Full wwPDB EM Validation Report

Mar 9, 2026 – 12:27 PM UTC

PDB ID	:	7QV1 / pdb_00007qv1
EMDB ID	:	EMD-14157
Title	:	Bacillus subtilis collided disome (Leading 70S)
Authors	:	Filbeck, S.; Pfeffer, S.
Deposited on	:	2022-01-19
Resolution	:	3.50 Å(reported)

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

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

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

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

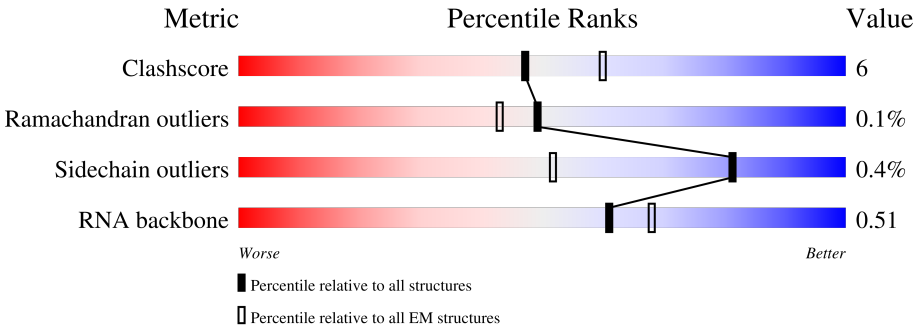
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

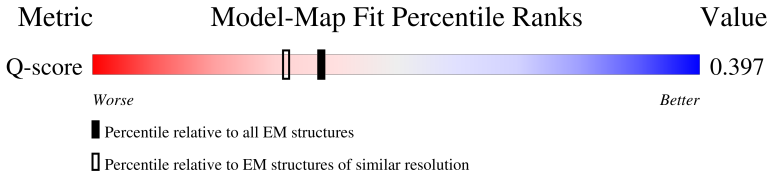
1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	0	59	81% 8% 8%
2	1	49	6% 78% 20%
3	2	44	91% 9%

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Mol	Chain	Length	Quality of chain
4	3	66	83% 14%
5	4	37	14% 81% 19%
6	6	66	71% 86% 9% 5%
7	B	112	61% 29% 10%
8	C	277	5% 85% 13%
9	D	209	84% 14%
10	E	207	14% 94% 5%
11	F	179	46% 85% 13%
12	G	179	56% 81% 17%
13	H	77	66% 27% 6%
14	I	24	100% 83% 17%
15	J	145	85% 13%
16	K	122	5% 83% 17%
17	L	146	14% 86% 14%
18	M	144	7% 83% 10% 6%
19	N	120	84% 15%
20	O	120	12% 90% 10%
21	P	115	8% 90% 10%
22	Q	119	87% 11%
23	R	102	8% 82% 17%
24	S	113	85% 12%
25	T	95	5% 86% 8% 5%
26	U	103	11% 81% 17%
27	V	2928	5% 59% 31% 9%
28	W	94	6% 80% 7% 13%

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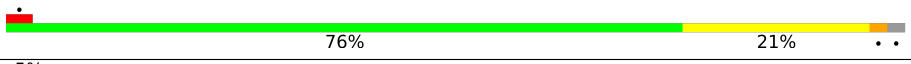
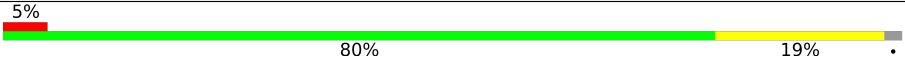
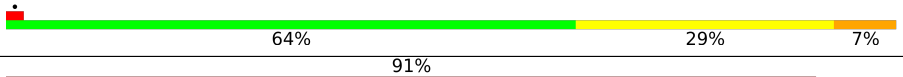
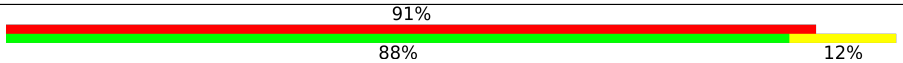
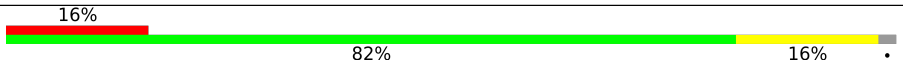
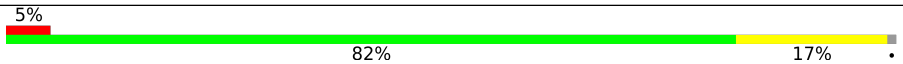
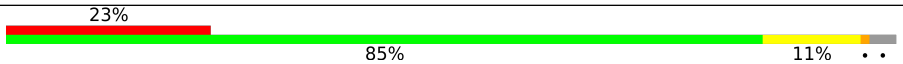
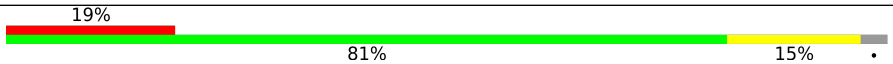
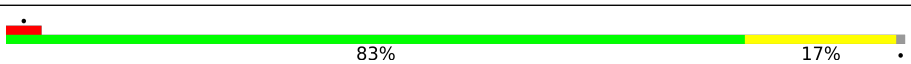
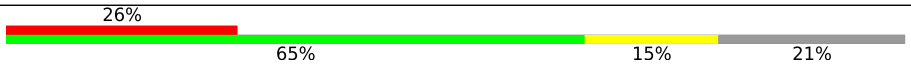
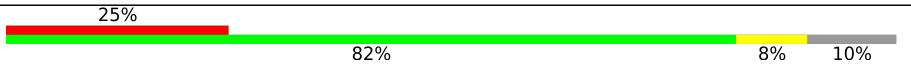
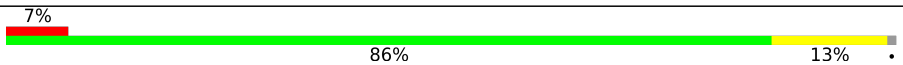
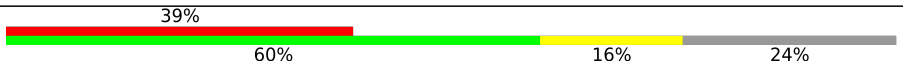
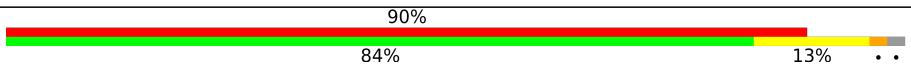
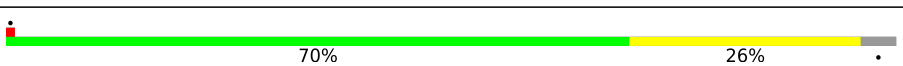
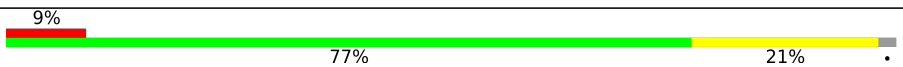
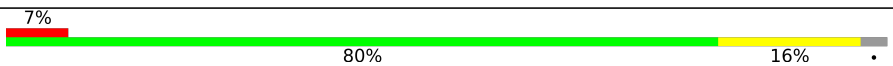
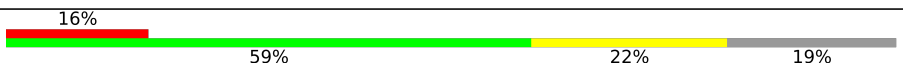
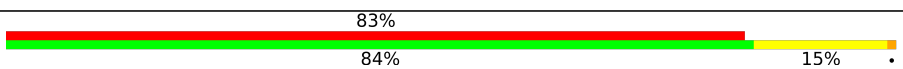
Mol	Chain	Length	Quality of chain
29	Y	66	
30	Z	59	
31	a	1533	
32	b	57	
33	c	218	
34	d	200	
35	e	166	
36	f	95	
37	g	156	
38	h	132	
39	i	130	
40	j	102	
41	k	131	
42	l	138	
43	m	121	
44	n	61	
45	o	89	
46	p	90	
47	q	87	
48	r	79	
49	s	92	
50	t	88	
51	u	62	
52	X	149	
53	A	26	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 140774 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	54	426	262	86	71	7	0	0

- Molecule 2 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	48	401	244	80	73	4	0	0

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	44	367	222	89	54	2	0	0

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	64	512	321	107	82	2	0	0

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	37	296	186	60	45	5	0	0

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	6	63	499	312	91	91	5	0	0

- Molecule 7 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

- Molecule 8 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	272	Total	C	N	O	S	0	0
			2083	1296	408	373	6		

- Molecule 9 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 10 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 11 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	176	Total	C	N	O	S	0	0
			1386	882	241	256	7		

- Molecule 12 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 13 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		

- Molecule 14 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	I	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	135	Total	C	N	O	S	0	0
			1076	690	205	176	5		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	115	Total	C	N	O	S	0	0
			944	600	185	158	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 23 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	101	Total	C	N	O	0	0
			786	501	139	146		

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 27 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	2887	Total	C	N	O	P	0	0
			61998	27661	11460	19993	2884		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	243	G	A	conflict	GB 1491848961
V	325	A	-	insertion	GB 1491848961
V	326	A	-	insertion	GB 1491848961
V	327	G	-	insertion	GB 1491848961
V	328	G	-	insertion	GB 1491848961
V	640	U	C	conflict	GB 1491848961
V	2232	A	G	conflict	GB 1491848961

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	W	82	Total	C	N	O	0	0
			630	390	123	117		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 30 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 31 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	1533	Total	C	N	O	P	0	0
			32891	14667	6034	10657	1533		

- Molecule 32 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	57	Total	C	N	O	S	0	0
			476	295	97	83	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	30	ALA	GLN	conflict	UNP P21478

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	206	Total	C	N	O	S	0	0
			1619	1011	304	301	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	195	Total	C	N	O	S	0	0
			1568	991	291	284	2		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	164	Total	C	N	O	S	0	0
			1218	767	225	224	2		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	92	Total	C	N	O	S	0	0
			755	476	132	146	1		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	151	Total	C	N	O	S	0	0
			1203	755	224	218	6		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	131	Total	C	N	O	S	0	0
			1036	655	191	187	3		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	i	103	Total	C	N	O	0	0
			784	485	151	148		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	95	Total	C	N	O	S	0	0
			761	479	139	141	2		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	118	Total	C	N	O	S	0	0
			871	537	171	161	2		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	136	Total	C	N	O	S	0	0
			1052	653	211	186	2		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	m	92	Total	C	N	O	0	0
			740	459	145	136		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	60	Total	C	N	O	S	0	0
			497	317	98	77	5		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	85	Total	C	N	O	S	0	0
			710	436	144	129	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	88	Total	C	N	O	S	0	0
			695	441	128	124	2		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	84	Total	C	N	O	S	0	0
			691	435	128	126	2		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	64	Total	C	N	O	S	0	0
			518	332	96	88	2		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	77	Total	C	N	O	S	0	0
			624	403	110	109	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	83	Total	C	N	O	S	0	0
			637	390	130	116	1		

- Molecule 51 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 52 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	X	149	Total	C	N	O	S	0	0
			1151	726	205	219	1		

- Molecule 53 is a RNA chain called mRNA.

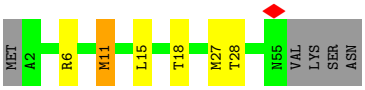
Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	26	Total	C	N	O	P	0	0
			559	251	106	176	26		

3 Residue-property plots (i)

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

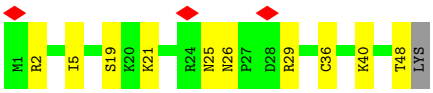
• Molecule 1: 50S ribosomal protein L32

Chain 0:



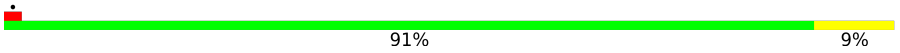
• Molecule 2: 50S ribosomal protein L33 1

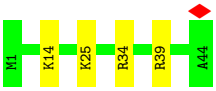
Chain 1:



• Molecule 3: 50S ribosomal protein L34

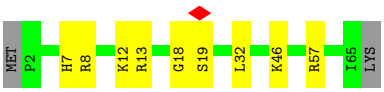
Chain 2:





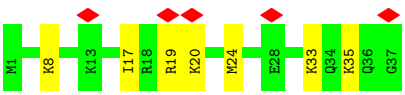
• Molecule 4: 50S ribosomal protein L35

Chain 3:



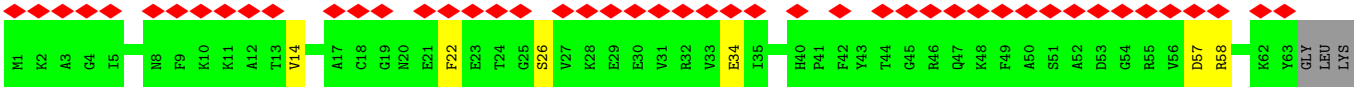
• Molecule 5: 50S ribosomal protein L36

Chain 4:



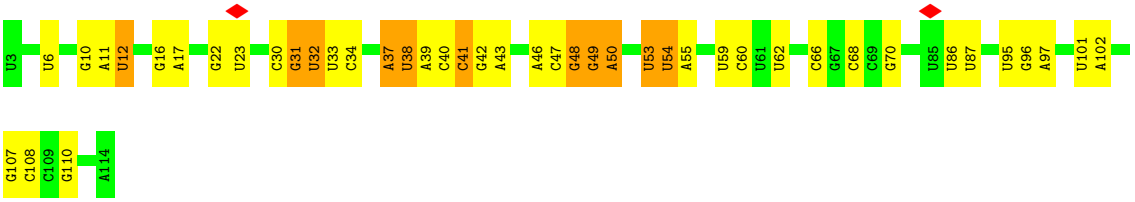
• Molecule 6: 50S ribosomal protein L31

Chain 6:



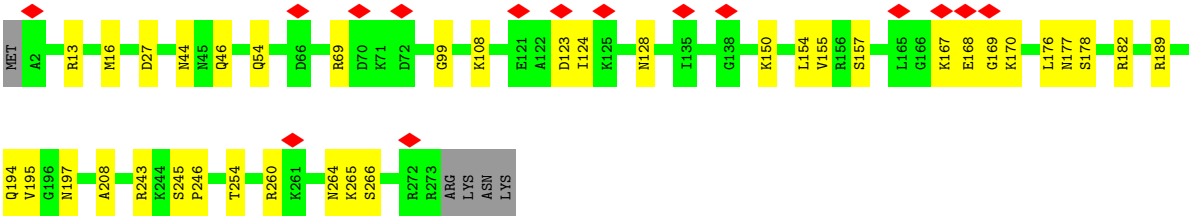
• Molecule 7: 5S ribosomal RNA

Chain B:



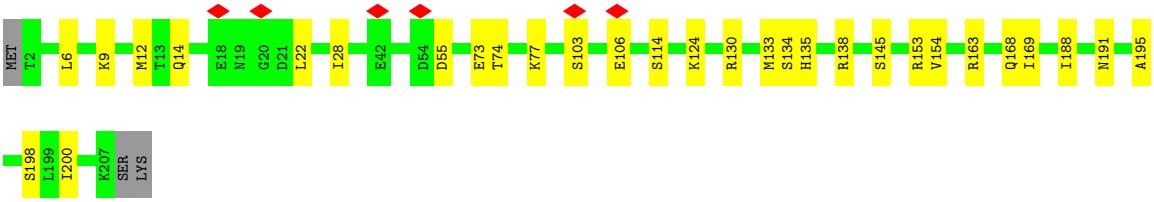
• Molecule 8: 50S ribosomal protein L2

Chain C:



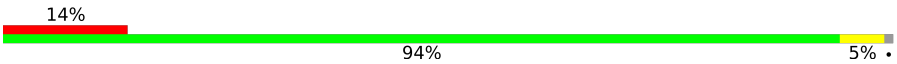
• Molecule 9: 50S ribosomal protein L3

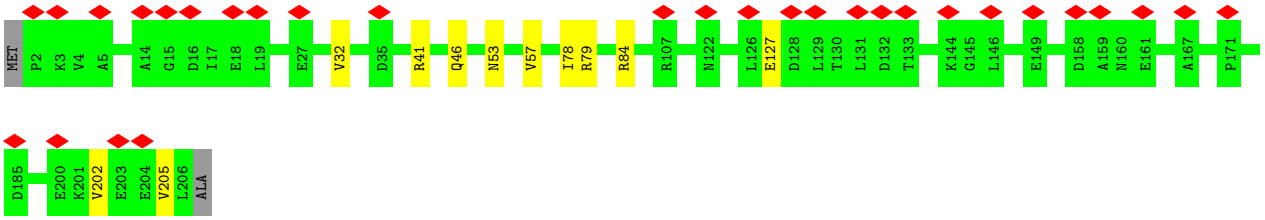
Chain D:



• Molecule 10: 50S ribosomal protein L4

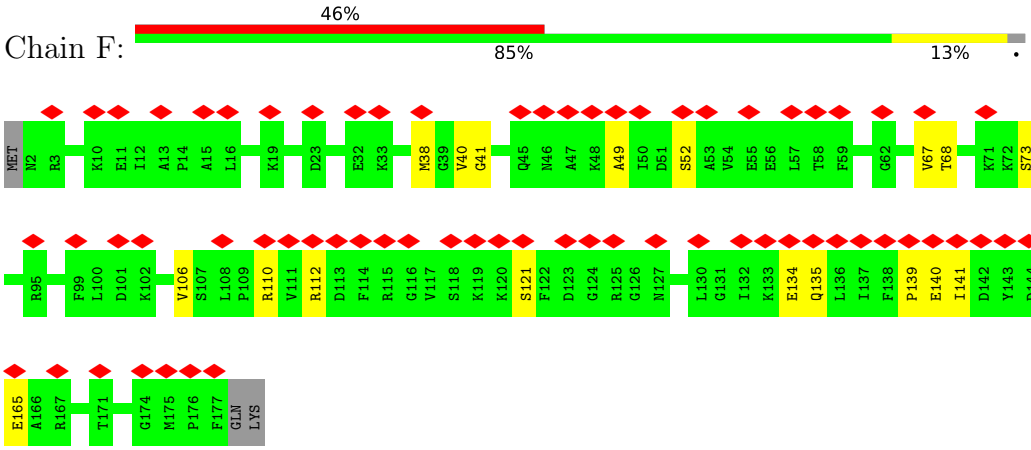
Chain E:





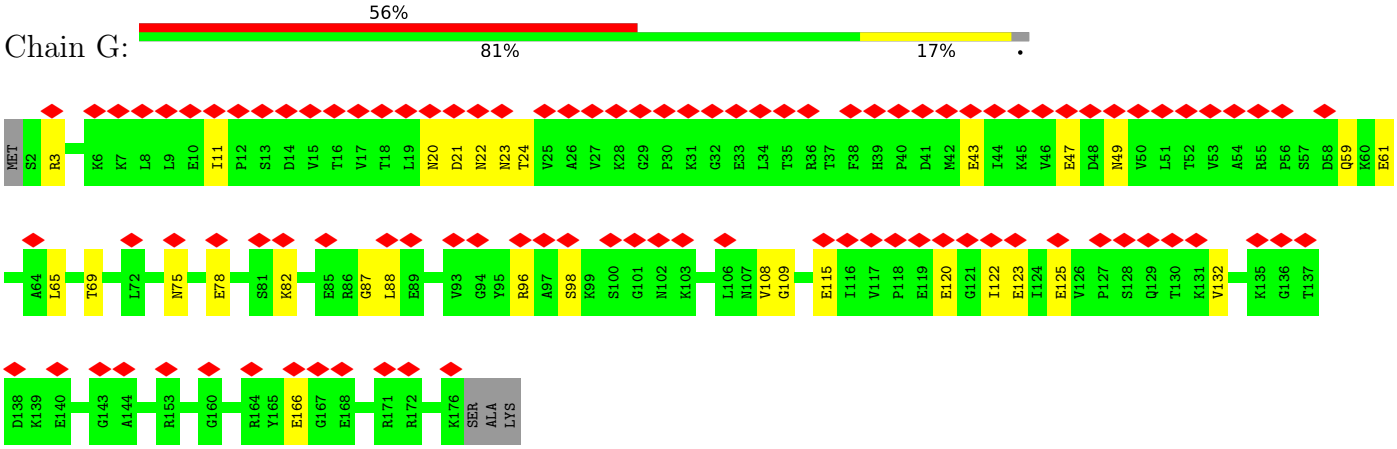
• Molecule 11: 50S ribosomal protein L5

Chain F:



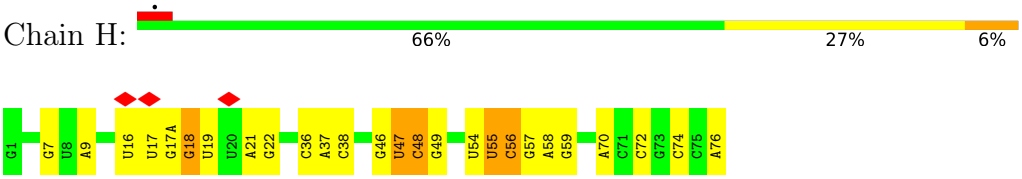
• Molecule 12: 50S ribosomal protein L6

Chain G:



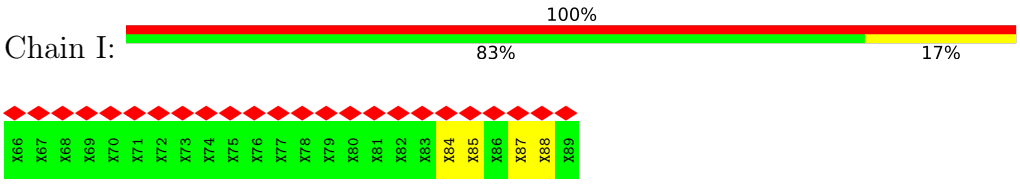
• Molecule 13: P-site tRNA

Chain H:



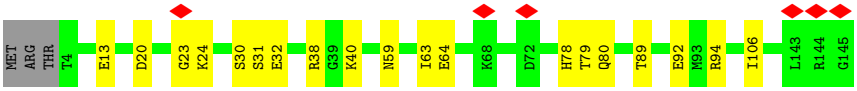
• Molecule 14: Nascent chain

Chain I:



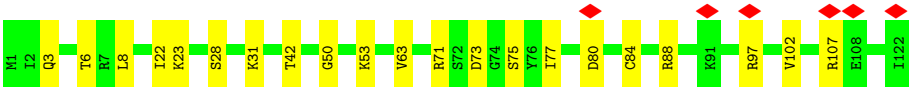
• Molecule 15: 50S ribosomal protein L13

Chain J:



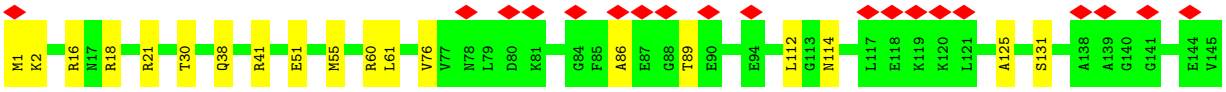
• Molecule 16: 50S ribosomal protein L14

Chain K:



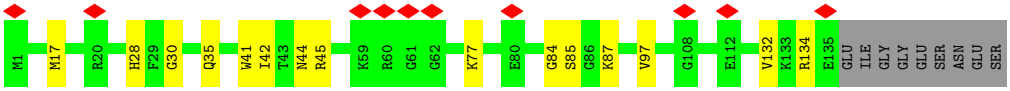
• Molecule 17: 50S ribosomal protein L15

Chain L:



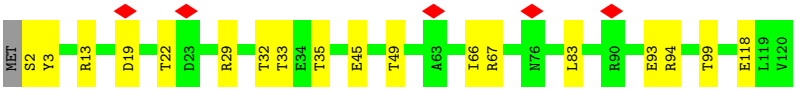
• Molecule 18: 50S ribosomal protein L16

Chain M:



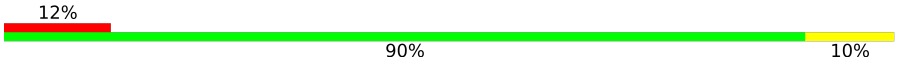
• Molecule 19: 50S ribosomal protein L17

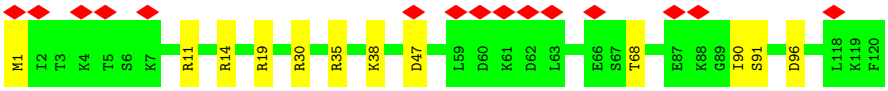
Chain N:



• Molecule 20: 50S ribosomal protein L18

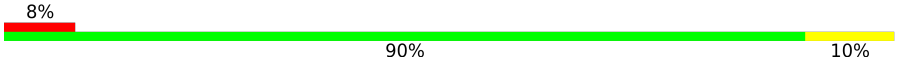
Chain O:

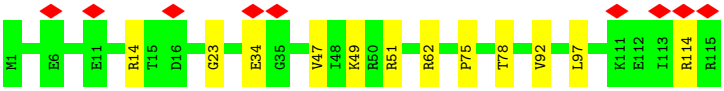




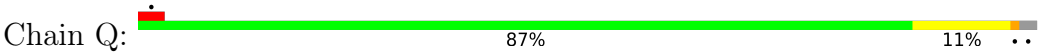
• Molecule 21: 50S ribosomal protein L19

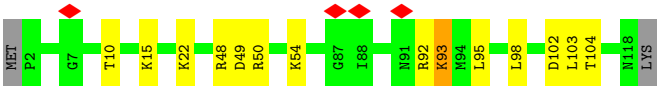
Chain P:



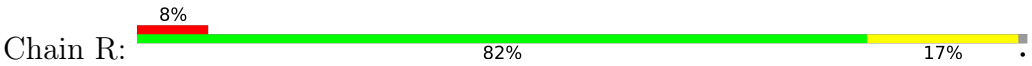


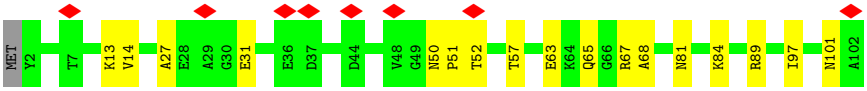
• Molecule 22: 50S ribosomal protein L20



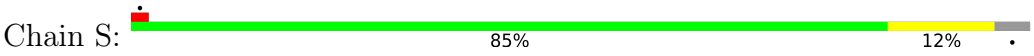


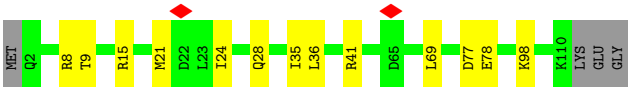
• Molecule 23: 50S ribosomal protein L21



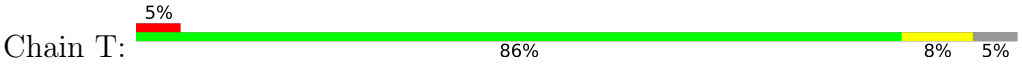


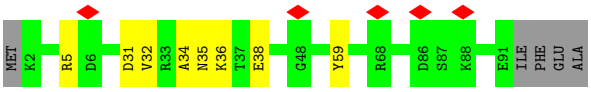
• Molecule 24: 50S ribosomal protein L22



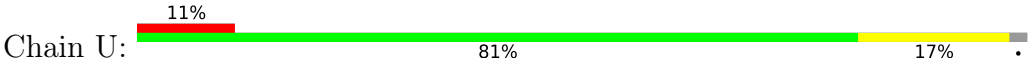


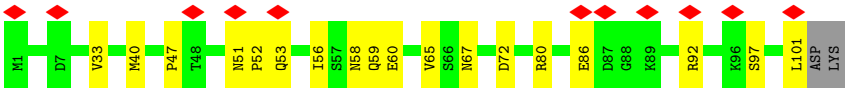
• Molecule 25: 50S ribosomal protein L23



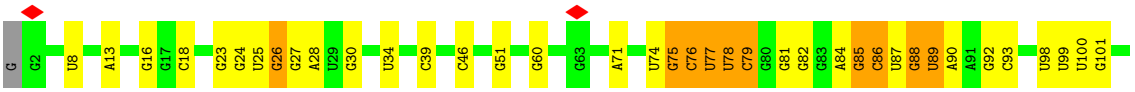


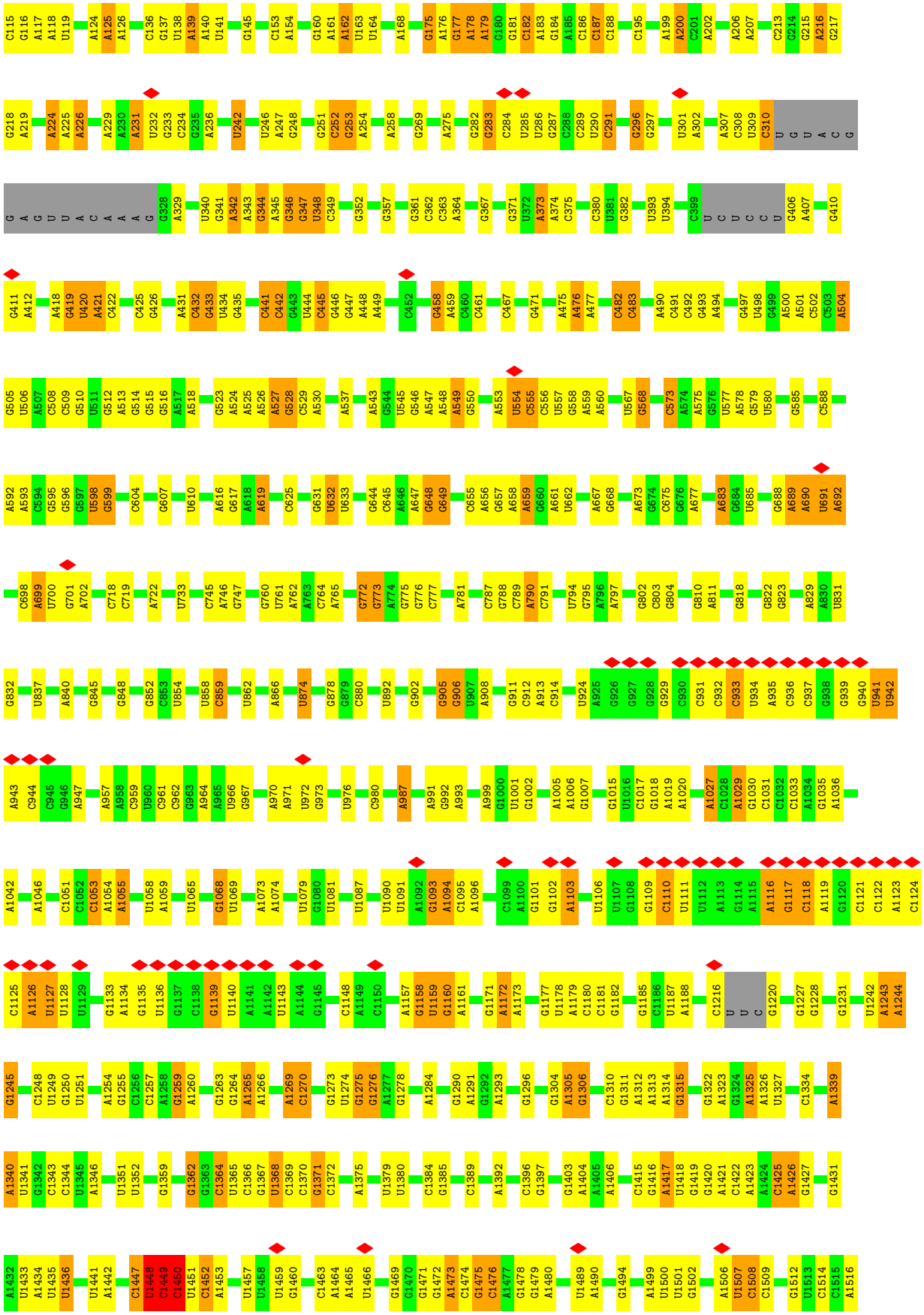
• Molecule 26: 50S ribosomal protein L24

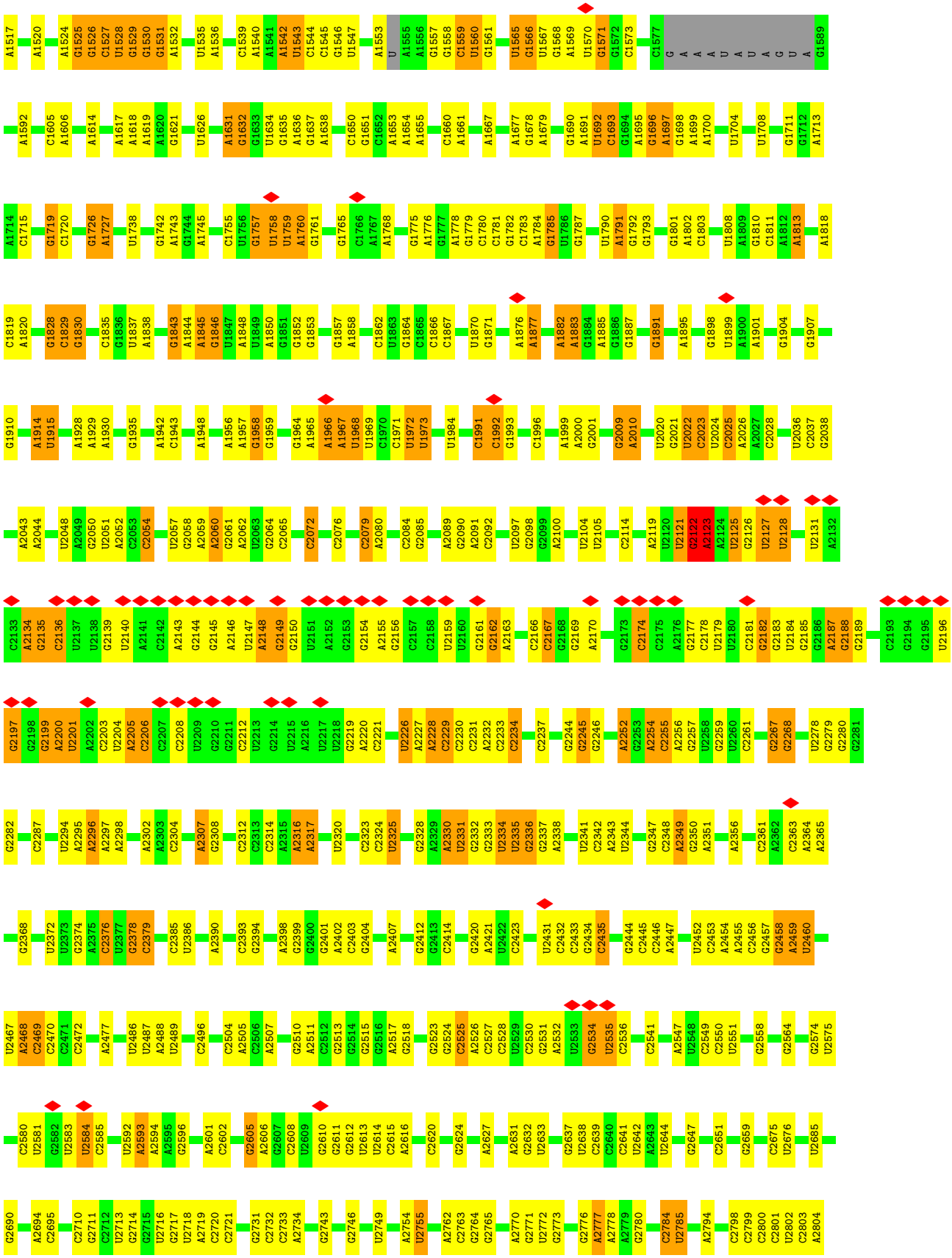


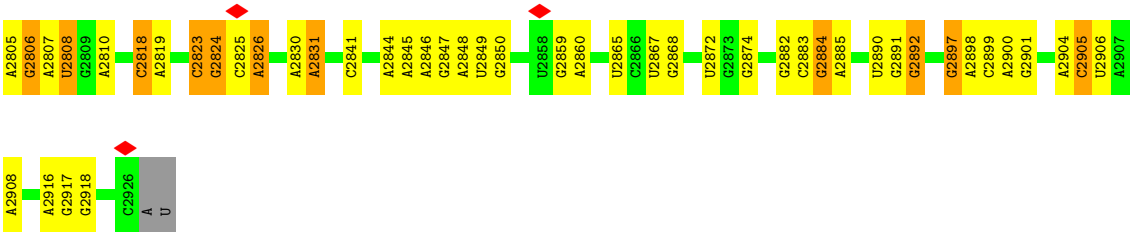


• Molecule 27: 23S ribosomal RNA



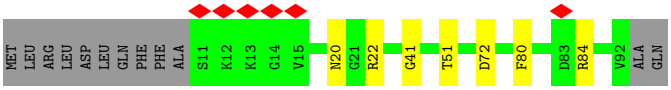

C115 G116 A117 A118 U119 A124 A125 A126 C136 G137 U138 A139 A140 U141 G145 C153 A154 G160 A161 A162 U163 U164 A168 G175 A176 G177 A178 A179 G180 G181 C182 A183 G184 A185 C186 C187 C188 C195 A199 A200 C201 A202 A206 A207 C213 G214 G215 A216 G217
G218 A219 A224 A225 A226 A229 A230 A231 U232 G233 C234 G235 A236 U242 U246 A247 G248 G251 C252 G253 A254 A258 G269 A275 G282 G283 C284 U285 U286 G287 C288 C289 U290 C291 G296 G297 U301 A302 A307 C308 U309 C310 U G U A C G
G A A G U U A C A A A G G328 A329 U340 G341 A342 A343 G344 A345 G346 G347 U348 C349 G352 G357 G361 C362 C363 A364 G367 G371 U372 A373 A374 C375 C380 U381 G382 U393 U394 C399 U C U C C U G406 A407 G410
G411 A412 A418 G419 U420 A421 C422 C425 G426 A431 C432 G433 U434 G435 C441 C442 G443 U444 C445 G446 G447 A448 A449 C452 G458 A459 C460 C461 C467 G471 A475 A476 A477 C482 C483 A490 C491 C492 G493 A494 G497 U498 C499 A500 A501 C502 C503 A504
G505 U506 A507 C508 C509 C510 U511 G512 A513 G514 C515 C516 A517 A518 G523 A524 A525 A526 A527 G528 C529 A530 A537 A543 G544 U545 C546 A547 A548 A549 G550 A553 U554 C555 C556 U557 C558 A559 A560 U567 G568 C573 A574 A575 G576 U577 A578 G579 U580 G585 C588
A592 A593 C594 G595 G596 G597 U598 G599 C604 G607 U610 A616 G617 A618 A619 C625 G631 U632 U633 G644 C645 A646 A647 G648 G649 C655 A656 G657 A658 A659 G660 A661 U662 A667 G668 A673 G674 C675 G676 A677 A683 G684 U685 G688 A689 A690 U691 A692
C698 A699 U700 G701 A702 C718 C719 A722 U733 C745 A746 G747 G760 U761 A762 A763 C764 A765 G772 G773 A774 G775 G776 C777 A781 C787 G788 C789 A790 C791 U794 G795 A796 A797 G802 C803 G804 G810 A811 G818 G822 G823 A829 A830 U831
G832 U837 A840 G845 G848 G852 C853 U854 U858 C859 U862 A866 U874 G878 G879 C880 U892 G902 G905 G906 U907 A908 G911 C912 A913 C914 U924 A925 G926 G927 G928 G929 C930 C931 C932 C933 U934 A935 C936 C937 G938 G939 G940 U941 U942
A943 C944 C945 G946 A947 A957 A958 C959 U960 C961 C962 G963 A964 A965 U966 G967 A970 A971 U972 G973 U976 C980 A987 A991 G992 A993 A999 G1000 U1001 G1002 A1005 A1006 G1007 G1015 U1016 C1017 G1018 A1019 A1020 A1027 C1028 A1029 G1030 C1031 C1032 C1033 A1034 G1035 A1036
A1042 A1046 C1051 C1052 C1053 A1054 A1055 U1058 A1059 U1065 G1068 U1069 A1073 A1074 U1079 G1080 U1081 U1087 U1090 U1091 A1092 G1093 A1094 C1095 A1096 C1099 A1100 G1101 G1102 A1103 U1106 U1107 G1108 G1109 C1110 U1111 U1112 A1113 G1114 A1115 A1116 G1117 C1118 A1119 G1120 C1121 C1122 A1123 C1124
C1125 A1126 U1127 U1128 U1129 G1133 A1134 G1135 U1136 G1137 C1138 G1139 U1140 A1141 A1142 U1143 A1144 G1145 C1148 A1149 C1150 A1157 G1158 U1159 G1160 A1161 G1171 A1172 A1173 G1177 U1178 A1179 C1180 C1181 G1182 G1185 C1186 U1187 A1188 C1216 U U C G1220 G1227 G1228 G1231 U1242 A1243 A1244
G1245 C1248 U1249 G1250 U1251 A1254 G1255 C1256 C1257 A1258 G1259 A1260 G1263 G1264 A1265 A1266 A1269 C1270 G1273 U1274 G1275 G1276 A1277 G1278 A1284 G1290 A1291 G1292 A1293 G1296 G1304 A1305 G1306 C1310 G1311 A1312 A1313 A1314 G1315 G1322 A1323 G1324 A1325 A1326 U1327 C1334 A1339
A1340 U1341 G1342 C1343 C1344 U1345 A1346 U1351 U1352 G1359 G1362 G1363 C1364 U1365 C1366 G1367 U1368 C1369 C1370 G1371 C1372 A1375 U1379 U1380 C1384 G1385 C1389 A1392 C1396 G1397 G1403 A1404 A1405 A1406 C1415 G1416 A1417 U1418 G1419 G1420 A1421 C1422 A1423 A1424 C1425 A1426 G1427 G1431
A1432 U1433 A1434 U1435 U1436 U1441 A1442 C1447 U1448 C1449 C1450 U1451 C1452 A1453 U1457 U1458 U1459 G1460 C1463 A1464 A1465 U1466 G1469 G1470 G1471 G1472 A1473 C1474 G1475 C1476 A1477 G1478 G1479 A1480 U1489 A1490 G1494 A1499 U1500 U1501 G1502 A1506 U1507 C1508 C1509 G1512 U1513 C1514 C1515 A1516





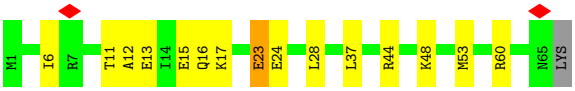
• Molecule 28: 50S ribosomal protein L27

Chain W:



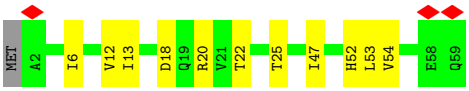
• Molecule 29: 50S ribosomal protein L29

Chain Y:



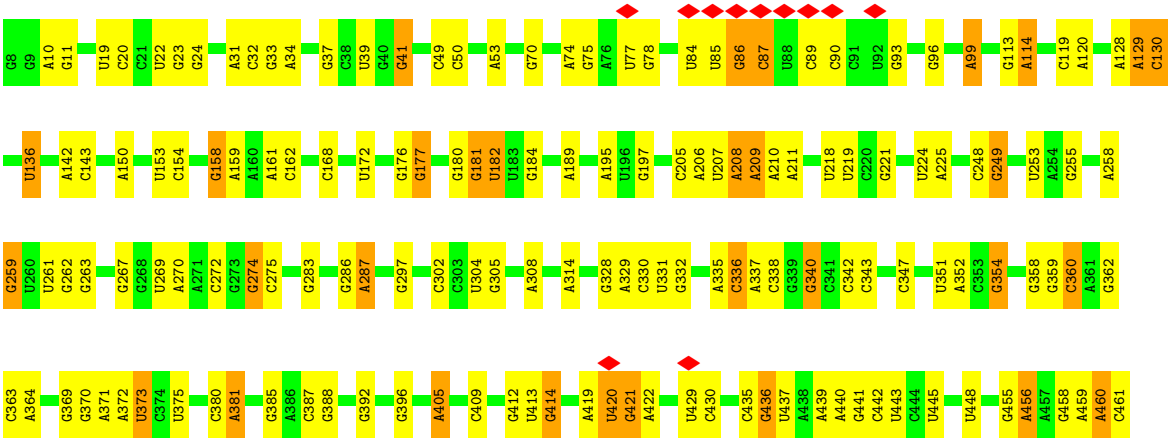
• Molecule 30: 50S ribosomal protein L30

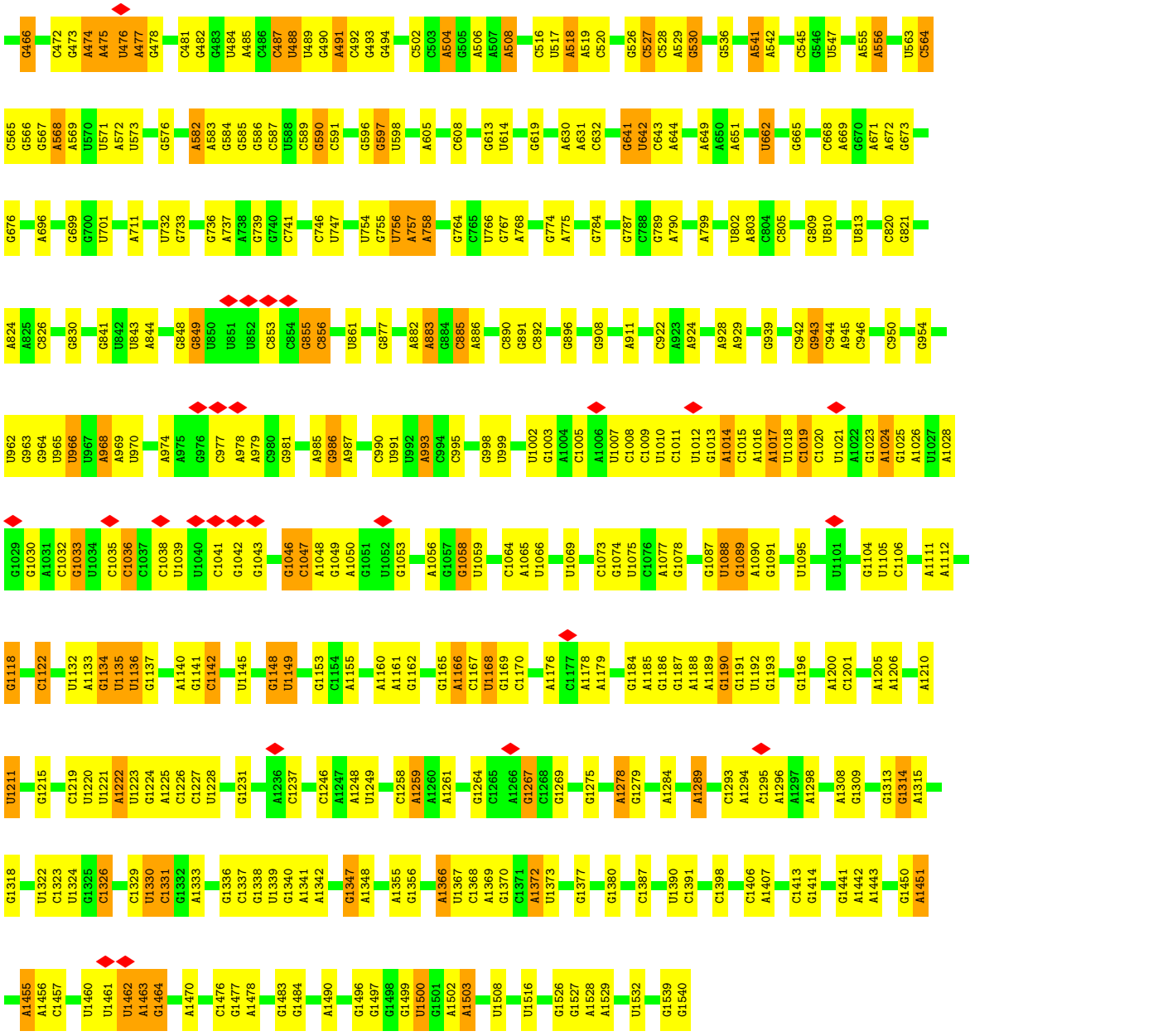
Chain Z:



• Molecule 31: 16S ribosomal RNA

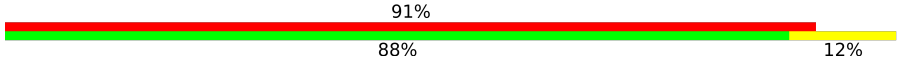
Chain a:

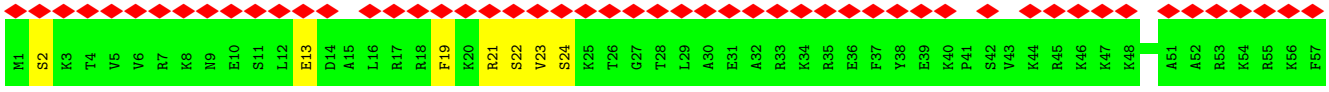




• Molecule 32: 30S ribosomal protein S21

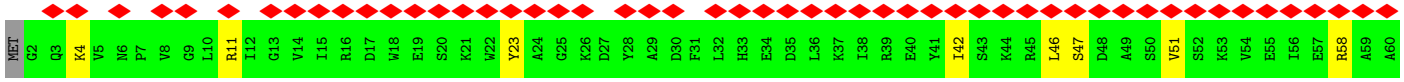
Chain b:

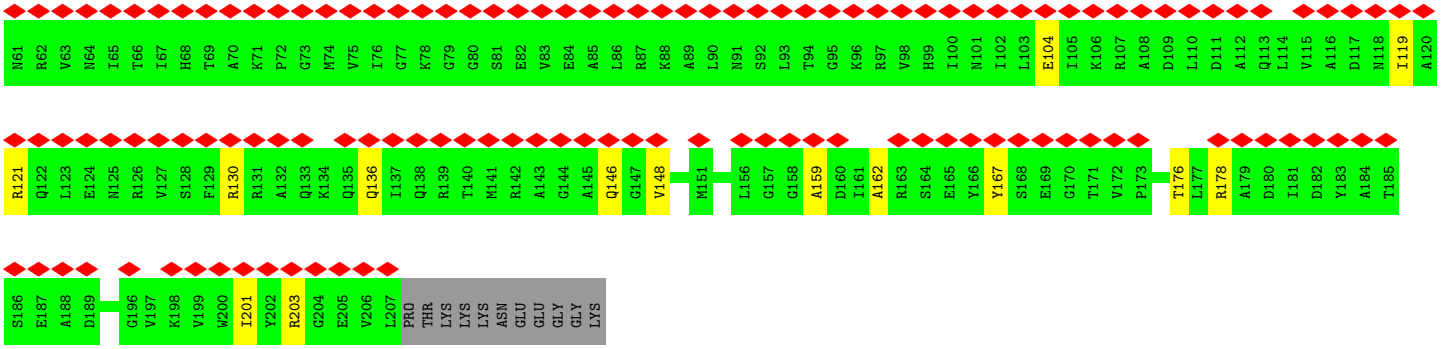




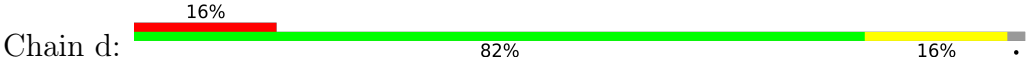
• Molecule 33: 30S ribosomal protein S3

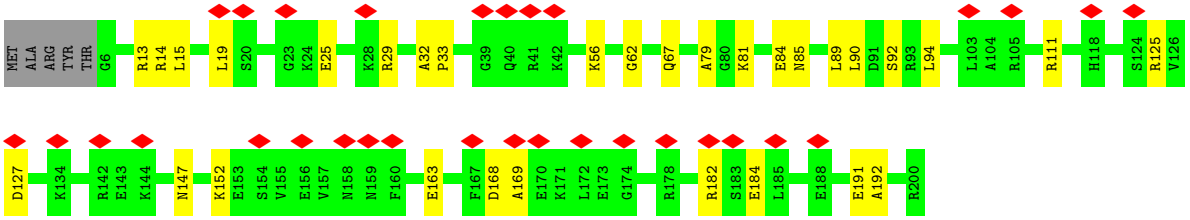
Chain c:



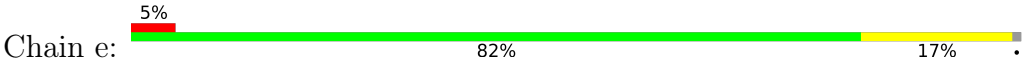


• Molecule 34: 30S ribosomal protein S4

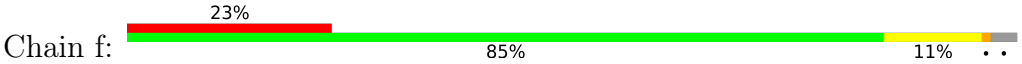


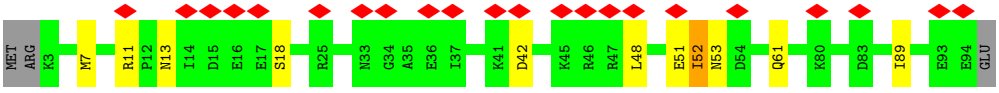


• Molecule 35: 30S ribosomal protein S5

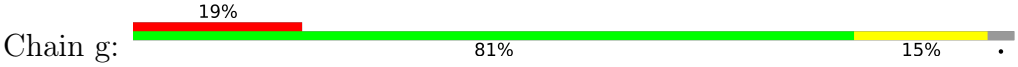


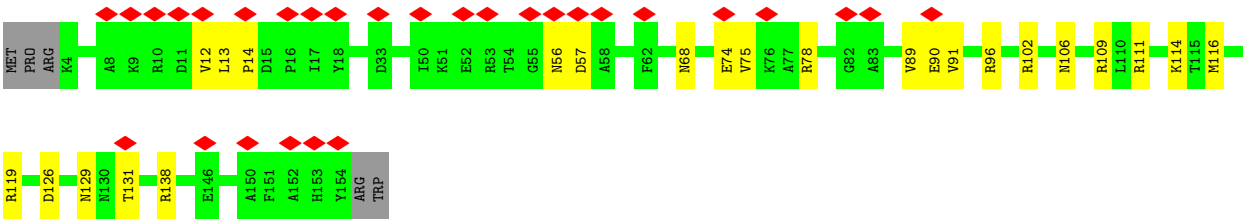
• Molecule 36: 30S ribosomal protein S6





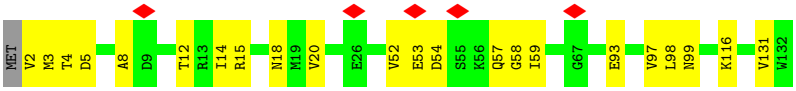
• Molecule 37: 30S ribosomal protein S7





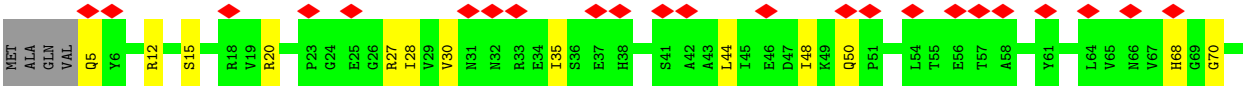
• Molecule 38: 30S ribosomal protein S8

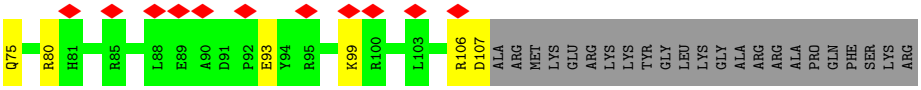
Chain h:



• Molecule 39: 30S ribosomal protein S9

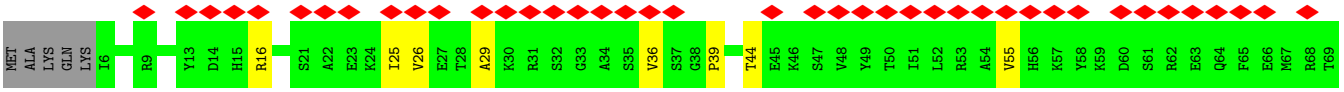
Chain i:

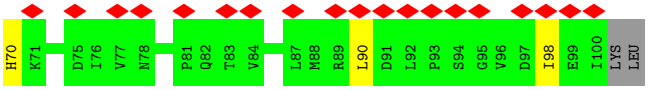




• Molecule 40: 30S ribosomal protein S10

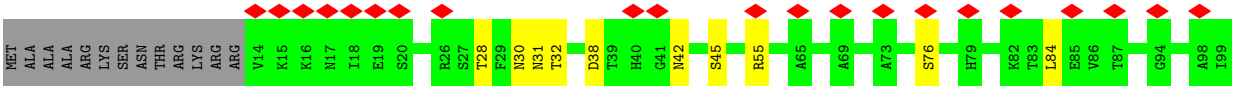
Chain j:

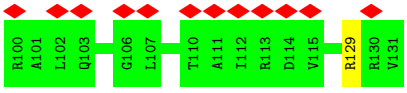




• Molecule 41: 30S ribosomal protein S11

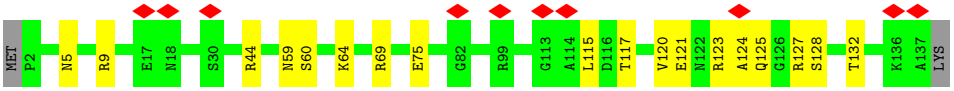
Chain k:





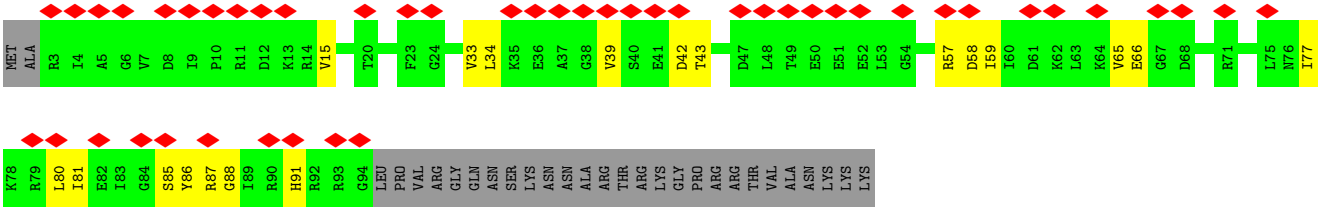
• Molecule 42: 30S ribosomal protein S12

Chain l:

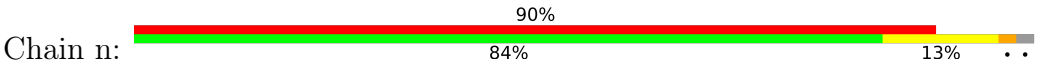


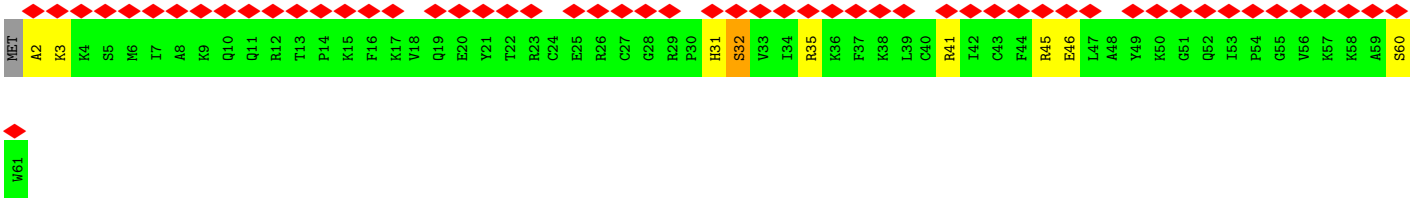
• Molecule 43: 30S ribosomal protein S13

Chain m:

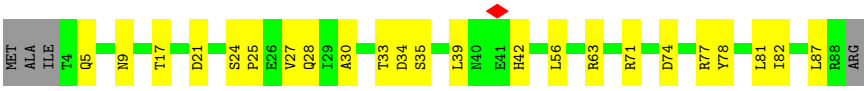


• Molecule 44: 30S ribosomal protein S14

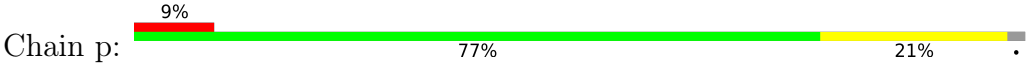


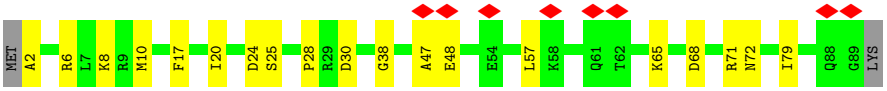


• Molecule 45: 30S ribosomal protein S15

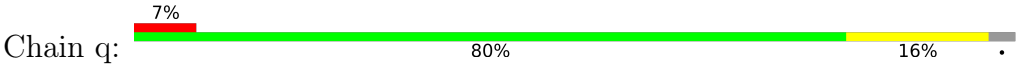


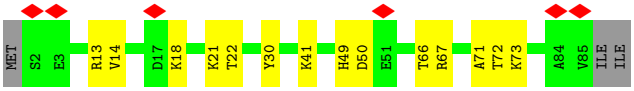
• Molecule 46: 30S ribosomal protein S16



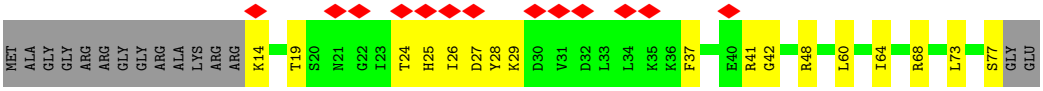


• Molecule 47: 30S ribosomal protein S17



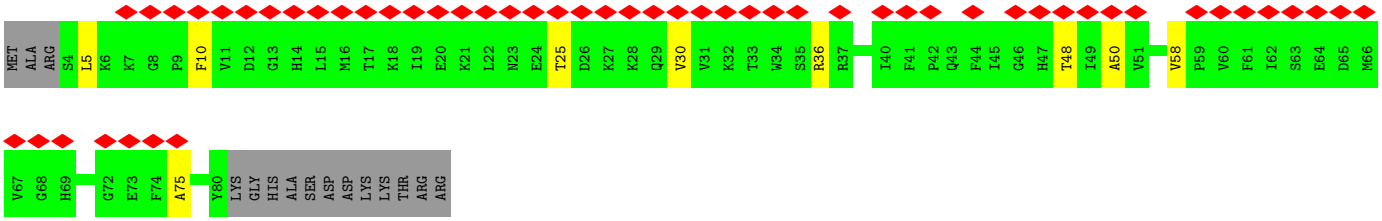


• Molecule 48: 30S ribosomal protein S18



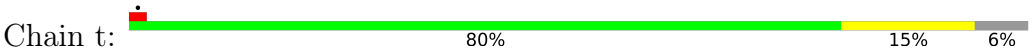
• Molecule 49: 30S ribosomal protein S19

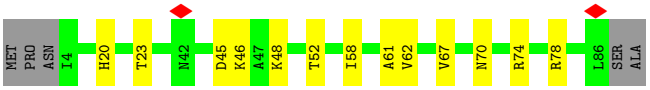
Chain s:



• Molecule 50: 30S ribosomal protein S20

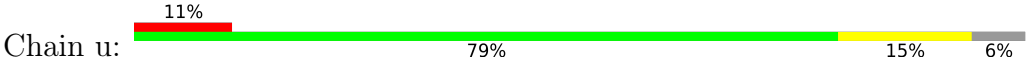
Chain t:

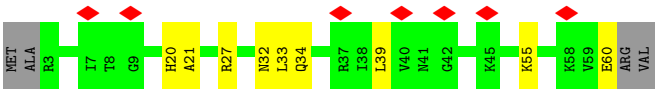




• Molecule 51: 50S ribosomal protein L28

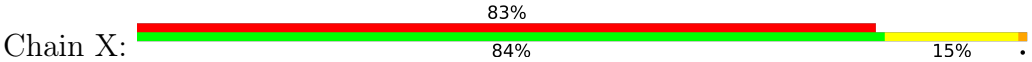
Chain u:

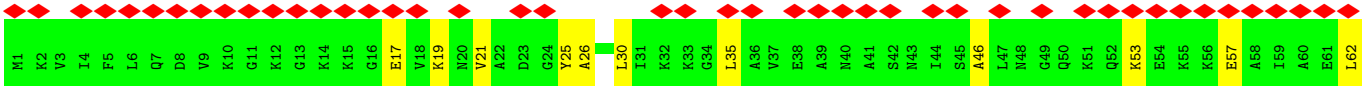


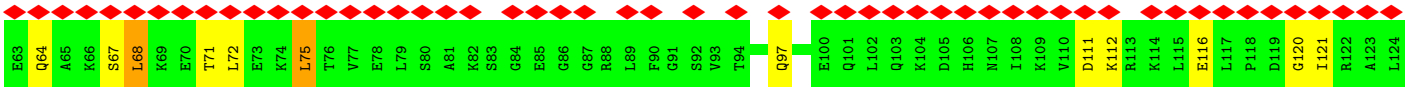


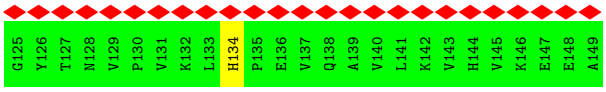
• Molecule 52: 50S ribosomal protein L9

Chain X:



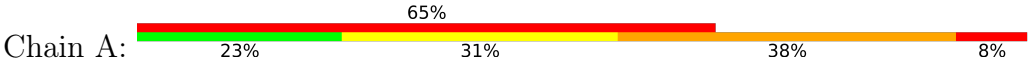






• Molecule 53: mRNA

Chain A:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27833	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	46.5	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	43.238	Depositor
Minimum map value	-15.141	Depositor
Average map value	-0.028	Depositor
Map value standard deviation	1.347	Depositor
Recommended contour level	5	Depositor
Map size (Å)	590.64, 590.64, 590.64	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.605, 1.605, 1.605	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	0	0.12	0/433	0.28	0/574
2	1	0.14	0/406	0.27	0/540
3	2	0.18	0/370	0.31	0/483
4	3	0.13	0/519	0.34	0/680
5	4	0.15	0/299	0.25	0/393
6	6	0.12	0/509	0.24	0/678
7	B	0.08	0/2675	0.21	0/4170
8	C	0.13	0/2120	0.30	0/2845
9	D	0.15	0/1591	0.34	0/2132
10	E	0.11	0/1580	0.28	0/2132
11	F	0.11	0/1405	0.32	0/1887
12	G	0.10	0/1360	0.24	0/1832
13	H	0.07	0/1834	0.21	0/2858
15	J	0.13	0/1146	0.28	0/1542
16	K	0.15	0/927	0.29	0/1245
17	L	0.13	0/1093	0.28	0/1457
18	M	0.12	0/1099	0.25	0/1468
19	N	0.12	0/960	0.28	0/1284
20	O	0.12	0/921	0.26	0/1236
21	P	0.14	0/957	0.29	0/1279
22	Q	0.15	0/952	0.34	0/1266
23	R	0.11	0/797	0.29	0/1070
24	S	0.13	0/851	0.32	0/1146
25	T	0.12	0/731	0.24	0/974
26	U	0.13	0/772	0.27	0/1032
27	V	0.11	0/69444	0.27	12/108334 (0.0%)
28	W	0.13	0/638	0.31	0/847
29	Y	0.14	0/531	0.25	0/707
30	Z	0.11	0/457	0.29	0/613
31	a	0.09	0/36826	0.22	0/57450
32	b	0.16	0/480	0.33	0/628
33	c	0.13	0/1641	0.30	0/2208
34	d	0.13	0/1598	0.31	0/2147
35	e	0.12	0/1230	0.27	0/1655

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
36	f	0.12	0/766	0.28	0/1031
37	g	0.11	0/1220	0.29	0/1637
38	h	0.14	0/1048	0.33	0/1407
39	i	0.12	0/794	0.30	0/1074
40	j	0.11	0/773	0.28	0/1044
41	k	0.13	0/885	0.30	0/1196
42	l	0.14	0/1069	0.33	0/1435
43	m	0.14	0/744	0.35	0/994
44	n	0.12	0/507	0.32	0/672
45	o	0.12	0/718	0.30	0/960
46	p	0.13	0/708	0.32	0/950
47	q	0.12	0/699	0.30	0/933
48	r	0.13	0/526	0.34	0/705
49	s	0.11	0/640	0.27	0/861
50	t	0.12	0/639	0.34	0/852
51	u	0.13	0/448	0.30	0/596
52	X	0.12	0/1162	0.38	0/1551
53	A	0.66	4/627 (0.6%)	0.85	5/975 (0.5%)
All	All	0.12	4/153125 (0.0%)	0.27	17/229665 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	A	41	C	C1'-N1	5.46	1.56	1.48
53	A	42	A	C1'-N9	-5.36	1.40	1.48
53	A	39	U	C1'-N1	5.35	1.55	1.47
53	A	50	C	C1'-N1	5.22	1.56	1.48

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
27	V	138	U	OP1-P-O3'	-29.77	18.68	108.00
53	A	32	U	P-O3'-C3'	-7.69	108.67	120.20
27	V	1449	C	P-O3'-C3'	-6.97	109.74	120.20
53	A	37	G	P-O3'-C3'	-6.92	109.82	120.20
27	V	1450	C	P-O3'-C3'	-6.87	109.89	120.20
53	A	38	A	P-O3'-C3'	-6.85	109.93	120.20
27	V	1447	C	P-O3'-C3'	-6.70	110.15	120.20
27	V	2123	A	P-O3'-C3'	-6.57	110.35	120.20
27	V	139	A	OP1-P-OP2	-6.37	100.50	119.60
53	A	35	A	P-O3'-C3'	-5.72	111.62	120.20
27	V	2122	G	P-O3'-C3'	-5.50	111.95	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
27	V	1448	U	C4'-C3'-O3'	5.45	117.58	109.40
27	V	2226	U	P-O3'-C3'	-5.22	112.38	120.20
27	V	1452	C	P-O3'-C3'	-5.19	112.41	120.20
27	V	2060	A	C2'-C3'-O3'	5.19	117.28	109.50
53	A	31	A	P-O3'-C3'	-5.14	112.48	120.20
27	V	420	U	P-O3'-C3'	-5.12	112.53	120.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	426	0	445	4	0
2	1	401	0	413	6	0
3	2	367	0	410	4	0
4	3	512	0	564	12	0
5	4	296	0	342	6	0
6	6	499	0	491	4	0
7	B	2392	0	1213	30	0
8	C	2083	0	2168	31	0
9	D	1569	0	1637	20	0
10	E	1561	0	1647	8	0
11	F	1386	0	1446	17	0
12	G	1342	0	1388	23	0
13	H	1643	0	831	14	0
14	I	120	0	28	3	0
15	J	1123	0	1162	17	0
16	K	920	0	977	18	0
17	L	1081	0	1132	17	0
18	M	1076	0	1145	10	0
19	N	953	0	983	13	0
20	O	912	0	947	9	0
21	P	944	0	1020	11	0
22	Q	940	0	1005	10	0
23	R	786	0	826	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	S	842	0	899	11	0
25	T	725	0	770	5	0
26	U	762	0	821	11	0
27	V	61998	0	31209	575	0
28	W	630	0	644	7	0
29	Y	530	0	568	10	0
30	Z	455	0	491	8	0
31	a	32891	0	16559	321	0
32	b	476	0	521	6	0
33	c	1619	0	1658	14	0
34	d	1568	0	1604	19	0
35	e	1218	0	1300	20	0
36	f	755	0	746	8	0
37	g	1203	0	1251	18	0
38	h	1036	0	1095	19	0
39	i	784	0	803	14	0
40	j	761	0	795	8	0
41	k	871	0	895	10	0
42	l	1052	0	1112	18	0
43	m	740	0	787	15	0
44	n	497	0	531	8	0
45	o	710	0	735	16	0
46	p	695	0	721	14	0
47	q	691	0	728	11	0
48	r	518	0	555	13	0
49	s	624	0	636	8	0
50	t	637	0	696	10	0
51	u	444	0	487	8	0
52	X	1151	0	1222	16	0
53	A	559	0	281	20	0
All	All	140774	0	93340	1330	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 (1330) 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)
27:V:310:C:O2	27:V:406:G:N2	1.93	1.01
31:a:890:C:H5”	42:l:9:ARG:NH1	1.74	1.00
31:a:1406:C:O2’	53:A:50:C:N4	1.95	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:28:A:N6	27:V:558:G:O2'	2.00	0.93
31:a:474:A:O2'	31:a:475:A:O5'	1.87	0.92
31:a:1461:U:O2'	31:a:1462:U:OP1	1.88	0.91
31:a:209:A:O2'	31:a:210:A:O4'	1.89	0.90
31:a:413:U:OP1	31:a:414:G:O2'	1.88	0.89
27:V:1216:C:O2	27:V:1220:G:N2	2.05	0.89
27:V:1866:C:O2'	27:V:1956:A:N3	2.06	0.89
31:a:1038:C:O2	31:a:1043:G:N2	2.05	0.88
31:a:1258:C:O2'	39:i:70:GLY:O	1.91	0.86
31:a:207:U:O2'	31:a:208:A:O5'	1.94	0.86
27:V:2287:C:O2'	27:V:2456:C:OP2	1.92	0.86
27:V:125:A:O2'	27:V:126:A:O4'	1.92	0.86
27:V:2610:G:OP2	27:V:2610:G:N2	2.08	0.85
27:V:2144:G:N2	27:V:2148:A:OP1	2.10	0.84
27:V:1808:U:OP2	27:V:1813:A:N6	2.09	0.84
46:p:6:ARG:NH2	46:p:28:PRO:O	2.11	0.84
17:L:21:ARG:NH1	27:V:1290:G:OP2	2.09	0.84
27:V:2135:G:N2	27:V:2212:C:O2	2.10	0.84
31:a:262:G:O3'	47:q:73:LYS:NZ	2.09	0.84
31:a:1414:G:O2'	31:a:1528:A:O2'	1.96	0.84
27:V:2386:U:O2	27:V:2390:A:N6	2.11	0.84
8:C:99:GLY:O	27:V:1546:G:O2'	1.96	0.83
27:V:1359:G:OP2	27:V:1359:G:N2	2.11	0.83
27:V:2294:U:OP2	27:V:2295:A:O2'	1.96	0.83
4:3:8:ARG:NH2	27:V:246:U:OP2	2.12	0.83
13:H:17(A):G:O2'	13:H:18:G:OP1	1.96	0.83
27:V:1968:U:OP1	27:V:2633:U:O2'	1.97	0.83
37:g:68:ASN:O	37:g:138:ARG:NH2	2.12	0.83
31:a:181:G:O2'	31:a:182:U:OP1	1.97	0.83
31:a:1135:U:O2'	31:a:1136:U:O5'	1.96	0.83
2:1:21:LYS:NZ	2:1:26:ASN:O	2.11	0.82
2:1:2:ARG:NH2	27:V:2314:C:OP2	2.11	0.82
31:a:699:G:O6	41:k:55:ARG:NH2	2.12	0.82
31:a:225:A:OP1	31:a:472:C:O2'	1.97	0.82
27:V:1364:C:OP1	27:V:1692:U:O2'	1.97	0.82
27:V:1742:G:OP2	27:V:1743:A:O2'	1.97	0.82
7:B:49:G:O2'	7:B:50:A:O5'	1.98	0.81
27:V:2361:C:OP1	28:W:84:ARG:NH1	2.13	0.81
31:a:986:G:OP2	31:a:1367:U:O2'	1.98	0.81
50:t:61:ALA:HB1	50:t:67:VAL:HG21	1.62	0.81
5:4:8:LYS:NZ	27:V:2496:C:OP1	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:516:C:OP2	31:a:517:U:O2'	1.99	0.81
27:V:1991:C:O2'	27:V:1992:C:O5'	1.98	0.81
43:m:85:SER:O	43:m:88:GLY:N	2.13	0.80
27:V:1243:A:O2'	27:V:1244:A:OP1	1.98	0.80
27:V:1726:G:O2'	27:V:1727:A:OP1	1.98	0.80
52:X:17:GLU:OE2	52:X:19:LYS:HD2	1.80	0.80
31:a:1132:U:O4	31:a:1133:A:N6	2.14	0.80
31:a:1170:C:O2	31:a:1184:G:N2	2.16	0.79
31:a:372:A:O2'	31:a:373:U:O5'	2.01	0.79
34:d:32:ALA:HB3	34:d:33:PRO:HD3	1.63	0.79
24:S:28:GLN:NE2	24:S:69:LEU:O	2.16	0.79
27:V:1509:C:HO2'	27:V:2731:G:HO2'	1.16	0.79
6:6:26:SER:OG	11:F:140:GLU:OE2	1.99	0.79
7:B:37:A:O2'	7:B:38:U:O5'	2.00	0.79
27:V:2890:U:OP2	27:V:2891:G:O2'	2.00	0.78
27:V:905:G:O2'	27:V:906:G:OP1	2.01	0.78
41:k:45:SER:OG	41:k:76:SER:OG	1.99	0.78
31:a:567:G:OP2	31:a:568:A:O2'	2.00	0.78
31:a:1318:G:OP1	43:m:91:HIS:NE2	2.16	0.78
27:V:2372:U:HO2'	27:V:2402:A:HO2'	1.32	0.78
31:a:582:A:O2'	31:a:583:A:O4'	1.99	0.78
27:V:698:C:O2'	27:V:699:A:O4'	2.02	0.78
27:V:2551:U:O2'	27:V:2676:U:OP1	2.02	0.78
31:a:466:G:O6	31:a:484:U:C2	2.36	0.78
31:a:1347:G:O2'	31:a:1348:A:O4'	2.00	0.78
31:a:150:A:OP2	31:a:168:C:N4	2.16	0.78
49:s:36:ARG:NH2	49:s:75:ALA:O	2.17	0.78
25:T:59:TYR:OH	27:V:1379:U:OP2	2.02	0.77
27:V:1139:G:O2'	27:V:1140:U:O4'	2.02	0.77
24:S:41:ARG:NH1	27:V:2038:G:OP1	2.18	0.77
19:N:94:ARG:NH1	27:V:2905:C:O2'	2.17	0.77
31:a:1275:G:N2	31:a:1278:A:OP2	2.16	0.77
31:a:269:U:OP2	50:t:74:ARG:NH2	2.18	0.77
27:V:458:G:OP2	27:V:2435:C:O2'	2.01	0.77
27:V:2135:G:N1	27:V:2212:C:N3	2.33	0.77
27:V:1509:C:O2'	27:V:2731:G:O2'	1.94	0.77
27:V:1695:A:HO2'	27:V:1696:G:P	2.08	0.77
15:J:31:SER:OG	15:J:32:GLU:OE2	2.02	0.77
4:3:7:HIS:NE2	27:V:254:A:OP1	2.18	0.77
11:F:68:THR:OG1	11:F:85:ILE:O	2.02	0.77
31:a:1056:A:N6	31:a:1220:U:O2	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:645:C:O2'	27:V:649:G:OP1	2.02	0.76
27:V:1964:G:O2'	27:V:1966:A:N1	2.17	0.76
31:a:977:C:OP2	31:a:978:A:O2'	2.02	0.76
31:a:1337:C:N4	31:a:1338:G:O6	2.19	0.76
27:V:77:U:O2'	27:V:78:U:O5'	2.04	0.76
31:a:1390:U:O2'	37:g:78:ARG:NH1	2.18	0.76
16:K:97:ARG:NE	31:a:347:C:OP2	2.19	0.76
25:T:34:ALA:HA	25:T:38:GLU:OE1	1.85	0.76
15:J:38:ARG:NH1	27:V:1053:C:OP1	2.18	0.76
27:V:619:A:OP2	27:V:2528:C:O2'	2.03	0.76
27:V:1118:C:O2'	27:V:1143:U:OP1	2.04	0.76
27:V:1033:C:O2'	27:V:1046:A:N3	2.18	0.75
27:V:1116:A:O2'	27:V:1117:G:OP1	2.04	0.75
31:a:1089:G:O2'	31:a:1090:A:O4'	2.01	0.75
10:E:41:ARG:NH2	27:V:1242:U:O2'	2.18	0.75
21:P:114:ARG:NH2	31:a:1451:A:O2'	2.20	0.75
15:J:38:ARG:NH1	27:V:1053:C:H5'	2.02	0.75
27:V:2844:A:O2'	27:V:2846:A:N7	2.17	0.75
31:a:1069:U:O3'	44:n:45:ARG:NH2	2.20	0.75
13:H:38:C:O2'	31:a:799:A:OP1	2.04	0.75
16:K:6:THR:HG22	27:V:1711:G:O2'	1.87	0.75
31:a:890:C:H5"	42:l:9:ARG:HH12	1.50	0.75
27:V:116:G:OP2	27:V:118:A:O2'	2.05	0.74
13:H:16:U:O4'	13:H:59:G:N2	2.20	0.74
45:o:34:ASP:OD1	45:o:35:SER:N	2.20	0.74
31:a:1024:A:O2'	31:a:1025:G:O4'	2.00	0.74
39:i:27:ARG:NH1	39:i:28:ILE:O	2.21	0.74
31:a:954:G:N2	31:a:1348:A:OP2	2.21	0.74
31:a:1269:G:OP1	31:a:1293:C:O2'	2.05	0.74
27:V:745:C:O2'	27:V:781:A:N6	2.21	0.73
31:a:1508:U:OP2	53:A:43:G:O2'	2.05	0.73
4:3:13:ARG:NH1	17:L:61:LEU:O	2.22	0.73
31:a:805:C:O3'	41:k:129:ARG:NH1	2.21	0.73
31:a:458:G:OP2	31:a:459:A:O2'	2.06	0.73
27:V:790:A:O2'	27:V:1704:U:OP1	2.07	0.73
11:F:75:ALA:N	13:H:56:C:O2'	2.21	0.73
31:a:343:C:O2'	31:a:1442:A:N3	2.21	0.73
27:V:160:G:O2'	27:V:168:A:N6	2.20	0.73
27:V:1087:U:O2	27:V:1160:G:O6	2.07	0.73
27:V:425:C:N4	27:V:426:G:O6	2.22	0.73
27:V:1090:U:O2'	27:V:1157:A:N1	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:1695:A:O2'	27:V:1696:G:O5'	2.07	0.72
31:a:890:C:H5"	42:l:9:ARG:HH11	1.53	0.72
27:V:1542:A:O2'	27:V:1544:C:N4	2.21	0.72
9:D:130:ARG:NH1	9:D:133:MET:SD	2.62	0.72
27:V:161:A:N3	27:V:2237:C:O2'	2.20	0.72
27:V:1843:G:OP2	27:V:1844:A:O2'	2.06	0.72
16:K:88:ARG:O	16:K:88:ARG:HG3	1.88	0.72
9:D:153:ARG:NH1	27:V:2054:C:OP1	2.22	0.72
31:a:1077:A:N1	31:a:1118:G:O2'	2.20	0.72
40:j:55:VAL:O	44:n:41:ARG:NH1	2.23	0.72
44:n:31:HIS:O	44:n:32:SER:OG	2.05	0.72
3:2:34:ARG:NH2	27:V:513:A:OP1	2.23	0.72
31:a:436:G:O2'	34:d:29:ARG:NH1	2.22	0.71
13:H:22:G:N7	13:H:46:G:N2	2.33	0.71
26:U:80:ARG:NH1	27:V:343:A:OP2	2.22	0.71
34:d:147:ASN:O	34:d:152:LYS:NZ	2.19	0.71
27:V:1765:G:N2	27:V:1768:A:OP2	2.23	0.71
27:V:2841:C:O2	27:V:2908:A:O2'	2.06	0.71
4:3:13:ARG:NH2	27:V:253:G:OP1	2.22	0.71
27:V:1525:G:O2'	27:V:1526:G:OP1	2.07	0.71
31:a:591:C:OP2	31:a:767:G:N1	2.23	0.71
24:S:8:ARG:O	24:S:9:THR:OG1	2.06	0.71
27:V:2143:A:N3	27:V:2196:U:O2'	2.19	0.71
31:a:775:A:OP2	31:a:821:G:N2	2.23	0.71
17:L:55:MET:O	17:L:60:ARG:NH2	2.24	0.71
8:C:260:ARG:NH1	27:V:1828:G:OP1	2.22	0.70
12:G:3:ARG:NH1	27:V:2778:A:OP1	2.24	0.70
23:R:68:ALA:O	23:R:89:ARG:NE	2.23	0.70
27:V:1171:G:OP2	27:V:1172:A:O2'	2.08	0.70
27:V:2159:U:O2'	27:V:2187:A:N1	2.22	0.70
12:G:96:ARG:NH1	12:G:98:SER:OG	2.25	0.70
27:V:560:A:N3	27:V:625:C:O2'	2.21	0.70
31:a:1324:U:O2'	31:a:1369:A:N3	2.24	0.70
31:a:22:U:O2'	31:a:582:A:N6	2.24	0.70
46:p:8:LYS:NZ	46:p:30:ASP:OD1	2.23	0.70
27:V:2135:G:N2	27:V:2212:C:C2	2.59	0.70
27:V:1783:C:N4	27:V:2746:G:O4'	2.25	0.70
7:B:47:C:N4	7:B:48:G:O6	2.25	0.70
9:D:145:SER:OG	27:V:2541:C:O2	2.09	0.70
6:6:14:VAL:N	6:6:22:PHE:O	2.25	0.70
31:a:409:C:O2'	31:a:630:A:N3	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:598:U:O2'	38:h:57:GLN:OE1	2.09	0.70
31:a:1036:C:N4	31:a:1046:G:O6	2.25	0.69
31:a:1087:G:N2	31:a:1090:A:OP2	2.25	0.69
23:R:67:ARG:NH2	23:R:89:ARG:O	2.25	0.69
31:a:754:U:OP1	31:a:861:U:O2'	2.09	0.69
31:a:184:G:O6	31:a:206:A:N6	2.25	0.69
50:t:48:LYS:O	50:t:52:THR:HG23	1.92	0.69
27:V:1715:C:O2	27:V:2022:U:O2'	2.09	0.69
4:3:57:ARG:NH2	17:L:51:GLU:OE1	2.25	0.69
27:V:482:C:O2'	27:V:483:C:O5'	2.09	0.69
47:q:22:THR:HG21	47:q:73:LYS:NZ	2.08	0.69
31:a:136:U:OP1	46:p:65:LYS:NZ	2.22	0.69
27:V:229:A:O2'	27:V:231:A:N1	2.26	0.69
28:W:41:GLY:N	28:W:72:ASP:OD1	2.26	0.69
31:a:1005:C:N3	31:a:1056:A:O2'	2.25	0.69
27:V:2105:U:OP2	27:V:2267:G:N2	2.25	0.69
27:V:162:A:OP2	27:V:163:U:O2'	2.10	0.68
31:a:159:A:N6	31:a:354:G:O6	2.25	0.68
31:a:466:G:O6	31:a:484:U:O2	2.11	0.68
27:V:1263:G:N2	27:V:1266:A:OP2	2.24	0.68
27:V:1453:A:N1	27:V:1635:G:C6	2.61	0.68
27:V:2127:U:O2'	27:V:2128:U:OP1	2.09	0.68
31:a:1016:A:O2'	31:a:1017:A:OP1	2.10	0.68
31:a:1160:A:H5"	40:j:44:THR:HG23	1.76	0.68
33:c:119:ILE:HG12	33:c:136:GLN:HG3	1.73	0.68
9:D:73:GLU:O	9:D:74:THR:HG23	1.94	0.68
27:V:528:G:O2'	27:V:553:A:N6	2.26	0.68
27:V:689:A:O2'	27:V:690:A:OP1	2.12	0.68
33:c:146:GLN:NE2	33:c:203:ARG:O	2.26	0.68
31:a:283:G:O5'	47:q:18:LYS:NZ	2.26	0.68
31:a:886:A:H1'	38:h:12:THR:HG21	1.76	0.68
7:B:53:U:O2'	7:B:54:U:O4'	2.11	0.68
27:V:2772:U:OP2	27:V:2784:C:N4	2.27	0.68
31:a:1066:U:OP1	33:c:162:ALA:N	2.27	0.68
38:h:14:ILE:O	38:h:18:ASN:ND2	2.26	0.68
31:a:475:A:O2'	31:a:476:U:O5'	2.11	0.68
31:a:1249:U:OP1	37:g:119:ARG:NH1	2.27	0.68
27:V:2818:C:O2'	27:V:2917:G:N2	2.27	0.67
11:F:121:SER:O	27:V:2332:G:O2'	2.12	0.67
13:H:55:U:O2'	13:H:56:C:OP1	2.11	0.67
35:e:36:LEU:HD21	35:e:134:ILE:HG12	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:28:SER:HG	27:V:2592:U:HO2'	1.40	0.67
27:V:1122:C:O2'	27:V:1123:A:N7	2.27	0.67
27:V:2404:G:N2	27:V:2407:A:OP2	2.27	0.67
31:a:1073:C:OP2	31:a:1074:G:O2'	2.10	0.67
31:a:1330:U:H4'	31:a:1331:C:OP2	1.95	0.67
27:V:2149:G:O2'	27:V:2150:G:O4'	2.09	0.67
15:J:78:HIS:ND1	15:J:79:THR:O	2.27	0.67
19:N:49:THR:HG21	27:V:2865:U:H5"	1.77	0.66
27:V:1845:A:O2'	27:V:1846:G:OP1	2.12	0.66
27:V:1972:U:O2'	27:V:1973:U:OP2	2.13	0.66
16:K:22:ILE:HG22	16:K:23:LYS:H	1.59	0.66
7:B:12:U:OP2	7:B:68:C:O2'	2.13	0.66
24:S:78:GLU:OE1	27:V:24:G:N2	2.28	0.66
31:a:455:G:O2'	31:a:456:A:O5'	2.11	0.66
31:a:968:A:O2'	31:a:995:C:O2'	2.00	0.66
7:B:16:G:O6	7:B:17:A:N6	2.29	0.66
31:a:1059:U:OP1	44:n:2:ALA:N	2.29	0.66
34:d:191:GLU:OE1	34:d:191:GLU:N	2.29	0.66
40:j:98:ILE:H	40:j:98:ILE:HD12	1.60	0.66
27:V:722:A:N3	27:V:2472:C:O2'	2.29	0.66
15:J:63:ILE:O	15:J:94:ARG:NH1	2.28	0.66
27:V:2200:A:O2'	27:V:2201:U:OP2	2.14	0.66
31:a:129:A:O2'	31:a:130:C:O5'	2.14	0.66
13:H:18:G:O2'	13:H:57:G:N2	2.29	0.65
31:a:1456:A:OP1	31:a:1457:C:N4	2.23	0.65
36:f:11:ARG:NH2	36:f:13:ASN:O	2.29	0.65
18:M:77:LYS:HE3	27:V:1002:G:H5"	1.78	0.65
24:S:15:ARG:NH2	27:V:1306:G:OP1	2.30	0.65
27:V:2009:G:O2'	27:V:2010:A:OP1	2.12	0.65
38:h:54:ASP:OD1	38:h:58:GLY:N	2.28	0.65
26:U:86:GLU:N	26:U:86:GLU:OE1	2.29	0.65
31:a:855:G:O2'	31:a:856:C:OP1	2.14	0.65
31:a:1264:G:O2'	31:a:1267:G:N3	2.27	0.65
1:0:11:MET:SD	27:V:16:G:O2'	2.54	0.65
31:a:1170:C:N3	31:a:1184:G:N1	2.45	0.65
48:r:42:GLY:O	48:r:68:ARG:NH2	2.29	0.65
42:l:59:ASN:OD1	42:l:60:SER:N	2.30	0.65
23:R:57:THR:O	23:R:101:ASN:ND2	2.29	0.65
25:T:35:ASN:OD1	25:T:36:LYS:N	2.30	0.65
8:C:13:ARG:NH1	8:C:16:MET:SD	2.71	0.64
27:V:2072:C:OP1	27:V:2806:G:O2'	2.15	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:2825:C:N3	27:V:2826:A:N6	2.45	0.64
31:a:518:A:O2'	31:a:519:A:O4'	2.08	0.64
27:V:2244:G:HO2'	27:V:2245:G:P	2.19	0.64
47:q:13:ARG:NH1	47:q:14:VAL:O	2.30	0.64
27:V:226:A:O2'	27:V:467:C:O2	2.15	0.64
27:V:76:C:O2'	27:V:77:U:OP2	2.14	0.64
27:V:2651:C:O2'	27:V:2850:G:N7	2.30	0.64
23:R:89:ARG:NH2	27:V:1263:G:OP2	2.31	0.64
27:V:688:G:O2'	27:V:2378:G:O2'	2.16	0.64
45:o:5:GLN:O	45:o:9:ASN:OD1	2.14	0.64
27:V:482:C:O2'	27:V:483:C:O4'	2.16	0.64
27:V:2584:U:O2'	27:V:2585:C:O4'	2.15	0.64
27:V:344:G:O2'	27:V:346:G:OP2	2.12	0.63
35:e:132:THR:OG1	35:e:135:ASN:OD1	2.12	0.63
30:Z:6:ILE:HG23	30:Z:54:VAL:HG13	1.79	0.63
52:X:67:SER:O	52:X:71:THR:HG23	1.98	0.63
7:B:30:C:N4	7:B:31:G:O6	2.31	0.63
27:V:1304:G:OP2	27:V:1305:A:O2'	2.14	0.63
27:V:2244:G:O2'	27:V:2245:G:O5'	2.15	0.63
31:a:302:C:OP1	31:a:619:G:O2'	2.08	0.63
16:K:107:ARG:NH2	21:P:34:GLU:OE1	2.31	0.63
27:V:1314:A:N1	27:V:1334:C:O2'	2.30	0.63
31:a:1463:A:O2'	31:a:1464:G:O5'	2.12	0.63
27:V:1310:C:O2'	27:V:1693:C:OP2	2.14	0.63
8:C:69:ARG:O	8:C:189:ARG:NH1	2.32	0.63
16:K:31:LYS:NZ	27:V:2025:C:OP1	2.25	0.63
48:r:37:PHE:HD1	48:r:60:LEU:HD21	1.63	0.63
30:Z:12:VAL:HG22	30:Z:20:ARG:HD2	1.80	0.63
31:a:1313:G:H21	31:a:1342:A:H62	1.45	0.63
31:a:1508:U:O2'	53:A:44:A:OP1	2.14	0.63
48:r:41:ARG:O	48:r:77:SER:OG	2.11	0.63
20:O:14:ARG:NH1	27:V:2324:C:OP1	2.32	0.62
27:V:177:G:O2'	27:V:178:A:O5'	2.16	0.62
27:V:2847:G:O2'	27:V:2849:U:OP2	2.17	0.62
9:D:124:LYS:NZ	27:V:2028:C:OP1	2.31	0.62
12:G:3:ARG:NH1	27:V:2780:G:OP2	2.32	0.62
27:V:342:A:O2'	27:V:343:A:O4'	2.15	0.62
31:a:1106:C:O2	31:a:1179:A:O2'	2.17	0.62
1:0:6:ARG:NH1	27:V:2048:U:OP2	2.32	0.62
27:V:675:C:O2	27:V:685:U:O2'	2.17	0.62
31:a:1259:A:OP1	39:i:68:HIS:ND1	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:4:33:LYS:NZ	27:V:2772:U:OP1	2.33	0.62
20:O:30:ARG:NH1	20:O:96:ASP:OD2	2.32	0.62
31:a:587:C:O2'	31:a:737:A:N3	2.31	0.62
31:a:304:U:O2'	31:a:565:C:O2	2.17	0.62
31:a:1088:U:O2'	31:a:1089:G:OP1	2.17	0.62
31:a:530:G:O2'	31:a:545:C:O2'	2.18	0.62
31:a:774:G:H1	31:a:821:G:HO2'	1.48	0.62
42:l:5:ASN:O	42:l:9:ARG:HG2	1.98	0.62
22:Q:92:ARG:O	22:Q:95:LEU:N	2.33	0.61
27:V:2148:A:N6	27:V:2199:G:N7	2.48	0.61
27:V:1103:A:N6	27:V:1133:G:OP2	2.33	0.61
31:a:1065:A:O2'	33:c:159:ALA:O	2.17	0.61
41:k:31:ASN:OD1	41:k:32:THR:N	2.34	0.61
52:X:72:LEU:O	52:X:75:LEU:HD22	2.00	0.61
27:V:1474:C:N4	27:V:1618:A:OP2	2.26	0.61
12:G:20:ASN:OD1	12:G:24:THR:OG1	2.19	0.61
3:2:14:LYS:NZ	27:V:818:G:OP1	2.30	0.61
38:h:8:ALA:O	38:h:12:THR:HG23	2.01	0.61
27:V:1971:C:OP2	27:V:1972:U:O2'	2.09	0.61
27:V:2057:U:H2'	27:V:2058:G:C8	2.35	0.61
7:B:48:G:O2'	7:B:49:G:O5'	2.18	0.61
10:E:57:VAL:HG11	10:E:79:ARG:HB3	1.82	0.61
20:O:14:ARG:NH2	27:V:2323:C:O3'	2.34	0.61
27:V:1216:C:N3	27:V:1220:G:N1	2.44	0.61
27:V:2169:G:N2	27:V:2181:C:O2	2.33	0.61
27:V:1380:U:OP2	27:V:1433:U:O2'	2.16	0.61
31:a:1455:A:O2'	31:a:1456:A:O4'	2.16	0.61
40:j:44:THR:HG22	40:j:70:HIS:HA	1.82	0.60
7:B:46:A:OP1	20:O:35:ARG:NH1	2.34	0.60
17:L:30:THR:OG1	27:V:1231:G:OP1	2.19	0.60
19:N:19:ASP:OD1	19:N:67:ARG:NH1	2.34	0.60
29:Y:6:ILE:O	29:Y:60:ARG:NH2	2.34	0.60
6:6:34:GLU:OE1	43:m:57:ARG:NE	2.33	0.60
31:a:541:A:N6	31:a:1215:G:O2'	2.35	0.60
31:a:1187:G:N2	31:a:1190:G:OP2	2.34	0.60
2:1:25:ASN:ND2	27:V:2314:C:OP1	2.34	0.60
27:V:2365:A:H61	28:W:51:THR:HG21	1.67	0.60
31:a:224:U:O2'	31:a:477:A:N6	2.35	0.60
5:4:20:LYS:NZ	27:V:2770:A:OP1	2.35	0.60
27:V:1074:A:N3	27:V:2515:G:O2'	2.31	0.60
16:K:3:GLN:NE2	27:V:2024:U:O2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:2162:G:O2'	27:V:2187:A:N1	2.32	0.60
31:a:1413:C:O2	31:a:1529:A:O2'	2.19	0.60
51:u:60:GLU:N	51:u:60:GLU:OE1	2.34	0.60
7:B:49:G:HO2'	7:B:50:A:C5'	2.11	0.60
27:V:747:G:O2'	27:V:1677:A:N3	2.28	0.60
27:V:500:A:N3	27:V:504:A:O2'	2.35	0.59
31:a:855:G:OP2	48:r:19:THR:OG1	2.08	0.59
15:J:24:LYS:N	15:J:64:GLU:OE2	2.35	0.59
31:a:332:G:N1	31:a:335:A:OP2	2.34	0.59
31:a:977:C:P	31:a:978:A:HO2'	2.24	0.59
27:V:559:A:O2'	27:V:1257:C:OP1	2.20	0.59
27:V:689:A:N6	27:V:2398:A:O2'	2.26	0.59
46:p:2:ALA:N	46:p:24:ASP:OD1	2.35	0.59
51:u:39:LEU:H	51:u:39:LEU:HD23	1.67	0.59
12:G:108:VAL:HG13	12:G:109:GLY:H	1.68	0.59
17:L:41:ARG:NH2	27:V:854:U:OP2	2.36	0.59
27:V:2685:U:O2	27:V:2694:A:N7	2.35	0.59
21:P:49:LYS:NZ	27:V:2714:G:OP1	2.35	0.59
21:P:92:VAL:HG21	21:P:97:LEU:HD21	1.85	0.59
31:a:387:C:N4	31:a:388:G:O6	2.35	0.59
17:L:18:ARG:NH2	27:V:1290:G:N7	2.50	0.59
27:V:441:C:O2'	27:V:442:C:OP1	2.17	0.59
27:V:2717:G:N1	27:V:2749:U:OP2	2.31	0.59
31:a:181:G:HO2'	31:a:182:U:P	2.22	0.59
31:a:1330:U:OP2	31:a:1331:C:H2'	2.03	0.59
42:l:69:ARG:NH1	42:l:75:GLU:OE1	2.36	0.59
27:V:2806:G:OP1	27:V:2810:A:O2'	2.16	0.58
31:a:1248:A:O2'	37:g:114:LYS:O	2.21	0.58
34:d:19:LEU:N	34:d:25:GLU:OE2	2.35	0.58
27:V:1473:A:N6	27:V:1619:A:OP2	2.32	0.58
38:h:93:GLU:N	38:h:93:GLU:OE1	2.36	0.58
31:a:641:G:O2'	31:a:642:U:O5'	2.18	0.58
39:i:70:GLY:O	39:i:75:GLN:OE1	2.21	0.58
26:U:51:ASN:O	26:U:53:GLN:N	2.35	0.58
27:V:88:G:O2'	27:V:89:U:OP1	2.21	0.58
27:V:1109:G:O2'	27:V:1110:C:O5'	2.20	0.58
4:3:32:LEU:HD12	27:V:2421:A:OP1	2.04	0.58
7:B:34:C:N4	7:B:47:C:O2	2.35	0.58
27:V:2535:U:OP2	27:V:2605:G:N1	2.35	0.58
8:C:150:LYS:NZ	27:V:1830:G:OP2	2.36	0.58
19:N:49:THR:HG21	27:V:2865:U:C5'	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:135:GLN:O	11:F:141:ILE:HG21	2.03	0.58
27:V:2605:G:O2'	27:V:2608:C:OP2	2.14	0.58
11:F:161:ASN:N	11:F:165:GLU:OE2	2.37	0.58
27:V:1469:G:HO2'	27:V:1545:C:HO2'	1.46	0.58
31:a:1186:G:OP1	39:i:99:LYS:NZ	2.35	0.58
21:P:51:ARG:NH1	27:V:2713:U:OP2	2.36	0.58
31:a:789:G:N1	31:a:810:U:OP2	2.37	0.57
36:f:51:GLU:OE1	36:f:51:GLU:N	2.36	0.57
27:V:248:G:O2'	27:V:431:A:N1	2.37	0.57
27:V:1867:C:N4	27:V:1928:A:O4'	2.38	0.57
27:V:2517:A:N6	27:V:2518:G:O6	2.36	0.57
31:a:492:C:OP2	31:a:493:G:O2'	2.11	0.57
23:R:31:GLU:N	23:R:31:GLU:OE1	2.38	0.57
45:o:74:ASP:OD2	45:o:74:ASP:N	2.38	0.57
51:u:33:LEU:HD12	51:u:33:LEU:O	2.03	0.57
31:a:993:A:H2	31:a:1231:G:H22	1.53	0.57
33:c:11:ARG:NH2	33:c:176:THR:O	2.37	0.57
10:E:127:GLU:N	10:E:127:GLU:OE1	2.37	0.57
27:V:573:C:N4	27:V:2808:U:OP2	2.37	0.57
27:V:275:A:H62	27:V:296:G:N2	2.03	0.57
27:V:1265:A:C6	27:V:1266:A:N1	2.73	0.57
23:R:84:LYS:NZ	27:V:862:U:OP1	2.37	0.57
31:a:596:G:O2'	31:a:597:G:OP2	2.19	0.57
7:B:41:C:O2'	7:B:43:A:N7	2.35	0.57
35:e:164:LEU:O	38:h:116:LYS:NZ	2.21	0.57
27:V:1158:G:O2'	27:V:1159:U:O5'	2.22	0.56
31:a:37:G:O2'	42:l:128:SER:O	2.17	0.56
31:a:1088:U:HO2'	31:a:1089:G:P	2.27	0.56
13:H:7:G:O2'	13:H:49:G:O4'	2.22	0.56
27:V:971:A:O2'	27:V:972:U:O4'	2.22	0.56
23:R:81:ASN:ND2	27:V:610:U:OP1	2.37	0.56
27:V:648:G:O2'	27:V:649:G:OP2	2.20	0.56
27:V:1065:U:OP1	27:V:1081:U:O2'	2.22	0.56
27:V:1159:U:O2'	27:V:1160:G:OP2	2.20	0.56
29:Y:13:GLU:N	29:Y:13:GLU:OE1	2.37	0.56
31:a:473:G:N2	31:a:476:U:OP2	2.38	0.56
31:a:569:A:C6	35:e:128:LEU:HD13	2.40	0.56
31:a:790:A:OP2	31:a:809:G:N1	2.36	0.56
48:r:14:LYS:NZ	48:r:48:ARG:O	2.35	0.56
38:h:53:GLU:N	38:h:53:GLU:OE1	2.39	0.56
8:C:182:ARG:NH1	27:V:1829:C:OP1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:563:U:O2'	31:a:564:C:OP1	2.23	0.56
31:a:1503:A:N6	53:A:47:G:O6	2.38	0.56
34:d:14:ARG:HA	34:d:32:ALA:HB1	1.87	0.56
5:4:19:ARG:NE	27:V:2785:U:OP2	2.36	0.56
8:C:108:LYS:N	8:C:194:GLN:O	2.36	0.56
27:V:840:A:OP2	27:V:2100:A:O2'	2.23	0.56
31:a:422:A:H62	31:a:439:A:H1'	1.71	0.56
31:a:1526:G:N2	31:a:1529:A:OP2	2.27	0.56
27:V:1425:C:O2'	27:V:1426:A:OP2	2.21	0.56
27:V:2534:G:O2'	27:V:2535:U:O5'	2.23	0.56
32:b:2:SER:HG	32:b:22:SER:CB	2.17	0.56
11:F:73:SER:OG	13:H:56:C:O4'	2.21	0.56
16:K:8:LEU:HD13	16:K:84:CYS:SG	2.46	0.56
7:B:31:G:O2'	7:B:32:U:OP1	2.23	0.56
7:B:49:G:HO2'	7:B:50:A:P	2.29	0.56
15:J:40:LYS:NZ	27:V:1055:A:OP2	2.28	0.56
27:V:85:G:O2'	27:V:86:C:OP2	2.20	0.56
27:V:529:C:O2'	27:V:543:A:N1	2.37	0.56
27:V:1898:G:N2	27:V:1901:A:OP2	2.31	0.56
31:a:261:U:O4'	31:a:283:G:N2	2.30	0.55
4:3:8:ARG:NH1	27:V:247:A:OP2	2.39	0.55
31:a:330:C:N3	31:a:340:G:N2	2.52	0.55
35:e:36:LEU:HD21	35:e:134:ILE:CG1	2.35	0.55
25:T:31:ASP:OD1	25:T:32:VAL:N	2.40	0.55
27:V:252:C:OP2	27:V:2423:C:O2'	2.20	0.55
27:V:976:U:O2'	30:Z:25:THR:O	2.20	0.55
31:a:1168:U:O4'	31:a:1191:G:N2	2.39	0.55
4:3:57:ARG:NH1	27:V:880:C:O2'	2.38	0.55
27:V:1116:A:HO2'	27:V:1117:G:P	2.28	0.55
27:V:1244:A:O2'	27:V:1245:G:OP1	2.23	0.55
27:V:290:U:O2'	27:V:291:C:O5'	2.22	0.55
31:a:329:A:O2'	31:a:330:C:O4'	2.16	0.55
8:C:44:ASN:ND2	27:V:1835:C:O2	2.40	0.55
36:f:52:ILE:HG22	36:f:53:ASN:H	1.71	0.55
49:s:58:VAL:HG13	49:s:58:VAL:O	2.07	0.55
27:V:421:A:C8	27:V:422:C:C6	2.95	0.55
27:V:1828:G:N2	27:V:1848:A:OP2	2.36	0.55
31:a:701:U:OP2	41:k:30:ASN:ND2	2.39	0.55
18:M:42:ILE:HD12	18:M:97:VAL:HG21	1.89	0.55
27:V:1713:A:O2'	27:V:1719:G:N7	2.31	0.55
27:V:2320:U:O2'	27:V:2403:C:O2	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:2593:A:O2'	27:V:2594:A:O4'	2.21	0.55
48:r:26:ILE:HD11	48:r:60:LEU:HD12	1.89	0.55
7:B:48:G:O2'	7:B:49:G:P	2.65	0.55
27:V:18:C:O2'	27:V:598:U:OP1	2.25	0.55
27:V:2119:A:N6	27:V:2259:G:O6	2.40	0.55
24:S:77:ASP:OD2	24:S:78:GLU:N	2.40	0.54
31:a:986:G:N2	31:a:1372:A:OP2	2.40	0.54
12:G:108:VAL:HG13	12:G:109:GLY:N	2.22	0.54
27:V:217:G:O2'	27:V:218:G:O5'	2.24	0.54
27:V:1068:G:N2	27:V:1069:U:O4	2.30	0.54
31:a:445:U:O4	31:a:504:A:N7	2.40	0.54
31:a:848:G:O2'	31:a:849:G:P	2.65	0.54
31:a:1018:U:O2'	31:a:1019:C:P	2.65	0.54
39:i:93:GLU:OE1	39:i:93:GLU:N	2.38	0.54
4:3:18:GLY:O	4:3:19:SER:OG	2.20	0.54
27:V:309:U:H3'	27:V:310:C:H5"	1.88	0.54
27:V:2163:A:N3	27:V:2188:G:O2'	2.39	0.54
20:O:90:ILE:O	20:O:91:SER:OG	2.17	0.54
27:V:524:A:N6	27:V:547:A:OP1	2.41	0.54
27:V:1126:A:O2'	27:V:1127:U:OP2	2.23	0.54
31:a:351:U:O2'	31:a:354:G:O6	2.22	0.54
31:a:1298:A:N1	31:a:1380:G:O2'	2.37	0.54
31:a:1356:G:N7	39:i:107:ASP:CG	2.64	0.54
27:V:688:G:N2	27:V:691:U:OP2	2.28	0.54
27:V:859:C:O2'	27:V:1266:A:O2'	2.24	0.54
27:V:2330:A:O2'	27:V:2331:U:OP1	2.24	0.54
20:O:19:ARG:NH1	20:O:47:ASP:OD2	2.41	0.54
31:a:70:G:H22	31:a:99:A:H62	1.54	0.54
31:a:665:G:O2'	45:o:28:GLN:NE2	2.41	0.54
53:A:31:A:C6	53:A:32:U:C4	2.94	0.54
8:C:243:ARG:NH1	27:V:2268:G:OP1	2.41	0.54
27:V:689:A:HO2'	27:V:690:A:P	2.29	0.54
27:V:1139:G:O2'	27:V:1140:U:O5'	2.25	0.54
32:b:2:SER:OG	32:b:22:SER:OG	2.03	0.54
9:D:9:LYS:HB2	9:D:200:ILE:HD13	1.90	0.54
27:V:1525:G:O2'	27:V:1526:G:P	2.66	0.54
27:V:1530:G:O2'	27:V:1531:G:OP1	2.24	0.54
27:V:2182:G:H2'	27:V:2183:G:O4'	2.08	0.54
34:d:13:ARG:NE	34:d:32:ALA:O	2.41	0.54
35:e:94:ILE:HD11	35:e:136:MET:SD	2.48	0.54
8:C:168:GLU:N	8:C:168:GLU:OE1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:38:ARG:HH12	27:V:1053:C:H5'	1.72	0.53
27:V:1158:G:HO2'	27:V:1159:U:C5'	2.20	0.53
27:V:2135:G:C2	27:V:2212:C:O2	2.61	0.53
31:a:1499:G:O2'	31:a:1500:U:P	2.66	0.53
35:e:95:LEU:HD23	35:e:128:LEU:HD11	1.90	0.53
8:C:243:ARG:NH2	27:V:2104:U:OP1	2.39	0.53
27:V:285:U:H1'	52:X:46:ALA:HB2	1.90	0.53
45:o:71:ARG:NH2	45:o:78:TYR:OH	2.39	0.53
7:B:31:G:O2'	7:B:32:U:P	2.66	0.53
27:V:446:G:OP2	51:u:55:LYS:NZ	2.38	0.53
27:V:1269:A:O2'	27:V:1270:C:OP1	2.26	0.53
27:V:2022:U:C2'	27:V:2023:C:OP1	2.57	0.53
36:f:42:ASP:OD1	36:f:61:GLN:OE1	2.25	0.53
17:L:16:ARG:NH2	27:V:633:U:OP2	2.39	0.53
20:O:38:LYS:O	20:O:68:THR:HG22	2.09	0.53
27:V:775:G:H3'	27:V:776:G:H5'	1.89	0.53
52:X:35:LEU:HD23	52:X:35:LEU:O	2.08	0.53
27:V:27:G:N2	27:V:559:A:OP2	2.23	0.53
27:V:1339:A:H4'	27:V:1340:A:H5'	1.88	0.53
27:V:2043:A:O2'	27:V:2044:A:O4'	2.21	0.53
11:F:67:VAL:O	11:F:67:VAL:HG13	2.08	0.53
14:I:87:UNK:HA	14:I:88:UNK:C	2.38	0.53
27:V:1605:C:OP2	27:V:1606:A:O2'	2.16	0.53
31:a:1330:U:O4	49:s:36:ARG:NH2	2.34	0.53
31:a:1462:U:O2'	31:a:1463:A:OP1	2.26	0.53
33:c:47:SER:O	33:c:121:ARG:NH2	2.42	0.53
4:3:46:LYS:NZ	27:V:2379:C:OP1	2.37	0.53
27:V:510:G:N2	27:V:513:A:OP2	2.39	0.53
31:a:563:U:O2'	31:a:564:C:P	2.67	0.53
31:a:757:A:HO2'	31:a:758:A:P	2.31	0.53
15:J:32:GLU:OE2	15:J:32:GLU:N	2.42	0.53
27:V:2135:G:C2	27:V:2212:C:C2	2.97	0.53
27:V:2166:C:H2'	27:V:2167:C:C1'	2.39	0.53
27:V:2308:G:N7	28:W:22:ARG:NH2	2.56	0.53
31:a:1025:G:O2'	31:a:1026:A:O4'	2.24	0.53
27:V:25:U:C2'	27:V:26:G:O5'	2.57	0.53
27:V:84:A:N1	27:V:98:U:O2'	2.42	0.53
27:V:1542:A:O2'	27:V:1543:U:OP2	2.25	0.53
31:a:1032:C:O2'	31:a:1033:G:OP1	2.24	0.52
27:V:1820:A:N6	27:V:1857:G:O2'	2.40	0.52
31:a:113:G:H4'	31:a:114:A:O5'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:699:G:OP2	41:k:31:ASN:ND2	2.40	0.52
31:a:1246:C:O2'	31:a:1309:G:N2	2.38	0.52
46:p:24:ASP:OD1	46:p:25:SER:N	2.43	0.52
31:a:855:G:HO2'	31:a:856:C:P	2.32	0.52
31:a:1330:U:H2'	31:a:1331:C:C5	2.45	0.52
27:V:874:U:O2'	27:V:2097:U:N3	2.42	0.52
47:q:22:THR:HG22	47:q:49:HIS:HA	1.91	0.52
48:r:27:ASP:O	48:r:29:LYS:N	2.43	0.52
27:V:2228:A:C8	27:V:2229:C:C5	2.97	0.52
31:a:1269:G:O2'	31:a:1284:A:N6	2.43	0.52
31:a:1315:A:N6	31:a:1340:G:O2'	2.42	0.52
7:B:31:G:HO2'	7:B:32:U:P	2.33	0.52
15:J:38:ARG:NH1	27:V:1053:C:C5'	2.73	0.52
27:V:136:C:N4	27:V:137:G:O6	2.43	0.52
27:V:187:C:N3	27:V:216:A:N6	2.58	0.52
27:V:421:A:C2	27:V:448:A:C4	2.97	0.52
27:V:1530:G:O2'	27:V:1531:G:P	2.68	0.52
16:K:22:ILE:HD11	16:K:42:THR:HG23	1.91	0.52
27:V:905:G:O2'	27:V:2297:A:O2'	2.27	0.52
27:V:2079:C:H2'	27:V:2080:A:O4'	2.09	0.52
27:V:2254:A:H1'	27:V:2255:C:OP2	2.10	0.52
31:a:1499:G:O2'	31:a:1500:U:OP1	2.27	0.52
7:B:6:U:OP1	20:O:11:ARG:NH1	2.42	0.52
7:B:49:G:H4'	7:B:50:A:OP1	2.10	0.52
17:L:131:SER:OG	27:V:683:A:OP1	2.21	0.52
19:N:22:THR:HG22	19:N:66:ILE:HG23	1.91	0.52
26:U:72:ASP:OD2	26:U:97:SER:OG	2.24	0.52
27:V:200:A:N6	27:V:2459:A:O2'	2.40	0.52
27:V:746:A:N3	27:V:1678:G:O2'	2.38	0.52
28:W:80:PHE:N	28:W:84:ARG:O	2.36	0.52
31:a:1406:C:OP2	35:e:29:ARG:NH2	2.43	0.52
47:q:22:THR:HG21	47:q:73:LYS:CE	2.39	0.52
10:E:53:ASN:ND2	27:V:848:G:O6	2.41	0.52
27:V:557:U:O2'	27:V:1255:G:N2	2.43	0.52
27:V:1882:A:O2'	27:V:1883:A:P	2.68	0.52
31:a:855:G:O2'	31:a:856:C:P	2.68	0.52
31:a:1013:G:N2	31:a:1014:A:O2'	2.42	0.52
33:c:23:TYR:O	33:c:58:ARG:NH2	2.44	0.52
31:a:487:C:O2'	31:a:488:U:OP1	2.25	0.51
37:g:74:GLU:O	37:g:89:VAL:N	2.43	0.51
23:R:27:ALA:O	23:R:65:GLN:NE2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:2092:C:N4	27:V:2530:C:O2	2.42	0.51
33:c:148:VAL:HG12	33:c:201:ILE:HG23	1.91	0.51
27:V:1565:U:HO2'	27:V:1566:G:P	2.33	0.51
27:V:2021:G:N2	27:V:2025:C:O2'	2.44	0.51
27:V:2754:A:O2'	27:V:2755:U:OP2	2.23	0.51
41:k:38:ASP:OD1	41:k:42:ASN:N	2.43	0.51
27:V:966:U:C2	27:V:967:G:C8	2.99	0.51
27:V:2278:U:N3	27:V:2282:G:OP2	2.42	0.51
27:V:2606:A:O4'	27:V:2641:C:N4	2.43	0.51
31:a:739:G:O2'	31:a:775:A:O4'	2.26	0.51
31:a:939:G:O6	31:a:1398:C:N4	2.43	0.51
27:V:1177:G:O2'	27:V:2054:C:O2'	2.27	0.51
31:a:37:G:H21	42:l:128:SER:HB2	1.75	0.51
31:a:372:A:H4'	31:a:373:U:OP1	2.11	0.51
31:a:1187:G:O2'	31:a:1189:A:N7	2.38	0.51
37:g:131:THR:O	37:g:131:THR:HG23	2.11	0.51
53:A:35:A:C5	53:A:36:U:C5	2.99	0.51
14:I:87:UNK:N	27:V:2091:A:N1	2.58	0.51
16:K:50:GLY:O	16:K:53:LYS:NZ	2.41	0.51
27:V:1017:C:O2'	27:V:1029:A:N3	2.41	0.51
27:V:1757:G:O2'	27:V:1758:U:O5'	2.24	0.51
27:V:2324:C:O2'	27:V:2325:U:O5'	2.26	0.51
47:q:71:ALA:O	47:q:72:THR:OG1	2.25	0.51
53:A:35:A:C4	53:A:36:U:C6	2.99	0.51
6:6:57:ASP:OD1	6:6:58:ARG:N	2.44	0.51
24:S:98:LYS:NZ	27:V:1362:G:OP1	2.44	0.51
27:V:1371:G:N7	27:V:1654:A:O2'	2.37	0.51
27:V:2324:C:HO2'	27:V:2325:U:P	2.33	0.51
52:X:111:ASP:OD1	52:X:112:LYS:N	2.44	0.51
15:J:13:GLU:N	15:J:13:GLU:OE2	2.44	0.51
27:V:1565:U:O2'	27:V:1566:G:P	2.68	0.51
31:a:965:U:O2'	31:a:966:U:P	2.68	0.51
43:m:87:ARG:O	43:m:91:HIS:ND1	2.39	0.51
52:X:97:GLN:OE1	52:X:97:GLN:N	2.42	0.51
27:V:1529:G:O2'	27:V:1530:G:P	2.69	0.51
31:a:896:G:O6	31:a:922:C:N4	2.44	0.51
31:a:1148:G:H4'	31:a:1149:U:O5'	2.11	0.51
9:D:163:ARG:NH2	27:V:2850:G:O6	2.44	0.51
11:F:38:MET:HG3	11:F:40:VAL:HG13	1.93	0.51
15:J:79:THR:OG1	15:J:80:GLN:N	2.42	0.51
27:V:140:A:HO2'	27:V:1447:C:HO2'	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:1914:A:O2'	27:V:1915:U:OP1	2.26	0.51
27:V:2823:C:H2'	27:V:2824:G:H8	1.76	0.51
18:M:77:LYS:HE3	27:V:1002:G:C5'	2.42	0.50
27:V:39:C:O2'	27:V:659:A:N1	2.41	0.50
27:V:343:A:O2'	27:V:362:C:O2	2.24	0.50
31:a:662:U:O4	38:h:57:GLN:NE2	2.40	0.50
27:V:393:U:O2	27:V:394:U:C5	2.64	0.50
27:V:1524:A:N6	27:V:1561:G:O2'	2.43	0.50
31:a:757:A:O2'	31:a:758:A:O5'	2.25	0.50
46:p:47:ALA:O	46:p:48:GLU:HG2	2.12	0.50
31:a:584:G:O2'	31:a:830:G:OP2	2.20	0.50
50:t:62:VAL:HG22	50:t:67:VAL:O	2.10	0.50
11:F:112:ARG:NH2	11:F:134:GLU:OE2	2.44	0.50
27:V:987:A:N3	27:V:1231:G:O2'	2.44	0.50
27:V:1027:A:O2'	27:V:2065:C:O2'	2.25	0.50
27:V:2824:G:H22	27:V:2826:A:H3'	1.76	0.50
22:Q:98:LEU:HD21	23:R:13:LYS:CE	2.42	0.50
27:V:1002:G:N2	27:V:1006:A:OP2	2.44	0.50
4:3:12:LYS:NZ	27:V:252:C:O2	2.44	0.50
8:C:123:ASP:O	8:C:128:ASN:ND2	2.42	0.50
27:V:1929:A:O2'	27:V:1930:A:OP1	2.25	0.50
27:V:2229:C:O2'	27:V:2256:A:N1	2.44	0.50
29:Y:28:LEU:HD13	29:Y:37:LEU:HD11	1.94	0.50
31:a:946:C:O2'	31:a:1391:C:N3	2.44	0.50
27:V:88:G:O2'	27:V:89:U:P	2.69	0.50
31:a:41:G:N3	31:a:412:G:N2	2.58	0.50
7:B:37:A:C2	7:B:42:G:C2	3.00	0.50
32:b:19:PHE:O	32:b:23:VAL:HG13	2.12	0.50
2:1:29:ARG:NH1	2:1:48:THR:O	2.44	0.50
26:U:33:VAL:CG2	26:U:65:VAL:HG22	2.41	0.50
27:V:588:C:N4	27:V:596:G:O6	2.45	0.50
31:a:790:A:O2'	31:a:1532:U:O2	2.30	0.50
31:a:843:U:O4	31:a:844:A:N6	2.45	0.50
2:1:5:ILE:N	2:1:19:SER:O	2.42	0.49
21:P:75:PRO:HB2	21:P:78:THR:HG23	1.94	0.49
27:V:30:G:O2'	27:V:1254:A:N3	2.43	0.49
31:a:1148:G:H1'	31:a:1149:U:OP2	2.12	0.49
27:V:545:U:H2'	27:V:546:G:O4'	2.12	0.49
30:Z:52:HIS:ND1	30:Z:53:LEU:HD12	2.27	0.49
31:a:207:U:HO2'	31:a:208:A:P	2.31	0.49
31:a:1406:C:C2'	53:A:50:C:N4	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:X:64:GLN:O	52:X:68:LEU:HD23	2.11	0.49
18:M:28:HIS:O	18:M:134:ARG:NH2	2.43	0.49
27:V:644:G:N2	27:V:649:G:O3'	2.46	0.49
31:a:39:U:O2'	31:a:556:A:N1	2.44	0.49
31:a:270:A:O2'	50:t:70:ASN:OD1	2.18	0.49
41:k:28:THR:OG1	41:k:31:ASN:O	2.24	0.49
22:Q:48:ARG:NH2	27:V:604:C:O2	2.46	0.49
27:V:2882:G:N2	27:V:2885:A:OP2	2.40	0.49
5:4:35:LYS:NZ	27:V:2771:G:OP1	2.36	0.49
12:G:59:GLN:OE1	12:G:61:GLU:N	2.45	0.49
31:a:848:G:HO2'	31:a:849:G:P	2.35	0.49
1:0:27:MET:HE1	24:S:35:ILE:HG13	1.93	0.49
12:G:78:GLU:OE1	12:G:82:LYS:NZ	2.44	0.49
14:I:84:UNK:O	14:I:85:UNK:C	2.61	0.49
19:N:13:ARG:NH1	27:V:2719:A:OP2	2.45	0.49
27:V:285:U:C2	27:V:289:C:H1'	2.46	0.49
27:V:2125:U:H2'	27:V:2126:G:O4'	2.13	0.49
31:a:358:G:O2'	31:a:359:G:O4'	2.24	0.49
44:n:46:GLU:OE2	44:n:46:GLU:HA	2.11	0.49
21:P:14:ARG:NH1	21:P:78:THR:O	2.43	0.49
27:V:282:G:O2'	27:V:283:G:O5'	2.31	0.49
27:V:902:G:N1	27:V:970:A:C2	2.80	0.49
27:V:2385:C:H2'	27:V:2386:U:O4'	2.13	0.49
27:V:2716:U:H2'	27:V:2717:G:O4'	2.13	0.49
37:g:75:VAL:O	37:g:75:VAL:HG13	2.12	0.49
18:M:45:ARG:NH2	27:V:2513:G:OP1	2.41	0.49
27:V:432:C:O2'	27:V:435:G:N2	2.46	0.49
31:a:259:G:N2	31:a:261:U:O4	2.46	0.49
31:a:455:G:O2'	31:a:456:A:P	2.70	0.49
31:a:820:C:O2'	31:a:911:A:N1	2.46	0.49
52:X:53:LYS:HE3	52:X:57:GLU:OE2	2.13	0.49
8:C:264:ASN:OD1	8:C:265:LYS:N	2.46	0.49
13:H:54:U:O4	13:H:58:A:N7	2.46	0.49
27:V:482:C:O2'	27:V:483:C:C5'	2.61	0.49
27:V:2398:A:N6	27:V:2399:G:O6	2.45	0.49
31:a:885:C:O2'	38:h:15:ARG:NH1	2.45	0.49
31:a:1450:G:O2'	31:a:1470:A:N6	2.42	0.49
32:b:13:GLU:HB3	53:A:33:A:C5	2.48	0.49
36:f:48:LEU:HD13	36:f:52:ILE:HD11	1.94	0.49
37:g:12:VAL:HG13	37:g:12:VAL:O	2.12	0.49
27:V:1713:A:N3	27:V:1715:C:N4	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:2170:A:H61	27:V:2179:U:H3	1.61	0.49
36:f:48:LEU:HD13	36:f:52:ILE:CD1	2.43	0.49
26:U:56:ILE:O	26:U:56:ILE:HG22	2.13	0.48
27:V:924:U:O2'	27:V:947:A:N6	2.46	0.48
27:V:1876:A:O2'	27:V:1877:A:N7	2.45	0.48
11:F:49:ALA:O	11:F:52:SER:OG	2.26	0.48
22:Q:10:THR:OG1	27:V:1291:A:OP1	2.26	0.48
27:V:76:C:OP1	29:Y:48:LYS:NZ	2.45	0.48
27:V:772:G:O3'	27:V:773:G:O4'	2.31	0.48
27:V:2122:G:O6	27:V:2254:A:C8	2.65	0.48
31:a:508:A:N1	31:a:555:A:O2'	2.40	0.48
31:a:1249:U:H5	37:g:116:MET:HE3	1.78	0.48
38:h:20:VAL:HG12	38:h:20:VAL:O	2.13	0.48
27:V:445:C:OP1	51:u:32:ASN:ND2	2.45	0.48
27:V:508:C:H2'	27:V:509:C:O4'	2.13	0.48
31:a:1149:U:H2'	31:a:1149:U:O2	2.12	0.48
31:a:1188:A:O2'	39:i:106:ARG:NH2	2.45	0.48
27:V:195:C:N4	27:V:206:A:O2'	2.46	0.48
27:V:688:G:H21	27:V:692:A:H62	1.59	0.48
27:V:1243:A:H61	27:V:1284:A:N6	2.11	0.48
27:V:1819:C:OP2	27:V:1857:G:N1	2.44	0.48
27:V:2159:U:O2'	27:V:2162:G:O2'	2.31	0.48
37:g:102:ARG:O	37:g:106:ASN:ND2	2.46	0.48
45:o:24:SER:O	45:o:27:VAL:N	2.46	0.48
53:A:31:A:C5	53:A:32:U:C5	3.01	0.48
53:A:45:C:O2'	53:A:46:A:O5'	2.16	0.48
23:R:50:ASN:O	23:R:51:PRO:C	2.56	0.48
31:a:267:G:OP1	50:t:78:ARG:NH1	2.47	0.48
31:a:1499:G:HO2'	31:a:1500:U:P	2.35	0.48
46:p:48:GLU:CG	46:p:48:GLU:O	2.61	0.48
11:F:141:ILE:HG22	11:F:141:ILE:O	2.13	0.48
12:G:47:GLU:N	12:G:47:GLU:OE2	2.47	0.48
17:L:21:ARG:NH2	27:V:631:G:OP1	2.45	0.48
31:a:445:U:H3	31:a:504:A:H62	1.61	0.48
15:J:23:GLY:N	15:J:64:GLU:OE1	2.42	0.48
31:a:205:C:N4	31:a:206:A:H62	2.11	0.48
43:m:42:ASP:O	43:m:43:THR:HG23	2.14	0.48
31:a:631:A:OP2	31:a:632:C:N4	2.39	0.48
31:a:1210:A:H1'	31:a:1211:U:OP2	2.13	0.48
31:a:1322:U:OP1	49:s:5:LEU:HD13	2.13	0.48
12:G:87:GLY:N	12:G:166:GLU:OE2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:123:GLU:OE2	12:G:123:GLU:N	2.44	0.48
27:V:224:A:O4'	27:V:236:A:O2'	2.30	0.48
27:V:1441:U:O2'	27:V:1517:A:N1	2.37	0.48
30:Z:47:ILE:HD12	30:Z:54:VAL:HG11	1.96	0.48
31:a:890:C:C5'	42:l:9:ARG:NH1	2.64	0.48
7:B:34:C:N3	7:B:47:C:O2'	2.42	0.48
27:V:242:U:HO2'	27:V:668:G:HO2'	1.61	0.48
27:V:1966:A:O2'	27:V:1968:U:OP2	2.27	0.48
29:Y:15:GLU:OE1	29:Y:16:GLN:NE2	2.44	0.48
31:a:746:C:C2	31:a:747:U:C5	3.02	0.48
31:a:1046:G:O2'	31:a:1047:C:O4'	2.32	0.48
31:a:1136:U:O2'	31:a:1289:A:H2'	2.13	0.48
52:X:21:VAL:HG23	52:X:26:ALA:HB2	1.94	0.48
27:V:505:G:O2'	27:V:516:G:O6	2.28	0.47
27:V:546:G:N1	27:V:549:A:OP2	2.39	0.47
27:V:1529:G:O2'	27:V:1530:G:O5'	2.30	0.47
31:a:1091:G:OP2	35:e:32:ARG:NH1	2.47	0.47
12:G:125:GLU:N	12:G:125:GLU:OE1	2.47	0.47
27:V:1135:G:N2	27:V:1136:U:O4	2.47	0.47
31:a:180:G:C2	31:a:209:A:C2	3.02	0.47
31:a:473:G:H21	31:a:477:A:H2	1.62	0.47
31:a:1463:A:O2'	31:a:1464:G:P	2.72	0.47
7:B:40:C:N4	7:B:41:C:H41	2.12	0.47
12:G:115:GLU:OE2	12:G:115:GLU:N	2.47	0.47
27:V:2580:C:N4	27:V:2581:U:O4	2.47	0.47
31:a:371:A:OP1	42:l:44:ARG:N	2.41	0.47
34:d:163:GLU:N	34:d:184:GLU:OE2	2.46	0.47
39:i:50:GLN:OE1	39:i:80:ARG:NH2	2.47	0.47
50:t:45:ASP:OD1	50:t:46:LYS:N	2.47	0.47
53:A:45:C:HO2'	53:A:46:A:P	2.33	0.47
12:G:22:ASN:OD1	12:G:23:ASN:N	2.47	0.47
27:V:2830:A:O2'	27:V:2831:A:OP2	2.23	0.47
38:h:97:VAL:HG12	38:h:98:LEU:HG	1.95	0.47
27:V:88:G:HO2'	27:V:89:U:P	2.36	0.47
27:V:2139:G:O2'	27:V:2149:G:OP1	2.33	0.47
27:V:2536:C:O2	27:V:2612:G:N2	2.47	0.47
31:a:269:U:N3	31:a:272:C:OP2	2.42	0.47
31:a:527:C:O2'	42:l:60:SER:OG	2.03	0.47
31:a:613:G:O6	31:a:644:A:N6	2.47	0.47
31:a:1018:U:O2'	31:a:1019:C:O5'	2.32	0.47
12:G:65:LEU:O	12:G:69:THR:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:J:20:ASP:OD1	15:J:59:ASN:ND2	2.44	0.47
27:V:585:G:O6	27:V:599:G:N2	2.48	0.47
27:V:775:G:H3'	27:V:776:G:C5'	2.44	0.47
27:V:1093:G:O2'	27:V:1094:A:O5'	2.32	0.47
27:V:1380:U:OP1	27:V:1436:U:N3	2.44	0.47
31:a:908:G:N2	31:a:911:A:OP2	2.48	0.47
31:a:1078:G:N2	31:a:1200:A:N3	2.59	0.47
31:a:1463:A:HO2'	31:a:1464:G:P	2.36	0.47
36:f:7:MET:HE2	48:r:29:LYS:HZ2	1.80	0.47
38:h:52:VAL:N	38:h:59:ILE:O	2.40	0.47
45:o:34:ASP:OD1	45:o:34:ASP:C	2.57	0.47
8:C:157:SER:O	8:C:195:VAL:HG21	2.14	0.47
27:V:1417:A:O2'	27:V:1419:G:N7	2.26	0.47
27:V:2487:U:O2'	27:V:2489:U:O4	2.32	0.47
31:a:886:A:C1'	38:h:12:THR:HG21	2.45	0.47
9:D:138:ARG:NH2	27:V:791:C:OP2	2.47	0.47
18:M:84:GLY:O	18:M:85:SER:OG	2.23	0.47
19:N:45:GLU:O	19:N:49:THR:HG23	2.15	0.47
21:P:23:GLY:N	21:P:47:VAL:O	2.44	0.47
27:V:677:A:N3	27:V:2444:G:O2'	2.47	0.47
27:V:1015:G:N2	27:V:1031:C:OP1	2.39	0.47
27:V:1322:G:N2	27:V:1325:A:OP2	2.46	0.47
27:V:2616:A:N6	27:V:2637:G:O2'	2.47	0.47
27:V:2799:C:H2'	27:V:2799:C:O2	2.15	0.47
31:a:113:G:H1'	31:a:114:A:OP2	2.15	0.47
31:a:261:U:C1'	31:a:283:G:H21	2.27	0.47
37:g:109:ARG:CB	37:g:116:MET:HE1	2.44	0.47
40:j:29:ALA:HB1	40:j:36:VAL:HG21	1.97	0.47
7:B:37:A:H4'	7:B:38:U:OP1	2.14	0.47
19:N:35:THR:HG21	27:V:1696:G:H3'	1.96	0.47
19:N:93:GLU:OE1	19:N:93:GLU:N	2.38	0.47
31:a:784:G:N2	31:a:813:U:O4	2.47	0.47
37:g:13:LEU:N	37:g:14:PRO:HD2	2.30	0.47
38:h:5:ASP:N	38:h:5:ASP:OD1	2.46	0.47
45:o:63:ARG:HD2	45:o:87:LEU:HD11	1.97	0.47
7:B:70:G:H21	7:B:102:A:H62	1.62	0.46
9:D:168:GLN:NE2	27:V:2802:U:OP1	2.44	0.46
11:F:106:VAL:HG12	11:F:110:ARG:HG3	1.97	0.46
27:V:2732:C:C2	27:V:2733:C:C5	3.04	0.46
37:g:116:MET:HE2	37:g:119:ARG:HH11	1.81	0.46
39:i:44:LEU:O	39:i:48:ILE:HG13	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:p:20:ILE:N	46:p:38:GLY:O	2.45	0.46
18:M:30:GLY:O	18:M:134:ARG:NH2	2.47	0.46
27:V:497:G:N1	27:V:501:A:OP2	2.43	0.46
31:a:766:U:H2'	31:a:767:G:O4'	2.15	0.46
31:a:890:C:OP1	42:l:9:ARG:NH1	2.48	0.46
31:a:1186:G:H2'	31:a:1187:G:O4'	2.14	0.46
52:X:116:GLU:OE1	52:X:116:GLU:N	2.48	0.46
27:V:648:G:O2'	27:V:649:G:P	2.74	0.46
27:V:1027:A:HO2'	27:V:2065:C:HO2'	1.59	0.46
27:V:2036:U:C2	27:V:2037:C:C5	3.04	0.46
27:V:2295:A:H4'	27:V:2296:A:OP2	2.15	0.46
27:V:2897:G:O2'	27:V:2898:A:O4'	2.27	0.46
31:a:342:C:O2'	31:a:1443:A:O2'	2.31	0.46
31:a:590:G:N2	31:a:768:A:OP2	2.45	0.46
31:a:1162:G:OP1	40:j:16:ARG:NH2	2.45	0.46
31:a:1462:U:O2'	31:a:1463:A:P	2.73	0.46
8:C:260:ARG:NH2	8:C:266:SER:OG	2.45	0.46
12:G:20:ASN:OD1	12:G:21:ASP:N	2.49	0.46
27:V:1450:C:C4	27:V:1451:U:C5	3.03	0.46
27:V:1475:G:HO2'	27:V:1476:C:H6	1.60	0.46
27:V:1692:U:O3'	27:V:1693:C:H4'	2.16	0.46
27:V:2534:G:HO2'	27:V:2535:U:P	2.37	0.46
31:a:848:G:O2'	31:a:849:G:O5'	2.32	0.46
31:a:1313:G:O3'	31:a:1314:G:O4'	2.32	0.46
48:r:64:ILE:CD1	48:r:73:LEU:HD13	2.45	0.46
11:F:158:THR:O	20:O:1:MET:N	2.47	0.46
27:V:1315:G:OP2	27:V:1690:G:O2'	2.33	0.46
27:V:2525:C:O2'	27:V:2526:A:O5'	2.25	0.46
31:a:474:A:HO2'	31:a:475:A:C5'	2.23	0.46
31:a:589:C:H2'	31:a:590:G:O4'	2.16	0.46
8:C:27:ASP:OD1	8:C:27:ASP:N	2.42	0.46
8:C:170:LYS:NZ	27:V:2252:A:OP1	2.40	0.46
29:Y:24:GLU:O	29:Y:28:LEU:HD23	2.16	0.46
45:o:78:TYR:CZ	45:o:82:ILE:HD11	2.51	0.46
46:p:68:ASP:O	46:p:72:ASN:ND2	2.48	0.46
48:r:37:PHE:CD1	48:r:60:LEU:HD21	2.47	0.46
49:s:30:VAL:HG22	49:s:48:THR:HG23	1.98	0.46
3:2:39:ARG:NH2	27:V:515:G:N7	2.63	0.46
22:Q:49:ASP:OD2	27:V:580:U:O2'	2.34	0.46
27:V:1818:A:H2'	27:V:1819:C:O4'	2.15	0.46
31:a:641:G:O2'	31:a:642:U:P	2.74	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:30:C:C2	7:B:49:G:N2	2.84	0.46
24:S:77:ASP:OD1	27:V:24:G:O2'	2.26	0.46
27:V:1403:G:N2	27:V:1406:A:OP2	2.49	0.46
27:V:1525:G:HO2'	27:V:1526:G:P	2.35	0.46
27:V:2162:G:N2	27:V:2187:A:OP2	2.42	0.46
12:G:75:ASN:ND2	27:V:2776:G:OP1	2.46	0.46
13:H:47:U:H1'	13:H:48:C:OP2	2.16	0.46
18:M:35:GLN:HB2	18:M:132:VAL:HG21	1.98	0.46
27:V:1450:C:C2	27:V:1451:U:C6	3.03	0.46
27:V:2122:G:H4'	52:X:25:TYR:HB3	1.96	0.46
8:C:154:LEU:HD13	8:C:176:LEU:HD21	1.97	0.46
31:a:381:A:N3	31:a:491:A:N6	2.64	0.46
31:a:1318:G:H5"	43:m:91:HIS:NE2	2.31	0.46
34:d:32:ALA:HB3	34:d:33:PRO:CD	2.39	0.46
34:d:79:ALA:O	34:d:85:ASN:ND2	2.46	0.46
27:V:139:A:C2	27:V:1449:C:C5	3.03	0.45
33:c:130:ARG:NH1	33:c:167:TYR:OH	2.48	0.45
37:g:111:ARG:NH2	37:g:126:ASP:OD2	2.50	0.45
8:C:208:ALA:HB2	27:V:1819:C:O2'	2.15	0.45
19:N:32:THR:OG1	19:N:33:THR:N	2.48	0.45
31:a:965:U:O2'	31:a:966:U:O5'	2.32	0.45
31:a:1441:G:N2	31:a:1478:A:OP2	2.42	0.45
38:h:97:VAL:HG11	38:h:131:VAL:O	2.16	0.45
27:V:175:G:N1	27:V:177:G:O6	2.49	0.45
29:Y:17:LYS:HB3	29:Y:53:MET:HE3	1.99	0.45
8:C:245:SER:O	8:C:245:SER:OG	2.30	0.45
10:E:84:ARG:NH2	27:V:518:A:OP1	2.41	0.45
27:V:340:U:H2'	27:V:341:G:O4'	2.17	0.45
27:V:514:G:H2'	27:V:515:G:C8	2.52	0.45
27:V:1527:C:C2'	27:V:1528:U:OP1	2.64	0.45
31:a:158:G:N2	31:a:161:A:OP2	2.36	0.45
31:a:547:U:OP1	42:l:124:ALA:N	2.43	0.45
31:a:1165:G:HO2'	31:a:1189:A:N6	2.14	0.45
31:a:1366:A:OP1	31:a:1368:C:N4	2.48	0.45
45:o:30:ALA:O	45:o:33:THR:OG1	2.32	0.45
47:q:21:LYS:O	47:q:50:ASP:N	2.50	0.45
53:A:35:A:C6	53:A:36:U:C2	3.04	0.45
12:G:120:GLU:HB2	12:G:122:ILE:HD11	1.99	0.45
22:Q:22:LYS:NZ	27:V:1259:G:OP1	2.41	0.45
27:V:25:U:H2'	27:V:26:G:O5'	2.17	0.45
27:V:2220:A:H2'	27:V:2221:C:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:2349:A:N3	27:V:2349:A:H2'	2.32	0.45
27:V:2731:G:C2	27:V:2732:C:C6	3.05	0.45
31:a:1326:C:HO2'	49:s:10:PHE:HZ	1.63	0.45
40:j:26:VAL:HG21	40:j:39:PRO:HD3	1.98	0.45
8:C:54:GLN:NE2	27:V:1852:G:OP1	2.49	0.45
25:T:5:ARG:NH2	29:Y:23:GLU:OE2	2.50	0.45
27:V:632:U:H2'	27:V:633:U:C6	2.51	0.45
27:V:1392:A:OP2	27:V:1416:G:N1	2.41	0.45
27:V:1559:C:H3'	27:V:1560:U:H5"	1.99	0.45
27:V:2228:A:N7	27:V:2229:C:C4	2.84	0.45
31:a:420:U:O2'	31:a:421:G:O5'	2.28	0.45
31:a:668:C:N4	31:a:669:A:N6	2.65	0.45
18:M:87:LYS:NZ	27:V:1001:U:OP1	2.35	0.45
27:V:1116:A:O2'	27:V:1118:C:N4	2.43	0.45
27:V:1631:A:C4'	27:V:1632:G:OP1	2.64	0.45
27:V:2695:C:O2	27:V:2695:C:O4'	2.35	0.45
31:a:757:A:O2'	31:a:758:A:P	2.73	0.45
33:c:104:GLU:N	33:c:104:GLU:OE2	2.50	0.45
45:o:17:THR:OG1	45:o:21:ASP:OD2	2.34	0.45
9:D:12:MET:HE1	9:D:191:ASN:OD1	2.16	0.45
15:J:89:THR:HG23	15:J:92:GLU:H	1.81	0.45
27:V:1018:G:OP2	27:V:1019:A:O2'	2.27	0.45
27:V:2121:U:N3	27:V:2255:C:OP2	2.50	0.45
27:V:2228:A:N7	27:V:2229:C:C5	2.85	0.45
27:V:2295:A:C3'	27:V:2296:A:H5'	2.46	0.45
37:g:56:ASN:OD1	37:g:57:ASP:N	2.50	0.45
42:l:127:ARG:O	42:l:132:THR:OG1	2.28	0.45
27:V:75:G:O5'	29:Y:44:ARG:NH2	2.50	0.45
27:V:275:A:N6	27:V:296:G:N2	2.65	0.45
27:V:441:C:C2'	27:V:442:C:OP1	2.64	0.45
27:V:494:A:N1	27:V:501:A:O2'	2.40	0.45
53:A:39:U:O2	53:A:39:U:O4'	2.34	0.45
31:a:993:A:N3	31:a:993:A:H2'	2.31	0.45
36:f:7:MET:HE2	48:r:29:LYS:NZ	2.32	0.45
5:4:17:ILE:O	5:4:24:MET:N	2.44	0.44
27:V:115:C:H2'	27:V:116:G:O4'	2.16	0.44
27:V:689:A:H61	27:V:2398:A:C2'	2.27	0.44
27:V:1471:G:N2	27:V:1621:G:N7	2.65	0.44
27:V:2022:U:O2'	27:V:2023:C:OP1	2.35	0.44
27:V:2420:G:O2'	27:V:2458:G:N2	2.50	0.44
31:a:74:A:C2	31:a:96:G:O6	2.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:d:62:GLY:O	34:d:111:ARG:NH2	2.43	0.44
34:d:125:ARG:NH2	34:d:127:ASP:OD2	2.44	0.44
43:m:58:ASP:OD1	43:m:59:ILE:N	2.50	0.44
10:E:78:ILE:HG23	10:E:79:ARG:HG2	2.00	0.44
21:P:75:PRO:HD2	21:P:78:THR:HG21	2.00	0.44
27:V:1957:A:H2'	27:V:1958:G:O4'	2.17	0.44
27:V:2182:G:H2'	27:V:2183:G:C8	2.52	0.44
31:a:528:C:H2'	31:a:529:A:O4'	2.16	0.44
31:a:1336:G:H2'	31:a:1337:C:O4'	2.17	0.44
9:D:28:ILE:HD12	9:D:188:ILE:HD13	1.99	0.44
23:R:63:GLU:N	23:R:63:GLU:OE2	2.51	0.44
27:V:1877:A:N7	31:a:711:A:N6	2.61	0.44
27:V:2467:U:O3'	27:V:2468:A:H3'	2.16	0.44
31:a:207:U:H4'	31:a:208:A:OP1	2.18	0.44
31:a:676:G:OP1	31:a:741:C:O2'	2.31	0.44
31:a:1165:G:O2'	31:a:1189:A:N6	2.50	0.44
3:2:25:LYS:NZ	27:V:213:C:OP1	2.47	0.44
12:G:11:ILE:O	12:G:49:ASN:ND2	2.49	0.44
27:V:432:C:O2'	27:V:433:G:OP2	2.35	0.44
27:V:2615:C:OP2	27:V:2637:G:N1	2.44	0.44
35:e:99:ALA:HB1	35:e:103:THR:HG21	1.99	0.44
50:t:20:HIS:O	50:t:23:THR:OG1	2.30	0.44
53:A:31:A:C4	53:A:32:U:C6	3.05	0.44
12:G:88:LEU:N	12:G:132:VAL:O	2.43	0.44
16:K:80:ASP:OD2	21:P:62:ARG:NH2	2.43	0.44
27:V:492:C:H2'	27:V:493:G:O4'	2.17	0.44
27:V:1494:G:O2'	27:V:1592:A:N3	2.41	0.44
27:V:1697:A:H2'	27:V:1698:G:O4'	2.17	0.44
27:V:2819:A:O2'	27:V:2917:G:O2'	2.35	0.44
40:j:25:ILE:HD13	40:j:90:LEU:HD13	2.00	0.44
42:l:115:LEU:C	42:l:117:THR:N	2.76	0.44
27:V:475:A:C2'	27:V:476:A:O5'	2.66	0.44
27:V:790:A:N6	27:V:802:G:O6	2.51	0.44
27:V:1479:G:H2'	27:V:1480:A:O4'	2.17	0.44
31:a:286:G:H4'	31:a:287:A:OP1	2.18	0.44
31:a:405:A:N7	31:a:556:A:O2'	2.51	0.44
4:3:32:LEU:HD13	27:V:2420:G:OP2	2.18	0.44
15:J:38:ARG:HH12	27:V:1053:C:C5'	2.29	0.44
16:K:97:ARG:HE	31:a:347:C:P	2.41	0.44
27:V:1243:A:H2'	27:V:1244:A:N3	2.33	0.44
43:m:33:VAL:HG13	43:m:59:ILE:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:p:48:GLU:O	46:p:48:GLU:HG3	2.18	0.44
52:X:17:GLU:O	52:X:19:LYS:HG3	2.18	0.44
9:D:114:SER:HB3	9:D:169:ILE:HD12	1.99	0.44
16:K:71:ARG:NH1	16:K:77:ILE:HG22	2.32	0.44
27:V:347:G:O2'	27:V:348:U:OP1	2.31	0.44
27:V:993:A:O2'	27:V:1030:G:N2	2.46	0.44
27:V:1451:U:H2'	27:V:1452:C:C6	2.52	0.44
31:a:1496:G:H2'	31:a:1497:G:O4'	2.18	0.44
35:e:25:VAL:HG12	35:e:26:LYS:N	2.32	0.44
22:Q:92:ARG:O	22:Q:93:LYS:C	2.60	0.44
26:U:40:MET:HE1	26:U:60:GLU:HG3	1.99	0.44
27:V:78:U:C2	27:V:79:C:C5	3.06	0.44
27:V:181:G:O2'	27:V:182:C:O5'	2.36	0.44
31:a:1184:G:H2'	31:a:1185:A:C8	2.52	0.44
27:V:419:G:N2	27:V:448:A:OP2	2.51	0.43
27:V:1451:U:C2	27:V:1637:G:N1	2.86	0.43
27:V:2307:A:OP2	28:W:20:ASN:ND2	2.51	0.43
27:V:2803:C:H2'	27:V:2804:A:O4'	2.18	0.43
53:A:30:A:C2	53:A:31:A:H1'	2.53	0.43
27:V:275:A:N6	27:V:296:G:H21	2.16	0.43
27:V:2446:C:C2	27:V:2447:A:C8	3.06	0.43
27:V:2486:U:H2'	27:V:2487:U:O4'	2.18	0.43
7:B:37:A:N1	7:B:42:G:C6	2.86	0.43
31:a:755:G:H2'	31:a:756:U:C4'	2.48	0.43
31:a:998:G:H1'	31:a:1025:G:H22	1.83	0.43
31:a:1087:G:O2'	31:a:1089:G:O6	2.35	0.43
31:a:1122:C:O2'	33:c:178:ARG:NH2	2.41	0.43
31:a:1141:G:H3'	31:a:1142:C:C5'	2.48	0.43
39:i:28:ILE:HD13	39:i:35:ILE:HD11	2.00	0.43
46:p:10:MET:N	46:p:17:PHE:O	2.49	0.43
48:r:24:THR:O	48:r:25:HIS:C	2.60	0.43
12:G:87:GLY:C	12:G:88:LEU:HD22	2.43	0.43
27:V:657:G:N2	27:V:661:A:OP2	2.46	0.43
27:V:1785:G:H4'	27:V:1787:G:O4'	2.19	0.43
27:V:2196:U:O3'	27:V:2197:G:O4'	2.35	0.43
31:a:1196:G:N3	44:n:60:SER:OG	2.42	0.43
31:a:1441:G:O2'	31:a:1477:G:O6	2.34	0.43
9:D:55:ASP:OD2	9:D:77:LYS:NZ	2.39	0.43
17:L:86:ALA:O	17:L:89:THR:HG22	2.18	0.43
27:V:1882:A:O2'	27:V:1883:A:OP1	2.37	0.43
31:a:1462:U:O2'	31:a:1463:A:O4'	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Q:15:LYS:NZ	27:V:1257:C:OP2	2.43	0.43
24:S:21:MET:HA	24:S:24:ILE:HD12	2.01	0.43
27:V:140:A:O2'	27:V:1447:C:O2'	2.28	0.43
27:V:514:G:H2'	27:V:515:G:O4'	2.19	0.43
27:V:1463:C:H2'	27:V:1464:A:O4'	2.19	0.43
27:V:2378:G:H3'	27:V:2379:C:H5"	1.98	0.43
31:a:442:C:C2	31:a:443:U:C5	3.06	0.43
31:a:613:G:H2'	31:a:614:U:O4'	2.18	0.43
31:a:891:G:H2'	31:a:892:C:O4'	2.19	0.43
34:d:81:LYS:NZ	35:e:101:GLU:O	2.49	0.43
23:R:50:ASN:O	23:R:52:THR:N	2.52	0.43
27:V:1243:A:O2'	27:V:1244:A:P	2.76	0.43
45:o:74:ASP:OD1	45:o:77:ARG:NE	2.52	0.43
47:q:66:THR:HG22	47:q:67:ARG:N	2.33	0.43
21:P:14:ARG:NH2	21:P:78:THR:O	2.51	0.43
27:V:2295:A:N6	27:V:2302:A:OP2	2.52	0.43
31:a:736:G:N2	31:a:739:G:OP2	2.45	0.43
31:a:1048:A:H2'	31:a:1049:G:O4'	2.19	0.43
53:A:44:A:C2'	53:A:45:C:H5'	2.48	0.43
27:V:371:G:N2	27:V:380:C:N3	2.67	0.43
27:V:554:U:C4'	27:V:555:C:OP2	2.66	0.43
27:V:1565:U:O2'	27:V:1566:G:OP1	2.27	0.43
27:V:1569:A:H5'	27:V:1571:G:C4	2.53	0.43
31:a:86:G:H2'	31:a:87:C:O4'	2.18	0.43
31:a:209:A:HO2'	31:a:210:A:C1'	2.20	0.43
31:a:928:A:H2'	31:a:929:A:O4'	2.19	0.43
31:a:939:G:N1	31:a:1398:C:N3	2.66	0.43
46:p:47:ALA:O	46:p:48:GLU:CG	2.67	0.43
17:L:38:GLN:OE1	27:V:878:G:O2'	2.31	0.43
27:V:461:C:O3'	27:V:1907:G:N2	2.52	0.43
27:V:508:C:H2'	27:V:509:C:C6	2.54	0.43
27:V:1420:G:O6	27:V:1421:A:N6	2.52	0.43
27:V:2534:G:O2'	27:V:2535:U:P	2.77	0.43
31:a:420:U:HO2'	31:a:421:G:P	2.41	0.43
31:a:1155:A:H2'	31:a:1155:A:N3	2.34	0.43
42:l:120:VAL:HG22	42:l:121:GLU:N	2.34	0.43
8:C:124:ILE:O	8:C:124:ILE:HG23	2.18	0.42
9:D:154:VAL:HG21	27:V:2647:G:H21	1.84	0.42
26:U:58:ASN:OD1	26:U:59:GLN:N	2.51	0.42
27:V:242:U:O2'	27:V:668:G:O2'	2.36	0.42
27:V:1520:A:N6	27:V:1566:G:O6	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:1696:G:O2'	27:V:1697:A:OP2	2.30	0.42
31:a:331:U:H2'	31:a:332:G:O4'	2.19	0.42
31:a:1058:G:OP1	44:n:3:LYS:N	2.52	0.42
31:a:1188:A:H2'	31:a:1189:A:O4'	2.19	0.42
39:i:12:ARG:O	39:i:15:SER:OG	2.35	0.42
52:X:62:LEU:HD22	52:X:134:HIS:NE2	2.33	0.42
19:N:2:SER:OG	19:N:3:TYR:N	2.43	0.42
27:V:419:G:H22	27:V:447:G:H3'	1.84	0.42
27:V:2279:G:OP1	27:V:2304:C:O2'	2.34	0.42
27:V:2341:U:N3	27:V:2342:C:C5	2.87	0.42
31:a:263:G:O6	31:a:274:G:O6	2.37	0.42
34:d:15:LEU:HD13	34:d:56:LYS:HA	2.01	0.42
37:g:90:GLU:OE2	37:g:90:GLU:HA	2.19	0.42
27:V:1759:U:O2'	27:V:1760:A:O5'	2.37	0.42
27:V:1870:U:C2	27:V:1871:G:C8	3.06	0.42
27:V:2295:A:H3'	27:V:2296:A:H5'	2.00	0.42
43:m:85:SER:O	43:m:86:TYR:C	2.62	0.42
24:S:24:ILE:HD11	24:S:36:LEU:HD21	2.01	0.42
27:V:349:C:N4	27:V:357:G:O6	2.52	0.42
27:V:655:C:N4	27:V:656:A:H62	2.17	0.42
27:V:1273:G:C2	27:V:1274:U:C4	3.08	0.42
27:V:1757:G:HO2'	27:V:1758:U:P	2.42	0.42
27:V:2036:U:N3	27:V:2037:C:C5	2.87	0.42
27:V:2076:C:O2'	27:V:2848:A:N1	2.46	0.42
31:a:23:G:H2'	31:a:24:G:C8	2.55	0.42
48:r:26:ILE:CD1	48:r:60:LEU:HD12	2.49	0.42
49:s:30:VAL:HG13	49:s:48:THR:O	2.18	0.42
50:t:58:ILE:O	50:t:62:VAL:HG23	2.19	0.42
8:C:177:ASN:O	8:C:178:SER:OG	2.32	0.42
8:C:265:LYS:NZ	27:V:2255:C:O2	2.41	0.42
27:V:421:A:N7	27:V:422:C:C6	2.88	0.42
27:V:2037:C:O2	27:V:2038:G:C8	2.72	0.42
27:V:2524:G:C2'	27:V:2525:C:H5'	2.50	0.42
27:V:2777:A:H2'	27:V:2778:A:O4'	2.19	0.42
30:Z:18:ASP:O	30:Z:22:THR:HG23	2.19	0.42
52:X:120:GLY:O	52:X:121:ILE:C	2.63	0.42
53:A:31:A:C2	53:A:32:U:C2	3.07	0.42
11:F:41:GLY:N	27:V:2336:G:O6	2.44	0.42
27:V:285:U:C1'	52:X:46:ALA:HB2	2.48	0.42
27:V:1275:G:H4'	27:V:1276:G:OP1	2.19	0.42
27:V:1801:G:N2	27:V:1803:C:H5"	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:a:1225:A:C2	31:a:1226:C:C5	3.08	0.42
49:s:30:VAL:HG11	49:s:50:ALA:HB2	2.01	0.42
31:a:360:C:O2	31:a:363:C:N4	2.51	0.42
35:e:82:PRO:O	38:h:99:ASN:ND2	2.48	0.42
43:m:65:VAL:HG12	43:m:66:GLU:N	2.35	0.42
51:u:20:HIS:O	51:u:21:ALA:HB3	2.19	0.42
8:C:245:SER:O	8:C:246:PRO:C	2.62	0.42
17:L:125:ALA:O	17:L:146:ILE:N	2.46	0.42
22:Q:102:ASP:O	22:Q:104:THR:N	2.53	0.42
26:U:67:ASN:ND2	27:V:373:A:OP2	2.52	0.42
27:V:85:G:O2'	27:V:86:C:H5'	2.20	0.42
27:V:1244:A:C2'	27:V:1245:G:OP1	2.67	0.42
27:V:1265:A:C2	27:V:1266:A:C2	3.08	0.42
27:V:1305:A:H4'	27:V:1306:G:O5'	2.20	0.42
27:V:1452:C:N3	27:V:1636:A:N1	2.67	0.42
27:V:2205:A:H4'	27:V:2206:C:OP1	2.20	0.42
31:a:1323:C:N4	31:a:1333:A:N1	2.67	0.42
31:a:1483:G:H2'	31:a:1484:G:C8	2.54	0.42
33:c:46:LEU:HD13	33:c:51:VAL:HG21	2.02	0.42
35:e:12:GLU:O	35:e:13:GLU:C	2.62	0.42
37:g:91:VAL:O	37:g:96:ARG:NE	2.52	0.42
12:G:122:ILE:HD12	12:G:122:ILE:N	2.34	0.42
19:N:29:ARG:NH2	19:N:118:GLU:OE2	2.53	0.42
27:V:1942:A:N3	27:V:1942:A:H2'	2.35	0.42
27:V:1968:U:O4'	27:V:2620:C:O2'	2.27	0.42
27:V:2459:A:N3	27:V:2459:A:H2'	2.35	0.42
31:a:877:G:O2'	31:a:883:A:N1	2.42	0.42
31:a:990:C:C5	31:a:991:U:C4	3.08	0.42
34:d:191:GLU:O	34:d:192:ALA:HB3	2.20	0.42
35:e:107:ALA:HB2	35:e:125:SER:OG	2.20	0.42
41:k:84:LEU:HD23	41:k:84:LEU:H	1.83	0.42
7:B:31:G:O6	7:B:48:G:O6	2.37	0.42
11:F:106:VAL:HG11	11:F:139:PRO:HD3	2.00	0.42
27:V:1843:G:OP2	27:V:1844:A:C2'	2.67	0.42
27:V:2134:A:N6	27:V:2135:G:O6	2.53	0.42
27:V:2135:G:N1	27:V:2212:C:C2	2.87	0.42
27:V:2140:U:OP2	27:V:2174:C:N4	2.49	0.42
31:a:248:C:HO2'	31:a:249:G:H8	1.66	0.42
31:a:440:A:C5	31:a:441:G:C8	3.08	0.42
43:m:34:LEU:HD22	43:m:39:VAL:HG21	2.02	0.42
9:D:6:LEU:N	9:D:6:LEU:HD23	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:760:G:H2'	27:V:761:U:C6	2.54	0.41
27:V:1305:A:H1'	27:V:1306:G:OP2	2.20	0.41
27:V:2022:U:O2'	27:V:2023:C:P	2.78	0.41
31:a:369:G:H2'	31:a:370:G:O4'	2.20	0.41
31:a:1020:C:C2	31:a:1021:U:C5	3.08	0.41
34:d:84:GLU:OE2	34:d:182:ARG:NE	2.53	0.41
47:q:30:TYR:HB3	47:q:41:LYS:HA	2.02	0.41
53:A:32:U:H2'	53:A:33:A:C8	2.55	0.41
8:C:167:LYS:O	8:C:169:GLY:N	2.53	0.41
27:V:81:G:H2'	27:V:82:G:O4'	2.20	0.41
27:V:2445:C:N3	27:V:2446:C:C5	2.88	0.41
31:a:305:G:N2	31:a:308:A:OP2	2.45	0.41
31:a:1499:G:H2'	31:a:1500:U:C6	2.55	0.41
38:h:3:MET:O	38:h:4:THR:OG1	2.35	0.41
27:V:153:C:H2'	27:V:154:A:H8	1.85	0.41
27:V:797:A:OP1	27:V:1660:C:N4	2.52	0.41
27:V:1478:G:H2'	27:V:1479:G:C8	2.55	0.41
27:V:2365:A:H61	28:W:51:THR:CG2	2.32	0.41
31:a:328:G:H2'	31:a:329:A:C8	2.55	0.41
31:a:459:A:H4'	31:a:460:A:O5'	2.20	0.41
31:a:641:G:H4'	31:a:642:U:OP1	2.21	0.41
31:a:1318:G:O6	31:a:1338:G:O6	2.38	0.41
31:a:1339:U:H2'	31:a:1340:G:O4'	2.20	0.41
41:k:84:LEU:HD23	41:k:84:LEU:N	2.35	0.41
45:o:81:LEU:C	45:o:81:LEU:HD23	2.45	0.41
10:E:46:GLN:N	27:V:490:A:OP1	2.54	0.41
13:H:55:U:HO2'	13:H:56:C:P	2.38	0.41
18:M:17:MET:HE3	18:M:41:TRP:CD1	2.56	0.41
22:Q:50:ARG:O	22:Q:54:LYS:NZ	2.52	0.41
23:R:14:VAL:HG13	23:R:97:ILE:HD13	2.01	0.41
27:V:911:G:H2'	27:V:912:C:C6	2.56	0.41
27:V:1087:U:O2	27:V:1160:G:C6	2.72	0.41
27:V:2296:A:OP2	27:V:2296:A:H3'	2.21	0.41
27:V:2459:A:C3'	27:V:2460:U:H5'	2.51	0.41
27:V:2550:C:H2'	27:V:2551:U:O4'	2.20	0.41
34:d:67:GLN:OE1	34:d:67:GLN:N	2.46	0.41
42:l:123:ARG:NE	42:l:125:GLN:O	2.54	0.41
46:p:57:LEU:CD1	46:p:79:ILE:HG23	2.50	0.41
27:V:24:G:C2	27:V:25:U:C5	3.09	0.41
27:V:2624:G:N2	27:V:2627:A:OP2	2.46	0.41
27:V:2874:G:N7	27:V:2892:G:N2	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:e:85:ILE:HD11	35:e:146:GLU:HB3	2.02	0.41
50:t:61:ALA:CB	50:t:67:VAL:HG21	2.42	0.41
8:C:254:THR:HG21	27:V:1853:G:O2'	2.20	0.41
9:D:134:SER:OG	9:D:135:HIS:N	2.54	0.41
26:U:47:PRO:O	26:U:52:PRO:HB3	2.21	0.41
27:V:567:U:H2'	27:V:568:G:C8	2.55	0.41
27:V:2178:C:H2'	27:V:2179:U:O4'	2.21	0.41
27:V:2721:C:O2	27:V:2872:U:O2'	2.38	0.41
29:Y:11:THR:OG1	29:Y:12:ALA:N	2.53	0.41
30:Z:47:ILE:CD1	30:Z:54:VAL:HG11	2.50	0.41
34:d:168:ASP:OD1	34:d:169:ALA:N	2.53	0.41
35:e:46:VAL:HG22	35:e:47:GLY:N	2.35	0.41
39:i:30:VAL:O	39:i:30:VAL:HG23	2.21	0.41
43:m:87:ARG:C	43:m:91:HIS:HD1	2.27	0.41
11:F:79:LEU:HD22	11:F:85:ILE:HD11	2.03	0.41
27:V:2334:U:O2'	27:V:2335:U:O4'	2.35	0.41
27:V:2374:G:C5	27:V:2376:C:C5	3.09	0.41
31:a:41:G:C2	31:a:412:G:C2	3.08	0.41
31:a:1169:G:N2	31:a:1185:A:N1	2.68	0.41
31:a:1222:A:O2'	31:a:1224:G:N7	2.42	0.41
2:1:36:CYS:O	2:1:40:LYS:N	2.49	0.41
8:C:123:ASP:OD2	8:C:124:ILE:N	2.54	0.41
16:K:22:ILE:O	16:K:23:LYS:C	2.63	0.41
17:L:114:ASN:OD1	17:L:114:ASN:N	2.52	0.41
19:N:99:THR:O	27:V:2906:U:O2'	2.38	0.41
27:V:932:C:H2'	27:V:933:C:C1'	2.51	0.41
27:V:2316:A:HO2'	27:V:2317:A:C5'	2.33	0.41
31:a:472:C:H3'	31:a:473:G:C8	2.56	0.41
31:a:572:A:H2'	31:a:576:G:C8	2.56	0.41
31:a:608:C:N4	31:a:649:A:H61	2.19	0.41
31:a:1227:C:H2'	31:a:1228:U:C6	2.56	0.41
31:a:1330:U:H2'	31:a:1331:C:C4	2.56	0.41
33:c:42:ILE:HG12	33:c:46:LEU:HD12	2.03	0.41
35:e:105:VAL:HG13	35:e:121:ALA:O	2.20	0.41
43:m:77:ILE:HG22	43:m:81:ILE:HD12	2.02	0.41
8:C:154:LEU:O	8:C:155:VAL:C	2.63	0.41
9:D:14:GLN:CG	9:D:22:LEU:HD22	2.51	0.41
9:D:106:GLU:OE1	9:D:106:GLU:N	2.40	0.41
12:G:43:GLU:N	12:G:43:GLU:OE1	2.53	0.41
15:J:30:SER:HB2	15:J:106:ILE:HD13	2.02	0.41
16:K:63:VAL:HG13	16:K:102:VAL:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:K:73:ASP:OD2	16:K:75:SER:OG	2.34	0.41
27:V:523:G:C4	27:V:525:A:OP2	2.74	0.41
27:V:526:A:H4'	27:V:527:A:OP1	2.21	0.41
27:V:762:A:C6	45:o:56:LEU:HD22	2.55	0.41
27:V:789:C:H4'	27:V:1720:C:O2'	2.21	0.41
27:V:1095:C:C2	27:V:1096:A:C8	3.08	0.41
27:V:1227:G:H2'	27:V:1228:G:O4'	2.21	0.41
27:V:1346:A:N7	27:V:1667:A:N6	2.69	0.41
27:V:2468:A:H1'	27:V:2469:C:OP2	2.21	0.41
27:V:2733:C:H2'	27:V:2734:A:O4'	2.21	0.41
27:V:2874:G:H1'	27:V:2891:G:H21	1.86	0.41
31:a:335:A:O2'	31:a:336:C:O4'	2.32	0.41
31:a:942:C:HO2'	31:a:943:G:H8	1.65	0.41
31:a:962:U:O3'	31:a:974:A:N6	2.46	0.41
31:a:1088:U:O2'	31:a:1089:G:P	2.78	0.41
31:a:1135:U:N3	31:a:1137:G:C8	2.89	0.41
31:a:1476:C:H2'	31:a:1477:G:O4'	2.21	0.41
32:b:13:GLU:CB	53:A:33:A:C5	3.04	0.41
35:e:25:VAL:HG12	35:e:26:LYS:H	1.86	0.41
37:g:126:ASP:O	37:g:129:ASN:O	2.39	0.41
43:m:15:VAL:HG23	43:m:43:THR:O	2.20	0.41
17:L:21:ARG:HA	27:V:858:U:H2'	2.03	0.41
27:V:310:C:H4'	27:V:310:C:OP1	2.20	0.41
27:V:803:C:H2'	27:V:804:G:O4'	2.21	0.41
27:V:2135:G:H2'	27:V:2136:C:O4'	2.21	0.41
27:V:2234:C:O2	27:V:2234:C:H2'	2.20	0.41
31:a:482:G:OP2	46:p:71:ARG:NH1	2.53	0.41
34:d:89:LEU:O	34:d:92:SER:OG	2.34	0.41
45:o:39:LEU:HD22	45:o:56:LEU:HD12	2.03	0.41
7:B:49:G:O2'	7:B:50:A:O4'	2.37	0.40
27:V:178:A:O2'	27:V:179:A:C8	2.73	0.40
27:V:448:A:H2'	27:V:449:A:C8	2.56	0.40
27:V:1447:C:H2'	27:V:1448:U:C6	2.56	0.40
27:V:1755:C:O4'	27:V:2884:G:N2	2.54	0.40
27:V:1891:G:C6	27:V:1910:G:C6	3.08	0.40
27:V:1967:A:O2'	27:V:1968:U:H5"	2.22	0.40
27:V:2122:G:C2	27:V:2123:A:N7	2.89	0.40
27:V:2799:C:N3	27:V:2800:C:C5	2.89	0.40
31:a:195:A:N1	47:q:66:THR:HG23	2.36	0.40
31:a:363:C:C4	31:a:364:A:N7	2.89	0.40
31:a:1133:A:H2'	31:a:1134:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:m:80:LEU:O	43:m:85:SER:HB3	2.21	0.40
9:D:103:SER:N	9:D:106:GLU:OE2	2.52	0.40
9:D:195:ALA:O	9:D:198:SER:OG	2.35	0.40
16:K:88:ARG:O	16:K:88:ARG:CG	2.64	0.40
17:L:1:MET:SD	17:L:2:LYS:N	2.94	0.40
27:V:216:A:C2'	27:V:217:G:O5'	2.69	0.40
27:V:1650:C:H2'	27:V:1651:G:O4'	2.22	0.40
27:V:2261:C:OP2	51:u:27:ARG:NH2	2.54	0.40
27:V:2433:C:H2'	27:V:2434:G:O4'	2.21	0.40
27:V:2574:G:H2'	27:V:2575:U:O4'	2.21	0.40
27:V:2800:C:C2	27:V:2801:C:C5	3.09	0.40
31:a:22:U:H2'	31:a:23:G:O4'	2.21	0.40
31:a:176:G:O2'	31:a:177:G:OP1	2.25	0.40
31:a:672:A:H2'	31:a:673:G:O4'	2.21	0.40
1:0:15:LEU:O	1:0:18:THR:OG1	2.24	0.40
8:C:13:ARG:HE	27:V:775:G:H4'	1.86	0.40
13:H:17(A):G:HO2'	13:H:18:G:P	2.36	0.40
26:U:92:ARG:O	26:U:101:LEU:N	2.48	0.40
27:V:941:U:O3'	27:V:942:U:O4'	2.40	0.40
27:V:967:G:H21	27:V:2298:A:H8	1.68	0.40
27:V:1325:A:N1	27:V:1368:U:O2'	2.46	0.40
27:V:1396:C:H2'	27:V:1397:G:O4'	2.22	0.40
27:V:1790:U:O2'	27:V:1791:A:O5'	2.36	0.40
27:V:2159:U:O2	27:V:2188:G:C6	2.75	0.40
31:a:19:U:H2'	31:a:20:C:C6	2.57	0.40
31:a:207:U:H2'	31:a:208:A:C8	2.55	0.40
31:a:1166:A:H4'	31:a:1167:C:O4'	2.21	0.40
31:a:1201:C:OP1	33:c:4:LYS:NZ	2.49	0.40
32:b:21:ARG:O	32:b:24:SER:OG	2.35	0.40
45:o:24:SER:O	45:o:25:PRO:C	2.64	0.40
7:B:31:G:H2'	7:B:32:U:C6	2.55	0.40
17:L:76:VAL:HG13	17:L:112:LEU:CD1	2.51	0.40
27:V:1035:G:C8	30:Z:13:ILE:HD11	2.57	0.40
27:V:1494:G:C6	27:V:1512:G:C6	3.09	0.40
27:V:2257:G:N2	51:u:34:GLN:OE1	2.54	0.40
31:a:530:G:OP2	42:l:64:LYS:NZ	2.39	0.40
31:a:1018:U:O2'	31:a:1019:C:OP1	2.39	0.40
31:a:1088:U:O2	35:e:135:ASN:ND2	2.54	0.40
31:a:1369:A:OP2	44:n:35:ARG:NH2	2.54	0.40
39:i:5:GLN:OE1	39:i:20:ARG:NH1	2.52	0.40
7:B:95:U:H2'	7:B:96:G:O4'	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:46:GLN:OE1	27:V:1835:C:O2'	2.25	0.40
10:E:202:VAL:HA	10:E:205:VAL:HG12	2.04	0.40
13:H:54:U:H3	13:H:58:A:H62	1.69	0.40
27:V:363:C:H2'	27:V:364:A:O4'	2.22	0.40
27:V:1306:G:OP2	27:V:1306:G:O4'	2.39	0.40
27:V:1366:C:H2'	27:V:1367:G:O4'	2.22	0.40
27:V:1507:U:C5'	27:V:1508:C:O5'	2.70	0.40
27:V:1819:C:H2'	27:V:1820:A:C8	2.57	0.40
27:V:2393:C:H2'	27:V:2394:G:O4'	2.21	0.40
27:V:2798:C:H2'	27:V:2799:C:H5'	2.03	0.40
31:a:566:G:H2'	31:a:567:G:O4'	2.20	0.40
31:a:671:A:H2'	31:a:672:A:C8	2.56	0.40
31:a:1087:G:H3'	31:a:1088:U:H5"	2.04	0.40
31:a:1219:C:H2'	31:a:1220:U:O4'	2.21	0.40
38:h:2:VAL:O	38:h:3:MET:HB3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	52/59 (88%)	50 (96%)	2 (4%)	0	100	100
2	1	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
3	2	42/44 (96%)	42 (100%)	0	0	100	100
4	3	62/66 (94%)	60 (97%)	2 (3%)	0	100	100
5	4	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
6	6	61/66 (92%)	60 (98%)	1 (2%)	0	100	100
8	C	270/277 (98%)	260 (96%)	10 (4%)	0	100	100
9	D	204/209 (98%)	193 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	E	203/207 (98%)	193 (95%)	10 (5%)	0	100	100
11	F	174/179 (97%)	165 (95%)	9 (5%)	0	100	100
12	G	173/179 (97%)	165 (95%)	8 (5%)	0	100	100
15	J	140/145 (97%)	133 (95%)	7 (5%)	0	100	100
16	K	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
17	L	144/146 (99%)	139 (96%)	5 (4%)	0	100	100
18	M	133/144 (92%)	132 (99%)	1 (1%)	0	100	100
19	N	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
20	O	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
21	P	113/115 (98%)	108 (96%)	5 (4%)	0	100	100
22	Q	115/119 (97%)	107 (93%)	6 (5%)	2 (2%)	7	35
23	R	99/102 (97%)	88 (89%)	11 (11%)	0	100	100
24	S	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
25	T	88/95 (93%)	87 (99%)	1 (1%)	0	100	100
26	U	99/103 (96%)	92 (93%)	7 (7%)	0	100	100
28	W	80/94 (85%)	76 (95%)	4 (5%)	0	100	100
29	Y	63/66 (96%)	62 (98%)	1 (2%)	0	100	100
30	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
32	b	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
33	c	204/218 (94%)	194 (95%)	10 (5%)	0	100	100
34	d	193/200 (96%)	176 (91%)	17 (9%)	0	100	100
35	e	162/166 (98%)	155 (96%)	7 (4%)	0	100	100
36	f	90/95 (95%)	87 (97%)	3 (3%)	0	100	100
37	g	149/156 (96%)	144 (97%)	5 (3%)	0	100	100
38	h	129/132 (98%)	116 (90%)	13 (10%)	0	100	100
39	i	101/130 (78%)	95 (94%)	6 (6%)	0	100	100
40	j	93/102 (91%)	87 (94%)	6 (6%)	0	100	100
41	k	116/131 (88%)	110 (95%)	6 (5%)	0	100	100
42	l	134/138 (97%)	124 (92%)	10 (8%)	0	100	100
43	m	90/121 (74%)	85 (94%)	5 (6%)	0	100	100
44	n	58/61 (95%)	52 (90%)	5 (9%)	1 (2%)	7	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
45	o	83/89 (93%)	79 (95%)	4 (5%)	0	100 100
46	p	86/90 (96%)	81 (94%)	5 (6%)	0	100 100
47	q	82/87 (94%)	76 (93%)	6 (7%)	0	100 100
48	r	62/79 (78%)	56 (90%)	5 (8%)	1 (2%)	7 36
49	s	75/92 (82%)	69 (92%)	6 (8%)	0	100 100
50	t	81/88 (92%)	79 (98%)	2 (2%)	0	100 100
51	u	56/62 (90%)	54 (96%)	2 (4%)	0	100 100
52	X	147/149 (99%)	135 (92%)	12 (8%)	0	100 100
All	All	5160/5478 (94%)	4894 (95%)	262 (5%)	4 (0%)	49 79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	Q	103	LEU
48	r	28	TYR
44	n	32	SER
22	Q	93	LYS

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	0	48/53 (91%)	46 (96%)	2 (4%)	26 52
2	1	46/47 (98%)	46 (100%)	0	100 100
3	2	39/39 (100%)	39 (100%)	0	100 100
4	3	54/56 (96%)	54 (100%)	0	100 100
5	4	35/35 (100%)	35 (100%)	0	100 100
6	6	53/55 (96%)	53 (100%)	0	100 100
8	C	220/225 (98%)	219 (100%)	1 (0%)	81 80
9	D	167/170 (98%)	167 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
10	E	169/170 (99%)	168 (99%)	1 (1%)	78 79
11	F	151/154 (98%)	151 (100%)	0	100 100
12	G	148/151 (98%)	148 (100%)	0	100 100
15	J	120/123 (98%)	120 (100%)	0	100 100
16	K	101/101 (100%)	101 (100%)	0	100 100
17	L	110/110 (100%)	110 (100%)	0	100 100
18	M	109/116 (94%)	108 (99%)	1 (1%)	70 76
19	N	99/100 (99%)	98 (99%)	1 (1%)	68 75
20	O	93/93 (100%)	93 (100%)	0	100 100
21	P	100/100 (100%)	100 (100%)	0	100 100
22	Q	96/98 (98%)	96 (100%)	0	100 100
23	R	83/84 (99%)	83 (100%)	0	100 100
24	S	90/93 (97%)	90 (100%)	0	100 100
25	T	81/85 (95%)	81 (100%)	0	100 100
26	U	85/87 (98%)	85 (100%)	0	100 100
28	W	64/74 (86%)	64 (100%)	0	100 100
29	Y	56/57 (98%)	55 (98%)	1 (2%)	51 69
30	Z	52/53 (98%)	52 (100%)	0	100 100
32	b	51/51 (100%)	51 (100%)	0	100 100
33	c	168/178 (94%)	168 (100%)	0	100 100
34	d	169/173 (98%)	167 (99%)	2 (1%)	63 73
35	e	128/130 (98%)	127 (99%)	1 (1%)	73 77
36	f	81/84 (96%)	78 (96%)	3 (4%)	30 56
37	g	127/132 (96%)	127 (100%)	0	100 100
38	h	111/112 (99%)	111 (100%)	0	100 100
39	i	81/102 (79%)	81 (100%)	0	100 100
40	j	86/92 (94%)	86 (100%)	0	100 100
41	k	90/100 (90%)	90 (100%)	0	100 100
42	l	114/116 (98%)	114 (100%)	0	100 100
43	m	80/104 (77%)	80 (100%)	0	100 100
44	n	53/54 (98%)	53 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
45	o	80/83 (96%)	79 (99%)	1 (1%)	61 72
46	p	74/76 (97%)	74 (100%)	0	100 100
47	q	77/80 (96%)	77 (100%)	0	100 100
48	r	56/64 (88%)	56 (100%)	0	100 100
49	s	69/81 (85%)	68 (99%)	1 (1%)	59 71
50	t	66/70 (94%)	66 (100%)	0	100 100
51	u	47/50 (94%)	47 (100%)	0	100 100
52	X	124/124 (100%)	121 (98%)	3 (2%)	43 64
All	All	4401/4585 (96%)	4383 (100%)	18 (0%)	81 81

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	11	MET
1	0	28	THR
8	C	197	ASN
10	E	32	VAL
18	M	44	ASN
19	N	83	LEU
29	Y	23	GLU
34	d	90	LEU
34	d	94	LEU
35	e	120	VAL
36	f	18	SER
36	f	52	ILE
36	f	89	ILE
45	o	42	HIS
49	s	25	THR
52	X	30	LEU
52	X	68	LEU
52	X	75	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
2	1	22	ASN
6	6	6	HIS
8	C	53	HIS

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Mol	Chain	Res	Type
8	C	90	ASN
10	E	82	GLN
11	F	63	GLN
17	L	17	ASN
17	L	35	HIS
17	L	70	ASN
19	N	27	ASN
22	Q	38	GLN
24	S	28	GLN
25	T	55	ASN
33	c	99	HIS
33	c	101	ASN
35	e	45	HIS
36	f	28	ASN
36	f	61	GLN
37	g	153	HIS
40	j	78	ASN
42	l	6	GLN
42	l	86	ASN
46	p	72	ASN
46	p	77	GLN
49	s	29	GLN
52	X	43	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	H	76/77 (98%)	14 (18%)	2 (2%)
27	V	2881/2928 (98%)	637 (22%)	62 (2%)
31	a	1532/1533 (99%)	266 (17%)	0
53	A	25/26 (96%)	12 (48%)	5 (20%)
7	B	111/112 (99%)	28 (25%)	4 (3%)
All	All	4625/4676 (98%)	957 (20%)	73 (1%)

All (957) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	B	10	G
7	B	11	A
7	B	12	U
7	B	22	G

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Mol	Chain	Res	Type
7	B	23	U
7	B	31	G
7	B	32	U
7	B	33	U
7	B	38	U
7	B	39	A
7	B	41	C
7	B	48	G
7	B	49	G
7	B	50	A
7	B	53	U
7	B	54	U
7	B	55	A
7	B	59	U
7	B	60	C
7	B	62	U
7	B	66	C
7	B	86	U
7	B	87	U
7	B	97	A
7	B	101	U
7	B	107	G
7	B	108	C
7	B	110	G
13	H	9	A
13	H	17	U
13	H	18	G
13	H	19	U
13	H	21	A
13	H	36	C
13	H	37	A
13	H	48	C
13	H	55	U
13	H	56	C
13	H	70	A
13	H	72	C
13	H	74	C
13	H	76	A
27	V	8	U
27	V	13	A
27	V	23	G
27	V	26	G

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Mol	Chain	Res	Type
27	V	34	U
27	V	46	C
27	V	51	G
27	V	60	G
27	V	71	A
27	V	74	U
27	V	75	G
27	V	76	C
27	V	77	U
27	V	78	U
27	V	79	C
27	V	85	G
27	V	86	C
27	V	87	U
27	V	89	U
27	V	90	A
27	V	92	G
27	V	93	C
27	V	99	U
27	V	100	U
27	V	101	G
27	V	117	A
27	V	119	U
27	V	124	A
27	V	125	A
27	V	141	U
27	V	145	G
27	V	162	A
27	V	164	U
27	V	175	G
27	V	176	A
27	V	177	G
27	V	178	A
27	V	179	A
27	V	182	C
27	V	184	G
27	V	186	C
27	V	187	C
27	V	188	C
27	V	199	A
27	V	200	A
27	V	202	A

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Mol	Chain	Res	Type
27	V	207	A
27	V	215	G
27	V	216	A
27	V	219	A
27	V	224	A
27	V	225	A
27	V	226	A
27	V	231	A
27	V	232	U
27	V	233	G
27	V	234	C
27	V	242	U
27	V	251	G
27	V	252	C
27	V	253	G
27	V	258	A
27	V	269	G
27	V	283	G
27	V	284	C
27	V	286	U
27	V	287	G
27	V	291	C
27	V	296	G
27	V	297	G
27	V	301	U
27	V	302	A
27	V	307	A
27	V	308	C
27	V	310	C
27	V	329	A
27	V	342	A
27	V	344	G
27	V	345	A
27	V	346	G
27	V	348	U
27	V	352	G
27	V	361	G
27	V	367	G
27	V	373	A
27	V	374	A
27	V	375	C
27	V	382	G

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Mol	Chain	Res	Type
27	V	407	A
27	V	410	G
27	V	411	G
27	V	412	A
27	V	418	A
27	V	419	G
27	V	420	U
27	V	421	A
27	V	432	C
27	V	433	G
27	V	434	U
27	V	442	C
27	V	444	U
27	V	445	C
27	V	458	G
27	V	459	A
27	V	471	G
27	V	476	A
27	V	477	A
27	V	482	C
27	V	483	C
27	V	491	C
27	V	498	U
27	V	502	C
27	V	504	A
27	V	506	U
27	V	512	G
27	V	527	A
27	V	528	G
27	V	530	A
27	V	537	A
27	V	548	A
27	V	550	G
27	V	554	U
27	V	555	C
27	V	556	C
27	V	568	G
27	V	573	C
27	V	575	A
27	V	577	U
27	V	578	A
27	V	579	G

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Mol	Chain	Res	Type
27	V	592	A
27	V	593	A
27	V	595	G
27	V	598	U
27	V	599	G
27	V	607	G
27	V	616	A
27	V	617	G
27	V	619	A
27	V	632	U
27	V	647	A
27	V	648	G
27	V	649	G
27	V	658	A
27	V	659	A
27	V	662	U
27	V	667	A
27	V	673	A
27	V	683	A
27	V	690	A
27	V	691	U
27	V	692	A
27	V	699	A
27	V	700	U
27	V	701	G
27	V	702	A
27	V	718	C
27	V	719	C
27	V	733	U
27	V	764	C
27	V	765	A
27	V	773	G
27	V	777	C
27	V	787	C
27	V	788	G
27	V	790	A
27	V	794	U
27	V	795	G
27	V	810	G
27	V	811	A
27	V	822	G
27	V	823	G

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Mol	Chain	Res	Type
27	V	829	A
27	V	831	U
27	V	832	G
27	V	837	U
27	V	845	G
27	V	852	G
27	V	859	C
27	V	866	A
27	V	874	U
27	V	892	U
27	V	906	G
27	V	908	A
27	V	913	A
27	V	914	C
27	V	929	G
27	V	931	C
27	V	933	C
27	V	934	U
27	V	935	A
27	V	936	C
27	V	937	C
27	V	939	G
27	V	940	G
27	V	941	U
27	V	942	U
27	V	943	A
27	V	944	C
27	V	957	A
27	V	959	C
27	V	961	C
27	V	962	C
27	V	964	A
27	V	973	G
27	V	980	C
27	V	987	A
27	V	991	A
27	V	992	G
27	V	999	A
27	V	1005	A
27	V	1007	G
27	V	1020	A
27	V	1027	A

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Mol	Chain	Res	Type
27	V	1029	A
27	V	1036	A
27	V	1042	A
27	V	1051	C
27	V	1053	C
27	V	1054	A
27	V	1055	A
27	V	1058	U
27	V	1059	A
27	V	1068	G
27	V	1073	A
27	V	1079	U
27	V	1091	U
27	V	1094	A
27	V	1101	G
27	V	1102	G
27	V	1103	A
27	V	1106	U
27	V	1110	C
27	V	1111	U
27	V	1116	A
27	V	1117	G
27	V	1118	C
27	V	1119	A
27	V	1121	C
27	V	1124	C
27	V	1125	C
27	V	1126	A
27	V	1127	U
27	V	1128	U
27	V	1134	A
27	V	1139	G
27	V	1148	C
27	V	1158	G
27	V	1159	U
27	V	1160	G
27	V	1161	A
27	V	1173	A
27	V	1178	U
27	V	1179	A
27	V	1180	C
27	V	1181	C

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Mol	Chain	Res	Type
27	V	1182	G
27	V	1185	G
27	V	1187	U
27	V	1188	A
27	V	1243	A
27	V	1244	A
27	V	1245	G
27	V	1248	C
27	V	1249	U
27	V	1251	U
27	V	1259	G
27	V	1260	A
27	V	1264	G
27	V	1265	A
27	V	1270	C
27	V	1275	G
27	V	1276	G
27	V	1278	G
27	V	1293	A
27	V	1296	G
27	V	1306	G
27	V	1311	G
27	V	1312	A
27	V	1313	A
27	V	1315	G
27	V	1323	A
27	V	1325	A
27	V	1326	A
27	V	1327	U
27	V	1339	A
27	V	1340	A
27	V	1341	U
27	V	1343	C
27	V	1344	C
27	V	1351	U
27	V	1352	U
27	V	1362	G
27	V	1364	C
27	V	1365	U
27	V	1368	U
27	V	1369	C
27	V	1370	C

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Mol	Chain	Res	Type
27	V	1371	G
27	V	1372	C
27	V	1375	A
27	V	1384	C
27	V	1385	G
27	V	1389	C
27	V	1404	A
27	V	1415	C
27	V	1417	A
27	V	1418	U
27	V	1422	C
27	V	1423	A
27	V	1425	C
27	V	1426	A
27	V	1427	G
27	V	1431	G
27	V	1434	A
27	V	1435	U
27	V	1436	U
27	V	1442	A
27	V	1449	C
27	V	1450	C
27	V	1457	U
27	V	1459	U
27	V	1460	G
27	V	1465	A
27	V	1466	U
27	V	1472	G
27	V	1473	A
27	V	1475	G
27	V	1476	C
27	V	1489	U
27	V	1490	A
27	V	1499	A
27	V	1500	U
27	V	1501	U
27	V	1502	G
27	V	1506	A
27	V	1507	U
27	V	1508	C
27	V	1514	C
27	V	1516	A

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Mol	Chain	Res	Type
27	V	1525	G
27	V	1526	G
27	V	1527	C
27	V	1528	U
27	V	1529	G
27	V	1530	G
27	V	1531	G
27	V	1532	A
27	V	1536	A
27	V	1539	C
27	V	1540	A
27	V	1542	A
27	V	1543	U
27	V	1547	U
27	V	1553	A
27	V	1557	G
27	V	1558	G
27	V	1559	C
27	V	1560	U
27	V	1566	G
27	V	1568	G
27	V	1570	U
27	V	1571	G
27	V	1573	C
27	V	1614	A
27	V	1617	A
27	V	1626	U
27	V	1632	G
27	V	1634	U
27	V	1638	A
27	V	1653	A
27	V	1655	A
27	V	1661	A
27	V	1679	A
27	V	1691	A
27	V	1692	U
27	V	1693	C
27	V	1696	G
27	V	1697	A
27	V	1699	A
27	V	1700	A
27	V	1708	U

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Mol	Chain	Res	Type
27	V	1719	G
27	V	1727	A
27	V	1738	U
27	V	1745	A
27	V	1757	G
27	V	1758	U
27	V	1759	U
27	V	1760	A
27	V	1761	G
27	V	1775	G
27	V	1776	A
27	V	1778	A
27	V	1779	G
27	V	1780	C
27	V	1781	C
27	V	1782	G
27	V	1785	G
27	V	1791	A
27	V	1792	G
27	V	1793	G
27	V	1802	A
27	V	1810	G
27	V	1811	C
27	V	1813	A
27	V	1829	C
27	V	1830	G
27	V	1837	U
27	V	1838	A
27	V	1843	G
27	V	1845	A
27	V	1846	G
27	V	1850	A
27	V	1858	A
27	V	1862	C
27	V	1864	G
27	V	1877	A
27	V	1883	A
27	V	1885	A
27	V	1887	G
27	V	1891	G
27	V	1895	A
27	V	1899	U

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Mol	Chain	Res	Type
27	V	1904	G
27	V	1915	U
27	V	1935	G
27	V	1943	C
27	V	1948	A
27	V	1958	G
27	V	1959	G
27	V	1965	A
27	V	1966	A
27	V	1967	A
27	V	1968	U
27	V	1969	U
27	V	1973	U
27	V	1984	U
27	V	1992	C
27	V	1993	G
27	V	1996	C
27	V	1999	A
27	V	2000	A
27	V	2001	G
27	V	2010	A
27	V	2020	U
27	V	2022	U
27	V	2023	C
27	V	2025	C
27	V	2026	A
27	V	2050	G
27	V	2051	U
27	V	2052	A
27	V	2054	C
27	V	2059	A
27	V	2060	A
27	V	2061	G
27	V	2062	A
27	V	2064	G
27	V	2072	C
27	V	2079	C
27	V	2084	C
27	V	2085	G
27	V	2089	A
27	V	2090	G
27	V	2098	G

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Mol	Chain	Res	Type
27	V	2114	C
27	V	2121	U
27	V	2122	G
27	V	2123	A
27	V	2125	U
27	V	2128	U
27	V	2131	U
27	V	2134	A
27	V	2135	G
27	V	2136	C
27	V	2145	G
27	V	2146	A
27	V	2147	U
27	V	2148	A
27	V	2149	G
27	V	2154	G
27	V	2156	G
27	V	2161	G
27	V	2162	G
27	V	2167	C
27	V	2174	C
27	V	2177	G
27	V	2182	G
27	V	2184	U
27	V	2185	G
27	V	2187	A
27	V	2188	G
27	V	2189	G
27	V	2197	G
27	V	2199	G
27	V	2200	A
27	V	2201	U
27	V	2203	C
27	V	2204	U
27	V	2205	A
27	V	2206	C
27	V	2208	C
27	V	2219	G
27	V	2226	U
27	V	2227	A
27	V	2228	A
27	V	2229	C

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Mol	Chain	Res	Type
27	V	2230	C
27	V	2231	C
27	V	2232	A
27	V	2233	C
27	V	2234	C
27	V	2245	G
27	V	2246	G
27	V	2252	A
27	V	2254	A
27	V	2255	C
27	V	2267	G
27	V	2268	G
27	V	2280	G
27	V	2296	A
27	V	2307	A
27	V	2312	C
27	V	2316	A
27	V	2317	A
27	V	2325	U
27	V	2328	G
27	V	2331	U
27	V	2333	G
27	V	2334	U
27	V	2335	U
27	V	2336	G
27	V	2337	G
27	V	2338	A
27	V	2343	A
27	V	2344	U
27	V	2347	G
27	V	2348	C
27	V	2349	A
27	V	2350	G
27	V	2351	A
27	V	2356	A
27	V	2363	C
27	V	2364	A
27	V	2368	G
27	V	2376	C
27	V	2378	G
27	V	2379	C
27	V	2401	G

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Mol	Chain	Res	Type
27	V	2412	G
27	V	2414	C
27	V	2431	U
27	V	2432	C
27	V	2435	C
27	V	2452	U
27	V	2453	C
27	V	2454	A
27	V	2455	A
27	V	2457	G
27	V	2458	G
27	V	2459	A
27	V	2460	U
27	V	2469	C
27	V	2470	C
27	V	2477	A
27	V	2488	A
27	V	2504	C
27	V	2505	A
27	V	2507	A
27	V	2511	A
27	V	2523	G
27	V	2525	C
27	V	2527	C
27	V	2531	G
27	V	2532	A
27	V	2534	G
27	V	2535	U
27	V	2547	A
27	V	2549	C
27	V	2558	G
27	V	2564	G
27	V	2583	U
27	V	2584	U
27	V	2593	A
27	V	2596	G
27	V	2601	A
27	V	2602	C
27	V	2605	G
27	V	2611	G
27	V	2613	U
27	V	2614	U

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Mol	Chain	Res	Type
27	V	2631	A
27	V	2632	G
27	V	2638	U
27	V	2639	C
27	V	2642	U
27	V	2644	U
27	V	2659	G
27	V	2675	C
27	V	2690	G
27	V	2711	G
27	V	2718	U
27	V	2720	C
27	V	2743	G
27	V	2755	U
27	V	2762	A
27	V	2763	C
27	V	2764	G
27	V	2765	G
27	V	2773	G
27	V	2777	A
27	V	2784	C
27	V	2785	U
27	V	2794	A
27	V	2806	G
27	V	2807	A
27	V	2808	U
27	V	2818	C
27	V	2823	C
27	V	2824	G
27	V	2826	A
27	V	2831	A
27	V	2845	A
27	V	2859	G
27	V	2860	A
27	V	2867	U
27	V	2868	G
27	V	2884	G
27	V	2892	G
27	V	2897	G
27	V	2899	C
27	V	2900	A
27	V	2901	G

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Mol	Chain	Res	Type
27	V	2905	C
27	V	2916	A
27	V	2918	G
31	a	10	A
31	a	11	G
31	a	31	A
31	a	32	C
31	a	33	G
31	a	34	A
31	a	41	G
31	a	49	C
31	a	50	C
31	a	53	A
31	a	75	G
31	a	77	U
31	a	78	G
31	a	84	U
31	a	85	U
31	a	86	G
31	a	87	C
31	a	89	C
31	a	90	C
31	a	93	G
31	a	99	A
31	a	114	A
31	a	119	C
31	a	120	A
31	a	128	A
31	a	129	A
31	a	130	C
31	a	136	U
31	a	142	A
31	a	143	C
31	a	153	U
31	a	154	C
31	a	158	G
31	a	162	C
31	a	172	U
31	a	177	G
31	a	181	G
31	a	182	U
31	a	189	A

Continued on next page...

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Mol	Chain	Res	Type
31	a	197	G
31	a	208	A
31	a	209	A
31	a	211	A
31	a	218	U
31	a	219	U
31	a	221	G
31	a	249	G
31	a	253	U
31	a	255	G
31	a	258	A
31	a	259	G
31	a	274	G
31	a	275	C
31	a	287	A
31	a	297	G
31	a	314	A
31	a	336	C
31	a	337	A
31	a	338	C
31	a	340	G
31	a	352	A
31	a	354	G
31	a	360	C
31	a	362	G
31	a	373	U
31	a	375	U
31	a	380	C
31	a	381	A
31	a	385	G
31	a	392	G
31	a	396	G
31	a	405	A
31	a	414	G
31	a	419	A
31	a	420	U
31	a	421	G
31	a	429	U
31	a	430	C
31	a	435	C
31	a	436	G
31	a	437	U

Continued on next page...

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Mol	Chain	Res	Type
31	a	448	U
31	a	456	A
31	a	460	A
31	a	461	C
31	a	466	G
31	a	474	A
31	a	475	A
31	a	476	U
31	a	477	A
31	a	478	G
31	a	481	C
31	a	485	A
31	a	487	C
31	a	488	U
31	a	489	U
31	a	490	G
31	a	491	A
31	a	494	G
31	a	502	C
31	a	504	A
31	a	506	A
31	a	508	A
31	a	518	A
31	a	520	C
31	a	526	G
31	a	527	C
31	a	530	G
31	a	536	G
31	a	541	A
31	a	542	A
31	a	556	A
31	a	564	C
31	a	568	A
31	a	571	U
31	a	573	U
31	a	582	A
31	a	585	G
31	a	586	G
31	a	590	G
31	a	597	G
31	a	605	A
31	a	641	G

Continued on next page...

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Mol	Chain	Res	Type
31	a	642	U
31	a	643	C
31	a	651	A
31	a	662	U
31	a	696	A
31	a	732	U
31	a	733	G
31	a	756	U
31	a	757	A
31	a	758	A
31	a	764	G
31	a	787	G
31	a	802	U
31	a	803	A
31	a	824	A
31	a	826	C
31	a	841	G
31	a	849	G
31	a	853	C
31	a	855	G
31	a	856	C
31	a	882	A
31	a	883	A
31	a	885	C
31	a	924	A
31	a	943	G
31	a	944	C
31	a	945	A
31	a	950	C
31	a	963	G
31	a	964	G
31	a	966	U
31	a	968	A
31	a	969	A
31	a	970	U
31	a	979	A
31	a	981	G
31	a	985	A
31	a	986	G
31	a	987	A
31	a	993	A
31	a	999	U

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Mol	Chain	Res	Type
31	a	1002	U
31	a	1003	G
31	a	1007	U
31	a	1008	C
31	a	1009	C
31	a	1010	U
31	a	1011	C
31	a	1012	U
31	a	1014	A
31	a	1015	C
31	a	1017	A
31	a	1019	C
31	a	1023	G
31	a	1024	A
31	a	1028	A
31	a	1030	G
31	a	1033	G
31	a	1035	C
31	a	1036	C
31	a	1039	U
31	a	1041	C
31	a	1042	G
31	a	1046	G
31	a	1047	C
31	a	1050	A
31	a	1053	G
31	a	1058	G
31	a	1064	C
31	a	1075	U
31	a	1088	U
31	a	1089	G
31	a	1095	U
31	a	1104	G
31	a	1105	U
31	a	1111	A
31	a	1112	A
31	a	1118	G
31	a	1122	C
31	a	1134	G
31	a	1135	U
31	a	1136	U
31	a	1140	A

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Mol	Chain	Res	Type
31	a	1142	C
31	a	1145	U
31	a	1148	G
31	a	1149	U
31	a	1153	G
31	a	1161	A
31	a	1166	A
31	a	1168	U
31	a	1176	A
31	a	1178	A
31	a	1190	G
31	a	1192	U
31	a	1193	G
31	a	1205	A
31	a	1206	A
31	a	1211	U
31	a	1221	U
31	a	1222	A
31	a	1223	U
31	a	1237	C
31	a	1259	A
31	a	1261	A
31	a	1267	G
31	a	1278	A
31	a	1279	G
31	a	1289	A
31	a	1294	A
31	a	1295	C
31	a	1296	A
31	a	1308	A
31	a	1314	G
31	a	1326	C
31	a	1329	C
31	a	1330	U
31	a	1331	C
31	a	1341	A
31	a	1347	G
31	a	1355	A
31	a	1366	A
31	a	1370	G
31	a	1372	A
31	a	1373	U

Continued on next page...

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Mol	Chain	Res	Type
31	a	1377	G
31	a	1387	C
31	a	1407	A
31	a	1451	A
31	a	1455	A
31	a	1460	U
31	a	1462	U
31	a	1463	A
31	a	1464	G
31	a	1490	A
31	a	1500	U
31	a	1502	A
31	a	1503	A
31	a	1516	U
31	a	1527	G
31	a	1539	G
31	a	1540	G
53	A	33	A
53	A	34	A
53	A	35	A
53	A	37	G
53	A	38	A
53	A	39	U
53	A	40	G
53	A	43	G
53	A	45	C
53	A	46	A
53	A	47	G
53	A	49	A

All (73) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	B	31	G
7	B	37	A
7	B	48	G
7	B	49	G
13	H	47	U
13	H	55	U
27	V	88	G
27	V	183	A
27	V	252	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	V	347	G
27	V	411	G
27	V	441	C
27	V	444	U
27	V	549	A
27	V	554	U
27	V	689	A
27	V	772	G
27	V	810	G
27	V	905	G
27	V	1093	G
27	V	1172	A
27	V	1243	A
27	V	1244	A
27	V	1250	G
27	V	1264	G
27	V	1269	A
27	V	1275	G
27	V	1305	A
27	V	1351	U
27	V	1435	U
27	V	1448	U
27	V	1507	U
27	V	1525	G
27	V	1527	C
27	V	1529	G
27	V	1530	G
27	V	1535	U
27	V	1565	U
27	V	1567	U
27	V	1570	U
27	V	1631	A
27	V	1726	G
27	V	1757	G
27	V	1784	A
27	V	1828	G
27	V	1882	A
27	V	1914	A
27	V	1972	U
27	V	1991	C
27	V	2009	G
27	V	2022	U

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Mol	Chain	Res	Type
27	V	2127	U
27	V	2155	A
27	V	2205	A
27	V	2254	A
27	V	2316	A
27	V	2330	A
27	V	2336	G
27	V	2452	U
27	V	2454	A
27	V	2468	A
27	V	2510	G
27	V	2534	G
27	V	2631	A
27	V	2710	C
27	V	2805	A
27	V	2883	C
27	V	2904	A
53	A	33	A
53	A	34	A
53	A	38	A
53	A	39	U
53	A	45	C

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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

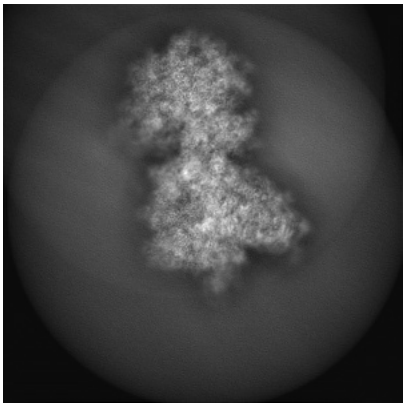
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-14157. These allow visual inspection of the internal detail of the map and identification of artifacts.

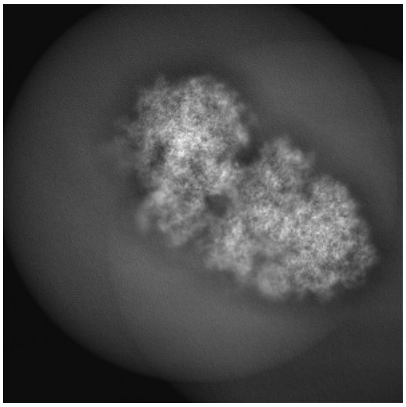
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

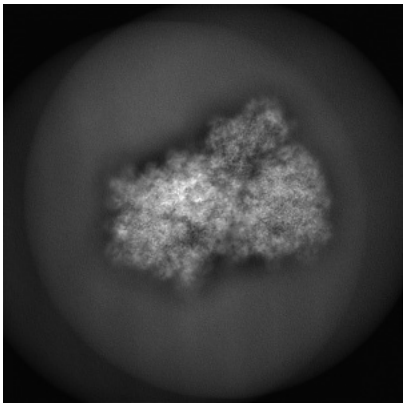
6.1.1 Primary map



X



Y

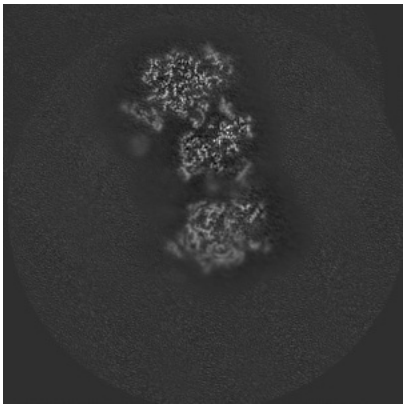


Z

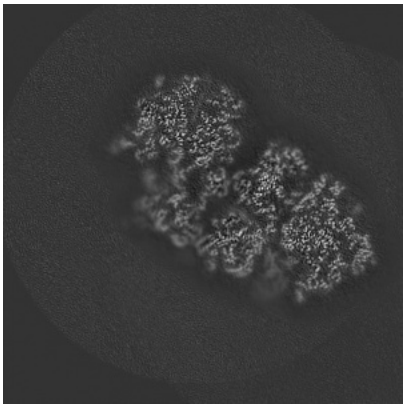
The images above show the map projected in three orthogonal directions.

6.2 Central slices

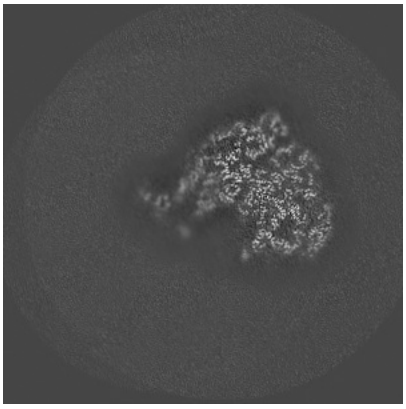
6.2.1 Primary map



X Index: 184



Y Index: 184

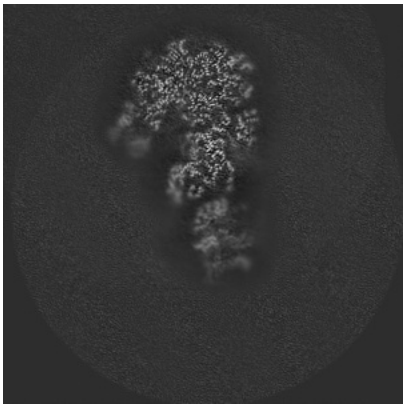


Z Index: 184

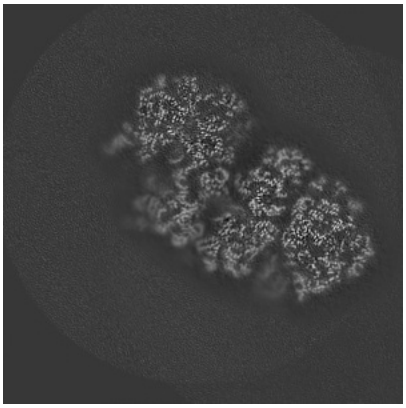
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

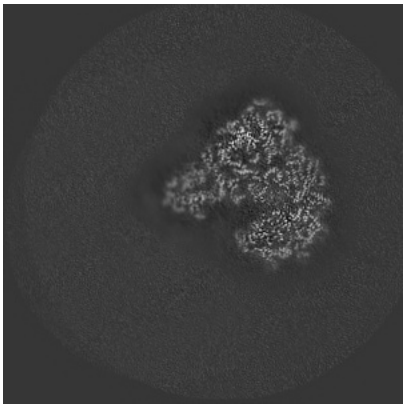
6.3.1 Primary map



X Index: 163



Y Index: 187

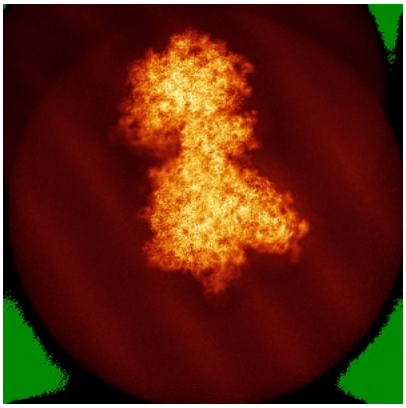


Z Index: 169

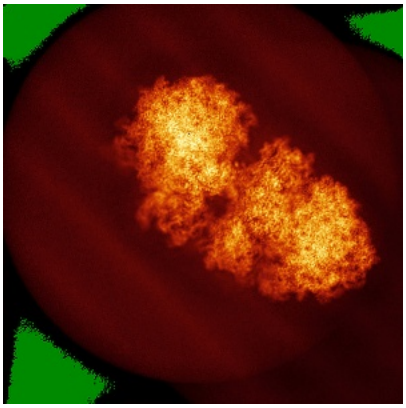
The images above show the largest variance slices of the map in three orthogonal directions.

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

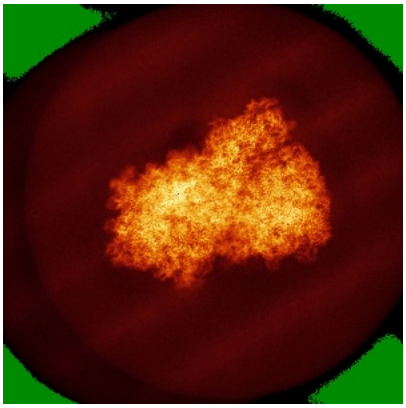
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

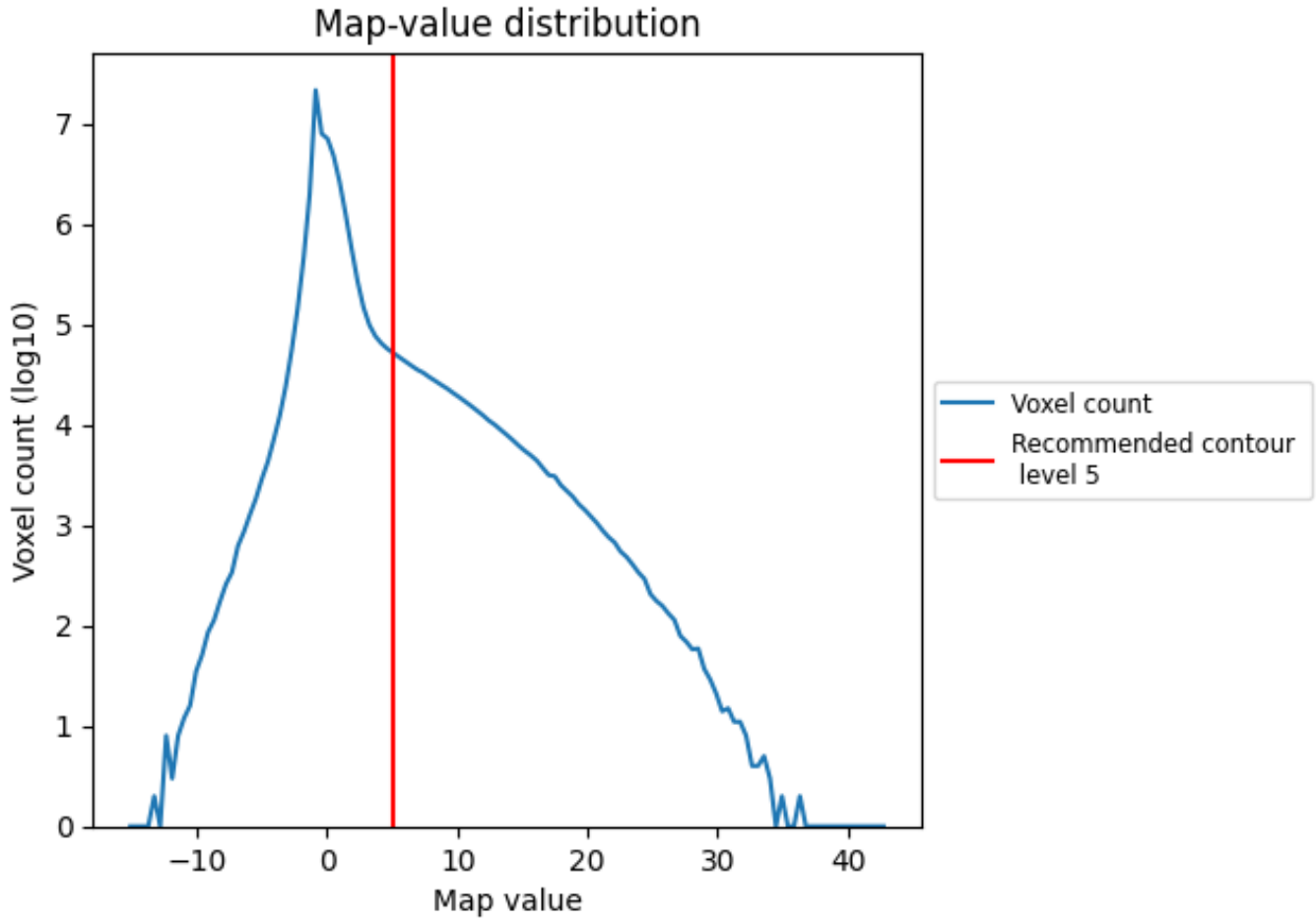
6.6 Mask visualisation (i)

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

7 Map analysis

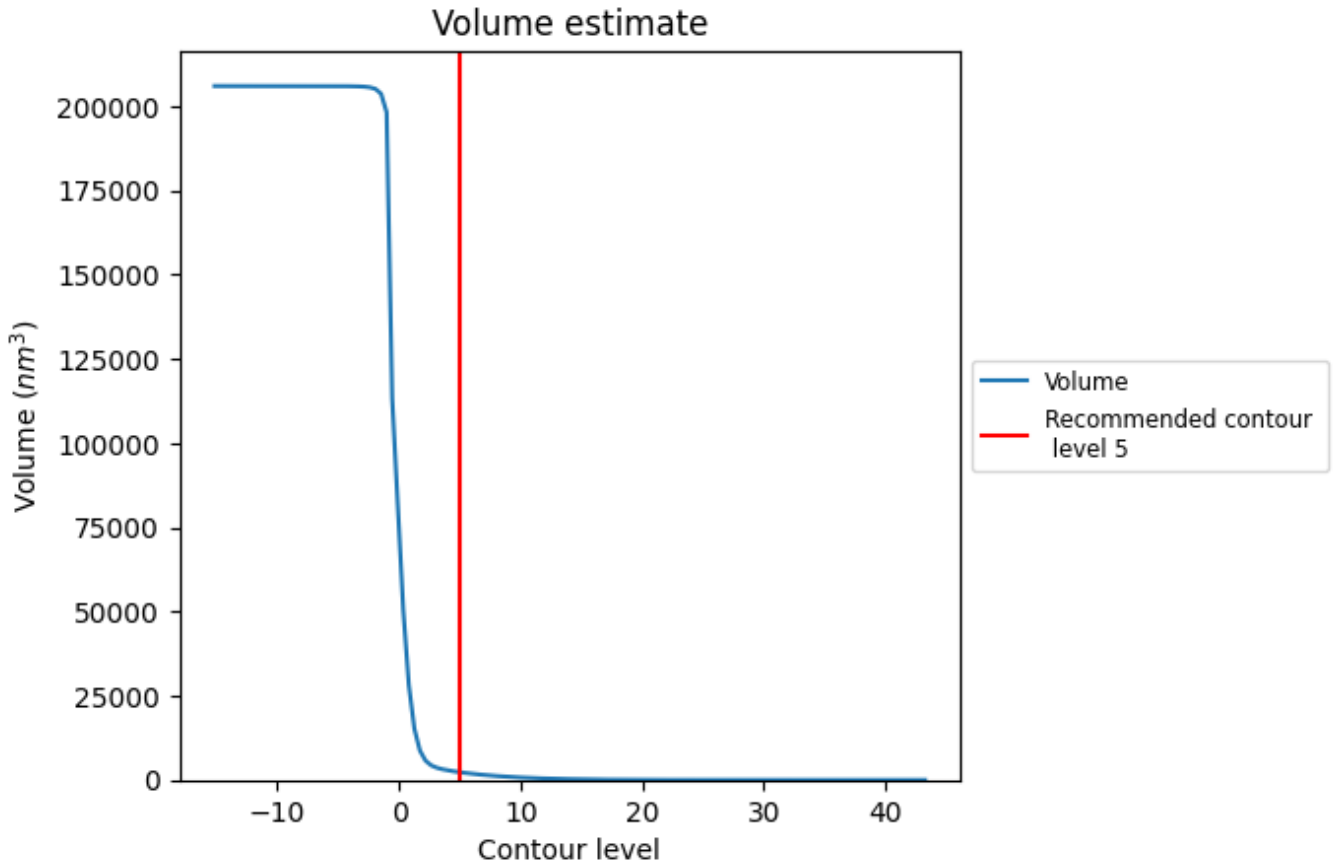
This section contains the results of statistical analysis of the map.

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.

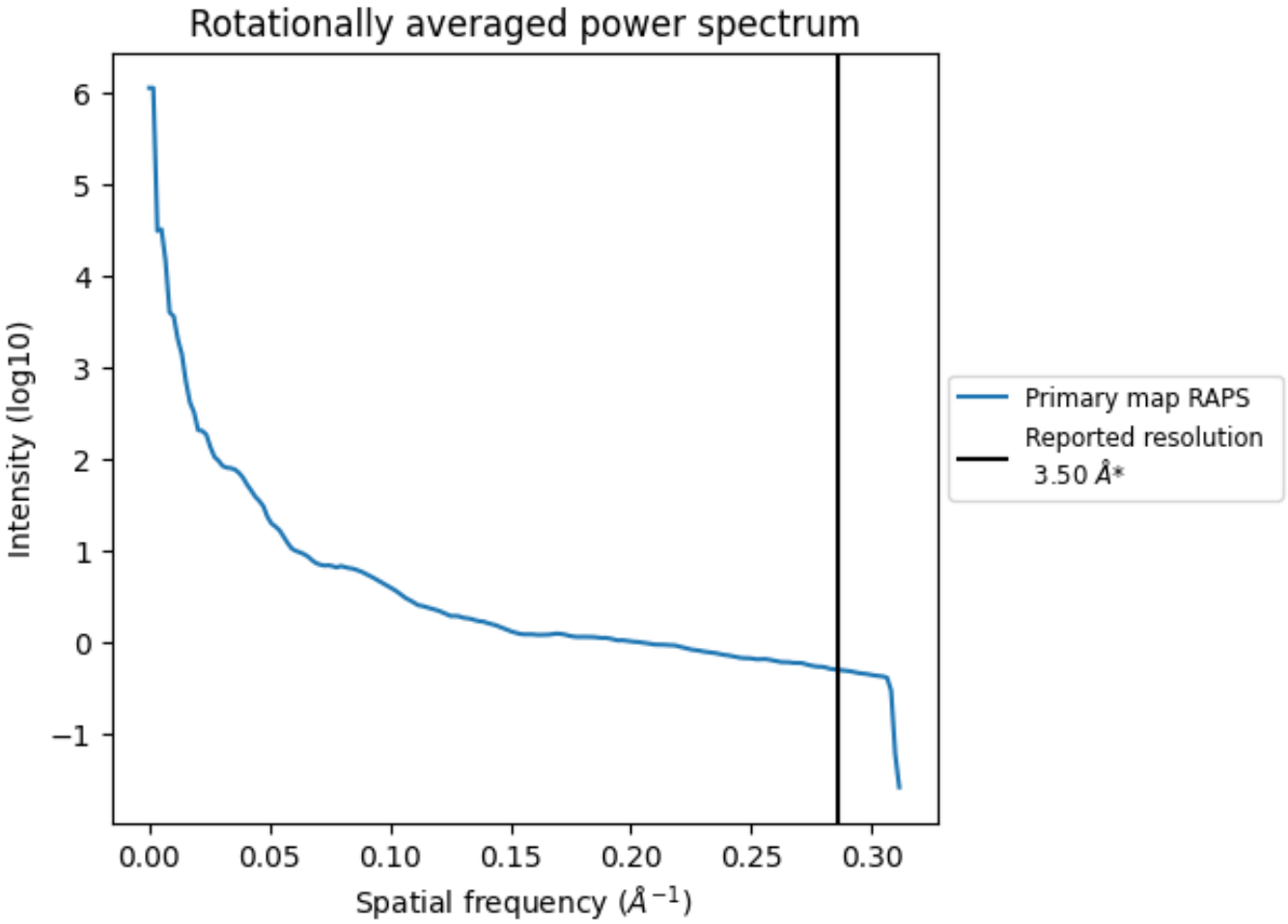
7.2 Volume estimate



The volume at the recommended contour level is 2302 nm^3; this corresponds to an approximate mass of 2079 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

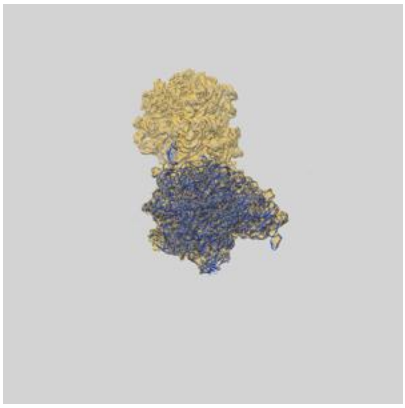
8 Fourier-Shell correlation

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

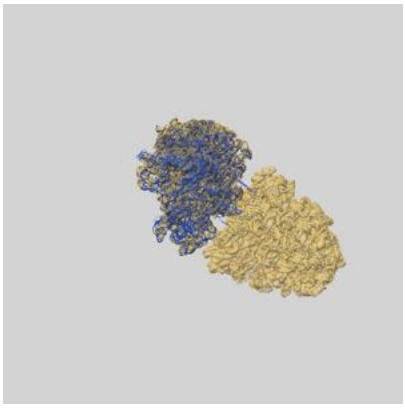
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-14157 and PDB model 7QV1. Per-residue inclusion information can be found in section 3 on page 13.

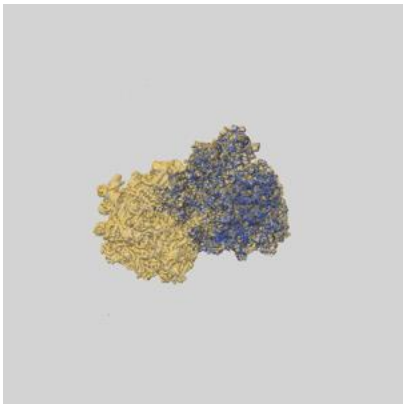
9.1 Map-model overlay



X



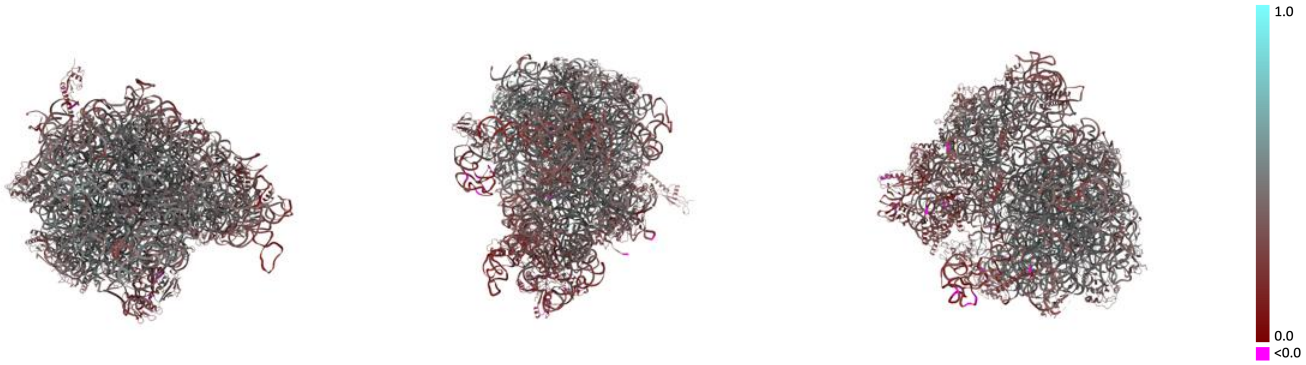
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

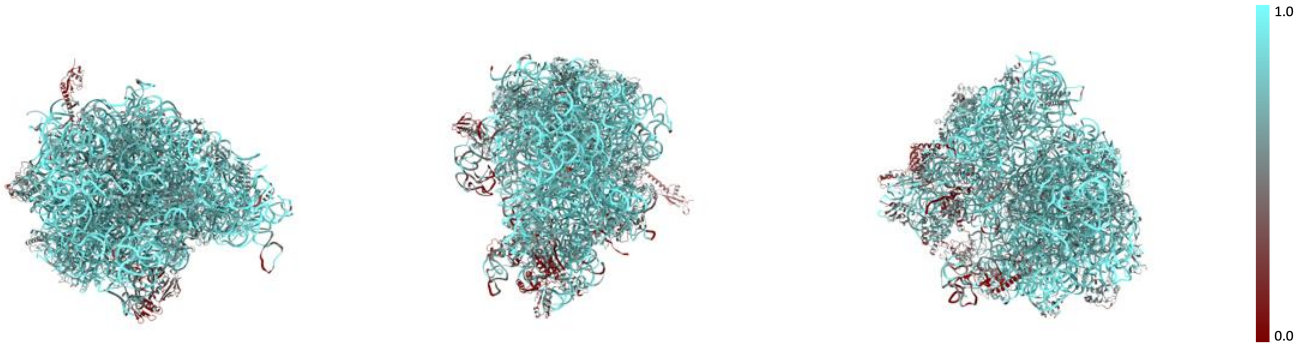
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

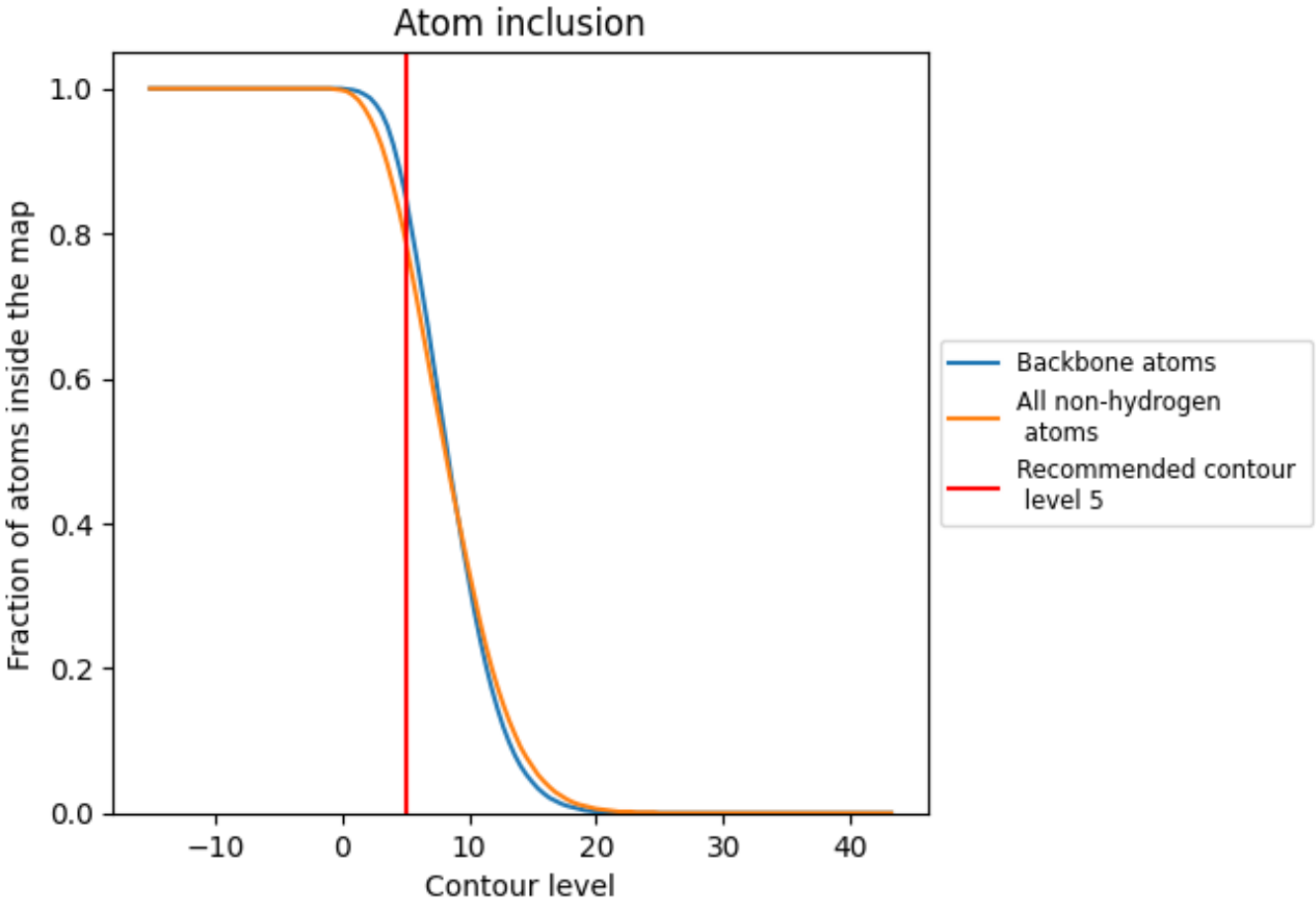
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (5).

9.4 Atom inclusion (i)



At the recommended contour level, 85% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7890	0.3970
0	0.7630	0.4840
1	0.6850	0.4460
2	0.8090	0.5000
3	0.7940	0.5060
4	0.6520	0.4430
6	0.2470	0.2700
A	0.3130	0.2370
B	0.8800	0.3830
C	0.6950	0.4620
D	0.7130	0.4770
E	0.6390	0.4250
F	0.4020	0.3070
G	0.3290	0.3280
H	0.8210	0.3310
I	0.0670	0.1630
J	0.7480	0.4690
K	0.6860	0.4570
L	0.6700	0.4510
M	0.6470	0.4270
N	0.6910	0.4260
O	0.6400	0.3770
P	0.6700	0.4260
Q	0.7680	0.4450
R	0.6560	0.4430
S	0.6960	0.4580
T	0.6820	0.4380
U	0.6540	0.4170
V	0.8730	0.4300
W	0.7270	0.4700
X	0.1740	0.2560
Y	0.6580	0.3690
Z	0.6670	0.4320
a	0.8900	0.3720
b	0.1360	0.2300

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Chain	Atom inclusion	Q-score
c	0.1380	0.2590
d	0.6180	0.3220
e	0.6780	0.4020
f	0.5460	0.3340
g	0.5330	0.2620
h	0.7340	0.3970
i	0.4990	0.2050
j	0.3570	0.2350
k	0.5220	0.3260
l	0.6730	0.3890
m	0.4040	0.2180
n	0.1670	0.2750
o	0.7150	0.3530
p	0.7010	0.3410
q	0.6670	0.3650
r	0.5780	0.3690
s	0.2330	0.2030
t	0.6750	0.3040
u	0.7110	0.4660