Full wwPDB EM Validation Report

Mar 12, 2026 – 09:46 PM UTC

PDB ID	:	8BHF / pdb_00008bhf
EMDB ID	:	EMD-16052
Title	:	Cryo-EM structure of stalled rabbit 80S ribosomes in complex with human CCR4-NOT and CNOT4
Authors	:	Absmeier, E.; Chandrasekaran, V.; O'Reilly, F.J.; Stowell, J.A.W.; Rappsilber, J.; Passmore, L.A.
Deposited on	:	2022-10-31
Resolution	:	3.10 Å(reported)

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

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

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

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

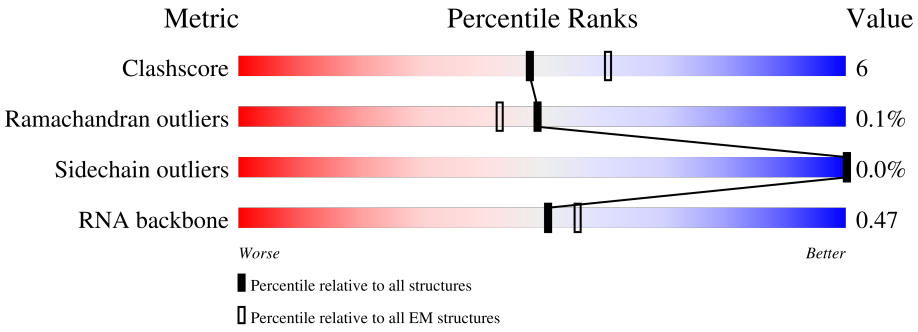
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

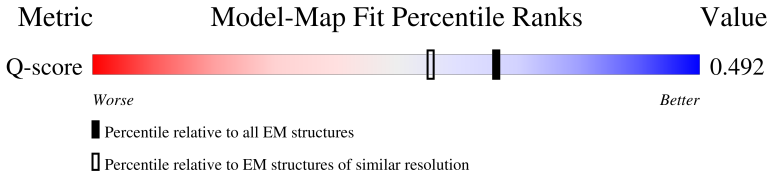
1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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

Mol	Chain	Length	Quality of chain
1	A1	203	85% 14%
2	B1	199	80% 20%
3	C1	153	82% 18%

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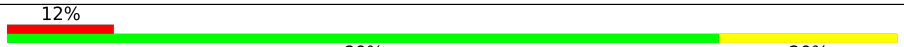
Mol	Chain	Length	Quality of chain
4	D1	187	
5	E1	180	
6	F1	176	
7	G1	159	
8	H1	99	
9	I1	139	
10	J1	106	
11	K1	118	
12	L1	134	
13	M1	135	
14	N1	147	
15	O1	116	
16	P1	98	
17	Q1	107	
18	R1	128	
19	S1	109	
20	T1	114	
21	U1	122	
22	V1	102	
23	W1	86	
24	X1	69	
25	Y1	50	
26	Z1	52	
27	a1	25	
28	b1	104	

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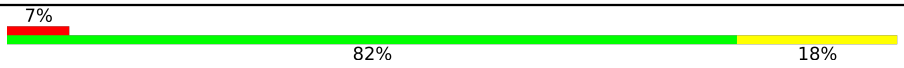
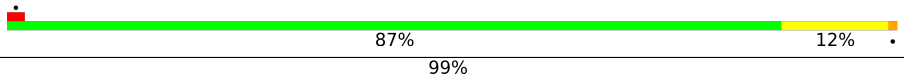
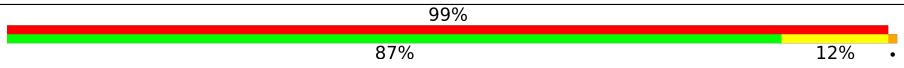
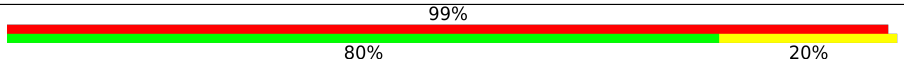
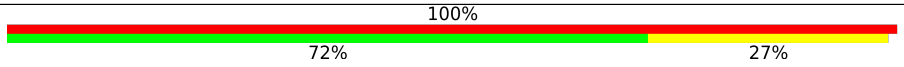
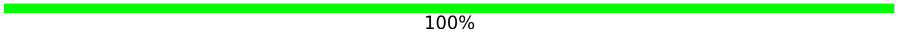
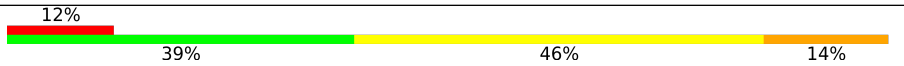
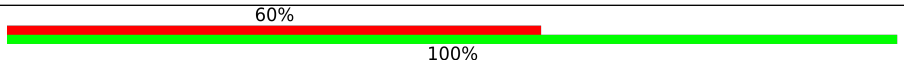
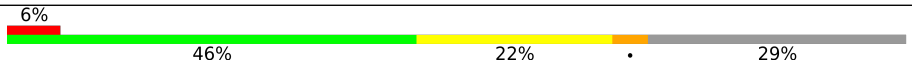
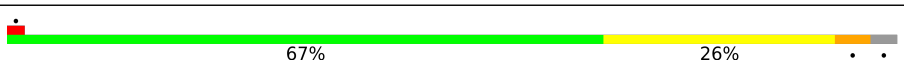
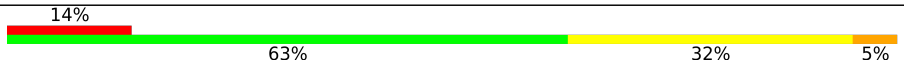
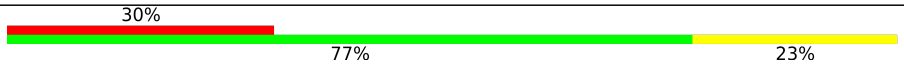
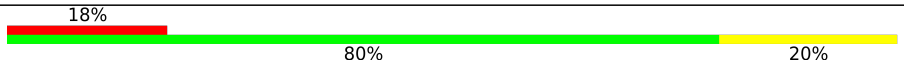
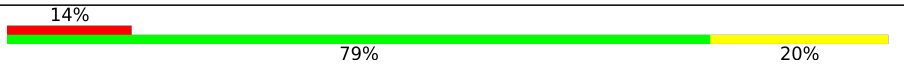
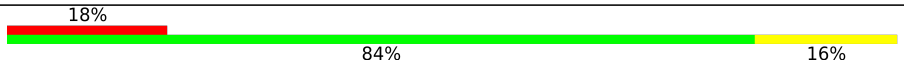
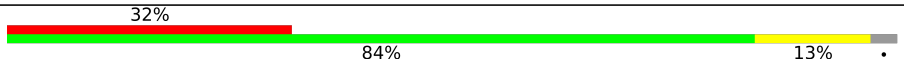
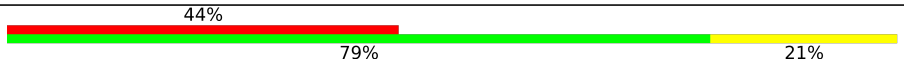
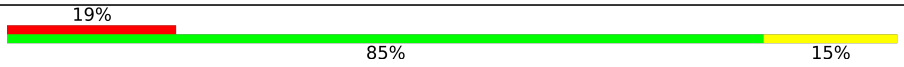
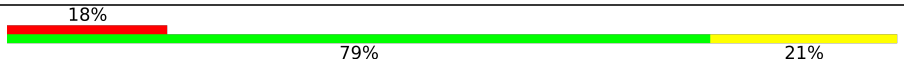
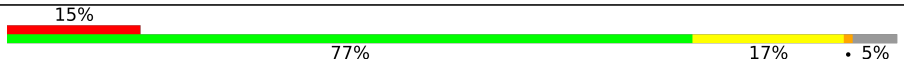
Mol	Chain	Length	Quality of chain
29	c1	91	
30	d1	124	
31	e1	196	
32	f1	153	
33	l1	206	
34	m1	3	
35	n1	236	
36	21	76	
37	11	5	
38	A2	5051	
39	B2	119	
40	C2	156	
41	A3	1697	
42	B3	217	
43	C3	213	
44	D3	221	
45	E3	228	
46	F3	262	
47	G3	191	
48	H3	237	
49	I3	189	
50	J3	206	
51	K3	185	
52	L3	96	
53	M3	151	

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Mol	Chain	Length	Quality of chain
54	N3	117	97% 77% 23%
55	O3	149	12% 86% 14%
56	P3	136	13% 74% 26%
57	Q3	129	51% 81% 19%
58	R3	142	35% 85% 15%
59	S3	132	55% 82% 18%
60	T3	144	46% 69% 31%
61	U3	141	35% 79% 20%
62	V3	100	53% 73% 27%
63	W3	83	31% 78% 22%
64	X3	129	78% 22%
65	Y3	141	12% 84% 15%
66	Z3	124	23% 83% 17%
67	a3	75	56% 83% 15%
68	b3	101	10% 83% 17%
69	c3	83	34% 81% 19%
70	d3	62	35% 77% 23%
71	e3	55	31% 89% 9%
72	f3	57	37% 91% 9%
73	g3	68	94% 87% 13%
74	h3	313	79% 69% 31%
75	j3	248	80% 20%
76	k3	394	80% 20%
77	l3	362	81% 19%
78	m3	293	83% 17%

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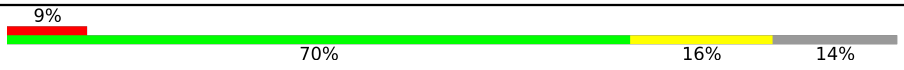
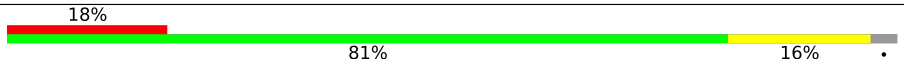
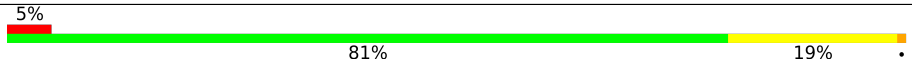
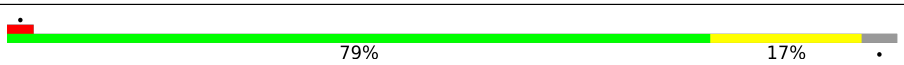
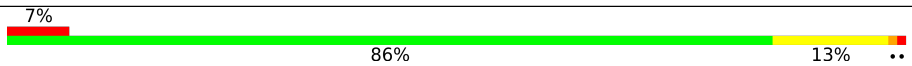
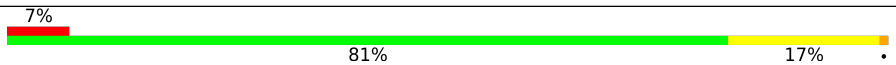
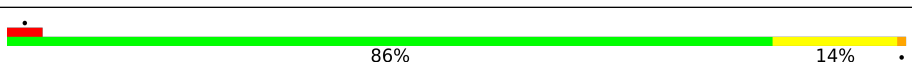
Mol	Chain	Length	Quality of chain
79	n3	251	
80	o3	225	
81	p3	240	
82	q3	190	
83	r3	213	
84	s3	170	
85	t3	210	
86	u3	138	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 219017 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A1	203	1701	1072	359	266	4	0	0

- Molecule 2 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B1	199	1630	1051	319	255	5	0	0

- Molecule 3 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C1	153	1242	777	241	215	9	0	0

- Molecule 4 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D1	187	1515	946	315	250	4	0	0

- Molecule 5 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E1	180	1508	933	328	238	9	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E1	38	ARG	HIS	conflict	UNP G1TYL6
E1	151	ARG	HIS	conflict	UNP G1TYL6

- Molecule 6 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F1	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 7 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G1	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 8 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H1	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 9 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I1	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 10 is a protein called TRASH domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J1	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 11 is a protein called Ribosomal protein L23/L25 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K1	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 12 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L1	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 13 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M1	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 14 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N1	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 15 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O1	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 16 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P1	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 17 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q1	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 18 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R1	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 19 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S1	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 20 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T1	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 21 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U1	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 22 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V1	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V1	31	GLY	ARG	conflict	UNP G1TBH2
V1	58	MET	ILE	conflict	UNP G1TBH2

- Molecule 23 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W1	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 24 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X1	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X1	24	LYS	ASN	conflict	UNP G1U001

- Molecule 25 is a protein called 60S ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y1	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 26 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z1	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 27 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a1	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 28 is a protein called Ribosomal protein L36a like.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b1	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 29 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c1	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 30 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d1	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 31 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e1	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 32 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f1	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 33 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l1	206	Total	C	N	O	S	0	0
			1654	1058	297	291	8		

- Molecule 34 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	m1	3	Total	C	N	O	P	0	0
			62	28	9	22	3		

- Molecule 35 is a protein called CCR4-NOT transcription complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n1	236	Total	C	N	O	S	0	0
			1948	1209	346	387	6		

- Molecule 36 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	21	76	Total	C	N	O	P	0	0
			1620	723	287	534	76		

- Molecule 37 is a protein called nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	11	5	Total	C	N	O	0	0
			34	23	5	6		

- Molecule 38 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A2	3603	Total	C	N	O	P	0	0
			77264	34409	14151	25101	3603		

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	B2	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 40 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	C2	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 41 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A3	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 42 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	B3	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 43 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	C3	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 44 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	D3	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 45 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	E3	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 46 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	F3	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F3	25	GLY	SER	conflict	UNP G1TK17
F3	51	ARG	LYS	conflict	UNP G1TK17
F3	78	THR	ALA	conflict	UNP G1TK17
F3	156	VAL	MET	conflict	UNP G1TK17

- Molecule 47 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	G3	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 48 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	H3	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 49 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	I3	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 50 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	J3	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J3	47	ARG	GLY	variant	UNP G1TJW1

- Molecule 51 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
51	K3	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 52 is a protein called Plectin/S10 N-terminal domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	L3	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 53 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	M3	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 54 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	N3	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 55 is a protein called ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	O3	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 56 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	P3	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 57 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Q3	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 58 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	R3	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 59 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	S3	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 60 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	T3	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 61 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	U3	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U3	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 62 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	V3	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 63 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	W3	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 64 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	X3	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 65 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Y3	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 66 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Z3	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 67 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	a3	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 68 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	b3	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 69 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	c3	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 70 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	d3	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 71 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	e3	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 72 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	f3	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 73 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	g3	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 74 is a protein called Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	h3	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 75 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	j3	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 76 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	k3	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 77 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	l3	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 78 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	m3	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 79 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	n3	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 80 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	o3	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 81 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	p3	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
p3	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 82 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	q3	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 83 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	r3	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 84 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	s3	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 85 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	t3	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
t3	74	ARG	HIS	conflict	UNP G1TKB3
t3	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 86 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	u3	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	C1	1	Total	Mg	0
			1	1	
87	I1	1	Total	Mg	0
			1	1	
87	N1	1	Total	Mg	0
			1	1	
87	T1	1	Total	Mg	0
			1	1	
87	A2	189	Total	Mg	0
			189	189	
87	B2	6	Total	Mg	0
			6	6	
87	C2	4	Total	Mg	0
			4	4	
87	A3	69	Total	Mg	0
			69	69	
87	M3	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
87	j3	1	Total Mg 1 1	0
87	r3	1	Total Mg 1 1	0

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
88	T1	1	Total Zn 1 1	0
88	W1	1	Total Zn 1 1	0
88	Z1	1	Total Zn 1 1	0
88	b1	1	Total Zn 1 1	0
88	c1	1	Total Zn 1 1	0
88	b3	1	Total Zn 1 1	0
88	e3	1	Total Zn 1 1	0

3 Residue-property plots (i)

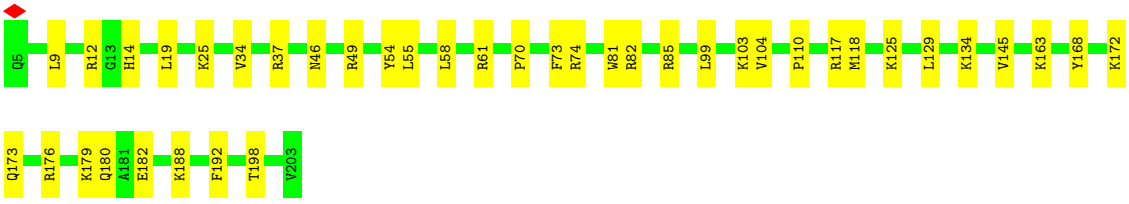
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: Ribosomal protein L15

Chain A1:

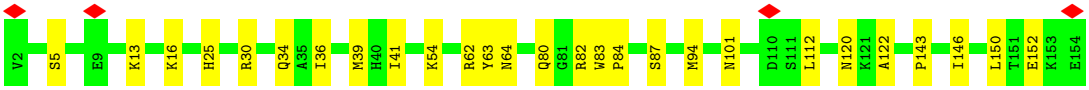
• Molecule 2: 60S ribosomal protein L13a

Chain B1:



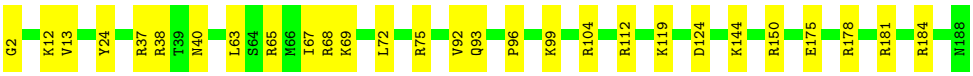
• Molecule 3: 60S ribosomal protein L17

Chain C1:



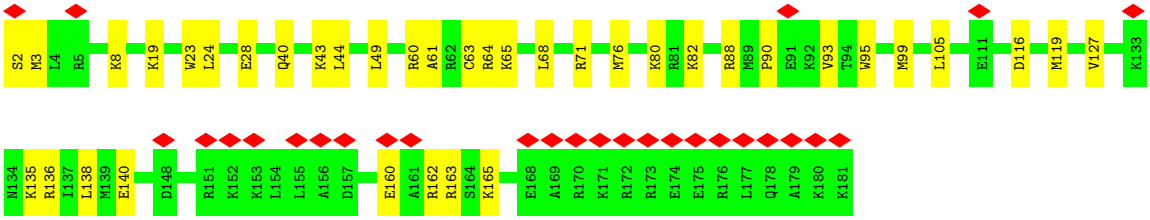
• Molecule 4: Ribosomal protein L18

Chain D1:



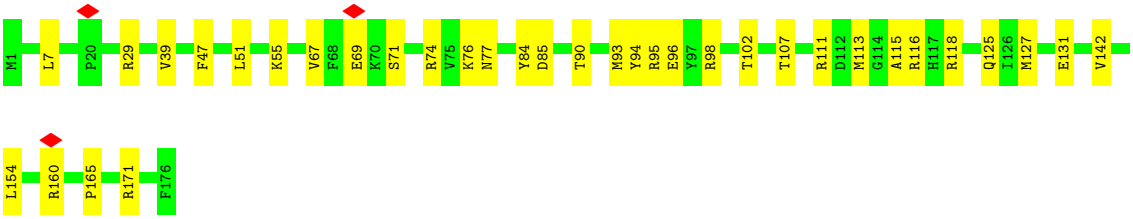
• Molecule 5: Ribosomal protein L19

Chain E1:



• Molecule 6: 60S ribosomal protein L18a

Chain F1:

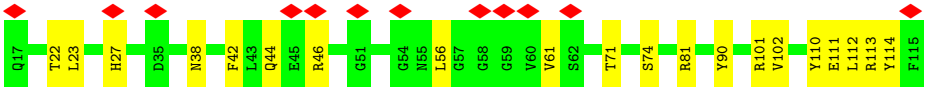


• Molecule 7: 60S ribosomal protein L21

Chain G1:

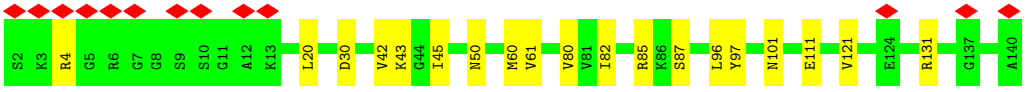
• Molecule 8: 60S ribosomal protein L22

Chain H1:



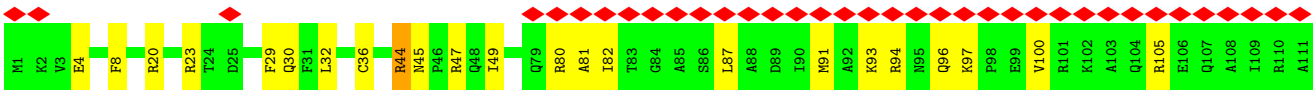
• Molecule 9: 60S ribosomal protein L23

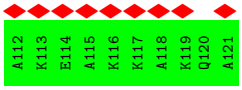
Chain I1:



• Molecule 10: TRASH domain-containing protein

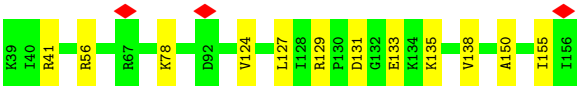
Chain J1:





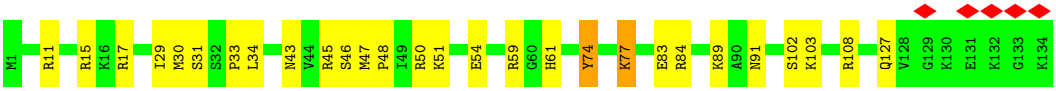
• Molecule 11: Ribosomal protein L23/L25 N-terminal domain-containing protein

Chain K1:



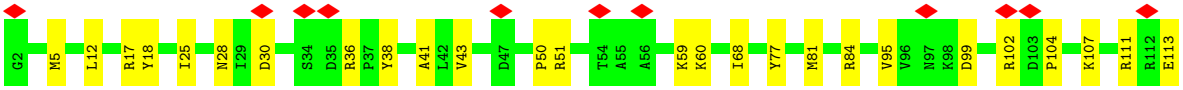
• Molecule 12: Ribosomal protein L26

Chain L1:



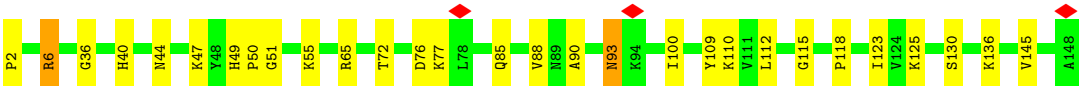
• Molecule 13: 60S ribosomal protein L27

Chain M1:



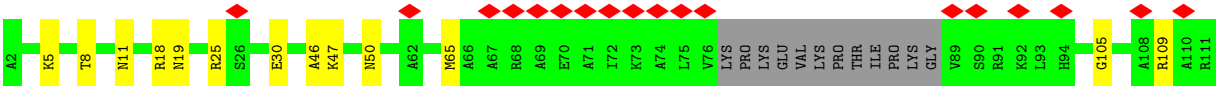
• Molecule 14: 60S ribosomal protein L27a

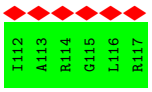
Chain N1:



• Molecule 15: 60S ribosomal protein L29

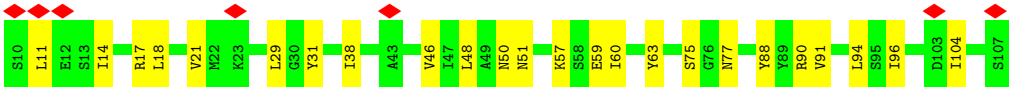
Chain O1:





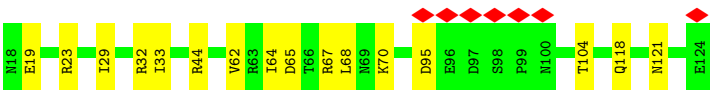
• Molecule 16: 60S ribosomal protein L30

Chain P1:



• Molecule 17: 60S ribosomal protein L31

Chain Q1:

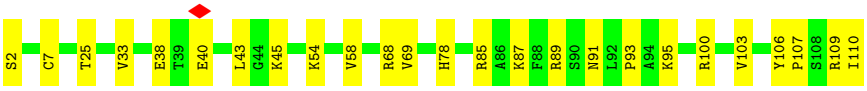


• Molecule 18: Ribosomal protein L32

Chain R1:

• Molecule 19: 60S ribosomal protein L35a

Chain S1:

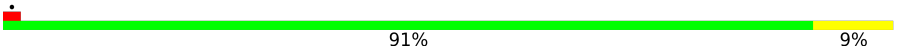


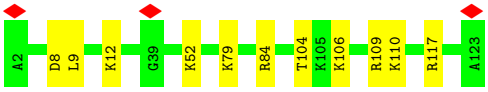
• Molecule 20: 60S ribosomal protein L34

Chain T1:

• Molecule 21: 60S ribosomal protein L35

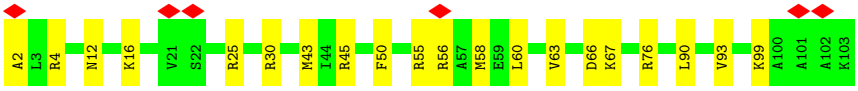
Chain U1:





• Molecule 22: 60S ribosomal protein L36

Chain V1:

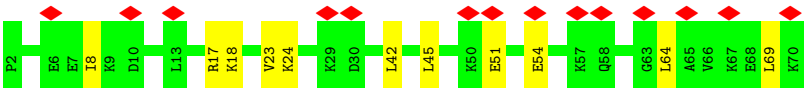


• Molecule 23: Ribosomal protein L37

Chain W1:

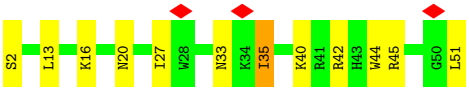
• Molecule 24: 60S ribosomal protein L38

Chain X1:



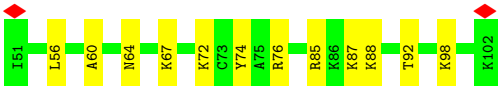
• Molecule 25: 60S ribosomal protein L39-like

Chain Y1:



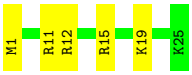
• Molecule 26: Ubiquitin-60S ribosomal protein L40

Chain Z1:



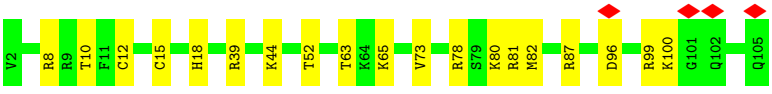
• Molecule 27: 60S ribosomal protein L41

Chain a1:



• Molecule 28: Ribosomal protein L36a like

Chain b1:

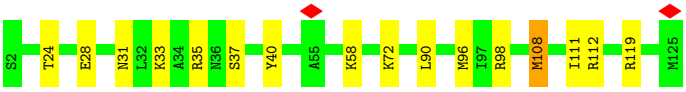


• Molecule 29: 60S ribosomal protein L37a

Chain c1:

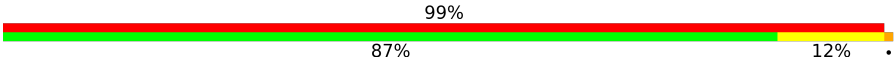
• Molecule 30: 60S ribosomal protein L28

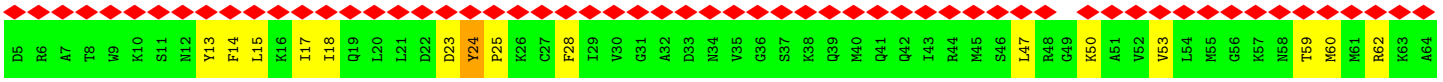
Chain d1:

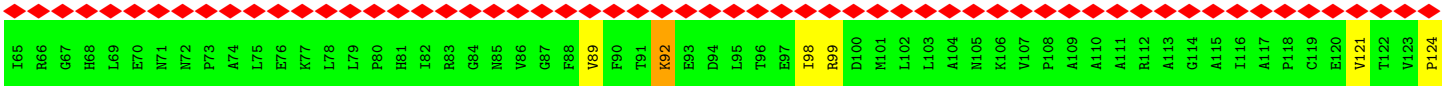


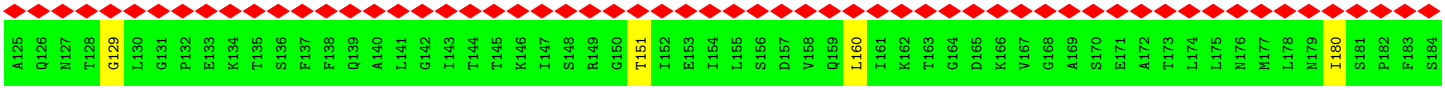
• Molecule 31: 60S acidic ribosomal protein P0

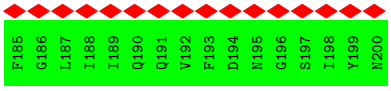
Chain e1:





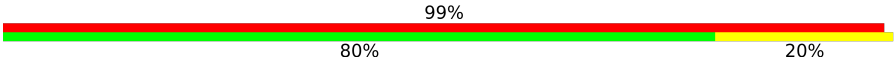


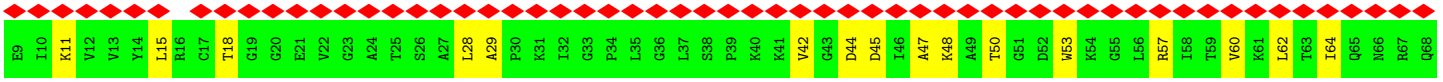


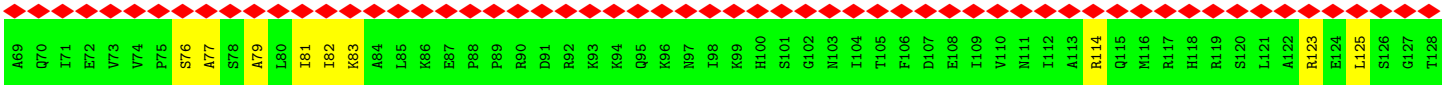


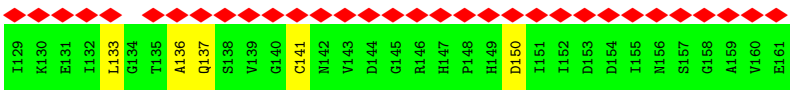
• Molecule 32: 60S ribosomal protein L12

Chain f1:



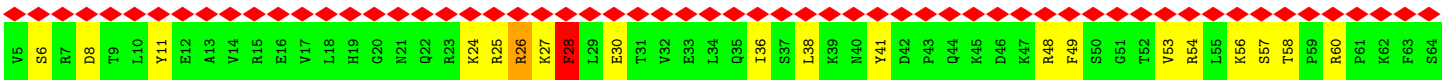


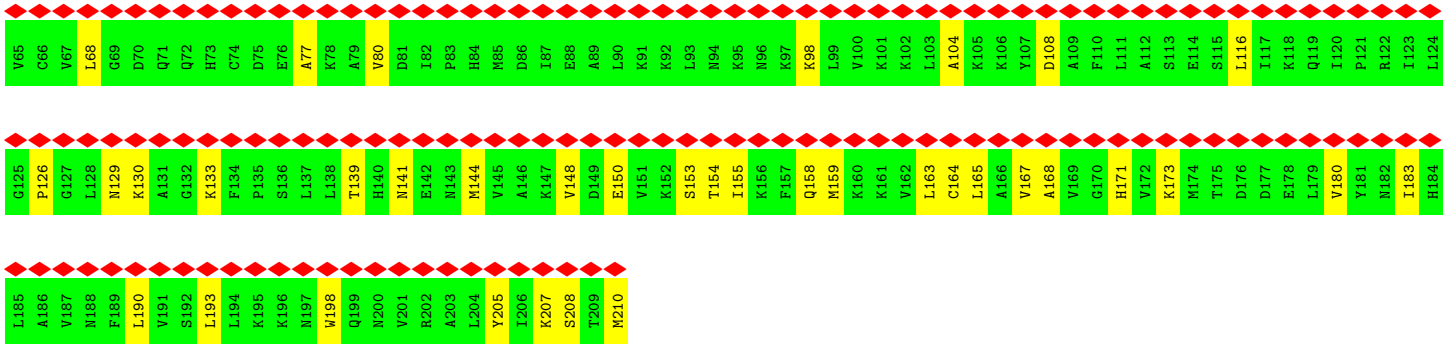




• Molecule 33: 60S ribosomal protein L10a

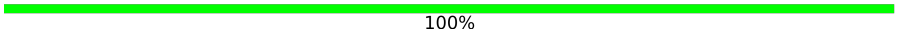
Chain l1:





• Molecule 34: mRNA

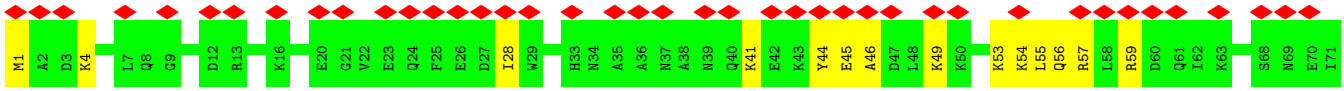
Chain m1:



There are no outlier residues recorded for this chain.

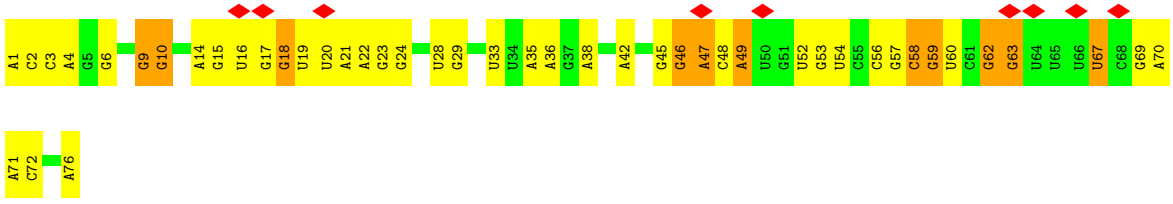
• Molecule 35: CCR4-NOT transcription complex subunit 3

Chain n1:



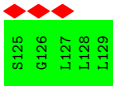
• Molecule 36: P-site tRNA

Chain 21:



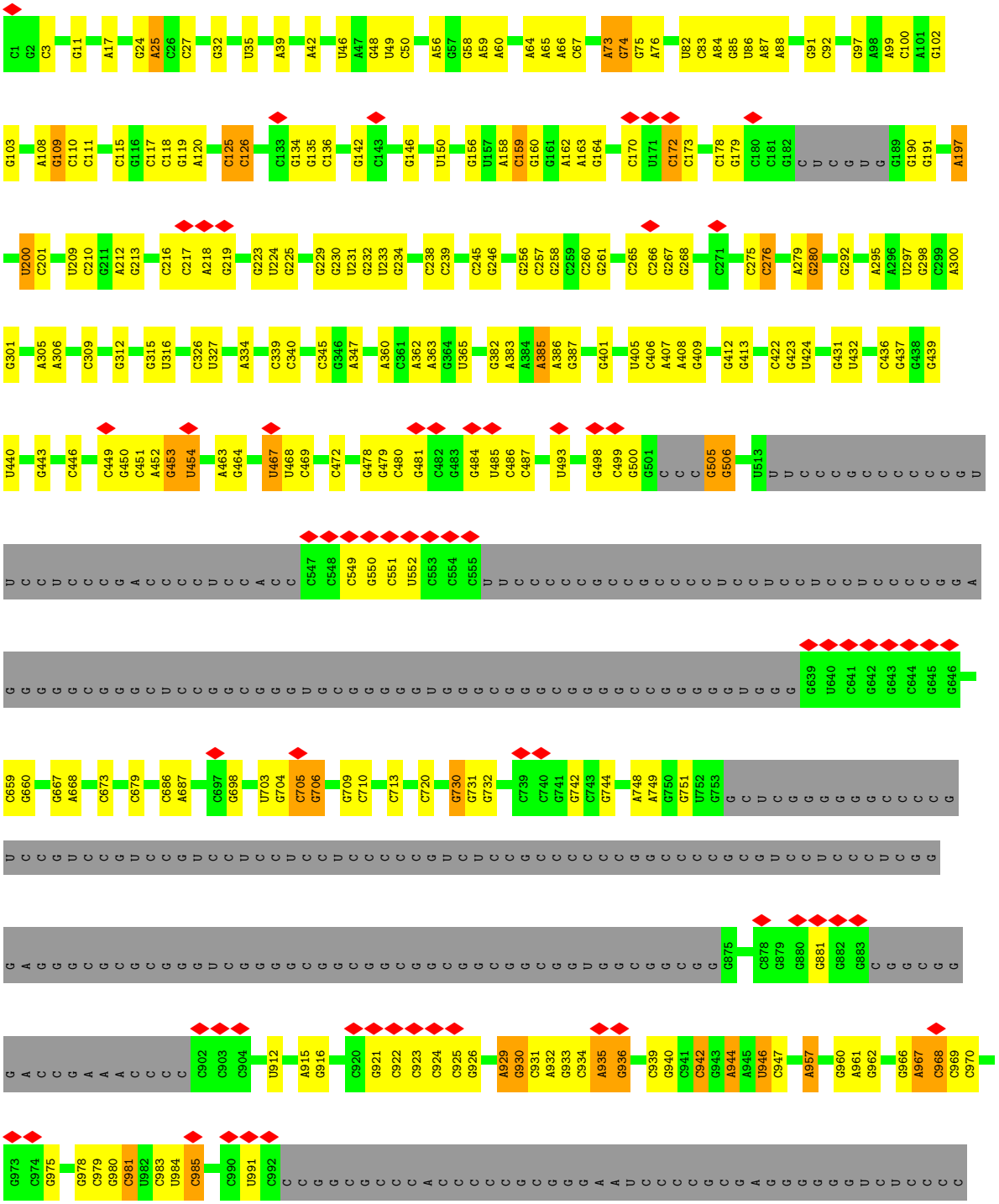
• Molecule 37: nascent chain

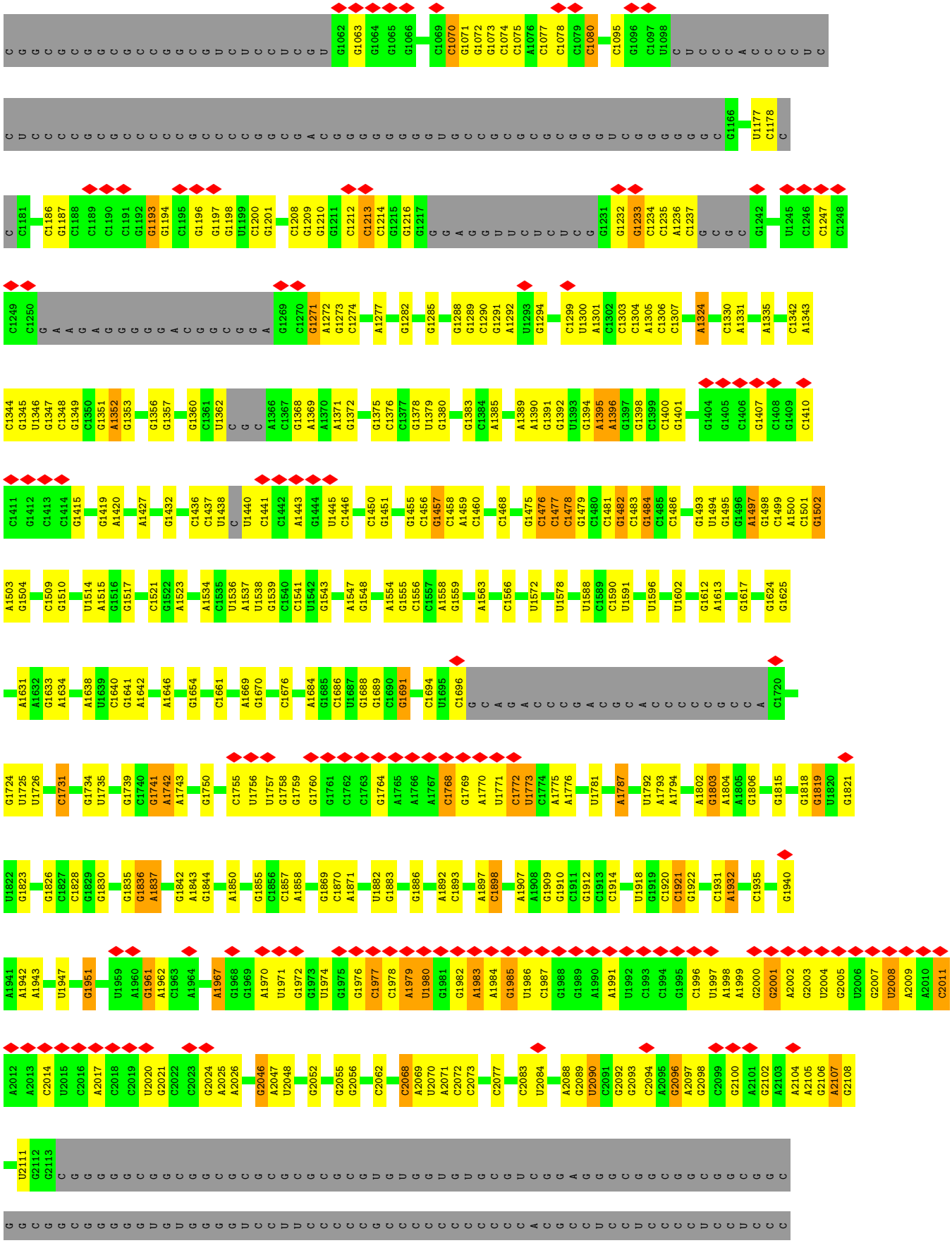
Chain 11:

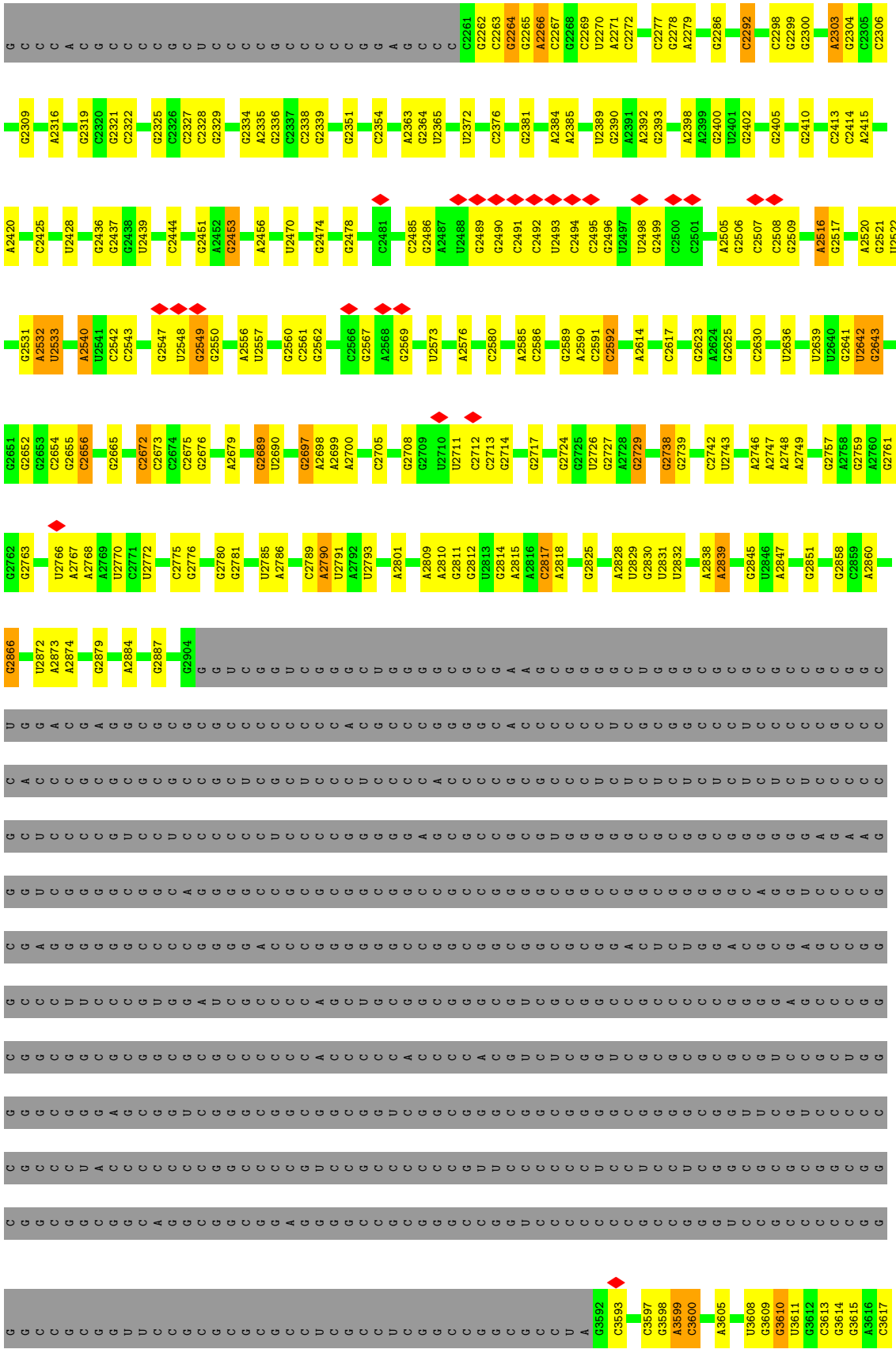


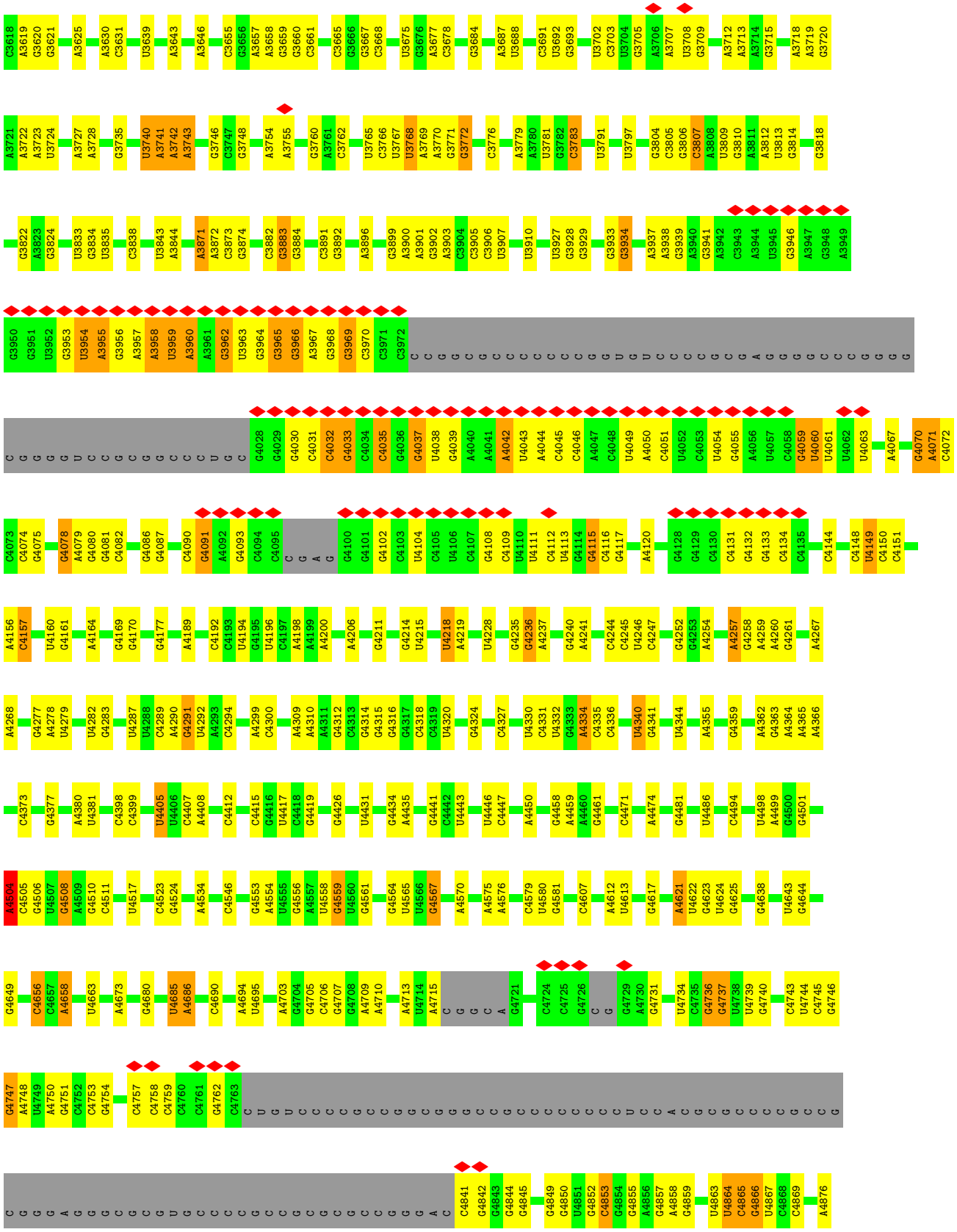
• Molecule 38: 28S ribosomal RNA

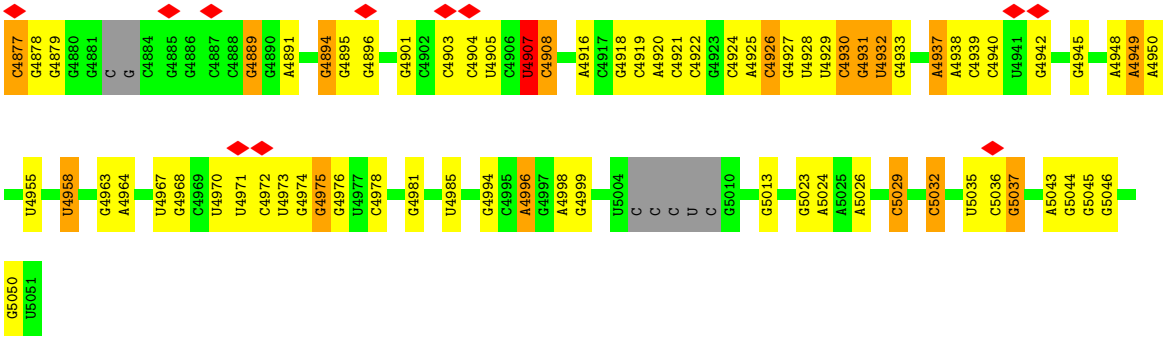
Chain A2:





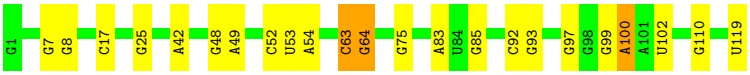






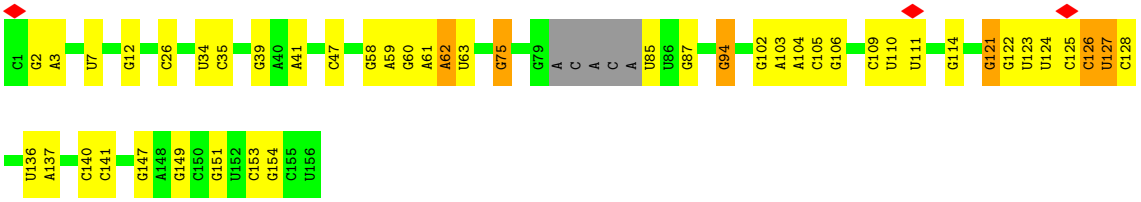
• Molecule 39: 5S ribosomal RNA

Chain B2:



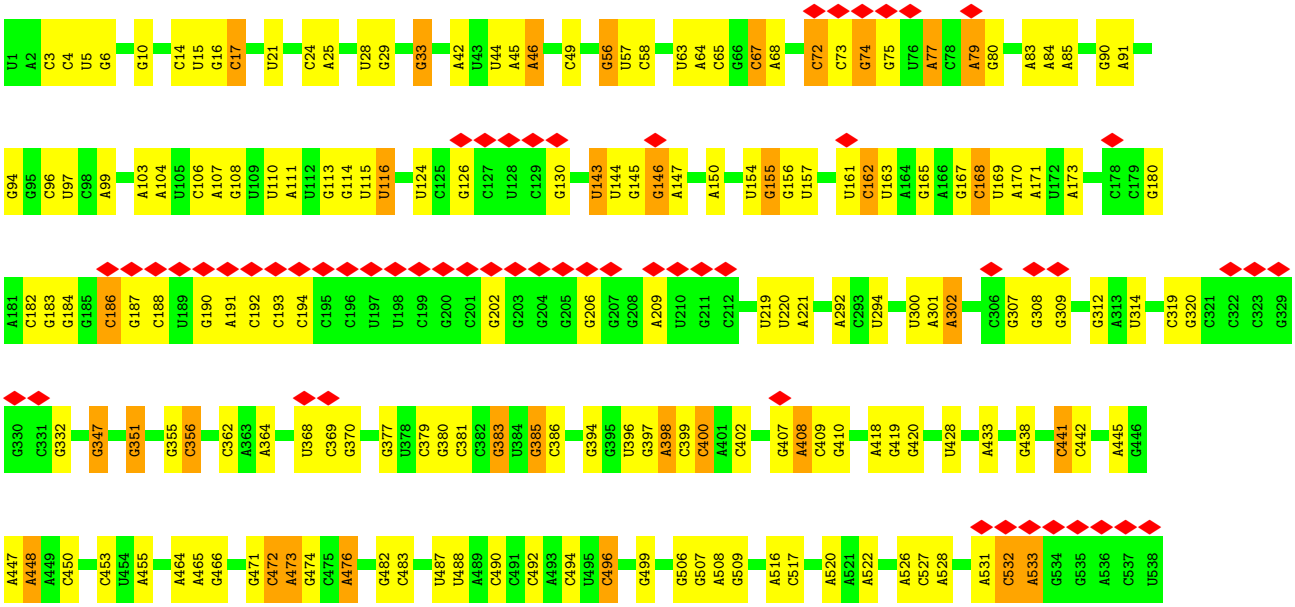
• Molecule 40: 5.8S ribosomal RNA

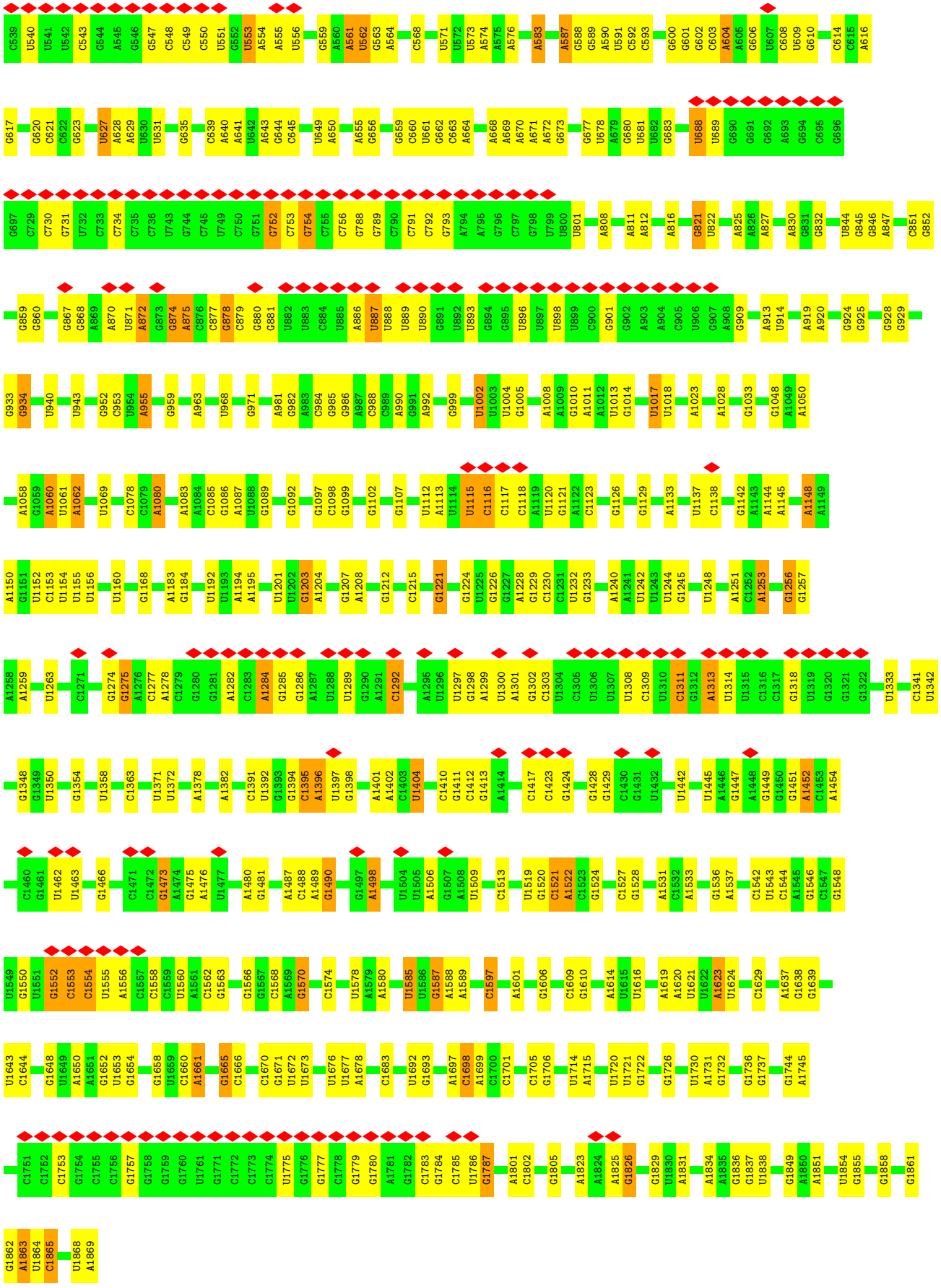
Chain C2:



• Molecule 41: 18S ribosomal RNA

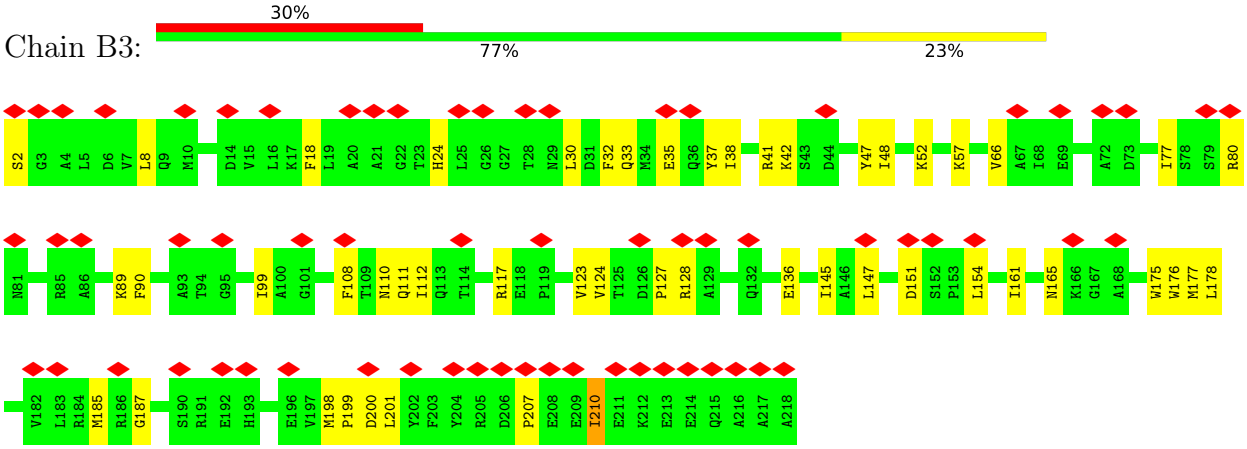
Chain A3:




C539 U540 U541 U542 C543 G544 A545 G546 G547 C548 C549 C550 U551 G552 U553 A554 A555 U556 G559 A560 A561 U562 G563 A564 C568 U571 U572 U573 A574 A575 A576 A583 A587 G588 G589 A590 U591 C592 C593 G600 G601 G602 C603 A604 A605 G606 U607 C608 U609 G610 C614 C615 A616
G617 G620 C621 C622 G623 U627 A628 A629 U630 U631 G635 C639 A640 A641 U642 A643 G644 C645 U649 A650 A655 G656 C659 C660 U661 G662 C663 A664 A668 A669 A670 A671 A672 G673 G677 U678 A679 G680 U681 U682 G683 U688 U689 G690 G691 G692 A693 G694 C695 G696
G697 C729 C730 G731 U732 C733 C734 C735 C736 U743 G744 C745 U749 C750 G751 G752 C753 G754 C755 C756 G788 G789 C790 C791 C792 G793 A794 A795 G796 C797 G798 U799 U800 U801 A808 A811 A812 A816 G821 U822 A825 A826 A827 A830 G831 G832 U844 G845 G846 A847 C851 G852
G859 G860 G867 G868 A869 A870 U871 A872 G873 G874 A875 C876 C877 G878 C879 G880 G881 U882 U883 C884 U885 A886 U887 U888 U889 U890 G891 U892 U893 G894 G895 U896 U897 U898 U899 C900 G901 G902 A903 A904 C905 U906 G907 A908 G909 A913 U914 A919 A920 G924 G925 G928 G929
G933 G934 U940 U943 G952 C953 U954 A955 G959 A963 U968 G971 A981 G982 A983 C984 G985 G986 A987 C988 C989 A990 G991 A992 G999 U1002 U1003 U1004 G1005 A1008 A1009 G1010 A1011 A1012 U1013 G1014 U1017 U1018 A1023 A1028 G1033 G1048 A1049 A1050
A1058 G1059 A1060 U1061 A1062 U1069 C1078 C1079 A1080 A1083 A1084 C1085 G1086 A1087 U1088 G1089 G1092 G1097 C1098 G1099 G1102 G1107 U1112 A1113 U1114 U1115 C1116 C1117 C1118 A1119 U1120 G1121 A1122 C1123 G1126 G1129 A1133 U1137 C1138 G1142 A1143 A1144 A1145 A1148 A1149
A1150 G1151 U1152 C1153 U1154 U1155 U1156 U1160 G1168 A1183 G1184 U1192 U1193 A1194 A1195 U1201 U1202 G1203 A1204 G1207 A1208 G1212 C1215 G1221 G1224 U1225 G1226 G1227 A1228 G1229 C1230 C1231 U1232 G1233 A1240 A1241 U1242 U1243 U1244 G1245 U1248 A1251 C1252 A1253 G1256 G1257
A1258 A1259 U1263 C1271 G1274 G1275 A1276 C1277 A1278 C1279 G1280 G1281 A1282 C1283 A1284 G1285 G1286 A1287 U1288 U1289 G1290 A1291 C1292 A1295 U1296 U1297 G1298 A1299 U1300 A1301 G1302 C1303 U1304 C1305 U1306 U1307 U1308 C1309 U1310 C1311 G1312 A1313 U1314 U1315 C1316 C1317 G1318 U1319 G1320 G1321 G1322 U1333 C1341 U1342
G1348 G1349 U1350 C1354 U1358 C1363 U1371 U1372 A1378 A1382 C1391 U1392 G1393 G1394 C1395 A1396 U1397 G1398 A1401 A1402 C1403 U1404 C1410 G1411 C1412 G1413 A1414 C1417 C1423 G1424 G1428 G1429 C1430 G1431 U1432 U1442 U1445 A1446 G1447 A1448 G1449 G1450 G1451 A1452 C1453 A1454
C1460 G1461 U1462 U1463 G1466 C1471 C1472 G1473 A1474 G1475 A1476 U1477 A1480 G1481 A1487 C1488 A1489 G1490 G1497 A1498 U1504 U1505 A1506 G1507 A1508 U1509 C1513 U1519 G1520 C1521 A1522 C1523 G1524 C1527 G1528 A1531 C1532 A1533 G1536 A1537 C1542 U1543 C1544 A1545 G1546 C1547 G1548
U1549 G1550 U1551 G1552 C1553 C1554 U1555 A1556 C1557 C1558 C1559 U1560 A1561 C1562 G1563 G1566 G1567 C1568 A1569 G1570 C1574 U1578 A1579 A1580 U1585 U1586 G1587 A1588 A1589 C1597 A1601 G1606 C1609 G1610 A1614 U1615 U1616 A1619 A1620 U1621 U1622 A1623 U1624 C1629 A1637 G1638 G1639
U1643 C1644 G1648 U1649 A1650 A1651 G1652 U1653 G1654 G1658 U1659 C1660 A1661 G1665 C1666 C1670 G1671 U1672 U1673 U1676 U1677 A1678 C1683 U1692 G1693 A1697 C1698 A1699 C1700 C1701 C1705 G1706 U1714 A1715 U1720 U1721 G1722 G1726 U1730 A1731 G1732 G1736 G1737 G1744 A1745
C1751 C1752 C1753 G1754 C1755 C1756 G1757 G1758 G1759 G1760 U1761 G1771 C1772 C1773 C1774 U1775 G1776 G1777 C1778 G1779 G1780 A1781 G1782 C1783 G1784 C1785 U1786 G1787 A1801 C1802 G1805 A1823 A1824 A1825 G1826 G1829 U1830 A1831 A1834 A1835 G1836 G1837 U1838 G1849 A1850 A1851 U1854 G1855 G1858 G1861
G1862 A1863 U1864 C1865 U1868 A1869

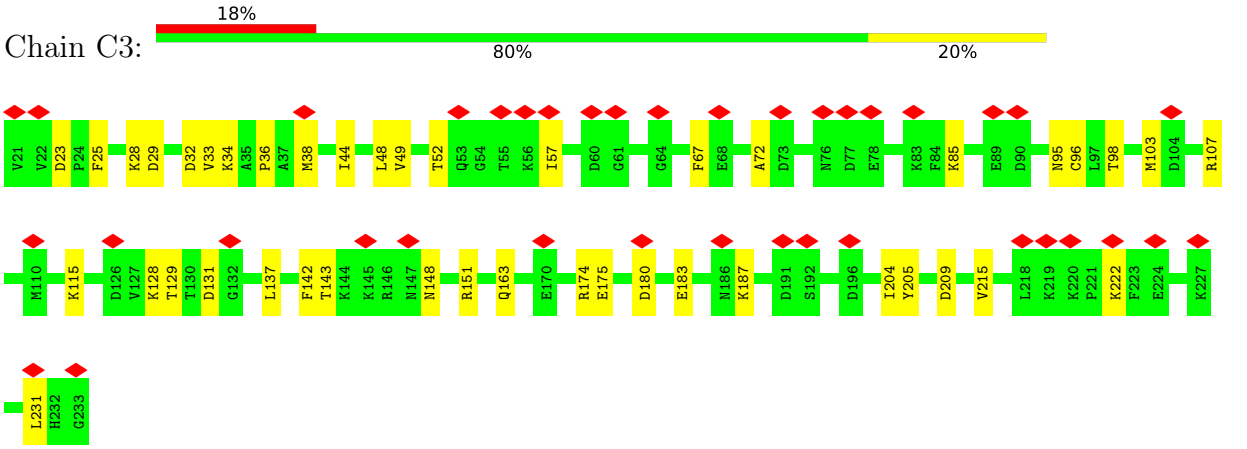
• Molecule 42: 40S_SA_C domain-containing protein

Chain B3:



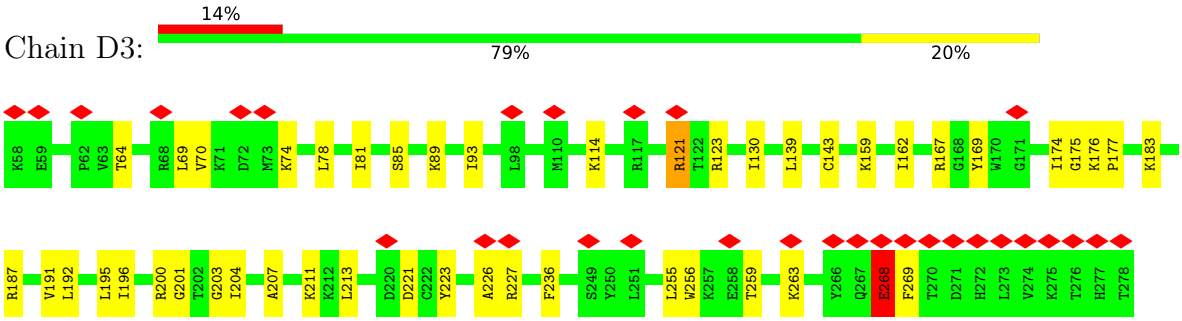
• Molecule 43: 40S ribosomal protein S3a

Chain C3:



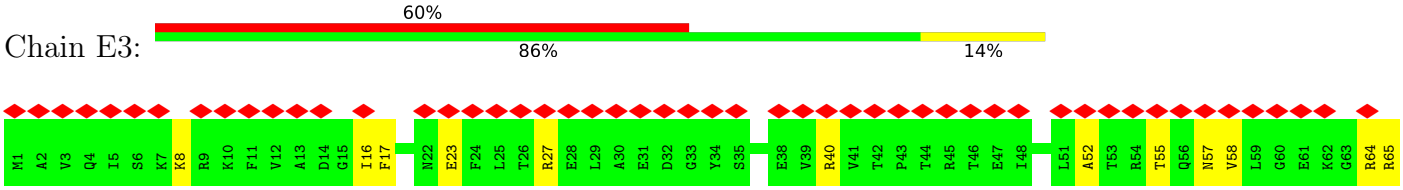
• Molecule 44: 40S ribosomal protein S2

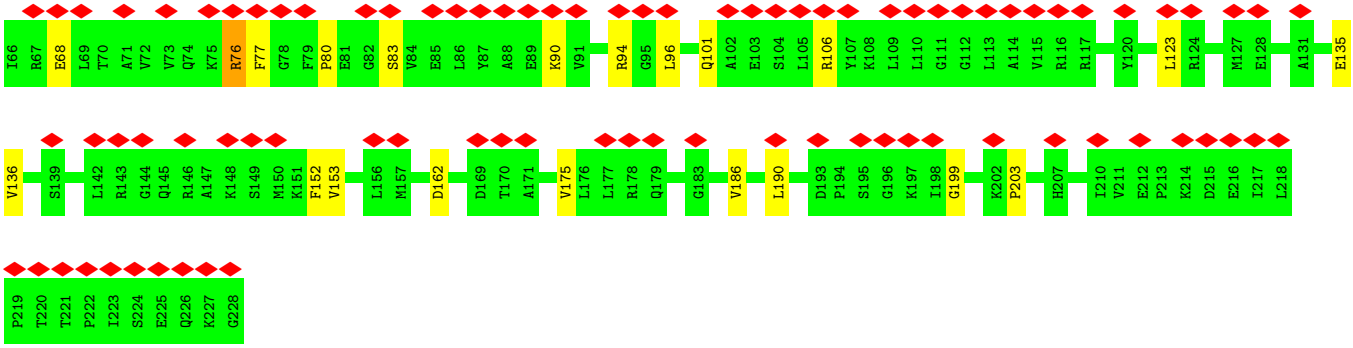
Chain D3:



• Molecule 45: Ribosomal protein S3

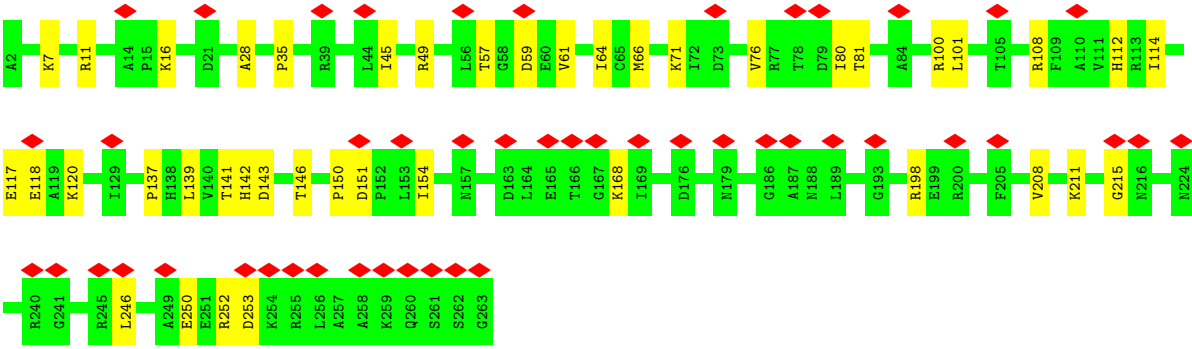
Chain E3:





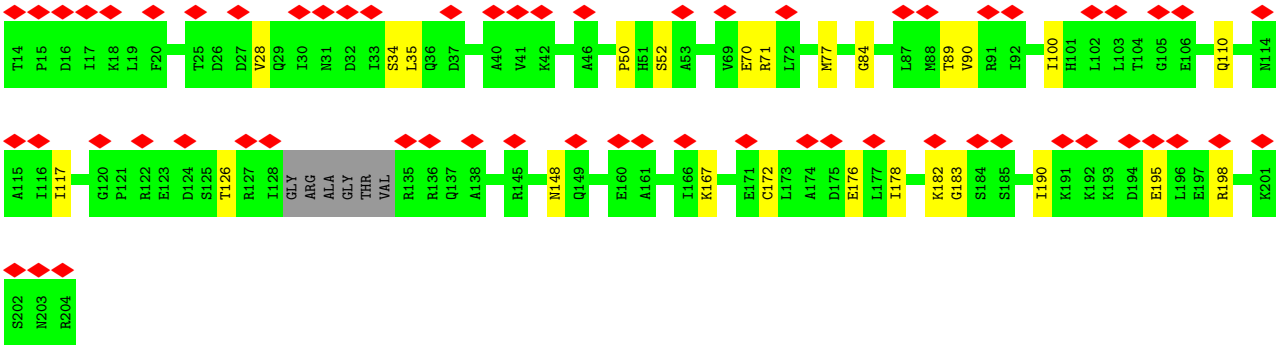
• Molecule 46: 40S ribosomal protein S4

Chain F3:



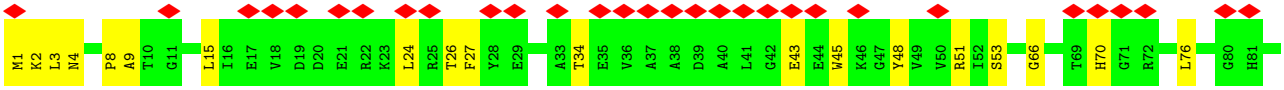
• Molecule 47: Ribosomal protein S5

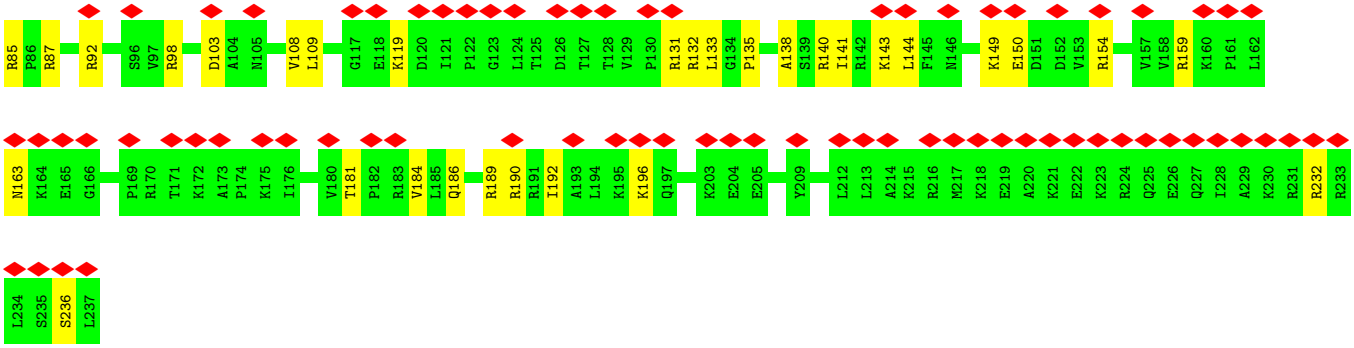
Chain G3:



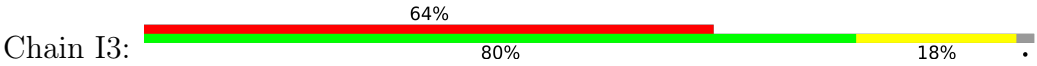
• Molecule 48: 40S ribosomal protein S6

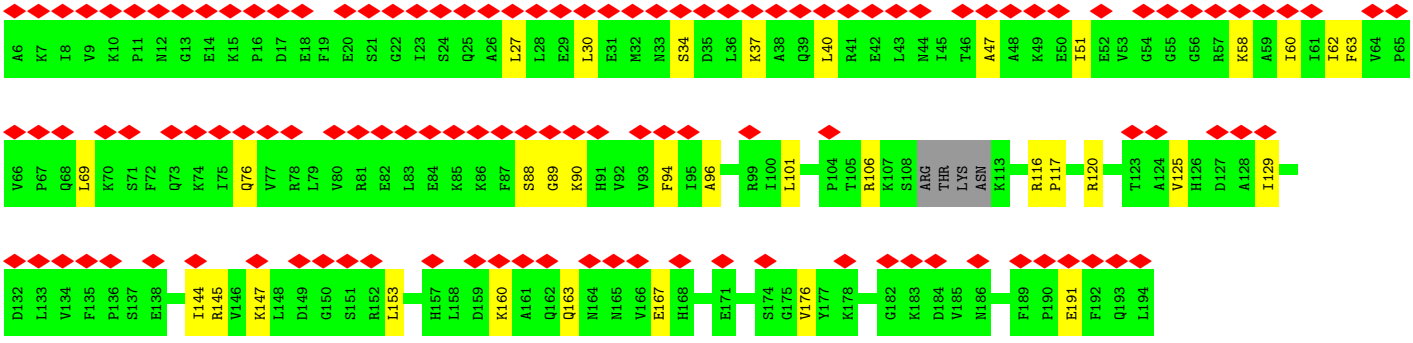
Chain H3:



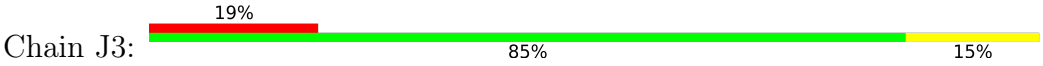


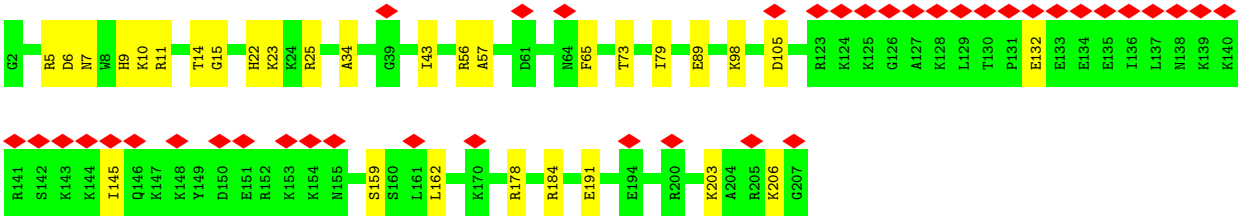
• Molecule 49: 40S ribosomal protein S7



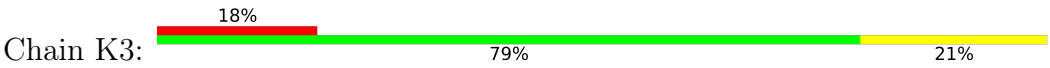


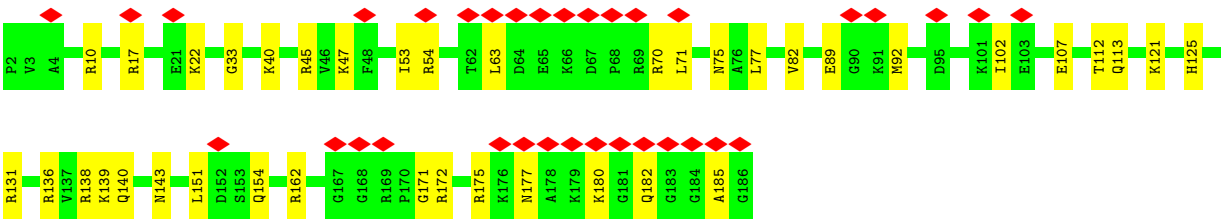
• Molecule 50: 40S ribosomal protein S8





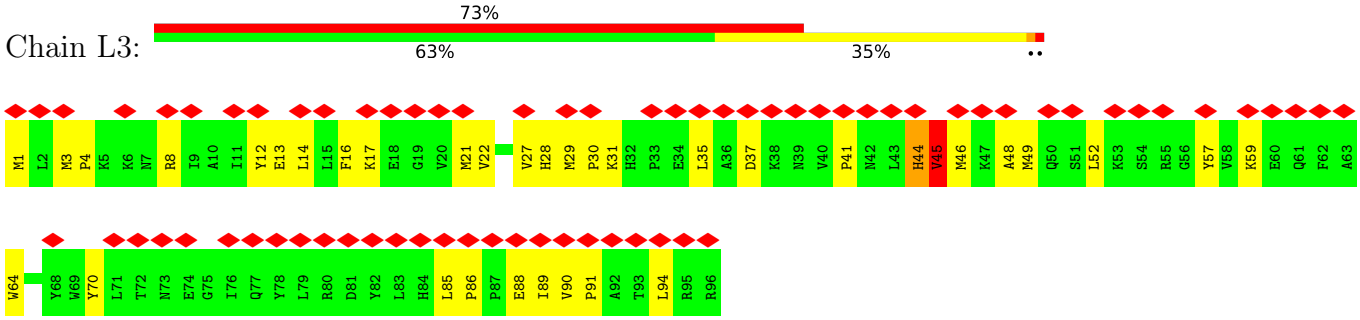
• Molecule 51: Ribosomal protein S9 (Predicted)





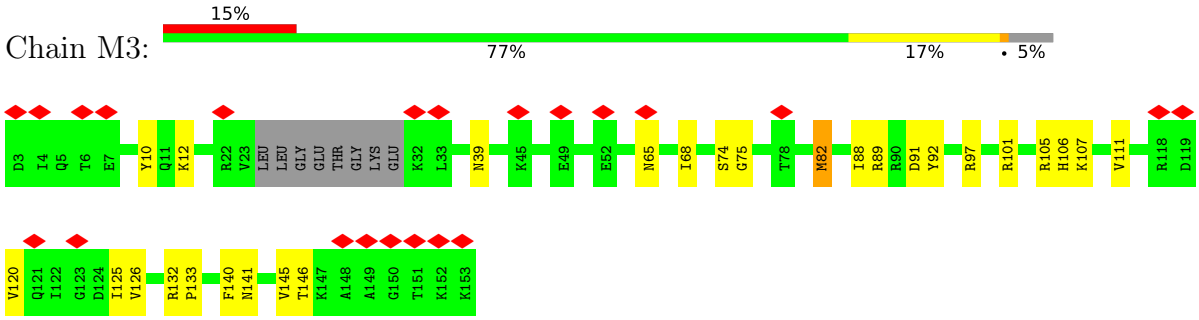
• Molecule 52: Plectin/S10 N-terminal domain-containing protein

Chain L3:



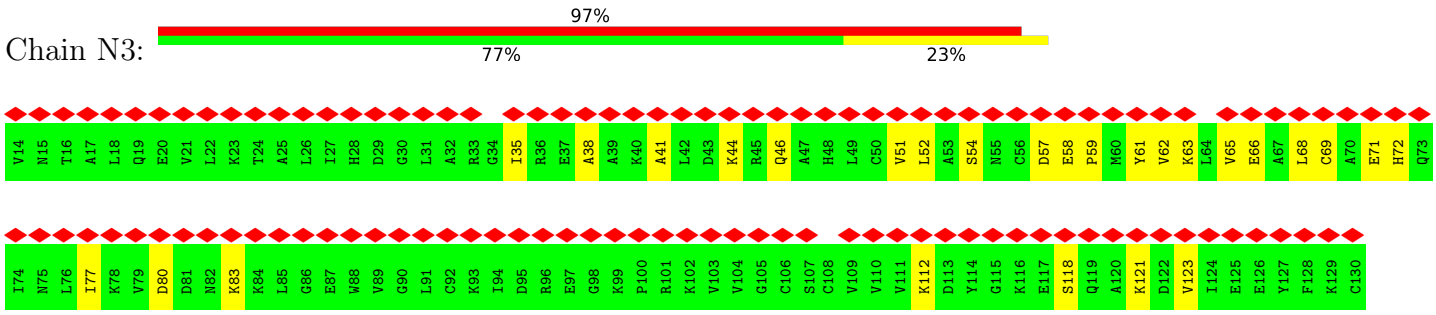
• Molecule 53: 40S ribosomal protein S11

Chain M3:



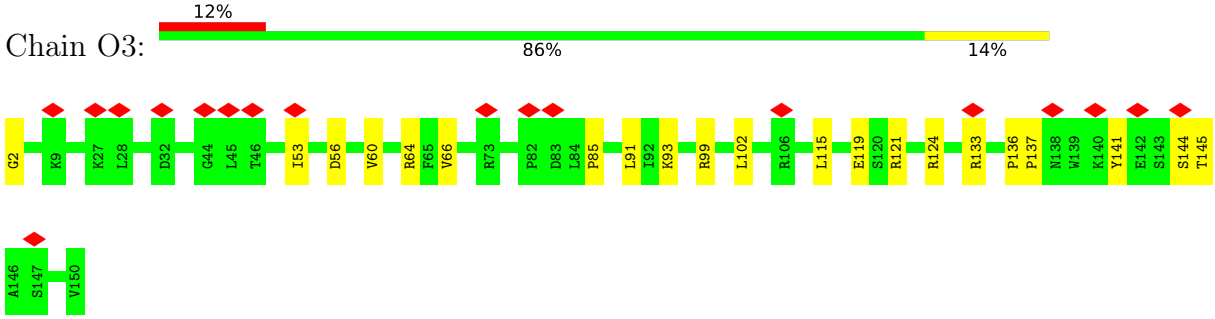
• Molecule 54: 40S ribosomal protein S12

Chain N3:



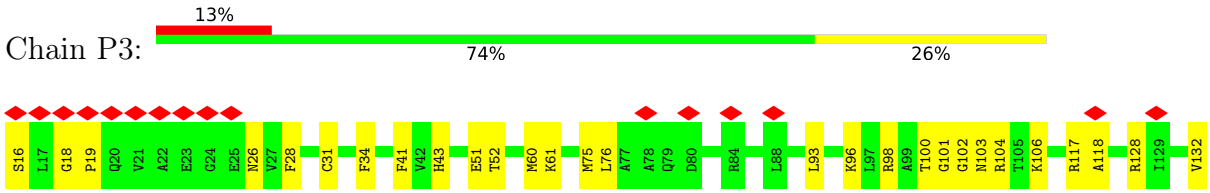
• Molecule 55: ribosomal protein uS15

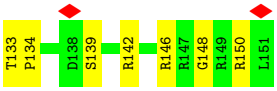
Chain O3:



• Molecule 56: Ribosomal protein S14

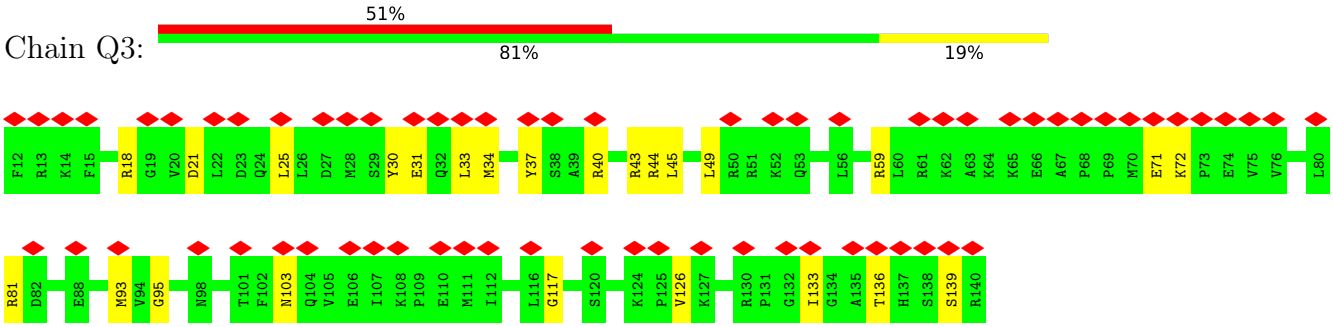
Chain P3:





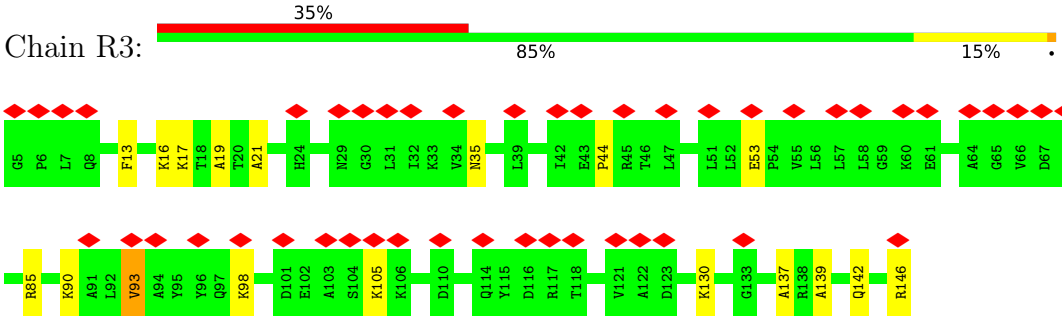
• Molecule 57: 40S ribosomal protein S15

Chain Q3:



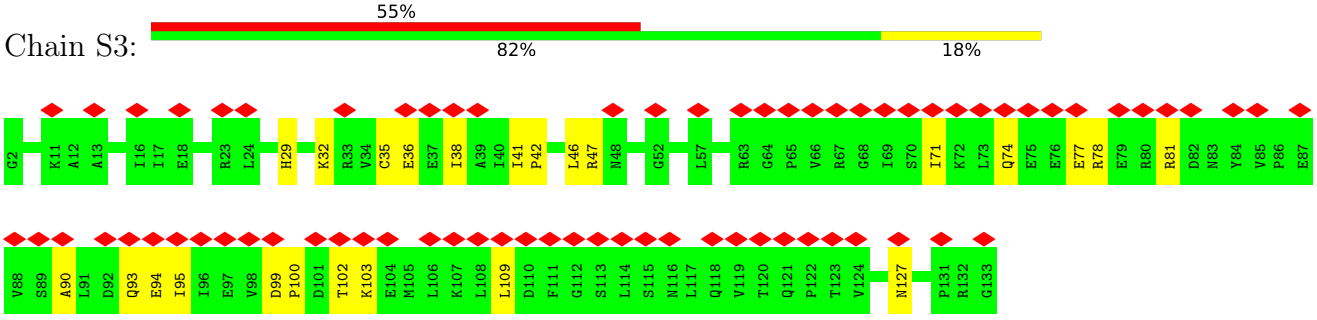
• Molecule 58: Ribosomal protein S16

Chain R3:



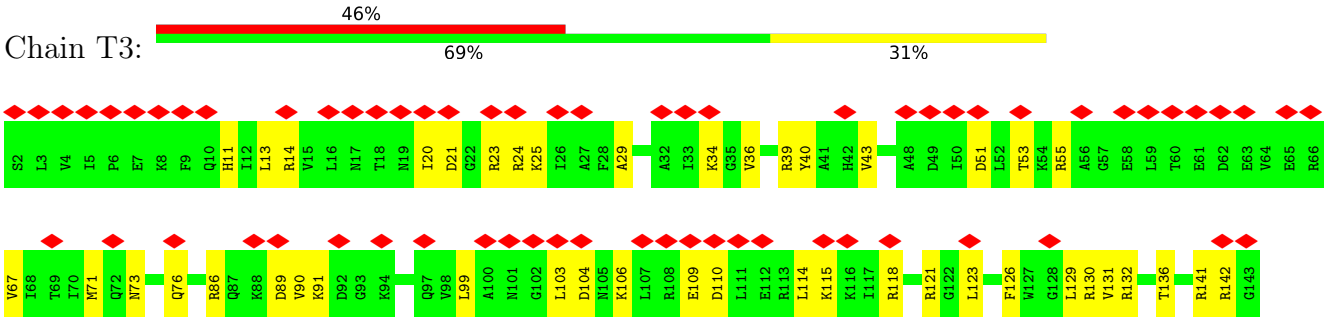
• Molecule 59: 40S ribosomal protein S17

Chain S3:



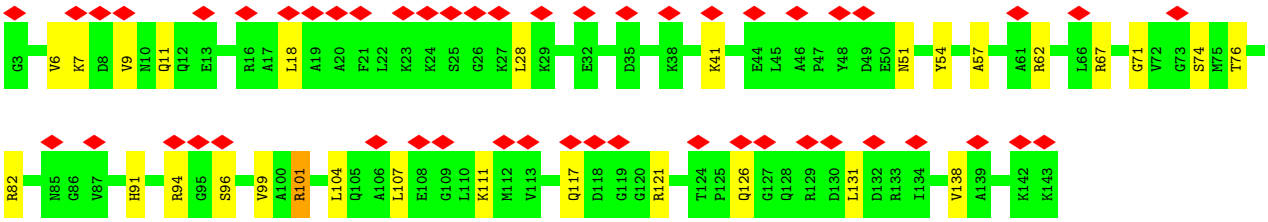
• Molecule 60: 40S ribosomal protein S18

Chain T3:



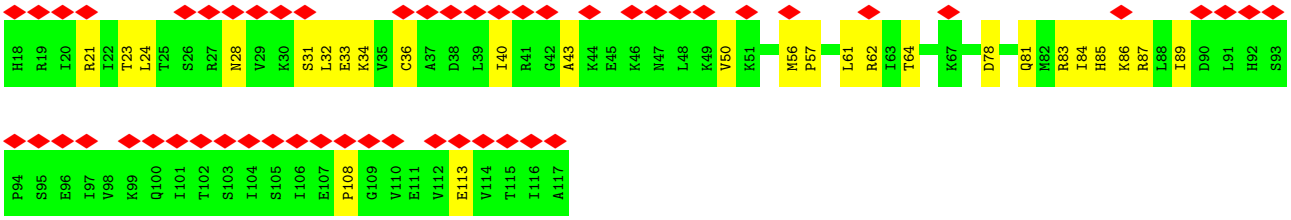
• Molecule 61: 40S ribosomal protein S19

Chain U3:



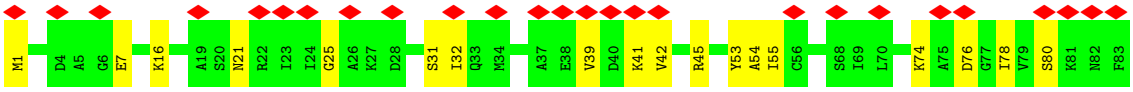
• Molecule 62: Ribosomal protein S20

Chain V3:



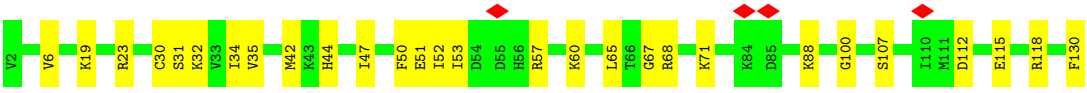
• Molecule 63: 40S ribosomal protein S21

Chain W3:



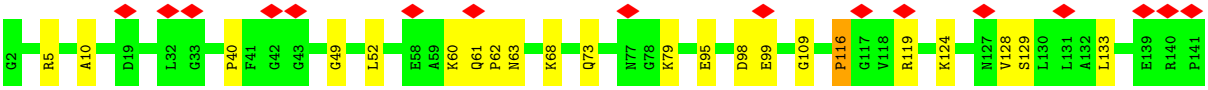
• Molecule 64: Ribosomal protein S15a

Chain X3:



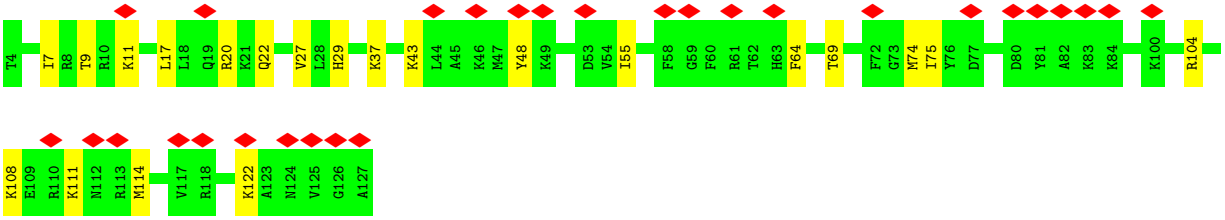
• Molecule 65: Ribosomal protein S23

Chain Y3:



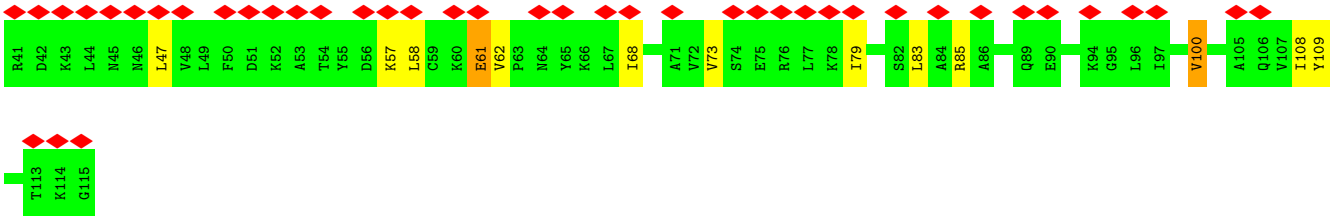
• Molecule 66: 40S ribosomal protein S24

Chain Z3:



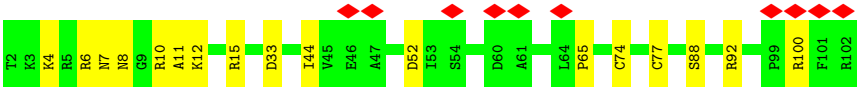
• Molecule 67: 40S ribosomal protein S25

Chain a3:



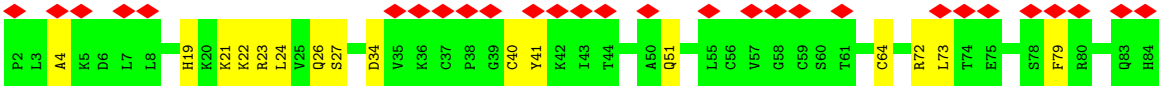
• Molecule 68: 40S ribosomal protein S26

Chain b3:



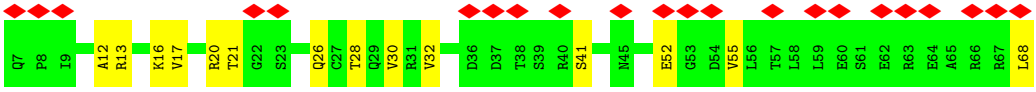
• Molecule 69: 40S ribosomal protein S27

Chain c3:



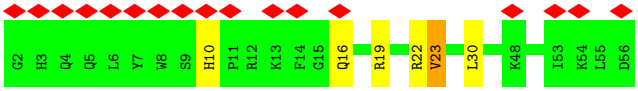
• Molecule 70: Ribosomal protein S28

Chain d3:



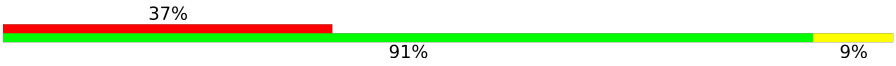
• Molecule 71: 40S ribosomal protein S29

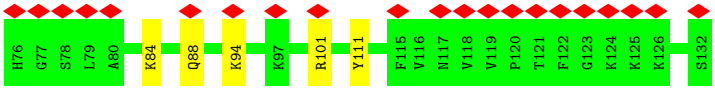
Chain e3:



• Molecule 72: Ubiquitin-like domain-containing protein

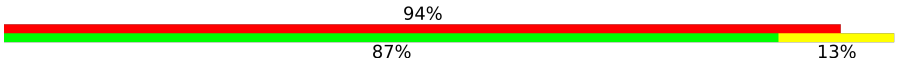
Chain f3:

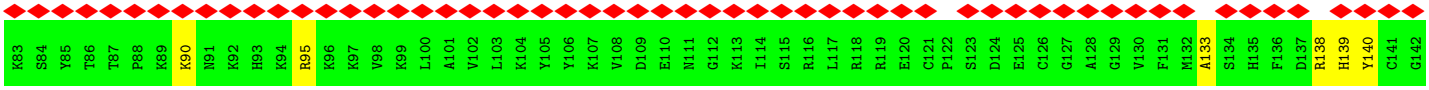




• Molecule 73: Ubiquitin-40S ribosomal protein S27a

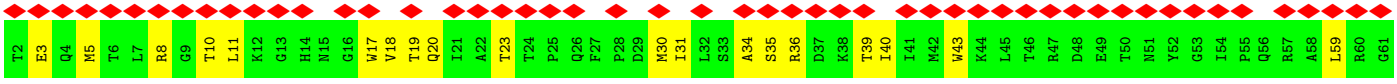
Chain g3:

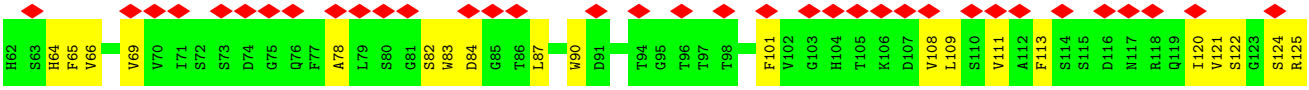


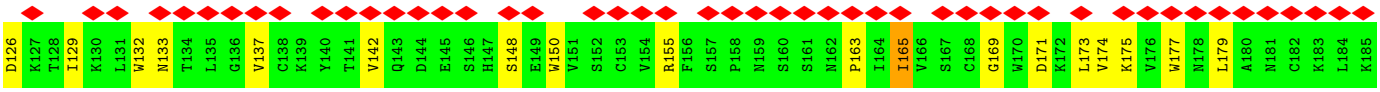


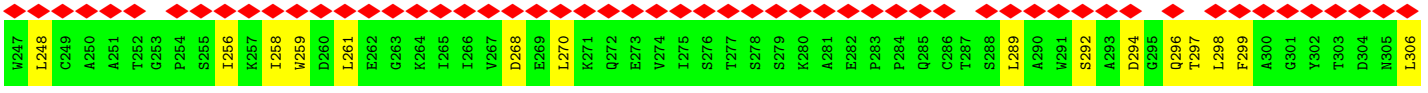
• Molecule 74: Ribosomal protein RACK1

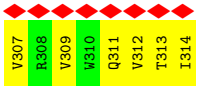
Chain h3:





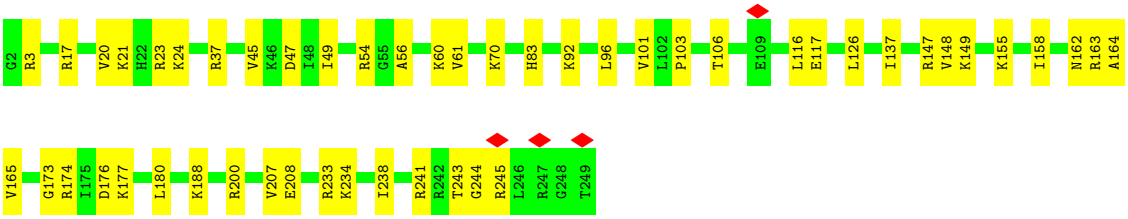






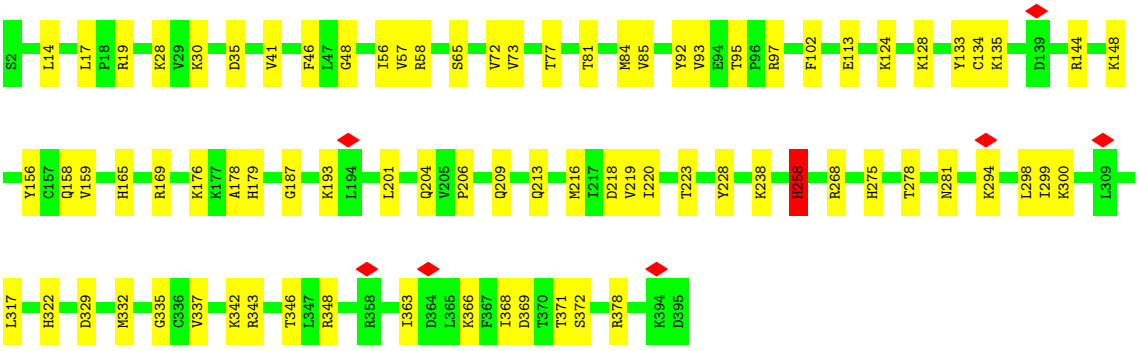
• Molecule 75: 60S ribosomal protein L8

Chain j3:



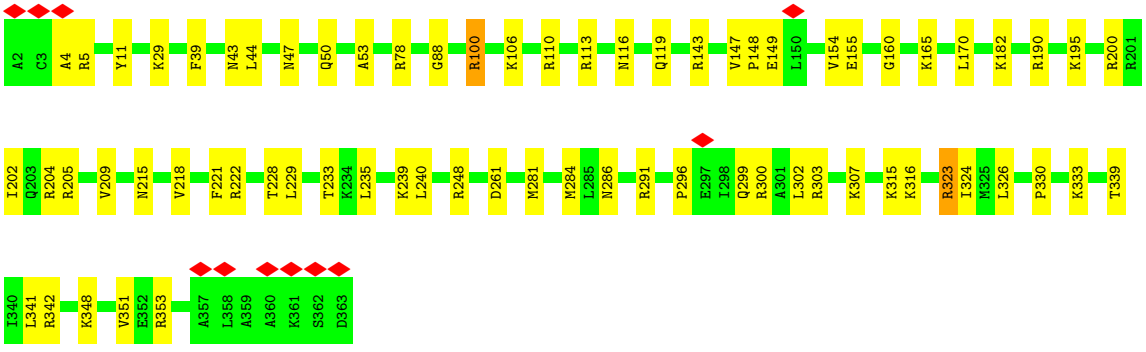
• Molecule 76: Ribosomal protein L3

Chain k3:



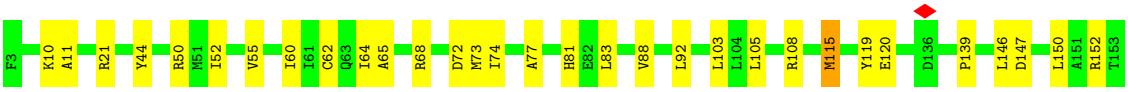
• Molecule 77: 60S ribosomal protein L4

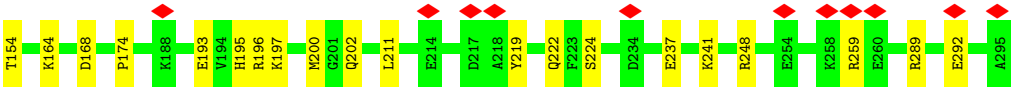
Chain l3:



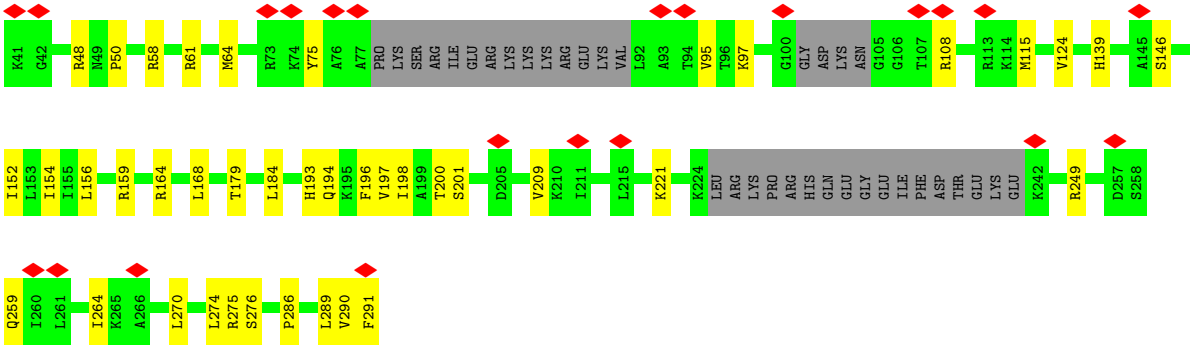
• Molecule 78: 60S ribosomal protein L5

Chain m3:

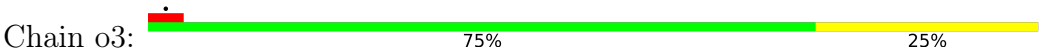


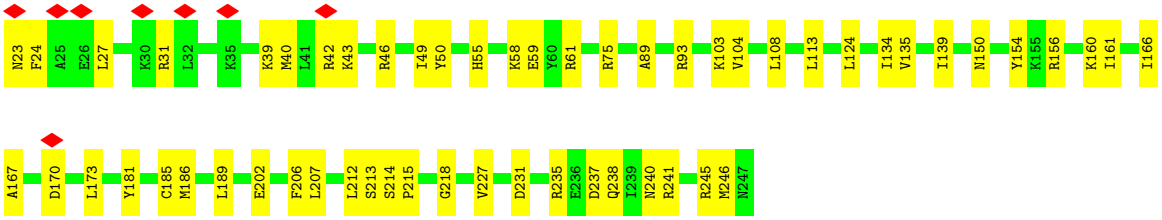


• Molecule 79: 60S ribosomal protein L6

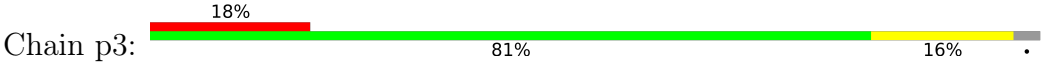


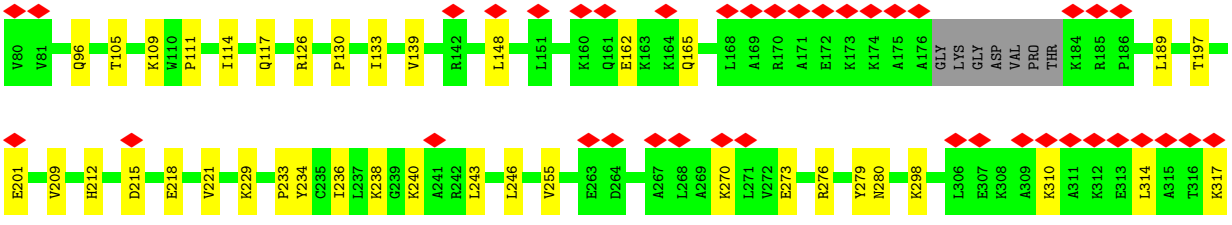
• Molecule 80: 60S ribosomal protein L7



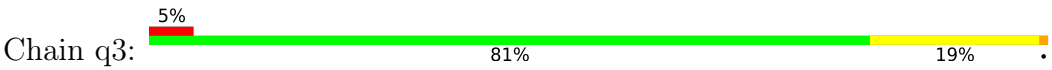


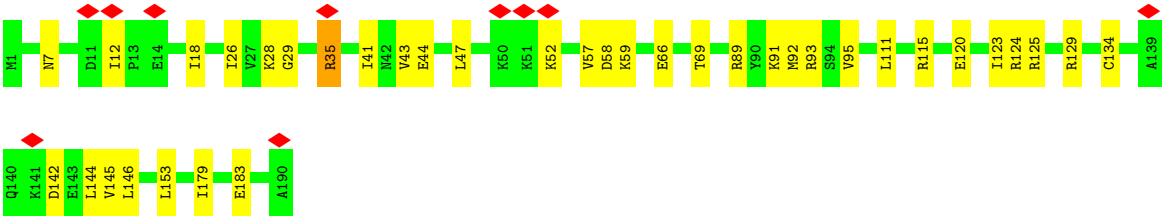
• Molecule 81: 60S ribosomal protein L7a



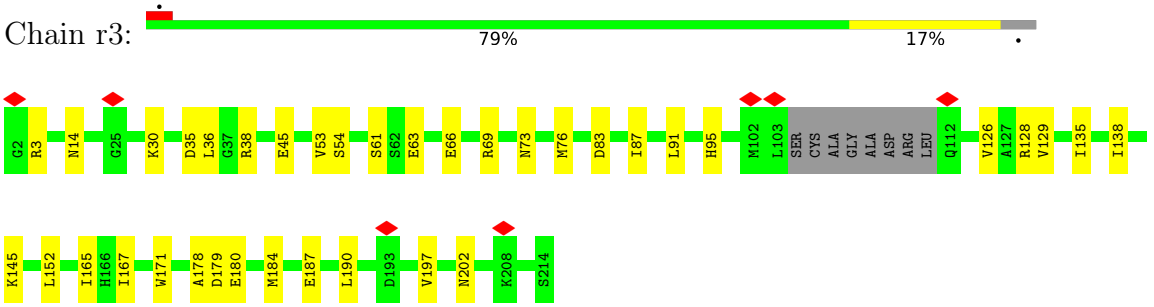


• Molecule 82: 60S ribosomal protein L9

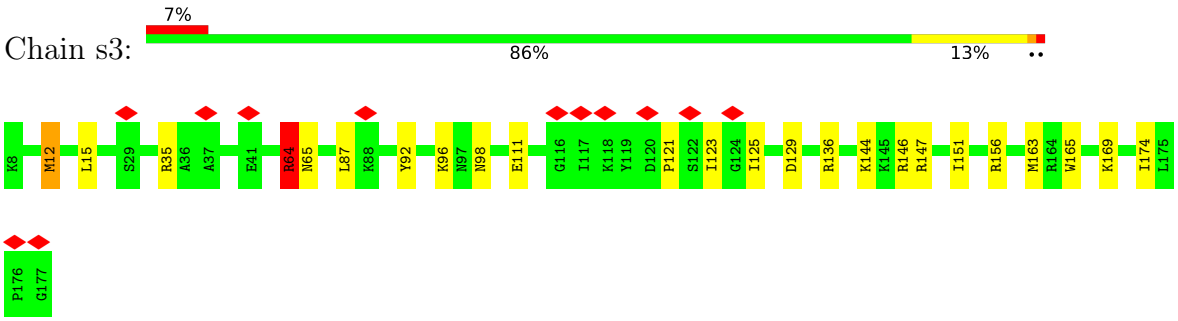




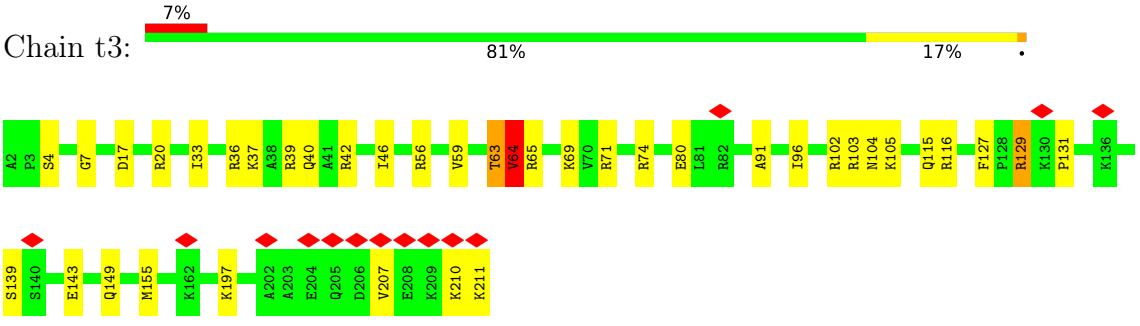
• Molecule 83: Ribosomal protein L10



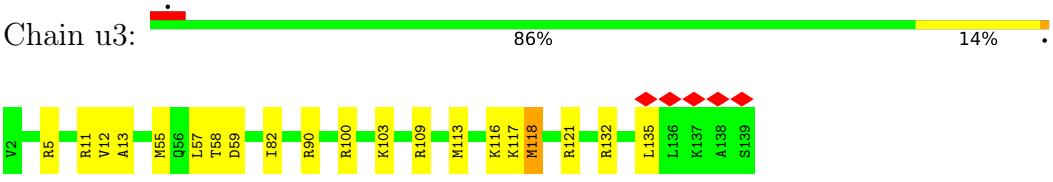
• Molecule 84: 60S ribosomal protein L11



• Molecule 85: 60S ribosomal protein L13



• Molecule 86: 60S ribosomal protein L14



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19437	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	47.5	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	414.5, 414.5, 414.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.829, 0.829, 0.829	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A1	0.42	0/1746	0.66	1/2338 (0.0%)
2	B1	0.37	0/1662	0.67	1/2222 (0.0%)
3	C1	0.39	0/1268	0.72	0/1700
4	D1	0.41	0/1539	0.70	0/2054
5	E1	0.35	0/1524	0.68	0/2013
6	F1	0.37	0/1501	0.69	2/2012 (0.1%)
7	G1	0.41	0/1326	0.67	0/1770
8	H1	0.34	0/823	0.75	0/1104
9	I1	0.35	0/1048	0.62	0/1402
10	J1	0.34	0/873	0.69	1/1158 (0.1%)
11	K1	0.32	0/984	0.60	0/1323
12	L1	0.40	0/1132	0.73	1/1504 (0.1%)
13	M1	0.31	0/1130	0.60	0/1507
14	N1	0.38	0/1191	0.59	0/1590
15	O1	0.38	0/861	0.68	0/1138
16	P1	0.39	0/771	0.66	0/1034
17	Q1	0.38	0/903	0.69	0/1216
18	R1	0.41	0/1071	0.64	2/1429 (0.1%)
19	S1	0.41	0/895	0.61	0/1198
20	T1	0.37	0/916	0.59	0/1220
21	U1	0.31	0/1021	0.62	0/1348
22	V1	0.27	0/841	0.67	1/1112 (0.1%)
23	W1	0.36	0/720	0.60	0/952
24	X1	0.36	0/575	0.66	0/761
25	Y1	0.53	1/459 (0.2%)	0.72	0/608
26	Z1	0.30	0/435	0.55	0/575
27	a1	0.40	0/240	0.63	0/305
28	b1	0.35	0/864	0.61	1/1140 (0.1%)
29	c1	0.38	0/718	0.70	0/953
30	d1	0.36	0/1010	0.69	1/1354 (0.1%)
31	e1	0.42	1/1530 (0.1%)	0.87	5/2064 (0.2%)
32	f1	0.41	1/1174 (0.1%)	0.76	1/1582 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	l1	0.48	1/1680 (0.1%)	0.89	4/2255 (0.2%)
34	m1	0.28	0/68	0.42	0/103
35	n1	0.42	0/1971	0.73	0/2639
36	21	0.25	0/1810	0.43	0/2819
37	11	0.20	0/33	0.67	0/43
38	A2	0.62	6/86400 (0.0%)	0.46	14/134684 (0.0%)
39	B2	0.31	0/2836	0.38	0/4421
40	C2	0.35	0/3581	0.45	2/5577 (0.0%)
41	A3	0.26	0/40502	0.43	4/63100 (0.0%)
42	B3	0.32	0/1747	0.69	2/2374 (0.1%)
43	C3	0.30	0/1756	0.63	0/2350
44	D3	0.35	0/1753	0.64	1/2369 (0.0%)
45	E3	0.35	0/1796	0.76	1/2417 (0.0%)
46	F3	0.27	0/2118	0.59	0/2849
47	G3	0.28	0/1492	0.67	0/2005
48	H3	0.29	0/1946	0.63	0/2590
49	I3	0.30	0/1510	0.72	0/2022
50	J3	0.30	0/1715	0.64	1/2287 (0.0%)
51	K3	0.31	0/1550	0.67	0/2069
52	L3	1.04	3/834 (0.4%)	1.49	9/1125 (0.8%)
53	M3	0.31	0/1195	0.60	1/1597 (0.1%)
54	N3	0.34	0/918	0.90	3/1233 (0.2%)
55	O3	0.73	2/1226 (0.2%)	1.07	5/1649 (0.3%)
56	P3	0.33	0/1029	0.66	0/1380
57	Q3	0.33	0/1079	0.72	2/1441 (0.1%)
58	R3	0.38	0/1146	0.79	1/1534 (0.1%)
59	S3	0.31	0/1082	0.73	0/1452
60	T3	0.35	0/1208	0.83	0/1618
61	U3	0.33	0/1115	0.74	2/1493 (0.1%)
62	V3	0.31	0/805	0.72	0/1081
63	W3	0.28	0/643	0.59	0/860
64	X3	0.36	0/1051	0.65	0/1406
65	Y3	0.28	0/1116	0.64	1/1490 (0.1%)
66	Z3	0.34	0/1028	0.65	0/1366
67	a3	0.34	0/604	0.84	3/810 (0.4%)
68	b3	0.30	0/828	0.62	0/1109
69	c3	0.26	0/665	0.65	0/891
70	d3	0.26	0/490	0.54	0/656
71	e3	0.27	0/470	0.68	1/623 (0.2%)
72	f3	0.27	0/462	0.56	0/607
73	g3	0.38	0/567	0.70	0/753
74	h3	0.39	1/2493 (0.0%)	0.83	6/3394 (0.2%)
75	j3	0.38	0/1936	0.66	1/2596 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	k3	0.38	0/3240	0.67	7/4339 (0.2%)
77	l3	0.39	0/2937	0.65	1/3946 (0.0%)
78	m3	0.32	0/2437	0.60	1/3264 (0.0%)
79	n3	0.30	0/1762	0.58	0/2362
80	o3	0.38	0/1911	0.69	0/2549
81	p3	0.33	0/1910	0.66	0/2569
82	q3	0.37	0/1535	0.70	0/2063
83	r3	0.39	0/1702	0.62	0/2272
84	s3	0.39	0/1385	0.73	3/1852 (0.2%)
85	t3	0.53	3/1733 (0.2%)	0.94	7/2316 (0.3%)
86	u3	0.37	0/1158	0.66	1/1547 (0.1%)
All	All	0.47	19/234715 (0.0%)	0.56	101/343902 (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
1	A1	0	1
12	L1	0	1
14	N1	0	1
17	Q1	0	1
19	S1	0	1
33	l1	0	2
42	B3	0	1
44	D3	0	2
52	L3	0	2
61	U3	0	1
65	Y3	0	1
76	k3	0	1
77	l3	0	3
82	q3	0	1
84	s3	0	1
85	t3	0	3
All	All	0	23

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A2	936	G	C5'-C4'	71.39	2.93	1.51
38	A2	935	A	N9-C8	64.07	2.65	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
38	A2	935	A	N7-C5	61.18	2.61	1.39
38	A2	935	A	N9-C4	59.28	2.56	1.37
38	A2	935	A	C8-N7	58.63	2.48	1.31
38	A2	935	A	C5-C4	51.44	2.41	1.38
52	L3	4	PRO	CG-CD	-22.36	0.74	1.50
55	O3	85	PRO	CG-CD	-21.90	0.76	1.50
52	L3	4	PRO	CB-CG	11.71	2.08	1.49
85	t3	131	PRO	CG-CD	-8.40	1.22	1.50
85	t3	131	PRO	CB-CG	-7.96	1.09	1.49
33	l1	198	TRP	CA-C	7.64	1.63	1.52
25	Y1	35	ILE	CG1-CD1	-7.38	1.23	1.51
74	h3	229	THR	CB-CG2	-6.13	1.32	1.52
32	f1	29	ALA	C-N	6.09	1.40	1.34
52	L3	4	PRO	N-CD	5.87	1.55	1.47
85	t3	131	PRO	N-CA	5.70	1.55	1.47
55	O3	85	PRO	N-CA	5.58	1.53	1.47
31	e1	24	TYR	CG-CD1	-5.21	1.28	1.39

All (101) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
52	L3	4	PRO	N-CD-CG	-29.06	59.62	103.20
55	O3	85	PRO	CB-CG-CD	23.08	179.95	106.10
85	t3	131	PRO	N-CD-CG	-21.39	71.12	103.20
52	L3	4	PRO	CA-CB-CG	-20.09	66.32	104.50
85	t3	131	PRO	CA-CB-CG	-19.97	66.55	104.50
55	O3	85	PRO	N-CD-CG	-18.88	74.88	103.20
55	O3	85	PRO	CA-CB-CG	-14.48	76.98	104.50
52	L3	30	PRO	CA-N-CD	-9.77	98.32	112.00
38	A2	936	G	C5'-C4'-C3'	9.75	135.50	116.00
38	A2	936	G	O5'-C5'-C4'	9.72	129.95	110.50
52	L3	4	PRO	N-CA-CB	-9.27	93.52	103.25
85	t3	131	PRO	CB-CG-CD	8.85	134.42	106.10
54	N3	57	ASP	CA-C-N	-8.71	113.13	122.89
54	N3	57	ASP	C-N-CA	-8.71	113.13	122.89
74	h3	229	THR	OG1-CB-CG2	-8.46	92.37	109.30
76	k3	258	HIS	N-CA-C	8.19	123.43	110.73
33	l1	28	PHE	N-CA-CB	7.34	121.33	109.28
28	b1	82	MET	CG-SD-CE	-7.24	84.97	100.90
31	e1	23	ASP	CA-C-N	-7.11	114.27	122.52
31	e1	23	ASP	C-N-CA	-7.11	114.27	122.52
52	L3	30	PRO	N-CD-CG	-7.03	92.65	103.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
65	Y3	116	PRO	CA-N-CD	-7.01	102.18	112.00
67	a3	100	VAL	CG1-CB-CG2	-6.94	95.53	110.80
74	h3	165	ILE	CG1-CB-CG2	-6.92	89.93	110.70
31	e1	24	TYR	OH-CZ-CE2	6.87	140.51	119.90
76	k3	201	LEU	CA-C-N	6.78	134.48	121.54
76	k3	201	LEU	C-N-CA	6.78	134.48	121.54
31	e1	92	LYS	CA-CB-CG	6.64	127.38	114.10
54	N3	123	VAL	N-CA-C	-6.40	106.28	112.29
52	L3	4	PRO	CB-CG-CD	-6.36	85.77	106.10
10	J1	44	ARG	CG-CD-NE	6.35	125.98	112.00
84	s3	12	MET	CG-SD-CE	-6.35	86.92	100.90
31	e1	24	TYR	CE1-CZ-OH	-6.34	100.87	119.90
38	A2	3968	G	C5'-C4'-C3'	6.32	125.47	116.00
33	l1	25	ARG	CA-C-N	6.30	129.65	120.71
33	l1	25	ARG	C-N-CA	6.30	129.65	120.71
30	d1	108	MET	CG-SD-CE	-6.25	87.15	100.90
44	D3	268	GLU	CG-CD-OE2	-6.21	104.11	118.40
85	t3	131	PRO	CA-N-CD	-6.21	103.31	112.00
12	L1	77	LYS	CB-CG-CD	6.17	125.50	111.30
50	J3	132	GLU	CA-CB-CG	6.11	126.33	114.10
18	R1	5	ARG	CB-CG-CD	-6.03	97.44	111.30
57	Q3	71	GLU	CA-C-N	6.00	130.62	121.03
57	Q3	71	GLU	C-N-CA	6.00	130.62	121.03
77	l3	281	MET	CG-SD-CE	-5.97	87.77	100.90
42	B3	127	PRO	N-CD-CG	-5.93	94.30	103.20
74	h3	229	THR	CA-CB-CG2	-5.91	100.46	110.50
75	j3	241	ARG	CG-CD-NE	5.87	124.92	112.00
84	s3	64	ARG	CB-CG-CD	5.84	124.73	111.30
78	m3	115	MET	CG-SD-CE	-5.83	88.07	100.90
86	u3	118	MET	CB-CG-SD	5.75	129.95	112.70
52	L3	4	PRO	CA-N-CD	-5.75	103.95	112.00
67	a3	61	GLU	CA-C-N	5.74	123.85	120.24
67	a3	61	GLU	C-N-CA	5.74	123.85	120.24
40	C2	75	G	N9-C1'-C2'	-5.71	103.44	112.00
18	R1	90	MET	CG-SD-CE	-5.70	88.37	100.90
84	s3	64	ARG	CA-CB-CG	-5.66	102.77	114.10
42	B3	210	ILE	CG1-CB-CG2	-5.63	93.82	110.70
71	e3	23	VAL	N-CA-C	-5.60	107.42	112.12
33	l1	26	ARG	N-CA-C	5.57	118.31	110.23
32	f1	123	ARG	CA-CB-CG	5.53	125.15	114.10
38	A2	4504	A	O5'-P-OP2	-5.51	91.46	108.00
74	h3	169	GLY	CA-C-N	-5.50	113.11	122.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
74	h3	169	GLY	C-N-CA	-5.50	113.11	122.56
38	A2	1070	C	P-O3'-C3'	5.44	128.35	120.20
45	E3	76	ARG	CG-CD-NE	5.41	123.91	112.00
38	A2	3883	G	C2'-C3'-O3'	5.40	121.81	113.70
22	V1	63	VAL	N-CA-C	-5.40	105.67	113.07
55	O3	144	SER	CA-C-N	-5.39	114.01	122.79
55	O3	144	SER	C-N-CA	-5.39	114.01	122.79
52	L3	45	VAL	CA-C-N	5.30	131.67	121.54
52	L3	45	VAL	C-N-CA	5.30	131.67	121.54
61	U3	117	GLN	CA-C-N	5.29	131.64	121.54
61	U3	117	GLN	C-N-CA	5.29	131.64	121.54
76	k3	213	GLN	CA-C-N	5.28	131.62	121.54
76	k3	213	GLN	C-N-CA	5.28	131.62	121.54
38	A2	2046	G	P-O3'-C3'	5.25	128.07	120.20
85	t3	131	PRO	N-CA-CB	-5.22	97.75	103.39
53	M3	82	MET	CG-SD-CE	-5.20	89.45	100.90
40	C2	75	G	C3'-C2'-O2'	5.15	118.42	110.70
38	A2	3954	U	P-O3'-C3'	5.15	127.92	120.20
85	t3	64	VAL	N-CA-C	5.15	120.04	109.34
74	h3	189	ILE	CG1-CB-CG2	-5.11	95.37	110.70
2	B1	110	PRO	N-CA-C	5.10	116.92	110.70
41	A3	752	G	P-O3'-C3'	5.09	127.84	120.20
58	R3	93	VAL	CA-CB-CG1	5.09	119.06	110.40
41	A3	553	U	P-O3'-C3'	5.09	127.83	120.20
85	t3	104	ASN	N-CA-CB	5.08	118.87	110.69
76	k3	65	SER	CA-C-N	-5.08	113.19	122.38
76	k3	65	SER	C-N-CA	-5.08	113.19	122.38
41	A3	627	U	P-O3'-C3'	5.08	127.81	120.20
38	A2	936	G	C5'-C4'-O4'	5.06	119.62	109.50
38	A2	2839	A	N9-C1'-C2'	5.06	119.58	112.00
41	A3	688	U	P-O3'-C3'	5.06	127.78	120.20
38	A2	4340	U	P-O3'-C3'	5.05	127.78	120.20
38	A2	4907	U	P-O3'-C3'	5.03	127.75	120.20
1	A1	19	MET	CG-SD-CE	-5.02	89.85	100.90
6	F1	165	PRO	CA-C-N	5.02	131.12	121.54
6	F1	165	PRO	C-N-CA	5.02	131.12	121.54
38	A2	1477	C	C2'-C3'-O3'	5.02	121.23	113.70
38	A2	3871	A	P-O3'-C3'	5.01	127.71	120.20

There are no chirality outliers.

All (23) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A1	108	ARG	Sidechain
42	B3	42	LYS	Peptide
44	D3	121	ARG	Sidechain
44	D3	268	GLU	Sidechain
12	L1	74	TYR	Sidechain
52	L3	3	MET	Mainchain
52	L3	44	HIS	Peptide
14	N1	6	ARG	Sidechain
17	Q1	95	ASP	Peptide
19	S1	106	TYR	Peptide
61	U3	101	ARG	Sidechain
65	Y3	61	GLN	Peptide
76	k3	258	HIS	Peptide
33	l1	27	LYS	Peptide
33	l1	28	PHE	Peptide
77	l3	100	ARG	Sidechain
77	l3	323	ARG	Sidechain
77	l3	339	THR	Peptide
82	q3	35	ARG	Sidechain
84	s3	64	ARG	Sidechain
85	t3	129	ARG	Sidechain
85	t3	42	ARG	Sidechain
85	t3	63	THR	Peptide

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	A1	1701	0	1749	23	0
2	B1	1630	0	1778	26	0
3	C1	1242	0	1274	17	0
4	D1	1515	0	1634	30	0
5	E1	1508	0	1664	29	0
6	F1	1462	0	1508	26	0
7	G1	1298	0	1366	25	0
8	H1	809	0	833	12	0
9	I1	1034	0	1097	16	0
10	J1	860	0	903	19	0
11	K1	967	0	1040	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	L1	1115	0	1205	20	0
13	M1	1107	0	1182	21	0
14	N1	1162	0	1209	29	0
15	O1	848	0	920	11	0
16	P1	761	0	794	17	0
17	Q1	888	0	930	11	0
18	R1	1053	0	1147	22	0
19	S1	876	0	912	18	0
20	T1	906	0	998	17	0
21	U1	1013	0	1147	8	0
22	V1	830	0	916	14	0
23	W1	705	0	737	7	0
24	X1	569	0	637	8	0
25	Y1	447	0	480	10	0
26	Z1	429	0	465	9	0
27	a1	239	0	289	6	0
28	b1	851	0	920	12	0
29	c1	708	0	756	18	0
30	d1	994	0	1051	15	0
31	e1	1507	0	1564	16	0
32	f1	1160	0	1218	16	0
33	l1	1654	0	1760	39	0
34	m1	62	0	32	0	0
35	n1	1948	0	1933	30	0
36	21	1620	0	817	28	0
37	11	34	0	40	0	0
38	A2	77264	0	39062	624	0
39	B2	2538	0	1286	12	0
40	C2	3208	0	1629	17	0
41	A3	36229	0	18307	291	0
42	B3	1710	0	1708	34	0
43	C3	1729	0	1803	32	0
44	D3	1716	0	1806	33	0
45	E3	1768	0	1866	22	0
46	F3	2076	0	2177	27	0
47	G3	1471	0	1522	15	0
48	H3	1923	0	2089	42	0
49	I3	1488	0	1582	22	0
50	J3	1686	0	1772	22	0
51	K3	1525	0	1640	27	0
52	L3	810	0	836	25	0
53	M3	1175	0	1249	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	N3	908	0	939	16	0
55	O3	1202	0	1289	13	0
56	P3	1016	0	1039	26	0
57	Q3	1058	0	1104	16	0
58	R3	1128	0	1195	15	0
59	S3	1068	0	1121	17	0
60	T3	1190	0	1249	36	0
61	U3	1097	0	1132	21	0
62	V3	795	0	862	18	0
63	W3	636	0	637	15	0
64	X3	1034	0	1080	23	0
65	Y3	1098	0	1167	15	0
66	Z3	1011	0	1083	20	0
67	a3	598	0	656	8	0
68	b3	814	0	864	13	0
69	c3	651	0	672	13	0
70	d3	488	0	514	9	0
71	e3	459	0	448	6	0
72	f3	457	0	502	4	0
73	g3	555	0	567	7	0
74	h3	2436	0	2393	63	0
75	j3	1898	0	1993	42	0
76	k3	3172	0	3310	55	0
77	l3	2883	0	3053	53	0
78	m3	2391	0	2424	37	0
79	n3	1729	0	1887	29	0
80	o3	1875	0	1995	39	0
81	p3	1879	0	2027	28	0
82	q3	1516	0	1597	21	0
83	r3	1664	0	1712	26	0
84	s3	1362	0	1399	16	0
85	t3	1702	0	1820	29	0
86	u3	1137	0	1211	17	0
87	A2	189	0	0	0	0
87	A3	69	0	0	0	0
87	B2	6	0	0	0	0
87	C1	1	0	0	0	0
87	C2	4	0	0	0	0
87	I1	1	0	0	0	0
87	M3	1	0	0	0	0
87	N1	1	0	0	0	0
87	T1	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	j3	1	0	0	0	0
87	r3	1	0	0	0	0
88	T1	1	0	0	0	0
88	W1	1	0	0	0	0
88	Z1	1	0	0	0	0
88	b1	1	0	0	0	0
88	b3	1	0	0	0	0
88	c1	1	0	0	0	0
88	e3	1	0	0	0	0
All	All	219017	0	164180	2123	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (2123) 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)
38:A2:935:A:C4	38:A2:936:G:H4'	1.82	1.14
38:A2:935:A:C4	38:A2:935:A:C5	2.41	1.08
38:A2:984:U:H3	38:A2:1271:G:H1	0.97	0.95
41:A3:1452:A:H61	41:A3:1473:G:H21	1.01	0.93
41:A3:1452:A:N6	41:A3:1473:G:H21	1.66	0.92
38:A2:742:G:O6	38:A2:921:G:N2	2.02	0.92
41:A3:1452:A:H61	41:A3:1473:G:N2	1.72	0.87
63:W3:32:ILE:O	63:W3:54:ALA:HA	1.75	0.87
38:A2:3960:A:H61	38:A2:4039:G:H21	1.22	0.86
38:A2:935:A:C8	38:A2:936:G:C5'	2.59	0.85
38:A2:3941:G:H1	38:A2:4061:U:H3	1.20	0.84
38:A2:3960:A:H61	38:A2:4039:G:N2	1.76	0.84
68:b3:88:SER:O	68:b3:92:ARG:HB2	1.79	0.83
38:A2:742:G:C6	38:A2:921:G:N2	2.46	0.82
38:A2:935:A:C4	38:A2:936:G:H5"	2.14	0.82
38:A2:935:A:C5	38:A2:936:G:C5'	2.62	0.82
33:l1:53:VAL:O	33:l1:154:THR:HA	1.79	0.81
38:A2:935:A:C8	38:A2:935:A:N7	2.48	0.81
38:A2:935:A:C4	38:A2:936:G:C5'	2.64	0.81
36:21:2:C:H42	36:21:71:A:H61	1.30	0.80
38:A2:3960:A:N6	38:A2:4039:G:H21	1.79	0.79
41:A3:1473:G:H2'	41:A3:1475:G:H22	1.49	0.78
38:A2:935:A:N7	38:A2:936:G:H5'	1.99	0.78
41:A3:821:G:N7	51:K3:138:ARG:NH2	2.32	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:A3:928:G:H1	41:A3:1013:U:H3	1.32	0.77
49:I3:30:LEU:O	49:I3:34:SER:HB3	1.85	0.77
38:A2:935:A:C8	38:A2:936:G:C4'	2.68	0.76
38:A2:935:A:N7	38:A2:936:G:C5'	2.49	0.76
38:A2:991:U:H3	38:A2:1063:G:H1	1.30	0.76
38:A2:935:A:N9	38:A2:936:G:C5'	2.49	0.75
7:G1:75:VAL:HA	7:G1:87:LYS:O	1.86	0.74
38:A2:935:A:C4	38:A2:935:A:N9	2.56	0.74
38:A2:742:G:C5	38:A2:921:G:N2	2.56	0.73
41:A3:952:G:H21	56:P3:52:THR:HG21	1.53	0.73
2:B1:173:GLN:HA	2:B1:176:ARG:HE	1.52	0.73
60:T3:25:LYS:HD3	60:T3:55:ARG:HE	1.52	0.73
41:A3:677:G:H21	41:A3:1028:A:H62	1.35	0.73
38:A2:935:A:N9	38:A2:936:G:H4'	2.03	0.73
44:D3:263:LYS:HE2	44:D3:268:GLU:HB3	1.69	0.73
74:h3:256:ILE:HB	74:h3:270:LEU:HB2	1.71	0.72
38:A2:935:A:C5	38:A2:936:G:C4'	2.73	0.72
7:G1:88:ARG:NH2	15:O1:30:GLU:OE2	2.23	0.72
10:J1:20:ARG:HE	10:J1:30:GLN:HB3	1.55	0.71
42:B3:187:GLY:HA2	63:W3:45:ARG:HE	1.53	0.71
41:A3:116:U:H3	41:A3:347:G:H1	1.36	0.71
67:a3:100:VAL:HG23	67:a3:108:ILE:HG13	1.72	0.71
35:n1:57:ARG:NH2	38:A2:3768:U:OP1	2.24	0.71
35:n1:59:ARG:HB2	35:n1:84:ILE:HG21	1.73	0.70
38:A2:4236:G:H5"	84:s3:98:ASN:HD22	1.56	0.70
16:P1:88:TYR:HE1	55:O3:145:THR:HB	1.56	0.70
38:A2:2650:A:H62	38:A2:2689:G:H8	1.38	0.70
80:o3:93:ARG:HE	80:o3:108:LEU:HD13	1.56	0.70
50:J3:203:LYS:HA	50:J3:206:LYS:HE2	1.74	0.70
41:A3:925:G:H1	41:A3:1017:U:H3	1.38	0.70
80:o3:218:GLY:O	80:o3:245:ARG:NH2	2.24	0.70
74:h3:206:LEU:HD23	74:h3:220:ASP:HB3	1.74	0.69
41:A3:1522:A:H5'	60:T3:144:ARG:HD2	1.73	0.69
13:M1:135:ARG:NH1	20:T1:98:GLU:OE2	2.21	0.69
38:A2:935:A:C5	38:A2:935:A:N7	2.61	0.69
38:A2:4504:A:N7	76:k3:258:HIS:NE2	2.40	0.69
21:U1:9:LEU:HD23	21:U1:12:LYS:HZ3	1.57	0.68
60:T3:23:ARG:O	60:T3:55:ARG:NH1	2.26	0.68
20:T1:66:ARG:HD3	38:A2:2542:C:H5"	1.74	0.68
41:A3:1757:G:H1	41:A3:1775:U:H3	1.41	0.68
35:n1:226:TYR:HB3	35:n1:231:LEU:HB2	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:h3:216:ALA:HB3	74:h3:230:LEU:HB2	1.75	0.68
38:A2:2264:G:H5'	79:n3:115:MET:HE1	1.76	0.68
36:21:3:C:H42	36:21:70:A:H61	1.41	0.67
43:C3:38:MET:HE1	43:C3:231:LEU:HD22	1.77	0.67
42:B3:210:ILE:HD11	59:S3:81:ARG:HG3	1.76	0.67
4:D1:104:ARG:NH2	38:A2:1351:G:N7	2.42	0.67
38:A2:3687:A:H62	38:A2:3818:G:H21	1.39	0.67
44:D3:255:LEU:O	63:W3:16:LYS:NZ	2.27	0.67
48:H3:98:ARG:NH2	48:H3:103:ASP:OD1	2.27	0.67
41:A3:394:G:O2'	53:M3:82:MET:SD	2.54	0.66
85:t3:116:ARG:NH2	85:t3:155:MET:O	2.28	0.66
38:A2:1819:G:H1'	78:m3:115:MET:HE1	1.77	0.66
38:A2:935:A:C4	38:A2:936:G:C4'	2.72	0.66
5:E1:71:ARG:HH22	38:A2:3599:A:H8	1.44	0.66
74:h3:10:THR:HB	74:h3:306:LEU:HD11	1.77	0.66
38:A2:1739:G:N3	38:A2:1742:A:N6	2.44	0.66
38:A2:1277:A:O2'	77:l3:323:ARG:NH2	2.29	0.66
45:E3:135:GLU:HG3	45:E3:153:VAL:HG22	1.78	0.66
76:k3:220:ILE:HB	76:k3:346:THR:HB	1.78	0.66
61:U3:18:LEU:HD11	61:U3:131:LEU:HD22	1.78	0.66
85:t3:56:ARG:O	85:t3:116:ARG:NH1	2.29	0.66
53:M3:97:ARG:NH1	53:M3:97:ARG:O	2.27	0.65
22:V1:55:ARG:HA	22:V1:58:MET:HE2	1.78	0.65
58:R3:90:LYS:HA	58:R3:93:VAL:HB	1.77	0.65
38:A2:935:A:N9	38:A2:936:G:C4'	2.60	0.65
47:G3:50:PRO:HG2	47:G3:90:VAL:HG22	1.78	0.65
1:A1:14:LYS:HA	1:A1:19:MET:HG2	1.78	0.65
10:J1:23:ARG:HE	10:J1:29:PHE:HE2	1.44	0.65
36:21:6:G:H1	36:21:67:U:H3	1.45	0.65
38:A2:4117:G:N2	81:p3:96:GLN:O	2.29	0.65
82:q3:44:GLU:HB2	82:q3:58:ASP:HB2	1.78	0.65
41:A3:433:A:H5"	50:J3:22:HIS:HB3	1.79	0.65
74:h3:226:HIS:NE2	74:h3:229:THR:OG1	2.30	0.65
29:c1:61:MET:SD	38:A2:2655:G:N2	2.70	0.65
4:D1:184:ARG:NH2	38:A2:4327:C:OP1	2.30	0.64
56:P3:34:PHE:HB3	56:P3:41:PHE:HB2	1.79	0.64
83:r3:91:LEU:HD21	83:r3:129:VAL:HB	1.78	0.64
13:M1:51:ARG:NH2	38:A2:2759:G:N7	2.45	0.64
38:A2:935:A:C8	38:A2:935:A:N9	2.65	0.64
41:A3:1521:C:O2'	60:T3:144:ARG:NH1	2.29	0.64
62:V3:31:SER:HA	62:V3:34:LYS:HG2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d1:98:ARG:NH2	38:A2:2265:G:OP2	2.30	0.64
38:A2:4287:U:OP2	38:A2:4289:C:N4	2.30	0.64
66:Z3:104:ARG:HG2	66:Z3:108:LYS:HE2	1.79	0.64
70:d3:32:VAL:O	70:d3:41:SER:HA	1.97	0.64
38:A2:4131:C:N3	38:A2:4132:G:N1	2.46	0.64
38:A2:150:U:H3	81:p3:215:ASP:HB2	1.61	0.64
61:U3:76:THR:HB	61:U3:94:ARG:HB3	1.80	0.64
78:m3:200:MET:HE3	78:m3:241:LYS:HE2	1.79	0.64
12:L1:74:TYR:CE2	12:L1:77:LYS:HG3	2.33	0.64
38:A2:4131:C:O2	38:A2:4132:G:N2	2.31	0.64
28:b1:81:ARG:NH2	38:A2:4279:U:O2'	2.31	0.64
38:A2:2303:A:N7	77:l3:143:ARG:NH1	2.45	0.64
54:N3:52:LEU:HD22	54:N3:65:VAL:HG11	1.78	0.64
14:N1:72:THR:HG22	14:N1:110:LYS:HB3	1.81	0.63
17:Q1:64:ILE:HG23	17:Q1:68:LEU:HD23	1.79	0.63
80:o3:161:ILE:HB	80:o3:166:ILE:HD13	1.80	0.63
38:A2:2523:C:O2	38:A2:2643:G:N2	2.31	0.63
41:A3:1192:U:OP2	65:Y3:119:ARG:NH2	2.31	0.63
75:j3:137:ILE:HD11	75:j3:149:LYS:HB2	1.79	0.63
38:A2:2556:A:H2	38:A2:2768:A:H62	1.46	0.63
38:A2:981:C:H42	38:A2:1274:C:H42	1.45	0.63
38:A2:4866:G:N7	79:n3:275:ARG:NH2	2.46	0.63
31:e1:13:TYR:OH	38:A2:1999:A:OP1	2.17	0.63
33:l1:54:ARG:HA	33:l1:154:THR:HG22	1.80	0.63
38:A2:935:A:N7	38:A2:936:G:C4'	2.61	0.63
38:A2:3746:G:H21	38:A2:3770:A:H8	1.47	0.63
41:A3:1542:C:OP1	61:U3:62:ARG:NE	2.32	0.63
46:F3:137:PRO:HB2	46:F3:150:PRO:HD2	1.80	0.63
38:A2:2300:G:P	77:l3:205:ARG:HH22	2.22	0.63
49:I3:160:LYS:HE2	49:I3:191:GLU:HA	1.79	0.63
76:k3:56:ILE:O	76:k3:73:VAL:HA	1.98	0.63
17:Q1:118:GLN:OE1	38:A2:5037:G:N2	2.32	0.62
21:U1:109:ARG:NH2	38:A2:156:G:OP2	2.32	0.62
20:T1:46:CYS:HB3	20:T1:82:MET:HE3	1.81	0.62
38:A2:223:G:N7	77:l3:165:LYS:NZ	2.45	0.62
5:E1:71:ARG:NH1	38:A2:3600:C:OP2	2.32	0.62
38:A2:1541:C:H5"	75:j3:21:LYS:HG2	1.81	0.62
67:a3:47:LEU:HB2	67:a3:79:ILE:HG22	1.82	0.62
75:j3:147:ARG:HE	75:j3:155:LYS:HE2	1.64	0.62
84:s3:165:TRP:O	84:s3:169:LYS:HB2	2.00	0.62
44:D3:196:ILE:HB	44:D3:223:TYR:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:k3:95:THR:HG22	76:k3:97:ARG:H	1.63	0.62
38:A2:1443:A:H61	38:A2:2111:U:H3	1.47	0.62
41:A3:754:G:H22	41:A3:791:C:H1'	1.64	0.62
45:E3:106:ARG:HG3	45:E3:175:VAL:HG12	1.81	0.62
36:21:33:U:H3'	58:R3:146:ARG:HH22	1.64	0.62
60:T3:13:LEU:HB2	60:T3:20:ILE:HB	1.81	0.62
14:N1:76:ASP:HB3	14:N1:115:GLY:HA3	1.80	0.62
41:A3:1543:U:OP2	61:U3:62:ARG:NH2	2.30	0.62
58:R3:93:VAL:HG22	58:R3:105:LYS:HE3	1.80	0.62
38:A2:1521:C:OP1	77:l3:100:ARG:NH2	2.31	0.62
42:B3:77:ILE:HD11	42:B3:124:VAL:HG22	1.80	0.62
6:F1:55:LYS:NZ	39:B2:99:G:N7	2.43	0.62
38:A2:4081:G:OP2	75:j3:37:ARG:NH2	2.32	0.61
32:f1:45:ASP:O	32:f1:48:LYS:NZ	2.33	0.61
6:F1:93:MET:SD	6:F1:95:ARG:NH1	2.73	0.61
18:R1:104:SER:HB3	38:A2:2306:C:H5"	1.82	0.61
24:X1:18:LYS:NZ	38:A2:2776:G:O2'	2.32	0.61
38:A2:1288:G:OP1	79:n3:221:LYS:NZ	2.34	0.61
44:D3:78:LEU:HD12	44:D3:81:ILE:HD12	1.82	0.61
51:K3:113:GLN:OE1	51:K3:154:GLN:NE2	2.34	0.61
38:A2:73:A:N7	85:t3:105:LYS:NZ	2.48	0.61
79:n3:264:ILE:HG23	79:n3:270:LEU:HD23	1.82	0.61
15:O1:105:GLY:O	15:O1:109:ARG:HB2	2.00	0.61
41:A3:91:A:OP1	46:F3:7:LYS:NZ	2.34	0.61
84:s3:87:LEU:HD12	84:s3:92:TYR:HA	1.82	0.61
5:E1:105:LEU:HD22	5:E1:135:LYS:HG3	1.81	0.61
64:X3:23:ARG:HD3	69:c3:4:ALA:HB2	1.83	0.61
4:D1:181:ARG:NH2	38:A2:1389:A:OP1	2.33	0.61
6:F1:154:LEU:HD12	86:u3:57:LEU:HD11	1.83	0.61
36:21:4:A:H2	36:21:69:G:H1	1.48	0.61
80:o3:170:ASP:HB2	80:o3:173:LEU:HG	1.82	0.61
38:A2:102:G:OP1	85:t3:71:ARG:NH1	2.34	0.61
74:h3:217:MET:HA	74:h3:229:THR:HG23	1.82	0.61
1:A1:31:ARG:NH1	38:A2:4072:C:OP1	2.34	0.60
38:A2:944:A:N7	80:o3:150:ASN:ND2	2.48	0.60
38:A2:1360:G:OP1	85:t3:39:ARG:NH2	2.34	0.60
38:A2:1979:A:H61	38:A2:1983:A:H3'	1.65	0.60
41:A3:1616:U:OP2	57:Q3:43:ARG:NH2	2.32	0.60
80:o3:104:VAL:HG13	80:o3:135:VAL:HG12	1.83	0.60
14:N1:65:ARG:NH1	38:A2:86:U:O2'	2.27	0.60
45:E3:94:ARG:O	45:E3:101:GLN:NE2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:F3:11:ARG:HA	46:F3:28:ALA:HB2	1.83	0.60
38:A2:2489:G:H2'	38:A2:2490:G:H8	1.66	0.60
38:A2:4399:C:H5	38:A2:4415:C:H42	1.47	0.60
69:c3:34:ASP:O	69:c3:79:PHE:HA	2.00	0.60
8:H1:44:GLN:HA	8:H1:56:LEU:HD13	1.83	0.60
35:n1:49:LYS:HD3	35:n1:91:PHE:HZ	1.66	0.60
43:C3:67:PHE:O	43:C3:85:LYS:HA	2.01	0.60
80:o3:215:PRO:HD3	80:o3:246:MET:HE3	1.83	0.60
2:B1:46:ASN:HA	2:B1:134:LYS:HG2	1.84	0.60
26:Z1:67:LYS:HD2	26:Z1:76:ARG:HG2	1.82	0.60
83:r3:36:LEU:HD21	83:r3:69:ARG:HH21	1.67	0.60
52:L3:59:LYS:HG3	52:L3:70:TYR:HB2	1.83	0.60
16:P1:21:VAL:HG11	16:P1:96:ILE:HD12	1.83	0.60
25:Y1:27:ILE:O	25:Y1:33:ASN:ND2	2.35	0.60
29:c1:4:ARG:NH2	38:A2:1555:G:O6	2.35	0.60
41:A3:1263:U:O2	71:e3:16:GLN:NE2	2.35	0.60
63:W3:41:LYS:HG3	63:W3:42:VAL:HG13	1.82	0.60
38:A2:2005:G:N2	38:A2:2014:C:O2	2.31	0.59
38:A2:3614:G:H22	38:A2:3619:A:H1'	1.65	0.59
2:B1:34:VAL:HG22	2:B1:103:LYS:HB2	1.84	0.59
2:B1:85:ARG:HG3	2:B1:99:LEU:HD11	1.84	0.59
41:A3:1498:A:OP2	45:E3:27:ARG:NH2	2.35	0.59
41:A3:1863:A:OP2	68:b3:4:LYS:NZ	2.35	0.59
43:C3:183:GLU:O	43:C3:187:LYS:NZ	2.35	0.59
4:D1:144:LYS:HG2	38:A2:1460:C:H5"	1.85	0.59
38:A2:978:G:H21	77:l3:323:ARG:NH1	2.00	0.59
41:A3:163:U:OP2	48:H3:87:ARG:NH2	2.34	0.59
41:A3:677:G:N2	41:A3:1028:A:H62	2.01	0.59
66:Z3:29:HIS:NE2	66:Z3:69:THR:OG1	2.34	0.59
12:L1:17:ARG:HH22	12:L1:29:ILE:HD11	1.66	0.59
41:A3:874:G:H2'	41:A3:875:A:H8	1.67	0.59
38:A2:4257:A:OP1	38:A2:4258:G:N2	2.35	0.59
9:I1:43:LYS:HD3	38:A2:4494:C:H5"	1.83	0.59
38:A2:4737:G:H1	38:A2:4930:C:H5	1.49	0.59
58:R3:93:VAL:HG13	58:R3:105:LYS:HE3	1.84	0.59
75:j3:234:LYS:HG2	75:j3:238:ILE:HD12	1.84	0.59
38:A2:4879:G:H1	38:A2:4905:U:H3	1.49	0.59
48:H3:2:LYS:HB2	48:H3:108:VAL:HG22	1.84	0.59
57:Q3:72:LYS:HB3	57:Q3:93:MET:HE1	1.85	0.59
74:h3:174:VAL:HB	74:h3:188:HIS:HB2	1.83	0.59
83:r3:76:MET:HE2	83:r3:138:ILE:HG21	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:d1:72:LYS:NZ	77:l3:149:GLU:OE1	2.36	0.59
38:A2:3957:A:N7	38:A2:4032:C:O2'	2.34	0.59
38:A2:4931:G:H4'	38:A2:4932:U:H5'	1.85	0.59
41:A3:67:C:H41	48:H3:163:ASN:HA	1.66	0.59
45:E3:136:VAL:HG22	45:E3:186:VAL:HG22	1.83	0.59
1:A1:11:TRP:HZ3	1:A1:120:TRP:HZ3	1.50	0.59
3:C1:36:ILE:HA	3:C1:39:MET:HG3	1.85	0.59
39:B2:8:G:O6	78:m3:21:ARG:NH2	2.35	0.59
41:A3:940:U:H3	41:A3:1002:U:H3	1.50	0.59
41:A3:1488:C:O2'	41:A3:1490:G:OP2	2.19	0.59
58:R3:53:GLU:OE1	58:R3:85:ARG:NH1	2.35	0.58
19:S1:43:LEU:O	19:S1:109:ARG:NH1	2.36	0.58
52:L3:1:MET:HE3	52:L3:45:VAL:HG23	1.83	0.58
59:S3:77:GLU:O	59:S3:81:ARG:NH1	2.32	0.58
9:I1:43:LYS:NZ	38:A2:4494:C:OP1	2.37	0.58
18:R1:107:ASN:ND2	38:A2:2306:C:OP1	2.35	0.58
41:A3:1152:U:O2'	64:X3:19:LYS:NZ	2.37	0.58
4:D1:37:ARG:NH2	38:A2:2088:A:OP2	2.35	0.58
41:A3:332:G:O6	48:H3:189:ARG:NH2	2.36	0.58
41:A3:1650:A:H5"	58:R3:139:ALA:HB2	1.85	0.58
74:h3:163:PRO:HB2	74:h3:179:LEU:HB2	1.84	0.58
83:r3:38:ARG:HG3	83:r3:83:ASP:HB2	1.83	0.58
86:u3:5:ARG:NE	86:u3:59:ASP:OD1	2.36	0.58
86:u3:11:ARG:NH1	86:u3:58:THR:O	2.36	0.58
21:U1:52:LYS:NZ	40:C2:62:A:OP1	2.37	0.58
29:c1:44:LYS:NZ	38:A2:2675:C:OP1	2.36	0.58
38:A2:4070:G:OP1	81:p3:126:ARG:NE	2.35	0.58
45:E3:190:LEU:HD23	45:E3:199:GLY:HA2	1.86	0.58
54:N3:58:GLU:HG2	54:N3:61:TYR:HB3	1.84	0.58
2:B1:81:TRP:HB2	2:B1:104:VAL:HG21	1.85	0.58
8:H1:22:THR:HG22	8:H1:71:THR:HG23	1.86	0.58
33:l1:68:LEU:HB3	33:l1:116:LEU:HD23	1.84	0.58
38:A2:935:A:C5	38:A2:936:G:H5"	2.38	0.58
38:A2:980:G:OP2	79:n3:61:ARG:NH2	2.35	0.58
41:A3:663:C:O2'	44:D3:227:ARG:NH2	2.37	0.58
41:A3:1148:A:OP2	68:b3:6:ARG:NH2	2.37	0.58
49:I3:144:ILE:HB	64:X3:52:ILE:HB	1.85	0.58
21:U1:117:ARG:NH2	85:t3:127:PHE:O	2.37	0.58
38:A2:3966:G:N2	38:A2:4044:A:H62	2.02	0.58
41:A3:1292:C:N3	73:g3:138:ARG:NH2	2.52	0.58
60:T3:86:ARG:NH1	60:T3:110:ASP:OD2	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:c3:40:CYS:SG	69:c3:41:TYR:N	2.77	0.58
12:L1:54:GLU:HB2	12:L1:108:ARG:HB3	1.84	0.58
18:R1:103:VAL:O	18:R1:108:ARG:NH1	2.37	0.58
30:d1:90:LEU:HD22	30:d1:111:ILE:HG23	1.85	0.58
13:M1:36:ARG:NH1	13:M1:38:TYR:OH	2.36	0.58
17:Q1:65:ASP:OD1	17:Q1:67:ARG:NH2	2.37	0.58
10:J1:44:ARG:NE	38:A2:3610:G:H21	2.01	0.57
41:A3:162:C:H5"	48:H3:87:ARG:HH22	1.68	0.57
77:l3:182:LYS:HG2	77:l3:204:ARG:HD3	1.85	0.57
41:A3:1658:G:OP2	41:A3:1660:C:N4	2.37	0.57
43:C3:33:VAL:HG12	43:C3:96:CYS:HB2	1.87	0.57
25:Y1:40:LYS:NZ	38:A2:365:U:O2'	2.37	0.57
38:A2:2001:G:H22	38:A2:2017:A:H1'	1.69	0.57
38:A2:4731:G:H1	38:A2:4937:A:H61	1.50	0.57
41:A3:332:G:OP1	48:H3:196:LYS:NZ	2.37	0.57
41:A3:1513:C:H5"	71:e3:10:HIS:HB2	1.85	0.57
44:D3:74:LYS:HB3	44:D3:269:PHE:CE2	2.39	0.57
32:f1:18:THR:HA	32:f1:57:ARG:HG3	1.85	0.57
41:A3:165:G:H4'	48:H3:53:SER:HB3	1.86	0.57
5:E1:8:LYS:HG2	5:E1:19:LYS:HG2	1.86	0.57
19:S1:89:ARG:NH2	38:A2:710:C:OP1	2.38	0.57
31:e1:28:PHE:HB2	31:e1:89:VAL:HB	1.86	0.57
46:F3:100:ARG:HH21	46:F3:118:GLU:HG2	1.69	0.57
75:j3:158:ILE:HB	75:j3:162:ASN:HD21	1.69	0.57
82:q3:93:ARG:NH1	82:q3:142:ASP:OD1	2.37	0.57
2:B1:117:ARG:NH2	38:A2:4744:U:O2'	2.37	0.57
4:D1:69:LYS:HD2	38:A2:1458:C:H5"	1.85	0.57
8:H1:81:ARG:NH2	38:A2:2625:G:O6	2.37	0.57
13:M1:84:ARG:HH22	20:T1:102:ILE:HG21	1.69	0.57
18:R1:34:ASN:ND2	38:A2:2325:G:OP2	2.36	0.57
41:A3:84:A:H5"	66:Z3:122:LYS:HD2	1.87	0.57
43:C3:28:LYS:NZ	56:P3:51:GLU:OE1	2.34	0.57
50:J3:6:ASP:OD1	50:J3:9:HIS:ND1	2.37	0.57
60:T3:89:ASP:OD2	60:T3:106:LYS:NZ	2.37	0.57
5:E1:64:ARG:NH1	38:A2:2636:U:OP1	2.37	0.57
29:c1:10:ILE:HD13	38:A2:1554:A:H4'	1.87	0.57
32:f1:53:TRP:HA	32:f1:83:LYS:HE3	1.87	0.57
35:n1:59:ARG:NH1	35:n1:85:GLU:HB2	2.20	0.57
38:A2:4958:U:O3'	76:k3:343:ARG:NH2	2.37	0.57
38:A2:5046:G:O6	76:k3:124:LYS:NZ	2.36	0.57
41:A3:754:G:N1	41:A3:791:C:O2	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:A3:1350:U:O2	42:B3:110:ASN:ND2	2.37	0.57
51:K3:63:LEU:O	51:K3:70:ARG:NH1	2.37	0.57
38:A2:4968:G:H5"	76:k3:176:LYS:HG2	1.87	0.57
42:B3:123:VAL:HG22	42:B3:145:ILE:HB	1.87	0.57
77:l3:78:ARG:HB3	77:l3:88:GLY:HA2	1.86	0.57
81:p3:111:PRO:HD2	81:p3:114:ILE:HD12	1.86	0.57
82:q3:91:LYS:HG2	82:q3:145:VAL:HG22	1.87	0.57
16:P1:50:ASN:ND2	16:P1:75:SER:O	2.37	0.57
27:a1:11:ARG:HE	41:A3:1183:A:H5'	1.69	0.57
33:l1:58:THR:HG23	33:l1:153:SER:HB3	1.87	0.57
39:B2:119:U:H3'	78:m3:259:ARG:HH22	1.69	0.57
53:M3:65:ASN:O	53:M3:132:ARG:NH1	2.35	0.57
61:U3:96:SER:HB3	61:U3:99:VAL:HG12	1.86	0.57
62:V3:56:MET:HB2	62:V3:86:LYS:HG3	1.87	0.57
74:h3:36:ARG:HG3	74:h3:65:PHE:CG	2.39	0.57
77:l3:5:ARG:NH2	77:l3:261:ASP:OD2	2.38	0.57
29:c1:29:ILE:HG21	75:j3:177:LYS:HB2	1.87	0.57
38:A2:984:U:O2	38:A2:1271:G:N2	2.31	0.57
42:B3:80:ARG:NH2	42:B3:165:ASN:O	2.38	0.57
60:T3:86:ARG:NH2	60:T3:109:GLU:OE2	2.38	0.57
74:h3:129:ILE:H	74:h3:142:VAL:HG22	1.69	0.57
78:m3:168:ASP:O	78:m3:248:ARG:NH2	2.37	0.57
79:n3:209:VAL:HG22	79:n3:259:GLN:HG2	1.87	0.57
14:N1:77:LYS:NZ	38:A2:1352:A:O2'	2.37	0.56
41:A3:616:A:OP1	65:Y3:68:LYS:NZ	2.38	0.56
2:B1:198:THR:O	86:u3:100:ARG:NH1	2.36	0.56
8:H1:113:ARG:NH1	38:A2:2705:C:O3'	2.38	0.56
12:L1:83:GLU:OE1	12:L1:84:ARG:NH2	2.33	0.56
38:A2:74:G:O6	85:t3:103:ARG:NH2	2.37	0.56
38:A2:2560:G:H1	38:A2:2573:U:H3	1.53	0.56
53:M3:89:ARG:NH1	53:M3:91:ASP:OD2	2.38	0.56
76:k3:219:VAL:HG11	76:k3:337:VAL:HB	1.86	0.56
1:A1:192:TRP:NE1	38:A2:48:G:OP1	2.38	0.56
12:L1:50:ARG:NH2	40:C2:85:U:O4	2.29	0.56
18:R1:98:GLU:HG3	18:R1:123:THR:HB	1.87	0.56
25:Y1:51:LEU:HD22	38:A2:2410:G:H22	1.69	0.56
26:Z1:56:LEU:HB3	82:q3:95:VAL:HG22	1.86	0.56
38:A2:1548:G:O2'	38:A2:2815:A:N3	2.38	0.56
38:A2:2839:A:H1'	76:k3:228:TYR:CE2	2.41	0.56
38:A2:3941:G:O6	38:A2:4061:U:O4	2.23	0.56
38:A2:4405:U:OP1	38:A2:4407:C:N4	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:A3:1314:U:O2'	52:L3:8:ARG:NH2	2.38	0.56
43:C3:137:LEU:HG	43:C3:215:VAL:HG22	1.87	0.56
49:I3:117:PRO:HG2	49:I3:120:ARG:HD3	1.87	0.56
50:J3:11:ARG:NH1	50:J3:15:GLY:O	2.38	0.56
77:l3:326:LEU:O	80:o3:46:ARG:NH2	2.39	0.56
12:L1:102:SER:OG	12:L1:103:LYS:NZ	2.34	0.56
32:f1:133:LEU:HD11	32:f1:150:ASP:HB3	1.87	0.56
35:n1:28:ILE:HG23	35:n1:44:TYR:HD1	1.70	0.56
38:A2:2761:G:O2'	38:A2:2768:A:N3	2.31	0.56
44:D3:176:LYS:NZ	63:W3:7:GLU:OE1	2.38	0.56
84:s3:144:LYS:HE2	84:s3:147:ARG:H	1.70	0.56
35:n1:56:GLN:HE21	35:n1:88:MET:HE3	1.71	0.56
36:21:47:A:N6	36:21:49:A:O2'	2.39	0.56
38:A2:469:C:N3	79:n3:108:ARG:NH2	2.48	0.56
38:A2:2531:G:H4'	38:A2:2786:A:H4'	1.87	0.56
38:A2:4703:A:OP2	76:k3:30:LYS:NZ	2.36	0.56
38:A2:4863:U:O4	86:u3:116:LYS:NZ	2.38	0.56
83:r3:152:LEU:HD12	83:r3:165:ILE:HG23	1.88	0.56
7:G1:2:THR:N	38:A2:4206:A:OP2	2.39	0.56
11:K1:124:VAL:HG22	11:K1:138:VAL:HG12	1.87	0.56
25:Y1:2:SER:N	38:A2:2410:G:O6	2.39	0.56
28:b1:99:ARG:NH2	28:b1:100:LYS:O	2.38	0.56
38:A2:109:G:OP2	85:t3:74:ARG:NH2	2.39	0.56
38:A2:2839:A:H1'	76:k3:228:TYR:HE2	1.70	0.56
38:A2:4417:U:OP2	83:r3:3:ARG:NH2	2.39	0.56
41:A3:64:A:H2	41:A3:83:A:H62	1.53	0.56
76:k3:92:TYR:HB2	76:k3:159:VAL:HB	1.87	0.56
82:q3:26:ILE:HG13	82:q3:35:ARG:HG3	1.86	0.56
1:A1:73:ARG:NH1	38:A2:32:G:OP1	2.38	0.56
16:P1:11:LEU:HA	16:P1:14:ILE:HG22	1.87	0.56
41:A3:506:G:OP1	66:Z3:108:LYS:NZ	2.36	0.56
52:L3:31:LYS:HA	52:L3:41:PRO:HA	1.87	0.56
54:N3:51:VAL:HG22	54:N3:77:ILE:HB	1.86	0.56
62:V3:28:ASN:OD1	62:V3:31:SER:OG	2.24	0.56
38:A2:3891:C:O2'	76:k3:268:ARG:NH2	2.39	0.56
38:A2:4087:G:H1	38:A2:4108:G:H22	1.54	0.56
49:I3:60:ILE:HD11	49:I3:90:LYS:HE2	1.88	0.56
61:U3:28:LEU:HD23	61:U3:54:TYR:HD1	1.70	0.56
65:Y3:60:LYS:HG3	65:Y3:116:PRO:HD3	1.88	0.56
73:g3:133:ALA:N	73:g3:140:TYR:O	2.39	0.56
1:A1:189:ARG:NH1	38:A2:49:U:OP1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:B3:198:MET:HG2	42:B3:200:ASP:H	1.71	0.56
76:k3:134:CYS:SG	76:k3:135:LYS:NZ	2.78	0.56
77:l3:4:ALA:O	77:l3:29:LYS:NZ	2.37	0.56
6:F1:71:SER:O	6:F1:76:LYS:NZ	2.39	0.55
22:V1:56:ARG:HH12	22:V1:60:LEU:HG	1.69	0.55
26:Z1:85:ARG:NH1	38:A2:4685:U:OP2	2.39	0.55
38:A2:946:U:OP1	77:l3:342:ARG:NH2	2.39	0.55
41:A3:351:G:OP1	50:J3:7:ASN:ND2	2.37	0.55
43:C3:36:PRO:HB2	43:C3:38:MET:HE3	1.88	0.55
20:T1:66:ARG:NH1	38:A2:2520:A:O2'	2.39	0.55
23:W1:46:LYS:NZ	38:A2:24:G:N7	2.54	0.55
41:A3:163:U:OP2	48:H3:85:ARG:NH1	2.39	0.55
42:B3:38:ILE:HD12	42:B3:47:TYR:HB3	1.87	0.55
81:p3:314:LEU:HA	81:p3:317:LYS:HG2	1.88	0.55
42:B3:24:HIS:O	42:B3:48:ILE:HA	2.06	0.55
48:H3:186:GLN:HA	48:H3:189:ARG:HE	1.71	0.55
59:S3:90:ALA:O	59:S3:93:GLN:NE2	2.39	0.55
13:M1:111:ARG:NH1	38:A2:2580:C:OP1	2.39	0.55
42:B3:111:GLN:HG2	42:B3:112:ILE:HG23	1.88	0.55
41:A3:1521:C:H3'	60:T3:129:LEU:HD11	1.87	0.55
41:A3:959:G:OP1	56:P3:104:ARG:NH2	2.40	0.55
42:B3:52:LYS:HB2	59:S3:109:LEU:HD11	1.89	0.55
74:h3:289:LEU:HD13	74:h3:298:LEU:HD11	1.88	0.55
81:p3:218:GLU:HA	81:p3:221:VAL:HG12	1.88	0.55
54:N3:59:PRO:HA	54:N3:62:VAL:HG22	1.89	0.55
15:O1:25:ARG:HH22	38:A2:1844:G:H5"	1.71	0.55
35:n1:41:LYS:O	35:n1:45:GLU:HB2	2.07	0.55
68:b3:44:ILE:HD12	68:b3:65:PRO:HG2	1.88	0.55
76:k3:216:MET:HE3	76:k3:281:ASN:HB3	1.88	0.55
78:m3:52:ILE:HA	78:m3:147:ASP:HB3	1.89	0.55
83:r3:38:ARG:NH2	83:r3:45:GLU:OE1	2.39	0.55
6:F1:111:ARG:NH2	38:A2:2062:C:O2'	2.39	0.55
6:F1:127:MET:HG2	7:G1:153:PRO:HB2	1.88	0.55
14:N1:85:GLN:HA	14:N1:88:VAL:HG22	1.88	0.55
14:N1:125:LYS:HG2	14:N1:145:VAL:HB	1.89	0.55
38:A2:983:C:H42	38:A2:1272:A:H61	1.54	0.55
41:A3:1156:U:OP1	64:X3:71:LYS:NZ	2.39	0.55
85:t3:33:ILE:HG13	85:t3:37:LYS:HE2	1.87	0.55
6:F1:69:GLU:OE2	6:F1:102:THR:HG22	2.05	0.55
12:L1:89:LYS:HE3	12:L1:91:ASN:HD21	1.72	0.55
19:S1:40:GLU:O	19:S1:109:ARG:NH2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:A3:5:U:H2'	41:A3:6:G:H8	1.72	0.55
41:A3:143:U:OP2	48:H3:149:LYS:NZ	2.37	0.55
53:M3:101:ARG:HB2	65:Y3:10:ALA:HB2	1.89	0.55
54:N3:65:VAL:O	54:N3:69:CYS:HB3	2.07	0.55
82:q3:115:ARG:HG2	82:q3:123:ILE:HG12	1.88	0.55
1:A1:8:GLN:NE2	38:A2:279:A:OP2	2.37	0.54
7:G1:50:LYS:NZ	38:A2:4314:G:OP1	2.36	0.54
26:Z1:98:LYS:NZ	38:A2:4459:A:OP1	2.39	0.54
31:e1:98:ILE:HG13	31:e1:99:ARG:HD2	1.88	0.54
38:A2:4091:G:O6	38:A2:4104:U:O4	2.25	0.54
38:A2:4690:C:O2'	82:q3:129:ARG:NH2	2.40	0.54
46:F3:57:THR:HG22	46:F3:59:ASP:H	1.72	0.54
48:H3:132:ARG:HG3	48:H3:133:LEU:HD12	1.89	0.54
55:O3:119:GLU:HG2	55:O3:141:TYR:HE2	1.72	0.54
31:e1:60:MET:HE3	38:A2:1961:G:H5"	1.88	0.54
76:k3:329:ASP:OD1	76:k3:329:ASP:N	2.40	0.54
82:q3:59:LYS:HE3	82:q3:66:GLU:HB3	1.89	0.54
33:l1:129:ASN:OD1	33:l1:129:ASN:N	2.38	0.54
38:A2:4151:C:OP1	81:p3:298:LYS:NZ	2.39	0.54
43:C3:25:PHE:HA	43:C3:28:LYS:HG2	1.88	0.54
57:Q3:21:ASP:O	57:Q3:25:LEU:HB2	2.07	0.54
62:V3:32:LEU:HD21	62:V3:87:ARG:HG2	1.88	0.54
75:j3:207:VAL:HG13	75:j3:208:GLU:HG3	1.89	0.54
85:t3:207:VAL:HG12	85:t3:211:LYS:HD2	1.89	0.54
26:Z1:88:LYS:NZ	38:A2:4471:C:O2'	2.40	0.54
38:A2:2789:C:H5"	38:A2:2790:A:H5'	1.90	0.54
38:A2:3939:G:H1	38:A2:4063:U:H3	1.55	0.54
38:A2:4567:G:H5'	76:k3:28:LYS:HE2	1.90	0.54
41:A3:1142:G:OP2	44:D3:187:ARG:NH1	2.39	0.54
41:A3:1566:G:N7	61:U3:101:ARG:NH1	2.55	0.54
50:J3:34:ALA:HB2	50:J3:56:ARG:HD2	1.89	0.54
60:T3:34:LYS:HG2	60:T3:103:LEU:HD23	1.88	0.54
69:c3:23:ARG:NH1	69:c3:27:SER:O	2.41	0.54
73:g3:139:HIS:O	73:g3:147:THR:HA	2.07	0.54
78:m3:83:LEU:HB3	78:m3:88:VAL:HB	1.89	0.54
33:l1:171:HIS:HD2	33:l1:173:LYS:HB3	1.71	0.54
38:A2:3966:G:H21	38:A2:4044:A:H62	1.53	0.54
41:A3:146:G:OP1	48:H3:143:LYS:NZ	2.41	0.54
41:A3:955:A:N1	41:A3:968:U:O2'	2.39	0.54
44:D3:64:THR:HG21	44:D3:89:LYS:HB2	1.90	0.54
82:q3:28:LYS:NZ	82:q3:29:GLY:O	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M1:99:ASP:O	13:M1:102:ARG:NH1	2.38	0.54
35:n1:46:ALA:HA	35:n1:49:LYS:HG2	1.89	0.54
38:A2:4071:A:N1	38:A2:4157:C:N4	2.52	0.54
41:A3:532:C:H2'	41:A3:533:A:C8	2.43	0.54
49:I3:58:LYS:HB2	49:I3:90:LYS:HG2	1.89	0.54
38:A2:2090:U:OP2	77:l3:307:LYS:NZ	2.39	0.54
41:A3:1228:A:H2'	41:A3:1229:G:C8	2.43	0.54
48:H3:34:THR:O	48:H3:51:ARG:HA	2.08	0.54
61:U3:111:LYS:O	61:U3:126:GLN:NE2	2.41	0.54
2:B1:61:ARG:HA	2:B1:70:PRO:HD2	1.90	0.54
10:J1:80:ARG:HH22	41:A3:167:G:H4'	1.73	0.54
12:L1:33:PRO:HD3	38:A2:239:C:H5'	1.90	0.54
38:A2:4876:A:H5"	38:A2:4877:C:H2'	1.88	0.54
50:J3:159:SER:HB3	50:J3:162:LEU:HD23	1.89	0.54
41:A3:1550:G:OP2	45:E3:8:LYS:NZ	2.37	0.54
64:X3:44:HIS:NE2	64:X3:112:ASP:OD2	2.37	0.54
8:H1:101:ARG:NH2	38:A2:2705:C:OP1	2.41	0.54
15:O1:47:LYS:HA	15:O1:50:ASN:HD22	1.73	0.54
28:b1:44:LYS:HE3	28:b1:52:THR:HB	1.90	0.54
38:A2:4863:U:OP1	86:u3:121:ARG:NH2	2.41	0.54
74:h3:245:ARG:HH22	74:h3:314:ILE:HG13	1.73	0.54
41:A3:46:A:N7	41:A3:97:U:O2'	2.41	0.53
41:A3:453:C:O2'	48:H3:92:ARG:O	2.24	0.53
41:A3:583:A:OP1	51:K3:162:ARG:NH2	2.41	0.53
41:A3:1624:U:H3	57:Q3:40:ARG:HH22	1.54	0.53
43:C3:103:MET:HG2	43:C3:215:VAL:HB	1.91	0.53
60:T3:25:LYS:NZ	60:T3:53:THR:OG1	2.41	0.53
3:C1:64:ASN:O	3:C1:80:GLN:NE2	2.41	0.53
15:O1:65:MET:HE1	38:A2:1830:G:H5'	1.90	0.53
30:d1:96:MET:HE2	38:A2:679:C:H4'	1.90	0.53
35:n1:55:LEU:HG	35:n1:84:ILE:HG23	1.91	0.53
38:A2:978:G:H22	38:A2:1277:A:H2	1.56	0.53
38:A2:2008:U:H1'	38:A2:2011:C:H5	1.73	0.53
38:A2:2780:G:H5"	38:A2:2781:G:H5'	1.91	0.53
60:T3:73:ASN:ND2	60:T3:76:GLN:OE1	2.42	0.53
60:T3:115:LYS:HE3	60:T3:126:PHE:HB2	1.90	0.53
77:l3:296:PRO:HB3	77:l3:300:ARG:HH12	1.73	0.53
2:B1:125:LYS:HG2	2:B1:129:LEU:HD12	1.89	0.53
4:D1:65:ARG:NH1	38:A2:1459:A:OP1	2.41	0.53
11:K1:78:LYS:NZ	11:K1:133:GLU:OE1	2.40	0.53
38:A2:1362:U:OP2	85:t3:36:ARG:NH2	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:h3:31:ILE:HG12	74:h3:43:TRP:HB2	1.88	0.53
84:s3:35:ARG:HB3	84:s3:123:ILE:HG23	1.89	0.53
8:H1:23:LEU:HD23	8:H1:110:TYR:HB2	1.90	0.53
33:l1:48:ARG:NH2	33:l1:159:MET:O	2.37	0.53
41:A3:72:C:O2'	41:A3:74:G:OP2	2.25	0.53
41:A3:1868:U:O2'	68:b3:100:ARG:NH1	2.42	0.53
60:T3:121:ARG:HG3	60:T3:131:VAL:HB	1.90	0.53
19:S1:78:HIS:HB2	19:S1:85:ARG:HG3	1.90	0.53
38:A2:3659:G:H2'	38:A2:3660:G:H8	1.73	0.53
67:a3:58:LEU:HD12	67:a3:62:VAL:HG21	1.90	0.53
6:F1:67:VAL:HA	38:A2:730:G:H1	1.71	0.53
33:l1:49:PHE:HB2	33:l1:193:LEU:HG	1.91	0.53
38:A2:4334:A:O2'	38:A2:4336:C:OP2	2.26	0.53
41:A3:302:A:H1'	50:J3:73:THR:HG23	1.90	0.53
41:A3:1396:A:O2'	41:A3:1398:G:N7	2.42	0.53
38:A2:2072:C:O2'	80:o3:212:LEU:O	2.25	0.53
38:A2:2742:C:O2	75:j3:188:LYS:NZ	2.40	0.53
38:A2:4624:U:OP1	38:A2:5026:A:O2'	2.25	0.53
38:A2:4841:C:H2'	38:A2:4842:G:H8	1.73	0.53
41:A3:587:A:H5'	41:A3:592:C:H41	1.74	0.53
5:E1:2:SER:OG	5:E1:3:MET:N	2.41	0.53
13:M1:59:LYS:HD3	38:A2:4134:C:H5"	1.90	0.53
22:V1:99:LYS:HE2	33:l1:6:SER:HB3	1.91	0.53
38:A2:5029:C:O2'	38:A2:5032:C:OP2	2.19	0.53
41:A3:1616:U:O4	57:Q3:40:ARG:NH1	2.40	0.53
42:B3:37:TYR:OH	42:B3:57:LYS:NZ	2.41	0.53
51:K3:177:ASN:HA	51:K3:180:LYS:HE2	1.90	0.53
62:V3:33:GLU:HA	62:V3:36:CYS:HB3	1.91	0.53
70:d3:20:ARG:NH1	70:d3:28:THR:OG1	2.41	0.53
17:Q1:23:ARG:HG2	17:Q1:121:ASN:HA	1.90	0.53
18:R1:117:GLN:O	30:d1:119:ARG:NH1	2.42	0.53
31:e1:47:LEU:HD22	31:e1:50:LYS:HD2	1.91	0.53
35:n1:150:SER:OG	35:n1:154:ARG:NH1	2.42	0.53
59:S3:36:GLU:OE2	59:S3:47:ARG:NH1	2.42	0.53
74:h3:125:ARG:HD2	74:h3:150:TRP:CE3	2.44	0.53
79:n3:48:ARG:HB2	79:n3:64:MET:HE1	1.91	0.53
83:r3:30:LYS:HG3	83:r3:63:GLU:HG3	1.91	0.53
3:C1:16:LYS:O	3:C1:101:ASN:ND2	2.40	0.53
5:E1:44:LEU:HD22	5:E1:49:LEU:HD12	1.91	0.53
19:S1:25:THR:OG1	19:S1:87:LYS:NZ	2.42	0.53
20:T1:26:PRO:HD2	38:A2:2524:G:H4'	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A2:2838:A:O2'	76:k3:228:TYR:O	2.27	0.53
49:I3:34:SER:O	49:I3:37:LYS:NZ	2.42	0.53
77:l3:116:ASN:HB2	77:l3:119:GLN:HG3	1.90	0.53
80:o3:24:PHE:HA	80:o3:27:LEU:HD12	1.91	0.53
3:C1:25:HIS:ND1	38:A2:2364:G:O6	2.42	0.52
15:O1:18:ARG:NH1	38:A2:1686:C:O2'	2.41	0.52
26:Z1:72:LYS:HG3	26:Z1:92:THR:HG21	1.90	0.52
38:A2:1982:G:N2	38:A2:2009:A:O3'	2.42	0.52
41:A3:1562:C:H2'	41:A3:1563:G:H8	1.73	0.52
42:B3:89:LYS:HE3	42:B3:201:LEU:HD22	1.91	0.52
59:S3:99:ASP:HB2	59:S3:102:THR:HG23	1.90	0.52
82:q3:12:ILE:HD13	82:q3:18:ILE:HG21	1.92	0.52
38:A2:1197:G:H2'	38:A2:1198:G:H8	1.73	0.52
57:Q3:45:LEU:HD13	57:Q3:49:LEU:HD21	1.91	0.52
74:h3:109:LEU:HD11	74:h3:125:ARG:HD3	1.91	0.52
17:Q1:70:LYS:HG3	38:A2:2392:A:H4'	1.90	0.52
18:R1:100:ALA:O	18:R1:108:ARG:NH2	2.43	0.52
41:A3:314:U:O4	48:H3:190:ARG:NH2	2.37	0.52
42:B3:30:LEU:HD21	42:B3:35:GLU:HG3	1.91	0.52
47:G3:77:MET:HB3	47:G3:89:THR:HG21	1.91	0.52
47:G3:126:THR:OG1	70:d3:26:GLN:NE2	2.42	0.52
60:T3:25:LYS:HD3	60:T3:55:ARG:NE	2.23	0.52
76:k3:41:VAL:HA	76:k3:187:GLY:HA3	1.90	0.52
81:p3:139:VAL:HG12	81:p3:236:ILE:HG22	1.92	0.52
18:R1:5:ARG:NH1	38:A2:454:U:O2	2.31	0.52
38:A2:2498:U:H2'	38:A2:2499:G:H8	1.73	0.52
45:E3:16:ILE:HG21	71:e3:22:ARG:HH11	1.75	0.52
62:V3:43:ALA:HB1	62:V3:50:VAL:HG11	1.92	0.52
74:h3:191:HIS:ND1	74:h3:193:GLY:O	2.42	0.52
78:m3:50:ARG:O	78:m3:64:ILE:HA	2.09	0.52
78:m3:103:LEU:HD11	78:m3:248:ARG:HE	1.74	0.52
7:G1:129:LYS:HB3	38:A2:1837:A:H5'	1.91	0.52
12:L1:45:ARG:NH2	38:A2:238:C:OP2	2.42	0.52
13:M1:12:LEU:HB2	13:M1:81:MET:HB3	1.90	0.52
16:P1:38:ILE:HG21	16:P1:63:TYR:HB3	1.90	0.52
38:A2:1802:A:O2'	38:A2:1837:A:OP1	2.28	0.52
58:R3:19:ALA:HB2	58:R3:75:GLY:HA3	1.91	0.52
77:l3:239:LYS:O	77:l3:248:ARG:NH1	2.43	0.52
78:m3:62:CYS:HB3	78:m3:105:LEU:HD22	1.92	0.52
83:r3:14:ASN:O	83:r3:128:ARG:NH2	2.31	0.52
13:M1:5:MET:O	13:M1:28:ASN:ND2	2.36	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:A3:190:G:O2'	41:A3:209:A:N6	2.42	0.52
41:A3:419:G:H4'	64:X3:88:LYS:HD2	1.91	0.52
51:K3:121:LYS:H	51:K3:125:HIS:CD2	2.27	0.52
76:k3:206:PRO:HG2	76:k3:209:GLN:HG3	1.91	0.52
78:m3:289:ARG:HA	78:m3:292:GLU:HG3	1.89	0.52
36:21:54:U:H3	36:21:58:C:H5	1.58	0.52
38:A2:2000:G:OP2	38:A2:2000:G:N2	2.42	0.52
41:A3:355:G:OP1	53:M3:105:ARG:NH1	2.40	0.52
7:G1:100:LYS:NZ	38:A2:1731:C:OP1	2.37	0.52
38:A2:2523:C:H2'	38:A2:2524:G:H8	1.74	0.52
38:A2:4093:G:H1	38:A2:4102:G:H1	1.55	0.52
38:A2:4922:C:O2'	79:n3:249:ARG:NH2	2.43	0.52
41:A3:1275:G:N2	41:A3:1506:A:OP2	2.37	0.52
41:A3:1289:U:H5	73:g3:95:ARG:HH12	1.58	0.52
56:P3:96:LYS:HE3	56:P3:132:VAL:HG11	1.92	0.52
67:a3:57:LYS:O	67:a3:61:GLU:HG2	2.10	0.52
73:g3:140:TYR:HA	73:g3:146:LEU:O	2.10	0.52
28:b1:63:THR:O	28:b1:87:ARG:NH1	2.43	0.52
30:d1:35:ARG:HG2	30:d1:37:SER:HB3	1.92	0.52
38:A2:1186:C:H2'	38:A2:1187:G:H8	1.75	0.52
38:A2:1967:A:N6	38:A2:2020:U:O4	2.43	0.52
38:A2:3783:C:N4	38:A2:3807:C:OP2	2.40	0.52
41:A3:788:G:H2'	41:A3:789:G:H8	1.75	0.52
42:B3:66:VAL:HG21	42:B3:185:MET:HB2	1.91	0.52
75:j3:20:VAL:HA	75:j3:23:ARG:HG3	1.92	0.52
77:l3:110:ARG:O	77:l3:113:ARG:NH1	2.43	0.52
5:E1:105:LEU:HD23	5:E1:138:LEU:HD23	1.92	0.52
6:F1:39:VAL:HG22	80:o3:227:VAL:HA	1.92	0.52
27:a1:1:MET:HG3	41:A3:1706:G:H5'	1.91	0.52
38:A2:4973:U:H2'	38:A2:4974:G:H8	1.74	0.52
41:A3:522:A:OP2	51:K3:45:ARG:NH2	2.43	0.52
58:R3:44:PRO:HD3	58:R3:77:HIS:HB3	1.92	0.52
81:p3:130:PRO:HD2	81:p3:133:ILE:HD12	1.91	0.52
2:B1:163:LYS:NZ	38:A2:4891:A:OP1	2.43	0.51
20:T1:4:ARG:NH2	38:A2:2400:G:O6	2.41	0.51
56:P3:31:CYS:HA	56:P3:43:HIS:O	2.10	0.51
1:A1:14:LYS:HE2	38:A2:280:G:H5"	1.91	0.51
38:A2:2548:U:H3'	38:A2:2549:G:H4'	1.92	0.51
41:A3:1013:U:OP1	41:A3:1129:G:O2'	2.29	0.51
41:A3:1568:C:OP1	61:U3:96:SER:OG	2.28	0.51
43:C3:32:ASP:O	43:C3:95:ASN:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:E3:23:GLU:OE1	45:E3:27:ARG:NE	2.37	0.51
47:G3:71:ARG:NH2	47:G3:148:ASN:OD1	2.42	0.51
56:P3:117:ARG:NE	68:b3:52:ASP:OD2	2.41	0.51
78:m3:150:LEU:HD12	84:s3:146:ARG:HA	1.91	0.51
80:o3:170:ASP:H	80:o3:173:LEU:HD12	1.75	0.51
9:I1:111:GLU:HB2	9:I1:131:ARG:HH11	1.75	0.51
15:O1:46:ALA:O	15:O1:50:ASN:ND2	2.43	0.51
25:Y1:20:ASN:ND2	25:Y1:42:ARG:O	2.41	0.51
41:A3:1585:U:O2'	41:A3:1587:G:OP2	2.28	0.51
47:G3:35:LEU:HD12	47:G3:117:ILE:HG12	1.91	0.51
49:I3:62:ILE:HB	49:I3:94:PHE:HD1	1.76	0.51
64:X3:47:ILE:HG22	64:X3:65:LEU:HD13	1.92	0.51
81:p3:148:LEU:HD21	81:p3:209:VAL:HG21	1.93	0.51
16:P1:38:ILE:HD11	16:P1:46:VAL:HG21	1.93	0.51
31:e1:53:VAL:HG22	31:e1:89:VAL:HG22	1.92	0.51
41:A3:540:U:O2'	41:A3:543:C:N4	2.43	0.51
44:D3:69:LEU:HD13	44:D3:269:PHE:HD2	1.76	0.51
16:P1:17:ARG:HB3	16:P1:104:ILE:HB	1.93	0.51
27:a1:19:LYS:NZ	38:A2:3776:C:OP1	2.38	0.51
38:A2:2872:U:O2'	38:A2:2884:A:N7	2.33	0.51
41:A3:90:G:OP1	41:A3:445:A:N6	2.44	0.51
41:A3:681:U:O2'	41:A3:1160:U:OP1	2.28	0.51
48:H3:192:ILE:HG22	48:H3:196:LYS:HE3	1.93	0.51
52:L3:16:PHE:HD1	52:L3:91:PRO:HG3	1.75	0.51
5:E1:71:ARG:HH12	38:A2:3599:A:H3'	1.76	0.51
10:J1:80:ARG:NH2	48:H3:8:PRO:O	2.43	0.51
19:S1:69:VAL:HG21	38:A2:4926:C:H1'	1.93	0.51
38:A2:4170:G:H5'	75:j3:233:ARG:HB2	1.92	0.51
38:A2:4508:G:O2'	38:A2:4511:C:OP2	2.28	0.51
39:B2:75:G:N2	39:B2:100:A:OP2	2.37	0.51
41:A3:106:C:H2'	41:A3:107:A:H8	1.76	0.51
41:A3:490:C:O2'	41:A3:574:A:N1	2.39	0.51
76:k3:113:GLU:HB3	76:k3:178:ALA:HB2	1.92	0.51
35:n1:188:ARG:NH2	47:G3:182:LYS:O	2.42	0.51
38:A2:115:C:O2'	38:A2:276:C:OP1	2.28	0.51
41:A3:872:A:O2'	41:A3:874:G:OP2	2.28	0.51
48:H3:3:LEU:HD13	48:H3:109:LEU:HB3	1.93	0.51
51:K3:107:GLU:HA	51:K3:112:THR:HG21	1.91	0.51
74:h3:292:SER:OG	74:h3:294:ASP:OD1	2.27	0.51
18:R1:124:ASN:ND2	38:A2:2328:C:O2'	2.44	0.51
27:a1:11:ARG:NH2	41:A3:1184:G:OP1	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:n1:125:GLY:HA2	35:n1:128:LEU:HD12	1.91	0.51
48:H3:135:PRO:HG2	48:H3:144:LEU:HD22	1.93	0.51
51:K3:71:LEU:O	51:K3:75:ASN:HB2	2.11	0.51
74:h3:111:VAL:HA	74:h3:121:VAL:O	2.11	0.51
74:h3:155:ARG:HG2	74:h3:198:VAL:HG13	1.93	0.51
5:E1:136:ARG:O	5:E1:140:GLU:HG3	2.11	0.51
7:G1:108:ARG:NH2	38:A2:1802:A:O2'	2.43	0.51
11:K1:56:ARG:HH12	40:C2:136:U:H5'	1.75	0.51
19:S1:91:ASN:ND2	38:A2:439:G:O3'	2.44	0.51
29:c1:73:THR:HG22	29:c1:75:SER:H	1.76	0.51
36:21:9:G:O2'	36:21:45:G:N2	2.44	0.51
41:A3:1481:G:N2	45:E3:162:ASP:OD2	2.44	0.51
46:F3:80:ILE:HG13	46:F3:81:THR:HG23	1.92	0.51
52:L3:86:PRO:HB2	52:L3:88:GLU:HG2	1.93	0.51
74:h3:82:SER:OG	74:h3:83:TRP:N	2.44	0.51
76:k3:220:ILE:HG12	76:k3:278:THR:HG23	1.93	0.51
4:D1:68:ARG:HH12	38:A2:1501:C:H2'	1.76	0.51
6:F1:94:TYR:OH	6:F1:96:GLU:OE1	2.26	0.51
29:c1:69:TRP:NE1	75:j3:173:GLY:O	2.38	0.51
33:l1:104:ALA:HB1	33:l1:133:LYS:HE3	1.93	0.51
36:21:52:U:H2'	36:21:53:G:H8	1.76	0.51
46:F3:71:LYS:HG2	46:F3:76:VAL:HG22	1.93	0.51
47:G3:195:GLU:OE1	47:G3:198:ARG:NH1	2.44	0.51
61:U3:57:ALA:HB1	61:U3:107:LEU:HD11	1.92	0.51
74:h3:87:LEU:HD11	74:h3:122:SER:HB3	1.91	0.51
75:j3:116:LEU:HB3	75:j3:126:LEU:HB2	1.92	0.51
38:A2:1324:A:OP2	38:A2:4431:U:O2'	2.29	0.50
40:C2:47:C:H1'	40:C2:61:A:H2'	1.94	0.50
41:A3:924:G:H1	41:A3:1018:U:H3	1.58	0.50
44:D3:121:ARG:HH12	44:D3:123:ARG:HH11	1.59	0.50
56:P3:98:ARG:HB2	56:P3:132:VAL:HG23	1.93	0.50
66:Z3:55:ILE:HG23	66:Z3:75:ILE:HG22	1.93	0.50
74:h3:133:ASN:ND2	74:h3:137:VAL:O	2.44	0.50
75:j3:24:LYS:HG3	75:j3:49:ILE:HD12	1.92	0.50
78:m3:68:ARG:HH21	78:m3:73:MET:HE2	1.75	0.50
4:D1:40:ASN:ND2	38:A2:1450:C:OP1	2.44	0.50
29:c1:4:ARG:NH1	38:A2:1554:A:OP2	2.41	0.50
38:A2:27:C:O2'	38:A2:60:A:N3	2.38	0.50
38:A2:88:A:HO2'	38:A2:292:G:HO2'	1.56	0.50
44:D3:139:LEU:HD13	44:D3:213:LEU:HD21	1.92	0.50
63:W3:74:LYS:NZ	63:W3:80:SER:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:k3:77:THR:OG1	76:k3:335:GLY:O	2.26	0.50
77:l3:291:ARG:NH1	77:l3:291:ARG:O	2.45	0.50
77:l3:341:LEU:HD21	79:n3:58:ARG:HG3	1.93	0.50
11:K1:129:ARG:NH2	11:K1:131:ASP:OD2	2.44	0.50
28:b1:80:LYS:NZ	38:A2:4332:U:OP1	2.44	0.50
38:A2:1942:A:H2'	38:A2:1943:A:C8	2.47	0.50
38:A2:4713:A:OP1	76:k3:133:TYR:N	2.44	0.50
41:A3:986:G:OP2	41:A3:988:C:N4	2.45	0.50
56:P3:102:GLY:O	56:P3:106:LYS:NZ	2.42	0.50
3:C1:112:LEU:HD22	3:C1:150:LEU:HB3	1.93	0.50
12:L1:61:HIS:N	38:A2:232:G:O6	2.43	0.50
33:l1:130:LYS:NZ	38:A2:4039:G:O6	2.45	0.50
38:A2:1342:C:H2'	38:A2:1343:A:H8	1.76	0.50
38:A2:3754:A:HO2'	41:A3:1826:G:HO2'	1.59	0.50
42:B3:33:GLN:HB3	42:B3:154:LEU:HD12	1.92	0.50
49:I3:101:LEU:HB3	49:I3:116:ARG:HD2	1.93	0.50
74:h3:245:ARG:NH2	74:h3:296:GLN:HE22	2.09	0.50
82:q3:92:MET:HE2	82:q3:179:ILE:HG22	1.94	0.50
2:B1:82:ARG:NH1	38:A2:3882:C:OP1	2.37	0.50
6:F1:171:ARG:O	38:A2:4853:C:N4	2.44	0.50
10:J1:8:PHE:HB3	10:J1:36:CYS:HB3	1.92	0.50
38:A2:1484:G:O2'	38:A2:1486:C:OP2	2.30	0.50
38:A2:2303:A:H5"	77:l3:182:LYS:HE3	1.92	0.50
38:A2:2641:G:H22	38:A2:2700:A:H61	1.59	0.50
41:A3:520:A:O2'	41:A3:825:A:N3	2.41	0.50
51:K3:107:GLU:O	51:K3:113:GLN:NE2	2.45	0.50
64:X3:30:CYS:SG	64:X3:31:SER:N	2.83	0.50
76:k3:58:ARG:HA	76:k3:366:LYS:HG2	1.94	0.50
83:r3:61:SER:HA	83:r3:126:VAL:HG22	1.92	0.50
9:I1:96:LEU:HD13	10:J1:20:ARG:HB3	1.93	0.50
33:l1:126:PRO:HA	33:l1:129:ASN:OD1	2.11	0.50
35:n1:75:ARG:HA	35:n1:78:ILE:HG22	1.94	0.50
38:A2:1517:G:O6	77:l3:106:LYS:NZ	2.36	0.50
46:F3:35:PRO:HB2	46:F3:143:ASP:HB2	1.94	0.50
46:F3:139:LEU:O	46:F3:146:THR:HA	2.11	0.50
78:m3:211:LEU:HB3	78:m3:219:TYR:HB2	1.94	0.50
80:o3:58:LYS:HA	80:o3:61:ARG:HG2	1.94	0.50
2:B1:55:LEU:HD23	2:B1:58:LEU:HD12	1.94	0.50
10:J1:4:GLU:HG3	10:J1:20:ARG:NH2	2.26	0.50
26:Z1:74:TYR:O	38:A2:4458:G:O2'	2.30	0.50
38:A2:4344:U:H4'	85:t3:197:LYS:HD3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:A3:623:G:O6	65:Y3:63:ASN:ND2	2.45	0.50
41:A3:1652:G:H1	41:A3:1672:U:H3	1.60	0.50
49:I3:163:GLN:O	49:I3:167:GLU:CB	2.60	0.50
63:W3:53:TYR:OH	63:W3:76:ASP:OD2	2.29	0.50
77:l3:218:VAL:O	77:l3:222:ARG:HB3	2.12	0.50
5:E1:82:LYS:O	38:A2:2866:G:O2'	2.28	0.50
11:K1:135:LYS:NZ	38:A2:2439:U:OP2	2.38	0.50
19:S1:110:ILE:O	79:n3:146:SER:OG	2.27	0.50
38:A2:383:A:N6	38:A2:405:U:O3'	2.44	0.50
38:A2:1371:A:OP1	77:l3:47:ASN:ND2	2.39	0.50
38:A2:1536:U:H2'	38:A2:1537:A:H8	1.76	0.50
38:A2:3655:C:H2'	38:A2:3677:A:H61	1.75	0.50
38:A2:4865:C:N4	79:n3:184:LEU:O	2.37	0.50
44:D3:201:GLY:N	44:D3:221:ASP:OD2	2.45	0.50
56:P3:103:ASN:HB2	56:P3:142:ARG:HG3	1.93	0.50
60:T3:51:ASP:OD1	60:T3:53:THR:HG22	2.11	0.50
75:j3:116:LEU:HD12	75:j3:164:ALA:HB2	1.94	0.50
79:n3:156:LEU:HD11	79:n3:198:ILE:HG13	1.93	0.50
4:D1:2:GLY:N	38:A2:2072:C:OP1	2.45	0.50
29:c1:26:VAL:HG21	75:j3:180:LEU:HD21	1.94	0.50
38:A2:1538:U:H2'	38:A2:1539:G:H8	1.76	0.50
38:A2:2727:G:O2'	38:A2:2729:G:OP2	2.27	0.50
38:A2:3955:A:N6	38:A2:3960:A:N7	2.60	0.50
41:A3:919:A:OP2	55:O3:64:ARG:NH2	2.34	0.50
61:U3:28:LEU:HD23	61:U3:54:TYR:CD1	2.47	0.50
61:U3:104:LEU:HD13	61:U3:121:ARG:HG3	1.93	0.50
64:X3:6:VAL:HG12	64:X3:34:ILE:HD11	1.94	0.50
32:f1:28:LEU:HG	32:f1:42:VAL:HB	1.93	0.49
38:A2:67:C:OP2	38:A2:312:G:N2	2.45	0.49
38:A2:74:G:H5'	85:t3:59:VAL:HB	1.92	0.49
38:A2:505:G:H2'	38:A2:506:G:H8	1.76	0.49
38:A2:4949:A:H2'	38:A2:4950:A:H8	1.76	0.49
41:A3:1546:G:N2	41:A3:1670:C:O2	2.41	0.49
42:B3:128:ARG:NH1	42:B3:151:ASP:O	2.45	0.49
46:F3:198:ARG:HG2	46:F3:208:VAL:HG22	1.94	0.49
74:h3:8:ARG:HB3	74:h3:309:VAL:HG23	1.93	0.49
74:h3:248:LEU:O	74:h3:258:ILE:HA	2.12	0.49
4:D1:72:LEU:HB2	4:D1:75:ARG:HD2	1.93	0.49
15:O1:50:ASN:OD1	38:A2:1826:G:N2	2.37	0.49
32:f1:114:ARG:HD2	32:f1:125:LEU:HD11	1.94	0.49
38:A2:731:G:OP2	80:o3:75:ARG:NE	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A2:4894:G:N2	76:k3:156:TYR:OH	2.46	0.49
41:A3:1232:U:H2'	41:A3:1233:G:C8	2.47	0.49
45:E3:203:PRO:HG2	59:S3:42:PRO:HB3	1.94	0.49
62:V3:40:ILE:HD11	62:V3:89:ILE:HD12	1.94	0.49
19:S1:7:CYS:HB2	19:S1:103:VAL:HB	1.94	0.49
52:L3:52:LEU:O	52:L3:57:TYR:N	2.43	0.49
74:h3:8:ARG:O	74:h3:8:ARG:NH1	2.37	0.49
3:C1:62:ARG:NH1	38:A2:423:G:OP1	2.45	0.49
5:E1:28:GLU:HG3	5:E1:49:LEU:HD22	1.93	0.49
6:F1:95:ARG:NH2	38:A2:1951:G:O2'	2.41	0.49
18:R1:37:LYS:HD3	18:R1:38:PRO:HD2	1.95	0.49
41:A3:1417:C:N3	41:A3:1423:C:N4	2.61	0.49
46:F3:252:ARG:HH21	46:F3:253:ASP:HB2	1.77	0.49
58:R3:35:ASN:O	61:U3:7:LYS:NZ	2.38	0.49
75:j3:45:VAL:HG22	75:j3:61:VAL:HG22	1.94	0.49
84:s3:111:GLU:HG3	84:s3:125:ILE:HG23	1.93	0.49
16:P1:29:LEU:HD22	16:P1:91:VAL:HG21	1.94	0.49
16:P1:48:LEU:HD21	16:P1:60:ILE:HG13	1.95	0.49
38:A2:985:C:OP1	79:n3:75:TYR:OH	2.27	0.49
38:A2:1769:G:H2'	38:A2:1770:A:H8	1.77	0.49
39:B2:17:C:OP1	84:s3:156:ARG:NH2	2.45	0.49
39:B2:49:A:H5"	78:m3:224:SER:HB3	1.94	0.49
41:A3:385:G:O2'	50:J3:10:LYS:NZ	2.42	0.49
41:A3:1060:A:O2'	41:A3:1062:A:N7	2.44	0.49
41:A3:1126:G:OP1	42:B3:41:ARG:NH1	2.43	0.49
51:K3:121:LYS:H	51:K3:125:HIS:HD2	1.61	0.49
66:Z3:114:MET:HE3	66:Z3:122:LYS:HB3	1.94	0.49
86:u3:100:ARG:HA	86:u3:103:LYS:HG2	1.95	0.49
3:C1:34:GLN:NE2	38:A2:424:U:OP1	2.46	0.49
10:J1:8:PHE:HZ	10:J1:49:ILE:HD12	1.77	0.49
13:M1:50:PRO:HD3	13:M1:68:ILE:HG12	1.95	0.49
18:R1:19:LYS:NZ	38:A2:2321:G:O6	2.45	0.49
38:A2:1759:G:H1	38:A2:1773:U:H3	1.61	0.49
38:A2:2523:C:H1'	38:A2:2643:G:H21	1.76	0.49
41:A3:635:G:OP1	72:f3:94:LYS:NZ	2.46	0.49
63:W3:21:ASN:HB2	64:X3:67:GLY:HA3	1.94	0.49
78:m3:164:LYS:HD3	78:m3:195:HIS:HE1	1.78	0.49
8:H1:38:ASN:OD1	8:H1:90:TYR:OH	2.31	0.49
32:f1:81:ILE:HD12	32:f1:136:ALA:HA	1.94	0.49
38:A2:3740:U:HO2'	75:j3:243:THR:H	1.60	0.49
61:U3:9:VAL:HG21	61:U3:138:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:h3:18:VAL:HA	74:h3:35:SER:HA	1.94	0.49
6:F1:74:ARG:O	6:F1:76:LYS:NZ	2.42	0.49
7:G1:116:LYS:NZ	38:A2:1836:G:O6	2.46	0.49
9:I1:30:ASP:OD1	9:I1:30:ASP:N	2.44	0.49
9:I1:60:MET:HG3	9:I1:80:VAL:HG22	1.95	0.49
38:A2:1503:A:H4'	38:A2:1504:G:H5'	1.94	0.49
38:A2:4877:C:O2	86:u3:132:ARG:NH1	2.36	0.49
46:F3:117:GLU:HA	46:F3:120:LYS:HE2	1.95	0.49
67:a3:79:ILE:HB	67:a3:83:LEU:HD23	1.95	0.49
76:k3:57:VAL:HG22	76:k3:73:VAL:HG22	1.95	0.49
83:r3:87:ILE:HG12	83:r3:138:ILE:HG12	1.95	0.49
4:D1:150:ARG:NH2	38:A2:1499:C:OP1	2.46	0.49
35:n1:54:LYS:HA	35:n1:57:ARG:HH21	1.77	0.49
38:A2:710:C:H1'	38:A2:4924:C:H5	1.77	0.49
38:A2:979:C:O2'	77:l3:333:LYS:NZ	2.41	0.49
41:A3:56:G:OP1	66:Z3:111:LYS:NZ	2.40	0.49
41:A3:1705:C:H2'	41:A3:1706:G:C8	2.48	0.49
52:L3:85:LEU:HB3	52:L3:89:ILE:HB	1.94	0.49
68:b3:11:ALA:HB3	68:b3:33:ASP:HB2	1.94	0.49
68:b3:12:LYS:HG3	68:b3:15:ARG:HB2	1.94	0.49
76:k3:35:ASP:OD2	76:k3:193:LYS:NZ	2.44	0.49
4:D1:13:VAL:HG12	38:A2:1691:G:H8	1.77	0.49
38:A2:453:G:O2'	38:A2:706:G:OP1	2.29	0.49
38:A2:1432:G:O2'	38:A2:1451:G:N2	2.37	0.49
38:A2:1563:A:N6	41:A3:1028:A:N1	2.61	0.49
41:A3:356:C:OP1	53:M3:105:ARG:NH2	2.44	0.49
41:A3:860:G:N2	64:X3:107:SER:OG	2.43	0.49
41:A3:1404:U:OP1	62:V3:21:ARG:NH2	2.33	0.49
53:M3:74:SER:HA	53:M3:126:VAL:O	2.13	0.49
74:h3:173:LEU:HD13	74:h3:175:LYS:HE3	1.95	0.49
77:l3:154:VAL:HG21	77:l3:170:LEU:HD11	1.94	0.49
80:o3:135:VAL:HG23	80:o3:139:ILE:HD13	1.95	0.49
4:D1:12:LYS:NZ	38:A2:2083:C:OP1	2.44	0.48
9:I1:42:VAL:HB	9:I1:45:ILE:HD12	1.94	0.48
35:n1:159:ASP:HB3	35:n1:162:LYS:HB2	1.95	0.48
38:A2:1394:G:O2'	38:A2:1468:C:O2'	2.25	0.48
38:A2:1558:A:H2'	38:A2:1559:G:H8	1.77	0.48
38:A2:4194:U:OP1	38:A2:4320:U:O2'	2.28	0.48
38:A2:4747:G:H2'	38:A2:4748:A:H8	1.77	0.48
41:A3:792:C:H2'	41:A3:793:G:C8	2.48	0.48
41:A3:1244:U:H2'	41:A3:1245:G:H8	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:E3:55:THR:HA	45:E3:58:VAL:HG12	1.94	0.48
50:J3:43:ILE:HG12	50:J3:57:ALA:HA	1.95	0.48
51:K3:47:LYS:HG3	51:K3:102:ILE:HD12	1.95	0.48
4:D1:175:GLU:O	38:A2:1497:A:N6	2.45	0.48
7:G1:87:LYS:NZ	38:A2:4287:U:OP2	2.46	0.48
33:l1:180:VAL:HA	33:l1:183:ILE:HG22	1.94	0.48
38:A2:957:A:O2'	38:A2:2077:C:OP1	2.24	0.48
38:A2:2298:C:H2'	38:A2:2299:G:H8	1.78	0.48
41:A3:63:U:O2'	41:A3:170:A:N3	2.41	0.48
41:A3:1086:G:OP2	68:b3:12:LYS:NZ	2.42	0.48
59:S3:77:GLU:OE1	59:S3:81:ARG:NH1	2.29	0.48
84:s3:163:MET:HE3	84:s3:174:ILE:HG21	1.94	0.48
4:D1:184:ARG:NH2	14:N1:55:LYS:O	2.46	0.48
5:E1:60:ARG:NH2	38:A2:2812:G:OP1	2.45	0.48
14:N1:47:LYS:NZ	38:A2:1684:A:OP1	2.45	0.48
22:V1:67:LYS:NZ	38:A2:3720:G:N7	2.47	0.48
38:A2:2489:G:H2'	38:A2:2490:G:C8	2.48	0.48
67:a3:68:ILE:HB	67:a3:109:TYR:HB2	1.94	0.48
76:k3:57:VAL:HA	76:k3:72:VAL:O	2.13	0.48
14:N1:93:ASN:C	14:N1:93:ASN:HD22	2.21	0.48
36:21:28:U:H2'	36:21:29:G:H8	1.78	0.48
38:A2:1980:U:O2'	38:A2:1982:G:O6	2.28	0.48
38:A2:2414:C:H2'	38:A2:2415:A:C8	2.49	0.48
64:X3:60:LYS:NZ	69:c3:23:ARG:O	2.46	0.48
78:m3:50:ARG:NH2	78:m3:72:ASP:OD1	2.47	0.48
10:J1:32:LEU:HD21	76:k3:378:ARG:HD3	1.95	0.48
30:d1:108:MET:HA	30:d1:111:ILE:HB	1.94	0.48
41:A3:846:G:OP2	46:F3:108:ARG:NH2	2.39	0.48
46:F3:246:LEU:HD23	46:F3:250:GLU:HB3	1.95	0.48
49:I3:147:LYS:HE3	49:I3:153:LEU:HD11	1.95	0.48
62:V3:24:LEU:O	62:V3:86:LYS:HA	2.14	0.48
74:h3:124:SER:OG	74:h3:126:ASP:OD1	2.29	0.48
81:p3:139:VAL:HG11	81:p3:238:LYS:HG3	1.93	0.48
8:H1:61:VAL:HG22	8:H1:74:SER:HB2	1.95	0.48
14:N1:77:LYS:HE2	38:A2:1502:G:H1	1.78	0.48
23:W1:59:THR:HG23	40:C2:41:A:H4'	1.96	0.48
38:A2:347:A:O2'	77:l3:50:GLN:NE2	2.40	0.48
38:A2:382:G:N1	38:A2:385:A:OP2	2.42	0.48
38:A2:3646:A:OP2	75:j3:200:ARG:NH2	2.45	0.48
38:A2:4059:G:H3'	38:A2:4060:U:C6	2.48	0.48
41:A3:377:G:H5'	50:J3:98:LYS:HD3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:d3:13:ARG:HG2	70:d3:55:VAL:HG22	1.94	0.48
77:l3:170:LEU:HD23	77:l3:221:PHE:HZ	1.78	0.48
21:U1:79:LYS:HE3	21:U1:84:ARG:HA	1.94	0.48
31:e1:24:TYR:CE1	31:e1:92:LYS:HB2	2.49	0.48
42:B3:8:LEU:HD11	63:W3:39:VAL:HG21	1.95	0.48
43:C3:28:LYS:HG3	43:C3:48:LEU:HD12	1.96	0.48
62:V3:64:THR:HA	62:V3:78:ASP:O	2.14	0.48
74:h3:148:SER:N	74:h3:171:ASP:OD2	2.43	0.48
76:k3:46:PHE:CE1	76:k3:84:MET:HG3	2.48	0.48
6:F1:95:ARG:HD2	6:F1:113:MET:HE1	1.95	0.48
70:d3:17:VAL:HG12	70:d3:30:VAL:HG12	1.96	0.48
74:h3:84:ASP:OD1	74:h3:84:ASP:N	2.45	0.48
76:k3:77:THR:HG21	76:k3:337:VAL:HG22	1.94	0.48
1:A1:18:VAL:HA	81:p3:130:PRO:HG2	1.95	0.48
6:F1:85:ASP:OD1	6:F1:90:THR:OG1	2.23	0.48
22:V1:12:ASN:OD1	22:V1:16:LYS:NZ	2.38	0.48
38:A2:1741:G:O2'	78:m3:10:LYS:NZ	2.46	0.48
38:A2:2338:C:H2'	38:A2:2339:G:H8	1.79	0.48
38:A2:2523:C:H2'	38:A2:2524:G:C8	2.49	0.48
38:A2:4091:G:H1	38:A2:4104:U:H3	1.60	0.48
41:A3:562:U:H2'	41:A3:563:G:C8	2.48	0.48
65:Y3:95:GLU:HG2	65:Y3:98:ASP:HB2	1.94	0.48
79:n3:200:THR:HG22	79:n3:291:PHE:HB2	1.94	0.48
79:n3:286:PRO:HA	79:n3:289:LEU:HG	1.95	0.48
7:G1:87:LYS:HZ3	38:A2:4291:G:H22	1.60	0.48
12:L1:15:ARG:NH1	38:A2:230:G:OP1	2.42	0.48
33:l1:8:ASP:N	33:l1:8:ASP:OD1	2.47	0.48
38:A2:1074:C:O2	38:A2:1233:G:N2	2.47	0.48
38:A2:1494:U:H2'	38:A2:1495:G:H8	1.78	0.48
38:A2:1743:A:H5'	78:m3:11:ALA:HB1	1.96	0.48
41:A3:677:G:OP1	55:O3:124:ARG:NH1	2.46	0.48
41:A3:1228:A:H2'	41:A3:1229:G:H8	1.77	0.48
44:D3:259:THR:HG23	63:W3:16:LYS:HE2	1.94	0.48
49:I3:47:ALA:HB3	49:I3:63:PHE:HB2	1.96	0.48
1:A1:26:ARG:HB3	1:A1:30:TYR:CZ	2.49	0.47
4:D1:92:VAL:O	4:D1:112:ARG:NH2	2.47	0.47
4:D1:178:ARG:H	14:N1:51:GLY:HA2	1.79	0.47
14:N1:44:ASN:ND2	85:t3:4:SER:O	2.46	0.47
18:R1:35:TRP:O	18:R1:36:ARG:NH1	2.45	0.47
32:f1:11:LYS:HB2	32:f1:64:ILE:HB	1.94	0.47
36:21:47:A:N6	36:21:49:A:HO2'	2.12	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A2:1726:U:OP1	80:o3:103:LYS:NZ	2.39	0.47
38:A2:3712:A:H2'	38:A2:3713:A:C8	2.49	0.47
41:A3:398:A:H5"	41:A3:400:C:H5'	1.96	0.47
41:A3:1451:G:H5'	74:h3:64:HIS:HE1	1.79	0.47
41:A3:1521:C:H5'	57:Q3:126:VAL:HB	1.95	0.47
45:E3:76:ARG:HB2	52:L3:22:VAL:HG11	1.96	0.47
48:H3:181:THR:H	48:H3:184:VAL:HG12	1.79	0.47
53:M3:125:ILE:HB	53:M3:146:THR:HB	1.96	0.47
80:o3:237:ASP:O	80:o3:240:ASN:ND2	2.46	0.47
7:G1:78:LYS:NZ	38:A2:4287:U:OP1	2.43	0.47
25:Y1:13:LEU:HD22	38:A2:2410:G:H2'	1.95	0.47
38:A2:3692:U:H5"	38:A2:3693:G:H5'	1.95	0.47
38:A2:4504:A:OP2	76:k3:258:HIS:HD2	1.97	0.47
41:A3:383:G:O2'	53:M3:133:PRO:O	2.26	0.47
41:A3:1014:G:N2	69:c3:51:GLN:OE1	2.47	0.47
81:p3:276:ARG:HG3	81:p3:280:ASN:HB2	1.95	0.47
83:r3:54:SER:HB2	83:r3:135:ILE:HD11	1.96	0.47
84:s3:96:LYS:HG3	84:s3:163:MET:HE1	1.96	0.47
1:A1:145:ASN:HB3	1:A1:148:THR:HG22	1.97	0.47
5:E1:95:TRP:CE2	38:A2:1572:U:H4'	2.49	0.47
13:M1:135:ARG:NH1	38:A2:4115:G:H22	2.11	0.47
38:A2:422:C:H2'	38:A2:423:G:H8	1.79	0.47
38:A2:4746:G:N1	38:A2:4753:C:OP1	2.32	0.47
38:A2:4949:A:H2'	38:A2:4950:A:C8	2.49	0.47
41:A3:94:G:HO2'	41:A3:508:A:HO2'	1.52	0.47
44:D3:200:ARG:O	51:K3:54:ARG:NH1	2.35	0.47
45:E3:123:LEU:HD11	45:E3:152:PHE:HB3	1.97	0.47
50:J3:79:ILE:HD11	50:J3:105:ASP:HB3	1.96	0.47
52:L3:49:MET:HE3	52:L3:49:MET:HB3	1.75	0.47
83:r3:190:LEU:HD13	83:r3:197:VAL:HG21	1.95	0.47
3:C1:30:ARG:HD2	3:C1:63:TYR:HE2	1.79	0.47
3:C1:120:ASN:ND2	40:C2:12:G:H21	2.12	0.47
11:K1:41:ARG:HG3	81:p3:105:THR:HG22	1.96	0.47
16:P1:31:TYR:OH	16:P1:59:GLU:OE1	2.30	0.47
38:A2:3615:G:OP1	38:A2:3617:C:N4	2.47	0.47
41:A3:981:A:H2'	41:A3:982:G:C8	2.50	0.47
4:D1:2:GLY:N	38:A2:1898:C:OP1	2.47	0.47
10:J1:97:LYS:HB2	10:J1:100:VAL:HG23	1.97	0.47
14:N1:112:LEU:HD23	14:N1:130:SER:HB2	1.96	0.47
15:O1:5:LYS:HE2	15:O1:8:THR:HB	1.96	0.47
31:e1:59:THR:HG23	31:e1:60:MET:HE2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:n1:197:VAL:HG12	35:n1:201:ARG:HE	1.79	0.47
36:21:9:G:O2'	36:21:10:G:N7	2.45	0.47
38:A2:1494:U:H2'	38:A2:1495:G:C8	2.50	0.47
38:A2:2748:A:H2'	38:A2:2749:A:C8	2.50	0.47
41:A3:816:A:OP1	51:K3:10:ARG:NH1	2.48	0.47
41:A3:953:C:OP1	43:C3:28:LYS:NZ	2.43	0.47
41:A3:1226:G:N1	41:A3:1639:G:OP2	2.36	0.47
74:h3:17:TRP:CE3	74:h3:36:ARG:HD2	2.49	0.47
79:n3:50:PRO:HG2	79:n3:58:ARG:HE	1.78	0.47
80:o3:189:LEU:HD21	80:o3:207:LEU:HD11	1.96	0.47
85:t3:36:ARG:O	85:t3:40:GLN:HG3	2.15	0.47
38:A2:1794:A:H5"	38:A2:4200:A:H61	1.79	0.47
41:A3:155:G:H2'	41:A3:156:G:H8	1.79	0.47
42:B3:90:PHE:HE1	42:B3:178:LEU:HB3	1.80	0.47
48:H3:232:ARG:O	48:H3:236:SER:OG	2.28	0.47
49:I3:51:ILE:HD11	49:I3:176:VAL:HG22	1.96	0.47
54:N3:35:ILE:HA	54:N3:38:ALA:HB3	1.95	0.47
74:h3:3:GLU:HB2	74:h3:313:THR:HB	1.96	0.47
10:J1:93:LYS:HA	10:J1:96:GLN:HB2	1.97	0.47
13:M1:104:PRO:HA	13:M1:107:LYS:HG2	1.97	0.47
18:R1:75:ARG:HB2	18:R1:95:TYR:CD1	2.50	0.47
21:U1:8:ASP:O	21:U1:12:LYS:NZ	2.44	0.47
28:b1:39:ARG:NH1	38:A2:295:A:OP2	2.44	0.47
36:21:23:G:H2'	36:21:24:G:C8	2.49	0.47
38:A2:1342:C:H2'	38:A2:1343:A:C8	2.50	0.47
38:A2:2451:G:O2'	75:j3:21:LYS:NZ	2.44	0.47
38:A2:3712:A:N3	38:A2:4164:A:O2'	2.44	0.47
38:A2:4260:A:H2'	38:A2:4261:G:C8	2.50	0.47
38:A2:4504:A:O5'	38:A2:4506:G:H4'	2.14	0.47
40:C2:102:G:OP2	40:C2:104:A:O2'	2.28	0.47
41:A3:57:U:O2'	41:A3:499:G:N3	2.45	0.47
41:A3:65:C:C5	48:H3:133:LEU:HD23	2.48	0.47
41:A3:1097:G:H4'	42:B3:32:PHE:CD1	2.49	0.47
42:B3:77:ILE:HG22	42:B3:99:ILE:HB	1.96	0.47
44:D3:85:SER:OG	63:W3:25:GLY:O	2.32	0.47
50:J3:65:PHE:O	50:J3:73:THR:HA	2.15	0.47
51:K3:53:ILE:HG23	51:K3:77:LEU:HD11	1.96	0.47
54:N3:41:ALA:HA	54:N3:44:LYS:HE2	1.97	0.47
57:Q3:81:ARG:NH2	57:Q3:117:GLY:O	2.48	0.47
74:h3:19:THR:N	74:h3:34:ALA:O	2.34	0.47
76:k3:298:LEU:HD22	76:k3:300:LYS:HD2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:m3:196:ARG:NH1	78:m3:237:GLU:OE2	2.47	0.47
83:r3:91:LEU:HD13	83:r3:135:ILE:HA	1.96	0.47
19:S1:54:LYS:NZ	38:A2:4734:U:OP1	2.35	0.47
32:f1:82:ILE:HD11	38:A2:1977:C:H4'	1.96	0.47
38:A2:86:U:H2'	38:A2:87:A:H8	1.79	0.47
38:A2:163:A:H2'	38:A2:164:G:H8	1.80	0.47
38:A2:4844:G:H2'	38:A2:4845:G:H8	1.80	0.47
41:A3:10:G:H21	44:D3:114:LYS:HA	1.80	0.47
41:A3:150:A:N6	41:A3:169:U:O2	2.47	0.47
41:A3:1253:A:N6	41:A3:1665:G:O2'	2.47	0.47
43:C3:48:LEU:HG	56:P3:51:GLU:HG2	1.96	0.47
48:H3:138:ALA:HA	48:H3:141:ILE:HD12	1.96	0.47
49:I3:88:SER:OG	49:I3:89:GLY:N	2.47	0.47
1:A1:114:ARG:NH1	1:A1:151:ILE:O	2.48	0.47
4:D1:93:GLN:HE21	14:N1:118:PRO:HD3	1.80	0.47
38:A2:4078:G:O6	75:j3:70:LYS:NZ	2.39	0.47
41:A3:5:U:H2'	41:A3:6:G:C8	2.49	0.47
41:A3:1394:G:H21	41:A3:1475:G:H1'	1.80	0.47
46:F3:45:ILE:HA	46:F3:61:VAL:HG11	1.97	0.47
76:k3:113:GLU:OE2	76:k3:169:ARG:N	2.46	0.47
9:I1:43:LYS:HG3	9:I1:60:MET:HE2	1.97	0.47
17:Q1:62:VAL:HG22	17:Q1:104:THR:HB	1.97	0.47
20:T1:49:CYS:HA	29:c1:61:MET:HE3	1.97	0.47
35:n1:222:ASN:HB3	35:n1:225:LEU:HG	1.98	0.47
38:A2:1351:G:O2'	38:A2:1353:G:O2'	2.30	0.47
38:A2:2520:A:N3	38:A2:2542:C:O2'	2.48	0.47
38:A2:3956:G:N2	38:A2:3958:A:N7	2.63	0.47
41:A3:1256:G:N2	71:e3:30:LEU:O	2.41	0.47
41:A3:1528:G:O2'	41:A3:1666:C:OP1	2.29	0.47
54:N3:54:SER:H	54:N3:80:ASP:HA	1.78	0.47
60:T3:40:TYR:HA	60:T3:43:VAL:HG12	1.97	0.47
6:F1:77:ASN:OD1	6:F1:98:ARG:NH1	2.47	0.46
28:b1:96:ASP:N	28:b1:96:ASP:OD1	2.47	0.46
38:A2:1193:G:H2'	38:A2:1194:G:C8	2.50	0.46
38:A2:1556:C:O2'	38:A2:2672:C:OP1	2.30	0.46
38:A2:1857:C:H2'	38:A2:1858:A:H8	1.79	0.46
38:A2:4553:G:OP1	76:k3:19:ARG:N	2.45	0.46
44:D3:70:VAL:HG21	44:D3:93:ILE:HG23	1.97	0.46
46:F3:112:HIS:NE2	46:F3:237:SER:O	2.46	0.46
46:F3:141:THR:OG1	46:F3:142:HIS:N	2.48	0.46
60:T3:24:ARG:HB2	60:T3:29:ALA:HB2	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:T3:36:VAL:HG13	60:T3:40:TYR:HD2	1.80	0.46
74:h3:78:ALA:HB3	74:h3:90:TRP:HB2	1.97	0.46
22:V1:66:ASP:N	22:V1:66:ASP:OD1	2.47	0.46
38:A2:3760:G:O2'	38:A2:3762:C:N4	2.49	0.46
38:A2:4973:U:H2'	38:A2:4974:G:C8	2.50	0.46
41:A3:4:C:H4'	44:D3:207:ALA:HB2	1.97	0.46
41:A3:532:C:H2'	41:A3:533:A:H8	1.79	0.46
41:A3:880:G:H2'	41:A3:881:G:H8	1.81	0.46
76:k3:165:HIS:HA	76:k3:179:HIS:O	2.16	0.46
4:D1:175:GLU:OE2	14:N1:50:PRO:HD2	2.15	0.46
24:X1:17:ARG:NH2	38:A2:2775:C:O2'	2.48	0.46
33:l1:26:ARG:HB3	33:l1:30:GLU:HG3	1.98	0.46
38:A2:3934:G:H1'	38:A2:4070:G:H22	1.80	0.46
41:A3:792:C:H2'	41:A3:793:G:H8	1.79	0.46
44:D3:130:ILE:HG23	44:D3:162:ILE:HD11	1.97	0.46
56:P3:75:MET:HG3	56:P3:118:ALA:HB2	1.97	0.46
57:Q3:31:GLU:HA	57:Q3:34:MET:HE3	1.97	0.46
85:t3:17:ASP:OD2	85:t3:20:ARG:HG3	2.15	0.46
2:B1:58:LEU:HD21	2:B1:74:ARG:HH12	1.81	0.46
2:B1:168:TYR:OH	38:A2:4754:G:OP1	2.24	0.46
9:I1:50:ASN:ND2	38:A2:4443:U:OP1	2.40	0.46
33:l1:26:ARG:HD2	33:l1:210:MET:HE2	1.97	0.46
33:l1:60:ARG:NH2	38:A2:3965:G:O2'	2.48	0.46
33:l1:77:ALA:HA	33:l1:80:VAL:HG12	1.97	0.46
38:A2:92:C:OP2	38:A2:4327:C:O2'	2.26	0.46
38:A2:1500:A:H5"	38:A2:1501:C:H5'	1.98	0.46
38:A2:1982:G:N2	38:A2:2009:A:O2'	2.47	0.46
38:A2:2414:C:H2'	38:A2:2415:A:H8	1.81	0.46
41:A3:96:C:O2	41:A3:473:A:O2'	2.33	0.46
41:A3:1102:G:OP2	43:C3:151:ARG:NH1	2.49	0.46
41:A3:1553:C:O2'	41:A3:1554:C:O4'	2.33	0.46
41:A3:1854:U:H2'	41:A3:1855:G:H8	1.80	0.46
48:H3:2:LYS:HB3	48:H3:15:LEU:HD11	1.97	0.46
60:T3:141:ARG:HE	60:T3:144:ARG:NH2	2.13	0.46
61:U3:82:ARG:HA	61:U3:91:HIS:O	2.15	0.46
68:b3:74:CYS:SG	68:b3:77:CYS:HB2	2.56	0.46
74:h3:174:VAL:O	74:h3:188:HIS:HB2	2.16	0.46
2:B1:49:ARG:NH2	38:A2:1932:A:OP2	2.48	0.46
12:L1:43:ASN:ND2	12:L1:127:GLN:OE1	2.49	0.46
13:M1:17:ARG:NH2	13:M1:18:TYR:OH	2.48	0.46
32:f1:47:ALA:HA	32:f1:50:THR:HG23	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A2:3937:A:H2'	38:A2:3938:A:H8	1.81	0.46
46:F3:64:ILE:HG23	66:Z3:17:LEU:HD12	1.98	0.46
47:G3:100:ILE:HA	47:G3:178:ILE:HD11	1.98	0.46
53:M3:92:TYR:OH	53:M3:107:LYS:NZ	2.43	0.46
76:k3:322:HIS:O	76:k3:342:LYS:NZ	2.41	0.46
77:l3:209:VAL:HB	77:l3:229:LEU:HD13	1.97	0.46
77:l3:228:THR:HB	77:l3:248:ARG:HH22	1.79	0.46
2:B1:54:TYR:CD1	2:B1:145:VAL:HG21	2.51	0.46
3:C1:122:ALA:HB3	3:C1:143:PRO:HG2	1.98	0.46
4:D1:99:LYS:HB2	4:D1:99:LYS:HE3	1.69	0.46
38:A2:549:C:H2'	38:A2:550:G:C8	2.50	0.46
38:A2:1352:A:N1	38:A2:1383:G:O2'	2.43	0.46
38:A2:1726:U:H5'	80:o3:134:ILE:HD11	1.97	0.46
38:A2:2642:U:H2'	38:A2:2697:G:H1	1.79	0.46
38:A2:4309:A:H2	78:m3:146:LEU:HB3	1.81	0.46
51:K3:172:ARG:HA	51:K3:175:ARG:HG2	1.97	0.46
55:O3:91:LEU:HD21	55:O3:121:ARG:HE	1.80	0.46
74:h3:120:ILE:HG13	74:h3:132:TRP:HB2	1.97	0.46
82:q3:129:ARG:HB3	82:q3:153:LEU:HD22	1.98	0.46
5:E1:90:PRO:HG2	5:E1:93:VAL:HG12	1.96	0.46
29:c1:86:LEU:HA	29:c1:89:LEU:HG	1.97	0.46
31:e1:15:LEU:HA	31:e1:18:ILE:HB	1.96	0.46
36:21:23:G:H2'	36:21:24:G:H8	1.81	0.46
38:A2:1396:A:H62	38:A2:1419:G:H21	1.63	0.46
38:A2:3772:G:O2'	38:A2:3810:G:O6	2.33	0.46
41:A3:1092:G:OP1	55:O3:2:GLY:N	2.49	0.46
41:A3:1673:U:O2'	47:G3:84:GLY:O	2.24	0.46
44:D3:174:ILE:O	44:D3:200:ARG:NH2	2.28	0.46
53:M3:88:ILE:HG21	53:M3:126:VAL:HG11	1.98	0.46
59:S3:29:HIS:HA	59:S3:32:LYS:HE2	1.97	0.46
75:j3:117:GLU:OE2	75:j3:163:ARG:NH2	2.43	0.46
80:o3:215:PRO:HB3	80:o3:246:MET:HG2	1.98	0.46
7:G1:106:LEU:HA	7:G1:109:VAL:HG22	1.98	0.46
32:f1:44:ASP:N	32:f1:44:ASP:OD1	2.49	0.46
35:n1:219:PHE:CE2	35:n1:221:GLU:HB2	2.51	0.46
38:A2:936:G:C5'	38:A2:936:G:C4'	2.93	0.46
38:A2:3804:G:OP2	38:A2:3804:G:N2	2.37	0.46
38:A2:3956:G:O2'	38:A2:4037:G:N2	2.41	0.46
38:A2:4246:U:H2'	38:A2:4247:C:C6	2.51	0.46
41:A3:851:C:O2'	41:A3:852:G:N2	2.49	0.46
43:C3:33:VAL:HG23	43:C3:44:ILE:HB	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
67:a3:73:VAL:HG12	67:a3:79:ILE:HD11	1.98	0.46
74:h3:109:LEU:HD21	74:h3:125:ARG:NE	2.31	0.46
77:l3:195:LYS:HG2	77:l3:200:ARG:HA	1.98	0.46
4:D1:67:ILE:HD12	4:D1:96:PRO:HD2	1.98	0.46
31:e1:25:PRO:HD2	31:e1:92:LYS:HE2	1.97	0.46
36:21:38:A:O2'	41:A3:1058:A:OP1	2.32	0.46
38:A2:966:G:N2	38:A2:2096:G:O2'	2.49	0.46
41:A3:1232:U:H2'	41:A3:1233:G:H8	1.80	0.46
48:H3:45:TRP:HA	48:H3:48:TYR:HD1	1.80	0.46
52:L3:21:MET:HE3	52:L3:22:VAL:H	1.80	0.46
55:O3:99:ARG:NH2	55:O3:119:GLU:OE2	2.39	0.46
58:R3:98:LYS:HA	58:R3:98:LYS:HD2	1.84	0.46
10:J1:81:ALA:HB2	10:J1:87:LEU:HB2	1.97	0.46
33:l1:24:LYS:HE3	33:l1:26:ARG:HD3	1.96	0.46
41:A3:1297:U:O4	57:Q3:59:ARG:NH2	2.48	0.46
41:A3:1552:G:OP1	41:A3:1578:U:N3	2.49	0.46
59:S3:94:GLU:HG2	59:S3:95:ILE:HG12	1.98	0.46
60:T3:118:ARG:HE	60:T3:123:LEU:HD21	1.81	0.46
65:Y3:52:LEU:HD11	65:Y3:73:GLN:HB2	1.98	0.46
80:o3:231:ASP:HA	80:o3:235:ARG:HH21	1.81	0.46
83:r3:171:TRP:HB2	83:r3:178:ALA:HA	1.98	0.46
4:D1:124:ASP:OD2	77:l3:286:ASN:N	2.47	0.45
7:G1:127:GLN:OE1	7:G1:128:LEU:N	2.49	0.45
14:N1:100:ILE:HA	14:N1:123:ILE:O	2.16	0.45
20:T1:76:ARG:NH1	38:A2:2585:A:OP1	2.46	0.45
24:X1:51:GLU:HA	24:X1:54:GLU:HG3	1.98	0.45
33:l1:56:LYS:NZ	33:l1:150:GLU:OE2	2.48	0.45
38:A2:942:C:OP2	80:o3:241:ARG:NH2	2.32	0.45
41:A3:402:C:OP1	50:J3:14:THR:OG1	2.33	0.45
43:C3:23:ASP:OD2	56:P3:16:SER:OG	2.27	0.45
46:F3:45:ILE:O	46:F3:49:ARG:HB3	2.16	0.45
47:G3:34:SER:HA	70:d3:55:VAL:HB	1.99	0.45
51:K3:89:GLU:HB3	51:K3:92:MET:HE3	1.98	0.45
74:h3:5:MET:SD	74:h3:312:VAL:HG22	2.56	0.45
35:n1:57:ARG:HH12	38:A2:3767:U:H5'	1.81	0.45
35:n1:197:VAL:HA	35:n1:200:ILE:HD12	1.98	0.45
38:A2:922:C:O2	38:A2:923:C:C2	2.69	0.45
38:A2:1346:U:H2'	38:A2:1347:G:H8	1.81	0.45
38:A2:4907:U:H4'	38:A2:4908:C:H5'	1.97	0.45
41:A3:408:A:O2'	41:A3:410:G:OP1	2.32	0.45
41:A3:1858:G:OP2	56:P3:146:ARG:NH2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:D3:167:ARG:HB3	44:D3:177:PRO:HB2	1.97	0.45
51:K3:140:GLN:NE2	66:Z3:64:PHE:O	2.39	0.45
52:L3:41:PRO:HB2	52:L3:44:HIS:H	1.80	0.45
12:L1:11:ARG:NH1	38:A2:229:G:OP1	2.49	0.45
19:S1:100:ARG:NH1	38:A2:4739:U:OP1	2.49	0.45
38:A2:86:U:H2'	38:A2:87:A:C8	2.51	0.45
38:A2:4715:A:OP2	38:A2:5050:G:N1	2.40	0.45
41:A3:1115:U:H1'	41:A3:1116:C:H2'	1.98	0.45
41:A3:1391:C:O3'	62:V3:83:ARG:NH2	2.48	0.45
41:A3:1527:C:OP1	58:R3:142:GLN:NE2	2.50	0.45
43:C3:222:LYS:HE3	43:C3:222:LYS:HB2	1.82	0.45
45:E3:17:PHE:HA	45:E3:77:PHE:HE1	1.82	0.45
51:K3:136:ARG:HD2	51:K3:139:LYS:HA	1.97	0.45
55:O3:53:ILE:HA	55:O3:56:ASP:HB2	1.98	0.45
55:O3:93:LYS:HE3	55:O3:93:LYS:HB3	1.70	0.45
56:P3:103:ASN:HB3	56:P3:139:SER:HB2	1.97	0.45
58:R3:130:LYS:HA	58:R3:137:ALA:HA	1.98	0.45
76:k3:332:MET:HE1	76:k3:368:ILE:HD13	1.98	0.45
22:V1:45:ARG:HD2	22:V1:45:ARG:HA	1.82	0.45
33:l1:11:TYR:HE2	33:l1:180:VAL:HG21	1.81	0.45
33:l1:164:CYS:SG	38:A2:3962:G:N2	2.89	0.45
35:n1:59:ARG:HH12	35:n1:85:GLU:HB2	1.80	0.45
41:A3:190:G:H5"	50:J3:145:ILE:HD13	1.98	0.45
45:E3:52:ALA:O	45:E3:90:LYS:HA	2.16	0.45
47:G3:28:VAL:HG13	47:G3:110:GLN:HA	1.99	0.45
54:N3:118:SER:HB3	54:N3:121:LYS:HG2	1.98	0.45
77:l3:160:GLY:HA2	77:l3:215:ASN:HB2	1.98	0.45
77:l3:315:LYS:HD2	80:o3:167:ALA:HB1	1.97	0.45
81:p3:212:HIS:ND1	81:p3:238:LYS:HA	2.31	0.45
83:r3:184:MET:HA	83:r3:187:GLU:HG2	1.98	0.45
14:N1:130:SER:OG	38:A2:1395:A:OP1	2.30	0.45
18:R1:78:LEU:HD11	38:A2:2327:C:H4'	1.99	0.45
33:l1:26:ARG:HG2	33:l1:30:GLU:HA	1.97	0.45
33:l1:28:PHE:H	38:A2:3969:G:H4'	1.82	0.45
33:l1:210:MET:SD	38:A2:4045:C:O2'	2.63	0.45
38:A2:1481:C:O2'	38:A2:1482:G:O4'	2.34	0.45
38:A2:2814:G:N1	38:A2:2817:C:OP2	2.36	0.45
38:A2:4974:G:H2'	38:A2:4975:G:C8	2.51	0.45
70:d3:16:LYS:NZ	70:d3:52:GLU:OE2	2.38	0.45
75:j3:148:VAL:O	75:j3:155:LYS:HA	2.17	0.45
23:W1:63:ARG:NH2	40:C2:58:G:N7	2.58	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A2:163:A:H2'	38:A2:164:G:C8	2.52	0.45
38:A2:984:U:O4	38:A2:1271:G:O6	2.33	0.45
38:A2:1857:C:H2'	38:A2:1858:A:C8	2.52	0.45
41:A3:49:C:H2'	41:A3:472:C:H41	1.81	0.45
41:A3:476:A:N3	41:A3:488:U:O2'	2.38	0.45
42:B3:210:ILE:HD13	42:B3:210:ILE:HG21	1.76	0.45
44:D3:204:ILE:O	44:D3:211:LYS:NZ	2.48	0.45
74:h3:239:LEU:HD22	74:h3:248:LEU:HD11	1.98	0.45
74:h3:289:LEU:HA	74:h3:299:PHE:O	2.17	0.45
75:j3:54:ARG:HG2	75:j3:56:ALA:H	1.82	0.45
79:n3:193:HIS:HB3	79:n3:196:PHE:HD2	1.81	0.45
4:D1:99:LYS:HE2	4:D1:119:LYS:HD2	1.98	0.45
7:G1:97:LYS:HD2	7:G1:97:LYS:HA	1.82	0.45
10:J1:105:ARG:NH1	48:H3:150:GLU:O	2.49	0.45
18:R1:48:ARG:O	38:A2:1883:G:O2'	2.33	0.45
19:S1:68:ARG:NH2	38:A2:443:G:OP1	2.47	0.45
20:T1:107:LEU:HA	20:T1:110:GLN:HG2	1.98	0.45
36:21:22:A:H62	36:21:46:G:H22	1.63	0.45
38:A2:978:G:H21	77:l3:323:ARG:CZ	2.29	0.45
38:A2:1075:C:OP1	38:A2:1213:C:O2'	2.32	0.45
38:A2:1400:C:H2'	38:A2:1401:G:H8	1.81	0.45
38:A2:4736:G:H2'	38:A2:4737:G:C8	2.51	0.45
38:A2:4985:U:OP2	76:k3:378:ARG:NH2	2.50	0.45
40:C2:126:C:O2'	40:C2:127:U:O5'	2.34	0.45
41:A3:106:C:H2'	41:A3:107:A:C8	2.52	0.45
41:A3:1203:G:H2'	41:A3:1204:A:C8	2.52	0.45
41:A3:1475:G:OP2	41:A3:1475:G:N2	2.40	0.45
41:A3:1745:A:H1'	48:H3:66:GLY:HA2	1.98	0.45
60:T3:67:VAL:HG12	60:T3:71:MET:HE3	1.98	0.45
60:T3:99:LEU:O	60:T3:103:LEU:N	2.42	0.45
77:l3:11:TYR:O	77:l3:155:GLU:N	2.50	0.45
2:B1:54:TYR:OH	2:B1:73:PHE:O	2.30	0.45
18:R1:62:SER:OG	38:A2:2322:C:OP2	2.33	0.45
25:Y1:16:LYS:O	25:Y1:42:ARG:NH2	2.50	0.45
30:d1:112:ARG:NH1	38:A2:2267:C:OP1	2.49	0.45
35:n1:53:LYS:O	35:n1:57:ARG:NE	2.47	0.45
36:21:29:G:H5"	57:Q3:136:THR:HG21	1.99	0.45
38:A2:1390:A:H2'	38:A2:1391:G:C8	2.52	0.45
38:A2:3742:A:H62	75:j3:245:ARG:NH2	2.15	0.45
41:A3:602:G:N2	41:A3:620:G:N7	2.61	0.45
42:B3:2:SER:OG	63:W3:78:ILE:O	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:B3:176:TRP:CD2	42:B3:199:PRO:HB3	2.52	0.45
49:I3:76:GLN:HG3	49:I3:94:PHE:CD2	2.52	0.45
56:P3:60:MET:HB3	56:P3:60:MET:HE2	1.67	0.45
64:X3:57:ARG:HE	69:c3:26:GLN:NE2	2.15	0.45
78:m3:164:LYS:NZ	78:m3:168:ASP:OD1	2.45	0.45
3:C1:41:ILE:HD13	3:C1:150:LEU:HD21	1.99	0.45
10:J1:4:GLU:HG3	10:J1:20:ARG:HH21	1.80	0.45
13:M1:115:LYS:NZ	38:A2:2576:A:O3'	2.42	0.45
28:b1:12:CYS:HB3	28:b1:15:CYS:HB2	1.99	0.45
32:f1:15:LEU:HD22	32:f1:28:LEU:HD12	1.99	0.45
32:f1:77:ALA:O	32:f1:81:ILE:HG12	2.17	0.45
36:21:58:C:O2'	36:21:60:U:OP2	2.31	0.45
38:A2:300:A:H2'	38:A2:301:G:H8	1.82	0.45
38:A2:2641:G:H22	38:A2:2700:A:N6	2.15	0.45
41:A3:17:C:O2'	41:A3:1194:A:N1	2.49	0.45
41:A3:144:U:H2'	41:A3:145:G:H8	1.81	0.45
41:A3:161:U:O2'	48:H3:87:ARG:NH1	2.38	0.45
41:A3:788:G:H2'	41:A3:789:G:C8	2.51	0.45
41:A3:1447:G:OP1	62:V3:85:HIS:ND1	2.41	0.45
41:A3:1570:G:O2'	41:A3:1614:A:O2'	2.29	0.45
42:B3:108:PHE:HB2	42:B3:136:GLU:HG2	1.99	0.45
54:N3:38:ALA:HA	54:N3:41:ALA:HB3	1.99	0.45
59:S3:74:GLN:O	59:S3:78:ARG:HG3	2.17	0.45
62:V3:62:ARG:HG2	62:V3:81:GLN:HG2	1.99	0.45
74:h3:87:LEU:HD21	74:h3:108:VAL:HG11	1.98	0.45
74:h3:165:ILE:HG12	74:h3:177:TRP:HB2	1.99	0.45
81:p3:189:LEU:HD22	81:p3:255:VAL:HB	1.99	0.45
1:A1:15:GLN:NE2	38:A2:305:A:OP2	2.49	0.45
17:Q1:32:ARG:NH1	38:A2:4978:C:OP1	2.44	0.45
38:A2:1481:C:O2'	38:A2:1482:G:O5'	2.35	0.45
38:A2:1558:A:H2'	38:A2:1559:G:C8	2.52	0.45
38:A2:1688:G:H2'	38:A2:1689:G:C8	2.52	0.45
38:A2:2522:U:O2'	38:A2:2533:U:O2	2.33	0.45
41:A3:300:U:H2'	41:A3:301:A:C8	2.52	0.45
41:A3:527:C:H2'	41:A3:528:A:H8	1.82	0.45
41:A3:1524:G:OP2	60:T3:141:ARG:NH1	2.50	0.45
43:C3:72:ALA:HB3	56:P3:128:ARG:HH22	1.82	0.45
44:D3:121:ARG:NH1	44:D3:123:ARG:HD3	2.32	0.45
45:E3:40:ARG:HD3	62:V3:108:PRO:HG3	1.99	0.45
49:I3:163:GLN:O	49:I3:167:GLU:HB2	2.17	0.45
57:Q3:95:GLY:HA2	57:Q3:103:ASN:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:h3:212:LYS:HA	74:h3:235:ILE:HG13	1.99	0.45
18:R1:90:MET:HG3	30:d1:33:LYS:HA	1.98	0.44
22:V1:76:ARG:HA	22:V1:76:ARG:HD3	1.82	0.44
29:c1:64:VAL:HG22	75:j3:83:HIS:HB3	1.99	0.44
38:A2:197:A:N1	38:A2:225:G:O2'	2.45	0.44
38:A2:703:U:H5'	79:n3:124:VAL:HG11	1.99	0.44
38:A2:1725:U:H2'	38:A2:1726:U:H6	1.81	0.44
38:A2:1870:C:H2'	38:A2:1871:A:H8	1.81	0.44
38:A2:1996:C:N4	38:A2:2000:G:H1	2.15	0.44
38:A2:3768:U:H2'	38:A2:3770:A:H2	1.81	0.44
41:A3:649:U:H2'	41:A3:650:A:C8	2.51	0.44
41:A3:1087:A:OP2	68:b3:8:ASN:ND2	2.49	0.44
41:A3:1395:C:H2'	41:A3:1396:A:N3	2.33	0.44
43:C3:180:ASP:OD1	43:C3:180:ASP:N	2.48	0.44
51:K3:33:GLY:HA3	72:f3:111:TYR:CG	2.52	0.44
54:N3:83:LYS:HA	54:N3:83:LYS:HD3	1.79	0.44
75:j3:47:ASP:HB3	75:j3:60:LYS:HB3	1.99	0.44
83:r3:145:LYS:HE3	83:r3:167:ILE:HG13	1.99	0.44
3:C1:84:PRO:HB2	3:C1:87:SER:HB2	1.99	0.44
9:I1:82:ILE:HD12	9:I1:121:VAL:HG22	1.99	0.44
10:J1:80:ARG:NE	48:H3:9:ALA:O	2.42	0.44
14:N1:2:PRO:HD2	38:A2:1509:C:H5"	1.98	0.44
16:P1:90:ARG:NH2	38:A2:2676:G:OP1	2.50	0.44
18:R1:108:ARG:NH2	38:A2:2329:G:OP1	2.50	0.44
24:X1:42:LEU:N	38:A2:2540:A:OP1	2.43	0.44
36:21:4:A:H2	36:21:69:G:H22	1.64	0.44
38:A2:704:G:H2'	38:A2:705:C:H4'	1.98	0.44
38:A2:3958:A:H2'	38:A2:3959:U:H2'	1.98	0.44
41:A3:1033:G:H1	41:A3:1080:A:HO2'	1.63	0.44
41:A3:1568:C:O3'	61:U3:41:LYS:NZ	2.51	0.44
41:A3:1692:U:H2'	41:A3:1693:G:C8	2.52	0.44
59:S3:100:PRO:HA	59:S3:103:LYS:HB2	1.99	0.44
74:h3:20:GLN:HG2	74:h3:69:VAL:H	1.83	0.44
74:h3:113:PHE:HA	74:h3:120:ILE:HG22	1.99	0.44
77:l3:348:LYS:HA	77:l3:351:VAL:HG22	1.98	0.44
78:m3:152:ARG:HG3	78:m3:154:THR:HG23	1.98	0.44
78:m3:197:LYS:HB3	78:m3:202:GLN:HB2	1.99	0.44
82:q3:7:ASN:HA	82:q3:57:VAL:O	2.16	0.44
83:r3:66:GLU:HA	83:r3:69:ARG:HG2	1.97	0.44
30:d1:24:THR:OG1	38:A2:2292:C:N4	2.51	0.44
35:n1:151:VAL:HG12	35:n1:155:LYS:HE2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A2:257:C:H2'	38:A2:258:G:H8	1.82	0.44
38:A2:1792:U:H3'	38:A2:1793:A:H8	1.82	0.44
41:A3:1731:A:H2'	41:A3:1732:G:C8	2.52	0.44
46:F3:66:MET:HE3	46:F3:66:MET:HB3	1.69	0.44
49:I3:76:GLN:HG3	49:I3:94:PHE:HD2	1.82	0.44
64:X3:115:GLU:HA	64:X3:118:ARG:HG2	1.98	0.44
76:k3:218:ASP:OD2	76:k3:348:ARG:NH2	2.33	0.44
78:m3:73:MET:HE3	78:m3:73:MET:HB3	1.80	0.44
79:n3:152:ILE:HD12	79:n3:274:LEU:HD21	1.99	0.44
13:M1:41:ALA:HB2	13:M1:77:TYR:HE1	1.82	0.44
14:N1:100:ILE:HG21	14:N1:125:LYS:HE2	1.99	0.44
16:P1:90:ARG:NH2	29:c1:44:LYS:HE2	2.33	0.44
30:d1:98:ARG:NH1	38:A2:2265:G:N7	2.66	0.44
38:A2:2591:C:H5"	38:A2:2592:C:H5"	1.99	0.44
38:A2:2873:A:H2'	38:A2:2874:A:C8	2.53	0.44
38:A2:3661:C:OP1	75:j3:234:LYS:NZ	2.40	0.44
38:A2:3727:A:H2'	38:A2:3728:A:C8	2.52	0.44
38:A2:3743:A:H5"	75:j3:243:THR:HB	1.98	0.44
39:B2:63:C:H5'	39:B2:64:G:H5"	1.99	0.44
41:A3:641:A:OP1	51:K3:40:LYS:NZ	2.42	0.44
41:A3:1697:A:H4'	41:A3:1698:C:H5"	1.98	0.44
42:B3:24:HIS:HB2	42:B3:48:ILE:HG23	1.99	0.44
43:C3:34:LYS:O	43:C3:98:THR:OG1	2.35	0.44
52:L3:27:VAL:HG23	52:L3:28:HIS:HD2	1.82	0.44
60:T3:39:ARG:HH11	60:T3:39:ARG:HG2	1.82	0.44
74:h3:296:GLN:O	74:h3:311:GLN:HA	2.17	0.44
77:l3:235:LEU:HD22	77:l3:240:LEU:HD11	1.99	0.44
81:p3:234:TYR:CZ	81:p3:279:TYR:HB3	2.52	0.44
83:r3:179:ASP:OD2	83:r3:180:GLU:N	2.50	0.44
4:D1:24:TYR:HD1	77:l3:284:MET:HG2	1.82	0.44
4:D1:178:ARG:N	14:N1:51:GLY:HA2	2.32	0.44
7:G1:143:THR:OG1	7:G1:146:LYS:O	2.34	0.44
28:b1:65:LYS:NZ	38:A2:4355:A:OP1	2.40	0.44
38:A2:3822:G:O2'	38:A2:3824:G:OP2	2.32	0.44
41:A3:801:U:O4	49:I3:106:ARG:NH2	2.50	0.44
41:A3:1010:G:H2'	41:A3:1011:A:C8	2.52	0.44
57:Q3:30:TYR:O	57:Q3:34:MET:HG3	2.18	0.44
66:Z3:20:ARG:NH2	66:Z3:22:GLN:OE1	2.50	0.44
76:k3:294:LYS:HB3	76:k3:299:ILE:HD13	1.99	0.44
80:o3:40:MET:HA	80:o3:43:LYS:HG2	1.99	0.44
81:p3:233:PRO:HG3	81:p3:276:ARG:HH21	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J1:91:MET:HA	10:J1:94:ARG:HG2	2.00	0.44
15:O1:19:ASN:ND2	38:A2:1686:C:OP1	2.43	0.44
16:P1:48:LEU:HD13	16:P1:57:LYS:HG3	2.00	0.44
36:21:1:A:H61	36:21:72:C:H42	1.64	0.44
38:A2:125:C:H2'	38:A2:126:C:H6	1.81	0.44
38:A2:480:C:O2'	38:A2:481:G:O6	2.24	0.44
38:A2:2742:C:OP1	75:j3:177:LYS:NZ	2.50	0.44
41:A3:219:U:O4'	50:J3:184:ARG:NH1	2.50	0.44
41:A3:1597:C:OP2	67:a3:85:ARG:NH2	2.41	0.44
41:A3:1623:A:C5	60:T3:132:ARG:HD3	2.52	0.44
66:Z3:7:ILE:HD12	66:Z3:43:LYS:HB3	2.00	0.44
80:o3:49:ILE:HD12	80:o3:185:CYS:SG	2.57	0.44
85:t3:91:ALA:HB1	85:t3:96:ILE:HB	2.00	0.44
8:H1:27:HIS:HB3	8:H1:114:TYR:HE1	1.82	0.44
16:P1:51:ASN:HB2	16:P1:77:ASN:HB2	2.00	0.44
33:l1:36:ILE:HG12	33:l1:190:LEU:HD22	1.99	0.44
38:A2:3:C:H42	40:C2:154:G:H1	1.66	0.44
38:A2:82:U:HO2'	38:A2:1380:G:HO2'	1.63	0.44
38:A2:1344:C:H2'	38:A2:1345:G:H8	1.83	0.44
38:A2:2617:C:O2'	38:A2:2811:G:OP1	2.30	0.44
38:A2:3960:A:N6	38:A2:4039:G:N2	2.48	0.44
38:A2:4038:U:O2'	38:A2:4042:A:N6	2.41	0.44
38:A2:4260:A:H2'	38:A2:4261:G:H8	1.83	0.44
41:A3:379:C:O2	50:J3:5:ARG:NE	2.50	0.44
51:K3:82:VAL:O	51:K3:151:LEU:HD23	2.18	0.44
76:k3:58:ARG:HE	76:k3:363:ILE:HG23	1.82	0.44
81:p3:197:THR:O	81:p3:201:GLU:HG2	2.18	0.44
82:q3:91:LYS:HB2	82:q3:183:GLU:HB2	2.00	0.44
2:B1:176:ARG:O	2:B1:180:GLN:HG3	2.17	0.44
7:G1:107:LYS:HA	7:G1:110:LYS:HG2	2.00	0.44
20:T1:17:SER:O	20:T1:17:SER:OG	2.34	0.44
22:V1:2:ALA:HB3	22:V1:4:ARG:HH12	1.83	0.44
25:Y1:33:ASN:OD1	25:Y1:35:ILE:N	2.43	0.44
38:A2:1330:C:H2'	38:A2:1331:A:H8	1.82	0.44
38:A2:2453:G:OP1	75:j3:17:ARG:NH1	2.50	0.44
38:A2:3718:A:H2'	38:A2:3719:A:C8	2.53	0.44
38:A2:3740:U:O2'	75:j3:243:THR:N	2.47	0.44
38:A2:4310:A:H4'	78:m3:174:PRO:HB2	1.99	0.44
41:A3:526:A:OP2	72:f3:101:ARG:NH2	2.36	0.44
41:A3:561:A:H5'	51:K3:171:GLY:HA3	1.99	0.44
41:A3:1587:G:C5	61:U3:67:ARG:HD3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:N3:65:VAL:HA	54:N3:68:LEU:HG	1.99	0.44
55:O3:102:LEU:HD21	55:O3:115:LEU:HD22	1.99	0.44
56:P3:101:GLY:HA3	56:P3:134:PRO:HG2	1.99	0.44
57:Q3:133:ILE:HA	57:Q3:139:SER:HB3	1.99	0.44
22:V1:90:LEU:HA	22:V1:93:VAL:HG12	2.00	0.44
30:d1:37:SER:HG	30:d1:40:TYR:H	1.62	0.44
38:A2:1850:A:N3	38:A2:2286:G:O2'	2.49	0.44
38:A2:2385:A:N1	38:A2:2832:U:O2'	2.41	0.44
41:A3:496:C:OP1	46:F3:49:ARG:NH2	2.49	0.44
43:C3:129:THR:OG1	43:C3:131:ASP:O	2.31	0.44
45:E3:80:PRO:O	45:E3:83:SER:OG	2.35	0.44
53:M3:75:GLY:HA3	53:M3:88:ILE:HD12	1.99	0.44
59:S3:71:ILE:HG13	59:S3:74:GLN:HB2	2.00	0.44
80:o3:160:LYS:N	80:o3:206:PHE:O	2.51	0.44
82:q3:41:ILE:HG22	82:q3:43:VAL:HG13	2.00	0.44
83:r3:36:LEU:HD11	83:r3:69:ARG:HE	1.81	0.44
33:l1:210:MET:HG3	38:A2:4046:C:H5'	1.99	0.43
38:A2:1372:G:O2'	77:l3:233:THR:O	2.36	0.43
38:A2:1427:A:OP2	38:A2:1457:G:N2	2.37	0.43
38:A2:1823:G:O2'	78:m3:44:TYR:O	2.35	0.43
38:A2:3715:G:H22	38:A2:3728:A:H2	1.66	0.43
38:A2:3939:G:N2	38:A2:4063:U:O2	2.39	0.43
38:A2:4054:U:H2'	38:A2:4055:G:C8	2.53	0.43
38:A2:4149:U:H5'	38:A2:4150:C:H5"	2.00	0.43
38:A2:5045:G:O6	76:k3:124:LYS:NZ	2.39	0.43
41:A3:639:C:H2'	41:A3:640:A:C8	2.53	0.43
41:A3:1731:A:H2'	41:A3:1732:G:H8	1.82	0.43
43:C3:29:ASP:N	43:C3:49:VAL:O	2.40	0.43
44:D3:191:VAL:HG11	44:D3:236:PHE:HA	1.99	0.43
44:D3:207:ALA:O	44:D3:211:LYS:HB2	2.19	0.43
58:R3:16:LYS:HG3	58:R3:17:LYS:HG3	2.00	0.43
61:U3:51:ASN:HB3	61:U3:54:TYR:CD2	2.53	0.43
75:j3:3:ARG:HB3	75:j3:207:VAL:HG22	2.00	0.43
13:M1:25:ILE:HA	13:M1:43:VAL:HG12	2.00	0.43
13:M1:30:ASP:OD1	13:M1:77:TYR:OH	2.29	0.43
30:d1:28:GLU:HB3	30:d1:31:ASN:HB2	2.00	0.43
33:l1:108:ASP:O	33:l1:133:LYS:NZ	2.49	0.43
38:A2:162:A:H2'	38:A2:163:A:C8	2.53	0.43
38:A2:4864:U:OP1	86:u3:117:LYS:NZ	2.42	0.43
41:A3:380:G:O6	50:J3:178:ARG:NH2	2.51	0.43
41:A3:609:U:H2'	41:A3:610:G:H8	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:U3:71:GLY:O	61:U3:74:SER:OG	2.29	0.43
62:V3:61:LEU:HD13	62:V3:84:ILE:HD13	2.01	0.43
64:X3:32:LYS:HA	64:X3:35:VAL:HG12	2.00	0.43
70:d3:12:ALA:HB1	70:d3:32:VAL:HB	2.00	0.43
80:o3:213:SER:OG	80:o3:214:SER:N	2.50	0.43
6:F1:74:ARG:NH2	6:F1:131:GLU:OE2	2.45	0.43
8:H1:111:GLU:OE2	8:H1:113:ARG:NE	2.52	0.43
9:I1:42:VAL:HG22	9:I1:61:VAL:HG12	2.01	0.43
21:U1:110:LYS:NZ	38:A2:111:C:OP1	2.47	0.43
36:21:15:G:H2'	36:21:59:G:H22	1.83	0.43
39:B2:83:A:O2'	39:B2:85:G:OP1	2.35	0.43
41:A3:1277:C:H2'	41:A3:1278:A:H8	1.82	0.43
41:A3:1616:U:H3	41:A3:1620:A:H2	1.65	0.43
41:A3:1779:G:H2'	41:A3:1780:G:C8	2.52	0.43
52:L3:85:LEU:HD22	52:L3:89:ILE:HG21	2.00	0.43
77:l3:299:GLN:OE1	77:l3:302:LEU:HD12	2.18	0.43
2:B1:168:TYR:CE2	2:B1:172:LYS:HD2	2.53	0.43
6:F1:95:ARG:HH21	6:F1:116:ARG:HH11	1.67	0.43
13:M1:60:LYS:HE3	13:M1:60:LYS:HB2	1.86	0.43
32:f1:60:VAL:HG11	32:f1:62:LEU:HD23	2.00	0.43
33:l1:205:TYR:HB3	33:l1:207:LYS:HD3	2.00	0.43
36:21:22:A:H62	36:21:46:G:N2	2.17	0.43
38:A2:172:C:C4'	85:t3:129:ARG:HH12	2.31	0.43
38:A2:4575:A:N1	38:A2:4607:C:O2'	2.47	0.43
38:A2:4580:U:H2'	38:A2:4581:G:H8	1.84	0.43
40:C2:121:G:H3'	40:C2:122:G:H8	1.83	0.43
41:A3:1536:G:H2'	41:A3:1537:A:H8	1.83	0.43
56:P3:150:ARG:H	56:P3:150:ARG:HG2	1.71	0.43
66:Z3:20:ARG:HD2	66:Z3:74:MET:HE3	2.00	0.43
74:h3:292:SER:OG	74:h3:297:THR:OG1	2.37	0.43
76:k3:317:LEU:HB2	76:k3:372:SER:HB2	2.00	0.43
79:n3:194:GLN:HA	79:n3:197:VAL:HG22	1.99	0.43
1:A1:11:TRP:HZ3	1:A1:120:TRP:CZ3	2.33	0.43
2:B1:9:LEU:HD23	2:B1:118:MET:HB2	2.01	0.43
30:d1:108:MET:HE1	38:A2:2266:A:H5"	2.00	0.43
38:A2:85:G:O2'	38:A2:97:G:O6	2.30	0.43
38:A2:212:A:H2'	38:A2:213:G:H8	1.83	0.43
41:A3:21:U:O2'	51:K3:17:ARG:O	2.36	0.43
52:L3:37:ASP:N	52:L3:37:ASP:OD1	2.52	0.43
60:T3:34:LYS:NZ	60:T3:104:ASP:OD2	2.51	0.43
64:X3:57:ARG:HE	69:c3:26:GLN:HE21	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:Y3:49:GLY:O	65:Y3:99:GLU:HA	2.19	0.43
75:j3:103:PRO:O	75:j3:106:THR:OG1	2.34	0.43
79:n3:201:SER:N	79:n3:291:PHE:O	2.38	0.43
79:n3:290:VAL:O	86:u3:109:ARG:NH2	2.52	0.43
19:S1:33:VAL:HG13	19:S1:38:GLU:HB2	2.00	0.43
19:S1:93:PRO:HB2	19:S1:95:LYS:HG2	1.99	0.43
20:T1:66:ARG:HH12	38:A2:2521:G:H5'	1.84	0.43
24:X1:23:VAL:HG23	24:X1:64:LEU:HD11	2.00	0.43
25:Y1:44:TRP:CZ3	25:Y1:45:ARG:HD3	2.54	0.43
29:c1:3:LYS:HE2	29:c1:3:LYS:HB3	1.87	0.43
29:c1:90:LYS:NZ	75:j3:106:THR:O	2.42	0.43
38:A2:713:C:H1'	79:n3:139:HIS:CE1	2.53	0.43
38:A2:2278:G:H2'	38:A2:2279:A:C8	2.54	0.43
38:A2:3906:C:H2'	38:A2:3907:U:H6	1.84	0.43
38:A2:4994:G:O2'	38:A2:4996:A:OP1	2.33	0.43
41:A3:186:C:H2'	41:A3:187:G:H8	1.84	0.43
41:A3:448:A:H5"	50:J3:25:ARG:HA	1.99	0.43
41:A3:1661:A:OP1	71:e3:19:ARG:NH2	2.49	0.43
43:C3:163:GLN:HB3	43:C3:204:ILE:HD13	2.01	0.43
44:D3:169:TYR:OH	44:D3:175:GLY:O	2.32	0.43
45:E3:64:ARG:O	45:E3:68:GLU:HG2	2.19	0.43
47:G3:172:CYS:O	47:G3:176:GLU:HB2	2.19	0.43
48:H3:143:LYS:HE3	48:H3:143:LYS:HB2	1.83	0.43
53:M3:120:VAL:HG22	53:M3:145:VAL:HG21	2.00	0.43
54:N3:35:ILE:HG21	54:N3:61:TYR:HE2	1.84	0.43
58:R3:13:PHE:HA	58:R3:21:ALA:O	2.18	0.43
64:X3:53:ILE:HD13	69:c3:24:LEU:HD11	2.01	0.43
78:m3:64:ILE:HG12	78:m3:105:LEU:HD11	2.01	0.43
79:n3:164:ARG:NH1	79:n3:276:SER:OG	2.52	0.43
82:q3:120:GLU:OE2	82:q3:124:ARG:NH1	2.41	0.43
84:s3:15:LEU:HD23	84:s3:136:ARG:HG2	2.01	0.43
84:s3:151:ILE:HD11	84:s3:156:ARG:HG2	2.00	0.43
1:A1:140:LYS:HA	1:A1:143:ARG:HB3	2.01	0.43
35:n1:59:ARG:NH1	35:n1:81:ARG:HG2	2.33	0.43
38:A2:83:C:O2'	38:A2:100:C:N4	2.52	0.43
38:A2:4131:C:N4	38:A2:4132:G:O6	2.52	0.43
38:A2:4331:C:H2'	38:A2:4332:U:C6	2.54	0.43
38:A2:4554:A:O2'	38:A2:4963:G:N7	2.51	0.43
41:A3:116:U:O4	41:A3:347:G:O6	2.36	0.43
41:A3:1033:G:N1	41:A3:1080:A:O2'	2.41	0.43
54:N3:71:GLU:OE1	54:N3:72:HIS:ND1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:X3:42:MET:HE2	64:X3:42:MET:HB3	1.76	0.43
77:l3:147:VAL:HA	77:l3:148:PRO:HD3	1.89	0.43
78:m3:50:ARG:NH1	78:m3:147:ASP:OD2	2.42	0.43
79:n3:168:LEU:HD11	79:n3:179:THR:HG22	2.01	0.43
2:B1:12:ARG:HB2	2:B1:37:ARG:HD2	1.99	0.43
5:E1:24:LEU:HD12	38:A2:2389:U:H5"	2.00	0.43
11:K1:150:ALA:HB1	11:K1:155:ILE:HG13	2.00	0.43
12:L1:30:MET:HE3	12:L1:30:MET:HB3	1.94	0.43
33:l1:38:LEU:HB2	33:l1:163:LEU:HG	2.00	0.43
35:n1:186:ILE:HD11	35:n1:231:LEU:HD11	2.00	0.43
38:A2:967:A:H4'	38:A2:968:C:H5"	2.01	0.43
38:A2:1344:C:H2'	38:A2:1345:G:C8	2.54	0.43
38:A2:1985:G:H1'	38:A2:2003:G:H2'	1.99	0.43
38:A2:2073:C:O2'	80:o3:156:ARG:NH1	2.42	0.43
38:A2:4033:G:H3'	38:A2:4035:C:H5	1.84	0.43
38:A2:4922:C:OP1	79:n3:159:ARG:NH1	2.52	0.43
41:A3:1129:G:OP1	69:c3:22:LYS:NZ	2.42	0.43
41:A3:1284:A:H61	41:A3:1313:A:H2'	1.84	0.43
47:G3:183:GLY:HA2	47:G3:190:ILE:HG13	2.00	0.43
74:h3:199:THR:HG21	74:h3:240:CYS:HA	2.00	0.43
75:j3:101:VAL:HG22	75:j3:165:VAL:HG22	2.00	0.43
77:l3:39:PHE:O	77:l3:43:ASN:ND2	2.43	0.43
1:A1:17:ASP:OD1	1:A1:18:VAL:N	2.52	0.43
6:F1:51:LEU:HD23	7:G1:151:LEU:HD22	2.00	0.43
6:F1:98:ARG:HG3	6:F1:142:VAL:HG13	2.00	0.43
7:G1:73:GLY:HA2	7:G1:89:ILE:O	2.19	0.43
8:H1:102:VAL:HG22	8:H1:112:LEU:HD22	2.01	0.43
28:b1:10:THR:HA	28:b1:18:HIS:HD2	1.83	0.43
38:A2:1688:G:H2'	38:A2:1689:G:H8	1.84	0.43
38:A2:2381:G:N2	38:A2:2384:A:OP2	2.51	0.43
38:A2:2623:G:H1	38:A2:2639:U:H3	1.65	0.43
38:A2:3722:A:H2'	38:A2:3723:A:C8	2.54	0.43
39:B2:48:G:O2'	78:m3:222:GLN:O	2.28	0.43
41:A3:934:G:H22	41:A3:1008:A:H2	1.65	0.43
44:D3:130:ILE:HD13	44:D3:159:LYS:HG3	2.00	0.43
48:H3:1:MET:HE3	48:H3:24:LEU:HD21	2.01	0.43
53:M3:10:TYR:CE2	53:M3:12:LYS:HB3	2.52	0.43
55:O3:60:VAL:HG13	55:O3:66:VAL:HG21	2.01	0.43
69:c3:19:HIS:CD2	69:c3:21:LYS:H	2.37	0.43
74:h3:40:ILE:HG12	74:h3:66:VAL:HG11	1.99	0.43
74:h3:206:LEU:HA	74:h3:220:ASP:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:l3:316:LYS:HB2	77:l3:324:ILE:HG13	2.00	0.43
82:q3:47:LEU:HD21	82:q3:52:LYS:HE3	2.01	0.43
4:D1:38:ARG:HB3	77:l3:302:LEU:HD22	2.00	0.43
5:E1:162:ARG:HA	5:E1:165:LYS:HG2	2.01	0.43
14:N1:36:GLY:HA3	14:N1:40:HIS:CE1	2.54	0.43
22:V1:25:ARG:NH2	38:A2:326:C:OP2	2.50	0.43
33:l1:155:ILE:HG21	33:l1:167:VAL:HG22	2.01	0.43
38:A2:35:U:O4	38:A2:46:U:O2'	2.31	0.43
38:A2:1330:C:H2'	38:A2:1331:A:C8	2.53	0.43
41:A3:1048:G:N1	41:A3:1069:U:OP2	2.42	0.43
45:E3:17:PHE:HD1	45:E3:77:PHE:CE1	2.37	0.43
50:J3:162:LEU:HD21	50:J3:191:GLU:HG2	2.01	0.43
63:W3:31:SER:HA	63:W3:55:ILE:O	2.19	0.43
76:k3:369:ASP:OD2	76:k3:371:THR:OG1	2.37	0.43
80:o3:27:LEU:O	80:o3:31:ARG:HG3	2.19	0.43
14:N1:93:ASN:C	14:N1:93:ASN:ND2	2.77	0.42
33:l1:26:ARG:HH21	33:l1:208:SER:HB2	1.84	0.42
38:A2:223:G:H4'	38:A2:225:G:N7	2.34	0.42
38:A2:3684:G:O2'	38:A2:3813:U:OP2	2.33	0.42
38:A2:4244:C:H2'	38:A2:4245:C:C6	2.54	0.42
41:A3:832:G:O6	66:Z3:11:LYS:NZ	2.50	0.42
52:L3:91:PRO:HD2	52:L3:94:LEU:HD23	2.02	0.42
64:X3:35:VAL:HG23	64:X3:50:PHE:HE1	1.84	0.42
78:m3:119:TYR:OH	78:m3:139:PRO:O	2.37	0.42
2:B1:192:PHE:CE1	86:u3:118:MET:HG2	2.54	0.42
5:E1:99:MET:HE1	5:E1:127:VAL:O	2.19	0.42
8:H1:42:PHE:O	8:H1:46:ARG:HB2	2.19	0.42
12:L1:59:ARG:NH1	38:A2:200:U:O2'	2.47	0.42
13:M1:121:ARG:HH12	13:M1:126:LYS:HD2	1.83	0.42
14:N1:109:TYR:OH	85:t3:64:VAL:O	2.36	0.42
38:A2:158:A:N1	38:A2:276:C:O2'	2.42	0.42
38:A2:436:C:H2'	38:A2:437:G:H8	1.84	0.42
38:A2:467:U:O2	38:A2:687:A:N6	2.52	0.42
38:A2:478:G:H2'	38:A2:479:G:H8	1.83	0.42
38:A2:1371:A:H5"	77:l3:44:LEU:HD13	2.00	0.42
38:A2:1478:C:H2'	38:A2:1479:G:H8	1.83	0.42
38:A2:1970:A:H5"	38:A2:1971:U:H5'	2.00	0.42
38:A2:2531:G:H21	38:A2:2532:A:H5"	1.83	0.42
38:A2:4656:C:O2'	38:A2:4658:A:OP2	2.30	0.42
38:A2:4963:G:H3'	38:A2:4964:A:H8	1.83	0.42
41:A3:494:C:N4	41:A3:509:G:H21	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:A3:867:G:H2'	41:A3:868:G:C8	2.55	0.42
41:A3:1098:C:H2'	41:A3:1099:G:C8	2.55	0.42
42:B3:187:GLY:HA2	63:W3:45:ARG:NE	2.30	0.42
57:Q3:33:LEU:HG	57:Q3:37:TYR:HE1	1.84	0.42
60:T3:114:LEU:HD21	60:T3:121:ARG:HB3	2.00	0.42
68:b3:7:ASN:ND2	68:b3:10:ARG:O	2.52	0.42
10:J1:45:ASN:HD21	10:J1:47:ARG:HD3	1.85	0.42
35:n1:147:GLU:O	35:n1:151:VAL:HG23	2.19	0.42
41:A3:104:A:H62	41:A3:356:C:H5	1.66	0.42
41:A3:292:A:O2'	53:M3:39:ASN:O	2.31	0.42
41:A3:1521:C:OP2	60:T3:136:THR:OG1	2.25	0.42
52:L3:90:VAL:HB	52:L3:94:LEU:HB2	2.01	0.42
55:O3:133:ARG:NH1	55:O3:133:ARG:O	2.52	0.42
60:T3:14:ARG:HA	60:T3:14:ARG:HD2	1.71	0.42
64:X3:23:ARG:HE	64:X3:23:ARG:HB3	1.67	0.42
79:n3:95:VAL:HG12	79:n3:97:LYS:HG3	2.00	0.42
3:C1:94:MET:HE1	3:C1:146:ILE:HB	2.02	0.42
4:D1:38:ARG:NH2	77:l3:303:ARG:O	2.40	0.42
5:E1:40:GLN:HA	5:E1:43:LYS:HG2	2.01	0.42
10:J1:82:ILE:HG12	48:H3:131:ARG:HE	1.83	0.42
14:N1:100:ILE:HG12	14:N1:123:ILE:HB	2.00	0.42
33:l1:98:LYS:HE2	38:A2:4038:U:H5	1.84	0.42
38:A2:451:C:OP2	38:A2:1292:A:N6	2.53	0.42
41:A3:28:U:H2'	41:A3:29:G:H8	1.84	0.42
41:A3:600:G:H2'	41:A3:601:G:H8	1.84	0.42
41:A3:1112:U:H2'	41:A3:1113:A:H8	1.85	0.42
41:A3:1445:U:H4'	62:V3:57:PRO:HG3	2.01	0.42
43:C3:115:LYS:HB3	43:C3:115:LYS:HE2	1.86	0.42
49:I3:69:LEU:HD22	49:I3:96:ALA:HB2	2.01	0.42
50:J3:22:HIS:ND1	50:J3:23:LYS:O	2.44	0.42
52:L3:12:TYR:CE1	52:L3:52:LEU:HD11	2.53	0.42
74:h3:11:LEU:HD23	74:h3:43:TRP:CD2	2.53	0.42
83:r3:36:LEU:HD13	83:r3:73:ASN:HB2	2.01	0.42
86:u3:113:MET:O	86:u3:117:LYS:HB2	2.18	0.42
9:I1:20:LEU:HD23	9:I1:20:LEU:HA	1.88	0.42
24:X1:8:ILE:HD13	24:X1:45:LEU:HD21	2.00	0.42
32:f1:137:GLN:NE2	32:f1:141:CYS:O	2.47	0.42
35:n1:55:LEU:HD11	35:n1:84:ILE:HG12	2.02	0.42
38:A2:103:G:OP1	85:t3:69:LYS:NZ	2.37	0.42
38:A2:505:G:H2'	38:A2:506:G:C8	2.53	0.42
38:A2:929:A:H3'	38:A2:930:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A2:1304:C:H2'	38:A2:1305:A:H8	1.84	0.42
38:A2:2402:G:O2'	38:A2:2825:G:O2'	2.34	0.42
38:A2:4747:G:H2'	38:A2:4748:A:C8	2.54	0.42
41:A3:397:G:OP1	53:M3:106:HIS:NE2	2.53	0.42
41:A3:441:C:H2'	41:A3:442:C:C6	2.54	0.42
41:A3:641:A:O2'	41:A3:645:C:OP1	2.36	0.42
41:A3:1120:U:O5'	69:c3:72:ARG:NH1	2.53	0.42
41:A3:1589:A:N3	41:A3:1653:U:O2'	2.44	0.42
77:l3:190:ARG:HB2	77:l3:202:ILE:HG23	2.02	0.42
78:m3:120:GLU:O	78:m3:248:ARG:NH1	2.52	0.42
82:q3:134:CYS:SG	82:q3:144:LEU:HD11	2.60	0.42
2:B1:25:LYS:NZ	38:A2:1914:C:OP1	2.42	0.42
6:F1:115:ALA:O	6:F1:118:ARG:NH1	2.52	0.42
9:I1:87:SER:HA	9:I1:97:TYR:HB3	2.01	0.42
14:N1:49:HIS:NE2	85:t3:7:GLY:O	2.38	0.42
17:Q1:33:ILE:HG22	17:Q1:44:ARG:HG2	2.02	0.42
24:X1:24:LYS:HE3	24:X1:69:LEU:HD11	2.01	0.42
38:A2:178:C:H2'	38:A2:179:G:C8	2.54	0.42
38:A2:1072:G:H2'	38:A2:1073:G:C8	2.54	0.42
38:A2:1769:G:H2'	38:A2:1770:A:C8	2.53	0.42
38:A2:1802:A:H5"	38:A2:1803:G:H5'	2.00	0.42
38:A2:1886:G:O2'	38:A2:1909:G:O2'	2.32	0.42
40:C2:26:C:O2'	77:l3:53:ALA:O	2.31	0.42
41:A3:1550:G:O2'	41:A3:1558:C:O2	2.29	0.42
41:A3:1643:U:H2'	41:A3:1644:C:C6	2.54	0.42
44:D3:203:GLY:N	44:D3:221:ASP:OD1	2.32	0.42
49:I3:27:LEU:HD12	49:I3:40:LEU:HD21	2.02	0.42
83:r3:95:HIS:HB3	83:r3:126:VAL:O	2.20	0.42
1:A1:179:LYS:NZ	38:A2:298:G:OP1	2.37	0.42
3:C1:82:ARG:NH2	38:A2:2365:U:OP1	2.42	0.42
12:L1:50:ARG:HG2	12:L1:51:LYS:H	1.84	0.42
17:Q1:29:ILE:O	17:Q1:33:ILE:HG12	2.20	0.42
23:W1:67:LEU:HA	23:W1:67:LEU:HD12	1.80	0.42
38:A2:32:G:H21	38:A2:50:C:H5	1.68	0.42
38:A2:930:G:O5'	77:l3:353:ARG:NH1	2.52	0.42
38:A2:1771:U:H2'	38:A2:1772:C:C6	2.55	0.42
38:A2:2561:C:H2'	38:A2:2562:G:H8	1.85	0.42
38:A2:4580:U:H2'	38:A2:4581:G:C8	2.55	0.42
39:B2:92:C:H2'	39:B2:93:G:H8	1.84	0.42
48:H3:135:PRO:HB3	48:H3:140:ARG:HG2	2.01	0.42
76:k3:156:TYR:O	76:k3:158:GLN:NE2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:l3:330:PRO:HB2	80:o3:50:TYR:HD2	1.84	0.42
86:u3:12:VAL:HG21	86:u3:82:ILE:HD13	2.00	0.42
5:E1:160:GLU:OE1	5:E1:163:ARG:NH1	2.52	0.42
6:F1:29:ARG:NE	7:G1:147:GLU:OE2	2.52	0.42
6:F1:84:TYR:CE1	6:F1:93:MET:HE3	2.54	0.42
15:O1:11:ASN:ND2	38:A2:1669:A:OP1	2.45	0.42
16:P1:18:LEU:HD12	16:P1:18:LEU:HA	1.84	0.42
20:T1:25:THR:HG22	38:A2:2524:G:H5"	2.01	0.42
20:T1:53:LEU:HA	20:T1:53:LEU:HD23	1.82	0.42
22:V1:30:ARG:NH1	38:A2:327:U:O2'	2.43	0.42
31:e1:124:PRO:HG2	31:e1:180:ILE:HD12	2.01	0.42
36:21:62:G:H2'	36:21:63:G:C8	2.55	0.42
38:A2:260:C:H2'	38:A2:261:G:C8	2.55	0.42
38:A2:3702:U:H2'	38:A2:3703:C:H6	1.85	0.42
38:A2:3727:A:H2'	38:A2:3728:A:H8	1.85	0.42
38:A2:4523:C:H2'	38:A2:4524:G:C8	2.55	0.42
41:A3:730:C:H2'	41:A3:731:G:H8	1.85	0.42
42:B3:99:ILE:HD11	42:B3:117:ARG:NH1	2.35	0.42
56:P3:31:CYS:HB2	56:P3:93:LEU:HD13	2.02	0.42
60:T3:11:HIS:ND1	84:s3:121:PRO:HG3	2.35	0.42
66:Z3:27:VAL:HB	66:Z3:69:THR:HB	2.01	0.42
76:k3:238:LYS:HE2	76:k3:238:LYS:HB2	1.77	0.42
36:21:18:G:H1'	36:21:57:G:H22	1.85	0.42
38:A2:551:C:H2'	38:A2:552:U:C6	2.54	0.42
38:A2:4926:C:H5'	38:A2:4927:G:H5'	2.02	0.42
41:A3:604:A:H5'	51:K3:22:LYS:HG3	2.01	0.42
41:A3:812:A:H5'	46:F3:16:LYS:HD2	2.02	0.42
41:A3:1004:U:H2'	41:A3:1005:G:C8	2.55	0.42
41:A3:1619:A:H4'	57:Q3:44:ARG:HE	1.85	0.42
42:B3:147:LEU:HD13	42:B3:161:ILE:HB	2.02	0.42
48:H3:70:HIS:HA	48:H3:98:ARG:HH12	1.85	0.42
53:M3:68:ILE:HD11	53:M3:141:ASN:HD22	1.84	0.42
66:Z3:9:THR:HG21	66:Z3:48:TYR:HE2	1.85	0.42
75:j3:92:LYS:HG3	75:j3:106:THR:HG21	2.02	0.42
1:A1:47:LYS:HE3	1:A1:51:LEU:HD11	2.01	0.42
14:N1:65:ARG:NH2	38:A2:87:A:H5'	2.35	0.42
23:W1:27:TYR:HA	23:W1:34:CYS:HA	2.01	0.42
29:c1:21:SER:OG	38:A2:3688:U:O3'	2.34	0.42
36:21:35:A:H2'	36:21:36:A:C8	2.55	0.42
41:A3:33:G:O2'	41:A3:564:A:O2'	2.37	0.42
41:A3:77:A:C8	48:H3:154:ARG:HD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:F3:168:LYS:HD3	46:F3:168:LYS:HA	1.81	0.42
56:P3:18:GLY:HA2	56:P3:19:PRO:HD2	1.93	0.42
65:Y3:124:LYS:HA	65:Y3:129:SER:HA	2.01	0.42
76:k3:128:LYS:HE3	76:k3:128:LYS:HB3	1.75	0.42
80:o3:89:ALA:HB2	80:o3:124:LEU:HD11	2.01	0.42
3:C1:13:LYS:HB3	3:C1:152:GLU:HG2	2.02	0.41
14:N1:136:LYS:NZ	38:A2:1396:A:OP1	2.48	0.41
19:S1:85:ARG:NH2	38:A2:2068:C:OP2	2.53	0.41
22:V1:50:PHE:O	22:V1:55:ARG:NH1	2.53	0.41
38:A2:25:A:N3	38:A2:339:C:O2'	2.47	0.41
38:A2:1080:C:N4	38:A2:1216:G:O6	2.53	0.41
38:A2:2542:C:H2'	38:A2:2543:C:C6	2.55	0.41
38:A2:3608:U:H2'	38:A2:3609:G:C8	2.55	0.41
38:A2:3741:A:H5"	75:j3:244:GLY:HA3	2.02	0.41
38:A2:4132:G:H2'	38:A2:4133:G:H8	1.85	0.41
40:C2:106:G:H4'	40:C2:137:A:H5'	2.02	0.41
41:A3:79:A:H3'	41:A3:80:G:H8	1.85	0.41
41:A3:1801:A:H2'	41:A3:1802:C:C6	2.55	0.41
45:E3:96:LEU:HD21	45:E3:190:LEU:HG	2.01	0.41
54:N3:46:GLN:OE1	54:N3:112:LYS:NZ	2.35	0.41
56:P3:148:GLY:O	56:P3:150:ARG:NH1	2.46	0.41
76:k3:144:ARG:O	76:k3:148:LYS:HD3	2.19	0.41
85:t3:210:LYS:HE2	85:t3:210:LYS:HB2	1.90	0.41
86:u3:13:ALA:HB1	86:u3:55:MET:HB2	2.02	0.41
1:A1:184:ILE:HD12	38:A2:99:A:H5"	2.02	0.41
5:E1:61:ALA:HB1	5:E1:65:LYS:NZ	2.35	0.41
18:R1:75:ARG:HD2	18:R1:95:TYR:HE1	1.84	0.41
18:R1:98:GLU:OE1	38:A2:2327:C:O2'	2.32	0.41
26:Z1:60:ALA:O	26:Z1:64:ASN:ND2	2.53	0.41
31:e1:59:THR:HA	31:e1:62:ARG:HG2	2.02	0.41
38:A2:190:G:H2'	38:A2:191:G:C8	2.55	0.41
38:A2:1346:U:H2'	38:A2:1347:G:C8	2.54	0.41
38:A2:4558:U:O2'	38:A2:4559:G:O4'	2.37	0.41
41:A3:571:U:H5"	66:Z3:37:LYS:HG3	2.03	0.41
41:A3:656:G:H5'	41:A3:662:G:N2	2.35	0.41
41:A3:1221:G:O2'	41:A3:1676:U:O2	2.29	0.41
41:A3:1277:C:H2'	41:A3:1278:A:C8	2.55	0.41
48:H3:43:GLU:OE2	48:H3:119:LYS:NZ	2.52	0.41
56:P3:34:PHE:HE1	56:P3:100:THR:HA	1.85	0.41
74:h3:220:ASP:OD1	74:h3:220:ASP:N	2.53	0.41
80:o3:93:ARG:HB2	80:o3:113:LEU:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C1:54:LYS:HA	3:C1:83:TRP:CD1	2.55	0.41
5:E1:76:MET:HE3	5:E1:76:MET:HB3	1.91	0.41
13:M1:135:ARG:NH2	38:A2:4116:C:O2	2.53	0.41
16:P1:18:LEU:HD11	16:P1:94:LEU:HD21	2.02	0.41
27:a1:11:ARG:HH21	41:A3:1184:G:P	2.42	0.41
31:e1:121:VAL:O	31:e1:160:LEU:N	2.53	0.41
31:e1:129:GLY:HA2	31:e1:151:THR:HG22	2.02	0.41
38:A2:408:A:H4'	38:A2:409:G:H3'	2.00	0.41
38:A2:3791:U:O2'	41:A3:1720:U:O2'	2.32	0.41
38:A2:3843:U:H2'	38:A2:3844:A:H8	1.85	0.41
38:A2:3937:A:H2'	38:A2:3938:A:C8	2.55	0.41
38:A2:4621:A:H2	38:A2:4649:G:H21	1.69	0.41
41:A3:220:U:H2'	41:A3:221:A:C8	2.55	0.41
41:A3:1786:U:H2'	41:A3:1787:G:H8	1.85	0.41
78:m3:55:VAL:HG22	78:m3:60:ILE:HD13	2.02	0.41
1:A1:31:ARG:HH12	38:A2:4072:C:P	2.44	0.41
5:E1:119:MET:HE3	5:E1:119:MET:HB2	1.98	0.41
9:I1:4:ARG:HG2	38:A2:4580:U:H4'	2.02	0.41
9:I1:42:VAL:HA	9:I1:61:VAL:HA	2.03	0.41
9:I1:85:ARG:H	9:I1:101:ASN:ND2	2.18	0.41
17:Q1:19:GLU:OE1	17:Q1:19:GLU:N	2.52	0.41
28:b1:73:VAL:O	28:b1:78:ARG:NH1	2.53	0.41
31:e1:24:TYR:HE1	31:e1:92:LYS:HB2	1.84	0.41
33:l1:158:GLN:H	33:l1:165:LEU:HD21	1.85	0.41
38:A2:1617:G:H1'	38:A2:2516:A:N6	2.35	0.41
38:A2:2298:C:H2'	38:A2:2299:G:C8	2.54	0.41
38:A2:2393:G:H22	38:A2:2828:A:H2	1.68	0.41
38:A2:3678:C:O2'	75:j3:174:ARG:NH2	2.53	0.41
38:A2:4160:U:H2'	38:A2:4161:G:H8	1.85	0.41
40:C2:149:G:H21	81:p3:117:GLN:HE22	1.68	0.41
41:A3:15:U:H2'	41:A3:16:G:O4'	2.20	0.41
42:B3:123:VAL:HG12	42:B3:175:TRP:CH2	2.55	0.41
43:C3:174:ARG:NH2	43:C3:175:GLU:OE2	2.53	0.41
44:D3:123:ARG:HB3	44:D3:143:CYS:SG	2.60	0.41
44:D3:192:LEU:O	44:D3:226:ALA:HA	2.21	0.41
46:F3:151:ASP:HB3	46:F3:154:ILE:HG13	2.02	0.41
51:K3:131:ARG:NH1	51:K3:143:ASN:O	2.53	0.41
52:L3:14:LEU:HD22	52:L3:35:LEU:HG	2.03	0.41
52:L3:29:MET:HB2	52:L3:29:MET:HE3	1.85	0.41
52:L3:64:TRP:CD2	71:e3:23:VAL:HG22	2.55	0.41
60:T3:91:LYS:HB2	60:T3:91:LYS:HE3	1.79	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:k3:14:LEU:HD22	76:k3:17:LEU:HD13	2.02	0.41
77:l3:291:ARG:HD2	77:l3:291:ARG:HA	1.80	0.41
86:u3:132:ARG:HA	86:u3:135:LEU:HG	2.02	0.41
1:A1:104:GLU:HA	1:A1:160:GLU:HG3	2.03	0.41
1:A1:178:HIS:HA	1:A1:181:HIS:NE2	2.35	0.41
2:B1:14:HIS:CD2	2:B1:19:LEU:HD13	2.55	0.41
7:G1:87:LYS:HD3	7:G1:87:LYS:HA	1.86	0.41
7:G1:108:ARG:NH1	38:A2:1837:A:OP1	2.53	0.41
18:R1:77:PHE:HB3	18:R1:88:LEU:HD11	2.01	0.41
19:S1:2:SER:O	38:A2:4928:U:O2'	2.29	0.41
20:T1:105:LYS:HB2	20:T1:105:LYS:HE2	1.84	0.41
38:A2:922:C:C2	38:A2:923:C:N3	2.88	0.41
38:A2:4244:C:H2'	38:A2:4245:C:H6	1.85	0.41
38:A2:4504:A:OP1	38:A2:4506:G:O2'	2.37	0.41
39:B2:63:C:H42	83:r3:202:ASN:HD22	1.69	0.41
41:A3:107:A:H2'	41:A3:108:G:C8	2.56	0.41
41:A3:399:C:H5	41:A3:680:G:H5"	1.85	0.41
41:A3:661:U:OP1	65:Y3:5:ARG:NH1	2.54	0.41
41:A3:756:C:N4	41:A3:788:G:O6	2.53	0.41
43:C3:107:ARG:NH2	56:P3:133:THR:O	2.53	0.41
52:L3:41:PRO:HD2	52:L3:44:HIS:HB2	2.03	0.41
65:Y3:128:VAL:HG13	65:Y3:133:LEU:HD11	2.01	0.41
80:o3:154:TYR:HD1	80:o3:186:MET:HE3	1.86	0.41
6:F1:160:ARG:HB3	38:A2:1921:C:H1'	2.02	0.41
7:G1:36:LYS:HA	7:G1:36:LYS:HD3	1.86	0.41
12:L1:46:SER:OG	38:A2:239:C:OP1	2.36	0.41
23:W1:49:TRP:O	38:A2:1646:A:O2'	2.34	0.41
30:d1:58:LYS:HA	30:d1:58:LYS:HD3	1.85	0.41
38:A2:1590:C:H4'	38:A2:2860:A:H5'	2.03	0.41
38:A2:1755:C:O2'	38:A2:1757:U:OP2	2.39	0.41
38:A2:2000:G:H4'	38:A2:2017:A:H2	1.86	0.41
38:A2:2738:G:H2'	38:A2:2739:G:H8	1.86	0.41
38:A2:3765:U:H2'	38:A2:3766:C:C6	2.56	0.41
41:A3:85:A:OP1	66:Z3:122:LYS:NZ	2.42	0.41
41:A3:507:G:OP1	66:Z3:108:LYS:NZ	2.46	0.41
41:A3:874:G:H2'	41:A3:875:A:C8	2.51	0.41
41:A3:1230:C:OP1	60:T3:130:ARG:NH2	2.42	0.41
41:A3:1392:U:OP1	62:V3:83:ARG:NH1	2.51	0.41
42:B3:207:PRO:HA	42:B3:210:ILE:HG22	2.02	0.41
43:C3:148:ASN:HB2	59:S3:127:ASN:ND2	2.35	0.41
45:E3:57:ASN:O	45:E3:65:ARG:NH1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:L3:45:VAL:HG11	52:L3:48:ALA:HB3	2.03	0.41
59:S3:41:ILE:HG23	59:S3:46:LEU:HD23	2.02	0.41
66:Z3:74:MET:HE3	66:Z3:74:MET:HB2	1.87	0.41
78:m3:193:GLU:O	78:m3:197:LYS:HG2	2.21	0.41
80:o3:55:HIS:NE2	80:o3:59:GLU:OE2	2.53	0.41
81:p3:243:LEU:HD12	81:p3:246:LEU:HD12	2.03	0.41
17:Q1:64:ILE:O	38:A2:2376:C:O2'	2.30	0.41
27:a1:12:ARG:HG2	27:a1:15:ARG:HH22	1.86	0.41
28:b1:8:ARG:NH1	38:A2:4218:U:O4	2.41	0.41
33:l1:139:THR:HG23	33:l1:141:ASN:H	1.86	0.41
33:l1:144:MET:HE2	33:l1:148:VAL:HG21	2.03	0.41
38:A2:2654:C:O2'	38:A2:2656:C:OP1	2.37	0.41
38:A2:3928:G:H2'	38:A2:3929:G:H8	1.86	0.41
38:A2:4850:G:H5"	86:u3:90:ARG:NH1	2.35	0.41
40:C2:140:C:H2'	40:C2:141:C:C6	2.56	0.41
41:A3:154:U:O2	48:H3:4:ASN:ND2	2.42	0.41
41:A3:604:A:N3	41:A3:639:C:O2'	2.50	0.41
41:A3:649:U:H2'	41:A3:650:A:H8	1.85	0.41
41:A3:928:G:H2'	41:A3:929:G:C8	2.55	0.41
41:A3:1677:U:H2'	41:A3:1678:A:H8	1.86	0.41
41:A3:1834:A:H2	41:A3:1837:G:H1	1.67	0.41
42:B3:18:PHE:CE1	42:B3:177:MET:HE2	2.56	0.41
47:G3:52:SER:OG	47:G3:70:GLU:OE1	2.37	0.41
59:S3:35:CYS:HA	59:S3:38:ILE:HG12	2.03	0.41
78:m3:77:ALA:O	78:m3:108:ARG:NH1	2.54	0.41
2:B1:179:LYS:HA	2:B1:182:GLU:OE1	2.20	0.41
2:B1:188:LYS:HB3	2:B1:188:LYS:HE3	1.91	0.41
6:F1:7:LEU:HG	6:F1:107:THR:HB	2.02	0.41
7:G1:158:PHE:HZ	83:r3:53:VAL:HG11	1.85	0.41
19:S1:58:VAL:O	38:A2:4926:C:N4	2.54	0.41
20:T1:29:ARG:NH1	38:A2:2525:G:OP1	2.54	0.41
26:Z1:87:LYS:HB2	26:Z1:87:LYS:HE3	1.84	0.41
33:l1:41:TYR:H	33:l1:163:LEU:HD21	1.85	0.41
38:A2:1303:C:OP1	40:C2:7:U:O2'	2.39	0.41
38:A2:1787:A:N3	38:A2:4196:U:O2'	2.53	0.41
38:A2:3905:C:H2'	38:A2:3906:C:C6	2.56	0.41
38:A2:4330:U:H2'	38:A2:4331:C:C6	2.55	0.41
42:B3:57:LYS:HA	42:B3:57:LYS:HD2	1.80	0.41
43:C3:143:THR:HB	43:C3:205:TYR:CE2	2.56	0.41
61:U3:6:VAL:O	61:U3:11:GLN:NE2	2.49	0.41
65:Y3:40:PRO:HB3	65:Y3:79:LYS:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:o3:39:LYS:HA	80:o3:42:ARG:HE	1.86	0.41
85:t3:46:ILE:O	85:t3:149:GLN:NE2	2.54	0.41
85:t3:139:SER:HB3	85:t3:143:GLU:HG3	2.03	0.41
3:C1:5:SER:OG	38:A2:423:G:N2	2.54	0.41
5:E1:68:LEU:HD23	5:E1:68:LEU:HA	1.94	0.41
12:L1:34:LEU:HD21	12:L1:47:MET:HB2	2.03	0.41
14:N1:6:ARG:NH1	38:A2:1510:G:OP2	2.54	0.41
14:N1:90:ALA:HA	14:N1:93:ASN:OD1	2.20	0.41
25:Y1:35:ILE:HA	25:Y1:35:ILE:HD12	1.80	0.41
29:c1:46:LYS:HE3	29:c1:46:LYS:HB3	1.85	0.41
31:e1:14:PHE:HA	31:e1:17:ILE:HD12	2.03	0.41
38:A2:150:U:O4	81:p3:240:LYS:NZ	2.44	0.41
38:A2:158:A:H5"	38:A2:159:C:H2'	2.03	0.41
38:A2:967:A:H1'	38:A2:969:C:N4	2.35	0.41
38:A2:979:C:H1'	77:l3:323:ARG:HD3	2.03	0.41
38:A2:1200:C:H2'	38:A2:1201:G:H8	1.85	0.41
38:A2:1348:C:H2'	38:A2:1349:G:C8	2.56	0.41
38:A2:1755:C:O2'	38:A2:1768:C:N4	2.54	0.41
38:A2:1758:G:H2'	38:A2:1759:G:C8	2.56	0.41
38:A2:4086:G:H3'	38:A2:4087:G:H8	1.84	0.41
38:A2:4564:G:H2'	38:A2:4565:U:C6	2.56	0.41
38:A2:4685:U:H1'	38:A2:4686:A:H5"	2.01	0.41
38:A2:4889:G:N2	38:A2:4895:G:H2'	2.36	0.41
41:A3:1004:U:H2'	41:A3:1005:G:H8	1.86	0.41
41:A3:1714:U:H2'	41:A3:1715:A:C8	2.55	0.41
46:F3:100:ARG:HB2	46:F3:114:ILE:HD13	2.03	0.41
47:G3:167:LYS:NZ	47:G3:172:CYS:SG	2.92	0.41
48:H3:26:THR:HG23	48:H3:27:PHE:HD2	1.85	0.41
49:I3:145:ARG:NH2	64:X3:51:GLU:OE2	2.52	0.41
56:P3:26:ASN:HB2	56:P3:28:PHE:HE1	1.85	0.41
60:T3:21:ASP:HB3	60:T3:24:ARG:HG3	2.03	0.41
63:W3:1:MET:HE2	63:W3:1:MET:HB2	1.93	0.41
65:Y3:109:GLY:HA2	65:Y3:119:ARG:HD3	2.03	0.41
66:Z3:27:VAL:HG12	66:Z3:29:HIS:HD2	1.86	0.41
73:g3:90:LYS:HA	73:g3:90:LYS:HD3	1.92	0.41
80:o3:181:TYR:CZ	80:o3:202:GLU:HG2	2.56	0.41
85:t3:63:THR:O	85:t3:65:ARG:N	2.54	0.41
85:t3:80:GLU:OE1	85:t3:102:ARG:NH2	2.54	0.41
86:u3:113:MET:HE3	86:u3:113:MET:HB3	2.00	0.41
1:A1:54:LYS:HA	1:A1:54:LYS:HD3	1.72	0.41
12:L1:103:LYS:NZ	38:A2:231:U:O2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S1:45:LYS:HD3	19:S1:107:PRO:HD2	2.02	0.41
20:T1:56:VAL:HG13	20:T1:72:LYS:HA	2.02	0.41
23:W1:84:PRO:HD3	40:C2:94:G:C5	2.56	0.41
33:l1:144:MET:HB2	33:l1:148:VAL:HG23	2.02	0.41
35:n1:1:MET:HG3	35:n1:4:LYS:HE3	2.03	0.41
38:A2:3712:A:H2'	38:A2:3713:A:H8	1.85	0.41
38:A2:4074:C:H2'	38:A2:4075:G:H8	1.86	0.41
38:A2:4579:C:H2'	38:A2:4580:U:H6	1.86	0.41
38:A2:4686:A:H2	82:q3:69:THR:HG22	1.86	0.41
39:B2:52:C:O2'	84:s3:12:MET:HE1	2.21	0.41
41:A3:1201:U:O2'	41:A3:1358:U:O2'	2.31	0.41
41:A3:1244:U:H2'	41:A3:1245:G:C8	2.56	0.41
43:C3:131:ASP:N	43:C3:131:ASP:OD1	2.54	0.41
49:I3:125:VAL:O	49:I3:129:ILE:HD12	2.21	0.41
52:L3:13:GLU:HG3	52:L3:17:LYS:NZ	2.35	0.41
55:O3:136:PRO:HA	55:O3:137:PRO:HD3	1.95	0.41
70:d3:21:THR:HB	70:d3:68:LEU:HD11	2.03	0.41
74:h3:5:MET:HG3	74:h3:268:ASP:OD2	2.21	0.41
81:p3:270:LYS:HA	81:p3:273:GLU:HG2	2.01	0.41
82:q3:111:LEU:HD21	82:q3:125:ARG:HG2	2.03	0.41
12:L1:31:SER:HA	12:L1:48:PRO:HA	2.03	0.40
35:n1:45:GLU:HG2	35:n1:49:LYS:NZ	2.36	0.40
36:21:28:U:H2'	36:21:29:G:C8	2.55	0.40
36:21:35:A:H2'	36:21:36:A:H8	1.85	0.40
38:A2:3927:U:H2'	38:A2:3928:G:C8	2.55	0.40
38:A2:4446:U:H2'	38:A2:4447:C:C6	2.56	0.40
41:A3:1144:A:H2'	41:A3:1145:A:C8	2.55	0.40
41:A3:1609:C:H2'	41:A3:1610:G:H8	1.85	0.40
43:C3:142:PHE:HD2	43:C3:209:ASP:HB2	1.86	0.40
44:D3:256:TRP:CD1	64:X3:68:ARG:HG2	2.55	0.40
46:F3:211:LYS:HE2	46:F3:215:GLY:HA2	2.03	0.40
64:X3:100:GLY:HA2	64:X3:130:PHE:HB3	2.03	0.40
74:h3:11:LEU:HB2	74:h3:307:VAL:HG13	2.03	0.40
74:h3:30:MET:HA	74:h3:43:TRP:O	2.20	0.40
78:m3:81:HIS:HA	78:m3:92:LEU:HD13	2.03	0.40
79:n3:154:ILE:HB	79:n3:198:ILE:HB	2.02	0.40
83:r3:184:MET:HG3	83:r3:190:LEU:HG	2.02	0.40
5:E1:63:CYS:SG	38:A2:2812:G:H5"	2.61	0.40
38:A2:1870:C:H2'	38:A2:1871:A:C8	2.56	0.40
38:A2:1996:C:H42	38:A2:2000:G:H1	1.68	0.40
38:A2:3718:A:H2'	38:A2:3719:A:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A2:4709:A:H2'	38:A2:4710:A:C8	2.56	0.40
41:A3:28:U:H2'	41:A3:29:G:C8	2.57	0.40
41:A3:886:A:H3'	41:A3:887:U:H5"	2.03	0.40
41:A3:1865:C:O2	68:b3:92:ARG:HG2	2.21	0.40
59:S3:103:LYS:HD2	59:S3:103:LYS:HA	1.95	0.40
60:T3:142:ARG:HD3	60:T3:142:ARG:HA	1.89	0.40
65:Y3:40:PRO:HA	65:Y3:79:LYS:HE3	2.02	0.40
72:f3:84:LYS:O	72:f3:88:GLN:HG2	2.21	0.40
74:h3:197:THR:HG21	74:h3:239:LEU:H	1.86	0.40
5:E1:23:TRP:CD1	38:A2:2390:G:H5"	2.57	0.40
6:F1:47:PHE:HE1	6:F1:125:GLN:HG2	1.86	0.40
11:K1:127:LEU:HD11	11:K1:135:LYS:HE2	2.03	0.40
21:U1:104:THR:HG22	21:U1:106:LYS:H	1.86	0.40
29:c1:90:LYS:HD2	75:j3:96:LEU:HD22	2.04	0.40
33:l1:60:ARG:HD3	33:l1:168:ALA:HB1	2.03	0.40
38:A2:172:C:H4'	85:t3:129:ARG:HH12	1.85	0.40
38:A2:2107:A:N3	80:o3:31:ARG:HD2	2.36	0.40
38:A2:2485:C:H2'	38:A2:2486:G:C8	2.57	0.40
38:A2:3687:A:H62	38:A2:3818:G:N2	2.14	0.40
38:A2:4079:A:H5"	81:p3:109:LYS:HB2	2.03	0.40
41:A3:155:G:H2'	41:A3:156:G:C8	2.56	0.40
41:A3:1412:C:H2'	41:A3:1413:G:H8	1.86	0.40
41:A3:1536:G:H2'	41:A3:1537:A:C8	2.56	0.40
41:A3:1736:G:H2'	41:A3:1737:G:H8	1.87	0.40
44:D3:183:LYS:HA	44:D3:195:LEU:O	2.21	0.40
54:N3:63:LYS:HA	54:N3:66:GLU:HB2	2.03	0.40
65:Y3:60:LYS:HE3	65:Y3:116:PRO:HD3	2.02	0.40
69:c3:64:CYS:HB3	69:c3:73:LEU:HD23	2.03	0.40
74:h3:39:THR:HA	74:h3:59:LEU:O	2.22	0.40
76:k3:85:VAL:HG22	76:k3:204:GLN:HG2	2.03	0.40
76:k3:223:THR:HB	76:k3:275:HIS:H	1.86	0.40
80:o3:23:ASN:HB3	80:o3:24:PHE:H	1.63	0.40
81:p3:310:LYS:HA	81:p3:310:LYS:HD2	1.91	0.40
82:q3:89:ARG:HA	82:q3:146:LEU:O	2.21	0.40
4:D1:63:LEU:O	4:D1:67:ILE:HG12	2.22	0.40
5:E1:116:ASP:OD2	5:E1:119:MET:HG2	2.22	0.40
7:G1:78:LYS:HD3	7:G1:87:LYS:HE3	2.02	0.40
18:R1:15:LYS:NZ	18:R1:59:GLY:O	2.50	0.40
22:V1:43:MET:HE1	81:p3:229:LYS:HD3	2.04	0.40
24:X1:24:LYS:HE3	24:X1:24:LYS:HB3	1.81	0.40
36:21:52:U:H2'	36:21:53:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:A2:75:G:C6	85:t3:102:ARG:HA	2.57	0.40
38:A2:1306:C:H2'	38:A2:1307:C:C6	2.56	0.40
38:A2:2847:A:O2'	38:A2:4617:G:H4'	2.22	0.40
38:A2:3605:A:O2'	50:J3:89:GLU:OE2	2.40	0.40
38:A2:3765:U:H2'	38:A2:3766:C:H6	1.87	0.40
38:A2:4087:G:H22	38:A2:4108:G:N2	2.19	0.40
38:A2:4236:G:O2'	84:s3:129:ASP:OD2	2.28	0.40
38:A2:4955:U:H1'	38:A2:4968:G:C2	2.57	0.40
38:A2:4975:G:H2'	38:A2:4976:G:H8	1.86	0.40
41:A3:168:C:O2'	48:H3:133:LEU:O	2.36	0.40
41:A3:193:C:H2'	41:A3:194:C:C6	2.57	0.40
41:A3:640:A:H2'	41:A3:641:A:C8	2.56	0.40
41:A3:877:C:H2'	41:A3:878:G:C8	2.57	0.40
41:A3:1311:C:H5"	73:g3:143:LYS:NZ	2.36	0.40
43:C3:128:LYS:NZ	43:C3:129:THR:O	2.46	0.40
52:L3:12:TYR:OH	52:L3:52:LEU:HD11	2.21	0.40
56:P3:61:LYS:HD2	56:P3:76:LEU:HB3	2.04	0.40
60:T3:90:VAL:HG23	60:T3:91:LYS:HG3	2.02	0.40
61:U3:11:GLN:OE1	61:U3:62:ARG:HD2	2.22	0.40
75:j3:149:LYS:HB2	75:j3:149:LYS:HE3	1.90	0.40
76:k3:48:GLY:HA3	76:k3:81:THR:HG22	2.03	0.40
76:k3:93:VAL:HG13	76:k3:102:PHE:HB2	2.04	0.40
78:m3:65:ALA:HB2	78:m3:74:ILE:HD13	2.02	0.40
80:o3:235:ARG:HB2	80:o3:238:GLN:HB2	2.04	0.40
81:p3:162:GLU:HA	81:p3:165:GLN:HG3	2.03	0.40
81:p3:246:LEU:HD23	81:p3:246:LEU:HA	1.92	0.40
5:E1:80:LYS:HD2	5:E1:80:LYS:HA	1.88	0.40
5:E1:88:ARG:HG2	38:A2:2815:A:H5'	2.03	0.40
13:M1:95:VAL:HG11	13:M1:113:GLU:HG3	2.03	0.40
16:P1:29:LEU:HD23	16:P1:94:LEU:HD13	2.04	0.40
32:f1:76:SER:HB2	32:f1:79:ALA:H	1.87	0.40
38:A2:551:C:O2'	85:t3:115:GLN:OE1	2.29	0.40
38:A2:1475:G:H2'	38:A2:1476:C:C6	2.57	0.40
41:A3:74:G:H22	48:H3:159:ARG:HH22	1.69	0.40
41:A3:1410:C:H2'	41:A3:1411:G:H8	1.85	0.40
43:C3:52:THR:HG23	43:C3:57:ILE:HA	2.03	0.40
46:F3:101:LEU:HA	46:F3:101:LEU:HD23	1.87	0.40
48:H3:76:LEU:HD12	48:H3:76:LEU:HA	1.92	0.40
51:K3:182:GLN:HA	51:K3:185:ALA:HB3	2.03	0.40
53:M3:111:VAL:HG12	53:M3:140:PHE:HB2	2.04	0.40
58:R3:72:VAL:HG21	58:R3:80:GLN:HG3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:V3:23:THR:HB	62:V3:113:GLU:HB3	2.02	0.40
74:h3:23:THR:HG22	74:h3:31:ILE:HG22	2.03	0.40
74:h3:87:LEU:HB2	74:h3:101:PHE:HB2	2.04	0.40
74:h3:230:LEU:HD22	74:h3:259:TRP:CE3	2.56	0.40
74:h3:246:TYR:CE2	74:h3:261:LEU:HB2	2.56	0.40
75:j3:173:GLY:O	75:j3:176:ASP:HB2	2.21	0.40
83:r3:35:ASP:HA	83:r3:87:ILE:O	2.21	0.40
84:s3:64:ARG:HG2	84:s3:65:ASN:N	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
2	B1	197/199 (99%)	191 (97%)	6 (3%)	0	100	100
3	C1	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
4	D1	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
5	E1	178/180 (99%)	174 (98%)	4 (2%)	0	100	100
6	F1	174/176 (99%)	164 (94%)	10 (6%)	0	100	100
7	G1	157/159 (99%)	153 (98%)	4 (2%)	0	100	100
8	H1	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
9	I1	137/139 (99%)	134 (98%)	3 (2%)	0	100	100
10	J1	102/106 (96%)	101 (99%)	1 (1%)	0	100	100
11	K1	116/118 (98%)	114 (98%)	2 (2%)	0	100	100
12	L1	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
13	M1	133/135 (98%)	127 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	N1	145/147 (99%)	136 (94%)	9 (6%)	0	100	100
15	O1	100/116 (86%)	98 (98%)	2 (2%)	0	100	100
16	P1	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
17	Q1	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
18	R1	126/128 (98%)	121 (96%)	5 (4%)	0	100	100
19	S1	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
20	T1	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
21	U1	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
22	V1	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
23	W1	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
24	X1	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
25	Y1	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
26	Z1	50/52 (96%)	50 (100%)	0	0	100	100
27	a1	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
28	b1	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
29	c1	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
30	d1	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
31	e1	194/196 (99%)	176 (91%)	18 (9%)	0	100	100
32	f1	151/153 (99%)	134 (89%)	17 (11%)	0	100	100
33	l1	204/206 (99%)	173 (85%)	30 (15%)	1 (0%)	24	57
35	n1	234/236 (99%)	229 (98%)	5 (2%)	0	100	100
37	11	3/5 (60%)	1 (33%)	2 (67%)	0	100	100
42	B3	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
43	C3	211/213 (99%)	202 (96%)	9 (4%)	0	100	100
44	D3	219/221 (99%)	212 (97%)	7 (3%)	0	100	100
45	E3	226/228 (99%)	216 (96%)	10 (4%)	0	100	100
46	F3	260/262 (99%)	249 (96%)	11 (4%)	0	100	100
47	G3	181/191 (95%)	173 (96%)	8 (4%)	0	100	100
48	H3	235/237 (99%)	226 (96%)	9 (4%)	0	100	100
49	I3	181/189 (96%)	174 (96%)	7 (4%)	0	100	100
50	J3	204/206 (99%)	193 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	K3	183/185 (99%)	180 (98%)	3 (2%)	0	100	100
52	L3	94/96 (98%)	83 (88%)	9 (10%)	2 (2%)	5	25
53	M3	139/151 (92%)	129 (93%)	10 (7%)	0	100	100
54	N3	115/117 (98%)	102 (89%)	13 (11%)	0	100	100
55	O3	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
56	P3	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
57	Q3	127/129 (98%)	123 (97%)	3 (2%)	1 (1%)	16	47
58	R3	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
59	S3	130/132 (98%)	124 (95%)	6 (5%)	0	100	100
60	T3	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
61	U3	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
62	V3	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
63	W3	81/83 (98%)	81 (100%)	0	0	100	100
64	X3	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
65	Y3	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	18	49
66	Z3	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
67	a3	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
68	b3	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
69	c3	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
70	d3	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
71	e3	53/55 (96%)	51 (96%)	2 (4%)	0	100	100
72	f3	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
73	g3	66/68 (97%)	59 (89%)	7 (11%)	0	100	100
74	h3	311/313 (99%)	287 (92%)	24 (8%)	0	100	100
75	j3	246/248 (99%)	233 (95%)	13 (5%)	0	100	100
76	k3	392/394 (100%)	373 (95%)	19 (5%)	0	100	100
77	l3	360/362 (99%)	345 (96%)	15 (4%)	0	100	100
78	m3	291/293 (99%)	282 (97%)	9 (3%)	0	100	100
79	n3	208/251 (83%)	199 (96%)	9 (4%)	0	100	100
80	o3	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
81	p3	229/240 (95%)	221 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
82	q3	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
83	r3	201/213 (94%)	195 (97%)	6 (3%)	0	100	100
84	s3	168/170 (99%)	168 (100%)	0	0	100	100
85	t3	208/210 (99%)	197 (95%)	10 (5%)	1 (0%)	24	57
86	u3	136/138 (99%)	131 (96%)	5 (4%)	0	100	100
All	All	11979/12239 (98%)	11459 (96%)	514 (4%)	6 (0%)	49	78

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	l1	57	SER
52	L3	45	VAL
52	L3	46	MET
57	Q3	18	ARG
85	t3	64	VAL
65	Y3	62	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A1	171/171 (100%)	171 (100%)	0	100	100
2	B1	171/171 (100%)	171 (100%)	0	100	100
3	C1	134/134 (100%)	134 (100%)	0	100	100
4	D1	164/164 (100%)	164 (100%)	0	100	100
5	E1	159/159 (100%)	159 (100%)	0	100	100
6	F1	157/157 (100%)	157 (100%)	0	100	100
7	G1	139/139 (100%)	139 (100%)	0	100	100
8	H1	89/89 (100%)	89 (100%)	0	100	100
9	I1	106/106 (100%)	106 (100%)	0	100	100
10	J1	86/86 (100%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	K1	106/106 (100%)	106 (100%)	0	100	100
12	L1	124/124 (100%)	124 (100%)	0	100	100
13	M1	117/117 (100%)	117 (100%)	0	100	100
14	N1	119/119 (100%)	118 (99%)	1 (1%)	73	81
15	O1	84/95 (88%)	84 (100%)	0	100	100
16	P1	84/84 (100%)	84 (100%)	0	100	100
17	Q1	98/98 (100%)	98 (100%)	0	100	100
18	R1	114/114 (100%)	114 (100%)	0	100	100
19	S1	88/88 (100%)	88 (100%)	0	100	100
20	T1	98/98 (100%)	98 (100%)	0	100	100
21	U1	109/109 (100%)	109 (100%)	0	100	100
22	V1	86/86 (100%)	86 (100%)	0	100	100
23	W1	73/73 (100%)	73 (100%)	0	100	100
24	X1	64/64 (100%)	64 (100%)	0	100	100
25	Y1	47/47 (100%)	47 (100%)	0	100	100
26	Z1	48/48 (100%)	48 (100%)	0	100	100
27	a1	24/24 (100%)	24 (100%)	0	100	100
28	b1	92/92 (100%)	92 (100%)	0	100	100
29	c1	74/74 (100%)	74 (100%)	0	100	100
30	d1	108/108 (100%)	108 (100%)	0	100	100
31	e1	164/164 (100%)	164 (100%)	0	100	100
32	f1	126/126 (100%)	126 (100%)	0	100	100
33	l1	186/186 (100%)	186 (100%)	0	100	100
35	n1	213/219 (97%)	213 (100%)	0	100	100
37	11	4/4 (100%)	4 (100%)	0	100	100
42	B3	180/181 (99%)	180 (100%)	0	100	100
43	C3	194/194 (100%)	194 (100%)	0	100	100
44	D3	187/187 (100%)	187 (100%)	0	100	100
45	E3	190/190 (100%)	190 (100%)	0	100	100
46	F3	224/224 (100%)	224 (100%)	0	100	100
47	G3	158/161 (98%)	158 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	H3	207/207 (100%)	207 (100%)	0	100	100
49	I3	165/169 (98%)	165 (100%)	0	100	100
50	J3	178/178 (100%)	178 (100%)	0	100	100
51	K3	161/161 (100%)	161 (100%)	0	100	100
52	L3	87/87 (100%)	87 (100%)	0	100	100
53	M3	130/136 (96%)	130 (100%)	0	100	100
54	N3	99/99 (100%)	99 (100%)	0	100	100
55	O3	130/130 (100%)	130 (100%)	0	100	100
56	P3	106/106 (100%)	106 (100%)	0	100	100
57	Q3	115/115 (100%)	115 (100%)	0	100	100
58	R3	117/117 (100%)	117 (100%)	0	100	100
59	S3	119/119 (100%)	119 (100%)	0	100	100
60	T3	125/125 (100%)	125 (100%)	0	100	100
61	U3	111/111 (100%)	111 (100%)	0	100	100
62	V3	92/92 (100%)	92 (100%)	0	100	100
63	W3	67/67 (100%)	67 (100%)	0	100	100
64	X3	112/112 (100%)	112 (100%)	0	100	100
65	Y3	113/113 (100%)	113 (100%)	0	100	100
66	Z3	107/107 (100%)	107 (100%)	0	100	100
67	a3	66/66 (100%)	66 (100%)	0	100	100
68	b3	88/88 (100%)	88 (100%)	0	100	100
69	c3	75/75 (100%)	75 (100%)	0	100	100
70	d3	55/55 (100%)	55 (100%)	0	100	100
71	e3	48/48 (100%)	48 (100%)	0	100	100
72	f3	47/47 (100%)	47 (100%)	0	100	100
73	g3	61/61 (100%)	61 (100%)	0	100	100
74	h3	272/272 (100%)	272 (100%)	0	100	100
75	j3	190/190 (100%)	190 (100%)	0	100	100
76	k3	342/342 (100%)	342 (100%)	0	100	100
77	l3	302/302 (100%)	302 (100%)	0	100	100
78	m3	247/247 (100%)	247 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
79	n3	190/223 (85%)	190 (100%)	0	100	100
80	o3	196/196 (100%)	196 (100%)	0	100	100
81	p3	200/205 (98%)	200 (100%)	0	100	100
82	q3	169/169 (100%)	169 (100%)	0	100	100
83	r3	175/180 (97%)	175 (100%)	0	100	100
84	s3	143/143 (100%)	143 (100%)	0	100	100
85	t3	175/175 (100%)	175 (100%)	0	100	100
86	u3	117/117 (100%)	117 (100%)	0	100	100
All	All	10458/10532 (99%)	10457 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	N1	93	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (99) such sidechains are listed below:

Mol	Chain	Res	Type
1	A1	182	HIS
2	B1	50	ASN
2	B1	96	GLN
2	B1	167	HIS
3	C1	10	ASN
3	C1	72	GLN
3	C1	133	HIS
4	D1	7	HIS
4	D1	125	GLN
4	D1	162	HIS
5	E1	178	GLN
7	G1	77	ASN
9	I1	101	ASN
10	J1	45	ASN
12	L1	91	ASN
13	M1	78	ASN
14	N1	39	HIS
21	U1	96	ASN
21	U1	108	GLN
23	W1	66	HIS

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Mol	Chain	Res	Type
25	Y1	4	HIS
28	b1	25	GLN
28	b1	76	ASN
28	b1	105	GLN
30	d1	6	GLN
31	e1	72	ASN
31	e1	126	GLN
33	l1	143	ASN
35	n1	8	GLN
35	n1	30	GLN
35	n1	87	GLN
35	n1	236	GLN
42	B3	193	HIS
43	C3	92	GLN
43	C3	158	HIS
44	D3	277	HIS
45	E3	101	GLN
45	E3	159	HIS
46	F3	98	ASN
46	F3	232	ASN
47	G3	74	ASN
47	G3	203	ASN
48	H3	65	GLN
48	H3	110	ASN
48	H3	177	GLN
49	I3	76	GLN
49	I3	168	HIS
50	J3	35	ASN
50	J3	87	ASN
50	J3	155	ASN
51	K3	154	GLN
52	L3	61	GLN
53	M3	5	GLN
53	M3	11	GLN
54	N3	19	GLN
54	N3	48	HIS
54	N3	73	GLN
55	O3	62	GLN
57	Q3	32	GLN
57	Q3	41	GLN
60	T3	42	HIS
60	T3	73	ASN

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Mol	Chain	Res	Type
61	U3	51	ASN
61	U3	128	GLN
63	W3	82	ASN
64	X3	56	HIS
65	Y3	16	HIS
65	Y3	73	GLN
66	Z3	19	GLN
68	b3	72	HIS
72	f3	88	GLN
74	h3	51	ASN
74	h3	296	GLN
75	j3	95	GLN
75	j3	205	ASN
76	k3	123	HIS
76	k3	145	GLN
77	l3	215	ASN
77	l3	231	ASN
77	l3	338	ASN
78	m3	122	GLN
78	m3	138	GLN
78	m3	175	HIS
78	m3	202	GLN
79	n3	269	GLN
80	o3	130	ASN
80	o3	199	HIS
81	p3	117	GLN
81	p3	153	HIS
81	p3	194	ASN
82	q3	42	ASN
83	r3	166	HIS
84	s3	42	GLN
84	s3	71	HIS
84	s3	104	ASN
84	s3	112	HIS
85	t3	40	GLN
85	t3	149	GLN
85	t3	188	ASN

5.3.3 RNA

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	m1	2/3 (66%)	0	0
36	21	75/76 (98%)	21 (28%)	0
38	A2	3556/5051 (70%)	732 (20%)	58 (1%)
39	B2	118/119 (99%)	11 (9%)	0
40	C2	149/156 (95%)	28 (18%)	1 (0%)
41	A3	1680/1697 (98%)	351 (20%)	15 (0%)
All	All	5580/7102 (78%)	1143 (20%)	74 (1%)

All (1143) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
36	21	9	G
36	21	10	G
36	21	14	A
36	21	16	U
36	21	17	G
36	21	18	G
36	21	19	U
36	21	20	U
36	21	21	A
36	21	42	A
36	21	46	G
36	21	47	A
36	21	48	C
36	21	49	A
36	21	56	C
36	21	58	C
36	21	59	G
36	21	62	G
36	21	63	G
36	21	67	U
36	21	76	A
38	A2	11	G
38	A2	17	A
38	A2	25	A
38	A2	39	A
38	A2	42	A
38	A2	56	A
38	A2	58	G
38	A2	59	A
38	A2	64	A

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Mol	Chain	Res	Type
38	A2	65	A
38	A2	66	A
38	A2	73	A
38	A2	74	G
38	A2	76	A
38	A2	84	A
38	A2	91	G
38	A2	108	A
38	A2	109	G
38	A2	110	C
38	A2	117	C
38	A2	118	C
38	A2	119	G
38	A2	120	A
38	A2	126	C
38	A2	134	G
38	A2	135	G
38	A2	136	C
38	A2	142	G
38	A2	146	G
38	A2	159	C
38	A2	160	G
38	A2	170	C
38	A2	172	C
38	A2	173	C
38	A2	197	A
38	A2	200	U
38	A2	201	C
38	A2	209	U
38	A2	210	C
38	A2	216	C
38	A2	217	C
38	A2	218	A
38	A2	219	G
38	A2	224	U
38	A2	233	U
38	A2	234	G
38	A2	246	G
38	A2	256	G
38	A2	265	C
38	A2	266	C
38	A2	267	G

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Mol	Chain	Res	Type
38	A2	268	G
38	A2	276	C
38	A2	280	G
38	A2	297	U
38	A2	306	A
38	A2	309	C
38	A2	315	G
38	A2	316	U
38	A2	334	A
38	A2	340	C
38	A2	345	C
38	A2	360	A
38	A2	362	A
38	A2	363	A
38	A2	386	A
38	A2	387	G
38	A2	401	G
38	A2	407	A
38	A2	412	G
38	A2	413	G
38	A2	431	G
38	A2	432	U
38	A2	440	U
38	A2	446	C
38	A2	449	C
38	A2	450	G
38	A2	452	A
38	A2	453	G
38	A2	454	U
38	A2	463	A
38	A2	464	G
38	A2	467	U
38	A2	468	U
38	A2	472	C
38	A2	484	G
38	A2	485	U
38	A2	486	C
38	A2	487	C
38	A2	493	U
38	A2	498	G
38	A2	499	C
38	A2	500	G

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Mol	Chain	Res	Type
38	A2	506	G
38	A2	659	C
38	A2	660	G
38	A2	667	G
38	A2	668	A
38	A2	673	C
38	A2	686	C
38	A2	698	G
38	A2	705	C
38	A2	706	G
38	A2	709	G
38	A2	720	C
38	A2	730	G
38	A2	732	G
38	A2	744	G
38	A2	748	A
38	A2	749	A
38	A2	751	G
38	A2	881	G
38	A2	912	U
38	A2	915	A
38	A2	916	G
38	A2	924	C
38	A2	925	C
38	A2	926	G
38	A2	929	A
38	A2	931	C
38	A2	932	A
38	A2	933	G
38	A2	934	C
38	A2	939	C
38	A2	940	G
38	A2	942	C
38	A2	944	A
38	A2	946	U
38	A2	947	C
38	A2	957	A
38	A2	960	G
38	A2	961	A
38	A2	962	G
38	A2	967	A
38	A2	968	C

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Mol	Chain	Res	Type
38	A2	970	C
38	A2	975	G
38	A2	981	C
38	A2	985	C
38	A2	1070	C
38	A2	1071	G
38	A2	1077	C
38	A2	1078	C
38	A2	1080	C
38	A2	1095	C
38	A2	1177	U
38	A2	1178	C
38	A2	1193	G
38	A2	1196	G
38	A2	1208	C
38	A2	1209	G
38	A2	1210	G
38	A2	1212	C
38	A2	1213	C
38	A2	1214	C
38	A2	1232	G
38	A2	1233	G
38	A2	1234	C
38	A2	1235	C
38	A2	1237	C
38	A2	1247	C
38	A2	1271	G
38	A2	1273	G
38	A2	1282	G
38	A2	1285	G
38	A2	1290	C
38	A2	1291	G
38	A2	1294	G
38	A2	1299	C
38	A2	1300	U
38	A2	1301	A
38	A2	1324	A
38	A2	1335	A
38	A2	1352	A
38	A2	1356	G
38	A2	1357	G
38	A2	1368	G

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Mol	Chain	Res	Type
38	A2	1369	A
38	A2	1375	G
38	A2	1376	C
38	A2	1378	G
38	A2	1379	U
38	A2	1385	A
38	A2	1392	G
38	A2	1395	A
38	A2	1396	A
38	A2	1398	G
38	A2	1407	G
38	A2	1410	C
38	A2	1415	G
38	A2	1420	A
38	A2	1436	C
38	A2	1437	C
38	A2	1438	U
38	A2	1441	C
38	A2	1445	U
38	A2	1446	C
38	A2	1456	C
38	A2	1457	G
38	A2	1476	C
38	A2	1477	C
38	A2	1478	C
38	A2	1482	G
38	A2	1483	C
38	A2	1484	G
38	A2	1493	G
38	A2	1497	A
38	A2	1498	G
38	A2	1502	G
38	A2	1514	U
38	A2	1515	A
38	A2	1523	A
38	A2	1534	A
38	A2	1543	G
38	A2	1547	A
38	A2	1566	C
38	A2	1578	U
38	A2	1588	U
38	A2	1591	U

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Mol	Chain	Res	Type
38	A2	1596	U
38	A2	1602	U
38	A2	1612	G
38	A2	1613	A
38	A2	1624	G
38	A2	1625	G
38	A2	1631	A
38	A2	1633	G
38	A2	1634	A
38	A2	1638	A
38	A2	1640	C
38	A2	1641	G
38	A2	1642	A
38	A2	1654	G
38	A2	1661	C
38	A2	1670	G
38	A2	1676	C
38	A2	1691	G
38	A2	1694	C
38	A2	1696	C
38	A2	1724	G
38	A2	1731	C
38	A2	1734	G
38	A2	1735	U
38	A2	1741	G
38	A2	1742	A
38	A2	1750	G
38	A2	1756	U
38	A2	1760	G
38	A2	1764	G
38	A2	1768	C
38	A2	1772	C
38	A2	1773	U
38	A2	1775	A
38	A2	1776	A
38	A2	1781	U
38	A2	1787	A
38	A2	1803	G
38	A2	1804	A
38	A2	1806	G
38	A2	1815	G
38	A2	1819	G

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Mol	Chain	Res	Type
38	A2	1821	G
38	A2	1828	C
38	A2	1835	G
38	A2	1836	G
38	A2	1837	A
38	A2	1842	G
38	A2	1843	A
38	A2	1855	G
38	A2	1869	G
38	A2	1882	U
38	A2	1892	A
38	A2	1893	C
38	A2	1897	A
38	A2	1898	C
38	A2	1907	A
38	A2	1910	G
38	A2	1912	G
38	A2	1918	U
38	A2	1920	C
38	A2	1921	C
38	A2	1922	G
38	A2	1931	C
38	A2	1932	A
38	A2	1935	C
38	A2	1940	G
38	A2	1947	U
38	A2	1951	G
38	A2	1961	G
38	A2	1962	A
38	A2	1967	A
38	A2	1972	G
38	A2	1974	U
38	A2	1976	G
38	A2	1977	C
38	A2	1978	C
38	A2	1980	U
38	A2	1984	A
38	A2	1985	G
38	A2	1986	U
38	A2	1987	C
38	A2	1991	A
38	A2	1997	U

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Mol	Chain	Res	Type
38	A2	1998	A
38	A2	2001	G
38	A2	2002	A
38	A2	2004	U
38	A2	2007	G
38	A2	2008	U
38	A2	2011	C
38	A2	2021	G
38	A2	2024	G
38	A2	2025	A
38	A2	2026	A
38	A2	2046	G
38	A2	2047	A
38	A2	2048	U
38	A2	2052	G
38	A2	2055	G
38	A2	2056	G
38	A2	2069	A
38	A2	2070	U
38	A2	2071	A
38	A2	2084	U
38	A2	2089	G
38	A2	2090	U
38	A2	2092	G
38	A2	2093	G
38	A2	2094	C
38	A2	2096	G
38	A2	2097	A
38	A2	2098	G
38	A2	2100	G
38	A2	2102	G
38	A2	2104	A
38	A2	2105	A
38	A2	2106	G
38	A2	2107	A
38	A2	2108	G
38	A2	2262	G
38	A2	2263	C
38	A2	2264	G
38	A2	2266	A
38	A2	2270	U
38	A2	2271	A

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Mol	Chain	Res	Type
38	A2	2272	C
38	A2	2277	C
38	A2	2292	C
38	A2	2303	A
38	A2	2304	G
38	A2	2309	G
38	A2	2316	A
38	A2	2319	G
38	A2	2334	G
38	A2	2335	A
38	A2	2336	G
38	A2	2351	G
38	A2	2354	C
38	A2	2363	A
38	A2	2372	U
38	A2	2398	A
38	A2	2405	G
38	A2	2413	C
38	A2	2420	A
38	A2	2425	C
38	A2	2428	U
38	A2	2436	G
38	A2	2437	G
38	A2	2444	C
38	A2	2453	G
38	A2	2456	A
38	A2	2470	U
38	A2	2474	G
38	A2	2478	G
38	A2	2491	C
38	A2	2492	C
38	A2	2493	U
38	A2	2494	C
38	A2	2495	C
38	A2	2496	G
38	A2	2506	G
38	A2	2507	C
38	A2	2508	C
38	A2	2509	G
38	A2	2516	A
38	A2	2517	G
38	A2	2523	C

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Mol	Chain	Res	Type
38	A2	2532	A
38	A2	2533	U
38	A2	2540	A
38	A2	2547	G
38	A2	2549	G
38	A2	2550	G
38	A2	2557	U
38	A2	2567	G
38	A2	2569	G
38	A2	2586	C
38	A2	2589	G
38	A2	2590	A
38	A2	2592	C
38	A2	2614	A
38	A2	2630	C
38	A2	2643	G
38	A2	2650	A
38	A2	2652	G
38	A2	2656	C
38	A2	2665	G
38	A2	2672	C
38	A2	2673	C
38	A2	2679	A
38	A2	2689	G
38	A2	2690	U
38	A2	2697	G
38	A2	2698	A
38	A2	2699	A
38	A2	2708	G
38	A2	2711	U
38	A2	2712	C
38	A2	2713	C
38	A2	2714	G
38	A2	2717	G
38	A2	2724	G
38	A2	2726	U
38	A2	2729	G
38	A2	2738	G
38	A2	2743	U
38	A2	2746	A
38	A2	2747	A
38	A2	2757	G

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Mol	Chain	Res	Type
38	A2	2763	G
38	A2	2766	U
38	A2	2767	A
38	A2	2770	U
38	A2	2772	U
38	A2	2785	U
38	A2	2790	A
38	A2	2791	U
38	A2	2793	U
38	A2	2801	A
38	A2	2809	A
38	A2	2810	A
38	A2	2817	C
38	A2	2818	A
38	A2	2829	U
38	A2	2830	G
38	A2	2831	U
38	A2	2845	G
38	A2	2851	G
38	A2	2858	G
38	A2	2866	G
38	A2	2879	G
38	A2	2887	G
38	A2	3593	C
38	A2	3597	C
38	A2	3599	A
38	A2	3600	C
38	A2	3610	G
38	A2	3611	U
38	A2	3613	C
38	A2	3620	G
38	A2	3621	G
38	A2	3625	A
38	A2	3630	A
38	A2	3631	C
38	A2	3639	U
38	A2	3643	A
38	A2	3657	A
38	A2	3658	A
38	A2	3665	C
38	A2	3668	C
38	A2	3675	U

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Mol	Chain	Res	Type
38	A2	3691	C
38	A2	3707	A
38	A2	3708	U
38	A2	3709	G
38	A2	3724	U
38	A2	3735	G
38	A2	3740	U
38	A2	3741	A
38	A2	3742	A
38	A2	3743	A
38	A2	3748	G
38	A2	3755	A
38	A2	3768	U
38	A2	3769	A
38	A2	3771	G
38	A2	3772	G
38	A2	3779	A
38	A2	3781	U
38	A2	3783	C
38	A2	3797	U
38	A2	3805	C
38	A2	3806	G
38	A2	3807	C
38	A2	3809	U
38	A2	3812	A
38	A2	3814	G
38	A2	3833	U
38	A2	3834	G
38	A2	3835	U
38	A2	3838	C
38	A2	3871	A
38	A2	3872	A
38	A2	3873	C
38	A2	3874	G
38	A2	3884	G
38	A2	3892	G
38	A2	3896	A
38	A2	3900	A
38	A2	3901	A
38	A2	3902	G
38	A2	3903	A
38	A2	3910	U

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Mol	Chain	Res	Type
38	A2	3933	G
38	A2	3934	G
38	A2	3946	G
38	A2	3953	G
38	A2	3954	U
38	A2	3955	A
38	A2	3958	A
38	A2	3959	U
38	A2	3960	A
38	A2	3962	G
38	A2	3963	U
38	A2	3964	G
38	A2	3965	G
38	A2	3966	G
38	A2	3967	A
38	A2	3969	G
38	A2	3970	C
38	A2	4031	C
38	A2	4032	C
38	A2	4033	G
38	A2	4035	C
38	A2	4037	G
38	A2	4042	A
38	A2	4043	U
38	A2	4049	U
38	A2	4050	A
38	A2	4051	C
38	A2	4060	U
38	A2	4067	A
38	A2	4070	G
38	A2	4071	A
38	A2	4078	G
38	A2	4080	G
38	A2	4082	C
38	A2	4090	C
38	A2	4091	G
38	A2	4109	C
38	A2	4111	U
38	A2	4112	C
38	A2	4113	U
38	A2	4115	G
38	A2	4120	A

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Mol	Chain	Res	Type
38	A2	4144	C
38	A2	4148	C
38	A2	4149	U
38	A2	4156	A
38	A2	4157	C
38	A2	4169	G
38	A2	4177	G
38	A2	4189	A
38	A2	4192	C
38	A2	4198	A
38	A2	4211	G
38	A2	4214	G
38	A2	4215	U
38	A2	4218	U
38	A2	4219	A
38	A2	4228	U
38	A2	4235	G
38	A2	4236	G
38	A2	4237	A
38	A2	4240	G
38	A2	4241	A
38	A2	4252	G
38	A2	4254	A
38	A2	4257	A
38	A2	4259	A
38	A2	4267	A
38	A2	4268	A
38	A2	4277	G
38	A2	4278	A
38	A2	4282	U
38	A2	4283	G
38	A2	4290	A
38	A2	4291	G
38	A2	4292	U
38	A2	4294	C
38	A2	4299	A
38	A2	4300	C
38	A2	4312	G
38	A2	4315	G
38	A2	4316	G
38	A2	4318	C
38	A2	4324	G

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Mol	Chain	Res	Type
38	A2	4334	A
38	A2	4335	C
38	A2	4340	U
38	A2	4341	G
38	A2	4359	G
38	A2	4362	A
38	A2	4363	G
38	A2	4364	A
38	A2	4365	A
38	A2	4366	A
38	A2	4373	C
38	A2	4377	G
38	A2	4380	A
38	A2	4381	U
38	A2	4398	C
38	A2	4405	U
38	A2	4408	A
38	A2	4412	C
38	A2	4419	G
38	A2	4426	G
38	A2	4434	G
38	A2	4435	A
38	A2	4441	G
38	A2	4450	A
38	A2	4461	G
38	A2	4474	A
38	A2	4481	G
38	A2	4486	U
38	A2	4498	U
38	A2	4499	A
38	A2	4501	G
38	A2	4504	A
38	A2	4505	C
38	A2	4508	G
38	A2	4510	G
38	A2	4517	U
38	A2	4534	A
38	A2	4546	C
38	A2	4556	G
38	A2	4559	G
38	A2	4561	G
38	A2	4567	G

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Mol	Chain	Res	Type
38	A2	4570	A
38	A2	4576	A
38	A2	4612	A
38	A2	4613	U
38	A2	4621	A
38	A2	4622	U
38	A2	4623	G
38	A2	4625	G
38	A2	4638	G
38	A2	4643	U
38	A2	4644	G
38	A2	4656	C
38	A2	4658	A
38	A2	4663	U
38	A2	4673	A
38	A2	4680	G
38	A2	4686	A
38	A2	4694	A
38	A2	4695	U
38	A2	4705	G
38	A2	4706	C
38	A2	4707	G
38	A2	4736	G
38	A2	4737	G
38	A2	4740	G
38	A2	4743	C
38	A2	4745	C
38	A2	4747	G
38	A2	4750	A
38	A2	4751	G
38	A2	4757	C
38	A2	4758	C
38	A2	4759	C
38	A2	4762	G
38	A2	4849	G
38	A2	4852	G
38	A2	4853	C
38	A2	4855	G
38	A2	4857	G
38	A2	4858	A
38	A2	4859	G
38	A2	4864	U

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Mol	Chain	Res	Type
38	A2	4865	C
38	A2	4867	U
38	A2	4869	C
38	A2	4877	C
38	A2	4878	G
38	A2	4889	G
38	A2	4894	G
38	A2	4896	G
38	A2	4901	G
38	A2	4903	C
38	A2	4904	C
38	A2	4908	C
38	A2	4916	A
38	A2	4919	C
38	A2	4920	A
38	A2	4921	C
38	A2	4925	A
38	A2	4926	C
38	A2	4929	U
38	A2	4930	C
38	A2	4931	G
38	A2	4932	U
38	A2	4933	G
38	A2	4937	A
38	A2	4938	A
38	A2	4939	C
38	A2	4940	C
38	A2	4942	G
38	A2	4945	G
38	A2	4948	A
38	A2	4949	A
38	A2	4958	U
38	A2	4967	U
38	A2	4970	U
38	A2	4971	U
38	A2	4972	C
38	A2	4975	G
38	A2	4981	G
38	A2	4996	A
38	A2	4998	A
38	A2	4999	G
38	A2	5013	G

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Mol	Chain	Res	Type
38	A2	5023	G
38	A2	5024	A
38	A2	5029	C
38	A2	5032	C
38	A2	5035	U
38	A2	5036	C
38	A2	5037	G
38	A2	5043	A
38	A2	5044	G
39	B2	7	G
39	B2	25	G
39	B2	42	A
39	B2	53	U
39	B2	54	A
39	B2	63	C
39	B2	64	G
39	B2	97	G
39	B2	100	A
39	B2	102	U
39	B2	110	G
40	C2	2	G
40	C2	3	A
40	C2	34	U
40	C2	35	C
40	C2	39	G
40	C2	59	A
40	C2	60	G
40	C2	62	A
40	C2	63	U
40	C2	75	G
40	C2	87	G
40	C2	94	G
40	C2	103	A
40	C2	105	C
40	C2	109	C
40	C2	110	U
40	C2	111	U
40	C2	114	G
40	C2	121	G
40	C2	123	U
40	C2	124	U
40	C2	125	C

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Mol	Chain	Res	Type
40	C2	126	C
40	C2	127	U
40	C2	128	C
40	C2	147	G
40	C2	151	G
40	C2	153	C
41	A3	3	C
41	A3	14	C
41	A3	17	C
41	A3	25	A
41	A3	33	G
41	A3	42	A
41	A3	44	U
41	A3	45	A
41	A3	46	A
41	A3	56	G
41	A3	58	C
41	A3	67	C
41	A3	68	A
41	A3	72	C
41	A3	73	C
41	A3	74	G
41	A3	75	G
41	A3	77	A
41	A3	79	A
41	A3	99	A
41	A3	103	A
41	A3	110	U
41	A3	111	A
41	A3	113	G
41	A3	114	G
41	A3	115	U
41	A3	116	U
41	A3	124	U
41	A3	126	G
41	A3	130	G
41	A3	143	U
41	A3	146	G
41	A3	147	A
41	A3	155	G
41	A3	157	U
41	A3	162	C

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Mol	Chain	Res	Type
41	A3	168	C
41	A3	171	A
41	A3	173	A
41	A3	180	G
41	A3	182	C
41	A3	183	G
41	A3	184	G
41	A3	186	C
41	A3	188	C
41	A3	191	A
41	A3	192	C
41	A3	202	G
41	A3	206	G
41	A3	294	U
41	A3	302	A
41	A3	307	G
41	A3	308	G
41	A3	309	G
41	A3	312	G
41	A3	319	C
41	A3	320	G
41	A3	347	G
41	A3	351	G
41	A3	356	C
41	A3	362	C
41	A3	364	A
41	A3	368	U
41	A3	369	C
41	A3	370	G
41	A3	381	C
41	A3	383	G
41	A3	385	G
41	A3	386	C
41	A3	396	U
41	A3	398	A
41	A3	400	C
41	A3	407	G
41	A3	408	A
41	A3	409	C
41	A3	418	A
41	A3	420	G
41	A3	428	U

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Mol	Chain	Res	Type
41	A3	438	G
41	A3	441	C
41	A3	447	A
41	A3	448	A
41	A3	450	C
41	A3	455	A
41	A3	464	A
41	A3	465	A
41	A3	466	G
41	A3	471	G
41	A3	472	C
41	A3	473	A
41	A3	474	G
41	A3	476	A
41	A3	482	G
41	A3	483	C
41	A3	487	U
41	A3	492	C
41	A3	496	C
41	A3	516	A
41	A3	517	C
41	A3	531	A
41	A3	532	C
41	A3	533	A
41	A3	547	G
41	A3	548	C
41	A3	549	C
41	A3	550	C
41	A3	551	U
41	A3	554	A
41	A3	555	A
41	A3	556	U
41	A3	559	G
41	A3	561	A
41	A3	562	U
41	A3	568	C
41	A3	573	U
41	A3	576	A
41	A3	583	A
41	A3	587	A
41	A3	588	G
41	A3	589	G

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Mol	Chain	Res	Type
41	A3	590	A
41	A3	591	U
41	A3	593	C
41	A3	603	C
41	A3	604	A
41	A3	606	G
41	A3	608	C
41	A3	614	C
41	A3	617	G
41	A3	621	C
41	A3	627	U
41	A3	628	A
41	A3	629	A
41	A3	631	U
41	A3	643	A
41	A3	644	G
41	A3	655	A
41	A3	659	G
41	A3	660	C
41	A3	664	A
41	A3	668	A
41	A3	669	A
41	A3	670	A
41	A3	671	A
41	A3	672	A
41	A3	673	G
41	A3	678	U
41	A3	683	G
41	A3	689	U
41	A3	734	C
41	A3	752	G
41	A3	753	C
41	A3	754	G
41	A3	808	A
41	A3	811	A
41	A3	821	G
41	A3	822	U
41	A3	827	A
41	A3	830	A
41	A3	844	U
41	A3	845	G
41	A3	847	A

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Mol	Chain	Res	Type
41	A3	859	G
41	A3	870	A
41	A3	871	U
41	A3	872	A
41	A3	874	G
41	A3	875	A
41	A3	878	G
41	A3	879	C
41	A3	887	U
41	A3	888	U
41	A3	889	U
41	A3	890	U
41	A3	893	U
41	A3	896	U
41	A3	898	U
41	A3	901	G
41	A3	909	G
41	A3	913	A
41	A3	914	U
41	A3	920	A
41	A3	933	G
41	A3	934	G
41	A3	943	U
41	A3	955	A
41	A3	963	A
41	A3	971	G
41	A3	984	C
41	A3	985	G
41	A3	990	A
41	A3	992	A
41	A3	999	G
41	A3	1002	U
41	A3	1017	U
41	A3	1023	A
41	A3	1050	A
41	A3	1060	A
41	A3	1062	A
41	A3	1078	C
41	A3	1080	A
41	A3	1083	A
41	A3	1085	C
41	A3	1089	G

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Mol	Chain	Res	Type
41	A3	1107	G
41	A3	1115	U
41	A3	1116	C
41	A3	1117	C
41	A3	1118	C
41	A3	1121	G
41	A3	1123	C
41	A3	1133	A
41	A3	1138	C
41	A3	1148	A
41	A3	1150	A
41	A3	1153	C
41	A3	1154	U
41	A3	1155	U
41	A3	1168	G
41	A3	1195	A
41	A3	1203	G
41	A3	1207	G
41	A3	1208	A
41	A3	1212	G
41	A3	1215	C
41	A3	1221	G
41	A3	1224	G
41	A3	1240	A
41	A3	1242	U
41	A3	1248	U
41	A3	1251	A
41	A3	1253	A
41	A3	1256	G
41	A3	1257	G
41	A3	1259	A
41	A3	1274	G
41	A3	1275	G
41	A3	1282	A
41	A3	1284	A
41	A3	1285	G
41	A3	1286	G
41	A3	1292	C
41	A3	1298	G
41	A3	1299	A
41	A3	1300	U
41	A3	1301	A

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Mol	Chain	Res	Type
41	A3	1302	G
41	A3	1303	C
41	A3	1308	U
41	A3	1309	C
41	A3	1311	C
41	A3	1313	A
41	A3	1318	G
41	A3	1333	U
41	A3	1341	C
41	A3	1342	U
41	A3	1348	G
41	A3	1354	G
41	A3	1363	C
41	A3	1371	U
41	A3	1372	U
41	A3	1378	A
41	A3	1382	A
41	A3	1395	C
41	A3	1396	A
41	A3	1397	U
41	A3	1401	A
41	A3	1402	A
41	A3	1404	U
41	A3	1424	G
41	A3	1428	G
41	A3	1429	G
41	A3	1442	U
41	A3	1449	G
41	A3	1452	A
41	A3	1454	A
41	A3	1462	U
41	A3	1463	U
41	A3	1466	G
41	A3	1473	G
41	A3	1476	A
41	A3	1480	A
41	A3	1487	A
41	A3	1489	A
41	A3	1490	G
41	A3	1498	A
41	A3	1509	U
41	A3	1519	U

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Mol	Chain	Res	Type
41	A3	1520	G
41	A3	1521	C
41	A3	1522	A
41	A3	1531	A
41	A3	1533	A
41	A3	1544	C
41	A3	1548	G
41	A3	1552	G
41	A3	1553	C
41	A3	1554	C
41	A3	1555	U
41	A3	1556	A
41	A3	1560	U
41	A3	1570	G
41	A3	1574	C
41	A3	1580	A
41	A3	1585	U
41	A3	1587	G
41	A3	1588	A
41	A3	1597	C
41	A3	1601	A
41	A3	1606	G
41	A3	1621	U
41	A3	1623	A
41	A3	1629	C
41	A3	1637	A
41	A3	1638	G
41	A3	1648	G
41	A3	1654	G
41	A3	1661	A
41	A3	1665	G
41	A3	1671	G
41	A3	1683	C
41	A3	1698	C
41	A3	1699	A
41	A3	1701	C
41	A3	1721	U
41	A3	1722	G
41	A3	1726	G
41	A3	1730	U
41	A3	1744	G
41	A3	1753	C

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Mol	Chain	Res	Type
41	A3	1777	G
41	A3	1783	C
41	A3	1784	G
41	A3	1785	C
41	A3	1787	G
41	A3	1805	G
41	A3	1823	A
41	A3	1825	A
41	A3	1826	G
41	A3	1829	G
41	A3	1831	A
41	A3	1836	G
41	A3	1838	U
41	A3	1849	G
41	A3	1851	A
41	A3	1861	G
41	A3	1862	G
41	A3	1863	A
41	A3	1864	U
41	A3	1865	C
41	A3	1869	A

All (74) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A2	125	C
38	A2	134	G
38	A2	217	C
38	A2	245	C
38	A2	265	C
38	A2	267	G
38	A2	275	C
38	A2	385	A
38	A2	406	C
38	A2	449	C
38	A2	486	C
38	A2	505	G
38	A2	930	G
38	A2	960	G
38	A2	1070	C
38	A2	1209	G
38	A2	1234	C

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Mol	Chain	Res	Type
38	A2	1236	A
38	A2	1289	G
38	A2	1368	G
38	A2	1440	U
38	A2	1445	U
38	A2	1455	G
38	A2	1477	C
38	A2	1633	G
38	A2	1818	G
38	A2	1979	A
38	A2	1983	A
38	A2	2046	G
38	A2	2068	C
38	A2	2089	G
38	A2	2269	C
38	A2	2505	A
38	A2	2642	U
38	A2	2698	A
38	A2	3598	G
38	A2	3620	G
38	A2	3667	G
38	A2	3705	G
38	A2	3871	A
38	A2	3883	G
38	A2	3899	G
38	A2	3954	U
38	A2	3969	G
38	A2	4030	G
38	A2	4059	G
38	A2	4112	C
38	A2	4218	U
38	A2	4340	U
38	A2	4364	A
38	A2	4381	U
38	A2	4434	G
38	A2	4685	U
38	A2	4705	G
38	A2	4866	G
38	A2	4907	U
38	A2	4918	G
38	A2	4929	U
40	C2	124	U

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Mol	Chain	Res	Type
41	A3	24	C
41	A3	110	U
41	A3	465	A
41	A3	532	C
41	A3	553	U
41	A3	561	A
41	A3	627	U
41	A3	688	U
41	A3	752	G
41	A3	870	A
41	A3	874	G
41	A3	1061	U
41	A3	1137	U
41	A3	1395	C
41	A3	1637	A

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 282 ligands modelled in this entry, 282 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
38	A2	27
41	A3	18
10	J1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J1	63:GLN	C	79:GLN	N	38.60
1	A2	1403:C	O3'	1404:G	P	20.34
1	A2	1407:G	O3'	1408:C	P	19.15
1	A2	1408:C	O3'	1409:G	P	17.91
1	A2	1404:G	O3'	1405:G	P	17.70
1	A3	697:G	O3'	729:C	P	17.34
1	A2	4131:C	O3'	4132:G	P	17.24
1	A3	834:C	O3'	841:G	P	17.04
1	A3	1761:U	O3'	1771:G	P	16.73
1	A3	130:G	O3'	141:A	P	16.21
1	A3	756:C	O3'	788:G	P	15.47
1	A3	1417:C	O3'	1423:C	P	14.74
1	A3	323:C	O3'	329:G	P	14.37
1	A2	919:C	O3'	920:C	P	13.26
1	A2	481:G	O3'	482:C	P	10.77
1	A2	920:C	O3'	921:G	P	10.22
1	A2	739:C	O3'	740:C	P	9.43
1	A2	482:C	O3'	483:G	P	8.98
1	A2	480:C	O3'	481:G	P	8.17
1	A3	745:C	O3'	749:U	P	8.08
1	A2	936:G	O3'	937:C	P	7.91
1	A2	973:G	O3'	974:C	P	7.66
1	A2	972:U	O3'	973:G	P	7.59
1	A2	1411:C	O3'	1412:G	P	7.49
1	A2	935:A	O3'	936:G	P	7.31
1	A3	225:G	O3'	287:U	P	7.10
1	A2	971:G	O3'	972:U	P	6.71
1	A3	736:C	O3'	743:U	P	6.58
1	A3	689:U	O3'	690:G	P	6.30
1	A2	922:C	O3'	923:C	P	6.29
1	A2	4058:C	O3'	4059:G	P	6.27
1	A3	322:C	O3'	323:C	P	6.10
1	A2	1956:A	O3'	1957:U	P	5.80

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A2	738:C	O3'	739:C	P	5.73
1	A3	798:G	O3'	799:U	P	5.24
1	A2	934:C	O3'	935:A	P	5.05
1	A2	740:C	O3'	741:G	P	4.93
1	A2	3943:C	O3'	3944:A	P	4.37
1	A3	304:C	O3'	305:U	P	4.25
1	A3	1432:U	O3'	1438:A	P	4.24
1	A2	1957:U	O3'	1958:A	P	4.06
1	A3	902:G	O3'	903:A	P	4.02
1	A2	5002:G	O3'	5003:C	P	3.56
1	A3	886:A	O3'	887:U	P	3.32
1	A2	170:C	O3'	171:U	P	3.25
1	A3	903:A	O3'	904:A	P	3.25

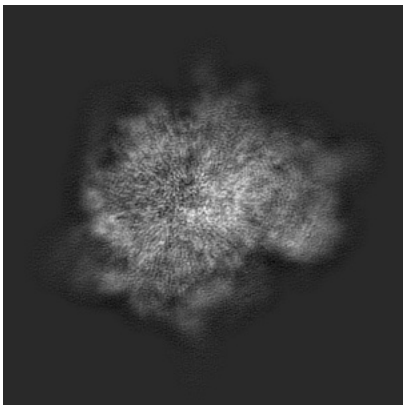
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-16052. These allow visual inspection of the internal detail of the map and identification of artifacts.

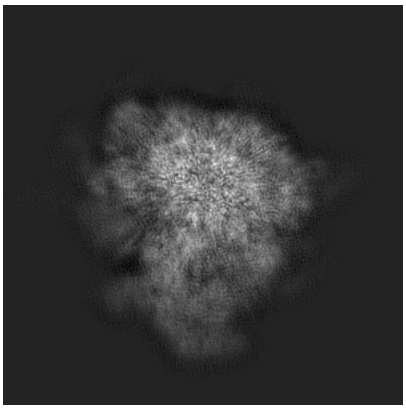
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

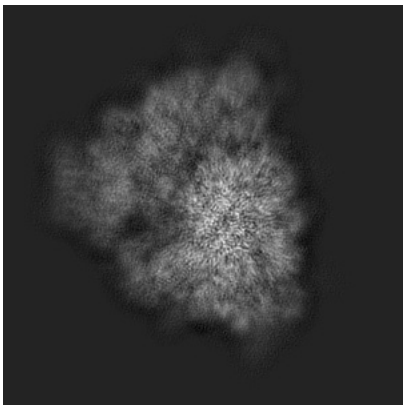
6.1.1 Primary map



X

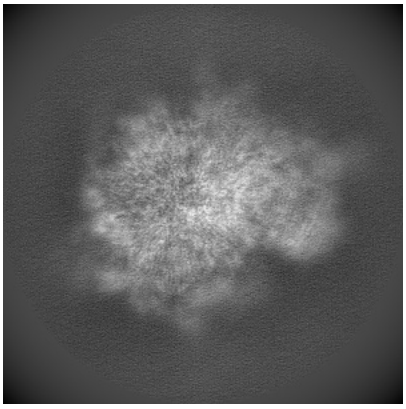


Y

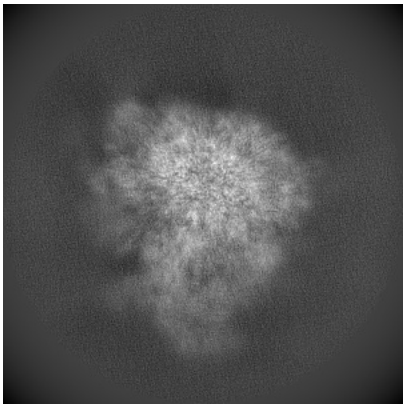


Z

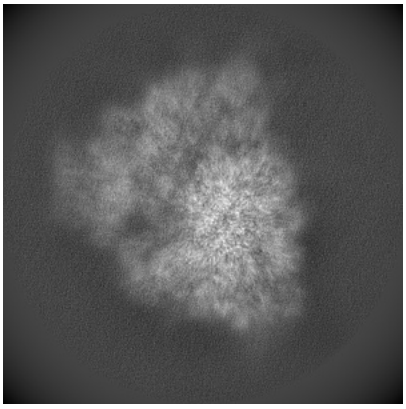
6.1.2 Raw map



X



Y

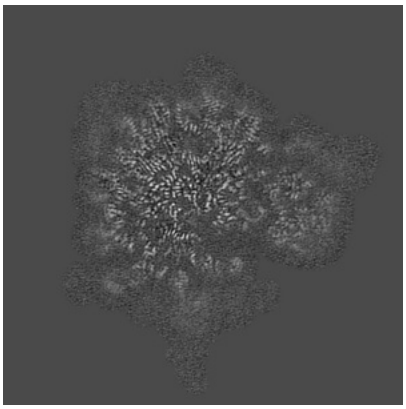


Z

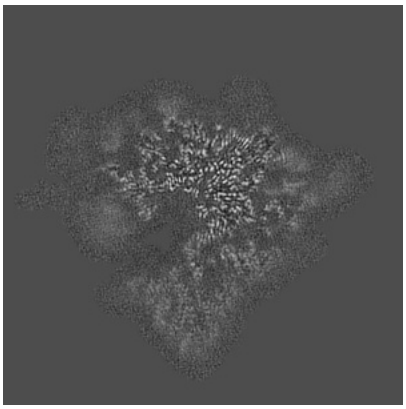
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

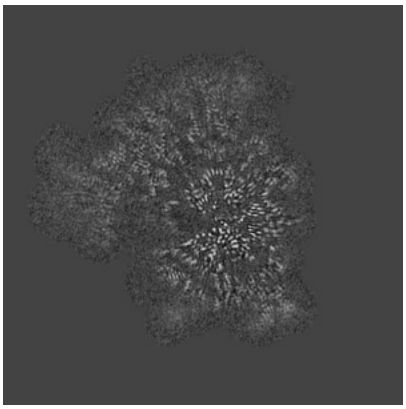
6.2.1 Primary map



X Index: 250

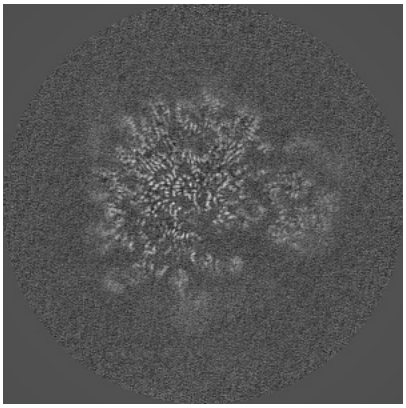


Y Index: 250

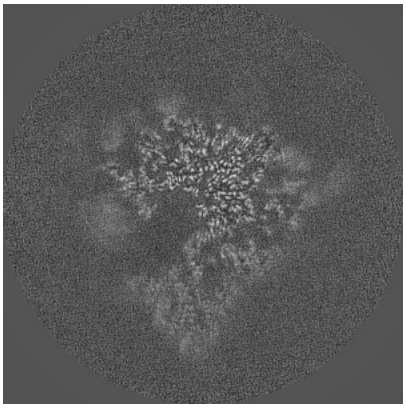


Z Index: 250

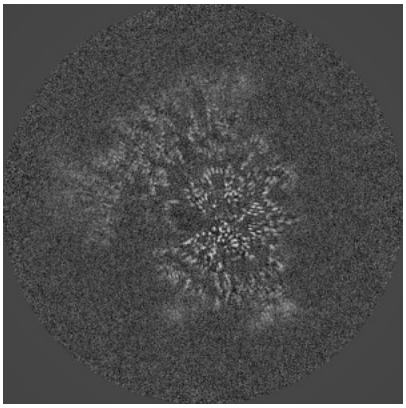
6.2.2 Raw map



X Index: 250



Y Index: 250

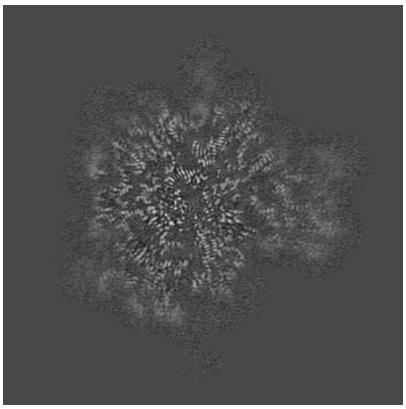


Z Index: 250

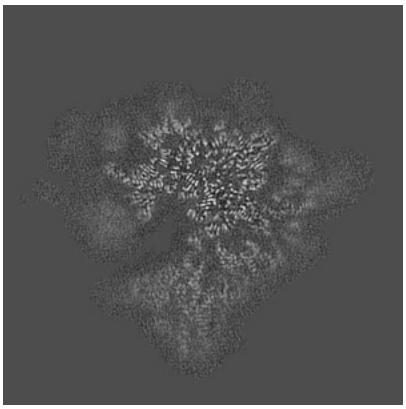
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

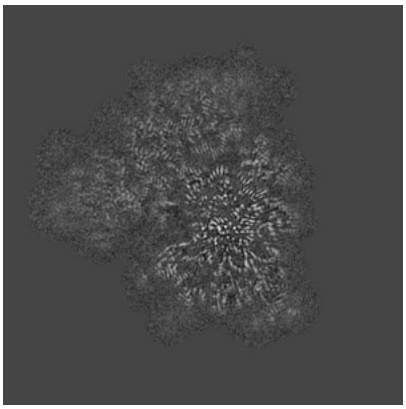
6.3.1 Primary map



X Index: 276

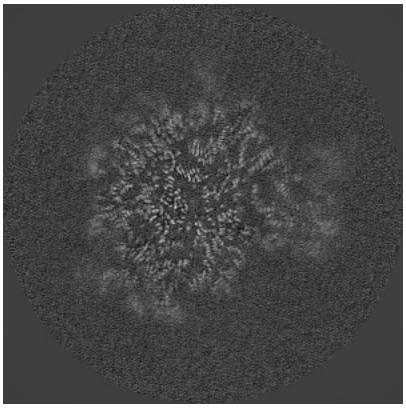


Y Index: 255

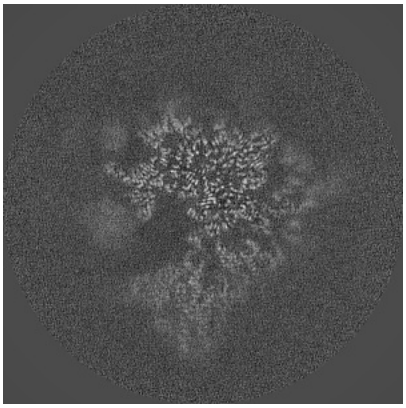


Z Index: 244

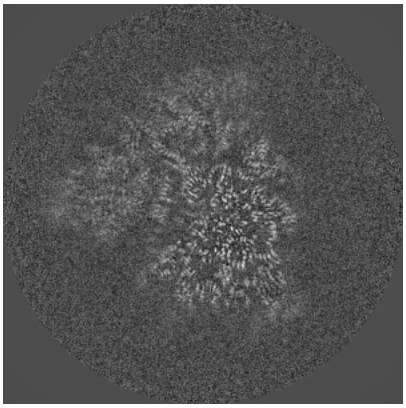
6.3.2 Raw map



X Index: 275



Y Index: 255

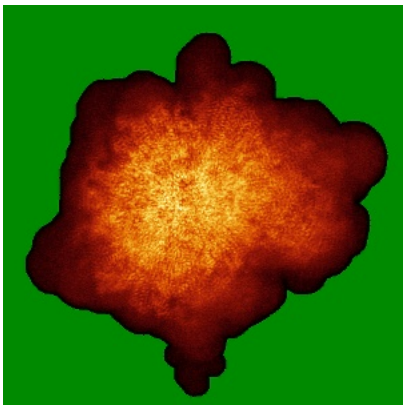


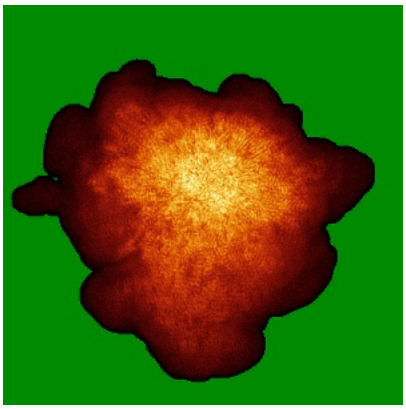
Z Index: 241

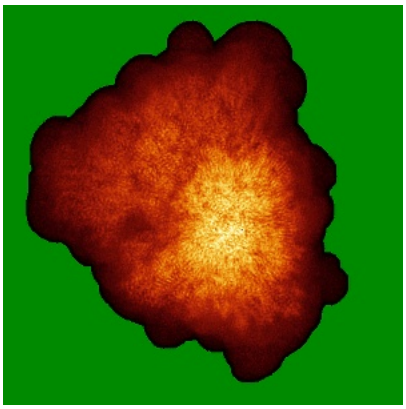
The images above show the largest variance slices of the map in three orthogonal directions.

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

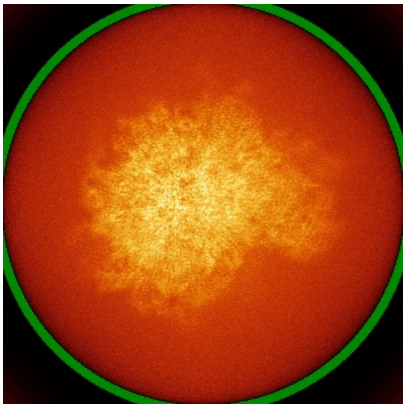
6.4.1 Primary map

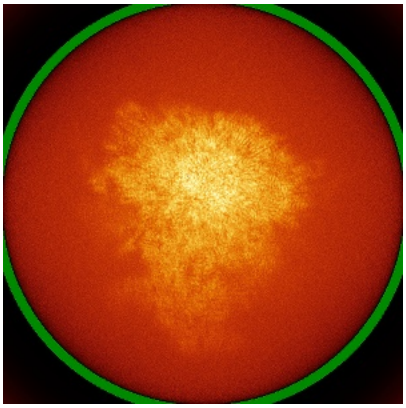

X

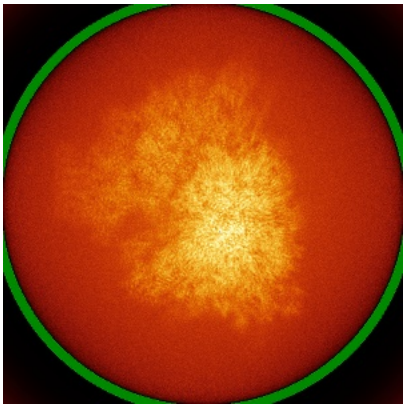

Y


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.

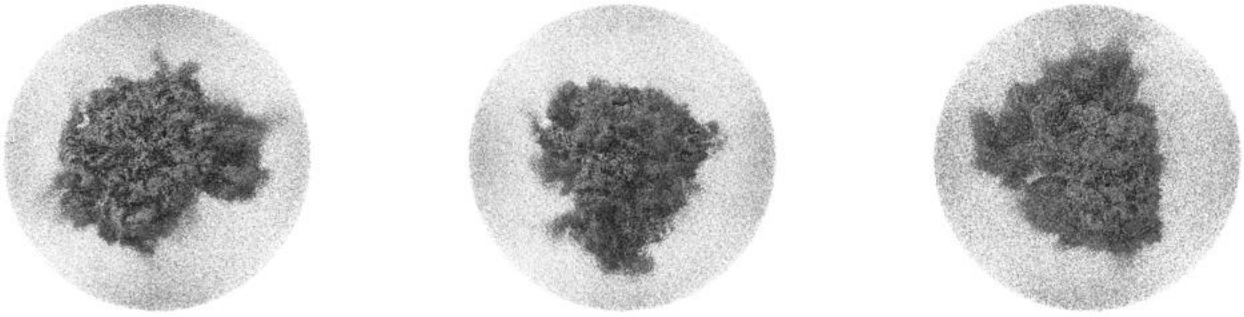
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

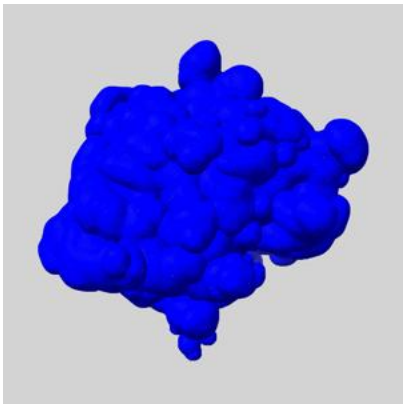
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

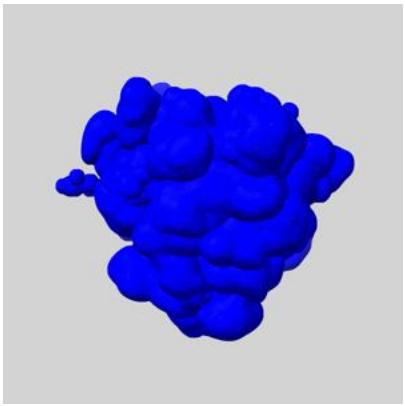
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

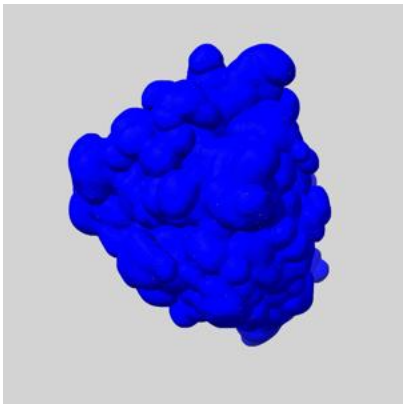
6.6.1 emd_16052_msk_1.map (i)



X



Y

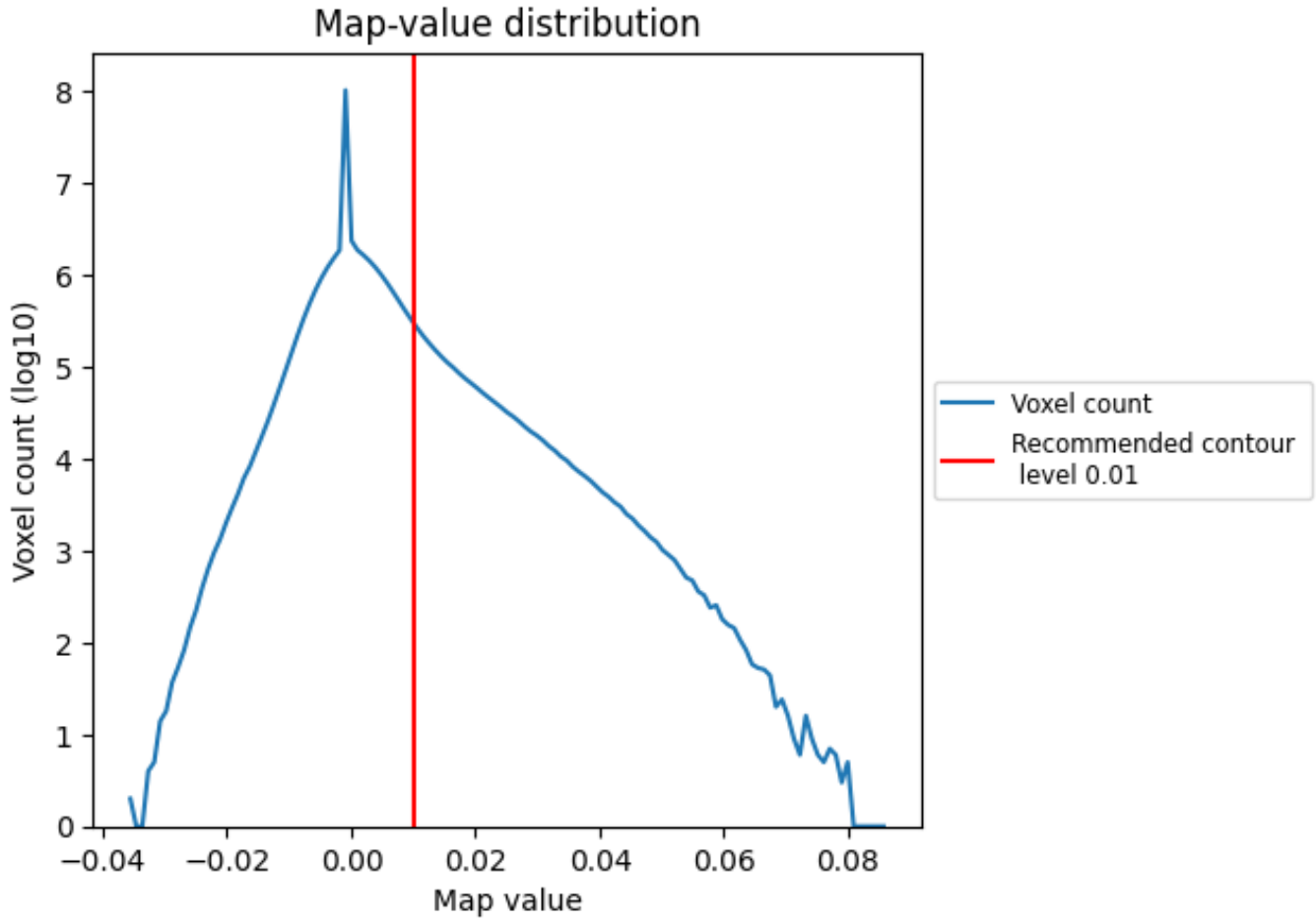


Z

7 Map analysis

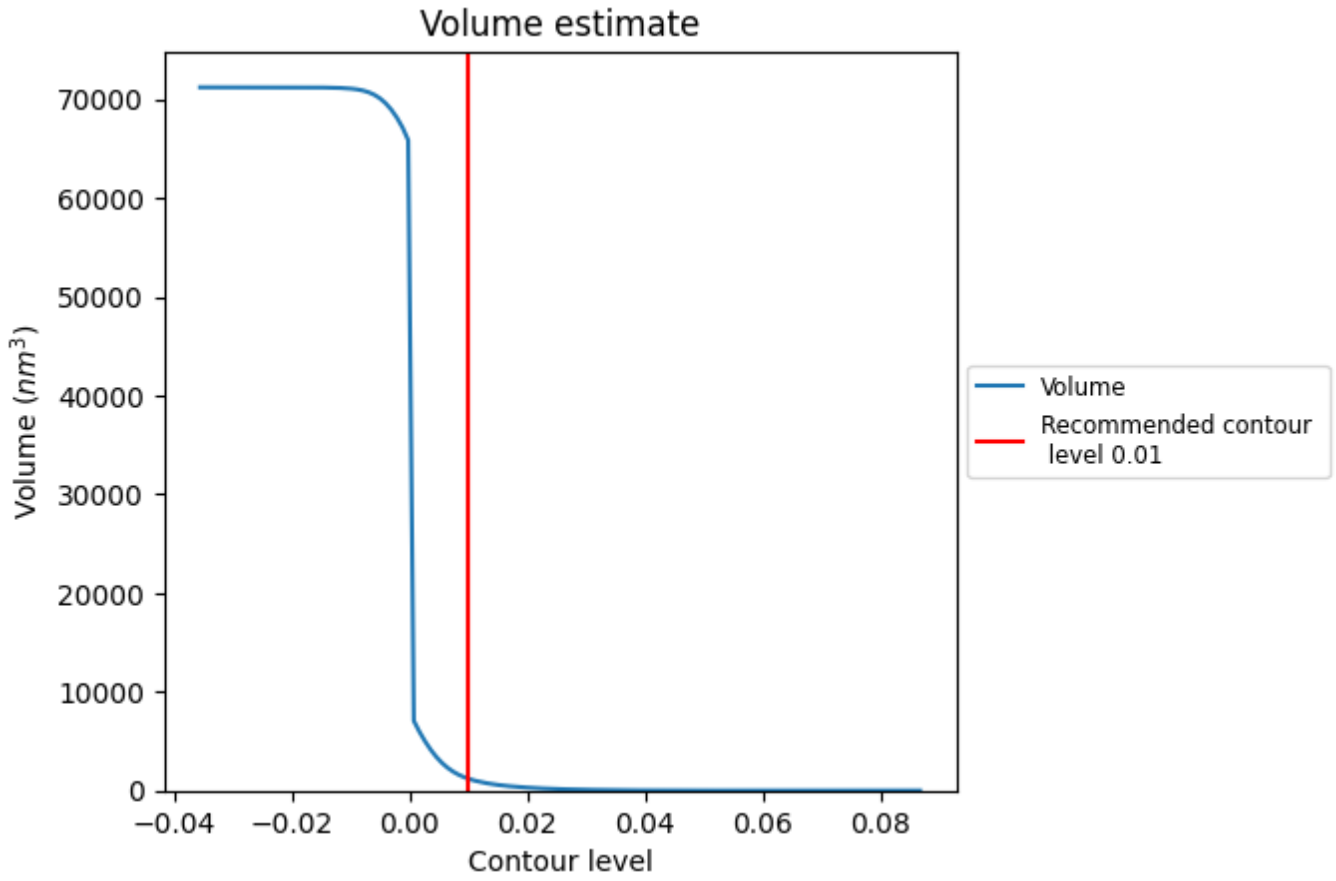
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

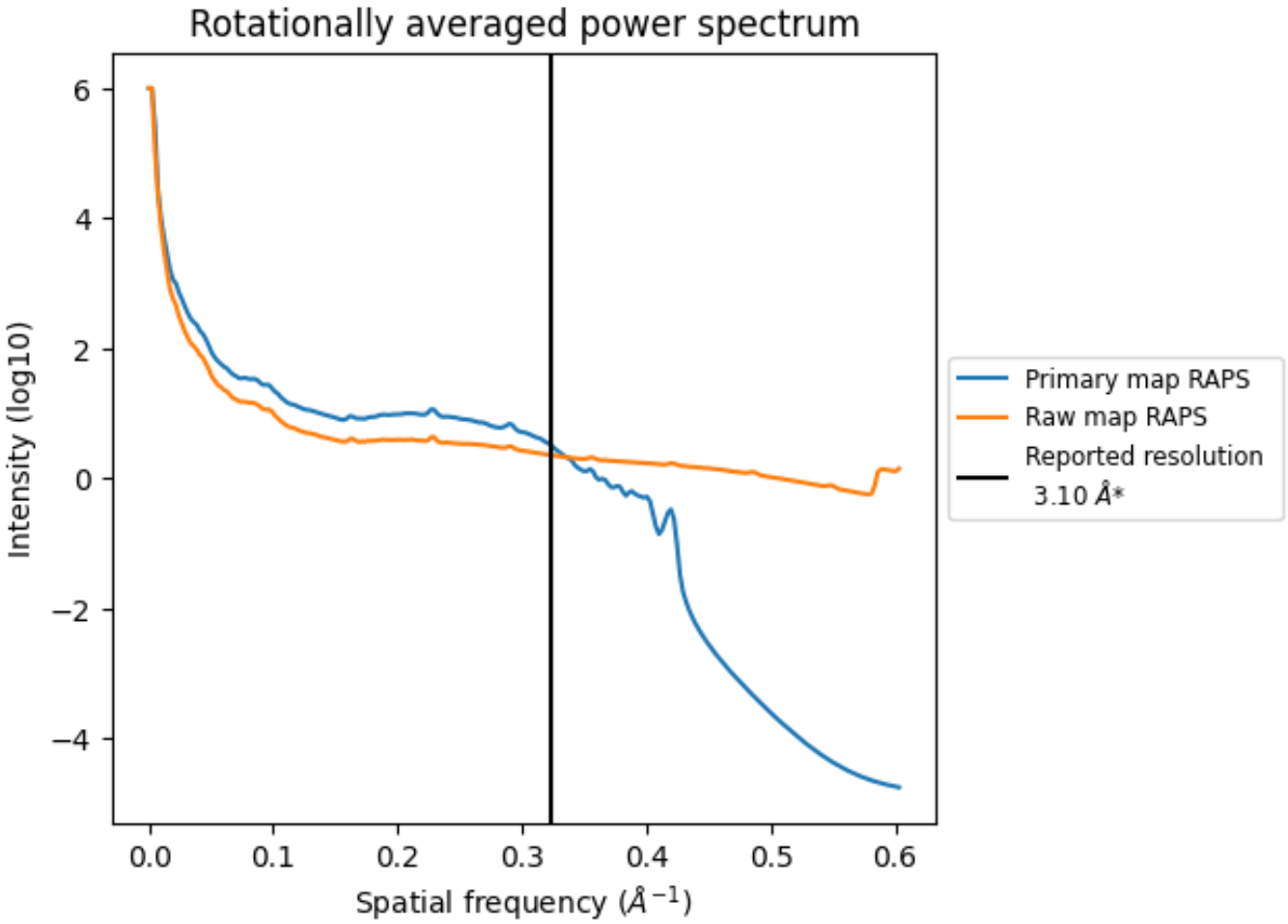
7.2 Volume estimate (i)



The volume at the recommended contour level is 1202 nm^3; this corresponds to an approximate mass of 1086 kDa.

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

7.3 Rotationally averaged power spectrum (i)

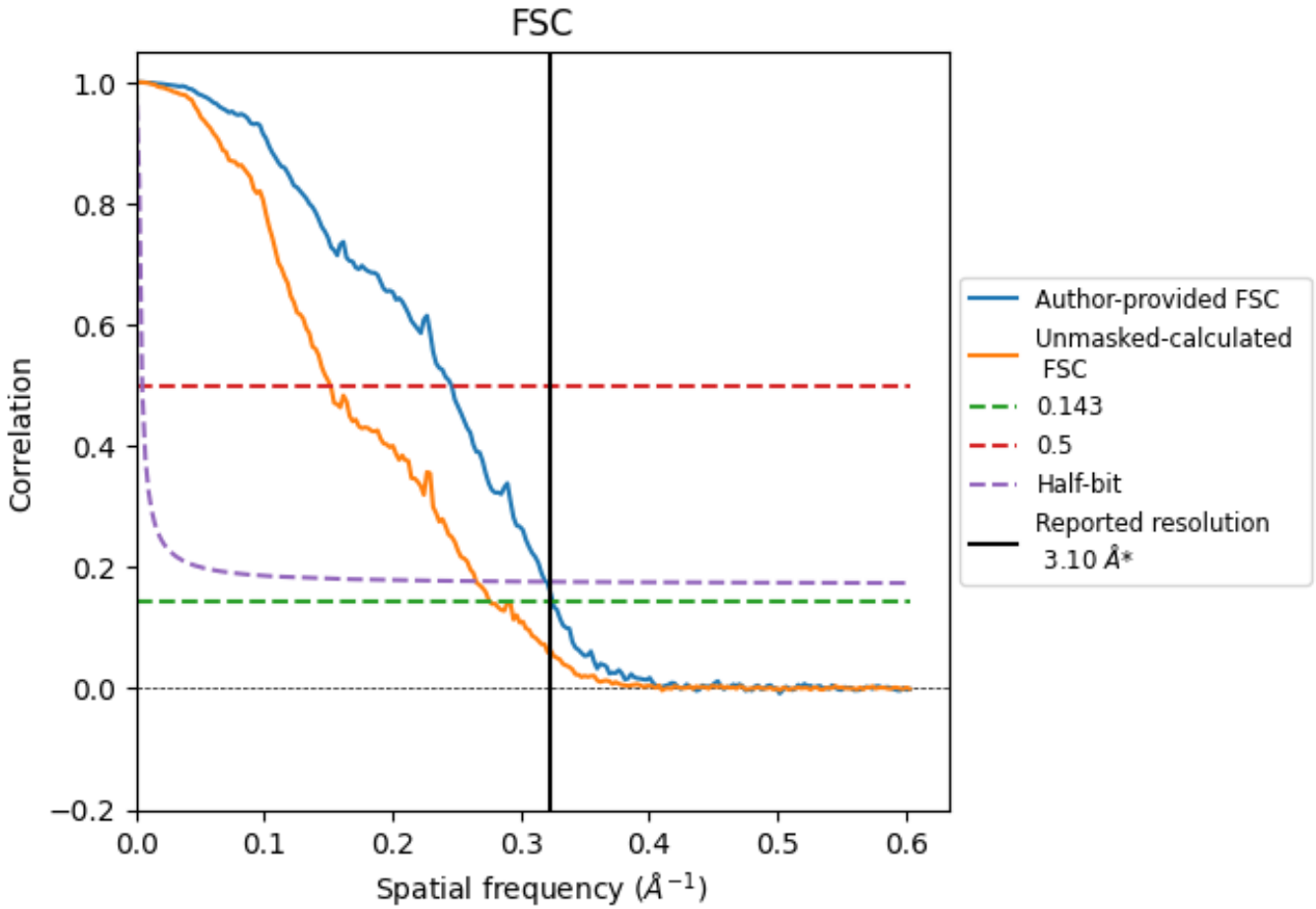


*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.323 $Å^{-1}$

8.2 Resolution estimates (i)

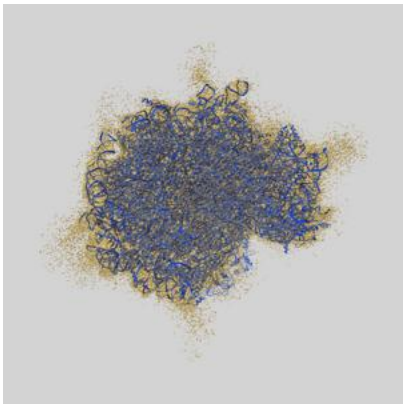
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.08	4.07	3.13
Unmasked-calculated*	3.62	6.61	3.77

*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 3.62 differs from the reported value 3.1 by more than 10 %

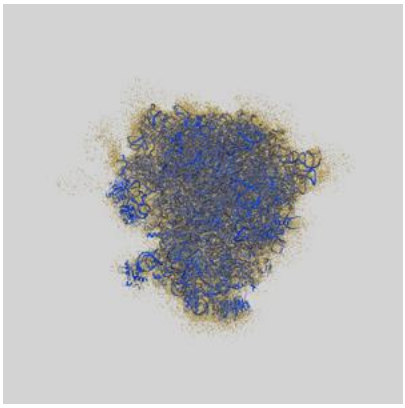
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-16052 and PDB model 8BHF. Per-residue inclusion information can be found in section 3 on page 22.

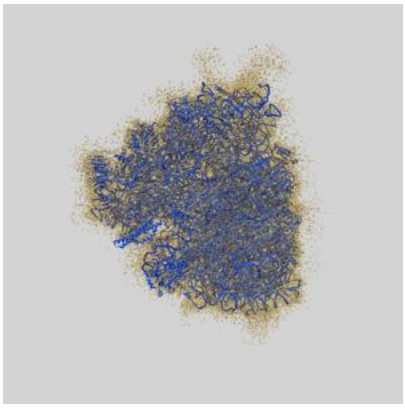
9.1 Map-model overlay



X



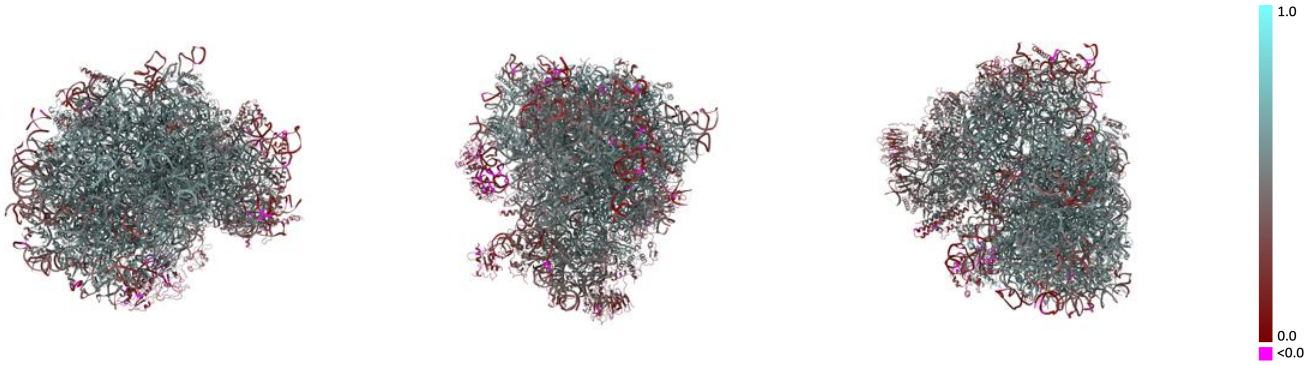
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

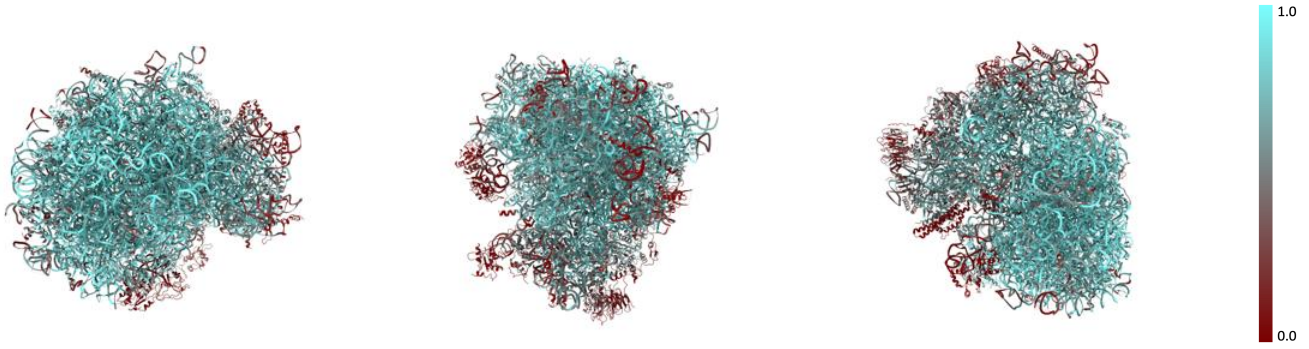
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

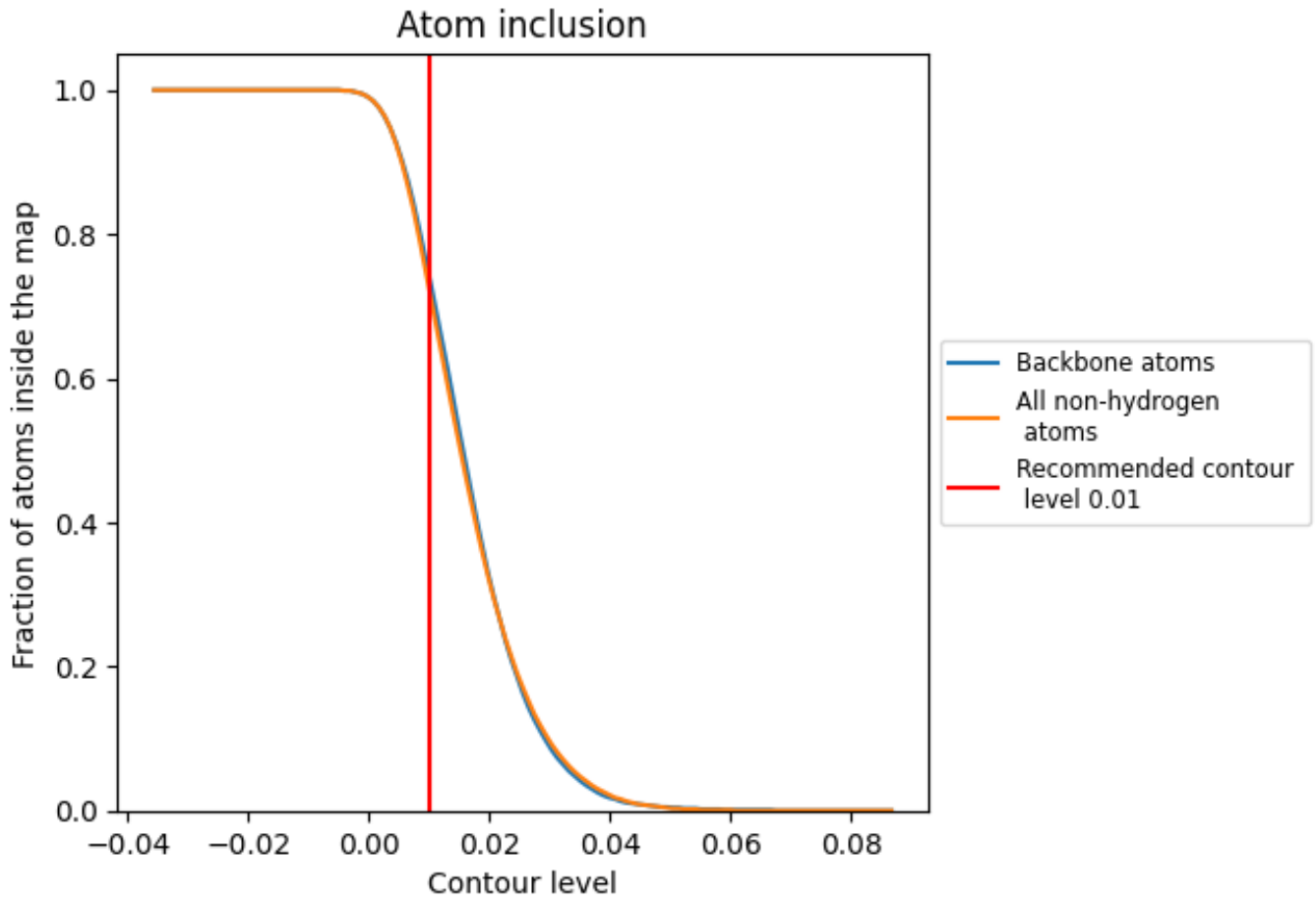
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 74% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7250	0.4920
11	0.3240	0.3870
21	0.6740	0.4480
A1	0.8670	0.5820
A2	0.8330	0.5090
A3	0.7330	0.4720
B1	0.8360	0.5710
B2	0.9380	0.5760
B3	0.5220	0.4700
C1	0.8330	0.5680
C2	0.9040	0.5530
C3	0.6090	0.4970
D1	0.8330	0.5700
D3	0.6360	0.5010
E1	0.7340	0.5220
E3	0.3540	0.3690
F1	0.8320	0.5700
F3	0.6040	0.4890
G1	0.7820	0.5450
G3	0.5350	0.4560
H1	0.6550	0.4750
H3	0.4400	0.3870
I1	0.7610	0.5480
I3	0.3260	0.3730
J1	0.5200	0.4220
J3	0.6090	0.5010
K1	0.7810	0.5430
K3	0.6350	0.4830
L1	0.8100	0.5470
L3	0.2720	0.3370
M1	0.7550	0.5370
M3	0.6720	0.5450
N1	0.8700	0.5850
N3	0.0650	0.2000
O1	0.6580	0.5030

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Chain	Atom inclusion	Q-score
O3	0.6690	0.5200
P1	0.7610	0.5420
P3	0.6680	0.5140
Q1	0.7600	0.5370
Q3	0.4030	0.3740
R1	0.8500	0.5750
R3	0.5150	0.4300
S1	0.8470	0.5750
S3	0.3960	0.3910
T1	0.7590	0.5510
T3	0.4570	0.4090
U1	0.7770	0.5460
U3	0.4880	0.4100
V1	0.7510	0.5420
V3	0.3810	0.4100
W1	0.9120	0.5920
W3	0.5390	0.4760
X1	0.6500	0.4800
X3	0.7350	0.5470
Y1	0.7960	0.5440
Y3	0.6650	0.5310
Z1	0.8100	0.5610
Z3	0.5560	0.4400
a1	0.7890	0.5860
a3	0.3960	0.4130
b1	0.7930	0.5690
b3	0.6970	0.5340
c1	0.7630	0.5470
c3	0.5380	0.4480
d1	0.8110	0.5620
d3	0.5060	0.4760
e1	0.0490	0.1620
e3	0.5320	0.4550
f1	0.0550	0.1720
f3	0.4570	0.4340
g3	0.0870	0.2050
h3	0.2280	0.2930
j3	0.8360	0.5790
k3	0.8320	0.5730
l1	0.0220	0.1540
l3	0.8320	0.5660
m1	0.8710	0.5660

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Chain	Atom inclusion	Q-score
m3	0.8030	0.5430
n1	0.1820	0.3090
n3	0.7290	0.5140
o3	0.8040	0.5550
p3	0.6620	0.4980
q3	0.7460	0.5350
r3	0.7860	0.5530
s3	0.7130	0.5150
t3	0.7640	0.5430
u3	0.7940	0.5490