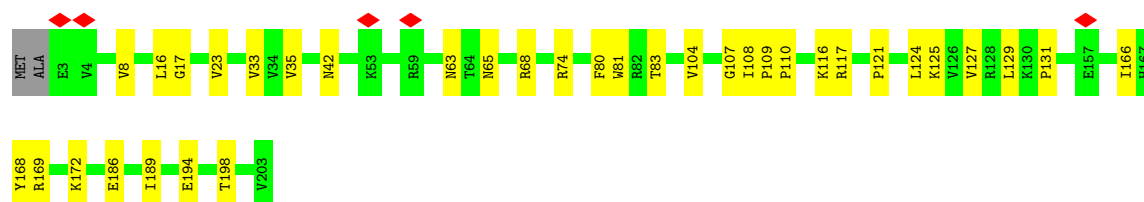
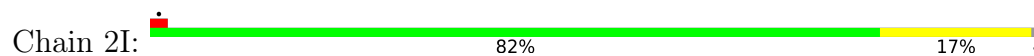


• Molecule 16: 60S ribosomal protein L15

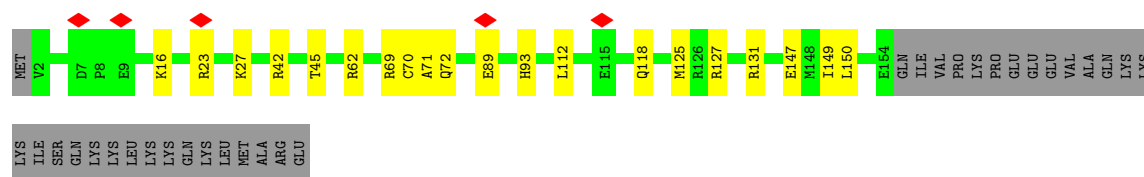




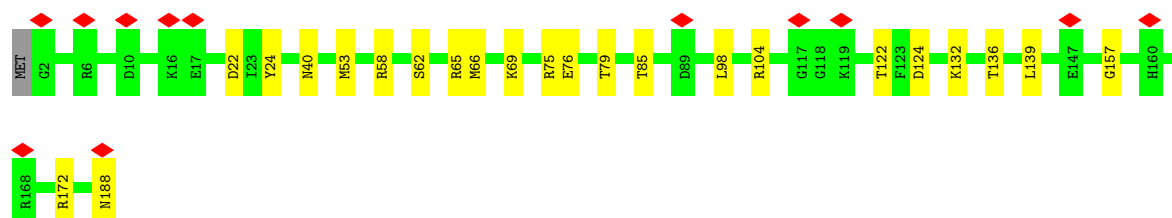
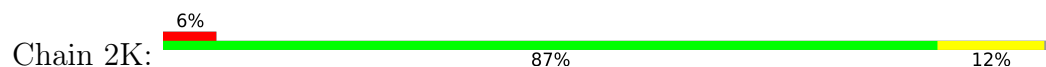
- Molecule 17: 60S ribosomal protein L13a



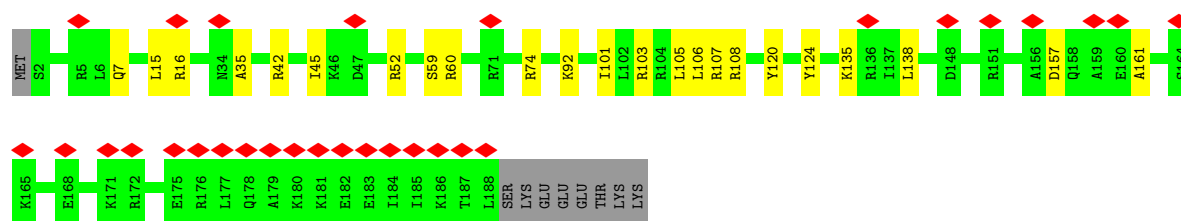
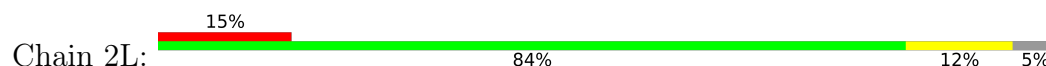
- Molecule 18: 60S ribosomal protein L17



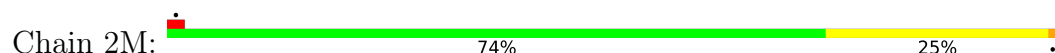
- Molecule 19: 60S ribosomal protein L18

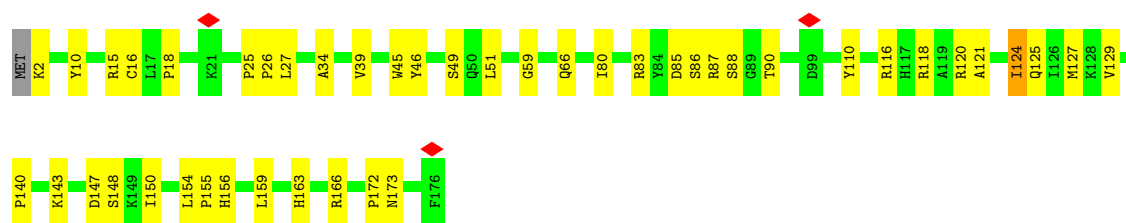


- Molecule 20: 60S ribosomal protein L19

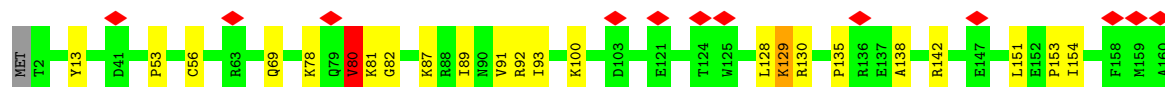
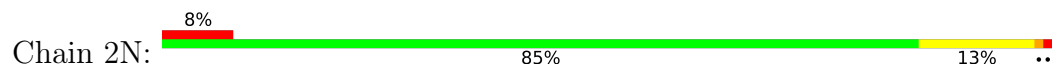


- Molecule 21: 60S ribosomal protein L18a

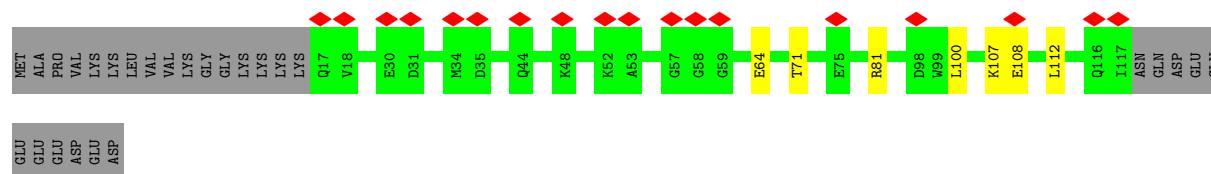
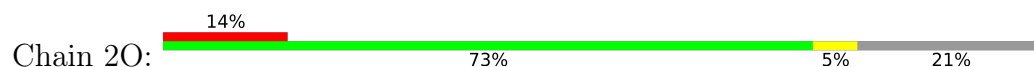




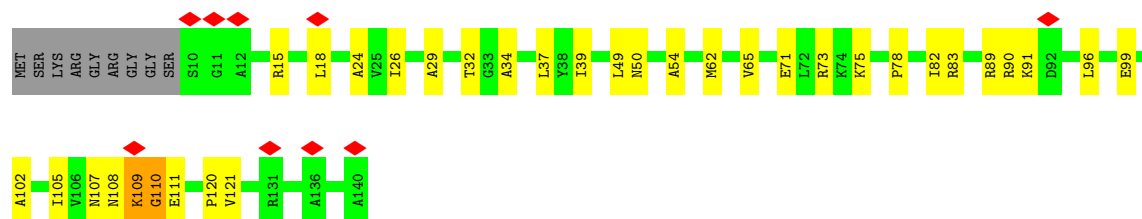
- Molecule 22: 60S ribosomal protein L21



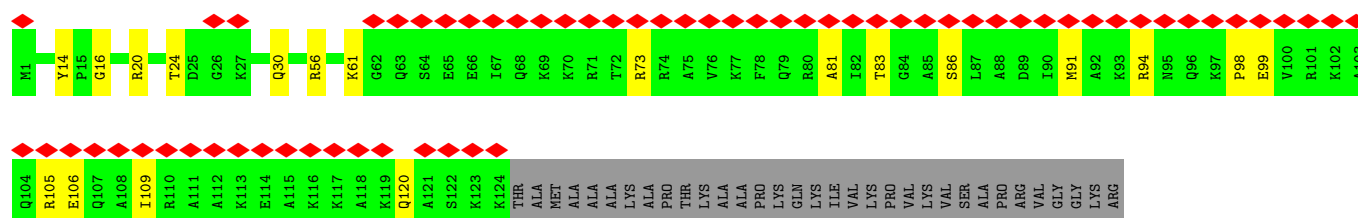
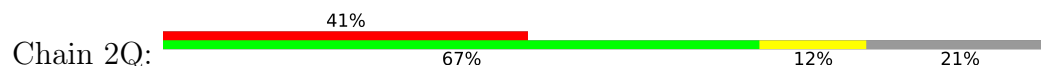
- Molecule 23: 60S ribosomal protein L22



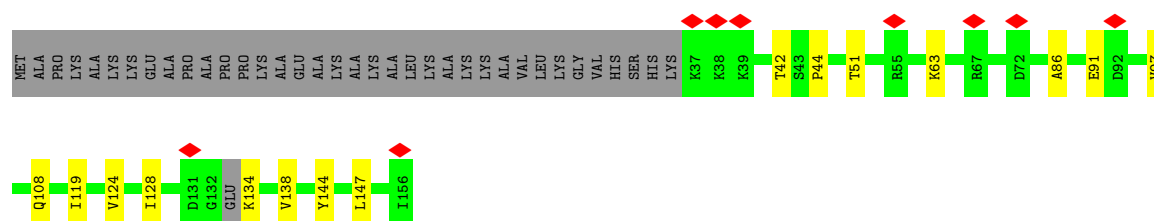
- Molecule 24: 60S ribosomal protein L23



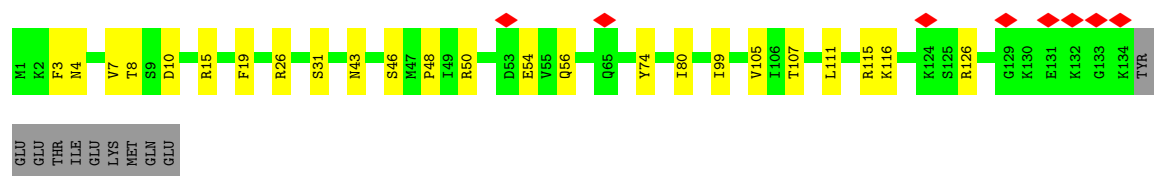
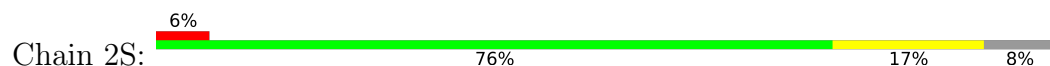
- Molecule 25: 60S ribosomal protein L24



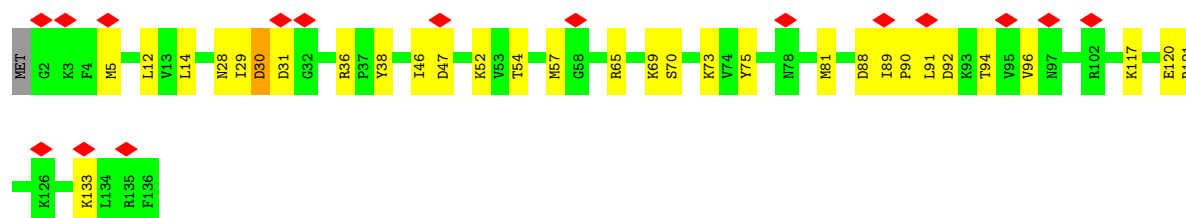
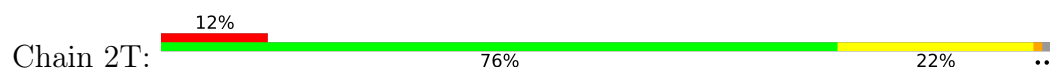
- Molecule 26: 60S ribosomal protein L23a



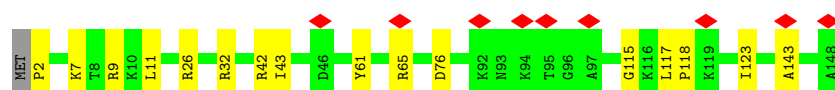
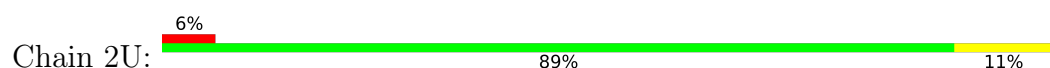
- Molecule 27: 60S ribosomal protein L26



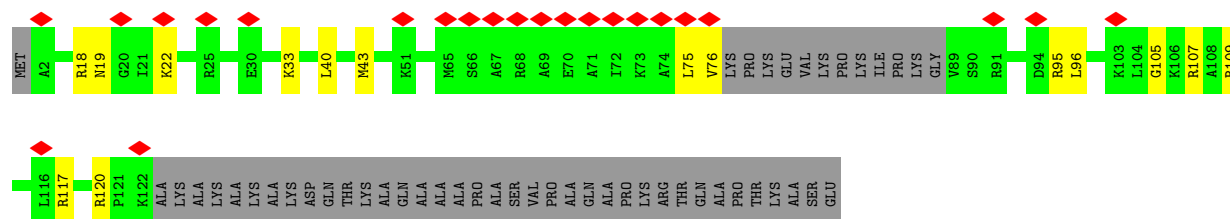
- Molecule 28: 60S ribosomal protein L27



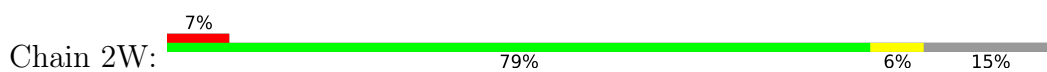
- Molecule 29: 60S ribosomal protein L27a



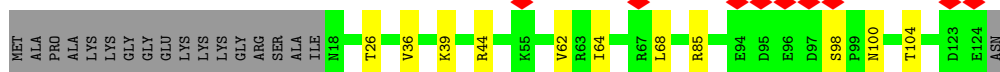
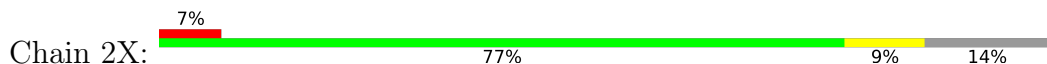
- Molecule 30: 60S ribosomal protein L29



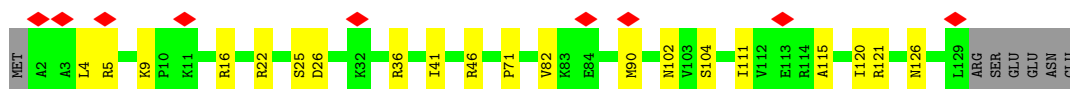
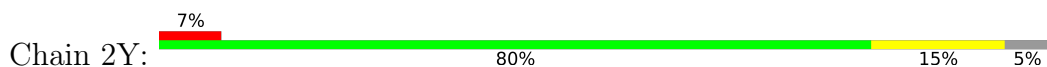
- Molecule 31: 60S ribosomal protein L30



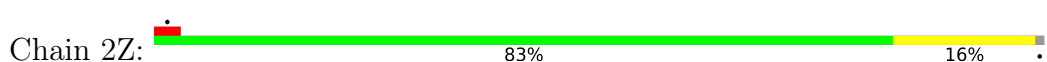
- Molecule 32: 60S ribosomal protein L31



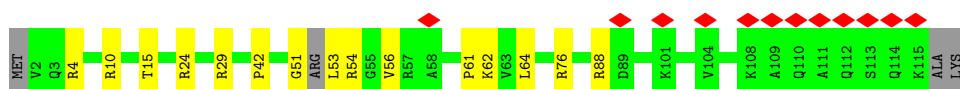
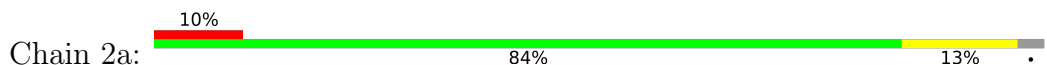
- Molecule 33: 60S ribosomal protein L32



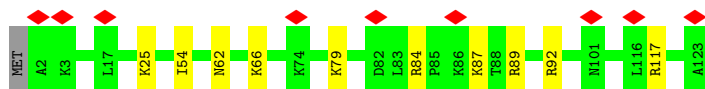
- Molecule 34: 60S ribosomal protein L35a



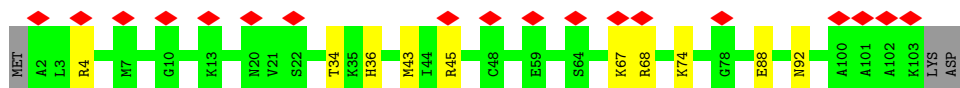
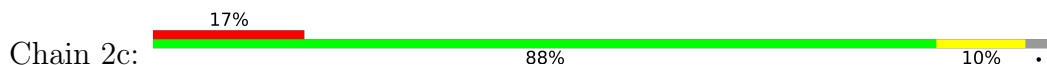
- Molecule 35: 60S ribosomal protein L34



- Molecule 36: 60S ribosomal protein L35



- Molecule 37: 60S ribosomal protein L36



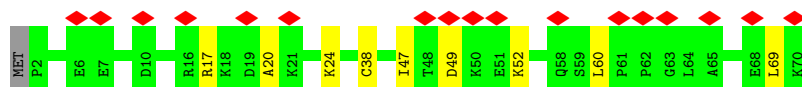
- Molecule 38: 60S ribosomal protein L37

Chain 2d:  67% 21% 11%



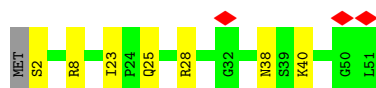
- Molecule 39: 60S ribosomal protein L38

Chain 2e:  24% 86% 13%



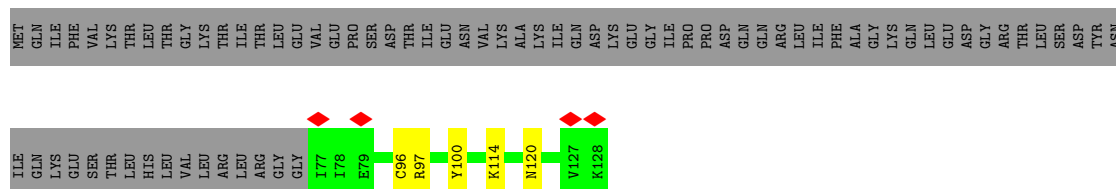
- Molecule 40: 60S ribosomal protein L39

Chain 2f:  6% 84% 14%

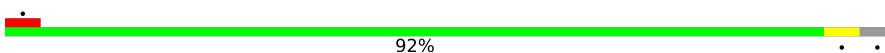


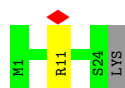
- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain 2g:  37% 59%



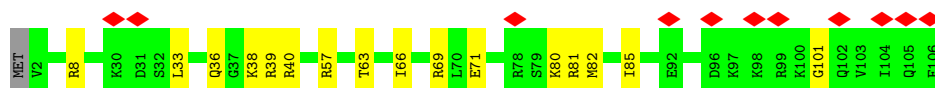
- Molecule 42: 60S ribosomal protein L41

Chain 2h:  92%

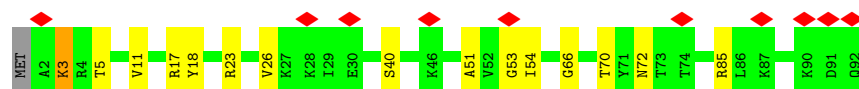


- Molecule 43: 60S ribosomal protein L36a

Chain 2i:  10% 84% 15%



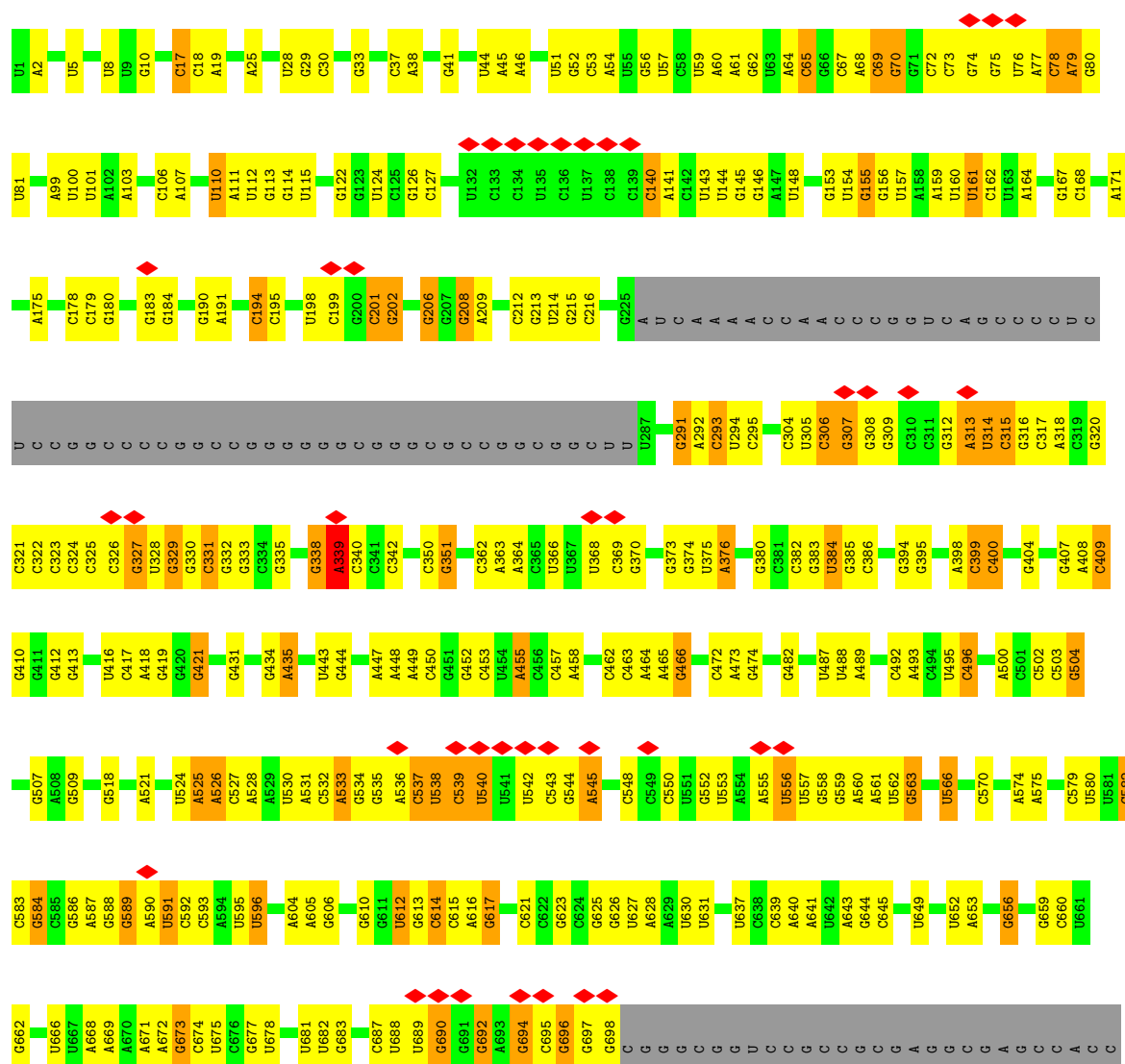
- Molecule 44: 60S ribosomal protein L37a

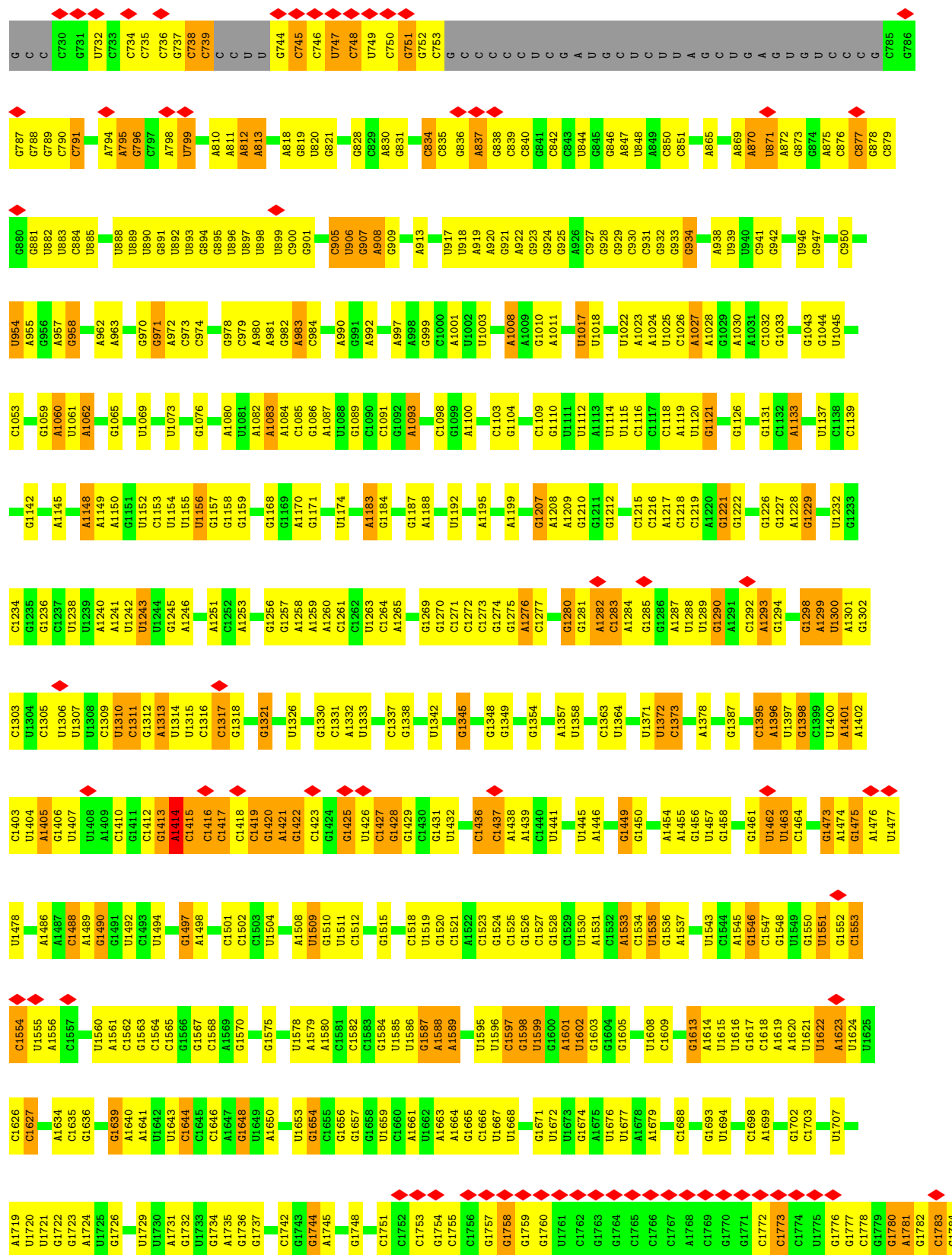


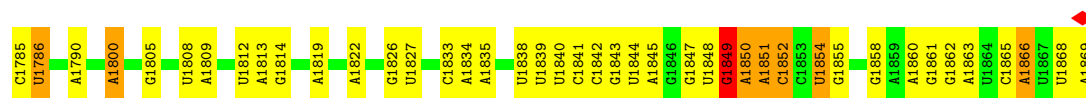
Chain 2k: 5% 78% 12% 9%



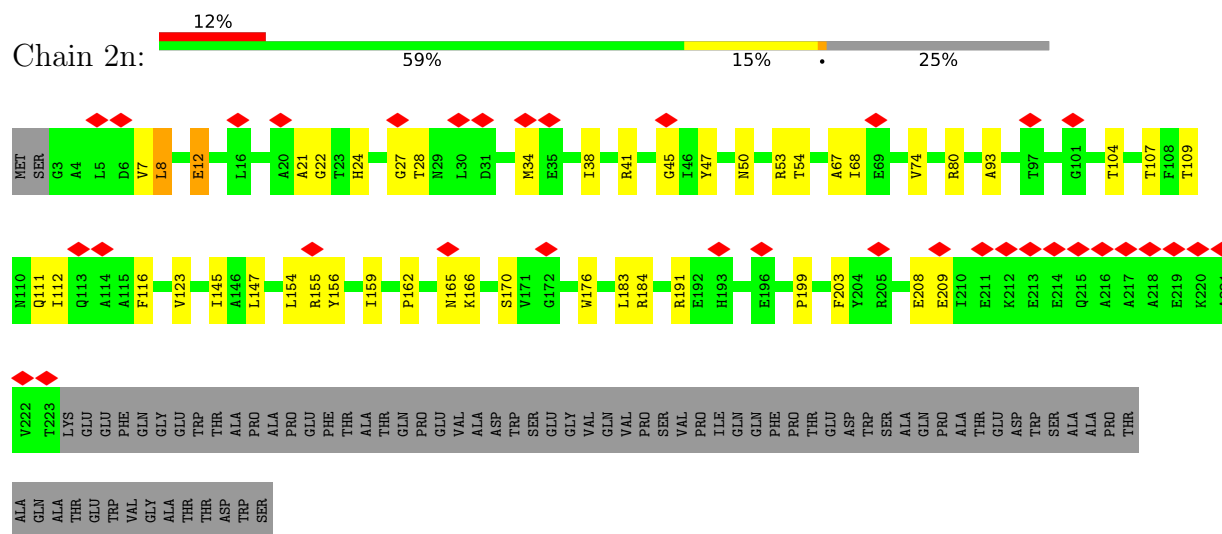
Chain 2m:



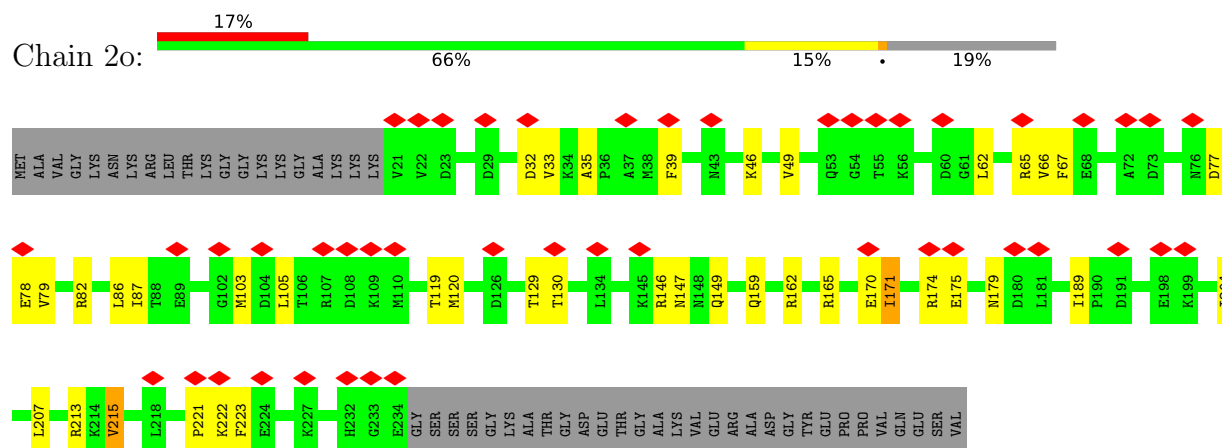




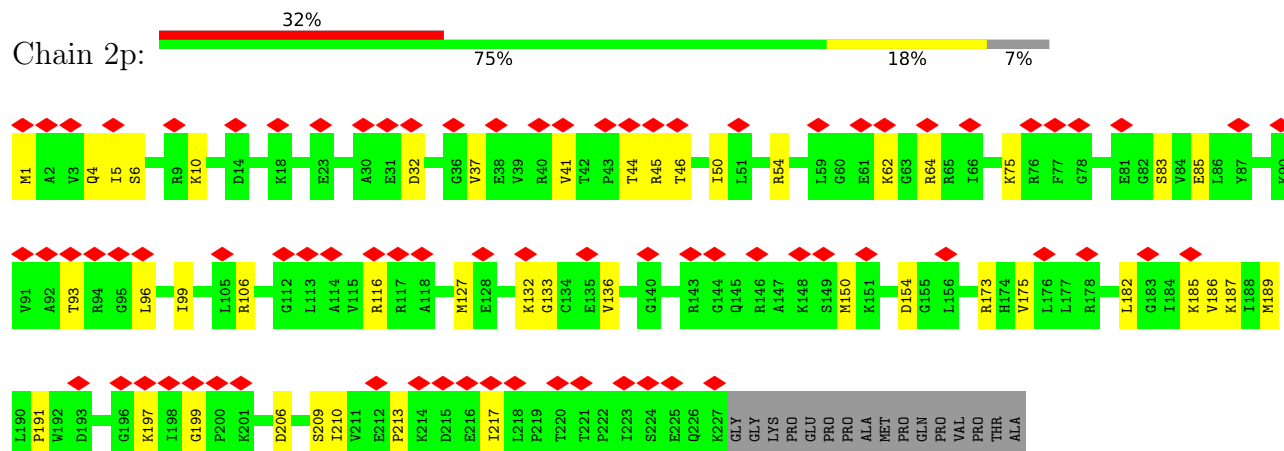
• Molecule 47: 40S ribosomal protein SA



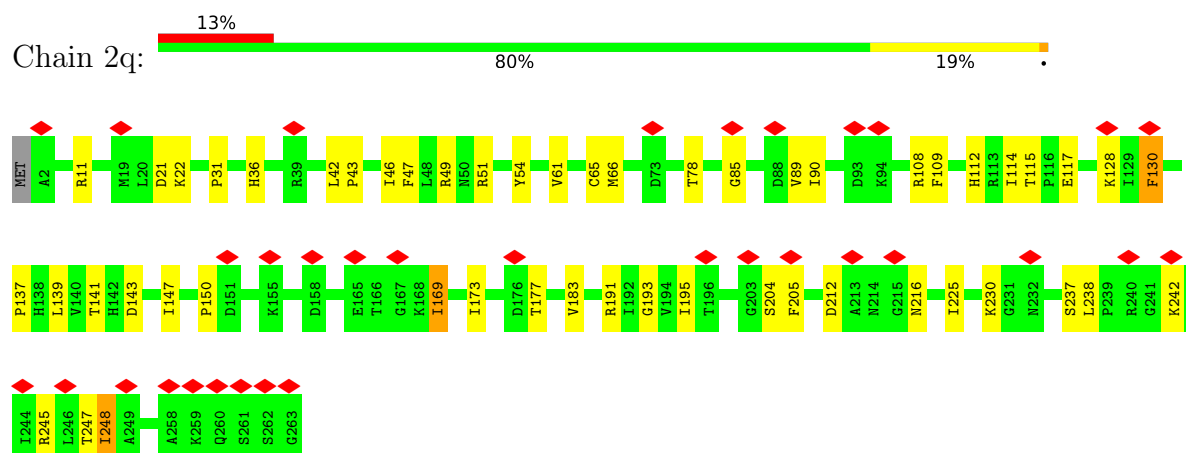
• Molecule 48: 40S ribosomal protein S3a



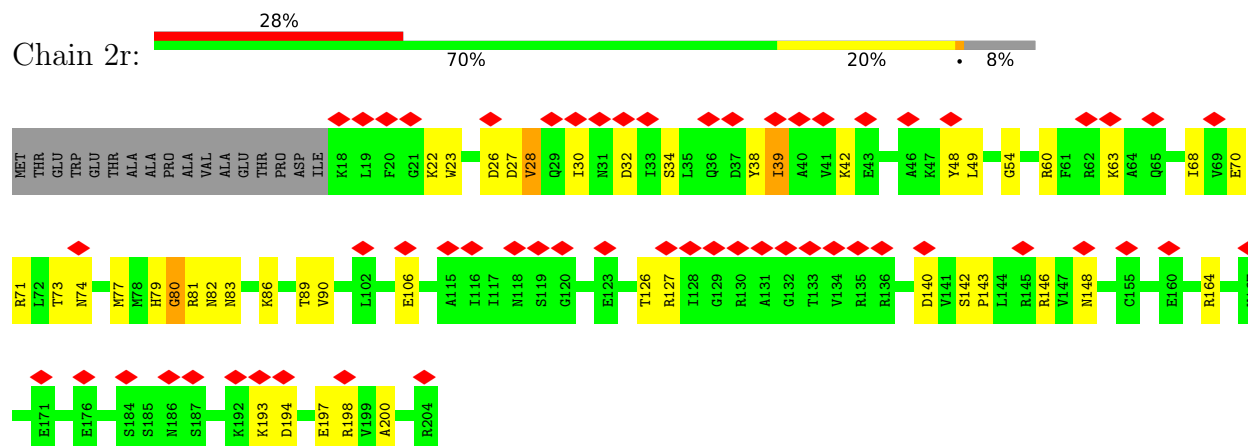
• Molecule 49: 40S ribosomal protein S3



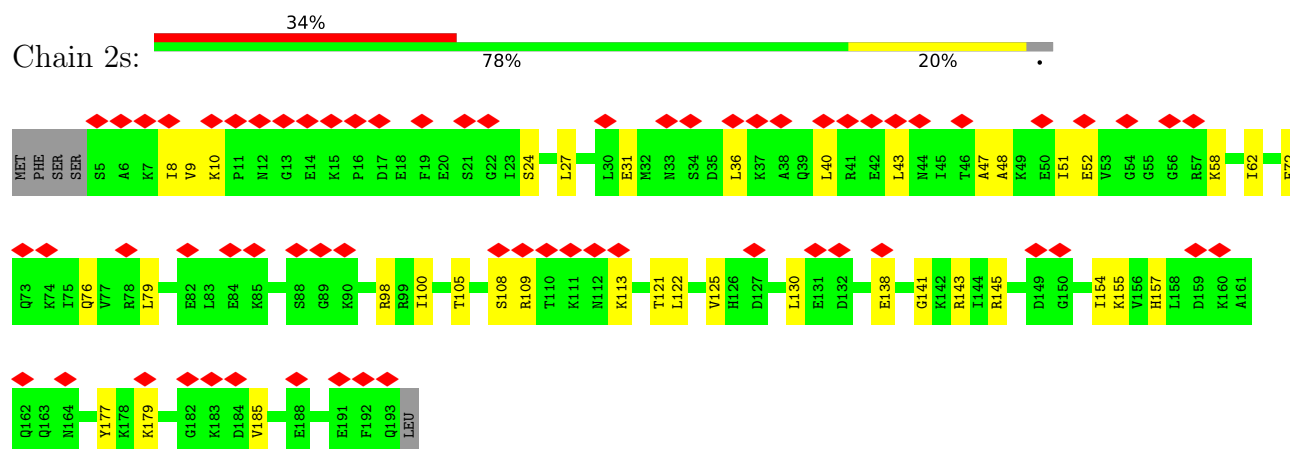
- Molecule 50: 40S ribosomal protein S4, X isoform



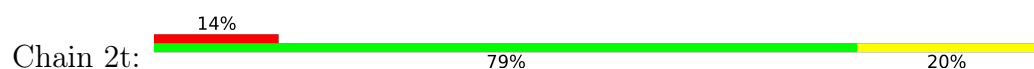
- Molecule 51: 40S ribosomal protein S5

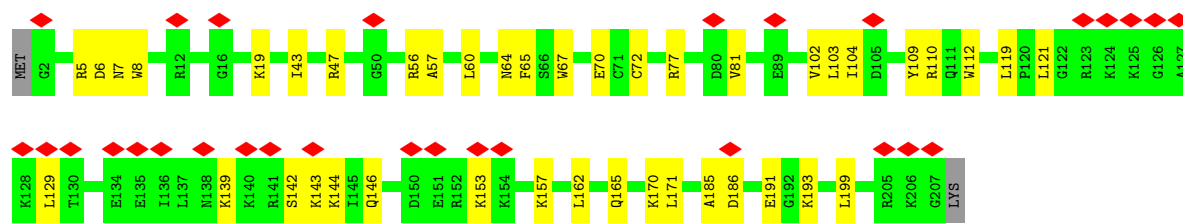


- Molecule 52: 40S ribosomal protein S7

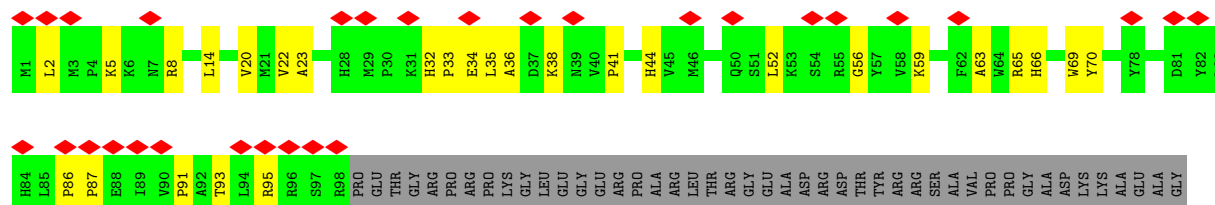


- Molecule 53: 40S ribosomal protein S8

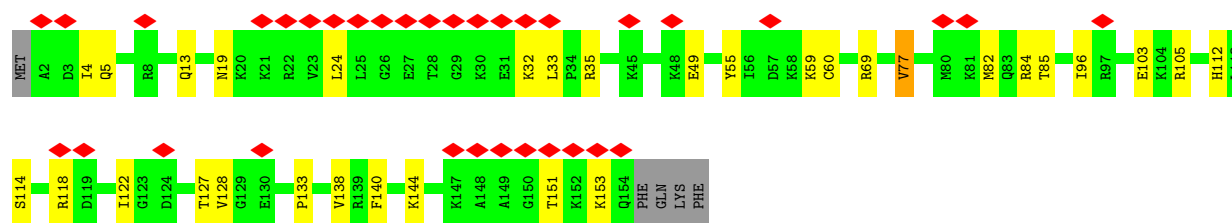
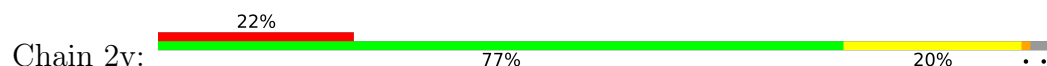




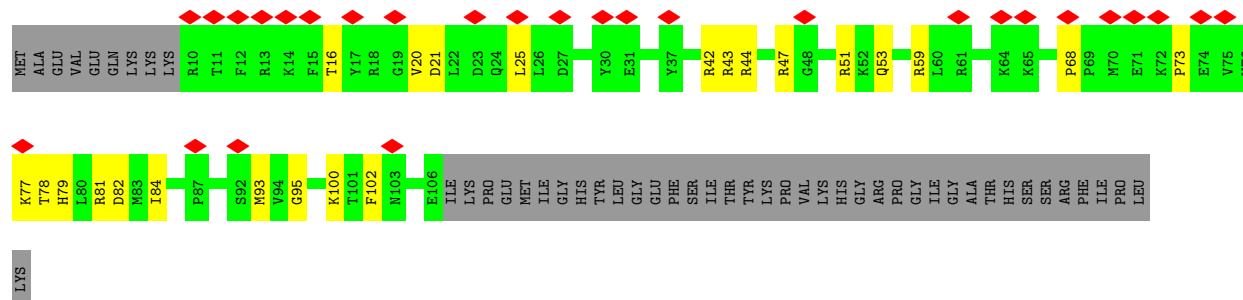
• Molecule 54: 40S ribosomal protein S10



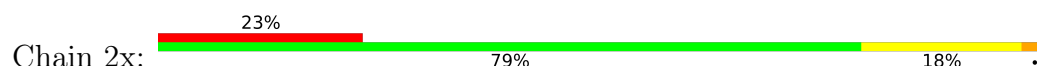
• Molecule 55: 40S ribosomal protein S11

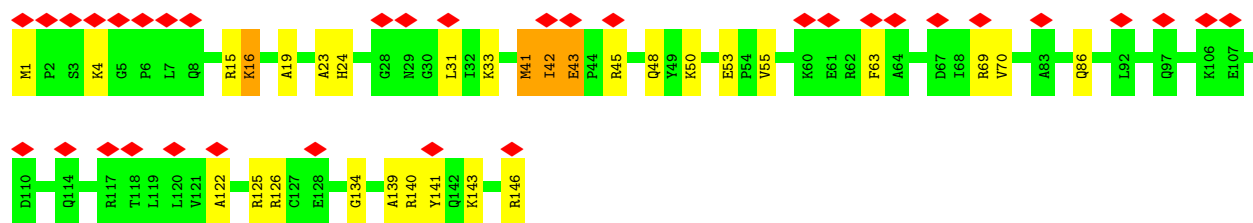


• Molecule 56: 40S ribosomal protein S15

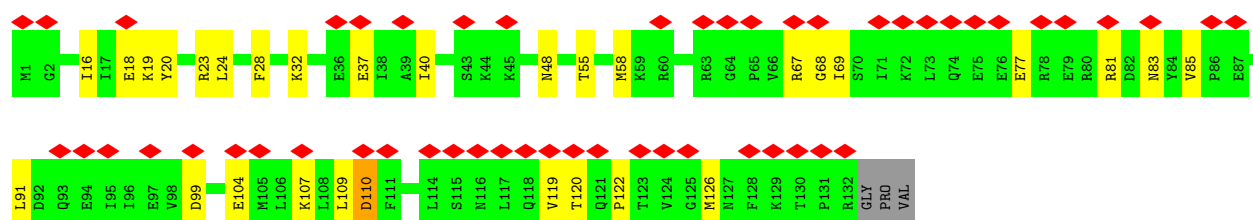
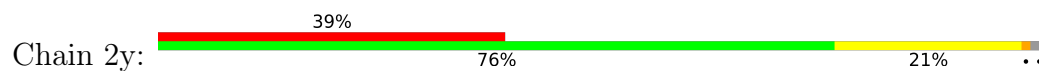


• Molecule 57: 40S ribosomal protein S16

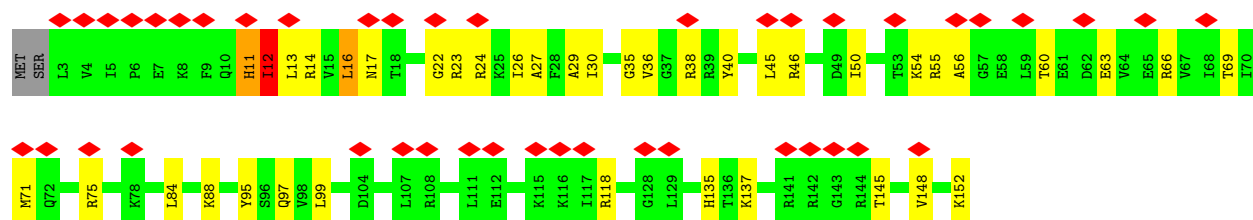
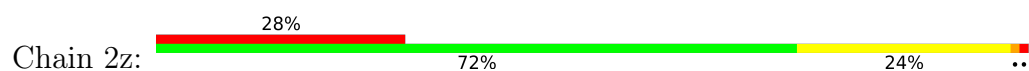




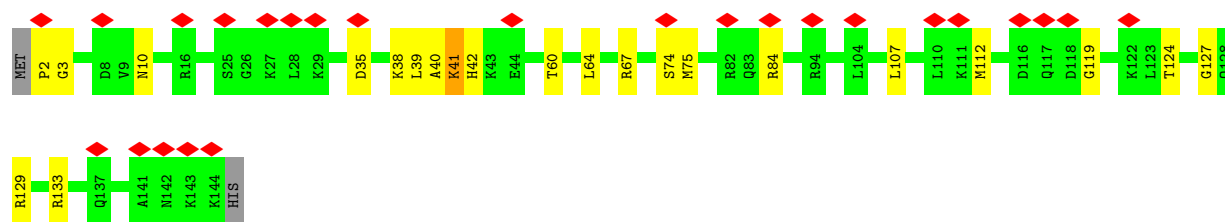
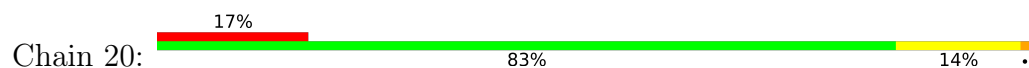
• Molecule 58: 40S ribosomal protein S17



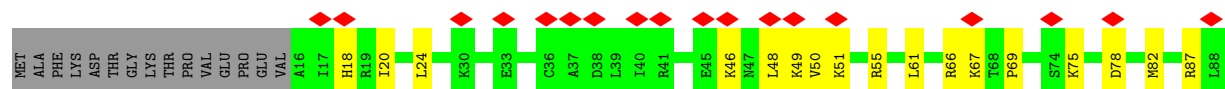
• Molecule 59: 40S ribosomal protein S18

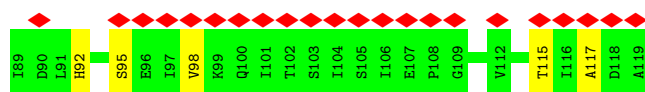


• Molecule 60: 40S ribosomal protein S19

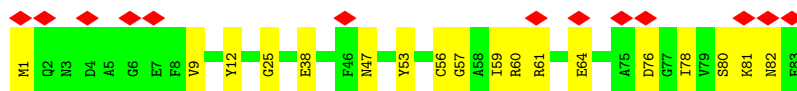
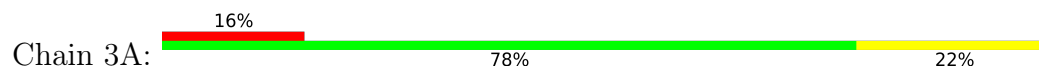


• Molecule 61: 40S ribosomal protein S20

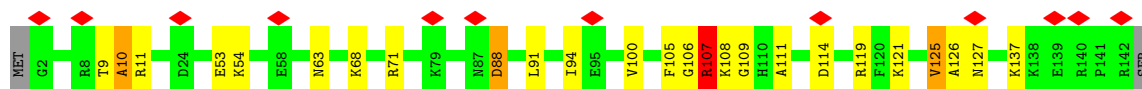
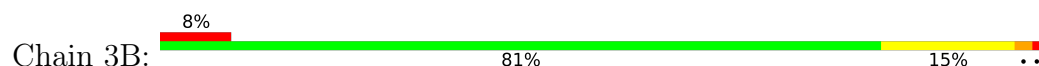




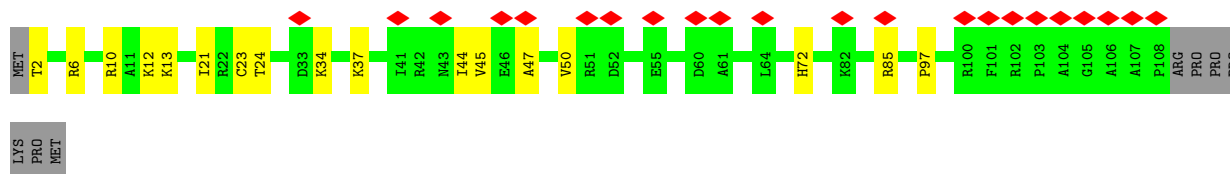
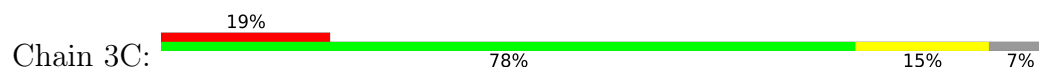
- Molecule 62: 40S ribosomal protein S21



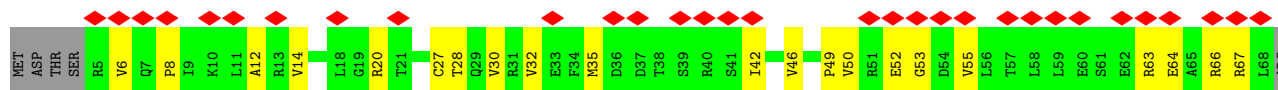
- Molecule 63: 40S ribosomal protein S23



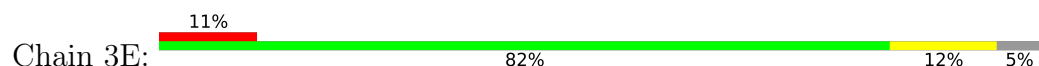
- Molecule 64: 40S ribosomal protein S26



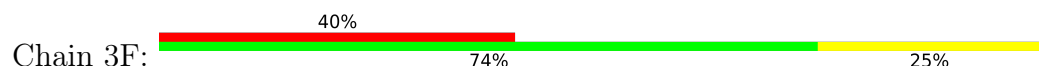
- Molecule 65: 40S ribosomal protein S28

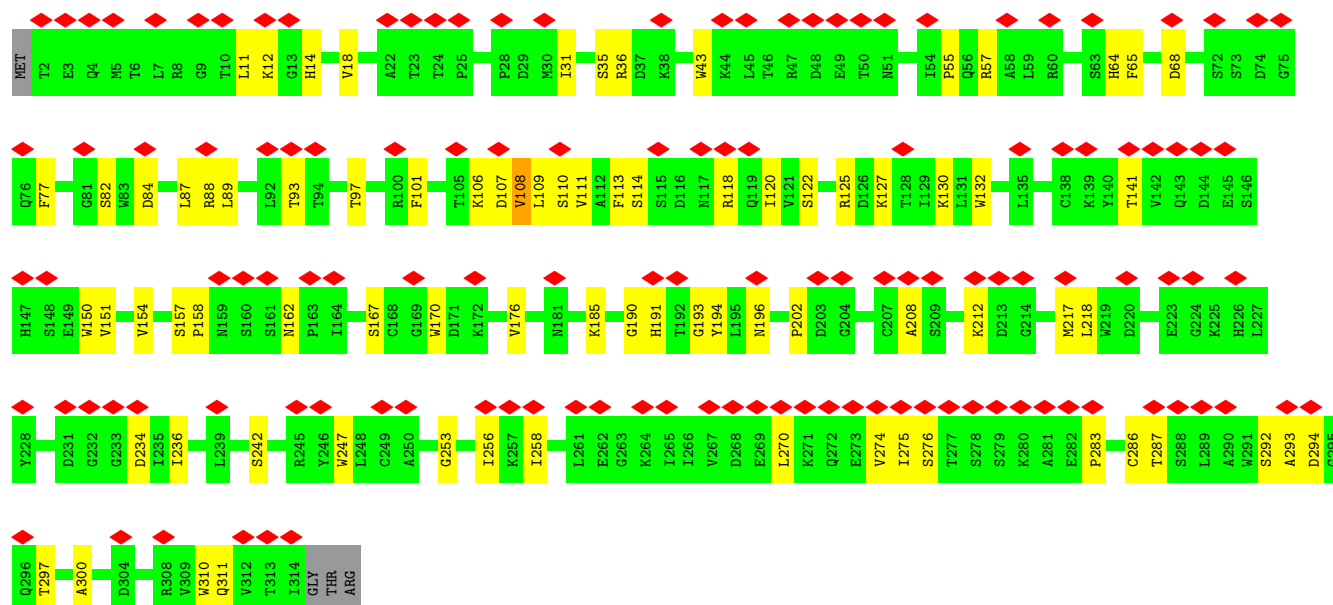


- Molecule 66: 40S ribosomal protein S29

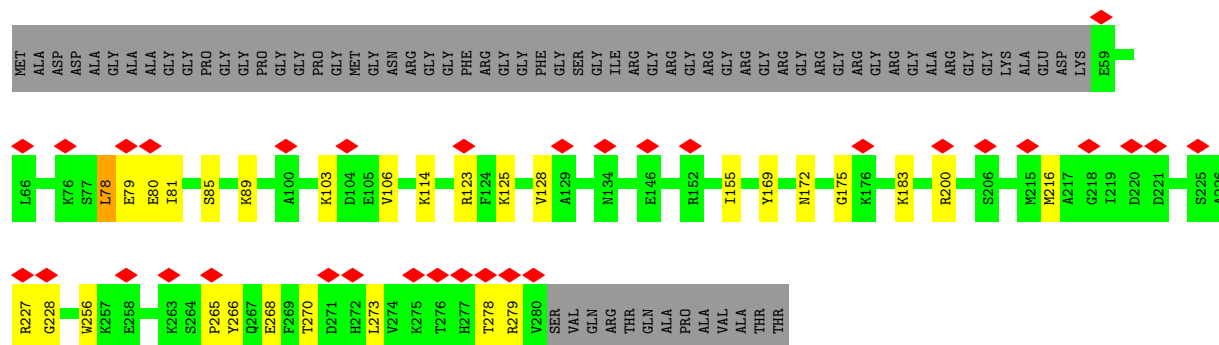


- Molecule 67: Receptor of activated protein C kinase 1

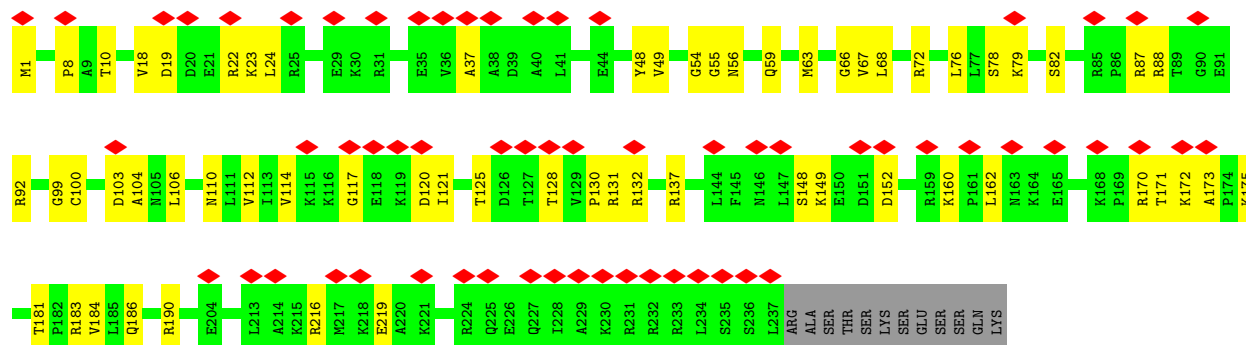
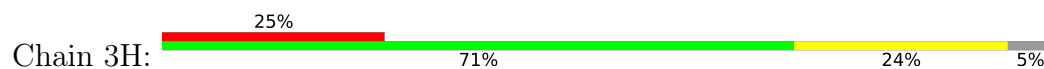




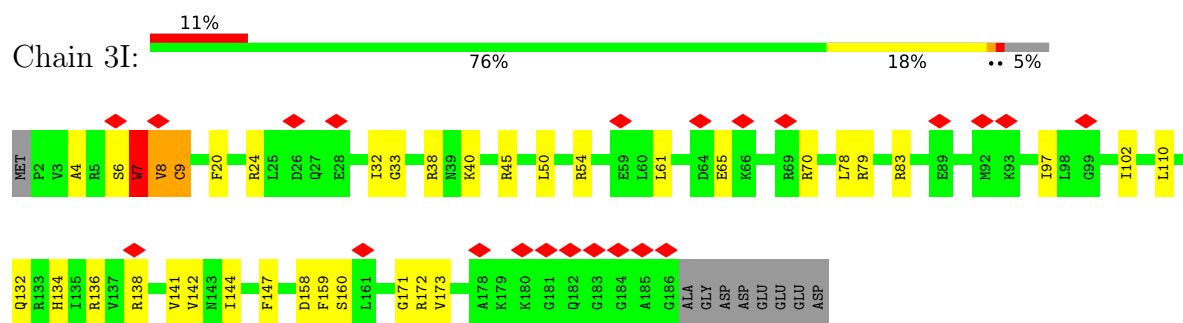
- Molecule 68: 40S ribosomal protein S2



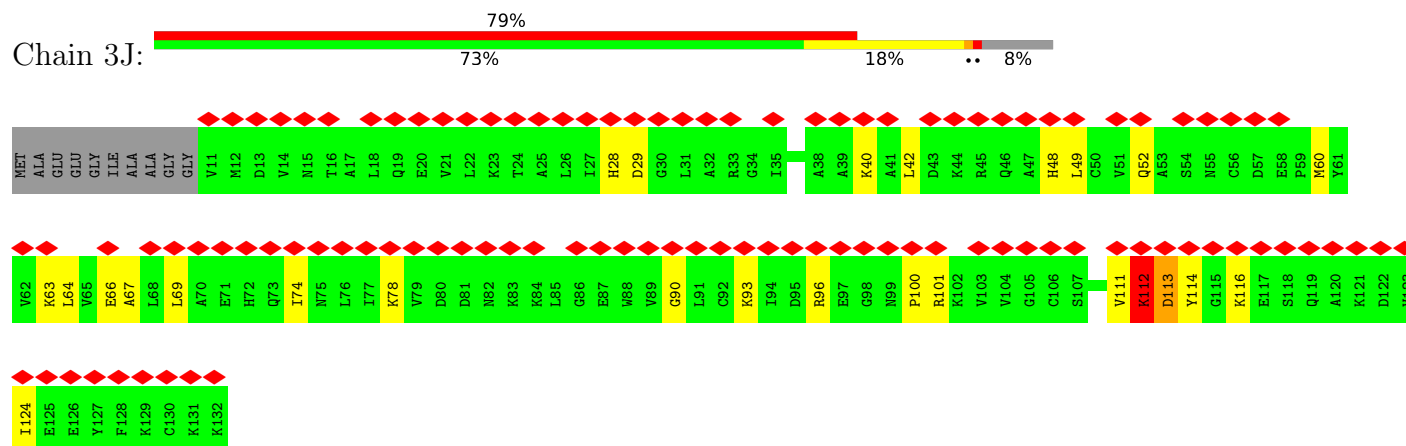
- Molecule 69: 40S ribosomal protein S6



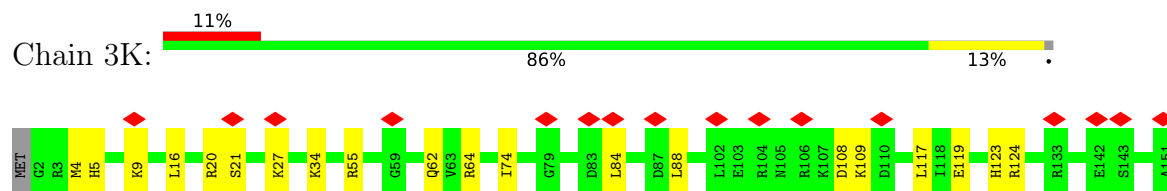
- Molecule 70: 40S ribosomal protein S9



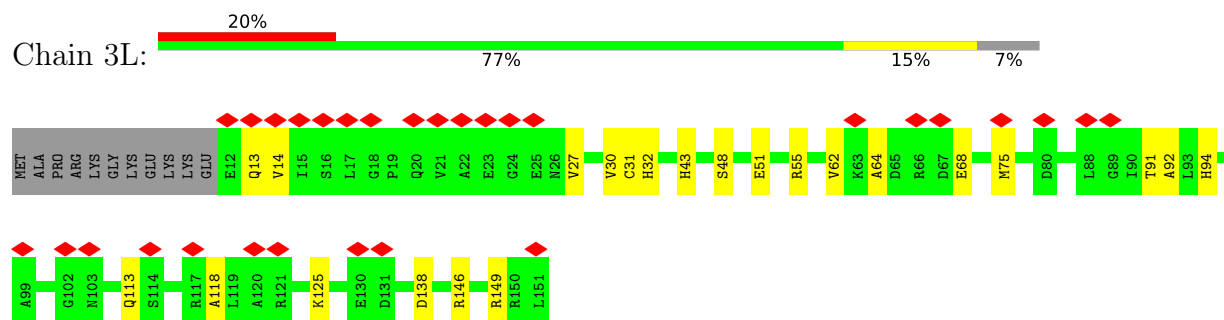
- Molecule 71: 40S ribosomal protein S12



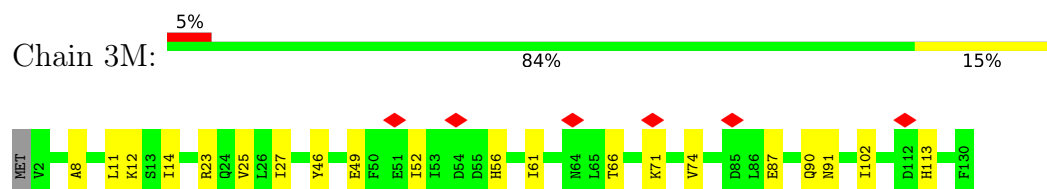
- Molecule 72: 40S ribosomal protein S13



- Molecule 73: 40S ribosomal protein S14



- Molecule 74: 40S ribosomal protein S15a



Chain 3N:

Category	Percentage
Red	17%
Green	83%
Yellow	16%

Sequence: MET, N2, D3, T4, 17, R8, T9, M13, T14, N15, R16, Q22, D26, A33, K37, L40, K43, K49, D53, R61, M74, I75, Y76, D77, S78, Y81, A82, K83, E86, R93, R94, G95, K99, K100, K101, T102, K122, A123, N124, Y125, G126, A127, G128, K129, K130, P131, K132, GLU.

Chain 30:

26% 44% 15% 40%

MET PRO PRO LYS ASP ASP LYS LYS LYS LYS ASP ALA GLY LYS SER LYS LYS LYS ASP ASP PRO VAL ASN LYS SER GLY GLY LYS ALA LYS LYS LYS LYS TRP SER LYS GLY LYS VAL R41 D42 K43 L44 M45 N46 L47 V48 L49 F50 D51 K52 Y55 D56 K57 L58 G59 K60 T61

Chain 3P:

Category	Percentage
Red	24%
Green	79%
Yellow	19%

Chain 3Q:

Chain 3R:

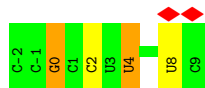
32%
35%
8%
57%

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

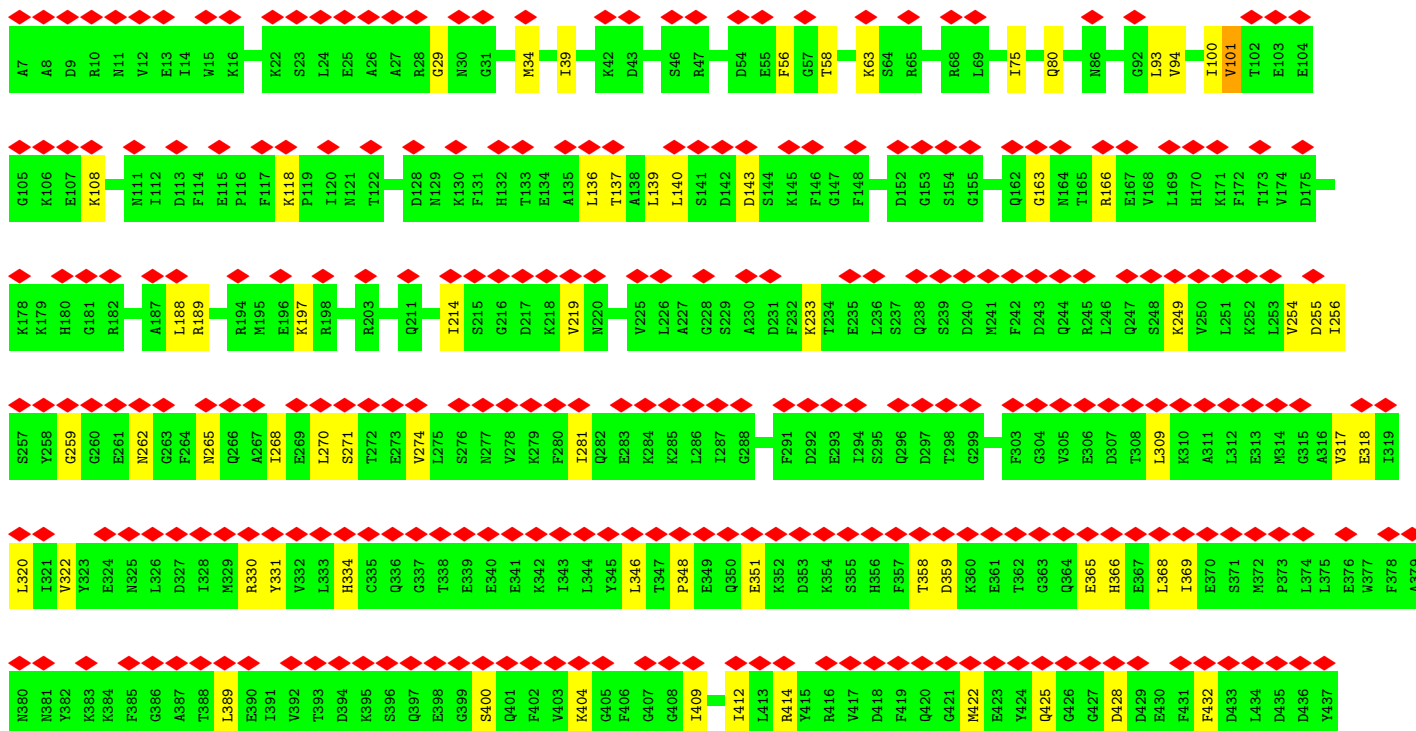
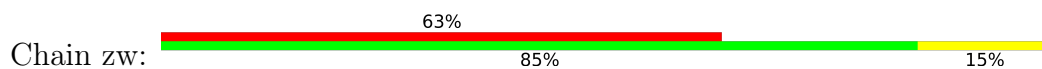
ILE GLN LYS GLU SER THR LEU VAL ARG GLY GLY ALA LYS LYS ARG LYS LYS SER Y85 T86 T87 T88 P89 X90 N91 X92 X93 X94 X95 X96 X97 X98 X99 Y100 A101 V102 L103 K104 Y105 Y106 K107 V108 D109 E110 N111 G112 K113 I114 S115 R116 L117 R118 R119 F120

G121 P122 S123 D124 E125 C126 G127 A128 G129 V130 A133 R138 H139 Y140 K143 C144 C145 Y146 Y148 C149 F150 N151 LYS PRO PRD GLU ASP LYS

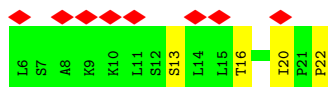
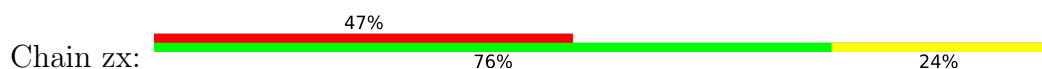
- Molecule 80: mRNA



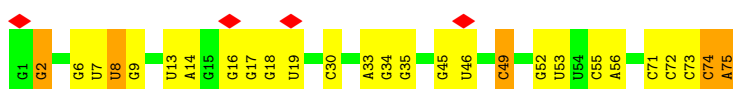
- Molecule 81: Eukaryotic peptide chain release factor subunit 1



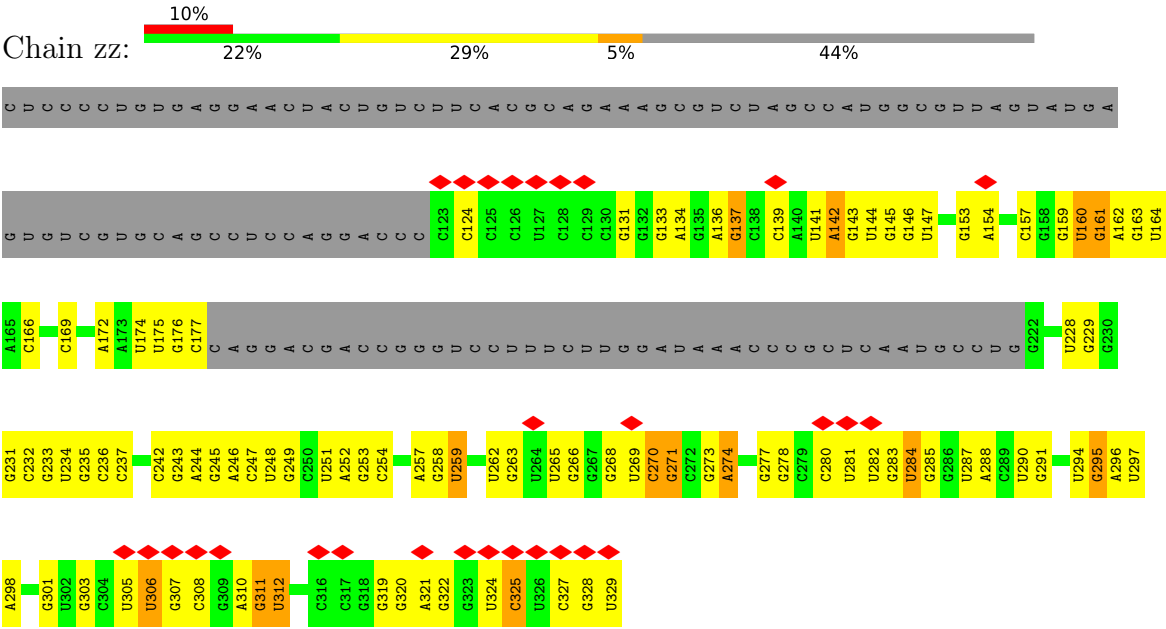
- Molecule 82: nascent peptide



- Molecule 83: P-site tRNA



- Molecule 84: HCV-IRES RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	48923	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	33557	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.269	Depositor
Minimum map value	-0.145	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	625.8, 625.8, 625.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.49, 1.49, 1.49	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1A	0.31	0/87922	0.45	10/137154 (0.0%)
2	1B	0.29	0/2858	0.41	0/4455
3	1C	0.30	0/3701	0.46	0/5766
4	1D	0.33	0/1936	0.69	1/2596 (0.0%)
5	1E	0.34	0/3306	0.74	5/4424 (0.1%)
6	1F	0.31	0/2981	0.68	4/4002 (0.1%)
7	1G	0.28	0/2428	0.66	2/3252 (0.1%)
8	1H	0.38	0/1951	0.81	4/2618 (0.2%)
9	2A	0.37	0/1905	0.70	4/2539 (0.2%)
10	2B	0.30	0/1960	0.68	2/2637 (0.1%)
11	2C	0.30	0/1537	0.71	1/2066 (0.0%)
12	2D	0.30	0/1751	0.68	0/2340
13	2E	0.29	0/1433	0.72	0/1915
14	2F	0.30	0/1732	0.72	3/2315 (0.1%)
15	2G	0.31	0/1161	0.64	1/1554 (0.1%)
16	2H	0.34	0/1746	0.70	2/2338 (0.1%)
17	2I	0.36	0/1682	0.64	1/2250 (0.0%)
18	2J	0.35	0/1268	0.65	0/1701
19	2K	0.32	0/1537	0.65	2/2052 (0.1%)
20	2L	0.29	0/1582	0.63	0/2091
21	2M	0.34	0/1493	0.62	0/2003
22	2N	0.32	0/1326	0.71	2/1770 (0.1%)
23	2O	0.27	0/839	0.67	0/1126
24	2P	0.31	0/993	0.72	1/1332 (0.1%)
25	2Q	0.32	0/1030	0.75	2/1364 (0.1%)
26	2R	0.28	0/992	0.61	0/1330
27	2S	0.29	0/1132	0.67	0/1504
28	2T	0.28	0/1130	0.64	1/1507 (0.1%)
29	2U	0.32	0/1191	0.64	0/1591
30	2V	0.26	0/889	0.64	0/1175
31	2W	0.27	0/774	0.57	0/1038
32	2X	0.30	0/903	0.61	0/1216
33	2Y	0.32	0/1071	0.62	0/1429
34	2Z	0.35	0/895	0.70	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	2a	0.28	0/904	0.62	0/1203
36	2b	0.27	0/1023	0.69	0/1351
37	2c	0.24	0/843	0.60	0/1115
38	2d	0.33	0/720	0.75	0/952
39	2e	0.28	0/575	0.72	0/761
40	2f	0.33	0/454	0.73	0/599
41	2g	0.31	0/435	0.64	0/575
42	2h	0.28	0/231	0.70	0/294
43	2i	0.30	0/876	0.66	2/1156 (0.2%)
44	2j	0.28	0/718	0.65	2/953 (0.2%)
45	2k	0.35	0/1017	0.68	0/1364
46	2m	0.28	0/41243	0.47	3/64257 (0.0%)
47	2n	0.30	0/1778	0.67	0/2416
48	2o	0.28	0/1765	0.69	3/2362 (0.1%)
49	2p	0.28	0/1793	0.71	1/2414 (0.0%)
50	2q	0.29	0/2118	0.72	3/2849 (0.1%)
51	2r	0.28	0/1500	0.80	2/2015 (0.1%)
52	2s	0.28	0/1544	0.64	0/2068
53	2t	0.30	0/1715	0.70	1/2287 (0.0%)
54	2u	0.30	0/851	0.72	0/1147
55	2v	0.31	0/1268	0.66	0/1696
56	2w	0.43	1/815 (0.1%)	0.81	3/1087 (0.3%)
57	2x	0.29	0/1177	0.73	2/1575 (0.1%)
58	2y	0.27	0/1086	0.68	0/1457
59	2z	0.35	0/1253	0.85	2/1676 (0.1%)
60	20	0.26	0/1131	0.70	1/1515 (0.1%)
61	2l	0.31	0/831	0.74	0/1115
62	3A	0.30	0/643	0.81	0/860
63	3B	0.33	0/1116	0.80	4/1490 (0.3%)
64	3C	0.40	1/863 (0.1%)	0.78	1/1159 (0.1%)
65	3D	0.29	0/508	0.84	0/680
66	3E	0.26	0/455	0.67	0/603
67	3F	0.30	0/2493	0.77	1/3394 (0.0%)
68	3G	0.31	0/1762	0.67	0/2381
69	3H	0.29	0/1946	0.80	4/2590 (0.2%)
70	3I	0.30	0/1550	0.83	9/2069 (0.4%)
71	3J	0.28	0/962	0.76	2/1290 (0.2%)
72	3K	0.28	0/1232	0.61	0/1656
73	3L	0.28	0/1062	0.71	0/1425
74	3M	0.30	0/1051	0.69	0/1406
75	3N	0.28	0/1083	0.62	0/1438
76	3O	0.32	0/604	0.88	1/810 (0.1%)
77	3P	0.30	0/665	0.71	0/891

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	3Q	0.24	0/465	0.62	0/612
79	3R	0.23	0/560	0.70	0/745
80	zv	0.29	0/273	0.57	0/421
81	zw	0.26	0/3467	0.60	0/4661
82	zx	0.36	0/131	0.76	0/176
83	zy	0.24	0/1786	0.45	1/2784 (0.0%)
84	zz	0.24	0/3902	0.51	0/6084
All	All	0.30	2/239278 (0.0%)	0.56	96/351532 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	1D	0	1
5	1E	0	2
7	1G	0	2
8	1H	0	4
9	2A	0	1
11	2C	0	3
14	2F	0	3
15	2G	0	1
18	2J	0	1
22	2N	0	2
24	2P	0	2
28	2T	0	1
38	2d	0	1
48	2o	0	2
50	2q	0	3
51	2r	0	1
55	2v	0	1
57	2x	0	3
58	2y	0	1
59	2z	0	3
60	2o	0	1
63	3B	0	2
64	3C	0	1
68	3G	0	1
70	3I	0	3
71	3J	0	1
76	3O	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
77	3P	0	1
All	All	0	49

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	2w	68	PRO	CA-C	-7.57	1.47	1.51
64	3C	97	PRO	CA-C	7.45	1.57	1.52

All (96) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	1E	299	ILE	N-CA-C	-9.43	104.76	113.71
16	2H	148	THR	N-CA-C	-8.14	104.22	114.56
64	3C	97	PRO	O-C-N	7.91	124.87	121.15
60	20	39	LEU	N-CA-C	-7.03	98.27	109.59
70	3I	4	ALA	CB-CA-C	7.02	124.39	110.42
7	1G	57	ASN	CA-C-N	6.99	132.20	120.81
7	1G	57	ASN	C-N-CA	6.99	132.20	120.81
70	3I	4	ALA	CA-C-N	6.89	134.11	121.70
70	3I	4	ALA	C-N-CA	6.89	134.11	121.70
63	3B	106	GLY	CA-C-O	-6.80	117.40	122.37
63	3B	106	GLY	N-CA-C	-6.51	105.51	112.08
9	2A	196	THR	CA-C-N	6.37	129.28	120.49
9	2A	196	THR	C-N-CA	6.37	129.28	120.49
70	3I	7	TRP	CA-C-N	6.28	133.26	121.97
70	3I	7	TRP	C-N-CA	6.28	133.26	121.97
5	1E	304	SER	CA-C-N	6.22	133.41	121.54
5	1E	304	SER	C-N-CA	6.22	133.41	121.54
53	2t	139	LYS	N-CA-C	6.18	118.28	110.24
1	1A	4731	G	P-O3'-C3'	6.16	129.44	120.20
49	2p	199	GLY	N-CA-C	6.12	124.81	112.34
15	2G	95	ILE	N-CA-C	-6.10	103.40	110.05
5	1E	257	TRP	CA-C-N	-6.09	116.07	122.28
5	1E	257	TRP	C-N-CA	-6.09	116.07	122.28
46	2m	1414	A	C4'-C3'-O3'	6.05	118.47	109.40
83	zy	74	C	C2'-C3'-O3'	6.00	122.70	113.70
67	3F	275	ILE	N-CA-C	-5.99	106.58	111.91
50	2q	248	ILE	N-CA-C	5.91	116.57	110.36
43	2i	101	GLY	CA-C-N	5.82	132.17	121.70
43	2i	101	GLY	C-N-CA	5.82	132.17	121.70
11	2C	106	GLN	N-CA-C	5.81	117.79	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	2P	110	GLY	N-CA-C	5.81	126.95	113.18
51	2r	38	TYR	CA-C-N	5.76	132.34	121.97
51	2r	38	TYR	C-N-CA	5.76	132.34	121.97
48	2o	86	LEU	N-CA-C	5.71	117.59	110.91
16	2H	142	ILE	N-CA-C	-5.70	107.72	113.20
4	1D	124	GLY	N-CA-C	5.70	126.69	113.18
71	3J	112	LYS	CA-C-N	5.68	132.38	121.54
71	3J	112	LYS	C-N-CA	5.68	132.38	121.54
6	1F	230	LEU	CA-C-N	5.67	129.75	121.31
6	1F	230	LEU	C-N-CA	5.67	129.75	121.31
70	3I	8	VAL	N-CA-C	5.63	121.04	109.34
8	1H	95	PRO	CA-C-N	5.60	131.79	121.70
8	1H	95	PRO	C-N-CA	5.60	131.79	121.70
46	2m	339	A	P-O3'-C3'	5.58	128.56	120.20
70	3I	4	ALA	N-CA-C	-5.55	98.98	110.80
14	2F	5	ARG	N-CA-C	5.49	122.50	110.80
6	1F	109	ARG	CA-C-N	5.48	132.00	121.54
6	1F	109	ARG	C-N-CA	5.48	132.00	121.54
46	2m	1849	G	P-O3'-C3'	5.46	128.38	120.20
70	3I	171	GLY	CA-C-N	5.42	128.95	120.82
70	3I	171	GLY	C-N-CA	5.42	128.95	120.82
50	2q	247	THR	CA-C-N	5.37	127.53	120.60
50	2q	247	THR	C-N-CA	5.37	127.53	120.60
9	2A	162	ILE	CA-C-N	5.37	131.79	121.54
9	2A	162	ILE	C-N-CA	5.37	131.79	121.54
56	2w	73	PRO	CA-C-N	5.36	131.35	121.70
56	2w	73	PRO	C-N-CA	5.36	131.35	121.70
59	2z	16	LEU	CA-C-N	5.35	131.77	121.54
59	2z	16	LEU	C-N-CA	5.35	131.77	121.54
19	2K	76	GLU	CA-C-N	5.34	131.74	121.54
19	2K	76	GLU	C-N-CA	5.34	131.74	121.54
28	2T	30	ASP	N-CA-C	5.30	122.10	110.80
44	2j	3	LYS	CA-C-N	5.30	131.67	121.54
44	2j	3	LYS	C-N-CA	5.30	131.67	121.54
1	1A	456	C	O4'-C1'-N1	5.28	116.12	108.20
17	2I	127	VAL	N-CA-C	-5.26	108.38	113.53
22	2N	80	VAL	CA-C-N	5.25	131.56	121.54
22	2N	80	VAL	C-N-CA	5.25	131.56	121.54
69	3H	23	LYS	CA-C-N	-5.23	115.32	121.90
69	3H	23	LYS	C-N-CA	-5.23	115.32	121.90
1	1A	485	C	C2-N1-C1'	5.22	134.47	118.80
56	2w	68	PRO	O-C-N	-5.22	118.91	121.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
63	3B	107	ARG	CA-C-N	5.21	131.49	121.54
63	3B	107	ARG	C-N-CA	5.21	131.49	121.54
14	2F	4	SER	CA-C-N	5.21	131.49	121.54
14	2F	4	SER	C-N-CA	5.21	131.49	121.54
48	2o	77	ASP	CA-C-N	5.20	131.48	121.54
48	2o	77	ASP	C-N-CA	5.20	131.48	121.54
25	2Q	81	ALA	CA-C-N	5.20	127.31	120.60
25	2Q	81	ALA	C-N-CA	5.20	127.31	120.60
76	3O	108	ILE	N-CA-C	5.17	116.08	109.30
1	1A	2760	G	P-O3'-C3'	5.17	127.95	120.20
69	3H	171	THR	CA-C-N	5.16	131.39	121.54
69	3H	171	THR	C-N-CA	5.16	131.39	121.54
1	1A	1082	C	P-O3'-C3'	5.13	127.89	120.20
1	1A	2854	G	P-O3'-C3'	5.12	127.89	120.20
1	1A	3908	A	P-O3'-C3'	5.10	127.85	120.20
1	1A	2695	A	P-O3'-C3'	5.09	127.84	120.20
10	2B	140	VAL	N-CA-C	-5.06	108.91	113.71
10	2B	80	ILE	N-CA-C	-5.05	107.91	112.96
1	1A	2033	A	P-O3'-C3'	5.05	127.78	120.20
1	1A	914	U	P-O3'-C3'	5.04	127.77	120.20
8	1H	109	LEU	CA-C-N	5.04	131.17	121.54
8	1H	109	LEU	C-N-CA	5.04	131.17	121.54
57	2x	16	LYS	CA-C-N	5.03	131.15	121.54
57	2x	16	LYS	C-N-CA	5.03	131.15	121.54

There are no chirality outliers.

All (49) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	1D	239	ALA	Peptide
5	1E	258	HIS	Peptide
5	1E	305	THR	Peptide
7	1G	124	GLU	Peptide
7	1G	43	LYS	Peptide
8	1H	110	ARG	Peptide
8	1H	111	LYS	Peptide
8	1H	130	LYS	Peptide
8	1H	132	PRO	Peptide
60	20	38	LYS	Peptide
9	2A	163	ASN	Peptide
11	2C	106	GLN	Peptide
11	2C	59	LYS	Peptide

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Mol	Chain	Res	Type	Group
11	2C	60	TRP	Peptide
14	2F	4	SER	Peptide
14	2F	47	ALA	Peptide
14	2F	54	PRO	Peptide
15	2G	64	PHE	Peptide
18	2J	131	ARG	Peptide
22	2N	128	LEU	Peptide
22	2N	80	VAL	Peptide
24	2P	108	ASN	Peptide
24	2P	109	LYS	Peptide
28	2T	29	ILE	Peptide
38	2d	39	TYR	Peptide
48	2o	189	ILE	Peptide
48	2o	221	PRO	Peptide
50	2q	130	PHE	Peptide
50	2q	169	ILE	Peptide
50	2q	89	VAL	Peptide
51	2r	106	GLU	Peptide
55	2v	33	LEU	Peptide
57	2x	41	MET	Peptide
57	2x	42	ILE	Peptide
57	2x	43	GLU	Peptide
58	2y	122	PRO	Peptide
59	2z	11	HIS	Peptide
59	2z	12	ILE	Peptide
59	2z	16	LEU	Peptide
63	3B	107	ARG	Peptide
63	3B	125	VAL	Peptide
64	3C	47	ALA	Peptide
68	3G	172	ASN	Peptide
70	3I	138	ARG	Peptide
70	3I	7	TRP	Peptide
70	3I	9	CYS	Peptide
71	3J	112	LYS	Peptide
76	3O	99	LEU	Peptide
77	3P	19	HIS	Mainchain

5.2 Too-close contacts

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	78599	0	39719	648	0
2	1B	2558	0	1296	22	0
3	1C	3314	0	1683	29	0
4	1D	1898	0	1993	36	0
5	1E	3238	0	3376	47	0
6	1F	2927	0	3104	31	0
7	1G	2382	0	2410	17	0
8	1H	1913	0	2067	25	0
9	2A	1870	0	1996	31	0
10	2B	1927	0	2074	22	0
11	2C	1518	0	1601	25	0
12	2D	1711	0	1749	31	0
13	2E	1410	0	1441	20	0
14	2F	1701	0	1818	23	0
15	2G	1138	0	1204	15	0
16	2H	1701	0	1749	30	0
17	2I	1650	0	1794	25	0
18	2J	1242	0	1269	12	0
19	2K	1513	0	1628	15	0
20	2L	1566	0	1729	18	0
21	2M	1453	0	1490	32	0
22	2N	1298	0	1366	16	0
23	2O	825	0	850	4	0
24	2P	979	0	1039	19	0
25	2Q	1015	0	1079	14	0
26	2R	976	0	1059	9	0
27	2S	1115	0	1205	17	0
28	2T	1107	0	1182	16	0
29	2U	1162	0	1213	14	0
30	2V	876	0	948	12	0
31	2W	764	0	804	4	0
32	2X	888	0	930	6	0
33	2Y	1053	0	1147	16	0
34	2Z	876	0	912	11	0
35	2a	895	0	988	12	0
36	2b	1015	0	1148	7	0
37	2c	832	0	917	8	0
38	2d	705	0	741	15	0
39	2e	569	0	637	5	0
40	2f	444	0	483	5	0
41	2g	429	0	469	5	0
42	2h	230	0	276	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	2i	862	0	933	12	0
44	2j	708	0	760	13	0
45	2k	1002	0	1068	14	0
46	2m	36900	0	18599	387	0
47	2n	1741	0	1746	30	0
48	2o	1738	0	1809	22	0
49	2p	1765	0	1865	27	0
50	2q	2076	0	2177	29	0
51	2r	1479	0	1534	32	0
52	2s	1521	0	1616	23	0
53	2t	1686	0	1772	29	0
54	2u	827	0	854	18	0
55	2v	1247	0	1323	23	0
56	2w	804	0	841	20	0
57	2x	1158	0	1232	22	0
58	2y	1072	0	1130	21	0
59	2z	1235	0	1309	31	0
60	20	1112	0	1146	16	0
61	21	821	0	883	17	0
62	3A	636	0	637	11	0
63	3B	1098	0	1167	18	0
64	3C	847	0	899	13	0
65	3D	506	0	536	14	0
66	3E	445	0	442	5	0
67	3F	2436	0	2393	43	0
68	3G	1725	0	1813	19	0
69	3H	1923	0	2089	44	0
70	3I	1525	0	1640	21	0
71	3J	952	0	983	15	0
72	3K	1208	0	1294	16	0
73	3L	1049	0	1073	17	0
74	3M	1034	0	1080	13	0
75	3N	1065	0	1142	14	0
76	3O	598	0	656	14	0
77	3P	651	0	672	9	0
78	3Q	459	0	503	5	0
79	3R	548	0	555	9	0
80	zv	247	0	130	2	0
81	zw	3410	0	3419	40	0
82	zx	129	0	148	3	0
83	zy	1599	0	809	9	0
84	zz	3492	0	1761	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	222618	0	165021	2063	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 6.

All (2063) 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)
2:1B:30:C:C2	2:1B:48:G:N2	2.26	1.02
46:2m:1533:A:H62	46:2m:1602:U:H3	1.00	0.98
1:1A:512:U:H3	1:1A:647:G:H1	1.09	0.93
84:zz:145:G:H1	84:zz:248:U:H3	1.21	0.88
46:2m:1533:A:N6	46:2m:1602:U:H3	1.70	0.87
1:1A:2557:G:H1	1:1A:2570:U:H3	1.19	0.87
1:1A:4633:G:H21	1:1A:4665:A:H62	1.17	0.85
84:zz:259:U:N3	84:zz:274:A:C8	2.43	0.85
46:2m:1656:G:H1	46:2m:1668:U:H3	1.25	0.82
2:1B:30:C:N3	2:1B:48:G:N1	2.28	0.82
46:2m:831:G:H1	46:2m:844:U:H3	1.33	0.76
1:1A:4421:C:H42	1:1A:4475:G:H22	1.33	0.76
46:2m:878:G:O6	46:2m:908:A:N6	2.18	0.76
1:1A:3869:C:H1'	17:2I:68:ARG:HH22	1.53	0.74
2:1B:30:C:C2	2:1B:48:G:C2	2.75	0.74
46:2m:878:G:C6	46:2m:908:A:N1	2.56	0.74
1:1A:2316:G:N2	1:1A:2324:C:C2	2.57	0.73
1:1A:4421:C:N4	1:1A:4475:G:H22	1.86	0.72
46:2m:1550:G:H3'	46:2m:1579:A:H61	1.56	0.71
1:1A:4421:C:H42	1:1A:4475:G:N2	1.87	0.71
46:2m:694:G:C6	46:2m:737:G:N2	2.58	0.71
46:2m:1234:C:H42	46:2m:1525:C:H42	1.38	0.71
51:2r:80:GLY:HA2	51:2r:83:ASN:HB2	1.72	0.71
3:1C:96:C:H5''	36:2b:66:LYS:HD2	1.73	0.70
46:2m:1657:G:H1	46:2m:1667:U:H3	1.35	0.70
27:2S:43:ASN:HB3	27:2S:126:ARG:HD3	1.73	0.70
51:2r:39:ILE:HG23	51:2r:68:ILE:HG21	1.74	0.70
76:3O:97:ILE:HD11	76:3O:110:THR:H	1.55	0.70
84:zz:294:U:H2'	84:zz:295:G:H2'	1.72	0.69
55:2v:60:CYS:HG	55:2v:114:SER:HG	1.39	0.69
46:2m:1644:C:H4'	57:2x:140:ARG:HB2	1.75	0.68
46:2m:318:A:H2	46:2m:332:G:H1	1.40	0.68
1:1A:1098:G:H1	1:1A:1197:C:H42	1.39	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:2B:82:GLN:HE21	10:2B:171:PRO:HG2	1.58	0.68
9:2A:94:ARG:HB2	9:2A:114:LEU:HD23	1.74	0.68
1:1A:505:G:H1	1:1A:653:U:H3	1.40	0.67
2:1B:75:G:H22	2:1B:99:G:H2'	1.58	0.67
46:2m:1694:U:HO2'	46:2m:1833:C:HO2'	1.43	0.67
1:1A:1100:U:H3	1:1A:1195:G:H1	1.42	0.67
26:2R:86:ALA:HB1	26:2R:97:VAL:HG11	1.76	0.67
17:2I:186:GLU:HA	17:2I:189:ILE:HG22	1.76	0.67
46:2m:925:G:H1	46:2m:1017:U:H3	1.42	0.67
2:1B:30:C:O2	2:1B:48:G:C2	2.48	0.66
1:1A:279:A:OP2	16:2H:12:ARG:NH2	2.28	0.66
31:2W:26:LYS:H	31:2W:98:ASP:HB3	1.59	0.66
81:zw:94:VAL:HG11	81:zw:136:LEU:HD11	1.76	0.66
1:1A:4769:G:H1	1:1A:4865:C:H42	1.41	0.66
46:2m:443:U:H3	46:2m:447:A:H62	1.41	0.66
1:1A:1252:C:H2'	1:1A:1254:A:H62	1.61	0.66
46:2m:70:G:H21	46:2m:79:A:H62	1.44	0.66
1:1A:489:C:H42	1:1A:664:G:H1	1.42	0.65
49:2p:1:MET:HB2	49:2p:4:GLN:HB3	1.79	0.65
1:1A:2896:G:C6	1:1A:3604:A:N6	2.64	0.65
60:20:60:THR:O	60:20:64:LEU:HB2	1.97	0.65
1:1A:4886:C:H41	8:1H:272:ARG:HH22	1.43	0.65
48:2o:170:GLU:HB3	48:2o:174:ARG:HH21	1.61	0.65
1:1A:1570:G:N7	44:2j:3:LYS:NZ	2.45	0.65
1:1A:2845:A:H61	1:1A:3843:C:H42	1.45	0.65
73:3L:43:HIS:HD2	73:3L:55:ARG:HD3	1.62	0.65
67:3F:87:LEU:HB3	67:3F:101:PHE:HB2	1.78	0.65
11:2C:148:GLY:HA3	11:2C:154:VAL:HG21	1.79	0.65
16:2H:115:VAL:HG11	16:2H:160:GLU:HB3	1.78	0.65
73:3L:62:VAL:HG12	73:3L:64:ALA:H	1.62	0.64
46:2m:383:G:H21	55:2v:133:PRO:HG2	1.61	0.64
69:3H:8:PRO:HG3	69:3H:112:VAL:HG13	1.80	0.64
1:1A:4633:G:N2	1:1A:4665:A:H62	1.94	0.64
1:1A:4765:G:H22	1:1A:4869:U:H3	1.45	0.64
46:2m:493:A:H1'	46:2m:574:A:H5'	1.80	0.64
46:2m:1707:U:O2'	46:2m:1849:G:N2	2.30	0.64
46:2m:38:A:H5'	70:3I:6:SER:HB2	1.79	0.64
28:2T:46:ILE:HA	28:2T:70:SER:HA	1.80	0.64
46:2m:878:G:O6	46:2m:908:A:C6	2.50	0.64
50:2q:11:ARG:NH1	50:2q:21:ASP:OD1	2.31	0.64
1:1A:1780:A:O2'	12:2D:198:LYS:NZ	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:2D:90:ARG:HH21	12:2D:134:VAL:HG11	1.64	0.63
25:2Q:73:ARG:NH1	46:2m:1782:G:N7	2.46	0.63
13:2E:113:ILE:HB	59:2z:13:LEU:HD21	1.79	0.63
46:2m:366:U:H3	46:2m:394:G:H1	1.46	0.63
47:2n:8:LEU:HB3	47:2n:191:ARG:HH22	1.63	0.63
2:1B:47:G:H21	7:1G:222:GLN:HE22	1.46	0.63
7:1G:125:VAL:HG12	7:1G:127:GLY:H	1.63	0.63
24:2P:32:THR:HG21	24:2P:105:ILE:HD12	1.80	0.63
4:1D:58:LEU:HD13	4:1D:75:LEU:HD21	1.79	0.63
19:2K:53:MET:O	19:2K:58:ARG:NH1	2.32	0.63
46:2m:831:G:N2	46:2m:844:U:O2	2.29	0.63
46:2m:1422:G:N2	46:2m:1425:G:OP2	2.31	0.63
49:2p:37:VAL:HG12	49:2p:50:ILE:HA	1.81	0.63
11:2C:44:GLU:HB3	11:2C:58:ASP:HB2	1.81	0.63
37:2c:34:THR:HG22	37:2c:36:HIS:H	1.64	0.63
67:3F:190:GLY:HA3	67:3F:217:MET:HE1	1.80	0.63
16:2H:73:ARG:HB3	16:2H:89:VAL:HG23	1.80	0.63
1:1A:753:C:H41	1:1A:910:G:H1	1.47	0.63
48:2o:66:VAL:HG22	48:2o:87:ILE:HG22	1.81	0.63
64:3C:45:VAL:HG11	64:3C:50:VAL:HB	1.79	0.63
1:1A:114:G:H22	1:1A:158:A:H61	1.45	0.63
1:1A:4980:C:N3	18:2J:69:ARG:NH2	2.46	0.63
46:2m:694:G:O6	46:2m:737:G:C2	2.51	0.63
47:2n:109:THR:O	68:3G:89:LYS:NZ	2.32	0.63
1:1A:1306:C:H2'	1:1A:1307:A:H8	1.63	0.62
48:2o:67:PHE:HB3	73:3L:48:SER:HA	1.80	0.62
9:2A:236:ARG:HH22	9:2A:243:LEU:HD13	1.62	0.62
46:2m:878:G:O6	46:2m:908:A:N1	2.31	0.62
46:2m:1421:A:N6	46:2m:1427:C:O2	2.31	0.62
1:1A:4302:U:OP2	1:1A:4303:C:N4	2.31	0.62
21:2M:46:TYR:OH	21:2M:125:GLN:NE2	2.33	0.62
46:2m:587:A:OP2	70:3I:172:ARG:NH2	2.32	0.62
1:1A:3759:A:N7	1:1A:3763:A:N6	2.47	0.62
16:2H:159:ARG:HH21	16:2H:165:THR:HG22	1.65	0.62
46:2m:65:C:H1'	69:3H:172:LYS:HE3	1.79	0.62
32:2X:62:VAL:HG12	32:2X:104:THR:HB	1.81	0.62
1:1A:1656:U:OP2	29:2U:26:ARG:NH2	2.33	0.62
72:3K:34:LYS:HE2	72:3K:74:ILE:HD11	1.82	0.62
1:1A:729:G:N2	21:2M:66:GLN:O	2.33	0.62
1:1A:4670:C:O2'	1:1A:4672:A:OP2	2.18	0.62
46:2m:1419:C:H5'	60:20:129:ARG:HA	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1100:U:O2	1:1A:1195:G:N2	2.32	0.62
8:1H:46:ARG:HG3	8:1H:62:MET:HE1	1.81	0.62
8:1H:107:VAL:HG13	8:1H:108:LYS:HB3	1.81	0.62
46:2m:124:U:H3	46:2m:339:A:H61	1.47	0.62
50:2q:31:PRO:HB3	50:2q:43:PRO:HB3	1.81	0.62
54:2u:5:LYS:HB2	71:3J:29:ASP:HB2	1.82	0.62
1:1A:2599:G:N2	1:1A:2747:U:O4	2.33	0.62
5:1E:115:LYS:NZ	5:1E:129:ALA:O	2.32	0.62
47:2n:54:THR:HG22	47:2n:162:PRO:HG2	1.81	0.62
1:1A:2711:G:H5''	1:1A:2712:G:H5''	1.81	0.61
1:1A:3786:U:OP1	1:1A:4550:G:O2'	2.17	0.61
12:2D:162:ARG:NH1	21:2M:88:SER:OG	2.28	0.61
50:2q:139:LEU:HD23	50:2q:150:PRO:HB3	1.82	0.61
1:1A:974:C:OP1	9:2A:40:LYS:NZ	2.32	0.61
1:1A:4886:C:H42	1:1A:4934:A:H61	1.48	0.61
75:3N:8:ARG:HB3	75:3N:26:ASP:HB3	1.82	0.61
46:2m:1358:U:H5'	68:3G:114:LYS:HD3	1.81	0.61
72:3K:55:ARG:NH2	77:3P:51:GLN:OE1	2.33	0.61
1:1A:300:A:H2'	1:1A:301:G:H8	1.65	0.61
61:21:61:LEU:HB2	61:21:82:MET:HB3	1.82	0.61
1:1A:2522:G:OP1	35:2a:29:ARG:NH1	2.33	0.61
10:2B:180:PRO:HA	10:2B:227:ASN:HD21	1.66	0.61
20:2L:16:ARG:HH22	35:2a:29:ARG:HH21	1.47	0.61
9:2A:105:VAL:HG13	9:2A:136:VAL:HG12	1.83	0.61
1:1A:2482:C:N3	1:1A:2497:C:N4	2.48	0.61
1:1A:2653:C:OP1	35:2a:54:ARG:NH2	2.32	0.61
1:1A:2303:C:H5''	33:2Y:104:SER:HB3	1.81	0.61
1:1A:2485:U:OP1	1:1A:2486:G:N2	2.33	0.61
1:1A:4745:G:H22	1:1A:4954:G:H22	1.48	0.61
21:2M:147:ASP:HB3	21:2M:150:ILE:HG13	1.83	0.61
67:3F:57:ARG:NH2	67:3F:93:THR:O	2.34	0.61
1:1A:2474:G:N2	1:1A:2502:G:O2'	2.34	0.61
21:2M:85:ASP:HB3	21:2M:90:THR:HG22	1.83	0.61
1:1A:4376:A:O2'	29:2U:42:ARG:NH1	2.34	0.61
46:2m:1060:A:O2'	46:2m:1062:A:N7	2.33	0.61
46:2m:1310:U:O4	79:3R:99:LYS:NZ	2.34	0.61
2:1B:30:C:O2	2:1B:48:G:N2	2.33	0.60
24:2P:82:ILE:HD12	24:2P:121:VAL:HG22	1.83	0.60
46:2m:1387:G:N2	49:2p:206:ASP:OD1	2.34	0.60
1:1A:382:G:O2'	1:1A:407:A:N6	2.30	0.60
1:1A:1700:G:H5''	1:1A:1704:C:H42	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:280:G:OP1	16:2H:47:LYS:NZ	2.33	0.60
1:1A:992:C:N4	1:1A:994:G:N7	2.49	0.60
24:2P:24:ALA:HB3	24:2P:39:ILE:HD12	1.83	0.60
28:2T:12:LEU:HB2	28:2T:81:MET:HB3	1.83	0.60
1:1A:1763:C:H41	1:1A:1764:G:H21	1.49	0.60
10:2B:58:PRO:HD2	10:2B:61:ILE:HD11	1.82	0.60
10:2B:100:HIS:O	10:2B:103:ARG:NH1	2.34	0.60
18:2J:89:GLU:O	18:2J:93:HIS:ND1	2.31	0.60
46:2m:1622:U:H3	59:2z:152:LYS:HB2	1.65	0.60
22:2N:56:CYS:SG	22:2N:78:LYS:NZ	2.73	0.60
46:2m:191:A:N6	46:2m:208:G:O2'	2.34	0.60
59:2z:36:VAL:HG23	59:2z:40:TYR:HD2	1.67	0.60
63:3B:63:ASN:ND2	63:3B:114:ASP:OD2	2.33	0.60
71:3J:52:GLN:HE21	71:3J:78:LYS:HB2	1.67	0.60
46:2m:1848:U:H2'	46:2m:1849:G:H2'	1.84	0.60
60:20:67:ARG:NH2	60:20:74:SER:OG	2.35	0.60
84:zz:259:U:O2	84:zz:274:A:N7	2.35	0.60
1:1A:4741:C:H2'	1:1A:4742:G:H8	1.65	0.60
46:2m:560:A:N6	46:2m:588:G:O6	2.35	0.60
46:2m:1091:C:N3	46:2m:1159:G:N1	2.49	0.60
1:1A:1844:G:OP1	30:2V:22:LYS:NZ	2.35	0.60
1:1A:3598:C:H2'	1:1A:3599:A:H8	1.67	0.60
1:1A:5040:U:OP2	5:1E:396:ARG:NH2	2.35	0.60
3:1C:71:A:H62	3:1C:87:G:H21	1.50	0.60
71:3J:28:HIS:HB2	71:3J:116:LYS:HG3	1.84	0.59
1:1A:512:U:O4	1:1A:647:G:O6	2.20	0.59
1:1A:1674:C:H1'	29:2U:43:ILE:HD11	1.84	0.59
1:1A:4558:U:OP2	5:1E:246:ARG:NH2	2.33	0.59
28:2T:36:ARG:NH1	28:2T:38:TYR:OH	2.34	0.59
51:2r:63:LYS:HE2	51:2r:71:ARG:HE	1.67	0.59
46:2m:927:C:O2	77:3P:51:GLN:NE2	2.35	0.59
1:1A:3762:U:H5'	81:zw:166:ARG:HH21	1.68	0.59
46:2m:331:C:N4	69:3H:186:GLN:OE1	2.35	0.59
76:3O:60:LYS:O	76:3O:64:ASN:ND2	2.36	0.59
1:1A:230:G:OP1	27:2S:15:ARG:NH1	2.35	0.59
1:1A:1653:A:OP1	29:2U:32:ARG:NH2	2.36	0.59
1:1A:2845:A:H61	1:1A:3843:C:N4	2.00	0.59
46:2m:1156:U:H5''	74:3M:71:LYS:HE2	1.84	0.59
46:2m:1236:G:O6	59:2z:137:LYS:NZ	2.35	0.59
47:2n:45:GLY:HA3	58:2y:126:MET:HB2	1.84	0.59
19:2K:85:THR:HG21	19:2K:104:ARG:HH11	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:2a:51:GLY:O	35:2a:53:LEU:N	2.36	0.59
46:2m:1032:C:H5'	72:3K:109:LYS:HD2	1.85	0.59
46:2m:1290:G:H5'	66:3E:4:GLN:HE22	1.66	0.59
46:2m:744:G:N2	52:2s:105:THR:O	2.36	0.59
1:1A:2838:G:H5'	5:1E:247:GLY:HA2	1.85	0.59
8:1H:221:LYS:HE2	8:1H:223:ARG:HB2	1.85	0.59
13:2E:111:GLU:OE2	59:2z:14:ARG:NH2	2.33	0.59
20:2L:7:GLN:NE2	20:2L:35:ALA:O	2.32	0.59
46:2m:351:G:OP1	53:2t:7:ASN:ND2	2.35	0.59
1:1A:1972:G:H1	1:1A:1993:C:H42	1.50	0.59
67:3F:196:ASN:ND2	67:3F:236:ILE:O	2.36	0.59
1:1A:86:U:HO2'	29:2U:65:ARG:HH11	1.51	0.58
7:1G:19:LYS:O	7:1G:24:ARG:NH2	2.36	0.58
39:2e:17:ARG:NH1	39:2e:38:CYS:SG	2.76	0.58
52:2s:40:LEU:HG	52:2s:43:LEU:HD11	1.84	0.58
46:2m:934:G:H1	46:2m:1008:A:H2	1.48	0.58
51:2r:74:ASN:HA	51:2r:77:MET:HE3	1.85	0.58
1:1A:1661:C:OP1	33:2Y:36:ARG:NH2	2.36	0.58
1:1A:4103:C:O2'	1:1A:4106:G:N2	2.37	0.58
18:2J:23:ARG:NH2	18:2J:125:MET:SD	2.76	0.58
31:2W:51:ASN:ND2	44:2j:40:SER:O	2.36	0.58
46:2m:1142:G:N2	46:2m:1145:A:OP2	2.34	0.58
46:2m:1402:A:N6	46:2m:1441:U:O2	2.36	0.58
49:2p:175:VAL:HG22	49:2p:182:LEU:H	1.69	0.58
1:1A:436:C:H2'	1:1A:437:G:H8	1.69	0.58
50:2q:212:ASP:OD1	50:2q:216:ASN:N	2.37	0.58
57:2x:31:LEU:HD21	57:2x:33:LYS:HE3	1.85	0.58
1:1A:438:G:OP1	33:2Y:16:ARG:NH2	2.35	0.58
1:1A:942:G:OP1	9:2A:245:ARG:NH1	2.36	0.58
1:1A:2300:A:N6	6:1F:178:ASN:OD1	2.36	0.58
1:1A:4525:C:OP1	5:1E:246:ARG:NH1	2.36	0.58
15:2G:31:ILE:HD11	15:2G:37:LEU:HB2	1.85	0.58
1:1A:3766:A:N6	46:2m:1850:A:N3	2.52	0.58
18:2J:112:LEU:HD23	18:2J:150:LEU:HD13	1.85	0.58
47:2n:80:ARG:HH22	47:2n:166:LYS:HA	1.68	0.58
57:2x:41:MET:SD	60:20:10:ASN:ND2	2.76	0.58
1:1A:375:G:OP2	38:2d:52:LYS:NZ	2.37	0.58
1:1A:712:C:OP1	8:1H:139:LYS:NZ	2.36	0.58
1:1A:2743:A:O2'	4:1D:21:LYS:NZ	2.37	0.58
11:2C:91:LYS:HG2	11:2C:145:ILE:HG13	1.85	0.58
58:2y:77:GLU:OE1	58:2y:81:ARG:NH2	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:2z:23:ARG:HD2	76:3O:48:VAL:HG11	1.85	0.58
1:1A:20:U:OP2	3:1C:36:G:N2	2.37	0.58
1:1A:3842:C:OP1	5:1E:238:LYS:NZ	2.36	0.58
1:1A:4293:U:O2'	43:2i:81:ARG:NH2	2.37	0.58
1:1A:4566:U:O2'	5:1E:269:ALA:O	2.20	0.58
9:2A:113:ARG:HH21	9:2A:210:PRO:HD3	1.69	0.58
9:2A:228:VAL:O	21:2M:2:LYS:N	2.37	0.58
46:2m:317:C:H5''	69:3H:183:ARG:HH22	1.69	0.58
1:1A:2553:A:H2	1:1A:2764:A:H62	1.51	0.57
1:1A:3717:A:OP2	1:1A:3735:G:N2	2.36	0.57
1:1A:4393:G:N2	1:1A:4396:A:OP2	2.36	0.57
14:2F:170:THR:HG22	14:2F:172:GLU:H	1.69	0.57
21:2M:140:PRO:HA	21:2M:143:LYS:HB2	1.86	0.57
59:2z:11:HIS:HA	59:2z:12:ILE:HG23	1.85	0.57
1:1A:1599:A:OP1	1:1A:2795:A:N6	2.37	0.57
1:1A:2395:A:N3	1:1A:2806:A:O2'	2.37	0.57
1:1A:4433:G:N7	12:2D:7:ARG:NH1	2.50	0.57
9:2A:26:ALA:HA	9:2A:29:LYS:HG2	1.84	0.57
46:2m:78:C:O2	69:3H:175:LYS:NZ	2.37	0.57
46:2m:1421:A:N1	46:2m:1427:C:O2'	2.37	0.57
46:2m:1240:A:N6	59:2z:152:LYS:O	2.36	0.57
65:3D:6:VAL:HG13	65:3D:8:PRO:HD3	1.84	0.57
1:1A:493:G:O6	1:1A:660:A:N1	2.37	0.57
46:2m:678:U:OP2	46:2m:1026:C:N4	2.37	0.57
79:3R:139:HIS:HB2	79:3R:148:TYR:HB3	1.86	0.57
1:1A:2112:G:H4'	1:1A:2251:G:H1	1.68	0.57
3:1C:75:G:OP2	27:2S:74:TYR:OH	2.22	0.57
46:2m:747:U:O2	46:2m:791:C:N4	2.38	0.57
47:2n:156:TYR:O	62:3A:60:ARG:NH2	2.37	0.57
81:zw:331:TYR:HB2	81:zw:346:LEU:HD13	1.85	0.57
1:1A:1351:G:OP1	6:1F:33:ARG:NH1	2.32	0.57
46:2m:1533:A:N7	46:2m:1602:U:O4	2.37	0.57
46:2m:1677:U:OP2	51:2r:63:LYS:NZ	2.36	0.57
1:1A:2322:G:OP1	33:2Y:36:ARG:NH1	2.36	0.57
4:1D:30:ARG:O	4:1D:163:ARG:NH2	2.36	0.57
13:2E:16:ARG:HH12	13:2E:137:PRO:HG3	1.70	0.57
15:2G:119:ARG:HA	17:2I:189:ILE:HD11	1.86	0.57
16:2H:120:TRP:HZ2	16:2H:123:GLU:HB2	1.69	0.57
21:2M:83:ARG:NH1	21:2M:125:GLN:OE1	2.37	0.57
46:2m:1283:C:N3	46:2m:1313:A:N6	2.53	0.57
46:2m:1403:C:OP2	46:2m:1405:A:N6	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:2w:53:GLN:NE2	56:2w:82:ASP:OD2	2.38	0.57
77:3P:33:MET:HE2	77:3P:48:SER:HA	1.86	0.57
1:1A:90:G:OP2	43:2i:40:ARG:NH2	2.37	0.57
1:1A:4620:U:OP2	1:1A:4670:C:N4	2.35	0.57
51:2r:140:ASP:HB3	65:3D:46:VAL:HG12	1.85	0.57
51:2r:197:GLU:HA	51:2r:200:ALA:HB3	1.86	0.57
1:1A:10:A:H2'	1:1A:11:G:H8	1.69	0.57
1:1A:2754:G:OP2	28:2T:133:LYS:NZ	2.30	0.57
42:2h:11:ARG:NH2	46:2m:1184:G:OP1	2.38	0.57
46:2m:681:U:H4'	63:3B:9:THR:HG22	1.86	0.57
46:2m:924:G:H1	46:2m:1018:U:H3	1.52	0.57
75:3N:76:TYR:HE2	75:3N:86:GLU:HB3	1.69	0.57
1:1A:3684:G:OP1	4:1D:174:ARG:NH2	2.38	0.57
1:1A:4873:G:OP2	15:2G:94:LYS:NZ	2.34	0.57
2:1B:30:C:N3	2:1B:48:G:C2	2.73	0.57
3:1C:155:C:OP2	10:2B:89:ARG:NH1	2.38	0.57
46:2m:314:U:O4	46:2m:338:G:N2	2.38	0.57
50:2q:42:LEU:HD21	50:2q:47:PHE:HB2	1.86	0.57
5:1E:153:MET:HE3	5:1E:194:LEU:HD11	1.87	0.56
5:1E:224:LYS:HE2	5:1E:340:THR:HG23	1.87	0.56
46:2m:1227:G:N2	46:2m:1635:C:O2'	2.37	0.56
76:3O:63:PRO:HB2	76:3O:112:ASN:HD21	1.69	0.56
15:2G:62:LEU:HD21	15:2G:82:ILE:HD11	1.87	0.56
46:2m:291:G:N2	46:2m:293:C:OP2	2.36	0.56
52:2s:122:LEU:HA	52:2s:125:VAL:HB	1.85	0.56
59:2z:30:ILE:HD12	59:2z:45:LEU:HD11	1.86	0.56
63:3B:107:ARG:NH1	63:3B:111:ALA:O	2.36	0.56
1:1A:3660:C:OP1	4:1D:241:ARG:NH2	2.38	0.56
1:1A:4431:U:OP2	12:2D:3:ARG:NH2	2.39	0.56
1:1A:4485:C:O2'	41:2g:114:LYS:NZ	2.38	0.56
46:2m:637:U:O2	78:3Q:56:ASN:ND2	2.38	0.56
46:2m:934:G:O6	46:2m:1008:A:N1	2.38	0.56
57:2x:50:LYS:HA	57:2x:53:GLU:HG3	1.86	0.56
67:3F:109:LEU:HD23	67:3F:110:SER:H	1.70	0.56
84:zz:137:G:O6	84:zz:287:U:C2	2.59	0.56
84:zz:259:U:C2	84:zz:274:A:N7	2.73	0.56
1:1A:4520:G:N2	5:1E:253:CYS:SG	2.78	0.56
31:2W:9:LYS:N	31:2W:12:GLU:OE1	2.37	0.56
46:2m:1357:A:OP1	68:3G:125:LYS:NZ	2.37	0.56
47:2n:7:VAL:HG12	47:2n:191:ARG:HH21	1.70	0.56
65:3D:42:ILE:HD11	65:3D:64:GLU:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
72:3K:27:LYS:NZ	84:zz:233:G:OP1	2.38	0.56
1:1A:3901:A:H5'	1:1A:3902:A:H5'	1.87	0.56
46:2m:190:G:O2'	46:2m:209:A:N6	2.38	0.56
1:1A:28:C:OP2	16:2H:189:ARG:NH1	2.38	0.56
1:1A:307:A:OP1	37:2c:45:ARG:NH1	2.39	0.56
1:1A:4077:A:N1	1:1A:4171:C:N4	2.49	0.56
1:1A:4213:A:H5''	1:1A:4214:A:H5''	1.86	0.56
4:1D:137:ILE:HD11	4:1D:149:LYS:HB2	1.88	0.56
28:2T:91:LEU:HD23	28:2T:96:VAL:HG21	1.87	0.56
46:2m:1400:U:O2	61:21:55:ARG:NH2	2.38	0.56
55:2v:49:GLU:OE2	55:2v:118:ARG:NH2	2.38	0.56
1:1A:2898:G:OP2	20:2L:135:LYS:NZ	2.38	0.56
46:2m:1562:C:H4'	60:20:119:GLY:HA3	1.88	0.56
46:2m:1598:G:H5''	76:3O:82:SER:HB3	1.87	0.56
54:2u:59:LYS:HB3	54:2u:70:TYR:HB2	1.88	0.56
74:3M:14:ILE:HG22	74:3M:25:VAL:HG21	1.86	0.56
19:2K:85:THR:HG22	19:2K:104:ARG:HB3	1.88	0.56
46:2m:1781:A:O2'	46:2m:1782:G:N7	2.38	0.56
1:1A:2647:A:H62	1:1A:2686:G:H8	1.52	0.56
1:1A:4476:C:O2	11:2C:173:ARG:NH2	2.39	0.56
46:2m:1414:A:H3'	46:2m:1416:C:H4'	1.88	0.56
52:2s:8:ILE:HG23	52:2s:9:VAL:HG23	1.87	0.56
1:1A:1552:G:O2'	1:1A:1574:G:N2	2.39	0.56
46:2m:1137:U:O2'	47:2n:155:ARG:NH1	2.39	0.56
51:2r:48:TYR:HD2	57:2x:53:GLU:HG2	1.71	0.56
1:1A:1973:G:H8	1:1A:1974:U:H2'	1.71	0.55
1:1A:2903:G:O2'	1:1A:3591:C:N4	2.39	0.55
5:1E:59:GLU:HB2	5:1E:366:LYS:HE2	1.88	0.55
46:2m:1199:A:OP1	64:3C:2:THR:OG1	2.24	0.55
46:2m:1605:G:OP1	60:20:84:ARG:NH2	2.40	0.55
50:2q:137:PRO:HG2	50:2q:150:PRO:HD2	1.87	0.55
57:2x:1:MET:HB3	57:2x:4:LYS:HB2	1.88	0.55
58:2y:18:GLU:HG3	58:2y:19:LYS:HG3	1.88	0.55
5:1E:10:ARG:NH1	5:1E:265:SER:O	2.32	0.55
17:2I:35:VAL:HB	17:2I:104:VAL:HG12	1.87	0.55
28:2T:88:ASP:OD1	28:2T:121:ARG:NH2	2.40	0.55
46:2m:202:G:OP2	53:2t:143:LYS:NZ	2.40	0.55
46:2m:1417:C:H41	46:2m:1429:G:H22	1.53	0.55
77:3P:59:CYS:SG	77:3P:60:SER:N	2.80	0.55
46:2m:140:C:H42	46:2m:144:U:H1'	1.72	0.55
46:2m:539:C:H5''	46:2m:540:U:H5''	1.86	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2m:1183:A:H2'	46:2m:1184:G:H8	1.70	0.55
49:2p:127:MET:HE1	49:2p:133:GLY:HA2	1.88	0.55
52:2s:145:ARG:NH2	74:3M:49:GLU:OE1	2.39	0.55
63:3B:105:PHE:HD1	63:3B:121:LYS:HB3	1.71	0.55
1:1A:2316:G:C2	1:1A:2324:C:C2	2.94	0.55
1:1A:4232:U:O4	43:2i:8:ARG:NH1	2.38	0.55
5:1E:234:ARG:NH1	5:1E:268:ARG:O	2.39	0.55
24:2P:18:LEU:HD23	24:2P:54:ALA:HB3	1.87	0.55
46:2m:659:G:O2'	46:2m:662:G:O2'	2.25	0.55
52:2s:24:SER:HA	52:2s:27:LEU:HD13	1.89	0.55
1:1A:1668:A:OP2	1:1A:2280:G:N2	2.34	0.55
1:1A:3861:A:H2'	1:1A:3862:A:H8	1.71	0.55
6:1F:31:PRO:HB3	19:2K:24:TYR:HE2	1.72	0.55
7:1G:80:ALA:HA	7:1G:83:LEU:HD13	1.88	0.55
9:2A:222:LYS:HB3	9:2A:231:GLY:HA2	1.88	0.55
12:2D:162:ARG:HH12	21:2M:88:SER:HG	1.52	0.55
51:2r:28:VAL:O	51:2r:42:LYS:NZ	2.39	0.55
57:2x:24:HIS:HE2	57:2x:69:ARG:HB3	1.72	0.55
61:21:69:PRO:O	66:3E:41:GLN:NE2	2.39	0.55
1:1A:4235:G:N2	1:1A:4290:U:O2	2.36	0.55
1:1A:4635:A:H2	1:1A:4663:G:H21	1.55	0.55
16:2H:61:ILE:HG22	16:2H:133:ILE:HA	1.87	0.55
21:2M:118:ARG:O	21:2M:120:ARG:NH1	2.40	0.55
34:2Z:77:ALA:HA	34:2Z:84:VAL:HG12	1.87	0.55
46:2m:1280:G:H5''	71:3J:101:ARG:HD2	1.88	0.55
50:2q:128:LYS:HE2	50:2q:130:PHE:HB3	1.89	0.55
60:20:124:THR:HG23	60:20:127:GLY:H	1.71	0.55
1:1A:2449:A:H5'	4:1D:21:LYS:HD3	1.87	0.55
33:2Y:22:ARG:HB3	33:2Y:25:SER:HB3	1.88	0.55
38:2d:70:VAL:HA	38:2d:73:ARG:HG2	1.87	0.55
46:2m:1641:A:HO2'	83:zy:30:C:HO2'	1.52	0.55
84:zz:262:U:O2	84:zz:271:G:O6	2.25	0.55
1:1A:4086:G:O6	10:2B:48:LYS:NZ	2.40	0.55
5:1E:117:ARG:HD2	5:1E:177:LYS:HG2	1.88	0.55
1:1A:2520:C:H2'	1:1A:2521:G:H8	1.72	0.55
1:1A:4601:U:O2	1:1A:4610:A:N7	2.40	0.55
21:2M:83:ARG:NH2	22:2N:154:ILE:O	2.39	0.55
22:2N:78:LYS:HE3	22:2N:80:VAL:HG13	1.88	0.55
46:2m:412:G:N2	46:2m:812:A:H61	2.05	0.55
50:2q:61:VAL:O	50:2q:65:CYS:HB2	2.07	0.55
1:1A:1699:A:O2'	6:1F:306:ARG:NH1	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2622:G:O6	23:2O:81:ARG:NH2	2.31	0.55
6:1F:334:THR:O	6:1F:338:ASN:ND2	2.40	0.55
15:2G:104:MET:HE3	15:2G:109:ARG:HG2	1.87	0.55
46:2m:171:A:OP1	69:3H:137:ARG:NH1	2.40	0.55
46:2m:399:C:O3'	63:3B:11:ARG:NH1	2.39	0.55
46:2m:457:C:H2'	46:2m:458:A:H8	1.71	0.55
71:3J:67:ALA:HB1	79:3R:114:ILE:HD11	1.89	0.55
1:1A:2484:A:N6	1:1A:2495:U:O2	2.38	0.54
1:1A:3904:G:H21	1:1A:4557:U:H3	1.55	0.54
25:2Q:120:GLN:NE2	46:2m:327:G:N7	2.55	0.54
46:2m:206:G:O6	53:2t:144:LYS:NZ	2.39	0.54
46:2m:1192:U:OP2	63:3B:119:ARG:NH2	2.39	0.54
69:3H:76:LEU:HD21	69:3H:92:ARG:HD2	1.89	0.54
70:3I:134:HIS:O	70:3I:160:SER:N	2.40	0.54
1:1A:2552:G:N2	1:1A:2766:A:N7	2.54	0.54
3:1C:104:A:OP2	38:2d:42:LYS:NZ	2.40	0.54
5:1E:119:TYR:OH	5:1E:129:ALA:N	2.39	0.54
14:2F:129:ARG:HB2	36:2b:117:ARG:HH12	1.72	0.54
39:2e:49:ASP:HB3	39:2e:52:LYS:HG2	1.90	0.54
1:1A:2907:G:N2	1:1A:2909:C:OP1	2.40	0.54
8:1H:155:GLY:O	8:1H:158:ARG:NH1	2.39	0.54
46:2m:1533:A:N6	46:2m:1602:U:N3	2.41	0.54
55:2v:151:THR:OG1	55:2v:153:LYS:NZ	2.40	0.54
65:3D:66:ARG:HG2	65:3D:67:ARG:HG2	1.90	0.54
1:1A:4292:A:O2'	43:2i:8:ARG:NH2	2.41	0.54
4:1D:113:VAL:HG12	4:1D:166:VAL:HA	1.88	0.54
6:1F:195:LYS:HB2	6:1F:200:ARG:HD2	1.90	0.54
7:1G:198:HIS:ND1	7:1G:203:ASN:OD1	2.39	0.54
9:2A:225:THR:OG1	9:2A:229:GLU:OE1	2.25	0.54
12:2D:177:ASN:ND2	12:2D:180:GLU:OE2	2.38	0.54
46:2m:380:G:OP1	53:2t:56:ARG:NH2	2.41	0.54
1:1A:293:G:H1	16:2H:181:HIS:HD2	1.54	0.54
1:1A:4622:A:H4'	5:1E:13:SER:HB2	1.89	0.54
1:1A:4770:U:N3	1:1A:4863:G:N7	2.55	0.54
25:2Q:20:ARG:HE	25:2Q:30:GLN:HE21	1.53	0.54
46:2m:1358:U:OP2	68:3G:123:ARG:NH1	2.40	0.54
49:2p:75:LYS:NZ	54:2u:20:VAL:O	2.37	0.54
77:3P:65:GLN:HB2	77:3P:72:ARG:HB3	1.89	0.54
1:1A:423:G:OP1	18:2J:62:ARG:NH2	2.41	0.54
2:1B:8:G:OP1	7:1G:33:ARG:NH2	2.40	0.54
12:2D:76:MET:HE3	12:2D:151:ALA:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2m:395:G:H5'	55:2v:82:MET:HE3	1.89	0.54
46:2m:412:G:H21	46:2m:812:A:H61	1.56	0.54
81:zw:29:GLY:HA2	81:zw:101:VAL:HG12	1.90	0.54
1:1A:1727:U:OP1	9:2A:131:ASN:ND2	2.41	0.54
1:1A:1918:U:O4'	1:1A:2065:G:N2	2.40	0.54
1:1A:4389:C:H2'	1:1A:4390:A:H8	1.71	0.54
7:1G:146:LEU:HD12	7:1G:163:LEU:HD13	1.89	0.54
7:1G:152:ARG:NH1	7:1G:153:THR:O	2.41	0.54
25:2Q:56:ARG:HE	25:2Q:61:LYS:HB2	1.73	0.54
25:2Q:83:THR:O	69:3H:128:THR:OG1	2.23	0.54
46:2m:882:U:O4	46:2m:905:C:N3	2.41	0.54
1:1A:19:G:OP2	36:2b:89:ARG:NH2	2.37	0.54
1:1A:442:G:OP1	34:2Z:68:ARG:NH1	2.38	0.54
1:1A:1176:C:H42	1:1A:1184:A:H61	1.55	0.54
1:1A:2811:G:N1	1:1A:2814:C:OP2	2.40	0.54
1:1A:3890:A:N6	1:1A:4570:G:O2'	2.41	0.54
1:1A:4096:C:N3	1:1A:4113:U:O2'	2.41	0.54
35:2a:42:PRO:HD2	35:2a:56:VAL:HG21	1.90	0.54
46:2m:114:G:O2'	46:2m:382:C:O2'	2.25	0.54
46:2m:178:C:H3'	46:2m:313:A:H61	1.72	0.54
46:2m:694:G:O6	46:2m:737:G:N1	2.41	0.54
46:2m:1311:C:N4	46:2m:1312:G:O6	2.40	0.54
60:20:107:LEU:HB3	60:20:112:MET:HB2	1.88	0.54
62:3A:59:ILE:HG23	62:3A:64:GLU:HB3	1.89	0.54
1:1A:1857:C:H2'	1:1A:1858:A:H8	1.73	0.54
1:1A:3745:U:O2'	4:1D:243:THR:O	2.25	0.54
12:2D:72:ALA:HB2	12:2D:155:ALA:HB2	1.88	0.54
48:2o:159:GLN:OE1	48:2o:162:ARG:NH2	2.40	0.54
1:1A:1321:G:N2	1:1A:3876:A:O4'	2.41	0.54
1:1A:4704:C:H2'	1:1A:4705:A:H8	1.72	0.54
46:2m:30:C:O2'	46:2m:596:U:OP1	2.25	0.54
1:1A:1346:C:H2'	1:1A:1347:G:H8	1.73	0.53
1:1A:4212:A:N6	1:1A:4219:A:OP2	2.41	0.53
1:1A:5018:C:H2'	1:1A:5019:A:H8	1.73	0.53
20:2L:106:LEU:HB3	20:2L:120:TYR:HE1	1.72	0.53
46:2m:1488:C:O2'	46:2m:1490:G:OP2	2.21	0.53
51:2r:193:LYS:NZ	51:2r:197:GLU:OE2	2.41	0.53
58:2y:37:GLU:OE1	67:3F:150:TRP:NE1	2.40	0.53
79:3R:117:LEU:HD23	79:3R:118:ARG:HE	1.71	0.53
84:zz:144:U:O2	84:zz:249:G:O6	2.25	0.53
1:1A:3689:G:O2'	1:1A:3818:U:OP2	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2p:62:LYS:O	54:2u:95:ARG:NH2	2.41	0.53
49:2p:64:ARG:HB2	54:2u:93:THR:HG21	1.91	0.53
49:2p:116:ARG:HG2	49:2p:150:MET:HE1	1.90	0.53
73:3L:92:ALA:HB2	73:3L:125:LYS:HB2	1.90	0.53
1:1A:4141:G:O2'	1:1A:4143:G:N7	2.37	0.53
1:1A:4767:C:O2'	1:1A:4874:A:N6	2.41	0.53
46:2m:1093:A:H61	46:2m:1152:U:H3	1.56	0.53
49:2p:132:LYS:HE2	49:2p:191:PRO:HB3	1.89	0.53
55:2v:4:ILE:HG23	55:2v:5:GLN:HG2	1.90	0.53
67:3F:256:ILE:HB	67:3F:270:LEU:HD22	1.89	0.53
1:1A:667:A:O2'	45:2k:46:ARG:NH2	2.41	0.53
1:1A:2276:A:OP1	9:2A:166:ARG:NH1	2.41	0.53
1:1A:4454:G:H2'	1:1A:4455:G:H8	1.74	0.53
43:2i:33:LEU:HA	43:2i:38:LYS:HG2	1.89	0.53
62:3A:25:GLY:O	68:3G:85:SER:OG	2.26	0.53
81:zw:322:VAL:HG22	81:zw:409:ILE:HG13	1.89	0.53
1:1A:974:C:O2'	6:1F:327:LYS:NZ	2.41	0.53
1:1A:1703:C:O2'	9:2A:39:GLN:NE2	2.42	0.53
1:1A:4940:C:OP2	8:1H:219:LYS:NZ	2.36	0.53
9:2A:226:HIS:HA	9:2A:233:ALA:HB3	1.91	0.53
21:2M:34:ALA:HB1	21:2M:39:VAL:HG13	1.90	0.53
46:2m:656:G:O5'	46:2m:662:G:N2	2.42	0.53
46:2m:1337:C:H2'	46:2m:1338:G:H8	1.73	0.53
1:1A:1837:A:OP2	22:2N:130:ARG:NH2	2.42	0.53
7:1G:115:MET:HE1	7:1G:141:ALA:HA	1.89	0.53
10:2B:94:GLN:HA	10:2B:97:LYS:HE3	1.91	0.53
11:2C:59:LYS:HE2	11:2C:67:LEU:HA	1.90	0.53
46:2m:1091:C:C2	46:2m:1159:G:N2	2.77	0.53
46:2m:1617:G:O6	56:2w:43:ARG:NH1	2.42	0.53
57:2x:43:GLU:OE1	57:2x:45:ARG:NE	2.40	0.53
69:3H:37:ALA:HA	69:3H:49:VAL:HA	1.90	0.53
69:3H:66:GLY:N	69:3H:100:CYS:SG	2.80	0.53
1:1A:38:A:H61	1:1A:41:C:H3'	1.72	0.53
1:1A:1100:U:O3'	1:1A:1167:C:N4	2.42	0.53
1:1A:2487:G:O6	1:1A:2492:C:N4	2.41	0.53
1:1A:2583:C:OP2	35:2a:76:ARG:NH1	2.41	0.53
8:1H:208:ILE:HD11	8:1H:212:LEU:HD22	1.89	0.53
26:2R:91:GLU:HG2	26:2R:147:LEU:HD21	1.90	0.53
63:3B:68:LYS:HG2	63:3B:91:LEU:HD22	1.90	0.53
1:1A:935:A:H1'	15:2G:44:GLN:HB3	1.89	0.53
1:1A:1968:G:OP2	1:1A:1970:A:N6	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2406:G:N7	40:2f:2:SER:N	2.57	0.53
53:2t:67:TRP:CD1	53:2t:70:GLU:H	2.27	0.53
58:2y:32:LYS:NZ	58:2y:48:ASN:OD1	2.34	0.53
67:3F:120:ILE:HB	67:3F:132:TRP:HB2	1.91	0.53
1:1A:1790:U:OP2	22:2N:13:TYR:OH	2.27	0.53
14:2F:91:ALA:HB1	14:2F:96:ILE:HB	1.91	0.53
27:2S:4:ASN:HB3	27:2S:7:VAL:HG22	1.91	0.53
46:2m:1396:A:O2'	46:2m:1398:G:N7	2.42	0.53
46:2m:1613:G:H5''	56:2w:42:ARG:HH21	1.74	0.53
47:2n:22:GLY:O	47:2n:24:HIS:ND1	2.41	0.53
47:2n:147:LEU:O	47:2n:165:ASN:ND2	2.42	0.53
48:2o:35:ALA:HB1	48:2o:39:PHE:HD2	1.74	0.53
82:zx:22:PRO:HB2	83:zy:75:A:H4'	1.90	0.53
1:1A:88:A:OP2	19:2K:172:ARG:NH2	2.32	0.53
1:1A:1290:G:H5''	8:1H:219:LYS:HD2	1.91	0.53
1:1A:2378:G:N2	1:1A:2381:A:OP2	2.42	0.53
1:1A:2907:G:H1'	1:1A:3589:G:H1	1.73	0.53
2:1B:30:C:N3	2:1B:48:G:N2	2.57	0.53
10:2B:83:PHE:HB3	10:2B:159:HIS:HB2	1.91	0.53
12:2D:61:SER:OG	12:2D:63:GLU:OE1	2.26	0.53
14:2F:128:PRO:HB3	14:2F:134:PRO:HD3	1.90	0.53
46:2m:521:A:OP1	70:3I:45:ARG:NH1	2.38	0.53
1:1A:450:G:H1	1:1A:1297:U:H3	1.57	0.52
1:1A:2897:G:H4'	20:2L:101:ILE:HD13	1.89	0.52
46:2m:1421:A:H61	46:2m:1427:C:H1'	1.74	0.52
48:2o:175:GLU:O	48:2o:179:ASN:ND2	2.41	0.52
53:2t:65:PHE:HD2	53:2t:104:ILE:HD13	1.73	0.52
53:2t:119:LEU:HD11	53:2t:153:LYS:HG2	1.91	0.52
54:2u:33:PRO:HA	54:2u:36:ALA:HB2	1.90	0.52
59:2z:55:ARG:HE	76:3O:83:LEU:HD11	1.74	0.52
70:3I:79:ARG:HH22	70:3I:83:ARG:HH21	1.57	0.52
81:zw:233:LYS:NZ	81:zw:255:ASP:OD1	2.38	0.52
1:1A:1573:G:OP1	20:2L:92:LYS:NZ	2.42	0.52
1:1A:2057:A:N6	17:2I:17:GLY:O	2.40	0.52
1:1A:2557:G:N2	1:1A:2570:U:O2	2.39	0.52
5:1E:58:ARG:NH1	5:1E:285:TYR:OH	2.42	0.52
46:2m:1086:G:OP2	64:3C:12:LYS:NZ	2.43	0.52
59:2z:45:LEU:HD22	59:2z:50:ILE:HD11	1.90	0.52
61:21:66:ARG:HH22	61:21:75:LYS:HG2	1.75	0.52
1:1A:425:U:H2'	1:1A:426:A:H8	1.74	0.52
1:1A:707:C:O2'	1:1A:4943:A:N1	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2399:G:N2	35:2a:4:ARG:HE	2.07	0.52
1:1A:2613:C:OP1	35:2a:24:ARG:NH2	2.42	0.52
1:1A:4103:C:H1'	1:1A:4106:G:H1	1.74	0.52
46:2m:1603:G:O4'	59:2z:38:ARG:NH2	2.43	0.52
81:zw:358:THR:HA	81:zw:365:GLU:HG2	1.91	0.52
1:1A:1591:U:OP2	5:1E:243:LYS:NZ	2.38	0.52
1:1A:2369:U:O2	32:2X:39:LYS:NZ	2.36	0.52
46:2m:1293:A:H5''	79:3R:147:THR:HG21	1.91	0.52
47:2n:104:THR:OG1	47:2n:107:THR:OG1	2.28	0.52
52:2s:43:LEU:HD13	52:2s:72:PHE:HE1	1.74	0.52
53:2t:110:ARG:NH1	53:2t:121:LEU:O	2.42	0.52
54:2u:2:LEU:HD23	54:2u:8:ARG:HD2	1.90	0.52
1:1A:2891:U:OP2	20:2L:74:ARG:NE	2.42	0.52
1:1A:4174:U:H2'	1:1A:4175:G:H8	1.75	0.52
2:1B:64:G:H2'	2:1B:65:G:H8	1.75	0.52
5:1E:150:PHE:HD1	5:1E:194:LEU:HD21	1.74	0.52
37:2c:88:GLU:O	37:2c:92:ASN:ND2	2.43	0.52
49:2p:209:SER:HB2	58:2y:40:ILE:HB	1.91	0.52
53:2t:110:ARG:HH21	53:2t:129:LEU:HD11	1.74	0.52
59:2z:35:GLY:HA3	59:2z:99:LEU:HA	1.91	0.52
71:3J:90:GLY:HA2	71:3J:93:LYS:HD3	1.90	0.52
76:3O:61:GLU:HA	76:3O:64:ASN:HD22	1.74	0.52
1:1A:387:G:O2'	1:1A:412:G:O6	2.23	0.52
1:1A:1094:G:H1	1:1A:1201:U:H3	1.56	0.52
11:2C:93:ARG:HG2	11:2C:182:SER:HB2	1.92	0.52
35:2a:61:PRO:HA	35:2a:64:LEU:HD13	1.90	0.52
46:2m:556:U:O2'	46:2m:558:G:OP2	2.27	0.52
58:2y:28:PHE:HA	58:2y:55:THR:HG21	1.92	0.52
1:1A:243:A:H5''	27:2S:3:PHE:HB2	1.92	0.52
1:1A:725:G:H2'	1:1A:726:G:H8	1.75	0.52
1:1A:2361:G:N2	1:1A:3860:A:OP2	2.38	0.52
1:1A:4429:C:N3	12:2D:158:LYS:NZ	2.57	0.52
9:2A:83:VAL:HG23	22:2N:138:ALA:HB1	1.91	0.52
14:2F:54:PRO:HD2	14:2F:56:ARG:HH12	1.75	0.52
19:2K:40:ASN:OD1	19:2K:132:LYS:NZ	2.42	0.52
25:2Q:91:MET:HA	25:2Q:94:ARG:HG2	1.92	0.52
46:2m:984:C:O2'	73:3L:138:ASP:OD2	2.26	0.52
46:2m:1395:C:O2	46:2m:1474:A:N6	2.43	0.52
52:2s:143:ARG:HB2	52:2s:155:LYS:HB2	1.91	0.52
52:2s:154:ILE:HB	52:2s:185:VAL:HG12	1.92	0.52
6:1F:152:LEU:HD23	6:1F:251:ILE:HG12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:2H:116:LEU:O	16:2H:159:ARG:NH2	2.42	0.52
28:2T:14:LEU:HD23	35:2a:88:ARG:HB2	1.90	0.52
46:2m:555:A:OP1	78:3Q:25:LYS:NZ	2.42	0.52
46:2m:1091:C:C2	46:2m:1159:G:C2	2.97	0.52
61:21:18:HIS:HA	61:21:117:ALA:HB2	1.92	0.52
1:1A:4693:C:OP1	11:2C:64:ARG:NH2	2.35	0.52
8:1H:66:LYS:HD2	8:1H:68:MET:HE2	1.92	0.52
33:2Y:9:LYS:NZ	33:2Y:71:PRO:O	2.43	0.52
46:2m:111:A:O2'	55:2v:69:ARG:NH1	2.43	0.52
46:2m:315:C:H42	46:2m:335:G:H1	1.57	0.52
46:2m:1457:U:H2'	46:2m:1458:G:H8	1.73	0.52
46:2m:1614:A:OP2	56:2w:42:ARG:NH2	2.38	0.52
67:3F:88:ARG:HE	67:3F:97:THR:HG21	1.75	0.52
81:zw:271:SER:HA	81:zw:274:VAL:HG22	1.91	0.52
1:1A:2574:G:N1	1:1A:2762:G:O6	2.32	0.52
1:1A:4457:U:OP1	24:2P:50:ASN:ND2	2.43	0.52
4:1D:216:HIS:HB2	4:1D:218:HIS:HD2	1.75	0.52
5:1E:384:GLU:OE2	25:2Q:14:TYR:OH	2.28	0.52
15:2G:70:GLN:HA	15:2G:73:VAL:HG12	1.91	0.52
20:2L:157:ASP:O	20:2L:161:ALA:N	2.43	0.52
46:2m:1309:C:OP1	79:3R:118:ARG:NH2	2.43	0.52
12:2D:79:SER:OG	12:2D:80:CYS:N	2.43	0.51
46:2m:1232:U:OP2	59:2z:135:HIS:ND1	2.43	0.51
48:2o:171:ILE:HA	48:2o:174:ARG:HG2	1.92	0.51
50:2q:112:HIS:NE2	50:2q:237:SER:O	2.43	0.51
57:2x:134:GLY:HA2	57:2x:141:TYR:HB2	1.92	0.51
67:3F:176:VAL:HB	67:3F:185:LYS:HB3	1.92	0.51
70:3I:61:LEU:HA	70:3I:70:ARG:HH12	1.75	0.51
1:1A:449:C:N3	33:2Y:126:ASN:ND2	2.59	0.51
1:1A:1442:C:N4	1:1A:2104:G:H21	2.08	0.51
24:2P:26:ILE:HB	24:2P:37:LEU:HB2	1.93	0.51
46:2m:563:G:N7	46:2m:586:G:N2	2.58	0.51
46:2m:745:C:H5''	46:2m:746:C:H5''	1.92	0.51
49:2p:45:ARG:HD2	49:2p:85:GLU:HG2	1.93	0.51
53:2t:6:ASP:OD2	53:2t:8:TRP:NE1	2.43	0.51
54:2u:52:LEU:O	54:2u:56:GLY:N	2.43	0.51
1:1A:2318:G:N2	1:1A:2321:G:OP2	2.41	0.51
1:1A:2809:G:OP1	20:2L:60:ARG:NH2	2.43	0.51
7:1G:30:TYR:O	7:1G:34:LYS:HB2	2.09	0.51
38:2d:18:LEU:HA	38:2d:25:LYS:HA	1.92	0.51
46:2m:350:C:O2'	46:2m:383:G:N1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2m:1588:A:H61	46:2m:1672:U:H1'	1.74	0.51
58:2y:24:LEU:HB2	58:2y:58:MET:HE1	1.92	0.51
81:zw:309:LEU:HD21	81:zw:330:ARG:HH22	1.75	0.51
84:zz:137:G:O6	84:zz:287:U:O2	2.28	0.51
1:1A:2611:A:H5'	1:1A:2688:G:H4'	1.92	0.51
1:1A:4229:U:OP1	43:2i:63:THR:OG1	2.28	0.51
1:1A:4419:U:OP1	1:1A:4475:G:N2	2.43	0.51
46:2m:1238:U:O2'	59:2z:148:VAL:O	2.29	0.51
67:3F:77:PHE:HB3	67:3F:89:LEU:HD11	1.92	0.51
1:1A:2600:A:N6	1:1A:2745:A:OP2	2.32	0.51
20:2L:105:LEU:HD23	20:2L:138:LEU:HD23	1.91	0.51
46:2m:1243:U:OP2	46:2m:1518:C:O2'	2.27	0.51
46:2m:1402:A:H4'	61:21:51:LYS:HE3	1.93	0.51
59:2z:60:THR:OG1	59:2z:63:GLU:OE1	2.28	0.51
69:3H:48:TYR:OH	69:3H:114:VAL:N	2.33	0.51
1:1A:1437:C:O2'	1:1A:2099:G:OP2	2.26	0.51
1:1A:2747:U:O2'	35:2a:62:LYS:NZ	2.44	0.51
1:1A:3705:G:H21	4:1D:224:THR:HG21	1.76	0.51
39:2e:24:LYS:HD2	39:2e:69:LEU:HD21	1.93	0.51
1:1A:1646:A:O2'	38:2d:49:TRP:O	2.29	0.51
1:1A:1730:U:H4'	22:2N:100:LYS:HB2	1.91	0.51
1:1A:3924:C:H4'	43:2i:57:ARG:HH12	1.76	0.51
1:1A:4414:A:OP1	12:2D:154:ARG:NH1	2.43	0.51
8:1H:281:ILE:HD13	8:1H:286:LEU:HD21	1.92	0.51
12:2D:149:ILE:HD11	12:2D:167:ILE:HD11	1.92	0.51
21:2M:127:MET:HB3	22:2N:153:PRO:HG2	1.93	0.51
49:2p:136:VAL:HG22	49:2p:186:VAL:HG13	1.92	0.51
53:2t:142:SER:O	53:2t:146:GLN:N	2.40	0.51
59:2z:71:MET:HG3	59:2z:99:LEU:HD13	1.92	0.51
67:3F:108:VAL:HA	67:3F:125:ARG:H	1.76	0.51
69:3H:19:ASP:OD2	69:3H:22:ARG:NH1	2.44	0.51
5:1E:220:ILE:HD11	5:1E:348:ARG:HE	1.75	0.51
11:2C:114:ILE:HB	11:2C:124:ARG:HB2	1.92	0.51
19:2K:157:GLY:O	19:2K:188:ASN:ND2	2.44	0.51
20:2L:42:ARG:HA	20:2L:45:ILE:HD12	1.93	0.51
27:2S:8:THR:HG22	27:2S:10:ASP:H	1.75	0.51
46:2m:690:G:O6	46:2m:739:C:N4	2.43	0.51
46:2m:877:C:H5'	46:2m:878:G:H5''	1.92	0.51
47:2n:12:GLU:HG3	58:2y:109:LEU:HD23	1.92	0.51
47:2n:156:TYR:HE1	62:3A:61:ARG:HG2	1.75	0.51
56:2w:20:VAL:HG12	56:2w:25:LEU:HD12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:3A:1:MET:H1	62:3A:9:VAL:H	1.59	0.51
79:3R:133:ALA:N	79:3R:140:TYR:O	2.39	0.51
81:zw:334:HIS:HB2	81:zw:369:ILE:HD11	1.93	0.51
1:1A:1269:G:H5'	30:2V:107:ARG:HH22	1.76	0.51
1:1A:1700:G:OP2	1:1A:1704:C:N4	2.44	0.51
1:1A:1785:C:OP1	12:2D:133:GLN:NE2	2.44	0.51
1:1A:2438:A:O2'	1:1A:2440:U:OP2	2.28	0.51
1:1A:3635:A:H61	44:2j:18:TYR:HD1	1.58	0.51
2:1B:54:A:O2'	13:2E:13:ARG:NH2	2.44	0.51
84:zz:145:G:N2	84:zz:248:U:O2	2.33	0.51
1:1A:1951:G:H5'	21:2M:116:ARG:HH11	1.76	0.51
1:1A:2402:G:O2'	35:2a:10:ARG:O	2.28	0.51
1:1A:2553:A:N6	1:1A:2764:A:OP2	2.43	0.51
1:1A:2637:U:HO2'	1:1A:2718:U:HO2'	1.59	0.51
46:2m:1782:G:H2'	46:2m:1783:C:H4'	1.92	0.51
51:2r:142:SER:OG	65:3D:49:PRO:O	2.26	0.51
62:3A:12:TYR:HB3	68:3G:79:GLU:HG3	1.93	0.51
70:3I:132:GLN:HG3	70:3I:134:HIS:CE1	2.46	0.51
2:1B:28:C:OP1	13:2E:144:LYS:NZ	2.42	0.50
10:2B:61:ILE:HA	10:2B:64:GLN:HG2	1.93	0.50
46:2m:612:U:O2'	78:3Q:11:LYS:NZ	2.43	0.50
46:2m:692:G:N2	46:2m:738:C:O2'	2.45	0.50
46:2m:748:C:H1'	46:2m:794:A:H61	1.76	0.50
73:3L:27:VAL:O	73:3L:91:THR:OG1	2.29	0.50
1:1A:4670:C:H2'	24:2P:15:ARG:HH22	1.76	0.50
11:2C:115:ARG:O	11:2C:117:PHE:N	2.44	0.50
46:2m:1285:G:H1'	79:3R:101:ALA:HB1	1.93	0.50
46:2m:1533:A:OP1	51:2r:164:ARG:NH1	2.45	0.50
68:3G:200:ARG:O	70:3I:54:ARG:NH2	2.44	0.50
1:1A:4935:C:H2'	1:1A:4936:G:C8	2.47	0.50
11:2C:92:MET:HB2	11:2C:144:LEU:HB2	1.93	0.50
30:2V:75:LEU:HD23	30:2V:76:VAL:HG23	1.92	0.50
46:2m:106:C:H2'	46:2m:107:A:H8	1.76	0.50
46:2m:1091:C:O2	46:2m:1159:G:C2	2.64	0.50
46:2m:1723:G:N1	46:2m:1812:U:O2	2.44	0.50
46:2m:1745:A:H1'	69:3H:68:LEU:HD11	1.93	0.50
46:2m:1760:G:N2	46:2m:1773:C:OP2	2.44	0.50
69:3H:149:LYS:HE2	69:3H:152:ASP:H	1.76	0.50
76:3O:63:PRO:O	76:3O:112:ASN:ND2	2.44	0.50
81:zw:400:SER:O	81:zw:404:LYS:HB2	2.12	0.50
1:1A:85:G:O2'	1:1A:97:G:O6	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2361:G:O2'	1:1A:3859:G:O6	2.30	0.50
4:1D:248:GLY:HA3	46:2m:1069:U:H5''	1.93	0.50
31:2W:47:ILE:HD12	31:2W:94:LEU:HD11	1.93	0.50
33:2Y:90:MET:HG2	45:2k:33:LYS:HG2	1.94	0.50
46:2m:155:G:H2'	46:2m:156:G:H8	1.76	0.50
46:2m:617:G:H4'	63:3B:88:ASP:HB3	1.94	0.50
46:2m:1258:A:H62	46:2m:1659:U:H2'	1.75	0.50
46:2m:1298:G:O2'	46:2m:1299:A:O4'	2.26	0.50
47:2n:34:MET:HE3	47:2n:154:LEU:HD11	1.92	0.50
1:1A:3921:U:OP1	4:1D:221:LYS:NZ	2.40	0.50
16:2H:159:ARG:HG2	16:2H:164:LEU:HB2	1.92	0.50
21:2M:86:SER:OG	21:2M:87:ARG:N	2.44	0.50
50:2q:141:THR:OG1	50:2q:143:ASP:O	2.26	0.50
62:3A:38:GLU:HG3	62:3A:78:ILE:HD11	1.92	0.50
67:3F:234:ASP:HB3	67:3F:253:GLY:HA3	1.93	0.50
1:1A:1326:A:OP2	1:1A:4445:U:O2'	2.29	0.50
1:1A:4940:C:OP1	8:1H:156:ARG:NH2	2.36	0.50
46:2m:1415:C:H2'	46:2m:1417:C:H4'	1.93	0.50
46:2m:1420:G:N2	46:2m:1427:C:O2'	2.45	0.50
49:2p:210:ILE:HD13	58:2y:16:ILE:HD12	1.94	0.50
55:2v:60:CYS:SG	55:2v:114:SER:OG	2.63	0.50
74:3M:27:ILE:HB	74:3M:61:ILE:HB	1.93	0.50
1:1A:496:G:H2'	1:1A:498:C:H5''	1.94	0.50
1:1A:989:U:O2'	1:1A:990:C:O4'	2.28	0.50
1:1A:3870:C:H2'	1:1A:3871:A:H8	1.76	0.50
3:1C:110:U:OP2	40:2f:8:ARG:NH1	2.45	0.50
5:1E:292:LEU:HD13	5:1E:298:LEU:HD11	1.92	0.50
23:2O:107:LYS:HG3	23:2O:108:GLU:HG2	1.94	0.50
46:2m:535:G:N2	46:2m:536:A:N7	2.60	0.50
46:2m:1133:A:H4'	64:3C:13:LYS:HG2	1.93	0.50
84:zz:283:G:OP1	84:zz:283:G:N2	2.42	0.50
34:2Z:50:VAL:HG12	34:2Z:69:VAL:HG12	1.94	0.50
46:2m:834:C:N4	75:3N:9:THR:O	2.44	0.50
46:2m:1218:C:H2'	46:2m:1219:C:H6	1.75	0.50
46:2m:1734:G:O2'	46:2m:1800:A:N6	2.44	0.50
56:2w:81:ARG:NH2	56:2w:84:ILE:O	2.45	0.50
81:zw:348:PRO:HA	81:zw:351:GLU:HB2	1.94	0.50
1:1A:1270:A:O2'	1:1A:1439:C:O2	2.29	0.50
1:1A:1555:G:H1	1:1A:1572:U:H3	1.60	0.50
1:1A:2896:G:N1	1:1A:3604:A:N6	2.60	0.50
1:1A:4415:A:O2'	12:2D:74:LYS:NZ	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:2F:106:SER:OG	14:2F:107:THR:N	2.45	0.50
46:2m:652:U:H2'	46:2m:653:A:H8	1.77	0.50
56:2w:16:THR:OG1	56:2w:21:ASP:OD1	2.30	0.50
70:3I:144:ILE:HB	70:3I:147:PHE:HB2	1.93	0.50
73:3L:31:CYS:SG	73:3L:32:HIS:N	2.85	0.50
80:zv:4:U:H4'	81:zv:58:THR:HG23	1.93	0.50
1:1A:951:G:H2'	1:1A:952:G:H8	1.77	0.49
1:1A:2075:G:H2'	1:1A:2076:G:H8	1.75	0.49
1:1A:3765:G:N2	1:1A:3767:C:OP1	2.45	0.49
1:1A:4354:U:O4	29:2U:61:TYR:N	2.45	0.49
12:2D:57:TYR:OH	12:2D:128:ARG:NH2	2.45	0.49
16:2H:42:PRO:HG3	16:2H:61:ILE:HG12	1.94	0.49
46:2m:375:U:OP2	55:2v:59:LYS:NZ	2.42	0.49
49:2p:6:SER:O	49:2p:10:LYS:N	2.43	0.49
50:2q:191:ARG:HH11	50:2q:245:ARG:HD2	1.77	0.49
51:2r:70:GLU:OE2	51:2r:74:ASN:ND2	2.45	0.49
1:1A:2406:G:OP2	38:2d:14:LYS:NZ	2.43	0.49
1:1A:2896:G:N2	1:1A:3604:A:N7	2.58	0.49
6:1F:135:ALA:HB1	45:2k:44:ILE:HG13	1.93	0.49
45:2k:26:SER:OG	45:2k:28:GLU:OE1	2.24	0.49
46:2m:677:G:N1	46:2m:1027:A:OP2	2.34	0.49
47:2n:21:ALA:O	47:2n:170:SER:OG	2.30	0.49
67:3F:31:ILE:HG23	67:3F:43:TRP:HB2	1.93	0.49
67:3F:208:ALA:HB2	67:3F:218:LEU:HG	1.94	0.49
1:1A:1265:G:OP1	30:2V:95:ARG:NH1	2.45	0.49
1:1A:2459:G:H1'	1:1A:2463:G:H22	1.76	0.49
1:1A:2740:U:O2'	1:1A:2742:G:N2	2.45	0.49
1:1A:4775:C:N4	1:1A:4861:G:O6	2.44	0.49
5:1E:222:VAL:O	5:1E:343:ARG:NH1	2.46	0.49
12:2D:105:CYS:O	81:zv:197:LYS:NZ	2.45	0.49
29:2U:123:ILE:HG12	29:2U:143:ALA:HB3	1.94	0.49
50:2q:112:HIS:NE2	50:2q:237:SER:OG	2.39	0.49
67:3F:68:ASP:HB2	67:3F:110:SER:HA	1.94	0.49
69:3H:67:VAL:HB	69:3H:99:GLY:HA2	1.94	0.49
71:3J:60:MET:HB3	71:3J:64:LEU:HD13	1.93	0.49
1:1A:318:A:H2'	1:1A:319:A:H8	1.77	0.49
1:1A:4087:G:N7	4:1D:67:TYR:OH	2.39	0.49
4:1D:121:GLY:HA2	4:1D:163:ARG:HH12	1.77	0.49
5:1E:293:ILE:HD12	5:1E:297:LYS:HB3	1.94	0.49
9:2A:94:ARG:HA	9:2A:140:ILE:HG22	1.94	0.49
28:2T:117:LYS:HA	28:2T:120:GLU:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:2X:26:THR:HB	32:2X:85:ARG:HH11	1.76	0.49
36:2b:79:LYS:O	36:2b:84:ARG:NH2	2.40	0.49
46:2m:201:C:H3'	46:2m:202:G:H8	1.78	0.49
46:2m:375:U:H2'	46:2m:376:A:C8	2.48	0.49
46:2m:1616:U:H3	46:2m:1620:A:H2	1.60	0.49
46:2m:1679:A:H2'	51:2r:60:ARG:HD2	1.95	0.49
46:2m:1757:G:N2	46:2m:1758:G:N3	2.60	0.49
47:2n:80:ARG:NH1	47:2n:165:ASN:O	2.45	0.49
48:2o:146:ARG:HB3	48:2o:149:GLN:HB2	1.94	0.49
59:2z:75:ARG:NH2	59:2z:95:TYR:O	2.45	0.49
68:3G:256:TRP:HZ2	74:3M:46:TYR:HE1	1.60	0.49
72:3K:108:ASP:N	72:3K:108:ASP:OD1	2.43	0.49
75:3N:37:LYS:HA	75:3N:40:ILE:HG22	1.94	0.49
84:zz:268:G:OP2	84:zz:270:C:N4	2.46	0.49
1:1A:1175:A:H2	1:1A:1185:G:H1	1.58	0.49
3:1C:71:A:H62	3:1C:87:G:N2	2.09	0.49
30:2V:40:LEU:HA	30:2V:43:MET:HG2	1.92	0.49
46:2m:1528:G:O2'	46:2m:1666:C:OP1	2.30	0.49
48:2o:103:MET:HG2	48:2o:215:VAL:HG22	1.93	0.49
81:zw:254:VAL:HG13	81:zw:270:LEU:HD22	1.93	0.49
1:1A:1541:C:H5''	4:1D:21:LYS:HG2	1.93	0.49
1:1A:2390:G:O6	1:1A:2825:A:N1	2.46	0.49
4:1D:54:ARG:HG3	4:1D:56:ALA:H	1.78	0.49
21:2M:15:ARG:HB3	21:2M:27:LEU:HD23	1.94	0.49
23:2O:100:LEU:HD23	23:2O:112:LEU:HD23	1.93	0.49
28:2T:5:MET:O	28:2T:28:ASN:ND2	2.45	0.49
45:2k:28:GLU:HG2	45:2k:31:ASN:HB2	1.93	0.49
1:1A:1940:G:N1	1:1A:4435:U:OP1	2.46	0.49
1:1A:3848:U:H2'	1:1A:3849:A:H8	1.76	0.49
2:1B:7:G:OP1	7:1G:33:ARG:NE	2.39	0.49
5:1E:297:LYS:HG3	5:1E:299:ILE:HD11	1.95	0.49
12:2D:32:ARG:HG3	12:2D:33:ILE:HG12	1.95	0.49
46:2m:1657:G:N2	46:2m:1667:U:O2	2.42	0.49
55:2v:35:ARG:NH1	55:2v:55:TYR:O	2.41	0.49
67:3F:111:VAL:HG23	67:3F:122:SER:HA	1.94	0.49
1:1A:1557:C:H2'	1:1A:1558:A:H8	1.77	0.49
1:1A:3725:G:N2	1:1A:3728:A:OP2	2.32	0.49
1:1A:4910:G:H22	17:2I:107:GLY:HA3	1.76	0.49
4:1D:120:PRO:HA	4:1D:162:ASN:HB3	1.94	0.49
24:2P:83:ARG:NH2	24:2P:120:PRO:O	2.42	0.49
46:2m:466:G:O2'	69:3H:72:ARG:NH2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2m:527:C:H2'	46:2m:528:A:H8	1.76	0.49
46:2m:1348:G:H2'	46:2m:1349:G:H8	1.76	0.49
46:2m:1780:G:H3'	46:2m:1781:A:H8	1.77	0.49
49:2p:106:ARG:HG3	49:2p:175:VAL:HG12	1.95	0.49
50:2q:66:MET:SD	50:2q:78:THR:OG1	2.70	0.49
71:3J:69:LEU:HG	71:3J:74:ILE:HB	1.94	0.49
81:zw:428:ASP:O	81:zw:432:PHE:HB2	2.12	0.49
1:1A:66:A:N6	1:1A:282:C:O2'	2.43	0.49
1:1A:2296:G:O2'	6:1F:242:PRO:O	2.30	0.49
1:1A:3805:U:H2'	1:1A:3806:G:H8	1.78	0.49
3:1C:53:G:O3'	40:2f:40:LYS:NZ	2.38	0.49
6:1F:122:TYR:HD1	6:1F:280:PRO:HG2	1.78	0.49
16:2H:4:TYR:HA	16:2H:7:ILE:HG12	1.94	0.49
16:2H:108:ARG:HH11	16:2H:161:MET:HE1	1.77	0.49
73:3L:13:GLN:HA	73:3L:14:VAL:HA	1.62	0.49
9:2A:116:GLN:HG2	9:2A:119:ASN:HD21	1.78	0.49
17:2I:121:PRO:HA	17:2I:124:LEU:HD13	1.94	0.49
34:2Z:4:ARG:NE	34:2Z:6:TRP:O	2.45	0.49
46:2m:1053:C:O2	46:2m:1065:G:N2	2.36	0.49
46:2m:1221:G:H2'	46:2m:1222:G:H8	1.76	0.49
61:21:46:LYS:HE2	61:21:98:VAL:HB	1.95	0.49
1:1A:75:G:O6	14:2F:103:ARG:NH1	2.46	0.48
1:1A:1502:G:OP2	19:2K:62:SER:OG	2.31	0.48
1:1A:3904:G:O6	1:1A:3905:A:N6	2.46	0.48
1:1A:4094:G:H2'	1:1A:4095:G:C8	2.48	0.48
46:2m:835:C:H2'	46:2m:837:A:H1'	1.94	0.48
46:2m:923:G:H2'	46:2m:924:G:H8	1.78	0.48
81:zw:39:ILE:HD12	81:zw:93:LEU:HD23	1.94	0.48
1:1A:4691:A:H5'	11:2C:71:ARG:HH11	1.77	0.48
5:1E:53:MET:HE1	5:1E:336:CYS:HA	1.94	0.48
38:2d:67:LEU:HA	38:2d:70:VAL:HG12	1.95	0.48
51:2r:194:ASP:O	51:2r:198:ARG:N	2.47	0.48
61:21:48:LEU:HD23	61:21:50:VAL:HG12	1.94	0.48
1:1A:1207:C:H2'	1:1A:1208:G:H8	1.77	0.48
1:1A:3727:A:O3'	37:2c:74:LYS:NZ	2.46	0.48
32:2X:64:ILE:HB	32:2X:68:LEU:HD23	1.95	0.48
52:2s:108:SER:OG	52:2s:109:ARG:N	2.46	0.48
74:3M:102:ILE:H	74:3M:113:HIS:HD2	1.60	0.48
81:zw:214:ILE:HA	81:zw:219:VAL:HA	1.95	0.48
1:1A:1241:C:H6	30:2V:120:ARG:H	1.60	0.48
1:1A:1253:G:O2'	1:1A:1255:A:OP1	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:4745:G:H1	1:1A:4954:G:H1	1.62	0.48
10:2B:57:TRP:O	10:2B:62:ARG:NH1	2.47	0.48
46:2m:164:A:OP1	69:3H:82:SER:OG	2.31	0.48
49:2p:99:ILE:HG23	49:2p:173:ARG:HH21	1.79	0.48
71:3J:96:ARG:HG2	71:3J:100:PRO:HB3	1.94	0.48
75:3N:119:GLY:O	75:3N:124:ASN:ND2	2.45	0.48
81:zw:118:LYS:HB3	81:zw:139:LEU:HD22	1.94	0.48
1:1A:347:A:O2'	6:1F:50:GLN:NE2	2.44	0.48
1:1A:363:A:H61	1:1A:376:A:H5''	1.79	0.48
1:1A:1700:G:H4'	6:1F:306:ARG:HH22	1.76	0.48
1:1A:2299:G:O6	6:1F:188:ARG:NH2	2.46	0.48
1:1A:2360:A:O2'	18:2J:27:LYS:NZ	2.46	0.48
1:1A:3715:U:H5	1:1A:3738:G:H1	1.60	0.48
1:1A:4300:U:H5''	22:2N:87:LYS:HE3	1.95	0.48
1:1A:4395:U:O2'	1:1A:4447:C:N4	2.47	0.48
1:1A:4646:U:OP1	20:2L:59:SER:N	2.46	0.48
1:1A:4727:A:H5'	5:1E:129:ALA:HA	1.95	0.48
7:1G:42:ASN:ND2	22:2N:69:GLN:OE1	2.45	0.48
10:2B:138:ALA:O	10:2B:142:THR:OG1	2.26	0.48
11:2C:59:LYS:NZ	11:2C:66:GLU:O	2.38	0.48
13:2E:76:GLY:HA2	13:2E:79:ALA:HB3	1.95	0.48
14:2F:171:GLU:HA	14:2F:174:LYS:HD3	1.96	0.48
20:2L:15:LEU:O	20:2L:52:ARG:NH2	2.46	0.48
1:1A:2816:G:O2'	1:1A:3622:C:O2'	2.29	0.48
3:1C:150:C:N4	10:2B:52:THR:O	2.46	0.48
14:2F:31:ARG:HA	14:2F:34:ARG:HG2	1.95	0.48
16:2H:65:ARG:HG3	16:2H:129:PHE:HE1	1.78	0.48
24:2P:29:ALA:HB2	24:2P:102:ALA:HB1	1.94	0.48
43:2i:71:GLU:HB3	43:2i:80:LYS:HG2	1.96	0.48
46:2m:412:G:H21	46:2m:812:A:N6	2.11	0.48
46:2m:870:A:H4'	46:2m:871:U:H3'	1.96	0.48
46:2m:1860:A:N7	64:3C:34:LYS:NZ	2.62	0.48
51:2r:127:ARG:NH2	65:3D:27:CYS:SG	2.80	0.48
52:2s:138:GLU:OE2	72:3K:21:SER:OG	2.31	0.48
59:2z:26:ILE:HG12	59:2z:56:ALA:HA	1.95	0.48
81:zw:143:ASP:OD2	81:zw:163:GLY:N	2.46	0.48
1:1A:4985:U:OP1	5:1E:175:GLN:NE2	2.47	0.48
3:1C:122:G:C8	3:1C:123:U:H1'	2.49	0.48
5:1E:56:ILE:HG22	5:1E:368:ILE:HA	1.95	0.48
12:2D:188:LYS:HE2	12:2D:213:HIS:H	1.78	0.48
14:2F:116:ARG:HH11	14:2F:155:MET:HB2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:2M:110:TYR:HE1	21:2M:124:ILE:HD11	1.77	0.48
46:2m:384:U:O4	53:2t:5:ARG:NH1	2.43	0.48
46:2m:955:A:N6	46:2m:971:G:O2'	2.46	0.48
46:2m:1337:C:H2'	46:2m:1338:G:C8	2.48	0.48
66:3E:21:CYS:SG	66:3E:25:SER:N	2.86	0.48
75:3N:37:LYS:HE3	75:3N:93:ARG:HE	1.78	0.48
1:1A:1645:C:H2'	1:1A:1646:A:C8	2.49	0.48
1:1A:1795:A:N3	2:1B:79:U:O2'	2.46	0.48
1:1A:3692:A:H62	1:1A:3823:G:H21	1.60	0.48
1:1A:3786:U:O2	1:1A:4537:C:O2'	2.32	0.48
1:1A:4084:G:N7	4:1D:72:ARG:NH2	2.61	0.48
1:1A:5006:U:H4'	1:1A:5007:A:H5'	1.95	0.48
1:1A:5047:C:O2'	1:1A:5050:C:OP2	2.28	0.48
2:1B:74:A:N6	2:1B:101:A:OP2	2.40	0.48
4:1D:180:LEU:HD22	44:2j:18:TYR:HB3	1.96	0.48
17:2I:194:GLU:O	17:2I:198:THR:OG1	2.28	0.48
18:2J:16:LYS:HB3	18:2J:149:ILE:HG22	1.95	0.48
19:2K:122:THR:OG1	19:2K:124:ASP:OD1	2.27	0.48
46:2m:110:U:H3	46:2m:351:G:H1	1.61	0.48
46:2m:1537:A:H5''	60:20:84:ARG:HH12	1.77	0.48
1:1A:323:C:H2'	1:1A:324:A:H8	1.79	0.48
1:1A:1509:C:H5''	29:2U:2:PRO:HG2	1.96	0.48
1:1A:2295:C:H2'	1:1A:2296:G:C8	2.49	0.48
1:1A:4321:U:H2'	1:1A:4322:G:C8	2.49	0.48
4:1D:249:THR:HG23	46:2m:1044:G:H2'	1.94	0.48
7:1G:166:ALA:HB1	7:1G:171:LEU:HD12	1.96	0.48
8:1H:240:TYR:OH	8:1H:246:ARG:NH1	2.47	0.48
46:2m:496:C:OP1	50:2q:49:ARG:NH1	2.37	0.48
46:2m:527:C:H2'	46:2m:528:A:C8	2.49	0.48
46:2m:958:G:N2	73:3L:68:GLU:OE2	2.47	0.48
46:2m:1221:G:H2'	46:2m:1222:G:C8	2.49	0.48
46:2m:1245:G:O2'	46:2m:1492:U:OP1	2.30	0.48
46:2m:1417:C:H41	46:2m:1429:G:N2	2.11	0.48
56:2w:77:LYS:HA	56:2w:95:GLY:HA3	1.95	0.48
70:3I:50:LEU:HD13	70:3I:102:ILE:HD13	1.95	0.48
77:3P:14:GLU:HG2	77:3P:18:LYS:HE2	1.96	0.48
1:1A:1958:A:O2'	1:1A:2025:A:N1	2.43	0.48
1:1A:3723:A:OP2	37:2c:68:ARG:NH1	2.39	0.48
3:1C:90:C:H2'	3:1C:91:A:C8	2.49	0.48
20:2L:103:ARG:NH1	20:2L:124:TYR:OH	2.47	0.48
28:2T:89:ILE:HD11	28:2T:117:LYS:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:2d:20:ARG:HH11	38:2d:39:TYR:HE2	1.62	0.48
45:2k:51:VAL:HG23	45:2k:62:VAL:HG22	1.96	0.48
46:2m:1785:C:O2'	46:2m:1786:U:O4'	2.32	0.48
47:2n:28:THR:HG21	58:2y:126:MET:HE1	1.96	0.48
59:2z:24:ARG:HB3	59:2z:29:ALA:HB2	1.95	0.48
46:2m:1413:G:H2'	46:2m:1414:A:H4'	1.96	0.47
46:2m:1808:U:H2'	46:2m:1809:A:H8	1.79	0.47
77:3P:36:LYS:HB2	77:3P:78:SER:HB2	1.96	0.47
1:1A:297:U:O2'	16:2H:179:LYS:O	2.32	0.47
1:1A:490:C:H2'	1:1A:491:G:H8	1.79	0.47
1:1A:2049:G:H2'	1:1A:2050:G:C8	2.49	0.47
1:1A:2339:G:H21	6:1F:45:ARG:HH12	1.61	0.47
1:1A:4478:G:O2'	1:1A:4602:A:N1	2.43	0.47
1:1A:5002:U:OP2	5:1E:385:LYS:NZ	2.41	0.47
3:1C:8:U:H2'	3:1C:9:A:C8	2.49	0.47
3:1C:30:U:OP1	14:2F:34:ARG:NH2	2.47	0.47
10:2B:137:ARG:HG3	10:2B:146:LEU:HD11	1.95	0.47
27:2S:19:PHE:O	27:2S:26:ARG:NH2	2.47	0.47
45:2k:28:GLU:HG3	45:2k:42:GLY:HA3	1.96	0.47
46:2m:449:A:N1	69:3H:88:ARG:NH1	2.61	0.47
52:2s:48:ALA:HA	52:2s:62:ILE:HA	1.96	0.47
53:2t:162:LEU:HD12	53:2t:165:GLN:HE21	1.79	0.47
57:2x:15:ARG:HA	57:2x:19:ALA:HB3	1.96	0.47
65:3D:12:ALA:HB1	65:3D:32:VAL:HB	1.97	0.47
84:zz:259:U:N3	84:zz:274:A:H8	2.08	0.47
1:1A:2741:U:O2	1:1A:2742:G:O6	2.32	0.47
1:1A:3937:C:H1'	16:2H:125:SER:HB3	1.94	0.47
1:1A:4419:U:OP1	1:1A:4421:C:N4	2.47	0.47
8:1H:254:ASP:HA	8:1H:257:ILE:HG22	1.97	0.47
13:2E:23:ASN:HB3	13:2E:129:ASP:HB2	1.96	0.47
46:2m:110:U:O2	46:2m:351:G:N2	2.39	0.47
46:2m:453:C:O2'	69:3H:92:ARG:O	2.29	0.47
46:2m:1421:A:H5'	60:20:2:PRO:HB3	1.96	0.47
46:2m:1562:C:H2'	46:2m:1563:G:H8	1.79	0.47
49:2p:32:ASP:HA	49:2p:54:ARG:HD2	1.96	0.47
68:3G:265:PRO:HA	68:3G:268:GLU:HB2	1.96	0.47
70:3I:110:LEU:HB2	70:3I:147:PHE:HB3	1.95	0.47
74:3M:11:LEU:HD23	74:3M:14:ILE:HD11	1.96	0.47
81:zw:318:GLU:N	81:zw:412:ILE:O	2.34	0.47
5:1E:29:VAL:HG12	5:1E:31:SER:H	1.77	0.47
6:1F:296:PRO:HA	6:1F:299:GLN:HB2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:2C:93:ARG:HA	11:2C:143:GLU:HA	1.97	0.47
46:2m:979:C:H2'	46:2m:980:A:C8	2.50	0.47
46:2m:1234:C:H4'	46:2m:1246:A:H61	1.79	0.47
51:2r:26:ASP:HA	51:2r:27:ASP:HA	1.67	0.47
1:1A:1633:G:O6	1:1A:3918:G:O2'	2.33	0.47
1:1A:4313:A:OP1	22:2N:92:ARG:NH2	2.35	0.47
17:2I:166:ILE:HA	17:2I:169:ARG:HG2	1.96	0.47
24:2P:71:GLU:O	24:2P:75:LYS:NZ	2.47	0.47
50:2q:115:THR:OG1	50:2q:117:GLU:O	2.30	0.47
81:zw:359:ASP:OD2	81:zw:366:HIS:ND1	2.45	0.47
1:1A:267:G:H2'	1:1A:268:G:H8	1.79	0.47
1:1A:4101:C:H4'	1:1A:4109:G:H22	1.80	0.47
3:1C:151:G:OP2	10:2B:65:ARG:NE	2.47	0.47
9:2A:228:VAL:HB	21:2M:39:VAL:HG23	1.96	0.47
46:2m:374:G:H4'	55:2v:84:ARG:HG3	1.96	0.47
46:2m:380:G:N1	46:2m:383:G:OP2	2.42	0.47
58:2y:119:VAL:HA	58:2y:120:THR:HA	1.73	0.47
1:1A:198:A:OP1	27:2S:126:ARG:NH2	2.41	0.47
1:1A:1442:C:O2'	1:1A:1443:A:O4'	2.30	0.47
1:1A:1669:A:OP1	30:2V:18:ARG:NH1	2.48	0.47
1:1A:1907:A:H4'	9:2A:223:LYS:HD3	1.95	0.47
1:1A:2848:G:O2'	1:1A:3838:U:O4	2.31	0.47
1:1A:2875:C:OP1	44:2j:23:ARG:NH2	2.42	0.47
1:1A:4093:G:H2'	1:1A:4094:G:C8	2.49	0.47
3:1C:121:G:H2'	3:1C:122:G:C8	2.50	0.47
7:1G:128:ASP:HB3	7:1G:130:TYR:H	1.80	0.47
8:1H:163:VAL:HG23	8:1H:271:LEU:HD21	1.96	0.47
13:2E:160:GLU:HA	13:2E:163:MET:HE2	1.97	0.47
25:2Q:106:GLU:HA	25:2Q:109:ILE:HD12	1.97	0.47
40:2f:25:GLN:OE1	40:2f:28:ARG:NH2	2.47	0.47
44:2j:53:GLY:O	44:2j:66:GLY:N	2.46	0.47
46:2m:51:U:H2'	46:2m:52:G:H8	1.78	0.47
46:2m:1858:G:OP2	73:3L:146:ARG:NH2	2.48	0.47
49:2p:185:LYS:HD3	49:2p:187:LYS:HE2	1.96	0.47
53:2t:103:LEU:HD23	53:2t:170:LYS:HG2	1.97	0.47
63:3B:53:GLU:HB3	63:3B:71:ARG:HB3	1.97	0.47
67:3F:127:LYS:HA	67:3F:151:VAL:HG23	1.97	0.47
1:1A:46:U:H5''	14:2F:16:LYS:HG3	1.96	0.47
13:2E:115:LEU:HA	13:2E:116:GLY:HA3	1.58	0.47
16:2H:122:GLY:HA3	16:2H:129:PHE:HB2	1.96	0.47
45:2k:32:LEU:HD11	45:2k:50:GLY:HA2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:2v:77:VAL:HG12	55:2v:122:ILE:HA	1.97	0.47
61:21:49:LYS:H	61:21:92:HIS:CD2	2.33	0.47
67:3F:65:PHE:O	67:3F:82:SER:OG	2.27	0.47
77:3P:38:PRO:O	77:3P:40:CYS:N	2.48	0.47
1:1A:109:G:OP2	14:2F:74:ARG:NH2	2.45	0.47
1:1A:2041:A:N7	1:1A:4434:C:O2'	2.47	0.47
1:1A:5026:U:O2'	53:2t:77:ARG:NH2	2.48	0.47
5:1E:44:THR:HG22	5:1E:349:LYS:HD3	1.97	0.47
12:2D:93:PRO:HB2	12:2D:125:THR:HG22	1.97	0.47
46:2m:1428:G:H2'	46:2m:1429:G:C8	2.50	0.47
46:2m:1842:C:H2'	46:2m:1843:G:H8	1.79	0.47
57:2x:41:MET:O	57:2x:48:GLN:NE2	2.48	0.47
68:3G:103:LYS:HB2	68:3G:216:MET:HE1	1.97	0.47
70:3I:142:VAL:HG12	70:3I:144:ILE:H	1.80	0.47
1:1A:1836:G:H4'	22:2N:129:LYS:HD3	1.97	0.47
1:1A:2295:C:H2'	1:1A:2296:G:H8	1.79	0.47
1:1A:2749:C:H2'	1:1A:2750:G:H8	1.80	0.47
1:1A:3848:U:O2'	1:1A:4634:U:O4	2.32	0.47
1:1A:4730:C:H1'	1:1A:4731:G:H5''	1.96	0.47
3:1C:94:G:C6	38:2d:84:PRO:HG3	2.50	0.47
17:2I:23:VAL:HG13	17:2I:33:VAL:HG11	1.97	0.47
28:2T:54:THR:HG22	28:2T:57:MET:HE3	1.97	0.47
41:2g:97:ARG:HD2	41:2g:120:ASN:HB3	1.97	0.47
46:2m:1723:G:H2'	46:2m:1724:A:H8	1.80	0.47
49:2p:127:MET:HE3	49:2p:154:ASP:HB3	1.97	0.47
50:2q:42:LEU:HG	50:2q:46:ILE:HD11	1.96	0.47
50:2q:147:ILE:HG21	50:2q:169:ILE:HD11	1.96	0.47
53:2t:193:LYS:HE2	55:2v:32:LYS:HZ1	1.79	0.47
67:3F:88:ARG:NH2	67:3F:97:THR:OG1	2.47	0.47
1:1A:235:A:OP1	6:1F:201:ARG:NH2	2.48	0.46
1:1A:679:C:H2'	1:1A:680:G:H8	1.80	0.46
1:1A:1188:C:H2'	1:1A:1189:G:C8	2.51	0.46
6:1F:33:ARG:NE	19:2K:22:ASP:OD1	2.49	0.46
15:2G:57:LEU:HD11	21:2M:154:LEU:HD12	1.96	0.46
33:2Y:115:ALA:HB1	33:2Y:120:ILE:HB	1.96	0.46
50:2q:173:ILE:HD12	50:2q:230:LYS:HG2	1.96	0.46
72:3K:84:LEU:HD11	72:3K:88:LEU:HD23	1.97	0.46
1:1A:67:C:OP2	1:1A:312:G:N2	2.49	0.46
1:1A:1459:A:OP1	19:2K:65:ARG:NH2	2.47	0.46
1:1A:1508:A:OP1	6:1F:110:ARG:NH1	2.48	0.46
1:1A:1935:C:OP1	1:1A:2048:U:O2'	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2486:G:O6	1:1A:2493:G:O6	2.32	0.46
1:1A:4389:C:H2'	1:1A:4390:A:C8	2.51	0.46
9:2A:50:ILE:HG12	9:2A:186:CYS:HB3	1.96	0.46
9:2A:131:ASN:OD1	9:2A:134:ARG:NH2	2.49	0.46
46:2m:1345:G:OP1	46:2m:1688:C:O2'	2.33	0.46
46:2m:1854:U:H2'	46:2m:1855:G:H8	1.79	0.46
50:2q:54:TYR:O	75:3N:15:ASN:ND2	2.48	0.46
56:2w:78:THR:HA	56:2w:95:GLY:HA3	1.97	0.46
70:3I:20:PHE:H	70:3I:24:ARG:HH21	1.62	0.46
70:3I:65:GLU:HA	70:3I:70:ARG:HD3	1.97	0.46
84:zz:262:U:H2'	84:zz:263:G:H8	1.80	0.46
84:zz:319:G:H2'	84:zz:320:G:H8	1.80	0.46
1:1A:451:C:H3'	1:1A:1294:A:H2	1.80	0.46
1:1A:1603:C:H2'	1:1A:1604:G:H8	1.79	0.46
1:1A:4252:C:H42	13:2E:25:CYS:HB3	1.81	0.46
1:1A:4991:U:H2'	1:1A:4992:G:H8	1.80	0.46
45:2k:66:ARG:NE	45:2k:68:SER:OG	2.48	0.46
46:2m:882:U:N3	46:2m:905:C:O2	2.42	0.46
46:2m:1216:C:O2'	57:2x:143:LYS:NZ	2.43	0.46
49:2p:93:THR:HB	49:2p:96:LEU:HD13	1.96	0.46
59:2z:22:GLY:HA2	59:2z:56:ALA:HB3	1.97	0.46
63:3B:54:LYS:HE2	63:3B:94:ILE:HG23	1.98	0.46
65:3D:20:ARG:HD2	65:3D:28:THR:HG22	1.97	0.46
67:3F:35:SER:OG	67:3F:36:ARG:N	2.47	0.46
67:3F:286:CYS:SG	67:3F:287:THR:N	2.89	0.46
69:3H:103:ASP:H	69:3H:106:LEU:HD13	1.79	0.46
1:1A:86:U:H2'	1:1A:87:A:H8	1.80	0.46
1:1A:123:C:H2'	1:1A:124:C:H6	1.81	0.46
1:1A:1334:A:H2'	1:1A:1335:G:H8	1.80	0.46
1:1A:2258:C:O4'	8:1H:88:VAL:N	2.48	0.46
1:1A:2845:A:N6	1:1A:3843:C:H42	2.09	0.46
1:1A:3917:A:H2'	1:1A:3918:G:H8	1.80	0.46
18:2J:70:CYS:SG	18:2J:71:ALA:N	2.87	0.46
46:2m:614:C:O2'	46:2m:626:G:N2	2.46	0.46
46:2m:1024:A:OP2	72:3K:124:ARG:NH2	2.48	0.46
46:2m:1601:A:O4'	46:2m:1636:G:N2	2.48	0.46
46:2m:1866:A:H61	64:3C:85:ARG:H	1.63	0.46
72:3K:20:ARG:HE	74:3M:56:HIS:CE1	2.32	0.46
75:3N:114:MET:HE3	75:3N:124:ASN:HB3	1.97	0.46
1:1A:4084:G:H5''	1:1A:4084:G:H8	1.81	0.46
1:1A:4274:A:H2'	1:1A:4275:G:H8	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:2K:79:THR:HB	19:2K:136:THR:HG22	1.98	0.46
36:2b:25:LYS:HG2	36:2b:54:ILE:HD11	1.96	0.46
46:2m:53:C:H2'	46:2m:54:A:H8	1.81	0.46
46:2m:545:A:N1	46:2m:548:C:N4	2.63	0.46
46:2m:1731:A:H2'	46:2m:1732:G:H8	1.80	0.46
47:2n:67:ALA:HA	62:3A:47:ASN:HD21	1.80	0.46
73:3L:30:VAL:HG12	73:3L:94:HIS:HB2	1.97	0.46
1:1A:2561:C:N4	1:1A:2562:G:O6	2.49	0.46
1:1A:2601:A:N6	1:1A:2744:A:OP2	2.49	0.46
1:1A:4088:C:H2'	1:1A:4089:G:C8	2.51	0.46
1:1A:5024:C:N4	1:1A:5028:G:H21	2.13	0.46
4:1D:103:PRO:HA	4:1D:163:ARG:HA	1.96	0.46
11:2C:88:PHE:HE2	11:2C:151:ILE:HB	1.80	0.46
46:2m:973:C:H42	73:3L:55:ARG:HH22	1.63	0.46
46:2m:1018:U:OP1	72:3K:62:GLN:NE2	2.49	0.46
53:2t:72:CYS:HG	53:2t:112:TRP:CG	2.34	0.46
54:2u:34:GLU:HA	54:2u:35:LEU:HA	1.67	0.46
72:3K:119:GLU:O	72:3K:123:HIS:ND1	2.45	0.46
75:3N:78:SER:HB2	75:3N:81:TYR:HD2	1.80	0.46
1:1A:1332:C:H2'	1:1A:1333:A:H8	1.81	0.46
1:1A:2550:G:H2'	1:1A:2551:A:H8	1.81	0.46
3:1C:9:A:H2'	3:1C:10:G:H8	1.81	0.46
6:1F:65:GLU:OE2	6:1F:80:ARG:NH1	2.49	0.46
13:2E:64:ARG:NH2	83:zy:55:C:O4'	2.48	0.46
51:2r:54:GLY:O	57:2x:125:ARG:NH1	2.48	0.46
51:2r:71:ARG:NH1	51:2r:148:ASN:OD1	2.47	0.46
52:2s:51:ILE:HG12	52:2s:179:LYS:HD3	1.97	0.46
54:2u:32:HIS:CD2	54:2u:34:GLU:H	2.32	0.46
55:2v:13:GLN:HE22	55:2v:35:ARG:HG3	1.80	0.46
55:2v:96:ILE:HD12	63:3B:10:ALA:HB1	1.97	0.46
67:3F:193:GLY:HA3	67:3F:212:LYS:HB3	1.96	0.46
84:zz:277:G:H2'	84:zz:278:G:C8	2.50	0.46
1:1A:163:A:H2'	1:1A:164:G:H8	1.80	0.46
1:1A:2666:U:OP1	20:2L:107:ARG:NH2	2.49	0.46
1:1A:3951:G:N2	1:1A:4061:G:O6	2.49	0.46
8:1H:50:LEU:HD12	8:1H:51:VAL:HG23	1.97	0.46
21:2M:45:TRP:O	21:2M:49:SER:OG	2.30	0.46
38:2d:21:ARG:NH2	38:2d:37:CYS:O	2.48	0.46
46:2m:28:U:H2'	46:2m:29:G:H8	1.80	0.46
46:2m:1551:U:OP2	46:2m:1579:A:N6	2.48	0.46
63:3B:100:VAL:HG12	63:3B:125:VAL:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:3F:292:SER:OG	67:3F:293:ALA:N	2.48	0.46
68:3G:169:TYR:OH	68:3G:175:GLY:O	2.31	0.46
81:zw:39:ILE:HB	81:zw:93:LEU:HB3	1.96	0.46
1:1A:338:A:OP1	14:2F:31:ARG:NH1	2.49	0.46
1:1A:366:A:H62	1:1A:375:G:H21	1.64	0.46
1:1A:407:A:N7	1:1A:410:A:N6	2.64	0.46
1:1A:2449:A:H62	1:1A:2510:G:N2	2.13	0.46
1:1A:3697:U:H5''	1:1A:3698:G:H5'	1.98	0.46
11:2C:126:VAL:HG11	11:2C:161:ILE:HG22	1.97	0.46
46:2m:339:A:H62	46:2m:342:C:N4	2.14	0.46
46:2m:750:C:H3'	46:2m:751:G:H4'	1.98	0.46
46:2m:1171:G:O2'	46:2m:1187:G:O6	2.29	0.46
1:1A:1857:C:H2'	1:1A:1858:A:C8	2.51	0.46
1:1A:1973:G:OP1	1:1A:1984:A:O2'	2.33	0.46
1:1A:3651:A:H5'	4:1D:199:VAL:HG12	1.98	0.46
1:1A:4235:G:N2	1:1A:4292:A:OP1	2.39	0.46
11:2C:104:VAL:HG13	11:2C:106:GLN:HG2	1.98	0.46
14:2F:55:ILE:HG23	14:2F:76:PHE:HE2	1.81	0.46
17:2I:8:VAL:HG23	17:2I:117:ARG:HA	1.97	0.46
28:2T:92:ASP:OD2	28:2T:94:THR:OG1	2.32	0.46
43:2i:82:MET:HB2	43:2i:82:MET:HE3	1.80	0.46
44:2j:85:ARG:NH2	46:2m:938:A:O2'	2.36	0.46
46:2m:533:A:H61	46:2m:550:C:H42	1.64	0.46
46:2m:1065:G:OP1	73:3L:149:ARG:NH1	2.49	0.46
58:2y:107:LYS:HA	58:2y:110:ASP:HB3	1.98	0.46
76:3O:50:PHE:HE2	76:3O:55:TYR:HD1	1.62	0.46
1:1A:14:C:H2'	1:1A:15:A:C8	2.51	0.45
24:2P:62:MET:HA	24:2P:78:PRO:HA	1.97	0.45
46:2m:373:G:H4'	55:2v:85:THR:HG21	1.97	0.45
46:2m:1126:G:OP1	47:2n:41:ARG:NH1	2.39	0.45
46:2m:1546:G:H22	46:2m:1654:G:N2	2.15	0.45
46:2m:1847:G:O6	46:2m:1852:C:N4	2.49	0.45
1:1A:3658:C:O2'	4:1D:238:ILE:O	2.34	0.45
1:1A:3827:G:O2'	1:1A:3829:G:OP2	2.25	0.45
1:1A:4704:C:H2'	1:1A:4705:A:C8	2.49	0.45
76:3O:58:LEU:HA	76:3O:62:VAL:HB	1.98	0.45
83:zy:8:U:H2'	83:zy:45:G:H21	1.81	0.45
84:zz:307:G:O6	84:zz:329:U:O2	2.34	0.45
1:1A:2843:U:O2'	1:1A:4632:U:OP1	2.35	0.45
13:2E:54:ARG:HH21	13:2E:55:TYR:HE1	1.64	0.45
17:2I:42:ASN:HD22	17:2I:125:LYS:HD3	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:2S:31:SER:HA	27:2S:48:PRO:HA	1.97	0.45
44:2j:11:VAL:HG11	44:2j:26:VAL:HG23	1.99	0.45
46:2m:443:U:O4	46:2m:447:A:N7	2.49	0.45
46:2m:1462:U:H5'	46:2m:1463:U:C2	2.52	0.45
46:2m:1597:C:H3'	76:3O:82:SER:HB2	1.97	0.45
61:21:24:LEU:HB3	61:21:87:ARG:HB2	1.97	0.45
1:1A:10:A:H2'	1:1A:11:G:C8	2.49	0.45
1:1A:146:G:H2'	1:1A:147:A:H8	1.81	0.45
1:1A:461:G:H2'	1:1A:462:G:H8	1.81	0.45
1:1A:1933:G:H2'	1:1A:1934:A:C8	2.52	0.45
1:1A:2028:C:H2'	1:1A:2029:A:C8	2.52	0.45
53:2t:191:GLU:O	55:2v:19:ASN:ND2	2.49	0.45
55:2v:103:GLU:OE2	55:2v:105:ARG:NH2	2.43	0.45
69:3H:181:THR:HG22	69:3H:184:VAL:HG23	1.98	0.45
1:1A:499:G:H2'	1:1A:504:G:H22	1.82	0.45
1:1A:1655:C:OP1	1:1A:1679:A:O2'	2.35	0.45
8:1H:118:THR:OG1	33:2Y:90:MET:O	2.28	0.45
29:2U:7:LYS:HG2	29:2U:11:LEU:HD13	1.99	0.45
46:2m:69:C:H3'	46:2m:70:G:H8	1.82	0.45
46:2m:339:A:H62	46:2m:342:C:H42	1.64	0.45
46:2m:1473:G:N2	46:2m:1475:G:OP2	2.50	0.45
46:2m:1613:G:H5''	56:2w:42:ARG:NH2	2.31	0.45
81:zw:137:THR:HG22	81:zw:140:LEU:HD12	1.99	0.45
1:1A:1876:U:H2'	1:1A:1877:G:C8	2.52	0.45
1:1A:2743:A:H2'	1:1A:2744:A:C8	2.52	0.45
1:1A:4474:A:OP2	1:1A:4476:C:N4	2.49	0.45
12:2D:57:TYR:HD1	12:2D:130:HIS:HA	1.82	0.45
25:2Q:83:THR:HG22	69:3H:10:THR:HG23	1.98	0.45
32:2X:36:VAL:HG11	32:2X:44:ARG:HD3	1.98	0.45
46:2m:878:G:N3	46:2m:909:G:N1	2.65	0.45
50:2q:36:HIS:NE2	50:2q:143:ASP:OD1	2.49	0.45
67:3F:130:LYS:HD2	67:3F:141:THR:HG23	1.98	0.45
76:3O:106:GLN:HB2	76:3O:108:ILE:HG13	1.98	0.45
1:1A:170:C:N3	1:1A:266:C:N4	2.65	0.45
1:1A:1557:C:H2'	1:1A:1558:A:C8	2.52	0.45
1:1A:1735:U:H2'	1:1A:1736:A:H8	1.82	0.45
1:1A:2262:G:OP2	45:2k:107:ARG:NH2	2.49	0.45
1:1A:2562:G:H1'	1:1A:2566:G:H1	1.80	0.45
1:1A:4573:G:N2	1:1A:4722:G:OP2	2.49	0.45
1:1A:4981:G:H3'	1:1A:4982:A:H8	1.82	0.45
15:2G:11:ARG:HB2	15:2G:27:ILE:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:2U:9:ARG:HD3	29:2U:9:ARG:HA	1.77	0.45
46:2m:194:C:H2'	46:2m:195:C:H6	1.81	0.45
46:2m:878:G:N1	46:2m:908:A:C2	2.84	0.45
46:2m:921:G:C4	77:3P:22:LYS:HG2	2.52	0.45
46:2m:928:G:H2'	46:2m:929:G:C8	2.51	0.45
46:2m:1533:A:OP2	51:2r:164:ARG:NH2	2.46	0.45
53:2t:157:LYS:HB2	55:2v:24:LEU:HD21	1.99	0.45
56:2w:79:HIS:N	56:2w:95:GLY:O	2.50	0.45
60:20:2:PRO:HA	60:20:3:GLY:HA2	1.64	0.45
1:1A:506:C:H2'	1:1A:507:G:H8	1.82	0.45
1:1A:1577:G:OP1	44:2j:17:ARG:NH1	2.46	0.45
1:1A:1911:C:H1'	1:1A:1917:A:H2'	1.97	0.45
1:1A:5018:C:H2'	1:1A:5019:A:C8	2.52	0.45
21:2M:154:LEU:HA	21:2M:154:LEU:HD23	1.82	0.45
26:2R:124:VAL:HG12	26:2R:138:VAL:HG22	1.98	0.45
43:2i:69:ARG:HH21	43:2i:80:LYS:HD3	1.82	0.45
46:2m:919:A:H5'	72:3K:16:LEU:HD13	1.99	0.45
46:2m:1597:C:H2'	46:2m:1598:G:C8	2.52	0.45
53:2t:81:VAL:HG22	53:2t:102:VAL:HG12	1.99	0.45
54:2u:35:LEU:HD12	54:2u:38:LYS:H	1.81	0.45
81:zw:331:TYR:HB3	81:zw:368:LEU:HD11	1.97	0.45
1:1A:908:G:H2'	1:1A:909:A:H8	1.82	0.45
1:1A:2749:C:H2'	1:1A:2750:G:C8	2.52	0.45
14:2F:170:THR:HB	14:2F:173:GLU:HG2	1.99	0.45
16:2H:22:LEU:HB3	16:2H:26:ARG:HH12	1.82	0.45
18:2J:70:CYS:SG	18:2J:72:GLN:N	2.88	0.45
20:2L:106:LEU:HB3	20:2L:120:TYR:CE1	2.51	0.45
23:2O:64:GLU:HB3	23:2O:71:THR:HB	1.99	0.45
24:2P:82:ILE:HB	24:2P:121:VAL:HG13	1.99	0.45
46:2m:333:G:N7	69:3H:190:ARG:NH1	2.63	0.45
46:2m:1420:G:N2	46:2m:1421:A:N1	2.53	0.45
46:2m:1568:C:O2	46:2m:1627:C:O2'	2.34	0.45
47:2n:38:ILE:HD11	47:2n:47:TYR:HB3	1.99	0.45
50:2q:183:VAL:HG12	50:2q:225:ILE:HD13	1.99	0.45
54:2u:23:ALA:HB3	54:2u:69:TRP:HZ3	1.82	0.45
67:3F:170:TRP:CG	67:3F:194:TYR:HB2	2.52	0.45
1:1A:4745:G:N2	1:1A:4954:G:H22	2.14	0.45
28:2T:47:ASP:N	28:2T:69:LYS:O	2.40	0.45
46:2m:1083:A:N7	46:2m:1841:C:O2'	2.49	0.45
46:2m:1228:A:H2'	46:2m:1229:G:C8	2.51	0.45
46:2m:1808:U:H2'	46:2m:1809:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:3F:297:THR:HG23	67:3F:311:GLN:HE21	1.82	0.45
70:3I:32:ILE:HD11	70:3I:40:LYS:HA	1.98	0.45
81:zw:29:GLY:HA3	81:zw:34:MET:HE2	1.98	0.45
1:1A:1954:U:H2'	1:1A:1955:G:H8	1.83	0.44
8:1H:153:LEU:HD11	8:1H:195:ILE:HG13	1.99	0.44
8:1H:168:LEU:HD21	8:1H:174:LEU:HD22	1.99	0.44
9:2A:93:ILE:HD12	9:2A:240:ILE:HD11	1.99	0.44
11:2C:88:PHE:N	11:2C:148:GLY:O	2.42	0.44
46:2m:19:A:H5''	63:3B:107:ARG:HG3	1.99	0.44
46:2m:409:C:H2'	46:2m:410:G:H8	1.82	0.44
46:2m:687:C:H4'	52:2s:121:THR:HG21	1.99	0.44
46:2m:1226:G:N1	46:2m:1639:G:OP2	2.50	0.44
67:3F:294:ASP:OD2	67:3F:297:THR:OG1	2.31	0.44
1:1A:35:U:O2'	1:1A:1525:A:N1	2.51	0.44
1:1A:3637:U:OP1	1:1A:3826:C:O2'	2.34	0.44
1:1A:3805:U:H2'	1:1A:3806:G:C8	2.53	0.44
1:1A:3929:G:OP1	16:2H:72:LYS:NZ	2.49	0.44
1:1A:4628:U:O2'	25:2Q:16:GLY:O	2.36	0.44
15:2G:20:HIS:CD2	15:2G:48:GLN:HE22	2.35	0.44
24:2P:89:ARG:HG2	24:2P:91:LYS:H	1.82	0.44
44:2j:70:THR:HG22	44:2j:72:ASN:H	1.81	0.44
46:2m:157:U:H4'	69:3H:59:GLN:HA	1.98	0.44
46:2m:507:G:OP2	75:3N:104:ARG:NH2	2.48	0.44
46:2m:537:C:H3'	46:2m:538:U:H5'	1.99	0.44
46:2m:930:C:O2'	46:2m:1104:G:OP1	2.34	0.44
49:2p:44:THR:O	49:2p:83:SER:OG	2.32	0.44
52:2s:130:LEU:HD23	52:2s:177:TYR:CZ	2.52	0.44
69:3H:54:GLY:O	69:3H:110:ASN:ND2	2.50	0.44
69:3H:181:THR:HG23	69:3H:183:ARG:H	1.83	0.44
1:1A:703:G:O2'	33:2Y:5:ARG:NH2	2.49	0.44
1:1A:1798:G:H2'	1:1A:1799:G:H8	1.82	0.44
1:1A:2557:G:O6	1:1A:2570:U:O4	2.35	0.44
1:1A:2837:U:OP1	5:1E:249:ARG:NE	2.49	0.44
3:1C:134:G:OP1	26:2R:63:LYS:NZ	2.48	0.44
4:1D:112:ILE:HG22	4:1D:135:THR:HG22	1.99	0.44
10:2B:55:VAL:HG12	26:2R:44:PRO:HA	1.98	0.44
10:2B:80:ILE:HG23	10:2B:164:ILE:HG21	1.99	0.44
10:2B:120:LYS:HE3	10:2B:125:LYS:HG3	1.99	0.44
46:2m:106:C:OP1	46:2m:431:G:O2'	2.34	0.44
51:2r:30:ILE:HG13	51:2r:32:ASP:H	1.82	0.44
51:2r:49:LEU:HD12	57:2x:50:LYS:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:3F:274:VAL:HG12	67:3F:276:SER:H	1.82	0.44
1:1A:1514:U:H2'	1:1A:1515:A:C8	2.52	0.44
1:1A:1779:U:H2'	1:1A:1780:A:C8	2.52	0.44
1:1A:1967:A:H2'	1:1A:1968:G:C8	2.52	0.44
1:1A:3620:G:OP1	1:1A:3622:C:N4	2.49	0.44
1:1A:4072:C:H2'	1:1A:4073:A:H8	1.81	0.44
1:1A:4881:U:O2'	1:1A:4882:U:O4'	2.36	0.44
2:1B:7:G:H2'	2:1B:8:G:H8	1.82	0.44
5:1E:46:PHE:HZ	5:1E:84:MET:H	1.66	0.44
33:2Y:82:VAL:HG22	33:2Y:111:ILE:HG13	1.99	0.44
46:2m:1280:G:H1	46:2m:1317:C:H41	1.65	0.44
46:2m:1736:G:H2'	46:2m:1737:G:H8	1.83	0.44
51:2r:34:SER:HA	65:3D:55:VAL:HG21	2.00	0.44
71:3J:63:LYS:HA	71:3J:66:GLU:HG2	1.98	0.44
81:zw:422:MET:O	81:zw:425:GLN:N	2.49	0.44
84:zz:160:U:H2'	84:zz:161:G:C8	2.52	0.44
1:1A:268:G:H2'	1:1A:269:G:C8	2.53	0.44
1:1A:1270:A:H8	1:1A:2106:G:H21	1.66	0.44
1:1A:1995:G:N7	1:1A:2000:G:N2	2.65	0.44
1:1A:3671:G:H2'	1:1A:3672:G:C8	2.53	0.44
1:1A:4405:G:O2'	12:2D:4:ARG:NE	2.50	0.44
3:1C:23:C:OP2	27:2S:15:ARG:NE	2.39	0.44
6:1F:116:ASN:HB2	6:1F:119:GLN:HG2	1.99	0.44
9:2A:48:LYS:HG2	30:2V:96:LEU:HD21	1.99	0.44
19:2K:66:MET:HE2	19:2K:98:LEU:HD13	1.99	0.44
38:2d:34:CYS:HB3	38:2d:39:TYR:H	1.82	0.44
46:2m:363:A:N6	46:2m:400:C:O2'	2.51	0.44
46:2m:375:U:H2'	46:2m:376:A:H8	1.82	0.44
46:2m:795:A:H2'	46:2m:796:G:H8	1.81	0.44
46:2m:1017:U:H5'	72:3K:55:ARG:HD3	1.98	0.44
47:2n:27:GLY:HA3	47:2n:28:THR:HA	1.68	0.44
81:zw:56:PHE:HB2	81:zw:75:ILE:HG21	1.98	0.44
1:1A:162:A:H2'	1:1A:163:A:H8	1.82	0.44
1:1A:382:G:N1	1:1A:385:A:OP2	2.49	0.44
1:1A:748:G:O3'	21:2M:148:SER:OG	2.32	0.44
1:1A:4425:G:OP1	41:2g:100:TYR:OH	2.26	0.44
1:1A:4910:G:H1	17:2I:108:ILE:H	1.66	0.44
1:1A:4992:G:H2'	1:1A:4993:G:C8	2.53	0.44
1:1A:5051:C:H4'	5:1E:324:GLY:HA2	1.99	0.44
5:1E:298:LEU:HD13	5:1E:301:ASN:HD22	1.83	0.44
11:2C:103:VAL:HG11	11:2C:144:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:2G:42:CYS:SG	15:2G:77:TRP:NE1	2.91	0.44
46:2m:1446:A:H1'	61:21:55:ARG:HD2	1.99	0.44
50:2q:51:ARG:NH2	50:2q:109:PHE:O	2.51	0.44
52:2s:98:ARG:HG3	52:2s:125:VAL:HG13	2.00	0.44
55:2v:127:THR:HG21	55:2v:144:LYS:HE2	2.00	0.44
84:zz:311:G:H3'	84:zz:312:U:H6	1.81	0.44
1:1A:6:C:H2'	1:1A:7:C:C6	2.53	0.44
1:1A:358:C:H2'	1:1A:359:A:C8	2.53	0.44
1:1A:474:C:H2'	1:1A:475:G:C8	2.53	0.44
1:1A:1327:C:H2'	1:1A:1328:G:C8	2.53	0.44
1:1A:2028:C:H2'	1:1A:2029:A:H8	1.82	0.44
1:1A:4094:G:H2'	1:1A:4095:G:H8	1.82	0.44
1:1A:4889:G:H21	1:1A:4931:G:H22	1.66	0.44
2:1B:57:C:H2'	2:1B:58:A:H8	1.83	0.44
11:2C:45:LEU:HD23	11:2C:57:VAL:HG12	1.99	0.44
39:2e:47:ILE:HD11	39:2e:52:LYS:HD2	2.00	0.44
46:2m:318:A:H2	46:2m:332:G:H22	1.66	0.44
68:3G:80:GLU:HB3	68:3G:266:TYR:HE2	1.82	0.44
1:1A:2079:G:H2'	1:1A:2080:U:C6	2.53	0.44
1:1A:4361:U:H2'	1:1A:4362:A:H8	1.81	0.44
1:1A:4911:A:OP2	5:1E:100:ARG:NE	2.43	0.44
46:2m:524:U:O4	70:3I:38:ARG:NH2	2.47	0.44
46:2m:1420:G:OP2	60:20:133:ARG:NH2	2.51	0.44
46:2m:1445:U:O2'	61:21:55:ARG:O	2.33	0.44
46:2m:1497:G:H21	54:2u:63:ALA:H	1.65	0.44
56:2w:93:MET:HG3	56:2w:102:PHE:HB2	1.99	0.44
59:2z:26:ILE:HD11	59:2z:54:LYS:HB2	2.00	0.44
61:21:95:SER:HA	61:21:98:VAL:HG12	1.99	0.44
68:3G:227:ARG:HG3	68:3G:228:GLY:H	1.83	0.44
1:1A:505:G:O6	1:1A:653:U:O4	2.36	0.44
1:1A:2741:U:O2	1:1A:2742:G:C6	2.71	0.44
1:1A:2792:C:O2	1:1A:2800:G:N2	2.51	0.44
1:1A:3872:A:H2'	1:1A:3873:G:H8	1.83	0.44
27:2S:111:LEU:HD23	27:2S:116:LYS:HA	1.99	0.44
46:2m:652:U:H2'	46:2m:653:A:C8	2.52	0.44
46:2m:1627:C:H5'	60:20:41:LYS:HD2	1.99	0.44
54:2u:14:LEU:HD11	54:2u:35:LEU:HB3	1.98	0.44
56:2w:81:ARG:HG2	59:2z:118:ARG:CZ	2.48	0.44
69:3H:160:LYS:HE2	69:3H:172:LYS:HG2	1.99	0.44
82:zx:13:SER:O	82:zx:16:THR:OG1	2.32	0.44
1:1A:493:G:H1	1:1A:660:A:H2	1.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:1442:C:H42	1:1A:2105:A:H1'	1.82	0.43
1:1A:4518:A:N7	5:1E:257:TRP:NE1	2.66	0.43
1:1A:4522:G:O2'	1:1A:4525:C:OP2	2.31	0.43
21:2M:15:ARG:HH12	21:2M:18:PRO:HG3	1.83	0.43
21:2M:163:HIS:HD2	21:2M:166:ARG:HE	1.64	0.43
45:2k:16:PHE:O	45:2k:26:SER:OG	2.35	0.43
46:2m:78:C:H4'	69:3H:173:ALA:HB1	2.00	0.43
46:2m:525:A:H2'	46:2m:526:A:C8	2.53	0.43
46:2m:982:G:H2'	46:2m:983:A:C8	2.53	0.43
46:2m:1462:U:OP2	46:2m:1463:U:N3	2.51	0.43
50:2q:36:HIS:CD2	50:2q:85:GLY:HA3	2.53	0.43
73:3L:75:MET:HG3	73:3L:118:ALA:HB2	2.00	0.43
81:zw:320:LEU:HD23	81:zw:389:LEU:HD13	1.98	0.43
1:1A:490:C:H2'	1:1A:491:G:C8	2.53	0.43
1:1A:1743:A:H1'	7:1G:15:ARG:HH21	1.81	0.43
1:1A:2648:G:H2'	1:1A:2649:G:H8	1.83	0.43
1:1A:2778:G:H1	3:1C:113:C:P	2.41	0.43
1:1A:2902:G:N2	1:1A:3597:G:H22	2.16	0.43
1:1A:4064:C:H2'	1:1A:4065:G:C8	2.53	0.43
1:1A:4734:A:H2'	1:1A:4735:G:C8	2.53	0.43
4:1D:107:MET:HE1	4:1D:113:VAL:HG11	2.00	0.43
6:1F:110:ARG:O	6:1F:112:HIS:N	2.45	0.43
27:2S:50:ARG:HD3	27:2S:115:ARG:HH21	1.82	0.43
32:2X:98:SER:OG	32:2X:100:ASN:O	2.26	0.43
38:2d:2:THR:HG22	38:2d:4:GLY:H	1.83	0.43
46:2m:382:C:H41	53:2t:5:ARG:HH22	1.66	0.43
46:2m:1207:G:H22	80:zv:0:G:H3'	1.84	0.43
46:2m:1428:G:C6	46:2m:1429:G:O6	2.71	0.43
55:2v:103:GLU:HB3	63:3B:10:ALA:HB3	2.00	0.43
67:3F:12:LYS:O	67:3F:14:HIS:N	2.49	0.43
83:zy:46:U:O2'	83:zy:49:C:OP1	2.35	0.43
83:zy:71:C:H2'	83:zy:72:C:C2	2.53	0.43
84:zz:306:U:O4	84:zz:327:C:N4	2.44	0.43
1:1A:161:G:H2'	1:1A:162:A:C8	2.54	0.43
1:1A:1457:G:O2'	19:2K:75:ARG:NH2	2.50	0.43
1:1A:2420:A:OP2	18:2J:127:ARG:NH1	2.51	0.43
1:1A:2895:A:H2'	1:1A:2896:G:H8	1.84	0.43
1:1A:2899:C:OP1	20:2L:108:ARG:NH2	2.51	0.43
1:1A:4088:C:H2'	1:1A:4089:G:H8	1.82	0.43
3:1C:132:G:H2'	3:1C:133:G:H8	1.83	0.43
33:2Y:41:ILE:HA	33:2Y:46:ARG:HH21	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:2i:36:GLN:HA	43:2i:39:ARG:HE	1.83	0.43
45:2k:21:ASN:N	45:2k:21:ASN:OD1	2.52	0.43
46:2m:124:U:C4	46:2m:339:A:N1	2.87	0.43
46:2m:306:C:H5''	46:2m:307:G:C5	2.53	0.43
46:2m:1276:A:H62	46:2m:1321:G:H8	1.64	0.43
48:2o:105:LEU:HD13	48:2o:213:ARG:HA	2.00	0.43
64:3C:37:LYS:HE3	64:3C:72:HIS:HE1	1.83	0.43
74:3M:87:GLU:OE1	74:3M:90:GLN:NE2	2.47	0.43
1:1A:116:G:H2'	1:1A:117:C:C6	2.54	0.43
1:1A:499:G:N3	1:1A:504:G:N1	2.66	0.43
1:1A:1481:C:N4	37:2c:4:ARG:HE	2.16	0.43
1:1A:1558:A:H2'	1:1A:1559:G:H8	1.83	0.43
1:1A:2648:G:H2'	1:1A:2649:G:C8	2.53	0.43
1:1A:2669:C:O2'	1:1A:2670:C:O5'	2.36	0.43
1:1A:4731:G:O2'	1:1A:4734:A:OP2	2.36	0.43
12:2D:11:TYR:O	12:2D:59:GLN:NE2	2.52	0.43
24:2P:96:LEU:HD12	25:2Q:20:ARG:HD2	1.99	0.43
27:2S:56:GLN:HB3	27:2S:105:VAL:HG13	2.00	0.43
28:2T:52:LYS:O	28:2T:65:ARG:NE	2.43	0.43
46:2m:980:A:H2'	46:2m:981:A:C8	2.54	0.43
46:2m:1850:A:H2'	46:2m:1851:A:C8	2.53	0.43
52:2s:52:GLU:HG3	52:2s:58:LYS:HD3	2.00	0.43
60:20:64:LEU:HD12	60:20:75:MET:HE1	2.01	0.43
61:21:20:ILE:HG23	61:21:115:THR:H	1.84	0.43
75:3N:7:ILE:HD11	75:3N:43:LYS:HB3	1.98	0.43
1:1A:252:C:H2'	1:1A:253:G:C8	2.53	0.43
1:1A:2869:U:O2'	1:1A:2881:A:N7	2.47	0.43
1:1A:3667:C:H2'	1:1A:3668:C:C6	2.53	0.43
1:1A:4725:C:H2'	1:1A:4726:G:C8	2.53	0.43
1:1A:5055:G:H2'	1:1A:5056:A:C8	2.54	0.43
3:1C:46:G:N2	3:1C:47:C:O2	2.52	0.43
6:1F:140:LYS:O	6:1F:204:ARG:NH1	2.51	0.43
15:2G:64:PHE:CZ	15:2G:73:VAL:HG23	2.53	0.43
21:2M:2:LYS:NZ	21:2M:121:ALA:O	2.40	0.43
39:2e:17:ARG:HB2	39:2e:20:ALA:HB2	2.01	0.43
41:2g:96:CYS:SG	41:2g:97:ARG:N	2.90	0.43
46:2m:957:A:O3'	46:2m:973:C:O2'	2.37	0.43
46:2m:1091:C:OP1	72:3K:9:LYS:NZ	2.46	0.43
46:2m:1401:A:H2'	46:2m:1402:A:C8	2.53	0.43
46:2m:1429:G:OP2	57:2x:69:ARG:NH2	2.51	0.43
46:2m:1504:U:H1'	46:2m:1509:U:H5	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2m:1617:G:N7	56:2w:47:ARG:NH2	2.56	0.43
48:2o:82:ARG:HH21	48:2o:103:MET:HE1	1.84	0.43
49:2p:132:LYS:HB2	49:2p:189:MET:HG2	2.01	0.43
51:2r:140:ASP:H	65:3D:63:ARG:HH12	1.67	0.43
57:2x:86:GLN:HE22	57:2x:122:ALA:HA	1.82	0.43
64:3C:10:ARG:HB3	64:3C:34:LYS:HB2	2.00	0.43
64:3C:23:CYS:SG	64:3C:24:THR:N	2.92	0.43
75:3N:13:MET:HB3	75:3N:22:GLN:HE21	1.82	0.43
81:zw:100:ILE:HD11	81:zw:108:LYS:HE3	1.99	0.43
1:1A:695:G:O2'	1:1A:697:G:O5'	2.36	0.43
1:1A:2044:U:O3'	17:2I:63:ASN:ND2	2.52	0.43
1:1A:4523:A:H5''	1:1A:4524:G:H5'	2.01	0.43
1:1A:4762:A:H2	21:2M:173:ASN:HA	1.82	0.43
2:1B:46:C:H2'	2:1B:47:G:C8	2.53	0.43
6:1F:184:TYR:HE1	6:1F:225:PRO:HG2	1.84	0.43
9:2A:80:ASN:HD21	22:2N:142:ARG:HA	1.82	0.43
14:2F:12:PRO:HB2	14:2F:14:PHE:HD2	1.83	0.43
17:2I:80:PHE:HD2	17:2I:104:VAL:HG11	1.84	0.43
21:2M:16:CYS:HA	21:2M:59:GLY:HA2	2.01	0.43
25:2Q:105:ARG:HD2	69:3H:149:LYS:HD3	2.00	0.43
45:2k:105:ASP:OD1	45:2k:105:ASP:N	2.50	0.43
46:2m:318:A:H2	46:2m:332:G:N1	2.14	0.43
46:2m:931:C:H2'	46:2m:932:G:C8	2.54	0.43
46:2m:1010:G:H2'	46:2m:1011:A:C8	2.54	0.43
46:2m:1260:A:H4'	46:2m:1623:A:H62	1.84	0.43
46:2m:1599:U:OP1	76:3O:46:ASN:ND2	2.51	0.43
46:2m:1676:U:H5'	51:2r:74:ASN:HB3	2.00	0.43
52:2s:76:GLN:HA	52:2s:79:LEU:HB3	1.99	0.43
52:2s:141:GLY:HA3	52:2s:157:HIS:HB2	2.00	0.43
66:3E:6:LEU:HA	66:3E:7:TYR:HA	1.70	0.43
69:3H:170:ARG:HH21	69:3H:172:LYS:HA	1.83	0.43
84:zz:142:A:H2'	84:zz:143:G:C8	2.53	0.43
1:1A:6:C:H2'	1:1A:7:C:H6	1.84	0.43
1:1A:158:A:N1	1:1A:276:C:O2'	2.45	0.43
1:1A:251:C:H2'	1:1A:252:C:C6	2.53	0.43
1:1A:1802:A:H5''	1:1A:1803:G:H5'	2.01	0.43
1:1A:1850:A:N3	1:1A:2283:G:O2'	2.51	0.43
1:1A:1972:G:H1	1:1A:1993:C:N4	2.16	0.43
1:1A:3722:G:H2'	1:1A:3723:A:C8	2.54	0.43
1:1A:3725:G:O6	37:2c:67:LYS:NZ	2.44	0.43
1:1A:4209:G:O6	1:1A:4224:A:N6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1C:132:G:OP1	26:2R:108:GLN:NE2	2.52	0.43
34:2Z:12:ALA:H	34:2Z:28:LEU:HA	1.84	0.43
46:2m:954:U:O2	73:3L:55:ARG:NH2	2.52	0.43
46:2m:1372:U:O2'	46:2m:1373:C:O4'	2.37	0.43
46:2m:1648:G:O6	57:2x:16:LYS:NZ	2.38	0.43
47:2n:68:ILE:HG21	47:2n:74:VAL:HG13	2.00	0.43
48:2o:129:THR:OG1	48:2o:130:THR:N	2.52	0.43
48:2o:222:LYS:HG3	48:2o:223:PHE:H	1.82	0.43
53:2t:43:ILE:HG12	53:2t:57:ALA:HA	2.00	0.43
69:3H:78:SER:OG	69:3H:79:LYS:N	2.52	0.43
69:3H:216:ARG:NH2	69:3H:219:GLU:OE1	2.52	0.43
1:1A:21:G:OP2	38:2d:43:ARG:NH2	2.52	0.43
1:1A:246:G:H2'	1:1A:247:G:C8	2.53	0.43
1:1A:725:G:OP2	6:1F:350:ARG:NH2	2.52	0.43
1:1A:2535:G:H2'	1:1A:2536:A:C8	2.54	0.43
1:1A:3658:C:H2'	1:1A:3659:G:C8	2.54	0.43
12:2D:111:LEU:HD13	83:zy:2:G:H1'	2.01	0.43
27:2S:54:GLU:OE1	27:2S:107:THR:OG1	2.33	0.43
30:2V:105:GLY:O	30:2V:109:ARG:NH1	2.52	0.43
36:2b:87:LYS:O	36:2b:92:ARG:NH1	2.52	0.43
46:2m:927:C:H2'	46:2m:928:G:H8	1.83	0.43
1:1A:679:C:H2'	1:1A:680:G:C8	2.53	0.43
1:1A:1637:A:H2	38:2d:11:ARG:HH12	1.67	0.43
1:1A:1818:G:OP2	1:1A:1818:G:N2	2.38	0.43
1:1A:2521:G:H2'	1:1A:2522:G:C8	2.54	0.43
1:1A:4413:C:N4	1:1A:4414:A:N1	2.67	0.43
1:1A:5040:U:H4'	1:1A:5041:G:H5'	2.00	0.43
13:2E:158:SER:HB3	13:2E:161:GLU:HG2	2.00	0.43
15:2G:24:LEU:HD11	15:2G:86:TRP:CD2	2.54	0.43
34:2Z:40:GLU:HA	34:2Z:43:LEU:HB2	2.00	0.43
46:2m:30:C:O3'	63:3B:137:LYS:NZ	2.45	0.43
46:2m:918:U:OP1	72:3K:64:ARG:NH2	2.51	0.43
46:2m:927:C:H2'	46:2m:928:G:C8	2.54	0.43
46:2m:1589:A:N3	46:2m:1653:U:O2'	2.41	0.43
54:2u:65:ARG:HB2	54:2u:66:HIS:CD2	2.53	0.43
67:3F:191:HIS:CE1	67:3F:217:MET:HB3	2.54	0.43
1:1A:318:A:H2'	1:1A:319:A:C8	2.53	0.43
1:1A:346:G:OP1	27:2S:8:THR:OG1	2.34	0.43
1:1A:1359:G:H4'	16:2H:203:TYR:HB2	2.01	0.43
1:1A:1629:G:H1	4:1D:208:GLU:CD	2.26	0.43
1:1A:1870:C:H2'	1:1A:1871:A:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:2112:G:O2'	1:1A:2250:C:N4	2.47	0.43
1:1A:3950:U:H5''	1:1A:3951:G:N7	2.34	0.43
1:1A:4165:C:OP1	10:2B:53:ARG:NH2	2.51	0.43
1:1A:4769:G:H22	1:1A:4865:C:H42	1.67	0.43
1:1A:5055:G:H2'	1:1A:5056:A:H8	1.84	0.43
13:2E:32:ARG:HA	13:2E:35:ARG:HE	1.83	0.43
13:2E:100:SER:HB3	13:2E:104:ASN:H	1.83	0.43
17:2I:80:PHE:HA	17:2I:83:THR:HG22	2.00	0.43
21:2M:80:ILE:HG12	21:2M:129:VAL:HG23	2.01	0.43
46:2m:322:C:N4	46:2m:329:G:O6	2.52	0.43
46:2m:560:A:C8	70:3I:173:VAL:HG11	2.54	0.43
46:2m:1616:U:OP2	56:2w:43:ARG:NH2	2.52	0.43
48:2o:32:ASP:OD1	48:2o:46:LYS:NZ	2.39	0.43
58:2y:68:GLY:HA3	58:2y:69:ILE:HG13	2.01	0.43
67:3F:113:PHE:HD1	67:3F:120:ILE:HG12	1.83	0.43
67:3F:158:PRO:HG2	67:3F:202:PRO:HA	2.00	0.43
68:3G:78:LEU:HD23	68:3G:81:ILE:HD12	2.01	0.43
1:1A:941:C:OP2	9:2A:242:ARG:NH2	2.52	0.42
1:1A:1273:G:C8	30:2V:117:ARG:HG2	2.54	0.42
1:1A:2360:A:H2	1:1A:2361:G:H21	1.67	0.42
1:1A:4519:C:H42	81:zw:188:LEU:HD11	1.84	0.42
46:2m:1148:A:OP1	64:3C:6:ARG:NH2	2.52	0.42
46:2m:1844:U:H2'	46:2m:1845:A:C8	2.53	0.42
47:2n:93:ALA:HB1	47:2n:183:LEU:HD11	2.00	0.42
49:2p:75:LYS:HB2	54:2u:22:VAL:HG11	2.01	0.42
57:2x:146:ARG:NH2	83:zy:33:A:O3'	2.52	0.42
59:2z:66:ARG:O	59:2z:69:THR:OG1	2.33	0.42
68:3G:106:VAL:HG12	68:3G:128:VAL:HG22	2.00	0.42
69:3H:131:ARG:HB3	69:3H:132:ARG:H	1.50	0.42
69:3H:162:LEU:HB2	69:3H:170:ARG:HD3	2.01	0.42
71:3J:48:HIS:NE2	71:3J:111:VAL:O	2.52	0.42
74:3M:8:ALA:HA	74:3M:74:VAL:HG11	2.01	0.42
1:1A:161:G:H2'	1:1A:162:A:H8	1.83	0.42
1:1A:178:C:H2'	1:1A:179:G:C8	2.54	0.42
1:1A:1686:C:OP1	30:2V:19:ASN:ND2	2.50	0.42
1:1A:2609:G:H2'	1:1A:2610:G:H8	1.84	0.42
1:1A:3866:C:H42	1:1A:3880:G:H1	1.65	0.42
1:1A:4299:U:H2'	1:1A:4300:U:H6	1.84	0.42
10:2B:154:LEU:HB3	10:2B:204:PHE:HD2	1.83	0.42
16:2H:71:ARG:HD2	16:2H:94:PHE:HD1	1.84	0.42
21:2M:159:LEU:HD21	21:2M:172:PRO:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:2U:117:LEU:HD12	29:2U:118:PRO:HD2	2.00	0.42
47:2n:184:ARG:HD3	47:2n:191:ARG:HD2	2.01	0.42
50:2q:193:GLY:HA3	50:2q:212:ASP:HA	2.01	0.42
1:1A:383:A:HO2'	1:1A:384:A:H8	1.66	0.42
1:1A:1723:A:O3'	9:2A:107:LYS:NZ	2.52	0.42
1:1A:1972:G:H22	1:1A:1994:C:H5	1.68	0.42
13:2E:141:ILE:HA	13:2E:144:LYS:HE3	2.01	0.42
15:2G:27:ILE:HA	15:2G:38:VAL:HG23	2.00	0.42
46:2m:566:U:H3	46:2m:584:G:H1	1.67	0.42
46:2m:1103:C:H2'	46:2m:1104:G:H8	1.84	0.42
51:2r:143:PRO:HA	51:2r:146:ARG:HG2	2.01	0.42
68:3G:128:VAL:HG11	68:3G:155:ILE:HG12	2.02	0.42
82:zx:16:THR:O	82:zx:20:ILE:HG12	2.19	0.42
1:1A:175:C:H2'	1:1A:176:G:C8	2.54	0.42
1:1A:384:A:H61	1:1A:405:U:H4'	1.84	0.42
1:1A:699:C:H2'	1:1A:700:G:H8	1.84	0.42
1:1A:1794:A:H5''	1:1A:4214:A:H61	1.83	0.42
1:1A:1973:G:C8	1:1A:1974:U:H2'	2.52	0.42
1:1A:2610:G:H2'	1:1A:2611:A:H8	1.84	0.42
1:1A:2809:G:O2'	1:1A:4644:G:OP1	2.37	0.42
1:1A:4177:C:OP1	16:2H:93:LYS:NZ	2.38	0.42
8:1H:107:VAL:HA	8:1H:108:LYS:HA	1.85	0.42
9:2A:41:MET:HE3	9:2A:41:MET:HB2	1.88	0.42
46:2m:616:A:H62	46:2m:625:G:H21	1.66	0.42
46:2m:1121:G:O2'	48:2o:204:ILE:O	2.32	0.42
53:2t:65:PHE:O	53:2t:109:TYR:OH	2.34	0.42
58:2y:20:TYR:HD1	58:2y:23:ARG:HD3	1.84	0.42
65:3D:35:MET:HE1	65:3D:55:VAL:HG13	2.01	0.42
65:3D:52:GLU:HG3	65:3D:53:GLY:H	1.84	0.42
69:3H:1:MET:HE1	69:3H:104:ALA:HA	2.02	0.42
1:1A:713:C:H2'	1:1A:714:G:C8	2.55	0.42
1:1A:1390:G:N2	1:1A:1393:G:OP2	2.49	0.42
1:1A:1440:U:H3	1:1A:2105:A:H2	1.68	0.42
1:1A:1870:C:H2'	1:1A:1871:A:C8	2.54	0.42
1:1A:3667:C:H4'	4:1D:8:GLN:HA	2.00	0.42
1:1A:4524:G:N3	5:1E:252:ALA:HB1	2.34	0.42
5:1E:162:VAL:O	5:1E:183:ILE:N	2.49	0.42
13:2E:119:TYR:HD2	59:2z:12:ILE:HD11	1.85	0.42
24:2P:32:THR:HG23	24:2P:34:ALA:H	1.85	0.42
24:2P:99:GLU:HB3	25:2Q:24:THR:HG23	2.02	0.42
46:2m:1754:G:C6	46:2m:1780:G:H1'	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:2w:78:THR:HG1	56:2w:95:GLY:C	2.26	0.42
68:3G:183:LYS:NZ	74:3M:91:ASN:O	2.52	0.42
69:3H:117:GLY:H	69:3H:121:ILE:HD11	1.85	0.42
1:1A:62:A:N3	1:1A:77:U:O2'	2.46	0.42
1:1A:1244:G:H2'	1:1A:1245:C:H6	1.85	0.42
1:1A:2608:G:H2'	1:1A:2609:G:H8	1.85	0.42
1:1A:2864:A:H2'	1:1A:2865:U:C6	2.55	0.42
1:1A:3650:C:H2'	1:1A:3651:A:C8	2.55	0.42
1:1A:3873:G:H2'	1:1A:3874:G:C8	2.55	0.42
1:1A:3916:G:C6	1:1A:4388:A:C6	3.07	0.42
3:1C:60:G:O6	36:2b:62:ASN:ND2	2.53	0.42
4:1D:28:ARG:HB2	4:1D:123:ARG:HB3	2.00	0.42
7:1G:131:ASN:OD1	7:1G:175:HIS:NE2	2.52	0.42
9:2A:113:ARG:NH1	9:2A:206:ASN:OD1	2.51	0.42
12:2D:145:GLU:HA	12:2D:148:VAL:HG22	2.01	0.42
13:2E:136:ARG:NH1	13:2E:155:HIS:O	2.53	0.42
16:2H:64:ILE:HD11	16:2H:102:ALA:HB1	2.00	0.42
46:2m:106:C:H2'	46:2m:107:A:C8	2.54	0.42
55:2v:112:HIS:HB2	55:2v:138:VAL:HG11	2.01	0.42
67:3F:43:TRP:HD1	67:3F:55:PRO:HA	1.84	0.42
69:3H:130:PRO:HA	69:3H:131:ARG:HA	1.86	0.42
69:3H:148:SER:HA	69:3H:149:LYS:HA	1.75	0.42
84:zz:305:U:O2	84:zz:325:C:N4	2.53	0.42
1:1A:1248:C:H2'	1:1A:1249:C:H6	1.84	0.42
1:1A:1695:U:H2'	1:1A:1696:C:C6	2.54	0.42
1:1A:4659:G:H2'	1:1A:4660:G:C8	2.54	0.42
1:1A:5002:U:H2'	1:1A:5003:U:C6	2.55	0.42
3:1C:147:G:H2'	3:1C:148:A:H8	1.84	0.42
5:1E:295:ASP:HA	5:1E:296:GLY:HA2	1.85	0.42
17:2I:109:PRO:HA	17:2I:110:PRO:HD3	1.94	0.42
18:2J:118:GLN:NE2	18:2J:147:GLU:OE2	2.49	0.42
44:2j:51:ALA:HB3	44:2j:54:ILE:HB	2.01	0.42
46:2m:1562:C:H2'	46:2m:1563:G:C8	2.55	0.42
47:2n:123:VAL:HG12	47:2n:145:ILE:HG23	2.01	0.42
59:2z:46:ARG:HG2	60:20:35:ASP:HB3	2.02	0.42
59:2z:84:LEU:HG	59:2z:97:GLN:HB2	2.01	0.42
61:21:49:LYS:H	61:21:92:HIS:HD2	1.66	0.42
62:3A:80:SER:O	62:3A:82:ASN:N	2.52	0.42
64:3C:44:ILE:O	73:3L:113:GLN:NE2	2.50	0.42
67:3F:18:VAL:HA	67:3F:35:SER:HA	2.00	0.42
68:3G:270:THR:HA	68:3G:273:LEU:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:3M:23:ARG:HH22	74:3M:66:THR:HA	1.84	0.42
1:1A:97:G:OP1	14:2F:16:LYS:NZ	2.52	0.42
1:1A:974:C:H41	1:1A:1281:G:H21	1.68	0.42
1:1A:1739:G:N3	1:1A:1742:A:N6	2.67	0.42
1:1A:3847:C:H2'	1:1A:3848:U:H6	1.84	0.42
1:1A:3872:A:H2'	1:1A:3873:G:C8	2.55	0.42
1:1A:4299:U:OP1	30:2V:33:LYS:NZ	2.52	0.42
1:1A:4991:U:H2'	1:1A:4992:G:C8	2.55	0.42
3:1C:82:A:H62	3:1C:84:A:H3'	1.85	0.42
8:1H:59:ARG:O	8:1H:63:TYR:HB2	2.20	0.42
9:2A:125:LEU:HD22	9:2A:130:ILE:HG22	2.02	0.42
16:2H:120:TRP:NE1	16:2H:122:GLY:O	2.53	0.42
34:2Z:14:TYR:OH	34:2Z:92:LEU:O	2.29	0.42
38:2d:63:ARG:HH12	38:2d:65:ARG:HD3	1.84	0.42
46:2m:17:C:H2'	46:2m:18:C:H6	1.85	0.42
46:2m:525:A:H2'	46:2m:526:A:H8	1.85	0.42
46:2m:1518:C:H5''	46:2m:1519:U:H5''	2.01	0.42
47:2n:111:GLN:HA	47:2n:116:PHE:CG	2.54	0.42
48:2o:65:ARG:NH2	73:3L:51:GLU:OE2	2.53	0.42
51:2r:126:THR:HB	51:2r:127:ARG:H	1.67	0.42
59:2z:27:ALA:HA	59:2z:45:LEU:HD12	2.02	0.42
65:3D:30:VAL:HG11	65:3D:50:VAL:HG11	2.02	0.42
84:zz:133:G:H2'	84:zz:134:A:C8	2.54	0.42
1:1A:86:U:HO2'	29:2U:65:ARG:NH1	2.16	0.42
1:1A:513:U:H3'	1:1A:514:U:H4'	2.01	0.42
1:1A:1506:G:O2'	6:1F:116:ASN:ND2	2.47	0.42
1:1A:1971:C:N4	1:1A:2001:G:O4'	2.53	0.42
1:1A:2640:G:H2'	1:1A:2641:A:H8	1.85	0.42
1:1A:2776:G:H2'	1:1A:2777:G:H8	1.85	0.42
12:2D:32:ARG:HG3	12:2D:33:ILE:H	1.85	0.42
26:2R:119:ILE:HG13	26:2R:144:TYR:HD2	1.84	0.42
46:2m:101:U:H5''	53:2t:19:LYS:HE2	2.02	0.42
46:2m:1300:U:O2	56:2w:51:ARG:NE	2.52	0.42
46:2m:1535:U:H2'	51:2r:82:ASN:HD22	1.85	0.42
49:2p:213:PRO:HD3	58:2y:19:LYS:HD2	2.01	0.42
51:2r:79:HIS:O	51:2r:81:ARG:N	2.53	0.42
56:2w:77:LYS:HA	56:2w:78:THR:HA	1.57	0.42
58:2y:83:ASN:HB3	58:2y:85:VAL:HG22	2.02	0.42
71:3J:113:ASP:HB3	71:3J:114:TYR:H	1.73	0.42
1:1A:14:C:H2'	1:1A:15:A:H8	1.84	0.42
1:1A:66:A:H61	1:1A:282:C:HO2'	1.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:239:C:H5''	27:2S:46:SER:HB3	2.01	0.42
1:1A:1687:U:H2'	1:1A:1688:G:C8	2.55	0.42
1:1A:4633:G:H21	1:1A:4665:A:N6	2.00	0.42
17:2I:168:TYR:CE2	17:2I:172:LYS:HD2	2.55	0.42
46:2m:589:G:H21	46:2m:591:U:H3	1.67	0.42
48:2o:33:VAL:HG11	48:2o:67:PHE:HZ	1.84	0.42
52:2s:10:LYS:HE3	52:2s:47:ALA:HA	2.00	0.42
53:2t:60:LEU:HD22	53:2t:185:ALA:HB2	2.00	0.42
57:2x:55:VAL:HA	57:2x:63:PHE:HE2	1.85	0.42
58:2y:67:ARG:HA	58:2y:68:GLY:HA3	1.67	0.42
61:21:67:LYS:HB2	61:21:78:ASP:HB2	2.01	0.42
67:3F:170:TRP:CD1	67:3F:194:TYR:HB2	2.54	0.42
70:3I:78:LEU:HD13	70:3I:97:ILE:HD11	2.02	0.42
1:1A:156:G:N2	1:1A:157:U:O4	2.52	0.41
1:1A:1902:G:OP1	34:2Z:24:HIS:NE2	2.53	0.41
1:1A:3597:G:H2'	1:1A:3598:C:C6	2.55	0.41
1:1A:4238:G:H2'	1:1A:4239:A:C8	2.55	0.41
1:1A:4424:A:OP2	41:2g:97:ARG:NH2	2.53	0.41
13:2E:164:ARG:HA	13:2E:167:GLN:HG2	2.01	0.41
46:2m:409:C:H2'	46:2m:410:G:C8	2.55	0.41
46:2m:416:U:O2	46:2m:421:G:O6	2.37	0.41
46:2m:813:A:O3'	50:2q:22:LYS:NZ	2.42	0.41
71:3J:124:ILE:H	71:3J:124:ILE:HG13	1.65	0.41
1:1A:163:A:H2'	1:1A:164:G:C8	2.55	0.41
1:1A:278:G:H4'	16:2H:50:ARG:HH21	1.85	0.41
1:1A:441:G:H2'	1:1A:442:G:H8	1.86	0.41
1:1A:1725:U:H2'	1:1A:1726:U:H6	1.84	0.41
1:1A:2669:C:O2'	1:1A:2670:C:O4'	2.33	0.41
1:1A:4440:G:OP1	81:zw:189:ARG:NH2	2.53	0.41
4:1D:79:ALA:H	4:1D:82:ILE:HD12	1.84	0.41
5:1E:17:LEU:O	5:1E:19:ARG:N	2.53	0.41
11:2C:90:TYR:HE2	11:2C:155:SER:HB2	1.85	0.41
12:2D:177:ASN:HB2	12:2D:180:GLU:HG2	2.03	0.41
14:2F:90:VAL:O	14:2F:93:THR:OG1	2.26	0.41
25:2Q:86:SER:HB3	69:3H:130:PRO:HB2	2.02	0.41
33:2Y:4:LEU:HD23	33:2Y:121:ARG:HB2	2.01	0.41
46:2m:51:U:H2'	46:2m:52:G:C8	2.54	0.41
46:2m:57:U:H4'	46:2m:504:G:H21	1.84	0.41
46:2m:155:G:N2	69:3H:56:ASN:OD1	2.45	0.41
46:2m:906:U:H2'	46:2m:907:G:C8	2.55	0.41
46:2m:934:G:C6	46:2m:1008:A:N1	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
84:zz:146:G:H2'	84:zz:147:U:C6	2.54	0.41
84:zz:319:G:H2'	84:zz:320:G:C8	2.55	0.41
1:1A:440:U:O2'	34:2Z:91:ASN:O	2.32	0.41
1:1A:1633:G:O4'	4:1D:205:ASN:ND2	2.54	0.41
1:1A:2475:G:N1	26:2R:51:THR:O	2.41	0.41
9:2A:117:ILE:HG12	9:2A:118:PHE:CD2	2.56	0.41
22:2N:53:PRO:HB3	22:2N:91:VAL:HG22	2.01	0.41
40:2f:23:ILE:HD11	40:2f:38:ASN:N	2.35	0.41
46:2m:145:G:H2'	46:2m:146:G:C8	2.55	0.41
46:2m:582:C:H1'	75:3N:33:ALA:HB2	2.03	0.41
46:2m:846:G:N7	50:2q:108:ARG:NH1	2.69	0.41
46:2m:946:U:H2'	46:2m:947:G:H8	1.85	0.41
46:2m:1457:U:H2'	46:2m:1458:G:C8	2.53	0.41
47:2n:208:GLU:HG3	47:2n:209:GLU:HG3	2.02	0.41
49:2p:5:ILE:HB	49:2p:10:LYS:HB2	2.01	0.41
50:2q:238:LEU:HD13	50:2q:242:LYS:HA	2.02	0.41
54:2u:41:PRO:HG2	54:2u:44:HIS:HB2	2.03	0.41
63:3B:9:THR:OG1	63:3B:10:ALA:N	2.53	0.41
67:3F:64:HIS:CD2	67:3F:84:ASP:HB2	2.56	0.41
67:3F:300:ALA:HB2	67:3F:310:TRP:HZ3	1.86	0.41
71:3J:49:LEU:HG	71:3J:74:ILE:HA	2.01	0.41
81:zw:94:VAL:HG21	81:zw:136:LEU:HD21	2.03	0.41
1:1A:164:G:H2'	1:1A:165:A:H8	1.86	0.41
1:1A:268:G:H2'	1:1A:269:G:H8	1.85	0.41
1:1A:1732:C:H2'	1:1A:1733:G:C8	2.56	0.41
1:1A:1974:U:H4'	1:1A:1975:G:H2'	2.02	0.41
1:1A:2775:C:H2'	1:1A:2776:G:C8	2.56	0.41
1:1A:4064:C:H2'	1:1A:4065:G:H8	1.84	0.41
1:1A:4237:C:H2'	1:1A:4238:G:C8	2.55	0.41
1:1A:4565:C:OP1	17:2I:65:ASN:ND2	2.45	0.41
1:1A:4679:G:H2'	1:1A:4680:G:C8	2.55	0.41
1:1A:4975:G:O2'	1:1A:4977:A:N6	2.53	0.41
2:1B:64:G:H2'	2:1B:65:G:C8	2.54	0.41
8:1H:111:LYS:HD2	8:1H:111:LYS:HA	1.73	0.41
10:2B:155:VAL:HG12	10:2B:157:ILE:HG13	2.01	0.41
14:2F:169:ILE:HG12	29:2U:123:ILE:HD11	2.02	0.41
24:2P:90:ARG:HH22	24:2P:96:LEU:HD13	1.84	0.41
46:2m:673:G:H2'	46:2m:674:C:C6	2.55	0.41
46:2m:1403:C:H42	46:2m:1436:C:H5''	1.85	0.41
48:2o:49:VAL:HB	48:2o:62:LEU:HD13	2.02	0.41
53:2t:64:ASN:N	53:2t:186:ASP:OD1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:2z:88:LYS:H	59:2z:95:TYR:HD1	1.68	0.41
1:1A:85:G:N2	1:1A:98:A:OP2	2.40	0.41
1:1A:1738:A:H2'	1:1A:1739:G:H8	1.86	0.41
1:1A:2395:A:N6	1:1A:2820:C:O2	2.54	0.41
1:1A:4238:G:H2'	1:1A:4239:A:H8	1.85	0.41
4:1D:96:LEU:HA	4:1D:102:LEU:HD21	2.02	0.41
8:1H:162:VAL:HG13	8:1H:177:GLY:N	2.34	0.41
9:2A:25:PHE:HB3	9:2A:26:ALA:H	1.73	0.41
17:2I:16:LEU:HD12	17:2I:80:PHE:HD1	1.86	0.41
24:2P:107:ASN:HB2	24:2P:111:GLU:HG3	2.03	0.41
29:2U:76:ASP:HB2	29:2U:115:GLY:HA3	2.02	0.41
46:2m:212:C:H2'	46:2m:213:G:H8	1.86	0.41
46:2m:1501:C:H2'	46:2m:1502:C:C6	2.56	0.41
46:2m:1777:G:H2'	46:2m:1778:C:O4'	2.20	0.41
48:2o:119:THR:HG22	48:2o:120:MET:H	1.84	0.41
67:3F:106:LYS:HG2	67:3F:107:ASP:H	1.86	0.41
69:3H:120:ASP:O	69:3H:125:THR:OG1	2.31	0.41
70:3I:136:ARG:HA	70:3I:141:VAL:HA	2.02	0.41
72:3K:5:HIS:HB3	72:3K:117:LEU:HD21	2.02	0.41
75:3N:22:GLN:HB3	75:3N:74:MET:HE3	2.03	0.41
81:zw:262:ASN:HA	81:zw:265:ASN:HD22	1.86	0.41
84:zz:284:U:H2'	84:zz:285:G:C8	2.56	0.41
1:1A:74:G:O2'	14:2F:71:ARG:NH2	2.53	0.41
1:1A:699:C:H2'	1:1A:700:G:C8	2.55	0.41
1:1A:1332:C:H2'	1:1A:1333:A:C8	2.55	0.41
1:1A:1350:C:H2'	1:1A:1351:G:H8	1.85	0.41
1:1A:1756:U:O2'	1:1A:1758:G:OP2	2.28	0.41
1:1A:2583:C:H2'	1:1A:2584:G:H8	1.86	0.41
1:1A:2768:C:H3'	1:1A:2769:U:H5'	2.02	0.41
1:1A:3621:A:O2'	1:1A:4658:G:O2'	2.30	0.41
1:1A:4769:G:O2'	1:1A:4771:C:N4	2.54	0.41
2:1B:12:U:OP2	2:1B:67:C:O2'	2.37	0.41
3:1C:142:U:OP1	16:2H:38:ARG:NH2	2.53	0.41
11:2C:88:PHE:HD1	11:2C:186:THR:HG22	1.85	0.41
15:2G:94:LYS:HE3	15:2G:94:LYS:HB2	1.85	0.41
17:2I:125:LYS:HG3	17:2I:129:LEU:HD12	2.01	0.41
19:2K:69:LYS:HB2	19:2K:139:LEU:HD21	2.02	0.41
24:2P:65:VAL:HG23	24:2P:73:ARG:HA	2.03	0.41
46:2m:941:C:H2'	46:2m:942:G:H8	1.84	0.41
46:2m:1299:A:H5'	56:2w:59:ARG:HH21	1.85	0.41
46:2m:1403:C:N4	46:2m:1437:C:OP2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:2p:41:VAL:HG23	49:2p:46:THR:HG22	2.02	0.41
50:2q:177:THR:HA	50:2q:195:ILE:HB	2.03	0.41
52:2s:31:GLU:HA	52:2s:36:LEU:HB2	2.03	0.41
57:2x:125:ARG:O	57:2x:126:ARG:NH2	2.43	0.41
59:2z:12:ILE:HD12	59:2z:13:LEU:HA	2.03	0.41
61:21:49:LYS:HG2	61:21:92:HIS:HD2	1.86	0.41
67:3F:114:SER:OG	67:3F:118:ARG:N	2.48	0.41
67:3F:154:VAL:HG12	67:3F:167:SER:HA	2.02	0.41
67:3F:242:SER:HB2	67:3F:247:TRP:HB2	2.03	0.41
76:3O:88:LEU:HB3	76:3O:109:TYR:HE2	1.86	0.41
1:1A:1333:A:H2'	1:1A:1334:A:C8	2.56	0.41
1:1A:1554:A:OP1	44:2j:5:THR:OG1	2.32	0.41
1:1A:1566:C:H2'	1:1A:1567:U:H6	1.86	0.41
1:1A:1864:G:OP1	12:2D:98:ARG:NH1	2.52	0.41
1:1A:1954:U:H2'	1:1A:1955:G:C8	2.56	0.41
1:1A:2307:A:H5'	33:2Y:102:ASN:HD22	1.84	0.41
1:1A:3633:C:H2'	1:1A:3634:G:C8	2.56	0.41
1:1A:3664:G:H2'	1:1A:3665:G:H8	1.85	0.41
1:1A:3796:U:H2'	1:1A:3797:C:H6	1.85	0.41
1:1A:4237:C:H2'	1:1A:4238:G:H8	1.85	0.41
1:1A:4580:U:O2'	5:1E:182:GLU:OE2	2.35	0.41
1:1A:4594:U:H2'	1:1A:4595:G:H8	1.85	0.41
28:2T:89:ILE:HA	28:2T:90:PRO:HD3	1.86	0.41
46:2m:1723:G:H2'	46:2m:1724:A:C8	2.55	0.41
47:2n:50:ASN:HD21	47:2n:53:ARG:HG3	1.85	0.41
63:3B:114:ASP:OD1	63:3B:114:ASP:N	2.54	0.41
81:zw:219:VAL:HG21	81:zw:249:LYS:HE2	2.03	0.41
1:1A:102:G:H2'	1:1A:103:G:H8	1.85	0.41
1:1A:1528:U:H2'	1:1A:1529:G:C8	2.56	0.41
1:1A:1579:C:H2'	1:1A:1580:C:H6	1.85	0.41
1:1A:1825:A:H2'	1:1A:1826:G:C8	2.56	0.41
1:1A:2449:A:H62	1:1A:2510:G:H21	1.69	0.41
1:1A:3658:C:H2'	1:1A:3659:G:H8	1.86	0.41
1:1A:3834:C:H2'	1:1A:3835:C:H6	1.85	0.41
1:1A:5054:C:H4'	1:1A:5055:G:H8	1.86	0.41
1:1A:5062:G:H2'	1:1A:5063:G:H8	1.84	0.41
3:1C:90:C:H2'	3:1C:91:A:H8	1.85	0.41
4:1D:80:GLU:HB3	4:1D:168:VAL:HG23	2.03	0.41
5:1E:20:LYS:O	5:1E:275:HIS:ND1	2.52	0.41
8:1H:234:ASP:OD1	8:1H:234:ASP:N	2.54	0.41
46:2m:444:G:N7	53:2t:47:ARG:NH1	2.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2m:640:A:H2'	46:2m:641:A:C8	2.56	0.41
46:2m:1033:G:N1	46:2m:1080:A:O2'	2.44	0.41
46:2m:1209:A:O2'	64:3C:85:ARG:NH2	2.48	0.41
47:2n:176:TRP:CD2	47:2n:199:PRO:HG3	2.55	0.41
62:3A:56:CYS:SG	62:3A:57:GLY:N	2.94	0.41
65:3D:14:VAL:HG12	65:3D:32:VAL:HG12	2.03	0.41
69:3H:55:GLY:O	69:3H:63:MET:HG2	2.20	0.41
81:zw:256:ILE:HD12	81:zw:259:GLY:HA2	2.03	0.41
81:zw:317:VAL:O	81:zw:414:ARG:NE	2.47	0.41
1:1A:93:G:H2'	1:1A:94:A:C8	2.56	0.41
1:1A:323:C:H2'	1:1A:324:A:C8	2.56	0.41
1:1A:443:G:H5''	34:2Z:54:LYS:HE3	2.03	0.41
1:1A:662:C:H2'	1:1A:663:G:C8	2.56	0.41
1:1A:948:C:H2'	1:1A:949:G:H8	1.86	0.41
1:1A:1281:G:H5'	6:1F:323:ARG:HB3	2.03	0.41
1:1A:3680:U:OP1	4:1D:54:ARG:NH2	2.54	0.41
1:1A:4631:G:N1	1:1A:4668:U:C2	2.84	0.41
1:1A:5041:G:N1	5:1E:389:MET:O	2.53	0.41
11:2C:59:LYS:HA	11:2C:59:LYS:HD2	1.86	0.41
13:2E:51:SER:HB2	13:2E:69:ALA:HB3	2.03	0.41
14:2F:134:PRO:HD2	14:2F:137:GLY:HA2	2.03	0.41
18:2J:42:ARG:HA	18:2J:45:THR:HG22	2.03	0.41
22:2N:89:ILE:HD12	22:2N:89:ILE:HG23	1.91	0.41
46:2m:434:G:H2'	46:2m:435:A:C8	2.56	0.41
46:2m:531:A:N6	46:2m:552:G:O6	2.54	0.41
46:2m:639:C:H2'	46:2m:640:A:C8	2.56	0.41
46:2m:1396:A:N7	46:2m:1449:G:O6	2.54	0.41
46:2m:1553:C:H4'	46:2m:1554:C:H5	1.86	0.41
46:2m:1619:A:H4'	56:2w:44:ARG:HE	1.85	0.41
46:2m:1744:G:O4'	46:2m:1790:A:N6	2.54	0.41
46:2m:1849:G:H1'	46:2m:1850:A:H5'	2.03	0.41
47:2n:203:PHE:HE2	58:2y:91:LEU:HD11	1.85	0.41
53:2t:165:GLN:HG3	53:2t:171:LEU:HD23	2.01	0.41
55:2v:128:VAL:HG12	55:2v:140:PHE:HB3	2.02	0.41
57:2x:23:ALA:HB2	57:2x:70:VAL:HG13	2.02	0.41
58:2y:104:GLU:HA	58:2y:107:LYS:HG3	2.03	0.41
63:3B:68:LYS:HE3	78:3Q:6:LEU:HB2	2.03	0.41
64:3C:21:ILE:HD12	64:3C:21:ILE:HA	1.95	0.41
70:3I:158:ASP:OD1	70:3I:159:PHE:N	2.54	0.41
71:3J:40:LYS:HD3	71:3J:42:LEU:HD12	2.01	0.41
84:zz:295:G:N2	84:zz:298:A:C2	2.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:66:A:N1	1:1A:311:G:O2'	2.54	0.41
1:1A:1543:G:OP1	1:1A:2514:G:O2'	2.38	0.41
1:1A:1548:G:O2'	1:1A:2812:A:N3	2.47	0.41
1:1A:1628:C:H2'	1:1A:1629:G:C8	2.56	0.41
2:1B:57:C:H2'	2:1B:58:A:C8	2.55	0.41
4:1D:116:LEU:HB2	4:1D:126:LEU:HB2	2.03	0.41
11:2C:48:LEU:HD22	11:2C:56:ARG:HB2	2.03	0.41
12:2D:71:CYS:SG	12:2D:72:ALA:N	2.94	0.41
16:2H:94:PHE:HE2	16:2H:96:ARG:HB2	1.85	0.41
16:2H:98:LEU:HD23	16:2H:128:LYS:HD3	2.02	0.41
46:2m:694:G:H8	46:2m:696:G:H1	1.69	0.41
46:2m:799:U:OP1	52:2s:113:LYS:NZ	2.39	0.41
46:2m:1003:U:H5''	48:2o:165:ARG:NH2	2.35	0.41
46:2m:1003:U:H5''	48:2o:165:ARG:HH22	1.86	0.41
46:2m:1650:A:H5''	57:2x:139:ALA:HB2	2.03	0.41
48:2o:147:ASN:ND2	84:zz:301:G:OP1	2.54	0.41
51:2r:22:LYS:HG3	51:2r:23:TRP:CG	2.56	0.41
59:2z:23:ARG:HA	59:2z:23:ARG:HD3	1.88	0.41
1:1A:197:A:N1	1:1A:225:G:O2'	2.41	0.40
1:1A:267:G:H2'	1:1A:268:G:C8	2.55	0.40
1:1A:710:G:H2'	1:1A:711:A:C8	2.56	0.40
1:1A:1269:G:O2'	1:1A:1440:U:O3'	2.31	0.40
1:1A:1866:U:OP1	12:2D:4:ARG:NH2	2.48	0.40
5:1E:189:THR:HG23	5:1E:192:GLU:H	1.86	0.40
6:1F:36:ILE:HG21	6:1F:122:TYR:HD2	1.86	0.40
20:2L:15:LEU:HD23	20:2L:52:ARG:HB2	2.03	0.40
21:2M:10:TYR:HD1	21:2M:66:GLN:HA	1.85	0.40
28:2T:73:LYS:HD2	28:2T:75:TYR:CZ	2.56	0.40
46:2m:674:C:H2'	46:2m:675:U:C6	2.56	0.40
46:2m:923:G:H2'	46:2m:924:G:C8	2.55	0.40
51:2r:86:LYS:O	51:2r:89:THR:OG1	2.31	0.40
67:3F:157:SER:OG	67:3F:162:ASN:O	2.35	0.40
84:zz:144:U:H2'	84:zz:145:G:C8	2.56	0.40
84:zz:262:U:H2'	84:zz:263:G:C8	2.56	0.40
1:1A:68:U:OP1	16:2H:178:HIS:ND1	2.46	0.40
1:1A:710:G:H2'	1:1A:711:A:H8	1.85	0.40
1:1A:928:C:H2'	1:1A:929:A:C8	2.56	0.40
1:1A:1743:A:N1	1:1A:1789:C:O2'	2.52	0.40
1:1A:2111:G:O6	1:1A:2251:G:O2'	2.39	0.40
1:1A:2547:G:H2'	1:1A:2548:C:C6	2.56	0.40
1:1A:2758:G:O2'	1:1A:2764:A:N3	2.46	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1A:3731:C:H2'	1:1A:3732:A:C8	2.57	0.40
1:1A:4894:A:N7	1:1A:4895:C:N4	2.68	0.40
1:1A:5014:A:H2	1:1A:5035:U:H3	1.68	0.40
6:1F:348:LYS:HA	6:1F:351:VAL:HG12	2.03	0.40
17:2I:81:TRP:HB2	17:2I:104:VAL:HG21	2.02	0.40
21:2M:25:PRO:HA	21:2M:26:PRO:HD3	1.88	0.40
26:2R:128:ILE:HG12	26:2R:134:LYS:HG2	2.03	0.40
44:2j:85:ARG:NH1	46:2m:939:U:O5'	2.51	0.40
46:2m:161:U:O2'	69:3H:87:ARG:NH2	2.40	0.40
46:2m:1093:A:H2	74:3M:12:LYS:HD2	1.86	0.40
46:2m:1236:G:H4'	81:zw:80:GLN:HG3	2.03	0.40
52:2s:100:ILE:HD11	52:2s:125:VAL:HG11	2.03	0.40
53:2t:199:LEU:HD23	53:2t:199:LEU:HA	1.96	0.40
62:3A:53:TYR:OH	62:3A:76:ASP:OD2	2.31	0.40
83:zy:34:G:H2'	83:zy:35:G:H8	1.86	0.40
1:1A:1616:U:H2'	1:1A:1617:G:H8	1.87	0.40
1:1A:4679:G:H2'	1:1A:4680:G:H8	1.86	0.40
1:1A:4876:U:H3	17:2I:116:LYS:NZ	2.20	0.40
4:1D:117:GLU:OE1	4:1D:121:GLY:N	2.53	0.40
5:1E:80:GLU:OE1	5:1E:323:TYR:OH	2.33	0.40
6:1F:209:ILE:HD13	6:1F:251:ILE:HB	2.02	0.40
7:1G:76:CYS:SG	7:1G:77:ALA:N	2.94	0.40
10:2B:176:LYS:HE2	37:2c:43:MET:HE1	2.03	0.40
33:2Y:26:ASP:OD1	33:2Y:26:ASP:N	2.48	0.40
46:2m:455:A:O2'	46:2m:1735:A:N3	2.51	0.40
46:2m:683:G:N1	46:2m:1022:U:OP2	2.39	0.40
46:2m:1263:U:H4'	66:3E:27:ARG:HG3	2.03	0.40
46:2m:1331:C:N4	81:zw:63:LYS:O	2.54	0.40
46:2m:1587:G:O2'	60:20:67:ARG:NH1	2.54	0.40
50:2q:204:SER:OG	50:2q:205:PHE:N	2.53	0.40
58:2y:99:ASP:OD1	58:2y:99:ASP:N	2.49	0.40
1:1A:75:G:H3'	14:2F:74:ARG:HD2	2.04	0.40
1:1A:691:C:H2'	1:1A:692:A:C8	2.56	0.40
1:1A:1759:G:O6	1:1A:1760:G:N2	2.54	0.40
1:1A:2520:C:H2'	1:1A:2521:G:C8	2.53	0.40
1:1A:3871:A:H2'	1:1A:3872:A:C8	2.57	0.40
1:1A:4146:G:H2'	1:1A:4147:G:H8	1.86	0.40
21:2M:51:LEU:HD13	22:2N:151:LEU:HB3	2.03	0.40
43:2i:66:ILE:HB	43:2i:85:ILE:HB	2.02	0.40
46:2m:820:U:H3	46:2m:828:G:H1	1.69	0.40
51:2r:73:THR:HG21	51:2r:90:VAL:HG22	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:3G:278:THR:HA	68:3G:279:ARG:HA	1.69	0.40
69:3H:18:VAL:HG11	69:3H:24:LEU:HD21	2.04	0.40
70:3I:33:GLY:HA3	78:3Q:38:TYR:CG	2.57	0.40
1:1A:662:C:H2'	1:1A:663:G:H8	1.87	0.40
1:1A:921:C:H2'	1:1A:922:C:C6	2.57	0.40
1:1A:1978:C:C4	1:1A:1979:A:H1'	2.56	0.40
1:1A:2306:G:O2'	1:1A:2330:G:O6	2.39	0.40
1:1A:2763:U:H2'	1:1A:2764:A:C8	2.57	0.40
1:1A:4586:G:OP2	17:2I:74:ARG:NH1	2.34	0.40
6:1F:289:LEU:HB2	45:2k:4:HIS:CE1	2.57	0.40
10:2B:69:ILE:HD13	10:2B:69:ILE:HG21	1.93	0.40
11:2C:37:ASP:OD1	11:2C:39:ASN:ND2	2.54	0.40
11:2C:42:ASN:HD21	17:2I:131:PRO:HB2	1.86	0.40
27:2S:80:ILE:HD13	27:2S:80:ILE:HG21	1.91	0.40
34:2Z:45:LYS:HA	34:2Z:107:PRO:HD2	2.03	0.40
46:2m:306:C:H5''	46:2m:307:G:C6	2.57	0.40
46:2m:1282:A:N6	46:2m:1287:A:O2'	2.54	0.40
54:2u:86:PRO:HA	54:2u:87:PRO:HD3	1.93	0.40
79:3R:126:CYS:HA	79:3R:143:LYS:HD2	2.04	0.40
81:zw:265:ASN:HA	81:zw:268:ILE:HD12	2.03	0.40
84:zz:307:G:C6	84:zz:329:U:O2	2.74	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	
4	1D	246/257 (96%)	224 (91%)	21 (8%)	1 (0%)	30	64
5	1E	400/403 (99%)	371 (93%)	27 (7%)	2 (0%)	24	59
6	1F	366/427 (86%)	347 (95%)	18 (5%)	1 (0%)	36	69
7	1G	291/297 (98%)	277 (95%)	12 (4%)	2 (1%)	18	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	1H	233/288 (81%)	206 (88%)	25 (11%)	2 (1%)	14	47
9	2A	223/248 (90%)	208 (93%)	15 (7%)	0	100	100
10	2B	239/266 (90%)	219 (92%)	19 (8%)	1 (0%)	30	64
11	2C	188/192 (98%)	169 (90%)	15 (8%)	4 (2%)	5	31
12	2D	211/214 (99%)	187 (89%)	23 (11%)	1 (0%)	24	59
13	2E	174/178 (98%)	162 (93%)	12 (7%)	0	100	100
14	2F	208/211 (99%)	194 (93%)	11 (5%)	3 (1%)	9	38
15	2G	137/215 (64%)	127 (93%)	10 (7%)	0	100	100
16	2H	201/204 (98%)	194 (96%)	7 (4%)	0	100	100
17	2I	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
18	2J	151/184 (82%)	141 (93%)	10 (7%)	0	100	100
19	2K	185/188 (98%)	178 (96%)	7 (4%)	0	100	100
20	2L	185/196 (94%)	180 (97%)	5 (3%)	0	100	100
21	2M	173/176 (98%)	159 (92%)	12 (7%)	2 (1%)	10	41
22	2N	157/160 (98%)	144 (92%)	9 (6%)	4 (2%)	4	29
23	2O	99/128 (77%)	93 (94%)	6 (6%)	0	100	100
24	2P	129/140 (92%)	118 (92%)	8 (6%)	3 (2%)	5	30
25	2Q	122/157 (78%)	115 (94%)	5 (4%)	2 (2%)	7	36
26	2R	115/156 (74%)	105 (91%)	9 (8%)	1 (1%)	14	47
27	2S	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
28	2T	133/136 (98%)	126 (95%)	5 (4%)	2 (2%)	8	37
29	2U	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
30	2V	105/159 (66%)	97 (92%)	8 (8%)	0	100	100
31	2W	96/115 (84%)	94 (98%)	2 (2%)	0	100	100
32	2X	105/125 (84%)	100 (95%)	5 (5%)	0	100	100
33	2Y	126/135 (93%)	119 (94%)	7 (6%)	0	100	100
34	2Z	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
35	2a	109/117 (93%)	108 (99%)	1 (1%)	0	100	100
36	2b	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
37	2c	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
38	2d	84/97 (87%)	77 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	2e	67/70 (96%)	60 (90%)	7 (10%)	0	100	100
40	2f	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	2g	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
42	2h	22/25 (88%)	22 (100%)	0	0	100	100
43	2i	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
44	2j	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
45	2k	123/137 (90%)	115 (94%)	8 (6%)	0	100	100
47	2n	219/295 (74%)	201 (92%)	16 (7%)	2 (1%)	14	47
48	2o	212/264 (80%)	194 (92%)	17 (8%)	1 (0%)	24	59
49	2p	225/243 (93%)	206 (92%)	18 (8%)	1 (0%)	30	64
50	2q	260/263 (99%)	235 (90%)	24 (9%)	1 (0%)	30	64
51	2r	185/204 (91%)	168 (91%)	15 (8%)	2 (1%)	11	43
52	2s	187/194 (96%)	177 (95%)	10 (5%)	0	100	100
53	2t	204/208 (98%)	189 (93%)	15 (7%)	0	100	100
54	2u	96/165 (58%)	82 (85%)	13 (14%)	1 (1%)	12	45
55	2v	151/158 (96%)	140 (93%)	11 (7%)	0	100	100
56	2w	95/145 (66%)	78 (82%)	16 (17%)	1 (1%)	11	43
57	2x	144/146 (99%)	134 (93%)	9 (6%)	1 (1%)	18	53
58	2y	130/135 (96%)	116 (89%)	13 (10%)	1 (1%)	16	50
59	2z	148/152 (97%)	132 (89%)	14 (10%)	2 (1%)	9	38
60	20	141/145 (97%)	130 (92%)	8 (6%)	3 (2%)	5	31
61	21	102/119 (86%)	95 (93%)	7 (7%)	0	100	100
62	3A	81/83 (98%)	69 (85%)	11 (14%)	1 (1%)	10	41
63	3B	139/143 (97%)	126 (91%)	7 (5%)	6 (4%)	2	20
64	3C	105/115 (91%)	98 (93%)	7 (7%)	0	100	100
65	3D	62/69 (90%)	54 (87%)	8 (13%)	0	100	100
66	3E	51/56 (91%)	51 (100%)	0	0	100	100
67	3F	311/317 (98%)	266 (86%)	44 (14%)	1 (0%)	36	69
68	3G	220/293 (75%)	210 (96%)	9 (4%)	1 (0%)	24	59
69	3H	235/249 (94%)	213 (91%)	22 (9%)	0	100	100
70	3I	183/194 (94%)	166 (91%)	14 (8%)	3 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	3J	120/132 (91%)	108 (90%)	10 (8%)	2 (2%)	7	35
72	3K	148/151 (98%)	137 (93%)	10 (7%)	1 (1%)	18	53
73	3L	138/151 (91%)	124 (90%)	14 (10%)	0	100	100
74	3M	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
75	3N	129/133 (97%)	125 (97%)	4 (3%)	0	100	100
76	3O	73/125 (58%)	64 (88%)	9 (12%)	0	100	100
77	3P	81/84 (96%)	71 (88%)	7 (9%)	3 (4%)	2	22
78	3Q	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
79	3R	65/156 (42%)	55 (85%)	10 (15%)	0	100	100
81	zw	429/431 (100%)	389 (91%)	40 (9%)	0	100	100
82	zx	15/17 (88%)	14 (93%)	1 (7%)	0	100	100
All	All	11763/13136 (90%)	10869 (92%)	829 (7%)	65 (1%)	23	55

All (65) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1E	393	LYS
8	1H	111	LYS
11	2C	61	TRP
14	2F	5	ARG
22	2N	81	LYS
24	2P	110	GLY
28	2T	30	ASP
48	2o	78	GLU
51	2r	39	ILE
59	2z	17	ASN
62	3A	81	LYS
63	3B	108	LYS
63	3B	126	ALA
70	3I	8	VAL
71	3J	113	ASP
4	1D	124	GLY
7	1G	59	ASP
11	2C	116	ASN
28	2T	31	ASP
47	2n	12	GLU
51	2r	80	GLY
56	2w	100	LYS

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Mol	Chain	Res	Type
60	20	41	LYS
63	3B	88	ASP
63	3B	109	GLY
63	3B	127	ASN
68	3G	78	LEU
70	3I	9	CYS
6	1F	111	TRP
8	1H	127	SER
11	2C	60	TRP
22	2N	82	GLY
22	2N	129	LYS
24	2P	109	LYS
26	2R	42	THR
58	2y	110	ASP
60	20	40	ALA
67	3F	283	PRO
70	3I	7	TRP
71	3J	112	LYS
72	3K	4	MET
77	3P	19	HIS
14	2F	54	PRO
21	2M	156	HIS
49	2p	197	LYS
54	2u	91	PRO
63	3B	10	ALA
77	3P	20	LYS
5	1E	294	LYS
10	2B	106	THR
25	2Q	99	GLU
24	2P	49	LEU
50	2q	90	ILE
59	2z	145	THR
60	20	42	HIS
77	3P	39	GLY
7	1G	125	VAL
47	2n	159	ILE
12	2D	15	LYS
21	2M	155	PRO
22	2N	135	PRO
11	2C	105	ILE
14	2F	62	PRO
57	2x	42	ILE

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Mol	Chain	Res	Type
25	2Q	98	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	1D	190/199 (96%)	190 (100%)	0	100	100
5	1E	348/349 (100%)	345 (99%)	3 (1%)	70	75
6	1F	306/348 (88%)	306 (100%)	0	100	100
7	1G	246/250 (98%)	246 (100%)	0	100	100
8	1H	210/252 (83%)	209 (100%)	1 (0%)	81	82
9	2A	194/215 (90%)	194 (100%)	0	100	100
10	2B	203/223 (91%)	203 (100%)	0	100	100
11	2C	169/171 (99%)	167 (99%)	2 (1%)	63	72
12	2D	180/181 (99%)	178 (99%)	2 (1%)	65	74
13	2E	148/149 (99%)	147 (99%)	1 (1%)	76	78
14	2F	176/177 (99%)	176 (100%)	0	100	100
15	2G	118/161 (73%)	116 (98%)	2 (2%)	53	68
16	2H	171/172 (99%)	171 (100%)	0	100	100
17	2I	173/174 (99%)	173 (100%)	0	100	100
18	2J	134/163 (82%)	134 (100%)	0	100	100
19	2K	164/165 (99%)	164 (100%)	0	100	100
20	2L	166/175 (95%)	166 (100%)	0	100	100
21	2M	156/157 (99%)	155 (99%)	1 (1%)	78	80
22	2N	139/140 (99%)	138 (99%)	1 (1%)	76	78
23	2O	91/115 (79%)	91 (100%)	0	100	100
24	2P	101/107 (94%)	101 (100%)	0	100	100
25	2Q	103/126 (82%)	103 (100%)	0	100	100
26	2R	107/133 (80%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	2S	124/135 (92%)	123 (99%)	1 (1%)	73	77
28	2T	117/118 (99%)	117 (100%)	0	100	100
29	2U	120/121 (99%)	120 (100%)	0	100	100
30	2V	88/126 (70%)	88 (100%)	0	100	100
31	2W	83/97 (86%)	83 (100%)	0	100	100
32	2X	98/110 (89%)	98 (100%)	0	100	100
33	2Y	114/121 (94%)	114 (100%)	0	100	100
34	2Z	88/89 (99%)	88 (100%)	0	100	100
35	2a	97/100 (97%)	96 (99%)	1 (1%)	68	75
36	2b	109/110 (99%)	109 (100%)	0	100	100
37	2c	86/89 (97%)	86 (100%)	0	100	100
38	2d	73/80 (91%)	73 (100%)	0	100	100
39	2e	64/65 (98%)	63 (98%)	1 (2%)	55	69
40	2f	47/48 (98%)	47 (100%)	0	100	100
41	2g	48/116 (41%)	48 (100%)	0	100	100
42	2h	23/24 (96%)	23 (100%)	0	100	100
43	2i	93/94 (99%)	93 (100%)	0	100	100
44	2j	74/75 (99%)	74 (100%)	0	100	100
45	2k	109/121 (90%)	108 (99%)	1 (1%)	70	75
47	2n	183/243 (75%)	181 (99%)	2 (1%)	65	74
48	2o	195/231 (84%)	191 (98%)	4 (2%)	47	65
49	2p	190/202 (94%)	189 (100%)	1 (0%)	81	82
50	2q	224/225 (100%)	222 (99%)	2 (1%)	70	75
51	2r	157/170 (92%)	156 (99%)	1 (1%)	78	80
52	2s	169/174 (97%)	169 (100%)	0	100	100
53	2t	178/180 (99%)	178 (100%)	0	100	100
54	2u	89/136 (65%)	89 (100%)	0	100	100
55	2v	137/142 (96%)	136 (99%)	1 (1%)	76	78
56	2w	87/130 (67%)	87 (100%)	0	100	100
57	2x	121/121 (100%)	121 (100%)	0	100	100
58	2y	120/122 (98%)	120 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	2z	130/132 (98%)	129 (99%)	1 (1%)	73	77
60	20	113/115 (98%)	113 (100%)	0	100	100
61	21	94/107 (88%)	94 (100%)	0	100	100
62	3A	67/67 (100%)	67 (100%)	0	100	100
63	3B	113/115 (98%)	113 (100%)	0	100	100
64	3C	90/98 (92%)	90 (100%)	0	100	100
65	3D	57/62 (92%)	57 (100%)	0	100	100
66	3E	47/49 (96%)	47 (100%)	0	100	100
67	3F	272/275 (99%)	269 (99%)	3 (1%)	65	74
68	3G	188/225 (84%)	188 (100%)	0	100	100
69	3H	207/218 (95%)	207 (100%)	0	100	100
70	3I	161/168 (96%)	161 (100%)	0	100	100
71	3J	104/108 (96%)	104 (100%)	0	100	100
72	3K	130/131 (99%)	130 (100%)	0	100	100
73	3L	110/119 (92%)	110 (100%)	0	100	100
74	3M	112/113 (99%)	111 (99%)	1 (1%)	70	75
75	3N	113/115 (98%)	113 (100%)	0	100	100
76	3O	66/103 (64%)	66 (100%)	0	100	100
77	3P	75/76 (99%)	75 (100%)	0	100	100
78	3Q	47/48 (98%)	47 (100%)	0	100	100
79	3R	60/140 (43%)	60 (100%)	0	100	100
81	zw	371/371 (100%)	369 (100%)	2 (0%)	81	82
82	zx	16/16 (100%)	16 (100%)	0	100	100
All	All	10241/11188 (92%)	10206 (100%)	35 (0%)	84	85

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	1E	72	VAL
5	1E	89	ILE
5	1E	363	ILE
8	1H	152	ILE
11	2C	145	ILE
11	2C	176	LEU

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Mol	Chain	Res	Type
12	2D	60	LEU
12	2D	129	VAL
13	2E	15	LEU
15	2G	61	ILE
15	2G	122	ILE
21	2M	124	ILE
22	2N	93	ILE
27	2S	99	ILE
35	2a	15	THR
39	2e	60	LEU
45	2k	44	ILE
47	2n	8	LEU
47	2n	112	ILE
48	2o	79	VAL
48	2o	171	ILE
48	2o	207	LEU
48	2o	215	VAL
49	2p	217	ILE
50	2q	114	ILE
50	2q	248	ILE
51	2r	28	VAL
55	2v	77	VAL
59	2z	12	ILE
67	3F	11	LEU
67	3F	108	VAL
67	3F	258	ILE
74	3M	52	ILE
81	zw	101	VAL
81	zw	281	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (134) such sidechains are listed below:

Mol	Chain	Res	Type
4	1D	50	HIS
4	1D	218	HIS
5	1E	42	HIS
5	1E	167	GLN
5	1E	245	HIS
5	1E	301	ASN
5	1E	376	HIS
6	1F	41	HIS
6	1F	50	GLN

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Mol	Chain	Res	Type
6	1F	245	HIS
7	1G	195	HIS
7	1G	203	ASN
7	1G	222	GLN
7	1G	282	GLN
8	1H	101	ASN
9	2A	39	GLN
9	2A	119	ASN
10	2B	38	ASN
10	2B	100	HIS
10	2B	227	ASN
10	2B	240	ASN
11	2C	42	ASN
12	2D	112	GLN
14	2F	15	HIS
14	2F	149	GLN
15	2G	34	ASN
15	2G	48	GLN
15	2G	70	GLN
16	2H	8	GLN
16	2H	57	GLN
16	2H	91	GLN
16	2H	156	HIS
16	2H	181	HIS
17	2I	42	ASN
18	2J	80	GLN
18	2J	145	HIS
19	2K	7	HIS
21	2M	66	GLN
21	2M	77	ASN
21	2M	91	HIS
21	2M	146	HIS
21	2M	163	HIS
25	2Q	30	GLN
25	2Q	120	GLN
26	2R	73	HIS
27	2S	14	ASN
27	2S	24	HIS
27	2S	96	HIS
27	2S	127	GLN
28	2T	40	HIS
29	2U	14	HIS

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Mol	Chain	Res	Type
29	2U	17	HIS
29	2U	60	HIS
30	2V	6	ASN
30	2V	7	HIS
30	2V	61	ASN
31	2W	72	HIS
32	2X	34	HIS
33	2Y	80	HIS
34	2Z	20	ASN
34	2Z	56	ASN
34	2Z	99	HIS
36	2b	20	GLN
40	2f	33	ASN
40	2f	43	HIS
45	2k	4	HIS
45	2k	6	GLN
45	2k	45	HIS
47	2n	9	GLN
47	2n	113	GLN
48	2o	179	ASN
48	2o	186	ASN
49	2p	56	GLN
49	2p	74	GLN
51	2r	95	HIS
51	2r	110	GLN
51	2r	114	ASN
52	2s	91	HIS
53	2t	99	ASN
53	2t	146	GLN
53	2t	165	GLN
54	2u	32	HIS
55	2v	83	GLN
56	2w	32	GLN
57	2x	11	GLN
57	2x	86	GLN
58	2y	29	HIS
58	2y	83	ASN
58	2y	118	GLN
59	2z	85	ASN
59	2z	120	HIS
60	20	10	ASN
60	20	11	GLN

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Mol	Chain	Res	Type
60	20	128	GLN
61	21	18	HIS
61	21	92	HIS
62	3A	29	HIS
63	3B	20	GLN
63	3B	61	GLN
64	3C	17	HIS
64	3C	72	HIS
66	3E	4	GLN
66	3E	10	HIS
67	3F	20	GLN
67	3F	117	ASN
68	3G	136	HIS
68	3G	267	GLN
69	3H	177	GLN
70	3I	124	HIS
70	3I	140	GLN
71	3J	19	GLN
71	3J	28	HIS
71	3J	72	HIS
71	3J	82	ASN
71	3J	99	ASN
71	3J	119	GLN
72	3K	62	GLN
73	3L	43	HIS
73	3L	103	ASN
74	3M	91	ASN
74	3M	113	HIS
76	3O	64	ASN
76	3O	89	GLN
76	3O	112	ASN
77	3P	83	GLN
81	zw	67	ASN
81	zw	132	HIS
81	zw	162	GLN
81	zw	199	HIS
81	zw	211	GLN
81	zw	247	GLN
81	zw	265	ASN
81	zw	282	GLN
81	zw	350	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1A	3654/5070 (72%)	1053 (28%)	27 (0%)
2	1B	119/121 (98%)	23 (19%)	0
3	1C	155/157 (98%)	38 (24%)	3 (1%)
46	2m	1714/1869 (91%)	621 (36%)	0
80	zv	11/12 (91%)	4 (36%)	0
83	zy	74/75 (98%)	18 (24%)	0
84	zz	161/290 (55%)	72 (44%)	0
All	All	5888/7594 (77%)	1829 (31%)	30 (0%)

All (1829) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1A	3	C
1	1A	17	A
1	1A	18	C
1	1A	23	C
1	1A	25	A
1	1A	26	C
1	1A	30	C
1	1A	35	U
1	1A	36	U
1	1A	39	A
1	1A	42	A
1	1A	47	A
1	1A	48	G
1	1A	59	A
1	1A	64	A
1	1A	65	A
1	1A	66	A
1	1A	68	U
1	1A	70	A
1	1A	72	C
1	1A	73	A
1	1A	74	G
1	1A	84	A
1	1A	88	A
1	1A	90	G
1	1A	91	G
1	1A	98	A
1	1A	108	A
1	1A	109	G

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Mol	Chain	Res	Type
1	1A	117	C
1	1A	119	G
1	1A	120	A
1	1A	121	A
1	1A	122	U
1	1A	127	G
1	1A	128	C
1	1A	133	C
1	1A	134	G
1	1A	136	C
1	1A	143	C
1	1A	149	A
1	1A	159	C
1	1A	170	C
1	1A	171	U
1	1A	173	C
1	1A	179	G
1	1A	180	C
1	1A	181	C
1	1A	183	C
1	1A	184	U
1	1A	185	C
1	1A	186	G
1	1A	188	G
1	1A	189	G
1	1A	195	C
1	1A	200	U
1	1A	208	A
1	1A	209	U
1	1A	217	C
1	1A	218	A
1	1A	219	G
1	1A	220	C
1	1A	227	A
1	1A	229	G
1	1A	234	G
1	1A	246	G
1	1A	250	C
1	1A	255	C
1	1A	256	G
1	1A	265	C
1	1A	266	C

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Mol	Chain	Res	Type
1	1A	274	C
1	1A	275	C
1	1A	277	G
1	1A	278	G
1	1A	280	G
1	1A	295	A
1	1A	296	A
1	1A	297	U
1	1A	306	A
1	1A	315	G
1	1A	316	U
1	1A	326	C
1	1A	340	C
1	1A	346	G
1	1A	360	A
1	1A	363	A
1	1A	364	G
1	1A	383	A
1	1A	384	A
1	1A	387	G
1	1A	388	A
1	1A	395	A
1	1A	396	A
1	1A	399	G
1	1A	406	C
1	1A	407	A
1	1A	409	G
1	1A	410	A
1	1A	412	G
1	1A	413	G
1	1A	415	G
1	1A	418	A
1	1A	438	G
1	1A	440	U
1	1A	446	C
1	1A	449	C
1	1A	450	G
1	1A	452	A
1	1A	453	G
1	1A	454	U
1	1A	456	C
1	1A	457	G

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Mol	Chain	Res	Type
1	1A	464	G
1	1A	465	G
1	1A	467	U
1	1A	484	U
1	1A	485	C
1	1A	486	C
1	1A	489	C
1	1A	493	G
1	1A	494	U
1	1A	496	G
1	1A	497	G
1	1A	498	C
1	1A	500	G
1	1A	501	C
1	1A	502	C
1	1A	503	C
1	1A	504	G
1	1A	505	G
1	1A	506	C
1	1A	509	A
1	1A	510	U
1	1A	512	U
1	1A	513	U
1	1A	514	U
1	1A	516	C
1	1A	517	C
1	1A	518	G
1	1A	643	C
1	1A	644	G
1	1A	646	G
1	1A	653	U
1	1A	654	C
1	1A	656	C
1	1A	657	C
1	1A	659	G
1	1A	665	C
1	1A	666	G
1	1A	667	A
1	1A	668	C
1	1A	670	G
1	1A	673	C
1	1A	674	G

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Mol	Chain	Res	Type
1	1A	675	C
1	1A	685	C
1	1A	686	A
1	1A	687	U
1	1A	696	C
1	1A	697	G
1	1A	700	G
1	1A	703	G
1	1A	704	C
1	1A	708	G
1	1A	719	C
1	1A	731	G
1	1A	738	C
1	1A	739	G
1	1A	747	A
1	1A	753	C
1	1A	757	G
1	1A	758	G
1	1A	760	G
1	1A	904	C
1	1A	905	C
1	1A	910	G
1	1A	912	G
1	1A	913	U
1	1A	914	U
1	1A	915	A
1	1A	916	C
1	1A	917	A
1	1A	918	G
1	1A	923	C
1	1A	924	C
1	1A	925	C
1	1A	926	G
1	1A	932	A
1	1A	933	G
1	1A	934	C
1	1A	935	A
1	1A	936	C
1	1A	941	C
1	1A	943	A
1	1A	944	A
1	1A	945	U

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Mol	Chain	Res	Type
1	1A	946	C
1	1A	959	G
1	1A	960	A
1	1A	961	G
1	1A	962	C
1	1A	965	G
1	1A	966	A
1	1A	967	C
1	1A	968	C
1	1A	970	G
1	1A	971	U
1	1A	982	U
1	1A	983	C
1	1A	984	C
1	1A	989	U
1	1A	990	C
1	1A	991	C
1	1A	992	C
1	1A	993	G
1	1A	995	C
1	1A	1048	G
1	1A	1051	G
1	1A	1070	G
1	1A	1071	C
1	1A	1072	C
1	1A	1074	G
1	1A	1075	G
1	1A	1082	C
1	1A	1083	U
1	1A	1089	G
1	1A	1092	G
1	1A	1095	A
1	1A	1096	C
1	1A	1099	C
1	1A	1168	G
1	1A	1171	G
1	1A	1173	G
1	1A	1178	G
1	1A	1179	U
1	1A	1180	C
1	1A	1181	C
1	1A	1182	C

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Mol	Chain	Res	Type
1	1A	1183	C
1	1A	1184	A
1	1A	1187	G
1	1A	1191	C
1	1A	1192	C
1	1A	1196	G
1	1A	1198	G
1	1A	1200	G
1	1A	1202	C
1	1A	1203	G
1	1A	1210	C
1	1A	1211	G
1	1A	1214	C
1	1A	1215	C
1	1A	1216	C
1	1A	1217	G
1	1A	1218	G
1	1A	1219	G
1	1A	1220	G
1	1A	1222	A
1	1A	1239	C
1	1A	1241	C
1	1A	1243	C
1	1A	1253	G
1	1A	1254	A
1	1A	1255	A
1	1A	1260	G
1	1A	1261	G
1	1A	1262	G
1	1A	1265	G
1	1A	1266	G
1	1A	1269	G
1	1A	1270	A
1	1A	1271	G
1	1A	1272	C
1	1A	1273	G
1	1A	1274	A
1	1A	1275	G
1	1A	1277	G
1	1A	1279	A
1	1A	1280	C
1	1A	1284	G

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Mol	Chain	Res	Type
1	1A	1287	G
1	1A	1293	G
1	1A	1294	A
1	1A	1295	C
1	1A	1296	G
1	1A	1301	C
1	1A	1303	A
1	1A	1314	C
1	1A	1320	U
1	1A	1322	A
1	1A	1323	A
1	1A	1326	A
1	1A	1338	G
1	1A	1344	C
1	1A	1354	A
1	1A	1358	G
1	1A	1359	G
1	1A	1365	C
1	1A	1372	A
1	1A	1377	G
1	1A	1378	C
1	1A	1379	C
1	1A	1381	U
1	1A	1387	A
1	1A	1391	A
1	1A	1394	G
1	1A	1397	A
1	1A	1398	A
1	1A	1399	G
1	1A	1402	C
1	1A	1404	G
1	1A	1405	C
1	1A	1407	C
1	1A	1409	C
1	1A	1410	U
1	1A	1411	C
1	1A	1416	G
1	1A	1417	C
1	1A	1420	A
1	1A	1425	G
1	1A	1435	G
1	1A	1438	U

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Mol	Chain	Res	Type
1	1A	1439	C
1	1A	1440	U
1	1A	1441	C
1	1A	1443	A
1	1A	1444	G
1	1A	1445	U
1	1A	1446	C
1	1A	1447	C
1	1A	1457	G
1	1A	1472	C
1	1A	1482	G
1	1A	1483	C
1	1A	1497	A
1	1A	1498	G
1	1A	1518	A
1	1A	1523	A
1	1A	1525	A
1	1A	1534	A
1	1A	1547	A
1	1A	1549	G
1	1A	1564	A
1	1A	1566	C
1	1A	1574	G
1	1A	1578	U
1	1A	1582	U
1	1A	1591	U
1	1A	1596	U
1	1A	1609	U
1	1A	1614	C
1	1A	1624	G
1	1A	1625	G
1	1A	1631	A
1	1A	1633	G
1	1A	1634	A
1	1A	1638	A
1	1A	1641	G
1	1A	1649	U
1	1A	1650	A
1	1A	1654	G
1	1A	1658	G
1	1A	1660	U
1	1A	1661	C

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Mol	Chain	Res	Type
1	1A	1676	C
1	1A	1677	U
1	1A	1678	C
1	1A	1681	G
1	1A	1697	G
1	1A	1699	A
1	1A	1700	G
1	1A	1701	A
1	1A	1703	C
1	1A	1704	C
1	1A	1705	G
1	1A	1707	C
1	1A	1715	C
1	1A	1719	A
1	1A	1724	G
1	1A	1734	G
1	1A	1740	C
1	1A	1741	G
1	1A	1742	A
1	1A	1745	G
1	1A	1746	A
1	1A	1749	A
1	1A	1750	G
1	1A	1755	C
1	1A	1757	U
1	1A	1758	G
1	1A	1760	G
1	1A	1761	G
1	1A	1762	C
1	1A	1763	C
1	1A	1764	G
1	1A	1765	A
1	1A	1766	A
1	1A	1768	C
1	1A	1769	G
1	1A	1770	A
1	1A	1772	C
1	1A	1775	A
1	1A	1787	A
1	1A	1803	G
1	1A	1804	A
1	1A	1806	G

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Mol	Chain	Res	Type
1	1A	1810	G
1	1A	1821	G
1	1A	1822	U
1	1A	1823	G
1	1A	1836	G
1	1A	1837	A
1	1A	1842	G
1	1A	1843	A
1	1A	1852	U
1	1A	1855	G
1	1A	1866	U
1	1A	1869	G
1	1A	1881	C
1	1A	1889	U
1	1A	1893	C
1	1A	1897	A
1	1A	1898	C
1	1A	1918	U
1	1A	1919	G
1	1A	1920	C
1	1A	1921	C
1	1A	1922	G
1	1A	1925	G
1	1A	1931	C
1	1A	1932	A
1	1A	1935	C
1	1A	1936	C
1	1A	1939	A
1	1A	1945	G
1	1A	1948	G
1	1A	1959	U
1	1A	1960	A
1	1A	1961	G
1	1A	1962	A
1	1A	1965	G
1	1A	1966	C
1	1A	1967	A
1	1A	1968	G
1	1A	1969	G
1	1A	1970	A
1	1A	1973	G
1	1A	1974	U

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Mol	Chain	Res	Type
1	1A	1975	G
1	1A	1976	G
1	1A	1977	C
1	1A	1978	C
1	1A	1979	A
1	1A	1980	U
1	1A	1981	G
1	1A	1982	G
1	1A	1983	A
1	1A	1984	A
1	1A	1985	G
1	1A	1987	C
1	1A	1988	G
1	1A	1989	G
1	1A	1991	A
1	1A	1993	C
1	1A	1994	C
1	1A	1995	G
1	1A	1996	C
1	1A	1997	U
1	1A	1998	A
1	1A	1999	A
1	1A	2001	G
1	1A	2002	A
1	1A	2003	G
1	1A	2004	U
1	1A	2005	G
1	1A	2006	U
1	1A	2007	G
1	1A	2009	A
1	1A	2010	A
1	1A	2011	C
1	1A	2012	A
1	1A	2013	A
1	1A	2015	U
1	1A	2016	C
1	1A	2018	C
1	1A	2019	C
1	1A	2020	U
1	1A	2021	G
1	1A	2025	A
1	1A	2026	A

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Mol	Chain	Res	Type
1	1A	2033	A
1	1A	2034	G
1	1A	2038	U
1	1A	2040	A
1	1A	2043	A
1	1A	2046	G
1	1A	2048	U
1	1A	2052	G
1	1A	2054	U
1	1A	2055	G
1	1A	2056	G
1	1A	2062	C
1	1A	2069	A
1	1A	2084	C
1	1A	2085	G
1	1A	2089	G
1	1A	2090	U
1	1A	2091	C
1	1A	2093	A
1	1A	2094	G
1	1A	2095	A
1	1A	2096	G
1	1A	2097	U
1	1A	2098	G
1	1A	2101	C
1	1A	2102	G
1	1A	2106	G
1	1A	2107	C
1	1A	2108	G
1	1A	2111	G
1	1A	2112	G
1	1A	2252	G
1	1A	2253	A
1	1A	2255	C
1	1A	2256	C
1	1A	2259	G
1	1A	2260	C
1	1A	2262	G
1	1A	2266	C
1	1A	2268	A
1	1A	2287	G
1	1A	2289	C

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Mol	Chain	Res	Type
1	1A	2300	A
1	1A	2301	G
1	1A	2306	G
1	1A	2307	A
1	1A	2313	A
1	1A	2316	G
1	1A	2327	G
1	1A	2328	G
1	1A	2331	G
1	1A	2333	G
1	1A	2335	C
1	1A	2337	C
1	1A	2345	G
1	1A	2346	C
1	1A	2347	A
1	1A	2348	G
1	1A	2349	A
1	1A	2350	U
1	1A	2351	C
1	1A	2353	U
1	1A	2360	A
1	1A	2370	A
1	1A	2379	A
1	1A	2390	G
1	1A	2391	G
1	1A	2394	G
1	1A	2398	U
1	1A	2402	G
1	1A	2409	U
1	1A	2412	A
1	1A	2413	U
1	1A	2417	A
1	1A	2421	G
1	1A	2426	U
1	1A	2434	G
1	1A	2441	C
1	1A	2444	U
1	1A	2450	G
1	1A	2463	G
1	1A	2465	C
1	1A	2470	C
1	1A	2471	G

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Mol	Chain	Res	Type
1	1A	2474	G
1	1A	2475	G
1	1A	2476	G
1	1A	2478	C
1	1A	2483	G
1	1A	2485	U
1	1A	2488	C
1	1A	2489	C
1	1A	2490	U
1	1A	2491	C
1	1A	2494	U
1	1A	2495	U
1	1A	2496	G
1	1A	2498	C
1	1A	2499	C
1	1A	2503	G
1	1A	2504	C
1	1A	2505	C
1	1A	2506	G
1	1A	2507	A
1	1A	2511	A
1	1A	2513	A
1	1A	2514	G
1	1A	2529	A
1	1A	2537	A
1	1A	2543	A
1	1A	2544	G
1	1A	2546	G
1	1A	2547	G
1	1A	2553	A
1	1A	2554	U
1	1A	2556	G
1	1A	2563	C
1	1A	2567	G
1	1A	2569	G
1	1A	2572	C
1	1A	2573	A
1	1A	2575	U
1	1A	2576	G
1	1A	2583	C
1	1A	2587	A
1	1A	2588	C

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Mol	Chain	Res	Type
1	1A	2589	C
1	1A	2600	A
1	1A	2601	A
1	1A	2602	G
1	1A	2604	C
1	1A	2607	C
1	1A	2618	G
1	1A	2627	C
1	1A	2637	U
1	1A	2643	G
1	1A	2645	G
1	1A	2653	C
1	1A	2662	G
1	1A	2670	C
1	1A	2673	G
1	1A	2675	G
1	1A	2681	G
1	1A	2682	G
1	1A	2686	G
1	1A	2687	U
1	1A	2695	A
1	1A	2696	A
1	1A	2699	C
1	1A	2703	G
1	1A	2707	U
1	1A	2708	U
1	1A	2710	C
1	1A	2711	G
1	1A	2712	G
1	1A	2714	G
1	1A	2721	G
1	1A	2724	G
1	1A	2726	G
1	1A	2727	C
1	1A	2739	C
1	1A	2743	A
1	1A	2744	A
1	1A	2756	G
1	1A	2761	U
1	1A	2762	G
1	1A	2763	U
1	1A	2767	U

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Mol	Chain	Res	Type
1	1A	2768	C
1	1A	2769	U
1	1A	2770	C
1	1A	2772	C
1	1A	2776	G
1	1A	2787	A
1	1A	2788	U
1	1A	2789	A
1	1A	2793	G
1	1A	2794	C
1	1A	2795	A
1	1A	2796	G
1	1A	2797	C
1	1A	2798	A
1	1A	2826	U
1	1A	2827	G
1	1A	2833	A
1	1A	2838	G
1	1A	2842	G
1	1A	2855	G
1	1A	2856	C
1	1A	2860	C
1	1A	2872	C
1	1A	2875	C
1	1A	2876	G
1	1A	2899	C
1	1A	2902	G
1	1A	2903	G
1	1A	2905	C
1	1A	2906	G
1	1A	2907	G
1	1A	2908	U
1	1A	3585	G
1	1A	3591	C
1	1A	3592	G
1	1A	3593	C
1	1A	3595	U
1	1A	3596	A
1	1A	3597	G
1	1A	3600	G
1	1A	3602	C
1	1A	3605	C

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Mol	Chain	Res	Type
1	1A	3615	G
1	1A	3616	U
1	1A	3619	G
1	1A	3620	G
1	1A	3626	G
1	1A	3630	A
1	1A	3635	A
1	1A	3637	U
1	1A	3643	A
1	1A	3644	U
1	1A	3646	A
1	1A	3653	A
1	1A	3662	A
1	1A	3664	G
1	1A	3670	C
1	1A	3671	G
1	1A	3672	G
1	1A	3673	C
1	1A	3678	G
1	1A	3680	U
1	1A	3682	A
1	1A	3690	U
1	1A	3692	A
1	1A	3696	C
1	1A	3709	U
1	1A	3711	A
1	1A	3712	A
1	1A	3713	U
1	1A	3724	A
1	1A	3727	A
1	1A	3729	U
1	1A	3733	A
1	1A	3735	G
1	1A	3743	G
1	1A	3748	A
1	1A	3750	G
1	1A	3753	G
1	1A	3756	A
1	1A	3757	G
1	1A	3758	U
1	1A	3760	A
1	1A	3761	C

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Mol	Chain	Res	Type
1	1A	3765	G
1	1A	3766	A
1	1A	3767	C
1	1A	3768	U
1	1A	3769	C
1	1A	3770	U
1	1A	3773	U
1	1A	3774	A
1	1A	3775	A
1	1A	3776	G
1	1A	3777	G
1	1A	3784	A
1	1A	3785	A
1	1A	3786	U
1	1A	3803	A
1	1A	3811	G
1	1A	3812	C
1	1A	3813	A
1	1A	3814	U
1	1A	3817	A
1	1A	3818	U
1	1A	3819	G
1	1A	3822	U
1	1A	3828	A
1	1A	3839	G
1	1A	3840	U
1	1A	3867	A
1	1A	3869	C
1	1A	3877	A
1	1A	3878	C
1	1A	3879	G
1	1A	3885	G
1	1A	3889	G
1	1A	3890	A
1	1A	3892	U
1	1A	3901	A
1	1A	3902	A
1	1A	3906	A
1	1A	3907	G
1	1A	3908	A
1	1A	3909	C
1	1A	3915	U

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Mol	Chain	Res	Type
1	1A	3923	A
1	1A	3929	G
1	1A	3937	C
1	1A	3938	G
1	1A	3939	G
1	1A	3943	A
1	1A	3947	A
1	1A	3948	C
1	1A	3949	A
1	1A	3950	U
1	1A	3951	G
1	1A	3952	A
1	1A	4061	G
1	1A	4062	A
1	1A	4066	U
1	1A	4076	G
1	1A	4082	G
1	1A	4084	G
1	1A	4085	A
1	1A	4086	G
1	1A	4088	C
1	1A	4101	C
1	1A	4104	G
1	1A	4105	A
1	1A	4106	G
1	1A	4107	G
1	1A	4108	G
1	1A	4110	C
1	1A	4111	U
1	1A	4112	C
1	1A	4113	U
1	1A	4114	C
1	1A	4115	G
1	1A	4116	C
1	1A	4117	U
1	1A	4119	C
1	1A	4120	U
1	1A	4121	G
1	1A	4122	G
1	1A	4127	A
1	1A	4135	G
1	1A	4138	C

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Mol	Chain	Res	Type
1	1A	4140	C
1	1A	4141	G
1	1A	4142	C
1	1A	4143	G
1	1A	4144	C
1	1A	4145	C
1	1A	4162	C
1	1A	4163	U
1	1A	4170	A
1	1A	4173	G
1	1A	4183	G
1	1A	4188	U
1	1A	4191	G
1	1A	4194	U
1	1A	4195	G
1	1A	4196	G
1	1A	4197	G
1	1A	4203	A
1	1A	4204	C
1	1A	4205	A
1	1A	4212	A
1	1A	4214	A
1	1A	4222	G
1	1A	4229	U
1	1A	4233	A
1	1A	4235	G
1	1A	4244	A
1	1A	4250	G
1	1A	4251	A
1	1A	4253	A
1	1A	4254	G
1	1A	4256	A
1	1A	4265	U
1	1A	4273	A
1	1A	4280	A
1	1A	4286	C
1	1A	4288	C
1	1A	4291	G
1	1A	4302	U
1	1A	4303	C
1	1A	4305	G
1	1A	4306	U

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Mol	Chain	Res	Type
1	1A	4314	C
1	1A	4317	A
1	1A	4326	G
1	1A	4328	G
1	1A	4330	G
1	1A	4332	C
1	1A	4337	C
1	1A	4338	G
1	1A	4339	A
1	1A	4342	C
1	1A	4349	C
1	1A	4350	C
1	1A	4376	A
1	1A	4377	G
1	1A	4378	A
1	1A	4380	A
1	1A	4381	A
1	1A	4382	G
1	1A	4383	U
1	1A	4387	C
1	1A	4391	G
1	1A	4393	G
1	1A	4394	A
1	1A	4395	U
1	1A	4396	A
1	1A	4398	C
1	1A	4420	U
1	1A	4422	A
1	1A	4440	G
1	1A	4442	U
1	1A	4448	G
1	1A	4449	A
1	1A	4450	U
1	1A	4453	C
1	1A	4459	U
1	1A	4464	A
1	1A	4465	U
1	1A	4466	C
1	1A	4476	C
1	1A	4477	A
1	1A	4479	A
1	1A	4495	G

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Mol	Chain	Res	Type
1	1A	4500	U
1	1A	4510	A
1	1A	4512	U
1	1A	4513	A
1	1A	4518	A
1	1A	4519	C
1	1A	4523	A
1	1A	4524	G
1	1A	4528	G
1	1A	4531	U
1	1A	4532	U
1	1A	4537	C
1	1A	4548	A
1	1A	4549	G
1	1A	4555	U
1	1A	4556	U
1	1A	4560	C
1	1A	4565	C
1	1A	4567	G
1	1A	4573	G
1	1A	4574	U
1	1A	4575	G
1	1A	4581	G
1	1A	4583	C
1	1A	4589	A
1	1A	4590	A
1	1A	4591	U
1	1A	4600	G
1	1A	4601	U
1	1A	4617	G
1	1A	4624	A
1	1A	4633	G
1	1A	4636	U
1	1A	4637	G
1	1A	4639	G
1	1A	4646	U
1	1A	4648	A
1	1A	4652	G
1	1A	4670	C
1	1A	4694	G
1	1A	4695	C
1	1A	4707	A

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Mol	Chain	Res	Type
1	1A	4708	A
1	1A	4709	U
1	1A	4720	C
1	1A	4730	C
1	1A	4731	G
1	1A	4732	G
1	1A	4733	C
1	1A	4740	G
1	1A	4741	C
1	1A	4743	G
1	1A	4749	C
1	1A	4750	G
1	1A	4753	U
1	1A	4756	C
1	1A	4757	C
1	1A	4758	U
1	1A	4760	G
1	1A	4763	U
1	1A	4764	A
1	1A	4770	U
1	1A	4771	C
1	1A	4772	C
1	1A	4773	C
1	1A	4775	C
1	1A	4776	G
1	1A	4860	G
1	1A	4861	G
1	1A	4862	G
1	1A	4863	G
1	1A	4865	C
1	1A	4869	U
1	1A	4871	C
1	1A	4872	G
1	1A	4873	G
1	1A	4874	A
1	1A	4875	G
1	1A	4876	U
1	1A	4877	G
1	1A	4878	C
1	1A	4882	U
1	1A	4883	C
1	1A	4884	G

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Mol	Chain	Res	Type
1	1A	4887	C
1	1A	4888	U
1	1A	4890	G
1	1A	4894	A
1	1A	4895	C
1	1A	4897	G
1	1A	4899	G
1	1A	4900	C
1	1A	4901	G
1	1A	4910	G
1	1A	4911	A
1	1A	4912	G
1	1A	4913	G
1	1A	4914	C
1	1A	4925	U
1	1A	4926	C
1	1A	4927	G
1	1A	4928	C
1	1A	4932	U
1	1A	4934	A
1	1A	4937	C
1	1A	4940	C
1	1A	4941	G
1	1A	4943	A
1	1A	4944	C
1	1A	4949	G
1	1A	4950	U
1	1A	4951	G
1	1A	4960	G
1	1A	4963	G
1	1A	4966	A
1	1A	4975	G
1	1A	4976	U
1	1A	4977	A
1	1A	4979	A
1	1A	4985	U
1	1A	4988	U
1	1A	4989	U
1	1A	4991	U
1	1A	5004	C
1	1A	5014	A
1	1A	5016	A

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Mol	Chain	Res	Type
1	1A	5017	G
1	1A	5022	U
1	1A	5023	C
1	1A	5024	C
1	1A	5025	C
1	1A	5027	C
1	1A	5028	G
1	1A	5031	G
1	1A	5034	A
1	1A	5040	U
1	1A	5041	G
1	1A	5047	C
1	1A	5050	C
1	1A	5055	G
1	1A	5061	A
1	1A	5069	U
2	1B	7	G
2	1B	13	A
2	1B	22	A
2	1B	23	A
2	1B	25	G
2	1B	27	G
2	1B	29	C
2	1B	31	G
2	1B	33	U
2	1B	34	C
2	1B	35	U
2	1B	40	U
2	1B	47	G
2	1B	49	A
2	1B	53	U
2	1B	54	A
2	1B	63	C
2	1B	64	G
2	1B	74	A
2	1B	97	G
2	1B	100	A
2	1B	103	A
2	1B	120	U
3	1C	13	G
3	1C	23	C
3	1C	25	G

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Mol	Chain	Res	Type
3	1C	34	U
3	1C	35	C
3	1C	39	G
3	1C	52	A
3	1C	59	A
3	1C	63	U
3	1C	74	U
3	1C	79	G
3	1C	82	A
3	1C	83	C
3	1C	84	A
3	1C	86	U
3	1C	87	G
3	1C	88	A
3	1C	103	A
3	1C	104	A
3	1C	105	C
3	1C	107	C
3	1C	110	U
3	1C	111	U
3	1C	112	G
3	1C	113	C
3	1C	114	G
3	1C	123	U
3	1C	124	U
3	1C	125	C
3	1C	126	C
3	1C	127	U
3	1C	129	C
3	1C	150	C
3	1C	151	G
3	1C	153	C
3	1C	154	G
3	1C	155	C
3	1C	156	U
46	2m	2	A
46	2m	5	U
46	2m	8	U
46	2m	10	G
46	2m	17	C
46	2m	25	A
46	2m	33	G

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Mol	Chain	Res	Type
46	2m	37	C
46	2m	41	G
46	2m	44	U
46	2m	45	A
46	2m	46	A
46	2m	56	G
46	2m	59	U
46	2m	60	A
46	2m	61	A
46	2m	62	G
46	2m	64	A
46	2m	65	C
46	2m	67	C
46	2m	68	A
46	2m	69	C
46	2m	70	G
46	2m	72	C
46	2m	73	C
46	2m	74	G
46	2m	75	G
46	2m	76	U
46	2m	77	A
46	2m	78	C
46	2m	79	A
46	2m	80	G
46	2m	81	U
46	2m	99	A
46	2m	100	U
46	2m	103	A
46	2m	110	U
46	2m	112	U
46	2m	113	G
46	2m	115	U
46	2m	122	G
46	2m	126	G
46	2m	127	C
46	2m	140	C
46	2m	141	A
46	2m	143	U
46	2m	148	U
46	2m	153	G
46	2m	154	U

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Mol	Chain	Res	Type
46	2m	155	G
46	2m	159	A
46	2m	160	U
46	2m	161	U
46	2m	162	C
46	2m	167	G
46	2m	168	C
46	2m	175	A
46	2m	179	C
46	2m	180	G
46	2m	183	G
46	2m	184	G
46	2m	194	C
46	2m	198	U
46	2m	199	C
46	2m	201	C
46	2m	202	G
46	2m	206	G
46	2m	208	G
46	2m	214	U
46	2m	215	G
46	2m	216	C
46	2m	291	G
46	2m	292	A
46	2m	293	C
46	2m	294	U
46	2m	295	C
46	2m	304	C
46	2m	305	U
46	2m	306	C
46	2m	307	G
46	2m	308	G
46	2m	309	G
46	2m	312	G
46	2m	313	A
46	2m	314	U
46	2m	315	C
46	2m	316	G
46	2m	320	G
46	2m	321	C
46	2m	323	C
46	2m	324	C

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Mol	Chain	Res	Type
46	2m	325	C
46	2m	326	C
46	2m	327	G
46	2m	328	U
46	2m	329	G
46	2m	330	G
46	2m	331	C
46	2m	338	G
46	2m	339	A
46	2m	340	C
46	2m	351	G
46	2m	362	C
46	2m	364	A
46	2m	368	U
46	2m	369	C
46	2m	370	G
46	2m	376	A
46	2m	384	U
46	2m	385	G
46	2m	386	C
46	2m	398	A
46	2m	399	C
46	2m	400	C
46	2m	404	G
46	2m	407	G
46	2m	408	A
46	2m	409	C
46	2m	413	G
46	2m	417	C
46	2m	418	A
46	2m	419	G
46	2m	421	G
46	2m	435	A
46	2m	448	A
46	2m	450	C
46	2m	452	G
46	2m	455	A
46	2m	462	C
46	2m	463	C
46	2m	464	A
46	2m	465	A
46	2m	466	G

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Mol	Chain	Res	Type
46	2m	472	C
46	2m	473	A
46	2m	474	G
46	2m	482	G
46	2m	487	U
46	2m	488	U
46	2m	489	A
46	2m	492	C
46	2m	495	U
46	2m	496	C
46	2m	500	A
46	2m	502	C
46	2m	503	C
46	2m	504	G
46	2m	509	G
46	2m	518	G
46	2m	525	A
46	2m	526	A
46	2m	530	U
46	2m	532	C
46	2m	533	A
46	2m	534	G
46	2m	537	C
46	2m	538	U
46	2m	539	C
46	2m	540	U
46	2m	542	U
46	2m	543	C
46	2m	544	G
46	2m	545	A
46	2m	553	U
46	2m	556	U
46	2m	557	U
46	2m	559	G
46	2m	561	A
46	2m	562	U
46	2m	563	G
46	2m	566	U
46	2m	570	C
46	2m	575	A
46	2m	579	C
46	2m	580	U

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Mol	Chain	Res	Type
46	2m	582	C
46	2m	583	C
46	2m	584	G
46	2m	589	G
46	2m	590	A
46	2m	591	U
46	2m	592	C
46	2m	593	C
46	2m	595	U
46	2m	596	U
46	2m	604	A
46	2m	605	A
46	2m	606	G
46	2m	610	G
46	2m	612	U
46	2m	613	G
46	2m	614	C
46	2m	615	C
46	2m	617	G
46	2m	621	C
46	2m	623	G
46	2m	627	U
46	2m	628	A
46	2m	630	U
46	2m	631	U
46	2m	643	A
46	2m	644	G
46	2m	645	C
46	2m	649	U
46	2m	656	G
46	2m	660	C
46	2m	666	U
46	2m	668	A
46	2m	669	A
46	2m	671	A
46	2m	672	A
46	2m	673	G
46	2m	682	U
46	2m	688	U
46	2m	689	U
46	2m	690	G
46	2m	692	G

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Mol	Chain	Res	Type
46	2m	694	G
46	2m	695	C
46	2m	696	G
46	2m	697	G
46	2m	698	G
46	2m	732	U
46	2m	734	C
46	2m	735	C
46	2m	736	C
46	2m	738	C
46	2m	739	C
46	2m	745	C
46	2m	747	U
46	2m	748	C
46	2m	749	U
46	2m	751	G
46	2m	752	G
46	2m	753	C
46	2m	787	G
46	2m	788	G
46	2m	789	G
46	2m	790	C
46	2m	791	C
46	2m	795	A
46	2m	796	G
46	2m	798	A
46	2m	799	U
46	2m	810	A
46	2m	811	A
46	2m	812	A
46	2m	813	A
46	2m	818	A
46	2m	819	G
46	2m	821	G
46	2m	830	A
46	2m	834	C
46	2m	836	G
46	2m	837	A
46	2m	838	G
46	2m	839	C
46	2m	840	C
46	2m	842	C

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Mol	Chain	Res	Type
46	2m	847	A
46	2m	848	U
46	2m	850	C
46	2m	851	C
46	2m	865	A
46	2m	869	A
46	2m	870	A
46	2m	871	U
46	2m	872	A
46	2m	873	G
46	2m	875	A
46	2m	876	C
46	2m	877	C
46	2m	879	C
46	2m	881	G
46	2m	883	U
46	2m	884	C
46	2m	885	U
46	2m	888	U
46	2m	889	U
46	2m	890	U
46	2m	891	G
46	2m	892	U
46	2m	893	U
46	2m	894	G
46	2m	895	G
46	2m	896	U
46	2m	897	U
46	2m	898	U
46	2m	899	U
46	2m	900	C
46	2m	901	G
46	2m	905	C
46	2m	906	U
46	2m	907	G
46	2m	908	A
46	2m	913	A
46	2m	917	U
46	2m	920	A
46	2m	922	A
46	2m	933	G
46	2m	934	G

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Mol	Chain	Res	Type
46	2m	950	C
46	2m	954	U
46	2m	958	G
46	2m	962	A
46	2m	963	A
46	2m	970	G
46	2m	971	G
46	2m	972	A
46	2m	974	C
46	2m	978	G
46	2m	983	A
46	2m	990	A
46	2m	992	A
46	2m	997	A
46	2m	999	G
46	2m	1001	A
46	2m	1008	A
46	2m	1017	U
46	2m	1023	A
46	2m	1025	U
46	2m	1027	A
46	2m	1028	A
46	2m	1030	A
46	2m	1043	G
46	2m	1045	U
46	2m	1059	G
46	2m	1060	A
46	2m	1061	U
46	2m	1062	A
46	2m	1073	U
46	2m	1076	G
46	2m	1082	A
46	2m	1083	A
46	2m	1084	A
46	2m	1085	C
46	2m	1087	A
46	2m	1089	G
46	2m	1093	A
46	2m	1098	C
46	2m	1100	A
46	2m	1109	C
46	2m	1110	G

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Mol	Chain	Res	Type
46	2m	1112	U
46	2m	1114	U
46	2m	1115	U
46	2m	1116	C
46	2m	1118	C
46	2m	1119	A
46	2m	1120	U
46	2m	1121	G
46	2m	1131	G
46	2m	1133	A
46	2m	1139	C
46	2m	1148	A
46	2m	1149	A
46	2m	1150	A
46	2m	1153	C
46	2m	1154	U
46	2m	1155	U
46	2m	1156	U
46	2m	1157	G
46	2m	1158	G
46	2m	1168	G
46	2m	1170	A
46	2m	1174	U
46	2m	1183	A
46	2m	1188	A
46	2m	1195	A
46	2m	1207	G
46	2m	1208	A
46	2m	1210	G
46	2m	1212	G
46	2m	1215	C
46	2m	1217	A
46	2m	1221	G
46	2m	1229	G
46	2m	1241	A
46	2m	1242	U
46	2m	1243	U
46	2m	1251	A
46	2m	1253	A
46	2m	1256	G
46	2m	1257	G
46	2m	1259	A

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Mol	Chain	Res	Type
46	2m	1261	C
46	2m	1264	C
46	2m	1265	A
46	2m	1269	G
46	2m	1270	G
46	2m	1271	C
46	2m	1272	C
46	2m	1273	C
46	2m	1274	G
46	2m	1275	G
46	2m	1276	A
46	2m	1277	C
46	2m	1280	G
46	2m	1281	G
46	2m	1282	A
46	2m	1283	C
46	2m	1284	A
46	2m	1288	U
46	2m	1289	U
46	2m	1290	G
46	2m	1292	C
46	2m	1293	A
46	2m	1294	G
46	2m	1298	G
46	2m	1299	A
46	2m	1300	U
46	2m	1301	A
46	2m	1302	G
46	2m	1303	C
46	2m	1305	C
46	2m	1306	U
46	2m	1307	U
46	2m	1310	U
46	2m	1311	C
46	2m	1313	A
46	2m	1314	U
46	2m	1315	U
46	2m	1316	C
46	2m	1317	C
46	2m	1318	G
46	2m	1321	G
46	2m	1326	U

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Mol	Chain	Res	Type
46	2m	1330	G
46	2m	1332	A
46	2m	1333	U
46	2m	1342	U
46	2m	1345	G
46	2m	1354	G
46	2m	1363	C
46	2m	1364	U
46	2m	1371	U
46	2m	1372	U
46	2m	1373	C
46	2m	1378	A
46	2m	1395	C
46	2m	1396	A
46	2m	1397	U
46	2m	1398	G
46	2m	1401	A
46	2m	1404	U
46	2m	1405	A
46	2m	1406	G
46	2m	1407	U
46	2m	1410	C
46	2m	1412	C
46	2m	1413	G
46	2m	1414	A
46	2m	1415	C
46	2m	1416	C
46	2m	1417	C
46	2m	1418	C
46	2m	1419	C
46	2m	1420	G
46	2m	1421	A
46	2m	1422	G
46	2m	1423	C
46	2m	1425	G
46	2m	1426	U
46	2m	1427	C
46	2m	1428	G
46	2m	1431	G
46	2m	1432	U
46	2m	1436	C
46	2m	1437	C

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Mol	Chain	Res	Type
46	2m	1438	A
46	2m	1439	A
46	2m	1449	G
46	2m	1450	G
46	2m	1454	A
46	2m	1455	A
46	2m	1456	G
46	2m	1461	G
46	2m	1462	U
46	2m	1463	U
46	2m	1464	C
46	2m	1473	G
46	2m	1475	G
46	2m	1476	A
46	2m	1477	U
46	2m	1478	U
46	2m	1486	A
46	2m	1488	C
46	2m	1489	A
46	2m	1490	G
46	2m	1494	U
46	2m	1497	G
46	2m	1498	A
46	2m	1508	A
46	2m	1509	U
46	2m	1510	G
46	2m	1511	U
46	2m	1512	C
46	2m	1515	G
46	2m	1520	G
46	2m	1521	C
46	2m	1523	C
46	2m	1524	G
46	2m	1526	G
46	2m	1527	C
46	2m	1530	U
46	2m	1531	A
46	2m	1533	A
46	2m	1534	C
46	2m	1535	U
46	2m	1536	G
46	2m	1543	U

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Mol	Chain	Res	Type
46	2m	1545	A
46	2m	1546	G
46	2m	1547	C
46	2m	1548	G
46	2m	1551	U
46	2m	1552	G
46	2m	1553	C
46	2m	1554	C
46	2m	1555	U
46	2m	1556	A
46	2m	1560	U
46	2m	1561	A
46	2m	1564	C
46	2m	1565	C
46	2m	1567	G
46	2m	1570	G
46	2m	1575	G
46	2m	1578	U
46	2m	1580	A
46	2m	1582	C
46	2m	1584	G
46	2m	1585	U
46	2m	1586	U
46	2m	1587	G
46	2m	1588	A
46	2m	1589	A
46	2m	1595	U
46	2m	1596	U
46	2m	1597	C
46	2m	1598	G
46	2m	1599	U
46	2m	1601	A
46	2m	1602	U
46	2m	1608	U
46	2m	1609	C
46	2m	1613	G
46	2m	1615	U
46	2m	1618	C
46	2m	1621	U
46	2m	1622	U
46	2m	1623	A
46	2m	1624	U

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Mol	Chain	Res	Type
46	2m	1626	C
46	2m	1627	C
46	2m	1634	A
46	2m	1639	G
46	2m	1640	A
46	2m	1643	U
46	2m	1644	C
46	2m	1646	C
46	2m	1648	G
46	2m	1654	G
46	2m	1661	A
46	2m	1663	A
46	2m	1664	A
46	2m	1665	G
46	2m	1671	G
46	2m	1674	G
46	2m	1693	G
46	2m	1698	C
46	2m	1699	A
46	2m	1702	G
46	2m	1703	C
46	2m	1719	A
46	2m	1720	U
46	2m	1721	U
46	2m	1722	G
46	2m	1726	G
46	2m	1729	U
46	2m	1742	C
46	2m	1744	G
46	2m	1748	G
46	2m	1751	C
46	2m	1753	C
46	2m	1755	C
46	2m	1758	G
46	2m	1759	G
46	2m	1772	C
46	2m	1773	C
46	2m	1776	G
46	2m	1780	G
46	2m	1781	A
46	2m	1783	C
46	2m	1784	G

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Mol	Chain	Res	Type
46	2m	1786	U
46	2m	1800	A
46	2m	1805	G
46	2m	1813	A
46	2m	1814	G
46	2m	1819	A
46	2m	1822	A
46	2m	1826	G
46	2m	1827	U
46	2m	1834	A
46	2m	1835	A
46	2m	1838	U
46	2m	1839	U
46	2m	1840	U
46	2m	1849	G
46	2m	1850	A
46	2m	1851	A
46	2m	1852	C
46	2m	1854	U
46	2m	1861	G
46	2m	1862	G
46	2m	1863	A
46	2m	1865	C
46	2m	1866	A
46	2m	1868	U
46	2m	1869	A
80	zv	0	G
80	zv	2	C
80	zv	4	U
80	zv	8	U
83	zy	2	G
83	zy	6	G
83	zy	7	U
83	zy	8	U
83	zy	9	G
83	zy	13	U
83	zy	14	A
83	zy	16	G
83	zy	17	G
83	zy	18	G
83	zy	19	U
83	zy	49	C

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Mol	Chain	Res	Type
83	zy	52	G
83	zy	53	U
83	zy	56	A
83	zy	73	C
83	zy	74	C
83	zy	75	A
84	zz	124	C
84	zz	131	G
84	zz	136	A
84	zz	137	G
84	zz	139	C
84	zz	141	U
84	zz	142	A
84	zz	153	G
84	zz	154	A
84	zz	157	C
84	zz	159	G
84	zz	160	U
84	zz	161	G
84	zz	162	A
84	zz	163	G
84	zz	164	U
84	zz	166	C
84	zz	169	C
84	zz	172	A
84	zz	174	U
84	zz	175	U
84	zz	176	G
84	zz	177	C
84	zz	228	U
84	zz	229	G
84	zz	231	G
84	zz	232	C
84	zz	234	U
84	zz	235	G
84	zz	236	C
84	zz	237	C
84	zz	242	C
84	zz	243	G
84	zz	244	A
84	zz	245	G
84	zz	246	A

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Mol	Chain	Res	Type
84	zz	247	C
84	zz	251	U
84	zz	252	A
84	zz	253	G
84	zz	254	C
84	zz	257	A
84	zz	258	G
84	zz	259	U
84	zz	265	U
84	zz	266	G
84	zz	269	U
84	zz	270	C
84	zz	271	G
84	zz	273	G
84	zz	274	A
84	zz	280	C
84	zz	281	U
84	zz	282	U
84	zz	284	U
84	zz	288	A
84	zz	290	U
84	zz	291	G
84	zz	295	G
84	zz	296	A
84	zz	297	U
84	zz	303	G
84	zz	306	U
84	zz	308	C
84	zz	310	A
84	zz	311	G
84	zz	312	U
84	zz	321	A
84	zz	322	G
84	zz	324	U
84	zz	325	C
84	zz	328	G

All (30) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1A	179	G
1	1A	218	A

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Mol	Chain	Res	Type
1	1A	406	C
1	1A	417	G
1	1A	504	G
1	1A	914	U
1	1A	1082	C
1	1A	2019	C
1	1A	2033	A
1	1A	2443	G
1	1A	2695	A
1	1A	2760	G
1	1A	2775	C
1	1A	2854	G
1	1A	3614	G
1	1A	3767	C
1	1A	3773	U
1	1A	3810	C
1	1A	3888	G
1	1A	3908	A
1	1A	4452	U
1	1A	4547	C
1	1A	4600	G
1	1A	4730	C
1	1A	4731	G
1	1A	4913	G
1	1A	4949	G
3	1C	85	U
3	1C	86	U
3	1C	87	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](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

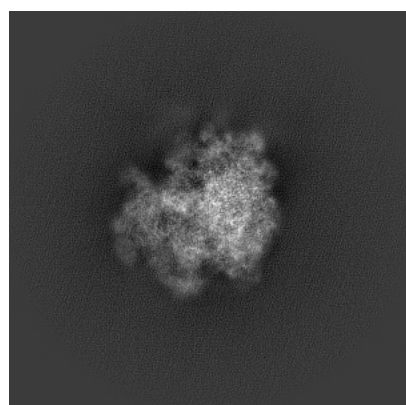
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9703. These allow visual inspection of the internal detail of the map and identification of artifacts.

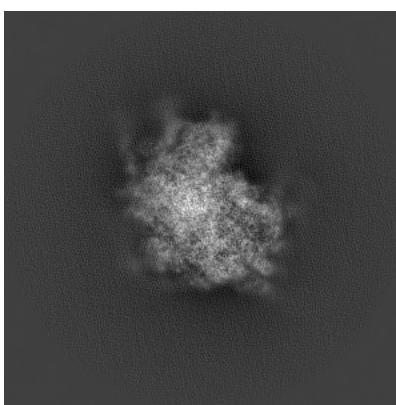
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

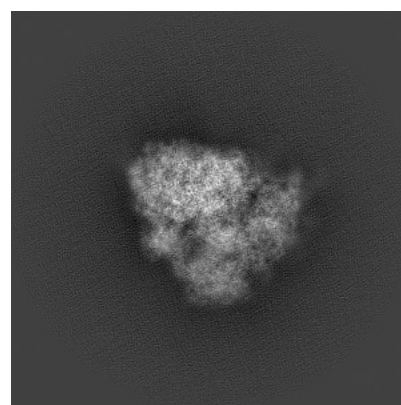
6.1.1 Primary map



X



Y

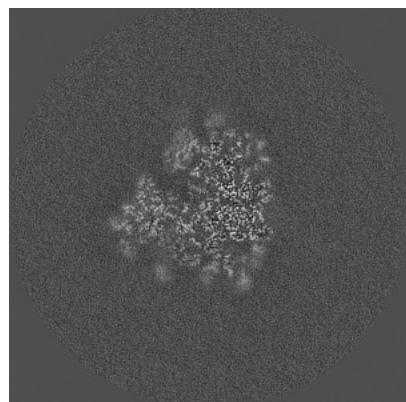


Z

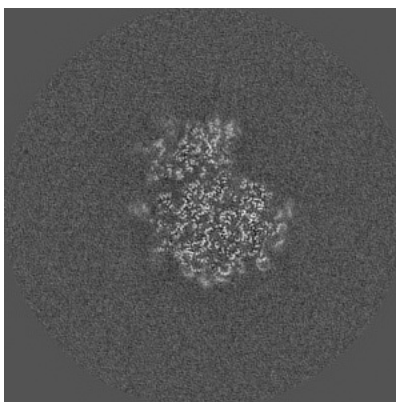
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

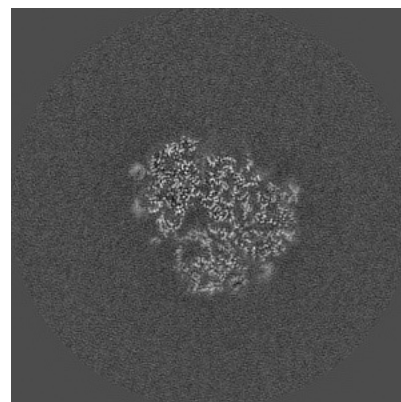
6.2.1 Primary map



X Index: 210



Y Index: 210

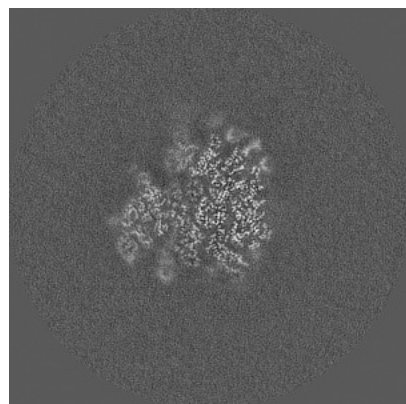


Z Index: 210

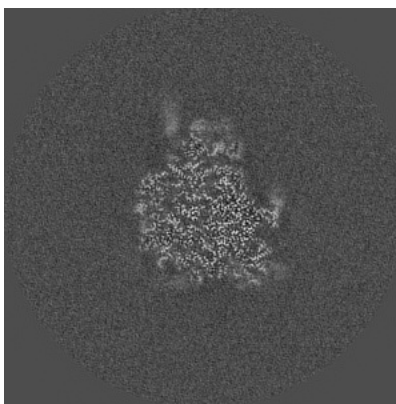
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

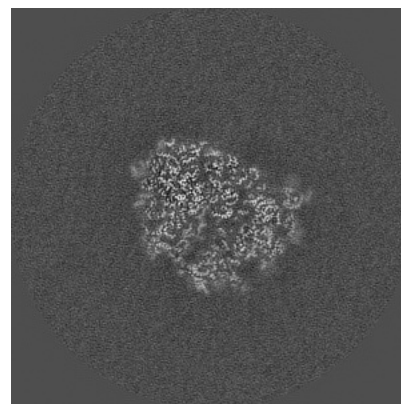
6.3.1 Primary map



X Index: 215



Y Index: 232

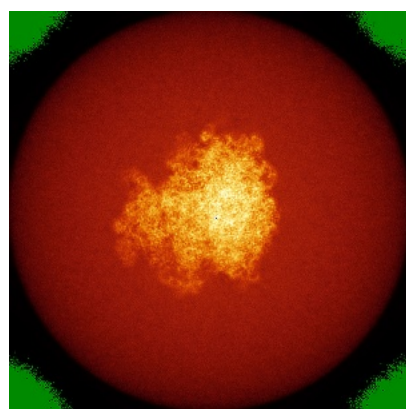


Z Index: 217

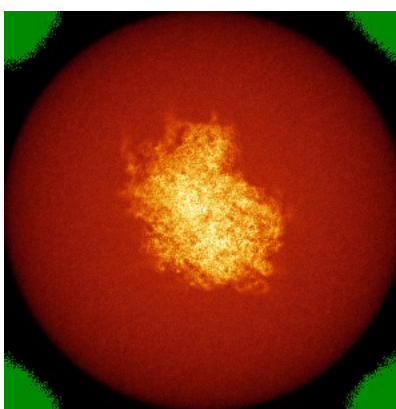
The images above show the largest variance slices of the map in three orthogonal directions.

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

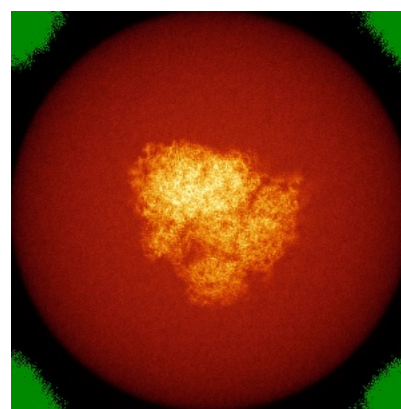
6.4.1 Primary map



X



Y

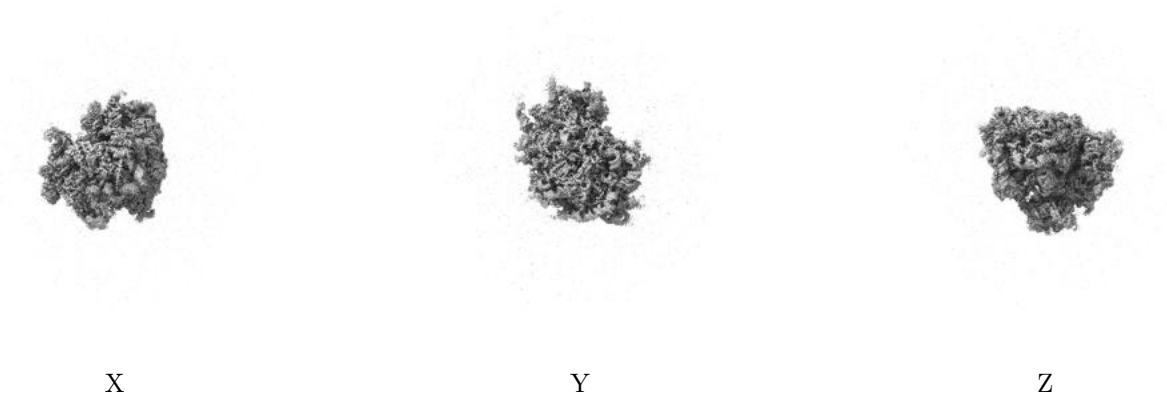


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

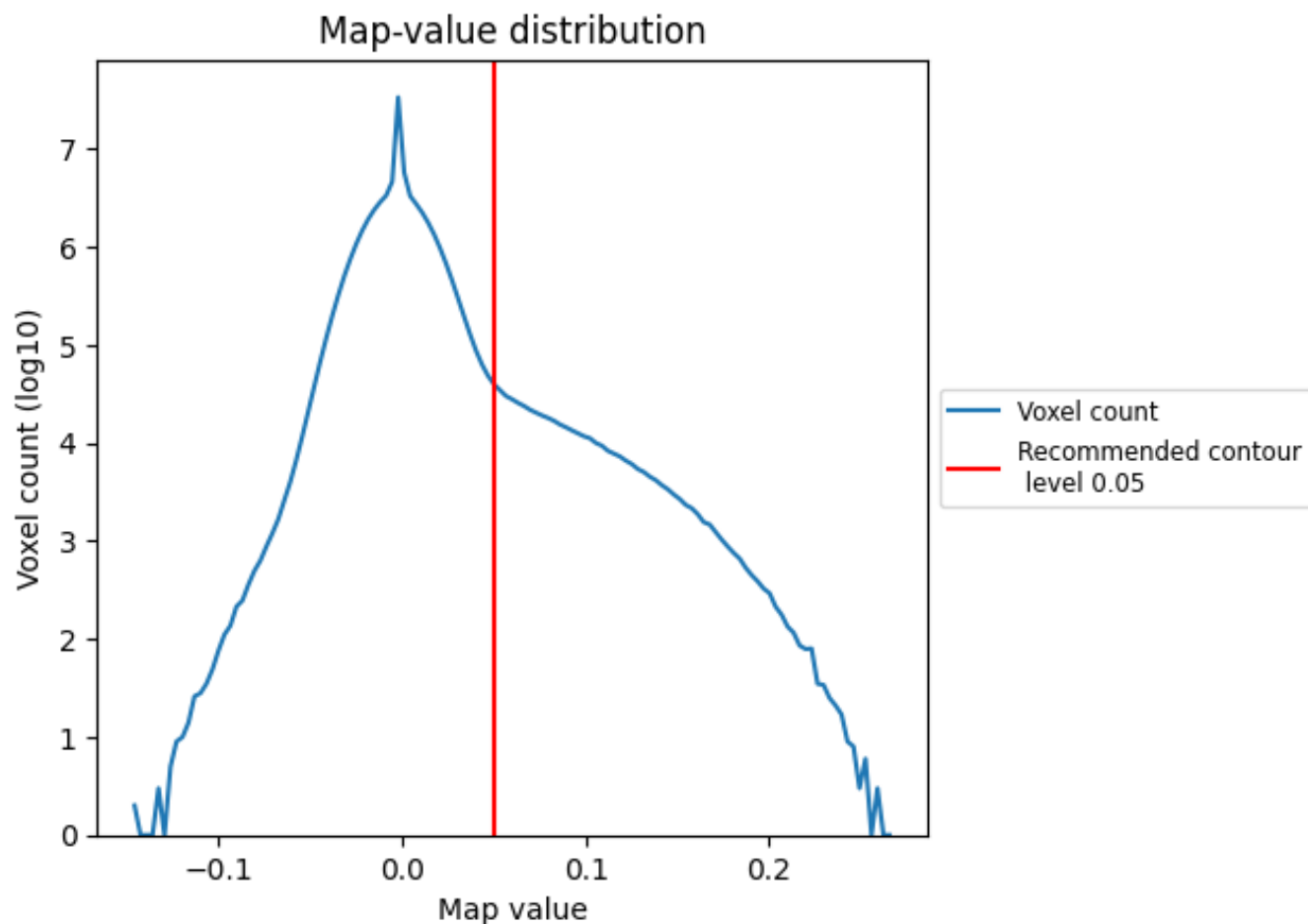
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

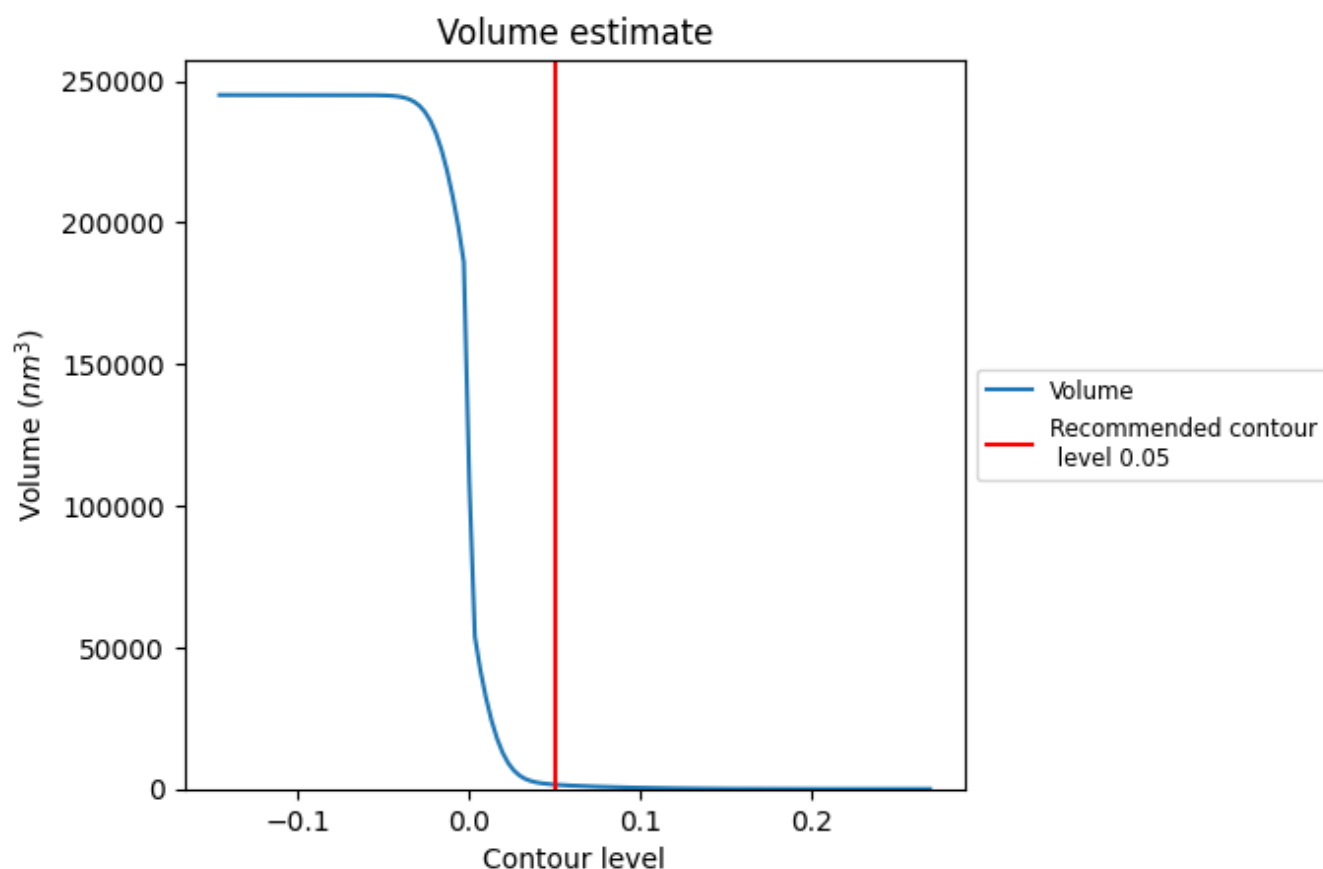
This section contains the results of statistical analysis of the map.

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.

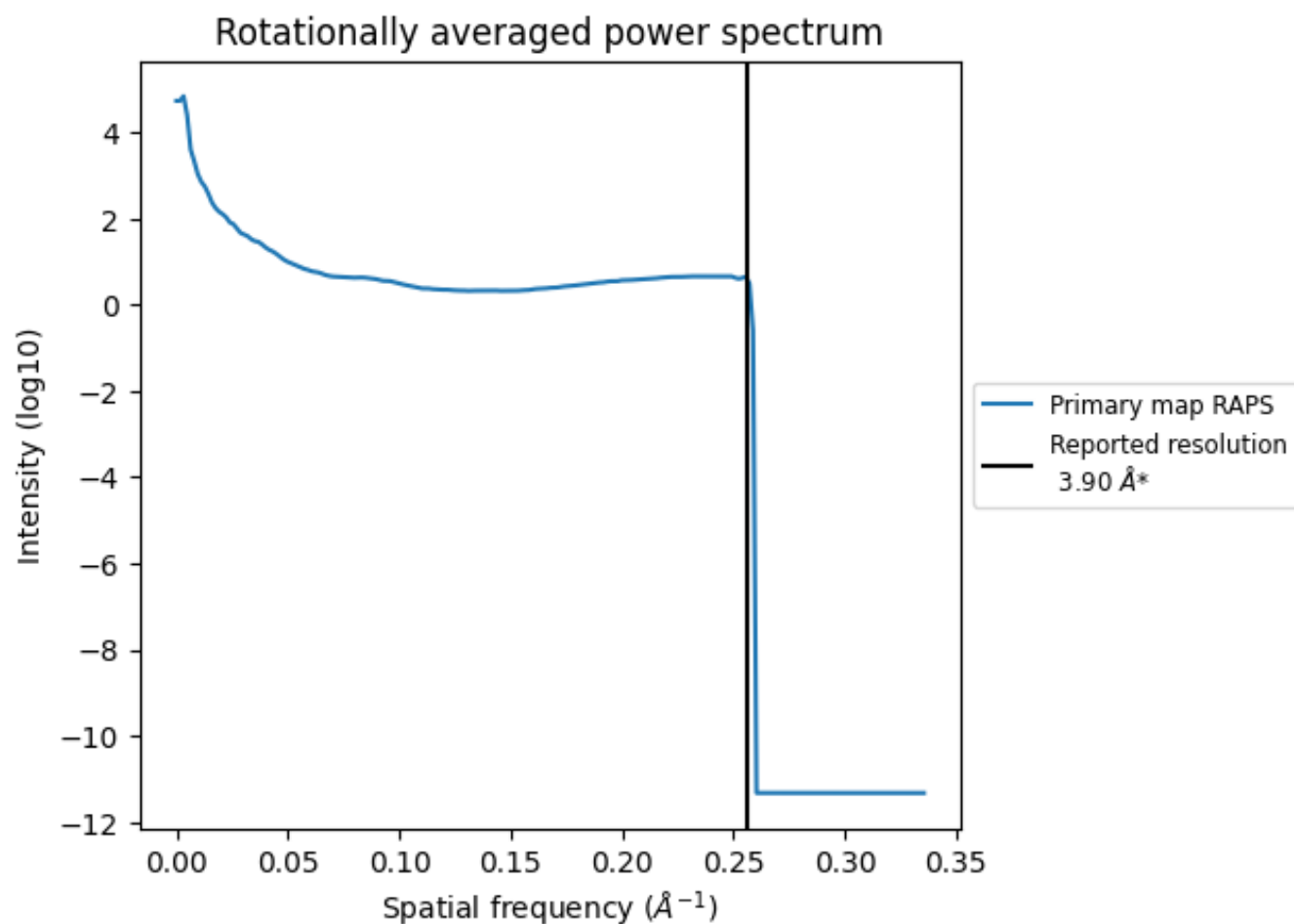
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1541 nm^3 ; this corresponds to an approximate mass of 1392 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

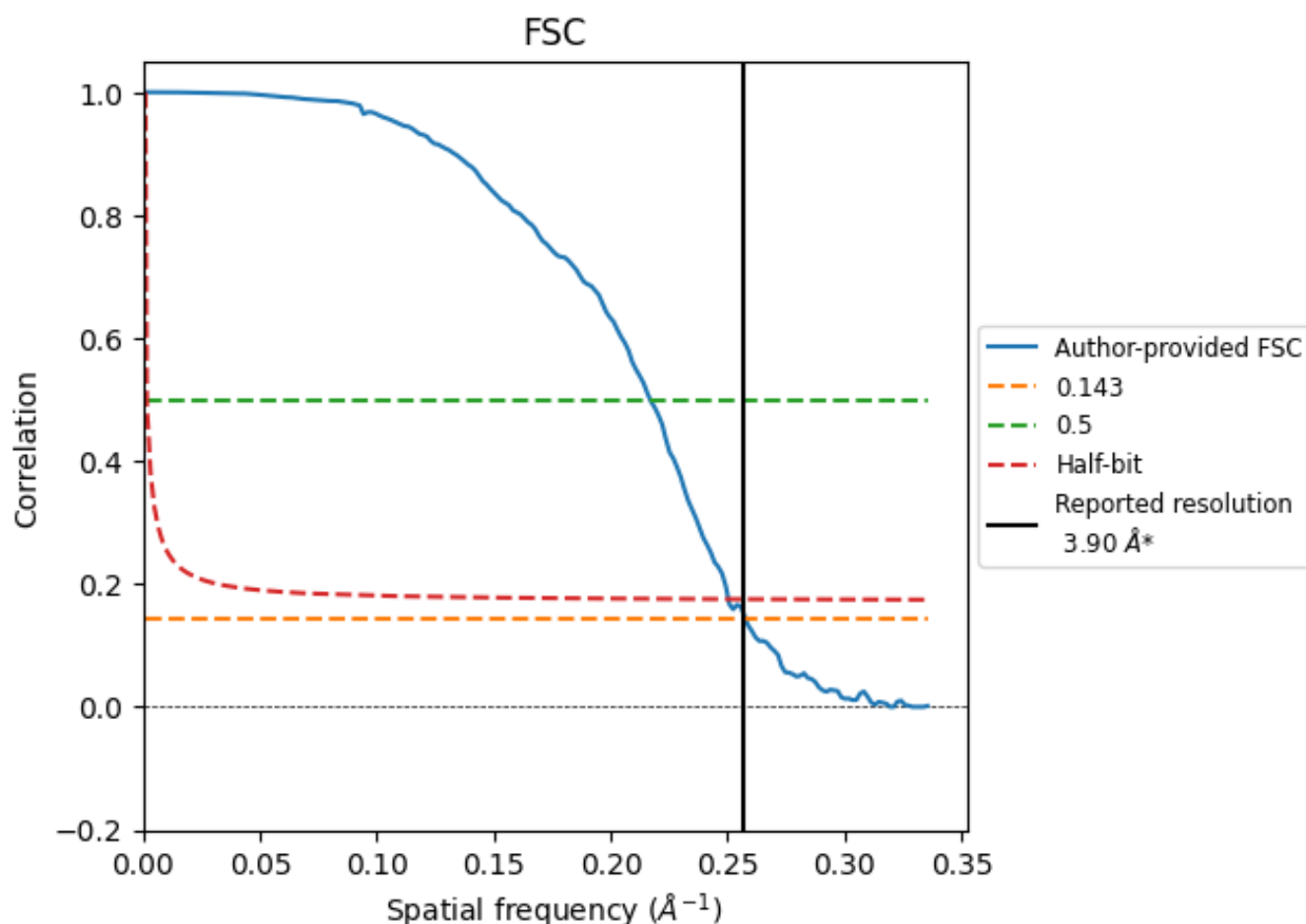


*Reported resolution corresponds to spatial frequency of 0.256 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

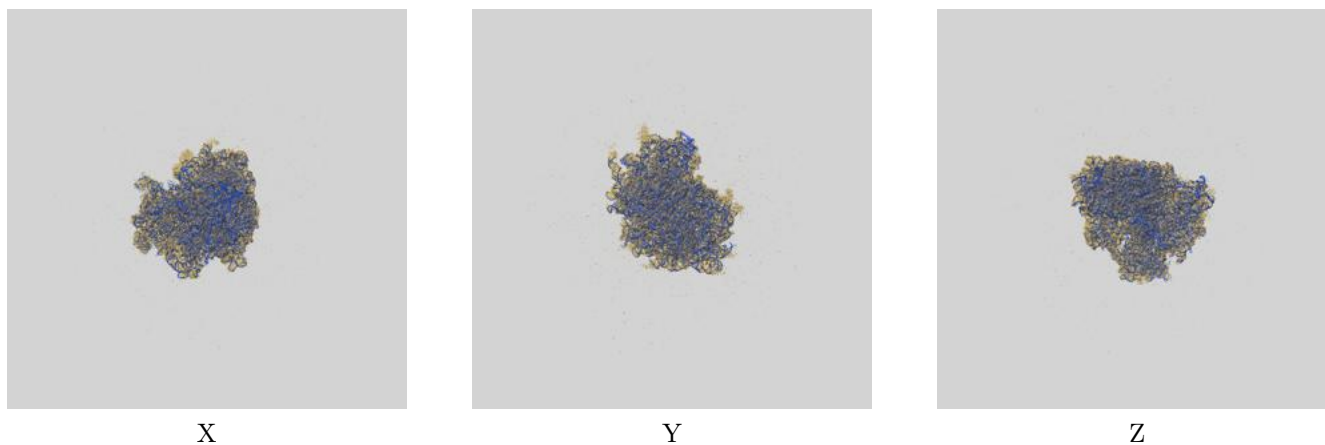
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.88	4.61	3.99
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

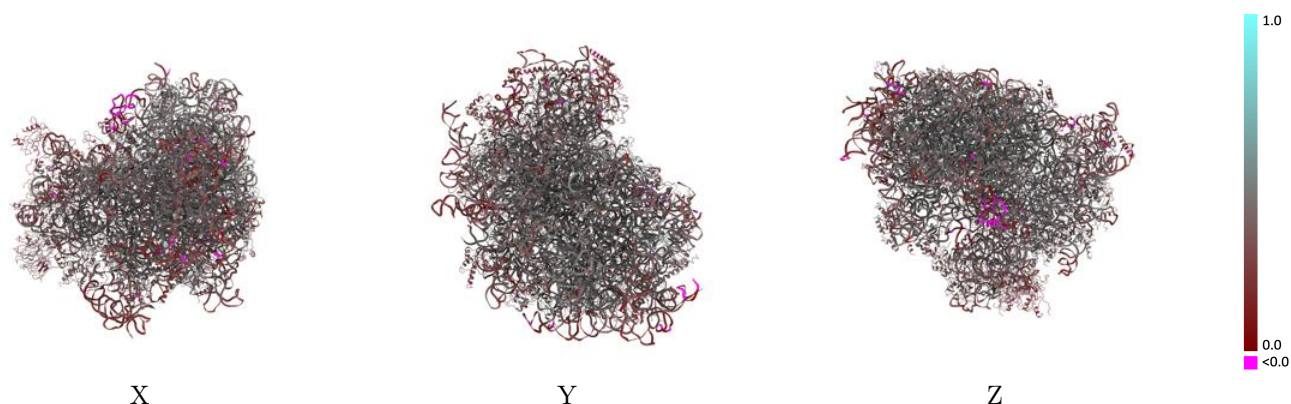
This section contains information regarding the fit between EMDB map EMD-9703 and PDB model 6IP8. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



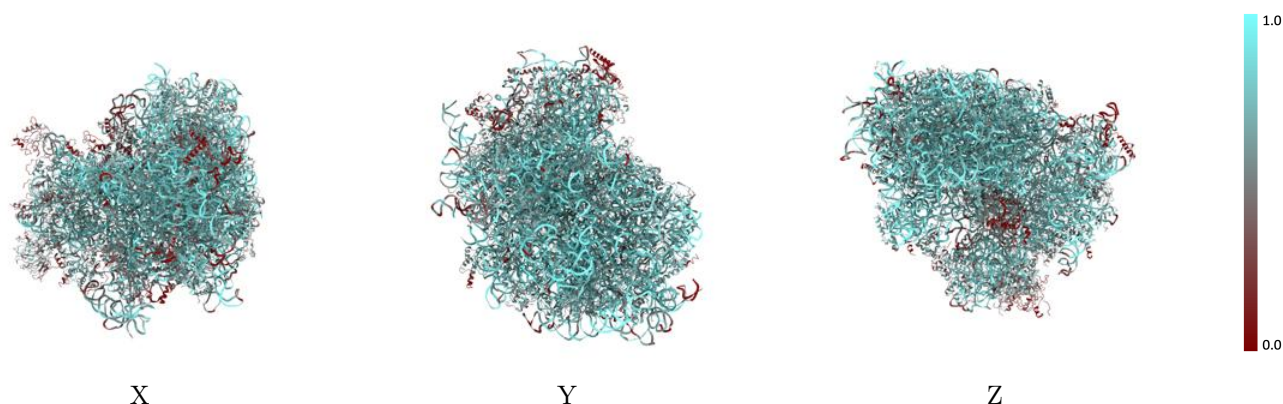
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



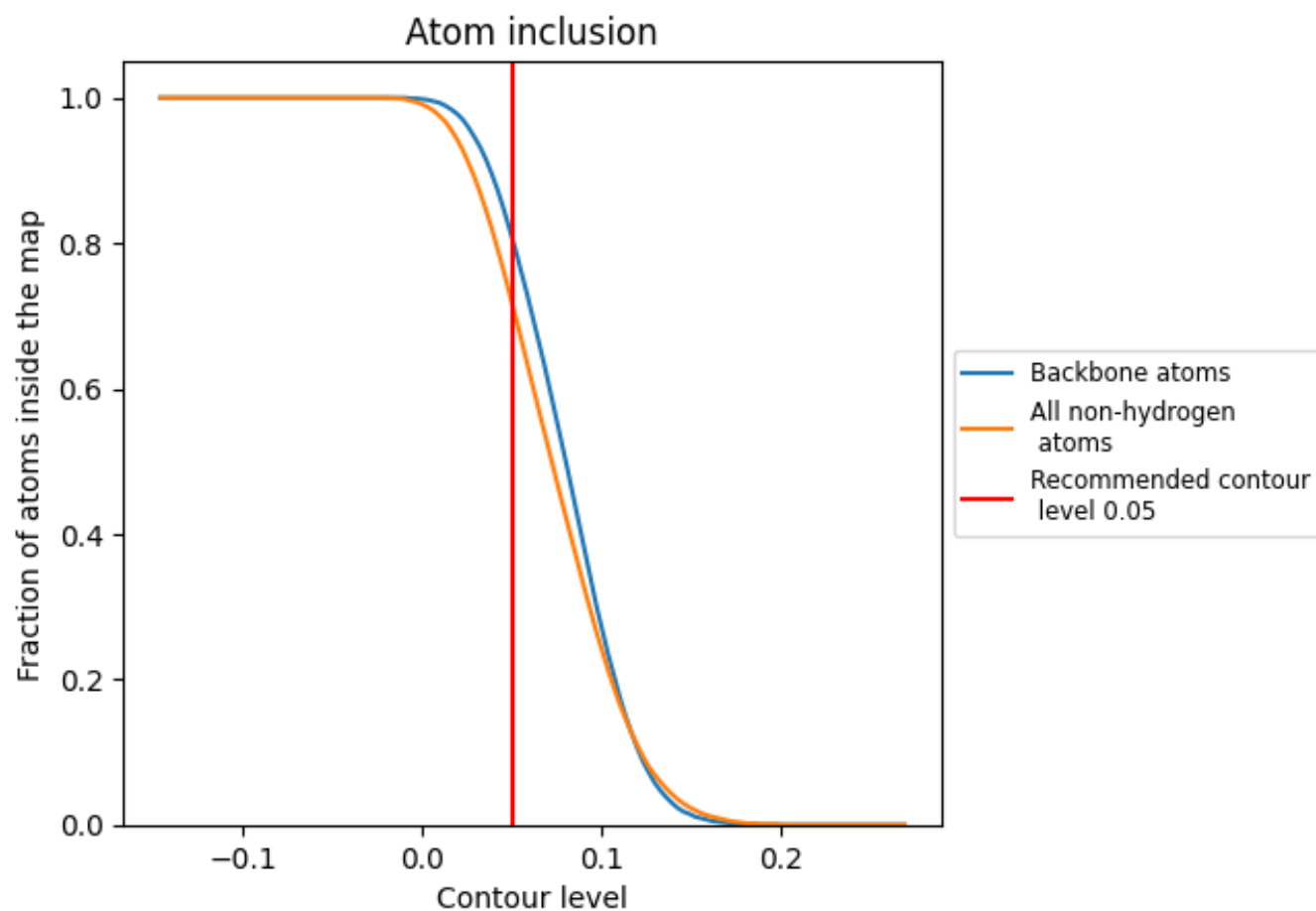
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

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

Chain	Atom inclusion	Q-score
All	 0.7200	 0.3970
1A	 0.8200	 0.3980
1B	 0.9120	 0.4410
1C	 0.8400	 0.4140
1D	 0.6600	 0.4570
1E	 0.6870	 0.4500
1F	 0.6800	 0.4520
1G	 0.6750	 0.3920
1H	 0.6240	 0.4050
20	 0.5980	 0.3660
21	 0.4630	 0.3410
2A	 0.7020	 0.4510
2B	 0.5390	 0.3790
2C	 0.6580	 0.4340
2D	 0.6120	 0.4210
2E	 0.6100	 0.3900
2F	 0.6270	 0.4140
2G	 0.7180	 0.4450
2H	 0.6960	 0.4480
2I	 0.6820	 0.4470
2J	 0.7030	 0.4570
2K	 0.6840	 0.4530
2L	 0.6290	 0.4090
2M	 0.7300	 0.4590
2N	 0.6660	 0.4380
2O	 0.5940	 0.3830
2P	 0.6540	 0.4630
2Q	 0.3600	 0.3140
2R	 0.6290	 0.4330
2S	 0.7000	 0.4380
2T	 0.6420	 0.4120
2U	 0.7090	 0.4490
2V	 0.5940	 0.3950
2W	 0.6280	 0.4230
2X	 0.6520	 0.4400



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Chain	Atom inclusion	Q-score
2Y	 0.7070	 0.4730
2Z	 0.7130	 0.4800
2a	 0.6550	 0.4390
2b	 0.6680	 0.4190
2c	 0.5970	 0.3960
2d	 0.7350	 0.4610
2e	 0.5530	 0.3830
2f	 0.6620	 0.4460
2g	 0.6720	 0.4510
2h	 0.6700	 0.4680
2i	 0.6300	 0.4260
2j	 0.6260	 0.4460
2k	 0.7240	 0.4500
2m	 0.8120	 0.3930
2n	 0.5990	 0.3920
2o	 0.5480	 0.4010
2p	 0.4880	 0.3560
2q	 0.6040	 0.4050
2r	 0.4960	 0.3520
2s	 0.4810	 0.3590
2t	 0.6260	 0.4050
2u	 0.4780	 0.3180
2v	 0.5730	 0.4100
2w	 0.5310	 0.3140
2x	 0.5480	 0.3540
2y	 0.4530	 0.3370
2z	 0.5520	 0.3480
3A	 0.5800	 0.3680
3B	 0.6190	 0.4390
3C	 0.5550	 0.4060
3D	 0.3970	 0.3510
3E	 0.6650	 0.4200
3F	 0.4600	 0.3010
3G	 0.6080	 0.4080
3H	 0.5400	 0.3390
3I	 0.6340	 0.3970
3J	 0.1760	 0.2110
3K	 0.6150	 0.4260
3L	 0.5350	 0.3860
3M	 0.6200	 0.4210
3N	 0.5860	 0.3620
3O	 0.4490	 0.3050

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Chain	Atom inclusion	Q-score
3P	 0.5480	 0.3840
3Q	 0.5180	 0.3860
3R	 0.2610	 0.2650
zV	 0.7000	 0.4220
zW	 0.3050	 0.3300
zX	 0.3830	 0.3040
zY	 0.7480	 0.3820
zZ	 0.6140	 0.2490