



Full wwPDB EM Validation Report ⓘ

Sep 21, 2026 – 12:50 PM EDT

PDB ID : 9YDE / pdb_00009yde
EMDB ID : EMD-72802
Title : Eukaryotic 80S ribosome with P/P tRNA from uL16 P-site loop mutants in bypass condition
Authors : Guan, K.; Taylor, D.W.
Deposited on : 2025-09-22
Resolution : 2.82 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:

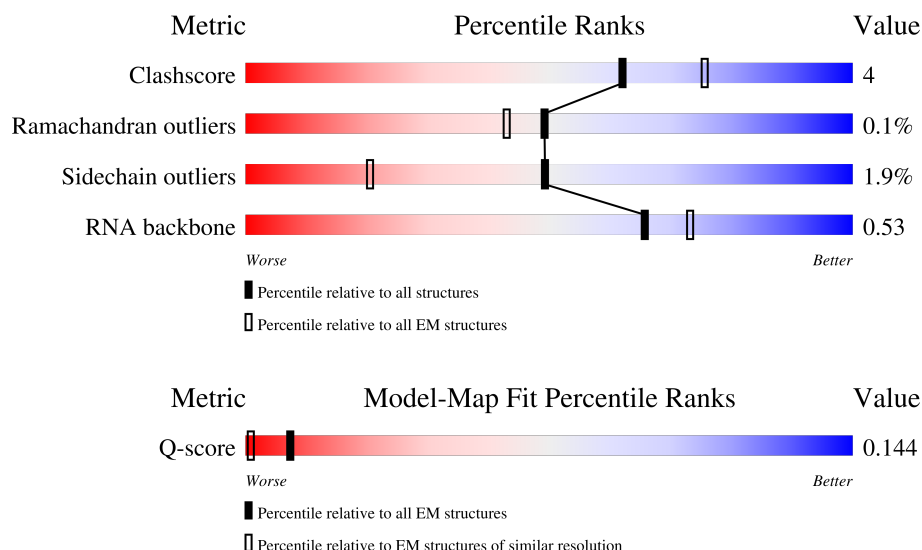
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.82 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	11795 (2.32 - 3.32)

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

Mol	Chain	Length	Quality of chain
1	A	3396	
2	B	121	
3	C	158	

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Mol	Chain	Length	Quality of chain
4	D	10	
5	E	1800	
6	LD	254	
7	LE	387	
8	LF	362	
9	LG	297	
10	LH	176	
11	LI	244	
12	LJ	256	
13	LK	191	
14	LL	210	
15	LM	174	
16	LN	199	
17	LO	138	
18	LP	204	
19	LQ	199	
20	LR	184	
21	LS	186	
22	LT	189	
23	LU	172	
24	LV	160	
25	LW	121	
26	LX	137	
27	LY	155	
28	LZ	142	

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Mol	Chain	Length	Quality of chain
29	La	127	
30	Lb	136	
31	Lc	149	
32	Ld	59	
33	Le	105	
34	Lf	113	
35	Lg	130	
36	Lh	107	
37	Li	121	
38	Lj	120	
39	Lk	100	
40	Ll	88	
41	Lm	78	
42	Ln	51	
43	Lo	128	
44	Lp	25	
45	Lq	106	
46	Lr	92	
47	SA	240	
48	SB	225	
49	SC	105	
50	SD	143	
51	SE	142	
52	SF	143	
53	SG	136	

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Mol	Chain	Length	Quality of chain
54	SH	146	
55	SI	144	
56	SJ	121	
57	SK	108	
58	SL	67	
59	SM	56	
60	SN	152	
61	SO	319	
62	SP	252	
63	SQ	255	
64	SR	254	
65	SS	261	
66	ST	236	
67	SU	190	
68	SV	200	
69	SW	197	
70	SX	156	
71	SY	151	
72	SZ	138	
73	Sa	87	
74	Sb	130	
75	Sc	145	
76	Sd	135	
77	Se	119	
78	Sf	82	

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Mol	Chain	Length	Quality of chain
79	Sg	63	54% 67% 19% • 13%
80	n	75	73% 36% 43% 9% 12%

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 192549 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3041	Total	C	N	O	P	0	0
			65056	29059	11741	21215	3041		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	493	U	G	conflict	GB 831416132

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 8S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	10	Total	C	N	O	P	0	0
			218	98	44	66	10		

- Molecule 5 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	1583	Total	C	N	O	P	0	0
			33767	15095	6008	11081	1583		

- Molecule 6 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LD	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LE	386	Total	C	N	O	S	0	0
			3079	1954	584	533	8		

- Molecule 8 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LF	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LG	292	Total	C	N	O	S	0	0
			2341	1478	408	453	2		

- Molecule 10 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	LH	156	Total	C	N	O	0	0
			1243	803	222	218		

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LI	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LJ	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 13 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LK	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	207	Total	C	N	O	S	0	0
			1686	1071	319	291	5		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LL	?	-	MET	deletion	UNP P41805
LL	?	-	LEU	deletion	UNP P41805
LL	?	-	SER	deletion	UNP P41805
LL	?	-	CYS	deletion	UNP P41805
LL	?	-	ALA	deletion	UNP P41805
LL	?	-	GLY	deletion	UNP P41805
LL	?	-	ALA	deletion	UNP P41805
LL	?	-	ASP	deletion	UNP P41805
LL	?	-	ARG	deletion	UNP P41805
LL	?	-	LEU	deletion	UNP P41805
LL	?	-	GLN	deletion	UNP P41805

- Molecule 15 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	168	Total	C	N	O	S	0	0
			1337	837	250	246	4		

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LN	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	172	Total	C	N	O	S	0	0
			1361	846	273	242			

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	174	Total	C	N	O	S	0	0
			1409	867	304	238			

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	LW	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 27 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	62	Total	C	N	O	S	0	0
			513	330	101	81	1		

- Molecule 28 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LZ	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	La	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Lb	133	Total	C	N	O	0	0
			1066	692	196	178		

- Molecule 31 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 32 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Ld	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Le	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	105	Total	C	N	O	S	0	0
			856	544	163	148	1		

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	126	Total	C	N	O	S	0	0
			1008	638	203	166	1		

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	110	Total	C	N	O	S	0	0
			866	536	176	150	4		

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lj	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lk	98	Total	C	N	O	S	0	0
			761	475	153	131	2		

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 41 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	77	Total	C	N	O	S	0	0
			608	388	114	106			

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 43 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	51	Total	C	N	O	S	0	0
			409	253	85	66	5		

- Molecule 44 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	24	Total	C	N	O	S	0	0
			224	136	61	26	1		

- Molecule 45 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lq	100	Total	C	N	O	S	0	0
			805	506	163	131	5		

- Molecule 46 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lr	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 47 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SA	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 48 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SB	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 49 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SC	83	Total	C	N	O	S	0	0
			708	461	113	132	2		

- Molecule 50 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SD	97	Total	C	N	O	S	0	0
			736	466	127	141	2		

- Molecule 51 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE	116	Total	C	N	O	S	0	0
			905	577	167	154	7		

- Molecule 52 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SF	141	Total	C	N	O		0	0
			1095	702	199	194			

- Molecule 53 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SG	114	Total	C	N	O	S	0	0
			908	573	169	164	2		

- Molecule 54 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SH	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 55 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SI	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 56 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SJ	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 57 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	SK	69	Total	C	N	O	0	0
			558	357	103	98		

- Molecule 58 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SL	62	Total	C	N	O	S	0	0
			486	300	95	90	1		

- Molecule 59 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SM	53	Total	C	N	O	S	0	0
			443	275	92	72	4		

- Molecule 60 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SN	56	Total	C	N	O	S	0	0
			429	271	84	70	4		

- Molecule 61 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SO	311	Total	C	N	O	S	0	0
			2375	1509	408	451	7		

- Molecule 62 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SP	205	Total	C	N	O	S	0	0
			1596	1025	283	286	2		

- Molecule 63 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SQ	225	Total	C	N	O	S	0	0
			1787	1131	328	324	4		

- Molecule 64 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SR	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 65 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SS	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 66 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	ST	218	Total	C	N	O	S	0	0
			1755	1102	337	313	3		

- Molecule 67 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
67	SU	180	Total	C	N	O		
			1451	932	259	260	0	0

- Molecule 68 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SV	186	Total	C	N	O	S		
			1471	913	294	262	2	0	0

- Molecule 69 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SW	184	Total	C	N	O	S		
			1479	935	285	258	1	0	0

- Molecule 70 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SX	141	Total	C	N	O	S		
			1137	730	216	188	3	0	0

- Molecule 71 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SY	150	Total	C	N	O	S		
			1192	759	224	207	2	0	0

- Molecule 72 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SZ	127	Total	C	N	O	S		
			923	568	185	167	3	0	0

- Molecule 73 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Sa	87	Total	C	N	O	S		
			673	415	125	131	2	0	0

- Molecule 74 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sb	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 75 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sc	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 76 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sd	131	Total	C	N	O	S	0	0
			1016	642	192	182			

- Molecule 77 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Se	97	Total	C	N	O	S	0	0
			765	473	160	127	5		

- Molecule 78 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sf	74	Total	C	N	O	S	0	0
			562	353	101	105	3		

- Molecule 79 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sg	55	Total	C	N	O	S	0	0
			437	276	89	71	1		

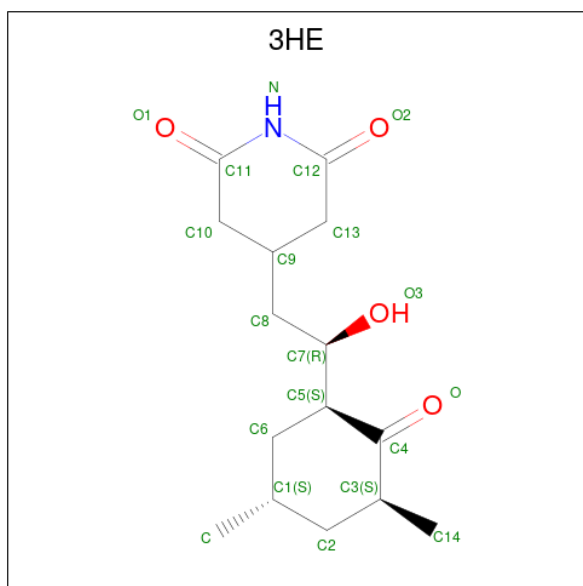
- Molecule 80 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	n	66	Total	C	N	O	P	0	0
			1409	628	257	458	66		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	10	A	G	conflict	GB 176433

- Molecule 81 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: $C_{15}H_{23}NO_4$) (labeled as "Ligand of Interest" by depositor).



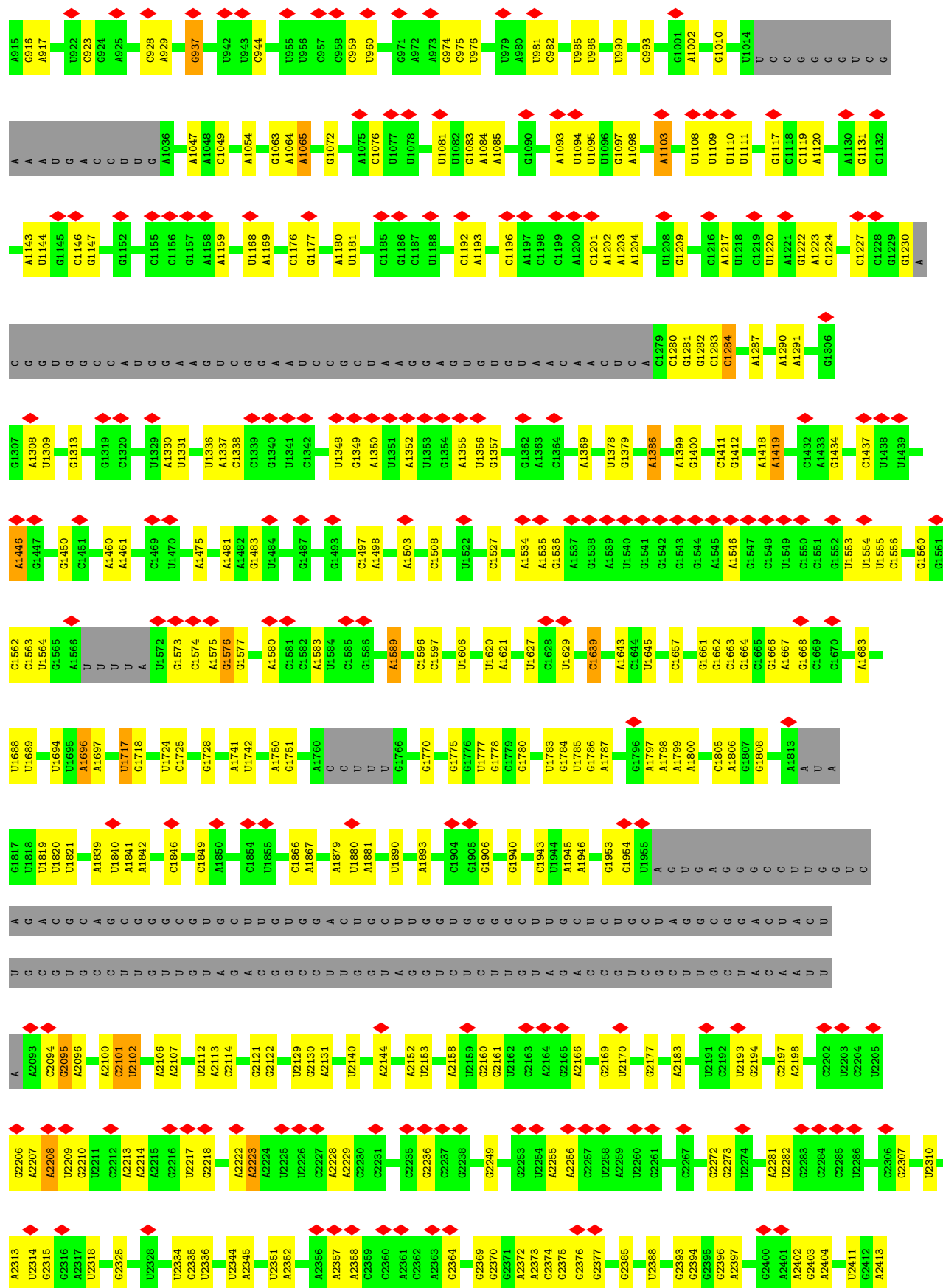
Mol	Chain	Residues	Atoms				AltConf
81	A	1	Total	C	N	O	0
			20	15	1	4	

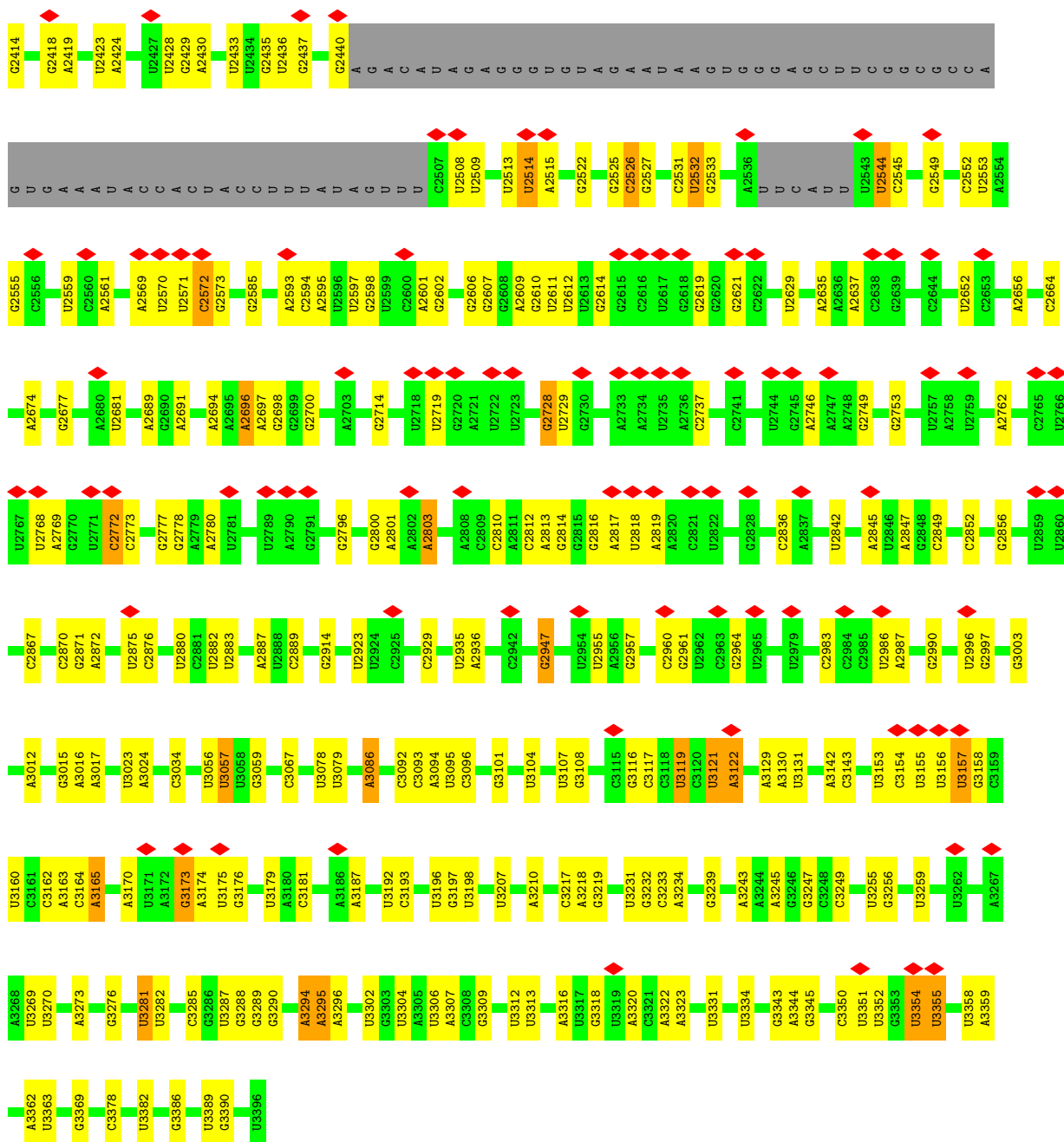
3 Residue-property plots

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

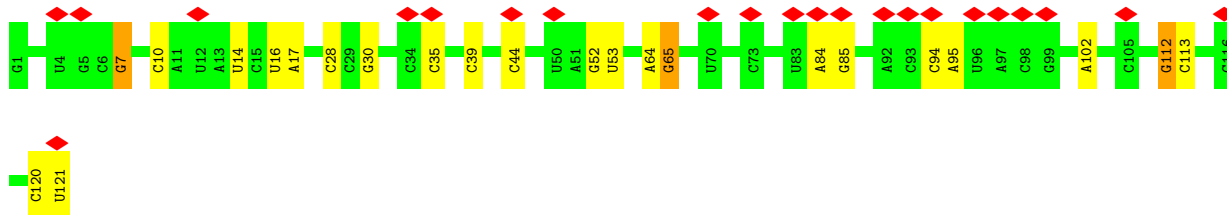
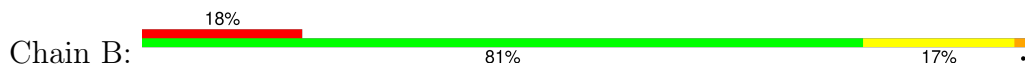
• Molecule 1: 25S RNA



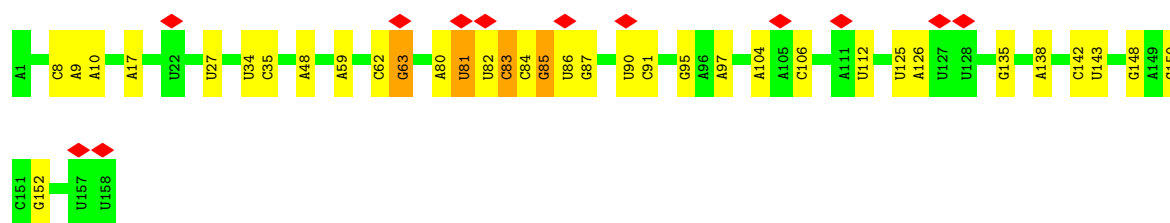


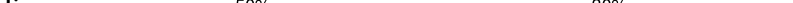


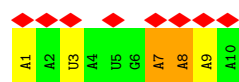
• Molecule 2: 5S RNA

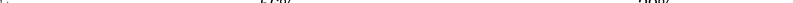


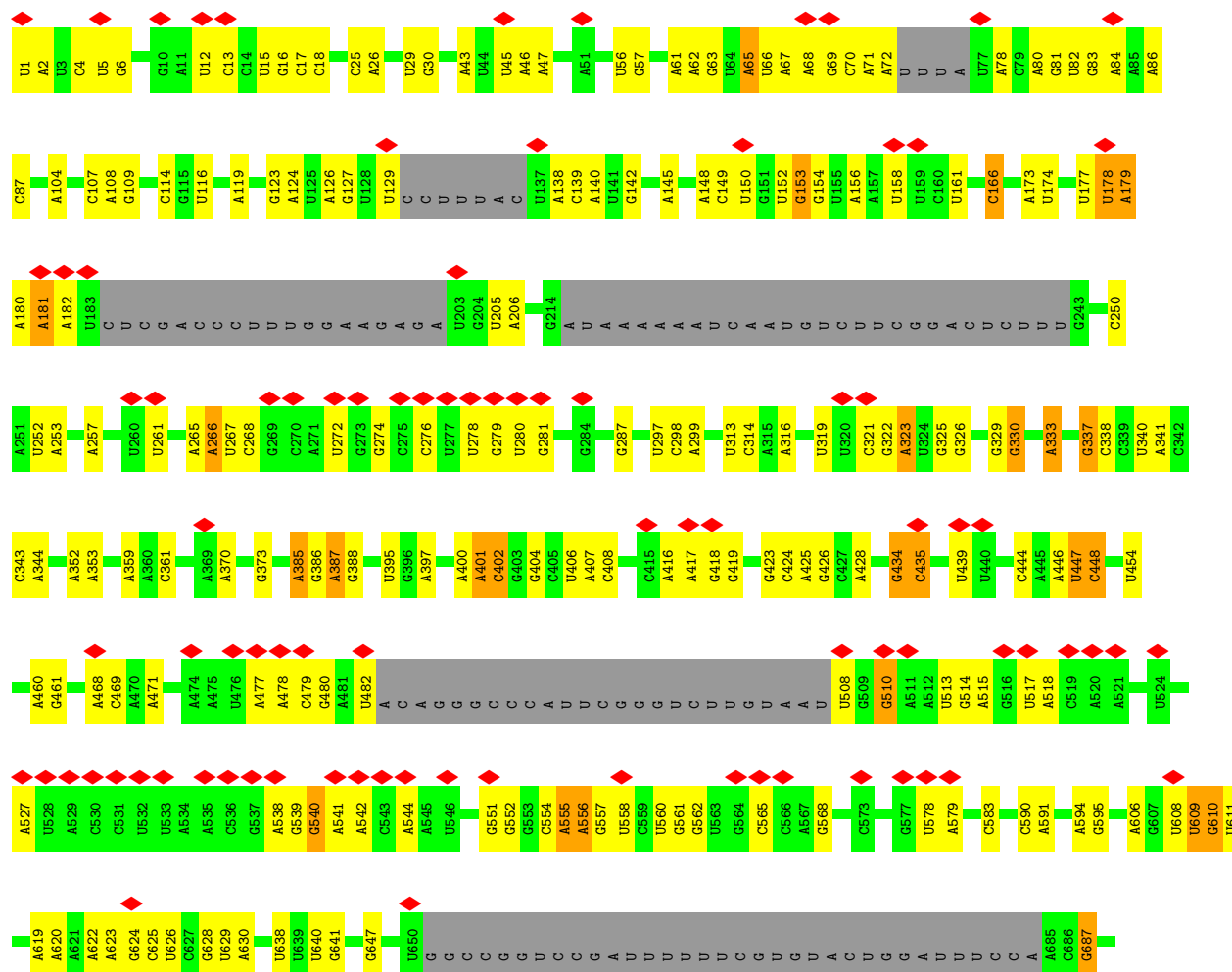
• Molecule 3: 8S RNA



- Chain D: 

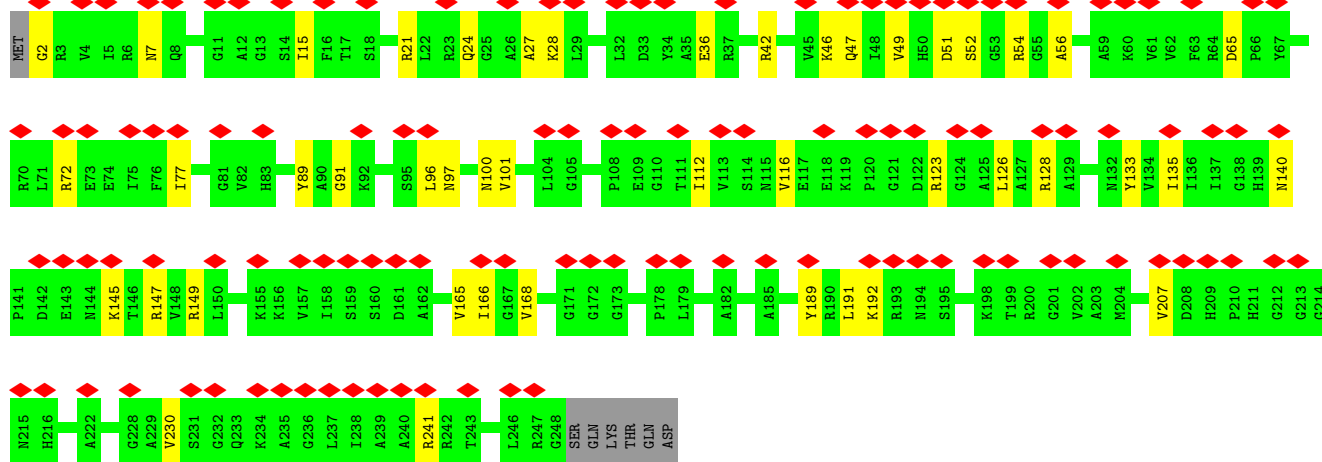


- Chain E: 



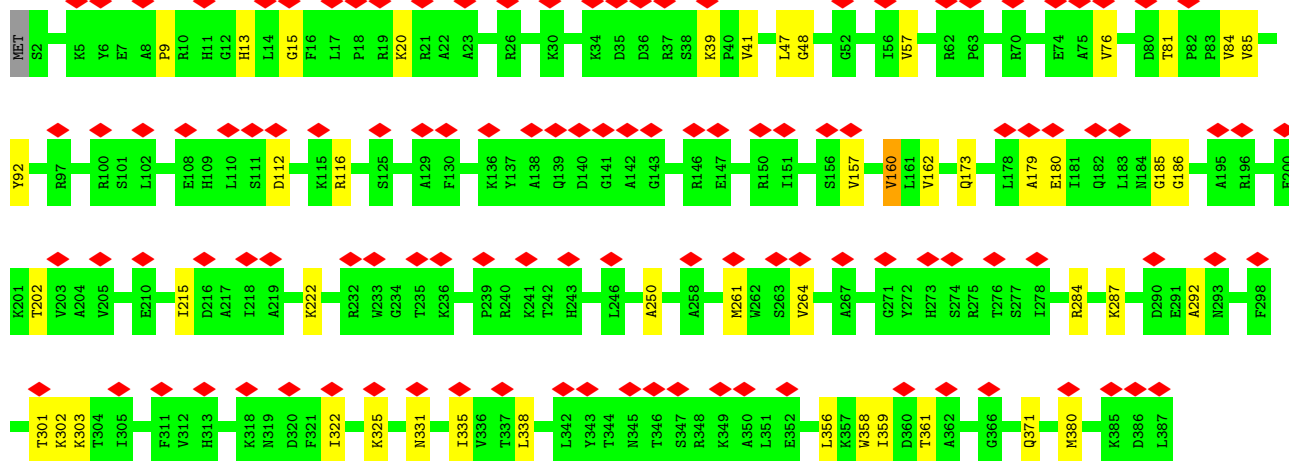


Chain LD:



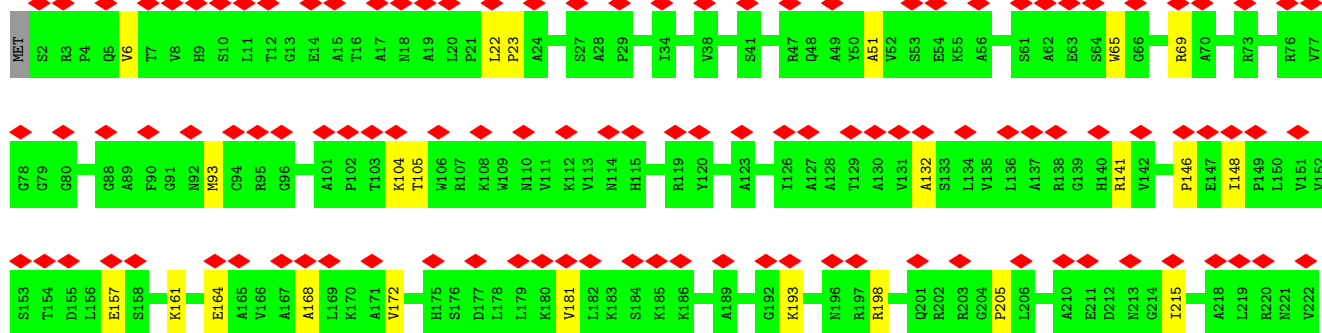
- Molecule 7: 60S ribosomal protein L3

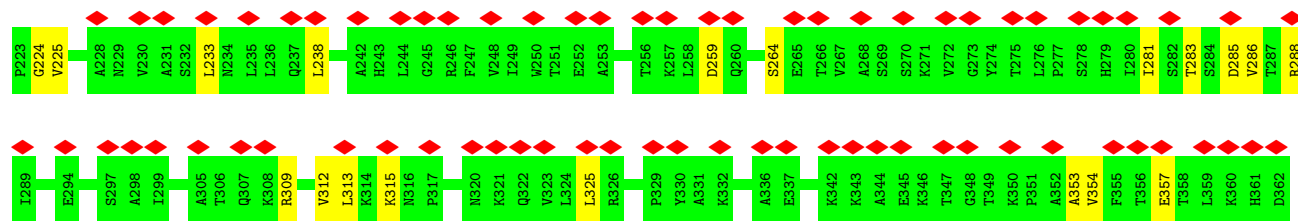
Chain LE:



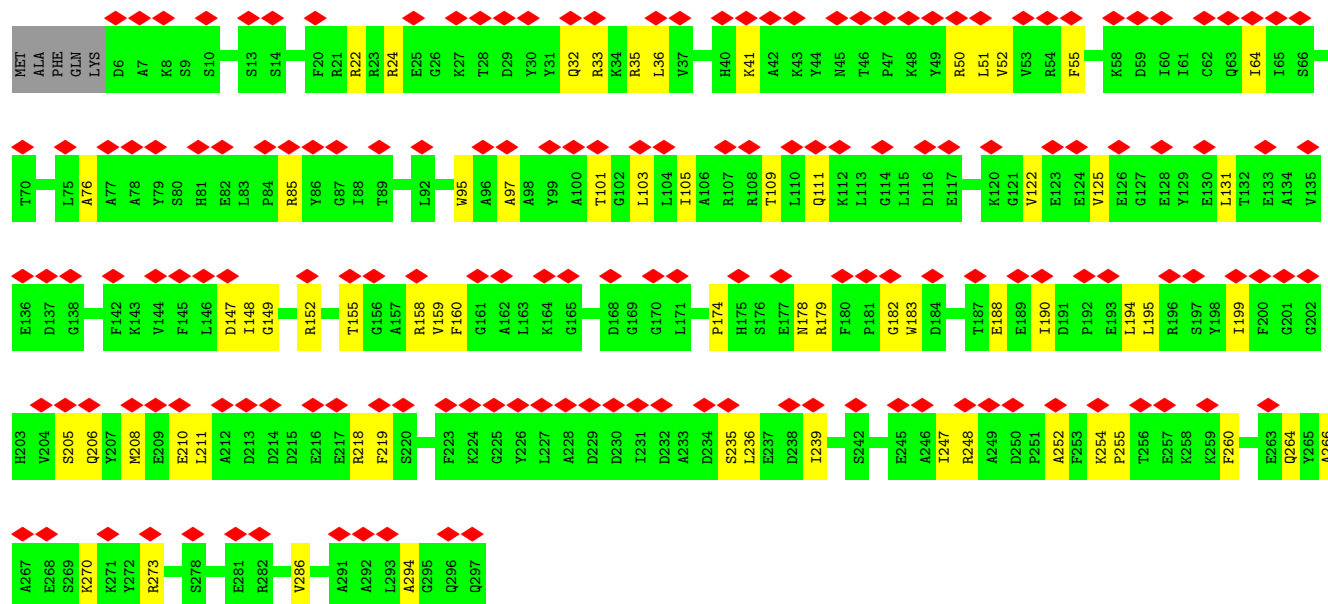
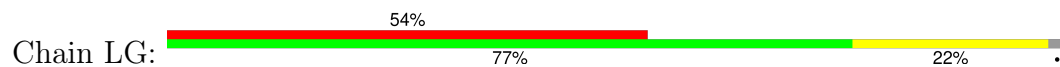
- Molecule 8: 60S ribosomal protein L4-A

Chain LF:

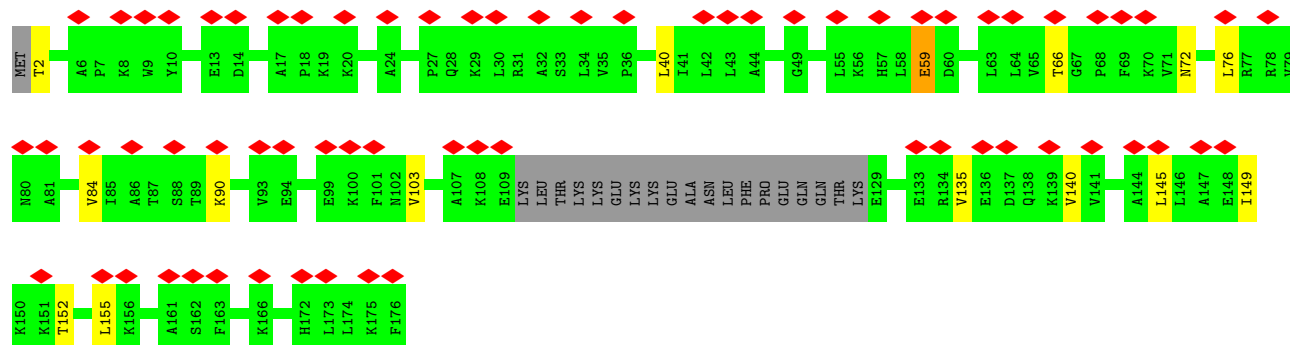
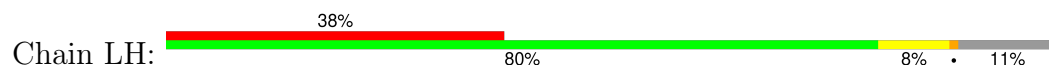




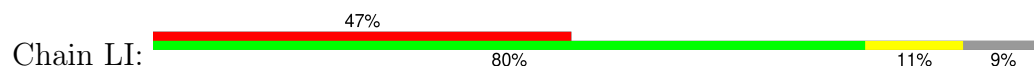
• Molecule 9: 60S ribosomal protein L5

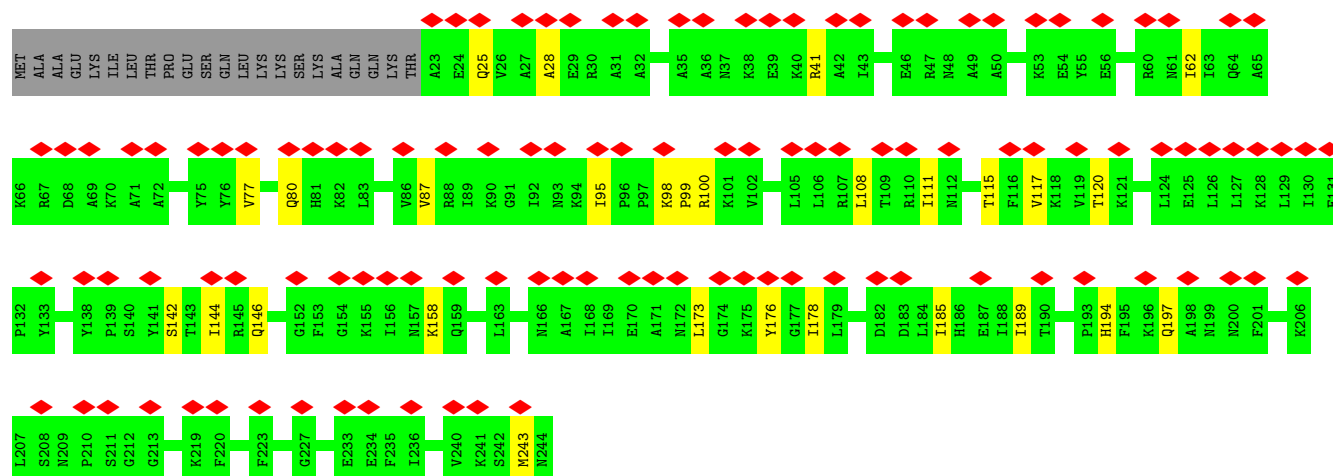


• Molecule 10: Large ribosomal subunit protein eL6B

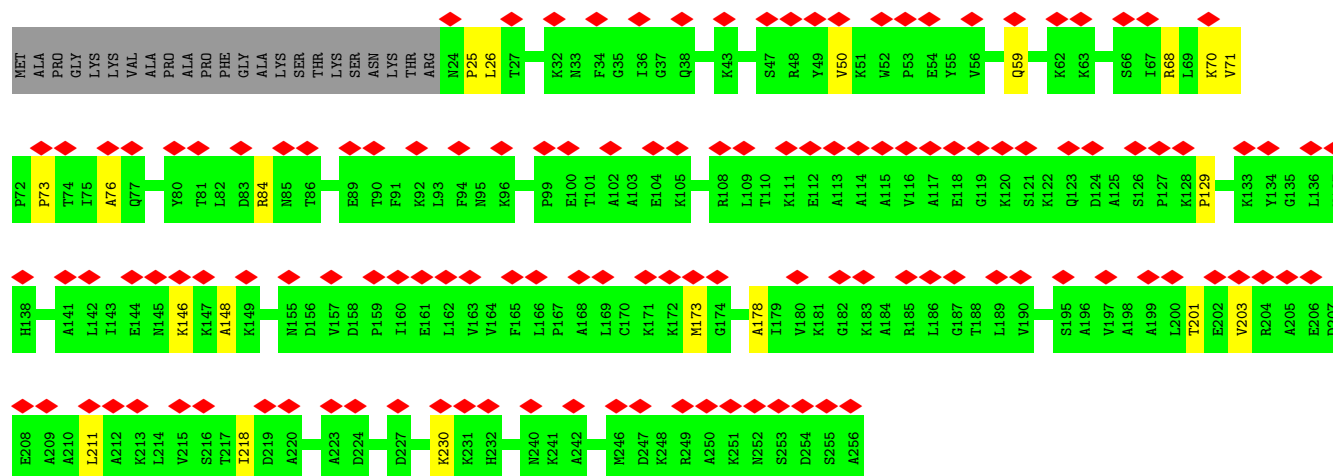
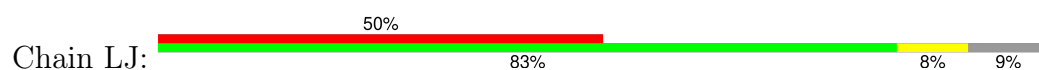


• Molecule 11: 60S ribosomal protein L7-A

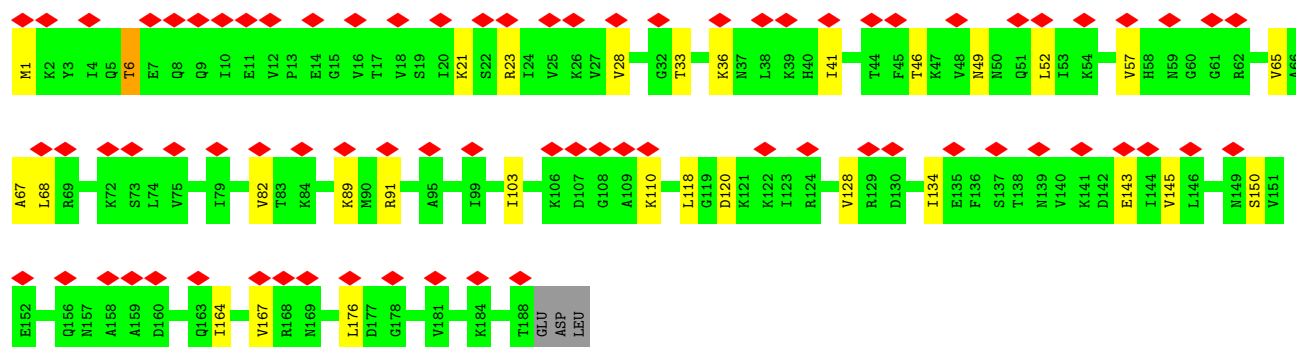
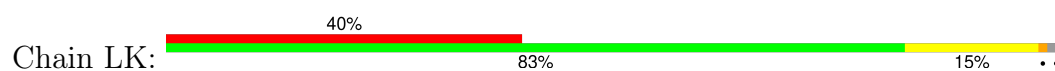




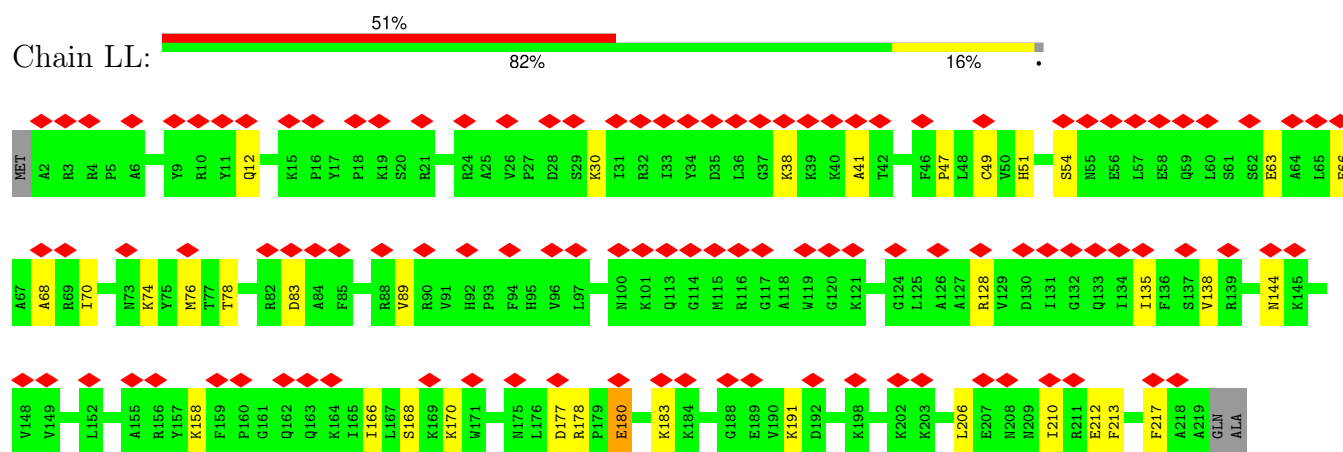
• Molecule 12: 60S ribosomal protein L8-A



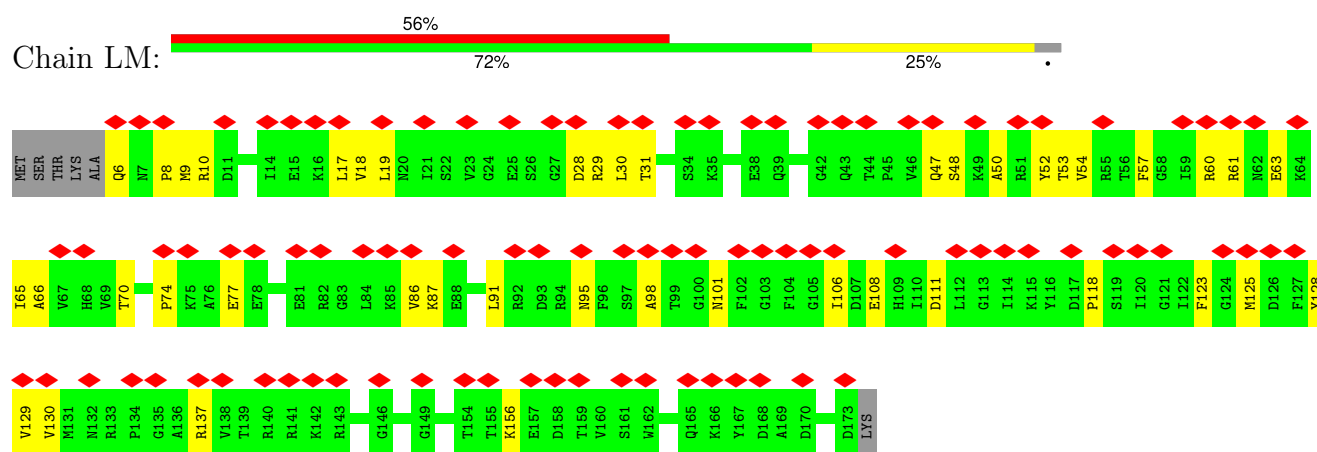
• Molecule 13: 60S ribosomal protein L9-A



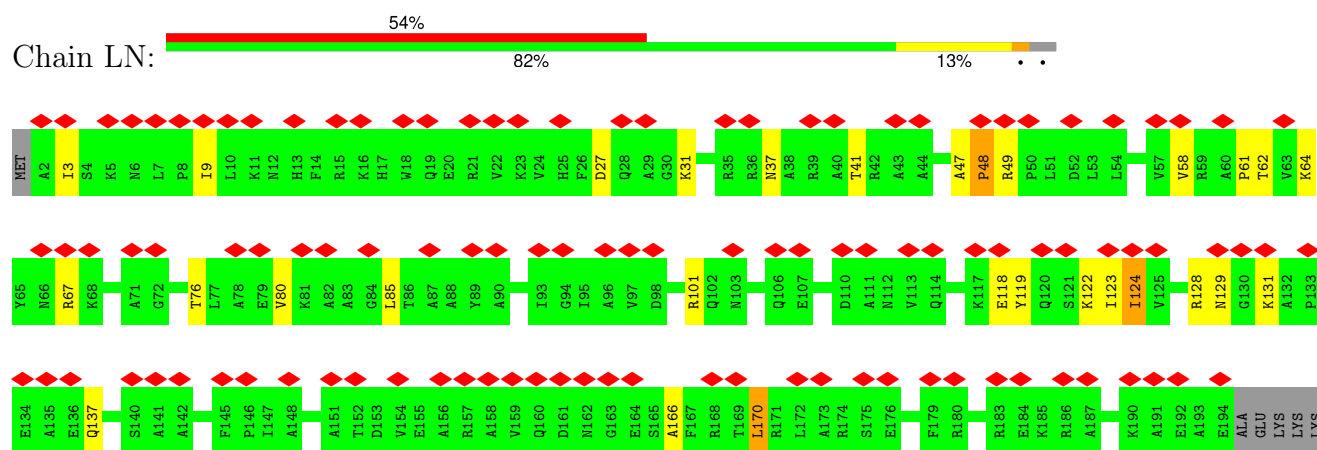
• Molecule 14: Large ribosomal subunit protein uL16



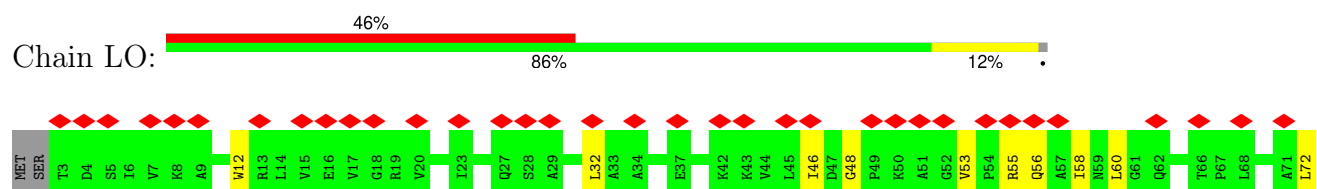
• Molecule 15: Large ribosomal subunit protein uL5B

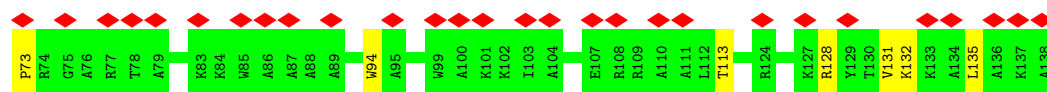


• Molecule 16: 60S ribosomal protein L13-A

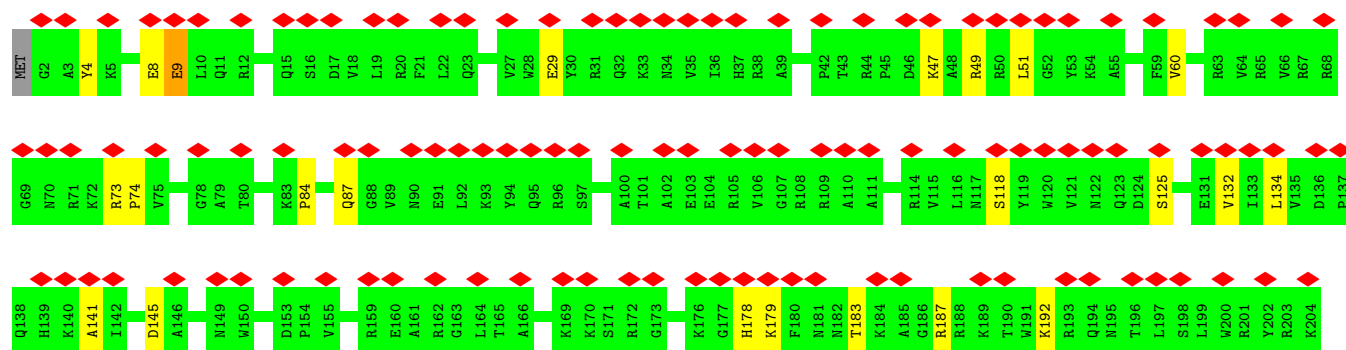
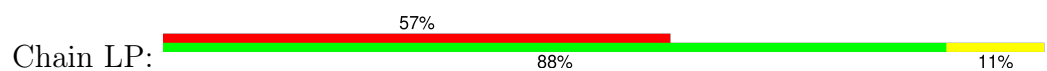


• Molecule 17: 60S ribosomal protein L14-A

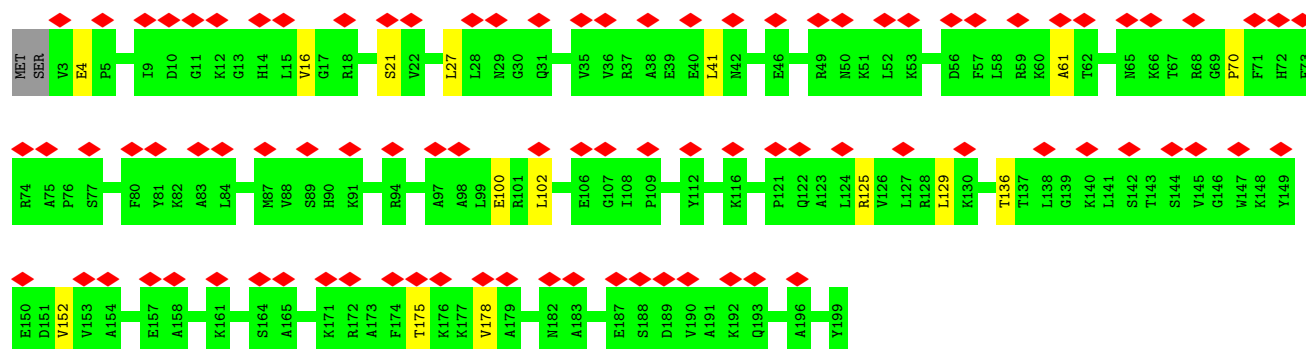




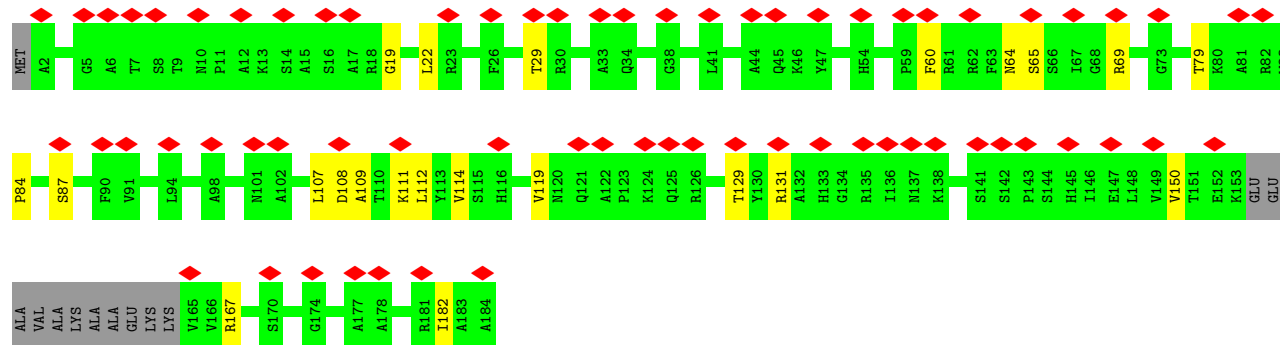
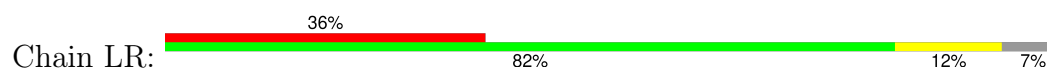
• Molecule 18: 60S ribosomal protein L15-A



• Molecule 19: 60S ribosomal protein L16-A

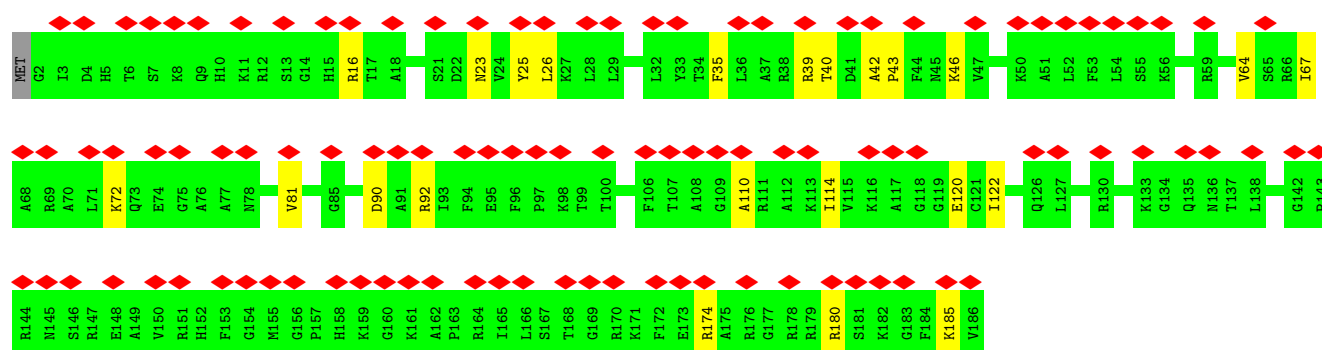


• Molecule 20: 60S ribosomal protein L17-A



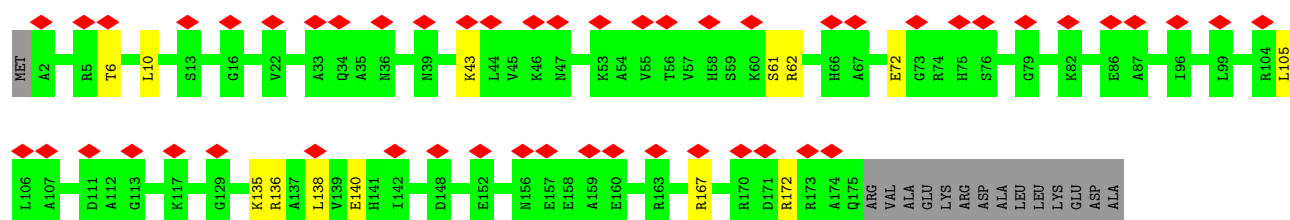
• Molecule 21: 60S ribosomal protein L18-A

Chain LS: 



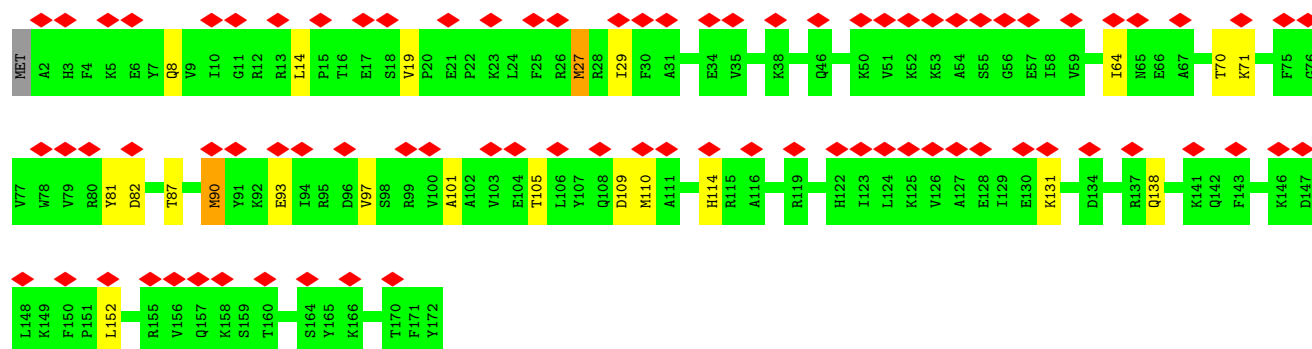
• Molecule 22: 60S ribosomal protein L19-A

Chain LT: 



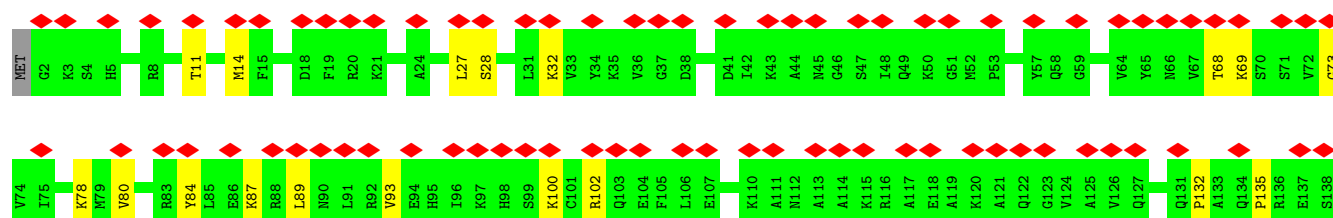
• Molecule 23: 60S ribosomal protein L20-A

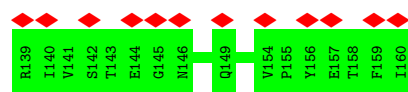
Chain LU: 



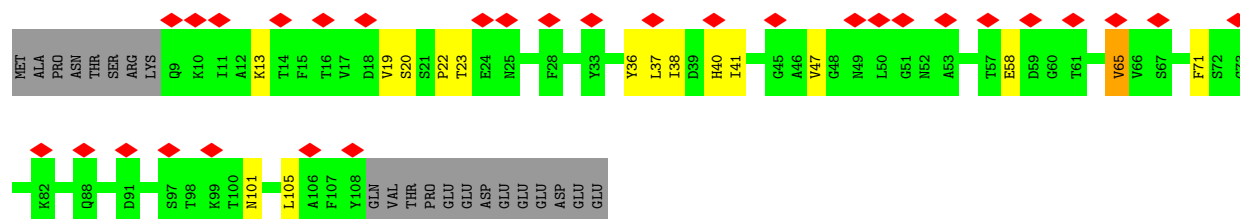
• Molecule 24: 60S ribosomal protein L21-A

Chain LV: 

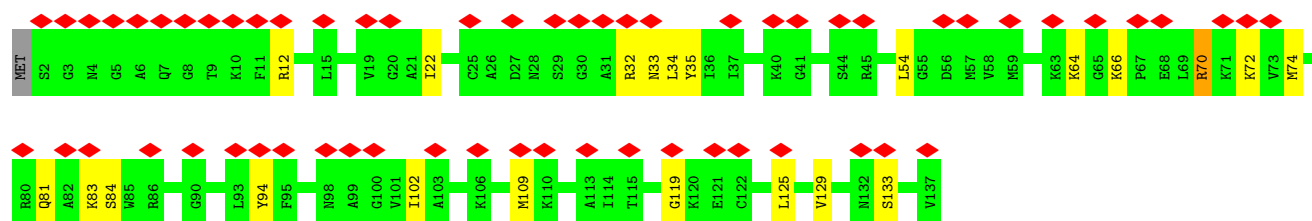
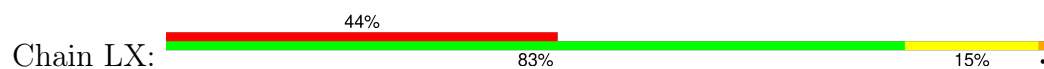




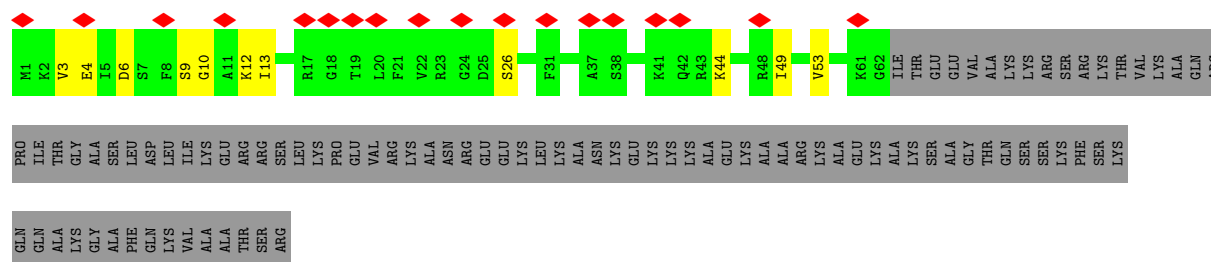
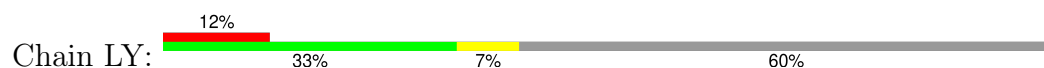
• Molecule 25: 60S ribosomal protein L22-A



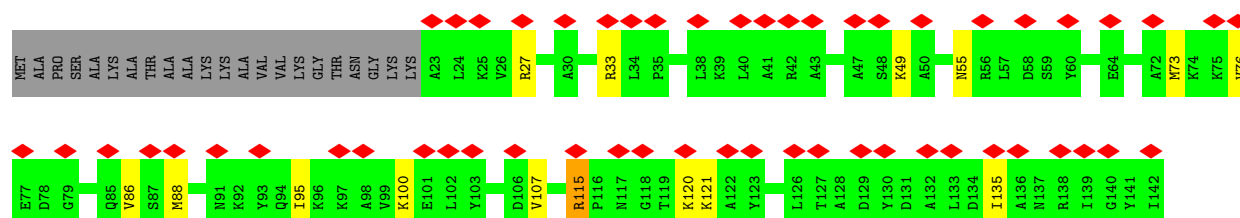
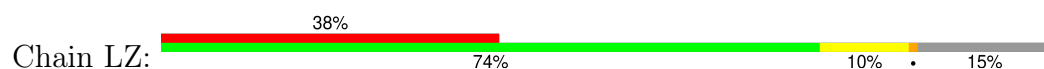
• Molecule 26: 60S ribosomal protein L23-A



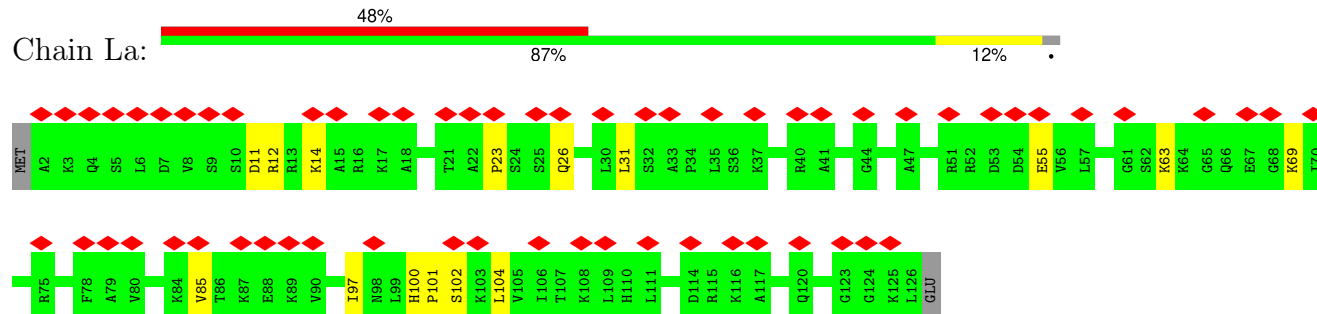
• Molecule 27: 60S ribosomal protein L24-A



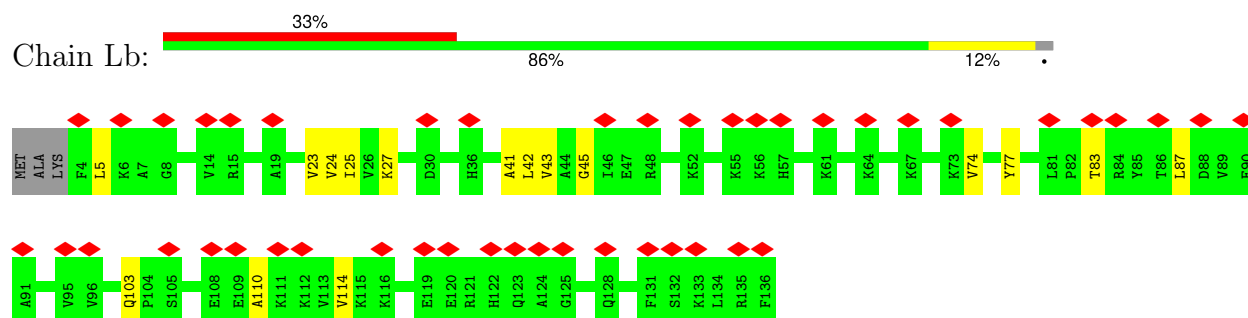
• Molecule 28: 60S ribosomal protein L25



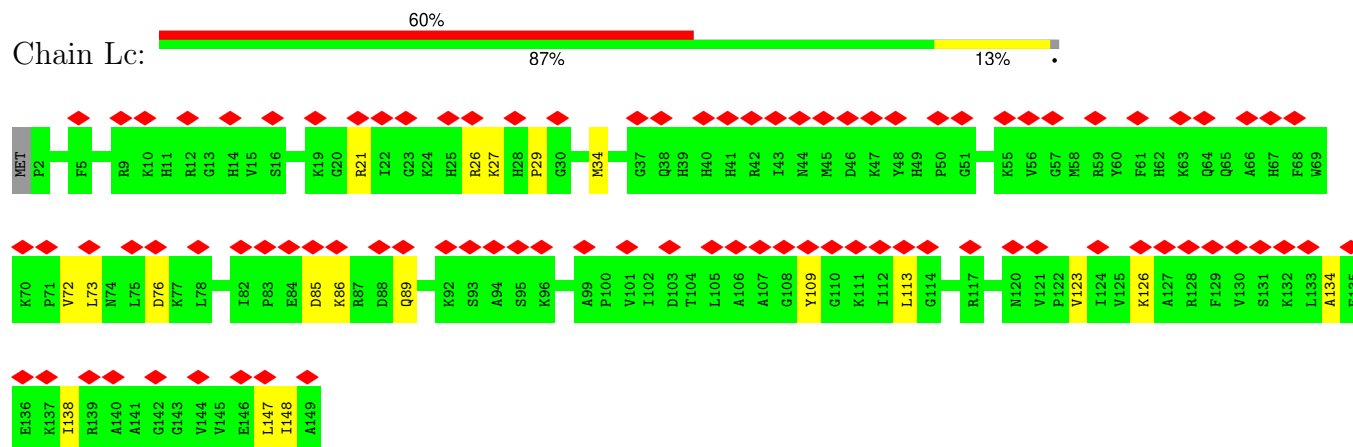
- Molecule 29: 60S ribosomal protein L26-A



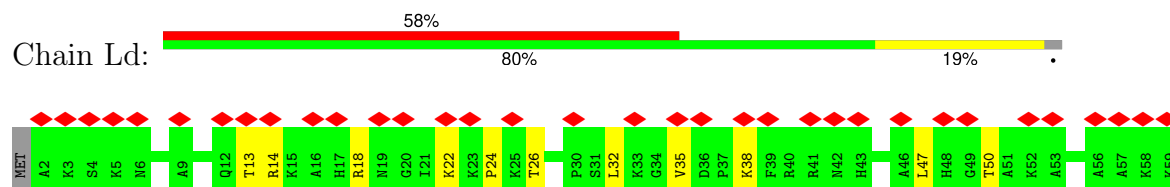
- Molecule 30: 60S ribosomal protein L27-A



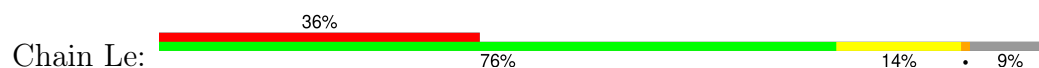
- Molecule 31: 60S ribosomal protein L28

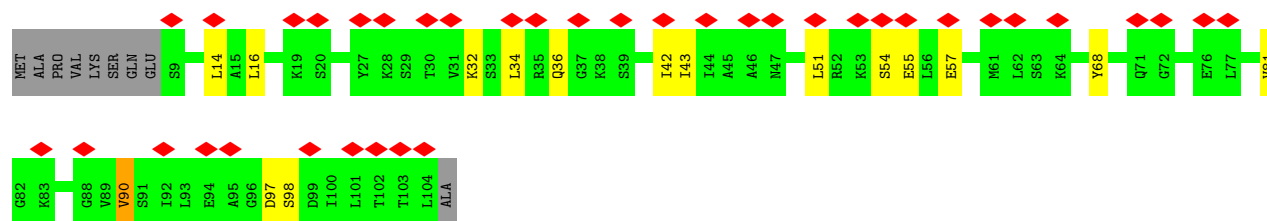


- Molecule 32: 60S ribosomal protein L29

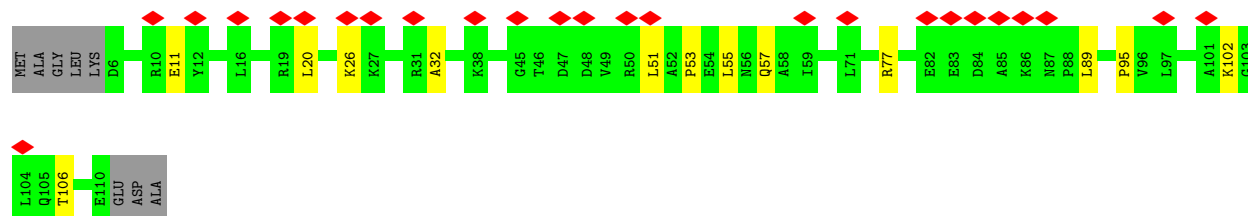
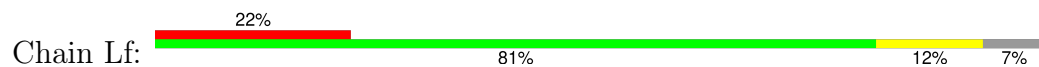


- Molecule 33: 60S ribosomal protein L30

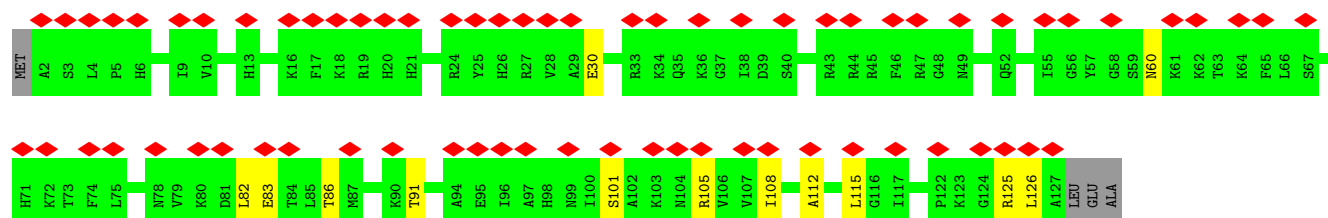
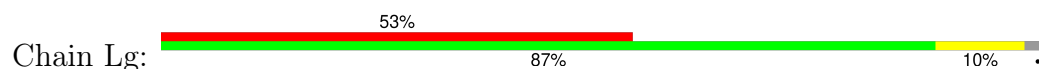




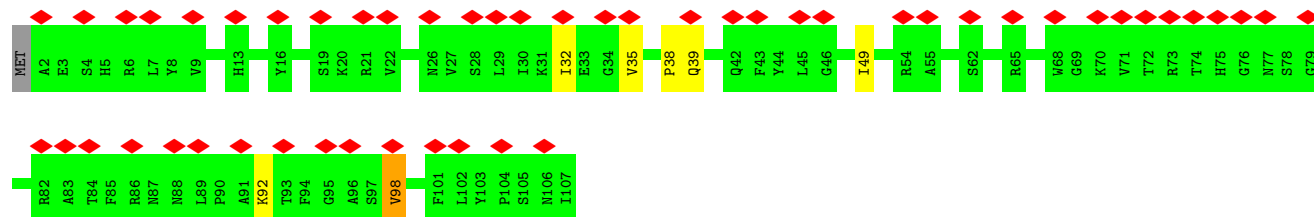
• Molecule 34: 60S ribosomal protein L31-A



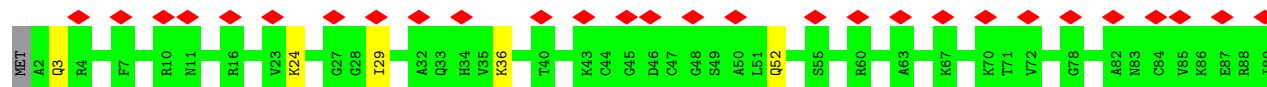
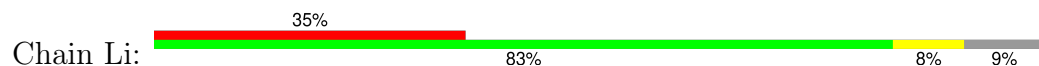
• Molecule 35: 60S ribosomal protein L32

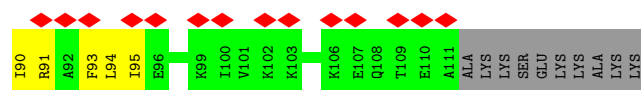


• Molecule 36: 60S ribosomal protein L33-A

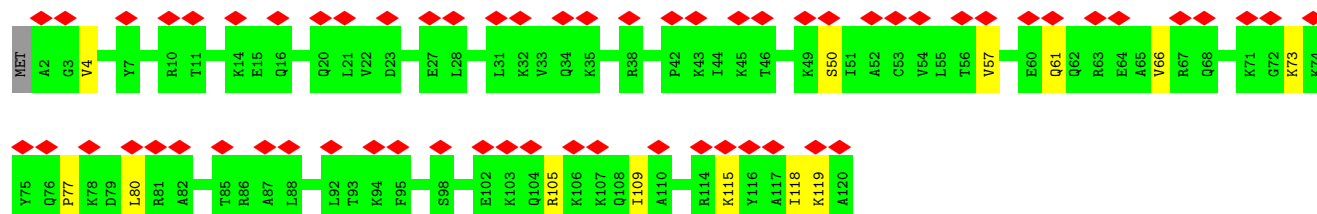
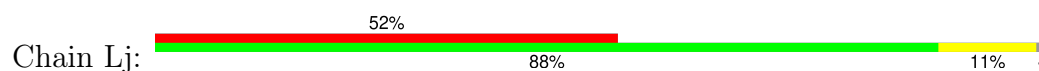


• Molecule 37: 60S ribosomal protein L34-A

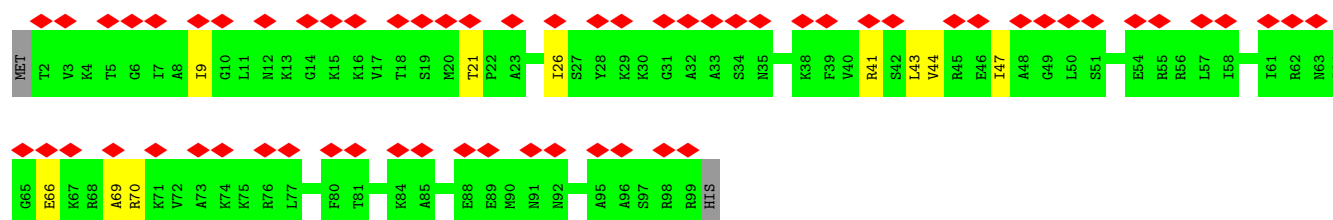




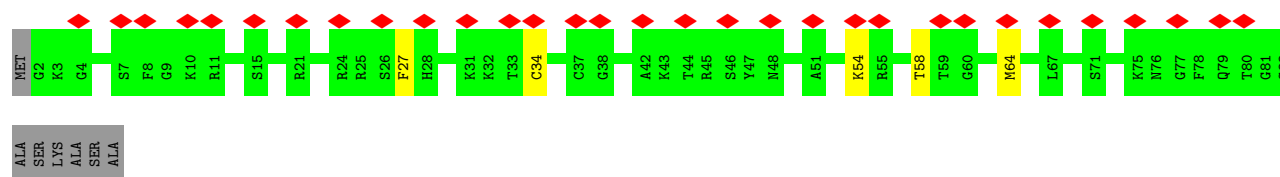
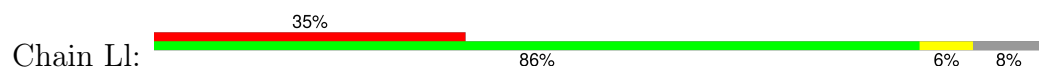
- Molecule 38: 60S ribosomal protein L35-A



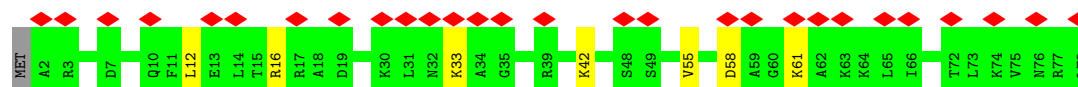
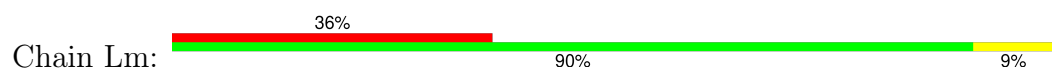
- Molecule 39: 60S ribosomal protein L36-A



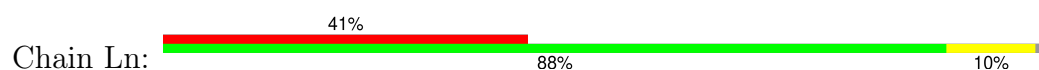
- Molecule 40: 60S ribosomal protein L37-A

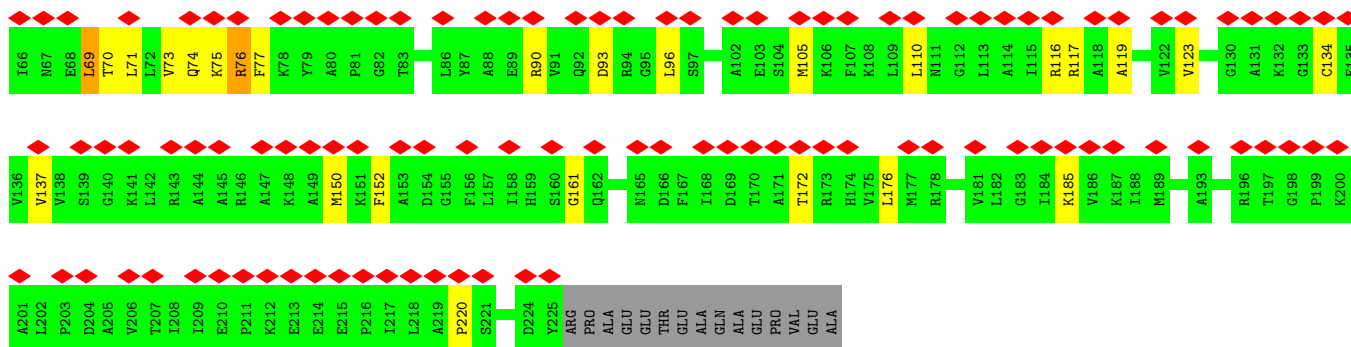


- Molecule 41: 60S ribosomal protein L38

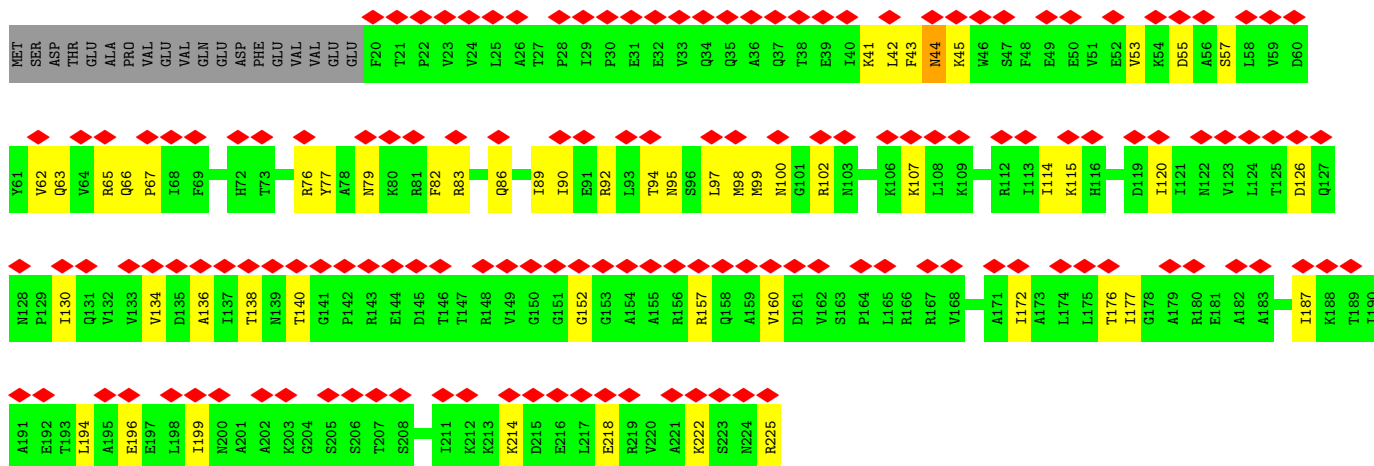


- Molecule 42: 60S ribosomal protein L39

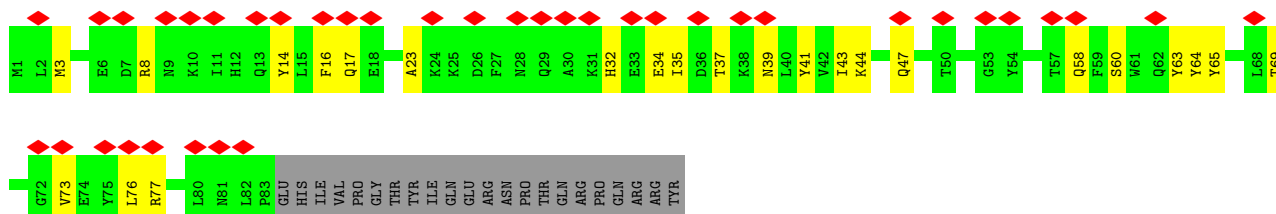




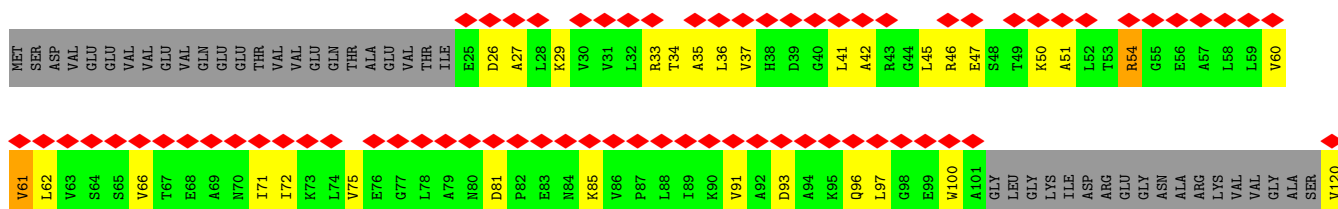
• Molecule 48: 40S ribosomal protein S5



• Molecule 49: 40S ribosomal protein S10-A



• Molecule 50: 40S ribosomal protein S12

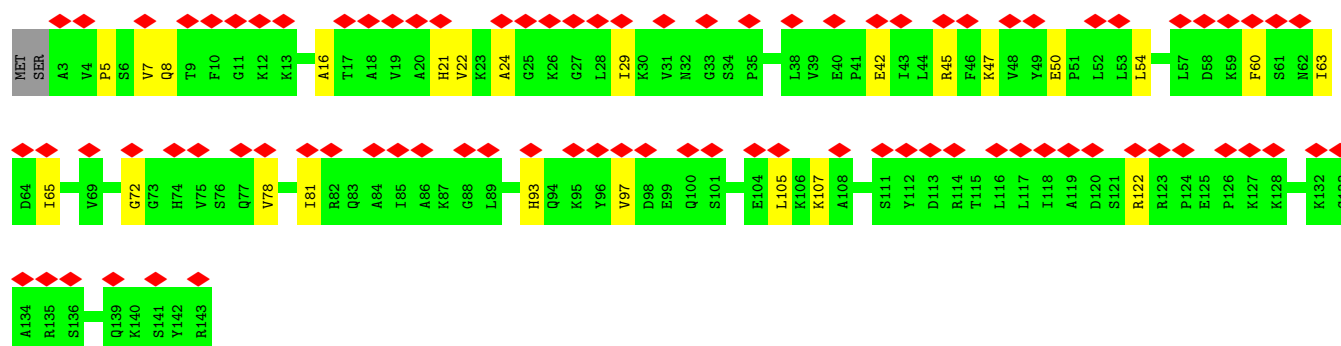
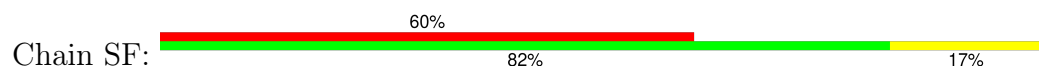




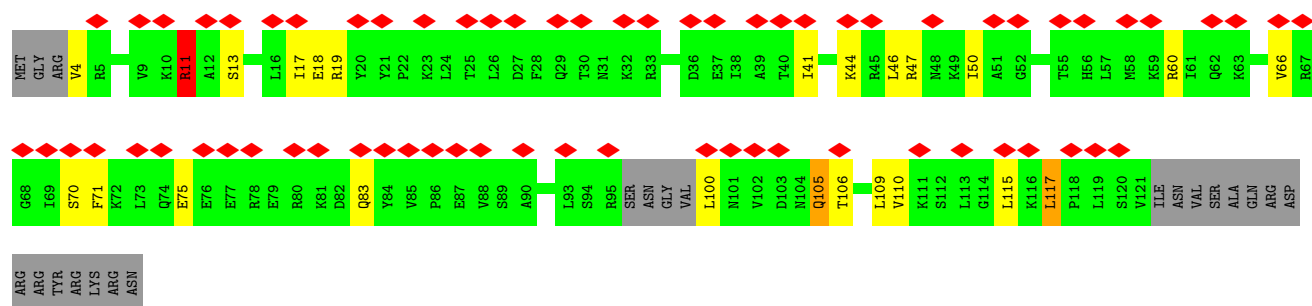
- Molecule 51: 40S ribosomal protein S15



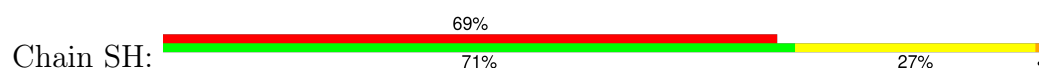
- Molecule 52: 40S ribosomal protein S16-A

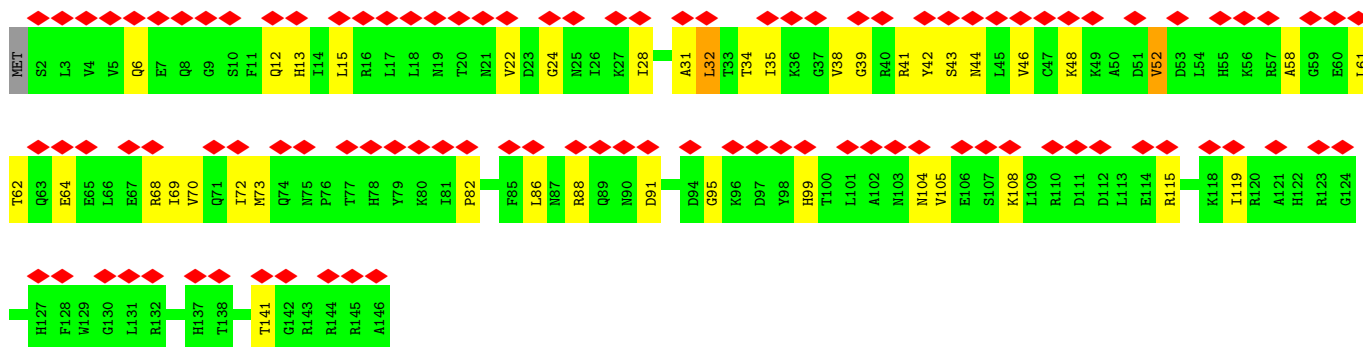


- Molecule 53: 40S ribosomal protein S17-B

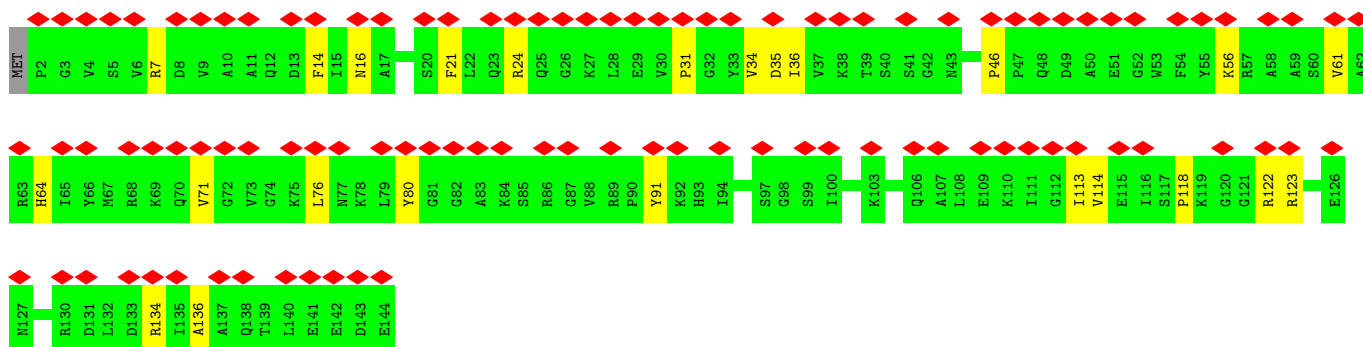
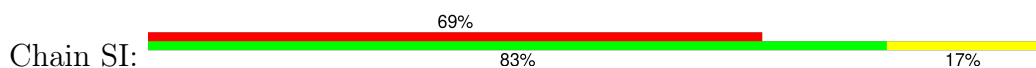


- Molecule 54: 40S ribosomal protein S18-A

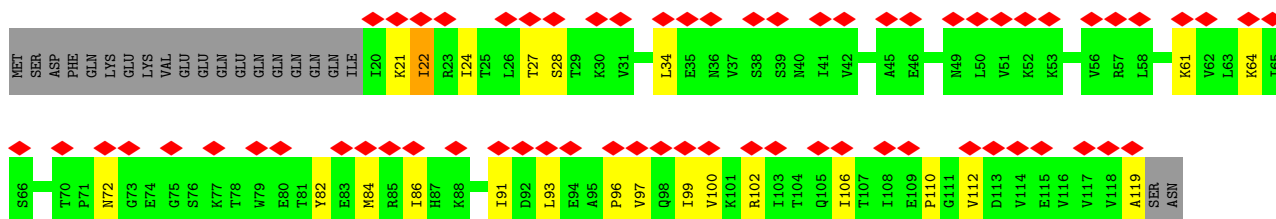




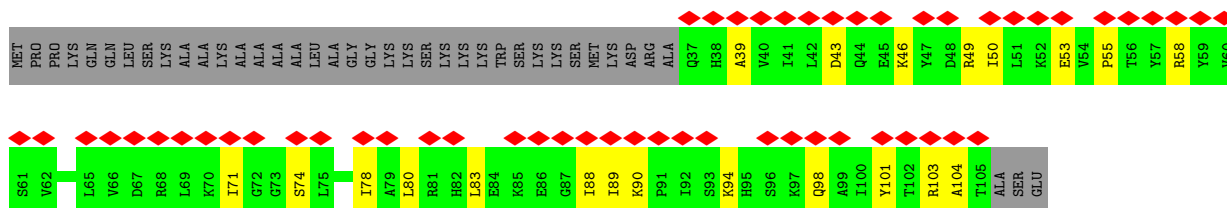
• Molecule 55: 40S ribosomal protein S19-A



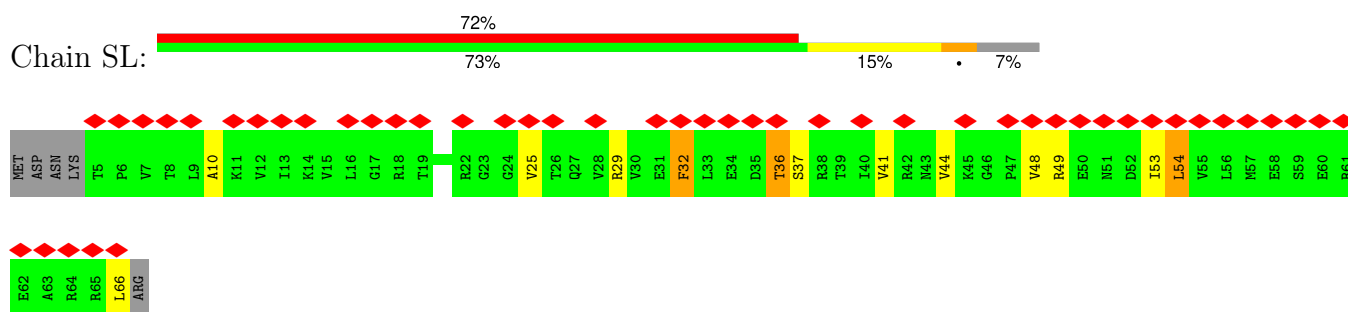
• Molecule 56: 40S ribosomal protein S20



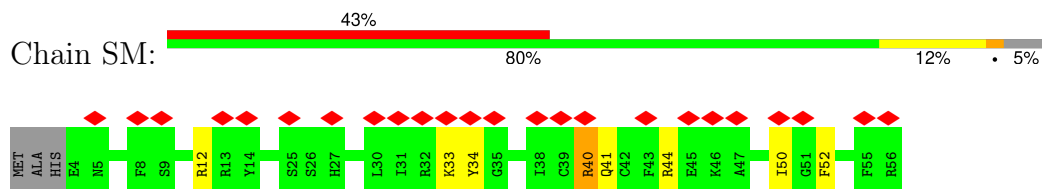
• Molecule 57: 40S ribosomal protein S25-A



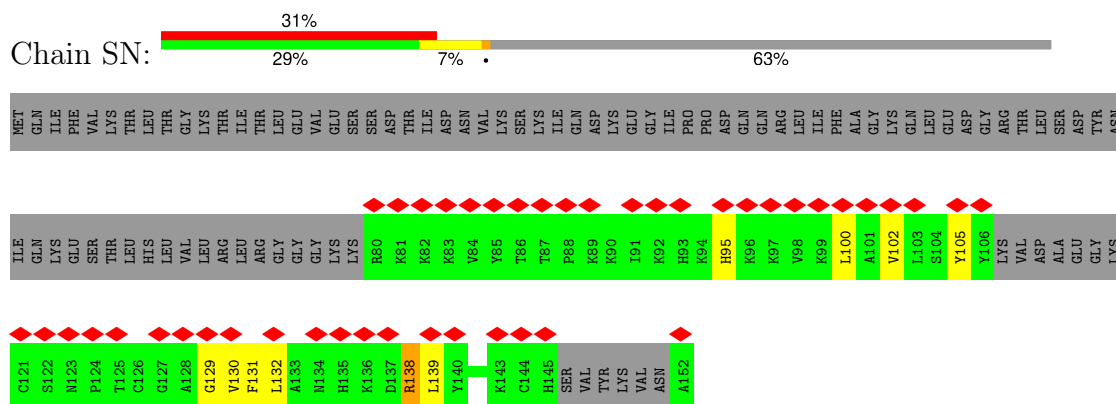
• Molecule 58: 40S ribosomal protein S28-A



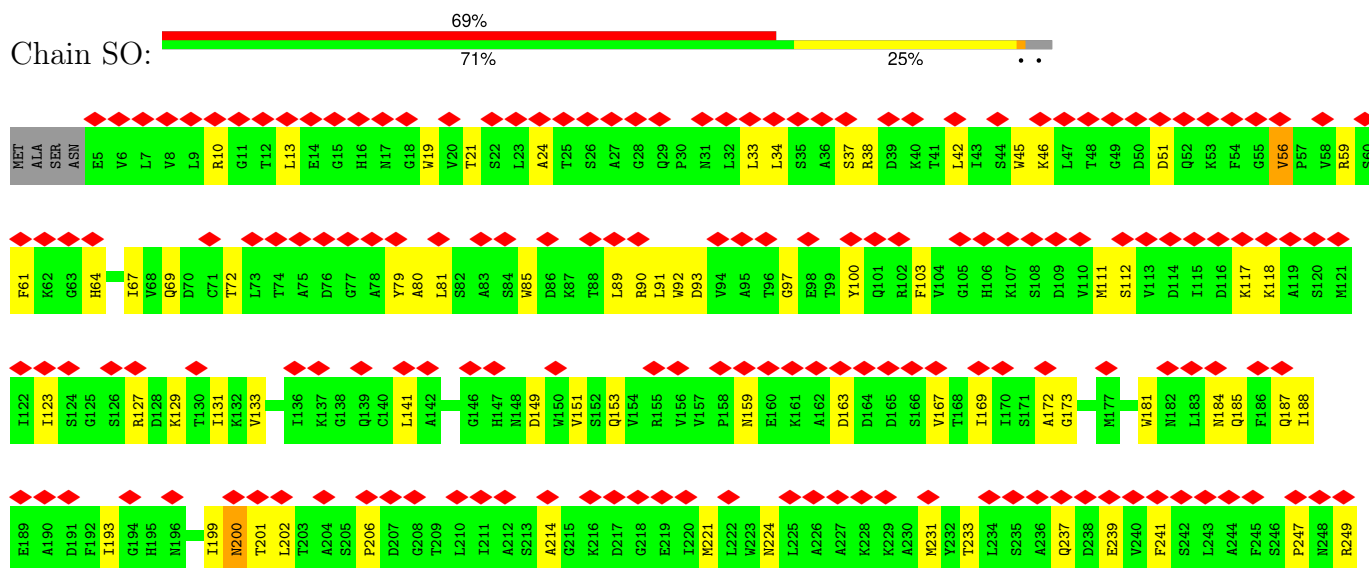
- Molecule 59: 40S ribosomal protein S29-A

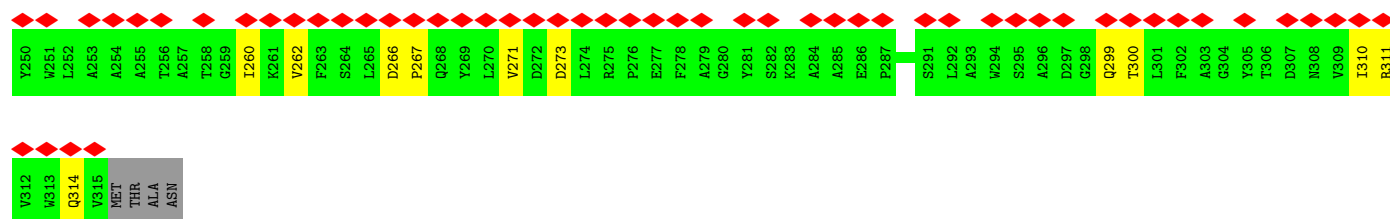


- Molecule 60: Ubiquitin-40S ribosomal protein S31

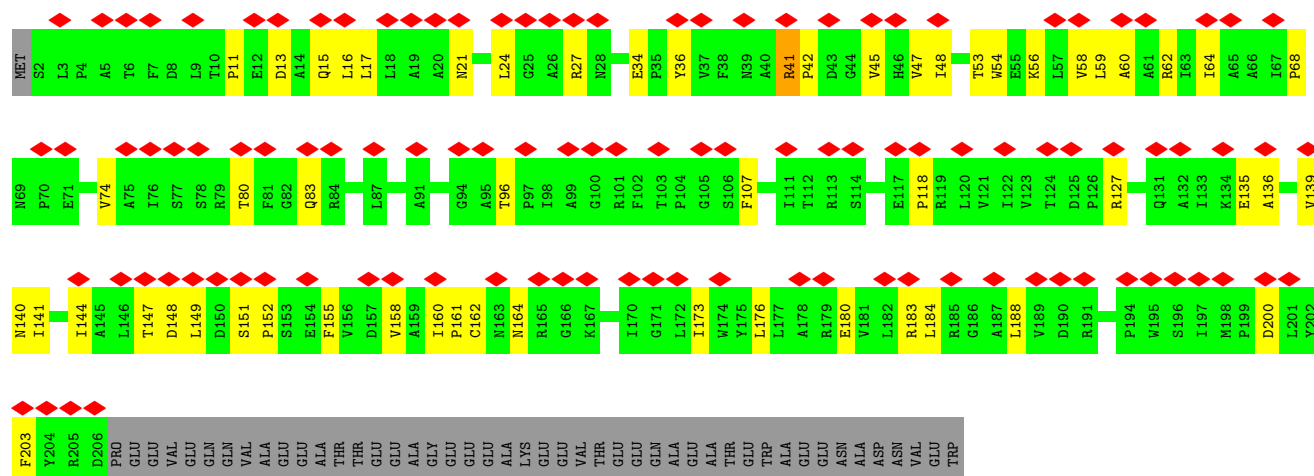
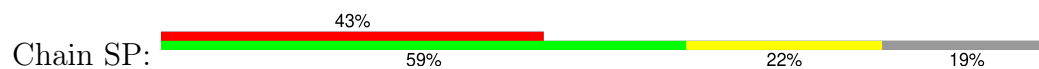


- Molecule 61: Guanine nucleotide-binding protein subunit beta-like protein

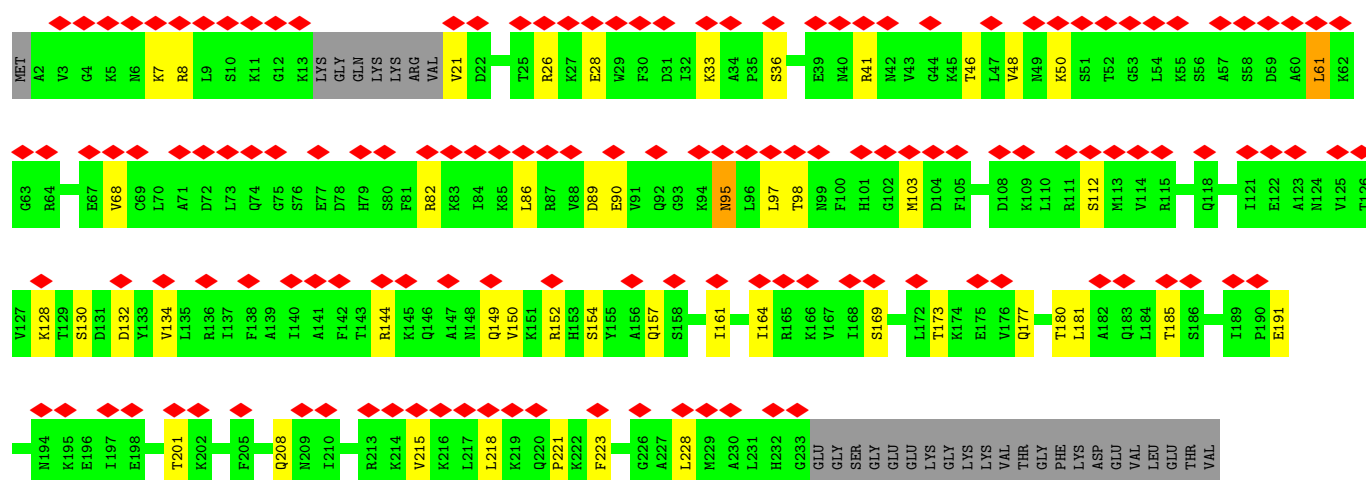




• Molecule 62: 40S ribosomal protein S0-A

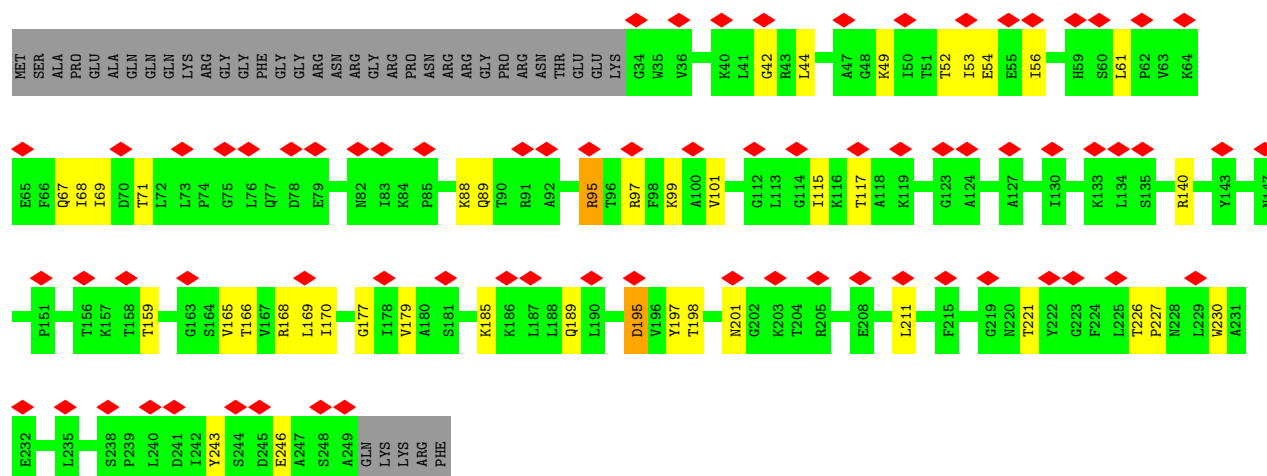


• Molecule 63: Small ribosomal subunit protein eS1A

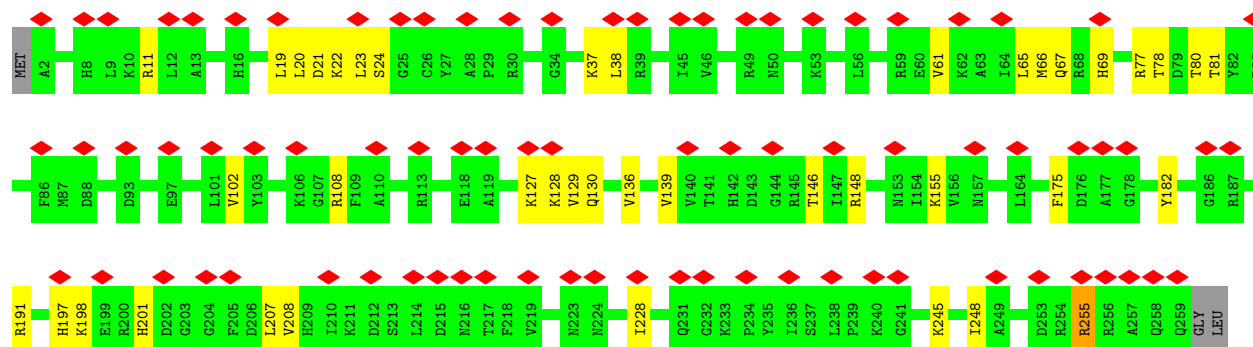
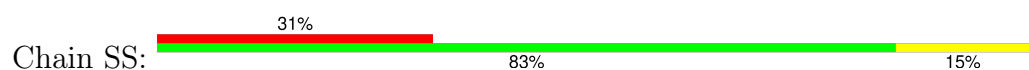


• Molecule 64: 40S ribosomal protein S2

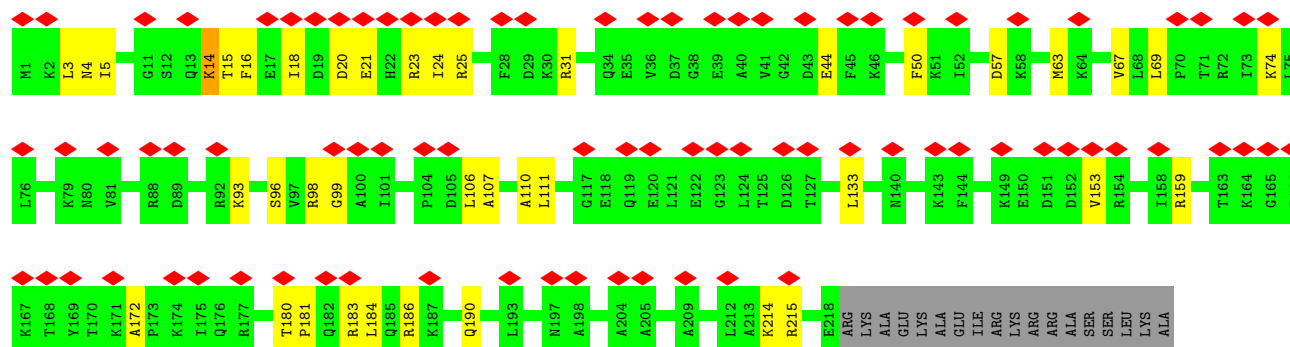
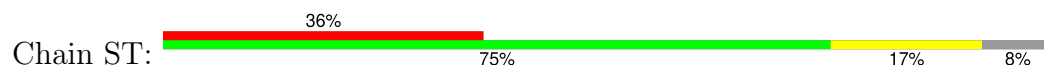




• Molecule 65: 40S ribosomal protein S4-A

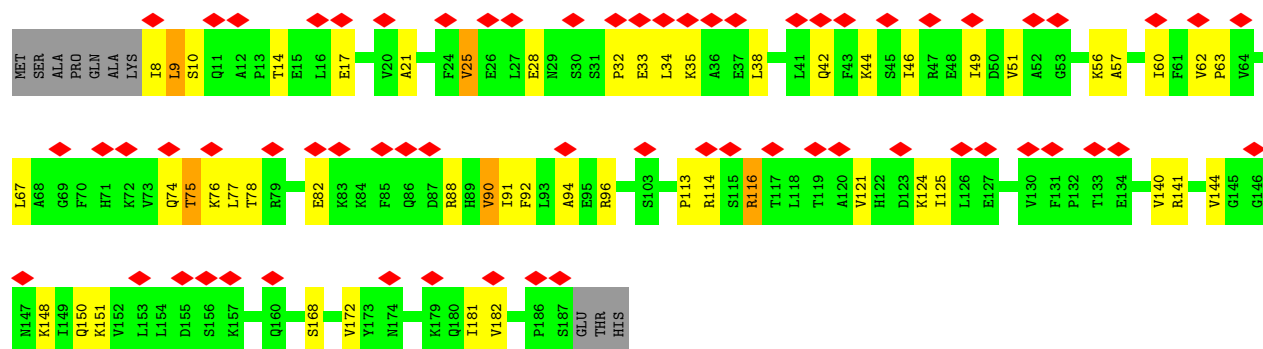


• Molecule 66: 40S ribosomal protein S6-A

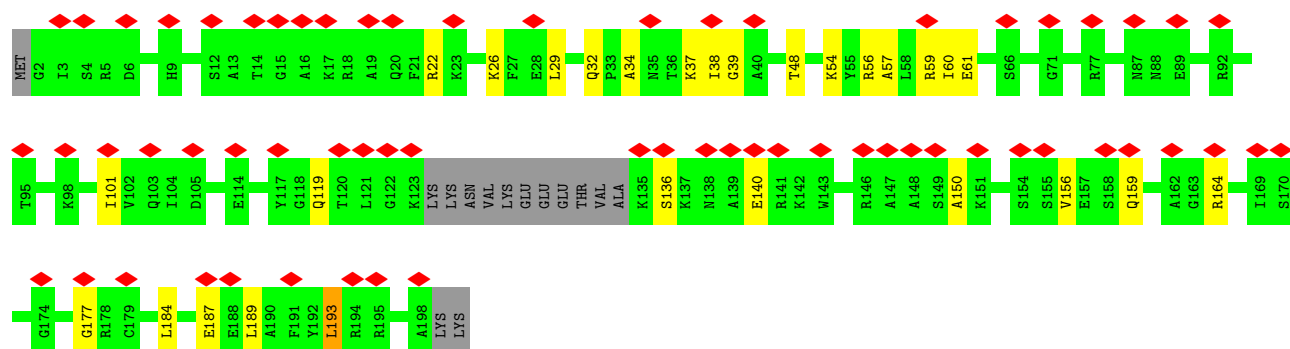
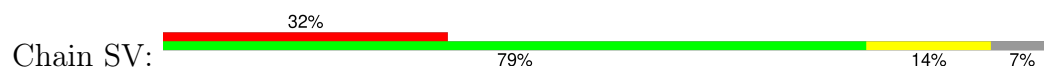


• Molecule 67: 40S ribosomal protein S7-A

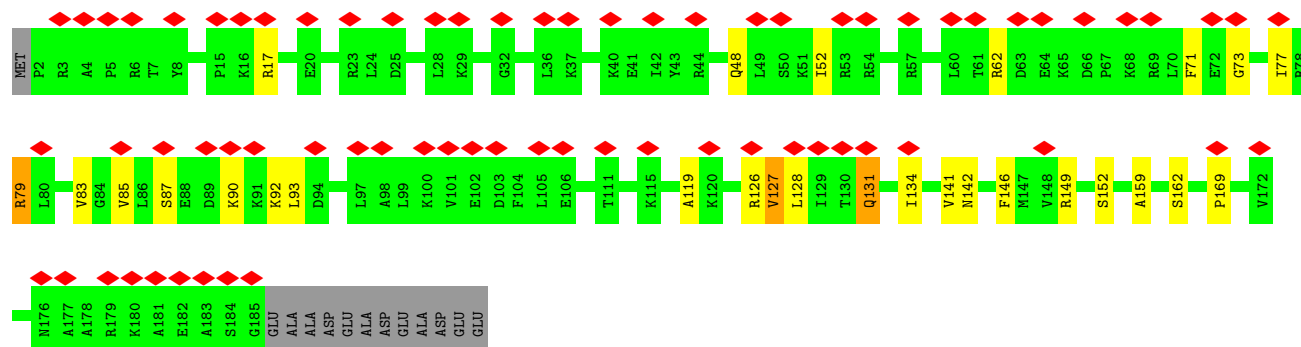
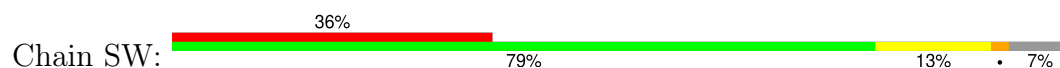




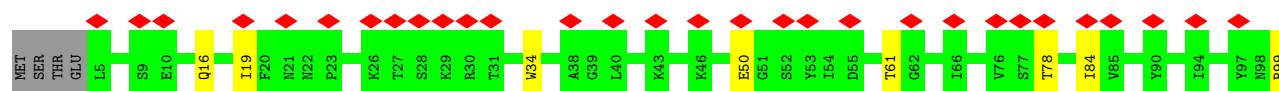
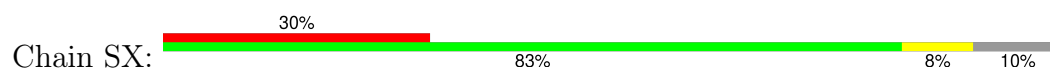
• Molecule 68: 40S ribosomal protein S8-A

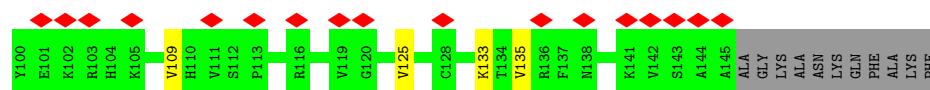


• Molecule 69: 40S ribosomal protein S9-A

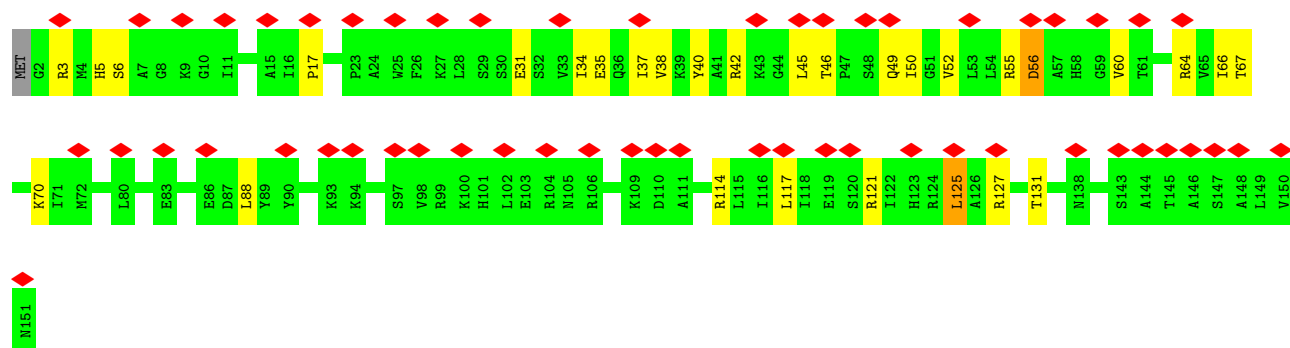
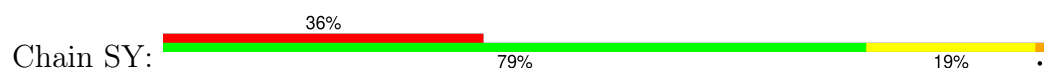


• Molecule 70: 40S ribosomal protein S11-A

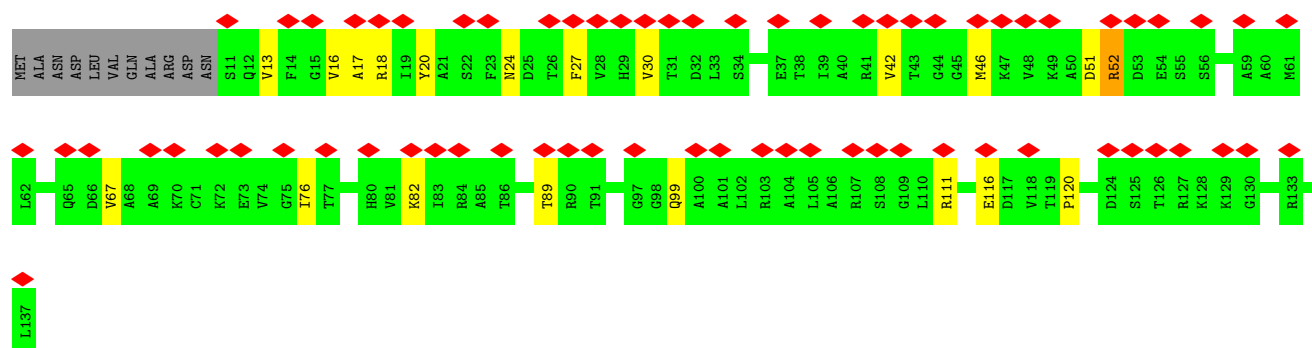
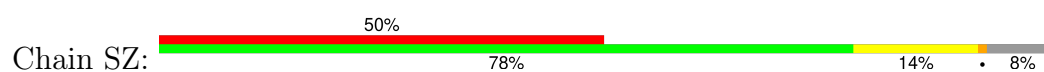




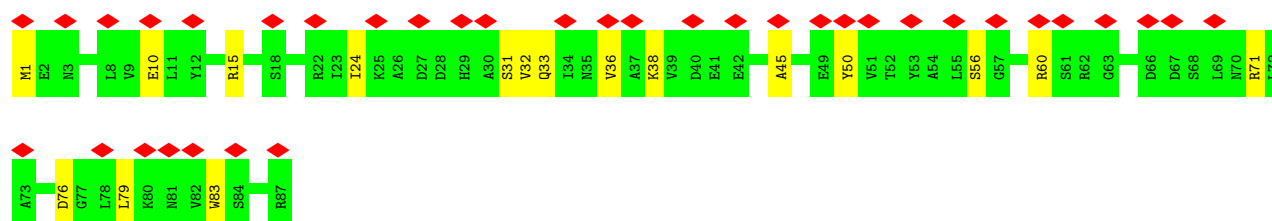
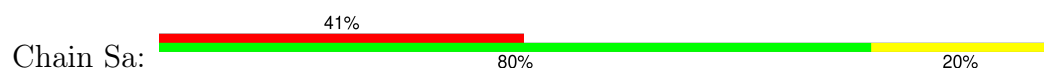
- Molecule 71: 40S ribosomal protein S13



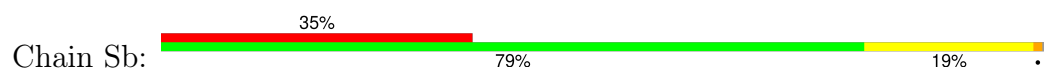
- Molecule 72: 40S ribosomal protein S14-B

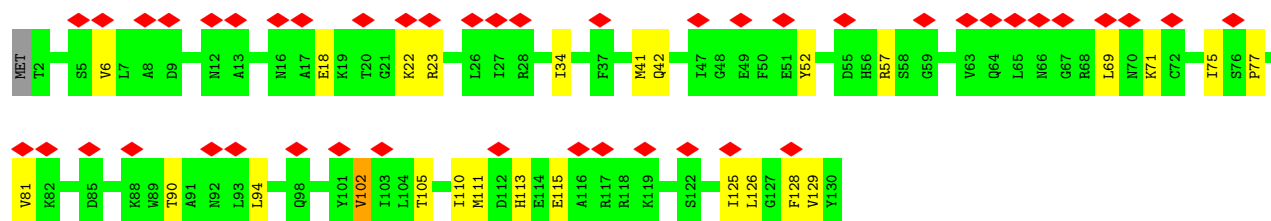


- Molecule 73: 40S ribosomal protein S21-A

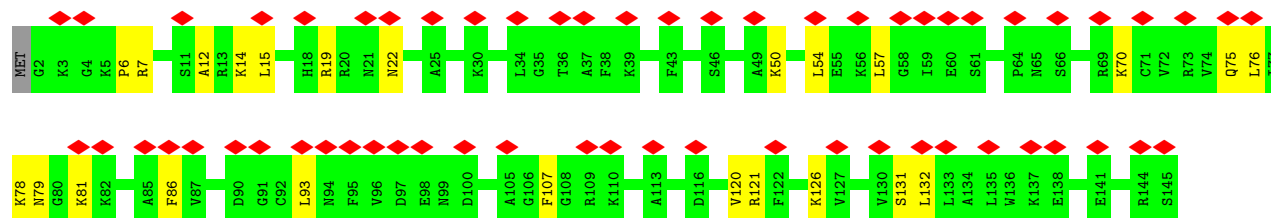
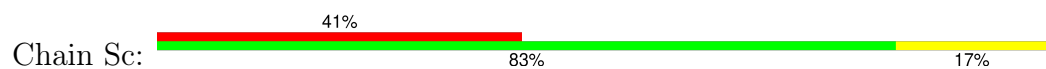


- Molecule 74: 40S ribosomal protein S22-A

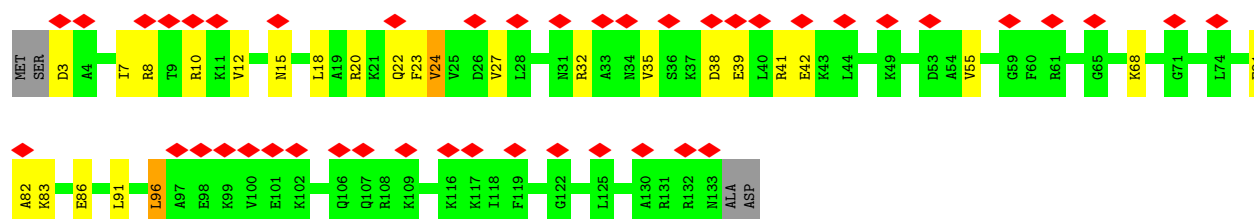
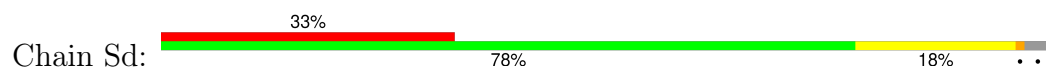




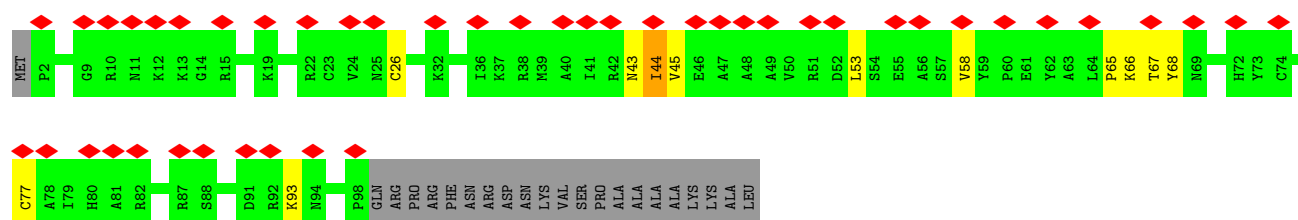
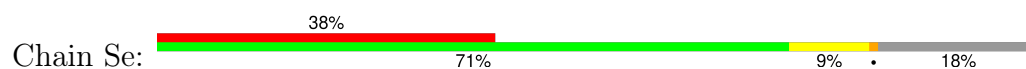
• Molecule 75: 40S ribosomal protein S23-A



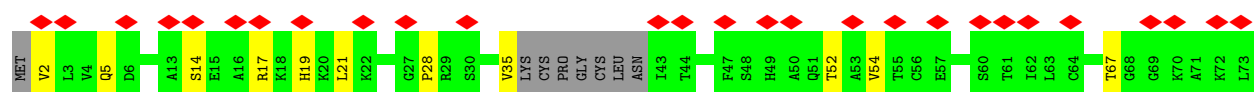
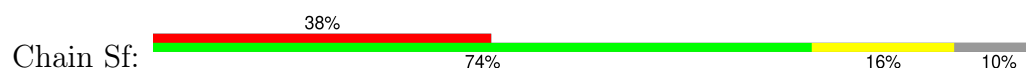
• Molecule 76: 40S ribosomal protein S24-A



• Molecule 77: Small ribosomal subunit protein eS26B

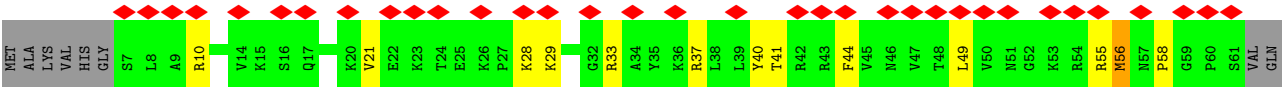


• Molecule 78: 40S ribosomal protein S27-A

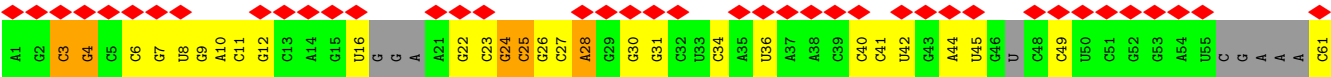




• Molecule 79: 40S ribosomal protein S30-A



• Molecule 80: P site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35555	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.782	Depositor
Minimum map value	-0.311	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	498.0, 498.0, 498.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3HE

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	A	0.25	0/72816	0.37	0/113508
2	B	0.22	0/2883	0.35	0/4491
3	C	0.25	0/3746	0.36	0/5832
4	D	0.24	0/245	0.52	0/378
5	E	0.23	0/37769	0.44	0/58836
6	LD	0.28	0/1912	0.58	0/2569
7	LE	0.26	0/3150	0.49	0/4236
8	LF	0.26	0/2801	0.53	0/3792
9	LG	0.28	0/2390	0.64	2/3225 (0.1%)
10	LH	0.30	0/1265	0.68	0/1706
11	LI	0.28	0/1821	0.55	0/2451
12	LJ	0.26	0/1836	0.58	0/2481
13	LK	0.27	0/1514	0.65	0/2039
14	LL	0.28	0/1723	0.62	0/2312
15	LM	0.31	0/1358	0.80	0/1823
16	LN	0.29	0/1568	0.58	0/2106
17	LO	0.28	0/1068	0.61	0/1438
18	LP	0.28	0/1757	0.53	0/2354
19	LQ	0.29	0/1585	0.55	0/2128
20	LR	0.26	0/1383	0.53	0/1858
21	LS	0.26	0/1465	0.55	0/1965
22	LT	0.27	0/1426	0.53	0/1901
23	LU	0.28	0/1473	0.59	0/1980
24	LV	0.28	0/1296	0.59	0/1739
25	LW	0.28	0/812	0.68	0/1099
26	LX	0.28	0/1018	0.55	0/1369
27	LY	0.30	0/525	0.61	0/696
28	LZ	0.27	0/974	0.65	0/1314
29	La	0.23	0/995	0.48	0/1329
30	Lb	0.28	0/1092	0.61	0/1467
31	Lc	0.27	0/1200	0.56	0/1607
32	Ld	0.23	0/473	0.49	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.30	0/745	0.61	0/1001
34	Lf	0.25	0/870	0.54	0/1168
35	Lg	0.24	0/1029	0.48	0/1379
36	Lh	0.26	0/868	0.55	0/1168
37	Li	0.30	0/876	0.60	0/1171
38	Lj	0.28	0/978	0.60	0/1301
39	Lk	0.28	0/767	0.69	0/1019
40	Ll	0.25	0/660	0.48	0/875
41	Lm	0.27	0/614	0.58	0/822
42	Ln	0.29	0/443	0.54	0/588
43	Lo	0.26	0/415	0.55	0/551
44	Lp	0.25	0/225	0.49	0/289
45	Lq	0.23	0/817	0.54	0/1078
46	Lr	0.25	0/701	0.51	0/934
47	SA	0.31	0/1754	0.71	0/2361
48	SB	0.28	0/1625	0.71	1/2197 (0.0%)
49	SC	0.36	0/725	0.94	0/978
50	SD	0.34	0/742	0.77	0/1005
51	SE	0.34	0/925	0.78	1/1245 (0.1%)
52	SF	0.26	0/1115	0.64	0/1499
53	SG	0.31	0/917	0.75	1/1229 (0.1%)
54	SH	0.31	0/1207	0.71	0/1623
55	SI	0.31	0/1130	0.80	0/1517
56	SJ	0.35	0/807	0.81	0/1091
57	SK	0.27	0/566	0.72	0/761
58	SL	0.27	0/488	0.70	0/656
59	SM	0.26	0/453	0.70	0/602
60	SN	0.53	0/437	0.74	0/585
61	SO	0.29	0/2428	0.78	1/3308 (0.0%)
62	SP	0.29	0/1636	0.68	0/2237
63	SQ	0.28	0/1812	0.68	0/2433
64	SR	0.30	0/1656	0.66	0/2251
65	SS	0.29	0/2097	0.74	1/2823 (0.0%)
66	ST	0.28	0/1779	0.69	0/2379
67	SU	0.31	0/1475	0.73	0/1987
68	SV	0.27	0/1496	0.61	0/1999
69	SW	0.30	0/1504	0.78	2/2016 (0.1%)
70	SX	0.27	0/1163	0.60	0/1568
71	SY	0.31	0/1215	0.68	0/1638
72	SZ	0.30	0/934	0.71	0/1257
73	Sa	0.26	0/682	0.59	0/921
74	Sb	0.33	0/1038	0.62	0/1395
75	Sc	0.24	0/1139	0.58	0/1518

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sd	0.27	0/1030	0.66	0/1379
77	Se	0.26	0/778	0.59	0/1042
78	Sf	0.26	0/570	0.63	0/769
79	Sg	0.28	0/444	0.78	0/591
80	n	0.24	0/1571	0.52	0/2440
All	All	0.26	0/206685	0.50	9/303302 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	LD	0	1
9	LG	0	2
13	LK	0	1
16	LN	0	2
21	LS	0	1
22	LT	0	1
26	LX	0	2
39	Lk	0	1
45	Lq	0	1
47	SA	0	4
48	SB	0	2
49	SC	0	1
50	SD	0	1
53	SG	0	2
54	SH	0	1
55	SI	0	2
56	SJ	0	1
57	SK	0	1
59	SM	0	2
60	SN	0	1
61	SO	0	1
62	SP	0	1
63	SQ	0	1
64	SR	0	1
66	ST	0	1
67	SU	0	1
69	SW	0	3
72	SZ	0	1
74	Sb	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
78	Sf	0	2
79	Sg	0	1
All	All	0	44

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	LG	188	GLU	CB-CG-CD	7.81	125.88	112.60
9	LG	188	GLU	CA-CB-CG	7.26	128.62	114.10
51	SE	61	ARG	CB-CG-CD	6.95	127.27	111.30
53	SG	11	ARG	CG-CD-NE	6.17	125.56	112.00
61	SO	237	GLN	CA-CB-CG	5.74	125.58	114.10
69	SW	92	LYS	CA-C-N	5.42	131.88	121.54
69	SW	92	LYS	C-N-CA	5.42	131.88	121.54
48	SB	99	MET	CB-CA-C	-5.33	106.83	114.87
65	SS	255	ARG	CB-CG-CD	5.00	122.81	111.30

There are no chirality outliers.

All (44) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	LD	241	ARG	Sidechain
9	LG	218	ARG	Sidechain
9	LG	85	ARG	Sidechain
13	LK	23	ARG	Sidechain
16	LN	49	ARG	Sidechain
16	LN	67	ARG	Sidechain
21	LS	16	ARG	Sidechain
22	LT	167	ARG	Sidechain
26	LX	12	ARG	Sidechain
26	LX	70	ARG	Sidechain
39	Lk	70	ARG	Sidechain
45	Lq	18	ARG	Sidechain
47	SA	116	ARG	Sidechain
47	SA	117	ARG	Sidechain
47	SA	76	ARG	Sidechain
47	SA	90	ARG	Sidechain
48	SB	102	ARG	Sidechain
48	SB	157	ARG	Sidechain
49	SC	8	ARG	Sidechain

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Mol	Chain	Res	Type	Group
50	SD	54	ARG	Sidechain
53	SG	11	ARG	Sidechain
53	SG	19	ARG	Sidechain
54	SH	88	ARG	Sidechain
55	SI	122	ARG	Sidechain
55	SI	7	ARG	Sidechain
56	SJ	102	ARG	Sidechain
57	SK	103	ARG	Sidechain
59	SM	12	ARG	Sidechain
59	SM	44	ARG	Sidechain
60	SN	118	ARG	Sidechain
61	SO	311	ARG	Sidechain
62	SP	41	ARG	Sidechain
63	SQ	26	ARG	Sidechain
64	SR	95	ARG	Sidechain
66	ST	31	ARG	Sidechain
67	SU	116	ARG	Sidechain
69	SW	17	ARG	Sidechain
69	SW	62	ARG	Sidechain
69	SW	79	ARG	Sidechain
72	SZ	52	ARG	Sidechain
74	Sb	57	ARG	Sidechain
78	Sf	80	ARG	Sidechain
78	Sf	81	ARG	Sidechain
79	Sg	10	ARG	Sidechain

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	A	65056	0	32701	255	0
2	B	2579	0	1304	9	0
3	C	3353	0	1695	13	0
4	D	218	0	109	3	0
5	E	33767	0	16988	218	0
6	LD	1878	0	1946	27	0
7	LE	3079	0	3158	30	0
8	LF	2749	0	2863	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	LG	2341	0	2290	43	0
10	LH	1243	0	1327	7	0
11	LI	1784	0	1862	15	0
12	LJ	1804	0	1877	15	0
13	LK	1493	0	1566	18	0
14	LL	1686	0	1725	21	0
15	LM	1337	0	1357	25	0
16	LN	1543	0	1608	18	0
17	LO	1053	0	1149	10	0
18	LP	1720	0	1779	14	0
19	LQ	1555	0	1659	7	0
20	LR	1361	0	1398	12	0
21	LS	1441	0	1543	15	0
22	LT	1409	0	1499	8	0
23	LU	1437	0	1475	12	0
24	LV	1272	0	1312	15	0
25	LW	796	0	812	8	0
26	LX	1003	0	1048	12	0
27	LY	513	0	540	5	0
28	LZ	959	0	1023	11	0
29	La	984	0	1075	8	0
30	Lb	1066	0	1104	9	0
31	Lc	1169	0	1211	13	0
32	Ld	462	0	491	7	0
33	Le	737	0	792	11	0
34	Lf	856	0	904	8	0
35	Lg	1008	0	1068	6	0
36	Lh	850	0	880	5	0
37	Li	866	0	927	10	0
38	Lj	969	0	1078	9	0
39	Lk	761	0	842	6	0
40	Ll	645	0	649	3	0
41	Lm	608	0	671	4	0
42	Ln	436	0	475	2	0
43	Lo	409	0	448	4	0
44	Lp	224	0	271	2	0
45	Lq	805	0	877	2	0
46	Lr	694	0	738	5	0
47	SA	1729	0	1812	23	0
48	SB	1605	0	1669	36	0
49	SC	708	0	701	16	0
50	SD	736	0	771	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	SE	905	0	928	18	0
52	SF	1095	0	1144	13	0
53	SG	908	0	961	13	0
54	SH	1188	0	1218	25	0
55	SI	1112	0	1124	13	0
56	SJ	797	0	863	17	0
57	SK	558	0	598	12	0
58	SL	486	0	522	11	0
59	SM	443	0	436	5	0
60	SN	429	0	412	6	0
61	SO	2375	0	2323	44	0
62	SP	1596	0	1603	34	0
63	SQ	1787	0	1870	27	0
64	SR	1626	0	1715	24	0
65	SS	2056	0	2140	28	0
66	ST	1755	0	1846	24	0
67	SU	1451	0	1538	33	0
68	SV	1471	0	1499	20	0
69	SW	1479	0	1556	13	0
70	SX	1137	0	1207	7	0
71	SY	1192	0	1255	17	0
72	SZ	923	0	948	14	0
73	Sa	673	0	662	11	0
74	Sb	1021	0	1060	15	0
75	Sc	1121	0	1196	15	0
76	Sd	1016	0	1032	15	0
77	Se	765	0	811	8	0
78	Sf	562	0	582	7	0
79	Sg	437	0	484	9	0
80	n	1409	0	721	15	0
81	A	20	0	23	0	0
All	All	192549	0	143344	1428	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 4.

All (1428) 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)
5:E:628:G:N2	5:E:971:A:H62	1.59	1.00
80:n:10:A:H61	80:n:25:C:H42	1.13	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:628:G:H21	5:E:971:A:N6	1.67	0.92
5:E:868:G:H1	5:E:960:U:H3	1.18	0.90
69:SW:127:VAL:O	69:SW:131:GLN:HB2	1.76	0.85
5:E:628:G:H21	5:E:971:A:H62	0.85	0.83
1:A:2208:A:C2	1:A:2236:G:N1	2.47	0.82
5:E:401:A:H3'	5:E:402:C:H4'	1.64	0.79
62:SP:148:ASP:HB2	62:SP:164:ASN:HB2	1.65	0.78
78:Sf:19:HIS:HD2	78:Sf:21:LEU:H	1.31	0.78
5:E:1499:G:H1	5:E:1508:U:H3	1.34	0.76
63:SQ:149:GLN:HE22	63:SQ:154:SER:HB3	1.51	0.75
47:SA:7:LYS:HD3	56:SJ:27:THR:HG21	1.69	0.74
53:SG:11:ARG:HH11	53:SG:11:ARG:HB2	1.52	0.74
71:SY:60:VAL:HG23	71:SY:66:ILE:HG13	1.70	0.73
56:SJ:28:SER:HB3	56:SJ:34:LEU:HD13	1.71	0.73
16:LN:9:ILE:HD12	31:Lc:34:MET:HE1	1.71	0.71
73:Sa:15:ARG:HH11	73:Sa:33:GLN:HE21	1.36	0.70
63:SQ:132:ASP:HB2	63:SQ:221:PRO:HB3	1.74	0.70
54:SH:91:ASP:HB3	54:SH:95:GLY:H	1.56	0.70
13:LK:41:ILE:HD11	13:LK:67:ALA:HB1	1.74	0.70
5:E:174:U:H3	5:E:266:A:H62	1.39	0.69
67:SU:140:VAL:HG12	67:SU:150:GLN:HG3	1.73	0.69
62:SP:53:THR:HG22	62:SP:161:PRO:HG2	1.74	0.69
64:SR:42:GLY:HA2	64:SR:68:ILE:HD11	1.75	0.69
72:SZ:42:VAL:HG12	72:SZ:67:VAL:HG23	1.73	0.69
74:Sb:105:THR:HG23	74:Sb:126:LEU:HD13	1.73	0.69
67:SU:75:THR:HG23	67:SU:76:LYS:HD2	1.74	0.69
47:SA:220:PRO:HA	61:SO:193:ILE:HD11	1.76	0.68
66:ST:20:ASP:HB3	66:ST:23:ARG:HB2	1.75	0.68
1:A:3165:A:H61	1:A:3285:C:H42	1.39	0.68
24:LV:11:THR:HG22	24:LV:14:MET:HE3	1.76	0.68
67:SU:46:ILE:HG12	67:SU:60:ILE:HG13	1.76	0.67
2:B:44:C:H4'	9:LG:152:ARG:HG3	1.77	0.67
5:E:647:G:H22	5:E:687:G:H1	1.40	0.67
53:SG:44:LYS:HG3	53:SG:47:ARG:HH21	1.59	0.67
47:SA:39:VAL:HA	47:SA:48:VAL:HG12	1.77	0.67
62:SP:107:PHE:HB2	62:SP:135:GLU:HG2	1.76	0.67
57:SK:55:PRO:HB3	57:SK:88:ILE:HD11	1.77	0.66
47:SA:40:ARG:HE	56:SJ:110:PRO:HG2	1.60	0.66
63:SQ:128:LYS:HB2	63:SQ:134:VAL:HG12	1.76	0.66
54:SH:69:ILE:HG22	54:SH:73:MET:HE2	1.78	0.66
1:A:990:U:H4'	24:LV:100:LYS:HB3	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SH:24:GLY:HA2	54:SH:58:ALA:HB3	1.77	0.66
1:A:2193:U:H5'	1:A:2194:G:H5'	1.77	0.65
5:E:1231:U:H3	5:E:1254:U:H3	1.43	0.65
33:Le:51:LEU:HD11	37:Li:90:ILE:HG22	1.77	0.65
50:SD:33:ARG:HH21	50:SD:36:LEU:HD22	1.60	0.65
72:SZ:20:TYR:HB3	72:SZ:27:PHE:HB2	1.78	0.65
18:LP:183:THR:HG22	18:LP:187:ARG:HG3	1.77	0.65
9:LG:64:ILE:HD12	9:LG:109:THR:HG21	1.77	0.65
48:SB:89:ILE:HD11	48:SB:134:VAL:HG12	1.77	0.65
49:SC:58:GLN:HE21	49:SC:60:SER:HB2	1.62	0.65
67:SU:144:VAL:HA	74:Sb:42:GLN:HE21	1.62	0.64
5:E:1217:A:H1'	49:SC:44:LYS:HE3	1.79	0.64
48:SB:41:LYS:HB2	48:SB:67:PRO:HB2	1.78	0.64
62:SP:13:ASP:HA	62:SP:16:LEU:HD12	1.77	0.64
64:SR:56:ILE:HG23	64:SR:61:LEU:HB2	1.79	0.64
67:SU:33:GLU:HG2	67:SU:34:LEU:HD22	1.79	0.64
1:A:1639:C:H5'	37:Li:52:GLN:HG2	1.78	0.64
67:SU:28:GLU:HB2	67:SU:38:LEU:HD11	1.80	0.64
69:SW:141:VAL:HG21	69:SW:146:PHE:HE2	1.63	0.63
12:LJ:203:VAL:HG21	12:LJ:211:LEU:HD22	1.81	0.63
16:LN:3:ILE:HD11	31:Lc:34:MET:HA	1.80	0.63
48:SB:98:MET:HE1	48:SB:107:LYS:HD2	1.79	0.63
30:Lb:27:LYS:HB3	30:Lb:42:LEU:HD12	1.81	0.63
5:E:1426:C:H3'	5:E:1427:A:H4'	1.80	0.63
61:SO:262:VAL:HG13	61:SO:271:VAL:HB	1.81	0.63
56:SJ:61:LYS:HB2	56:SJ:86:ILE:HB	1.79	0.63
56:SJ:96:PRO:HD2	56:SJ:99:ILE:HD12	1.81	0.63
22:LT:105:LEU:HD13	22:LT:138:LEU:HD23	1.81	0.62
13:LK:91:ARG:HD2	13:LK:143:GLU:HB2	1.80	0.62
49:SC:16:PHE:HB2	49:SC:76:LEU:HD11	1.80	0.62
14:LL:170:LYS:HA	14:LL:177:ASP:HA	1.81	0.62
67:SU:10:SER:HB2	67:SU:44:LYS:HA	1.80	0.62
64:SR:170:ILE:HB	64:SR:197:TYR:HB2	1.81	0.62
1:A:597:G:H2'	1:A:598:A:H8	1.64	0.62
72:SZ:99:GLN:HE22	77:Se:45:VAL:HA	1.65	0.62
49:SC:14:TYR:HD1	49:SC:17:GLN:HE21	1.46	0.61
60:SN:132:LEU:HD12	60:SN:139:LEU:HB3	1.82	0.61
5:E:385:A:H5''	68:SV:22:ARG:HG2	1.81	0.61
15:LM:48:SER:HB2	15:LM:66:ALA:HB3	1.81	0.61
67:SU:67:LEU:HG	67:SU:94:ALA:HB2	1.82	0.61
71:SY:37:ILE:HA	71:SY:50:ILE:HD11	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:1587:A:H2'	5:E:1588:G:H8	1.64	0.61
65:SS:255:ARG:HA	65:SS:255:ARG:HH11	1.64	0.61
69:SW:119:ALA:HB2	69:SW:128:LEU:HD22	1.82	0.61
70:SX:78:THR:HA	70:SX:84:ILE:HG22	1.81	0.61
5:E:970:A:H3'	5:E:971:A:H8	1.65	0.61
9:LG:41:LYS:HE3	24:LV:93:VAL:HG11	1.83	0.61
1:A:655:C:H2'	1:A:656:A:H8	1.66	0.61
1:A:2208:A:N1	1:A:2236:G:C6	2.69	0.61
65:SS:80:THR:HG23	65:SS:81:THR:HG23	1.81	0.61
66:ST:63:MET:HG2	66:ST:98:ARG:HH11	1.66	0.61
15:LM:91:LEU:HB3	15:LM:95:ASN:HD22	1.65	0.61
54:SH:6:GLN:HG3	57:SK:43:ASP:HA	1.82	0.61
8:LF:283:THR:HG21	8:LF:288:ARG:HH21	1.66	0.60
15:LM:50:ALA:HB2	15:LM:65:ILE:HG12	1.83	0.60
76:Sd:18:LEU:HB2	76:Sd:20:ARG:HD3	1.84	0.60
1:A:2208:A:H2	1:A:2236:G:N1	1.99	0.60
5:E:477:A:H62	5:E:540:G:H1	1.49	0.60
62:SP:48:ILE:HD12	62:SP:161:PRO:HB2	1.84	0.60
67:SU:113:PRO:HG2	67:SU:116:ARG:HB2	1.84	0.60
18:LP:9:GLU:HB3	39:Lk:44:VAL:HG21	1.83	0.60
48:SB:97:LEU:HD21	48:SB:194:LEU:HD11	1.83	0.60
5:E:205:U:H2'	5:E:206:A:H8	1.67	0.60
47:SA:93:ASP:HB3	47:SA:96:LEU:HD23	1.83	0.60
3:C:81:U:H1'	3:C:83:C:H5"	1.84	0.60
7:LE:292:ALA:HB2	7:LE:302:LYS:HD3	1.84	0.60
61:SO:131:ILE:HD11	61:SO:151:VAL:HG21	1.83	0.60
5:E:513:U:H2'	5:E:514:G:C8	2.37	0.60
5:E:153:G:H2'	5:E:154:G:H8	1.66	0.59
6:LD:36:GLU:HG3	6:LD:91:GLY:HA2	1.84	0.59
61:SO:46:LYS:HE3	61:SO:56:VAL:HB	1.83	0.59
5:E:1591:C:H2'	5:E:1592:A:H8	1.67	0.59
9:LG:286:VAL:HG23	14:LL:206:LEU:HD11	1.84	0.59
29:La:101:PRO:HA	29:La:104:LEU:HD12	1.85	0.59
31:Lc:72:VAL:HG13	31:Lc:113:LEU:HD23	1.82	0.59
66:ST:50:PHE:HB3	66:ST:111:LEU:HD22	1.84	0.59
69:SW:128:LEU:HG	69:SW:134:ILE:HG12	1.84	0.59
51:SE:86:VAL:HG12	51:SE:88:GLU:HG3	1.84	0.59
33:Le:55:GLU:HB2	37:Li:94:LEU:HD11	1.84	0.59
64:SR:101:VAL:HG12	64:SR:115:ILE:HG23	1.84	0.59
21:LS:180:ARG:HG3	21:LS:185:LYS:HB2	1.82	0.59
6:LD:52:SER:HB3	6:LD:191:LEU:HD22	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LF:283:THR:HG22	8:LF:285:ASP:H	1.66	0.59
9:LG:51:LEU:HD23	9:LG:64:ILE:HG12	1.83	0.59
48:SB:95:ASN:HA	48:SB:98:MET:HE2	1.84	0.59
57:SK:80:LEU:HD13	57:SK:101:TYR:HE2	1.67	0.59
48:SB:57:SER:HA	58:SL:53:ILE:HB	1.84	0.58
17:LO:46:ILE:HD11	17:LO:56:GLN:HE21	1.68	0.58
75:Sc:6:PRO:HG3	75:Sc:14:LYS:HG2	1.85	0.58
9:LG:182:GLY:HA2	9:LG:194:LEU:HD13	1.85	0.58
1:A:824:C:H5''	6:LD:21:ARG:HD3	1.84	0.58
5:E:800:U:H2'	5:E:801:G:H8	1.68	0.58
13:LK:57:VAL:HG12	13:LK:68:LEU:HD22	1.85	0.58
33:Le:54:SER:HA	33:Le:57:GLU:HG3	1.84	0.58
58:SL:10:ALA:HA	58:SL:32:PHE:HA	1.86	0.58
5:E:29:U:H2'	5:E:30:G:H8	1.69	0.58
15:LM:118:PRO:HD3	54:SH:13:HIS:HD2	1.68	0.58
75:Sc:70:LYS:HB3	75:Sc:93:LEU:HD22	1.86	0.58
34:Lf:20:LEU:HD11	34:Lf:32:ALA:HB2	1.85	0.58
68:SV:57:ALA:HB2	68:SV:177:GLY:HA2	1.84	0.58
1:A:2413:A:H2'	1:A:2414:G:H8	1.69	0.58
5:E:1:U:H5'	64:SR:179:VAL:HG13	1.86	0.58
13:LK:89:LYS:HG2	13:LK:145:VAL:HG22	1.84	0.58
50:SD:61:VAL:O	50:SD:120:VAL:HA	2.04	0.58
1:A:2514:U:H5'	12:LJ:68:ARG:HG3	1.86	0.58
48:SB:77:TYR:HA	48:SB:83:ARG:HG2	1.86	0.58
52:SF:78:VAL:HA	52:SF:81:ILE:HD12	1.84	0.58
61:SO:38:ARG:HG2	61:SO:67:ILE:HG23	1.85	0.58
32:Ld:14:ARG:HG2	32:Ld:18:ARG:HH21	1.67	0.57
1:A:2208:A:N1	1:A:2236:G:O6	2.37	0.57
50:SD:26:ASP:HA	50:SD:29:LYS:HG2	1.86	0.57
3:C:150:G:H21	12:LJ:59:GLN:HE22	1.52	0.57
50:SD:42:ALA:HB2	50:SD:124:LYS:HE3	1.86	0.57
50:SD:81:ASP:HB2	50:SD:85:LYS:HB2	1.86	0.57
80:n:10:A:H61	80:n:25:C:N4	1.95	0.57
6:LD:51:ASP:HB3	6:LD:54:ARG:HB3	1.86	0.57
8:LF:313:LEU:HD23	8:LF:315:LYS:HE2	1.85	0.57
54:SH:44:ASN:HD21	54:SH:48:LYS:HE3	1.69	0.57
71:SY:46:THR:H	71:SY:49:GLN:HE21	1.53	0.57
74:Sb:6:VAL:HG22	74:Sb:34:ILE:HD11	1.85	0.57
54:SH:86:LEU:HD23	54:SH:99:HIS:HB2	1.85	0.57
61:SO:69:GLN:HE21	61:SO:85:TRP:HE1	1.52	0.57
66:ST:67:VAL:HG23	66:ST:99:GLY:HA2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SQ:89:ASP:HB3	63:SQ:223:PHE:HE1	1.69	0.57
68:SV:39:GLY:HA2	68:SV:61:GLU:HG3	1.87	0.57
5:E:343:C:H2'	5:E:344:A:H8	1.70	0.57
48:SB:53:VAL:HG11	48:SB:62:VAL:HG11	1.87	0.57
64:SR:53:ILE:HA	64:SR:56:ILE:HD12	1.87	0.56
5:E:1556:A:H2'	51:SE:40:ARG:HH11	1.70	0.56
72:SZ:111:ARG:HE	77:Se:58:VAL:HG12	1.69	0.56
5:E:298:C:H5''	65:SS:38:LEU:HB2	1.87	0.56
8:LF:309:ARG:HH21	8:LF:312:VAL:HG12	1.70	0.56
12:LJ:148:ALA:HA	12:LJ:201:THR:HG22	1.86	0.56
15:LM:60:ARG:HB2	15:LM:63:GLU:HB2	1.87	0.56
76:Sd:32:ARG:HH21	76:Sd:35:VAL:HG12	1.71	0.56
46:Lr:30:GLU:HA	46:Lr:33:GLN:HG2	1.86	0.56
80:n:62:C:H2'	80:n:63:G:H8	1.70	0.56
5:E:1657:U:H5'	5:E:1658:G:H5''	1.88	0.56
30:Lb:25:ILE:HA	30:Lb:43:VAL:HG12	1.87	0.56
1:A:1661:G:H2'	1:A:1662:G:C8	2.40	0.56
7:LE:81:THR:HG21	7:LE:322:ILE:HD12	1.86	0.56
68:SV:34:ALA:HB2	68:SV:56:ARG:HD2	1.88	0.56
16:LN:124:ILE:HB	38:Lj:119:LYS:HE3	1.88	0.56
24:LV:84:TYR:HB2	32:Ld:24:PRO:HD3	1.88	0.56
67:SU:49:ILE:HB	67:SU:57:ALA:HB3	1.87	0.56
66:ST:159:ARG:HD2	66:ST:172:ALA:HB2	1.88	0.56
1:A:571:U:H2'	1:A:572:A:H8	1.70	0.56
5:E:1171:A:H2'	5:E:1172:G:C8	2.41	0.56
14:LL:30:LYS:HG2	14:LL:63:GLU:HG3	1.88	0.56
30:Lb:24:VAL:HG21	30:Lb:87:LEU:HB3	1.87	0.56
17:LO:48:GLY:HA3	17:LO:53:VAL:HB	1.87	0.56
51:SE:108:ARG:H	51:SE:111:MET:HE3	1.71	0.56
73:Sa:1:MET:HB3	73:Sa:10:GLU:HB2	1.88	0.56
5:E:514:G:H2'	5:E:515:A:H8	1.70	0.55
6:LD:112:ILE:HG13	46:Lr:79:VAL:HG22	1.87	0.55
5:E:297:U:H5''	65:SS:37:LYS:HD2	1.87	0.55
48:SB:126:ASP:HB2	57:SK:58:ARG:HH22	1.71	0.55
61:SO:249:ARG:HH21	61:SO:299:GLN:HE22	1.51	0.55
62:SP:41:ARG:HD2	62:SP:42:PRO:HD2	1.87	0.55
12:LJ:84:ARG:HG3	12:LJ:84:ARG:HH11	1.72	0.55
1:A:1103:A:H5''	11:LI:158:LYS:HD3	1.89	0.55
6:LD:189:TYR:HA	6:LD:192:LYS:HB2	1.88	0.55
8:LF:181:VAL:HG11	8:LF:224:GLY:HA3	1.87	0.55
67:SU:62:VAL:O	67:SU:94:ALA:HA	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LN:123:ILE:HG22	38:Lj:118:ILE:HG12	1.88	0.55
5:E:780:A:H2	76:Sd:8:ARG:HH12	1.54	0.55
48:SB:94:THR:HG22	48:SB:114:ILE:HG13	1.88	0.55
61:SO:221:MET:HG2	61:SO:233:THR:HG23	1.89	0.55
5:E:871:G:H2'	5:E:872:G:C8	2.41	0.55
5:E:891:A:H2'	5:E:892:A:H8	1.71	0.55
5:E:1171:A:H2'	5:E:1172:G:H8	1.72	0.55
5:E:1785:U:H2'	5:E:1786:G:H8	1.71	0.55
47:SA:172:THR:HG22	47:SA:185:LYS:HG3	1.87	0.55
50:SD:29:LYS:HE2	50:SD:100:TRP:CE2	2.41	0.55
1:A:598:A:H4'	8:LF:325:LEU:HD13	1.88	0.55
5:E:1588:G:H1	5:E:1608:U:H3	1.54	0.55
8:LF:193:LYS:HG2	8:LF:198:ARG:HG2	1.89	0.55
14:LL:76:MET:HE1	14:LL:144:ASN:HD21	1.71	0.55
1:A:2555:G:N7	37:Li:95:ILE:HD11	2.22	0.55
5:E:1483:A:H4'	52:SF:72:GLY:H	1.70	0.55
66:ST:57:ASP:HB3	66:ST:106:LEU:HD23	1.87	0.55
5:E:1727:G:H2'	5:E:1728:A:C8	2.42	0.55
26:LX:129:VAL:O	26:LX:133:SER:HB3	2.07	0.55
73:Sa:15:ARG:HH21	73:Sa:24:ILE:HG21	1.72	0.54
9:LG:211:LEU:HB3	9:LG:219:PHE:HB2	1.87	0.54
50:SD:54:ARG:HH22	60:SN:129:GLY:N	2.05	0.54
1:A:655:C:H2'	1:A:656:A:C8	2.43	0.54
5:E:148:A:N6	5:E:166:C:N3	2.55	0.54
5:E:1344:A:H2'	5:E:1345:A:C8	2.42	0.54
5:E:1586:A:H3'	5:E:1587:A:H8	1.71	0.54
23:LU:8:GLN:HB3	23:LU:64:ILE:HD11	1.88	0.54
56:SJ:24:ILE:HB	56:SJ:91:ILE:HG22	1.89	0.54
62:SP:155:PHE:HB3	73:Sa:60:ARG:HH21	1.73	0.54
1:A:2436:U:H4'	12:LJ:70:LYS:HD3	1.90	0.54
9:LG:111:GLN:HE22	9:LG:252:ALA:HB2	1.72	0.54
56:SJ:21:LYS:HE2	56:SJ:119:ALA:HB2	1.90	0.54
1:A:1553:U:H4'	1:A:1554:U:H5'	1.89	0.54
1:A:2364:G:H22	1:A:2396:G:H1'	1.72	0.54
15:LM:6:GLN:HB2	15:LM:8:PRO:HD3	1.89	0.54
41:Lm:12:LEU:HB3	41:Lm:16:ARG:HH21	1.73	0.54
66:ST:4:ASN:O	66:ST:110:ALA:HA	2.07	0.54
5:E:1402:G:H5'	53:SG:4:VAL:HG22	1.89	0.54
7:LE:160:VAL:O	7:LE:180:GLU:HA	2.08	0.54
52:SF:7:VAL:HG22	52:SF:22:VAL:HB	1.89	0.54
5:E:1549:C:H5''	51:SE:39:ALA:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LK:1:MET:HE1	23:LU:138:GLN:HG3	1.90	0.54
30:Lb:23:VAL:HG12	30:Lb:45:GLY:HA3	1.90	0.54
78:Sf:14:SER:HA	78:Sf:17:ARG:HG3	1.90	0.54
1:A:1786:G:H2'	1:A:1787:A:C8	2.42	0.53
5:E:153:G:H2'	5:E:154:G:C8	2.42	0.53
5:E:590:C:H2'	5:E:591:A:H8	1.72	0.53
11:LI:144:ILE:HD12	11:LI:189:ILE:HD12	1.89	0.53
27:LY:6:ASP:HB3	27:LY:10:GLY:H	1.72	0.53
16:LN:166:ALA:HB1	31:Lc:147:LEU:HD21	1.91	0.53
25:LW:19:VAL:HG12	25:LW:105:LEU:HD22	1.90	0.53
5:E:1587:A:H2'	5:E:1588:G:C8	2.42	0.53
6:LD:96:LEU:HD12	6:LD:166:ILE:HD13	1.89	0.53
8:LF:23:PRO:HB3	8:LF:259:ASP:HB2	1.91	0.53
15:LM:17:LEU:HD23	15:LM:129:VAL:HG22	1.90	0.53
74:Sb:111:MET:HG3	74:Sb:115:GLU:HB3	1.90	0.53
7:LE:13:HIS:CD2	7:LE:15:GLY:H	2.26	0.53
35:Lg:82:LEU:HD21	35:Lg:112:ALA:HB2	1.91	0.53
17:LO:55:ARG:HE	23:LU:70:THR:HB	1.74	0.53
68:SV:119:GLN:HG3	68:SV:150:ALA:HB2	1.91	0.53
5:E:924:A:H2'	5:E:925:G:C8	2.43	0.53
5:E:1662:G:H2'	5:E:1663:G:H8	1.74	0.53
31:Lc:86:LYS:HE3	31:Lc:89:GLN:HE21	1.72	0.53
5:E:319:U:H4'	5:E:323:A:C8	2.44	0.53
65:SS:182:TYR:HB2	65:SS:228:ILE:HD13	1.90	0.53
67:SU:60:ILE:HB	67:SU:92:PHE:HD1	1.72	0.53
46:Lr:36:ARG:HG2	46:Lr:48:LYS:HD3	1.90	0.53
53:SG:115:LEU:HB3	53:SG:117:LEU:HD23	1.91	0.53
1:A:728:G:H5''	21:LS:43:PRO:HB2	1.90	0.53
5:E:905:A:H5''	72:SZ:52:ARG:HG2	1.90	0.53
14:LL:51:HIS:CD2	14:LL:168:SER:HB2	2.44	0.53
1:A:3016:A:H2'	1:A:3017:A:H8	1.74	0.53
5:E:1672:G:H2'	5:E:1673:G:C8	2.44	0.53
15:LM:18:VAL:HG12	15:LM:70:THR:HG23	1.91	0.53
38:Lj:105:ARG:O	38:Lj:109:ILE:HD12	2.09	0.53
65:SS:175:PHE:HE1	65:SS:198:LYS:HD2	1.73	0.53
68:SV:101:ILE:HD12	68:SV:184:LEU:HD11	1.90	0.53
1:A:1717:U:H2'	1:A:1718:G:C8	2.44	0.52
3:C:8:C:H2'	3:C:9:A:H8	1.74	0.52
69:SW:159:ALA:HB3	69:SW:162:SER:HB3	1.90	0.52
5:E:65:A:H2	5:E:84:A:H62	1.56	0.52
5:E:1067:C:H5''	63:SQ:150:VAL:HG22	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:SA:70:THR:O	47:SA:74:GLN:HB2	2.09	0.52
55:SI:61:VAL:HG13	55:SI:76:LEU:HD11	1.90	0.52
63:SQ:90:GLU:HB3	63:SQ:97:LEU:HD12	1.92	0.52
76:Sd:27:VAL:O	76:Sd:68:LYS:HA	2.08	0.52
1:A:620:U:H4'	20:LR:167:ARG:HH22	1.74	0.52
1:A:1805:C:H2'	1:A:1806:A:H8	1.74	0.52
5:E:142:G:H22	5:E:173:A:H2	1.55	0.52
21:LS:23:ASN:HB3	21:LS:26:LEU:HB3	1.90	0.52
33:Le:34:LEU:HD21	33:Le:42:ILE:HG21	1.90	0.52
38:Lj:66:VAL:HG12	38:Lj:80:LEU:HD11	1.92	0.52
48:SB:63:GLN:HG3	48:SB:86:GLN:HA	1.90	0.52
1:A:1497:C:H2'	1:A:1498:A:H8	1.74	0.52
1:A:1689:U:H5''	22:LT:61:SER:HB3	1.92	0.52
61:SO:93:ASP:HB2	61:SO:100:TYR:HE1	1.74	0.52
61:SO:172:ALA:HB2	61:SO:202:LEU:HD13	1.92	0.52
61:SO:181:TRP:HD1	61:SO:188:ILE:HA	1.75	0.52
1:A:2424:A:H61	6:LD:230:VAL:HG11	1.74	0.52
5:E:513:U:H2'	5:E:514:G:H8	1.73	0.52
5:E:1210:C:H2'	5:E:1211:A:H8	1.75	0.52
62:SP:144:ILE:HG12	62:SP:158:VAL:HB	1.91	0.52
63:SQ:103:MET:HB3	63:SQ:215:VAL:HG22	1.90	0.52
63:SQ:164:ILE:HD12	63:SQ:201:THR:HB	1.92	0.52
67:SU:82:GLU:HG3	67:SU:90:VAL:HG12	1.90	0.52
35:Lg:101:SER:HA	35:Lg:125:ARG:HH21	1.75	0.52
56:SJ:82:TYR:HB3	59:SM:52:PHE:HB3	1.91	0.52
69:SW:149:ARG:HB2	69:SW:152:SER:HB3	1.90	0.52
1:A:597:G:H5''	11:LI:41:ARG:HD2	1.90	0.52
67:SU:32:PRO:HA	67:SU:35:LYS:HE3	1.91	0.52
72:SZ:16:VAL:HG12	72:SZ:18:ARG:HG2	1.90	0.52
1:A:1411:C:H2'	1:A:1412:G:H8	1.75	0.52
16:LN:76:THR:HG22	16:LN:101:ARG:HB3	1.91	0.52
33:Le:51:LEU:HD13	37:Li:91:ARG:HG2	1.91	0.52
1:A:3015:G:H2'	1:A:3016:A:H8	1.74	0.52
34:Lf:77:ARG:HD2	34:Lf:89:LEU:HD23	1.91	0.52
73:Sa:31:SER:HB2	73:Sa:56:SER:HA	1.91	0.52
1:A:3160:U:H3	1:A:3290:G:H1	1.57	0.52
5:E:868:G:N2	5:E:960:U:O2	2.31	0.52
15:LM:54:VAL:HG12	15:LM:57:PHE:H	1.74	0.52
19:LQ:125:ARG:HG3	19:LQ:129:LEU:HD22	1.91	0.52
35:Lg:82:LEU:HD22	35:Lg:108:ILE:HG23	1.92	0.52
72:SZ:17:ALA:HA	72:SZ:30:VAL:HG22	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:LL:30:LYS:HE2	14:LL:66:GLU:HG2	1.91	0.51
21:LS:67:ILE:HG23	21:LS:81:VAL:HG21	1.91	0.51
50:SD:62:LEU:HD11	50:SD:72:ILE:HD13	1.92	0.51
6:LD:135:ILE:HB	6:LD:149:ARG:HB3	1.92	0.51
56:SJ:64:LYS:HA	56:SJ:82:TYR:O	2.09	0.51
69:SW:73:GLY:O	69:SW:77:ILE:HG13	2.10	0.51
5:E:480:G:H1	5:E:508:U:H3	1.57	0.51
9:LG:33:ARG:HH11	24:LV:27:LEU:HG	1.75	0.51
29:La:100:HIS:CD2	29:La:102:SER:HB3	2.45	0.51
56:SJ:22:ILE:HG22	56:SJ:93:LEU:HB2	1.92	0.51
62:SP:155:PHE:HA	73:Sa:60:ARG:HE	1.75	0.51
70:SX:16:GLN:HE21	70:SX:61:THR:HG23	1.76	0.51
71:SY:17:PRO:HG3	78:Sf:28:PRO:HG3	1.91	0.51
1:A:664:U:H2'	1:A:665:A:C8	2.45	0.51
1:A:800:G:H1	8:LF:104:LYS:HZ1	1.58	0.51
1:A:1119:C:H2'	1:A:1120:A:H8	1.76	0.51
1:A:1798:A:H2'	1:A:1799:A:C8	2.45	0.51
1:A:2526:C:H2'	1:A:2527:G:H8	1.76	0.51
5:E:556:A:H4'	79:Sg:56:MET:HG2	1.92	0.51
5:E:560:U:H2'	5:E:561:G:H8	1.76	0.51
5:E:1606:C:H2'	5:E:1607:G:H8	1.75	0.51
9:LG:32:GLN:HE22	9:LG:149:GLY:H	1.59	0.51
15:LM:30:LEU:HD11	15:LM:47:GLN:HG2	1.91	0.51
1:A:289:A:H2'	1:A:290:G:H8	1.76	0.51
1:A:3343:G:H21	1:A:3362:A:H2	1.58	0.51
68:SV:26:LYS:HG3	68:SV:29:LEU:HD23	1.92	0.51
1:A:370:U:H4'	1:A:404:G:H5'	1.92	0.51
5:E:1535:U:H2'	48:SB:187:ILE:HD11	1.93	0.51
8:LF:161:LYS:HB2	8:LF:164:GLU:HG3	1.93	0.51
49:SC:23:ALA:HB3	49:SC:64:TYR:HB2	1.91	0.51
80:n:27:C:H2'	80:n:28:A:H8	1.75	0.51
1:A:1378:U:H2'	1:A:1379:G:H8	1.75	0.51
5:E:1474:G:H2'	5:E:1475:A:H8	1.76	0.51
11:LI:95:ILE:HB	11:LI:100:ARG:HG3	1.92	0.51
14:LL:74:LYS:O	14:LL:78:THR:HG23	2.10	0.51
34:Lf:55:LEU:HB2	34:Lf:95:PRO:HD3	1.93	0.51
54:SH:68:ARG:O	54:SH:72:ILE:HG12	2.10	0.51
15:LM:19:LEU:HD22	15:LM:125:MET:HE2	1.92	0.51
21:LS:67:ILE:HG12	21:LS:81:VAL:HG11	1.93	0.51
52:SF:5:PRO:HG2	52:SF:24:ALA:HB2	1.93	0.51
1:A:597:G:H2'	1:A:598:A:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1799:A:H2'	1:A:1800:A:H8	1.76	0.51
61:SO:206:PRO:HG3	61:SO:247:PRO:HA	1.93	0.51
74:Sb:105:THR:HG22	74:Sb:110:ILE:HG12	1.91	0.51
80:n:62:C:H2'	80:n:63:G:C8	2.45	0.51
19:LQ:27:LEU:HD11	19:LQ:102:LEU:HB2	1.93	0.50
28:LZ:33:ARG:HH11	28:LZ:33:ARG:HG2	1.77	0.50
46:Lr:26:VAL:O	46:Lr:30:GLU:HB2	2.11	0.50
61:SO:224:ASN:HB2	61:SO:231:MET:HE3	1.93	0.50
65:SS:198:LYS:HG2	65:SS:208:VAL:HG12	1.92	0.50
66:ST:18:ILE:HD11	66:ST:24:ILE:HD13	1.93	0.50
1:A:1369:A:H4'	31:Lc:21:ARG:HG3	1.93	0.50
5:E:778:G:H2'	5:E:779:U:H2'	1.92	0.50
71:SY:38:VAL:O	71:SY:42:ARG:HG2	2.11	0.50
5:E:849:C:H2'	5:E:850:A:H8	1.75	0.50
10:LH:40:LEU:HD13	10:LH:84:VAL:HG21	1.94	0.50
1:A:1666:G:H2'	1:A:1667:A:H8	1.76	0.50
1:A:2553:U:C4	37:Li:95:ILE:HG22	2.47	0.50
1:A:2697:A:H2'	1:A:2698:G:C8	2.46	0.50
5:E:1524:A:H2'	5:E:1525:A:C8	2.47	0.50
13:LK:118:LEU:HD21	13:LK:167:VAL:HG22	1.94	0.50
47:SA:12:VAL:HG12	56:SJ:84:MET:HE3	1.92	0.50
51:SE:41:VAL:HG23	51:SE:84:ILE:HD13	1.92	0.50
55:SI:21:PHE:HA	55:SI:24:ARG:HE	1.76	0.50
62:SP:27:ARG:HG2	62:SP:45:VAL:HG22	1.94	0.50
74:Sb:90:THR:O	74:Sb:94:LEU:HB2	2.10	0.50
1:A:2960:C:H2'	1:A:2961:G:C8	2.47	0.50
48:SB:120:ILE:HD11	57:SK:98:GLN:HE21	1.75	0.50
53:SG:46:LEU:O	53:SG:50:ILE:HG13	2.11	0.50
61:SO:112:SER:HB2	61:SO:153:GLN:HA	1.94	0.50
1:A:307:A:H2'	1:A:308:A:C8	2.47	0.50
53:SG:60:ARG:HH21	53:SG:66:VAL:HG23	1.75	0.50
54:SH:46:VAL:HG13	54:SH:72:ILE:HB	1.92	0.50
61:SO:10:ARG:HH12	61:SO:51:ASP:HA	1.77	0.50
62:SP:74:VAL:HG13	62:SP:118:PRO:HB3	1.92	0.50
70:SX:99:ARG:HG3	75:Sc:12:ALA:HB2	1.94	0.50
3:C:8:C:H2'	3:C:9:A:C8	2.46	0.50
5:E:1429:G:H21	56:SJ:72:ASN:ND2	2.10	0.50
66:ST:57:ASP:HA	66:ST:107:ALA:H	1.75	0.50
69:SW:48:GLN:O	69:SW:52:ILE:HD12	2.11	0.50
5:E:544:A:H4'	79:Sg:28:LYS:NZ	2.27	0.50
38:Lj:77:PRO:HD2	38:Lj:80:LEU:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2357:A:H2'	1:A:2358:A:H8	1.76	0.50
14:LL:66:GLU:O	14:LL:70:ILE:HG13	2.11	0.50
15:LM:101:ASN:HD22	15:LM:130:VAL:HA	1.77	0.50
56:SJ:28:SER:HB2	56:SJ:112:VAL:HA	1.94	0.50
60:SN:138:ARG:NE	60:SN:139:LEU:H	2.10	0.50
61:SO:91:LEU:HD23	61:SO:100:TYR:HB2	1.93	0.50
66:ST:181:PRO:HA	66:ST:184:LEU:HG	1.94	0.50
1:A:2344:U:H2'	1:A:2345:A:H8	1.76	0.49
5:E:337:G:H3'	70:SX:133:LYS:HB2	1.93	0.49
16:LN:37:ASN:O	16:LN:41:THR:HG23	2.12	0.49
17:LO:56:GLN:HG3	17:LO:58:ILE:HG23	1.94	0.49
17:LO:128:ARG:HA	17:LO:131:VAL:HG22	1.94	0.49
43:Lo:98:LYS:HG3	43:Lo:118:THR:HG21	1.92	0.49
52:SF:47:LYS:HA	52:SF:50:GLU:HG3	1.94	0.49
55:SI:31:PRO:HG2	55:SI:34:VAL:HB	1.94	0.49
72:SZ:13:VAL:HG23	72:SZ:76:ILE:HA	1.93	0.49
1:A:2101:C:HO2'	1:A:2102:U:H6	1.60	0.49
20:LR:29:THR:HG22	20:LR:119:VAL:HG21	1.94	0.49
29:La:11:ASP:HB3	29:La:14:LYS:HB2	1.93	0.49
47:SA:76:ARG:HG3	47:SA:77:PHE:HD2	1.77	0.49
61:SO:151:VAL:HA	61:SO:173:GLY:HA3	1.94	0.49
1:A:2555:G:C5	37:Li:95:ILE:HD11	2.47	0.49
5:E:800:U:H2'	5:E:801:G:C8	2.47	0.49
7:LE:41:VAL:HA	7:LE:185:GLY:HA3	1.94	0.49
7:LE:47:LEU:HD22	7:LE:335:ILE:HD11	1.93	0.49
9:LG:205:SER:HA	9:LG:208:MET:HE3	1.93	0.49
34:Lf:51:LEU:HB3	34:Lf:55:LEU:HD23	1.94	0.49
48:SB:89:ILE:HA	48:SB:92:ARG:HG3	1.93	0.49
51:SE:111:MET:HB3	54:SH:119:ILE:HG21	1.92	0.49
62:SP:80:THR:HA	62:SP:83:GLN:HG3	1.93	0.49
65:SS:61:VAL:O	65:SS:65:LEU:HD12	2.12	0.49
1:A:3023:U:H2'	1:A:3024:A:H8	1.75	0.49
5:E:891:A:H2'	5:E:892:A:C8	2.48	0.49
5:E:1210:C:H2'	5:E:1211:A:C8	2.47	0.49
5:E:1359:C:H5''	55:SI:134:ARG:HH21	1.77	0.49
5:E:1382:A:H2'	5:E:1383:G:C8	2.47	0.49
5:E:1606:C:H2'	5:E:1607:G:C8	2.47	0.49
9:LG:76:ALA:HB3	9:LG:109:THR:HG22	1.94	0.49
1:A:821:U:H2'	1:A:822:G:H8	1.77	0.49
3:C:9:A:H2'	3:C:10:A:C8	2.47	0.49
5:E:479:C:H2'	5:E:480:G:H8	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LG:50:ARG:O	9:LG:64:ILE:HA	2.13	0.49
53:SG:41:ILE:HG23	53:SG:46:LEU:HD23	1.94	0.49
62:SP:21:ASN:HB3	62:SP:24:LEU:HD23	1.95	0.49
62:SP:200:ASP:HA	62:SP:203:PHE:CD2	2.47	0.49
71:SY:5:HIS:HB3	71:SY:117:LEU:HD13	1.94	0.49
1:A:985:U:H2'	1:A:986:U:H6	1.77	0.49
1:A:2597:U:H2'	1:A:2598:G:H8	1.76	0.49
21:LS:43:PRO:HA	21:LS:46:LYS:HD2	1.94	0.49
55:SI:76:LEU:HD12	55:SI:80:TYR:HE2	1.77	0.49
65:SS:129:VAL:HG22	65:SS:139:VAL:HG12	1.93	0.49
80:n:75:C:H3'	80:n:76:A:H4'	1.95	0.49
1:A:1336:U:H2'	1:A:1337:A:H8	1.77	0.49
1:A:3057:U:H5'	1:A:3086:A:H61	1.78	0.49
3:C:150:G:H21	12:LJ:59:GLN:NE2	2.10	0.49
5:E:1063:U:H2'	5:E:1064:G:H8	1.77	0.49
42:Ln:15:LYS:O	42:Ln:19:GLN:HG2	2.13	0.49
48:SB:76:ARG:HE	52:SF:122:ARG:HD3	1.78	0.49
50:SD:60:VAL:HG22	50:SD:122:VAL:HG22	1.95	0.49
57:SK:90:LYS:HB2	57:SK:104:ALA:HA	1.93	0.49
61:SO:200:ASN:HD22	61:SO:241:PHE:HA	1.76	0.49
67:SU:151:LYS:HA	67:SU:182:VAL:O	2.13	0.49
1:A:1576:G:H2'	1:A:1577:G:C8	2.48	0.49
2:B:64:A:H5'	2:B:65:G:H5''	1.95	0.49
9:LG:260:PHE:HB3	9:LG:264:GLN:HE21	1.78	0.49
36:Lh:32:ILE:HB	36:Lh:35:VAL:HG22	1.95	0.49
57:SK:74:SER:O	57:SK:78:ILE:HG12	2.12	0.49
67:SU:8:ILE:HD11	67:SU:21:ALA:HB1	1.93	0.49
10:LH:66:THR:HB	10:LH:76:LEU:HD23	1.94	0.49
14:LL:49:CYS:SG	14:LL:168:SER:HB3	2.53	0.49
16:LN:47:ALA:HB1	16:LN:48:PRO:HD2	1.94	0.49
79:Sg:55:ARG:HH21	79:Sg:58:PRO:HA	1.78	0.49
1:A:567:G:H2'	1:A:568:G:C8	2.48	0.49
1:A:1497:C:H2'	1:A:1498:A:C8	2.47	0.49
1:A:3255:U:H2'	1:A:3256:G:H8	1.76	0.49
5:E:844:A:H2'	5:E:845:G:H8	1.78	0.49
14:LL:180:GLU:HA	14:LL:183:LYS:NZ	2.28	0.49
44:Lp:12:ARG:HH12	44:Lp:15:ARG:HH21	1.60	0.49
63:SQ:33:LYS:HE2	63:SQ:95:ASN:HB3	1.94	0.49
79:Sg:37:ARG:O	79:Sg:41:THR:HG23	2.13	0.49
1:A:627:U:H2'	1:A:628:A:C8	2.48	0.48
5:E:799:A:H4'	65:SS:201:HIS:CE1	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SD:62:LEU:HD13	50:SD:75:VAL:HG11	1.95	0.48
50:SD:91:VAL:HG21	50:SD:97:LEU:HD13	1.94	0.48
51:SE:20:VAL:HG21	51:SE:28:MET:HE1	1.94	0.48
67:SU:140:VAL:HG22	74:Sb:52:TYR:HB3	1.94	0.48
71:SY:40:TYR:HB3	71:SY:45:LEU:HD11	1.95	0.48
78:Sf:19:HIS:CD2	78:Sf:21:LEU:H	2.21	0.48
1:A:1799:A:H2'	1:A:1800:A:C8	2.48	0.48
5:E:1241:G:H4'	51:SE:78:THR:HA	1.95	0.48
9:LG:103:LEU:HD11	9:LG:248:ARG:HD3	1.93	0.48
16:LN:170:LEU:HD12	39:Lk:9:ILE:HG22	1.94	0.48
47:SA:123:VAL:HG23	47:SA:134:CYS:HB3	1.95	0.48
1:A:589:A:H1'	1:A:1337:A:H5''	1.95	0.48
1:A:1168:U:H2'	1:A:1169:A:H8	1.78	0.48
1:A:2836:C:H5	1:A:2852:C:H42	1.60	0.48
5:E:86:A:H2'	5:E:87:C:C6	2.49	0.48
5:E:387:A:H2'	5:E:402:C:H5'	1.95	0.48
5:E:478:A:N1	5:E:510:G:O6	2.46	0.48
19:LQ:175:THR:HA	19:LQ:178:VAL:HG12	1.94	0.48
56:SJ:97:VAL:HA	56:SJ:100:VAL:HG22	1.95	0.48
1:A:1419:A:H5''	8:LF:193:LYS:NZ	2.29	0.48
5:E:329:G:H2'	5:E:330:G:H8	1.78	0.48
5:E:1474:G:H2'	5:E:1475:A:C8	2.49	0.48
24:LV:28:SER:O	24:LV:32:LYS:HG2	2.14	0.48
27:LY:4:GLU:HB2	27:LY:13:ILE:HB	1.96	0.48
49:SC:77:ARG:HG2	49:SC:77:ARG:HH11	1.78	0.48
67:SU:49:ILE:HG21	67:SU:172:VAL:HG12	1.96	0.48
79:Sg:49:LEU:HB3	79:Sg:55:ARG:HB2	1.96	0.48
1:A:2351:U:H2'	1:A:2352:A:H8	1.78	0.48
5:E:590:C:H2'	5:E:591:A:C8	2.48	0.48
15:LM:101:ASN:HB3	15:LM:128:TYR:HE1	1.78	0.48
52:SF:42:GLU:HA	52:SF:45:ARG:HB2	1.95	0.48
58:SL:44:VAL:HG21	58:SL:48:VAL:HG21	1.95	0.48
65:SS:67:GLN:HB3	65:SS:69:HIS:CE1	2.48	0.48
78:Sf:2:VAL:HG13	78:Sf:5:GLN:HE21	1.77	0.48
1:A:68:C:H41	1:A:315:C:H5'	1.79	0.48
1:A:2621:G:H22	80:n:73:A:H5''	1.79	0.48
5:E:629:U:H2'	5:E:630:A:H8	1.78	0.48
50:SD:35:ALA:HB1	50:SD:41:LEU:HB2	1.96	0.48
57:SK:89:ILE:HB	57:SK:101:TYR:HB3	1.95	0.48
61:SO:33:LEU:HB3	61:SO:45:TRP:HB2	1.96	0.48
61:SO:123:ILE:HG21	61:SO:169:ILE:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:n:25:C:H3'	80:n:26:G:H8	1.78	0.48
1:A:629:U:H2'	1:A:630:A:C8	2.49	0.48
1:A:2768:U:H2'	1:A:2769:A:H8	1.78	0.48
1:A:3231:U:H2'	1:A:3232:G:H8	1.79	0.48
2:B:112:G:H2'	2:B:113:C:C6	2.48	0.48
5:E:1041:G:H2'	5:E:1042:G:C8	2.49	0.48
9:LG:178:ASN:HA	9:LG:183:TRP:CE3	2.49	0.48
29:La:63:LYS:HG2	29:La:85:VAL:HG13	1.95	0.48
47:SA:27:ARG:HD3	49:SC:58:GLN:HE22	1.78	0.48
50:SD:27:ALA:HB2	50:SD:135:MET:HE3	1.96	0.48
71:SY:52:VAL:O	71:SY:56:ASP:HB2	2.14	0.48
76:Sd:38:ASP:O	76:Sd:42:GLU:HG3	2.14	0.48
80:n:3:C:H2'	80:n:4:G:C8	2.48	0.48
2:B:28:C:H5''	15:LM:137:ARG:HG2	1.94	0.48
27:LY:44:LYS:HB3	27:LY:49:ILE:HD11	1.96	0.48
1:A:2160:G:H2'	1:A:2161:G:H8	1.79	0.48
5:E:325:G:H2'	5:E:326:G:H8	1.79	0.48
16:LN:128:ARG:C	16:LN:129:ASN:HD22	2.22	0.48
76:Sd:83:LYS:HD3	76:Sd:96:LEU:HD22	1.96	0.48
1:A:2107:A:H2	1:A:3344:A:H8	1.62	0.48
16:LN:62:THR:HG23	16:LN:64:LYS:H	1.79	0.48
26:LX:72:LYS:HB3	26:LX:72:LYS:HE3	1.58	0.48
48:SB:65:ARG:NH1	48:SB:66:GLN:HB2	2.28	0.48
55:SI:113:ILE:HG22	55:SI:114:VAL:HG13	1.95	0.48
56:SJ:22:ILE:HD12	56:SJ:22:ILE:HA	1.72	0.48
60:SN:138:ARG:HE	60:SN:139:LEU:H	1.60	0.48
61:SO:300:THR:HG22	61:SO:314:GLN:HB3	1.95	0.48
70:SX:19:ILE:HD11	70:SX:34:TRP:HB2	1.95	0.48
71:SY:34:ILE:O	71:SY:38:VAL:HG23	2.14	0.48
5:E:901:G:H3'	5:E:902:G:H8	1.79	0.47
5:E:1776:A:H2'	5:E:1777:G:C8	2.48	0.47
6:LD:116:VAL:HB	6:LD:126:LEU:HB2	1.96	0.47
48:SB:82:PHE:HB3	58:SL:49:ARG:NH2	2.29	0.47
49:SC:69:THR:O	49:SC:73:VAL:HG23	2.14	0.47
5:E:1477:G:H2'	5:E:1478:G:C8	2.50	0.47
24:LV:78:LYS:HD3	24:LV:87:LYS:HZ2	1.79	0.47
1:A:528:U:H2'	1:A:529:A:C8	2.49	0.47
1:A:2344:U:H2'	1:A:2345:A:C8	2.49	0.47
5:E:1607:G:H2'	5:E:1608:U:C6	2.48	0.47
5:E:1607:G:H2'	5:E:1608:U:H6	1.79	0.47
26:LX:54:LEU:HD21	26:LX:119:GLY:HA3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:SH:82:PRO:HG3	55:SI:36:ILE:HG21	1.97	0.47
59:SM:33:LYS:HG2	59:SM:34:TYR:CD2	2.49	0.47
63:SQ:169:SER:O	63:SQ:173:THR:HG23	2.15	0.47
1:A:2803:A:OP1	45:Lq:60:LYS:HE3	2.14	0.47
25:LW:36:TYR:O	25:LW:40:HIS:HB2	2.14	0.47
58:SL:25:VAL:HG11	58:SL:66:LEU:HD12	1.96	0.47
62:SP:184:LEU:HD22	73:Sa:45:ALA:HB2	1.97	0.47
80:n:27:C:H2'	80:n:28:A:C8	2.49	0.47
1:A:411:U:H2'	1:A:412:G:H8	1.79	0.47
1:A:2526:C:H2'	1:A:2527:G:C8	2.49	0.47
1:A:2571:U:H1'	1:A:2572:C:H2'	1.95	0.47
3:C:83:C:H1'	3:C:85:G:H21	1.79	0.47
35:Lg:101:SER:O	35:Lg:105:ARG:HG3	2.13	0.47
51:SE:24:LYS:HB2	51:SE:24:LYS:HE3	1.73	0.47
53:SG:106:THR:O	53:SG:110:VAL:HG23	2.14	0.47
57:SK:49:ARG:HH21	57:SK:53:GLU:HG2	1.79	0.47
68:SV:156:VAL:HA	68:SV:159:GLN:HG3	1.96	0.47
68:SV:189:LEU:HD13	68:SV:193:LEU:HG	1.95	0.47
77:Se:44:ILE:HG23	77:Se:67:THR:HB	1.95	0.47
1:A:3016:A:H2'	1:A:3017:A:C8	2.49	0.47
5:E:333:A:H5'	68:SV:48:THR:HB	1.96	0.47
5:E:447:U:H2'	5:E:448:C:O4'	2.15	0.47
5:E:1216:C:O2'	5:E:1217:A:H3'	2.13	0.47
47:SA:71:LEU:O	47:SA:75:LYS:HG2	2.14	0.47
48:SB:82:PHE:HB3	58:SL:49:ARG:HH21	1.79	0.47
62:SP:58:VAL:HG12	62:SP:180:GLU:HG3	1.96	0.47
68:SV:48:THR:HG21	68:SV:54:LYS:HE3	1.96	0.47
1:A:1083:G:H2'	1:A:1084:A:C8	2.50	0.47
1:A:2880:U:H1'	7:LE:250:ALA:HB3	1.96	0.47
1:A:3354:U:H5''	1:A:3355:U:H3'	1.97	0.47
5:E:1357:A:H2'	5:E:1358:G:C8	2.49	0.47
8:LF:132:ALA:HA	8:LF:148:ILE:HD11	1.95	0.47
9:LG:36:LEU:HD11	9:LG:147:ASP:HB2	1.97	0.47
9:LG:160:PHE:CE2	9:LG:179:ARG:HG2	2.50	0.47
12:LJ:71:VAL:HG23	12:LJ:76:ALA:HB2	1.95	0.47
26:LX:81:GLN:HE21	26:LX:83:LYS:HB3	1.79	0.47
50:SD:46:ARG:HH12	50:SD:50:LYS:HE3	1.80	0.47
63:SQ:130:SER:HB2	63:SQ:180:THR:HG22	1.95	0.47
1:A:50:U:H2'	1:A:51:A:H8	1.80	0.47
1:A:1694:U:H4'	37:Li:24:LYS:HE3	1.97	0.47
1:A:3121:U:H1'	1:A:3122:A:H5''	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3306:U:H2'	1:A:3307:A:H5''	1.96	0.47
5:E:406:U:H2'	5:E:407:A:C8	2.50	0.47
14:LL:191:LYS:HD3	14:LL:212:GLU:HB2	1.97	0.47
26:LX:32:ARG:HB3	26:LX:64:LYS:HG3	1.95	0.47
31:Lc:134:ALA:O	31:Lc:138:ILE:HG13	2.14	0.47
67:SU:44:LYS:HG3	67:SU:63:PRO:HD3	1.97	0.47
67:SU:74:GLN:O	67:SU:78:THR:HG23	2.15	0.47
1:A:1083:G:H2'	1:A:1084:A:H8	1.79	0.47
1:A:2960:C:H2'	1:A:2961:G:H8	1.80	0.47
5:E:890:C:H2'	5:E:891:A:H8	1.80	0.47
5:E:1357:A:H2'	5:E:1358:G:H8	1.80	0.47
6:LD:133:TYR:HB3	6:LD:168:VAL:HG12	1.97	0.47
7:LE:13:HIS:HD2	7:LE:15:GLY:H	1.62	0.47
22:LT:136:ARG:O	22:LT:140:GLU:HG3	2.15	0.47
54:SH:12:GLN:HG3	54:SH:15:LEU:HB3	1.97	0.47
79:Sg:29:LYS:HA	79:Sg:29:LYS:HD3	1.69	0.47
80:n:11:C:H2'	80:n:12:G:C8	2.50	0.47
1:A:873:C:H3'	1:A:874:U:H4'	1.98	0.47
1:A:3302:U:H3	1:A:3312:U:H3	1.63	0.47
5:E:1566:U:H5'	54:SH:39:GLY:HA3	1.97	0.47
9:LG:208:MET:HG2	9:LG:219:PHE:HE2	1.80	0.47
15:LM:86:VAL:HG11	15:LM:106:ILE:HD13	1.97	0.47
47:SA:76:ARG:HG3	47:SA:77:PHE:CD2	2.50	0.47
49:SC:32:HIS:CE1	49:SC:34:GLU:H	2.33	0.47
77:Se:44:ILE:HG12	77:Se:65:PRO:HG2	1.97	0.47
9:LG:270:LYS:HA	9:LG:273:ARG:HG2	1.98	0.46
64:SR:88:LYS:HD2	64:SR:95:ARG:NH2	2.30	0.46
65:SS:175:PHE:CE1	65:SS:198:LYS:HD2	2.51	0.46
75:Sc:79:ASN:HB2	75:Sc:81:LYS:HG3	1.97	0.46
1:A:631:U:H2'	1:A:632:G:C8	2.50	0.46
1:A:1203:A:H2'	1:A:1204:A:C8	2.50	0.46
5:E:70:C:H2'	5:E:71:A:H8	1.81	0.46
5:E:1331:A:H61	47:SA:161:GLY:HA2	1.80	0.46
5:E:1641:C:H2'	5:E:1642:G:C8	2.50	0.46
9:LG:206:GLN:O	9:LG:210:GLU:HG3	2.16	0.46
61:SO:111:MET:HE3	61:SO:127:ARG:HG3	1.98	0.46
72:SZ:16:VAL:O	72:SZ:30:VAL:HA	2.15	0.46
9:LG:294:ALA:HB1	14:LL:217:PHE:HB3	1.98	0.46
29:La:23:PRO:HG2	29:La:26:GLN:HG3	1.97	0.46
52:SF:60:PHE:HA	52:SF:63:ILE:HD11	1.96	0.46
62:SP:11:PRO:O	62:SP:15:GLN:HG3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:SQ:89:ASP:HB2	63:SQ:228:LEU:HD22	1.97	0.46
1:A:3322:A:H2'	1:A:3323:A:C8	2.50	0.46
5:E:12:U:H2'	5:E:13:C:C6	2.51	0.46
5:E:1506:G:H2'	5:E:1507:G:H8	1.80	0.46
6:LD:47:GLN:HG3	6:LD:49:VAL:HG13	1.97	0.46
19:LQ:61:ALA:HA	19:LQ:70:PRO:HD2	1.97	0.46
23:LU:27:MET:HE2	23:LU:29:ILE:HD11	1.98	0.46
47:SA:8:LYS:HE2	56:SJ:61:LYS:HB3	1.97	0.46
51:SE:87:PRO:HA	51:SE:90:ILE:HG13	1.97	0.46
54:SH:41:ARG:HH21	55:SI:46:PRO:HG3	1.80	0.46
67:SU:8:ILE:HA	67:SU:42:GLN:HG2	1.97	0.46
1:A:627:U:H2'	1:A:628:A:H8	1.81	0.46
1:A:656:A:H2'	1:A:657:A:C8	2.50	0.46
5:E:918:U:H4'	72:SZ:18:ARG:HD2	1.98	0.46
23:LU:81:TYR:CE1	23:LU:90:MET:HE3	2.51	0.46
47:SA:15:GLY:HA3	59:SM:50:ILE:HG23	1.97	0.46
1:A:2222:A:H2'	1:A:2223:A:C8	2.51	0.46
5:E:86:A:H2'	5:E:87:C:H6	1.80	0.46
5:E:766:U:H3	5:E:770:A:H62	1.62	0.46
5:E:939:A:H2'	5:E:940:A:C8	2.50	0.46
5:E:953:G:H2'	5:E:954:G:H8	1.81	0.46
13:LK:6:THR:HG23	13:LK:57:VAL:HG13	1.98	0.46
15:LM:9:MET:HB3	15:LM:10:ARG:H	1.39	0.46
24:LV:68:THR:HG22	24:LV:69:LYS:H	1.80	0.46
48:SB:214:LYS:O	48:SB:218:GLU:HG2	2.16	0.46
60:SN:105:TYR:HB3	60:SN:131:PHE:CD2	2.49	0.46
62:SP:54:TRP:HZ3	62:SP:176:LEU:HD12	1.79	0.46
74:Sb:102:VAL:HG13	74:Sb:113:HIS:HB3	1.97	0.46
1:A:417:A:H2'	1:A:418:A:C8	2.50	0.46
1:A:1576:G:H2'	1:A:1577:G:H8	1.79	0.46
1:A:3233:C:H2'	1:A:3234:A:C8	2.50	0.46
9:LG:36:LEU:HD22	9:LG:50:ARG:HG2	1.96	0.46
11:LI:25:GLN:HG3	11:LI:28:ALA:HB3	1.97	0.46
11:LI:142:SER:O	11:LI:146:GLN:HG3	2.16	0.46
12:LJ:70:LYS:HB3	12:LJ:70:LYS:HE3	1.81	0.46
50:SD:34:THR:HA	50:SD:37:VAL:HG22	1.97	0.46
50:SD:54:ARG:HH12	60:SN:129:GLY:HA3	1.79	0.46
62:SP:136:ALA:HA	62:SP:139:VAL:HG12	1.98	0.46
63:SQ:134:VAL:HG23	63:SQ:218:LEU:HB2	1.97	0.46
63:SQ:173:THR:O	63:SQ:177:GLN:HG3	2.16	0.46
64:SR:159:THR:HG22	64:SR:168:ARG:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2532:U:H2'	1:A:2533:G:C8	2.51	0.46
2:B:7:G:H5''	9:LG:22:ARG:HD3	1.97	0.46
5:E:5:U:H2'	5:E:6:G:H8	1.81	0.46
5:E:783:G:H8	76:Sd:12:VAL:HG12	1.81	0.46
5:E:1661:U:H2'	5:E:1662:G:C8	2.51	0.46
9:LG:122:VAL:HG23	9:LG:125:VAL:HG12	1.97	0.46
36:Lh:92:LYS:HE3	36:Lh:92:LYS:HB3	1.82	0.46
62:SP:48:ILE:HG22	62:SP:149:LEU:HD11	1.97	0.46
65:SS:155:LYS:HA	65:SS:155:LYS:HD3	1.74	0.46
80:n:61:C:H2'	80:n:62:C:C6	2.51	0.46
1:A:2129:U:H2'	1:A:2130:G:C8	2.50	0.46
5:E:252:U:H2'	5:E:253:A:C8	2.51	0.46
5:E:1511:U:H2'	5:E:1512:G:C8	2.51	0.46
15:LM:28:ASP:HA	15:LM:31:THR:HG22	1.98	0.46
21:LS:64:VAL:HA	21:LS:67:ILE:HD12	1.98	0.46
28:LZ:86:VAL:O	28:LZ:120:LYS:HB3	2.15	0.46
54:SH:70:VAL:HA	54:SH:73:MET:HE3	1.97	0.46
63:SQ:7:LYS:HG3	63:SQ:8:ARG:HG3	1.96	0.46
1:A:2213:A:H2'	1:A:2214:A:C8	2.51	0.46
1:A:3295:A:H2'	1:A:3296:A:C8	2.51	0.46
5:E:1268:G:H1'	5:E:1448:G:H5''	1.96	0.46
8:LF:205:PRO:HG2	8:LF:225:VAL:HG13	1.96	0.46
9:LG:95:TRP:HZ3	9:LG:199:ILE:HG12	1.80	0.46
1:A:876:A:H5''	1:A:1890:U:H5''	1.97	0.45
5:E:29:U:H2'	5:E:30:G:C8	2.49	0.45
13:LK:28:VAL:HG12	13:LK:33:THR:HG23	1.98	0.45
31:Lc:27:LYS:HD2	31:Lc:27:LYS:HA	1.69	0.45
62:SP:107:PHE:HB3	62:SP:139:VAL:HG11	1.97	0.45
64:SR:88:LYS:HG2	64:SR:89:GLN:H	1.81	0.45
74:Sb:71:LYS:HD3	74:Sb:128:PHE:HE2	1.81	0.45
1:A:215:G:H5''	29:La:12:ARG:HG3	1.97	0.45
1:A:900:G:H1'	1:A:1589:A:N6	2.31	0.45
1:A:2228:A:H2'	1:A:2229:A:C8	2.51	0.45
5:E:178:U:H4'	5:E:179:A:O5'	2.15	0.45
5:E:762:A:H2'	5:E:763:G:H8	1.81	0.45
12:LJ:73:PRO:HA	12:LJ:76:ALA:HB3	1.97	0.45
63:SQ:149:GLN:NE2	63:SQ:154:SER:HB3	2.27	0.45
1:A:19:U:H2'	1:A:20:A:C8	2.51	0.45
5:E:884:A:H2'	5:E:885:G:C8	2.51	0.45
5:E:1583:A:H1'	5:E:1585:U:C2	2.52	0.45
9:LG:103:LEU:HG	9:LG:247:ILE:HG21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:SV:37:LYS:HA	68:SV:37:LYS:HD3	1.64	0.45
1:A:243:G:H2'	1:A:244:G:O4'	2.16	0.45
1:A:1696:A:H2'	1:A:1697:A:C8	2.51	0.45
1:A:3067:C:H3'	22:LT:62:ARG:HH22	1.81	0.45
5:E:406:U:H2'	5:E:407:A:H8	1.82	0.45
5:E:816:G:H22	5:E:855:A:H2	1.64	0.45
5:E:844:A:H2'	5:E:845:G:C8	2.51	0.45
5:E:925:G:H2'	5:E:926:A:H8	1.81	0.45
5:E:1591:C:H2'	5:E:1592:A:C8	2.47	0.45
5:E:1667:A:H2'	5:E:1668:G:H8	1.82	0.45
48:SB:160:VAL:HG21	58:SL:25:VAL:HG22	1.97	0.45
5:E:514:G:H2'	5:E:515:A:C8	2.50	0.45
5:E:1160:A:H2'	5:E:1161:C:C6	2.51	0.45
5:E:1477:G:H2'	5:E:1478:G:H8	1.80	0.45
14:LL:49:CYS:HA	14:LL:138:VAL:O	2.16	0.45
23:LU:101:ALA:O	23:LU:105:THR:HG22	2.17	0.45
31:Lc:126:LYS:HB3	31:Lc:148:ILE:HD13	1.99	0.45
48:SB:42:LEU:HD13	48:SB:45:LYS:HA	1.98	0.45
48:SB:196:GLU:HA	48:SB:199:ILE:HD12	1.98	0.45
48:SB:222:LYS:HA	48:SB:225:ARG:HG3	1.98	0.45
53:SG:13:SER:O	53:SG:17:ILE:HG13	2.15	0.45
1:A:2772:C:H4'	1:A:2773:C:H5'	1.97	0.45
1:A:3313:U:H4'	7:LE:173:GLN:HG2	1.99	0.45
5:E:435:C:H5'	75:Sc:50:LYS:HD2	1.97	0.45
5:E:454:U:C2	65:SS:66:MET:HE1	2.52	0.45
5:E:1673:G:O6	5:E:1728:A:N1	2.50	0.45
6:LD:101:VAL:HG22	6:LD:165:VAL:HG22	1.99	0.45
8:LF:233:LEU:HD13	8:LF:238:LEU:HD11	1.99	0.45
17:LO:135:LEU:HD11	19:LQ:178:VAL:HA	1.99	0.45
28:LZ:100:LYS:HE3	28:LZ:100:LYS:HB3	1.83	0.45
36:Lh:38:PRO:HG2	36:Lh:39:GLN:NE2	2.32	0.45
67:SU:14:THR:HB	67:SU:17:GLU:HG3	1.97	0.45
72:SZ:82:LYS:HA	72:SZ:116:GLU:O	2.17	0.45
1:A:129:U:H2'	1:A:130:A:C8	2.51	0.45
5:E:454:U:N3	65:SS:66:MET:HE1	2.32	0.45
9:LG:155:THR:HA	9:LG:179:ARG:HG3	1.99	0.45
13:LK:176:LEU:HD12	43:Lo:90:ASN:HD22	1.81	0.45
25:LW:13:LYS:HE2	25:LW:101:ASN:HD21	1.82	0.45
33:Le:16:LEU:HD11	33:Le:97:ASP:HB2	1.99	0.45
46:Lr:82:THR:O	46:Lr:86:LEU:HG	2.17	0.45
47:SA:119:ALA:O	47:SA:123:VAL:HG12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:SD:42:ALA:HB1	50:SD:47:GLU:HB3	1.98	0.45
65:SS:128:LYS:HD2	65:SS:130:GLN:HE21	1.81	0.45
71:SY:64:ARG:HD2	71:SY:70:LYS:HD3	1.98	0.45
1:A:428:A:H2'	1:A:429:U:C6	2.52	0.45
1:A:584:G:H2'	1:A:585:A:H8	1.81	0.45
1:A:2428:U:H2'	1:A:2429:G:H8	1.81	0.45
1:A:2812:C:H2'	1:A:2813:A:C8	2.52	0.45
1:A:3015:G:H2'	1:A:3016:A:C8	2.51	0.45
5:E:340:U:H2'	5:E:341:A:H8	1.82	0.45
5:E:1681:A:H2	5:E:1720:G:H21	1.65	0.45
28:LZ:115:ARG:HD2	28:LZ:121:LYS:HD2	1.98	0.45
40:LI:27:PHE:HA	40:LI:34:CYS:HA	1.98	0.45
62:SP:62:ARG:HH21	73:Sa:38:LYS:HA	1.82	0.45
63:SQ:181:LEU:O	63:SQ:185:THR:HG23	2.16	0.45
80:n:63:G:H2'	80:n:64:A:H8	1.82	0.45
1:A:1119:C:H2'	1:A:1120:A:C8	2.52	0.45
1:A:1666:G:H2'	1:A:1667:A:C8	2.51	0.45
1:A:2197:C:H4'	1:A:2198:A:H5'	1.97	0.45
1:A:3119:U:H4'	43:Lo:104:PRO:HG2	1.98	0.45
14:LL:38:LYS:HB2	14:LL:83:ASP:HA	1.97	0.45
67:SU:56:LYS:HB2	67:SU:88:ARG:HD3	1.99	0.45
1:A:1667:A:H2'	1:A:1668:G:C8	2.52	0.45
5:E:874:C:H2'	5:E:875:G:C8	2.52	0.45
7:LE:47:LEU:HD11	7:LE:179:ALA:HB3	1.98	0.45
11:LI:80:GLN:HB2	24:LV:135:PRO:HB2	1.99	0.45
16:LN:48:PRO:HB3	16:LN:137:GLN:HB2	1.99	0.45
16:LN:118:GLU:O	16:LN:122:LYS:HB2	2.17	0.45
32:Ld:32:LEU:HD22	32:Ld:35:VAL:HG21	1.98	0.45
61:SO:64:HIS:CE1	61:SO:90:ARG:HE	2.34	0.45
76:Sd:10:ARG:HB2	76:Sd:24:VAL:HG13	1.99	0.45
1:A:1596:C:H2'	1:A:1597:C:C6	2.52	0.44
5:E:123:G:H21	65:SS:146:THR:HG21	1.82	0.44
5:E:152:U:O2'	66:ST:15:THR:HG23	2.16	0.44
5:E:898:A:H4'	72:SZ:46:MET:HE3	1.98	0.44
5:E:1488:G:H3'	5:E:1515:A:H61	1.82	0.44
5:E:1628:U:H2'	5:E:1629:G:C8	2.52	0.44
5:E:1650:U:H2'	5:E:1651:A:C8	2.52	0.44
15:LM:101:ASN:ND2	15:LM:130:VAL:HA	2.32	0.44
64:SR:97:ARG:HE	64:SR:117:THR:HG23	1.82	0.44
1:A:68:C:N4	1:A:315:C:H5'	2.33	0.44
5:E:902:G:H5''	72:SZ:24:ASN:ND2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:947:U:H2'	5:E:948:G:H8	1.81	0.44
14:LL:210:ILE:HD13	14:LL:210:ILE:HA	1.88	0.44
39:Lk:43:LEU:O	39:Lk:47:ILE:HG23	2.18	0.44
49:SC:3:MET:HE3	49:SC:41:TYR:HB3	1.98	0.44
49:SC:39:ASN:O	49:SC:43:ILE:HD12	2.17	0.44
54:SH:28:ILE:O	54:SH:32:LEU:HD22	2.18	0.44
67:SU:141:ARG:O	67:SU:148:LYS:HA	2.17	0.44
5:E:767:U:H5	69:SW:142:ASN:HB3	1.82	0.44
7:LE:380:MET:HE3	7:LE:380:MET:HB3	1.86	0.44
14:LL:47:PRO:HB2	14:LL:178:ARG:HH22	1.82	0.44
52:SF:16:ALA:HB2	52:SF:72:GLY:HA3	2.00	0.44
54:SH:52:VAL:HG21	54:SH:61:LEU:HD21	1.98	0.44
59:SM:50:ILE:H	59:SM:50:ILE:HD12	1.82	0.44
64:SR:99:LYS:HA	64:SR:117:THR:HA	1.99	0.44
66:ST:21:GLU:O	66:ST:25:ARG:HG2	2.17	0.44
76:Sd:41:ARG:HD2	76:Sd:55:VAL:HG23	1.99	0.44
80:n:23:C:H2'	80:n:24:G:O4'	2.17	0.44
1:A:314:U:H2'	1:A:315:C:C6	2.53	0.44
1:A:3294:A:H2'	1:A:3295:A:O4'	2.18	0.44
5:E:385:A:H2'	5:E:386:G:C8	2.52	0.44
5:E:1673:G:H1	5:E:1728:A:H2	1.61	0.44
11:LI:108:LEU:HD21	11:LI:115:THR:HG22	1.99	0.44
42:Ln:23:LEU:HD22	42:Ln:24:PRO:HD2	1.98	0.44
64:SR:140:ARG:HH21	64:SR:226:THR:HG21	1.82	0.44
65:SS:11:ARG:NH1	65:SS:20:LEU:HB3	2.32	0.44
73:Sa:71:ARG:HB2	73:Sa:83:TRP:CE2	2.53	0.44
79:Sg:56:MET:O	79:Sg:58:PRO:HD3	2.17	0.44
1:A:937:G:H5''	31:Lc:29:PRO:HA	1.98	0.44
1:A:1338:C:H4'	35:Lg:60:ASN:HD22	1.82	0.44
1:A:1777:U:H2'	1:A:1778:G:C8	2.52	0.44
1:A:3255:U:H2'	1:A:3256:G:C8	2.52	0.44
5:E:1483:A:H2'	5:E:1484:G:C8	2.53	0.44
6:LD:46:LYS:HD2	6:LD:46:LYS:HA	1.71	0.44
11:LI:120:THR:HB	24:LV:132:PRO:HB2	2.00	0.44
11:LI:176:TYR:HB3	11:LI:194:HIS:CG	2.53	0.44
18:LP:141:ALA:O	18:LP:145:ASP:HB2	2.18	0.44
20:LR:60:PHE:HB3	20:LR:64:ASN:HB3	2.00	0.44
52:SF:8:GLN:HE21	52:SF:21:HIS:HE1	1.66	0.44
55:SI:118:PRO:HD2	55:SI:123:ARG:HH21	1.82	0.44
57:SK:46:LYS:O	57:SK:50:ILE:HG12	2.17	0.44
71:SY:3:ARG:HB3	71:SY:6:SER:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:SY:31:GLU:O	71:SY:35:GLU:HG3	2.17	0.44
76:Sd:82:ALA:O	76:Sd:86:GLU:HB2	2.18	0.44
1:A:531:G:H2'	1:A:532:A:C8	2.53	0.44
1:A:541:U:H2'	1:A:542:G:C8	2.52	0.44
1:A:1108:U:H2'	1:A:1109:U:C6	2.53	0.44
1:A:1290:A:H2'	1:A:1291:A:C8	2.53	0.44
1:A:3107:U:H2'	1:A:3108:G:C8	2.52	0.44
4:D:1:A:C8	48:SB:152:GLY:HA3	2.53	0.44
28:LZ:86:VAL:HG11	28:LZ:95:ILE:HD11	1.99	0.44
30:Lb:41:ALA:HB2	30:Lb:77:TYR:HE1	1.82	0.44
55:SI:64:HIS:CD2	55:SI:71:VAL:HG21	2.52	0.44
61:SO:24:ALA:HB3	61:SO:34:LEU:HB3	2.00	0.44
61:SO:266:ASP:CG	61:SO:267:PRO:HD3	2.43	0.44
64:SR:67:GLN:O	64:SR:71:THR:HG22	2.17	0.44
76:Sd:20:ARG:HH21	76:Sd:22:GLN:HE22	1.66	0.44
1:A:307:A:H2'	1:A:308:A:H8	1.81	0.44
1:A:546:C:H4'	1:A:547:G:C4	2.53	0.44
1:A:700:C:H2'	1:A:701:G:H8	1.81	0.44
1:A:2376:G:H2'	1:A:2377:G:C8	2.53	0.44
1:A:2882:U:H2'	1:A:2883:U:C6	2.53	0.44
1:A:3162:C:H2'	1:A:3163:A:C8	2.52	0.44
9:LG:55:PHE:HE1	9:LG:159:VAL:HG23	1.83	0.44
18:LP:84:PRO:HA	18:LP:87:GLN:HG3	1.98	0.44
30:Lb:83:THR:HG22	37:Li:93:PHE:CZ	2.53	0.44
35:Lg:86:THR:HG23	35:Lg:115:LEU:HD22	2.00	0.44
47:SA:40:ARG:HA	56:SJ:110:PRO:HB3	2.00	0.44
49:SC:23:ALA:O	49:SC:63:TYR:HA	2.18	0.44
61:SO:42:LEU:HB2	61:SO:61:PHE:HD1	1.82	0.44
61:SO:123:ILE:HG22	61:SO:133:VAL:HG23	1.99	0.44
66:ST:14:LYS:HE3	66:ST:15:THR:H	1.83	0.44
74:Sb:41:MET:HG2	74:Sb:129:VAL:HG21	2.00	0.44
1:A:993:G:N3	1:A:2637:A:H2'	2.33	0.44
5:E:1675:C:H1'	68:SV:32:GLN:NE2	2.33	0.44
9:LG:35:ARG:H	9:LG:35:ARG:HD2	1.82	0.44
14:LL:54:SER:HB2	14:LL:135:ILE:HD11	1.99	0.44
17:LO:128:ARG:HG2	17:LO:132:LYS:HD2	1.99	0.44
26:LX:22:ILE:HD13	26:LX:35:TYR:HB2	2.00	0.44
55:SI:14:PHE:HE2	55:SI:136:ALA:HB2	1.83	0.44
1:A:2413:A:H2'	1:A:2414:G:C8	2.50	0.44
5:E:554:C:H1'	5:E:555:A:H2	1.83	0.44
7:LE:261:MET:HB2	7:LE:264:VAL:HG23	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:LG:235:SER:O	9:LG:239:ILE:HG12	2.18	0.44
33:Le:43:ILE:HG23	33:Le:68:TYR:HD2	1.82	0.44
37:Li:3:GLN:HE22	37:Li:29:ILE:HG22	1.83	0.44
39:Lk:66:GLU:HA	39:Lk:69:ALA:HB3	2.00	0.44
54:SH:61:LEU:HD12	54:SH:61:LEU:HA	1.84	0.44
62:SP:59:LEU:HD22	73:Sa:79:LEU:HD21	1.99	0.44
62:SP:74:VAL:HG12	62:SP:96:THR:HB	2.00	0.44
67:SU:21:ALA:O	67:SU:25:VAL:HG13	2.18	0.44
71:SY:88:LEU:HD13	71:SY:125:LEU:HD12	1.99	0.44
1:A:656:A:H2'	1:A:657:A:H8	1.83	0.43
1:A:2611:U:H2'	1:A:2612:U:C6	2.53	0.43
5:E:386:G:H2'	5:E:387:A:C8	2.53	0.43
5:E:1087:A:H2'	5:E:1088:A:C8	2.53	0.43
52:SF:93:HIS:HA	52:SF:97:VAL:HB	1.99	0.43
57:SK:39:ALA:HB3	57:SK:71:ILE:HA	2.00	0.43
61:SO:201:THR:HG23	61:SO:214:ALA:HB3	2.00	0.43
63:SQ:36:SER:HA	63:SQ:41:ARG:HH12	1.83	0.43
65:SS:19:LEU:HD11	65:SS:108:ARG:HD3	2.00	0.43
65:SS:66:MET:HA	65:SS:78:THR:HG23	2.00	0.43
65:SS:248:ILE:HG12	69:SW:71:PHE:CE2	2.53	0.43
75:Sc:126:LYS:HA	75:Sc:131:SER:HA	2.00	0.43
1:A:312:C:H2'	1:A:313:A:H8	1.82	0.43
5:E:107:C:H2'	5:E:108:A:H8	1.84	0.43
5:E:751:G:H2'	5:E:752:A:H8	1.83	0.43
5:E:925:G:H2'	5:E:926:A:C8	2.54	0.43
6:LD:27:ALA:HB1	6:LD:77:ILE:HG12	2.01	0.43
8:LF:353:ALA:O	8:LF:357:GLU:HG2	2.17	0.43
14:LL:38:LYS:HE3	14:LL:41:ALA:HB2	2.00	0.43
18:LP:60:VAL:HB	18:LP:134:LEU:HB2	2.00	0.43
18:LP:118:SER:HB3	18:LP:132:VAL:HG22	2.00	0.43
20:LR:69:ARG:HB3	20:LR:79:THR:HG22	2.00	0.43
30:Lb:5:LEU:HD12	30:Lb:5:LEU:HA	1.83	0.43
67:SU:96:ARG:HB2	67:SU:121:VAL:HG13	2.00	0.43
80:n:11:C:H2'	80:n:12:G:H8	1.83	0.43
1:A:928:C:H2'	1:A:929:A:C8	2.53	0.43
1:A:1076:C:H4'	32:Ld:38:LYS:HG2	2.00	0.43
1:A:2697:A:H2'	1:A:2698:G:H8	1.82	0.43
3:C:27:U:H4'	8:LF:51:ALA:HB3	1.99	0.43
5:E:1071:U:H2'	5:E:1072:C:C6	2.53	0.43
5:E:1222:C:H2'	5:E:1223:A:H8	1.83	0.43
6:LD:28:LYS:HB2	6:LD:123:ARG:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LD:54:ARG:HG2	6:LD:56:ALA:H	1.82	0.43
18:LP:47:LYS:HE3	18:LP:51:LEU:HD11	1.99	0.43
31:Lc:73:LEU:HB2	31:Lc:109:TYR:CD2	2.52	0.43
41:Lm:42:LYS:HG2	41:Lm:55:VAL:HG22	2.00	0.43
48:SB:90:ILE:O	48:SB:94:THR:HG23	2.18	0.43
54:SH:104:ASN:O	54:SH:108:LYS:HE2	2.18	0.43
61:SO:19:TRP:HB2	61:SO:38:ARG:HD2	2.00	0.43
61:SO:260:ILE:O	61:SO:273:ASP:HA	2.19	0.43
66:ST:133:LEU:HD23	66:ST:133:LEU:HA	1.84	0.43
75:Sc:86:PHE:HB2	75:Sc:120:VAL:HG11	2.01	0.43
78:Sf:2:VAL:HG13	78:Sf:5:GLN:NE2	2.33	0.43
1:A:1534:A:H2'	1:A:1535:A:C8	2.52	0.43
4:D:7:A:H2	4:D:8:A:H62	1.66	0.43
20:LR:129:THR:HG23	20:LR:131:ARG:HD3	1.99	0.43
48:SB:76:ARG:NH2	48:SB:79:ASN:HD21	2.16	0.43
53:SG:105:GLN:NE2	62:SP:41:ARG:HA	2.33	0.43
63:SQ:48:VAL:HG11	63:SQ:61:LEU:HD22	2.00	0.43
63:SQ:152:ARG:H	63:SQ:152:ARG:HG2	1.61	0.43
68:SV:159:GLN:NE2	68:SV:189:LEU:HD21	2.34	0.43
75:Sc:132:LEU:HD12	75:Sc:132:LEU:HA	1.83	0.43
1:A:595:G:H1	1:A:609:G:H5''	1.82	0.43
1:A:911:C:H5''	6:LD:15:ILE:HD13	1.99	0.43
1:A:1280:C:H2'	1:A:1281:G:C8	2.53	0.43
1:A:1663:C:H2'	1:A:1664:G:H8	1.83	0.43
1:A:2095:G:H2'	1:A:2096:A:C8	2.53	0.43
1:A:2433:U:H1'	18:LP:125:SER:HB2	2.00	0.43
1:A:3157:U:H4'	1:A:3158:G:H8	1.83	0.43
7:LE:85:VAL:HG22	7:LE:202:THR:HG22	1.99	0.43
38:Lj:4:VAL:HG22	38:Lj:50:SER:HB2	1.99	0.43
47:SA:5:ILE:HD11	47:SA:9:ARG:HE	1.83	0.43
48:SB:130:ILE:O	48:SB:134:VAL:HG13	2.18	0.43
79:Sg:40:TYR:O	79:Sg:44:PHE:HB3	2.19	0.43
1:A:159:A:H2'	1:A:160:G:H8	1.83	0.43
5:E:329:G:H2'	5:E:330:G:C8	2.54	0.43
5:E:561:G:H2'	5:E:562:G:H8	1.83	0.43
11:LI:173:LEU:HB3	11:LI:178:ILE:HB	2.01	0.43
13:LK:41:ILE:HD12	13:LK:41:ILE:HA	1.78	0.43
20:LR:114:VAL:HG12	20:LR:150:VAL:HG12	2.00	0.43
29:La:55:GLU:HA	29:La:69:LYS:HA	2.01	0.43
51:SE:57:MET:HE3	51:SE:57:MET:HB3	1.91	0.43
51:SE:94:VAL:HG23	51:SE:107:ILE:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:SP:176:LEU:HD13	62:SP:176:LEU:HA	1.85	0.43
1:A:2183:A:H5''	6:LD:7:ASN:HB2	2.01	0.43
1:A:3034:C:C2	13:LK:120:ASP:HB2	2.53	0.43
7:LE:301:THR:HG23	7:LE:303:LYS:HG2	2.01	0.43
8:LF:157:GLU:HA	8:LF:215:ILE:HB	2.01	0.43
8:LF:205:PRO:HD2	8:LF:225:VAL:HG22	2.00	0.43
18:LP:9:GLU:OE2	39:Lk:41:ARG:HG2	2.19	0.43
34:Lf:26:LYS:HD3	34:Lf:26:LYS:HA	1.81	0.43
61:SO:172:ALA:HB1	61:SO:199:ILE:HG21	1.99	0.43
63:SQ:144:ARG:HD3	63:SQ:208:GLN:HB3	2.01	0.43
71:SY:114:ARG:HE	71:SY:114:ARG:HB2	1.54	0.43
1:A:1146:C:H2'	1:A:1147:G:H8	1.83	0.43
5:E:848:C:H2'	5:E:849:C:C6	2.53	0.43
5:E:1505:A:H1'	5:E:1562:G:H21	1.83	0.43
14:LL:12:GLN:NE2	14:LL:128:ARG:HB3	2.33	0.43
18:LP:192:LYS:HB3	18:LP:192:LYS:HE2	1.78	0.43
20:LR:108:ASP:HB3	20:LR:111:LYS:HD2	1.99	0.43
26:LX:74:MET:HE2	26:LX:74:MET:HB3	1.81	0.43
26:LX:84:SER:HA	26:LX:94:TYR:HB3	2.00	0.43
38:Lj:57:VAL:O	38:Lj:61:GLN:HG3	2.19	0.43
65:SS:77:ARG:HA	65:SS:77:ARG:HD3	1.92	0.43
66:ST:5:ILE:HD12	66:ST:16:PHE:CE2	2.54	0.43
66:ST:44:GLU:H	66:ST:44:GLU:HG2	1.66	0.43
74:Sb:22:LYS:H	74:Sb:22:LYS:HG2	1.68	0.43
1:A:532:A:HO2'	1:A:533:A:H8	1.66	0.43
1:A:616:G:H2'	1:A:617:G:C8	2.53	0.43
1:A:2428:U:H2'	1:A:2429:G:C8	2.54	0.43
1:A:3164:C:O2'	1:A:3165:A:H8	2.01	0.43
1:A:3198:U:H1'	13:LK:21:LYS:HB3	2.01	0.43
5:E:953:G:H2'	5:E:954:G:C8	2.53	0.43
5:E:1358:G:H2'	5:E:1359:C:C6	2.54	0.43
7:LE:215:ILE:HD12	7:LE:338:LEU:HB3	2.00	0.43
19:LQ:16:VAL:HG23	19:LQ:41:LEU:HD13	2.01	0.43
20:LR:84:PRO:HB2	20:LR:87:SER:HB3	2.01	0.43
62:SP:183:ARG:HG2	62:SP:188:LEU:HD22	1.99	0.43
64:SR:140:ARG:HB3	64:SR:221:THR:HB	1.99	0.43
64:SR:169:LEU:HD23	64:SR:198:THR:HG22	2.01	0.43
65:SS:136:VAL:HG11	65:SS:148:ARG:NH2	2.33	0.43
66:ST:69:LEU:O	66:ST:99:GLY:HA3	2.19	0.43
74:Sb:77:PRO:HD3	75:Sc:7:ARG:HG3	2.00	0.43
77:Se:43:ASN:HA	77:Se:66:LYS:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:C:H2'	1:A:106:A:H8	1.84	0.43
1:A:2914:G:H5''	7:LE:9:PRO:HG3	2.01	0.43
5:E:1222:C:H2'	5:E:1223:A:C8	2.54	0.43
5:E:1579:U:H2'	5:E:1580:C:C6	2.54	0.43
8:LF:259:ASP:OD1	8:LF:264:SER:HB2	2.19	0.43
9:LG:41:LYS:HB2	24:LV:68:THR:O	2.19	0.43
27:LY:3:VAL:HG11	27:LY:12:LYS:HD2	2.00	0.43
28:LZ:73:MET:HA	28:LZ:76:VAL:HB	2.00	0.43
47:SA:69:LEU:O	47:SA:73:VAL:HG12	2.19	0.43
63:SQ:33:LYS:HD2	63:SQ:41:ARG:HG2	2.00	0.43
69:SW:126:ARG:HD3	79:Sg:33:ARG:HE	1.84	0.43
1:A:501:A:H2'	1:A:502:U:C6	2.54	0.42
5:E:15:U:H2'	5:E:16:G:O4'	2.19	0.42
5:E:340:U:H2'	5:E:341:A:C8	2.54	0.42
9:LG:148:ILE:HD13	9:LG:148:ILE:HA	1.81	0.42
13:LK:6:THR:HG21	13:LK:65:VAL:HG22	2.01	0.42
14:LL:191:LYS:HG3	14:LL:213:PHE:CE1	2.54	0.42
22:LT:105:LEU:HD12	22:LT:135:LYS:HG3	2.01	0.42
50:SD:51:ALA:HB2	50:SD:124:LYS:HE2	2.01	0.42
65:SS:22:LYS:HE2	65:SS:23:LEU:HD21	2.01	0.42
66:ST:3:LEU:HG	66:ST:5:ILE:HD11	2.01	0.42
66:ST:180:THR:HG22	66:ST:183:ARG:HG3	2.01	0.42
1:A:786:A:H4'	1:A:787:G:H5'	2.01	0.42
1:A:1280:C:H2'	1:A:1281:G:H8	1.83	0.42
1:A:2177:G:H2'	6:LD:128:ARG:HD3	2.00	0.42
3:C:63:G:H22	3:C:97:A:H2	1.67	0.42
5:E:17:C:H2'	5:E:18:C:H6	1.84	0.42
5:E:252:U:H2'	5:E:253:A:H8	1.84	0.42
5:E:1454:G:H4'	51:SE:122:THR:HG21	2.00	0.42
7:LE:84:VAL:O	7:LE:202:THR:HA	2.18	0.42
7:LE:92:TYR:HB2	7:LE:157:VAL:HB	2.01	0.42
9:LG:97:ALA:O	9:LG:101:THR:HG22	2.19	0.42
9:LG:105:ILE:O	9:LG:109:THR:HG23	2.20	0.42
12:LJ:25:PRO:HG2	12:LJ:26:LEU:HD22	2.01	0.42
13:LK:36:LYS:HE2	13:LK:36:LYS:HB2	1.74	0.42
27:LY:9:SER:O	27:LY:53:VAL:HG12	2.19	0.42
34:Lf:102:LYS:HB3	34:Lf:102:LYS:HE3	1.80	0.42
38:Lj:73:LYS:HB3	38:Lj:73:LYS:HE3	1.82	0.42
54:SH:39:GLY:O	54:SH:43:SER:HB3	2.18	0.42
63:SQ:157:GLN:O	63:SQ:161:ILE:HG12	2.19	0.42
1:A:286:U:H2'	1:A:287:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2728:G:C6	24:LV:80:VAL:HG11	2.54	0.42
8:LF:281:ILE:HG22	21:LS:25:TYR:HB3	2.02	0.42
9:LG:190:ILE:HD11	9:LG:195:LEU:HD22	2.00	0.42
25:LW:20:SER:HA	25:LW:23:THR:HG22	2.01	0.42
28:LZ:120:LYS:HB2	28:LZ:120:LYS:HE3	1.77	0.42
34:Lf:53:PRO:O	34:Lf:57:GLN:HG3	2.18	0.42
54:SH:42:TYR:O	54:SH:46:VAL:HG23	2.20	0.42
54:SH:115:ARG:O	54:SH:119:ILE:HG12	2.19	0.42
66:ST:186:ARG:O	66:ST:190:GLN:HG2	2.18	0.42
1:A:662:U:H2'	1:A:663:C:C6	2.54	0.42
1:A:1054:A:H5''	1:A:2637:A:H61	1.85	0.42
1:A:1084:A:H2'	1:A:1085:A:C8	2.54	0.42
1:A:2429:G:H2'	1:A:2430:A:H8	1.85	0.42
5:E:108:A:H2'	5:E:109:G:C8	2.53	0.42
6:LD:42:ARG:HG3	6:LD:89:TYR:CE1	2.54	0.42
6:LD:97:ASN:HB2	6:LD:100:ASN:ND2	2.33	0.42
7:LE:112:ASP:O	7:LE:116:ARG:HG3	2.19	0.42
15:LM:29:ARG:HD2	15:LM:123:PHE:HE1	1.84	0.42
16:LN:131:LYS:HE3	16:LN:131:LYS:HB2	1.89	0.42
21:LS:110:ALA:O	21:LS:114:ILE:HG13	2.19	0.42
33:Le:16:LEU:HD12	33:Le:98:SER:HB3	2.01	0.42
48:SB:214:LYS:HE2	48:SB:214:LYS:HB3	1.91	0.42
54:SH:31:ALA:O	54:SH:34:THR:HG22	2.19	0.42
64:SR:211:LEU:HD23	64:SR:211:LEU:HA	1.85	0.42
1:A:121:A:C6	12:LJ:129:PRO:HG3	2.54	0.42
1:A:157:A:N7	39:Lk:26:ILE:HG12	2.35	0.42
1:A:1945:A:H2'	1:A:1946:A:C8	2.54	0.42
1:A:2357:A:H2'	1:A:2358:A:C8	2.55	0.42
1:A:2544:U:H2'	1:A:2545:C:C6	2.55	0.42
2:B:16:U:H2'	2:B:17:A:C8	2.54	0.42
3:C:9:A:H2'	3:C:10:A:H8	1.84	0.42
5:E:968:U:H2'	5:E:969:C:O4'	2.20	0.42
5:E:1063:U:H2'	5:E:1064:G:C8	2.54	0.42
7:LE:361:THR:H	7:LE:371:GLN:NE2	2.17	0.42
10:LH:90:LYS:HB3	10:LH:90:LYS:HE3	1.62	0.42
14:LL:68:ALA:HB2	14:LL:158:LYS:HB2	2.01	0.42
18:LP:4:TYR:O	18:LP:8:GLU:HG2	2.19	0.42
22:LT:10:LEU:HD12	22:LT:10:LEU:HA	1.92	0.42
47:SA:150:MET:HG2	47:SA:152:PHE:CZ	2.54	0.42
51:SE:55:GLY:O	51:SE:59:LYS:HG3	2.19	0.42
54:SH:22:VAL:HG13	54:SH:31:ALA:HB1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:G:H2'	1:A:301:G:H8	1.84	0.42
7:LE:41:VAL:HG22	7:LE:186:GLY:H	1.84	0.42
18:LP:73:ARG:HA	18:LP:74:PRO:HD3	1.86	0.42
20:LR:19:GLY:HA3	20:LR:22:LEU:HD11	2.01	0.42
24:LV:102:ARG:HD2	24:LV:102:ARG:HA	1.83	0.42
41:Lm:33:LYS:HA	41:Lm:33:LYS:HD3	1.78	0.42
48:SB:55:ASP:HB2	48:SB:138:THR:HG23	2.01	0.42
58:SL:44:VAL:HG11	58:SL:54:LEU:HD11	2.02	0.42
64:SR:44:LEU:HD12	64:SR:49:LYS:HB2	2.00	0.42
1:A:138:U:H2'	1:A:139:G:H8	1.84	0.42
1:A:3309:G:H1'	20:LR:69:ARG:HD3	2.01	0.42
15:LM:98:ALA:HA	15:LM:156:LYS:HB2	2.02	0.42
62:SP:162:CYS:SG	62:SP:173:ILE:HG13	2.60	0.42
64:SR:227:PRO:HA	64:SR:230:TRP:CG	2.54	0.42
1:A:650:C:H2'	1:A:651:G:C8	2.55	0.42
5:E:119:A:H1'	5:E:397:A:C5	2.55	0.42
7:LE:48:GLY:O	7:LE:335:ILE:HA	2.19	0.42
8:LF:65:TRP:HB3	8:LF:69:ARG:HD3	2.02	0.42
15:LM:74:PRO:HA	15:LM:77:GLU:HG3	2.02	0.42
15:LM:87:LYS:HE2	15:LM:87:LYS:HB2	1.81	0.42
16:LN:80:VAL:HG12	16:LN:85:LEU:O	2.20	0.42
21:LS:72:LYS:HA	21:LS:72:LYS:HD2	1.88	0.42
31:Lc:26:ARG:HA	31:Lc:26:ARG:HD3	1.91	0.42
58:SL:36:THR:HG22	58:SL:37:SER:H	1.85	0.42
65:SS:201:HIS:HE1	65:SS:207:LEU:HD12	1.84	0.42
67:SU:150:GLN:HB3	67:SU:181:ILE:HG22	2.02	0.42
77:Se:93:LYS:H	77:Se:93:LYS:HG2	1.65	0.42
1:A:1460:A:H2'	1:A:1461:A:H8	1.85	0.42
5:E:1486:G:H2'	5:E:1487:A:C8	2.55	0.42
5:E:1667:A:H2'	5:E:1668:G:C8	2.55	0.42
6:LD:24:GLN:H	6:LD:24:GLN:HG2	1.63	0.42
7:LE:39:LYS:H	7:LE:39:LYS:HG2	1.67	0.42
22:LT:43:LYS:HE2	22:LT:43:LYS:HB2	1.60	0.42
25:LW:65:VAL:HG21	25:LW:71:PHE:HE2	1.84	0.42
49:SC:35:ILE:HG22	49:SC:37:THR:HG23	2.01	0.42
61:SO:59:ARG:HH22	61:SO:97:GLY:HA3	1.84	0.42
67:SU:9:LEU:HD21	67:SU:17:GLU:HB3	2.01	0.42
1:A:2429:G:H2'	1:A:2430:A:C8	2.55	0.42
2:B:14:U:H5''	9:LG:24:ARG:HD3	2.01	0.42
4:D:8:A:H2'	4:D:9:A:C8	2.55	0.42
5:E:826:U:H2'	5:E:827:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:1223:A:H2'	5:E:1224:A:H8	1.84	0.42
5:E:1450:U:H2'	5:E:1451:C:C6	2.55	0.42
7:LE:284:ARG:HE	7:LE:284:ARG:HB2	1.70	0.42
25:LW:38:ILE:HD13	25:LW:38:ILE:HA	1.85	0.42
48:SB:82:PHE:CE2	58:SL:49:ARG:HG2	2.55	0.42
52:SF:107:LYS:HB3	52:SF:107:LYS:HE3	1.72	0.42
55:SI:16:ASN:HD22	55:SI:16:ASN:HA	1.68	0.42
64:SR:68:ILE:HG22	64:SR:69:ILE:HD13	2.02	0.42
75:Sc:19:ARG:NH1	75:Sc:22:ASN:HD22	2.18	0.42
1:A:563:U:H2'	1:A:564:G:H8	1.84	0.41
1:A:2106:A:H2'	1:A:2107:A:H8	1.85	0.41
5:E:407:A:H2'	5:E:408:C:C6	2.55	0.41
5:E:1382:A:H2'	5:E:1383:G:H8	1.85	0.41
6:LD:2:GLY:HA2	6:LD:207:VAL:HG23	2.02	0.41
9:LG:254:LYS:HG2	9:LG:255:PRO:HD2	2.02	0.41
13:LK:110:LYS:HE3	13:LK:128:VAL:HG21	2.02	0.41
29:La:31:LEU:HB3	29:La:101:PRO:HG3	2.02	0.41
33:Le:32:LYS:O	33:Le:36:GLN:HG3	2.18	0.41
50:SD:126:TRP:NE1	50:SD:133:LEU:HD21	2.35	0.41
51:SE:26:LEU:HD23	51:SE:26:LEU:HA	1.87	0.41
62:SP:34:GLU:HB2	62:SP:36:TYR:HD2	1.85	0.41
63:SQ:112:SER:HA	77:Se:68:TYR:OH	2.20	0.41
66:ST:93:LYS:HB2	66:ST:93:LYS:HE2	1.83	0.41
68:SV:159:GLN:HE22	68:SV:189:LEU:HD21	1.84	0.41
78:Sf:52:THR:HG23	78:Sf:54:VAL:HG23	2.01	0.41
1:A:1783:U:H2'	1:A:1784:G:C8	2.56	0.41
1:A:1940:G:H21	1:A:3362:A:H8	1.68	0.41
1:A:2508:U:H2'	1:A:2509:U:C6	2.55	0.41
5:E:625:C:H2'	5:E:626:U:C6	2.55	0.41
5:E:1592:A:H2'	5:E:1593:A:H8	1.85	0.41
19:LQ:4:GLU:H	19:LQ:4:GLU:HG2	1.60	0.41
21:LS:35:PHE:CE1	21:LS:39:ARG:HD3	2.54	0.41
23:LU:27:MET:HE3	23:LU:27:MET:HB3	1.90	0.41
24:LV:69:LYS:HE3	24:LV:69:LYS:HB3	1.83	0.41
30:Lb:42:LEU:HD23	30:Lb:74:VAL:HG22	2.01	0.41
33:Le:14:LEU:HD21	33:Le:43:ILE:HD13	2.03	0.41
51:SE:74:ALA:HA	51:SE:75:PRO:HD3	1.92	0.41
61:SO:13:LEU:HB2	61:SO:310:ILE:HB	2.02	0.41
61:SO:79:TYR:HB3	61:SO:91:LEU:HD11	2.01	0.41
61:SO:80:ALA:HB3	61:SO:92:TRP:HB2	2.02	0.41
62:SP:60:ALA:O	62:SP:64:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SS:21:ASP:OD1	65:SS:24:SER:HB3	2.20	0.41
68:SV:39:GLY:O	68:SV:59:ARG:HB3	2.20	0.41
71:SY:40:TYR:HD2	71:SY:50:ILE:HG13	1.85	0.41
1:A:1065:A:N1	32:Ld:26:THR:HG23	2.34	0.41
1:A:3281:U:H2'	1:A:3282:U:C6	2.55	0.41
5:E:107:C:H2'	5:E:108:A:C8	2.55	0.41
5:E:923:A:H2'	5:E:924:A:C8	2.55	0.41
5:E:1196:A:H4'	5:E:1197:C:H5''	2.02	0.41
10:LH:59:GLU:OE2	10:LH:103:VAL:HG23	2.20	0.41
11:LI:144:ILE:HG22	11:LI:185:ILE:HG23	2.02	0.41
16:LN:27:ASP:O	16:LN:31:LYS:HB2	2.20	0.41
17:LO:60:LEU:HD13	23:LU:152:LEU:HD11	2.02	0.41
24:LV:73:GLY:HA2	24:LV:89:LEU:O	2.20	0.41
26:LX:125:LEU:HD12	26:LX:125:LEU:HA	1.91	0.41
36:Lh:49:ILE:HG23	36:Lh:98:VAL:HG13	2.02	0.41
50:SD:93:ASP:HB3	50:SD:96:GLN:HE21	1.85	0.41
66:ST:215:ARG:HD3	66:ST:215:ARG:HA	1.90	0.41
76:Sd:12:VAL:HA	76:Sd:23:PHE:HB3	2.02	0.41
1:A:631:U:H2'	1:A:632:G:H8	1.85	0.41
1:A:1283:C:H2'	1:A:1284:C:C6	2.56	0.41
1:A:1336:U:H2'	1:A:1337:A:C8	2.55	0.41
1:A:1446:A:H5''	20:LR:65:SER:HB2	2.01	0.41
1:A:2609:A:H2'	1:A:2610:G:C8	2.55	0.41
1:A:2819:A:N6	1:A:2870:C:O2	2.54	0.41
1:A:3358:U:H2'	1:A:3359:A:H8	1.84	0.41
5:E:551:G:H2'	5:E:552:G:H8	1.85	0.41
5:E:1590:G:OP1	55:SI:91:TYR:HB2	2.21	0.41
5:E:1647:U:H2'	5:E:1648:A:H8	1.86	0.41
5:E:1648:A:H2'	5:E:1649:G:C8	2.55	0.41
5:E:1776:A:H2'	5:E:1777:G:H8	1.84	0.41
18:LP:178:HIS:CE1	18:LP:179:LYS:HG2	2.55	0.41
21:LS:40:THR:HG22	21:LS:42:ALA:H	1.84	0.41
45:Lq:23:HIS:HA	45:Lq:73:GLU:O	2.20	0.41
52:SF:29:ILE:HG23	52:SF:65:ILE:HB	2.02	0.41
61:SO:117:LYS:HD3	61:SO:118:LYS:H	1.84	0.41
65:SS:127:LYS:HB3	65:SS:127:LYS:HE3	1.90	0.41
68:SV:164:ARG:HD3	68:SV:164:ARG:HA	1.75	0.41
69:SW:87:SER:HB3	69:SW:90:LYS:HE2	2.02	0.41
5:E:407:A:H2'	5:E:408:C:H6	1.85	0.41
5:E:1202:A:H1'	5:E:1207:C:N4	2.36	0.41
28:LZ:55:ASN:C	28:LZ:55:ASN:HD22	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:SA:76:ARG:C	47:SA:76:ARG:HH11	2.28	0.41
48:SB:44:ASN:HD21	48:SB:115:LYS:HD2	1.85	0.41
48:SB:177:ILE:HD13	48:SB:177:ILE:HA	1.94	0.41
51:SE:33:PHE:CD2	51:SE:87:PRO:HD3	2.56	0.41
53:SG:115:LEU:HD13	53:SG:115:LEU:HA	1.90	0.41
61:SO:72:THR:HG22	61:SO:81:LEU:HB2	2.02	0.41
65:SS:191:ARG:HD3	65:SS:245:LYS:HB2	2.01	0.41
69:SW:79:ARG:O	69:SW:83:VAL:HG23	2.19	0.41
71:SY:52:VAL:HG23	71:SY:55:ARG:HH12	1.86	0.41
74:Sb:18:GLU:OE1	74:Sb:69:LEU:HB3	2.19	0.41
76:Sd:15:ASN:ND2	76:Sd:18:LEU:H	2.19	0.41
1:A:148:G:H3'	18:LP:49:ARG:HH22	1.84	0.41
1:A:792:G:H2'	1:A:793:C:C6	2.55	0.41
5:E:846:G:H3'	5:E:847:A:H8	1.85	0.41
5:E:947:U:H2'	5:E:948:G:C8	2.55	0.41
9:LG:131:LEU:HD21	9:LG:174:PRO:HA	2.01	0.41
12:LJ:178:ALA:HB2	12:LJ:218:ILE:HD12	2.02	0.41
26:LX:34:LEU:HD21	26:LX:102:ILE:HG12	2.01	0.41
26:LX:66:LYS:O	26:LX:70:ARG:HG3	2.21	0.41
34:Lf:11:GLU:O	34:Lf:106:THR:HA	2.20	0.41
43:Lo:99:CYS:HB3	43:Lo:115:CYS:HB3	2.03	0.41
48:SB:115:LYS:HA	48:SB:115:LYS:HD3	1.84	0.41
58:SL:29:ARG:HE	58:SL:41:VAL:HG23	1.85	0.41
62:SP:56:LYS:HB3	62:SP:160:ILE:HD12	2.03	0.41
64:SR:165:VAL:HA	64:SR:201:ASN:O	2.19	0.41
68:SV:136:SER:O	68:SV:140:GLU:HG2	2.20	0.41
1:A:273:A:H2'	1:A:274:G:H8	1.85	0.41
1:A:664:U:H2'	1:A:665:A:H8	1.84	0.41
1:A:748:U:H2'	1:A:749:C:C6	2.56	0.41
1:A:2095:G:H2'	1:A:2096:A:H8	1.85	0.41
3:C:135:G:H5''	28:LZ:49:LYS:HD2	2.02	0.41
5:E:5:U:H2'	5:E:6:G:C8	2.56	0.41
5:E:82:U:H2'	5:E:83:G:O4'	2.20	0.41
5:E:267:U:H2'	5:E:268:C:C6	2.55	0.41
5:E:477:A:H2'	5:E:478:A:H8	1.86	0.41
5:E:887:A:H5''	72:SZ:120:PRO:HB2	2.03	0.41
5:E:1151:A:H2'	5:E:1152:A:H8	1.85	0.41
5:E:1564:U:H2'	5:E:1565:C:C6	2.55	0.41
8:LF:22:LEU:HD23	8:LF:22:LEU:HA	1.96	0.41
8:LF:93:MET:HE3	8:LF:93:MET:HB3	1.93	0.41
12:LJ:50:VAL:HG21	28:LZ:27:ARG:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:LN:119:TYR:O	16:LN:123:ILE:HG23	2.21	0.41
38:Lj:115:LYS:HE3	38:Lj:115:LYS:HB2	1.93	0.41
48:SB:172:ILE:O	48:SB:176:THR:HG23	2.20	0.41
49:SC:44:LYS:HD3	49:SC:44:LYS:HA	1.71	0.41
57:SK:94:LYS:HE3	57:SK:94:LYS:HB2	1.90	0.41
62:SP:147:THR:HB	62:SP:151:SER:OG	2.19	0.41
63:SQ:28:GLU:OE2	63:SQ:50:LYS:HA	2.21	0.41
63:SQ:86:LEU:HB3	63:SQ:98:THR:HB	2.02	0.41
76:Sd:3:ASP:N	76:Sd:32:ARG:HD3	2.36	0.41
1:A:791:A:H2'	1:A:792:G:H8	1.85	0.41
1:A:899:U:H2'	1:A:900:G:H8	1.85	0.41
1:A:975:C:H2'	1:A:976:U:C6	2.56	0.41
5:E:17:C:H2'	5:E:18:C:C6	2.56	0.41
5:E:1174:C:H42	5:E:1465:C:H42	1.69	0.41
5:E:1789:G:H2'	5:E:1790:A:H8	1.86	0.41
6:LD:65:ASP:HB2	6:LD:72:ARG:HG2	2.01	0.41
6:LD:140:ASN:HB2	6:LD:145:LYS:HB2	2.02	0.41
9:LG:236:LEU:HD12	9:LG:236:LEU:HA	1.86	0.41
30:Lb:110:ALA:O	30:Lb:114:VAL:HG12	2.20	0.41
40:Ll:64:MET:HE3	40:Ll:64:MET:HB3	1.87	0.41
41:Lm:61:LYS:HB3	41:Lm:61:LYS:HE2	1.78	0.41
49:SC:3:MET:HB3	49:SC:41:TYR:CD1	2.56	0.41
61:SO:129:LYS:HG2	61:SO:149:ASP:C	2.46	0.41
71:SY:127:ARG:O	71:SY:131:THR:HG22	2.21	0.41
74:Sb:75:ILE:HD13	74:Sb:75:ILE:HA	1.97	0.41
74:Sb:125:ILE:O	74:Sb:126:LEU:HD12	2.20	0.41
75:Sc:54:LEU:HD21	75:Sc:75:GLN:HB3	2.03	0.41
1:A:612:U:H2'	1:A:613:G:H8	1.85	0.41
1:A:710:A:H2'	1:A:711:A:C8	2.56	0.41
1:A:2217:U:H2'	1:A:2218:G:H8	1.85	0.41
1:A:2369:G:H2'	1:A:2370:G:C8	2.56	0.41
1:A:2597:U:H2'	1:A:2598:G:C8	2.55	0.41
1:A:2696:A:H2'	1:A:2697:A:C8	2.56	0.41
1:A:3095:U:H2'	1:A:3096:C:C6	2.56	0.41
1:A:3192:U:H2'	1:A:3193:C:C6	2.56	0.41
3:C:142:C:H2'	3:C:143:U:C6	2.56	0.41
5:E:843:U:H2'	5:E:844:A:H8	1.86	0.41
5:E:1727:G:H21	68:SV:32:GLN:NE2	2.19	0.41
7:LE:20:LYS:HE3	7:LE:20:LYS:HB2	1.89	0.41
7:LE:356:LEU:HD13	7:LE:359:ILE:HD11	2.03	0.41
9:LG:266:ALA:O	9:LG:270:LYS:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LH:145:LEU:O	10:LH:149:ILE:HG13	2.21	0.41
10:LH:149:ILE:HA	10:LH:155:LEU:HD23	2.03	0.41
11:LI:87:VAL:HG11	11:LI:243:MET:HE1	2.03	0.41
11:LI:98:LYS:HB3	11:LI:99:PRO:HD3	2.02	0.41
11:LI:197:GLN:HE21	11:LI:197:GLN:HB2	1.75	0.41
13:LK:49:ASN:HB3	13:LK:52:LEU:HD23	2.02	0.41
15:LM:53:THR:HG22	15:LM:61:ARG:N	2.36	0.41
21:LS:122:ILE:HD13	21:LS:122:ILE:HA	1.87	0.41
23:LU:14:LEU:HD23	23:LU:14:LEU:HA	1.90	0.41
47:SA:105:MET:HE1	47:SA:119:ALA:HB2	2.03	0.41
48:SB:136:ALA:O	48:SB:140:THR:HG22	2.21	0.41
48:SB:140:THR:HA	48:SB:214:LYS:NZ	2.36	0.41
61:SO:89:LEU:HB3	61:SO:103:PHE:HB2	2.02	0.41
61:SO:159:ASN:HB2	61:SO:163:ASP:H	1.86	0.41
61:SO:185:GLN:CD	61:SO:187:GLN:HE22	2.28	0.41
68:SV:60:ILE:HD13	68:SV:60:ILE:HA	1.86	0.41
75:Sc:121:ARG:H	75:Sc:121:ARG:HG2	1.64	0.41
77:Se:26:CYS:HB3	77:Se:77:CYS:SG	2.61	0.41
1:A:72:C:H1'	16:LN:61:PRO:O	2.21	0.41
1:A:254:A:H2'	1:A:255:A:C8	2.56	0.41
1:A:429:U:H2'	1:A:430:U:H6	1.85	0.41
1:A:1110:U:H2'	1:A:1111:U:C6	2.56	0.41
1:A:1460:A:H2'	1:A:1461:A:C8	2.55	0.41
1:A:1785:U:H2'	1:A:1786:G:C8	2.55	0.41
5:E:180:A:O2'	5:E:181:A:H8	2.03	0.41
8:LF:215:ILE:HD12	8:LF:215:ILE:HA	1.87	0.41
40:Ll:54:LYS:O	40:Ll:58:THR:HB	2.21	0.41
54:SH:62:THR:OG1	54:SH:64:GLU:HG2	2.21	0.41
64:SR:185:LYS:O	64:SR:189:GLN:HG3	2.21	0.41
66:ST:214:LYS:HE3	66:ST:214:LYS:HB3	1.85	0.41
67:SU:124:LYS:HD3	67:SU:124:LYS:HA	1.86	0.41
1:A:201:A:H2'	1:A:202:G:H8	1.86	0.40
1:A:407:A:C2	3:C:17:A:H1'	2.56	0.40
1:A:785:G:H1	21:LS:90:ASP:HA	1.86	0.40
1:A:2947:G:N3	7:LE:250:ALA:HB1	2.36	0.40
1:A:3173:G:O6	36:Lh:92:LYS:HD2	2.21	0.40
7:LE:76:VAL:HG12	7:LE:325:LYS:HA	2.03	0.40
12:LJ:146:LYS:HE2	12:LJ:173:MET:HE3	2.03	0.40
51:SE:96:ILE:HG12	51:SE:116:LEU:HD23	2.02	0.40
62:SP:140:ASN:ND2	73:Sa:32:VAL:HG12	2.36	0.40
64:SR:44:LEU:HD11	64:SR:243:TYR:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:SU:121:VAL:O	67:SU:125:ILE:HG23	2.21	0.40
76:Sd:7:ILE:HD13	76:Sd:27:VAL:HG12	2.03	0.40
1:A:2601:A:H2'	1:A:2602:G:H8	1.86	0.40
5:E:820:U:H6	5:E:820:U:H2'	1.72	0.40
6:LD:140:ASN:ND2	6:LD:147:ARG:HH11	2.20	0.40
15:LM:101:ASN:HB3	15:LM:128:TYR:CE1	2.56	0.40
17:LO:32:LEU:HD11	17:LO:94:TRP:CD1	2.56	0.40
21:LS:92:ARG:HG2	31:Lc:76:ASP:HB2	2.03	0.40
23:LU:110:MET:HE3	23:LU:110:MET:HB3	1.79	0.40
32:Ld:47:LEU:HA	32:Ld:50:THR:HG22	2.04	0.40
33:Le:43:ILE:HB	33:Le:90:VAL:HG13	2.03	0.40
50:SD:66:VAL:HG21	50:SD:71:ILE:HB	2.03	0.40
62:SP:127:ARG:NH2	62:SP:152:PRO:HD3	2.36	0.40
64:SR:52:THR:HB	64:SR:54:GLU:HG2	2.04	0.40
67:SU:77:LEU:HA	67:SU:77:LEU:HD13	1.83	0.40
67:SU:168:SER:O	67:SU:172:VAL:HG13	2.21	0.40
75:Sc:19:ARG:HH12	75:Sc:22:ASN:HD22	1.69	0.40
1:A:29:C:H4'	1:A:62:A:H4'	2.03	0.40
1:A:207:U:H2'	1:A:208:C:C6	2.57	0.40
1:A:671:U:H2'	1:A:672:A:H8	1.86	0.40
1:A:887:G:H2'	1:A:888:A:C8	2.56	0.40
1:A:1386:A:H5''	8:LF:141:ARG:HH22	1.87	0.40
1:A:2152:A:H2'	1:A:2153:U:H6	1.86	0.40
1:A:2986:U:H2'	1:A:2987:A:H8	1.87	0.40
5:E:16:G:H2'	5:E:17:C:C6	2.56	0.40
5:E:609:U:H5''	5:E:610:G:C5	2.56	0.40
5:E:1202:A:H1'	5:E:1207:C:H42	1.85	0.40
7:LE:222:LYS:HD3	7:LE:331:ASN:HB3	2.03	0.40
13:LK:103:ILE:HD11	13:LK:134:ILE:HG21	2.04	0.40
13:LK:164:ILE:HD12	13:LK:164:ILE:HA	1.91	0.40
17:LO:72:LEU:HD12	17:LO:73:PRO:HD2	2.02	0.40
23:LU:90:MET:HE1	23:LU:114:HIS:NE2	2.35	0.40
32:Ld:22:LYS:HB3	32:Ld:22:LYS:HE3	1.81	0.40
44:Lp:19:LYS:HB3	44:Lp:19:LYS:HE2	1.91	0.40
50:SD:45:LEU:H	50:SD:45:LEU:HD23	1.85	0.40
53:SG:18:GLU:HG2	53:SG:70:SER:H	1.86	0.40
61:SO:167:VAL:HG12	61:SO:184:ASN:HD21	1.85	0.40
64:SR:177:GLY:O	64:SR:195:ASP:HA	2.22	0.40
70:SX:99:ARG:HD2	75:Sc:15:LEU:HD12	2.03	0.40
1:A:207:U:H2'	1:A:208:C:H6	1.87	0.40
1:A:1176:C:H2'	1:A:1177:G:N2	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2746:A:N1	9:LG:148:ILE:HG12	2.36	0.40
2:B:84:A:H2'	2:B:85:G:C8	2.56	0.40
2:B:94:C:H2'	2:B:95:A:C8	2.56	0.40
5:E:149:C:H2'	5:E:150:U:C6	2.56	0.40
5:E:434:G:H5'	75:Sc:78:LYS:HB3	2.04	0.40
8:LF:168:ALA:O	8:LF:172:VAL:HG22	2.21	0.40
9:LG:95:TRP:CD1	9:LG:158:ARG:HA	2.57	0.40
10:LH:152:THR:OG1	10:LH:155:LEU:HB2	2.21	0.40
20:LR:109:ALA:HA	20:LR:112:LEU:HG	2.03	0.40
22:LT:172:ARG:HH11	22:LT:172:ARG:HG3	1.87	0.40
25:LW:22:PRO:HD3	25:LW:105:LEU:O	2.20	0.40
25:LW:37:LEU:O	25:LW:41:ILE:HG13	2.22	0.40
26:LX:33:ASN:ND2	26:LX:64:LYS:HG2	2.37	0.40
28:LZ:88:MET:HE3	28:LZ:88:MET:HB3	1.89	0.40
49:SC:44:LYS:HD3	49:SC:47:GLN:HE21	1.86	0.40
59:SM:40:ARG:HG3	59:SM:41:GLN:NE2	2.36	0.40
61:SO:13:LEU:HD23	61:SO:45:TRP:CD2	2.56	0.40
63:SQ:82:ARG:HH12	63:SQ:191:GLU:HG2	1.87	0.40
70:SX:109:VAL:HG21	70:SX:125:VAL:HG11	2.03	0.40
1:A:1283:C:H2'	1:A:1284:C:C5	2.56	0.40
1:A:2351:U:H2'	1:A:2352:A:C8	2.57	0.40
1:A:2423:U:H2'	1:A:2424:A:C8	2.57	0.40
5:E:980:G:H4'	5:E:1776:A:H4'	2.04	0.40
5:E:1410:A:H2'	5:E:1411:A:C8	2.56	0.40
7:LE:57:VAL:HB	7:LE:358:TRP:HB3	2.03	0.40
8:LF:141:ARG:HA	8:LF:141:ARG:HD3	1.97	0.40
15:LM:60:ARG:HE	15:LM:60:ARG:HB3	1.66	0.40
23:LU:71:LYS:HE2	23:LU:71:LYS:HB3	1.91	0.40
53:SG:71:PHE:O	53:SG:75:GLU:HG2	2.21	0.40
61:SO:21:THR:HG23	61:SO:37:SER:HA	2.04	0.40
66:ST:74:LYS:HG2	66:ST:96:SER:HB2	2.04	0.40
67:SU:114:ARG:HA	67:SU:114:ARG:HD3	1.86	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	
6	LD	245/254 (96%)	238 (97%)	7 (3%)	0	100	100
7	LE	384/387 (99%)	372 (97%)	12 (3%)	0	100	100
8	LF	359/362 (99%)	346 (96%)	12 (3%)	1 (0%)	36	64
9	LG	290/297 (98%)	286 (99%)	4 (1%)	0	100	100
10	LH	152/176 (86%)	143 (94%)	8 (5%)	1 (1%)	18	45
11	LI	220/244 (90%)	218 (99%)	2 (1%)	0	100	100
12	LJ	231/256 (90%)	224 (97%)	7 (3%)	0	100	100
13	LK	186/191 (97%)	178 (96%)	8 (4%)	0	100	100
14	LL	205/210 (98%)	197 (96%)	8 (4%)	0	100	100
15	LM	166/174 (95%)	164 (99%)	2 (1%)	0	100	100
16	LN	191/199 (96%)	184 (96%)	6 (3%)	1 (0%)	24	53
17	LO	134/138 (97%)	133 (99%)	1 (1%)	0	100	100
18	LP	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
19	LQ	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
20	LR	168/184 (91%)	163 (97%)	5 (3%)	0	100	100
21	LS	183/186 (98%)	179 (98%)	4 (2%)	0	100	100
22	LT	172/189 (91%)	169 (98%)	3 (2%)	0	100	100
23	LU	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
24	LV	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
25	LW	98/121 (81%)	94 (96%)	4 (4%)	0	100	100
26	LX	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
27	LY	60/155 (39%)	60 (100%)	0	0	100	100
28	LZ	118/142 (83%)	116 (98%)	2 (2%)	0	100	100
29	La	123/127 (97%)	123 (100%)	0	0	100	100
30	Lb	131/136 (96%)	127 (97%)	4 (3%)	0	100	100
31	Lc	146/149 (98%)	140 (96%)	6 (4%)	0	100	100
32	Ld	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
33	Le	94/105 (90%)	94 (100%)	0	0	100	100
34	Lf	103/113 (91%)	101 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Lg	124/130 (95%)	123 (99%)	1 (1%)	0	100	100
36	Lh	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
37	Li	108/121 (89%)	103 (95%)	5 (5%)	0	100	100
38	Lj	117/120 (98%)	116 (99%)	1 (1%)	0	100	100
39	Lk	96/100 (96%)	91 (95%)	4 (4%)	1 (1%)	12	36
40	Ll	79/88 (90%)	77 (98%)	2 (2%)	0	100	100
41	Lm	75/78 (96%)	75 (100%)	0	0	100	100
42	Ln	48/51 (94%)	48 (100%)	0	0	100	100
43	Lo	49/128 (38%)	49 (100%)	0	0	100	100
44	Lp	22/25 (88%)	22 (100%)	0	0	100	100
45	Lq	98/106 (92%)	96 (98%)	2 (2%)	0	100	100
46	Lr	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
47	SA	220/240 (92%)	213 (97%)	7 (3%)	0	100	100
48	SB	204/225 (91%)	189 (93%)	14 (7%)	1 (0%)	24	53
49	SC	81/105 (77%)	75 (93%)	6 (7%)	0	100	100
50	SD	93/143 (65%)	86 (92%)	7 (8%)	0	100	100
51	SE	114/142 (80%)	111 (97%)	3 (3%)	0	100	100
52	SF	139/143 (97%)	133 (96%)	6 (4%)	0	100	100
53	SG	110/136 (81%)	107 (97%)	3 (3%)	0	100	100
54	SH	143/146 (98%)	137 (96%)	6 (4%)	0	100	100
55	SI	141/144 (98%)	140 (99%)	1 (1%)	0	100	100
56	SJ	98/121 (81%)	97 (99%)	1 (1%)	0	100	100
57	SK	67/108 (62%)	64 (96%)	3 (4%)	0	100	100
58	SL	60/67 (90%)	55 (92%)	5 (8%)	0	100	100
59	SM	51/56 (91%)	47 (92%)	4 (8%)	0	100	100
60	SN	51/152 (34%)	47 (92%)	3 (6%)	1 (2%)	6	19
61	SO	309/319 (97%)	298 (96%)	11 (4%)	0	100	100
62	SP	203/252 (81%)	194 (96%)	8 (4%)	1 (0%)	24	53
63	SQ	221/255 (87%)	215 (97%)	6 (3%)	0	100	100
64	SR	214/254 (84%)	210 (98%)	4 (2%)	0	100	100
65	SS	256/261 (98%)	241 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	ST	216/236 (92%)	214 (99%)	2 (1%)	0	100	100
67	SU	178/190 (94%)	170 (96%)	8 (4%)	0	100	100
68	SV	182/200 (91%)	172 (94%)	10 (6%)	0	100	100
69	SW	182/197 (92%)	168 (92%)	12 (7%)	2 (1%)	11	34
70	SX	139/156 (89%)	134 (96%)	5 (4%)	0	100	100
71	SY	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
72	SZ	125/138 (91%)	121 (97%)	4 (3%)	0	100	100
73	Sa	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
74	Sb	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
75	Sc	142/145 (98%)	140 (99%)	2 (1%)	0	100	100
76	Sd	129/135 (96%)	127 (98%)	2 (2%)	0	100	100
77	Se	95/119 (80%)	92 (97%)	3 (3%)	0	100	100
78	Sf	70/82 (85%)	66 (94%)	4 (6%)	0	100	100
79	Sg	53/63 (84%)	44 (83%)	7 (13%)	2 (4%)	2	8
All	All	10726/11870 (90%)	10385 (97%)	330 (3%)	11 (0%)	49	75

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	48	PRO
60	SN	95	HIS
48	SB	100	ASN
62	SP	68	PRO
69	SW	93	LEU
10	LH	72	ASN
79	Sg	56	MET
8	LF	146	PRO
79	Sg	21	VAL
39	Lk	21	THR
69	SW	169	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	LD	189/196 (96%)	189 (100%)	0	100	100
7	LE	321/323 (99%)	318 (99%)	3 (1%)	70	89
8	LF	288/289 (100%)	284 (99%)	4 (1%)	59	84
9	LG	241/245 (98%)	240 (100%)	1 (0%)	84	94
10	LH	136/155 (88%)	132 (97%)	4 (3%)	37	71
11	LI	186/205 (91%)	182 (98%)	4 (2%)	45	77
12	LJ	187/208 (90%)	186 (100%)	1 (0%)	81	93
13	LK	168/171 (98%)	164 (98%)	4 (2%)	43	75
14	LL	177/179 (99%)	174 (98%)	3 (2%)	53	81
15	LM	144/151 (95%)	141 (98%)	3 (2%)	47	78
16	LN	154/159 (97%)	151 (98%)	3 (2%)	50	79
17	LO	107/109 (98%)	105 (98%)	2 (2%)	50	79
18	LP	175/176 (99%)	173 (99%)	2 (1%)	65	86
19	LQ	160/162 (99%)	156 (98%)	4 (2%)	42	74
20	LR	138/146 (94%)	136 (99%)	2 (1%)	59	84
21	LS	150/151 (99%)	148 (99%)	2 (1%)	61	85
22	LT	142/154 (92%)	140 (99%)	2 (1%)	59	84
23	LU	155/156 (99%)	146 (94%)	9 (6%)	18	47
24	LV	135/137 (98%)	135 (100%)	0	100	100
25	LW	87/107 (81%)	84 (97%)	3 (3%)	32	66
26	LX	104/105 (99%)	103 (99%)	1 (1%)	68	88
27	LY	54/129 (42%)	53 (98%)	1 (2%)	50	79
28	LZ	104/118 (88%)	101 (97%)	3 (3%)	37	71
29	La	108/110 (98%)	107 (99%)	1 (1%)	70	89
30	Lb	111/116 (96%)	110 (99%)	1 (1%)	70	89
31	Lc	117/119 (98%)	115 (98%)	2 (2%)	53	81
32	Ld	46/47 (98%)	45 (98%)	1 (2%)	45	77
33	Le	81/88 (92%)	79 (98%)	2 (2%)	42	74
34	Lf	92/97 (95%)	92 (100%)	0	100	100
35	Lg	107/111 (96%)	103 (96%)	4 (4%)	30	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	Lh	90/91 (99%)	89 (99%)	1 (1%)	65	86
37	Li	94/103 (91%)	93 (99%)	1 (1%)	65	86
38	Lj	104/105 (99%)	104 (100%)	0	100	100
39	Lk	80/82 (98%)	80 (100%)	0	100	100
40	Ll	67/71 (94%)	67 (100%)	0	100	100
41	Lm	67/69 (97%)	66 (98%)	1 (2%)	57	83
42	Ln	45/46 (98%)	44 (98%)	1 (2%)	45	77
43	Lo	46/116 (40%)	45 (98%)	1 (2%)	45	77
44	Lp	22/23 (96%)	22 (100%)	0	100	100
45	Lq	86/91 (94%)	84 (98%)	2 (2%)	44	76
46	Lr	71/72 (99%)	71 (100%)	0	100	100
47	SA	182/195 (93%)	178 (98%)	4 (2%)	45	77
48	SB	172/191 (90%)	170 (99%)	2 (1%)	63	86
49	SC	77/98 (79%)	76 (99%)	1 (1%)	61	85
50	SD	80/119 (67%)	79 (99%)	1 (1%)	61	85
51	SE	94/118 (80%)	92 (98%)	2 (2%)	47	78
52	SF	115/119 (97%)	113 (98%)	2 (2%)	53	81
53	SG	100/124 (81%)	95 (95%)	5 (5%)	22	53
54	SH	127/129 (98%)	121 (95%)	6 (5%)	23	55
55	SI	115/116 (99%)	113 (98%)	2 (2%)	53	81
56	SJ	93/114 (82%)	91 (98%)	2 (2%)	45	77
57	SK	61/89 (68%)	60 (98%)	1 (2%)	55	82
58	SL	55/60 (92%)	52 (94%)	3 (6%)	19	49
59	SM	47/49 (96%)	46 (98%)	1 (2%)	47	78
60	SN	42/135 (31%)	37 (88%)	5 (12%)	5	16
61	SO	249/262 (95%)	245 (98%)	4 (2%)	55	82
62	SP	169/210 (80%)	166 (98%)	3 (2%)	51	80
63	SQ	198/224 (88%)	193 (98%)	5 (2%)	42	74
64	SR	175/205 (85%)	172 (98%)	3 (2%)	53	81
65	SS	220/222 (99%)	218 (99%)	2 (1%)	70	89
66	ST	187/201 (93%)	185 (99%)	2 (1%)	65	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	SU	162/170 (95%)	156 (96%)	6 (4%)	30	63
68	SV	148/161 (92%)	145 (98%)	3 (2%)	48	79
69	SW	156/166 (94%)	153 (98%)	3 (2%)	50	79
70	SX	126/137 (92%)	124 (98%)	2 (2%)	55	82
71	SY	127/128 (99%)	123 (97%)	4 (3%)	35	69
72	SZ	90/105 (86%)	88 (98%)	2 (2%)	45	77
73	Sa	71/74 (96%)	68 (96%)	3 (4%)	26	59
74	Sb	110/111 (99%)	107 (97%)	3 (3%)	39	72
75	Sc	119/120 (99%)	116 (98%)	3 (2%)	42	74
76	Sd	101/113 (89%)	96 (95%)	5 (5%)	22	53
77	Se	82/100 (82%)	80 (98%)	2 (2%)	43	75
78	Sf	64/71 (90%)	62 (97%)	2 (3%)	35	69
79	Sg	47/54 (87%)	47 (100%)	0	100	100
All	All	9097/9978 (91%)	8924 (98%)	173 (2%)	49	79

All (173) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	LE	160	VAL
7	LE	162	VAL
7	LE	287	LYS
8	LF	6	VAL
8	LF	105	THR
8	LF	286	VAL
8	LF	354	VAL
9	LG	52	VAL
10	LH	2	THR
10	LH	59	GLU
10	LH	135	VAL
10	LH	140	VAL
11	LI	62	ILE
11	LI	77	VAL
11	LI	111	ILE
11	LI	117	VAL
12	LJ	230	LYS
13	LK	6	THR
13	LK	46	THR

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Mol	Chain	Res	Type
13	LK	82	VAL
13	LK	150	SER
14	LL	89	VAL
14	LL	166	ILE
14	LL	180	GLU
15	LM	52	TYR
15	LM	108	GLU
15	LM	111	ASP
16	LN	58	VAL
16	LN	124	ILE
16	LN	170	LEU
17	LO	12	TRP
17	LO	113	THR
18	LP	9	GLU
18	LP	29	GLU
19	LQ	21	SER
19	LQ	100	GLU
19	LQ	136	THR
19	LQ	152	VAL
20	LR	107	LEU
20	LR	182	ILE
21	LS	120	GLU
21	LS	174	ARG
22	LT	6	THR
22	LT	72	GLU
23	LU	19	VAL
23	LU	27	MET
23	LU	82	ASP
23	LU	87	THR
23	LU	90	MET
23	LU	93	GLU
23	LU	97	VAL
23	LU	109	ASP
23	LU	131	LYS
25	LW	47	VAL
25	LW	58	GLU
25	LW	65	VAL
26	LX	109	MET
27	LY	26	SER
28	LZ	107	VAL
28	LZ	115	ARG
28	LZ	135	ILE

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Mol	Chain	Res	Type
29	La	97	ILE
30	Lb	103	GLN
31	Lc	85	ASP
31	Lc	123	VAL
32	Ld	13	THR
33	Le	81	VAL
33	Le	90	VAL
35	Lg	30	GLU
35	Lg	83	GLU
35	Lg	91	THR
35	Lg	126	LEU
36	Lh	98	VAL
37	Li	36	LYS
41	Lm	58	ASP
42	Ln	29	LEU
43	Lo	82	LEU
45	Lq	34	SER
45	Lq	83	LEU
47	SA	69	LEU
47	SA	110	LEU
47	SA	137	VAL
47	SA	176	LEU
48	SB	43	PHE
48	SB	44	ASN
49	SC	65	TYR
50	SD	61	VAL
51	SE	35	LYS
51	SE	61	ARG
52	SF	54	LEU
52	SF	105	LEU
53	SG	83	GLN
53	SG	100	LEU
53	SG	105	GLN
53	SG	109	LEU
53	SG	117	LEU
54	SH	32	LEU
54	SH	35	ILE
54	SH	38	VAL
54	SH	52	VAL
54	SH	105	VAL
54	SH	141	THR
55	SI	35	ASP

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Mol	Chain	Res	Type
55	SI	56	LYS
56	SJ	22	ILE
56	SJ	106	ILE
57	SK	83	LEU
58	SL	32	PHE
58	SL	36	THR
58	SL	54	LEU
59	SM	40	ARG
60	SN	100	LEU
60	SN	102	VAL
60	SN	119	ARG
60	SN	130	VAL
60	SN	138	ARG
61	SO	56	VAL
61	SO	141	LEU
61	SO	200	ASN
61	SO	239	GLU
62	SP	17	LEU
62	SP	47	VAL
62	SP	141	ILE
63	SQ	21	VAL
63	SQ	46	THR
63	SQ	61	LEU
63	SQ	68	VAL
63	SQ	95	ASN
64	SR	166	THR
64	SR	195	ASP
64	SR	246	GLU
65	SS	102	VAL
65	SS	197	HIS
66	ST	14	LYS
66	ST	153	VAL
67	SU	9	LEU
67	SU	25	VAL
67	SU	51	VAL
67	SU	75	THR
67	SU	90	VAL
67	SU	91	ILE
68	SV	38	ILE
68	SV	187	GLU
68	SV	193	LEU
69	SW	85	VAL

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Mol	Chain	Res	Type
69	SW	127	VAL
69	SW	131	GLN
70	SX	50	GLU
70	SX	135	VAL
71	SY	56	ASP
71	SY	67	THR
71	SY	121	ARG
71	SY	125	LEU
72	SZ	51	ASP
72	SZ	89	THR
73	Sa	36	VAL
73	Sa	50	TYR
73	Sa	76	ASP
74	Sb	23	ARG
74	Sb	81	VAL
74	Sb	102	VAL
75	Sc	57	LEU
75	Sc	76	LEU
75	Sc	107	PHE
76	Sd	24	VAL
76	Sd	39	GLU
76	Sd	81	GLU
76	Sd	91	LEU
76	Sd	96	LEU
77	Se	44	ILE
77	Se	53	LEU
78	Sf	35	VAL
78	Sf	67	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (180) such sidechains are listed below:

Mol	Chain	Res	Type
6	LD	132	ASN
6	LD	140	ASN
7	LE	211	GLN
7	LE	345	ASN
7	LE	371	GLN
8	LF	140	HIS
8	LF	213	ASN
8	LF	221	ASN
9	LG	111	GLN
9	LG	244	HIS

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Mol	Chain	Res	Type
9	LG	264	GLN
10	LH	57	HIS
10	LH	61	ASN
10	LH	138	GLN
11	LI	104	GLN
11	LI	197	GLN
11	LI	225	GLN
12	LJ	45	ASN
12	LJ	59	GLN
12	LJ	77	GLN
13	LK	9	GLN
13	LK	58	HIS
13	LK	169	ASN
14	LL	23	ASN
14	LL	100	ASN
14	LL	123	HIS
14	LL	144	ASN
14	LL	163	GLN
15	LM	6	GLN
15	LM	43	GLN
15	LM	68	HIS
15	LM	90	GLN
15	LM	95	ASN
15	LM	101	ASN
16	LN	129	ASN
17	LO	56	GLN
17	LO	119	GLN
18	LP	23	GLN
18	LP	182	ASN
19	LQ	26	GLN
19	LQ	31	GLN
19	LQ	182	ASN
20	LR	45	GLN
20	LR	55	GLN
20	LR	97	ASN
21	LS	23	ASN
21	LS	136	ASN
22	LT	3	ASN
22	LT	68	GLN
22	LT	92	GLN
24	LV	90	ASN
24	LV	103	GLN

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Mol	Chain	Res	Type
24	LV	134	GLN
24	LV	149	GLN
25	LW	87	ASN
25	LW	101	ASN
26	LX	81	GLN
27	LY	42	GLN
28	LZ	85	GLN
29	La	81	GLN
29	La	98	ASN
30	Lb	123	GLN
31	Lc	62	HIS
31	Lc	89	GLN
32	Ld	6	ASN
32	Ld	19	ASN
34	Lf	17	HIS
34	Lf	87	ASN
35	Lg	52	GLN
36	Lh	39	GLN
37	Li	3	GLN
37	Li	61	GLN
38	Lj	34	GLN
38	Lj	68	GLN
38	Lj	113	GLN
39	Lk	12	ASN
40	Ll	13	ASN
40	Ll	69	HIS
40	Ll	76	ASN
41	Lm	28	ASN
41	Lm	40	GLN
41	Lm	67	GLN
41	Lm	76	ASN
42	Ln	19	GLN
42	Ln	43	ASN
43	Lo	90	ASN
43	Lo	109	ASN
43	Lo	120	GLN
45	Lq	27	GLN
45	Lq	82	GLN
45	Lq	90	HIS
46	Lr	32	GLN
46	Lr	34	HIS
47	SA	165	ASN

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Mol	Chain	Res	Type
48	SB	44	ASN
48	SB	66	GLN
48	SB	79	ASN
48	SB	158	GLN
49	SC	17	GLN
49	SC	47	GLN
49	SC	58	GLN
50	SD	80	ASN
50	SD	96	GLN
51	SE	114	HIS
52	SF	8	GLN
52	SF	83	GLN
52	SF	94	GLN
52	SF	139	GLN
53	SG	105	GLN
54	SH	13	HIS
54	SH	19	ASN
54	SH	21	ASN
54	SH	25	ASN
54	SH	44	ASN
54	SH	55	HIS
54	SH	104	ASN
55	SI	16	ASN
55	SI	43	ASN
55	SI	64	HIS
55	SI	106	GLN
57	SK	82	HIS
59	SM	37	ASN
59	SM	41	GLN
61	SO	64	HIS
61	SO	69	GLN
61	SO	147	HIS
61	SO	153	GLN
61	SO	182	ASN
61	SO	200	ASN
61	SO	268	GLN
61	SO	299	GLN
62	SP	15	GLN
62	SP	33	GLN
62	SP	92	HIS
62	SP	109	ASN
62	SP	140	ASN

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Mol	Chain	Res	Type
62	SP	168	HIS
63	SQ	40	ASN
63	SQ	42	ASN
63	SQ	148	ASN
63	SQ	149	GLN
63	SQ	177	GLN
64	SR	77	GLN
65	SS	69	HIS
65	SS	130	GLN
65	SS	216	ASN
66	ST	34	GLN
66	ST	56	ASN
66	ST	199	GLN
67	SU	160	GLN
67	SU	161	GLN
67	SU	174	ASN
68	SV	32	GLN
68	SV	52	ASN
68	SV	88	ASN
68	SV	175	GLN
69	SW	48	GLN
69	SW	124	HIS
69	SW	131	GLN
70	SX	14	GLN
70	SX	22	ASN
70	SX	106	ASN
71	SY	36	GLN
71	SY	49	GLN
71	SY	62	GLN
71	SY	69	ASN
72	SZ	99	GLN
73	Sa	33	GLN
73	Sa	81	ASN
74	Sb	12	ASN
74	Sb	80	ASN
75	Sc	22	ASN
75	Sc	99	ASN
76	Sd	15	ASN
77	Se	8	ASN
77	Se	11	ASN
77	Se	69	ASN
77	Se	94	ASN

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Mol	Chain	Res	Type
78	Sf	19	HIS
78	Sf	51	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3029/3396 (89%)	473 (15%)	23 (0%)
2	B	120/121 (99%)	11 (9%)	2 (1%)
3	C	157/158 (99%)	25 (15%)	1 (0%)
4	D	9/10 (90%)	3 (33%)	1 (11%)
5	E	1571/1800 (87%)	340 (21%)	44 (2%)
80	n	62/75 (82%)	28 (45%)	0
All	All	4948/5560 (88%)	880 (17%)	71 (1%)

All (880) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	14	U
1	A	26	A
1	A	40	A
1	A	43	A
1	A	49	A
1	A	59	G
1	A	60	A
1	A	65	A
1	A	66	A
1	A	74	G
1	A	77	A
1	A	92	G
1	A	110	G
1	A	111	C
1	A	116	A
1	A	117	U
1	A	121	A
1	A	122	A
1	A	135	C
1	A	136	G
1	A	156	G
1	A	157	A
1	A	166	C

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Mol	Chain	Res	Type
1	A	187	A
1	A	190	U
1	A	191	U
1	A	200	C
1	A	206	G
1	A	210	U
1	A	213	A
1	A	218	G
1	A	219	A
1	A	234	G
1	A	239	G
1	A	240	U
1	A	241	G
1	A	242	C
1	A	243	G
1	A	257	U
1	A	269	G
1	A	270	U
1	A	286	U
1	A	295	A
1	A	305	U
1	A	329	U
1	A	330	G
1	A	339	C
1	A	350	C
1	A	351	A
1	A	376	G
1	A	395	A
1	A	399	A
1	A	401	U
1	A	402	A
1	A	403	C
1	A	404	G
1	A	420	G
1	A	421	G
1	A	422	A
1	A	438	A
1	A	440	A
1	A	441	U
1	A	494	G
1	A	503	C
1	A	518	G

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Mol	Chain	Res	Type
1	A	521	A
1	A	523	A
1	A	533	A
1	A	535	G
1	A	543	C
1	A	544	C
1	A	545	U
1	A	546	C
1	A	549	U
1	A	555	U
1	A	557	A
1	A	559	A
1	A	560	G
1	A	579	G
1	A	592	A
1	A	604	G
1	A	609	G
1	A	611	A
1	A	620	U
1	A	621	A
1	A	637	C
1	A	649	A
1	A	660	A
1	A	677	A
1	A	681	U
1	A	683	U
1	A	691	A
1	A	705	A
1	A	712	G
1	A	715	A
1	A	716	A
1	A	719	U
1	A	720	A
1	A	721	G
1	A	727	G
1	A	742	G
1	A	758	C
1	A	764	U
1	A	765	C
1	A	766	U
1	A	767	U
1	A	776	U

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Mol	Chain	Res	Type
1	A	779	G
1	A	781	G
1	A	785	G
1	A	787	G
1	A	806	A
1	A	808	A
1	A	817	A
1	A	830	A
1	A	848	A
1	A	861	C
1	A	874	U
1	A	879	U
1	A	895	A
1	A	896	A
1	A	907	G
1	A	908	G
1	A	914	A
1	A	916	G
1	A	917	A
1	A	923	C
1	A	937	G
1	A	944	C
1	A	959	C
1	A	960	U
1	A	974	G
1	A	981	U
1	A	982	C
1	A	1002	A
1	A	1010	G
1	A	1047	A
1	A	1049	C
1	A	1063	G
1	A	1064	A
1	A	1065	A
1	A	1072	G
1	A	1081	U
1	A	1093	A
1	A	1094	U
1	A	1095	U
1	A	1097	G
1	A	1098	A
1	A	1103	A

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Mol	Chain	Res	Type
1	A	1117	G
1	A	1131	G
1	A	1143	A
1	A	1144	U
1	A	1159	A
1	A	1180	A
1	A	1181	U
1	A	1192	C
1	A	1193	A
1	A	1196	C
1	A	1201	C
1	A	1202	A
1	A	1209	G
1	A	1217	A
1	A	1220	U
1	A	1222	G
1	A	1223	A
1	A	1224	C
1	A	1227	C
1	A	1230	G
1	A	1282	G
1	A	1284	C
1	A	1287	A
1	A	1308	A
1	A	1309	U
1	A	1313	G
1	A	1330	A
1	A	1331	U
1	A	1348	U
1	A	1349	G
1	A	1350	A
1	A	1352	A
1	A	1355	A
1	A	1356	U
1	A	1357	G
1	A	1386	A
1	A	1399	A
1	A	1400	G
1	A	1418	A
1	A	1419	A
1	A	1434	G
1	A	1437	C

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Mol	Chain	Res	Type
1	A	1446	A
1	A	1450	G
1	A	1475	A
1	A	1481	A
1	A	1483	G
1	A	1503	A
1	A	1508	C
1	A	1527	C
1	A	1536	G
1	A	1546	A
1	A	1555	U
1	A	1556	C
1	A	1560	G
1	A	1563	C
1	A	1564	U
1	A	1573	G
1	A	1574	C
1	A	1575	A
1	A	1576	G
1	A	1580	A
1	A	1583	A
1	A	1589	A
1	A	1606	U
1	A	1620	U
1	A	1621	A
1	A	1627	U
1	A	1629	U
1	A	1639	C
1	A	1643	A
1	A	1645	U
1	A	1657	C
1	A	1683	A
1	A	1688	U
1	A	1696	A
1	A	1717	U
1	A	1724	U
1	A	1725	C
1	A	1728	G
1	A	1741	A
1	A	1742	U
1	A	1750	A
1	A	1751	G

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Mol	Chain	Res	Type
1	A	1770	G
1	A	1775	G
1	A	1780	G
1	A	1797	A
1	A	1808	G
1	A	1819	U
1	A	1820	U
1	A	1821	U
1	A	1839	A
1	A	1840	U
1	A	1841	A
1	A	1842	A
1	A	1846	C
1	A	1849	C
1	A	1866	C
1	A	1867	A
1	A	1879	A
1	A	1880	U
1	A	1881	A
1	A	1893	A
1	A	1906	G
1	A	1943	C
1	A	1953	G
1	A	1954	G
1	A	2094	C
1	A	2095	G
1	A	2100	A
1	A	2101	C
1	A	2102	U
1	A	2112	U
1	A	2113	A
1	A	2114	C
1	A	2121	G
1	A	2122	G
1	A	2131	A
1	A	2140	U
1	A	2144	A
1	A	2158	A
1	A	2166	A
1	A	2169	G
1	A	2170	U
1	A	2206	G

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Mol	Chain	Res	Type
1	A	2207	A
1	A	2208	A
1	A	2209	U
1	A	2210	G
1	A	2223	A
1	A	2249	G
1	A	2256	A
1	A	2272	G
1	A	2273	G
1	A	2281	A
1	A	2282	U
1	A	2307	G
1	A	2310	U
1	A	2313	A
1	A	2314	U
1	A	2315	G
1	A	2318	U
1	A	2325	G
1	A	2334	U
1	A	2335	G
1	A	2336	U
1	A	2372	A
1	A	2373	A
1	A	2374	C
1	A	2375	G
1	A	2385	G
1	A	2388	U
1	A	2393	G
1	A	2394	G
1	A	2397	A
1	A	2402	A
1	A	2403	G
1	A	2404	A
1	A	2411	U
1	A	2418	G
1	A	2419	A
1	A	2435	G
1	A	2437	G
1	A	2440	G
1	A	2514	U
1	A	2515	A
1	A	2522	G

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Mol	Chain	Res	Type
1	A	2525	G
1	A	2526	C
1	A	2531	C
1	A	2532	U
1	A	2544	U
1	A	2549	G
1	A	2552	C
1	A	2559	U
1	A	2561	A
1	A	2569	A
1	A	2570	U
1	A	2572	C
1	A	2573	G
1	A	2585	G
1	A	2593	A
1	A	2594	C
1	A	2595	A
1	A	2606	G
1	A	2607	G
1	A	2614	G
1	A	2619	G
1	A	2629	U
1	A	2635	A
1	A	2652	U
1	A	2656	A
1	A	2664	C
1	A	2674	A
1	A	2677	G
1	A	2681	U
1	A	2689	A
1	A	2691	A
1	A	2694	A
1	A	2696	A
1	A	2700	G
1	A	2714	G
1	A	2719	U
1	A	2728	G
1	A	2729	U
1	A	2737	C
1	A	2749	G
1	A	2753	G
1	A	2762	A

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Mol	Chain	Res	Type
1	A	2772	C
1	A	2777	G
1	A	2778	G
1	A	2780	A
1	A	2796	G
1	A	2800	G
1	A	2801	A
1	A	2803	A
1	A	2810	C
1	A	2814	G
1	A	2816	G
1	A	2817	A
1	A	2818	U
1	A	2842	U
1	A	2845	A
1	A	2847	A
1	A	2849	C
1	A	2856	G
1	A	2867	C
1	A	2871	G
1	A	2872	A
1	A	2875	U
1	A	2876	C
1	A	2887	A
1	A	2889	C
1	A	2923	U
1	A	2929	C
1	A	2935	U
1	A	2936	A
1	A	2947	G
1	A	2955	U
1	A	2957	G
1	A	2964	G
1	A	2983	C
1	A	2990	G
1	A	2996	U
1	A	2997	G
1	A	3003	G
1	A	3012	A
1	A	3056	U
1	A	3057	U
1	A	3059	G

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Mol	Chain	Res	Type
1	A	3078	U
1	A	3079	U
1	A	3086	A
1	A	3092	C
1	A	3093	C
1	A	3094	A
1	A	3101	G
1	A	3104	U
1	A	3116	G
1	A	3117	C
1	A	3119	U
1	A	3122	A
1	A	3129	A
1	A	3130	A
1	A	3131	U
1	A	3142	A
1	A	3143	C
1	A	3153	U
1	A	3154	C
1	A	3155	U
1	A	3156	U
1	A	3157	U
1	A	3165	A
1	A	3170	A
1	A	3173	G
1	A	3174	A
1	A	3175	U
1	A	3176	G
1	A	3179	U
1	A	3181	C
1	A	3187	A
1	A	3196	U
1	A	3197	G
1	A	3207	U
1	A	3210	A
1	A	3217	C
1	A	3218	A
1	A	3219	G
1	A	3239	G
1	A	3243	A
1	A	3245	A
1	A	3247	G

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Mol	Chain	Res	Type
1	A	3249	C
1	A	3259	U
1	A	3270	U
1	A	3273	A
1	A	3276	G
1	A	3281	U
1	A	3287	U
1	A	3288	G
1	A	3289	G
1	A	3294	A
1	A	3295	A
1	A	3304	U
1	A	3316	A
1	A	3318	G
1	A	3320	A
1	A	3331	U
1	A	3334	U
1	A	3345	G
1	A	3351	U
1	A	3352	U
1	A	3354	U
1	A	3355	U
1	A	3363	U
1	A	3369	G
1	A	3378	C
1	A	3382	U
1	A	3386	G
1	A	3389	U
1	A	3390	G
2	B	7	G
2	B	10	C
2	B	30	G
2	B	35	C
2	B	39	C
2	B	52	G
2	B	53	U
2	B	65	G
2	B	102	A
2	B	112	G
2	B	121	U
3	C	34	U
3	C	35	C

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Mol	Chain	Res	Type
3	C	48	A
3	C	59	A
3	C	62	C
3	C	63	G
3	C	80	A
3	C	81	U
3	C	82	U
3	C	83	C
3	C	84	C
3	C	85	G
3	C	86	U
3	C	87	G
3	C	90	U
3	C	91	C
3	C	95	G
3	C	104	A
3	C	106	C
3	C	112	U
3	C	125	U
3	C	126	A
3	C	138	A
3	C	148	G
3	C	152	G
4	D	3	U
4	D	7	A
4	D	8	A
5	E	2	A
5	E	4	C
5	E	25	C
5	E	26	A
5	E	43	A
5	E	45	U
5	E	46	A
5	E	47	A
5	E	56	U
5	E	57	G
5	E	61	A
5	E	62	A
5	E	63	G
5	E	66	U
5	E	67	A
5	E	68	A

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Mol	Chain	Res	Type
5	E	69	G
5	E	72	A
5	E	78	A
5	E	81	G
5	E	104	A
5	E	114	C
5	E	116	U
5	E	124	A
5	E	126	A
5	E	127	G
5	E	129	U
5	E	138	A
5	E	139	C
5	E	140	A
5	E	145	A
5	E	153	G
5	E	156	A
5	E	158	U
5	E	161	U
5	E	166	C
5	E	178	U
5	E	179	A
5	E	181	A
5	E	182	A
5	E	250	C
5	E	257	A
5	E	261	U
5	E	265	A
5	E	266	A
5	E	272	U
5	E	274	G
5	E	276	C
5	E	278	U
5	E	279	G
5	E	280	U
5	E	281	G
5	E	287	G
5	E	299	A
5	E	313	U
5	E	314	C
5	E	316	A
5	E	321	C

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Mol	Chain	Res	Type
5	E	322	G
5	E	323	A
5	E	330	G
5	E	333	A
5	E	337	G
5	E	338	C
5	E	352	A
5	E	353	A
5	E	359	A
5	E	361	C
5	E	370	A
5	E	373	G
5	E	385	A
5	E	387	A
5	E	388	G
5	E	395	U
5	E	400	A
5	E	401	A
5	E	402	C
5	E	404	G
5	E	416	A
5	E	417	A
5	E	418	G
5	E	419	G
5	E	423	G
5	E	424	C
5	E	425	A
5	E	426	G
5	E	428	A
5	E	434	G
5	E	435	C
5	E	439	U
5	E	444	C
5	E	446	A
5	E	447	U
5	E	448	C
5	E	460	A
5	E	461	G
5	E	468	A
5	E	469	C
5	E	471	A
5	E	482	U

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Mol	Chain	Res	Type
5	E	510	G
5	E	517	U
5	E	518	A
5	E	527	A
5	E	538	A
5	E	540	G
5	E	541	A
5	E	542	A
5	E	555	A
5	E	556	A
5	E	557	G
5	E	558	U
5	E	565	C
5	E	568	G
5	E	578	U
5	E	579	A
5	E	583	C
5	E	594	A
5	E	595	G
5	E	606	A
5	E	608	U
5	E	609	U
5	E	610	G
5	E	611	U
5	E	619	A
5	E	620	A
5	E	622	A
5	E	623	A
5	E	624	G
5	E	638	U
5	E	641	G
5	E	687	G
5	E	694	U
5	E	745	U
5	E	753	A
5	E	756	A
5	E	764	U
5	E	765	G
5	E	766	U
5	E	774	A
5	E	778	G
5	E	782	U

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Mol	Chain	Res	Type
5	E	783	G
5	E	784	C
5	E	789	A
5	E	803	A
5	E	804	A
5	E	812	A
5	E	813	U
5	E	814	A
5	E	815	G
5	E	816	G
5	E	820	U
5	E	821	U
5	E	823	G
5	E	846	G
5	E	847	A
5	E	848	C
5	E	856	A
5	E	863	A
5	E	873	U
5	E	876	G
5	E	881	A
5	E	886	U
5	E	898	A
5	E	899	G
5	E	902	G
5	E	904	G
5	E	912	U
5	E	913	G
5	E	929	A
5	E	933	A
5	E	935	U
5	E	942	G
5	E	945	U
5	E	951	A
5	E	960	U
5	E	966	A
5	E	988	A
5	E	989	U
5	E	993	A
5	E	1004	U
5	E	1005	A
5	E	1023	A

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Mol	Chain	Res	Type
5	E	1024	U
5	E	1025	A
5	E	1026	A
5	E	1028	C
5	E	1032	G
5	E	1039	A
5	E	1053	G
5	E	1066	C
5	E	1076	A
5	E	1081	A
5	E	1082	C
5	E	1092	A
5	E	1096	C
5	E	1097	U
5	E	1100	G
5	E	1113	A
5	E	1138	A
5	E	1150	G
5	E	1158	C
5	E	1160	A
5	E	1167	G
5	E	1170	G
5	E	1185	U
5	E	1186	U
5	E	1194	A
5	E	1199	G
5	E	1200	G
5	E	1208	A
5	E	1212	G
5	E	1214	U
5	E	1217	A
5	E	1218	G
5	E	1227	A
5	E	1229	G
5	E	1231	U
5	E	1241	G
5	E	1244	A
5	E	1245	G
5	E	1246	C
5	E	1252	C
5	E	1255	G
5	E	1256	A

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Mol	Chain	Res	Type
5	E	1257	U
5	E	1260	U
5	E	1263	G
5	E	1274	C
5	E	1276	U
5	E	1284	C
5	E	1285	U
5	E	1286	U
5	E	1301	U
5	E	1307	U
5	E	1308	G
5	E	1312	A
5	E	1314	U
5	E	1315	U
5	E	1316	G
5	E	1318	G
5	E	1321	A
5	E	1322	A
5	E	1344	A
5	E	1345	A
5	E	1346	A
5	E	1347	U
5	E	1348	A
5	E	1349	G
5	E	1361	U
5	E	1362	U
5	E	1363	U
5	E	1370	U
5	E	1371	A
5	E	1372	U
5	E	1373	C
5	E	1382	A
5	E	1383	G
5	E	1390	U
5	E	1395	G
5	E	1398	U
5	E	1399	C
5	E	1400	A
5	E	1402	G
5	E	1413	U
5	E	1414	U
5	E	1415	U

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Mol	Chain	Res	Type
5	E	1427	A
5	E	1431	C
5	E	1432	U
5	E	1433	G
5	E	1436	A
5	E	1446	A
5	E	1448	G
5	E	1458	G
5	E	1459	C
5	E	1460	A
5	E	1466	G
5	E	1469	A
5	E	1471	A
5	E	1472	C
5	E	1478	G
5	E	1496	U
5	E	1516	A
5	E	1520	U
5	E	1521	G
5	E	1523	G
5	E	1524	A
5	E	1528	U
5	E	1535	U
5	E	1536	G
5	E	1537	C
5	E	1538	U
5	E	1540	G
5	E	1543	A
5	E	1550	A
5	E	1557	U
5	E	1558	U
5	E	1559	A
5	E	1570	A
5	E	1572	G
5	E	1573	A
5	E	1574	G
5	E	1575	G
5	E	1577	A
5	E	1583	A
5	E	1584	G
5	E	1601	G
5	E	1608	U

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Mol	Chain	Res	Type
5	E	1609	U
5	E	1615	C
5	E	1616	G
5	E	1619	C
5	E	1633	A
5	E	1634	C
5	E	1635	A
5	E	1637	C
5	E	1657	U
5	E	1658	G
5	E	1680	G
5	E	1681	A
5	E	1717	G
5	E	1718	G
5	E	1731	A
5	E	1755	A
5	E	1757	G
5	E	1760	G
5	E	1762	A
5	E	1766	A
5	E	1767	G
5	E	1769	U
5	E	1780	G
5	E	1782	A
5	E	1783	C
5	E	1792	G
5	E	1793	G
5	E	1794	A
5	E	1796	C
5	E	1799	U
80	n	3	C
80	n	4	G
80	n	6	C
80	n	7	G
80	n	8	U
80	n	9	G
80	n	16	U
80	n	22	G
80	n	24	G
80	n	25	C
80	n	28	A
80	n	30	G

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Mol	Chain	Res	Type
80	n	31	G
80	n	34	C
80	n	36	U
80	n	40	C
80	n	41	C
80	n	42	U
80	n	44	A
80	n	45	U
80	n	49	C
80	n	68	G
80	n	69	C
80	n	70	G
80	n	71	C
80	n	72	U
80	n	75	C
80	n	76	A

All (71) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	73	C
1	A	186	U
1	A	636	C
1	A	763	G
1	A	916	G
1	A	1064	A
1	A	1097	G
1	A	1222	G
1	A	1348	U
1	A	1355	A
1	A	1562	C
1	A	1820	U
1	A	1821	U
1	A	2112	U
1	A	2255	A
1	A	2513	U
1	A	2525	G
1	A	3078	U
1	A	3121	U
1	A	3218	A
1	A	3269	U

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Mol	Chain	Res	Type
1	A	3350	C
2	B	52	G
2	B	120	C
3	C	85	G
4	D	7	A
5	E	65	A
5	E	68	A
5	E	80	A
5	E	139	C
5	E	177	U
5	E	178	U
5	E	279	G
5	E	313	U
5	E	321	C
5	E	322	G
5	E	352	A
5	E	387	A
5	E	539	G
5	E	541	A
5	E	609	U
5	E	640	U
5	E	783	G
5	E	803	A
5	E	814	A
5	E	819	G
5	E	912	U
5	E	913	G
5	E	928	U
5	E	1023	A
5	E	1217	A
5	E	1226	A
5	E	1255	G
5	E	1256	A
5	E	1273	G
5	E	1344	A
5	E	1362	U
5	E	1382	A
5	E	1430	U
5	E	1471	A
5	E	1535	U
5	E	1536	G
5	E	1556	A

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Mol	Chain	Res	Type
5	E	1557	U
5	E	1572	G
5	E	1573	A
5	E	1615	C
5	E	1633	A
5	E	1634	C
5	E	1636	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	3HE	A	3401	-	21,21,21	0.53	0	23,30,30	0.86	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	3HE	A	3401	-	-	2/8/36/36	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

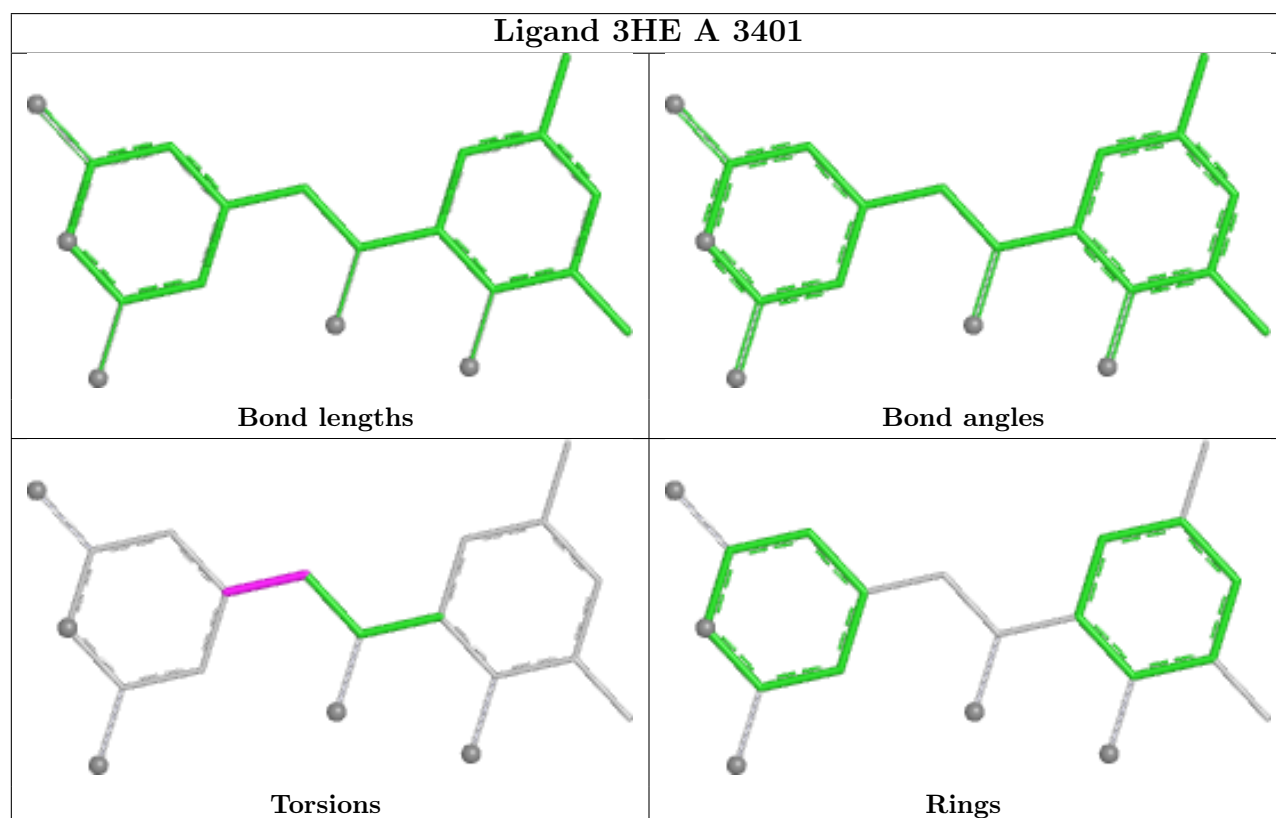
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	A	3401	3HE	C7-C8-C9-C10
81	A	3401	3HE	C7-C8-C9-C13

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

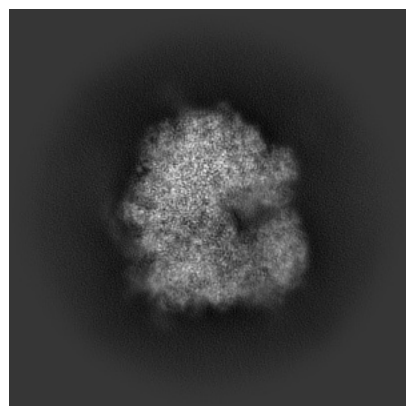
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72802. These allow visual inspection of the internal detail of the map and identification of artifacts.

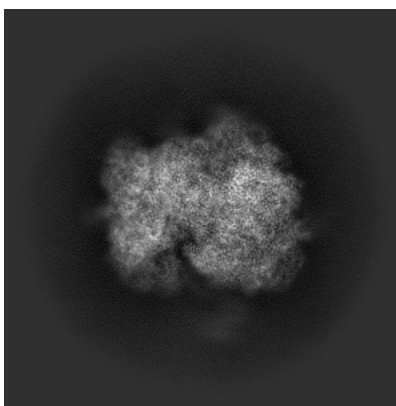
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

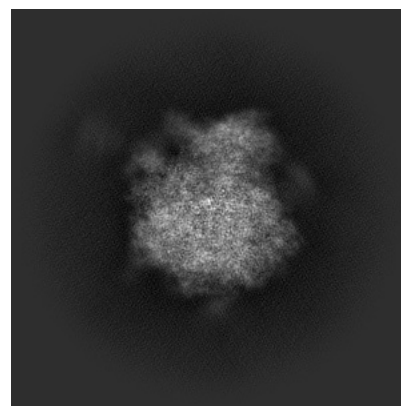
6.1.1 Primary map



X

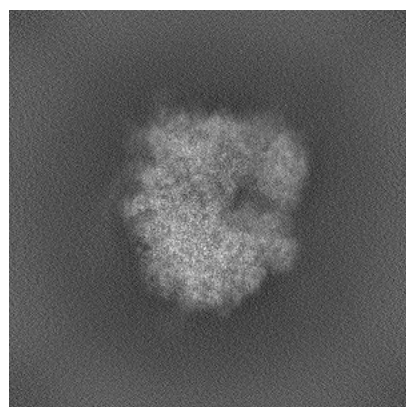


Y

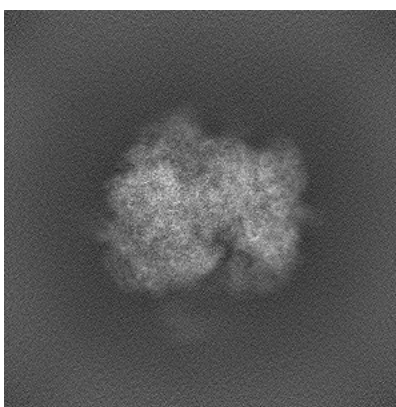


Z

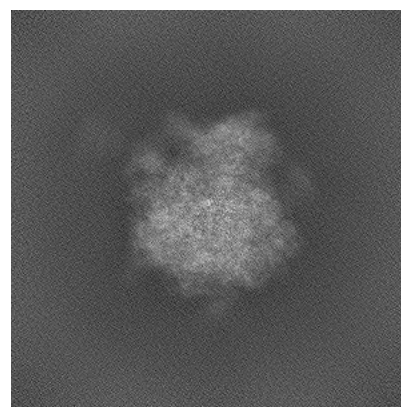
6.1.2 Raw map



X



Y

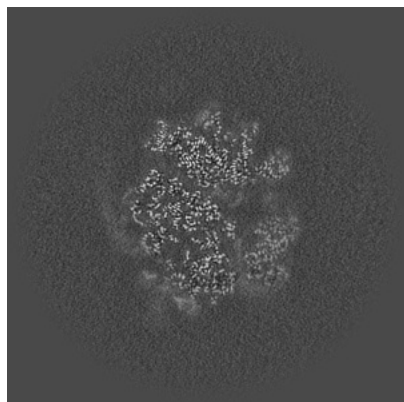


Z

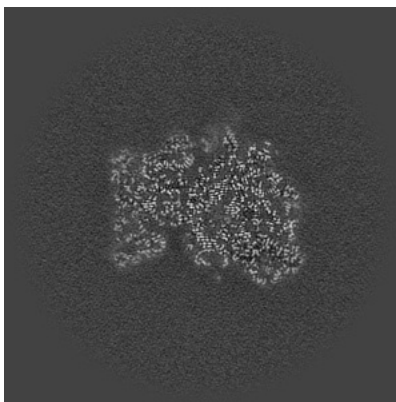
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

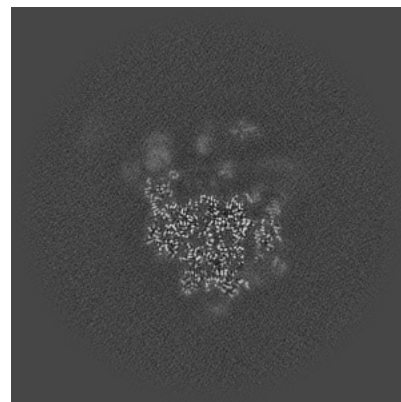
6.2.1 Primary map



X Index: 300

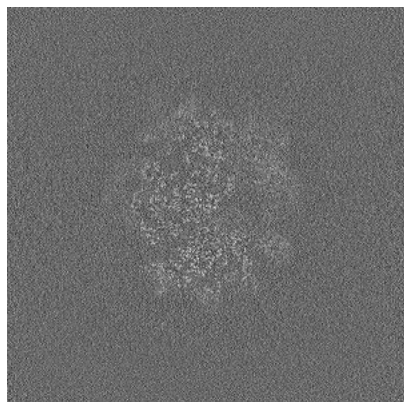


Y Index: 300

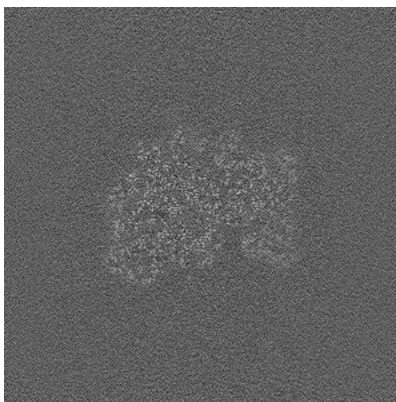


Z Index: 300

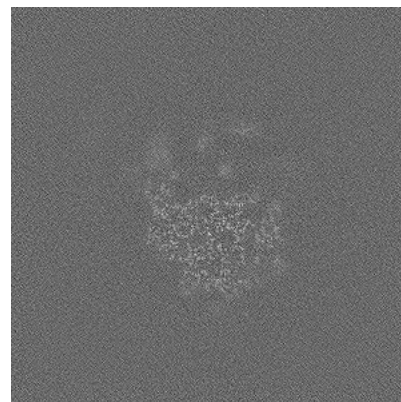
6.2.2 Raw map



X Index: 300



Y Index: 300

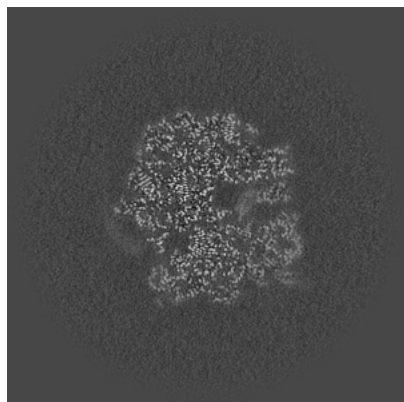


Z Index: 300

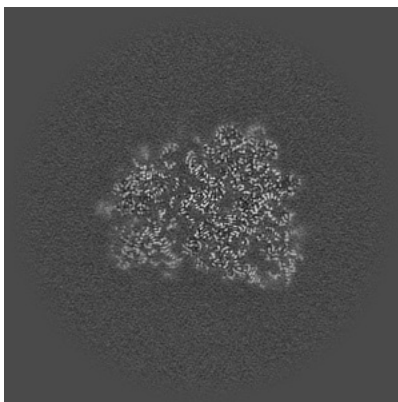
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

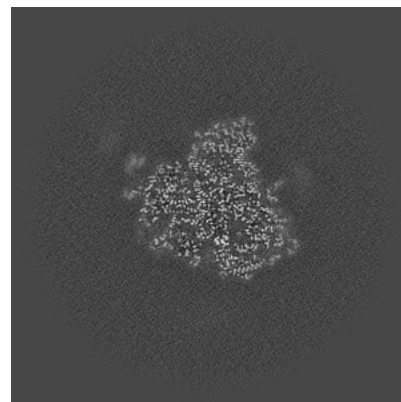
6.3.1 Primary map



X Index: 326

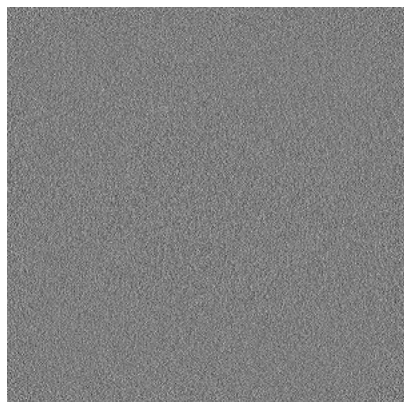


Y Index: 277

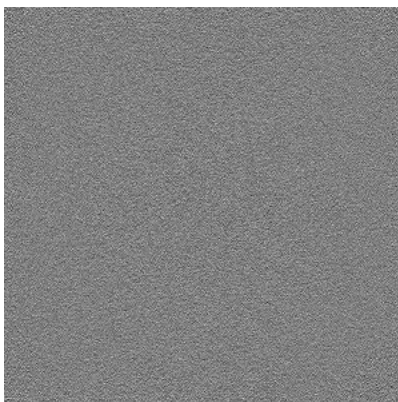


Z Index: 364

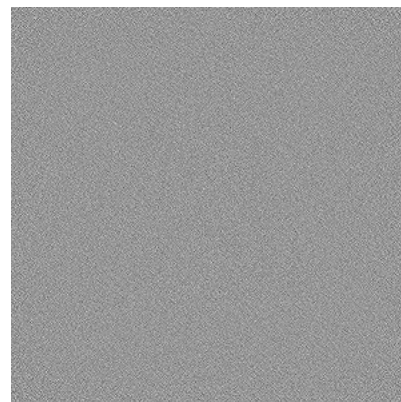
6.3.2 Raw map



X Index: 0



Y Index: 0

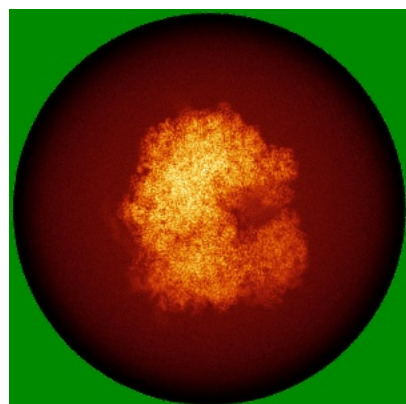


Z Index: 0

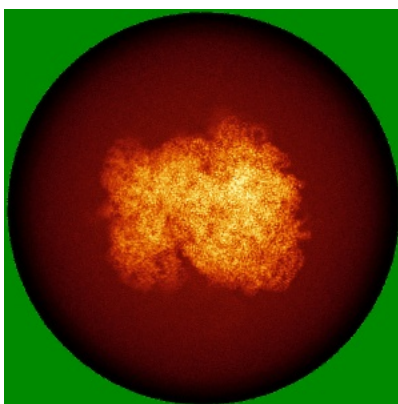
The images above show the largest variance slices of the map in three orthogonal directions.

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

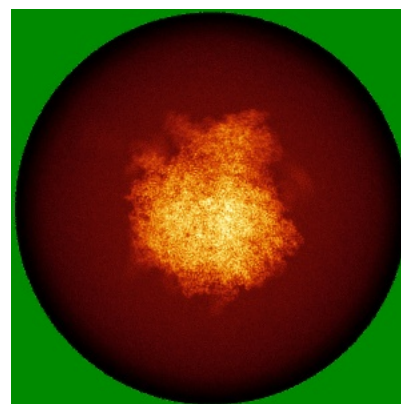
6.4.1 Primary map



X

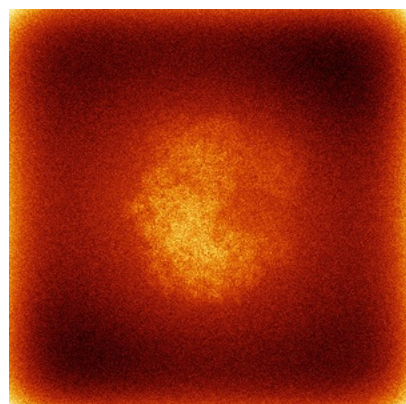


Y

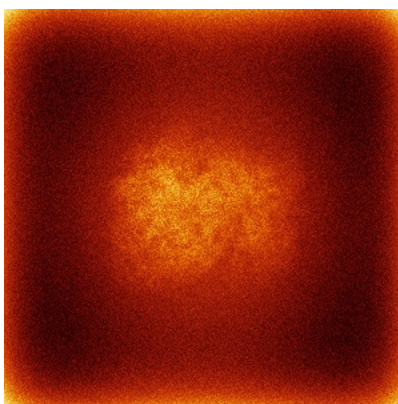


Z

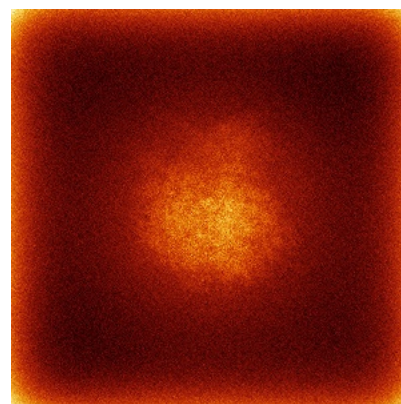
6.4.2 Raw map



X



Y

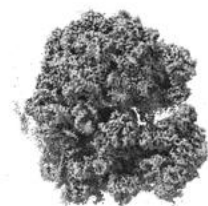


Z

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

6.5 Orthogonal surface views [i](#)

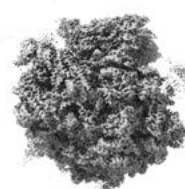
6.5.1 Primary map



X



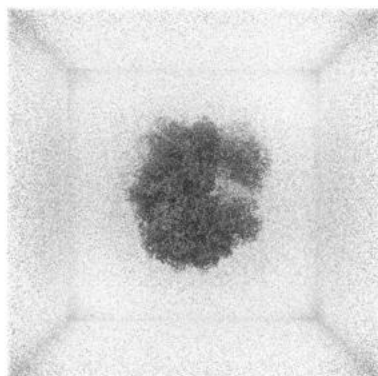
Y



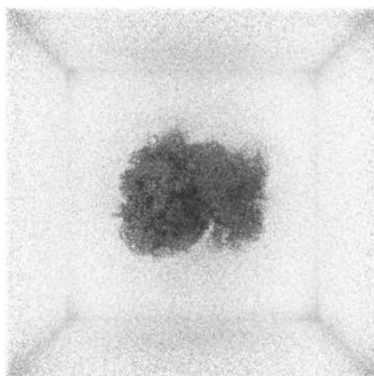
Z

The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

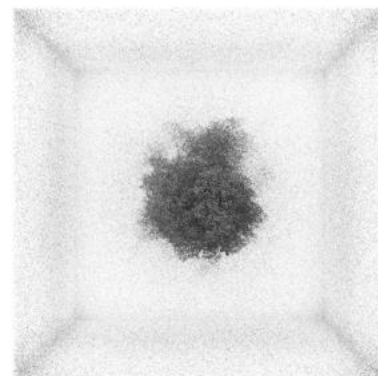
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

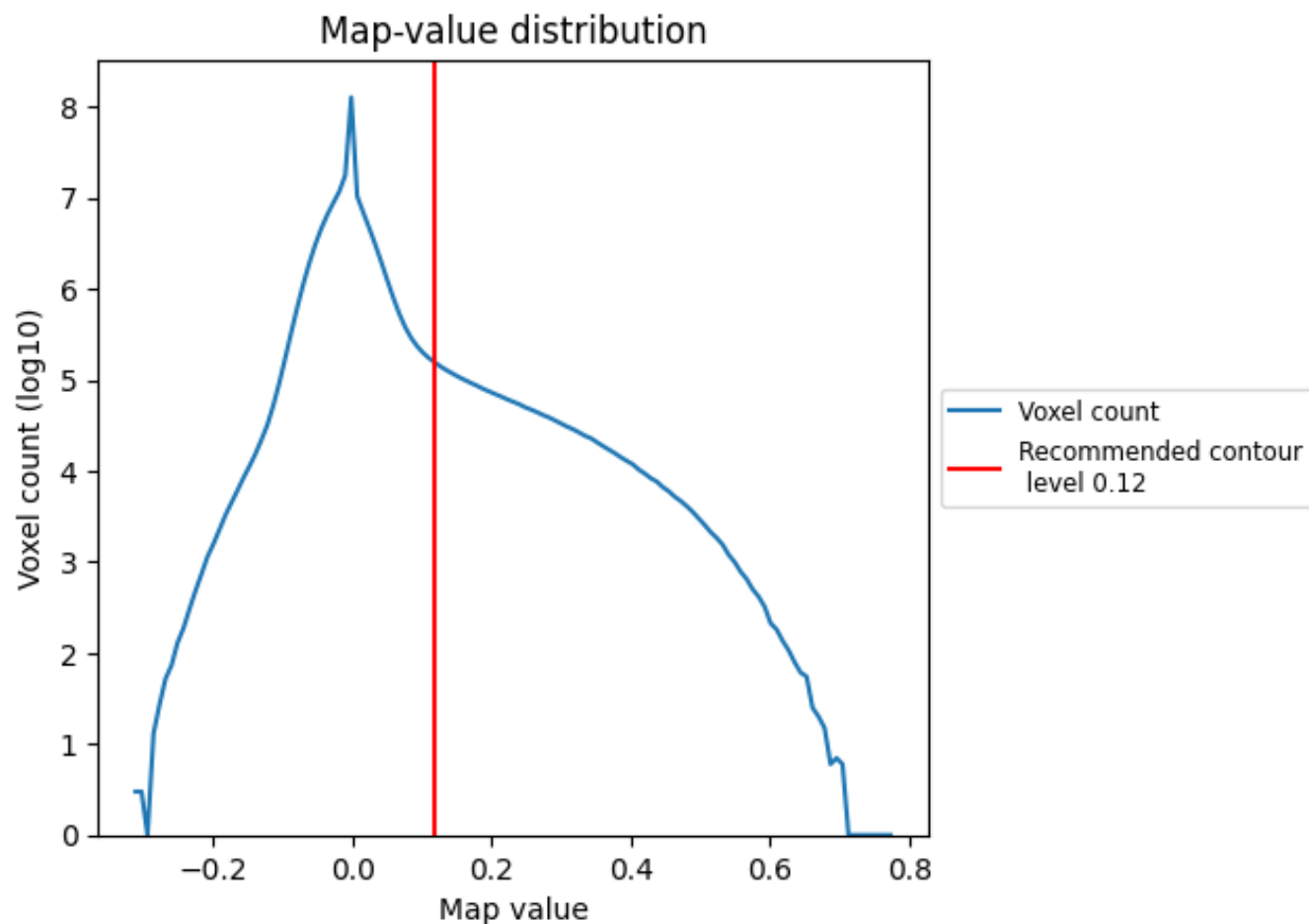
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

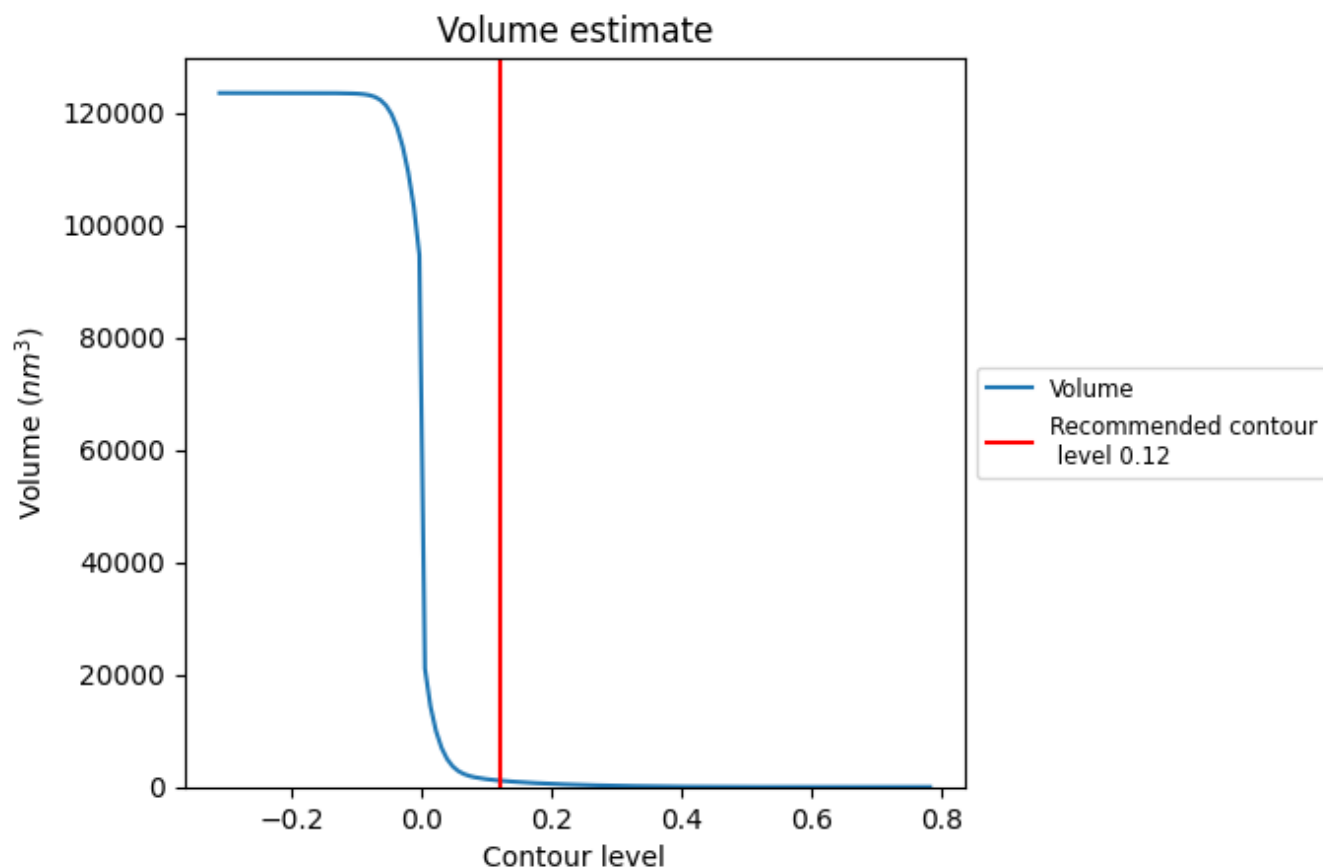
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

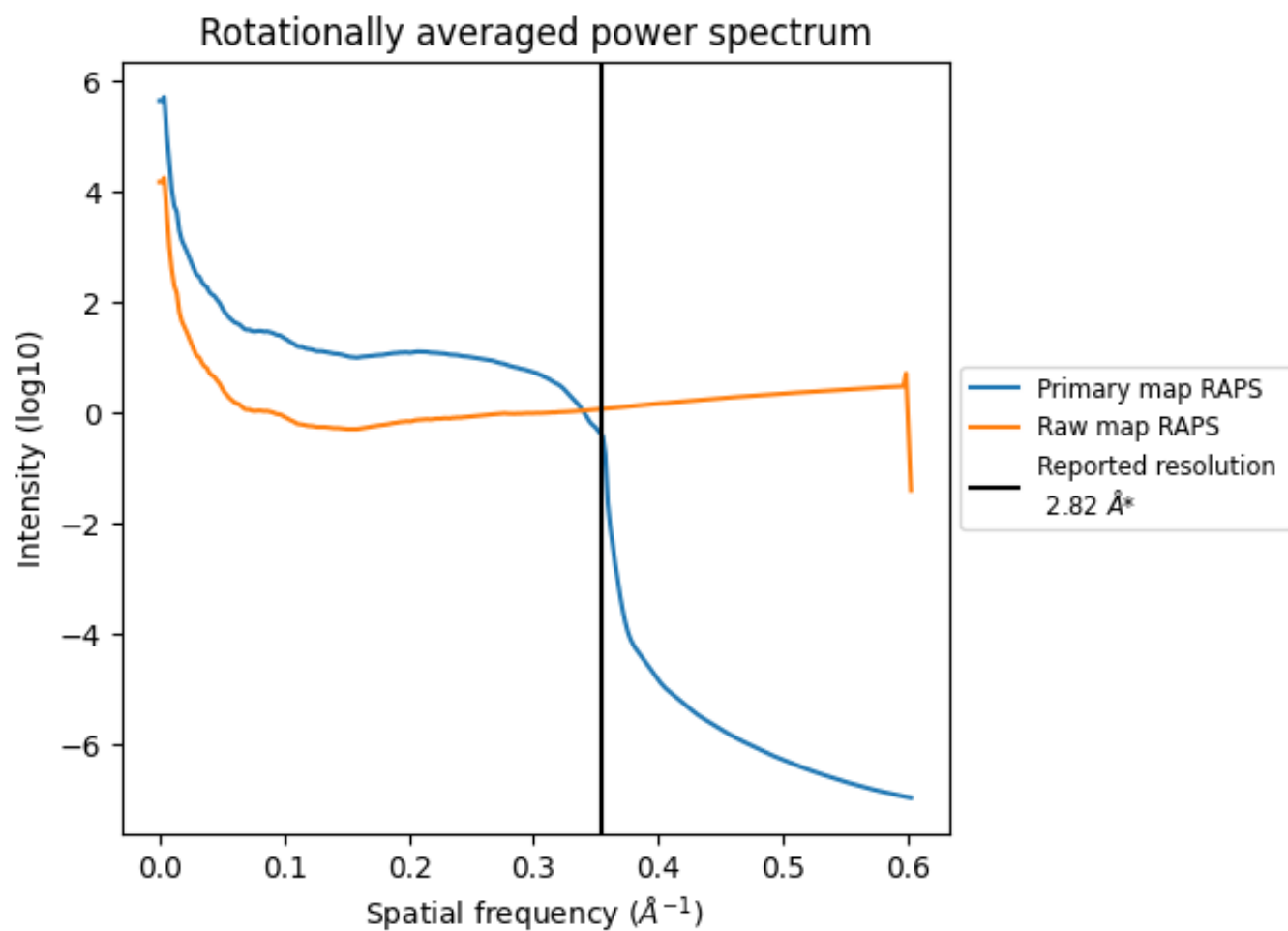
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1138 nm³; this corresponds to an approximate mass of 1028 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

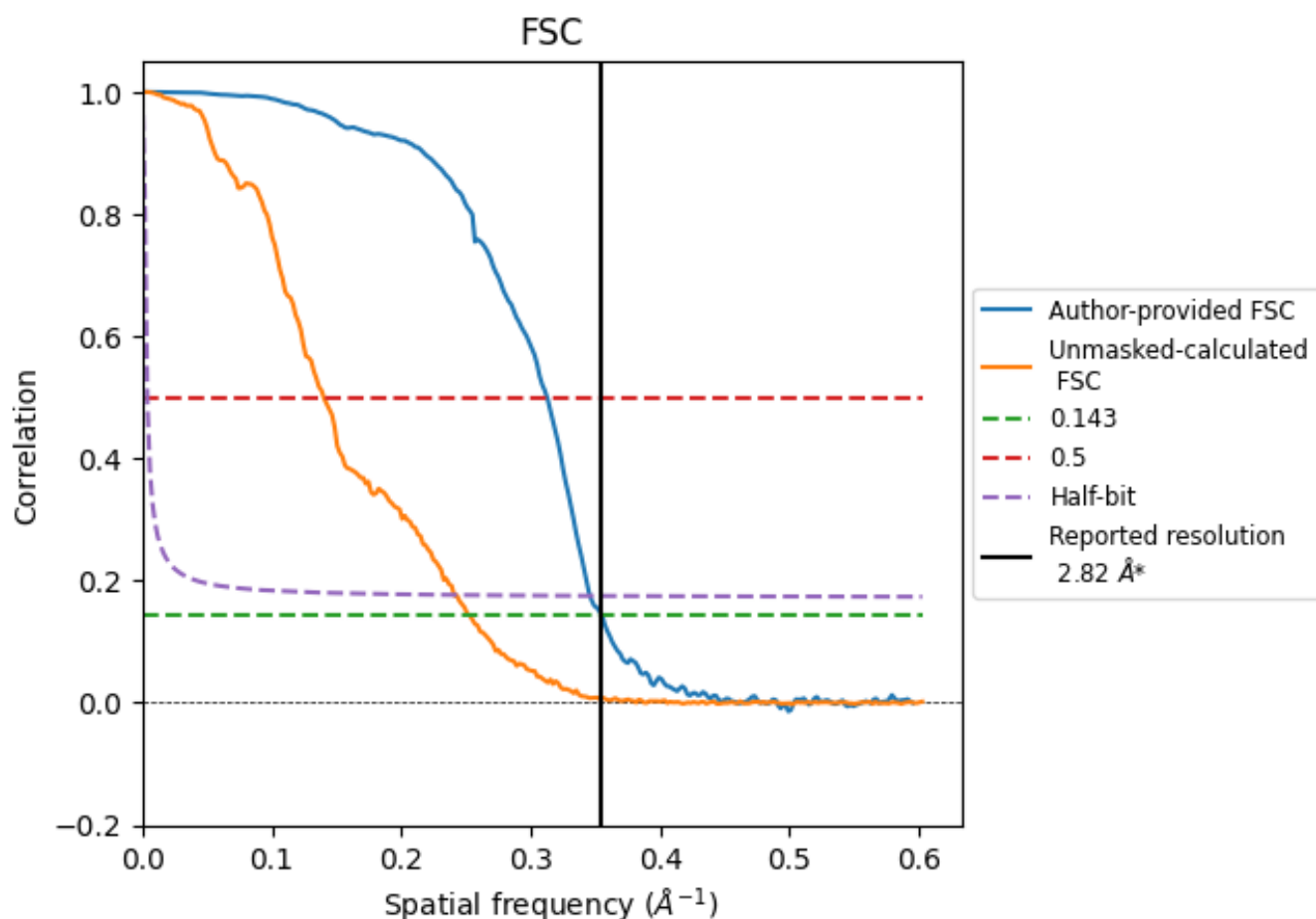


*Reported resolution corresponds to spatial frequency of 0.355 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.355 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

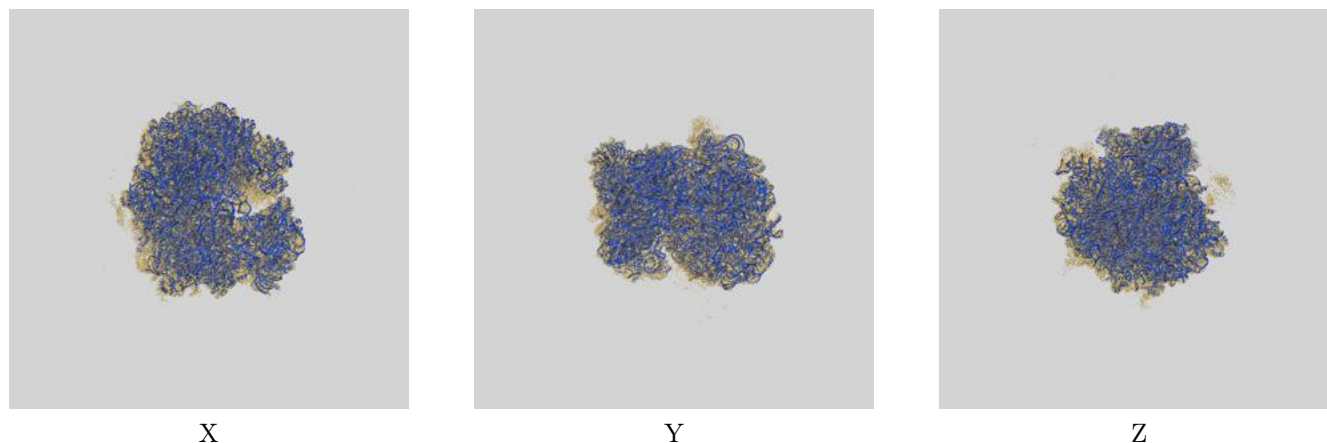
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.82	-	-
Author-provided FSC curve	2.82	3.20	2.89
Unmasked-calculated*	3.95	7.13	4.15

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.95 differs from the reported value 2.82 by more than 10 %

9 Map-model fit [i](#)

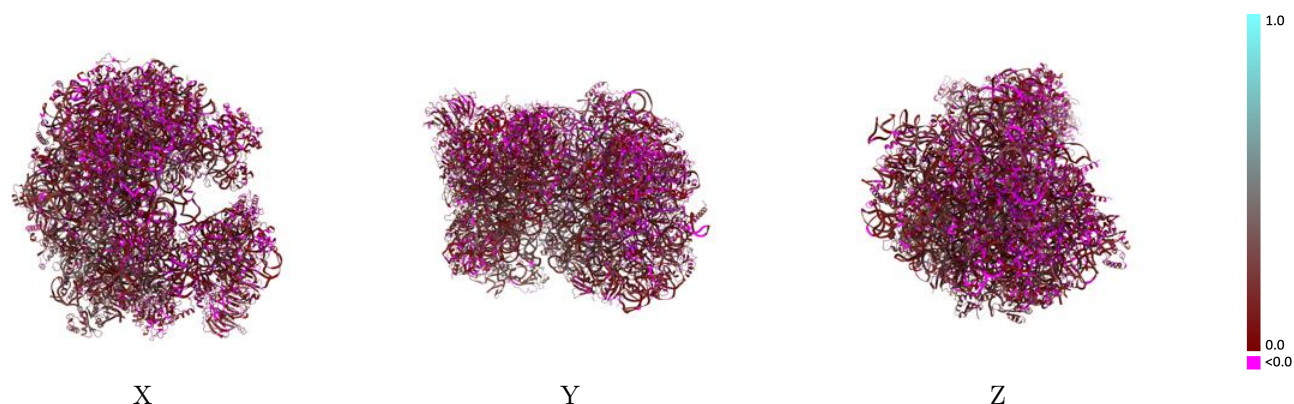
This section contains information regarding the fit between EMDB map EMD-72802 and PDB model 9YDE. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



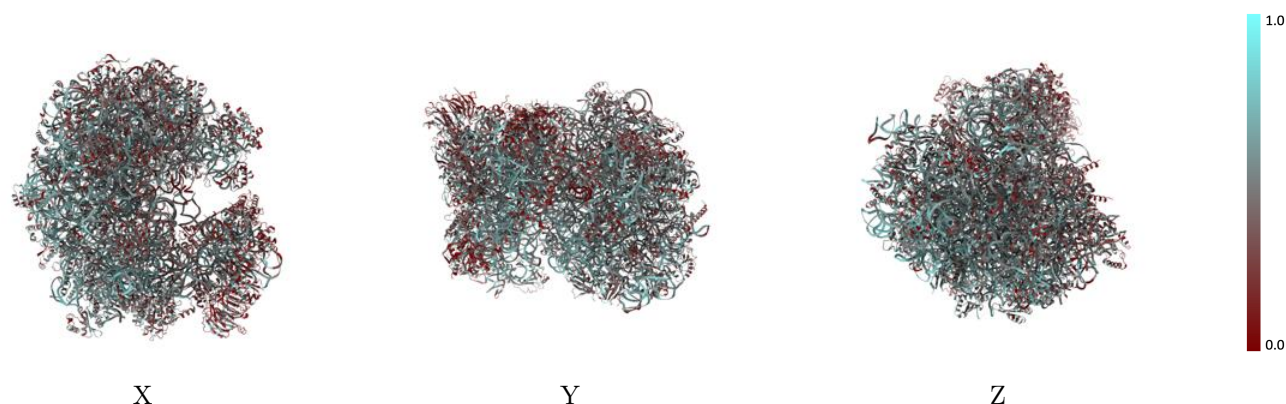
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



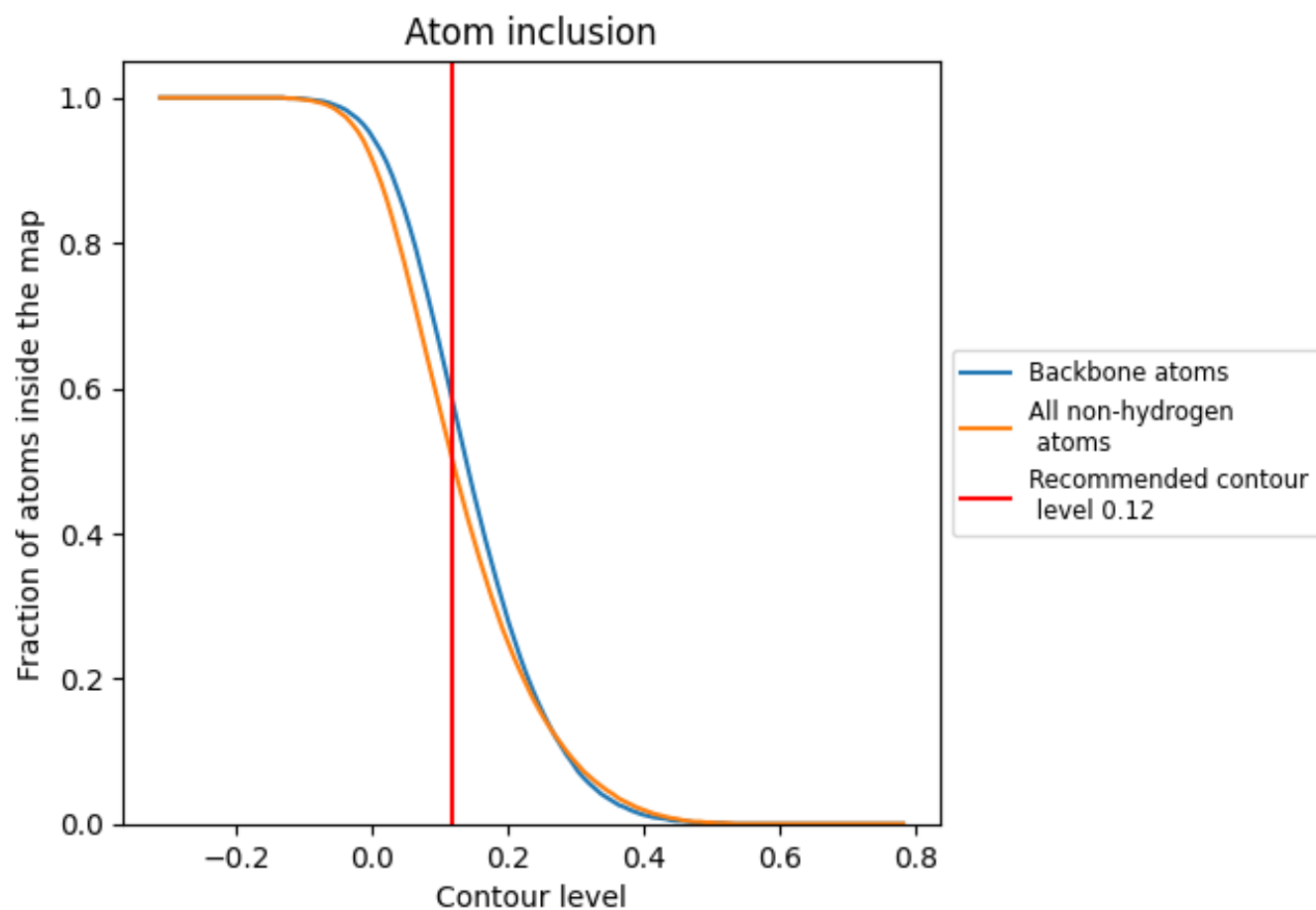
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 58% of all backbone atoms, 50% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4970	 0.1440
A	 0.5560	 0.1420
B	 0.5490	 0.0640
C	 0.5610	 0.1430
D	 0.2660	 0.0790
E	 0.5700	 0.1580
LD	 0.4400	 0.1270
LE	 0.5340	 0.2140
LF	 0.4200	 0.0860
LG	 0.3770	 0.0720
LH	 0.4430	 0.1380
LI	 0.4120	 0.0990
LJ	 0.4020	 0.1000
LK	 0.4660	 0.1680
LL	 0.3850	 0.1250
LM	 0.3700	 0.1240
LN	 0.3820	 0.0520
LO	 0.4600	 0.1290
LP	 0.3870	 0.0670
LQ	 0.4580	 0.1420
LR	 0.4750	 0.1420
LS	 0.3790	 0.0580
LT	 0.5480	 0.2420
LU	 0.4300	 0.1280
LV	 0.3720	 0.0820
LW	 0.5010	 0.2200
LX	 0.4680	 0.2190
LY	 0.5330	 0.2360
LZ	 0.4650	 0.1440
La	 0.4530	 0.1060
Lb	 0.4770	 0.1590
Lc	 0.3890	 0.0700
Ld	 0.3890	 0.1000
Le	 0.4590	 0.1510
Lf	 0.5350	 0.2230



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Chain	Atom inclusion	Q-score
Lg	 0.4020	 0.0940
Lh	 0.4400	 0.1150
Li	 0.4840	 0.1520
Lj	 0.4070	 0.0770
Lk	 0.3590	 0.0730
Ll	 0.4620	 0.1100
Lm	 0.4860	 0.2160
Ln	 0.5230	 0.1890
Lo	 0.4630	 0.1640
Lp	 0.4040	 0.1700
Lq	 0.3700	 0.0780
Lr	 0.4540	 0.1470
SA	 0.3430	 0.1290
SB	 0.3070	 0.0800
SC	 0.4210	 0.1970
SD	 0.1350	 0.1150
SE	 0.3220	 0.1430
SF	 0.3480	 0.1010
SG	 0.3610	 0.1170
SH	 0.2910	 0.0820
SI	 0.2950	 0.0670
SJ	 0.3180	 0.1200
SK	 0.2660	 0.0330
SL	 0.2760	 0.0760
SM	 0.4460	 0.1760
SN	 0.2210	 0.1400
SO	 0.2890	 0.1200
SP	 0.4130	 0.1130
SQ	 0.3400	 0.0880
SR	 0.4960	 0.2000
SS	 0.5240	 0.2760
ST	 0.4710	 0.2570
SU	 0.4900	 0.2570
SV	 0.5070	 0.2580
SW	 0.4740	 0.2130
SX	 0.5040	 0.2600
SY	 0.4940	 0.2080
SZ	 0.3760	 0.0980
Sa	 0.4660	 0.1670
Sb	 0.5020	 0.2130
Sc	 0.4530	 0.2190
Sd	 0.5040	 0.2540

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Chain	Atom inclusion	Q-score
Se	 0.4490	 0.1590
Sf	 0.4560	 0.1650
Sg	 0.3470	 0.1390
n	 0.2470	 0.0820