Full wwPDB EM Validation Report ⓘ

May 5, 2025 – 11:10 am BST

PDB ID	:	9GY4 / pdb_00009gy4
EMDB ID	:	EMD-51681
Title	:	60S ribosomal subunit in complex with E3-UFM1 ligase and RQC machinery components NEMF and LTN1 (Composite map)
Authors	:	Penchev, I.; Gumbin, S.; Becker, T.; Kopito, R.; Beckmann, R.
Deposited on	:	2024-10-01
Resolution	:	3.00 Å(reported)

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

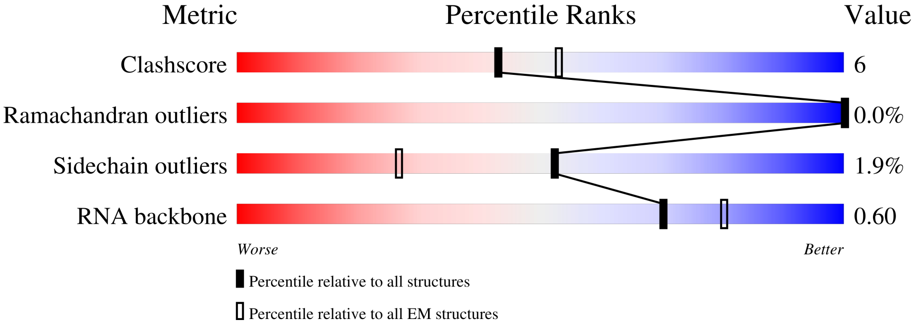
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline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

1 Overall quality at a glance ⓘ

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

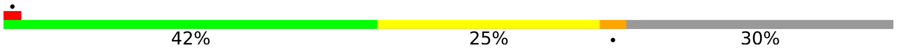
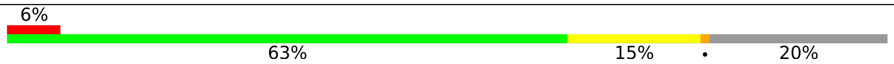
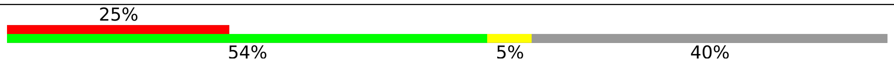
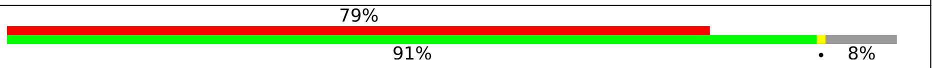
The reported resolution of this entry is 3.00 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	5	5070	
2	7	121	
3	8	157	
4	B	506	
5	C	314	
6	D	85	
7	E	794	

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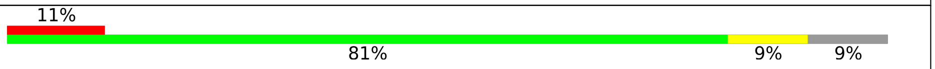
Mol	Chain	Length	Quality of chain
8	F	1766	
9	G	76	
10	LB	403	
11	LC	427	
12	LD	297	
13	LE	288	
14	LF	248	
15	LG	266	
16	LH	192	
17	LI	214	
18	LJ	178	
19	LL	211	
20	LM	215	
21	LN	204	
22	LO	203	
23	LP	184	
24	LQ	188	
25	LR	196	
26	LS	176	
27	LT	160	
28	LU	128	
29	LV	140	
30	LW	157	
31	LX	156	
32	LY	145	

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Mol	Chain	Length	Quality of chain
33	LZ	136	• 77% 21% ••
34	La	148	• 82% 18% •
35	Lb	159	8% 57% 12% 31%
36	Lc	115	5% 73% 12% 15%
37	Ld	125	• 74% 10% • 14%
38	Le	135	• 81% 12% • 5%
39	Lf	110	85% 14% ••
40	Lg	117	8% 86% 11% •
41	Lh	123	• 91% 8% •
42	Li	105	• 86% 10% • •
43	Lj	97	74% 14% 11%
44	Lk	70	10% 93% 6% •
45	Ll	51	82% 16% •
46	Lm	128	• 31% 9% 59%
47	Lo	106	• 92% 8% •
48	Lp	92	• 87% 11% ••
49	Lr	137	• 81% 10% 9%
50	Lz	217	76% 23% •
51	Z	1076	11% 52% 15% • 32%
52	a	257	• 81% 15% • •
53	s	317	39% 47% 15% • 37%
54	t	165	• 70% 16% 13%
55	A	7	14% 100%

2 Entry composition (i)

There are 57 unique types of molecules in this entry. The entry contains 169625 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	5	3528	75663	33699	13869	24568	3527	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	2113	C	G	conflict	GB 86475748
5	4906	U	C	conflict	GB 86475748
5	4910	A	G	conflict	GB 86475748

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	7	120	2561	1141	456	844	120	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	8	148	3152	1407	563	1035	147	0	0

- Molecule 4 is a protein called CDK5 regulatory subunit-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	B	403	3234	2049	545	624	16	0	0

- Molecule 5 is a protein called DDRGK domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	188	1547	954	279	313	1	0	0

- Molecule 6 is a protein called Ubiquitin-fold modifier 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	D	78	588	382	96	109	1	0	0

- Molecule 7 is a protein called E3 UFM1-protein ligase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	E	660	5251	3323	901	1009	18	0	0

- Molecule 8 is a protein called E3 ubiquitin-protein ligase listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	F	1679	13415	8627	2194	2514	80	0	0

- Molecule 9 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	G	76	1622	721	285	540	76	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	73	G	A	conflict	GB 2736373571
G	74	C	A	conflict	GB 2736373571
G	75	C	U	conflict	GB 2736373571
G	76	A	C	conflict	GB 2736373571

- Molecule 10 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LB	402	3239	2060	608	557	14	0	0

- Molecule 11 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LC	368	2927	1840	583	489	15	0	0

- Molecule 12 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LD	293	2382	1507	434	427	14	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LE	220	1765	1136	334	291	4	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 15 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	LG	241	1927	1228	371	324	4	0	0

- Molecule 16 is a protein called 60S ribosomal protein L9.

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

- Molecule 17 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	LI	213	1710	1083	329	284	14	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LI	87	ILE	MET	conflict	UNP Q96L21

- Molecule 18 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	LJ	175	1401	882	261	252	6	0	0

- Molecule 19 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	LL	194	1573	987	327	255	4	0	0

- Molecule 20 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	LM	136	1120	719	215	179	7	0	0

- Molecule 21 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	LN	203	1701	1072	359	266	4	0	0

- Molecule 22 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	LO	201	1650	1063	321	261	5	0	0

- Molecule 23 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	LP	153	1242	776	241	216	9	0	0

- Molecule 24 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	LQ	187	1513	944	314	250	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	LR	155	1294	808	278	199	9	0	0

- Molecule 26 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	LS	175	1453	925	283	235	10	0	0

- Molecule 27 is a protein called 60S ribosomal protein L21.

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

- Molecule 28 is a protein called 60S ribosomal protein L22.

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

- Molecule 29 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	LV	131	979	618	184	172	5	0	0

- Molecule 30 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	LW	62	519	332	101	83	3	0	0

- Molecule 31 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	LX	118	967	618	181	167	1	0	0

- Molecule 32 is a protein called 60S ribosomal protein L26.

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

- Molecule 33 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 34 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 36 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 37 is a protein called 60S ribosomal protein L31.

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

- Molecule 38 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 39 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	Lf	109	876	555	174	144	3	0	0

- Molecule 40 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Lg	114	906	566	187	147	6	0	0

- Molecule 41 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	Lh	122	1015	641	205	168	1	0	0

- Molecule 42 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	Li	102	832	521	177	129	5	0	0

- Molecule 43 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	Lj	86	705	434	155	111	5	0	0

- Molecule 44 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	Lk	69	569	366	103	99	1	0	0

- Molecule 45 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	Ll	50	444	281	98	64	1	0	0

- Molecule 46 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	Lm	52	429	266	90	67	6	0	0

- Molecule 47 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	Lo	105	863	542	175	140	6	0	0

- Molecule 48 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	Lp	91	708	445	136	120	7	0	0

- Molecule 49 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	Lr	125	1002	622	207	168	5	0	0

- Molecule 50 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	Lz	217	1744	1114	314	307	9	0	0

- Molecule 51 is a protein called Ribosome quality control complex subunit NEMF.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	Z	731	5891	3768	1012	1090	21	0	0

- Molecule 52 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	a	248	1898	1189	389	314	6	0	0

- Molecule 53 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	s	201	1545	983	268	285	9	0	0

- Molecule 54 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	t	143	1068	665	197	202	4	0	0

- Molecule 55 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
55	A	7	35	21	7	7	0	0

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
56	5	205	205	205	0
56	7	2	2	2	0
56	8	5	5	5	0
56	LI	1	1	1	0
56	LP	1	1	1	0
56	LV	1	1	1	0
56	Le	1	1	1	0
56	Lf	1	1	1	0
56	Lg	1	1	1	0
56	Lj	1	1	1	0

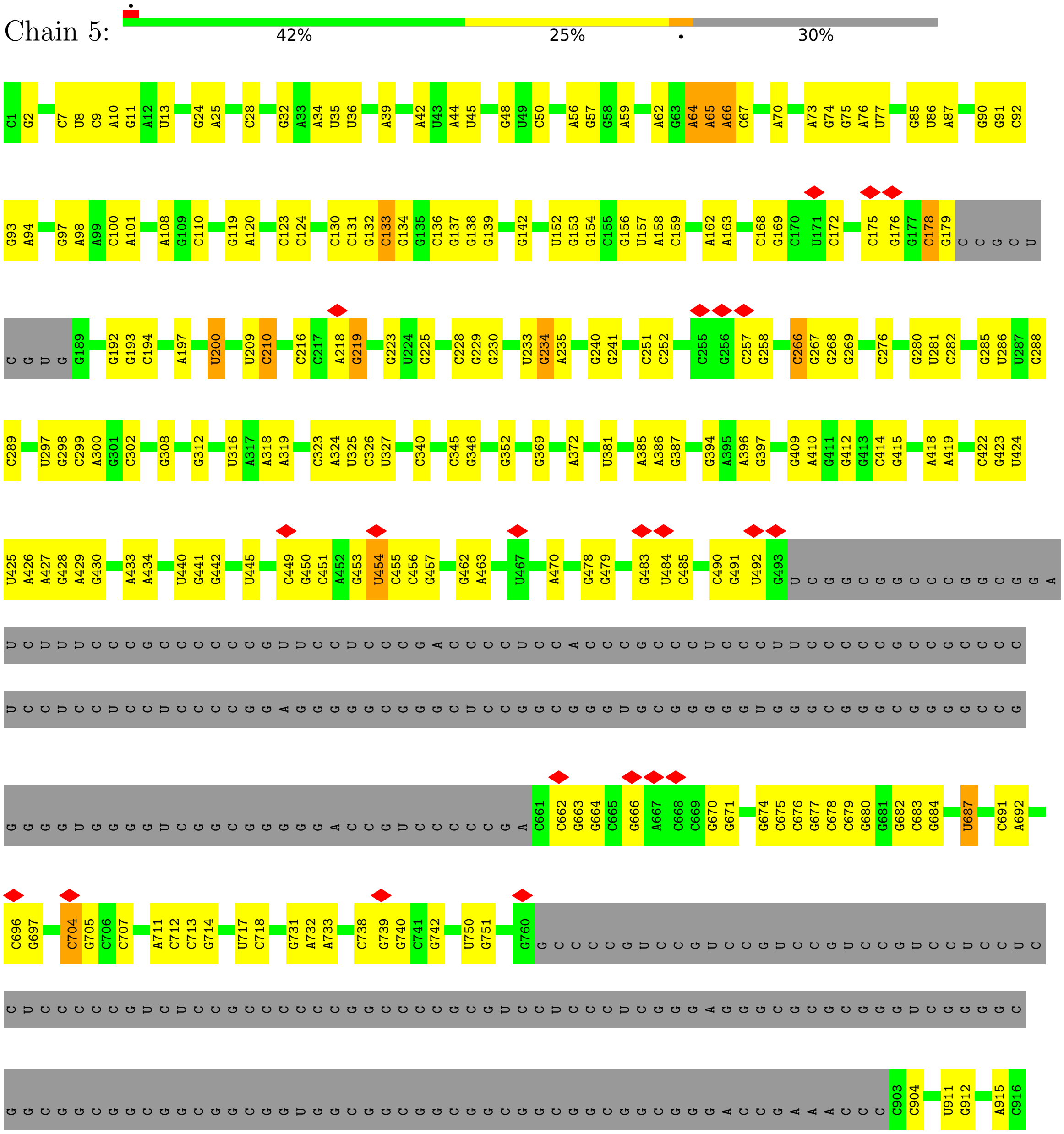
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

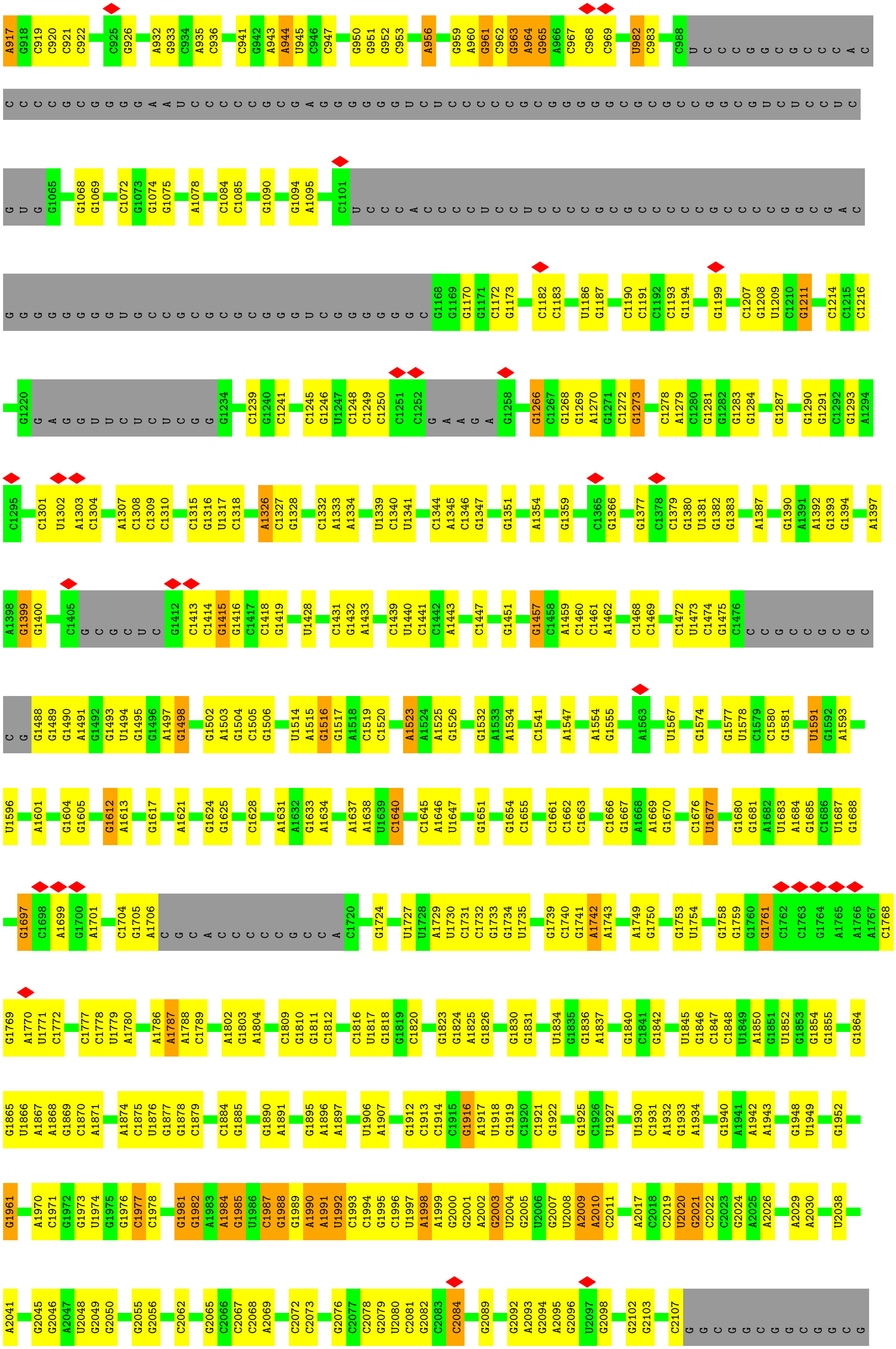
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
57	Lg	1	1	1	0
57	Lj	1	1	1	0
57	Lm	1	1	1	0
57	Lo	1	1	1	0
57	Lp	1	1	1	0

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 rRNA




A917 G918 C919 C920 C921 C922 C925 G926 A932 G933 C934 A935 C936 C941 G942 A943 A944 U945 C946 C947 G950 G951 G952 C953 A956 G959 A960 G961 C962 G963 A964 G965 A966 C967 C968 C969 U982 C983 C988 U C C C G G C G C C C A C
C C C C G C G G G G A A U C C C C C G C G A G G G G G G U C U C C C C C G G C G G G G G C G C G C C G G C G G U C U C C U C
G U G G1065 G1068 G1069 C1072 G1073 G1074 C1075 A1078 C1084 C1085 G1090 G1094 A1095 C1101 U C C C A C C C C U C C U C C C C G C G C C C C G C C C C G G C G A C
G G G G G G G G U G C C G C G C C G G G U C G G G G G C G1168 G1169 G1170 G1171 C1172 G1173 C1182 C1183 U1186 G1187 C1190 C1191 C1192 C1193 G1194 G1199 C1207 G1208 U1209 C1210 G1211 C1214 C1215 C1216
G1220 G A G G U U C U C U C G G G1234 C1239 G1240 C1241 C1245 G1246 U1247 C1248 C1249 C1250 C1251 C1252 G A A G A G1258 G1266 C1267 G1268 G1269 A1270 G1271 C1272 G1273 C1278 A1279 C1280 G1281 G1282 G1283 G1284 G1287 G1290 G1291 C1292 G1293 A1294
C1295 C1301 U1302 A1303 C1304 A1307 C1308 C1309 C1310 C1315 G1316 U1317 C1318 A1326 C1327 G1328 C1332 A1333 A1334 U1339 C1340 U1341 C1344 A1345 C1346 G1347 G1351 A1354 G1359 C1365 G1366 G1377 C1378 C1379 G1380 U1381 G1382 G1383 A1387 G1390 A1391 A1392 G1393 G1394 A1397
A1398 G1399 G1400 C1405 G C G C U C G1412 C1413 C1414 G1415 G1416 C1417 C1418 G1419 U1428 C1431 G1432 A1433 C1439 U1440 C1441 C1442 A1443 C1447 G1451 G1457 C1458 A1459 C1460 C1461 A1462 C1468 C1469 C1472 U1473 C1474 G1475 C1476 C C G C C G C G C
C G G1488 G1489 G1490 A1491 G1492 G1493 U1494 G1495 G1496 A1497 G1498 G1502 A1503 G1504 C1505 G1506 U1514 A1515 G1516 G1517 A1518 C1519 C1520 A1523 A1524 A1525 G1526 G1532 A1533 A1534 C1541 A1547 A1554 G1555 A1563 U1567 G1574 G1577 U1578 C1579 C1580 G1581 U1591 G1592 A1593
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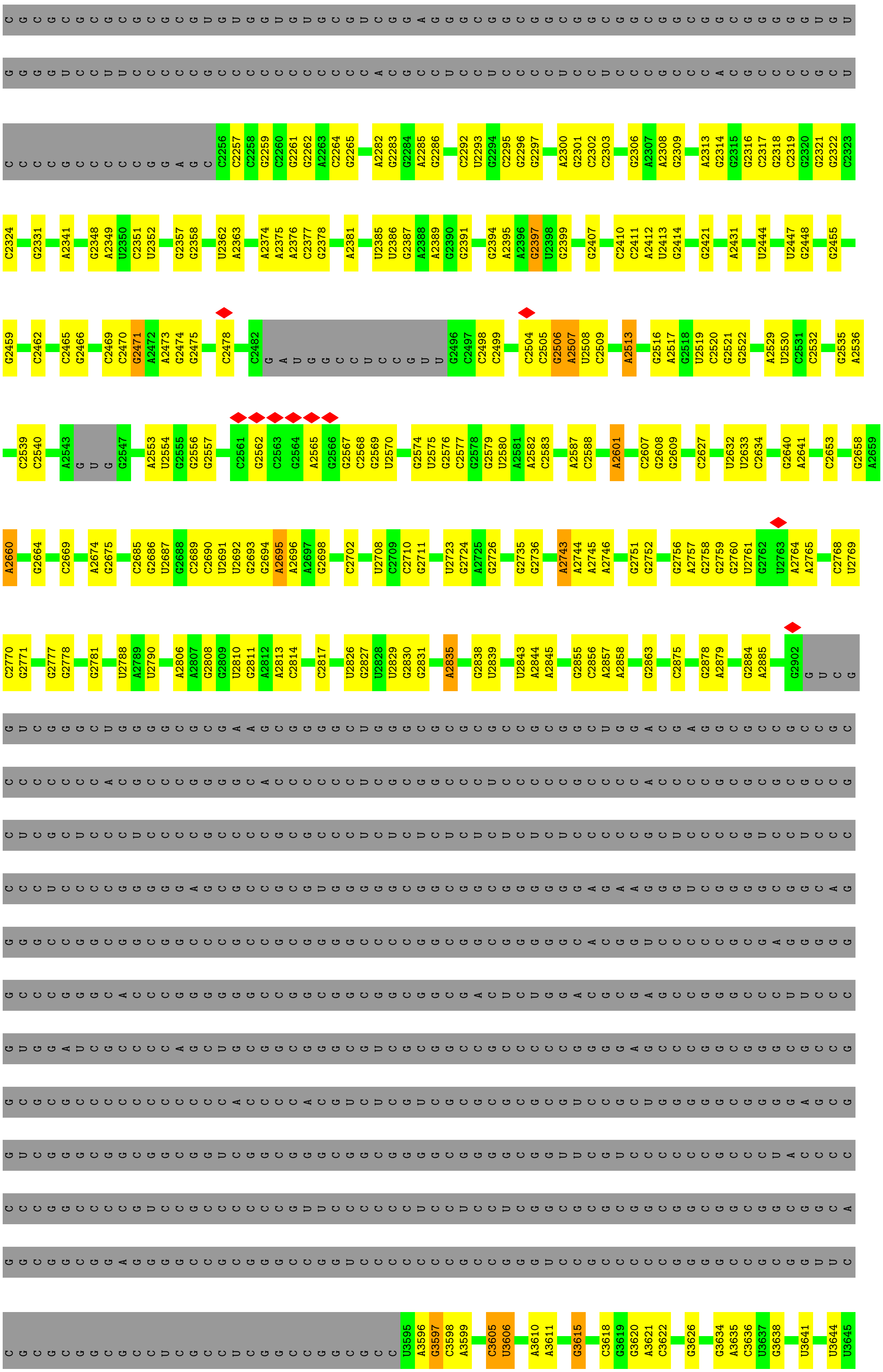
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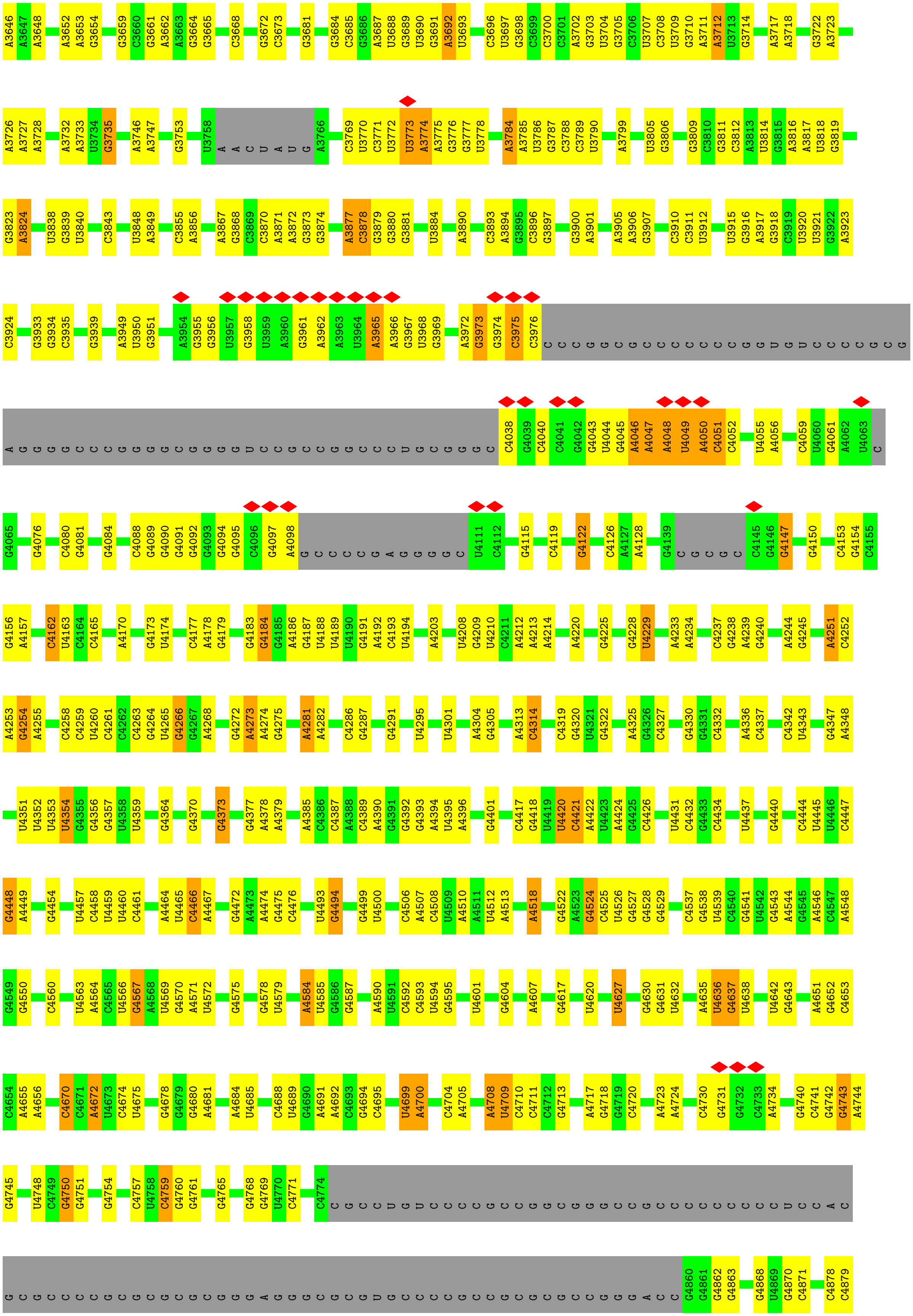
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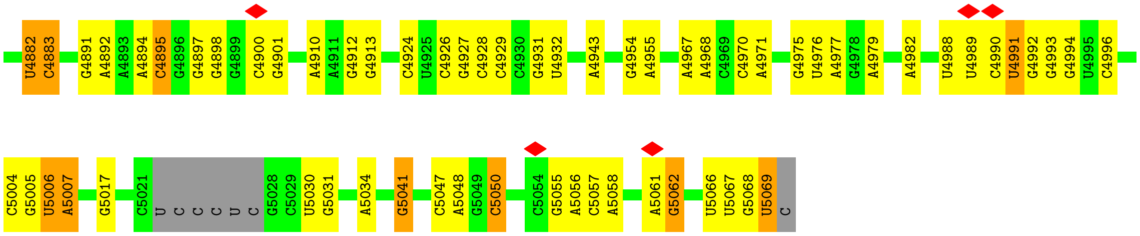
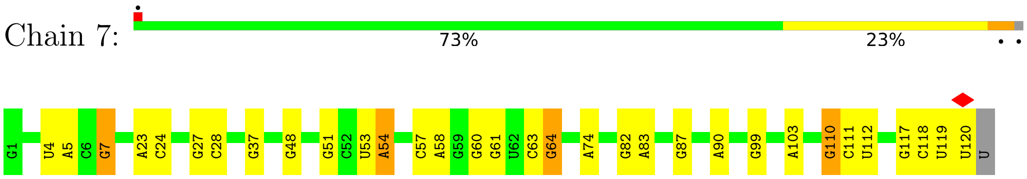


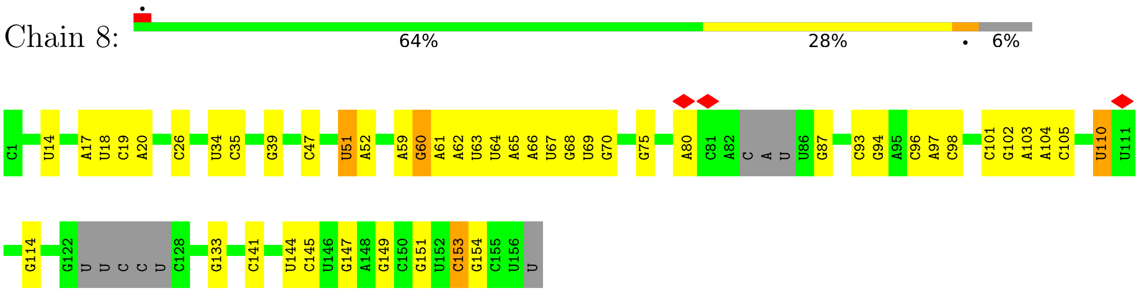
- Molecule 2: 5S rRNA

Chain 7:



- Molecule 3: 5.8S rRNA

Chain 8:



- Molecule 4: CDK5 regulatory subunit-associated protein 3

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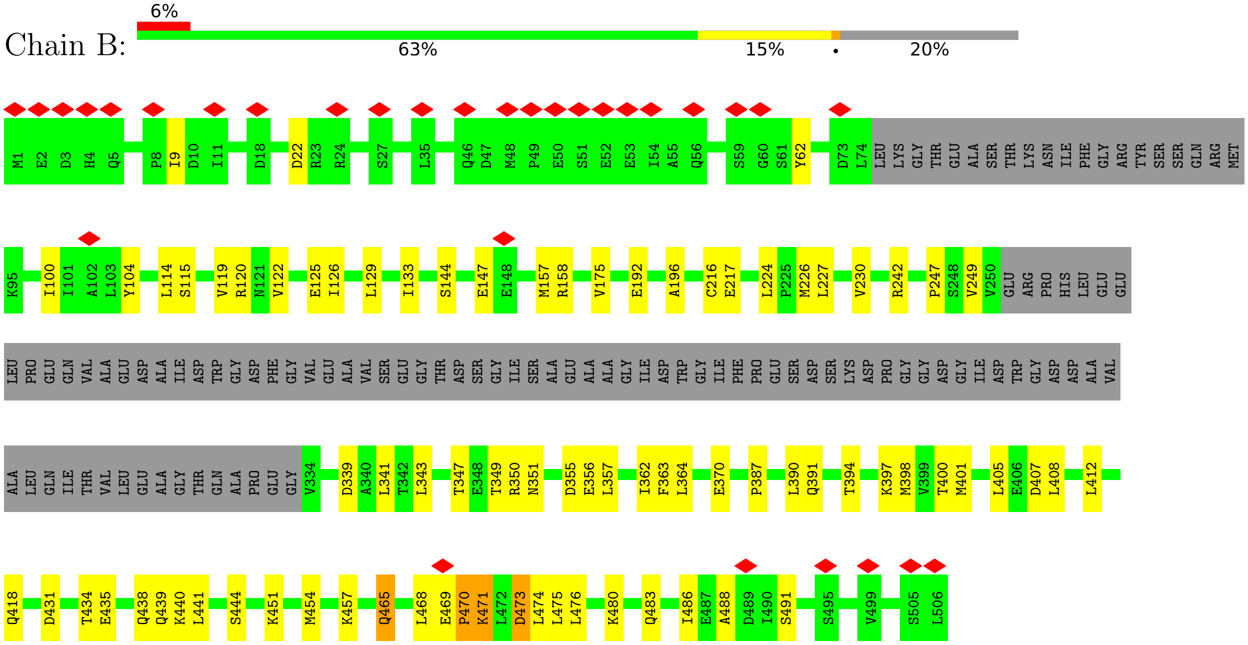

- Molecule 5: DDRGK domain-containing protein 1

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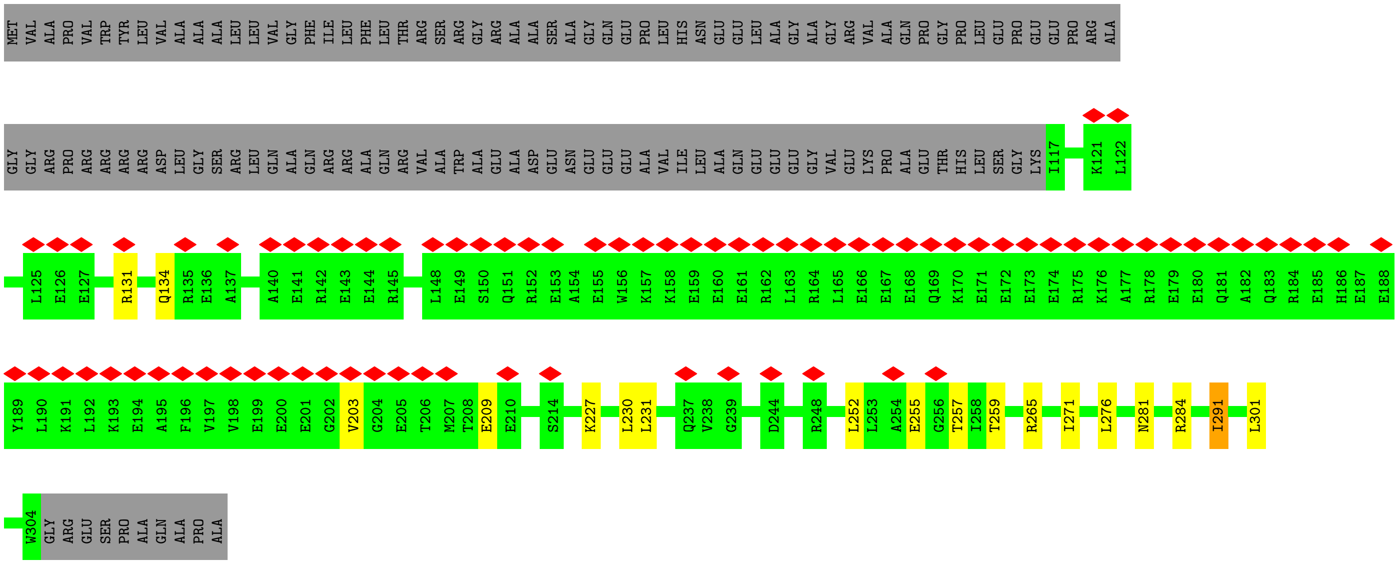

- Molecule 6: Ubiquitin-fold modifier 1

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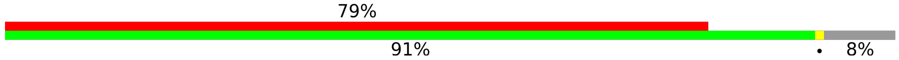

- Molecule 7: E3 UFM1-protein ligase 1

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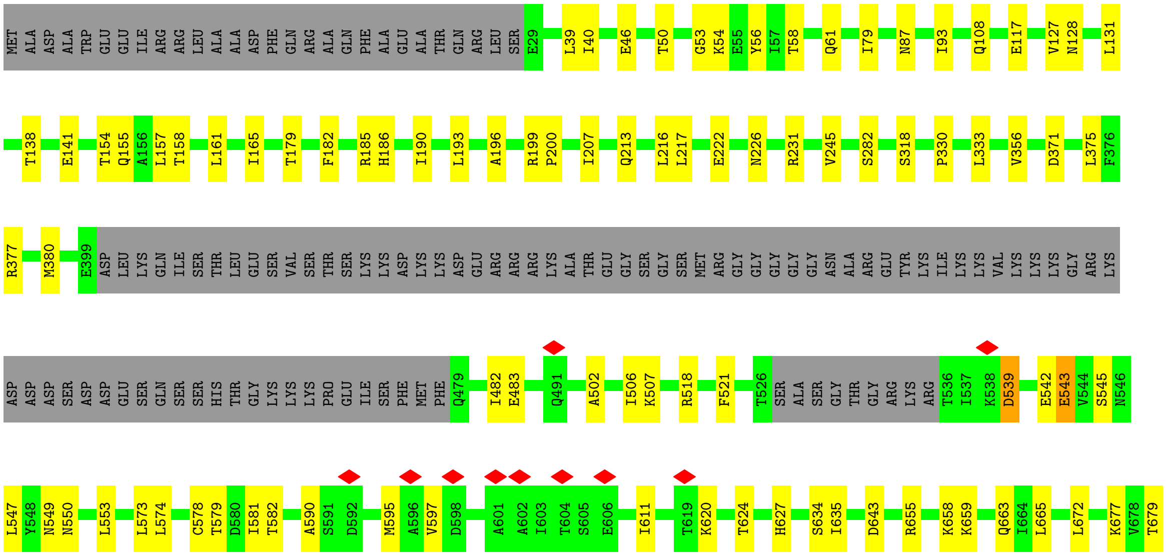

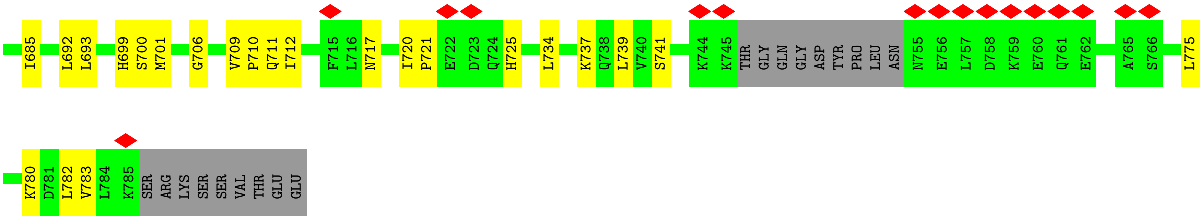

- Molecule 8: E3 ubiquitin-protein ligase listerin

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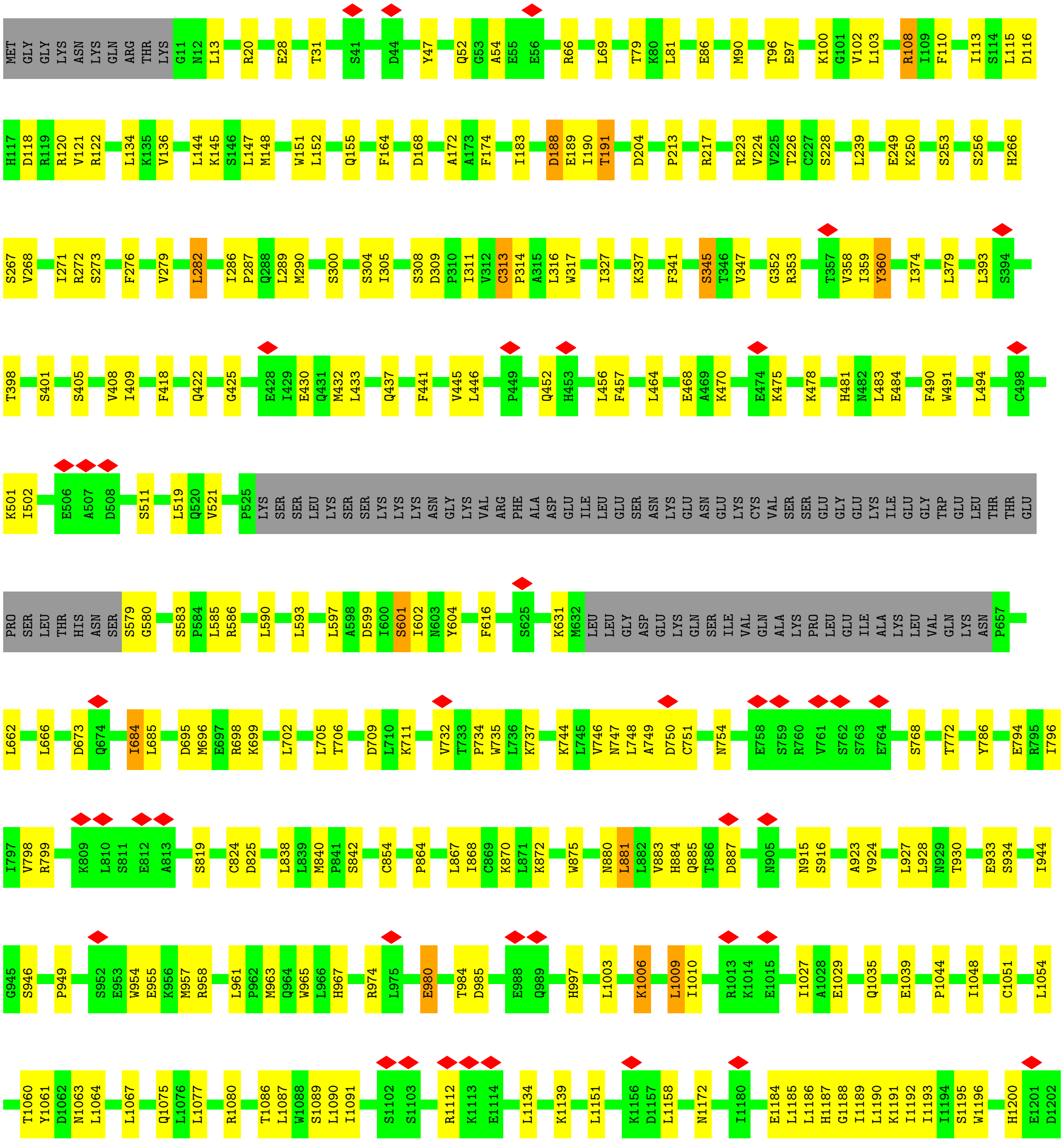

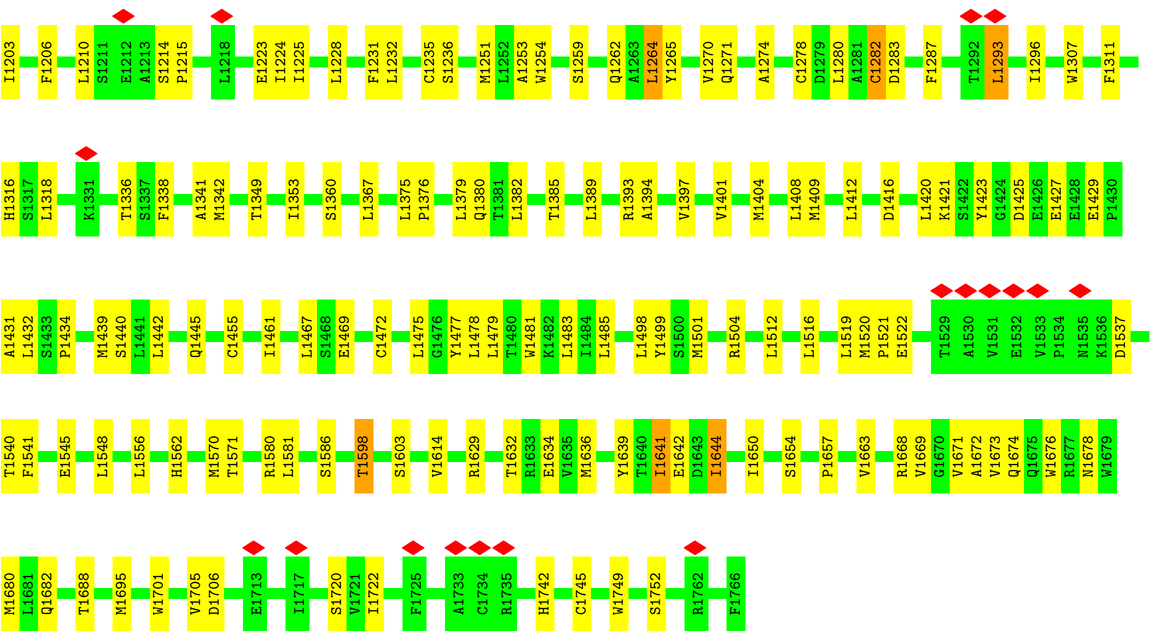

- Molecule 9: tRNA

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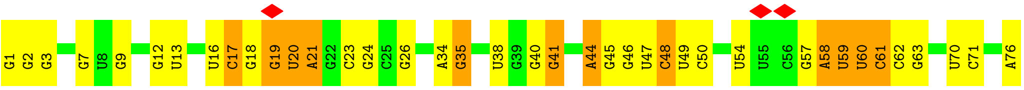

- Molecule 10: 60S ribosomal protein L3

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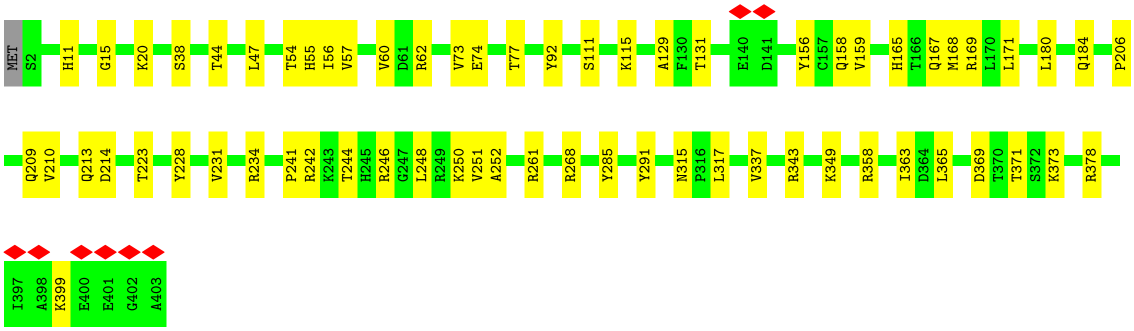
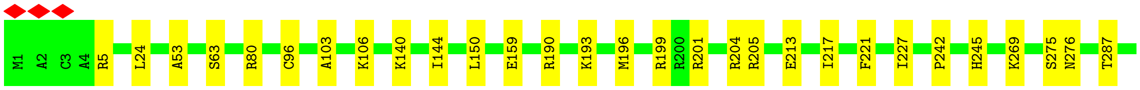


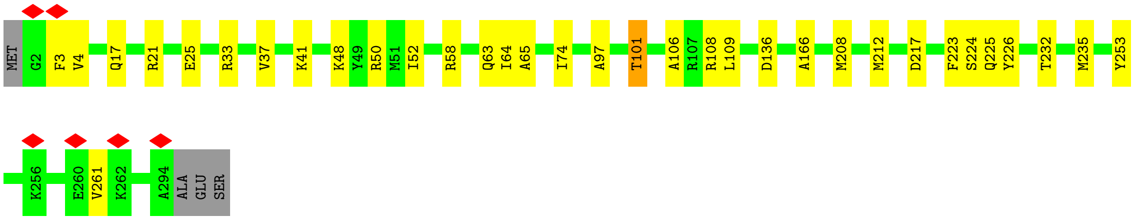
- Molecule 11: 60S ribosomal protein L4

Chain LC:



- Molecule 12: 60S ribosomal protein L5

Chain LD:



- Molecule 13: Large ribosomal subunit protein eL6

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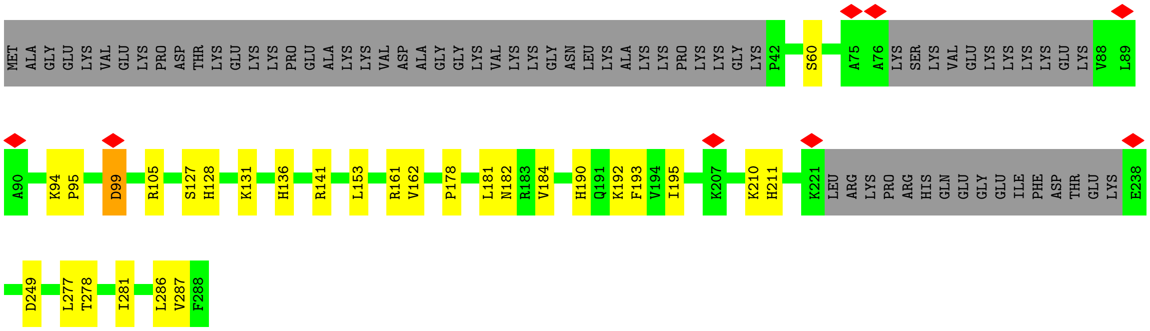

- Molecule 14: Large ribosomal subunit protein uL30

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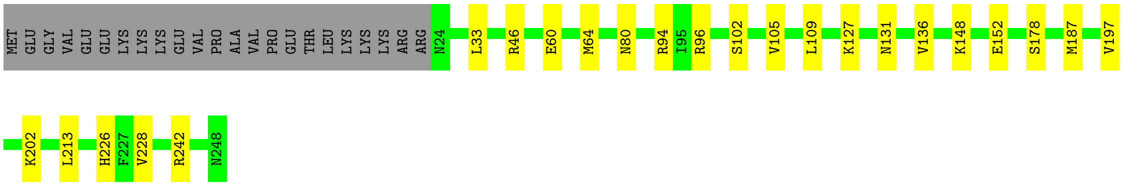

- Molecule 15: 60S ribosomal protein L7a

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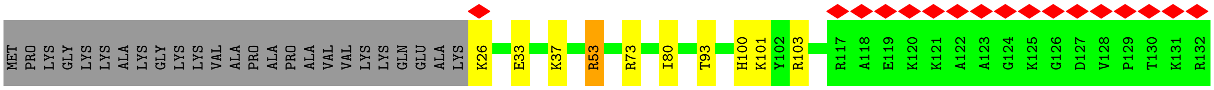
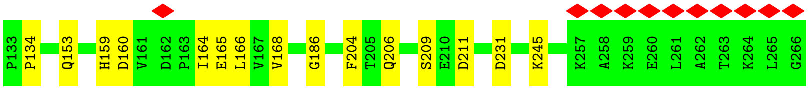
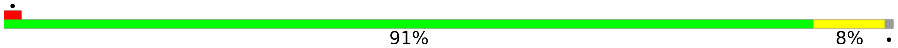
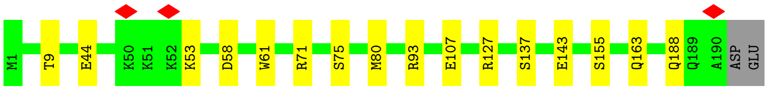




- Molecule 16: 60S ribosomal protein L9

Chain LH:





- Molecule 17: Ribosomal protein uL16-like

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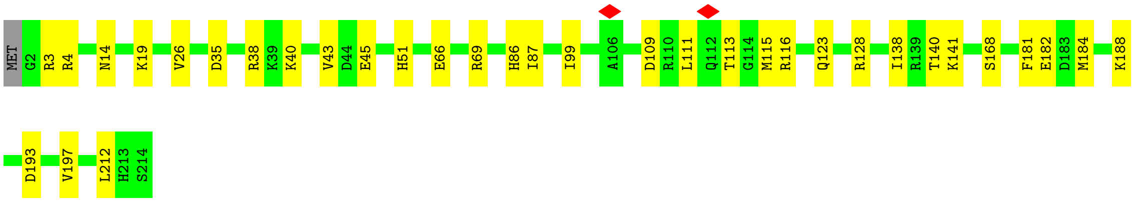

- Molecule 18: 60S ribosomal protein L11

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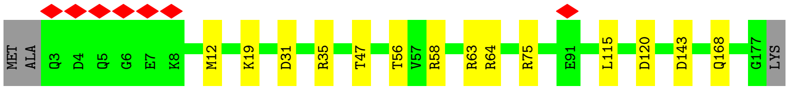

- Molecule 19: 60S ribosomal protein L13

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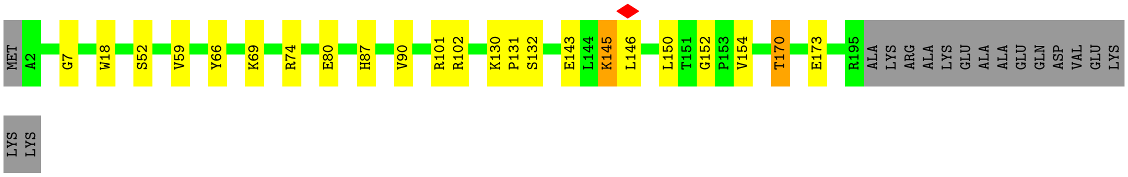
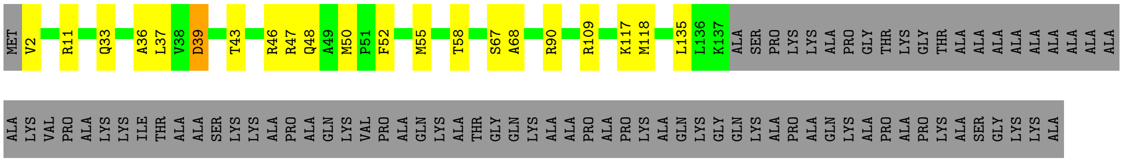
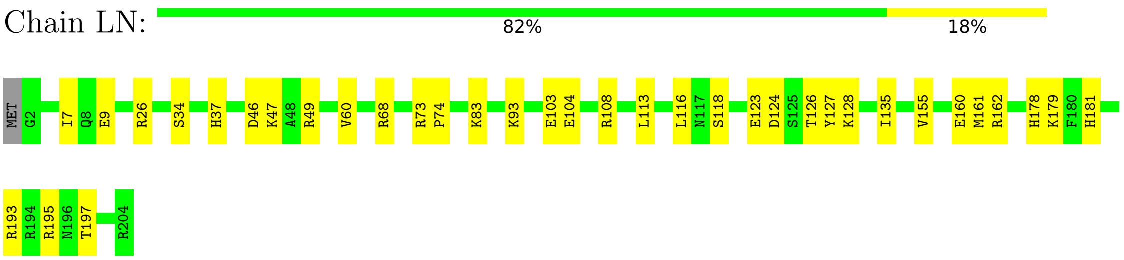


- Molecule 20: 60S ribosomal protein L14

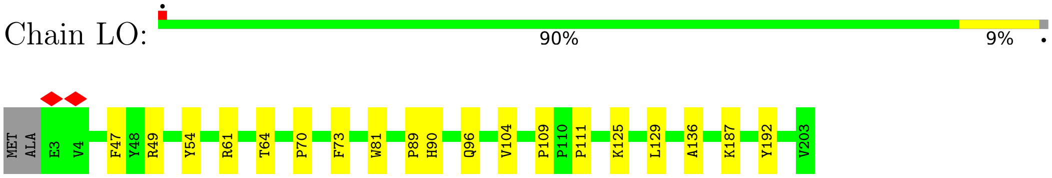
Chain LM:



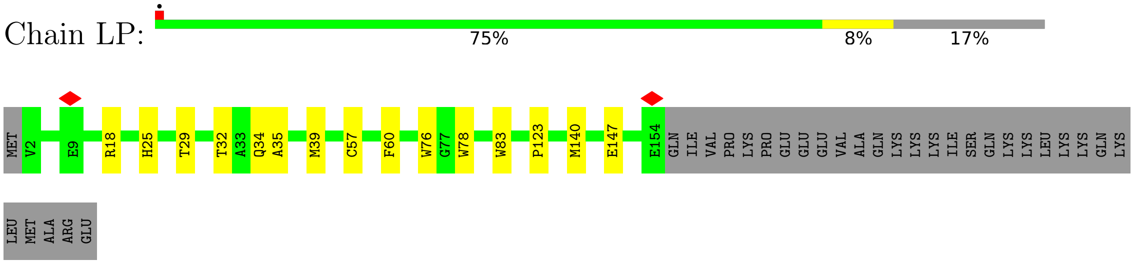
- Molecule 21: 60S ribosomal protein L15



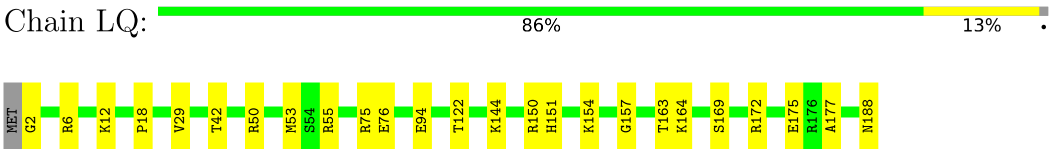
- Molecule 22: 60S ribosomal protein L13a



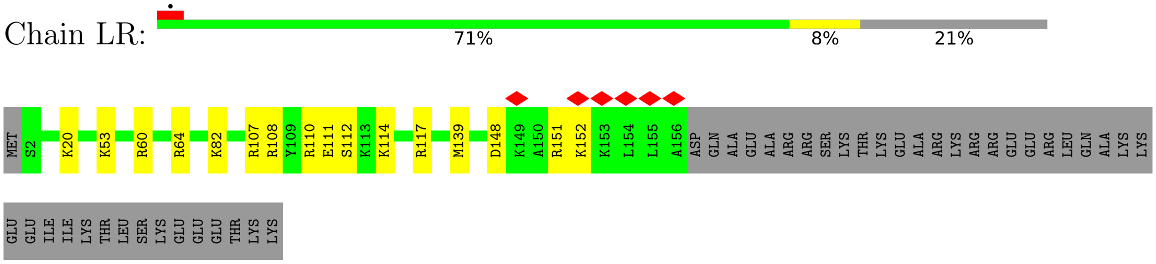
- Molecule 23: 60S ribosomal protein L17



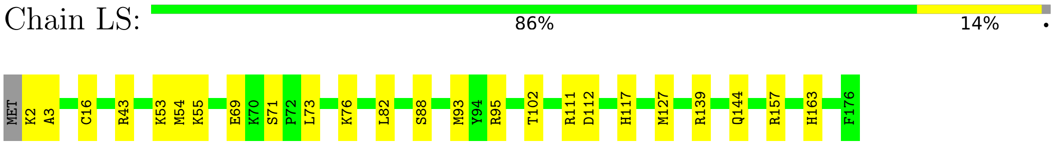
- Molecule 24: 60S ribosomal protein L18



- Molecule 25: 60S ribosomal protein L19



- Molecule 26: 60S ribosomal protein L18a



- Molecule 27: 60S ribosomal protein L21

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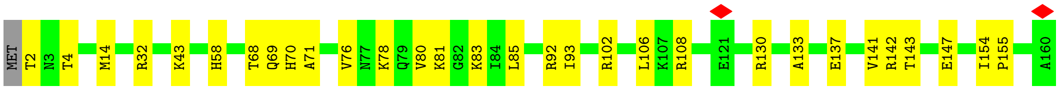
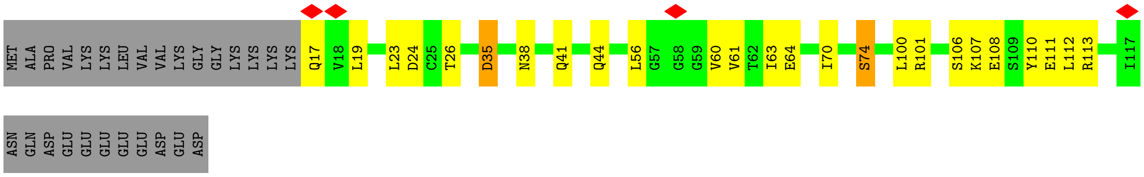


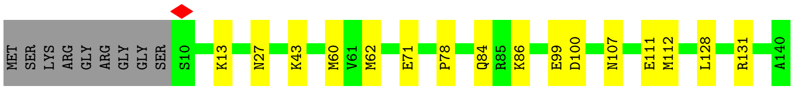
- Molecule 28: 60S ribosomal protein L22

Chain LU:



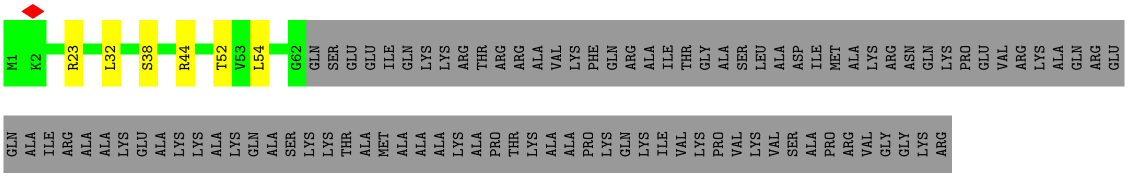
- Molecule 29: 60S ribosomal protein L23

Chain LV:



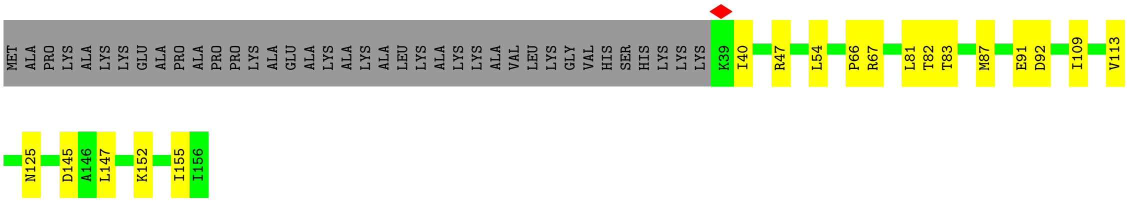
- Molecule 30: 60S ribosomal protein L24

Chain LW:



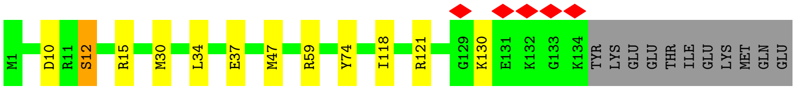
- Molecule 31: 60S ribosomal protein L23a

Chain LX:



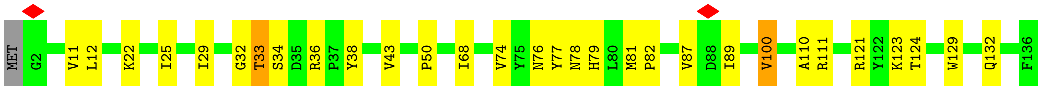
- Molecule 32: 60S ribosomal protein L26

Chain LY:



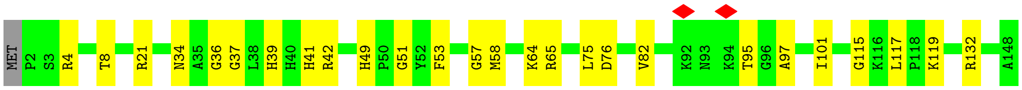
- Molecule 33: 60S ribosomal protein L27

Chain LZ:



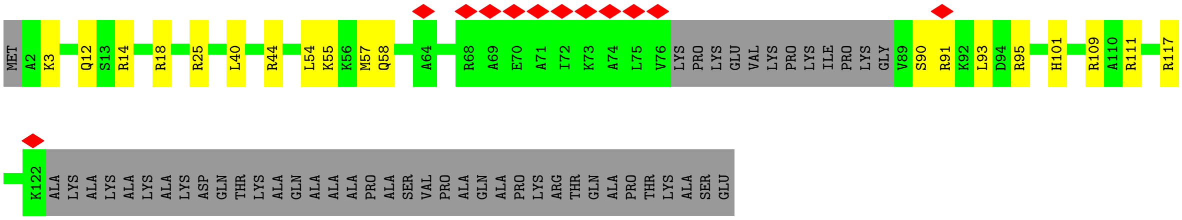
- Molecule 34: 60S ribosomal protein L27a

Chain La:



- Molecule 35: 60S ribosomal protein L29

Chain Lb:

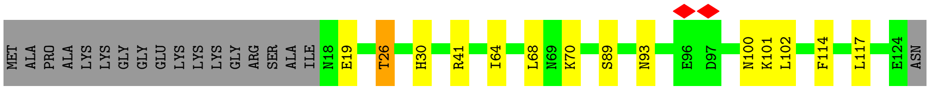


- Molecule 36: 60S ribosomal protein L30

Chain Lc:

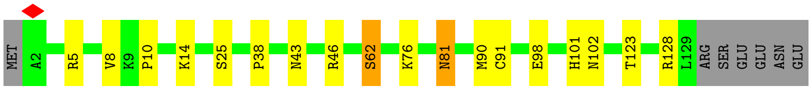
- Molecule 37: 60S ribosomal protein L31

Chain Ld:



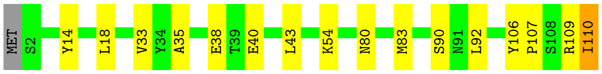
- Molecule 38: 60S ribosomal protein L32

Chain Le:



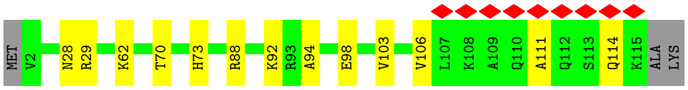
- Molecule 39: 60S ribosomal protein L35a

Chain Lf:



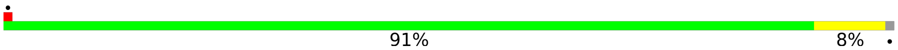
- Molecule 40: 60S ribosomal protein L34

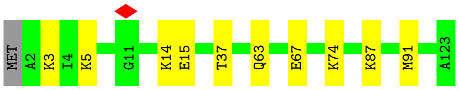
Chain Lg:



- Molecule 41: 60S ribosomal protein L35

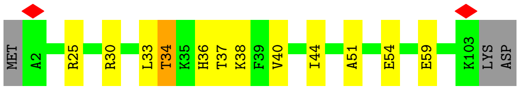
Chain Lh:





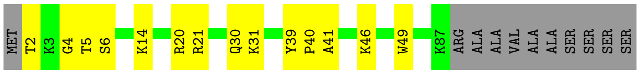
- Molecule 42: 60S ribosomal protein L36

Chain Li:



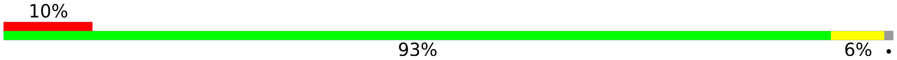
- Molecule 43: 60S ribosomal protein L37

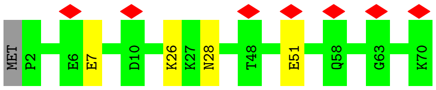
Chain Lj:



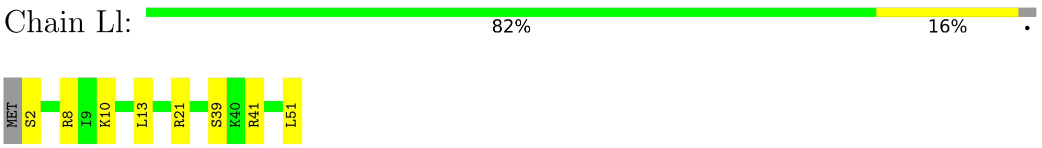
- Molecule 44: 60S ribosomal protein L38

Chain Lk:

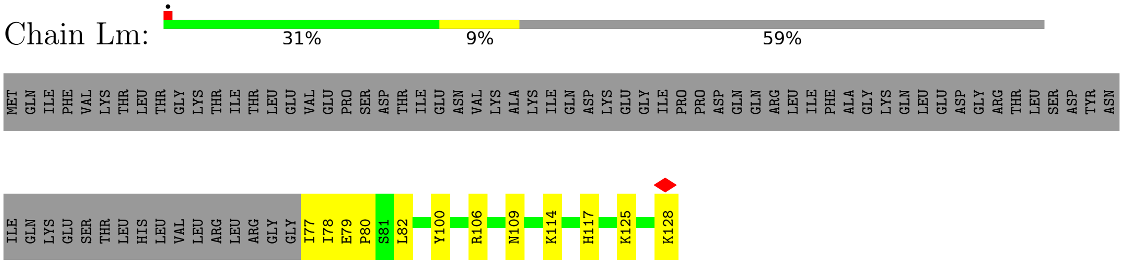




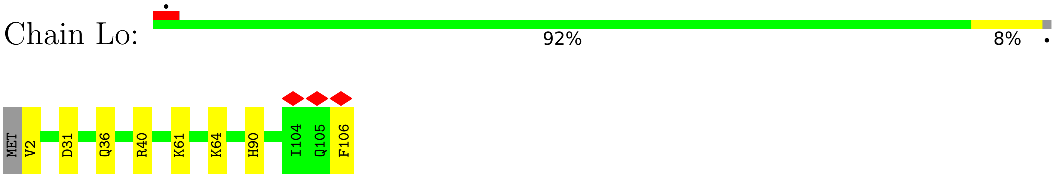
- Molecule 45: 60S ribosomal protein L39



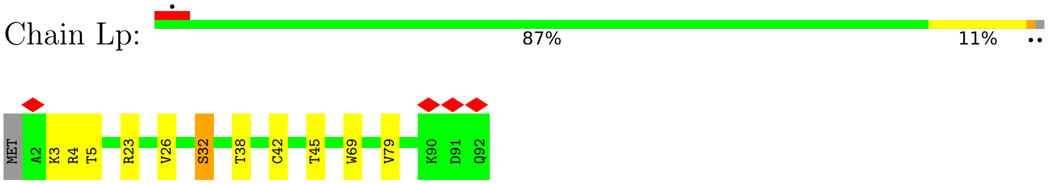
- Molecule 46: Ubiquitin-60S ribosomal protein L40



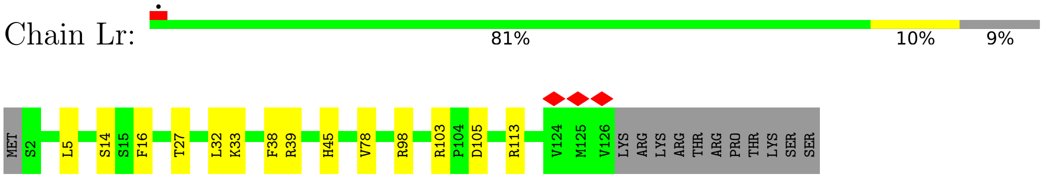
- Molecule 47: 60S ribosomal protein L36a



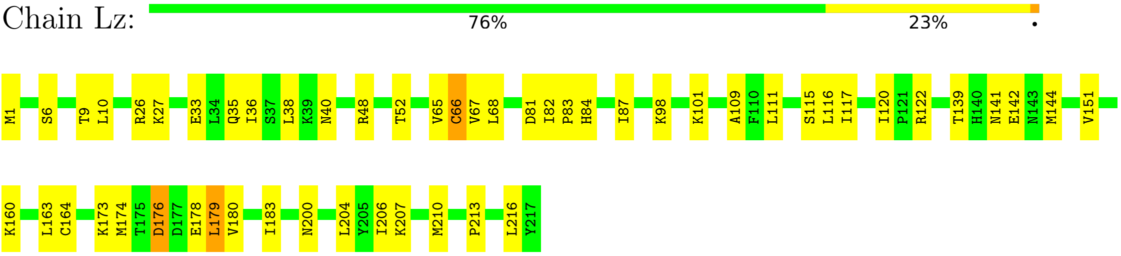
- Molecule 48: 60S ribosomal protein L37a



- Molecule 49: 60S ribosomal protein L28

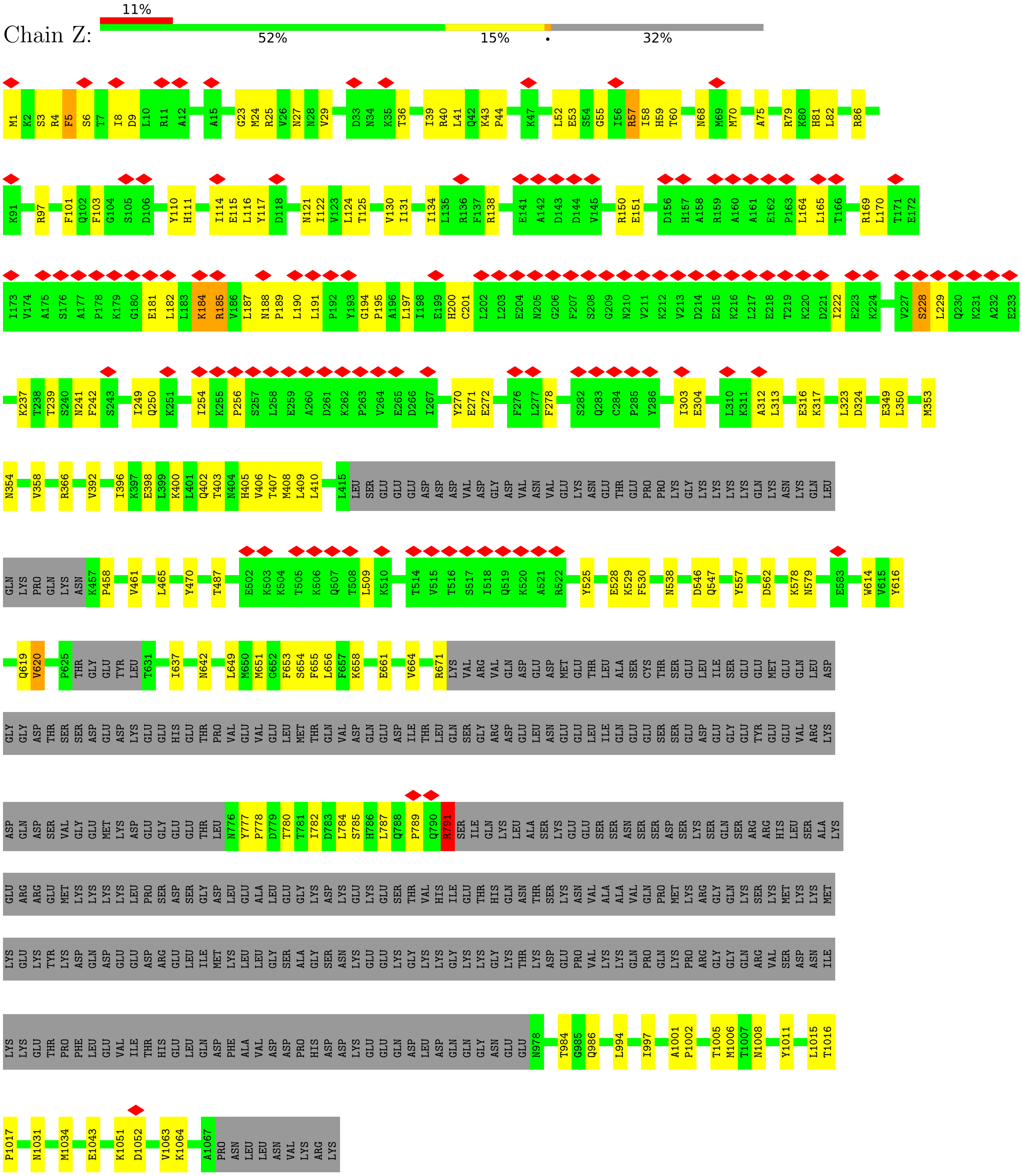


- Molecule 50: 60S ribosomal protein L10a



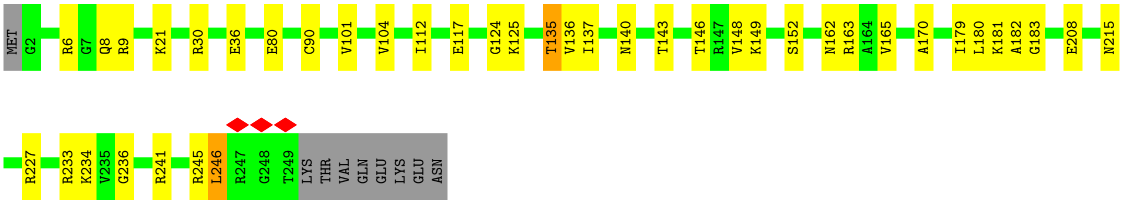
- Molecule 51: Ribosome quality control complex subunit NEMF

Chain Z:



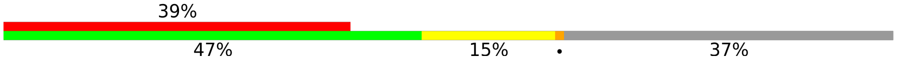
- Molecule 52: 60S ribosomal protein L8

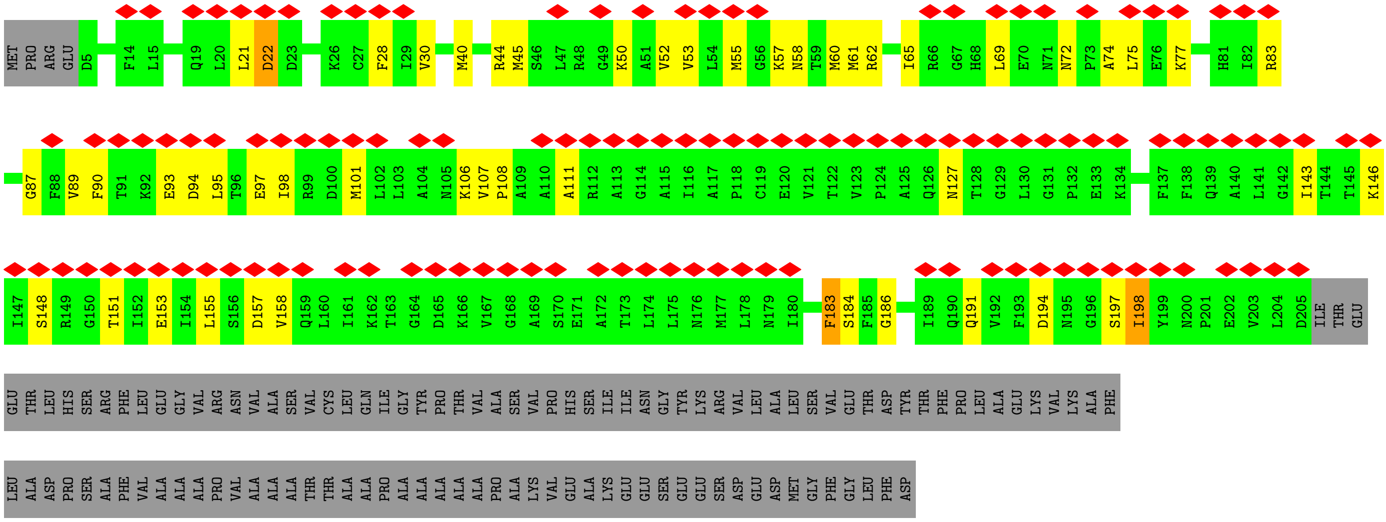
Chain a:



- Molecule 53: 60S acidic ribosomal protein P0

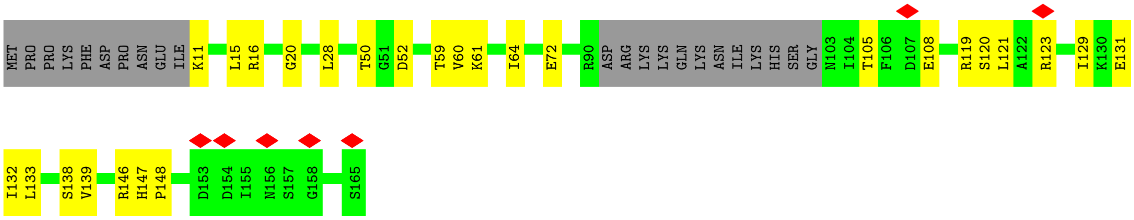
Chain s:





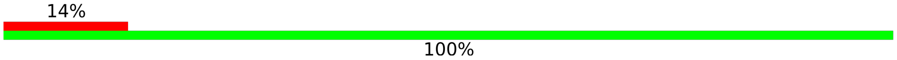
- Molecule 54: Large ribosomal subunit protein uL11

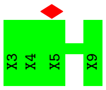
Chain t:



- Molecule 55: Nascent chain

Chain A:





4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8461	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\mathring{A}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	16.014	Depositor
Minimum map value	-13.967	Depositor
Average map value	0.033	Depositor
Map value standard deviation	1.069	Depositor
Recommended contour level	2.7	Depositor
Map size (Å)	436.2, 436.2, 436.2	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#|Z| >5$	RMSZ	$\#|Z| >5$
1	5	0.08	0/84644	0.21	0/132019
2	7	0.08	0/2861	0.19	0/4459
3	8	0.08	0/3520	0.21	0/5481
4	B	0.19	0/3280	0.42	1/4426 (0.0%)
5	C	0.11	0/1560	0.38	0/2085
6	D	0.11	0/601	0.33	0/818
7	E	0.13	0/5322	0.38	0/7181
8	F	0.16	0/13702	0.39	1/18567 (0.0%)
9	G	0.08	0/1810	0.21	0/2821
10	LB	0.11	0/3307	0.37	0/4424
11	LC	0.12	0/2981	0.42	0/4002
12	LD	0.11	0/2428	0.38	0/3252
13	LE	0.13	0/1799	0.41	0/2414
14	LF	0.11	0/1905	0.40	0/2539
15	LG	0.12	0/1960	0.41	0/2637
16	LH	0.11	0/1537	0.37	0/2066
17	LI	0.12	0/1750	0.41	0/2340
18	LJ	0.11	0/1424	0.41	0/1904
19	LL	0.14	0/1604	0.49	0/2149
20	LM	0.10	0/1142	0.37	0/1527
21	LN	0.13	0/1746	0.46	0/2338
22	LO	0.12	0/1682	0.41	0/2250
23	LP	0.11	0/1268	0.40	0/1701
24	LQ	0.14	0/1537	0.48	0/2052
25	LR	0.13	0/1310	0.48	0/1734
26	LS	0.14	0/1493	0.44	0/2003
27	LT	0.14	0/1326	0.44	0/1770
28	LU	0.16	0/839	0.47	0/1126
29	LV	0.11	0/993	0.39	0/1332
30	LW	0.11	0/532	0.40	0/708
31	LX	0.12	0/984	0.42	0/1323
32	LY	0.13	0/1132	0.45	0/1504

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	LZ	0.13	0/1130	0.41	0/1507
34	La	0.12	0/1191	0.42	0/1591
35	Lb	0.12	0/889	0.44	0/1175
36	Lc	0.11	0/774	0.34	0/1038
37	Ld	0.13	0/903	0.44	0/1216
38	Le	0.13	0/1071	0.46	0/1429
39	Lf	0.12	0/895	0.43	0/1198
40	Lg	0.13	0/916	0.47	0/1220
41	Lh	0.12	0/1023	0.43	0/1351
42	Li	0.12	0/843	0.46	0/1115
43	Lj	0.13	0/720	0.47	0/952
44	Lk	0.13	0/575	0.39	0/761
45	Ll	0.14	0/454	0.50	0/599
46	Lm	0.13	0/435	0.47	0/575
47	Lo	0.12	0/877	0.40	0/1156
48	Lp	0.10	0/718	0.37	0/953
49	Lr	0.13	0/1017	0.45	0/1364
50	Lz	0.12	0/1772	0.40	0/2375
51	Z	0.19	0/6010	0.42	0/8115
52	a	0.13	0/1936	0.44	0/2596
53	s	0.15	0/1569	0.42	1/2119 (0.0%)
54	t	0.14	0/1081	0.46	0/1460
All	All	0.11	0/180778	0.32	3/262817 (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
51	Z	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	470	PRO	N-CA-C	-6.77	103.79	113.47
53	s	108	PRO	CA-N-CD	-5.96	103.66	112.00
8	F	734	PRO	CA-N-CD	-5.89	103.75	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
51	Z	185	ARG	Sidechain
51	Z	791	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	5	75663	0	38217	887	0
2	7	2561	0	1295	24	0
3	8	3152	0	1601	33	0
4	B	3234	0	3287	48	0
5	C	1547	0	1543	12	0
6	D	588	0	616	0	0
7	E	5251	0	5358	73	0
8	F	13415	0	13576	248	0
9	G	1622	0	820	20	0
10	LB	3239	0	3376	41	0
11	LC	2927	0	3104	27	0
12	LD	2382	0	2410	26	0
13	LE	1765	0	1917	21	0
14	LF	1870	0	1996	15	0
15	LG	1927	0	2074	16	0
16	LH	1518	0	1601	11	0
17	LI	1710	0	1748	23	0
18	LJ	1401	0	1428	10	0
19	LL	1573	0	1681	16	0
20	LM	1120	0	1187	16	0
21	LN	1701	0	1749	25	0
22	LO	1650	0	1794	12	0
23	LP	1242	0	1269	9	0
24	LQ	1513	0	1628	19	0
25	LR	1294	0	1434	14	0
26	LS	1453	0	1490	15	0
27	LT	1298	0	1366	26	0
28	LU	825	0	850	18	0
29	LV	979	0	1039	12	0
30	LW	519	0	533	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	LX	967	0	1040	14	0
32	LY	1115	0	1205	12	0
33	LZ	1107	0	1182	18	0
34	La	1162	0	1213	22	0
35	Lb	876	0	948	17	0
36	Lc	764	0	804	8	0
37	Ld	888	0	930	9	0
38	Le	1053	0	1147	15	0
39	Lf	876	0	912	12	0
40	Lg	906	0	998	9	0
41	Lh	1015	0	1148	6	0
42	Li	832	0	917	8	0
43	Lj	705	0	737	11	0
44	Lk	569	0	637	3	0
45	Ll	444	0	483	10	0
46	Lm	429	0	465	12	0
47	Lo	863	0	929	5	0
48	Lp	708	0	756	10	0
49	Lr	1002	0	1068	8	0
50	Lz	1744	0	1859	31	0
51	Z	5891	0	5986	106	0
52	a	1898	0	1993	34	0
53	s	1545	0	1599	33	0
54	t	1068	0	1113	23	0
55	A	35	0	10	0	0
56	5	205	0	0	0	0
56	7	2	0	0	0	0
56	8	5	0	0	0	0
56	LI	1	0	0	0	0
56	LP	1	0	0	0	0
56	LV	1	0	0	0	0
56	Le	1	0	0	0	0
56	Lf	1	0	0	0	0
56	Lg	1	0	0	0	0
56	Lj	1	0	0	0	0
57	Lg	1	0	0	0	0
57	Lj	1	0	0	0	0
57	Lm	1	0	0	0	0
57	Lo	1	0	0	0	0
57	Lp	1	0	0	0	0
All	All	169625	0	132066	1852	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 (1852) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2520:C:O2	1:5:2640:G:N2	2.14	0.80
8:F:286:ILE:HD12	8:F:287:PRO:HD2	1.65	0.78
1:5:1293:G:OP2	1:5:1293:G:N2	2.16	0.78
51:Z:350:LEU:O	51:Z:354:ASN:ND2	2.17	0.78
26:LS:69:GLU:OE1	26:LS:102:THR:N	2.16	0.78
9:G:54:U:O2	9:G:58:A:N7	2.17	0.77
51:Z:784:LEU:HD13	51:Z:787:LEU:HB2	1.67	0.77
1:5:3653:A:O2’	52:a:179:ILE:O	2.03	0.77
1:5:3776:G:N2	1:5:3776:G:OP2	2.19	0.76
1:5:3809:G:N2	1:5:3809:G:OP2	2.18	0.75
1:5:941:C:OP2	14:LF:242:ARG:NH2	2.20	0.75
8:F:110:PHE:HA	8:F:113:ILE:HG22	1.69	0.75
7:E:574:LEU:HA	7:E:578:CYS:HB3	1.66	0.75
1:5:1845:U:H5”	35:Lb:25:ARG:HH12	1.52	0.74
8:F:1644:ILE:HG13	8:F:1669:VAL:HG21	1.69	0.74
11:LC:287:THR:HG21	49:Lr:5:LEU:HB2	1.69	0.74
7:E:207:ILE:HD11	7:E:217:LEU:HG	1.68	0.74
29:LV:71:GLU:OE1	29:LV:71:GLU:N	2.20	0.74
1:5:4115:G:N2	1:5:4115:G:OP2	2.20	0.74
24:LQ:94:GLU:N	24:LQ:94:GLU:OE1	2.21	0.73
1:5:1172:C:H3’	1:5:1173:G:H21	1.53	0.73
8:F:1632:THR:HG23	8:F:1634:GLU:HG2	1.70	0.73
1:5:1332:C:H2’	1:5:1333:A:H8	1.54	0.73
1:5:2845:A:H61	1:5:3843:C:H42	1.35	0.73
1:5:3641:U:OP2	1:5:3646:A:N6	2.22	0.73
1:5:3697:U:H5”	1:5:3698:G:H5’	1.71	0.73
2:7:51:G:H21	18:LJ:12:MET:HE1	1.52	0.73
3:8:110:U:OP2	45:Ll:8:ARG:NH1	2.22	0.73
1:5:1984:A:N7	1:5:2010:A:O2’	2.22	0.72
1:5:1750:G:N2	17:LI:193:ASP:OD1	2.22	0.72
1:5:74:G:H5’	19:LL:59:VAL:HB	1.71	0.72
4:B:401:MET:N	4:B:401:MET:SD	2.62	0.71
51:Z:349:GLU:HG2	51:Z:353:MET:HE1	1.72	0.71
1:5:1494:U:H2’	1:5:1495:G:H8	1.55	0.71
4:B:469:GLU:HB3	4:B:470:PRO:HD3	1.71	0.71
8:F:586:ARG:HD2	8:F:590:LEU:HD12	1.73	0.71
1:5:4052:C:O2	50:Lz:207:LYS:NZ	2.23	0.71
8:F:1228:LEU:HA	8:F:1231:PHE:HB3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1878:G:OP2	35:Lb:14:ARG:NH1	2.24	0.70
1:5:235:A:OP1	11:LC:201:ARG:NH1	2.25	0.70
1:5:67:C:OP2	1:5:312:G:N2	2.25	0.70
1:5:4620:U:OP2	1:5:4670:C:N4	2.23	0.70
1:5:308:G:N2	1:5:308:G:OP2	2.21	0.70
1:5:2431:A:OP1	45:Ll:41:ARG:NH1	2.25	0.69
7:E:699:HIS:ND1	7:E:699:HIS:O	2.26	0.69
2:7:27:G:N7	12:LD:58:ARG:NH1	2.40	0.69
8:F:1064:LEU:HD13	8:F:1067:LEU:HD12	1.75	0.69
1:5:1985:G:N2	1:5:2003:G:O2’	2.25	0.69
1:5:2407:G:N2	1:5:2407:G:OP2	2.26	0.69
1:5:4454:G:H1	1:5:4526:U:H3	1.39	0.69
7:E:739:LEU:HD13	51:Z:778:PRO:HG3	1.75	0.69
1:5:2601:A:N6	1:5:2744:A:OP2	2.26	0.68
8:F:69:LEU:HD11	8:F:102:VAL:HG23	1.74	0.68
8:F:191:THR:HG23	8:F:250:LYS:HE3	1.74	0.68
1:5:454:U:O2	38:Le:5:ARG:NH1	2.26	0.68
1:5:2296:G:O2’	11:LC:242:PRO:O	2.12	0.68
4:B:224:LEU:HD13	4:B:227:LEU:HD12	1.75	0.68
44:Lk:51:GLU:N	44:Lk:51:GLU:OE1	2.27	0.68
51:Z:1:MET:HE2	51:Z:1:MET:HA	1.74	0.68
1:5:3774:A:H2’	1:5:3775:A:C8	2.29	0.67
8:F:750:ASP:O	8:F:754:ASN:ND2	2.26	0.67
54:t:146:ARG:NE	54:t:147:HIS:H	1.92	0.67
1:5:1555:G:O6	48:Lp:4:ARG:NH1	2.28	0.67
23:LP:140:MET:HA	23:LP:140:MET:HE3	1.77	0.67
1:5:4527:G:N2	1:5:4527:G:OP2	2.27	0.67
4:B:391:GLN:O	50:Lz:1:MET:N	2.27	0.67
28:LU:108:GLU:OE1	28:LU:108:GLU:N	2.27	0.67
1:5:1645:C:OP1	11:LC:80:ARG:NH2	2.28	0.67
1:5:4047:A:OP1	50:Lz:101:LYS:NZ	2.27	0.67
8:F:631:LYS:HA	8:F:631:LYS:HE2	1.77	0.67
8:F:1434:PRO:HD2	8:F:1439:MET:HE1	1.77	0.67
51:Z:651:MET:HE2	51:Z:651:MET:HA	1.76	0.67
1:5:4472:G:O2’	46:Lm:100:TYR:O	2.13	0.66
7:E:709:VAL:HA	7:E:712:ILE:HG12	1.78	0.66
8:F:272:ARG:NH1	8:F:309:ASP:OD2	2.28	0.66
8:F:1035:GLN:HB3	8:F:1087:LEU:HD22	1.76	0.66
1:5:75:G:O2’	19:LL:101:ARG:NH2	2.28	0.66
1:5:4670:C:O2’	1:5:4672:A:OP2	2.13	0.66
51:Z:70:MET:H	51:Z:70:MET:HE2	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2660:A:OP1	25:LR:117:ARG:NH1	2.26	0.66
1:5:3700:C:O2'	1:5:3774:A:N3	2.24	0.66
8:F:1580:ARG:NH2	8:F:1657:PRO:O	2.28	0.66
1:5:1516:G:O2'	19:LL:18:TRP:NE1	2.29	0.66
8:F:662:LEU:HG	8:F:666:LEU:HD22	1.77	0.66
1:5:2262:G:OP2	49:Lr:98:ARG:NH2	2.28	0.66
1:5:3659:G:OP1	52:a:241:ARG:NH2	2.29	0.66
8:F:1439:MET:HA	8:F:1442:LEU:HB2	1.76	0.66
27:LT:43:LYS:O	27:LT:58:HIS:ND1	2.29	0.66
1:5:2580:U:HO2'	33:LZ:79:HIS:HD1	1.42	0.65
8:F:1389:LEU:HD22	8:F:1401:VAL:HG11	1.78	0.65
38:Le:90:MET:HE2	38:Le:90:MET:HA	1.79	0.65
51:Z:101:PHE:HB3	51:Z:103:PHE:HE1	1.60	0.65
16:LH:107:GLU:OE1	16:LH:127:ARG:NH2	2.30	0.65
24:LQ:50:ARG:HA	24:LQ:53:MET:HG3	1.78	0.65
51:Z:53:GLU:OE1	51:Z:57:ARG:NH2	2.29	0.65
1:5:1982:G:N2	1:5:2010:A:OP1	2.29	0.65
1:5:1326:A:OP2	1:5:4445:U:O2'	2.13	0.65
8:F:358:VAL:HG23	8:F:359:ILE:HG12	1.78	0.65
9:G:57:G:N2	9:G:60:U:O4	2.29	0.65
1:5:4313:A:OP1	27:LT:92:ARG:NH2	2.30	0.64
1:5:4954:G:H2'	1:5:4955:A:C8	2.32	0.64
54:t:15:LEU:HD21	54:t:28:LEU:HD11	1.77	0.64
1:5:1697:G:N2	1:5:2084:C:OP1	2.30	0.64
8:F:1650:ILE:HG12	8:F:1663:VAL:HG12	1.80	0.64
28:LU:23:LEU:HB2	28:LU:70:ILE:HB	1.79	0.64
28:LU:64:GLU:N	28:LU:64:GLU:OE1	2.31	0.64
1:5:454:U:H1'	38:Le:5:ARG:HH22	1.63	0.64
8:F:116:ASP:O	8:F:223:ARG:NH2	2.31	0.64
22:LO:109:PRO:HB2	22:LO:111:PRO:HD2	1.77	0.64
1:5:3689:G:O2'	1:5:3818:U:OP2	2.16	0.64
8:F:1172:ASN:ND2	8:F:1223:GLU:O	2.29	0.64
31:LX:82:THR:HG22	31:LX:155:ILE:HG23	1.80	0.64
1:5:1670:G:OP1	35:Lb:12:GLN:NE2	2.31	0.64
1:5:3962:A:N6	1:5:3965:A:O2'	2.29	0.64
1:5:1890:G:N2	1:5:1890:G:OP2	2.31	0.64
1:5:4165:C:OP1	15:LG:245:LYS:NZ	2.31	0.64
8:F:249:GLU:OE1	8:F:249:GLU:N	2.28	0.64
1:5:200:U:O2'	32:LY:59:ARG:NH1	2.31	0.64
26:LS:71:SER:O	26:LS:76:LYS:NZ	2.30	0.64
1:5:4122:G:N1	40:Lg:98:GLU:OE2	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4546:A:N7	52:a:215:ASN:ND2	2.45	0.63
51:Z:400:LYS:NZ	51:Z:407:THR:OG1	2.32	0.63
1:5:1933:G:H2'	1:5:1934:A:C8	2.32	0.63
1:5:2522:G:OP1	40:Lg:29:ARG:NH2	2.31	0.63
8:F:116:ASP:O	8:F:122:ARG:NH1	2.31	0.63
8:F:470:LYS:HD2	8:F:483:LEU:HD13	1.81	0.63
41:Lh:15:GLU:OE1	41:Lh:15:GLU:N	2.26	0.63
1:5:3823:G:N2	1:5:3823:G:OP2	2.31	0.63
7:E:46:GLU:N	7:E:46:GLU:OE1	2.31	0.63
1:5:62:A:N3	1:5:77:U:O2'	2.26	0.63
1:5:2520:C:H2'	1:5:2521:G:H8	1.64	0.63
16:LH:137:SER:HB3	16:LH:143:GLU:HB3	1.79	0.63
1:5:369:G:N2	1:5:372:A:OP2	2.27	0.63
8:F:432:MET:O	8:F:432:MET:HE3	1.98	0.63
1:5:4220:A:OP2	27:LT:2:THR:N	2.31	0.63
25:LR:108:ARG:HH21	25:LR:108:ARG:HG3	1.64	0.63
27:LT:137:GLU:OE1	27:LT:137:GLU:N	2.24	0.63
8:F:145:LYS:HA	8:F:148:MET:HE1	1.81	0.63
1:5:4563:U:H2'	1:5:4564:A:H8	1.63	0.62
7:E:692:LEU:HD13	7:E:783:VAL:HG11	1.81	0.62
1:5:419:A:N3	1:5:1332:C:O2'	2.30	0.62
7:E:131:LEU:HG	7:E:179:THR:HG22	1.79	0.62
7:E:377:ARG:HA	7:E:380:MET:HB2	1.82	0.62
9:G:17:C:O2	9:G:57:G:N2	2.33	0.62
13:LE:153:LEU:HD11	13:LE:195:ILE:HG13	1.80	0.62
42:Li:34:THR:HG22	42:Li:37:THR:H	1.63	0.62
1:5:2257:C:O2'	1:5:2259:G:OP2	2.13	0.62
8:F:1409:MET:HA	8:F:1412:LEU:HG	1.80	0.62
51:Z:97:ARG:HB3	51:Z:116:LEU:HB3	1.81	0.62
41:Lh:87:LYS:HB3	41:Lh:91:MET:HE2	1.81	0.62
1:5:4617:G:OP2	10:LB:358:ARG:NH1	2.33	0.62
2:7:48:G:OP1	12:LD:226:TYR:OH	2.15	0.62
1:5:4392:G:N2	1:5:4395:U:O2	2.31	0.62
1:5:1802:A:H5"	1:5:1803:G:H5'	1.80	0.62
1:5:2318:G:N2	1:5:2321:G:OP2	2.24	0.62
1:5:4474:A:OP2	1:5:4476:C:N4	2.32	0.62
54:t:133:LEU:HB3	54:t:148:PRO:HB3	1.81	0.62
1:5:1517:G:H22	11:LC:103:ALA:HA	1.65	0.61
1:5:1739:G:N3	1:5:1742:A:N6	2.48	0.61
1:5:1866:U:OP1	17:LI:4:ARG:NH2	2.25	0.61
1:5:2324:C:O2'	38:Le:98:GLU:OE1	2.17	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:440:LYS:O	4:B:444:SER:N	2.33	0.61
27:LT:68:THR:HG22	27:LT:69:GLN:H	1.65	0.61
51:Z:1016:THR:O	51:Z:1064:LYS:N	2.31	0.61
1:5:4566:U:O2'	10:LB:234:ARG:NH2	2.32	0.61
50:Lz:139:THR:OG1	50:Lz:141:ASN:OD1	2.17	0.61
1:5:1961:G:N2	1:5:2024:G:O2'	2.32	0.61
1:5:2588:C:OP1	1:5:2768:C:O2'	2.18	0.61
1:5:4524:G:C2	10:LB:252:ALA:HB1	2.35	0.61
50:Lz:48:ARG:NH2	50:Lz:160:LYS:O	2.33	0.61
1:5:2777:G:H5"	1:5:2778:G:H5'	1.81	0.61
1:5:4522:G:O2'	1:5:4525:C:OP2	2.18	0.61
1:5:4044:U:OP1	50:Lz:98:LYS:NZ	2.32	0.61
1:5:1930:U:OP2	22:LO:49:ARG:NH2	2.31	0.61
1:5:4272:G:OP2	1:5:4272:G:N2	2.23	0.61
48:Lp:79:VAL:HG22	52:a:112:ILE:HD13	1.81	0.61
1:5:2411:C:H2'	1:5:2412:A:H8	1.66	0.60
21:LN:193:ARG:O	21:LN:197:THR:OG1	2.18	0.60
1:5:323:C:H2'	1:5:324:A:H8	1.67	0.60
1:5:1779:U:H2'	1:5:1780:A:C8	2.36	0.60
15:LG:134:PRO:HB3	15:LG:206:GLN:HG3	1.83	0.60
28:LU:56:LEU:HD12	28:LU:61:VAL:HB	1.83	0.60
51:Z:27:ASN:O	51:Z:79:ARG:NH1	2.34	0.60
13:LE:99:ASP:OD1	13:LE:99:ASP:N	2.35	0.60
1:5:1332:C:H2'	1:5:1333:A:C8	2.37	0.60
8:F:425:GLY:N	8:F:430:GLU:OE2	2.34	0.60
8:F:732:VAL:HG22	8:F:735:TRP:HB3	1.82	0.60
1:5:1268:G:N7	35:Lb:111:ARG:NH1	2.49	0.60
8:F:1461:ILE:HD11	8:F:1521:PRO:HA	1.83	0.60
17:LI:14:ASN:O	17:LI:128:ARG:NH1	2.34	0.60
1:5:2562:G:N2	1:5:2565:A:OP2	2.35	0.60
1:5:2702:C:O3'	28:LU:113:ARG:NH1	2.35	0.60
1:5:3848:U:H2'	1:5:3849:A:H8	1.67	0.60
7:E:155:GLN:N	7:E:155:GLN:OE1	2.35	0.60
8:F:224:VAL:O	8:F:228:SER:OG	2.19	0.60
11:LC:144:ILE:HD13	11:LC:150:LEU:HD13	1.84	0.60
4:B:158:ARG:NH1	4:B:444:SER:OG	2.35	0.60
51:Z:1031:ASN:HA	51:Z:1034:MET:HE2	1.82	0.60
1:5:24:G:N7	43:Lj:46:LYS:NZ	2.50	0.60
1:5:4094:G:H2'	1:5:4095:G:C8	2.36	0.60
1:5:4541:G:N2	1:5:4544:A:OP2	2.29	0.60
1:5:947:C:OP1	11:LC:336:ARG:NH2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:507:LYS:NZ	7:E:507:LYS:O	2.35	0.59
8:F:1274:ALA:HB1	8:F:1342:MET:HE3	1.84	0.59
9:G:62:C:H2'	9:G:63:G:C8	2.36	0.59
24:LQ:6:ARG:NH1	35:Lb:18:ARG:O	2.35	0.59
53:s:106:LYS:HD3	53:s:107:VAL:H	1.66	0.59
3:8:67:U:H2'	3:8:68:G:H8	1.67	0.59
28:LU:17:GLN:HB3	28:LU:19:LEU:HD13	1.83	0.59
46:Lm:79:GLU:HB2	46:Lm:82:LEU:H	1.66	0.59
51:Z:40:ARG:NH1	51:Z:41:LEU:O	2.35	0.59
51:Z:97:ARG:HE	51:Z:117:TYR:HB3	1.66	0.59
1:5:1283:G:N1	1:5:2076:G:OP1	2.35	0.59
8:F:1029:GLU:OE2	8:F:1080:ARG:NH2	2.35	0.59
1:5:4301:U:OP1	27:LT:78:LYS:NZ	2.34	0.59
1:5:2735:G:H2'	1:5:2736:G:H8	1.66	0.59
1:5:1554:A:OP2	48:Lp:4:ARG:NH2	2.34	0.59
1:5:1646:A:O2'	43:Lj:49:TRP:O	2.21	0.59
50:Lz:65:VAL:HG12	50:Lz:109:ALA:HB3	1.85	0.59
51:Z:546:ASP:OD1	51:Z:547:GLN:N	2.35	0.59
1:5:2845:A:H61	1:5:3843:C:N4	1.99	0.59
1:5:4467:A:O2'	1:5:4510:A:N3	2.28	0.59
8:F:409:ILE:HG12	8:F:456:LEU:HD12	1.85	0.59
14:LF:105:VAL:HG13	14:LF:136:VAL:HG23	1.85	0.59
29:LV:43:LYS:HG3	29:LV:60:MET:HG2	1.84	0.59
1:5:1315:C:N4	1:5:1316:G:O6	2.35	0.59
8:F:915:ASN:OD1	8:F:916:SER:N	2.36	0.59
50:Lz:10:LEU:HD21	50:Lz:183:ILE:HB	1.85	0.59
51:Z:986:GLN:NE2	51:Z:1008:ASN:O	2.36	0.59
1:5:4694:G:N2	1:5:4694:G:OP1	2.32	0.59
12:LD:217:ASP:N	12:LD:217:ASP:OD1	2.35	0.59
2:7:7:G:OP1	12:LD:33:ARG:NH2	2.33	0.58
53:s:55:MET:N	53:s:55:MET:HE3	2.18	0.58
1:5:3661:G:N7	52:a:152:SER:OG	2.37	0.58
1:5:4699:U:H1'	1:5:4700:A:H5"	1.84	0.58
8:F:164:PHE:O	8:F:168:ASP:N	2.34	0.58
27:LT:80:VAL:HG23	27:LT:81:LYS:H	1.69	0.58
1:5:1613:A:H5'	52:a:183:GLY:HA2	1.85	0.58
1:5:4238:G:H2'	1:5:4239:A:H8	1.69	0.58
1:5:4364:G:H1'	34:La:58:MET:HE3	1.85	0.58
8:F:290:MET:HE2	8:F:327:ILE:HD11	1.85	0.58
27:LT:147:GLU:OE1	27:LT:147:GLU:N	2.36	0.58
1:5:130:C:N4	1:5:131:C:N4	2.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:327:U:O2'	42:Li:30:ARG:NH2	2.35	0.58
1:5:4996:C:H4'	37:Ld:26:THR:HG23	1.85	0.58
7:E:545:SER:O	7:E:549:ASN:ND2	2.36	0.58
8:F:1307:TRP:HA	8:F:1311:PHE:HB2	1.85	0.58
8:F:1639:TYR:OH	8:F:1706:ASP:OD1	2.20	0.58
1:5:2579:G:N2	1:5:2582:A:OP2	2.25	0.58
2:7:99:G:N7	26:LS:55:LYS:NZ	2.51	0.58
8:F:705:LEU:HA	8:F:709:ASP:HB2	1.85	0.58
1:5:956:A:H1'	1:5:2076:G:H5"	1.85	0.58
1:5:2413:U:H2'	1:5:2414:G:H8	1.69	0.58
1:5:4274:A:H2'	1:5:4275:G:H8	1.68	0.58
32:LY:37:GLU:N	32:LY:37:GLU:OE1	2.33	0.58
51:Z:43:LYS:HG3	51:Z:44:PRO:HD2	1.84	0.58
1:5:4567:G:H5'	10:LB:20:LYS:HB3	1.86	0.58
9:G:62:C:H2'	9:G:63:G:H8	1.67	0.58
42:Li:51:ALA:HB3	42:Li:54:GLU:HG3	1.85	0.58
8:F:103:LEU:HD21	8:F:136:VAL:HG11	1.86	0.58
1:5:1577:G:O2'	1:5:1612:G:H4'	2.04	0.57
8:F:696:MET:SD	8:F:696:MET:N	2.77	0.57
8:F:1282:CYS:HB3	8:F:1349:THR:HA	1.86	0.57
1:5:45:U:O4	21:LN:83:LYS:NZ	2.36	0.57
1:5:1988:G:H2'	1:5:1989:G:C8	2.39	0.57
1:5:4431:U:OP2	17:LI:3:ARG:NH1	2.37	0.57
46:Lm:77:ILE:HG23	46:Lm:78:ILE:HG13	1.86	0.57
1:5:85:G:O2'	1:5:97:G:O6	2.22	0.57
4:B:120:ARG:HH22	5:C:230:LEU:HD21	1.69	0.57
7:E:108:GLN:NE2	7:E:117:GLU:OE2	2.36	0.57
9:G:3:G:O6	9:G:71:C:N4	2.38	0.57
1:5:1279:A:O2'	1:5:1281:G:N7	2.37	0.57
1:5:2702:C:OP1	28:LU:101:ARG:NH1	2.35	0.57
1:5:3620:G:OP1	1:5:3622:C:N4	2.37	0.57
8:F:96:THR:HG22	8:F:100:LYS:HE2	1.86	0.57
51:Z:52:LEU:HA	51:Z:58:ILE:HG12	1.87	0.57
1:5:1732:C:H2'	1:5:1733:G:C8	2.40	0.57
34:La:39:HIS:O	34:La:42:ARG:N	2.37	0.57
51:Z:201:CYS:SG	51:Z:228:SER:OG	2.55	0.57
1:5:3873:G:H2'	1:5:3874:G:C8	2.39	0.57
21:LN:103:GLU:OE2	21:LN:118:SER:OG	2.23	0.57
1:5:1706:A:OP2	14:LF:46:ARG:NH1	2.29	0.57
1:5:4924:C:H1'	1:5:4926:C:H41	1.69	0.57
8:F:144:LEU:O	8:F:147:LEU:N	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Lc:34:THR:HG23	36:Lc:95:ALA:HB2	1.87	0.57
3:8:51:U:O3'	45:Ll:21:ARG:NH1	2.38	0.57
1:5:1779:U:H2'	1:5:1780:A:H8	1.70	0.56
3:8:70:G:OP1	32:LY:118:ILE:HD11	2.05	0.56
35:Lb:101:HIS:O	35:Lb:109:ARG:NH1	2.38	0.56
36:Lc:31:TYR:OH	36:Lc:59:GLU:OE2	2.21	0.56
1:5:32:G:H21	1:5:50:C:H5	1.53	0.56
10:LB:246:ARG:O	10:LB:250:LYS:NZ	2.28	0.56
12:LD:136:ASP:OD1	12:LD:136:ASP:N	2.35	0.56
51:Z:36:THR:HA	51:Z:53:GLU:HA	1.87	0.56
53:s:106:LYS:HD2	53:s:184:SER:HB2	1.86	0.56
1:5:1460:C:H2'	1:5:1461:C:H6	1.70	0.56
1:5:3893:C:O2'	1:5:4979:A:N1	2.36	0.56
1:5:4327:C:OP1	27:LT:70:HIS:NE2	2.39	0.56
8:F:1545:GLU:O	8:F:1562:HIS:NE2	2.37	0.56
21:LN:46:ASP:OD1	21:LN:47:LYS:N	2.39	0.56
28:LU:111:GLU:OE2	28:LU:113:ARG:HD3	2.05	0.56
36:Lc:38:ILE:HG21	36:Lc:63:TYR:HB3	1.88	0.56
43:Lj:14:LYS:NZ	45:Ll:51:LEU:O	2.38	0.56
1:5:4883:C:N4	13:LE:181:LEU:O	2.34	0.56
3:8:19:C:H2'	3:8:20:A:H8	1.70	0.56
4:B:122:VAL:HA	4:B:126:ILE:HD12	1.88	0.56
8:F:47:TYR:HD1	8:F:108:ARG:HE	1.51	0.56
8:F:204:ASP:OD1	8:F:217:ARG:NH2	2.38	0.56
1:5:1604:G:H2'	1:5:1605:G:C8	2.40	0.56
8:F:1501:MET:C	8:F:1501:MET:HE3	2.31	0.56
54:t:129:ILE:O	54:t:133:LEU:HD12	2.05	0.56
1:5:2378:G:N2	1:5:2381:A:OP2	2.36	0.56
1:5:3855:C:H2'	1:5:3856:A:H8	1.71	0.56
1:5:4156:G:OP2	1:5:4157:A:O2'	2.21	0.56
37:Ld:19:GLU:HG3	37:Ld:102:LEU:HD11	1.88	0.56
1:5:1591:U:OP2	1:5:2856:C:O2'	2.24	0.56
8:F:749:ALA:HB1	8:F:799:ARG:HD2	1.86	0.56
34:La:95:THR:HG23	34:La:97:ALA:H	1.69	0.56
1:5:1457:G:O2'	24:LQ:75:ARG:NH1	2.36	0.56
1:5:2863:G:O2'	25:LR:82:LYS:O	2.21	0.56
10:LB:378:ARG:HG2	30:LW:32:LEU:HD21	1.86	0.56
10:LB:399:LYS:C	10:LB:399:LYS:HD2	2.30	0.56
22:LO:54:TYR:OH	22:LO:73:PHE:O	2.22	0.56
48:Lp:32:SER:OG	48:Lp:69:TRP:O	2.23	0.56
15:LG:101:LYS:NZ	15:LG:211:ASP:OD1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1970:A:H5"	1:5:1971:C:H5'	1.86	0.56
8:F:1629:ARG:HH22	8:F:1636:MET:HE1	1.70	0.56
9:G:1:G:H2'	9:G:2:G:H8	1.70	0.56
53:s:57:LYS:HB2	53:s:60:MET:HB2	1.88	0.56
1:5:1333:A:H2'	1:5:1334:A:H8	1.71	0.55
1:5:1734:G:N2	1:5:1735:U:O4	2.35	0.55
1:5:2295:C:H2'	1:5:2296:G:H8	1.70	0.55
1:5:2296:G:OP2	11:LC:190:ARG:NH1	2.37	0.55
1:5:2745:A:H2'	1:5:2746:A:H8	1.71	0.55
53:s:53:VAL:HG12	53:s:89:VAL:HG22	1.87	0.55
1:5:158:A:N1	1:5:276:C:O2'	2.31	0.55
1:5:1850:A:N3	1:5:2283:G:O2'	2.38	0.55
1:5:2089:G:O2'	11:LC:307:LYS:NZ	2.29	0.55
8:F:151:TRP:CD1	8:F:155:GLN:HE21	2.24	0.55
1:5:5047:C:O2'	1:5:5050:C:OP2	2.25	0.55
2:7:110:G:H2'	2:7:111:C:C6	2.41	0.55
8:F:1077:LEU:HD13	8:F:1091:ILE:HD13	1.88	0.55
1:5:1415:G:H2'	1:5:1416:G:C8	2.42	0.55
1:5:1523:A:N3	1:5:4389:C:O2'	2.35	0.55
1:5:1741:G:O6	2:7:103:A:O2'	2.20	0.55
1:5:4992:G:H2'	1:5:4993:G:C8	2.41	0.55
3:8:110:U:H5'	45:Ll:8:ARG:NH1	2.21	0.55
8:F:980:GLU:HB2	8:F:1215:PRO:HG2	1.88	0.55
53:s:28:PHE:HB2	53:s:89:VAL:HB	1.88	0.55
53:s:111:ALA:HA	53:s:183:PHE:HE2	1.71	0.55
1:5:4045:G:N2	1:5:4048:A:OP2	2.37	0.55
8:F:928:LEU:HD13	8:F:1010:ILE:HG21	1.89	0.55
1:5:36:U:OP1	1:5:1651:G:N2	2.39	0.55
1:5:2519:U:O2'	1:5:2530:U:O2	2.24	0.55
1:5:4594:U:H2'	1:5:4595:G:H8	1.71	0.55
1:5:4688:C:HO2'	16:LH:155:SER:HG	1.50	0.55
38:Le:90:MET:HG3	49:Lr:33:LYS:HA	1.89	0.55
1:5:93:G:H2'	1:5:94:A:C8	2.41	0.55
1:5:679:C:H2'	1:5:680:G:H8	1.72	0.55
1:5:2049:G:O2'	1:5:3884:U:O2'	2.25	0.55
1:5:3786:U:OP1	1:5:4550:G:O2'	2.21	0.55
2:7:37:G:O6	7:E:658:LYS:NZ	2.39	0.55
34:La:82:VAL:HG13	34:La:101:ILE:HG23	1.89	0.55
1:5:2459:G:N2	1:5:2462:C:OP2	2.39	0.55
51:Z:406:VAL:HG23	51:Z:465:LEU:HD11	1.88	0.55
1:5:178:C:H41	1:5:258:G:H21	1.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4091:G:H2'	1:5:4092:G:H8	1.72	0.55
1:5:4239:A:H2'	1:5:4240:G:H8	1.71	0.55
1:5:4255:A:H61	9:G:20:U:H5	1.54	0.55
8:F:337:LYS:NZ	8:F:374:ILE:O	2.40	0.55
1:5:1273:G:N7	35:Lb:117:ARG:NH2	2.55	0.55
1:5:1786:A:O2'	1:5:1788:A:OP2	2.18	0.55
8:F:144:LEU:HB3	8:F:148:MET:SD	2.47	0.55
9:G:7:G:O2'	9:G:49:U:OP2	2.24	0.55
22:LO:61:ARG:HA	22:LO:70:PRO:HD2	1.89	0.55
34:La:75:LEU:HD22	34:La:117:LEU:HD11	1.89	0.55
1:5:1193:C:H3'	1:5:1194:G:H21	1.72	0.54
1:5:1351:G:O6	24:LQ:55:ARG:NH2	2.40	0.54
1:5:1461:C:H2'	1:5:1462:A:H8	1.71	0.54
1:5:1493:G:OP2	35:Lb:44:ARG:NH1	2.39	0.54
1:5:4343:U:O2'	47:Lo:31:ASP:OD1	2.25	0.54
15:LG:80:ILE:HG23	15:LG:164:ILE:HD13	1.89	0.54
9:G:40:G:O2'	9:G:41:G:O5'	2.25	0.54
14:LF:127:LYS:HB2	27:LT:133:ALA:HB3	1.89	0.54
54:t:16:ARG:NH2	54:t:59:THR:OG1	2.41	0.54
1:5:1474:C:H2'	1:5:1475:G:C8	2.42	0.54
1:5:3973:G:O2'	50:Lz:26:ARG:NH1	2.37	0.54
8:F:445:VAL:HG11	8:F:456:LEU:HD22	1.90	0.54
52:a:36:GLU:OE2	52:a:163:ARG:NH2	2.38	0.54
7:E:710:PRO:HD3	51:Z:777:TYR:HE2	1.73	0.54
10:LB:261:ARG:HB2	22:LO:64:THR:HG21	1.90	0.54
12:LD:223:PHE:HB3	12:LD:226:TYR:HB2	1.88	0.54
26:LS:127:MET:HE1	27:LT:155:PRO:HA	1.89	0.54
51:Z:653:PHE:HB2	51:Z:1015:LEU:HD11	1.89	0.54
1:5:676:C:H2'	1:5:677:G:H8	1.72	0.54
2:7:23:A:N3	2:7:118:C:O2'	2.34	0.54
4:B:431:ASP:HA	4:B:434:THR:HG22	1.89	0.54
5:C:291:ILE:HD11	7:E:56:TYR:CZ	2.42	0.54
35:Lb:55:LYS:HA	35:Lb:58:GLN:HE21	1.73	0.54
51:Z:29:VAL:HG22	51:Z:39:ILE:HD12	1.89	0.54
53:s:61:MET:O	53:s:65:ILE:HD13	2.06	0.54
1:5:1207:C:H2'	1:5:1208:G:H8	1.72	0.54
1:5:2386:U:H2'	1:5:2387:G:H8	1.72	0.54
1:5:4238:G:H2'	1:5:4239:A:C8	2.43	0.54
8:F:266:HIS:O	8:F:272:ARG:NH2	2.35	0.54
51:Z:1002:PRO:O	51:Z:1005:THR:OG1	2.24	0.54
1:5:1541:C:H5"	52:a:21:LYS:HG2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2845:A:N6	1:5:3843:C:H42	2.03	0.54
1:5:4094:G:H2'	1:5:4095:G:H8	1.72	0.54
1:5:4537:C:N4	1:5:4538:G:O6	2.41	0.54
1:5:4991:U:H2'	1:5:4992:G:H8	1.73	0.54
7:E:200:PRO:HG3	7:E:245:VAL:HG12	1.88	0.54
8:F:1280:LEU:HA	8:F:1283:ASP:HB2	1.90	0.54
8:F:1393:ARG:HH12	8:F:1469:GLU:HA	1.72	0.54
49:Lr:16:PHE:HB3	49:Lr:27:THR:H	1.73	0.54
51:Z:82:LEU:HD21	51:Z:124:LEU:HD13	1.90	0.54
1:5:1567:U:OP1	48:Lp:3:LYS:NZ	2.38	0.54
1:5:1802:A:HO2'	27:LT:108:ARG:HH12	1.54	0.54
1:5:4253:A:H5'	1:5:4254:G:C8	2.43	0.54
8:F:1086:THR:O	8:F:1089:SER:OG	2.26	0.54
8:F:1189:ILE:HA	8:F:1192:ILE:HD12	1.90	0.54
16:LH:44:GLU:OE2	20:LM:2:VAL:N	2.40	0.54
38:Le:81:ASN:N	38:Le:81:ASN:OD1	2.41	0.54
46:Lm:79:GLU:HG2	46:Lm:82:LEU:HD12	1.90	0.54
1:5:64:A:H1'	1:5:76:A:H1'	1.90	0.54
1:5:4088:C:H2'	1:5:4089:G:H8	1.72	0.54
4:B:435:GLU:O	4:B:439:GLN:N	2.41	0.54
5:C:255:GLU:OE1	5:C:257:THR:OG1	2.24	0.54
7:E:318:SER:OG	50:Lz:122:ARG:NH2	2.40	0.54
52:a:30:ARG:NH2	52:a:36:GLU:OE1	2.38	0.54
1:5:3769:C:H2'	1:5:3770:U:H6	1.74	0.53
1:5:4891:G:O6	1:5:4929:C:N4	2.41	0.53
8:F:226:THR:HG23	8:F:271:ILE:HD13	1.89	0.53
10:LB:156:TYR:O	10:LB:158:GLN:NE2	2.41	0.53
28:LU:61:VAL:HG22	28:LU:74:SER:HB2	1.90	0.53
37:Ld:93:ASN:ND2	37:Ld:100:ASN:O	2.39	0.53
1:5:1503:A:H4'	1:5:1504:G:H5'	1.90	0.53
1:5:2022:C:OP1	53:s:83:ARG:NH1	2.41	0.53
10:LB:369:ASP:OD1	10:LB:371:THR:OG1	2.27	0.53
50:Lz:67:VAL:HG21	50:Lz:144:MET:HE1	1.90	0.53
1:5:1996:C:H2'	1:5:1997:U:O4'	2.08	0.53
4:B:217:GLU:HG2	7:E:231:ARG:HH11	1.72	0.53
17:LI:182:GLU:H	17:LI:182:GLU:CD	2.17	0.53
1:5:7:C:H2'	1:5:8:U:C6	2.43	0.53
18:LJ:56:THR:OG1	18:LJ:64:ARG:N	2.41	0.53
1:5:152:U:OP2	21:LN:49:ARG:NH1	2.31	0.53
1:5:456:C:H2'	1:5:457:G:H8	1.73	0.53
1:5:2407:G:H2'	45:Ll:13:LEU:HD22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2758:G:O2'	1:5:2765:A:N3	2.32	0.53
1:5:3672:G:OP2	1:5:3672:G:N2	2.38	0.53
8:F:393:LEU:HB2	8:F:408:VAL:HG11	1.90	0.53
48:Lp:26:VAL:HG21	52:a:180:LEU:HD11	1.90	0.53
1:5:1743:A:N1	1:5:1789:C:O2'	2.37	0.53
1:5:3799:A:N3	1:5:4506:C:O2'	2.36	0.53
7:E:775:LEU:HD23	7:E:775:LEU:H	1.73	0.53
8:F:928:LEU:HD13	8:F:1010:ILE:HD13	1.89	0.53
8:F:1027:ILE:HG12	8:F:1064:LEU:HD12	1.90	0.53
20:LM:118:MET:HG2	22:LO:192:TYR:CZ	2.43	0.53
1:5:433:A:C8	1:5:3867:A:H4'	2.44	0.53
1:5:3732:A:H2'	1:5:3733:A:C8	2.44	0.53
8:F:747:ASN:O	8:F:751:CYS:N	2.39	0.53
20:LM:11:ARG:NH2	20:LM:58:THR:O	2.42	0.53
1:5:2308:A:N3	3:8:19:C:O2'	2.40	0.53
1:5:4635:A:OP1	1:5:4636:U:O2'	2.27	0.53
1:5:4680:G:H2'	1:5:4681:A:C8	2.43	0.53
50:Lz:81:ASP:OD1	50:Lz:81:ASP:N	2.41	0.53
1:5:1761:G:O6	1:5:1771:U:O2	2.27	0.53
1:5:2080:U:H2'	1:5:2081:C:C6	2.43	0.53
1:5:2080:U:H2'	1:5:2081:C:H6	1.74	0.53
1:5:2309:G:O2'	3:8:18:U:O2	2.26	0.53
17:LI:66:GLU:OE1	17:LI:69:ARG:NH1	2.42	0.53
1:5:4239:A:H2'	1:5:4240:G:C8	2.44	0.53
3:8:102:G:OP2	3:8:104:A:O2'	2.20	0.53
23:LP:18:ARG:NH1	23:LP:147:GLU:OE1	2.42	0.53
51:Z:170:LEU:HD23	51:Z:222:ILE:HG23	1.90	0.53
1:5:1818:G:OP2	1:5:1818:G:N2	2.23	0.52
1:5:1991:A:O2'	1:5:1992:U:O4'	2.27	0.52
1:5:2302:C:O2'	38:Le:102:ASN:O	2.26	0.52
4:B:129:LEU:HD21	4:B:468:LEU:HD22	1.91	0.52
12:LD:64:ILE:HD13	12:LD:109:LEU:HD22	1.91	0.52
22:LO:81:TRP:HB2	22:LO:104:VAL:HG21	1.91	0.52
1:5:325:U:H2'	1:5:326:C:C6	2.45	0.52
1:5:2009:A:O2'	1:5:2010:A:OP1	2.26	0.52
1:5:4274:A:H2'	1:5:4275:G:C8	2.43	0.52
1:5:4924:C:H1'	1:5:4926:C:N4	2.24	0.52
4:B:216:CYS:O	7:E:231:ARG:NE	2.41	0.52
8:F:20:ARG:NH1	46:Lm:128:LYS:OXT	2.42	0.52
19:LL:80:GLU:OE2	19:LL:102:ARG:NH1	2.39	0.52
20:LM:46:ARG:O	20:LM:48:GLN:NE2	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Lf:33:VAL:HG13	39:Lf:38:GLU:HB2	1.91	0.52
1:5:1847:C:H2’	1:5:1848:C:C6	2.44	0.52
1:5:2516:G:O2’	40:Lg:62:LYS:NZ	2.41	0.52
1:5:3610:A:H2’	1:5:3611:A:H8	1.75	0.52
1:5:3871:A:H2’	1:5:3872:A:C8	2.43	0.52
1:5:4642:U:H2’	1:5:4643:G:H8	1.75	0.52
1:5:4691:A:H5’	16:LH:71:ARG:HH21	1.75	0.52
7:E:50:THR:OG1	7:E:87:ASN:O	2.19	0.52
8:F:290:MET:O	8:F:290:MET:HE3	2.08	0.52
8:F:1641:ILE:HG23	8:F:1642:GLU:H	1.75	0.52
50:Lz:207:LYS:HB3	50:Lz:213:PRO:HA	1.90	0.52
51:Z:651:MET:HB3	51:Z:1015:LEU:HB2	1.90	0.52
1:5:1845:U:H5’	35:Lb:25:ARG:HH22	1.74	0.52
1:5:2875:C:OP1	48:Lp:23:ARG:NH1	2.42	0.52
4:B:125:GLU:HA	5:C:265:ARG:HH22	1.74	0.52
8:F:305:ILE:HA	8:F:316:LEU:HD11	1.91	0.52
8:F:954:TRP:HA	8:F:957:MET:HE2	1.90	0.52
20:LM:55:MET:O	26:LS:157:ARG:NH1	2.42	0.52
39:Lf:35:ALA:HB3	39:Lf:38:GLU:HG3	1.91	0.52
50:Lz:6:SER:OG	50:Lz:9:THR:OG1	2.26	0.52
1:5:1494:U:H2’	1:5:1495:G:C8	2.41	0.52
1:5:2520:C:H2’	1:5:2521:G:C8	2.44	0.52
1:5:2539:C:H2’	1:5:2540:C:C6	2.44	0.52
1:5:2568:C:H2’	1:5:2569:G:H8	1.75	0.52
1:5:4569:U:OP1	1:5:4982:A:O2’	2.23	0.52
3:8:19:C:H2’	3:8:20:A:C8	2.44	0.52
21:LN:104:GLU:HG2	21:LN:161:MET:HG2	1.90	0.52
51:Z:184:LYS:HB2	51:Z:195:PRO:HB3	1.91	0.52
1:5:267:G:H2’	1:5:268:G:H8	1.75	0.52
1:5:1503:A:H1’	1:5:1504:G:C8	2.44	0.52
1:5:1669:A:N3	1:5:1852:U:O2’	2.39	0.52
1:5:1818:G:O2’	1:5:1820:C:OP2	2.19	0.52
1:5:2878:G:OP2	1:5:2879:A:O2’	2.25	0.52
1:5:4208:U:OP2	27:LT:4:THR:OG1	2.24	0.52
4:B:362:ILE:HD11	7:E:193:LEU:HD12	1.91	0.52
1:5:223:G:O2’	1:5:225:G:OP2	2.26	0.52
1:5:425:U:H2’	1:5:426:A:H8	1.74	0.52
1:5:704:C:H42	1:5:707:C:H5	1.57	0.52
1:5:1317:U:H2’	1:5:1318:C:C6	2.45	0.52
1:5:1749:A:H2’	1:5:1750:G:C8	2.45	0.52
1:5:2094:G:N2	1:5:2095:A:H2’	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2830:G:H2’	1:5:2831:G:H8	1.75	0.52
1:5:4336:A:H5”	1:5:4337:C:H5’	1.92	0.52
8:F:464:LEU:HD11	8:F:490:PHE:HE2	1.74	0.52
29:LV:99:GLU:HG3	30:LW:23:ARG:HA	1.92	0.52
1:5:982:U:H2’	1:5:983:C:C6	2.44	0.52
1:5:1802:A:N3	27:LT:130:ARG:NH1	2.53	0.52
1:5:5057:C:H2’	1:5:5058:A:C8	2.45	0.52
8:F:501:LYS:HZ3	8:F:511:SER:HB3	1.75	0.52
8:F:1075:GLN:OE1	8:F:1112:ARG:NH1	2.43	0.52
8:F:1184:GLU:O	8:F:1188:GLY:N	2.39	0.52
51:Z:614:TRP:O	51:Z:642:ASN:ND2	2.40	0.52
1:5:10:A:H2’	1:5:11:G:C8	2.45	0.52
4:B:192:GLU:O	4:B:196:ALA:N	2.38	0.52
51:Z:4:ARG:NH2	51:Z:55:GLY:O	2.42	0.52
51:Z:8:ILE:HD12	51:Z:197:LEU:HD22	1.92	0.52
1:5:1245:C:H2’	1:5:1246:G:H8	1.75	0.52
1:5:1497:A:N6	24:LQ:175:GLU:O	2.43	0.52
1:5:2394:G:O4’	1:5:2397:G:N2	2.43	0.52
1:5:3711:A:O2’	1:5:3712:A:O4’	2.27	0.52
8:F:308:SER:O	8:F:308:SER:OG	2.21	0.52
8:F:490:PHE:CE1	8:F:494:LEU:HD23	2.45	0.52
51:Z:59:HIS:ND1	51:Z:60:THR:O	2.36	0.52
1:5:2407:G:O6	45:Ll:2:SER:N	2.44	0.51
1:5:3696:C:O2’	1:5:3816:A:N1	2.42	0.51
1:5:3848:U:H2’	1:5:3849:A:C8	2.45	0.51
1:5:153:G:H2’	1:5:154:G:H8	1.74	0.51
1:5:302:C:OP1	21:LN:68:ARG:NE	2.38	0.51
1:5:1317:U:OP1	34:La:21:ARG:NH2	2.40	0.51
1:5:2517:A:N3	1:5:2539:C:O2’	2.40	0.51
1:5:4260:U:H2’	1:5:4261:C:H6	1.75	0.51
1:5:5030:U:H2’	1:5:5031:G:H8	1.75	0.51
10:LB:210:VAL:O	10:LB:349:LYS:NZ	2.43	0.51
12:LD:41:LYS:NZ	27:LT:32:ARG:O	2.32	0.51
31:LX:152:LYS:NZ	31:LX:152:LYS:HB3	2.25	0.51
33:LZ:78:ASN:OD1	36:Lc:39:ARG:NH1	2.42	0.51
1:5:478:G:H2’	1:5:479:G:H8	1.75	0.51
1:5:1346:C:H2’	1:5:1347:G:H8	1.74	0.51
1:5:4048:A:O2’	1:5:4049:U:OP1	2.24	0.51
1:5:4420:U:OP2	1:5:4421:C:N4	2.42	0.51
5:C:131:ARG:HH22	5:C:134:GLN:HG3	1.76	0.51
49:Lr:39:ARG:O	49:Lr:103:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2532:C:OP1	31:LX:125:ASN:ND2	2.39	0.51
1:5:3598:C:H2'	1:5:3599:A:H8	1.74	0.51
1:5:4088:C:H2'	1:5:4089:G:C8	2.45	0.51
4:B:473:ASP:HA	4:B:476:LEU:HD12	1.92	0.51
8:F:491:TRP:HA	8:F:494:LEU:HG	1.90	0.51
8:F:1316:HIS:CG	8:F:1353:ILE:HD13	2.45	0.51
14:LF:148:LYS:O	14:LF:152:GLU:HG2	2.11	0.51
38:Le:8:VAL:HG23	38:Le:10:PRO:HD3	1.92	0.51
39:Lf:43:LEU:O	39:Lf:109:ARG:NH2	2.43	0.51
51:Z:649:LEU:HD23	51:Z:1017:PRO:HG3	1.92	0.51
52:a:117:GLU:O	52:a:162:ASN:ND2	2.41	0.51
1:5:1498:G:OP1	24:LQ:150:ARG:NH2	2.43	0.51
1:5:1824:G:H2'	1:5:1825:A:C8	2.46	0.51
1:5:2658:G:O2'	1:5:2675:G:N2	2.43	0.51
1:5:4584:A:H2'	1:5:4585:U:O4'	2.11	0.51
1:5:4604:G:N2	1:5:4607:A:OP2	2.42	0.51
4:B:247:PRO:HB2	4:B:249:VAL:HG22	1.91	0.51
8:F:441:PHE:CE1	8:F:456:LEU:HD11	2.45	0.51
9:G:19:G:H3'	18:LJ:58:ARG:HB2	1.93	0.51
1:5:2723:U:H2'	1:5:2724:G:C8	2.46	0.51
7:E:539:ASP:N	7:E:539:ASP:OD1	2.43	0.51
54:t:129:ILE:O	54:t:132:ILE:N	2.44	0.51
1:5:90:G:OP2	1:5:92:C:N4	2.44	0.51
1:5:1999:A:H2'	1:5:2000:G:C4	2.46	0.51
1:5:4353:U:H5"	1:5:4354:U:H5'	1.93	0.51
1:5:4991:U:H2'	1:5:4992:G:C8	2.46	0.51
3:8:144:U:H2'	3:8:145:C:C6	2.46	0.51
4:B:133:ILE:HG13	4:B:465:GLN:HG2	1.92	0.51
8:F:1485:LEU:HD13	8:F:1570:MET:HB2	1.93	0.51
19:LL:7:GLY:O	34:La:49:HIS:NE2	2.39	0.51
33:LZ:33:THR:OG1	33:LZ:34:SER:N	2.44	0.51
1:5:3597:G:OP1	25:LR:114:LYS:NZ	2.34	0.51
1:5:4708:A:N3	1:5:4709:U:H5'	2.25	0.51
8:F:1278:CYS:SG	8:F:1349:THR:OG1	2.63	0.51
1:5:1787:A:N3	1:5:4210:U:O2'	2.44	0.51
1:5:2577:C:OP1	33:LZ:111:ARG:NH1	2.44	0.51
1:5:2770:C:H2'	1:5:2771:G:H8	1.76	0.51
1:5:4370:G:H5"	47:Lo:64:LYS:HG2	1.92	0.51
1:5:4723:A:H2'	1:5:4724:A:C8	2.46	0.51
8:F:1416:ASP:OD2	8:F:1499:TYR:OH	2.26	0.51
49:Lr:32:LEU:O	49:Lr:113:ARG:NH2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Z:656:LEU:O	51:Z:997:ILE:N	2.43	0.51
1:5:1428:U:H5”	24:LQ:42:THR:HB	1.93	0.51
1:5:1876:U:H2’	1:5:1877:G:C8	2.46	0.51
1:5:2412:A:H2’	1:5:2413:U:C6	2.46	0.51
1:5:3823:G:H2’	1:5:3824:A:H8	1.76	0.51
8:F:1478:LEU:HD11	8:F:1519:LEU:HD23	1.92	0.51
51:Z:130:VAL:HG11	51:Z:150:ARG:NH1	2.26	0.51
1:5:133:C:H3’	41:Lh:74:LYS:HZ3	1.76	0.50
1:5:1239:C:H5	13:LE:60:SER:HB2	1.77	0.50
1:5:2094:G:H21	1:5:2095:A:H2’	1.76	0.50
1:5:4587:G:N2	10:LB:15:GLY:O	2.37	0.50
4:B:343:LEU:HG	4:B:349:THR:HG21	1.92	0.50
10:LB:214:ASP:OD2	10:LB:363:ILE:N	2.34	0.50
19:LL:145:LYS:HE3	19:LL:146:LEU:HB2	1.92	0.50
19:LL:170:THR:HB	19:LL:173:GLU:HG3	1.94	0.50
22:LO:90:HIS:O	22:LO:96:GLN:NE2	2.40	0.50
35:Lb:90:SER:OG	35:Lb:95:ARG:NH2	2.44	0.50
1:5:4967:A:H2’	1:5:4968:A:H8	1.76	0.50
33:LZ:50:PRO:HD3	33:LZ:68:ILE:HG12	1.92	0.50
1:5:3653:A:C2	1:5:3692:A:H4’	2.46	0.50
1:5:3896:C:O2’	10:LB:268:ARG:NH2	2.39	0.50
12:LD:21:ARG:O	12:LD:25:GLU:HG3	2.11	0.50
15:LG:165:GLU:HB3	21:LN:7:ILE:HG23	1.93	0.50
43:Lj:2:THR:HG22	43:Lj:4:GLY:H	1.77	0.50
1:5:1390:G:N2	1:5:1393:G:OP2	2.34	0.50
1:5:1865:G:N2	1:5:1868:A:OP2	2.31	0.50
1:5:1876:U:H2’	1:5:1877:G:H8	1.75	0.50
1:5:1942:A:H2’	1:5:1943:A:C8	2.46	0.50
1:5:4265:U:N3	12:LD:17:GLN:O	2.39	0.50
1:5:4743:G:H2’	1:5:4744:A:C8	2.46	0.50
4:B:147:GLU:O	4:B:451:LYS:NZ	2.44	0.50
1:5:1655:C:O2	1:5:4390:A:O2’	2.28	0.50
1:5:1845:U:H2’	1:5:1846:G:C8	2.46	0.50
3:8:110:U:H5’	45:Ll:8:ARG:HH12	1.77	0.50
8:F:437:GLN:O	8:F:441:PHE:HB3	2.11	0.50
8:F:464:LEU:HD13	8:F:586:ARG:HH11	1.76	0.50
8:F:1035:GLN:OE1	8:F:1061:TYR:OH	2.27	0.50
8:F:1580:ARG:NH1	8:F:1688:THR:O	2.44	0.50
8:F:1680:MET:N	8:F:1680:MET:SD	2.84	0.50
13:LE:178:PRO:HD2	13:LE:181:LEU:HD12	1.92	0.50
34:La:36:GLY:HA2	34:La:39:HIS:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:Z:409:LEU:HD21	51:Z:458:PRO:HB2	1.93	0.50
54:t:11:LYS:N	54:t:64:ILE:O	2.44	0.50
1:5:1339:U:H2'	1:5:1340:C:C6	2.47	0.50
1:5:1681:G:O2'	34:La:41:HIS:NE2	2.41	0.50
1:5:2413:U:H2'	1:5:2414:G:C8	2.46	0.50
8:F:1190:LEU:HA	8:F:1193:ILE:HG22	1.92	0.50
43:Lj:21:ARG:NH1	43:Lj:41:ALA:O	2.39	0.50
53:s:194:ASP:O	53:s:197:SER:OG	2.25	0.50
1:5:28:C:OP2	21:LN:193:ARG:NH1	2.38	0.50
1:5:424:U:H2'	1:5:425:U:C6	2.47	0.50
1:5:1468:C:OP1	34:La:132:ARG:NH1	2.45	0.50
1:5:1990:A:O2'	1:5:1991:A:OP1	2.26	0.50
1:5:4636:U:OP1	37:Ld:41:ARG:NH1	2.44	0.50
29:LV:111:GLU:HG3	29:LV:131:ARG:HG3	1.93	0.50
50:Lz:87:ILE:HD11	50:Lz:116:LEU:HD11	1.93	0.50
51:Z:358:VAL:HG22	51:Z:408:MET:HE1	1.93	0.50
1:5:429:A:H2'	1:5:430:G:H8	1.77	0.50
1:5:935:A:O2'	20:LM:46:ARG:NH2	2.45	0.50
1:5:1475:G:N2	1:5:1489:G:H22	2.09	0.50
1:5:3880:G:H2'	1:5:3881:G:C8	2.47	0.50
4:B:397:LYS:O	4:B:400:THR:OG1	2.29	0.50
12:LD:232:THR:HG23	12:LD:235:MET:HG3	1.93	0.50
1:5:2781:G:OP1	45:Ll:10:LYS:NZ	2.40	0.50
1:5:3933:G:H2'	1:5:3934:G:H8	1.77	0.50
8:F:31:THR:HA	46:Lm:80:PRO:HG3	1.94	0.50
1:5:470:A:N3	13:LE:105:ARG:NH2	2.56	0.49
1:5:4458:C:H2'	1:5:4459:U:C6	2.47	0.49
1:5:4617:G:OP1	10:LB:62:ARG:NH2	2.43	0.49
15:LG:165:GLU:OE1	21:LN:26:ARG:NH1	2.35	0.49
21:LN:9:GLU:HB3	42:Li:44:ILE:HG13	1.94	0.49
1:5:1952:G:OP1	26:LS:139:ARG:NE	2.44	0.49
1:5:2020:U:H2'	1:5:2021:G:C8	2.47	0.49
1:5:3917:A:H2'	1:5:3918:G:H8	1.76	0.49
1:5:4128:A:O2'	15:LG:33:GLU:O	2.26	0.49
1:5:4147:G:OP1	15:LG:26:LYS:NZ	2.40	0.49
51:Z:1015:LEU:HD22	51:Z:1063:VAL:HG11	1.94	0.49
1:5:678:C:H2'	1:5:679:C:H6	1.78	0.49
1:5:2693:G:H2'	1:5:2694:G:N2	2.26	0.49
1:5:3787:G:H1'	1:5:3789:C:H41	1.77	0.49
1:5:3911:C:H2'	1:5:3912:U:H6	1.77	0.49
1:5:4322:G:N2	1:5:4325:A:OP2	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:115:SER:O	4:B:119:VAL:N	2.39	0.49
8:F:1393:ARG:NH2	8:F:1472:CYS:SG	2.85	0.49
53:s:58:ASN:O	53:s:62:ARG:NE	2.40	0.49
1:5:2856:C:O2	10:LB:242:ARG:NH1	2.37	0.49
1:5:4967:A:H2’	1:5:4968:A:C8	2.46	0.49
3:8:52:A:H5’	45:Ll:21:ARG:NH1	2.27	0.49
33:LZ:89:ILE:HD11	33:LZ:121:ARG:HG2	1.94	0.49
1:5:2029:A:H2’	1:5:2030:A:C8	2.47	0.49
1:5:3688:U:OP2	52:a:6:ARG:NH1	2.45	0.49
1:5:3870:C:H2’	1:5:3871:A:H8	1.77	0.49
1:5:5004:C:H2’	1:5:5005:G:O4’	2.13	0.49
8:F:86:GLU:O	8:F:90:MET:HG3	2.13	0.49
12:LD:208:MET:O	12:LD:212:MET:HG2	2.12	0.49
1:5:1504:G:H2’	1:5:1505:C:C6	2.47	0.49
1:5:2009:A:HO2’	1:5:2010:A:P	2.36	0.49
1:5:2045:G:O6	1:5:3870:C:O2’	2.29	0.49
1:5:3732:A:H2’	1:5:3733:A:H8	1.78	0.49
1:5:4194:U:H5”	35:Lb:3:LYS:HD3	1.94	0.49
8:F:1742:HIS:HB2	8:F:1745:CYS:HB2	1.95	0.49
1:5:1942:A:H2’	1:5:1943:A:H8	1.76	0.49
1:5:1987:C:O2’	1:5:1988:G:OP1	2.28	0.49
1:5:3955:G:H2’	1:5:3956:G:C8	2.48	0.49
1:5:4162:C:N3	15:LG:73:ARG:NH2	2.49	0.49
8:F:300:SER:O	8:F:304:SER:OG	2.25	0.49
1:5:1733:G:N3	1:5:4214:A:H2’	2.28	0.49
1:5:3690:U:H2’	1:5:3691:G:O4’	2.13	0.49
1:5:3920:U:H2’	1:5:3921:U:H6	1.78	0.49
16:LH:61:TRP:CZ3	20:LM:33:GLN:HG3	2.48	0.49
24:LQ:18:PRO:HG3	24:LQ:29:VAL:HG21	1.95	0.49
1:5:1345:A:H2’	1:5:1346:C:C6	2.48	0.49
1:5:3687:A:O2’	52:a:236:GLY:N	2.44	0.49
1:5:3868:G:H22	1:5:3900:G:H1’	1.77	0.49
1:5:4882:U:OP1	20:LM:117:LYS:NZ	2.34	0.49
1:5:4993:G:H22	1:5:5058:A:H2	1.61	0.49
4:B:370:GLU:OE1	7:E:199:ARG:NE	2.46	0.49
4:B:471:LYS:O	4:B:474:LEU:HB2	2.13	0.49
10:LB:241:PRO:O	10:LB:244:THR:OG1	2.31	0.49
51:Z:410:LEU:HD23	51:Z:461:VAL:HB	1.93	0.49
1:5:1214:C:OP2	35:Lb:91:ARG:NH2	2.43	0.49
1:5:1727:U:OP1	14:LF:131:ASN:ND2	2.43	0.49
1:5:1977:C:H2’	1:5:1978:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8:67:U:H2’	3:8:68:G:C8	2.47	0.49
4:B:226:MET:O	4:B:230:VAL:N	2.35	0.49
4:B:355:ASP:OD1	7:E:185:ARG:HA	2.12	0.49
7:E:620:LYS:O	7:E:624:THR:OG1	2.25	0.49
8:F:794:GLU:HA	8:F:840:MET:HE1	1.94	0.49
8:F:1376:PRO:HG2	8:F:1379:LEU:HD12	1.94	0.49
19:LL:130:LYS:HD2	19:LL:131:PRO:HD2	1.95	0.49
24:LQ:154:LYS:O	24:LQ:163:THR:OG1	2.26	0.49
29:LV:107:ASN:HD21	29:LV:111:GLU:HB2	1.78	0.49
52:a:246:LEU:O	52:a:246:LEU:HD13	2.13	0.49
1:5:4759:C:H2’	1:5:4760:G:C8	2.47	0.48
53:s:94:ASP:OD1	53:s:95:LEU:N	2.46	0.48
1:5:381:U:H4’	1:5:415:G:H5’	1.94	0.48
1:5:423:G:H2’	1:5:424:U:C6	2.48	0.48
1:5:677:G:H2’	1:5:678:C:H6	1.78	0.48
1:5:1927:U:OP1	1:5:1949:U:O2’	2.16	0.48
1:5:1973:G:H2’	1:5:1974:U:C5	2.48	0.48
1:5:2411:C:H2’	1:5:2412:A:C8	2.47	0.48
1:5:4459:U:H2’	1:5:4460:U:C6	2.48	0.48
8:F:854:CYS:HG	8:F:875:TRP:CD1	2.30	0.48
8:F:1481:TRP:CD2	8:F:1512:LEU:HD22	2.48	0.48
18:LJ:56:THR:HG23	18:LJ:63:ARG:HA	1.93	0.48
28:LU:23:LEU:HD13	28:LU:110:TYR:HB2	1.95	0.48
52:a:135:THR:HG23	52:a:149:LYS:HB3	1.95	0.48
1:5:1981:G:O2’	1:5:1982:G:OP1	2.27	0.48
1:5:2038:U:O2’	46:Lm:114:LYS:O	2.24	0.48
1:5:2079:G:H2’	1:5:2080:U:C6	2.48	0.48
1:5:2640:G:H2’	1:5:2641:A:C8	2.48	0.48
1:5:3772:U:H2’	1:5:3773:U:H2’	1.94	0.48
2:7:87:G:N2	2:7:90:A:OP2	2.40	0.48
13:LE:141:ARG:NH1	39:Lf:110:ILE:O	2.46	0.48
27:LT:68:THR:HG22	27:LT:69:GLN:N	2.29	0.48
31:LX:81:LEU:HG	31:LX:83:THR:HG23	1.94	0.48
1:5:1333:A:H2’	1:5:1334:A:C8	2.48	0.48
2:7:82:G:H2’	2:7:83:A:C8	2.48	0.48
4:B:357:LEU:HD21	4:B:408:LEU:HD22	1.95	0.48
7:E:737:LYS:O	7:E:741:SER:OG	2.31	0.48
28:LU:106:SER:OG	28:LU:107:LYS:N	2.47	0.48
33:LZ:11:VAL:HG12	33:LZ:82:PRO:HA	1.96	0.48
33:LZ:87:VAL:HB	33:LZ:89:ILE:HD12	1.95	0.48
1:5:10:A:H2’	1:5:11:G:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:424:U:OP1	23:LP:34:GLN:NE2	2.46	0.48
8:F:1598:THR:O	8:F:1603:SER:N	2.39	0.48
9:G:21:A:N6	9:G:46:G:O2'	2.46	0.48
48:Lp:38:THR:HA	48:Lp:45:THR:HA	1.95	0.48
1:5:1683:U:H2'	1:5:1684:A:H8	1.79	0.48
1:5:4051:C:O2'	50:Lz:210:MET:SD	2.70	0.48
1:5:4458:C:OP1	10:LB:11:HIS:NE2	2.40	0.48
13:LE:278:THR:HB	13:LE:281:ILE:HG12	1.95	0.48
51:Z:254:ILE:HG22	51:Z:256:PRO:HD3	1.96	0.48
1:5:440:U:H2'	1:5:441:G:H8	1.79	0.48
1:5:4055:U:H2'	1:5:4056:A:C8	2.49	0.48
8:F:1151:LEU:H	8:F:1151:LEU:HD12	1.78	0.48
47:Lo:36:GLN:OE1	47:Lo:40:ARG:NH1	2.47	0.48
1:5:1328:G:O2'	1:5:2349:A:OP1	2.31	0.48
1:5:2693:G:H2'	1:5:2694:G:C2	2.49	0.48
1:5:3774:A:H2'	1:5:3775:A:H8	1.73	0.48
7:E:518:ARG:O	7:E:518:ARG:NH2	2.47	0.48
8:F:1293:LEU:HA	8:F:1296:ILE:HD12	1.96	0.48
26:LS:3:ALA:O	26:LS:111:ARG:NH1	2.47	0.48
28:LU:100:LEU:HD12	28:LU:112:LEU:HB3	1.95	0.48
51:Z:396:ILE:HA	51:Z:408:MET:HG2	1.95	0.48
52:a:136:VAL:HA	52:a:148:VAL:HG12	1.96	0.48
8:F:1629:ARG:HH22	8:F:1636:MET:CE	2.26	0.48
50:Lz:68:LEU:N	50:Lz:111:LEU:O	2.33	0.48
50:Lz:176:ASP:N	50:Lz:176:ASP:OD1	2.45	0.48
1:5:138:G:H2'	1:5:139:G:H8	1.79	0.48
1:5:1399:G:H2'	1:5:1400:G:C8	2.49	0.48
1:5:1517:G:O6	11:LC:106:LYS:NZ	2.41	0.48
1:5:2535:G:H2'	1:5:2536:A:C8	2.47	0.48
4:B:480:LYS:HA	4:B:483:GLN:HB3	1.96	0.48
7:E:581:ILE:HD12	7:E:582:THR:N	2.29	0.48
8:F:267:SER:OG	8:F:268:VAL:N	2.47	0.48
33:LZ:123:LYS:O	33:LZ:124:THR:OG1	2.26	0.48
36:Lc:105:ILE:O	36:Lc:106:ARG:HG2	2.13	0.48
50:Lz:10:LEU:HD23	50:Lz:180:VAL:HA	1.94	0.48
51:Z:5:PHE:HD1	51:Z:6:SER:H	1.62	0.48
53:s:45:MET:HE1	54:t:121:LEU:HD13	1.96	0.48
53:s:65:ILE:O	53:s:69:LEU:N	2.46	0.48
1:5:963:G:O2'	1:5:964:A:O4'	2.28	0.47
1:5:2633:U:OP1	25:LR:64:ARG:NH1	2.40	0.47
1:5:3771:C:H2'	1:5:3772:U:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4089:G:H2'	1:5:4090:G:H8	1.79	0.47
3:8:47:C:H1'	3:8:61:A:H2'	1.96	0.47
3:8:141:C:H5"	21:LN:60:VAL:HG11	1.96	0.47
8:F:695:ASP:OD1	8:F:698:ARG:NH2	2.46	0.47
8:F:872:LYS:HA	8:F:875:TRP:NE1	2.29	0.47
51:Z:658:LYS:O	51:Z:994:LEU:N	2.45	0.47
1:5:1187:G:OP2	1:5:1187:G:N2	2.25	0.47
1:5:1754:U:H4'	12:LD:3:PHE:HZ	1.79	0.47
1:5:1846:G:H2'	1:5:1847:C:C6	2.49	0.47
1:5:1919:G:N2	26:LS:163:HIS:O	2.43	0.47
1:5:2020:U:H2'	1:5:2021:G:H8	1.79	0.47
1:5:2521:G:H2'	1:5:2522:G:H8	1.79	0.47
1:5:4186:A:H2'	1:5:4187:G:C8	2.50	0.47
2:7:51:G:H21	18:LJ:12:MET:CE	2.25	0.47
8:F:744:LYS:O	8:F:748:LEU:N	2.35	0.47
11:LC:221:PHE:HB3	11:LC:227:ILE:HG21	1.96	0.47
24:LQ:151:HIS:ND1	24:LQ:164:LYS:O	2.48	0.47
53:s:148:SER:O	53:s:151:THR:OG1	2.29	0.47
1:5:1593:A:H5"	1:5:2839:U:H5"	1.95	0.47
1:5:1994:C:O2'	54:t:131:GLU:OE2	2.31	0.47
1:5:2608:G:H2'	1:5:2609:G:H8	1.80	0.47
1:5:3867:A:H2'	1:5:3868:G:C8	2.49	0.47
1:5:4508:C:H5"	29:LV:43:LYS:HD3	1.96	0.47
1:5:4578:G:H2'	1:5:4579:U:C6	2.49	0.47
51:Z:187:LEU:HB3	51:Z:191:LEU:HD12	1.96	0.47
51:Z:398:GLU:OE1	51:Z:400:LYS:NZ	2.38	0.47
1:5:4252:C:OP2	1:5:4253:A:O2'	2.25	0.47
8:F:967:HIS:ND1	8:F:1338:PHE:HB2	2.29	0.47
8:F:1200:HIS:HB3	8:F:1203:ILE:HD12	1.96	0.47
9:G:19:G:H5'	18:LJ:58:ARG:HG3	1.96	0.47
38:Le:101:HIS:O	38:Le:128:ARG:NH1	2.47	0.47
51:Z:616:TYR:N	51:Z:619:GLN:OE1	2.35	0.47
53:s:72:ASN:HB3	53:s:75:LEU:HD12	1.96	0.47
1:5:251:C:H2'	1:5:252:C:C6	2.49	0.47
1:5:1739:G:H2'	1:5:1740:C:C6	2.50	0.47
8:F:1432:LEU:HG	8:F:1498:LEU:HD12	1.95	0.47
1:5:2455:G:H1'	1:5:2471:G:C5	2.49	0.47
1:5:4493:U:H2'	1:5:4494:G:H8	1.80	0.47
8:F:579:SER:OG	8:F:580:GLY:N	2.46	0.47
20:LM:37:LEU:HD21	20:LM:47:ARG:HD3	1.96	0.47
42:Li:36:HIS:O	42:Li:40:VAL:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:86:U:O2'	34:La:65:ARG:NH1	2.47	0.47
1:5:175:C:H2'	1:5:176:G:H8	1.79	0.47
1:5:299:C:H2'	1:5:300:A:H8	1.80	0.47
1:5:429:A:H2'	1:5:430:G:C8	2.49	0.47
1:5:1532:G:OP2	43:Lj:31:LYS:NZ	2.48	0.47
1:5:1577:G:N7	52:a:181:LYS:HB3	2.30	0.47
1:5:1613:A:H5'	52:a:183:GLY:CA	2.45	0.47
1:5:1998:A:H2'	1:5:1999:A:C8	2.49	0.47
1:5:2062:C:OP1	26:LS:2:LYS:N	2.47	0.47
1:5:2506:G:O2'	1:5:2507:A:O5'	2.23	0.47
1:5:4080:C:H2'	1:5:4081:G:H8	1.79	0.47
1:5:4750:G:H2'	1:5:4751:G:H8	1.78	0.47
3:8:26:C:O2'	11:LC:53:ALA:O	2.29	0.47
11:LC:159:GLU:HA	11:LC:217:ILE:HB	1.97	0.47
23:LP:60:PHE:O	23:LP:78:TRP:NE1	2.48	0.47
29:LV:60:MET:HE3	29:LV:78:PRO:HB3	1.96	0.47
1:5:70:A:OP2	34:La:64:LYS:NZ	2.37	0.47
1:5:418:A:C2	3:8:17:A:H1'	2.50	0.47
1:5:676:C:H2'	1:5:677:G:C8	2.50	0.47
1:5:687:U:H1'	13:LE:94:LYS:HE2	1.96	0.47
1:5:1346:C:H2'	1:5:1347:G:C8	2.50	0.47
1:5:1617:G:H1'	1:5:2513:A:N6	2.28	0.47
1:5:2317:C:OP1	38:Le:14:LYS:NZ	2.44	0.47
1:5:2884:G:H2'	1:5:2885:A:H8	1.79	0.47
1:5:3911:C:H2'	1:5:3912:U:C6	2.50	0.47
1:5:5068:G:N2	1:5:5069:U:O4	2.36	0.47
3:8:14:U:H5”	23:LP:123:PRO:HG3	1.97	0.47
8:F:347:VAL:HG22	8:F:353:ARG:HH12	1.79	0.47
8:F:1283:ASP:O	8:F:1287:PHE:N	2.48	0.47
8:F:1467:LEU:HD21	8:F:1556:LEU:HD21	1.96	0.47
12:LD:65:ALA:HB2	12:LD:74:ILE:HD13	1.96	0.47
1:5:56:A:H2'	1:5:57:G:C8	2.50	0.47
1:5:4260:U:H2'	1:5:4261:C:C6	2.50	0.47
8:F:963:MET:HA	8:F:965:TRP:NE1	2.29	0.47
11:LC:140:LYS:HE3	11:LC:245:HIS:HB2	1.97	0.47
12:LD:37:VAL:HG12	12:LD:50:ARG:HD3	1.96	0.47
40:Lg:103:VAL:HA	40:Lg:106:VAL:HG22	1.97	0.47
44:Lk:7:GLU:OE1	44:Lk:7:GLU:HA	2.14	0.47
51:Z:6:SER:OG	51:Z:9:ASP:OD2	2.28	0.47
51:Z:188:ASN:C	51:Z:190:LEU:N	2.73	0.47
54:t:15:LEU:HB2	54:t:60:VAL:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:64:A:N1	1:5:108:A:O2'	2.38	0.47
1:5:2508:U:H2'	1:5:2509:C:H6	1.79	0.47
1:5:3664:G:H2'	1:5:3665:G:H8	1.80	0.47
1:5:3871:A:H2'	1:5:3872:A:H8	1.78	0.47
1:5:4258:C:H2'	1:5:4259:C:H6	1.80	0.47
1:5:4373:G:N7	47:Lo:61:LYS:NZ	2.62	0.47
8:F:360:TYR:CZ	8:F:408:VAL:HG22	2.50	0.47
1:5:230:G:OP1	32:LY:15:ARG:NH2	2.44	0.46
1:5:2473:A:OP1	31:LX:47:ARG:NH2	2.49	0.46
1:5:2557:G:H1	1:5:2570:U:H3	1.63	0.46
1:5:3681:G:C6	52:a:125:LYS:HB3	2.50	0.46
1:5:3920:U:H2'	1:5:3921:U:C6	2.50	0.46
1:5:4165:C:OP1	15:LG:53:ARG:NH1	2.48	0.46
1:5:4466:C:H2'	1:5:4467:A:H8	1.80	0.46
1:5:4768:G:H2'	1:5:4769:G:H8	1.80	0.46
4:B:347:THR:HG22	4:B:350:ARG:HH12	1.80	0.46
8:F:100:LYS:HA	8:F:103:LEU:HD23	1.96	0.46
8:F:183:ILE:HG21	8:F:239:LEU:HD21	1.97	0.46
8:F:1187:HIS:HA	8:F:1190:LEU:HB3	1.97	0.46
37:Ld:114:PHE:HA	37:Ld:117:LEU:HD12	1.96	0.46
51:Z:5:PHE:HD2	51:Z:57:ARG:HA	1.81	0.46
51:Z:1001:ALA:HB3	51:Z:1006:MET:HE2	1.96	0.46
1:5:433:A:H2'	1:5:434:A:O4'	2.15	0.46
1:5:478:G:H2'	1:5:479:G:C8	2.50	0.46
1:5:1344:C:H2'	1:5:1345:A:H8	1.80	0.46
1:5:1382:G:H2'	1:5:1383:G:H8	1.81	0.46
1:5:2835:A:O2'	10:LB:228:TYR:O	2.33	0.46
7:E:330:PRO:HG2	7:E:333:LEU:HG	1.97	0.46
8:F:840:MET:HE3	8:F:842:SER:OG	2.15	0.46
51:Z:24:MET:HE2	51:Z:43:LYS:NZ	2.30	0.46
51:Z:557:TYR:O	51:Z:578:LYS:NZ	2.44	0.46
52:a:80:GLU:HB2	52:a:170:ALA:HA	1.97	0.46
54:t:129:ILE:H	54:t:129:ILE:HD12	1.80	0.46
1:5:732:A:H2'	1:5:733:A:O4'	2.15	0.46
1:5:2078:C:H2'	1:5:2079:G:C8	2.50	0.46
1:5:4448:G:H5"	1:5:4449:A:H5"	1.97	0.46
3:8:101:C:O2'	43:Lj:20:ARG:HG2	2.15	0.46
7:E:595:MET:HE2	7:E:611:ILE:HG12	1.97	0.46
7:E:706:GLY:HA3	51:Z:780:THR:HB	1.97	0.46
7:E:720:ILE:HG13	7:E:721:PRO:HD2	1.96	0.46
8:F:1382:LEU:O	8:F:1385:THR:OG1	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:LM:39:ASP:OD2	20:LM:47:ARG:NE	2.43	0.46
1:5:325:U:H2'	1:5:326:C:H6	1.79	0.46
1:5:717:U:H2'	1:5:718:C:C6	2.50	0.46
1:5:1942:A:N3	1:5:4432:C:O2'	2.40	0.46
1:5:2632:U:H2'	1:5:2633:U:C6	2.51	0.46
1:5:3684:G:H2'	1:5:3685:C:C6	2.51	0.46
7:E:711:GLN:OE1	7:E:711:GLN:N	2.48	0.46
8:F:883:VAL:HG11	8:F:933:GLU:HB2	1.97	0.46
8:F:1225:ILE:HD11	8:F:1254:TRP:CE2	2.51	0.46
17:LI:188:LYS:HB3	17:LI:212:LEU:HD21	1.96	0.46
31:LX:83:THR:O	31:LX:87:MET:HG2	2.15	0.46
33:LZ:12:LEU:HB2	33:LZ:81:MET:HB3	1.96	0.46
49:Lr:105:ASP:OD1	49:Lr:105:ASP:N	2.48	0.46
51:Z:25:ARG:O	51:Z:41:LEU:HA	2.16	0.46
1:5:1504:G:H2'	1:5:1505:C:H6	1.80	0.46
1:5:2081:C:H2'	1:5:2082:G:H8	1.81	0.46
1:5:2724:G:O2'	1:5:2726:G:OP2	2.29	0.46
1:5:2843:U:O2'	1:5:4632:U:OP1	2.31	0.46
1:5:4635:A:H3'	1:5:4636:U:H4'	1.97	0.46
8:F:190:ILE:H	8:F:190:ILE:HD12	1.79	0.46
10:LB:206:PRO:HG2	10:LB:209:GLN:HG3	1.96	0.46
13:LE:131:LYS:O	13:LE:136:HIS:NE2	2.48	0.46
17:LI:51:HIS:CD2	17:LI:168:SER:HB2	2.51	0.46
17:LI:87:ILE:HG12	17:LI:138:ILE:HG12	1.97	0.46
38:Le:98:GLU:HG3	38:Le:123:THR:OG1	2.16	0.46
53:s:50:LYS:HE2	53:s:93:GLU:OE2	2.15	0.46
54:t:61:LYS:HE2	54:t:72:GLU:HB3	1.98	0.46
1:5:1998:A:H1'	1:5:2019:C:O2'	2.16	0.46
1:5:2072:C:O2'	14:LF:213:LEU:O	2.34	0.46
8:F:955:GLU:OE1	8:F:958:ARG:NH2	2.49	0.46
8:F:1210:LEU:HD12	8:F:1270:VAL:HG13	1.98	0.46
8:F:1404:MET:O	8:F:1408:LEU:HG	2.15	0.46
25:LR:107:ARG:O	25:LR:111:GLU:HG2	2.15	0.46
31:LX:109:ILE:O	31:LX:113:VAL:HG12	2.15	0.46
51:Z:165:LEU:HD22	51:Z:169:ARG:HG2	1.98	0.46
51:Z:188:ASN:HB3	51:Z:189:PRO:HD3	1.98	0.46
1:5:123:C:H2'	1:5:124:C:H6	1.81	0.46
1:5:440:U:H2'	1:5:441:G:C8	2.50	0.46
1:5:445:U:O4	1:5:1301:C:N3	2.48	0.46
1:5:2607:C:H2'	1:5:2608:G:H8	1.81	0.46
1:5:3610:A:H2'	1:5:3611:A:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4208:U:H2'	1:5:4209:G:H8	1.80	0.46
7:E:579:THR:O	7:E:582:THR:OG1	2.34	0.46
8:F:398:THR:O	8:F:405:SER:OG	2.27	0.46
10:LB:57:VAL:HG22	10:LB:73:VAL:HG22	1.98	0.46
14:LF:60:GLU:O	14:LF:64:MET:HG3	2.15	0.46
15:LG:160:ASP:OD1	15:LG:160:ASP:N	2.43	0.46
19:LL:143:GLU:OE1	19:LL:143:GLU:HA	2.16	0.46
23:LP:35:ALA:O	23:LP:39:MET:HE3	2.16	0.46
43:Lj:2:THR:HB	43:Lj:6:SER:HB2	1.97	0.46
1:5:234:G:N2	1:5:2303:C:N3	2.47	0.46
1:5:491:G:H2'	1:5:492:U:C6	2.51	0.46
1:5:674:G:H2'	1:5:675:C:C6	2.51	0.46
1:5:964:A:H2'	1:5:965:G:H4'	1.98	0.46
1:5:1870:C:H2'	1:5:1871:A:H8	1.79	0.46
1:5:2844:A:O2'	1:5:4631:G:H4'	2.16	0.46
1:5:3788:C:N4	1:5:3812:C:O4'	2.49	0.46
3:8:93:C:O2'	3:8:94:G:H8	1.99	0.46
13:LE:211:HIS:NE2	13:LE:249:ASP:OD1	2.48	0.46
51:Z:121:ASN:HD21	51:Z:134:ILE:HD11	1.80	0.46
1:5:441:G:H2'	1:5:442:G:H8	1.81	0.46
1:5:1190:C:H2'	1:5:1191:C:C6	2.51	0.46
1:5:1190:C:H2'	1:5:1191:C:H6	1.80	0.46
1:5:1207:C:H2'	1:5:1208:G:C8	2.51	0.46
1:5:1683:U:H2'	1:5:1684:A:C8	2.51	0.46
1:5:1730:U:H2'	1:5:1731:C:C6	2.51	0.46
1:5:2376:A:H2'	1:5:2377:C:C6	2.51	0.46
1:5:4862:G:H2'	1:5:4863:G:C8	2.50	0.46
1:5:4894:A:H5"	1:5:4895:C:H3'	1.96	0.46
3:8:60:G:O6	3:8:96:C:O2'	2.29	0.46
7:E:128:ASN:HB2	7:E:165:ILE:HD13	1.97	0.46
8:F:276:PHE:HA	8:F:279:VAL:HG22	1.97	0.46
8:F:1262:GLN:HA	8:F:1265:TYR:CE2	2.51	0.46
8:F:1420:LEU:HA	8:F:1423:TYR:CD2	2.51	0.46
8:F:1629:ARG:HH11	8:F:1634:GLU:HG3	1.80	0.46
24:LQ:172:ARG:HD2	34:La:57:GLY:HA3	1.98	0.46
1:5:919:C:H2'	1:5:920:C:H6	1.81	0.46
1:5:950:G:H2'	1:5:951:G:H8	1.81	0.46
1:5:1344:C:H2'	1:5:1345:A:C8	2.51	0.46
1:5:1884:C:H2'	1:5:1885:G:H8	1.81	0.46
1:5:1976:G:H21	54:t:138:SER:HB2	1.81	0.46
3:8:66:A:H2'	3:8:67:U:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:1264:LEU:HD12	8:F:1270:VAL:HG21	1.96	0.46
15:LG:166:LEU:HA	21:LN:7:ILE:HD11	1.97	0.46
21:LN:123:GLU:HB2	21:LN:128:LYS:HG2	1.98	0.46
1:5:326:C:OP1	42:Li:25:ARG:NH2	2.49	0.45
1:5:682:G:H2'	1:5:683:C:C6	2.51	0.45
1:5:1433:A:N6	1:5:1451:G:O2'	2.50	0.45
1:5:3621:A:C8	1:5:4642:U:H1'	2.50	0.45
1:5:3702:A:C2	1:5:3703:G:C8	3.04	0.45
1:5:3893:C:H2'	1:5:3894:A:C8	2.51	0.45
1:5:4194:U:O2'	17:LI:116:ARG:NH1	2.48	0.45
4:B:363:PHE:CD1	7:E:196:ALA:HB2	2.52	0.45
8:F:490:PHE:CD1	8:F:490:PHE:C	2.94	0.45
8:F:519:LEU:HD21	8:F:593:LEU:HD23	1.97	0.45
8:F:1224:ILE:O	8:F:1228:LEU:HD23	2.15	0.45
23:LP:25:HIS:O	23:LP:29:THR:OG1	2.23	0.45
36:Lc:78:ASN:OD1	36:Lc:78:ASN:N	2.46	0.45
1:5:2297:G:H4'	11:LC:242:PRO:HB2	1.97	0.45
2:7:57:C:H2'	2:7:58:A:C8	2.52	0.45
2:7:119:U:H2'	12:LD:261:VAL:HG11	1.98	0.45
4:B:387:PRO:HD2	4:B:390:LEU:HD23	1.98	0.45
8:F:282:LEU:O	8:F:286:ILE:HG22	2.17	0.45
8:F:468:GLU:HG2	8:F:585:LEU:HB2	1.98	0.45
8:F:974:ARG:NH1	8:F:1039:GLU:OE1	2.46	0.45
8:F:1206:PHE:HB3	8:F:1253:ALA:HB1	1.98	0.45
8:F:1429:GLU:OE2	8:F:1504:ARG:NH1	2.49	0.45
13:LE:287:VAL:O	20:LM:109:ARG:NH1	2.49	0.45
25:LR:20:LYS:O	25:LR:53:LYS:NZ	2.48	0.45
27:LT:83:LYS:HD2	27:LT:85:LEU:HD21	1.98	0.45
37:Ld:64:ILE:HG23	37:Ld:68:LEU:HD23	1.97	0.45
40:Lg:94:ALA:O	40:Lg:98:GLU:HG2	2.16	0.45
51:Z:75:ALA:O	51:Z:79:ARG:HG2	2.16	0.45
1:5:223:G:H4'	1:5:225:G:N7	2.32	0.45
1:5:352:G:O6	11:LC:196:MET:HB3	2.16	0.45
1:5:422:C:H2'	1:5:423:G:H8	1.82	0.45
1:5:4313:A:H4'	27:LT:71:ALA:HB3	1.99	0.45
2:7:60:G:H2'	2:7:61:G:H8	1.81	0.45
8:F:662:LEU:HD21	8:F:705:LEU:HD21	1.98	0.45
8:F:1251:MET:HE3	8:F:1251:MET:O	2.17	0.45
13:LE:162:VAL:HG11	13:LE:184:VAL:HG11	1.98	0.45
13:LE:210:LYS:HA	13:LE:210:LYS:HD2	1.61	0.45
18:LJ:31:ASP:OD2	18:LJ:35:ARG:NH1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:LL:87:HIS:HB3	19:LL:90:VAL:HG22	1.98	0.45
51:Z:181:GLU:HG2	51:Z:185:ARG:HH12	1.82	0.45
1:5:1415:G:H2'	1:5:1416:G:H8	1.82	0.45
1:5:1505:C:H2'	1:5:1506:G:H8	1.82	0.45
1:5:1613:A:N7	1:5:3638:G:H1'	2.32	0.45
1:5:1824:G:H2'	1:5:1825:A:H8	1.80	0.45
1:5:2078:C:H2'	1:5:2079:G:H8	1.80	0.45
1:5:3949:A:H2'	1:5:3950:U:C6	2.51	0.45
1:5:4089:G:H2'	1:5:4090:G:C8	2.51	0.45
1:5:4188:U:H2'	1:5:4189:U:C6	2.51	0.45
1:5:4418:G:O6	1:5:4421:C:H2'	2.17	0.45
1:5:4691:A:OP1	16:LH:75:SER:OG	2.31	0.45
1:5:4927:G:OP2	1:5:4927:G:N2	2.49	0.45
8:F:464:LEU:HD13	8:F:586:ARG:NH1	2.31	0.45
8:F:702:LEU:O	8:F:706:THR:N	2.40	0.45
8:F:824:CYS:HB3	8:F:870:LYS:HG3	1.99	0.45
8:F:1172:ASN:ND2	8:F:1223:GLU:OE1	2.49	0.45
10:LB:44:THR:OG1	10:LB:184:GLN:O	2.33	0.45
51:Z:182:LEU:HD12	51:Z:185:ARG:HE	1.80	0.45
1:5:240:G:C2	1:5:241:G:H1'	2.51	0.45
1:5:454:U:H2'	1:5:455:C:C6	2.51	0.45
1:5:1316:G:OP1	38:Le:43:ASN:ND2	2.40	0.45
1:5:1475:G:H22	1:5:1489:G:H1	1.65	0.45
1:5:1475:G:H22	1:5:1489:G:H22	1.63	0.45
1:5:1977:C:H5"	54:t:139:VAL:HG22	1.98	0.45
1:5:3668:C:OP1	52:a:8:GLN:NE2	2.49	0.45
1:5:3910:C:H2'	1:5:3911:C:H6	1.82	0.45
1:5:5061:A:H5"	1:5:5062:G:C8	2.52	0.45
3:8:133:G:O2'	31:LX:66:PRO:HB3	2.17	0.45
7:E:371:ASP:O	7:E:375:LEU:HD23	2.15	0.45
8:F:746:VAL:HG22	8:F:796:ILE:HG13	1.97	0.45
17:LI:99:ILE:HG22	17:LI:123:GLN:HB2	1.98	0.45
21:LN:104:GLU:OE2	21:LN:108:ARG:NH1	2.49	0.45
25:LR:112:SER:OG	25:LR:114:LYS:HG3	2.15	0.45
50:Lz:117:ILE:HA	50:Lz:120:ILE:HD13	1.98	0.45
1:5:130:C:N4	1:5:131:C:H41	2.13	0.45
1:5:299:C:H2'	1:5:300:A:C8	2.51	0.45
1:5:1459:A:H2'	1:5:1460:C:O4'	2.17	0.45
1:5:1505:C:H2'	1:5:1506:G:C8	2.51	0.45
1:5:4272:G:O2'	1:5:4273:A:H8	2.00	0.45
1:5:4688:C:H2'	1:5:4689:U:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:412:LEU:O	4:B:418:GLN:NE2	2.44	0.45
8:F:253:SER:O	8:F:256:SER:OG	2.25	0.45
8:F:1375:LEU:O	8:F:1380:GLN:NE2	2.50	0.45
30:LW:52:THR:HG22	30:LW:54:LEU:H	1.82	0.45
36:Lc:105:ILE:O	36:Lc:106:ARG:NH2	2.50	0.45
50:Lz:33:GLU:O	50:Lz:206:ILE:HA	2.17	0.45
50:Lz:66:CYS:HB2	50:Lz:83:PRO:HB2	1.99	0.45
1:5:713:C:H2'	1:5:714:G:H8	1.82	0.45
1:5:2374:A:H2'	1:5:2375:A:H8	1.80	0.45
1:5:2553:A:OP2	1:5:2574:G:O2'	2.30	0.45
1:5:2745:A:H2'	1:5:2746:A:C8	2.50	0.45
5:C:209:GLU:OE1	5:C:209:GLU:N	2.47	0.45
7:E:547:LEU:HA	7:E:550:ASN:HD22	1.82	0.45
8:F:379:LEU:HG	8:F:432:MET:HG2	1.99	0.45
8:F:433:LEU:HA	8:F:437:GLN:HG3	1.98	0.45
10:LB:231:VAL:HG21	10:LB:251:VAL:HG23	1.98	0.45
51:Z:654:SER:OG	51:Z:655:PHE:N	2.50	0.45
1:5:2465:C:H2'	1:5:2466:G:O4'	2.17	0.45
1:5:3634:G:N2	1:5:3636:C:H5"	2.31	0.45
1:5:3923:A:H2'	1:5:3924:C:C6	2.52	0.45
1:5:4237:C:H2'	1:5:4238:G:C8	2.51	0.45
7:E:643:ASP:OD1	7:E:655:ARG:NH1	2.47	0.45
8:F:1581:LEU:HD21	28:LU:38:ASN:HB2	1.99	0.45
16:LH:93:ARG:NH1	46:Lm:82:LEU:HD11	2.31	0.45
1:5:86:U:H2'	1:5:87:A:H8	1.81	0.45
1:5:1621:A:OP2	43:Lj:30:GLN:NE2	2.49	0.45
1:5:1637:A:OP1	1:5:1640:C:N4	2.41	0.45
1:5:1846:G:H2'	1:5:1847:C:H6	1.82	0.45
1:5:4695:C:O2	46:Lm:106:ARG:NH1	2.50	0.45
34:La:119:LYS:HB3	34:La:119:LYS:HE3	1.80	0.45
51:Z:661:GLU:O	51:Z:664:VAL:HG12	2.17	0.45
1:5:94:A:H5"	34:La:34:ASN:HB2	1.99	0.45
1:5:1601:A:OP1	43:Lj:5:THR:OG1	2.31	0.45
1:5:1687:U:H2'	1:5:1688:G:C8	2.52	0.45
1:5:1771:U:H2'	1:5:1772:C:C6	2.52	0.45
1:5:3916:G:H2'	1:5:3917:A:C8	2.51	0.45
1:5:4281:A:O2'	1:5:4282:A:O5'	2.34	0.45
1:5:4637:G:H2'	1:5:4638:U:C6	2.52	0.45
3:8:51:U:O2'	3:8:52:A:N7	2.50	0.45
3:8:149:G:O2'	3:8:151:G:OP2	2.34	0.45
8:F:864:PRO:HD2	8:F:867:LEU:HD12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:1134:LEU:HB2	8:F:1139:LYS:HE3	1.98	0.45
8:F:1720:SER:OG	8:F:1722:ILE:O	2.34	0.45
51:Z:312:ALA:O	51:Z:316:GLU:HG3	2.16	0.45
54:t:147:HIS:ND1	54:t:148:PRO:HD2	2.32	0.45
1:5:210:C:OP1	32:LY:59:ARG:NH2	2.49	0.44
1:5:1461:C:H2'	1:5:1462:A:C8	2.51	0.44
1:5:1704:C:O3'	14:LF:46:ARG:NH2	2.50	0.44
1:5:5006:U:H4'	1:5:5007:A:H5'	1.99	0.44
8:F:81:LEU:HD11	8:F:120:ARG:HB3	1.98	0.44
8:F:446:LEU:O	8:F:452:GLN:NE2	2.50	0.44
8:F:1516:LEU:O	8:F:1520:MET:HG2	2.16	0.44
15:LG:100:HIS:CE1	15:LG:103:ARG:HH11	2.35	0.44
16:LH:80:MET:HE3	16:LH:80:MET:HB2	1.89	0.44
17:LI:38:ARG:NH1	17:LI:45:GLU:OE1	2.50	0.44
33:LZ:76:ASN:OD1	33:LZ:77:TYR:N	2.50	0.44
39:Lf:106:TYR:HB2	39:Lf:107:PRO:HD3	1.99	0.44
1:5:216:C:OP2	1:5:219:G:O2'	2.33	0.44
1:5:1997:U:OP2	54:t:123:ARG:NH1	2.51	0.44
1:5:4543:G:H2'	1:5:4544:A:C8	2.52	0.44
21:LN:103:GLU:HB3	21:LN:160:GLU:HB2	1.98	0.44
50:Lz:40:ASN:O	50:Lz:200:ASN:ND2	2.49	0.44
51:Z:984:THR:HG23	51:Z:986:GLN:H	1.83	0.44
1:5:138:G:H2'	1:5:139:G:C8	2.53	0.44
1:5:423:G:H2'	1:5:424:U:H6	1.83	0.44
1:5:683:C:H2'	1:5:684:G:O4'	2.18	0.44
1:5:1753:G:H2'	1:5:1754:U:O4'	2.17	0.44
4:B:144:SER:HA	4:B:147:GLU:HG2	2.00	0.44
7:E:127:VAL:O	7:E:131:LEU:N	2.43	0.44
8:F:118:ASP:HB3	8:F:121:VAL:HG12	1.98	0.44
8:F:599:ASP:HA	8:F:602:ILE:HD12	1.99	0.44
8:F:1251:MET:HA	8:F:1254:TRP:HB2	1.98	0.44
10:LB:54:THR:OG1	10:LB:55:HIS:N	2.50	0.44
33:LZ:36:ARG:HG2	33:LZ:38:TYR:CZ	2.53	0.44
1:5:35:U:H4'	1:5:1525:A:C2	2.53	0.44
1:5:691:C:H2'	1:5:692:A:C8	2.53	0.44
1:5:1186:U:H2'	1:5:1187:G:N3	2.33	0.44
1:5:2352:U:H1'	11:LC:96:CYS:HA	1.97	0.44
1:5:3681:G:O6	52:a:125:LYS:HD3	2.17	0.44
1:5:4601:U:OP1	8:F:79:THR:OG1	2.24	0.44
4:B:438:GLN:HA	4:B:441:LEU:HB2	1.98	0.44
8:F:457:PHE:HB3	8:F:521:VAL:HG11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:48:C:H2'	9:G:59:U:H1'	1.99	0.44
26:LS:16:CYS:SG	26:LS:54:MET:HG2	2.57	0.44
39:Lf:83:MET:HE3	39:Lf:83:MET:HB3	1.79	0.44
51:Z:81:HIS:HB3	51:Z:110:TYR:CD2	2.52	0.44
51:Z:785:SER:C	51:Z:787:LEU:N	2.75	0.44
53:s:198:ILE:O	53:s:198:ILE:HD12	2.17	0.44
1:5:162:A:H2'	1:5:163:A:H8	1.83	0.44
1:5:268:G:H2'	1:5:269:G:H8	1.83	0.44
1:5:2539:C:H2'	1:5:2540:C:H6	1.80	0.44
1:5:2664:G:OP1	25:LR:110:ARG:NH2	2.50	0.44
1:5:4237:C:H2'	1:5:4238:G:H8	1.81	0.44
1:5:4578:G:H2'	1:5:4579:U:H6	1.83	0.44
8:F:481:HIS:HA	8:F:484:GLU:HB2	1.99	0.44
8:F:737:LYS:NZ	8:F:786:TYR:O	2.51	0.44
8:F:885:GLN:NE2	8:F:887:ASP:OD2	2.50	0.44
8:F:1235:CYS:SG	8:F:1236:SER:N	2.90	0.44
8:F:1389:LEU:HD21	8:F:1397:VAL:HG22	1.98	0.44
8:F:1416:ASP:OD1	8:F:1423:TYR:OH	2.34	0.44
53:s:106:LYS:HE2	53:s:186:GLY:HA3	1.99	0.44
1:5:1916:G:O6	39:Lf:18:LEU:HB2	2.18	0.44
1:5:2079:G:H2'	1:5:2080:U:H6	1.82	0.44
1:5:2282:A:H4'	34:La:21:ARG:HG3	1.99	0.44
1:5:2685:C:H2'	1:5:2686:G:O4'	2.18	0.44
1:5:4630:G:H2'	1:5:4631:G:H8	1.82	0.44
4:B:114:LEU:HB3	4:B:486:ILE:HG12	2.00	0.44
4:B:488:ALA:O	4:B:491:SER:OG	2.35	0.44
7:E:693:LEU:HD12	7:E:720:ILE:HD11	1.99	0.44
8:F:1425:ASP:O	8:F:1427:GLU:N	2.51	0.44
8:F:1461:ILE:HD12	8:F:1461:ILE:HA	1.79	0.44
8:F:1668:ARG:HD2	8:F:1672:ALA:HB2	1.99	0.44
8:F:1695:MET:HE2	8:F:1695:MET:HB3	1.84	0.44
17:LI:19:LYS:HD3	17:LI:26:VAL:HB	2.00	0.44
17:LI:111:LEU:HG	17:LI:113:THR:H	1.82	0.44
50:Lz:179:LEU:O	50:Lz:183:ILE:HG12	2.17	0.44
1:5:1245:C:H2'	1:5:1246:G:C8	2.51	0.44
1:5:1248:C:H2'	1:5:1249:C:C6	2.53	0.44
1:5:1895:G:O2'	1:5:1907:A:N3	2.46	0.44
1:5:2744:A:H2'	1:5:2745:A:C8	2.53	0.44
1:5:4080:C:H2'	1:5:4081:G:C8	2.53	0.44
1:5:4457:U:H1'	10:LB:252:ALA:HB3	2.00	0.44
3:8:98:C:OP2	31:LX:67:ARG:NH2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:227:LYS:NZ	5:C:301:LEU:O	2.39	0.44
8:F:352:GLY:O	8:F:353:ARG:HG2	2.18	0.44
28:LU:63:ILE:N	28:LU:63:ILE:HD12	2.32	0.44
51:Z:239:THR:HA	51:Z:242:PHE:HB2	2.00	0.44
53:s:127:ASN:HA	53:s:153:GLU:HA	2.00	0.44
1:5:385:A:H4’	1:5:386:A:H5’	1.99	0.44
1:5:1874:A:O4’	1:5:4213:A:N6	2.51	0.44
1:5:2082:G:H5”	24:LQ:12:LYS:HD2	2.00	0.44
1:5:2319:C:OP2	38:Le:62:SER:OG	2.28	0.44
1:5:2808:G:O3’	25:LR:60:ARG:NH2	2.51	0.44
1:5:3910:C:H2’	1:5:3911:C:C6	2.52	0.44
1:5:4048:A:HO2’	1:5:4049:U:P	2.41	0.44
1:5:4868:G:OP1	20:LM:90:ARG:NH1	2.51	0.44
4:B:476:LEU:O	4:B:480:LYS:HG2	2.17	0.44
7:E:677:LYS:HA	7:E:780:LYS:HD3	1.98	0.44
8:F:673:ASP:OD2	8:F:711:LYS:NZ	2.36	0.44
8:F:702:LEU:HA	8:F:705:LEU:HD12	1.99	0.44
10:LB:317:LEU:HD23	10:LB:317:LEU:HA	1.83	0.44
11:LC:328:LEU:HD22	14:LF:187:MET:HG3	2.00	0.44
32:LY:10:ASP:OD1	32:LY:12:SER:N	2.49	0.44
50:Lz:204:LEU:HB3	50:Lz:216:LEU:HB2	1.99	0.44
52:a:101:VAL:HG22	52:a:165:VAL:HG22	2.00	0.44
1:5:711:A:H2’	1:5:712:C:C6	2.53	0.44
1:5:1488:G:H2’	1:5:1489:G:C8	2.53	0.44
1:5:1490:G:H2’	1:5:1491:A:H8	1.83	0.44
1:5:1994:C:H2’	1:5:1995:G:H8	1.83	0.44
1:5:2041:A:N7	1:5:4434:C:O2’	2.51	0.44
1:5:3890:A:N6	1:5:4571:A:O4’	2.51	0.44
1:5:4043:G:H2’	1:5:4044:U:C6	2.53	0.44
1:5:4192:A:H2’	1:5:4193:C:H6	1.82	0.44
2:7:57:C:H2’	2:7:58:A:H8	1.83	0.44
8:F:13:LEU:HD13	51:Z:403:THR:HG22	2.00	0.44
9:G:35:G:OP1	51:Z:86:ARG:NE	2.50	0.44
10:LB:291:TYR:OH	10:LB:315:ASN:OD1	2.31	0.44
17:LI:109:ASP:OD1	17:LI:109:ASP:N	2.50	0.44
18:LJ:19:LYS:HB3	18:LJ:75:ARG:NH2	2.32	0.44
1:5:100:C:C2	1:5:101:A:C8	3.05	0.43
1:5:1580:C:H2’	1:5:1581:G:O4’	2.18	0.43
1:5:1750:G:H5”	17:LI:40:LYS:HD3	2.00	0.43
1:5:2065:G:O2’	39:Lf:80:ASN:OD1	2.30	0.43
1:5:4177:C:H2’	1:5:4178:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4184:G:H5'	52:a:233:ARG:HB2	2.00	0.43
1:5:4313:A:H2'	1:5:4314:C:O4'	2.17	0.43
1:5:4710:C:H2'	1:5:4711:C:C6	2.52	0.43
3:8:75:G:OP2	32:LY:74:TYR:OH	2.28	0.43
7:E:518:ARG:HH21	7:E:521:PHE:HB3	1.82	0.43
8:F:1278:CYS:SG	8:F:1282:CYS:N	2.91	0.43
10:LB:77:THR:HG21	10:LB:337:VAL:HG22	2.00	0.43
29:LV:13:LYS:HB2	29:LV:128:LEU:HD21	2.00	0.43
51:Z:23:GLY:C	51:Z:43:LYS:HE2	2.43	0.43
1:5:462:G:H2'	1:5:463:A:C8	2.53	0.43
1:5:1339:U:OP1	34:La:8:THR:OG1	2.33	0.43
1:5:2444:U:H4'	3:8:110:U:O2	2.18	0.43
1:5:3789:C:OP2	1:5:3790:U:O2'	2.32	0.43
1:5:4385:A:O2'	1:5:4546:A:OP1	2.33	0.43
1:5:4538:G:H2'	1:5:4539:U:C6	2.53	0.43
1:5:4954:G:H2'	1:5:4955:A:H8	1.80	0.43
2:7:117:G:OP1	12:LD:253:TYR:OH	2.22	0.43
8:F:286:ILE:HG23	8:F:290:MET:HB2	2.00	0.43
8:F:1006:LYS:HA	8:F:1006:LYS:HD2	1.47	0.43
28:LU:41:GLN:OE1	28:LU:44:GLN:NE2	2.49	0.43
51:Z:188:ASN:HB2	51:Z:195:PRO:HD3	2.00	0.43
51:Z:402:GLN:O	51:Z:402:GLN:NE2	2.51	0.43
51:Z:562:ASP:OD1	51:Z:579:ASN:N	2.49	0.43
1:5:956:A:N6	1:5:1283:G:H1'	2.33	0.43
1:5:1318:C:OP1	34:La:21:ARG:HB3	2.18	0.43
1:5:2081:C:H2'	1:5:2082:G:C8	2.53	0.43
1:5:2521:G:H5'	1:5:2640:G:H1'	2.01	0.43
1:5:3877:A:N3	1:5:4401:G:O2'	2.47	0.43
1:5:4651:A:H2'	1:5:4652:G:O4'	2.18	0.43
3:8:97:A:O3'	31:LX:67:ARG:NH1	2.52	0.43
7:E:482:ILE:HG22	7:E:483:GLU:HG2	2.01	0.43
8:F:1186:LEU:HB3	8:F:1231:PHE:CD1	2.53	0.43
10:LB:115:LYS:NZ	10:LB:129:ALA:O	2.36	0.43
29:LV:112:MET:HE2	29:LV:112:MET:HB3	1.78	0.43
50:Lz:174:MET:HE2	50:Lz:178:GLU:HG3	2.00	0.43
1:5:86:U:H2'	1:5:87:A:C8	2.53	0.43
1:5:426:A:H2'	1:5:427:A:H8	1.83	0.43
1:5:490:C:H2'	1:5:491:G:C8	2.53	0.43
1:5:1392:A:H2'	1:5:1393:G:C8	2.53	0.43
1:5:2072:C:OP1	24:LQ:2:GLY:N	2.51	0.43
1:5:3726:A:N6	1:5:4359:U:O2'	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4153:C:H2'	1:5:4154:G:H8	1.83	0.43
7:E:182:PHE:O	7:E:186:HIS:N	2.42	0.43
8:F:313:CYS:HB2	8:F:317:TRP:HZ3	1.83	0.43
8:F:949:PRO:HG2	8:F:957:MET:HE1	2.00	0.43
8:F:1186:LEU:HB3	8:F:1231:PHE:HD1	1.83	0.43
40:Lg:111:ALA:O	40:Lg:114:GLN:NE2	2.52	0.43
49:Lr:38:PHE:O	49:Lr:45:HIS:NE2	2.36	0.43
50:Lz:173:LYS:HB2	50:Lz:173:LYS:HE2	1.82	0.43
51:Z:188:ASN:O	51:Z:190:LEU:N	2.51	0.43
1:5:288:G:H2'	1:5:289:C:C6	2.53	0.43
1:5:1490:G:H2'	1:5:1491:A:C8	2.52	0.43
1:5:1777:C:H2'	1:5:1778:C:H6	1.82	0.43
1:5:2264:C:H2'	1:5:2265:G:O4'	2.18	0.43
1:5:4178:A:H2'	1:5:4179:G:H8	1.83	0.43
4:B:242:ARG:NH1	4:B:339:ASP:OD2	2.44	0.43
4:B:470:PRO:O	4:B:471:LYS:C	2.61	0.43
7:E:186:HIS:O	7:E:190:ILE:HG12	2.19	0.43
7:E:553:LEU:HD23	7:E:553:LEU:HA	1.74	0.43
8:F:115:LEU:HD21	8:F:223:ARG:HG2	2.01	0.43
8:F:1479:LEU:O	8:F:1483:LEU:HG	2.19	0.43
11:LC:140:LYS:O	11:LC:204:ARG:NH1	2.52	0.43
11:LC:269:LYS:HB3	11:LC:269:LYS:HE3	1.78	0.43
22:LO:125:LYS:HG3	22:LO:129:LEU:HD12	2.00	0.43
26:LS:73:LEU:HD23	26:LS:73:LEU:HA	1.78	0.43
43:Lj:39:TYR:CG	43:Lj:40:PRO:HA	2.53	0.43
1:5:1431:C:H2'	1:5:1432:G:O4'	2.17	0.43
1:5:1646:A:H2'	1:5:1647:U:C6	2.54	0.43
1:5:2698:G:H21	40:Lg:28:ASN:HD21	1.66	0.43
1:5:3717:A:H2'	1:5:3718:A:H8	1.84	0.43
1:5:3805:U:C2	1:5:3806:G:C8	3.06	0.43
1:5:4319:C:H2'	1:5:4320:G:H8	1.83	0.43
4:B:394:THR:O	4:B:398:MET:N	2.49	0.43
8:F:152:LEU:HA	8:F:155:GLN:HB2	2.01	0.43
8:F:1006:LYS:HA	8:F:1009:LEU:HD12	1.99	0.43
19:LL:52:SER:OG	19:LL:152:GLY:O	2.32	0.43
32:LY:34:LEU:HD21	32:LY:47:MET:HB2	2.00	0.43
36:Lc:51:ASN:ND2	36:Lc:78:ASN:OD1	2.45	0.43
51:Z:55:GLY:HA2	51:Z:116:LEU:HA	2.01	0.43
51:Z:114:ILE:HG23	51:Z:122:ILE:HG12	2.01	0.43
51:Z:313:LEU:O	51:Z:317:LYS:HG2	2.18	0.43
51:Z:323:LEU:HD23	51:Z:324:ASP:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:a:90:CYS:HB3	52:a:101:VAL:HB	2.00	0.43
52:a:117:GLU:HG2	52:a:124:GLY:H	1.83	0.43
54:t:146:ARG:HH11	54:t:147:HIS:HB2	1.83	0.43
1:5:162:A:H2'	1:5:163:A:C8	2.53	0.43
1:5:1440:U:H2'	1:5:1441:C:C6	2.54	0.43
1:5:1895:G:OP1	14:LF:96:ARG:NH1	2.51	0.43
1:5:4592:C:H2'	1:5:4593:C:C6	2.53	0.43
1:5:4891:G:C6	1:5:4892:A:C6	3.06	0.43
7:E:590:ALA:O	7:E:595:MET:N	2.39	0.43
9:G:1:G:H2'	9:G:2:G:C8	2.52	0.43
25:LR:148:ASP:C	25:LR:148:ASP:OD1	2.62	0.43
31:LX:145:ASP:OD1	31:LX:145:ASP:C	2.62	0.43
33:LZ:29:ILE:HG22	33:LZ:32:GLY:H	1.82	0.43
35:Lb:93:LEU:HD23	35:Lb:93:LEU:HA	1.81	0.43
39:Lf:40:GLU:O	39:Lf:109:ARG:NH1	2.50	0.43
53:s:93:GLU:N	53:s:93:GLU:OE1	2.52	0.43
1:5:911:U:H2'	1:5:912:G:O4'	2.19	0.43
1:5:1309:C:H2'	1:5:1310:C:C6	2.54	0.43
1:5:1468:C:H2'	1:5:1469:C:H6	1.84	0.43
1:5:2757:A:H2'	1:5:2758:G:C8	2.53	0.43
1:5:3717:A:OP2	1:5:3735:G:N2	2.42	0.43
1:5:4153:C:H2'	1:5:4154:G:C8	2.53	0.43
1:5:4177:C:OP1	21:LN:93:LYS:NZ	2.39	0.43
1:5:4266:G:N3	1:5:4266:G:H2'	2.34	0.43
1:5:4356:G:C2	1:5:4357:G:C8	3.07	0.43
7:E:710:PRO:HG3	51:Z:777:TYR:OH	2.18	0.43
8:F:446:LEU:HD11	8:F:501:LYS:NZ	2.34	0.43
8:F:502:ILE:HG13	8:F:597:LEU:HD22	2.01	0.43
8:F:768:SER:O	8:F:772:THR:OG1	2.31	0.43
8:F:825:ASP:OD1	8:F:870:LYS:NZ	2.35	0.43
8:F:881:LEU:HD13	8:F:881:LEU:HA	1.86	0.43
12:LD:97:ALA:O	12:LD:101:THR:OG1	2.36	0.43
28:LU:24:ASP:OD1	28:LU:26:THR:OG1	2.35	0.43
31:LX:67:ARG:HA	31:LX:67:ARG:HD2	1.71	0.43
35:Lb:58:GLN:H	35:Lb:58:GLN:HG2	1.69	0.43
51:Z:403:THR:O	51:Z:405:HIS:ND1	2.43	0.43
1:5:86:U:OP1	24:LQ:169:SER:OG	2.33	0.43
1:5:288:G:H2'	1:5:289:C:H6	1.83	0.43
1:5:424:U:H5"	23:LP:34:GLN:HE22	1.82	0.43
1:5:425:U:H2'	1:5:426:A:C8	2.54	0.43
1:5:1906:U:H2'	1:5:1907:A:H8	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1973:G:H5”	54:t:119:ARG:HH11	1.84	0.43
1:5:2694:G:H5’	1:5:2695:A:C2	2.54	0.43
1:5:2751:G:H2’	1:5:2752:G:H8	1.84	0.43
1:5:2756:G:H2’	1:5:2757:A:C8	2.54	0.43
1:5:4642:U:H2’	1:5:4643:G:C8	2.53	0.43
8:F:1185:LEU:O	8:F:1189:ILE:HG22	2.19	0.43
9:G:23:C:H2’	9:G:24:G:H8	1.84	0.43
10:LB:74:GLU:OE1	10:LB:285:TYR:OH	2.21	0.43
10:LB:168:MET:HA	10:LB:171:LEU:HD12	2.01	0.43
12:LD:208:MET:HE2	12:LD:208:MET:HB3	1.87	0.43
13:LE:277:LEU:HA	13:LE:281:ILE:HD11	2.00	0.43
1:5:483:G:H4’	1:5:484:U:H5”	2.00	0.43
1:5:1090:G:OP1	27:LT:142:ARG:NH2	2.47	0.43
1:5:1662:C:H2’	1:5:1663:C:C6	2.54	0.43
1:5:1730:U:H2’	1:5:1731:C:H6	1.83	0.43
1:5:1998:A:N7	53:s:55:MET:SD	2.92	0.43
1:5:2341:A:OP2	34:La:4:ARG:NH1	2.47	0.43
1:5:2508:U:H2’	1:5:2509:C:C6	2.54	0.43
1:5:3615:G:N3	30:LW:44:ARG:HD3	2.34	0.43
1:5:4347:G:H2’	1:5:4348:A:C8	2.53	0.43
1:5:4420:U:H3’	1:5:4421:C:C5	2.53	0.43
3:8:64:U:C2	3:8:65:A:C8	3.07	0.43
13:LE:281:ILE:HD13	13:LE:286:LEU:HD11	2.01	0.43
17:LI:140:THR:OG1	17:LI:141:LYS:N	2.51	0.43
20:LM:47:ARG:NH1	20:LM:68:ALA:O	2.48	0.43
32:LY:130:LYS:N	32:LY:130:LYS:HD2	2.34	0.43
44:Lk:26:LYS:NZ	44:Lk:28:ASN:OD1	2.47	0.43
47:Lo:2:VAL:N	47:Lo:90:HIS:O	2.51	0.43
51:Z:237:LYS:H	51:Z:237:LYS:HG2	1.56	0.43
53:s:30:VAL:O	53:s:87:GLY:N	2.47	0.43
1:5:1278:C:H2’	1:5:1279:A:O4’	2.19	0.42
1:5:1514:U:H2’	1:5:1515:A:C8	2.54	0.42
1:5:1825:A:H2’	1:5:1826:G:C8	2.53	0.42
1:5:4178:A:H2’	1:5:4179:G:C8	2.53	0.42
1:5:4351:U:H2’	1:5:4352:U:H6	1.85	0.42
1:5:4499:G:C2	1:5:4529:G:H1’	2.54	0.42
1:5:4592:C:H2’	1:5:4593:C:H6	1.84	0.42
1:5:4970:C:C2	1:5:4971:A:C8	3.07	0.42
8:F:1431:ALA:HB2	8:F:1501:MET:HE2	2.01	0.42
8:F:1540:THR:OG1	8:F:1541:PHE:N	2.52	0.42
19:LL:130:LYS:HZ2	19:LL:132:SER:H	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:LN:155:VAL:O	21:LN:162:ARG:NH1	2.50	0.42
25:LR:108:ARG:HG3	25:LR:108:ARG:NH2	2.31	0.42
28:LU:35:ASP:OD1	28:LU:35:ASP:C	2.62	0.42
33:LZ:22:LYS:NZ	33:LZ:132:GLN:O	2.45	0.42
52:a:227:ARG:O	52:a:234:LYS:NZ	2.35	0.42
1:5:394:G:N2	1:5:397:G:OP2	2.33	0.42
1:5:952:G:H2’	1:5:953:C:C6	2.55	0.42
1:5:1554:A:OP1	48:Lp:5:THR:OG1	2.36	0.42
1:5:1646:A:OP1	11:LC:63:SER:OG	2.30	0.42
1:5:1823:G:H2’	1:5:1824:G:C8	2.54	0.42
1:5:1914:C:H4’	22:LO:89:PRO:HD3	1.99	0.42
1:5:2580:U:O2’	33:LZ:79:HIS:ND1	2.39	0.42
1:5:2838:G:OP1	10:LB:248:LEU:N	2.52	0.42
1:5:3976:C:H42	1:5:4038:C:H5	1.67	0.42
1:5:4563:U:C2	1:5:4564:A:C8	3.08	0.42
1:5:4637:G:OP1	37:Ld:30:HIS:NE2	2.43	0.42
1:5:4878:C:H2’	1:5:4879:C:H6	1.84	0.42
1:5:5066:U:H2’	1:5:5067:U:C6	2.54	0.42
4:B:175:VAL:HG23	4:B:434:THR:OG1	2.18	0.42
4:B:454:MET:O	4:B:457:LYS:HG3	2.19	0.42
7:E:154:THR:O	7:E:158:THR:OG1	2.25	0.42
8:F:418:PHE:CE1	8:F:422:GLN:HG3	2.53	0.42
29:LV:43:LYS:HE2	29:LV:62:MET:HE3	2.02	0.42
31:LX:91:GLU:HG2	31:LX:92:ASP:OD1	2.19	0.42
34:La:37:GLY:HA3	34:La:53:PHE:HZ	1.84	0.42
1:5:44:A:N3	1:5:94:A:H2	2.17	0.42
1:5:137:G:C2	1:5:138:G:C5	3.07	0.42
1:5:1666:C:H2’	1:5:1667:G:O4’	2.20	0.42
1:5:2689:C:C2	1:5:2690:C:C5	3.07	0.42
1:5:4460:U:H2’	1:5:4461:C:H6	1.84	0.42
8:F:1445:GLN:HB3	8:F:1477:TYR:HB2	2.00	0.42
17:LI:43:VAL:HG21	17:LI:197:VAL:HG13	2.02	0.42
25:LR:151:ARG:HH22	25:LR:152:LYS:HA	1.84	0.42
1:5:1074:G:H2’	1:5:1075:G:H8	1.85	0.42
1:5:2743:A:H1’	52:a:21:LYS:HE3	2.00	0.42
7:E:542:GLU:O	7:E:543:GLU:C	2.62	0.42
7:E:581:ILE:HD12	7:E:581:ILE:C	2.44	0.42
7:E:717:ASN:HA	7:E:725:HIS:CD2	2.54	0.42
8:F:1086:THR:O	8:F:1090:LEU:HG	2.20	0.42
8:F:1271:GLN:NE2	8:F:1338:PHE:O	2.44	0.42
8:F:1336:THR:O	8:F:1336:THR:OG1	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:LD:41:LYS:HG3	27:LT:93:ILE:HG21	2.01	0.42
27:LT:14:MET:HE2	27:LT:58:HIS:CD2	2.55	0.42
41:Lh:3:LYS:HB3	41:Lh:5:LYS:HE2	2.01	0.42
51:Z:194:GLY:O	51:Z:195:PRO:C	2.62	0.42
51:Z:525:TYR:N	51:Z:528:GLU:OE1	2.36	0.42
1:5:194:C:O2	32:LY:121:ARG:NH1	2.48	0.42
1:5:677:G:H2’	1:5:678:C:C6	2.54	0.42
1:5:1418:C:H2’	1:5:1419:G:O4’	2.20	0.42
1:5:1460:C:H5”	24:LQ:144:LYS:HG2	2.00	0.42
1:5:1866:U:H2’	1:5:1867:A:O4’	2.20	0.42
1:5:2285:A:H2’	1:5:2286:G:H8	1.85	0.42
1:5:2556:G:H2’	1:5:2557:G:H8	1.83	0.42
4:B:341:LEU:HD23	4:B:341:LEU:H	1.85	0.42
4:B:364:LEU:HD23	4:B:398:MET:HE3	2.01	0.42
7:E:79:ILE:HG23	7:E:93:ILE:HG21	2.01	0.42
7:E:213:GLN:HB2	7:E:216:LEU:HB2	2.00	0.42
8:F:433:LEU:HA	8:F:437:GLN:HE21	1.85	0.42
8:F:1678:ASN:OD1	8:F:1682:GLN:NE2	2.50	0.42
10:LB:56:ILE:HD13	10:LB:365:LEU:HD22	2.01	0.42
10:LB:223:THR:O	10:LB:343:ARG:NH1	2.52	0.42
16:LH:53:LYS:HD3	16:LH:53:LYS:HA	1.67	0.42
19:LL:66:TYR:HB3	19:LL:69:LYS:HE2	2.02	0.42
22:LO:187:LYS:HE2	22:LO:187:LYS:HB3	1.95	0.42
26:LS:95:ARG:NH1	26:LS:112:ASP:OD2	2.49	0.42
51:Z:250:GLN:HG2	51:Z:270:TYR:HA	2.01	0.42
1:5:228:C:H2’	1:5:229:G:H8	1.85	0.42
1:5:396:A:H2’	1:5:397:G:C8	2.55	0.42
1:5:1840:G:OP2	14:LF:202:LYS:NZ	2.50	0.42
1:5:2292:C:H2’	1:5:2293:U:C6	2.54	0.42
1:5:2521:G:H2’	1:5:2522:G:C8	2.54	0.42
1:5:2691:U:H2’	1:5:2692:U:C6	2.54	0.42
1:5:4050:A:H5’	1:5:4050:A:N3	2.34	0.42
7:E:573:LEU:HD23	7:E:635:ILE:HD11	2.02	0.42
8:F:699:LYS:HG3	8:F:735:TRP:HD1	1.85	0.42
8:F:794:GLU:O	8:F:798:VAL:HG23	2.19	0.42
51:Z:249:ILE:N	51:Z:249:ILE:HD12	2.35	0.42
52:a:140:ASN:OD1	52:a:143:THR:HG22	2.19	0.42
54:t:52:ASP:OD1	54:t:52:ASP:N	2.51	0.42
1:5:298:G:OP1	21:LN:179:LYS:HD3	2.20	0.42
1:5:1724:G:N2	1:5:1876:U:OP1	2.52	0.42
1:5:1830:G:H2’	1:5:1831:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2019:C:H2’	1:5:2020:U:C6	2.54	0.42
1:5:2072:C:C2	1:5:2073:C:C5	3.07	0.42
1:5:4891:G:H3’	1:5:4892:A:H2	1.85	0.42
2:7:28:C:H1’	2:7:54:A:H61	1.85	0.42
2:7:111:C:H2’	2:7:112:U:O4’	2.19	0.42
8:F:1475:LEU:HD13	8:F:1479:LEU:HD23	2.02	0.42
12:LD:41:LYS:HB2	27:LT:68:THR:O	2.20	0.42
20:LM:50:MET:HE3	20:LM:50:MET:HB2	1.91	0.42
21:LN:178:HIS:HA	21:LN:181:HIS:NE2	2.34	0.42
25:LR:139:MET:HE3	25:LR:139:MET:HB2	1.86	0.42
54:t:108:GLU:C	54:t:108:GLU:OE1	2.63	0.42
1:5:713:C:H2’	1:5:714:G:C8	2.55	0.42
1:5:1677:U:H4’	1:5:1680:G:C2	2.55	0.42
1:5:2633:U:H2’	1:5:2634:C:C6	2.55	0.42
1:5:3856:A:H5”	23:LP:83:TRP:O	2.20	0.42
1:5:4263:C:H2’	1:5:4264:G:O4’	2.20	0.42
1:5:4507:A:H2’	1:5:4508:C:C6	2.54	0.42
8:F:28:GLU:OE2	51:Z:366:ARG:NH2	2.52	0.42
8:F:1271:GLN:OE1	8:F:1341:ALA:N	2.52	0.42
8:F:1394:ALA:HB3	8:F:1397:VAL:HG12	2.02	0.42
41:Lh:63:GLN:O	41:Lh:67:GLU:HG3	2.20	0.42
42:Li:33:LEU:HD11	42:Li:38:LYS:HB2	2.01	0.42
51:Z:271:GLU:HG3	51:Z:272:GLU:HG2	2.01	0.42
53:s:97:GLU:OE2	53:s:98:ILE:HG12	2.20	0.42
54:t:20:GLY:N	54:t:50:THR:OG1	2.52	0.42
1:5:67:C:N4	1:5:325:U:O2’	2.47	0.42
1:5:175:C:H2’	1:5:176:G:C8	2.54	0.42
1:5:285:G:H2’	1:5:286:U:C6	2.55	0.42
1:5:1068:G:H2’	1:5:1069:G:H8	1.84	0.42
1:5:1249:C:H2’	1:5:1250:C:C6	2.55	0.42
1:5:1811:G:H2’	1:5:1812:C:H6	1.85	0.42
1:5:2811:G:H22	1:5:2813:A:H3’	1.85	0.42
1:5:3605:C:H2’	1:5:3606:U:O4’	2.20	0.42
1:5:3727:A:H2’	1:5:3728:A:C8	2.54	0.42
1:5:4424:A:H8	46:Lm:125:LYS:HZ1	1.68	0.42
1:5:4524:G:N3	10:LB:252:ALA:HB1	2.35	0.42
1:5:4897:G:H2’	1:5:4898:G:H8	1.83	0.42
2:7:63:C:H5’	2:7:64:G:H5”	2.01	0.42
7:E:518:ARG:NH2	7:E:521:PHE:HB3	2.35	0.42
8:F:1232:LEU:HD11	8:F:1280:LEU:HD12	2.01	0.42
8:F:1421:LYS:HE2	8:F:1421:LYS:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LF:226:HIS:ND1	14:LF:228:VAL:HG22	2.35	0.42
21:LN:116:LEU:HD22	21:LN:135:ILE:HD11	2.02	0.42
53:s:97:GLU:O	53:s:101:MET:HG3	2.20	0.42
53:s:143:ILE:HD12	53:s:158:VAL:HG11	2.02	0.42
1:5:1399:G:H2'	1:5:1400:G:H8	1.84	0.42
1:5:1645:C:H2'	1:5:1646:A:C8	2.55	0.42
1:5:1809:C:H2'	1:5:1810:G:H8	1.85	0.42
1:5:2674:A:N6	48:Lp:42:CYS:HA	2.35	0.42
1:5:3654:G:O2'	1:5:3693:U:OP1	2.33	0.42
1:5:4319:C:H2'	1:5:4320:G:C8	2.54	0.42
1:5:4768:G:H2'	1:5:4769:G:C8	2.55	0.42
8:F:883:VAL:HG22	8:F:934:SER:HB3	2.00	0.42
9:G:60:U:H3'	9:G:61:C:H5'	2.02	0.42
13:LE:190:HIS:HB3	13:LE:193:PHE:HD2	1.84	0.42
16:LH:44:GLU:HB3	16:LH:58:ASP:HB2	2.02	0.42
17:LI:181:PHE:HE1	17:LI:197:VAL:HG21	1.84	0.42
32:LY:47:MET:HE3	32:LY:47:MET:HB3	1.79	0.42
37:Ld:101:LYS:O	37:Ld:102:LEU:HD23	2.20	0.42
51:Z:131:ILE:HG22	51:Z:151:GLU:O	2.20	0.42
51:Z:620:VAL:HB	51:Z:637:ILE:HG12	2.00	0.42
1:5:456:C:H2'	1:5:457:G:C8	2.53	0.41
1:5:670:G:H2'	1:5:671:G:H8	1.85	0.41
1:5:921:C:H2'	1:5:922:C:H6	1.85	0.41
1:5:1281:G:H5'	11:LC:323:ARG:HB2	2.02	0.41
1:5:1519:C:H2'	1:5:1520:C:H6	1.85	0.41
1:5:1875:C:H2'	1:5:1876:U:C6	2.54	0.41
1:5:2362:U:H2'	1:5:2363:A:C8	2.55	0.41
1:5:2374:A:H2'	1:5:2375:A:C8	2.54	0.41
1:5:2412:A:H2'	1:5:2413:U:H6	1.84	0.41
1:5:2817:C:H4'	1:5:4655:A:O2'	2.20	0.41
1:5:3878:C:N4	1:5:4518:A:O4'	2.53	0.41
1:5:4046:A:H2'	1:5:4047:A:C4	2.55	0.41
1:5:4493:U:H2'	1:5:4494:G:C8	2.54	0.41
1:5:4538:G:H2'	1:5:4539:U:H6	1.83	0.41
1:5:4699:U:H4'	1:5:4700:A:OP1	2.19	0.41
7:E:58:THR:HG23	7:E:61:GLN:H	1.85	0.41
7:E:672:LEU:HD22	51:Z:782:ILE:HD11	2.02	0.41
8:F:1187:HIS:O	8:F:1191:LYS:N	2.46	0.41
12:LD:52:ILE:N	12:LD:63:GLN:O	2.48	0.41
21:LN:181:HIS:O	21:LN:195:ARG:NH1	2.40	0.41
40:Lg:88:ARG:HG2	40:Lg:92:LYS:HE2	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:Lz:26:ARG:HE	50:Lz:27:LYS:H	1.68	0.41
51:Z:115:GLU:CD	51:Z:138:ARG:HH12	2.28	0.41
1:5:1266:G:C8	35:Lb:95:ARG:HG3	2.55	0.41
1:5:1327:C:H2’	1:5:1328:G:C8	2.56	0.41
1:5:1786:A:H2’	1:5:1789:C:C5	2.55	0.41
1:5:1878:G:H2’	1:5:1879:C:C6	2.55	0.41
1:5:2049:G:H2’	1:5:2050:G:H8	1.85	0.41
1:5:4228:G:H5”	1:5:4229:U:O4’	2.20	0.41
1:5:4691:A:H2’	1:5:4692:A:O4’	2.21	0.41
7:E:502:ALA:O	7:E:506:ILE:HG23	2.19	0.41
12:LD:106:ALA:HB2	12:LD:166:ALA:HA	2.02	0.41
27:LT:154:ILE:O	27:LT:154:ILE:HD12	2.20	0.41
51:Z:111:HIS:HB2	51:Z:125:THR:OG1	2.20	0.41
54:t:146:ARG:CZ	54:t:147:HIS:H	2.33	0.41
1:5:281:U:H2’	1:5:282:C:H6	1.85	0.41
1:5:1981:G:HO2’	1:5:1982:G:P	2.42	0.41
1:5:2049:G:H2’	1:5:2050:G:C8	2.55	0.41
1:5:2759:G:O2’	1:5:2760:G:O4’	2.24	0.41
1:5:2857:A:H2’	1:5:2858:A:O4’	2.20	0.41
1:5:3722:G:H2’	1:5:3723:A:H8	1.85	0.41
1:5:4126:C:OP1	15:LG:37:LYS:NZ	2.53	0.41
1:5:4173:G:H2’	1:5:4174:U:C6	2.54	0.41
1:5:4342:C:H2’	1:5:4343:U:H6	1.85	0.41
1:5:4748:U:H5”	39:Lf:54:LYS:HE3	2.02	0.41
11:LC:275:SER:C	11:LC:276:ASN:HD22	2.25	0.41
13:LE:94:LYS:HA	13:LE:95:PRO:HD3	1.97	0.41
24:LQ:76:GLU:H	24:LQ:76:GLU:CD	2.29	0.41
27:LT:102:ARG:O	27:LT:106:LEU:HD22	2.20	0.41
40:Lg:70:THR:HA	40:Lg:73:HIS:CD2	2.55	0.41
53:s:40:MET:HG3	53:s:44:ARG:HE	1.86	0.41
1:5:7:C:H2’	1:5:8:U:H6	1.84	0.41
1:5:9:C:OP1	21:LN:37:HIS:NE2	2.53	0.41
1:5:1084:C:H2’	1:5:1085:C:H6	1.86	0.41
1:5:1209:U:O2’	1:5:1211:G:H8	2.03	0.41
1:5:1307:A:H2’	1:5:1308:C:C6	2.55	0.41
1:5:1460:C:H2’	1:5:1461:C:C6	2.52	0.41
1:5:1879:C:O2’	1:5:1891:A:N3	2.50	0.41
1:5:2810:U:H2’	1:5:2811:G:O4’	2.19	0.41
1:5:4251:A:H2’	1:5:4252:C:C6	2.55	0.41
1:5:4351:U:H2’	1:5:4352:U:C6	2.56	0.41
1:5:4627:U:H4’	10:LB:373:LYS:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:8:68:G:H2'	3:8:69:U:O4'	2.21	0.41
8:F:54:ALA:HA	46:Lm:79:GLU:OE2	2.20	0.41
8:F:1409:MET:O	8:F:1412:LEU:N	2.49	0.41
10:LB:167:GLN:OE1	10:LB:169:ARG:NH2	2.46	0.41
11:LC:213:GLU:OE1	11:LC:213:GLU:HA	2.20	0.41
13:LE:161:ARG:O	13:LE:182:ASN:ND2	2.53	0.41
15:LG:159:HIS:CD2	15:LG:186:GLY:H	2.38	0.41
17:LI:184:MET:HE2	17:LI:184:MET:HB3	1.86	0.41
20:LM:135:LEU:HD12	20:LM:135:LEU:HA	1.82	0.41
51:Z:68:ASN:ND2	51:Z:70:MET:O	2.53	0.41
52:a:137:ILE:HD11	52:a:149:LYS:HB2	2.02	0.41
1:5:2640:G:H2'	1:5:2641:A:H8	1.84	0.41
1:5:3934:G:H2'	1:5:3935:C:C6	2.56	0.41
8:F:97:GLU:O	8:F:100:LYS:HG2	2.20	0.41
8:F:286:ILE:HG12	8:F:289:LEU:HB2	2.02	0.41
8:F:864:PRO:O	8:F:868:ILE:HG13	2.21	0.41
8:F:1537:ASP:OD1	8:F:1537:ASP:C	2.63	0.41
26:LS:2:LYS:HE3	26:LS:43:ARG:HD2	2.01	0.41
50:Lz:111:LEU:HD21	50:Lz:151:VAL:HG21	2.02	0.41
51:Z:538:ASN:H	51:Z:671:ARG:HD3	1.86	0.41
1:5:266:C:H2'	1:5:267:G:C8	2.56	0.41
1:5:1472:C:H2'	1:5:1473:U:C6	2.55	0.41
1:5:2391:G:OP1	1:5:4653:C:O2'	2.37	0.41
1:5:3704:U:C2	1:5:3705:G:C8	3.09	0.41
1:5:3747:A:C8	52:a:245:ARG:HB2	2.55	0.41
1:5:3975:C:H5'	50:Lz:26:ARG:CZ	2.51	0.41
1:5:4091:G:H2'	1:5:4092:G:C8	2.54	0.41
1:5:4342:C:H2'	1:5:4343:U:C6	2.55	0.41
1:5:4975:G:O2'	1:5:4977:A:N6	2.47	0.41
1:5:5061:A:H5"	1:5:5062:G:H8	1.85	0.41
2:7:4:U:H2'	2:7:5:A:H8	1.86	0.41
4:B:407:ASP:OD1	4:B:408:LEU:N	2.53	0.41
7:E:550:ASN:HD21	51:Z:787:LEU:HD22	1.86	0.41
8:F:961:LEU:HD11	8:F:997:HIS:ND1	2.35	0.41
8:F:1044:PRO:O	8:F:1048:ILE:HG13	2.20	0.41
17:LI:35:ASP:OD2	17:LI:86:HIS:NE2	2.54	0.41
53:s:21:LEU:HD11	53:s:75:LEU:HD21	2.02	0.41
1:5:76:A:H5'	19:LL:101:ARG:NH2	2.36	0.41
1:5:427:A:H2'	1:5:428:G:C8	2.55	0.41
1:5:941:C:O2'	1:5:944:A:N1	2.45	0.41
1:5:961:G:O2'	1:5:963:G:N7	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:1987:C:HO2'	1:5:1988:G:P	2.44	0.41
1:5:3770:U:C2	1:5:3771:C:C5	3.09	0.41
7:E:709:VAL:HA	7:E:712:ILE:CG1	2.49	0.41
8:F:189:GLU:OE1	8:F:189:GLU:N	2.53	0.41
8:F:1259:SER:HB3	8:F:1318:LEU:HD21	2.02	0.41
17:LI:111:LEU:O	17:LI:113:THR:HG23	2.20	0.41
51:Z:303:ILE:HD12	51:Z:304:GLU:N	2.36	0.41
51:Z:1051:LYS:HD2	51:Z:1052:ASP:HB2	2.03	0.41
1:5:66:A:O2'	1:5:326:C:O2	2.30	0.41
1:5:750:U:C2	1:5:751:G:C8	3.09	0.41
1:5:2385:U:H2'	1:5:2386:U:C6	2.55	0.41
1:5:3916:G:H2'	1:5:3917:A:H8	1.84	0.41
1:5:4048:A:O2'	1:5:4049:U:P	2.79	0.41
1:5:4460:U:H2'	1:5:4461:C:C6	2.55	0.41
1:5:4674:C:H2'	1:5:4675:U:C6	2.55	0.41
1:5:4927:G:OP1	1:5:4928:C:N4	2.48	0.41
5:C:231:LEU:HD12	5:C:231:LEU:HA	1.87	0.41
7:E:665:LEU:HA	7:E:701:MET:SD	2.61	0.41
8:F:134:LEU:HD21	8:F:172:ALA:HB1	2.03	0.41
8:F:923:ALA:O	8:F:924:VAL:C	2.63	0.41
8:F:1393:ARG:NH1	8:F:1469:GLU:HA	2.36	0.41
10:LB:165:HIS:HB3	10:LB:180:LEU:HD12	2.01	0.41
11:LC:190:ARG:NH2	11:LC:199:ARG:O	2.49	0.41
39:Lf:14:TYR:OH	39:Lf:92:LEU:O	2.26	0.41
51:Z:529:LYS:HG3	51:Z:530:PHE:CD2	2.55	0.41
54:t:146:ARG:NH2	54:t:146:ARG:HA	2.35	0.41
1:5:65:A:N6	1:5:75:G:H1'	2.36	0.41
1:5:192:G:H2'	1:5:193:G:H8	1.86	0.41
1:5:750:U:H1'	1:5:917:A:C8	2.55	0.41
1:5:1281:G:C6	13:LE:128:HIS:HB2	2.55	0.41
1:5:1290:G:H2'	1:5:1291:G:H8	1.85	0.41
1:5:1414:C:H2'	1:5:1415:G:H8	1.86	0.41
1:5:1816:C:N4	1:5:1817:U:O4	2.54	0.41
1:5:1895:G:H2'	1:5:1896:A:O4'	2.20	0.41
1:5:1912:G:H2'	1:5:1913:C:C6	2.56	0.41
1:5:2017:A:N3	1:5:2017:A:H2'	2.35	0.41
1:5:2021:G:H2'	1:5:2022:C:C6	2.56	0.41
1:5:2067:C:H2'	1:5:2068:C:C6	2.56	0.41
1:5:3652:A:O2'	52:a:182:ALA:HB2	2.21	0.41
1:5:3700:C:H2'	1:5:3746:A:H61	1.86	0.41
1:5:4048:A:H3'	1:5:4048:A:N3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4396:A:N6	1:5:4447:C:O2	2.54	0.41
1:5:4417:C:H2'	1:5:4418:G:O4'	2.20	0.41
1:5:4723:A:H2'	1:5:4724:A:H8	1.86	0.41
2:7:28:C:O2'	2:7:54:A:N1	2.54	0.41
4:B:351:ASN:O	4:B:355:ASP:HB2	2.20	0.41
8:F:188:ASP:OD1	8:F:188:ASP:N	2.53	0.41
8:F:213:PRO:O	8:F:217:ARG:HG3	2.21	0.41
8:F:491:TRP:CH2	8:F:593:LEU:HB2	2.56	0.41
8:F:601:SER:HA	8:F:604:TYR:HB2	2.02	0.41
8:F:1671:VAL:HG12	8:F:1676:TRP:HB2	2.03	0.41
9:G:26:G:H22	9:G:44:A:H2	1.68	0.41
9:G:70:U:H2'	9:G:71:C:C6	2.56	0.41
12:LD:224:SER:OG	12:LD:225:GLN:OE1	2.37	0.41
18:LJ:120:ASP:OD1	18:LJ:120:ASP:C	2.64	0.41
21:LN:73:ARG:HA	21:LN:74:PRO:HD3	1.95	0.41
31:LX:145:ASP:OD1	31:LX:147:LEU:N	2.49	0.41
33:LZ:22:LYS:NZ	33:LZ:129:TRP:O	2.42	0.41
51:Z:164:LEU:HD23	51:Z:164:LEU:H	1.86	0.41
53:s:22:ASP:N	53:s:22:ASP:OD1	2.53	0.41
1:5:75:G:H3'	19:LL:74:ARG:HD2	2.02	0.41
1:5:156:G:N2	1:5:157:U:O4	2.53	0.41
1:5:257:C:H2'	1:5:258:G:O4'	2.21	0.41
1:5:345:C:H2'	1:5:346:G:H8	1.86	0.41
1:5:424:U:H2'	1:5:425:U:H6	1.85	0.41
1:5:1628:C:OP2	52:a:9:ARG:HD2	2.21	0.41
1:5:2498:C:H2'	1:5:2499:C:H6	1.85	0.41
1:5:4457:U:H2'	1:5:4458:C:C6	2.56	0.41
1:5:4541:G:O2'	1:5:4543:G:O6	2.38	0.41
1:5:4717:A:H2'	1:5:4718:G:O4'	2.21	0.41
1:5:4931:G:C2	1:5:4932:U:C5	3.09	0.41
7:E:50:THR:HG23	7:E:53:GLY:H	1.86	0.41
8:F:478:LYS:HA	8:F:481:HIS:CE1	2.56	0.41
8:F:1749:TRP:O	8:F:1752:SER:OG	2.38	0.41
10:LB:213:GLN:HG3	10:LB:214:ASP:OD1	2.21	0.41
20:LM:36:ALA:HB2	20:LM:52:PHE:CZ	2.56	0.41
24:LQ:157:GLY:O	24:LQ:188:ASN:ND2	2.54	0.41
26:LS:93:MET:HE1	26:LS:117:HIS:CE1	2.56	0.41
29:LV:27:ASN:ND2	29:LV:100:ASP:OD2	2.54	0.41
29:LV:84:GLN:NE2	29:LV:86:LYS:O	2.46	0.41
33:LZ:25:ILE:HA	33:LZ:43:VAL:HG12	2.01	0.41
38:Le:38:PRO:HB2	38:Le:46:ARG:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:Lm:109:ASN:ND2	46:Lm:117:HIS:O	2.46	0.41
51:Z:270:TYR:CD1	51:Z:270:TYR:N	2.88	0.41
51:Z:791:ARG:HD3	51:Z:791:ARG:HA	1.83	0.41
53:s:52:VAL:O	53:s:90:PHE:N	2.52	0.41
1:5:1604:G:H2’	1:5:1605:G:H8	1.86	0.40
1:5:1933:G:H8	1:5:1933:G:O5’	2.04	0.40
1:5:2389:A:H4’	37:Ld:70:LYS:HG3	2.03	0.40
1:5:2575:U:H5”	1:5:2576:G:H5’	2.03	0.40
1:5:3707:U:H2’	1:5:3708:C:C6	2.56	0.40
1:5:3784:A:O2’	1:5:3785:A:H3’	2.21	0.40
1:5:4045:G:H2’	1:5:4047:A:OP2	2.22	0.40
1:5:4286:C:H2’	1:5:4287:G:C8	2.57	0.40
1:5:4678:G:N2	1:5:4713:G:H1’	2.36	0.40
1:5:4704:C:H2’	1:5:4705:A:H8	1.86	0.40
4:B:227:LEU:HG	4:B:356:GLU:HG3	2.02	0.40
5:C:281:ASN:HA	5:C:284:ARG:HD2	2.03	0.40
7:E:659:LYS:O	7:E:663:GLN:HG3	2.21	0.40
8:F:311:ILE:O	8:F:314:PRO:HD2	2.21	0.40
8:F:341:PHE:O	8:F:345:SER:OG	2.35	0.40
8:F:666:LEU:HD12	8:F:684:ILE:HG23	2.03	0.40
14:LF:94:ARG:HD2	14:LF:109:LEU:HD22	2.03	0.40
18:LJ:143:ASP:N	18:LJ:143:ASP:OD1	2.52	0.40
32:LY:30:MET:HE2	32:LY:30:MET:HB3	1.87	0.40
39:Lf:110:ILE:H	39:Lf:110:ILE:HG13	1.76	0.40
41:Lh:15:GLU:H	41:Lh:15:GLU:CD	2.25	0.40
51:Z:200:HIS:CE1	51:Z:278:PHE:HA	2.56	0.40
53:s:74:ALA:O	53:s:77:LYS:HG2	2.21	0.40
1:5:1729:A:H2’	1:5:1730:U:C6	2.56	0.40
1:5:1864:G:H21	17:LI:115:MET:HE2	1.87	0.40
1:5:2386:U:H2’	1:5:2387:G:C8	2.53	0.40
1:5:2397:G:C8	1:5:2399:G:C8	3.09	0.40
1:5:4594:U:H2’	1:5:4595:G:C8	2.54	0.40
2:7:74:A:H1’	26:LS:53:LYS:HZ3	1.86	0.40
5:C:291:ILE:HD13	7:E:54:LYS:C	2.46	0.40
8:F:1158:LEU:HD11	8:F:1196:TRP:CE2	2.56	0.40
8:F:1673:VAL:HG23	8:F:1674:GLN:H	1.86	0.40
10:LB:92:TYR:HB2	10:LB:159:VAL:HB	2.03	0.40
11:LC:5:ARG:HB3	11:LC:24:LEU:HB3	2.03	0.40
11:LC:204:ARG:NH2	11:LC:205:ARG:O	2.54	0.40
14:LF:80:ASN:HB3	27:LT:141:VAL:O	2.21	0.40
19:LL:150:LEU:HD23	19:LL:154:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:LZ:100:VAL:HG21	33:LZ:110:ALA:HB2	2.02	0.40
42:Li:59:GLU:HA	42:Li:59:GLU:OE1	2.21	0.40
1:5:34:A:O2’	1:5:1526:G:N3	2.53	0.40
1:5:1377:G:H21	1:5:1380:G:H5’	1.86	0.40
1:5:2357:G:H2’	1:5:2358:G:C8	2.57	0.40
1:5:2362:U:H2’	1:5:2363:A:H8	1.86	0.40
1:5:2447:U:H2’	1:5:2448:G:H8	1.85	0.40
1:5:4325:A:O2’	12:LD:48:LYS:NZ	2.40	0.40
1:5:5005:G:H22	1:5:5041:G:H1’	1.85	0.40
7:E:161:LEU:HA	7:E:165:ILE:HB	2.02	0.40
8:F:52:GLN:HB3	8:F:66:ARG:HD2	2.03	0.40
8:F:475:LYS:HE3	8:F:475:LYS:HB3	1.97	0.40
12:LD:108:ARG:CZ	12:LD:253:TYR:HB2	2.51	0.40
13:LE:190:HIS:HD2	13:LE:192:LYS:HB3	1.87	0.40
15:LG:153:GLN:N	15:LG:204:PHE:O	2.48	0.40
24:LQ:177:ALA:O	34:La:51:GLY:HA2	2.21	0.40
28:LU:56:LEU:HD11	28:LU:63:ILE:HD11	2.03	0.40
1:5:229:G:H2’	1:5:230:G:H8	1.86	0.40
1:5:1340:C:H2’	1:5:1341:U:C6	2.57	0.40
1:5:1414:C:H2’	1:5:1415:G:C8	2.57	0.40
1:5:1475:G:H22	1:5:1489:G:N2	2.19	0.40
1:5:1669:A:H4’	1:5:1685:G:N2	2.36	0.40
1:5:4244:A:H2’	1:5:4245:G:O4’	2.21	0.40
1:5:4314:C:OP1	27:LT:70:HIS:ND1	2.41	0.40
1:5:5055:G:H2’	1:5:5056:A:H8	1.86	0.40
5:C:259:THR:OG1	5:C:271:ILE:O	2.26	0.40
5:C:276:LEU:HG	7:E:39:LEU:HD12	2.03	0.40
7:E:138:THR:N	7:E:141:GLU:OE2	2.45	0.40
7:E:222:GLU:O	7:E:226:ASN:ND2	2.46	0.40
8:F:868:ILE:O	8:F:872:LYS:N	2.50	0.40
8:F:944:ILE:C	8:F:946:SER:N	2.77	0.40
8:F:1051:CYS:HA	8:F:1054:LEU:HG	2.03	0.40
10:LB:47:LEU:HD23	10:LB:47:LEU:HA	1.96	0.40
22:LO:47:PHE:HA	22:LO:136:ALA:HB2	2.03	0.40
35:Lb:40:LEU:HD23	35:Lb:40:LEU:HA	1.91	0.40
38:Le:76:LYS:HD2	38:Le:98:GLU:CD	2.47	0.40
51:Z:1011:TYR:OH	51:Z:1043:GLU:OE1	2.30	0.40
53:s:157:ASP:OD1	53:s:157:ASP:N	2.55	0.40
1:5:318:A:H2’	1:5:319:A:C8	2.57	0.40
1:5:1381:U:H2’	1:5:1382:G:O4’	2.21	0.40
1:5:2007:G:H2’	1:5:2008:U:O2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:4684:A:H2’	1:5:4685:U:O4’	2.22	0.40
2:7:23:A:H2’	2:7:24:C:C6	2.56	0.40
3:8:153:C:H2’	3:8:154:G:C8	2.57	0.40
7:E:679:THR:HG22	7:E:685:ILE:HG13	2.03	0.40
8:F:1701:TRP:O	8:F:1705:VAL:HG23	2.21	0.40
21:LN:124:ASP:OD1	21:LN:127:TYR:N	2.34	0.40
34:La:76:ASP:HB3	34:La:115:GLY:HA3	2.04	0.40
50:Lz:38:LEU:HB2	50:Lz:163:LEU:HB3	2.03	0.40
52:a:104:VAL:HG12	52:a:146:THR:HG21	2.04	0.40
53:s:146:LYS:HB2	53:s:155:LEU:HD21	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	B	397/506 (78%)	379 (96%)	18 (4%)	0	100	100
5	C	186/314 (59%)	186 (100%)	0	0	100	100
6	D	76/85 (89%)	75 (99%)	1 (1%)	0	100	100
7	E	652/794 (82%)	633 (97%)	19 (3%)	0	100	100
8	F	1673/1766 (95%)	1619 (97%)	53 (3%)	1 (0%)	48	81
10	LB	400/403 (99%)	395 (99%)	5 (1%)	0	100	100
11	LC	366/427 (86%)	354 (97%)	12 (3%)	0	100	100
12	LD	291/297 (98%)	286 (98%)	4 (1%)	1 (0%)	37	70
13	LE	214/288 (74%)	206 (96%)	8 (4%)	0	100	100
14	LF	223/248 (90%)	218 (98%)	4 (2%)	1 (0%)	30	66
15	LG	239/266 (90%)	232 (97%)	7 (3%)	0	100	100
16	LH	188/192 (98%)	185 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	LI	211/214 (99%)	206 (98%)	5 (2%)	0	100	100
18	LJ	173/178 (97%)	172 (99%)	1 (1%)	0	100	100
19	LL	192/211 (91%)	188 (98%)	4 (2%)	0	100	100
20	LM	134/215 (62%)	132 (98%)	2 (2%)	0	100	100
21	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
22	LO	199/203 (98%)	197 (99%)	2 (1%)	0	100	100
23	LP	151/184 (82%)	149 (99%)	2 (1%)	0	100	100
24	LQ	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
25	LR	153/196 (78%)	153 (100%)	0	0	100	100
26	LS	173/176 (98%)	169 (98%)	4 (2%)	0	100	100
27	LT	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
28	LU	99/128 (77%)	92 (93%)	7 (7%)	0	100	100
29	LV	129/140 (92%)	127 (98%)	2 (2%)	0	100	100
30	LW	60/157 (38%)	60 (100%)	0	0	100	100
31	LX	116/156 (74%)	115 (99%)	1 (1%)	0	100	100
32	LY	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
33	LZ	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
34	La	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
35	Lb	105/159 (66%)	102 (97%)	3 (3%)	0	100	100
36	Lc	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
37	Ld	105/125 (84%)	102 (97%)	3 (3%)	0	100	100
38	Le	126/135 (93%)	124 (98%)	2 (2%)	0	100	100
39	Lf	107/110 (97%)	107 (100%)	0	0	100	100
40	Lg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
41	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
42	Li	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
43	Lj	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
44	Lk	67/70 (96%)	67 (100%)	0	0	100	100
45	Ll	48/51 (94%)	48 (100%)	0	0	100	100
46	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
47	Lo	103/106 (97%)	102 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	Lp	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
49	Lr	123/137 (90%)	122 (99%)	1 (1%)	0	100	100
50	Lz	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
51	Z	721/1076 (67%)	700 (97%)	20 (3%)	1 (0%)	48	81
52	a	246/257 (96%)	239 (97%)	7 (3%)	0	100	100
53	s	199/317 (63%)	193 (97%)	6 (3%)	0	100	100
54	t	139/165 (84%)	136 (98%)	3 (2%)	0	100	100
All	All	10603/12427 (85%)	10348 (98%)	251 (2%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	F	360	TYR
12	LD	4	VAL
51	Z	789	PRO
14	LF	197	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	B	360/438 (82%)	349 (97%)	11 (3%)	35	68
5	C	162/254 (64%)	159 (98%)	3 (2%)	52	79
6	D	66/72 (92%)	65 (98%)	1 (2%)	60	83
7	E	593/704 (84%)	581 (98%)	12 (2%)	50	78
8	F	1533/1611 (95%)	1486 (97%)	47 (3%)	35	68
10	LB	348/349 (100%)	344 (99%)	4 (1%)	70	87
11	LC	306/348 (88%)	305 (100%)	1 (0%)	91	96
12	LD	246/250 (98%)	245 (100%)	1 (0%)	89	95
13	LE	194/252 (77%)	192 (99%)	2 (1%)	73	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	LF	194/215 (90%)	191 (98%)	3 (2%)	60	83
15	LG	203/223 (91%)	198 (98%)	5 (2%)	42	73
16	LH	169/171 (99%)	166 (98%)	3 (2%)	54	80
17	LI	179/181 (99%)	179 (100%)	0	100	100
18	LJ	147/149 (99%)	144 (98%)	3 (2%)	50	78
19	LL	164/177 (93%)	162 (99%)	2 (1%)	67	86
20	LM	116/161 (72%)	113 (97%)	3 (3%)	41	72
21	LN	171/172 (99%)	168 (98%)	3 (2%)	54	80
22	LO	173/174 (99%)	173 (100%)	0	100	100
23	LP	134/163 (82%)	131 (98%)	3 (2%)	47	76
24	LQ	164/165 (99%)	163 (99%)	1 (1%)	84	93
25	LR	138/175 (79%)	138 (100%)	0	100	100
26	LS	156/157 (99%)	153 (98%)	3 (2%)	52	79
27	LT	139/140 (99%)	137 (99%)	2 (1%)	62	83
28	LU	91/115 (79%)	88 (97%)	3 (3%)	33	67
29	LV	101/107 (94%)	101 (100%)	0	100	100
30	LW	54/126 (43%)	53 (98%)	1 (2%)	52	79
31	LX	106/133 (80%)	104 (98%)	2 (2%)	52	79
32	LY	124/135 (92%)	123 (99%)	1 (1%)	79	90
33	LZ	117/118 (99%)	114 (97%)	3 (3%)	41	72
34	La	120/121 (99%)	120 (100%)	0	100	100
35	Lb	88/126 (70%)	86 (98%)	2 (2%)	45	75
36	Lc	83/97 (86%)	80 (96%)	3 (4%)	30	64
37	Ld	98/110 (89%)	96 (98%)	2 (2%)	50	78
38	Le	114/121 (94%)	110 (96%)	4 (4%)	31	65
39	Lf	88/89 (99%)	86 (98%)	2 (2%)	45	75
40	Lg	98/100 (98%)	98 (100%)	0	100	100
41	Lh	109/110 (99%)	107 (98%)	2 (2%)	54	80
42	Li	86/89 (97%)	85 (99%)	1 (1%)	67	86
43	Lj	73/80 (91%)	73 (100%)	0	100	100
44	Lk	64/65 (98%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	Ll	47/48 (98%)	46 (98%)	1 (2%)	48	77
46	Lm	48/116 (41%)	48 (100%)	0	100	100
47	Lo	93/94 (99%)	92 (99%)	1 (1%)	70	87
48	Lp	74/75 (99%)	73 (99%)	1 (1%)	62	83
49	Lr	109/121 (90%)	107 (98%)	2 (2%)	54	80
50	Lz	196/196 (100%)	185 (94%)	11 (6%)	17	49
51	Z	645/962 (67%)	632 (98%)	13 (2%)	50	78
52	a	190/199 (96%)	187 (98%)	3 (2%)	58	82
53	s	169/258 (66%)	165 (98%)	4 (2%)	44	74
54	t	116/137 (85%)	114 (98%)	2 (2%)	56	81
All	All	9356/10749 (87%)	9179 (98%)	177 (2%)	52	79

All (177) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	9	ILE
4	B	22	ASP
4	B	62	TYR
4	B	100	ILE
4	B	104	TYR
4	B	157	MET
4	B	405	LEU
4	B	465	GLN
4	B	471	LYS
4	B	473	ASP
4	B	475	LEU
5	C	203	VAL
5	C	252	LEU
5	C	291	ILE
6	D	62	THR
7	E	40	ILE
7	E	157	LEU
7	E	282	SER
7	E	356	VAL
7	E	539	ASP
7	E	543	GLU
7	E	597	VAL
7	E	627	HIS

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Mol	Chain	Res	Type
7	E	634	SER
7	E	700	SER
7	E	734	LEU
7	E	782	LEU
8	F	108	ARG
8	F	174	PHE
8	F	188	ASP
8	F	191	THR
8	F	273	SER
8	F	282	LEU
8	F	313	CYS
8	F	345	SER
8	F	401	SER
8	F	583	SER
8	F	601	SER
8	F	616	PHE
8	F	684	ILE
8	F	685	LEU
8	F	819	SER
8	F	838	LEU
8	F	880	ASN
8	F	881	LEU
8	F	884	HIS
8	F	927	LEU
8	F	930	THR
8	F	980	GLU
8	F	984	THR
8	F	985	ASP
8	F	1003	LEU
8	F	1006	LYS
8	F	1009	LEU
8	F	1060	THR
8	F	1063	ASN
8	F	1195	SER
8	F	1214	SER
8	F	1264	LEU
8	F	1282	CYS
8	F	1293	LEU
8	F	1360	SER
8	F	1367	LEU
8	F	1440	SER
8	F	1455	CYS

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Mol	Chain	Res	Type
8	F	1522	GLU
8	F	1548	LEU
8	F	1571	THR
8	F	1586	SER
8	F	1598	THR
8	F	1614	VAL
8	F	1641	ILE
8	F	1644	ILE
8	F	1654	SER
10	LB	38	SER
10	LB	60	VAL
10	LB	111	SER
10	LB	131	THR
11	LC	193	LYS
12	LD	101	THR
13	LE	99	ASP
13	LE	127	SER
14	LF	33	LEU
14	LF	102	SER
14	LF	178	SER
15	LG	53	ARG
15	LG	93	THR
15	LG	168	VAL
15	LG	209	SER
15	LG	231	ASP
16	LH	9	THR
16	LH	163	GLN
16	LH	188	GLN
18	LJ	47	THR
18	LJ	115	LEU
18	LJ	168	GLN
19	LL	145	LYS
19	LL	170	THR
20	LM	39	ASP
20	LM	43	THR
20	LM	67	SER
21	LN	34	SER
21	LN	113	LEU
21	LN	126	THR
23	LP	32	THR
23	LP	57	CYS
23	LP	76	TRP

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Mol	Chain	Res	Type
24	LQ	122	THR
26	LS	82	LEU
26	LS	88	SER
26	LS	144	GLN
27	LT	76	VAL
27	LT	143	THR
28	LU	35	ASP
28	LU	60	VAL
28	LU	74	SER
30	LW	38	SER
31	LX	40	ILE
31	LX	54	LEU
32	LY	12	SER
33	LZ	33	THR
33	LZ	74	VAL
33	LZ	100	VAL
35	Lb	54	LEU
35	Lb	57	MET
36	Lc	10	SER
36	Lc	13	SER
36	Lc	68	LYS
37	Ld	26	THR
37	Ld	89	SER
38	Le	25	SER
38	Le	62	SER
38	Le	81	ASN
38	Le	91	CYS
39	Lf	90	SER
39	Lf	110	ILE
41	Lh	14	LYS
41	Lh	37	THR
42	Li	34	THR
45	Ll	39	SER
47	Lo	106	PHE
48	Lp	32	SER
49	Lr	14	SER
49	Lr	78	VAL
50	Lz	35	GLN
50	Lz	36	ILE
50	Lz	52	THR
50	Lz	66	CYS
50	Lz	82	ILE

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Mol	Chain	Res	Type
50	Lz	84	HIS
50	Lz	115	SER
50	Lz	142	GLU
50	Lz	164	CYS
50	Lz	176	ASP
50	Lz	179	LEU
51	Z	3	SER
51	Z	5	PHE
51	Z	57	ARG
51	Z	184	LYS
51	Z	228	SER
51	Z	229	LEU
51	Z	241	ASN
51	Z	392	VAL
51	Z	470	TYR
51	Z	487	THR
51	Z	509	LEU
51	Z	620	VAL
51	Z	791	ARG
52	a	135	THR
52	a	208	GLU
52	a	246	LEU
53	s	22	ASP
53	s	183	PHE
53	s	191	GLN
53	s	198	ILE
54	t	105	THR
54	t	120	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (66) such sidechains are listed below:

Mol	Chain	Res	Type
4	B	382	GLN
4	B	384	GLN
7	E	84	GLN
7	E	628	ASN
7	E	670	GLN
7	E	717	ASN
8	F	117	HIS
8	F	257	GLN
8	F	376	ASN
8	F	435	ASN

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Mol	Chain	Res	Type
8	F	452	GLN
8	F	729	HIS
8	F	747	ASN
8	F	1167	HIS
11	LC	21	ASN
11	LC	223	ASN
11	LC	276	ASN
11	LC	329	ASN
12	LD	45	ASN
12	LD	195	HIS
12	LD	222	GLN
14	LF	24	ASN
14	LF	151	ASN
15	LG	81	ASN
15	LG	82	GLN
15	LG	112	GLN
16	LH	39	ASN
16	LH	98	HIS
19	LL	19	GLN
19	LL	67	HIS
20	LM	66	HIS
21	LN	32	GLN
21	LN	156	HIS
22	LO	26	GLN
22	LO	167	HIS
23	LP	133	HIS
24	LQ	57	ASN
25	LR	40	GLN
25	LR	118	HIS
28	LU	95	ASN
32	LY	14	ASN
32	LY	43	ASN
37	Ld	100	ASN
38	Le	24	GLN
40	Lg	14	ASN
43	Lj	13	ASN
43	Lj	57	ASN
43	Lj	66	HIS
45	Ll	33	ASN
47	Lo	90	HIS
50	Lz	21	ASN
50	Lz	96	ASN

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Mol	Chain	Res	Type
50	Lz	200	ASN
51	Z	68	ASN
51	Z	274	HIS
51	Z	339	GLN
51	Z	402	GLN
51	Z	488	GLN
51	Z	788	GLN
51	Z	790	GLN
51	Z	1008	ASN
52	a	38	HIS
52	a	216	HIS
53	s	58	ASN
54	t	70	GLN
54	t	137	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3506/5070 (69%)	445 (12%)	12 (0%)
2	7	119/121 (98%)	6 (5%)	0
3	8	145/157 (92%)	16 (11%)	0
9	G	75/76 (98%)	22 (29%)	2 (2%)
All	All	3845/5424 (70%)	489 (12%)	14 (0%)

All (489) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	13	U
1	5	25	A
1	5	39	A
1	5	42	A
1	5	48	G
1	5	59	A
1	5	64	A
1	5	65	A
1	5	66	A
1	5	73	A
1	5	91	G
1	5	98	A
1	5	110	C

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Mol	Chain	Res	Type
1	5	119	G
1	5	120	A
1	5	132	G
1	5	133	C
1	5	134	G
1	5	136	C
1	5	142	G
1	5	159	C
1	5	168	C
1	5	169	G
1	5	172	C
1	5	178	C
1	5	179	G
1	5	197	A
1	5	200	U
1	5	209	U
1	5	210	C
1	5	218	A
1	5	219	G
1	5	233	U
1	5	234	G
1	5	266	C
1	5	280	G
1	5	297	U
1	5	316	U
1	5	340	C
1	5	387	G
1	5	409	G
1	5	410	A
1	5	412	G
1	5	414	C
1	5	449	C
1	5	450	G
1	5	451	C
1	5	453	G
1	5	454	U
1	5	485	C
1	5	662	C
1	5	663	G
1	5	664	G
1	5	666	G
1	5	687	U

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Mol	Chain	Res	Type
1	5	696	C
1	5	697	G
1	5	704	C
1	5	705	G
1	5	731	G
1	5	738	C
1	5	739	G
1	5	740	G
1	5	742	G
1	5	904	C
1	5	915	A
1	5	917	A
1	5	926	G
1	5	932	A
1	5	933	G
1	5	936	C
1	5	943	A
1	5	944	A
1	5	945	U
1	5	956	A
1	5	959	G
1	5	960	A
1	5	961	G
1	5	962	C
1	5	964	A
1	5	965	G
1	5	967	C
1	5	968	C
1	5	969	C
1	5	982	U
1	5	1072	C
1	5	1078	A
1	5	1094	G
1	5	1095	A
1	5	1170	G
1	5	1182	C
1	5	1183	C
1	5	1199	G
1	5	1211	G
1	5	1216	C
1	5	1241	C
1	5	1266	G

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Mol	Chain	Res	Type
1	5	1269	G
1	5	1270	A
1	5	1272	C
1	5	1273	G
1	5	1284	G
1	5	1287	G
1	5	1302	U
1	5	1303	A
1	5	1304	C
1	5	1326	A
1	5	1354	A
1	5	1359	G
1	5	1366	G
1	5	1379	C
1	5	1387	A
1	5	1394	G
1	5	1397	A
1	5	1399	G
1	5	1413	C
1	5	1415	G
1	5	1439	C
1	5	1443	A
1	5	1447	C
1	5	1457	G
1	5	1498	G
1	5	1502	G
1	5	1516	G
1	5	1523	A
1	5	1534	A
1	5	1547	A
1	5	1574	G
1	5	1578	U
1	5	1591	U
1	5	1596	U
1	5	1612	G
1	5	1624	G
1	5	1625	G
1	5	1631	A
1	5	1633	G
1	5	1634	A
1	5	1638	A
1	5	1640	C

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Mol	Chain	Res	Type
1	5	1654	G
1	5	1661	C
1	5	1676	C
1	5	1677	U
1	5	1697	G
1	5	1699	A
1	5	1701	A
1	5	1705	G
1	5	1742	A
1	5	1758	G
1	5	1759	G
1	5	1761	G
1	5	1768	C
1	5	1769	G
1	5	1770	A
1	5	1787	A
1	5	1804	A
1	5	1834	U
1	5	1836	G
1	5	1837	A
1	5	1842	G
1	5	1854	G
1	5	1855	G
1	5	1869	G
1	5	1897	A
1	5	1916	G
1	5	1917	A
1	5	1918	U
1	5	1921	C
1	5	1922	G
1	5	1925	G
1	5	1931	C
1	5	1932	A
1	5	1940	G
1	5	1948	G
1	5	1961	G
1	5	1977	C
1	5	1982	G
1	5	1984	A
1	5	1985	G
1	5	1987	C
1	5	1988	G

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Mol	Chain	Res	Type
1	5	1990	A
1	5	1991	A
1	5	1992	U
1	5	1993	C
1	5	1998	A
1	5	2001	G
1	5	2002	A
1	5	2003	G
1	5	2004	U
1	5	2005	G
1	5	2009	A
1	5	2010	A
1	5	2011	C
1	5	2021	G
1	5	2026	A
1	5	2046	G
1	5	2048	U
1	5	2055	G
1	5	2056	G
1	5	2069	A
1	5	2084	C
1	5	2092	G
1	5	2093	A
1	5	2096	G
1	5	2098	G
1	5	2102	G
1	5	2103	G
1	5	2107	C
1	5	2261	G
1	5	2300	A
1	5	2301	G
1	5	2306	G
1	5	2313	A
1	5	2314	G
1	5	2316	G
1	5	2322	G
1	5	2331	G
1	5	2348	G
1	5	2351	C
1	5	2395	A
1	5	2397	G
1	5	2410	C

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Mol	Chain	Res	Type
1	5	2421	G
1	5	2469	C
1	5	2470	C
1	5	2471	G
1	5	2474	G
1	5	2475	G
1	5	2478	C
1	5	2504	C
1	5	2505	C
1	5	2507	A
1	5	2513	A
1	5	2529	A
1	5	2554	U
1	5	2567	G
1	5	2583	C
1	5	2587	A
1	5	2601	A
1	5	2627	C
1	5	2653	C
1	5	2660	A
1	5	2669	C
1	5	2687	U
1	5	2695	A
1	5	2696	A
1	5	2708	U
1	5	2710	C
1	5	2711	G
1	5	2743	A
1	5	2761	U
1	5	2764	A
1	5	2769	U
1	5	2788	U
1	5	2790	U
1	5	2806	A
1	5	2814	C
1	5	2826	U
1	5	2827	G
1	5	2829	U
1	5	2835	A
1	5	2855	G
1	5	3596	A
1	5	3597	G

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Mol	Chain	Res	Type
1	5	3605	C
1	5	3606	U
1	5	3615	G
1	5	3618	C
1	5	3626	G
1	5	3635	A
1	5	3644	U
1	5	3648	A
1	5	3662	A
1	5	3673	C
1	5	3692	A
1	5	3709	U
1	5	3710	G
1	5	3712	A
1	5	3714	G
1	5	3735	G
1	5	3753	G
1	5	3773	U
1	5	3774	A
1	5	3777	G
1	5	3778	U
1	5	3784	A
1	5	3811	G
1	5	3814	U
1	5	3817	A
1	5	3819	G
1	5	3824	A
1	5	3838	U
1	5	3839	G
1	5	3840	U
1	5	3877	A
1	5	3878	C
1	5	3879	G
1	5	3897	G
1	5	3901	A
1	5	3905	A
1	5	3906	A
1	5	3907	G
1	5	3915	U
1	5	3939	G
1	5	3951	G
1	5	3958	G

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Mol	Chain	Res	Type
1	5	3961	G
1	5	3965	A
1	5	3966	A
1	5	3967	G
1	5	3968	U
1	5	3969	G
1	5	3972	A
1	5	3973	G
1	5	3974	G
1	5	3975	C
1	5	4040	C
1	5	4046	A
1	5	4047	A
1	5	4048	A
1	5	4049	U
1	5	4050	A
1	5	4051	C
1	5	4059	C
1	5	4061	G
1	5	4076	G
1	5	4084	G
1	5	4097	G
1	5	4098	A
1	5	4119	C
1	5	4122	G
1	5	4147	G
1	5	4150	G
1	5	4162	C
1	5	4163	U
1	5	4170	A
1	5	4183	G
1	5	4184	G
1	5	4191	G
1	5	4203	A
1	5	4212	A
1	5	4225	G
1	5	4229	U
1	5	4233	A
1	5	4234	A
1	5	4251	A
1	5	4254	G
1	5	4266	G

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Mol	Chain	Res	Type
1	5	4268	A
1	5	4273	A
1	5	4281	A
1	5	4291	G
1	5	4295	U
1	5	4304	A
1	5	4305	G
1	5	4314	C
1	5	4330	G
1	5	4332	C
1	5	4354	U
1	5	4373	G
1	5	4377	G
1	5	4378	A
1	5	4379	A
1	5	4387	C
1	5	4393	G
1	5	4394	A
1	5	4421	C
1	5	4422	A
1	5	4426	C
1	5	4437	U
1	5	4440	G
1	5	4444	C
1	5	4448	G
1	5	4464	A
1	5	4465	U
1	5	4466	C
1	5	4475	G
1	5	4494	G
1	5	4500	U
1	5	4512	U
1	5	4513	A
1	5	4518	A
1	5	4524	G
1	5	4528	G
1	5	4548	A
1	5	4560	C
1	5	4567	G
1	5	4570	G
1	5	4572	U
1	5	4575	G

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Mol	Chain	Res	Type
1	5	4584	A
1	5	4590	A
1	5	4627	U
1	5	4636	U
1	5	4637	G
1	5	4656	A
1	5	4670	C
1	5	4672	A
1	5	4700	A
1	5	4708	A
1	5	4709	U
1	5	4720	C
1	5	4730	C
1	5	4731	G
1	5	4734	A
1	5	4740	G
1	5	4741	C
1	5	4742	G
1	5	4743	G
1	5	4745	G
1	5	4750	G
1	5	4754	G
1	5	4757	C
1	5	4759	C
1	5	4761	G
1	5	4765	G
1	5	4771	C
1	5	4870	G
1	5	4871	C
1	5	4882	U
1	5	4883	C
1	5	4895	C
1	5	4900	C
1	5	4901	G
1	5	4910	A
1	5	4912	G
1	5	4913	G
1	5	4943	A
1	5	4976	U
1	5	4988	U
1	5	4989	U
1	5	4990	C

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Mol	Chain	Res	Type
1	5	4991	U
1	5	4994	G
1	5	5006	U
1	5	5007	A
1	5	5017	G
1	5	5034	A
1	5	5041	G
1	5	5048	A
1	5	5050	C
1	5	5062	G
1	5	5069	U
2	7	7	G
2	7	53	U
2	7	54	A
2	7	64	G
2	7	110	G
2	7	120	U
3	8	34	U
3	8	35	C
3	8	39	G
3	8	51	U
3	8	59	A
3	8	60	G
3	8	62	A
3	8	63	U
3	8	80	A
3	8	87	G
3	8	103	A
3	8	105	C
3	8	110	U
3	8	114	G
3	8	147	G
3	8	153	C
9	G	9	G
9	G	12	G
9	G	13	U
9	G	16	U
9	G	17	C
9	G	18	G
9	G	19	G
9	G	20	U
9	G	21	A

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Mol	Chain	Res	Type
9	G	34	A
9	G	35	G
9	G	38	U
9	G	41	G
9	G	45	G
9	G	47	U
9	G	48	C
9	G	50	C
9	G	58	A
9	G	59	U
9	G	60	U
9	G	61	C
9	G	76	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	963	G
1	5	1633	G
1	5	1981	G
1	5	1987	C
1	5	1990	A
1	5	2009	A
1	5	2020	U
1	5	2506	G
1	5	4048	A
1	5	4050	A
1	5	4420	U
1	5	4699	U
9	G	12	G
9	G	44	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 224 ligands modelled in this entry, 224 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

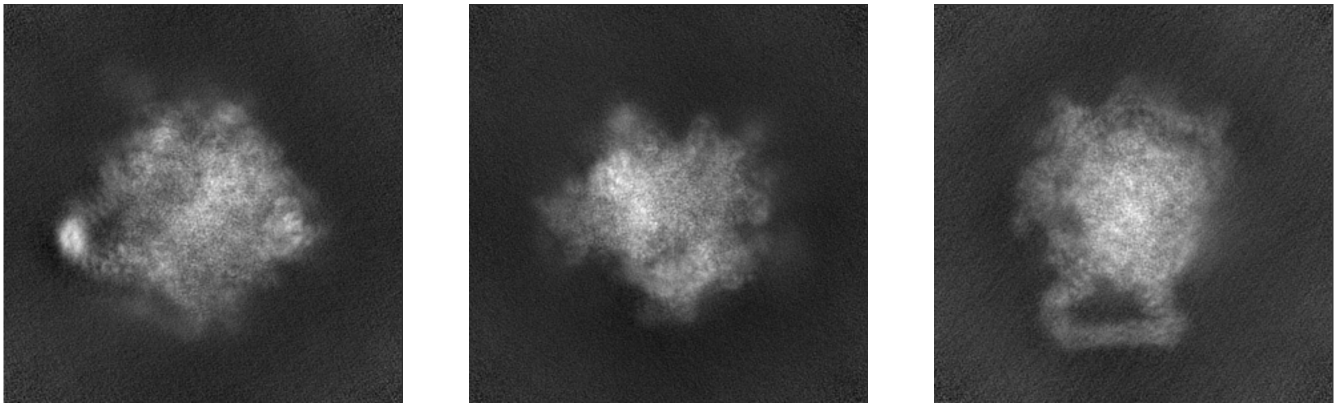
6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-51681. 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 ⓘ

6.1.1 Primary map

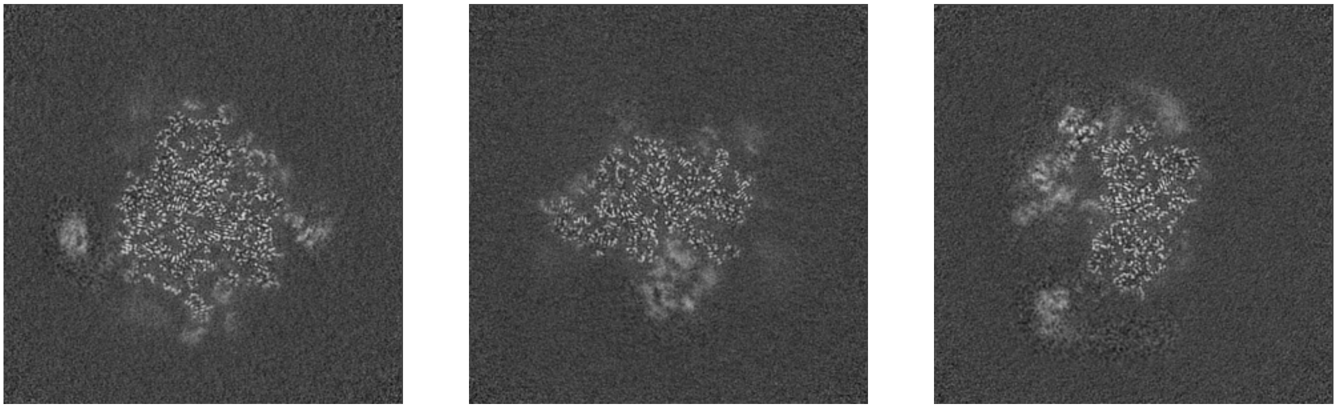


X Y Z

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

6.2 Central slices ⓘ

6.2.1 Primary map

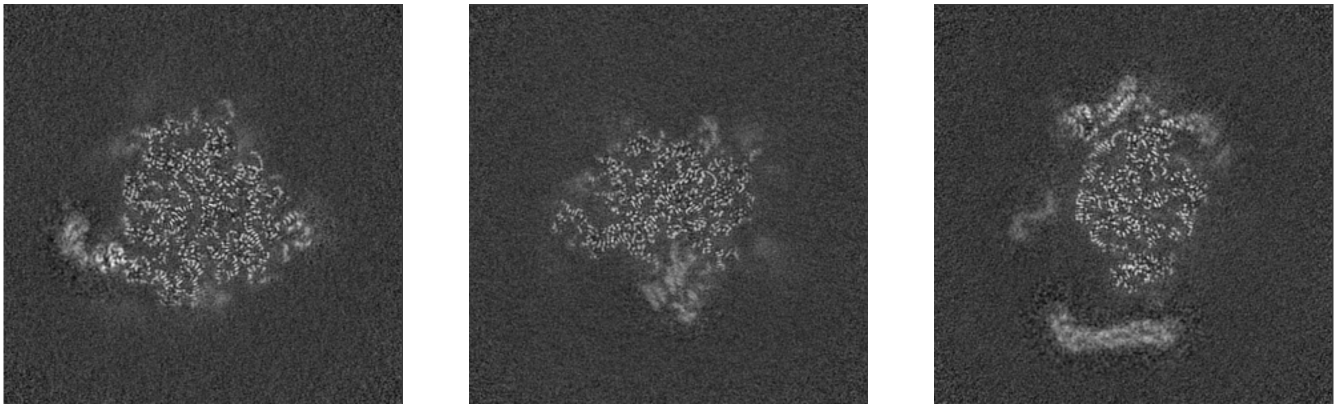


X Index: 300 Y Index: 300 Z Index: 300

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

6.3 Largest variance slices

6.3.1 Primary map

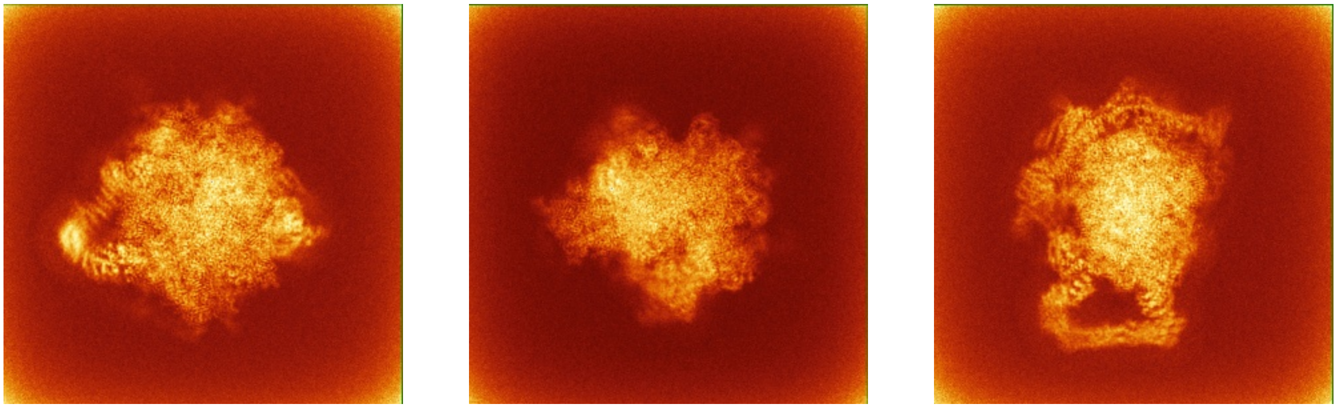


X Index: 321 Y Index: 310 Z Index: 261

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

6.4 Orthogonal standard-deviation projections (False-color)

6.4.1 Primary map



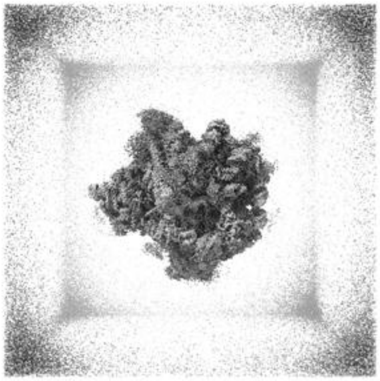
X Y Z

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.

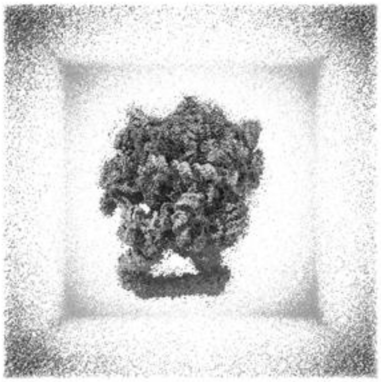
6.5 Orthogonal surface views ⓘ

6.5.1 Primary map

X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.7. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

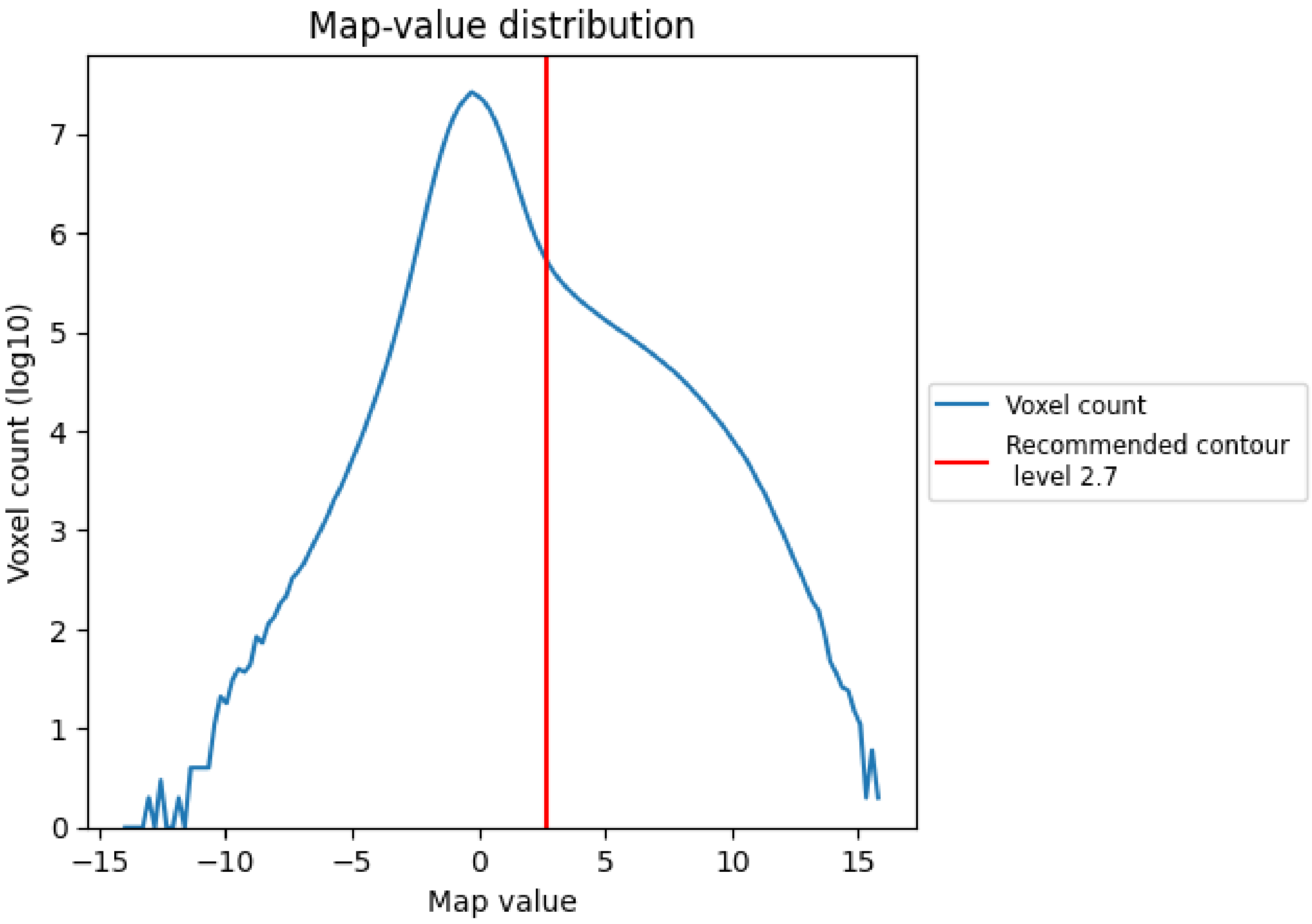
6.6 Mask visualisation ⓘ

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

7 Map analysis ⓘ

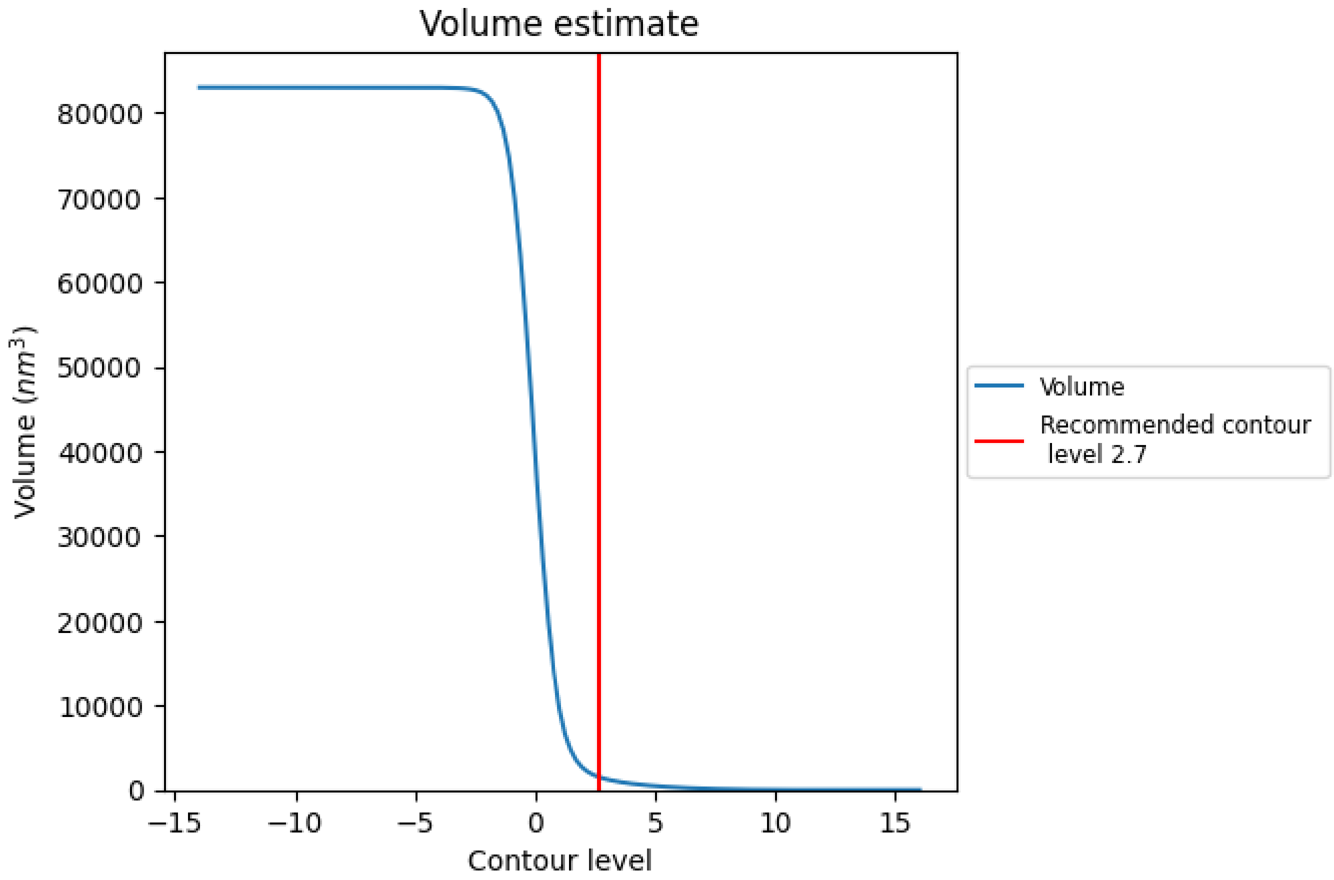
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

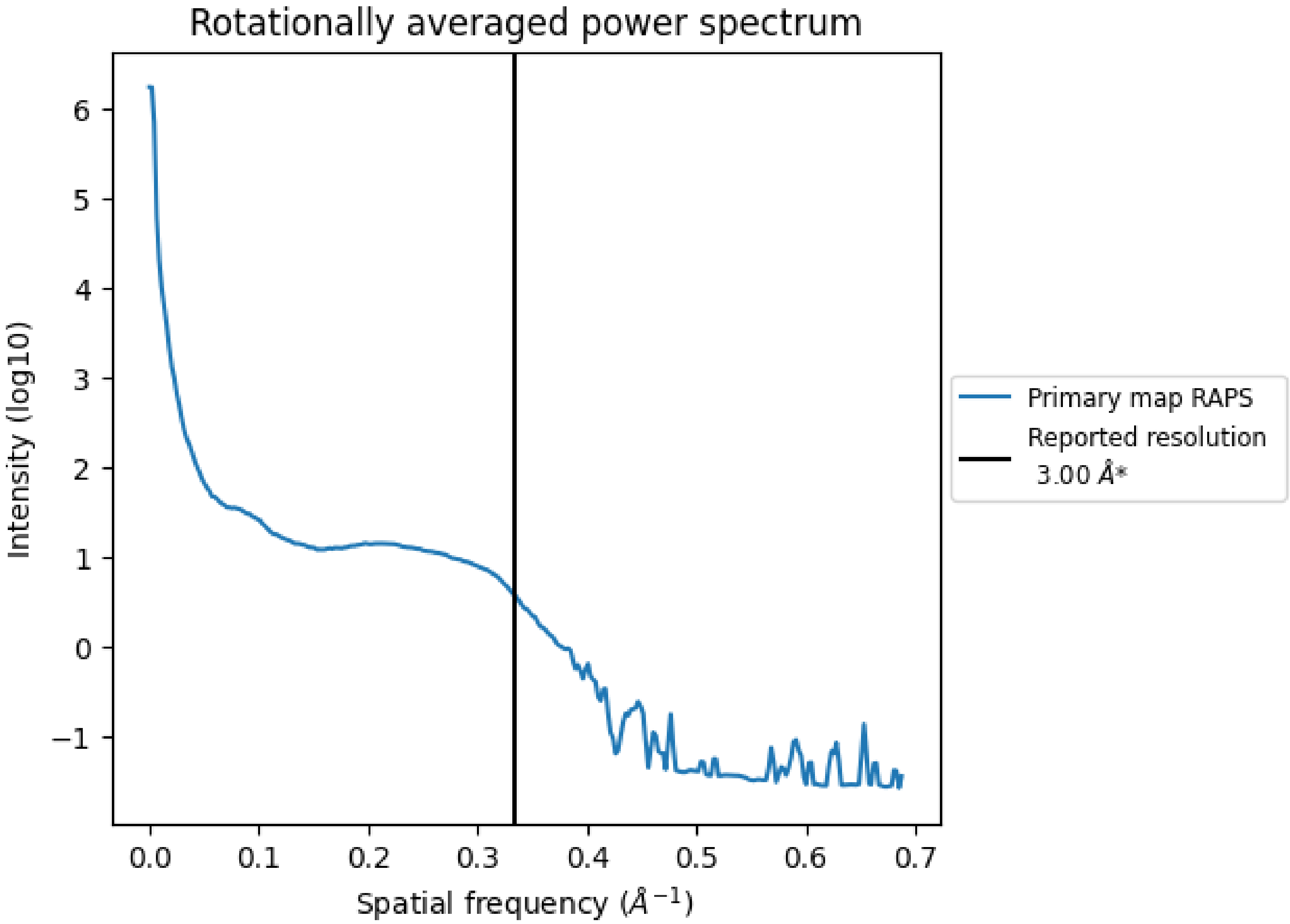
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 1497 nm^3; this corresponds to an approximate mass of 1352 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 0.333 Å^{-1}

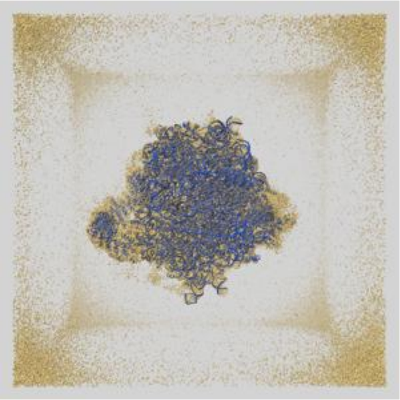
8 Fourier-Shell correlation ⓘ

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

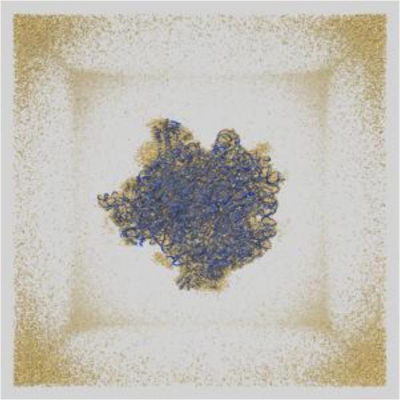
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-51681 and PDB model 9GY4. Per-residue inclusion information can be found in section 3 on page 15.

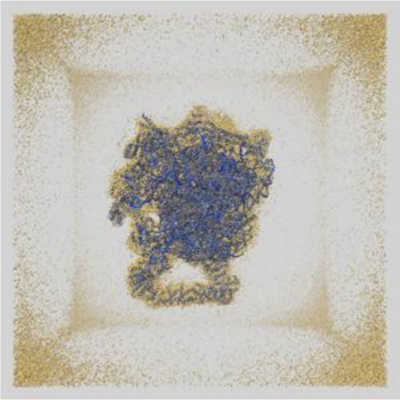
9.1 Map-model overlay



X



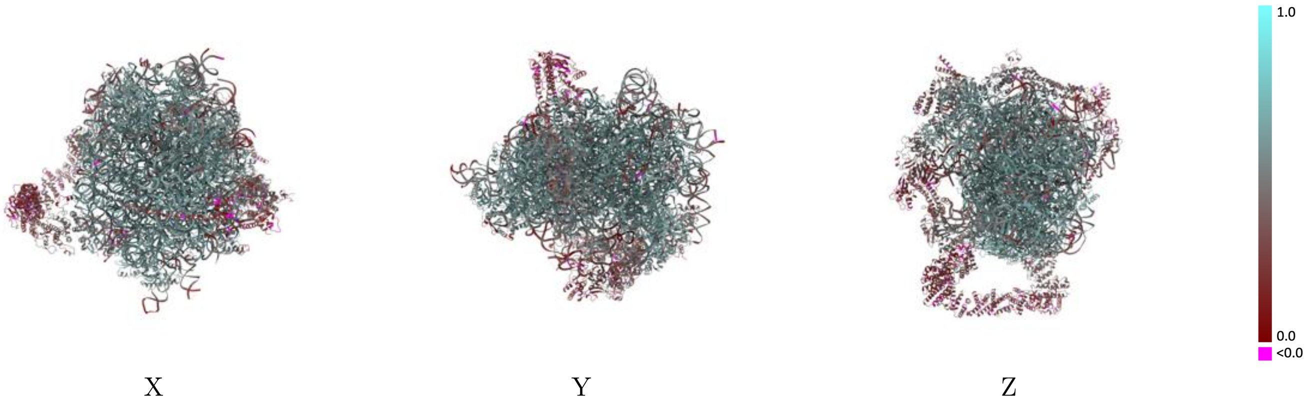
Y



Z

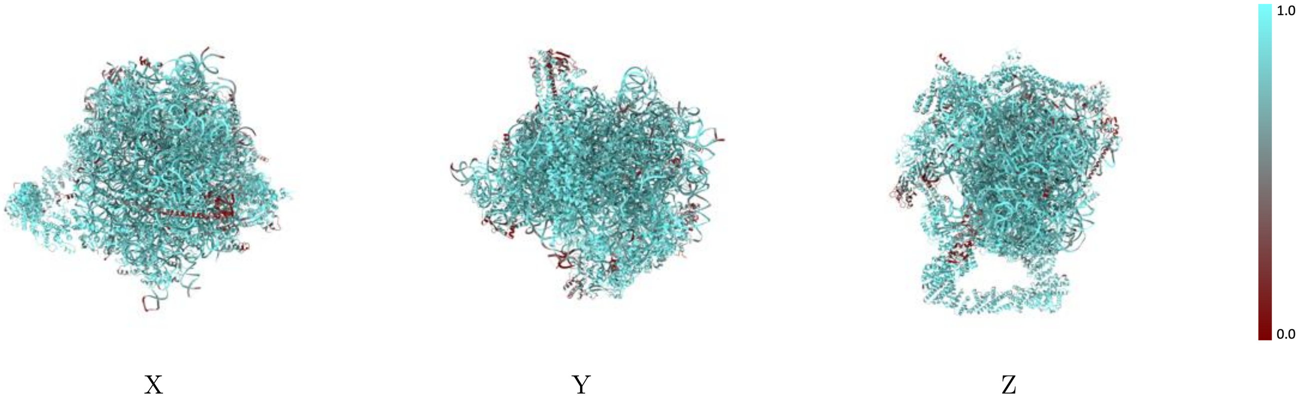
The images above show the 3D surface view of the map at the recommended contour level 2.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model



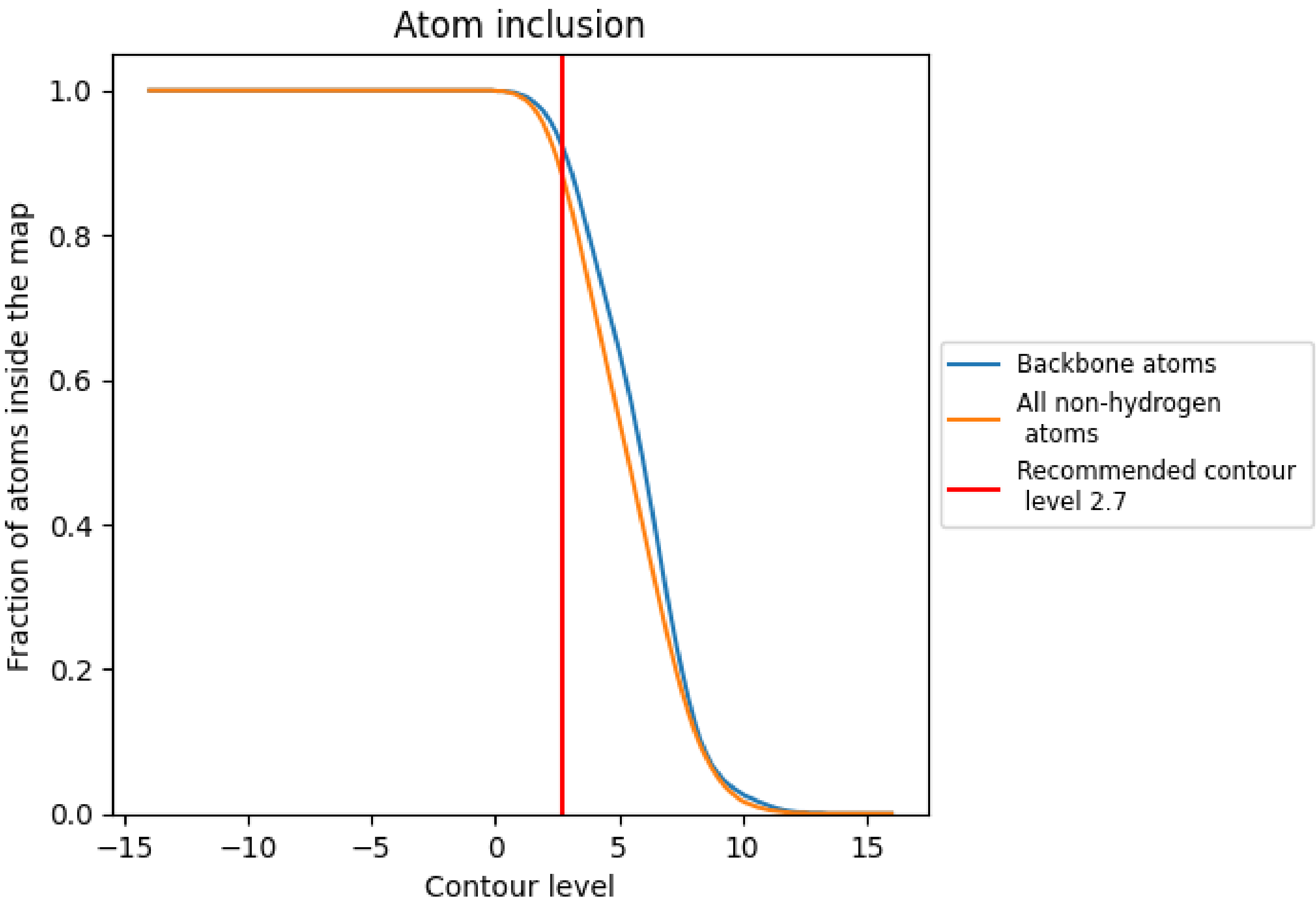
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model



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 (2.7).

9.4 Atom inclusion ⓘ



At the recommended contour level, 92% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (2.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8840	0.5170
5	0.9160	0.5490
7	0.9670	0.5860
8	0.9400	0.5730
A	0.6860	0.4700
B	0.8090	0.3180
C	0.5250	0.2670
D	0.1940	0.1560
E	0.8520	0.4260
F	0.8840	0.2680
G	0.8680	0.2640
LB	0.8980	0.6150
LC	0.8910	0.6040
LD	0.8700	0.5830
LE	0.8500	0.5820
LF	0.9190	0.6200
LG	0.7870	0.5580
LH	0.8880	0.6050
LI	0.8870	0.6020
LJ	0.8350	0.5400
LL	0.9140	0.5950
LM	0.9030	0.6090
LN	0.9600	0.6330
LO	0.9210	0.6180
LP	0.9170	0.6200
LQ	0.9360	0.6250
LR	0.8850	0.5940
LS	0.9300	0.6200
LT	0.8700	0.5930
LU	0.8690	0.5210
LV	0.8740	0.6140
LW	0.8860	0.6160
LX	0.8770	0.6010
LY	0.8970	0.6040
LZ	0.8750	0.5920

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Chain	Atom inclusion	Q-score
La	0.9160	0.6160
Lb	0.7770	0.5520
Lc	0.7960	0.5830
Ld	0.9250	0.5910
Le	0.9210	0.6160
Lf	0.9410	0.6290
Lg	0.8630	0.5890
Lh	0.8630	0.6050
Li	0.8780	0.5870
Lj	0.9630	0.6300
Lk	0.7380	0.5640
Ll	0.9080	0.6090
Lm	0.9130	0.5880
Lo	0.9150	0.6090
Lp	0.8460	0.6030
Lr	0.9090	0.6140
Lz	0.9150	0.4760
Z	0.7370	0.3290
a	0.9300	0.6230
s	0.3390	0.3290
t	0.8240	0.3820