Full wwPDB EM Validation Report

Mar 6, 2026 – 04:39 PM UTC

PDB ID	:	7OYC / pdb_00007oyc
EMDB ID	:	EMD-13113
Title	:	Cryo-EM structure of the Xenopus egg 80S ribosome
Authors	:	Leesch, F.; Lorenzo-Orts, L.; Grishkovskaya, I.; Kandolf, S.; Belacic, K.; Meinhart, A.; Haselbach, D.; Pauli, A.
Deposited on	:	2021-06-24
Resolution	:	2.40 Å(reported)

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

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

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

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

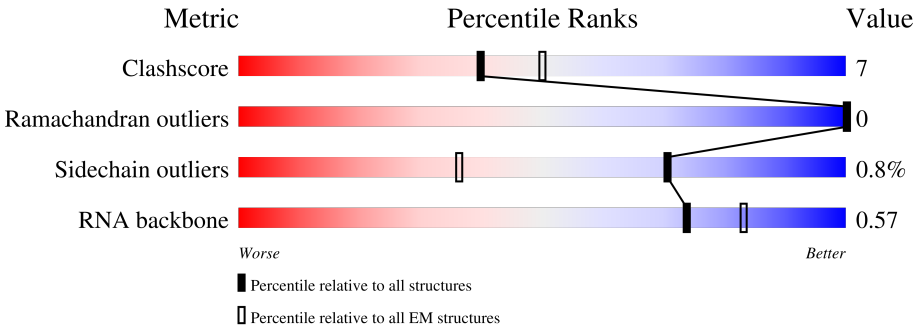
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

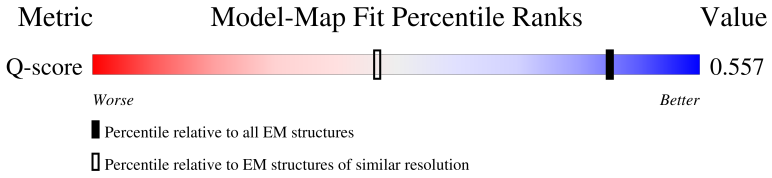
1 Overall quality at a glance

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

The reported resolution of this entry is 2.40 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	5628 (1.90 - 2.90)

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	11	154	49% 72% 16% • 12%
2	22	1826	51% 26% 5% 18%
3	51	4115	49% 25% 5% 21%

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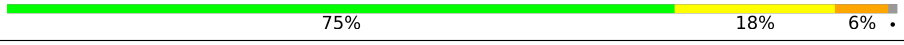
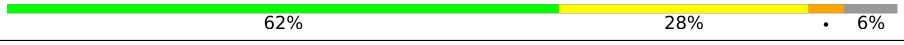
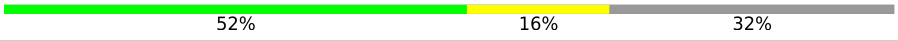
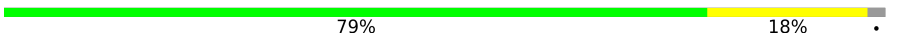
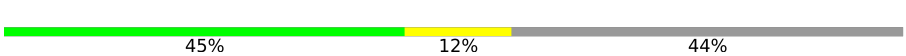
Mol	Chain	Length	Quality of chain
4	71	120	
5	81	156	
6	A1	257	
7	A2	306	
8	B1	403	
9	B2	264	
10	C1	401	
11	C2	281	
12	D1	296	
13	D2	246	
14	E1	258	
15	E2	263	
16	F1	246	
17	F2	203	
18	G1	266	
19	G2	249	
20	H1	192	
21	H2	194	
22	I1	215	
23	I2	208	
24	J1	177	
25	J2	194	
26	K2	165	
27	L1	211	
28	L2	158	

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Mol	Chain	Length	Quality of chain
29	M1	138	
30	N1	204	
31	N2	151	
32	O1	231	
33	O2	151	
34	P1	184	
35	P2	145	
36	Q1	188	
37	Q2	146	
38	R1	197	
39	R2	135	
40	S1	176	
41	S2	152	
42	T1	160	
43	T2	146	
44	U1	128	
45	U2	119	
46	V1	140	
47	V2	83	
48	W1	155	
49	W2	130	
50	X1	155	
51	X2	143	
52	Y1	145	
53	Y2	132	

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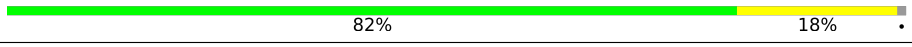
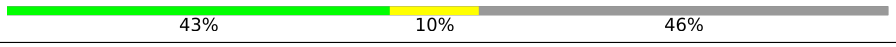
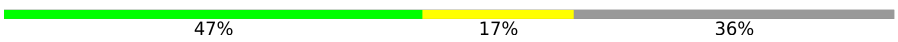
Mol	Chain	Length	Quality of chain
54	Z1	136	
55	Z2	125	
56	a1	148	
57	a2	115	
58	b1	75	
59	b2	84	
60	c1	116	
61	c2	69	
62	d1	125	
63	d2	86	
64	e1	135	
65	e2	133	
66	f1	110	
67	g1	117	
68	g2	317	
69	h1	123	
70	i1	105	
71	i2	378	
72	j1	97	
73	k1	70	
74	l1	51	
75	m1	128	
76	n1	25	
77	o1	106	
78	p1	92	

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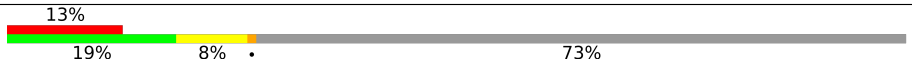
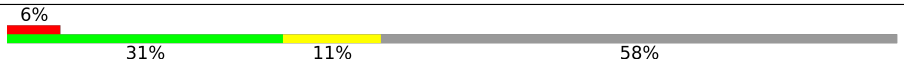
Mol	Chain	Length	Quality of chain
79	r1	137	
80	s1	113	
81	v2	858	

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 198947 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 Eukaryotic translation initiation factor 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	11	136	1033	644	178	200	11	0	0

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	22	1495	31922	14260	5748	10420	1494	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
22	287	C	U	conflict	GB X04025.1

- Molecule 3 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	51	3245	69603	30999	12763	22596	3245	0	0

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	71	119	2538	1133	457	830	118	0	0

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	81	147	3139	1399	564	1029	147	0	0

- Molecule 6 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A1	245	Total	C	N	O	S	0	0
			1868	1173	378	311	6		

- Molecule 7 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A2	208	Total	C	N	O	S	0	0
			1643	1046	289	299	9		

- Molecule 8 is a protein called Rpl3-prov protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B1	394	Total	C	N	O	S	0	0
			3170	2021	594	541	14		

- Molecule 9 is a protein called 40S ribosomal protein S3a-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B2	213	Total	C	N	O	S	0	0
			1734	1103	309	309	13		

- Molecule 10 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C1	351	Total	C	N	O	S	0	0
			2805	1763	557	469	16		

- Molecule 11 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C2	215	Total	C	N	O	S	0	0
			1663	1077	285	292	9		

- Molecule 12 is a protein called Rpl5-b protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	D1	289	Total	C	N	O	S	0	0
			2348	1493	427	421	7		

- Molecule 13 is a protein called DNA-(apurinic or apyrimidinic site) lyase.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D2	223	Total	C	N	O	S	0	0
			1732	1103	312	310	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D2	83	GLY	SER	conflict	UNP Q7ZYT3

- Molecule 14 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E1	214	Total	C	N	O	S	0	0
			1739	1123	332	280	4		

- Molecule 15 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E2	258	Total	C	N	O	S	0	0
			2055	1312	384	351	8		

- Molecule 16 is a protein called MGC130910 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F1	227	Total	C	N	O	S	0	0
			1877	1210	358	302	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F1	134	ALA	VAL	conflict	UNP Q3B8I3

- Molecule 17 is a protein called Ribosomal_S7 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	F2	182	Total	C	N	O	S	0	0
			1439	903	271	259	6		

- Molecule 18 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G1	210	Total	C	N	O	S	0	0
			1695	1088	320	283	4		

- Molecule 19 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	G2	222	Total	C	N	O	S	0	0
			1796	1120	358	312	6		

- Molecule 20 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	H1	190	Total	C	N	O	S	0	0
			1517	955	285	269	8		

- Molecule 21 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	H2	186	Total	C	N	O	S	0	0
			1494	952	277	264	1		

- Molecule 22 is a protein called Ribosomal_L16 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I1	202	Total	C	N	O	S	0	0
			1639	1042	316	268	13		

- Molecule 23 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	I2	198	Total	C	N	O	S	0	0
			1620	1017	319	279	5		

- Molecule 24 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	J1	167	Total	C	N	O	S	0	0
			1338	848	250	235	5		

- Molecule 25 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	J2	180	Total	C	N	O	S	0	0
			1497	955	298	242	2		

- Molecule 26 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	K2	93	Total	C	N	O	S	0	0
			779	513	133	128	5		

- Molecule 27 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L1	199	Total	C	N	O	S	0	0
			1608	1012	330	262	4		

- Molecule 28 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L2	140	Total	C	N	O	S	0	0
			1145	726	220	193	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L2	153	ALA	THR	conflict	UNP Q7SZ77

- Molecule 29 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	M1	134	Total	C	N	O	S	0	0
			1100	700	212	180	8		

- Molecule 30 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	N1	203	Total	C	N	O	S	0	0
			1691	1065	351	269	6		

- Molecule 31 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	N2	149	Total	C	N	O	S	0	0
			1204	770	230	203	1		

- Molecule 32 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	O1	199	Total	C	N	O	S	0	0
			1627	1054	314	255	4		

- Molecule 33 is a protein called Rps14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	O2	133	Total	C	N	O	S	0	0
			998	610	196	186	6		

- Molecule 34 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	P1	152	Total	C	N	O	S	0	0
			1234	772	241	212	9		

- Molecule 35 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	P2	116	Total	C	N	O	S	0	0
			955	607	177	163	8		

- Molecule 36 is a protein called Ribosomal_L18e/L15P domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Q1	180	Total	C	N	O	S	0	0
			1454	912	299	237	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q1	116	ALA	SER	conflict	UNP A0A1L8FN04

- Molecule 37 is a protein called Rps16 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Q2	134	Total	C	N	O	S	0	0
			1054	671	197	183	3		

- Molecule 38 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	R1	166	Total	C	N	O	S	0	0
			1382	858	298	217	9		

- Molecule 39 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R2	132	Total	C	N	O	S	0	0
			1066	669	199	194	4		

- Molecule 40 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S1	176	Total	C	N	O	S	0	0
			1455	934	280	232	9		

- Molecule 41 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S2	136	Total	C	N	O	S	0	0
			1129	708	228	192	1		

- Molecule 42 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T1	157	Total	C	N	O	S	0	0
			1291	814	257	215	5		

- Molecule 43 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	T2	137	Total	C	N	O	S	0	0
			1059	666	199	191	3		

- Molecule 44 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	U1	97	Total	C	N	O	S	0	0
			792	508	139	143	2		

- Molecule 45 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	U2	85	Total 684	C 429	N 133	O 118	S 4	0	0

- Molecule 46 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V1	129	Total 968	C 612	N 182	O 169	S 5	0	0

- Molecule 47 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	V2	83	Total 643	C 396	N 118	O 124	S 5	0	0

- Molecule 48 is a protein called TRASH domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W1	60	Total 502	C 321	N 98	O 81	S 2	0	0

- Molecule 49 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	W2	129	Total 1035	C 659	N 193	O 177	S 6	0	0

- Molecule 50 is a protein called Ribosomal_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	X1	119	Total 976	C 624	N 181	O 170	S 1	0	0

- Molecule 51 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	X2	139	Total 1077	C 679	N 213	O 182	S 3	0	0

- Molecule 52 is a protein called KOW domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Y1	125	Total	C	N	O	S	0	0
			1039	654	208	174	3		

- Molecule 53 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Y2	123	Total	C	N	O	S	0	0
			1004	637	195	167	5		

- Molecule 54 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Z1	135	Total	C	N	O	S	0	0
			1109	713	211	182	3		

- Molecule 55 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Z2	67	Total	C	N	O	S	0	0
			536	345	98	92	1		

- Molecule 56 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	a1	147	Total	C	N	O	S	0	0
			1164	741	233	186	4		

- Molecule 57 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	a2	98	Total	C	N	O	S	0	0
			780	484	161	130	5		

- Molecule 58 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	b1	63	Total	C	N	O	S	0	0
			527	328	112	84	3		

- Molecule 59 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	b2	81	Total	C	N	O	S	0	0
			631	397	116	111	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	c1	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 61 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	c2	59	Total	C	N	O	S	0	0
			459	279	89	89	2		

- Molecule 62 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	d1	106	Total	C	N	O	S	0	0
			884	558	173	152	1		

- Molecule 63 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	d2	55	Total	C	N	O	S	0	0
			455	282	95	72	6		

- Molecule 64 is a protein called Rpl32.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	e1	126	Total	C	N	O	S	0	0
			1037	657	209	166	5		

- Molecule 65 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	e2	51	Total	C	N	O	S	0	0
			407	250	90	66	1		

- Molecule 66 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	f1	107	Total	C	N	O	S	0	0
			869	551	174	140	4		

- Molecule 67 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	g1	104	Total	C	N	O	S	0	0
			830	520	171	133	6		

- Molecule 68 is a protein called Gnb2l1-prov protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	g2	310	Total	C	N	O	S	0	0
			2410	1516	421	460	13		

- Molecule 69 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	h1	120	Total	C	N	O	0	0
			995	627	203	165		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	i1	98	Total	C	N	O	S	0	0
			812	508	174	124	6		

- Molecule 71 is a protein called HABP4_PAI-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	i2	51	Total	C	N	O	S	0	0
			423	255	85	81	2		

- Molecule 72 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	j1	86	Total	C	N	O	S	0	0
			699	430	152	112	5		

- Molecule 73 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	k1	68	Total	C	N	O	S	0	0
			558	360	99	98	1		

- Molecule 74 is a protein called MGC116452 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	l1	50	Total	C	N	O	S	0	0
			441	281	96	63	1		

- Molecule 75 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	m1	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 76 is a protein called Rpl41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	n1	24	Total	C	N	O	S	0	0
			231	140	63	26	2		

- Molecule 77 is a protein called MGC85428 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	o1	102	Total	C	N	O	S	0	0
			835	519	173	137	6		

- Molecule 78 is a protein called Rpl37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	p1	91	Total	C	N	O	S	0	0
			707	447	134	119	7		

- Molecule 79 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	r1	118	Total	C	N	O	S	0	0
			945	590	193	159	3		

- Molecule 80 is a protein called Death-associated protein-like 1-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	s1	31	Total	C	N	O	S	0	0
			251	158	50	42	1		

- Molecule 81 is a protein called Eef2-prov protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	v2	360	Total	C	N	O	S	0	0
			2813	1776	493	530	14		

- Molecule 82 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	51	123	Total	Mg	0
			123	123	
82	71	2	Total	Mg	0
			2	2	
82	81	2	Total	Mg	0
			2	2	
82	A1	1	Total	Mg	0
			1	1	
82	B1	1	Total	Mg	0
			1	1	
82	C1	1	Total	Mg	0
			1	1	
82	V1	1	Total	Mg	0
			1	1	
82	a1	1	Total	Mg	0
			1	1	
82	e1	1	Total	Mg	0
			1	1	
82	m1	1	Total	Mg	0
			1	1	

- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	a2	1	Total	Zn	0
			1	1	
83	d2	1	Total	Zn	0
			1	1	
83	g1	1	Total	Zn	0
			1	1	

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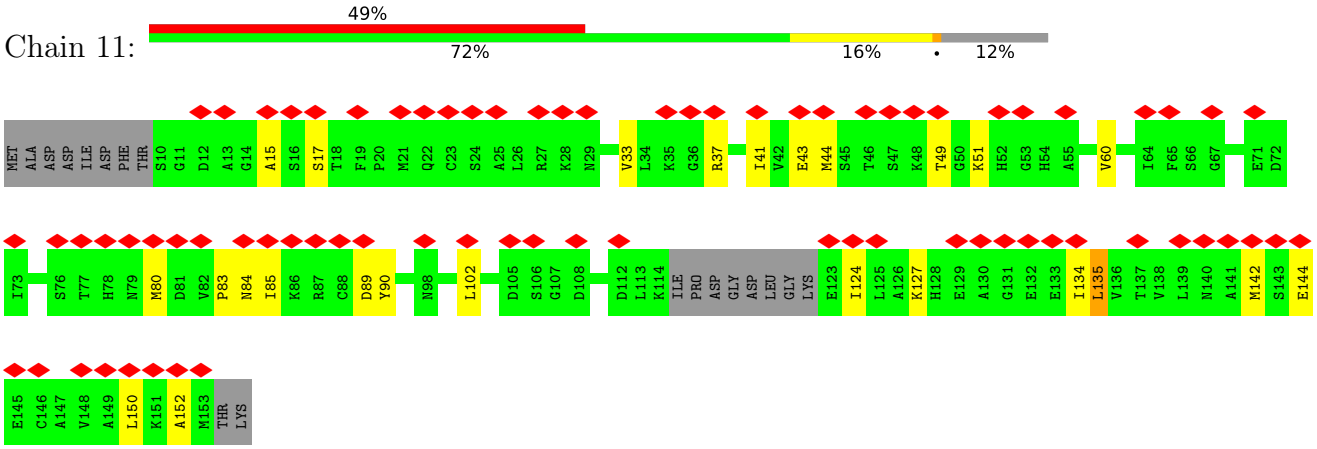
Mol	Chain	Residues	Atoms	AltConf
83	j1	1	Total Zn 1 1	0
83	m1	1	Total Zn 1 1	0
83	o1	1	Total Zn 1 1	0
83	p1	1	Total Zn 1 1	0

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.

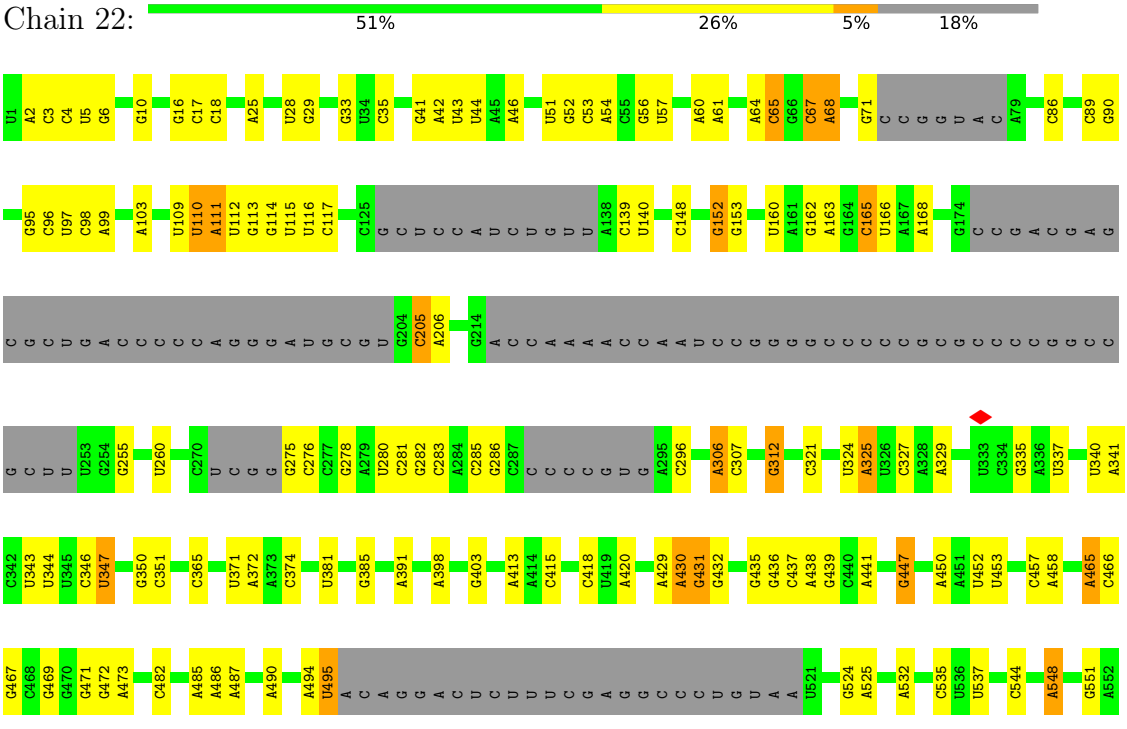
• Molecule 1: Eukaryotic translation initiation factor 5A

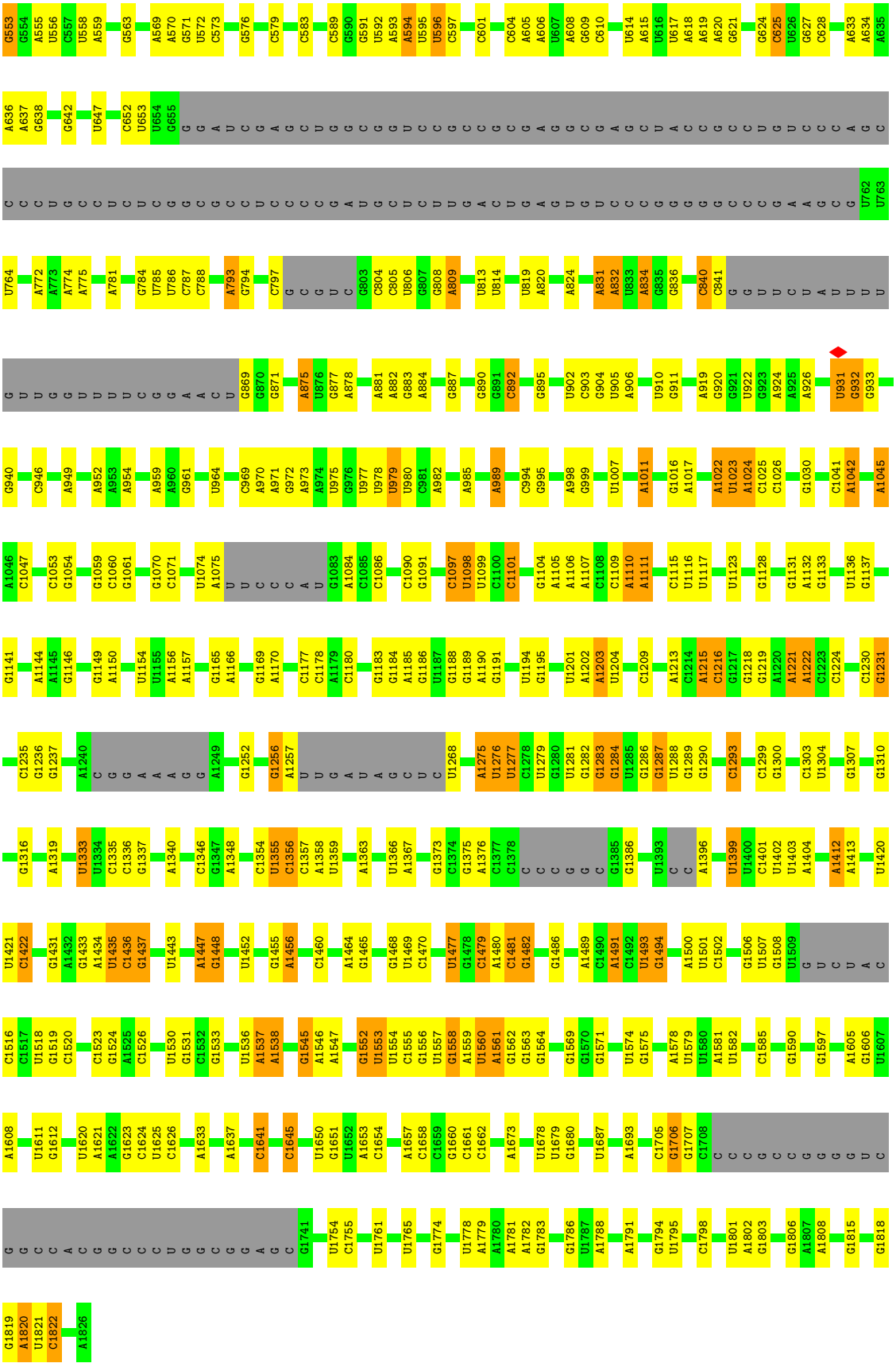
Chain 11:



• Molecule 2: 18S rRNA

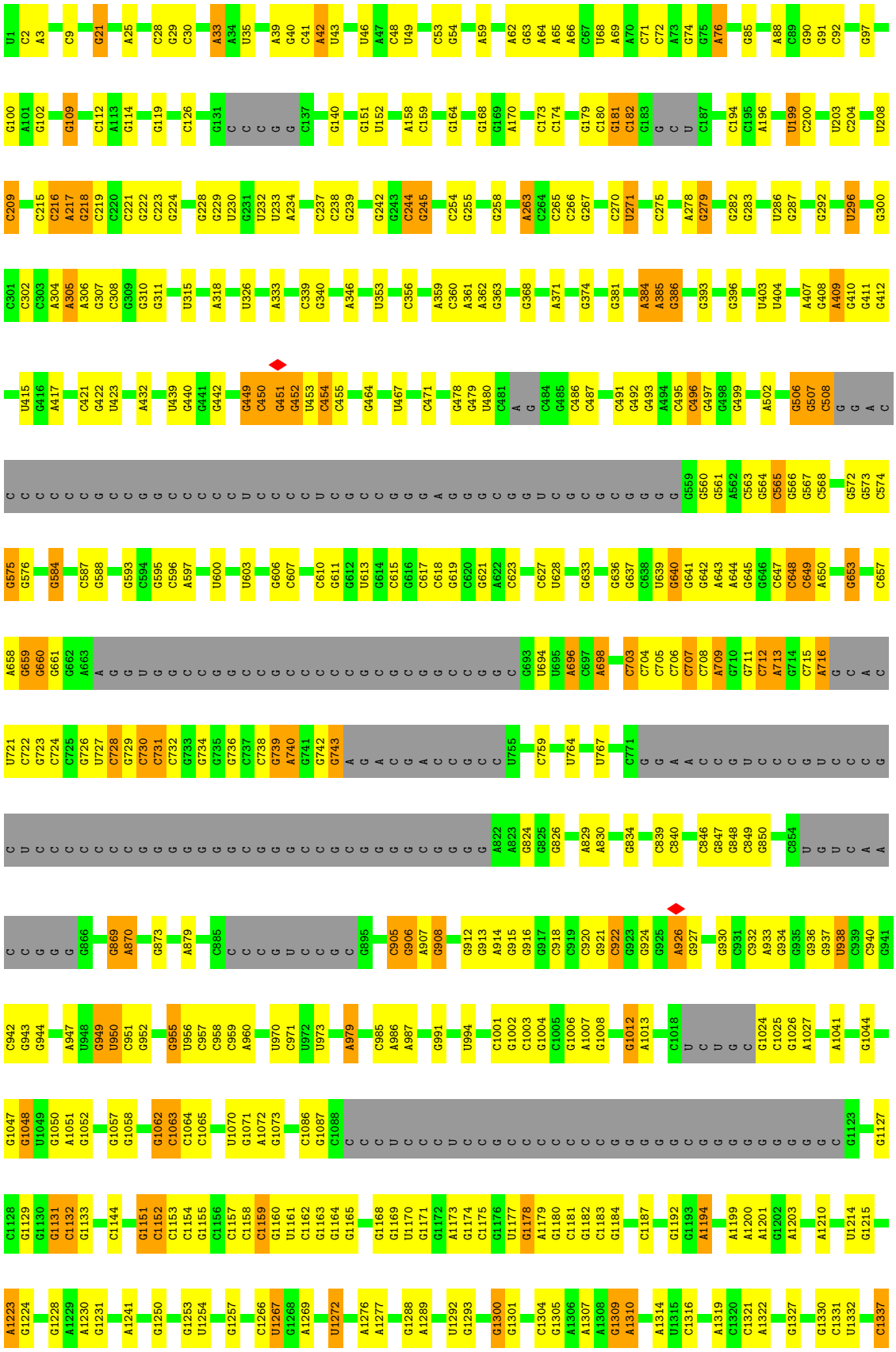
Chain 22:

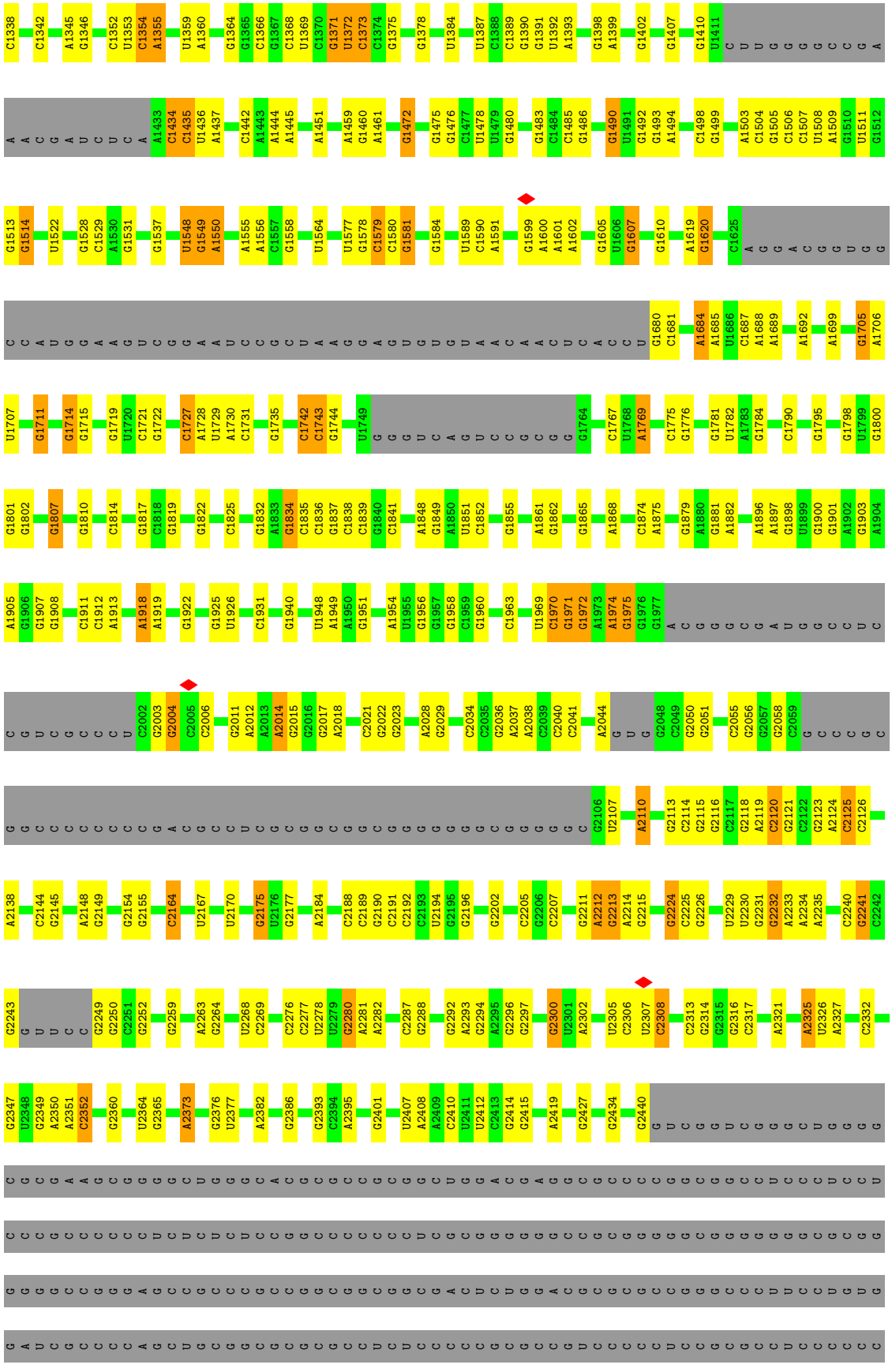


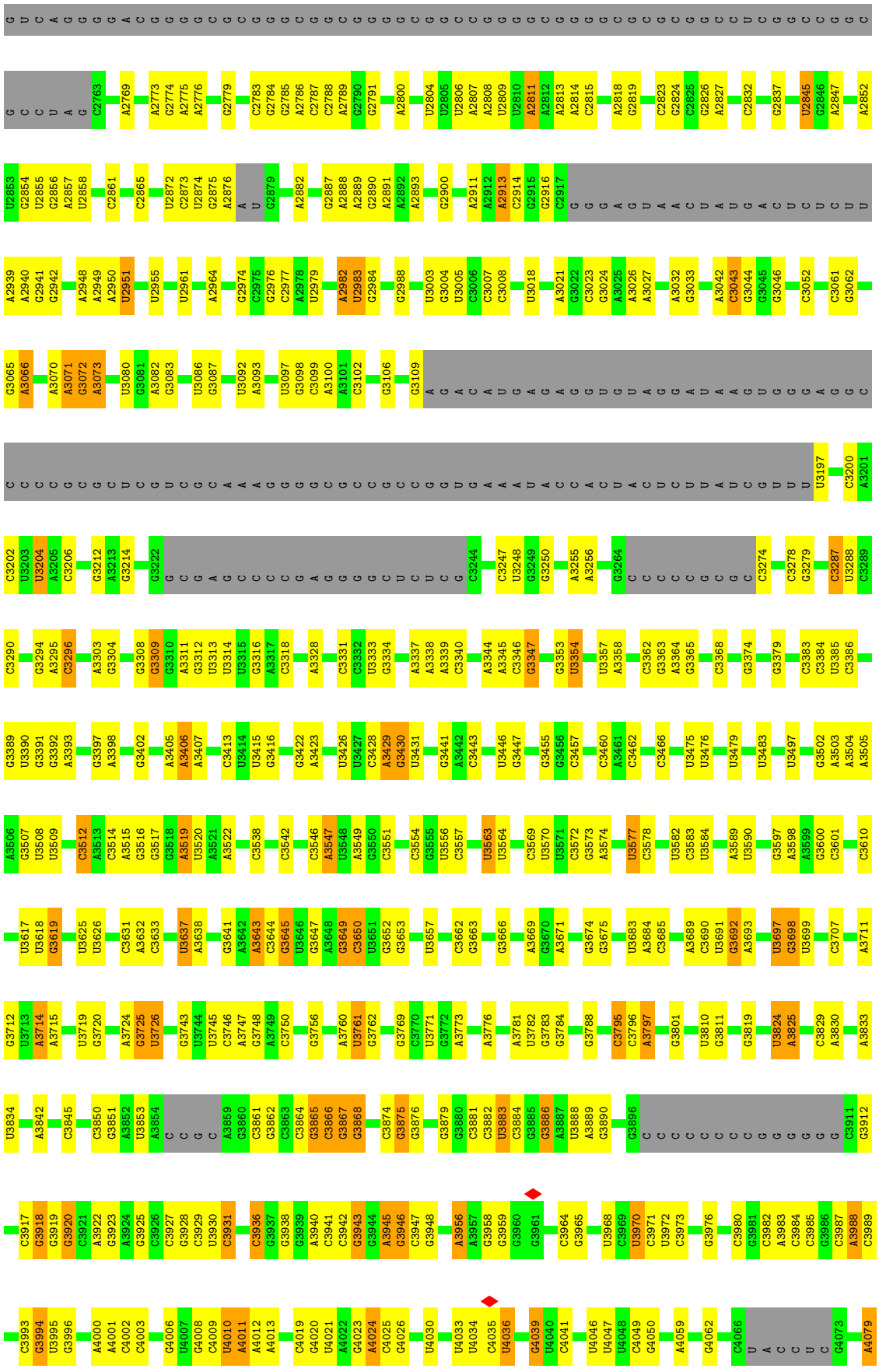


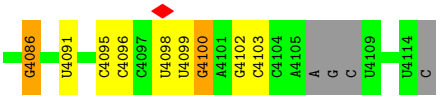
- Molecule 3: 28S rRNA

Chain 51:



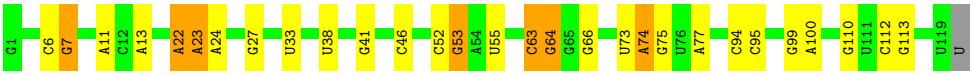






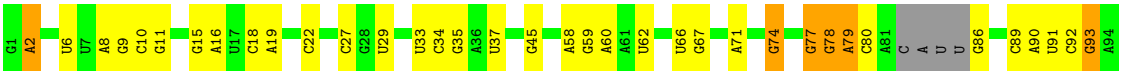
• Molecule 4: 5S rRNA

Chain 71:



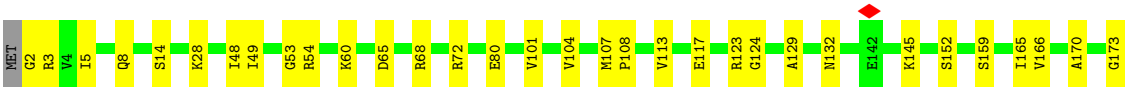
• Molecule 5: 5.8S rRNA

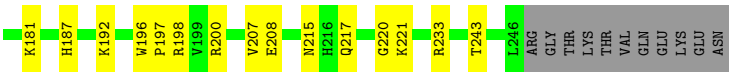
Chain 81:



• Molecule 6: 60S ribosomal protein L8

Chain A1:



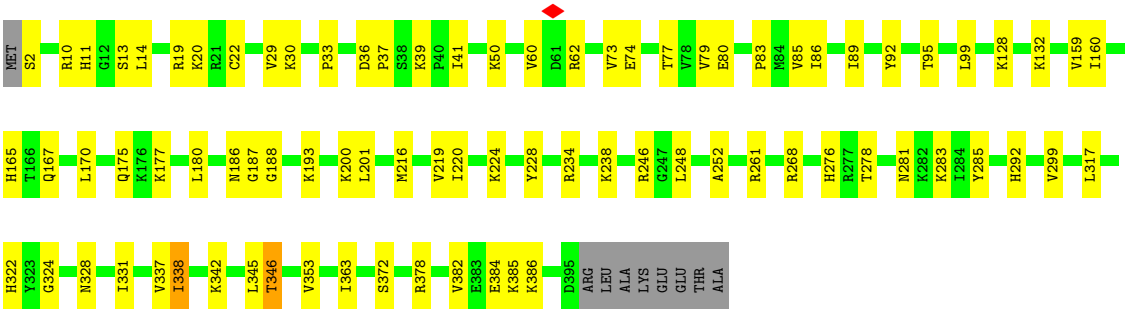


• Molecule 7: 40S ribosomal protein SA

Chain A2:

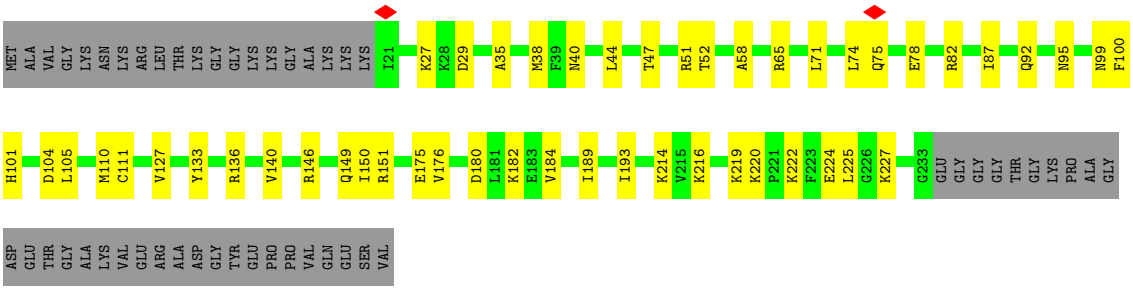
• Molecule 8: Rpl3-prov protein

Chain B1:



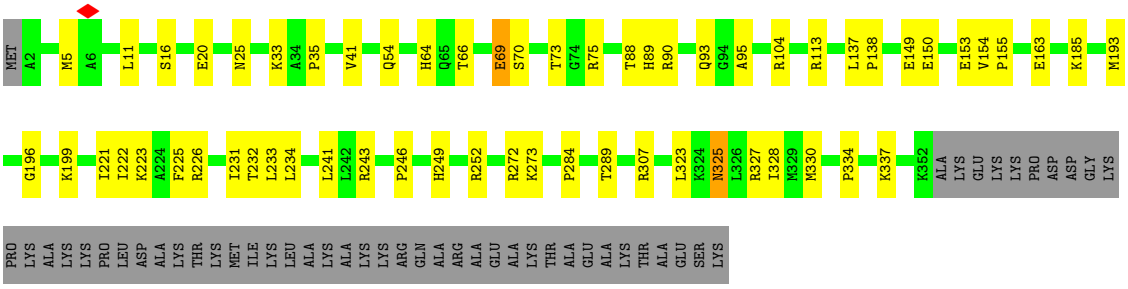
• Molecule 9: 40S ribosomal protein S3a-A

Chain B2:



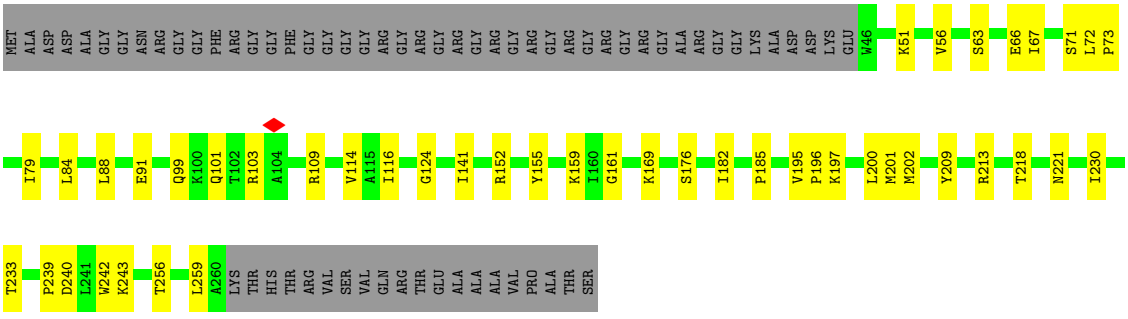
• Molecule 10: 60S ribosomal protein L4-B

Chain C1:



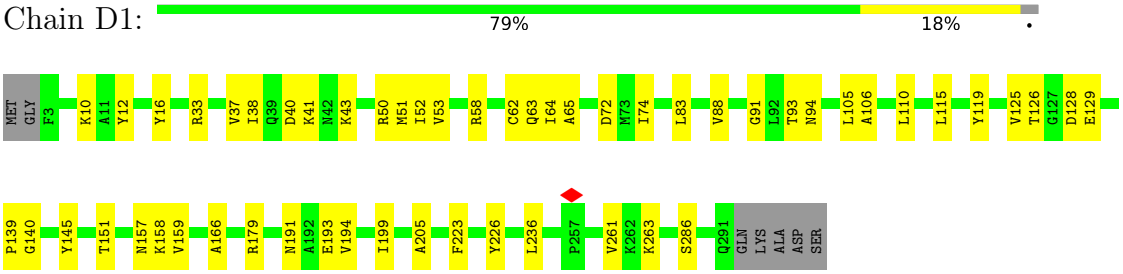
• Molecule 11: 40S ribosomal protein S2

Chain C2:



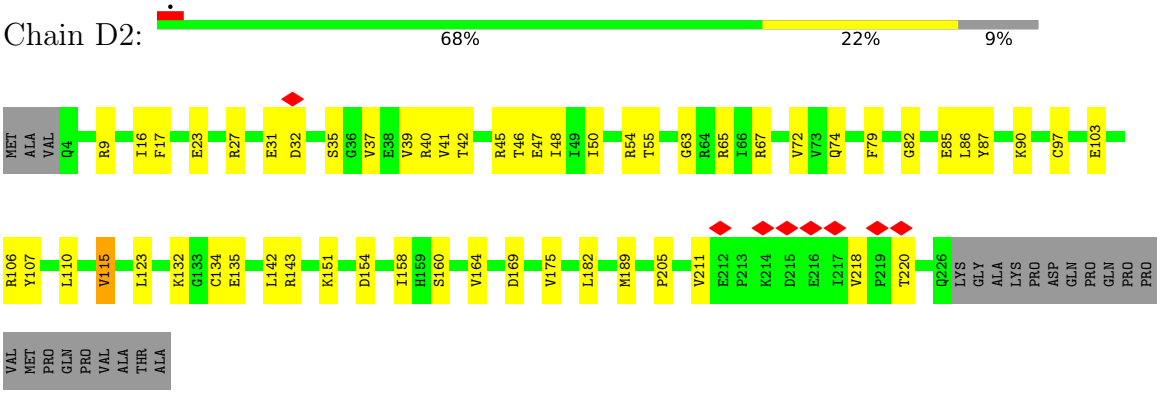
• Molecule 12: Rpl5-b protein

Chain D1:



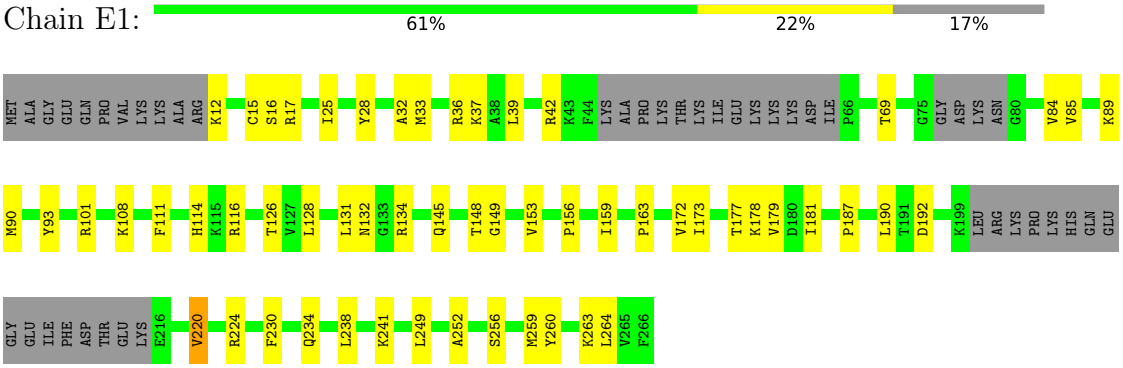
• Molecule 13: DNA-(apurinic or apyrimidinic site) lyase

Chain D2:



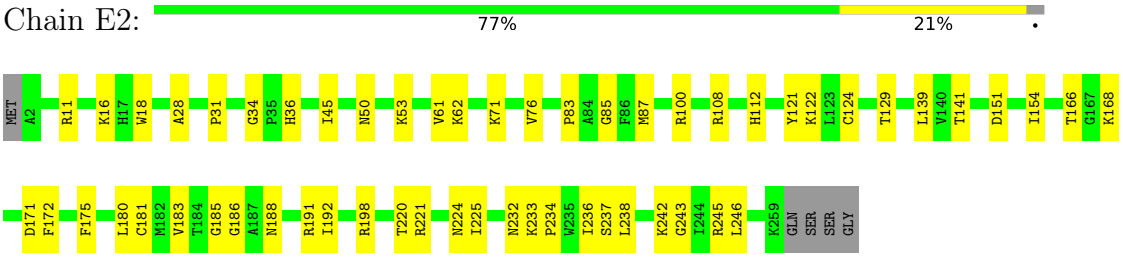
• Molecule 14: 60S ribosomal protein L6

Chain E1:



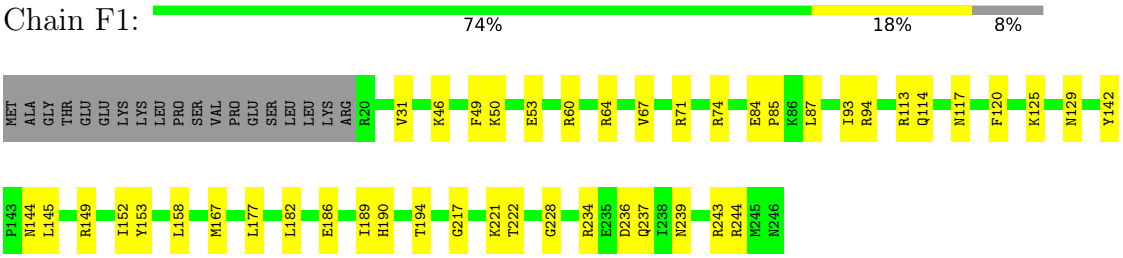
• Molecule 15: 40S ribosomal protein S4

Chain E2:



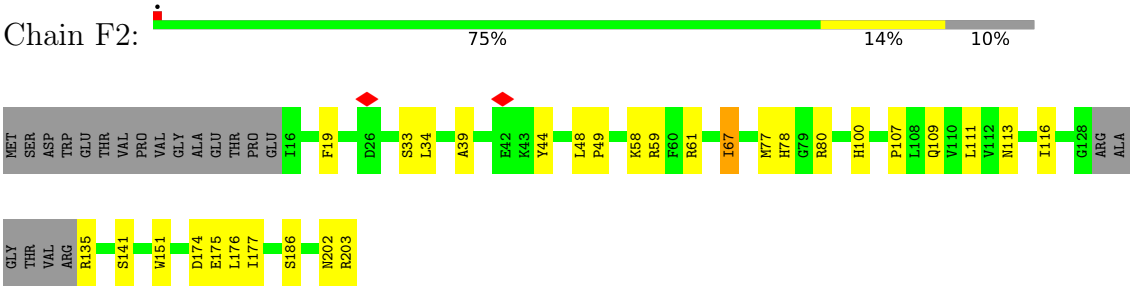
• Molecule 16: MGC130910 protein

Chain F1:



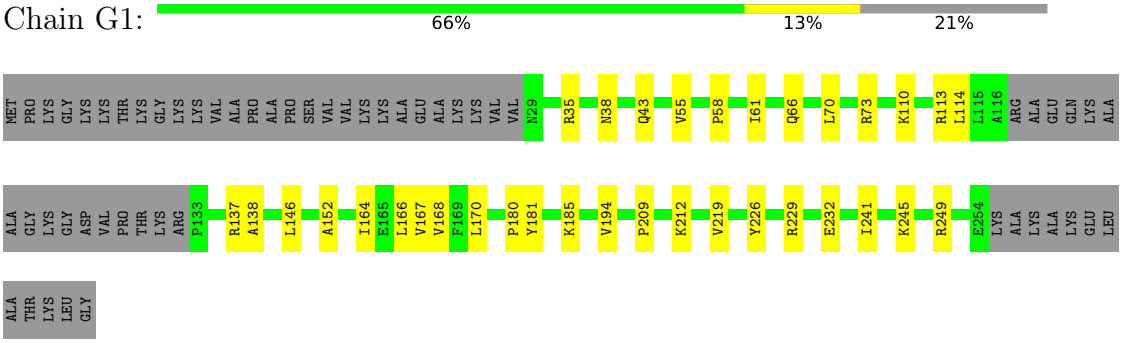
• Molecule 17: Ribosomal_S7 domain-containing protein

Chain F2:



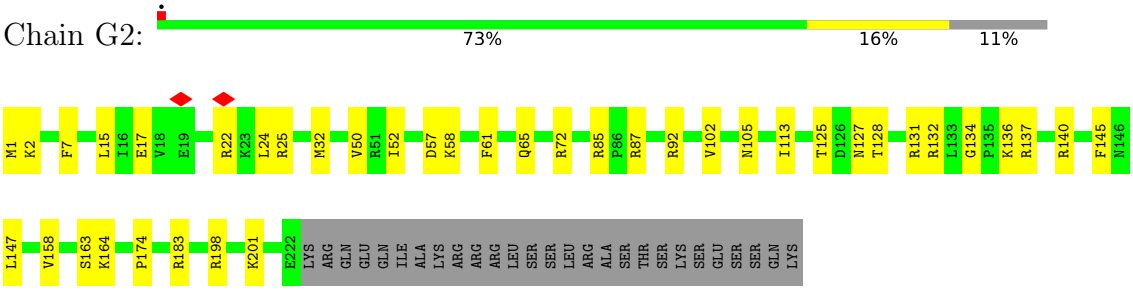
• Molecule 18: 60S ribosomal protein L7a

Chain G1:



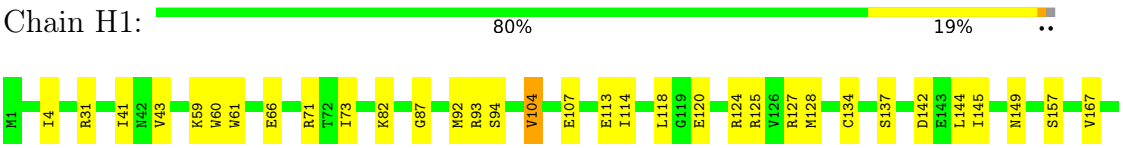
• Molecule 19: 40S ribosomal protein S6

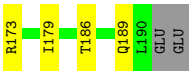
Chain G2:



• Molecule 20: 60S ribosomal protein L9

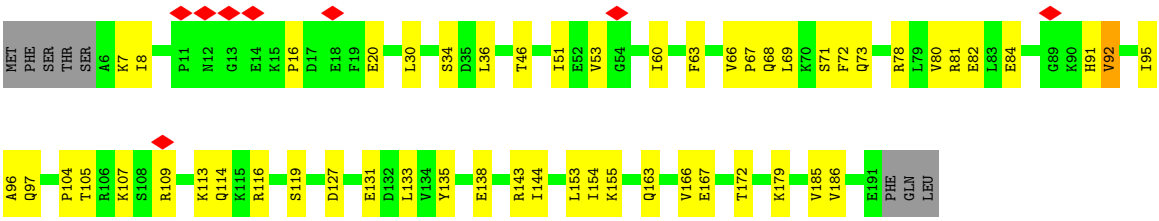
Chain H1:





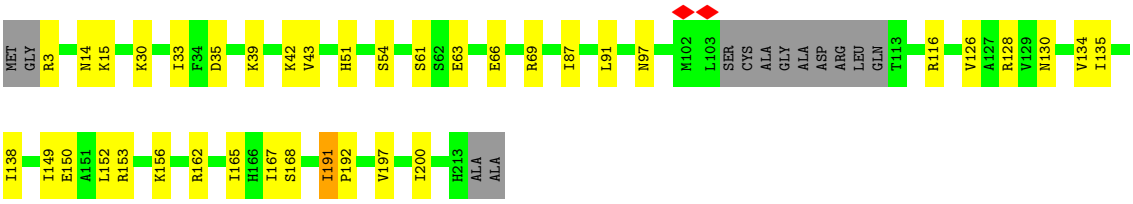
• Molecule 21: 40S ribosomal protein S7

Chain H2:



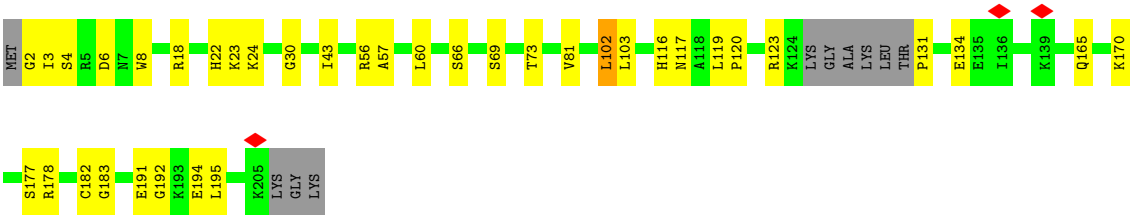
• Molecule 22: Ribosomal_L16 domain-containing protein

Chain I1:



• Molecule 23: 40S ribosomal protein S8

Chain I2:

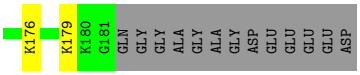


• Molecule 24: 60S ribosomal protein L11

Chain J1:

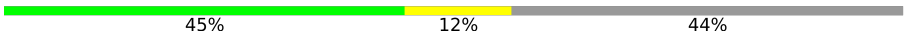
• Molecule 25: 40S ribosomal protein S9

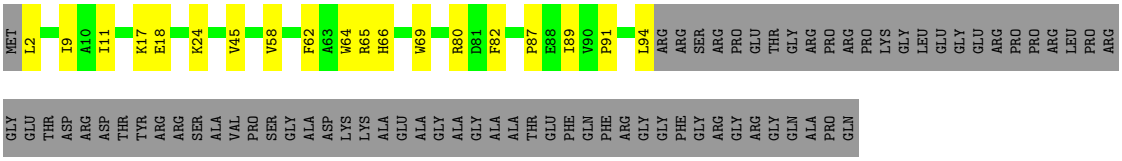
Chain J2:



• Molecule 26: 40S ribosomal protein S10

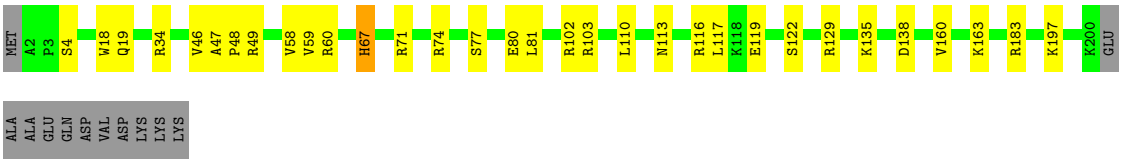
Chain K2:





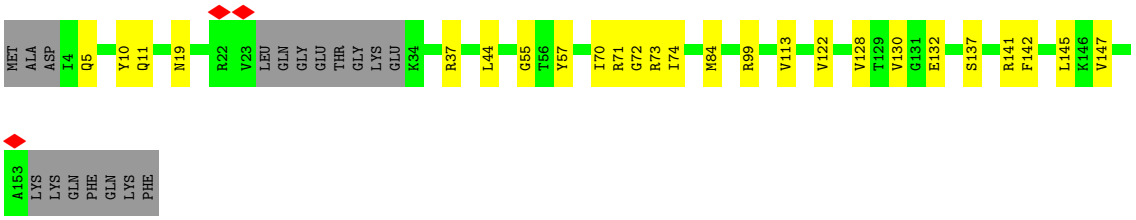
• Molecule 27: 60S ribosomal protein L13

Chain L1:



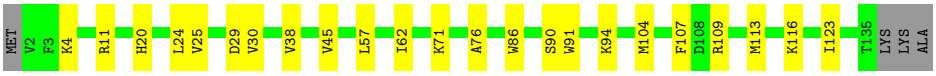
• Molecule 28: 40S ribosomal protein S11

Chain L2:



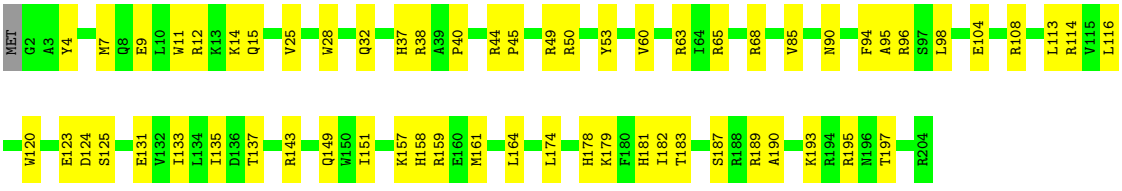
• Molecule 29: 60S ribosomal protein L14

Chain M1:



• Molecule 30: Ribosomal protein L15

Chain N1:

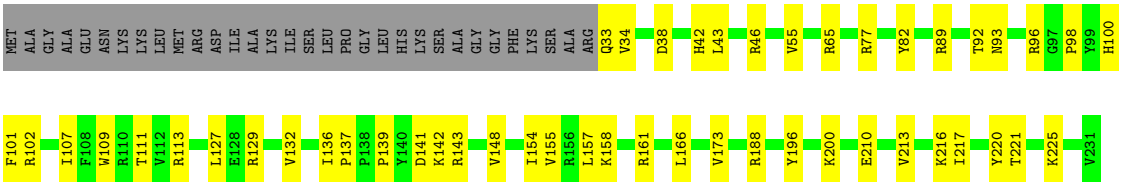


• Molecule 31: 40S ribosomal protein S13

Chain N2:

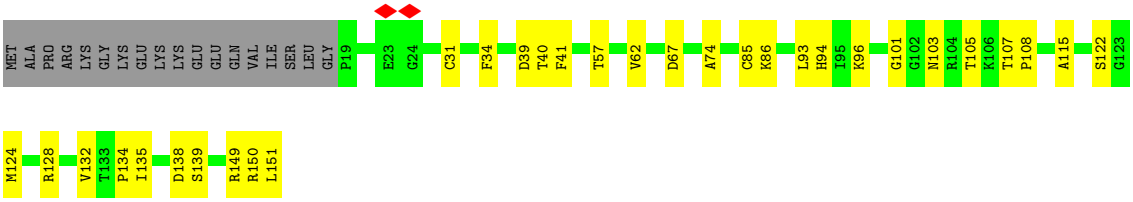
• Molecule 32: 60S ribosomal protein L13a

Chain O1:



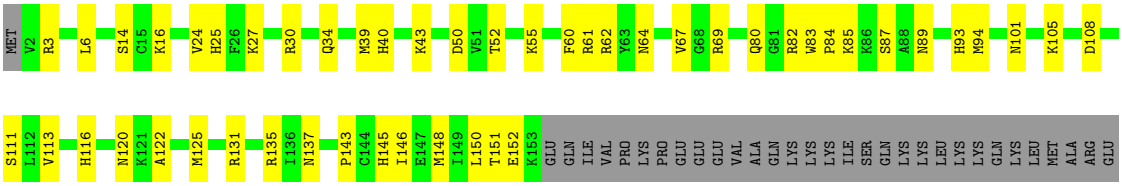
• Molecule 33: Rps14

Chain O2:



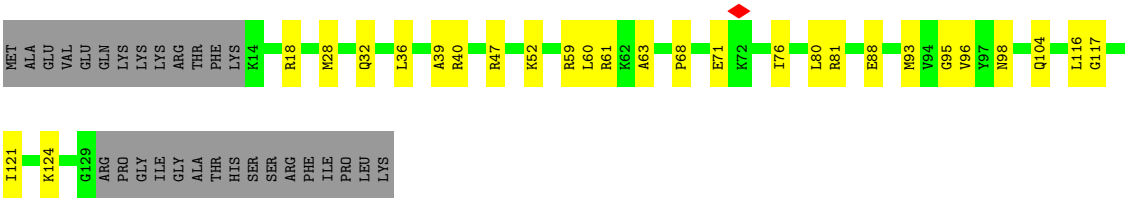
• Molecule 34: 60S ribosomal protein L17

Chain P1:



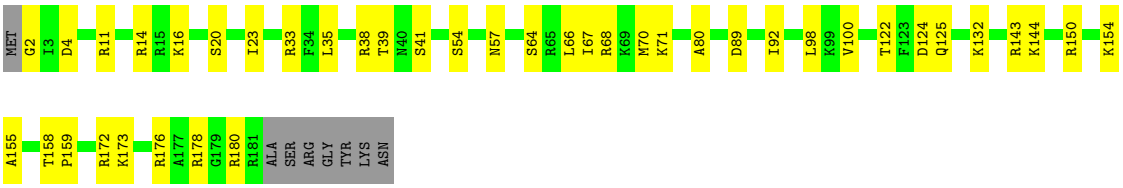
• Molecule 35: 40S ribosomal protein S15

Chain P2:



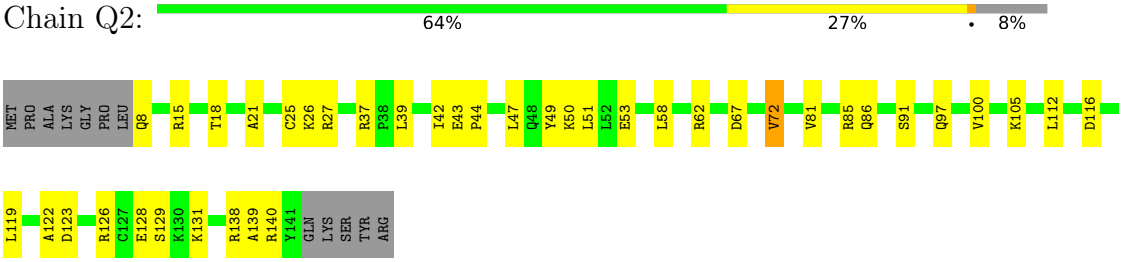
• Molecule 36: Ribosomal_L18e/L15P domain-containing protein

Chain Q1:



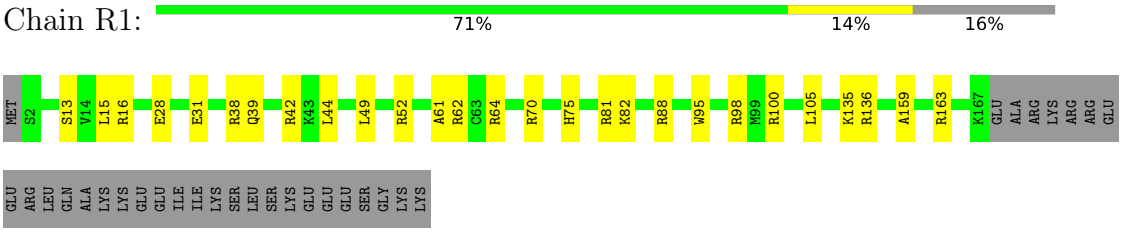
• Molecule 37: Rps16 protein

Chain Q2:



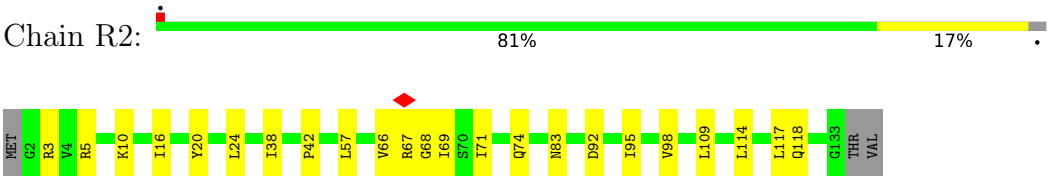
• Molecule 38: 60S ribosomal protein L19

Chain R1:



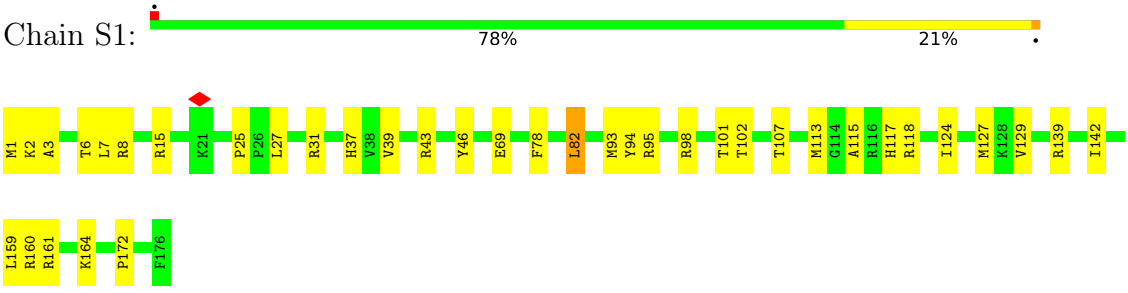
• Molecule 39: 40S ribosomal protein S17

Chain R2:



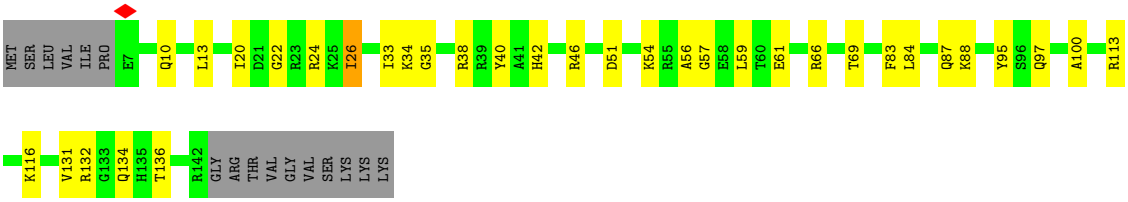
• Molecule 40: 60S ribosomal protein L18a

Chain S1:

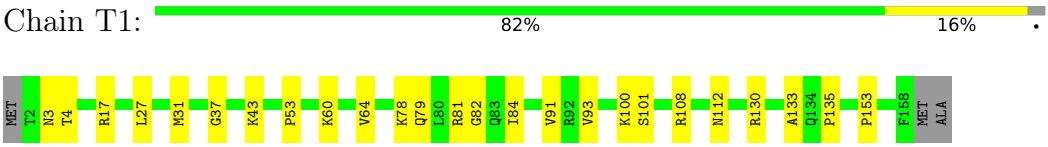


• Molecule 41: 40S ribosomal protein S18

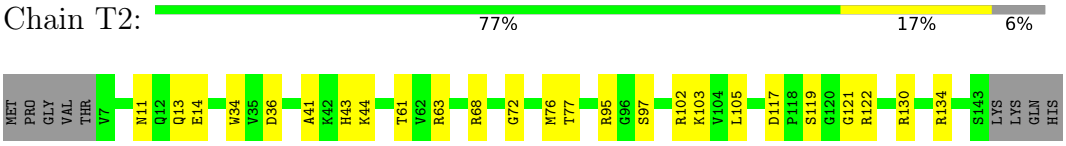
Chain S2:



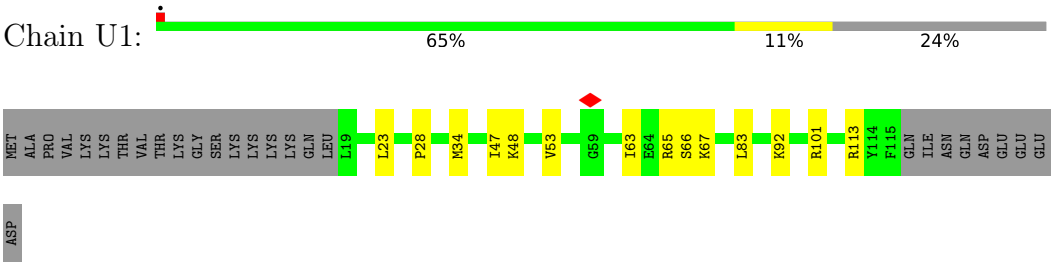
• Molecule 42: 60S ribosomal protein L21



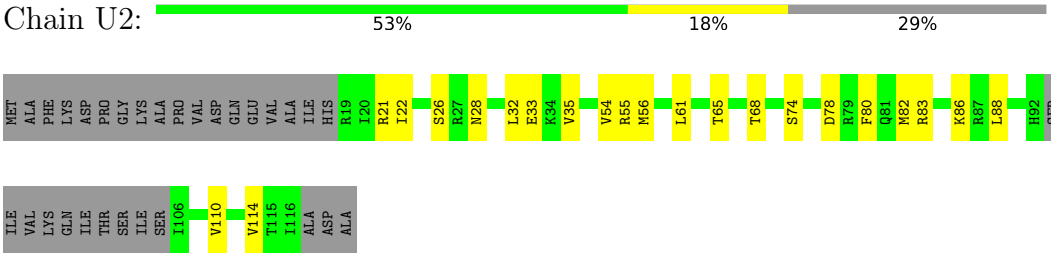
• Molecule 43: 40S ribosomal protein S19



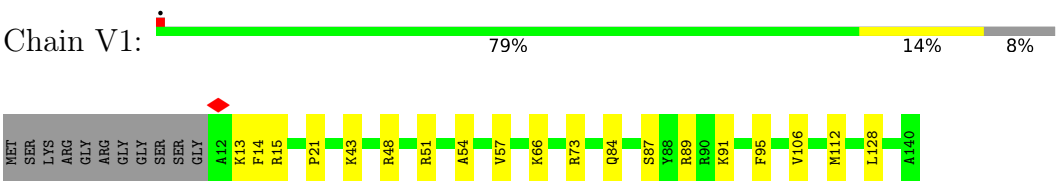
• Molecule 44: 60S ribosomal protein L22



• Molecule 45: 40S ribosomal protein S20

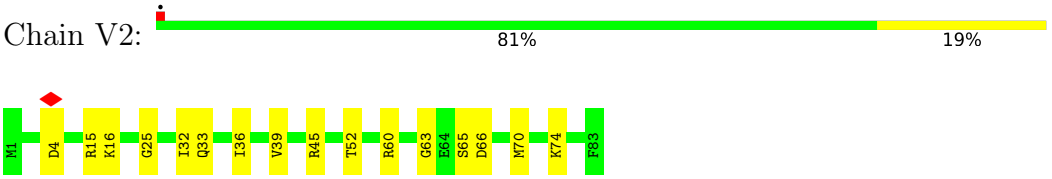


• Molecule 46: 60S ribosomal protein L23



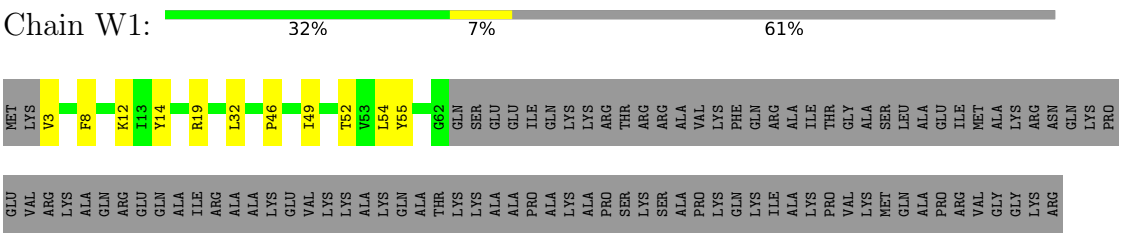
• Molecule 47: 40S ribosomal protein S21

Chain V2:



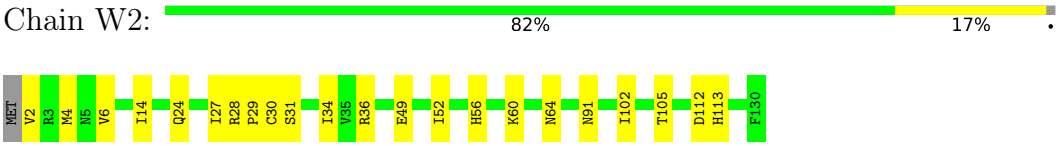
• Molecule 48: TRASH domain-containing protein

Chain W1:



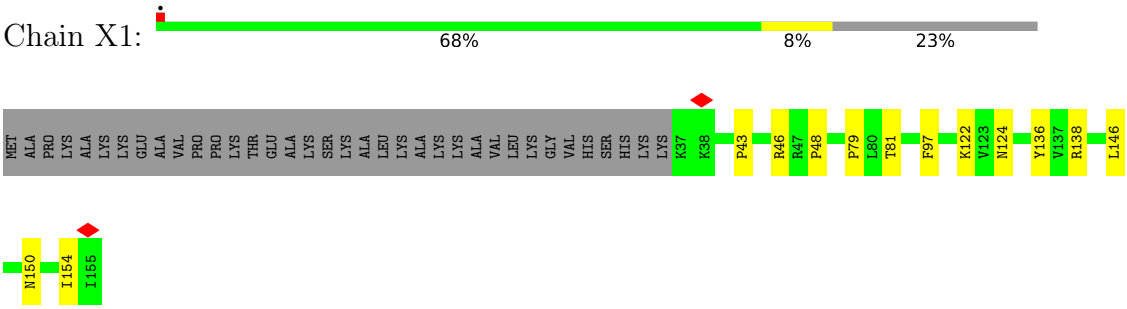
• Molecule 49: 40S ribosomal protein S15a

Chain W2:



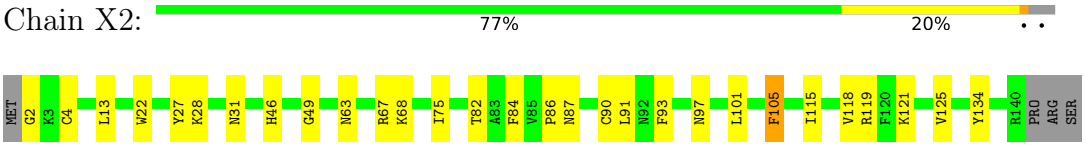
• Molecule 50: Ribosomal_L23eN domain-containing protein

Chain X1:



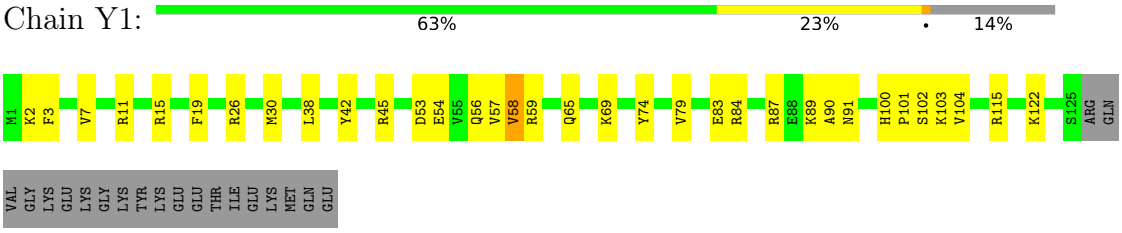
• Molecule 51: 40S ribosomal protein S23

Chain X2:



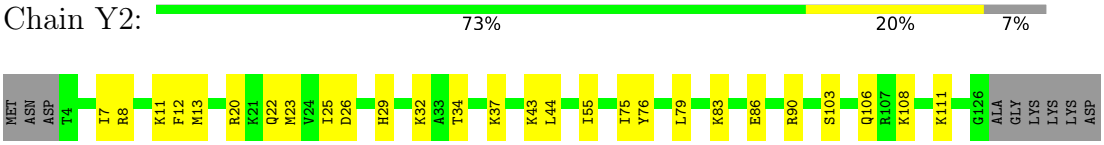
• Molecule 52: KOW domain-containing protein

Chain Y1:



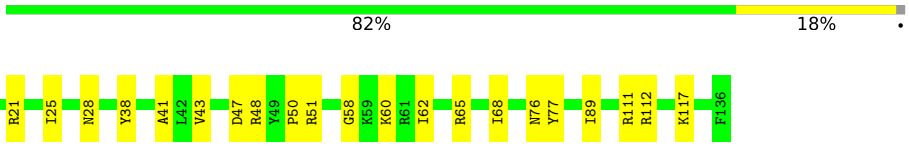
• Molecule 53: 40S ribosomal protein S24

Chain Y2:



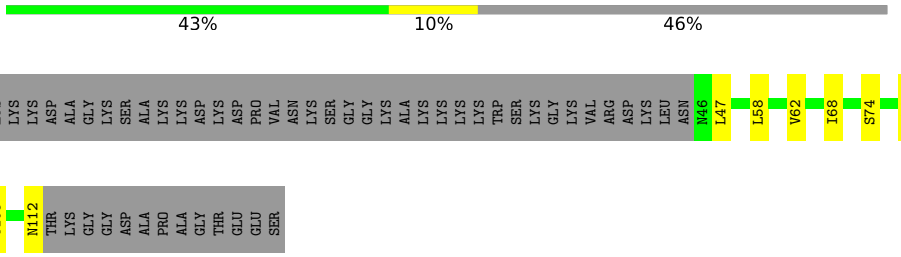
• Molecule 54: 60S ribosomal protein L27

Chain Z1:



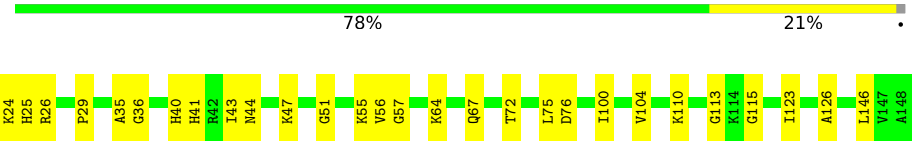
• Molecule 55: 40S ribosomal protein S25

Chain Z2:



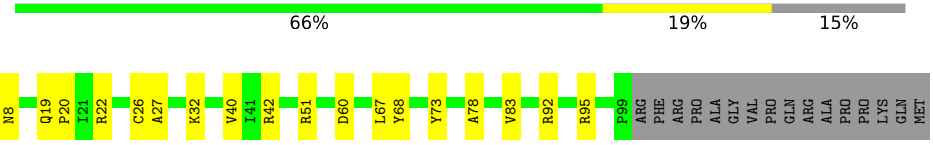
• Molecule 56: 60S ribosomal protein L27a

Chain a1:



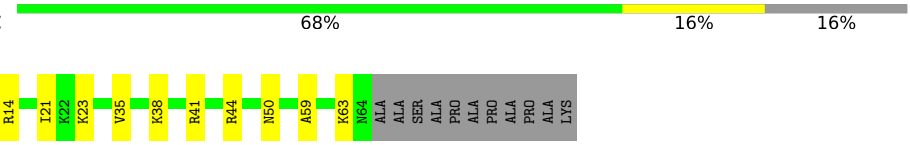
• Molecule 57: 40S ribosomal protein S26

Chain a2:



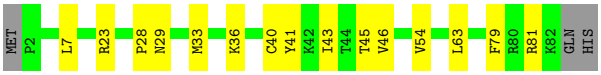
• Molecule 58: 60S ribosomal protein L29

Chain b1:



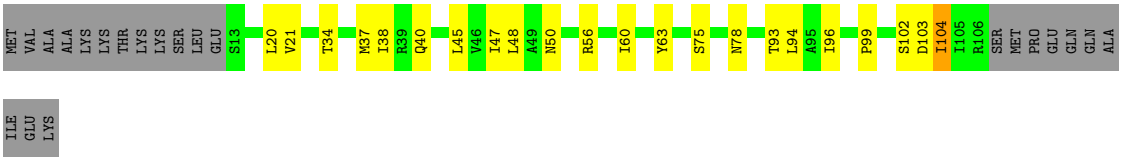
• Molecule 59: 40S ribosomal protein S27

Chain b2:



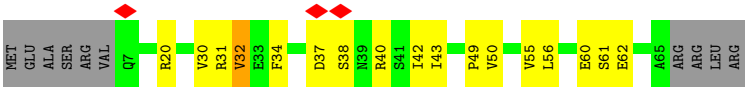
• Molecule 60: 60S ribosomal protein L30

Chain c1:



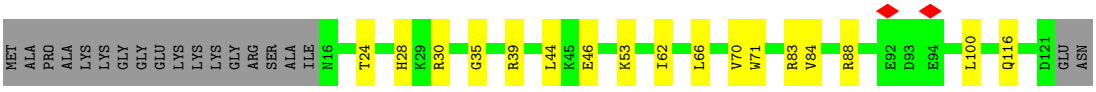
• Molecule 61: 40S ribosomal protein S28

Chain c2:



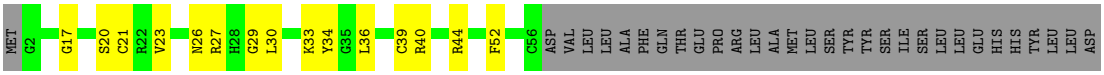
• Molecule 62: 60S ribosomal protein L31

Chain d1:



• Molecule 63: 40S ribosomal protein S29

Chain d2:

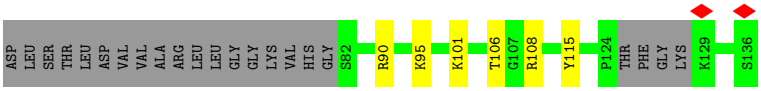


• Molecule 64: Rpl32

Chain e1:

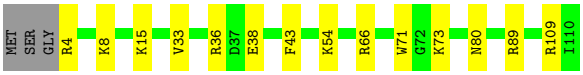
• Molecule 65: 40S ribosomal protein S30

Chain e2:



• Molecule 66: 60S ribosomal protein L35a

Chain f1:

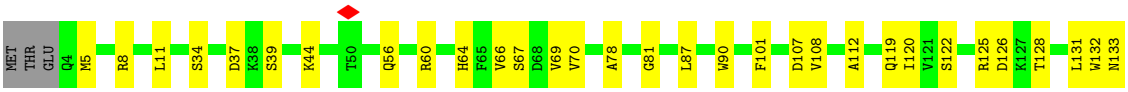


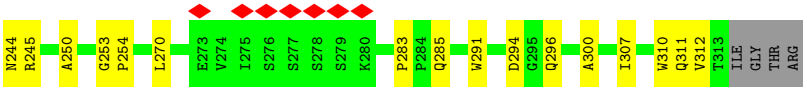
• Molecule 67: 60S ribosomal protein L34

Chain g1:

• Molecule 68: Gnb2l1-prov protein

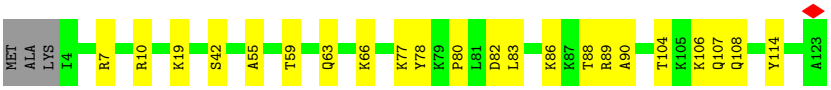
Chain g2:





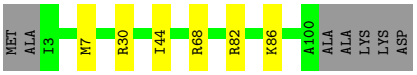
• Molecule 69: 60S ribosomal protein L35

Chain h1:



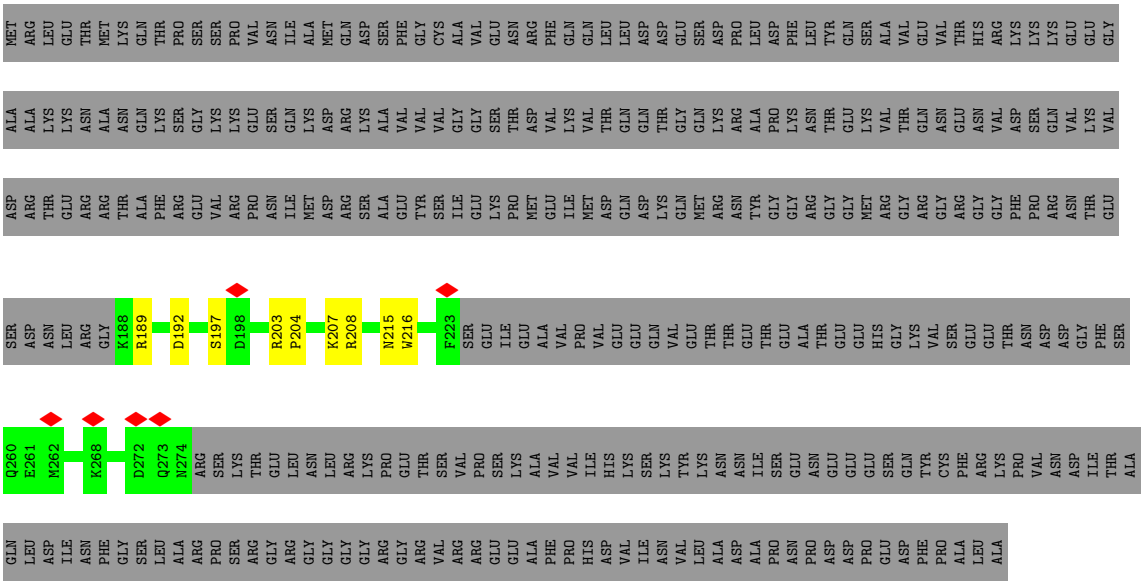
• Molecule 70: 60S ribosomal protein L36

Chain i1:



• Molecule 71: HABP4_PAI-RBP1 domain-containing protein

Chain i2:

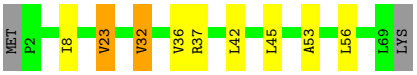


• Molecule 72: Ribosomal protein L37

Chain j1:

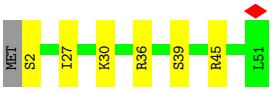
• Molecule 73: 60S ribosomal protein L38

Chain k1:



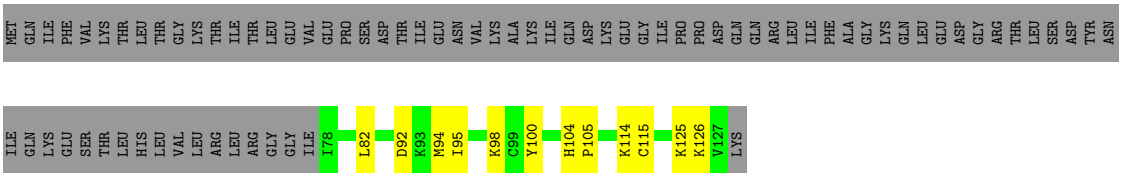
• Molecule 74: MGC116452 protein

Chain l1:



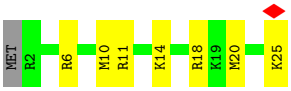
• Molecule 75: 60S ribosomal protein L40

Chain m1:



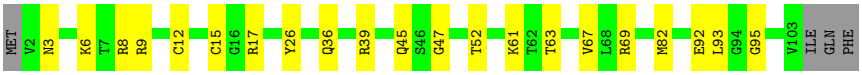
• Molecule 76: Rpl41

Chain n1:



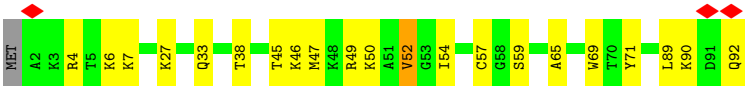
• Molecule 77: MGC85428 protein

Chain o1:



• Molecule 78: Rpl37a

Chain p1:

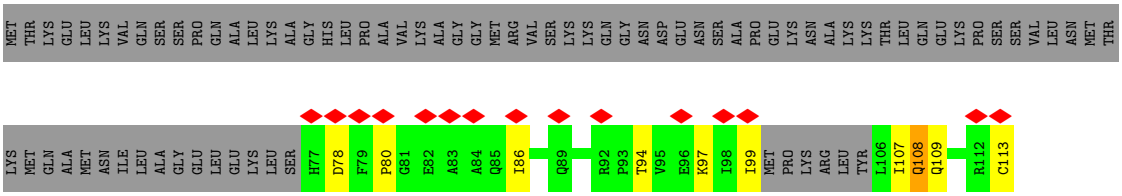


• Molecule 79: 60S ribosomal protein L28

Chain r1:

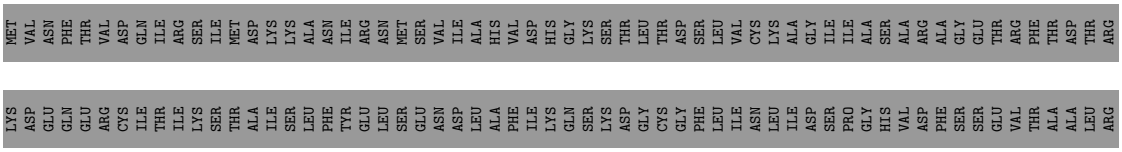
• Molecule 80: Death-associated protein-like 1-B

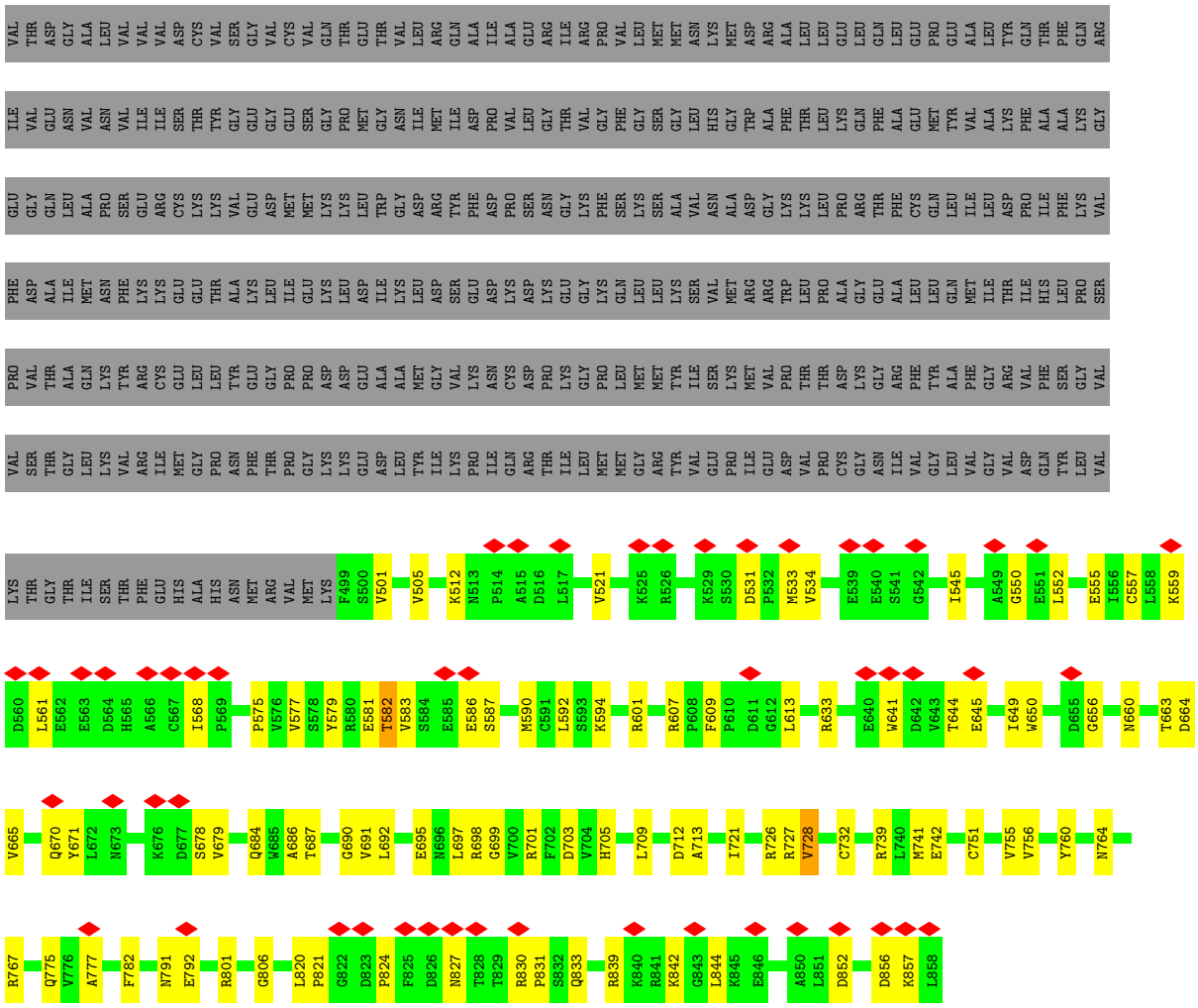
Chain s1:



• Molecule 81: Eef2-prov protein

Chain v2:




VAL THR ASP GLY ALA LEU VAL VAL VAL ASP CYS VAL SER GLY VAL CYS VAL GLN THR GLU THR VAL LEU ARG GLN ALA ILE ALA GLU ARG ILE ARG PRO VAL LEU MET MET ASN LYS MET ASP ARG ALA LEU LEU GLU LEU GLN LEU GLU PRO GLU ALA LEU TYR GLN THR PHE GLN ARG
ILE VAL GLU ASN VAL ASN VAL ILE ILE SER THR TYR GLY GLU GLY GLU SER GLY PRO MET GLY ASN ILE MET ILE ASP PRO VAL LEU GLY THR VAL GLY PHE GLY SER GLY LEU HIS GLY TRP ALA PHE THR LEU LYS GLN PHE ALA GLU MET TYR VAL ALA LYS PHE ALA ALA LYS GLY
GLU GLY GLN LEU ALA PRO SER GLU ARG CYS LYS LYS VAL GLU ASP MET MET LYS LYS LEU TRP GLY ASP ARG TYR PHE ASP PRO SER ASN GLY LYS PHE SER LYS SER ALA VAL ASN ALA ASP GLY LYS LYS LEU PRO LYS LEU PRO ARG THR PHE CYS GLN LEU LEU ILE LEU ASP PRO ILE LEU PHE LYS VAL
PHE ASP ALA ILE MET ASN PHE LYS LYS GLU GLU THR ALA LYS LEU ILE GLU LYS LEU ASP SER GLU ASP ILE LYS LEU LYS GLU GLY LYS GLN LEU LEU LYS SER VAL MET ARG ARG TRP LEU PRO ALA GLY GLU ALA LEU LEU GLN MET ILE THR ILE ILE HIS LEU PRO SER
PRO VAL THR ALA GLN LYS TYR ARG CYS GLU LEU LEU TYR GLU GLY PRO PRO ASP ASP GLU ALA ALA MET GLY VAL LYS ASN CYS ASP PRO LYS GLY PRO LEU MET MET TYR ILE SER LYS MET VAL PRO THR THR ASP LYS GLY GLU ALA ARG PHE TYR LEU PRO ALA GLY GLU ALA LEU LEU GLY ARG VAL ILE PHE SER GLY VAL
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LYS THR GLY THR ILE SER THR PHE GLU HIS ALA HIS ASN MET ARG VAL MET LYS F499 S500 V501 V505 K512 N513 P514 A515 D516 L517 V521 K525 R526 K529 S530 D531 P532 M533 V534 E539 E540 S541 G542 I545 A549 G550 E551 L552 E555 I556 C557 L558 K559
D560 L561 E562 E563 D564 H565 A566 G567 I568 P569 P575 V576 V577 S578 Y579 R580 E581 T582 V583 S584 E585 E586 S587 M590 C591 L592 S593 K594 R601 R607 P608 F609 P610 D611 G612 L613 R633 E640 W641 D642 V643 T644 E645 I649 W650 D655 G656 N660 T663 D664
V665 Q670 Y671 L672 N673 K676 D677 S678 V679 Q684 W685 A686 T687 G690 V691 L692 E695 N696 L697 R698 G699 V700 R701 F702 D703 V704 H705 L709 D712 A713 I721 R726 R727 V728 C732 R739 L740 M741 E742 C751 V755 V756 Y760 N764
R767 Q775 V776 A777 F782 N791 E792 R801 G806 L820 P821 G822 D823 P824 F825 D826 N827 T828 T829 R830 P831 S832 Q833 R839 K840 R841 K842 G843 L844 K845 E846 A850 L851 D852 D856 K857 L858

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	412340	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	6.789	Depositor
Minimum map value	-2.088	Depositor
Average map value	0.046	Depositor
Map value standard deviation	0.188	Depositor
Recommended contour level	0.55	Depositor
Map size (Å)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, 5CT

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	11	0.07	0/1030	0.25	0/1381
2	22	0.09	0/35698	0.17	0/55605
3	51	0.10	0/77857	0.17	0/121410
4	71	0.09	0/2837	0.14	0/4422
5	81	0.09	0/3506	0.15	0/5460
6	A1	0.11	0/1905	0.28	0/2554
7	A2	0.09	0/1680	0.25	0/2283
8	B1	0.10	0/3237	0.27	0/4329
9	B2	0.08	0/1762	0.28	0/2359
10	C1	0.11	0/2857	0.28	0/3836
11	C2	0.09	0/1699	0.24	0/2298
12	D1	0.09	0/2392	0.24	0/3206
13	D2	0.10	0/1760	0.26	0/2370
14	E1	0.09	0/1775	0.25	0/2373
15	E2	0.10	0/2098	0.28	0/2825
16	F1	0.10	0/1911	0.27	0/2549
17	F2	0.09	0/1459	0.28	0/1959
18	G1	0.10	0/1728	0.25	0/2328
19	G2	0.09	0/1820	0.27	0/2427
20	H1	0.09	0/1535	0.25	0/2061
21	H2	0.10	0/1516	0.29	0/2033
22	I1	0.10	0/1676	0.26	0/2238
23	I2	0.09	0/1648	0.26	0/2197
24	J1	0.09	0/1361	0.27	0/1821
25	J2	0.10	0/1522	0.27	0/2033
26	K2	0.08	0/803	0.28	0/1085
27	L1	0.11	0/1638	0.29	0/2192
28	L2	0.10	0/1165	0.28	0/1560
29	M1	0.09	0/1121	0.24	0/1496
30	N1	0.11	0/1732	0.29	0/2314
31	N2	0.09	0/1228	0.26	0/1652
32	O1	0.10	0/1659	0.27	0/2221

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	O2	0.10	0/1011	0.33	0/1355
34	P1	0.10	0/1260	0.28	0/1691
35	P2	0.08	0/972	0.24	0/1298
36	Q1	0.11	0/1476	0.30	0/1970
37	Q2	0.09	0/1070	0.26	0/1435
38	R1	0.10	0/1398	0.28	0/1849
39	R2	0.08	0/1080	0.24	0/1449
40	S1	0.11	0/1496	0.28	0/2011
41	S2	0.09	0/1146	0.27	0/1532
42	T1	0.10	0/1318	0.27	0/1761
43	T2	0.09	0/1078	0.24	0/1447
44	U1	0.10	0/807	0.28	0/1082
45	U2	0.09	0/691	0.26	0/924
46	V1	0.10	0/982	0.26	0/1317
47	V2	0.13	0/650	0.26	0/870
48	W1	0.11	0/515	0.29	0/687
49	W2	0.10	0/1052	0.25	0/1408
50	X1	0.09	0/993	0.24	0/1335
51	X2	0.09	0/1093	0.26	0/1460
52	Y1	0.10	0/1056	0.26	0/1406
53	Y2	0.09	0/1021	0.28	0/1356
54	Z1	0.09	0/1131	0.24	0/1508
55	Z2	0.09	0/542	0.25	0/729
56	a1	0.10	0/1196	0.25	0/1598
57	a2	0.11	0/793	0.28	0/1063
58	b1	0.09	0/538	0.23	0/708
59	b2	0.09	0/644	0.27	0/864
60	c1	0.09	0/742	0.21	0/996
61	c2	0.09	0/461	0.26	0/618
62	d1	0.10	0/899	0.30	0/1211
63	d2	0.09	0/466	0.27	0/619
64	e1	0.11	0/1055	0.29	0/1406
65	e2	0.10	0/410	0.30	0/537
66	f1	0.11	0/889	0.28	0/1192
67	g1	0.11	0/841	0.30	0/1121
68	g2	0.08	0/2467	0.24	0/3356
69	h1	0.09	0/1002	0.26	0/1323
70	i1	0.10	0/823	0.29	0/1089
71	i2	0.08	0/430	0.26	0/569
72	j1	0.11	0/713	0.30	0/942
73	k1	0.07	0/564	0.21	0/748
74	l1	0.11	0/451	0.28	0/596
75	m1	0.10	0/417	0.28	0/553

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	n1	0.13	0/232	0.37	0/295
77	o1	0.10	0/847	0.27	0/1117
78	p1	0.09	0/717	0.24	0/951
79	r1	0.10	0/959	0.29	0/1283
80	s1	0.58	0/256	0.68	1/344 (0.3%)
81	v2	0.09	0/2872	0.28	0/3889
All	All	0.10	0/213137	0.22	1/311745 (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
9	B2	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
80	s1	108	GLN	N-CA-C	8.26	122.79	111.39

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	B2	74	LEU	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	11	1033	0	1047	15	0
2	22	31922	0	16118	343	0
3	51	69603	0	35164	744	0
4	71	2538	0	1287	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	81	3139	0	1591	38	0
6	A1	1868	0	1965	40	0
7	A2	1643	0	1648	33	0
8	B1	3170	0	3316	65	0
9	B2	1734	0	1805	30	0
10	C1	2805	0	2967	49	0
11	C2	1663	0	1747	34	0
12	D1	2348	0	2395	36	0
13	D2	1732	0	1820	38	0
14	E1	1739	0	1889	37	0
15	E2	2055	0	2153	34	0
16	F1	1877	0	2024	32	0
17	F2	1439	0	1492	20	0
18	G1	1695	0	1811	25	0
19	G2	1796	0	1932	30	0
20	H1	1517	0	1606	26	0
21	H2	1494	0	1595	31	0
22	I1	1639	0	1697	27	0
23	I2	1620	0	1698	23	0
24	J1	1338	0	1374	11	0
25	J2	1497	0	1618	29	0
26	K2	779	0	796	12	0
27	L1	1608	0	1735	25	0
28	L2	1145	0	1206	18	0
29	M1	1100	0	1157	16	0
30	N1	1691	0	1747	55	0
31	N2	1204	0	1289	26	0
32	O1	1627	0	1778	33	0
33	O2	998	0	1021	21	0
34	P1	1234	0	1267	32	0
35	P2	955	0	1001	17	0
36	Q1	1454	0	1577	33	0
37	Q2	1054	0	1116	28	0
38	R1	1382	0	1524	27	0
39	R2	1066	0	1119	18	0
40	S1	1455	0	1513	30	0
41	S2	1129	0	1181	23	0
42	T1	1291	0	1347	24	0
43	T2	1059	0	1088	21	0
44	U1	792	0	811	10	0
45	U2	684	0	746	13	0
46	V1	968	0	1029	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	V2	643	0	642	13	0
48	W1	502	0	508	7	0
49	W2	1035	0	1080	17	0
50	X1	976	0	1050	10	0
51	X2	1077	0	1141	20	0
52	Y1	1039	0	1120	28	0
53	Y2	1004	0	1078	19	0
54	Z1	1109	0	1181	20	0
55	Z2	536	0	587	9	0
56	a1	1164	0	1206	23	0
57	a2	780	0	824	21	0
58	b1	527	0	553	9	0
59	b2	631	0	657	11	0
60	c1	732	0	769	13	0
61	c2	459	0	476	13	0
62	d1	884	0	932	16	0
63	d2	455	0	442	10	0
64	e1	1037	0	1127	16	0
65	e2	407	0	451	5	0
66	f1	869	0	898	9	0
67	g1	830	0	915	20	0
68	g2	2410	0	2361	45	0
69	h1	995	0	1123	16	0
70	i1	812	0	893	5	0
71	i2	423	0	398	9	0
72	j1	699	0	732	21	0
73	k1	558	0	624	6	0
74	l1	441	0	483	5	0
75	m1	411	0	441	10	0
76	n1	231	0	277	6	0
77	o1	835	0	897	14	0
78	p1	707	0	761	16	0
79	r1	945	0	1006	14	0
80	s1	251	0	256	13	0
81	v2	2813	0	2803	57	0
82	51	123	0	0	0	0
82	71	2	0	0	0	0
82	81	2	0	0	0	0
82	A1	1	0	0	0	0
82	B1	1	0	0	0	0
82	C1	1	0	0	0	0
82	V1	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
82	a1	1	0	0	0	0
82	e1	1	0	0	0	0
82	m1	1	0	0	0	0
83	a2	1	0	0	0	0
83	d2	1	0	0	0	0
83	g1	1	0	0	0	0
83	j1	1	0	0	0	0
83	m1	1	0	0	0	0
83	o1	1	0	0	0	0
83	p1	1	0	0	0	0
All	All	198947	0	150499	2246	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 7.

All (2246) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:995:G:H1	2:22:1042:A:HO2'	0.91	0.89
2:22:1053:C:HO2'	49:W2:2:VAL:N	1.71	0.87
3:51:2857:A:H62	3:51:2988:G:H21	1.23	0.86
3:51:2175:G:H1	3:51:2235:A:H61	1.26	0.84
3:51:653:G:H1	3:51:703:C:H42	1.30	0.80
32:O1:42:HIS:HE1	32:O1:148:VAL:H	1.30	0.78
3:51:628:U:H3	3:51:734:G:H1	1.31	0.78
22:I1:66:GLU:HG3	22:I1:69:ARG:HH21	1.49	0.78
3:51:1154:C:H5	3:51:1163:G:H1	1.33	0.77
2:22:841:C:H42	2:22:869:G:H1	1.30	0.77
2:22:116:U:H3	2:22:312:G:H1	1.31	0.77
2:22:890:G:H1	2:22:975:U:H3	1.32	0.77
6:A1:104:VAL:HA	6:A1:107:MET:HE2	1.67	0.76
18:G1:58:PRO:HD2	18:G1:61:ILE:HD12	1.68	0.75
2:22:887:G:H1	2:22:979:U:H3	1.34	0.75
15:E2:192:ILE:H	15:E2:243:GLY:HA3	1.52	0.75
3:51:3743:G:H5"	46:V1:15:ARG:HB3	1.67	0.74
30:N1:120:TRP:HE1	30:N1:123:GLU:HG3	1.52	0.74
3:51:3106:G:H1	3:51:3200:C:H42	1.34	0.74
46:V1:13:LYS:HD2	46:V1:128:LEU:HD11	1.69	0.74
3:51:640:G:H22	3:51:905:C:H5"	1.52	0.73
32:O1:158:LYS:HB2	32:O1:161:ARG:HG2	1.70	0.73
3:51:2806:U:OP2	3:51:2811:A:N6	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:1221:A:N6	2:22:1477:U:OP1	2.22	0.73
26:K2:64:TRP:HB3	63:d2:23:VAL:HA	1.69	0.73
2:22:906:A:H5"	33:O2:134:PRO:HB2	1.69	0.73
3:51:661:G:H22	3:51:696:A:H8	1.37	0.73
3:51:209:C:OP1	52:Y1:59:ARG:NH2	2.22	0.72
2:22:1520:C:H5'	43:T2:72:GLY:HA3	1.72	0.72
3:51:574:C:H2'	3:51:575:G:H4'	1.69	0.72
3:51:767:U:H3	3:51:826:G:H1	1.38	0.71
3:51:3881:C:H5	3:51:3925:G:H1	1.36	0.71
2:22:1524:G:N7	43:T2:102:ARG:NH1	2.38	0.71
37:Q2:86:GLN:HE22	37:Q2:122:ALA:HB2	1.55	0.71
35:P2:96:VAL:HG11	35:P2:116:LEU:HB3	1.72	0.71
3:51:3760:A:H2	3:51:3788:G:H21	1.37	0.70
2:22:1637:A:H2'	17:F2:59:ARG:HD3	1.72	0.70
2:22:1500:A:OP1	43:T2:63:ARG:NH1	2.25	0.70
9:B2:52:THR:HG22	9:B2:58:ALA:H	1.56	0.70
34:P1:122:ALA:HB3	34:P1:143:PRO:HB2	1.73	0.70
3:51:2243:G:H22	3:51:2249:G:H1	1.40	0.69
7:A2:38:ILE:HD11	7:A2:150:THR:HG22	1.74	0.69
38:R1:16:ARG:HH12	67:g1:29:ARG:HH11	1.39	0.69
2:22:1131:G:OP1	76:n1:6:ARG:NH1	2.26	0.69
3:51:174:C:H41	3:51:263:A:H62	1.38	0.69
3:51:2240:C:OP1	44:U1:101:ARG:NH2	2.25	0.69
20:H1:31:ARG:NH2	20:H1:149:ASN:OD1	2.26	0.69
9:B2:176:VAL:HG23	9:B2:184:VAL:HG11	1.75	0.69
19:G2:134:GLY:HA3	19:G2:158:VAL:HG21	1.74	0.69
3:51:1332:U:OP2	56:a1:26:ARG:NH2	2.26	0.69
26:K2:24:LYS:HE3	26:K2:65:ARG:HD3	1.75	0.69
3:51:471:C:H42	3:51:593:G:H1	1.40	0.68
22:I1:30:LYS:HG3	22:I1:63:GLU:HG3	1.74	0.68
15:E2:87:MET:HE1	15:E2:236:ILE:HD13	1.75	0.68
3:51:229:G:OP1	52:Y1:15:ARG:NH1	2.26	0.68
47:V2:70:MET:SD	47:V2:74:LYS:NZ	2.66	0.68
42:T1:27:LEU:HB3	42:T1:31:MET:HE3	1.75	0.68
3:51:636:G:OP1	3:51:905:C:N4	2.26	0.68
3:51:2058:G:H1	3:51:2107:U:H3	1.40	0.68
3:51:642:G:H22	3:51:721:U:H3	1.41	0.68
21:H2:69:LEU:HD22	21:H2:96:ALA:HB2	1.75	0.68
42:T1:82:GLY:HA2	58:b1:21:ILE:HG13	1.75	0.68
3:51:2115:G:N7	54:Z1:17:ARG:NH1	2.42	0.68
11:C2:116:ILE:HD11	11:C2:141:ILE:HG23	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:374:G:OP2	72:j1:52:LYS:NZ	2.26	0.68
19:G2:22:ARG:HG3	19:G2:25:ARG:HH22	1.58	0.67
68:g2:11:LEU:HB2	68:g2:307:ILE:HB	1.77	0.67
2:22:1501:U:H5"	37:Q2:37:ARG:HH12	1.59	0.67
3:51:278:A:N7	30:N1:12:ARG:NH1	2.42	0.67
3:51:1063:C:N4	3:51:1472:G:OP1	2.26	0.67
20:H1:41:ILE:HG13	20:H1:73:ILE:HD11	1.77	0.67
3:51:1050:G:HO2'	3:51:1144:C:HO2'	1.37	0.67
3:51:1378:G:H1	3:51:1498:C:H5	1.42	0.67
3:51:2148:A:H5'	3:51:2226:G:H4'	1.75	0.67
3:51:2327:A:O2'	74:l1:45:ARG:NH2	2.27	0.67
20:H1:94:SER:HB2	20:H1:142:ASP:HB3	1.77	0.67
26:K2:65:ARG:NH1	63:d2:20:SER:OG	2.28	0.67
33:O2:62:VAL:HG11	33:O2:67:ASP:HB2	1.76	0.67
49:W2:102:ILE:H	49:W2:113:HIS:HD2	1.39	0.67
3:51:199:U:O2'	52:Y1:59:ARG:NH1	2.28	0.67
6:A1:207:VAL:HG13	6:A1:208:GLU:HG3	1.77	0.67
3:51:318:A:H1'	3:51:2891:A:H8	1.60	0.66
3:51:2184:A:H62	3:51:2224:G:H8	1.43	0.66
14:E1:90:MET:O	79:r1:88:ARG:NH1	2.28	0.66
2:22:1506:G:N2	2:22:1506:G:OP2	2.29	0.66
8:B1:79:VAL:HB	8:B1:331:ILE:HG22	1.77	0.66
19:G2:85:ARG:O	19:G2:87:ARG:NH1	2.28	0.66
2:22:447:G:N1	2:22:450:A:OP2	2.28	0.66
8:B1:73:VAL:O	46:V1:89:ARG:NH2	2.28	0.66
2:22:485:A:O2'	2:22:788:C:O2	2.14	0.66
43:T2:77:THR:HG22	43:T2:95:ARG:HB3	1.77	0.66
2:22:162:G:N2	2:22:162:G:OP2	2.29	0.66
3:51:2120:C:OP2	67:g1:76:ARG:NH2	2.29	0.66
33:O2:34:PHE:HB3	33:O2:41:PHE:HB2	1.76	0.66
3:51:3406:A:H2'	3:51:3407:A:H8	1.60	0.66
61:c2:40:ARG:NH2	61:c2:61:SER:O	2.29	0.65
3:51:3671:A:N7	6:A1:215:ASN:ND2	2.44	0.65
10:C1:138:PRO:HG3	10:C1:154:VAL:HG21	1.78	0.65
33:O2:105:THR:HG22	33:O2:107:THR:H	1.60	0.65
14:E1:37:LYS:O	14:E1:42:ARG:NH1	2.29	0.65
53:Y2:29:HIS:HB2	53:Y2:32:LYS:HB2	1.79	0.65
28:L2:44:LEU:HD13	28:L2:74:ILE:HD11	1.78	0.65
36:Q1:54:SER:OG	36:Q1:57:ASN:ND2	2.28	0.65
81:v2:581:GLU:HG2	81:v2:692:LEU:HB2	1.78	0.65
19:G2:1:MET:HE2	19:G2:24:LEU:HD13	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:979:A:OP2	3:51:3570:U:O2'	2.13	0.65
3:51:1168:G:O2'	58:b1:41:ARG:NH1	2.29	0.65
2:22:385:G:O2'	2:22:625:C:N3	2.29	0.65
81:v2:760:TYR:O	81:v2:764:ASN:ND2	2.29	0.65
3:51:3666:G:N2	3:51:3669:A:OP2	2.28	0.64
23:I2:123:ARG:NH1	23:I2:134:GLU:OE2	2.30	0.64
3:51:636:G:H5"	3:51:905:C:H41	1.61	0.64
4:71:7:G:OP1	12:D1:33:ARG:NH2	2.29	0.64
55:Z2:58:LEU:HD12	55:Z2:62:VAL:HG21	1.78	0.64
10:C1:222:ILE:HA	10:C1:233:LEU:HD13	1.79	0.64
15:E2:122:LYS:NZ	15:E2:124:CYS:SG	2.69	0.64
2:22:1479:C:OP2	41:S2:136:THR:OG1	2.14	0.64
3:51:3018:U:O2'	3:51:4024:A:N3	2.31	0.64
3:51:3597:G:O2'	75:m1:100:TYR:O	2.15	0.64
23:I2:116:HIS:ND1	23:I2:117:ASN:OD1	2.31	0.64
68:g2:78:ALA:HB3	68:g2:90:TRP:HB2	1.78	0.64
79:r1:15:SER:HB3	79:r1:18:ILE:HG13	1.79	0.64
1:11:90:TYR:HB3	1:11:102:LEU:HB3	1.80	0.64
20:H1:92:MET:HB2	20:H1:144:LEU:HB2	1.80	0.64
28:L2:5:GLN:HE22	28:L2:11:GLN:H	1.42	0.64
3:51:3936:C:H1'	3:51:3976:G:H22	1.61	0.64
35:P2:18:ARG:NH1	41:S2:88:LYS:O	2.31	0.64
3:51:506:G:H1	3:51:560:G:H1	1.44	0.64
3:51:1970:C:O2'	3:51:1971:G:N7	2.29	0.64
68:g2:217:MET:HG2	68:g2:229:THR:HG22	1.80	0.64
3:51:922:C:OP2	16:F1:46:LYS:NZ	2.31	0.64
3:51:3866:C:O2'	3:51:3995:U:N3	2.31	0.64
37:Q2:42:ILE:HG22	37:Q2:44:PRO:HD2	1.80	0.64
13:D2:115:VAL:HG21	71:i2:216:TRP:HE3	1.61	0.64
18:G1:70:LEU:HD23	30:N1:25:VAL:HG23	1.80	0.64
21:H2:105:THR:HG22	21:H2:107:LYS:H	1.63	0.64
6:A1:5:ILE:H	6:A1:8:GLN:HE21	1.44	0.64
3:51:3748:G:OP1	8:B1:19:ARG:NH2	2.31	0.63
2:22:824:A:H4'	49:W2:36:ARG:HH12	1.63	0.63
3:51:1795:G:N2	3:51:1841:C:O2	2.30	0.63
3:51:3007:C:OP1	8:B1:238:LYS:NZ	2.31	0.63
37:Q2:53:GLU:OE2	37:Q2:85:ARG:NH2	2.31	0.63
3:51:2188:C:O2'	67:g1:54:ARG:NH2	2.32	0.63
3:51:3745:U:OP2	3:51:3795:C:N4	2.32	0.63
5:81:142:U:OP1	30:N1:38:ARG:NH2	2.31	0.63
6:A1:3:ARG:HG2	6:A1:207:VAL:HG22	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:67:C:H41	19:G2:163:SER:HA	1.63	0.63
2:22:343:U:OP2	23:I2:178:ARG:NH1	2.32	0.63
8:B1:170:LEU:O	8:B1:328:ASN:ND2	2.31	0.63
36:Q1:16:LYS:O	36:Q1:33:ARG:NH2	2.31	0.63
2:22:1620:U:O4	2:22:1621:A:N6	2.32	0.63
3:51:565:C:OP1	10:C1:273:LYS:NZ	2.31	0.63
3:51:3689:A:OP1	32:O1:96:ARG:NH2	2.31	0.63
13:D2:23:GLU:HG2	26:K2:64:TRP:HE1	1.63	0.63
3:51:3538:C:H5	3:51:3554:C:H42	1.47	0.63
25:J2:109:ARG:HH12	25:J2:111:GLN:HE21	1.46	0.63
32:O1:89:ARG:HA	32:O1:98:PRO:HD2	1.80	0.63
8:B1:36:ASP:HB3	8:B1:39:LYS:HE3	1.80	0.62
2:22:1144:A:OP1	76:n1:18:ARG:NH2	2.32	0.62
2:22:1335:C:O2'	39:R2:10:LYS:NZ	2.32	0.62
3:51:1159:C:OP1	3:51:1160:G:N2	2.32	0.62
12:D1:91:GLY:O	12:D1:94:ASN:ND2	2.32	0.62
31:N2:54:LEU:HD23	31:N2:58:HIS:HD2	1.64	0.62
68:g2:165:ILE:HG13	68:g2:177:TRP:HB2	1.81	0.62
12:D1:65:ALA:HB2	12:D1:74:ILE:HD13	1.80	0.62
16:F1:217:GLY:O	16:F1:244:ARG:NH2	2.32	0.62
3:51:2852:A:H3'	6:A1:198:ARG:HH22	1.63	0.62
3:51:1322:A:O2'	72:j1:49:TRP:O	2.16	0.62
3:51:2819:G:O2'	3:51:2858:U:OP1	2.15	0.62
3:51:3691:U:O2'	8:B1:234:ARG:NH2	2.32	0.62
8:B1:220:ILE:HG12	8:B1:278:THR:HG23	1.81	0.62
2:22:920:G:OP2	2:22:920:G:N2	2.28	0.62
3:51:3357:U:O4	77:o1:8:ARG:NH2	2.33	0.62
8:B1:41:ILE:HA	8:B1:187:GLY:HA3	1.81	0.62
13:D2:40:ARG:NH1	13:D2:47:GLU:OE2	2.32	0.62
21:H2:16:PRO:HB3	21:H2:20:GLU:HG2	1.80	0.62
38:R1:44:LEU:HD22	38:R1:49:LEU:HD12	1.81	0.62
3:51:1620:G:O2'	3:51:1684:A:N6	2.33	0.62
18:G1:167:VAL:HG12	18:G1:170:LEU:HD12	1.80	0.62
30:N1:63:ARG:NH1	30:N1:131:GLU:OE2	2.33	0.62
8:B1:37:PRO:HA	8:B1:188:GLY:HA2	1.82	0.62
24:J1:34:ARG:HD3	24:J1:122:ILE:HA	1.79	0.62
30:N1:53:TYR:HB2	30:N1:133:ILE:HD13	1.81	0.62
2:22:1518:U:H2'	2:22:1519:G:H8	1.65	0.62
3:51:3073:A:C2	80:s1:107:ILE:O	2.53	0.62
3:51:4023:G:OP2	3:51:4023:G:N2	2.28	0.62
51:X2:68:LYS:HB3	51:X2:91:LEU:HD22	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:1256:G:N2	2:22:1268:U:OP2	2.32	0.61
3:51:2854:G:O2'	3:51:2983:U:OP2	2.15	0.61
8:B1:220:ILE:HB	8:B1:346:THR:HG23	1.82	0.61
40:S1:115:ALA:O	40:S1:118:ARG:NH1	2.33	0.61
81:v2:824:PRO:HG3	81:v2:831:PRO:HB2	1.80	0.61
2:22:111:A:O2'	28:L2:71:ARG:NH1	2.34	0.61
2:22:1307:G:N7	2:22:1333:U:O2'	2.29	0.61
3:51:637:G:H1	3:51:723:G:H1	1.48	0.61
3:51:2373:A:O2'	8:B1:228:TYR:O	2.18	0.61
24:J1:98:PHE:O	24:J1:158:LYS:NZ	2.33	0.61
41:S2:51:ASP:HB3	41:S2:54:LYS:HE3	1.82	0.61
2:22:1316:G:N2	2:22:1319:A:OP2	2.31	0.61
2:22:1821:U:OP2	57:a2:5:ARG:NH1	2.30	0.61
3:51:3204:U:H5'	18:G1:73:ARG:HG2	1.81	0.61
22:I1:33:ILE:O	22:I1:69:ARG:NH1	2.33	0.61
40:S1:127:MET:HG2	42:T1:153:PRO:HB2	1.80	0.61
3:51:736:G:H5"	66:f1:73:LYS:HE2	1.82	0.61
7:A2:147:LEU:O	7:A2:165:ASN:ND2	2.33	0.61
14:E1:126:THR:HG22	14:E1:178:LYS:HG2	1.83	0.61
21:H2:36:LEU:HD21	21:H2:78:ARG:HD3	1.82	0.61
33:O2:74:ALA:HB1	33:O2:115:ALA:HB2	1.82	0.61
3:51:1360:A:OP1	56:a1:47:LYS:NZ	2.34	0.61
3:51:4050:G:N2	3:51:4086:G:O2'	2.34	0.61
31:N2:114:ARG:HD3	31:N2:117:LEU:HD12	1.83	0.61
34:P1:39:MET:HE2	34:P1:43:LYS:HE2	1.82	0.61
3:51:4100:G:N2	62:d1:116:GLN:OE1	2.33	0.61
23:I2:2:GLY:O	23:I2:24:LYS:NZ	2.33	0.61
10:C1:88:THR:HG22	10:C1:90:ARG:H	1.66	0.61
37:Q2:58:LEU:HB3	37:Q2:62:ARG:HD2	1.83	0.61
46:V1:66:LYS:O	46:V1:73:ARG:NH1	2.34	0.61
2:22:1500:A:O2'	37:Q2:43:GLU:OE2	2.18	0.61
3:51:326:U:O2'	70:i1:30:ARG:NH1	2.34	0.61
30:N1:181:HIS:O	30:N1:195:ARG:NH2	2.34	0.61
32:O1:33:GLN:HG3	32:O1:34:VAL:HG23	1.81	0.61
66:f1:43:PHE:O	66:f1:109:ARG:NH2	2.31	0.61
2:22:1045:A:O2'	2:22:1815:G:N2	2.34	0.61
2:22:1508:G:H3'	2:22:1537:A:H61	1.65	0.61
21:H2:143:ARG:HB2	21:H2:155:LYS:HB2	1.83	0.61
2:22:628:C:O2'	11:C2:213:ARG:NH1	2.35	0.60
3:51:2018:A:H5'	67:g1:62:LYS:HD2	1.83	0.60
3:51:2916:G:H21	3:51:2940:A:H8	1.48	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:81:74:G:OP2	52:Y1:74:TYR:OH	2.18	0.60
60:c1:37:MET:SD	60:c1:40:GLN:NE2	2.74	0.60
5:81:93:G:OP2	72:j1:72:ARG:NH2	2.35	0.60
22:I1:14:ASN:O	22:I1:128:ARG:NH2	2.30	0.60
2:22:977:U:O2'	31:N2:55:ARG:NH1	2.34	0.60
3:51:1368:C:H4'	36:Q1:143:ARG:HH22	1.64	0.60
3:51:2964:A:N3	3:51:3631:C:O2'	2.31	0.60
35:P2:60:LEU:HD23	35:P2:76:ILE:HD12	1.84	0.60
2:22:949:A:OP1	57:a2:32:LYS:NZ	2.34	0.60
2:22:979:U:H5'	31:N2:55:ARG:HD3	1.83	0.60
34:P1:64:ASN:ND2	34:P1:80:GLN:OE1	2.35	0.60
41:S2:38:ARG:O	41:S2:42:HIS:ND1	2.34	0.60
3:51:2292:G:O2'	54:Z1:51:ARG:NH1	2.35	0.60
10:C1:307:ARG:O	36:Q1:38:ARG:NH2	2.35	0.60
23:I2:4:SER:HB2	23:I2:24:LYS:HE3	1.84	0.60
45:U2:33:GLU:OE2	45:U2:55:ARG:NH1	2.34	0.60
55:Z2:74:SER:OG	55:Z2:79:ILE:O	2.18	0.60
62:d1:62:ILE:HG23	62:d1:66:LEU:HD23	1.84	0.60
22:I1:191:ILE:HG12	22:I1:200:ILE:HD11	1.81	0.60
47:V2:60:ARG:HA	47:V2:65:SER:HB2	1.82	0.60
3:51:4010:U:OP1	8:B1:132:LYS:NZ	2.35	0.60
42:T1:84:ILE:HD12	58:b1:23:LYS:HG2	1.83	0.60
2:22:17:C:O2'	2:22:1156:A:N1	2.33	0.60
3:51:381:G:N1	3:51:384:A:OP2	2.35	0.60
3:51:2434:G:OP1	38:R1:136:ARG:NH1	2.35	0.60
81:v2:586:GLU:HG2	81:v2:607:ARG:HB3	1.83	0.60
2:22:1412:A:H5"	39:R2:3:ARG:HD2	1.82	0.59
3:51:2116:G:N2	3:51:2119:A:OP2	2.33	0.59
3:51:3061:C:O2'	8:B1:268:ARG:NH2	2.35	0.59
8:B1:39:LYS:NZ	8:B1:186:ASN:O	2.35	0.59
38:R1:15:LEU:O	38:R1:52:ARG:NH1	2.35	0.59
2:22:1555:C:OP2	55:Z2:85:ARG:NH1	2.35	0.59
3:51:21:G:H5'	72:j1:43:ARG:HG2	1.83	0.59
3:51:307:G:OP2	3:51:307:G:N2	2.32	0.59
3:51:561:G:N2	3:51:561:G:OP2	2.33	0.59
3:51:2028:A:OP1	38:R1:38:ARG:NH2	2.34	0.59
13:D2:37:VAL:HG12	13:D2:50:ILE:HA	1.83	0.59
25:J2:127:ARG:HD2	65:e2:108:ARG:HD3	1.83	0.59
49:W2:49:GLU:O	49:W2:64:ASN:ND2	2.33	0.59
3:51:168:G:H1	3:51:266:C:H42	1.48	0.59
3:51:3340:C:O2	42:T1:60:LYS:NZ	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:81:141:C:H5”	30:N1:60:VAL:HG11	1.83	0.59
77:o1:36:GLN:OE1	77:o1:39:ARG:NH2	2.35	0.59
79:r1:64:VAL:HG22	79:r1:80:LYS:HG3	1.84	0.59
2:22:1166:A:OP1	11:C2:103:ARG:NH2	2.35	0.59
2:22:1443:U:OP1	13:D2:151:LYS:NZ	2.33	0.59
3:51:1908:G:OP2	3:51:1908:G:N2	2.32	0.59
50:X1:146:LEU:O	50:X1:150:ASN:ND2	2.31	0.59
3:51:712:C:O2’	3:51:713:A:O5’	2.20	0.59
3:51:1402:G:N2	3:51:1442:C:O2	2.35	0.59
3:51:2023:G:OP1	67:g1:29:ARG:NH2	2.34	0.59
57:a2:51:ARG:NH2	61:c2:62:GLU:OE2	2.35	0.59
59:b2:40:CYS:SG	59:b2:41:TYR:N	2.75	0.59
2:22:1526:C:OP1	43:T2:97:SER:OG	2.19	0.59
3:51:3522:A:H4’	80:s1:113:CYS:HA	1.84	0.59
3:51:3842:A:OP2	8:B1:30:LYS:NZ	2.29	0.59
14:E1:37:LYS:HE2	14:E1:39:LEU:HD21	1.84	0.59
30:N1:68:ARG:NH1	30:N1:124:ASP:O	2.35	0.59
3:51:3202:C:H5”	18:G1:249:ARG:HH22	1.68	0.59
11:C2:159:LYS:HB2	47:V2:4:ASP:HB2	1.83	0.59
54:Z1:21:ARG:NH1	54:Z1:47:ASP:OD1	2.34	0.59
2:22:595:U:O2	71:i2:208:ARG:NH1	2.36	0.59
2:22:601:C:OP1	65:e2:101:LYS:NZ	2.36	0.59
3:51:374:G:N7	72:j1:56:ARG:NH1	2.50	0.59
52:Y1:89:LYS:HD2	52:Y1:91:ASN:HD21	1.68	0.59
2:22:1523:C:OP2	43:T2:102:ARG:NH2	2.36	0.59
3:51:112:C:OP2	69:h1:106:LYS:NZ	2.30	0.59
3:51:412:G:OP2	74:l1:36:ARG:NH2	2.35	0.59
3:51:3746:C:OP1	46:V1:48:ARG:NE	2.34	0.59
3:51:3874:C:H5	3:51:3996:G:H1	1.51	0.59
9:B2:219:LYS:NZ	78:p1:92:GLN:OXT	2.36	0.59
10:C1:225:PHE:HB3	10:C1:231:ILE:HG21	1.85	0.59
33:O2:101:GLY:HA3	33:O2:134:PRO:HG2	1.84	0.59
75:m1:92:ASP:OD1	75:m1:126:LYS:NZ	2.36	0.59
3:51:1589:U:OP2	32:O1:77:ARG:NH1	2.32	0.58
7:A2:36:GLN:O	7:A2:53:ARG:NH1	2.35	0.58
13:D2:74:GLN:HA	13:D2:79:PHE:HB2	1.85	0.58
14:E1:17:ARG:HB2	14:E1:33:MET:HE1	1.84	0.58
20:H1:104:VAL:HG13	20:H1:113:GLU:HB2	1.85	0.58
32:O1:137:PRO:HB2	32:O1:139:PRO:HD2	1.85	0.58
68:g2:8:ARG:HD3	68:g2:311:GLN:HG3	1.83	0.58
20:H1:186:THR:O	20:H1:189:GLN:NE2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:368:G:N2	3:51:371:A:OP2	2.29	0.58
3:51:933:A:O2'	10:C1:325:ASN:ND2	2.36	0.58
3:51:3650:C:OP1	8:B1:246:ARG:NH2	2.36	0.58
3:51:3683:U:OP2	8:B1:246:ARG:NH1	2.36	0.58
30:N1:116:LEU:HD22	30:N1:135:ILE:HD11	1.84	0.58
36:Q1:23:ILE:HD12	79:r1:9:MET:HB3	1.84	0.58
81:v2:594:LYS:HG2	81:v2:601:ARG:HG2	1.85	0.58
2:22:1099:U:O2'	7:A2:155:ARG:NH1	2.37	0.58
2:22:1310:G:OP1	11:C2:109:ARG:NH2	2.36	0.58
11:C2:185:PRO:HB3	25:J2:98:LEU:HD13	1.86	0.58
43:T2:11:ASN:HB3	43:T2:14:GLU:HG2	1.84	0.58
30:N1:182:ILE:HG23	30:N1:183:THR:HG23	1.85	0.58
41:S2:35:GLY:O	41:S2:97:GLN:NE2	2.36	0.58
43:T2:11:ASN:HD22	43:T2:14:GLU:H	1.52	0.58
73:k1:8:ILE:HG13	73:k1:45:LEU:HD21	1.86	0.58
2:22:834:A:O2'	2:22:836:G:OP2	2.20	0.58
3:51:1192:G:O2'	27:L1:18:TRP:NE1	2.29	0.58
3:51:1490:G:O2'	3:51:1492:G:N2	2.37	0.58
3:51:3725:G:H4'	3:51:3726:U:O5'	2.03	0.58
13:D2:103:GLU:OE1	13:D2:106:ARG:NH2	2.36	0.58
2:22:65:C:N4	2:22:166:U:O2'	2.37	0.58
2:22:1045:A:N7	2:22:1798:C:O2'	2.34	0.58
3:51:35:U:O2'	3:51:1201:A:N1	2.37	0.58
3:51:43:U:H5"	30:N1:85:VAL:HG22	1.84	0.58
3:51:869:G:H2'	3:51:870:A:C8	2.38	0.58
3:51:1579:C:H42	3:51:1722:G:H1	1.52	0.58
3:51:2038:A:OP2	73:k1:37:ARG:NH2	2.36	0.58
3:51:4025:C:N3	34:P1:69:ARG:NH2	2.50	0.58
25:J2:121:LYS:H	25:J2:125:HIS:HD2	1.50	0.58
44:U1:65:ARG:NH1	44:U1:66:SER:O	2.37	0.58
77:o1:69:ARG:HG3	77:o1:82:MET:HE1	1.86	0.58
3:51:164:G:N2	3:51:271:U:O2	2.36	0.58
3:51:3397:G:OP2	3:51:3397:G:N2	2.30	0.58
25:J2:110:LEU:HB2	25:J2:147:PHE:HB3	1.85	0.58
37:Q2:128:GLU:OE2	37:Q2:138:ARG:NH2	2.36	0.58
81:v2:842:LYS:HG3	81:v2:844:LEU:HD23	1.85	0.58
3:51:3556:U:OP2	22:I1:3:ARG:NH2	2.37	0.58
22:I1:87:ILE:HG12	22:I1:138:ILE:HG12	1.85	0.58
81:v2:678:SER:HB3	81:v2:721:ILE:HB	1.86	0.58
2:22:905:U:OP1	9:B2:214:LYS:NZ	2.35	0.57
3:51:305:A:N3	70:i1:82:ARG:NH1	2.50	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:2845:U:OP1	6:A1:54:ARG:NH1	2.28	0.57
3:51:3383:C:H5'	24:J1:67:ILE:HD11	1.86	0.57
16:F1:125:LYS:HB2	42:T1:133:ALA:HB3	1.84	0.57
32:O1:213:VAL:HG22	32:O1:216:LYS:HB2	1.86	0.57
33:O2:103:ASN:HB3	33:O2:139:SER:HB3	1.85	0.57
45:U2:22:ILE:HG12	45:U2:114:VAL:HG12	1.85	0.57
53:Y2:76:TYR:OH	53:Y2:86:GLU:OE1	2.22	0.57
68:g2:87:LEU:HB2	68:g2:101:PHE:HB2	1.85	0.57
2:22:205:C:H42	2:22:275:G:H22	1.51	0.57
2:22:1436:C:HO2'	2:22:1437:G:H8	1.52	0.57
3:51:1711:G:H5'	32:O1:111:THR:HG23	1.84	0.57
5:81:10:C:O3'	34:P1:3:ARG:NH1	2.37	0.57
5:81:77:G:O2'	5:81:78:G:OP1	2.22	0.57
7:A2:60:LEU:HD11	47:V2:36:ILE:HD13	1.86	0.57
22:I1:61:SER:HA	22:I1:126:VAL:HG12	1.86	0.57
69:h1:88:THR:HG22	69:h1:90:ALA:H	1.69	0.57
2:22:999:G:H4'	2:22:1802:A:H4'	1.87	0.57
3:51:407:A:H4'	3:51:408:G:H3'	1.85	0.57
3:51:2887:G:OP2	70:i1:68:ARG:NH2	2.36	0.57
3:51:3004:G:N2	3:51:3008:C:O2'	2.38	0.57
5:81:95:C:H5"	69:h1:66:LYS:HG2	1.85	0.57
17:F2:175:GLU:OE1	17:F2:186:SER:OG	2.18	0.57
22:I1:61:SER:OG	22:I1:63:GLU:OE1	2.21	0.57
45:U2:78:ASP:OD2	63:d2:44:ARG:NH1	2.37	0.57
77:o1:3:ASN:HD22	77:o1:92:GLU:HG3	1.68	0.57
79:r1:40:ARG:O	79:r1:104:ARG:NH2	2.37	0.57
2:22:1561:A:OP1	41:S2:24:ARG:NH1	2.36	0.57
3:51:610:C:H2'	3:51:611:G:H8	1.68	0.57
3:51:973:U:O2'	3:51:1550:A:N1	2.32	0.57
3:51:1359:U:OP1	56:a1:44:ASN:ND2	2.37	0.57
12:D1:110:LEU:HG	12:D1:115:LEU:HB2	1.87	0.57
19:G2:2:LYS:HG2	19:G2:17:GLU:HG3	1.86	0.57
2:22:494:A:H2'	2:22:495:U:H4'	1.87	0.57
3:51:237:C:OP2	52:Y1:45:ARG:NH2	2.38	0.57
3:51:1834:G:H5"	10:C1:199:LYS:HE3	1.87	0.57
6:A1:117:GLU:HG2	6:A1:124:GLY:H	1.69	0.57
37:Q2:8:GLN:OE1	37:Q2:27:ARG:NH2	2.37	0.57
13:D2:55:THR:H	13:D2:90:LYS:HZ3	1.53	0.57
68:g2:126:ASP:OD1	68:g2:128:THR:OG1	2.18	0.57
2:22:548:A:OP1	25:J2:162:ARG:NH2	2.35	0.57
3:51:1901:G:H21	67:g1:6:THR:HG22	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:2138:A:N6	3:51:2282:A:OP2	2.36	0.57
8:B1:384:GLU:OE2	48:W1:14:TYR:OH	2.23	0.57
9:B2:71:LEU:HD11	9:B2:189:ILE:HG23	1.86	0.57
68:g2:214:GLY:HA2	68:g2:236:ILE:HG12	1.86	0.57
3:51:2263:A:N6	38:R1:88:ARG:O	2.38	0.57
3:51:3428:C:H2'	3:51:3430:G:H8	1.69	0.57
3:51:4096:C:H5'	8:B1:324:GLY:HA2	1.86	0.57
25:J2:35:TYR:O	25:J2:111:GLN:NE2	2.38	0.57
67:g1:101:LYS:O	67:g1:105:LYS:NZ	2.37	0.57
2:22:165:C:OP1	19:G2:131:ARG:NH1	2.38	0.57
3:51:126:C:OP2	69:h1:77:LYS:NZ	2.38	0.57
3:51:658:A:O2'	3:51:660:G:OP2	2.21	0.57
3:51:659:G:O6	40:S1:98:ARG:NH2	2.34	0.57
3:51:2154:G:OP1	38:R1:64:ARG:NH2	2.34	0.57
7:A2:77:ILE:HG12	7:A2:99:ILE:HB	1.86	0.57
17:F2:58:LYS:HB2	17:F2:61:ARG:HG2	1.87	0.57
27:L1:81:LEU:HD23	27:L1:117:LEU:HD21	1.87	0.57
39:R2:114:LEU:HB2	39:R2:117:LEU:HG	1.87	0.57
50:X1:81:THR:HG22	50:X1:154:ILE:HG23	1.87	0.57
54:Z1:89:ILE:HD11	54:Z1:117:LYS:HB3	1.87	0.57
2:22:98:C:OP2	2:22:391:A:O2'	2.23	0.56
2:22:111:A:H5'	28:L2:72:GLY:HA2	1.87	0.56
3:51:3093:A:OP1	30:N1:90:ASN:ND2	2.38	0.56
3:51:3956:A:H4'	8:B1:95:THR:HG22	1.87	0.56
8:B1:92:TYR:HB2	8:B1:159:VAL:HB	1.87	0.56
34:P1:64:ASN:O	34:P1:80:GLN:NE2	2.37	0.56
68:g2:174:VAL:HB	68:g2:188:HIS:HB2	1.87	0.56
2:22:537:U:OP2	53:Y2:37:LYS:NZ	2.38	0.56
3:51:3290:C:OP1	18:G1:245:LYS:NZ	2.38	0.56
12:D1:62:CYS:HB3	12:D1:105:LEU:HD22	1.87	0.56
53:Y2:7:ILE:HG23	53:Y2:25:ILE:HG23	1.87	0.56
2:22:606:A:OP1	25:J2:40:LYS:NZ	2.36	0.56
3:51:936:G:N1	3:51:1735:G:OP1	2.36	0.56
3:51:1907:G:N7	74:l1:2:SER:N	2.54	0.56
18:G1:110:LYS:HG3	18:G1:113:ARG:HH22	1.71	0.56
21:H2:144:ILE:HB	49:W2:52:ILE:HB	1.86	0.56
26:K2:80:ARG:HD3	26:K2:87:PRO:HA	1.86	0.56
34:P1:16:LYS:O	34:P1:101:ASN:ND2	2.35	0.56
37:Q2:26:LYS:O	37:Q2:67:ASP:N	2.34	0.56
68:g2:245:ARG:NH1	68:g2:296:GLN:OE1	2.38	0.56
3:51:643:A:H61	3:51:716:A:H61	1.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:1304:C:OP1	6:A1:14:SER:OG	2.22	0.56
3:51:2815:C:OP1	6:A1:200:ARG:NH2	2.35	0.56
3:51:4011:A:H5'	8:B1:128:LYS:HG3	1.87	0.56
20:H1:173:ARG:NH1	75:m1:125:LYS:O	2.38	0.56
23:I2:4:SER:OG	23:I2:6:ASP:OD2	2.21	0.56
67:g1:102:ILE:HA	67:g1:105:LYS:HZ3	1.70	0.56
2:22:1501:U:OP1	37:Q2:37:ARG:NH2	2.39	0.56
3:51:932:C:O2'	3:51:934:G:N7	2.39	0.56
3:51:2241:G:OP1	44:U1:113:ARG:NH1	2.38	0.56
81:v2:545:ILE:HD12	81:v2:575:PRO:HB3	1.86	0.56
81:v2:691:VAL:O	81:v2:839:ARG:NH2	2.37	0.56
2:22:471:G:OP1	53:Y2:108:LYS:NZ	2.36	0.56
2:22:840:C:N4	2:22:869:G:O6	2.26	0.56
2:22:1293:C:N4	71:i2:192:ASP:O	2.36	0.56
3:51:1300:G:H4'	3:51:1301:G:H5'	1.88	0.56
3:51:1819:G:N2	3:51:1822:G:OP2	2.32	0.56
3:51:4039:G:N2	3:51:4103:C:O2	2.38	0.56
33:O2:85:CYS:HB2	33:O2:124:MET:HE1	1.87	0.56
2:22:794:G:H1	2:22:805:C:H5	1.53	0.56
2:22:840:C:H3'	2:22:841:C:H2'	1.87	0.56
2:22:1820:A:OP2	57:a2:4:LYS:NZ	2.36	0.56
3:51:2386:G:O2'	3:51:3003:U:O4	2.19	0.56
3:51:3441:G:OP1	58:b1:38:LYS:NZ	2.36	0.56
11:C2:169:LYS:NZ	49:W2:91:ASN:O	2.38	0.56
47:V2:15:ARG:NH1	47:V2:33:GLN:OE1	2.38	0.56
3:51:1044:G:N2	3:51:1047:G:OP2	2.36	0.56
3:51:2382:A:N6	3:51:3004:G:O2'	2.39	0.56
3:51:3795:C:O2'	3:51:3797:A:OP2	2.24	0.56
8:B1:261:ARG:HB2	32:O1:92:THR:HG21	1.87	0.56
9:B2:99:ASN:OD1	9:B2:100:PHE:N	2.38	0.56
41:S2:34:LYS:HB2	41:S2:100:ALA:HA	1.88	0.56
41:S2:40:TYR:HA	41:S2:83:PHE:HE2	1.69	0.56
68:g2:120:ILE:HB	68:g2:132:TRP:HB2	1.86	0.56
2:22:114:G:O2'	2:22:347:U:O2'	2.16	0.56
2:22:1180:C:H1'	2:22:1641:C:H42	1.71	0.56
3:51:1266:C:H4'	3:51:2395:A:H5'	1.87	0.56
4:71:6:C:H4'	12:D1:52:ILE:HD13	1.87	0.56
15:E2:45:ILE:HA	15:E2:61:VAL:HG11	1.88	0.56
41:S2:132:ARG:HB2	41:S2:134:GLN:HE22	1.71	0.56
59:b2:23:ARG:NH2	59:b2:29:ASN:OD1	2.39	0.56
68:g2:5:MET:HG3	68:g2:270:LEU:HD21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:I2:43:ILE:HD11	23:I2:60:LEU:HD21	1.88	0.56
49:W2:14:ILE:HD11	49:W2:27:ILE:HD11	1.87	0.56
2:22:381:U:HO2'	2:22:617:U:HO2'	1.54	0.55
22:I1:91:LEU:HD12	22:I1:135:ILE:HG23	1.87	0.55
71:i2:189:ARG:NH2	81:v2:712:ASP:OD2	2.34	0.55
3:51:3617:U:O2'	3:51:3637:U:O2	2.20	0.55
43:T2:130:ARG:HD2	43:T2:134:ARG:HH21	1.71	0.55
2:22:875:A:N6	21:H2:119:SER:O	2.36	0.55
10:C1:153:GLU:HG2	10:C1:155:PRO:HD2	1.89	0.55
25:J2:107:GLU:O	25:J2:113:GLN:NE2	2.40	0.55
75:m1:94:MET:HG2	75:m1:105:PRO:HA	1.87	0.55
2:22:35:C:H5"	2:22:544:C:H5"	1.88	0.55
2:22:535:C:O2'	53:Y2:34:THR:O	2.15	0.55
3:51:90:G:OP2	3:51:92:C:N4	2.37	0.55
3:51:1071:G:OP1	36:Q1:71:LYS:NZ	2.38	0.55
3:51:1742:C:H5'	3:51:1743:C:H5"	1.88	0.55
11:C2:152:ARG:NH1	11:C2:240:ASP:OD1	2.39	0.55
32:O1:102:ARG:HG3	32:O1:173:VAL:HG23	1.88	0.55
3:51:1862:G:O2'	3:51:3024:G:O6	2.18	0.55
5:81:86:G:OP2	69:h1:7:ARG:NH1	2.40	0.55
49:W2:60:LYS:NZ	59:b2:23:ARG:O	2.40	0.55
2:22:487:A:H3'	25:J2:38:ARG:HH21	1.71	0.55
3:51:100:G:OP2	3:51:100:G:N2	2.28	0.55
3:51:600:U:OP2	14:E1:89:LYS:NZ	2.39	0.55
3:51:2785:G:OP1	3:51:2787:C:N4	2.40	0.55
3:51:3633:C:H5"	46:V1:43:LYS:HD2	1.88	0.55
3:51:3707:C:O2'	8:B1:99:LEU:O	2.19	0.55
6:A1:129:ALA:HB3	6:A1:132:ASN:HD22	1.71	0.55
10:C1:226:ARG:HD3	52:Y1:3:PHE:HZ	1.72	0.55
15:E2:124:CYS:HB3	15:E2:141:THR:HB	1.88	0.55
19:G2:52:ILE:HD13	19:G2:102:VAL:HG21	1.89	0.55
41:S2:22:GLY:HA2	41:S2:56:ALA:HB3	1.89	0.55
3:51:636:G:H1	3:51:724:C:H5	1.55	0.55
3:51:2022:G:H4'	67:g1:26:PRO:HD2	1.87	0.55
3:51:3714:A:N1	3:51:3746:C:O2'	2.40	0.55
3:51:3771:U:OP2	38:R1:62:ARG:NH2	2.39	0.55
4:71:63:C:H5'	4:71:64:G:H5"	1.89	0.55
7:A2:141:ASN:ND2	11:C2:71:SER:O	2.39	0.55
37:Q2:129:SER:O	37:Q2:131:LYS:NZ	2.32	0.55
49:W2:6:VAL:HG12	49:W2:34:ILE:HD11	1.88	0.55
81:v2:557:CYS:HA	81:v2:561:LEU:HB2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:v2:579:TYR:OH	81:v2:791:ASN:ND2	2.40	0.55
2:22:814:U:O2'	28:L2:99:ARG:NH2	2.40	0.55
3:51:3773:A:OP1	38:R1:62:ARG:NH1	2.40	0.55
14:E1:111:PHE:O	14:E1:116:ARG:NH2	2.40	0.55
21:H2:154:ILE:HB	21:H2:185:VAL:HG12	1.88	0.55
62:d1:24:THR:OG1	62:d1:83:ARG:NH1	2.37	0.55
2:22:1556:G:O6	55:Z2:85:ARG:NH2	2.40	0.55
3:51:1231:G:O6	78:p1:4:ARG:NH2	2.39	0.55
3:51:1305:G:H1	6:A1:208:GLU:HG2	1.72	0.55
3:51:3024:G:OP2	34:P1:25:HIS:NE2	2.36	0.55
5:81:101:G:OP2	5:81:103:A:O2'	2.24	0.55
28:L2:37:ARG:NH1	28:L2:57:TYR:O	2.36	0.55
36:Q1:122:THR:OG1	36:Q1:124:ASP:OD1	2.24	0.55
38:R1:105:LEU:HD13	38:R1:135:LYS:HE3	1.89	0.55
68:g2:283:PRO:O	68:g2:285:GLN:NE2	2.40	0.55
71:i2:197:SER:HA	81:v2:713:ALA:HB3	1.88	0.55
2:22:1022:A:H4'	2:22:1023:U:H5'	1.89	0.54
6:A1:5:ILE:HG12	6:A1:8:GLN:HE21	1.72	0.54
6:A1:173:GLY:O	78:p1:69:TRP:NE1	2.37	0.54
9:B2:38:MET:HE2	9:B2:182:LYS:HA	1.89	0.54
30:N1:9:GLU:HA	30:N1:12:ARG:HD2	1.88	0.54
2:22:1354:C:H41	2:22:1436:C:H41	1.53	0.54
3:51:619:G:N2	3:51:942:C:O2	2.40	0.54
3:51:985:C:H2'	3:51:986:A:C8	2.41	0.54
3:51:1360:A:O2'	42:T1:81:ARG:NH1	2.40	0.54
3:51:2347:G:O2'	3:51:3769:G:OP1	2.23	0.54
20:H1:114:ILE:HB	20:H1:124:ARG:HB2	1.88	0.54
23:I2:103:LEU:HD13	23:I2:170:LYS:HD3	1.88	0.54
33:O2:39:ASP:OD1	33:O2:40:THR:N	2.40	0.54
68:g2:156:PHE:HE2	68:g2:179:LEU:HD21	1.72	0.54
3:51:2882:A:OP2	3:51:2900:G:N2	2.36	0.54
3:51:4033:U:O2'	3:51:4036:U:O2	2.24	0.54
17:F2:34:LEU:HD12	17:F2:116:ILE:HD13	1.87	0.54
72:j1:27:TYR:HA	72:j1:34:CYS:HA	1.90	0.54
3:51:1277:A:OP2	3:51:2808:A:N6	2.41	0.54
7:A2:205:ARG:HH11	7:A2:210:ILE:HA	1.73	0.54
38:R1:95:TRP:HE3	38:R1:98:ARG:HH21	1.55	0.54
56:a1:3:SER:HA	56:a1:6:ARG:HG2	1.90	0.54
2:22:982:A:N7	31:N2:70:LYS:NZ	2.55	0.54
3:51:53:C:H2'	3:51:54:G:H8	1.73	0.54
3:51:2110:A:O2'	54:Z1:112:ARG:NH1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:4046:U:HO2'	8:B1:372:SER:HG	1.55	0.54
14:E1:128:LEU:HD13	14:E1:172:VAL:HG11	1.89	0.54
34:P1:89:ASN:O	34:P1:93:HIS:ND1	2.38	0.54
53:Y2:55:ILE:HG12	53:Y2:75:ILE:HG12	1.88	0.54
58:b1:59:ALA:O	58:b1:63:LYS:NZ	2.40	0.54
3:51:648:C:O3'	29:M1:71:LYS:NZ	2.41	0.54
3:51:1072:A:H4'	3:51:1073:G:H5'	1.90	0.54
66:f1:33:VAL:HG13	66:f1:38:GLU:HB2	1.90	0.54
3:51:1345:A:N3	3:51:1511:U:O2'	2.34	0.54
3:51:1800:G:H5'	79:r1:16:SER:HB2	1.90	0.54
3:51:2948:A:H2	3:51:2955:U:H3	1.54	0.54
3:51:3390:U:OP1	12:D1:12:TYR:OH	2.25	0.54
18:G1:38:ASN:ND2	18:G1:43:GLN:OE1	2.41	0.54
2:22:53:C:O2'	2:22:472:G:N7	2.34	0.54
3:51:3542:C:N4	3:51:3547:A:O2'	2.41	0.54
28:L2:137:SER:O	28:L2:141:ARG:NH1	2.40	0.54
40:S1:31:ARG:NH1	40:S1:129:VAL:O	2.41	0.54
3:51:306:A:OP1	70:i1:86:LYS:NZ	2.40	0.54
3:51:3867:G:H5'	3:51:3868:G:C8	2.43	0.54
3:51:3945:A:N6	3:51:3946:G:O6	2.41	0.54
11:C2:185:PRO:HG2	25:J2:58:ARG:HD2	1.90	0.54
12:D1:191:ASN:HD22	12:D1:194:VAL:H	1.55	0.54
56:a1:64:LYS:HD2	56:a1:67:GLN:HE21	1.72	0.54
3:51:267:G:OP1	69:h1:114:TYR:OH	2.25	0.54
3:51:1781:G:N2	3:51:1782:U:O4	2.41	0.54
3:51:3633:C:OP1	46:V1:43:LYS:NZ	2.41	0.54
3:51:3928:G:OP2	3:51:3928:G:N2	2.39	0.54
9:B2:71:LEU:HD22	9:B2:82:ARG:HD2	1.89	0.54
17:F2:48:LEU:HD12	37:Q2:50:LYS:HG2	1.90	0.54
24:J1:141:ALA:O	24:J1:147:ARG:NH1	2.40	0.54
68:g2:128:THR:HG22	68:g2:143:GLN:HB3	1.90	0.54
72:j1:2:THR:HG23	72:j1:4:GLY:H	1.73	0.54
3:51:442:G:H5"	66:f1:54:LYS:HD3	1.89	0.53
3:51:2051:G:H1	3:51:2305:U:H3	1.56	0.53
3:51:3987:C:H4'	14:E1:132:ASN:HB3	1.90	0.53
32:O1:221:THR:OG1	32:O1:225:LYS:NZ	2.40	0.53
54:Z1:41:ALA:HB2	54:Z1:77:TYR:HE1	1.73	0.53
2:22:324:U:OP1	51:X2:22:TRP:NE1	2.35	0.53
4:71:11:A:N6	12:D1:16:TYR:O	2.41	0.53
9:B2:136:ARG:HB3	9:B2:216:LYS:HB2	1.89	0.53
25:J2:107:GLU:HA	25:J2:112:THR:HG21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:R1:15:LEU:HD13	38:R1:52:ARG:HB2	1.90	0.53
62:d1:88:ARG:HD3	62:d1:100:LEU:HD13	1.89	0.53
2:22:1235:C:O2'	2:22:1464:A:N6	2.41	0.53
3:51:1475:G:OP2	3:51:1475:G:N2	2.33	0.53
3:51:3422:G:H2'	3:51:3423:A:H8	1.74	0.53
44:U1:23:LEU:HD11	44:U1:83:LEU:HD13	1.90	0.53
52:Y1:83:GLU:OE2	52:Y1:84:ARG:NH2	2.41	0.53
59:b2:33:MET:HB2	59:b2:79:PHE:HA	1.91	0.53
2:22:54:A:OP1	53:Y2:111:LYS:NZ	2.29	0.53
2:22:595:U:OP2	13:D2:143:ARG:NH2	2.42	0.53
3:51:109:G:OP2	27:L1:74:ARG:NH2	2.42	0.53
3:51:287:G:H5"	77:o1:47:GLY:HA2	1.91	0.53
5:81:93:G:H8	72:j1:82:THR:HG23	1.72	0.53
7:A2:37:TYR:OH	47:V2:66:ASP:OD1	2.24	0.53
13:D2:218:VAL:HG22	13:D2:220:THR:H	1.72	0.53
40:S1:69:GLU:HB2	40:S1:101:THR:HG23	1.91	0.53
43:T2:63:ARG:HB3	43:T2:63:ARG:HH11	1.73	0.53
67:g1:74:VAL:HG23	67:g1:76:ARG:H	1.72	0.53
81:v2:590:MET:HE1	81:v2:705:HIS:HD2	1.73	0.53
81:v2:663:THR:OG1	81:v2:703:ASP:OD1	2.26	0.53
81:v2:739:ARG:HD3	81:v2:821:PRO:HA	1.90	0.53
3:51:68:U:HO2'	3:51:100:G:HO2'	1.56	0.53
3:51:3337:A:N1	42:T1:3:ASN:ND2	2.45	0.53
3:51:3931:C:N4	14:E1:159:ILE:O	2.38	0.53
7:A2:108:PHE:HB2	7:A2:136:GLU:HG2	1.91	0.53
15:E2:71:LYS:HG2	15:E2:76:VAL:HG22	1.91	0.53
21:H2:104:PRO:HD3	21:H2:116:ARG:HD2	1.91	0.53
56:a1:72:THR:HG22	56:a1:110:LYS:HB3	1.91	0.53
3:51:158:A:N1	3:51:275:C:O2'	2.35	0.53
3:51:3443:C:H4'	77:o1:17:ARG:HA	1.90	0.53
6:A1:108:PRO:HD3	78:p1:90:LYS:HD2	1.91	0.53
77:o1:26:TYR:HB3	77:o1:67:VAL:HB	1.89	0.53
78:p1:33:GLN:OE1	78:p1:49:ARG:NH1	2.41	0.53
2:22:617:U:H2'	2:22:618:A:H8	1.72	0.53
2:22:1011:A:OP2	2:22:1030:G:N1	2.31	0.53
2:22:1299:C:H2'	2:22:1300:G:C8	2.44	0.53
3:51:829:A:N6	14:E1:36:ARG:O	2.40	0.53
3:51:3647:G:O2'	3:51:3650:C:OP2	2.20	0.53
7:A2:190:SER:HA	47:V2:45:ARG:HH21	1.74	0.53
35:P2:98:ASN:ND2	35:P2:121:ILE:O	2.37	0.53
60:c1:38:ILE:HG21	60:c1:63:TYR:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:919:A:OP1	33:O2:57:THR:OG1	2.21	0.53
2:22:1110:A:H4'	2:22:1111:A:O5'	2.08	0.53
3:51:1179:A:H4'	3:51:1180:G:H5'	1.90	0.53
3:51:3883:U:O2'	32:O1:143:ARG:O	2.27	0.53
11:C2:116:ILE:O	11:C2:124:GLY:N	2.39	0.53
13:D2:16:ILE:HD11	63:d2:36:LEU:HD23	1.91	0.53
43:T2:61:THR:HG23	43:T2:76:MET:HE2	1.90	0.53
1:11:49:THR:OG1	3:51:3508:U:OP1	2.25	0.53
2:22:604:C:H2'	2:22:605:A:C8	2.44	0.53
2:22:1188:G:N1	2:22:1597:G:OP2	2.40	0.53
2:22:1651:G:N2	2:22:1791:A:H8	2.06	0.53
3:51:633:G:N2	3:51:730:C:N3	2.56	0.53
3:51:3577:U:H3	80:s1:108:GLN:HA	1.74	0.53
19:G2:58:LYS:HE2	19:G2:105:ASN:HA	1.91	0.53
2:22:432:G:O5'	19:G2:72:ARG:NH1	2.41	0.53
3:51:1052:G:H1	3:51:1071:G:HO2'	1.56	0.53
3:51:1331:C:OP1	3:51:1355:A:O2'	2.27	0.53
3:51:1835:C:N4	10:C1:193:MET:O	2.35	0.53
3:51:2350:A:H5'	38:R1:88:ARG:HG2	1.90	0.53
22:I1:43:VAL:HG11	22:I1:197:VAL:HG13	1.91	0.53
23:I2:3:ILE:O	23:I2:30:GLY:N	2.41	0.53
78:p1:46:LYS:HD2	78:p1:59:SER:HB3	1.91	0.53
1:11:37:ARG:NH1	1:11:144:GLU:OE2	2.37	0.52
2:22:1299:C:H2'	2:22:1300:G:H8	1.75	0.52
3:51:2427:G:H21	3:51:4079:A:H8	1.57	0.52
3:51:3033:G:H22	3:51:3065:G:H1'	1.74	0.52
13:D2:35:SER:OG	13:D2:97:CYS:SG	2.64	0.52
25:J2:84:ILE:HA	25:J2:150:ARG:HA	1.90	0.52
30:N1:68:ARG:HA	30:N1:98:LEU:HD21	1.90	0.52
36:Q1:57:ASN:OD1	36:Q1:143:ARG:NH2	2.42	0.52
79:r1:29:GLU:HG3	79:r1:32:ASN:HB2	1.90	0.52
1:11:17:SER:HB2	1:11:142:MET:HB2	1.90	0.52
2:22:1084:A:N3	9:B2:146:ARG:NH2	2.57	0.52
2:22:1104:G:N2	2:22:1107:A:OP2	2.36	0.52
3:51:1855:G:OP1	10:C1:89:HIS:NE2	2.41	0.52
3:51:1903:G:O2'	67:g1:10:ARG:O	2.27	0.52
3:51:2951:U:OP1	3:51:3675:G:O2'	2.26	0.52
3:51:3212:G:O6	6:A1:72:ARG:NH2	2.41	0.52
20:H1:59:LYS:HE2	20:H1:66:GLU:HB3	1.90	0.52
2:22:975:U:OP1	2:22:1091:G:O2'	2.21	0.52
2:22:1074:U:H1'	9:B2:146:ARG:HH12	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:1403:U:O4	2:22:1404:A:N6	2.42	0.52
2:22:1460:C:O2	81:v2:670:GLN:NE2	2.42	0.52
3:51:3931:C:OP1	14:E1:252:ALA:N	2.41	0.52
14:E1:148:THR:OG1	14:E1:192:ASP:OD2	2.24	0.52
32:O1:55:VAL:O	32:O1:129:ARG:NH1	2.43	0.52
37:Q2:97:GLN:HE22	68:g2:60:ARG:HE	1.57	0.52
2:22:840:C:O2'	2:22:871:G:N2	2.42	0.52
2:22:905:U:O2'	33:O2:135:ILE:O	2.28	0.52
2:22:1431:G:O2'	2:22:1433:G:N2	2.43	0.52
3:51:1865:G:N2	3:51:3023:C:O2	2.41	0.52
7:A2:5:LEU:O	7:A2:9:GLN:NE2	2.39	0.52
19:G2:50:VAL:HG12	19:G2:113:ILE:HD13	1.91	0.52
22:I1:153:ARG:HA	22:I1:156:LYS:HE2	1.91	0.52
54:Z1:21:ARG:NH1	54:Z1:47:ASP:O	2.43	0.52
56:a1:26:ARG:HB2	56:a1:29:PRO:HG3	1.91	0.52
68:g2:44:LYS:HG3	68:g2:56:GLN:HB2	1.92	0.52
71:i2:207:LYS:O	71:i2:215:ASN:ND2	2.42	0.52
2:22:625:C:H5'	51:X2:13:LEU:HD13	1.92	0.52
2:22:1105:A:H5'	11:C2:176:SER:HB3	1.91	0.52
2:22:1413:A:OP1	39:R2:5:ARG:NH1	2.42	0.52
2:22:1456:A:OP2	13:D2:27:ARG:NH2	2.38	0.52
3:51:2125:C:H41	67:g1:70:THR:HG21	1.73	0.52
3:51:2296:G:O2'	3:51:2302:A:N3	2.31	0.52
3:51:3206:C:OP1	30:N1:32:GLN:NE2	2.42	0.52
3:51:3294:G:H4'	3:51:3296:C:C2	2.44	0.52
3:51:3346:C:N3	22:I1:116:ARG:NH2	2.58	0.52
3:51:3693:A:O2'	3:51:4026:G:N7	2.43	0.52
34:P1:131:ARG:HG3	34:P1:137:ASN:ND2	2.25	0.52
54:Z1:51:ARG:HB2	54:Z1:65:ARG:HB3	1.91	0.52
2:22:877:G:OP2	2:22:877:G:N2	2.36	0.52
2:22:1489:A:H4'	2:22:1563:G:H4'	1.90	0.52
3:51:1389:C:H5"	42:T1:43:LYS:HD2	1.91	0.52
3:51:4041:C:OP1	62:d1:30:ARG:NH1	2.33	0.52
14:E1:256:SER:H	14:E1:259:MET:HE2	1.75	0.52
46:V1:87:SER:HB2	48:W1:19:ARG:HH21	1.74	0.52
53:Y2:79:LEU:HG	53:Y2:83:LYS:HE3	1.91	0.52
78:p1:50:LYS:HE2	78:p1:54:ILE:HG21	1.91	0.52
81:v2:582:THR:HG22	81:v2:583:VAL:H	1.75	0.52
2:22:1022:A:O2'	2:22:1024:A:N7	2.31	0.52
2:22:1054:G:OP1	31:N2:2:GLY:N	2.41	0.52
2:22:1574:U:H3	2:22:1578:A:H2	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:71:73:U:H3'	4:71:74:A:H5"	1.92	0.52
12:D1:128:ASP:OD1	12:D1:129:GLU:N	2.41	0.52
31:N2:29:THR:OG1	31:N2:32:ASP:OD1	2.25	0.52
52:Y1:58:VAL:HG23	52:Y1:59:ARG:HG2	1.90	0.52
81:v2:501:VAL:HG23	81:v2:533:MET:HE3	1.92	0.52
3:51:3600:G:N7	75:m1:125:LYS:NZ	2.54	0.52
7:A2:8:LEU:HD11	47:V2:39:VAL:HG21	1.91	0.52
23:I2:131:PRO:HG2	23:I2:134:GLU:HB2	1.91	0.52
39:R2:66:VAL:HG12	39:R2:68:GLY:H	1.74	0.52
2:22:1201:U:H2'	2:22:1203:A:OP2	2.10	0.52
17:F2:19:PHE:HE2	17:F2:49:PRO:HD3	1.75	0.52
22:I1:54:SER:HB3	22:I1:135:ILE:HD11	1.91	0.52
30:N1:178:HIS:HA	30:N1:181:HIS:CE1	2.45	0.52
36:Q1:172:ARG:HD2	56:a1:57:GLY:HA3	1.92	0.52
50:X1:79:PRO:HA	50:X1:97:PHE:HA	1.92	0.52
50:X1:122:LYS:HE3	50:X1:124:ASN:HD21	1.75	0.52
2:22:1300:G:H4'	45:U2:74:SER:H	1.74	0.52
3:51:2050:G:H1	3:51:2308:C:H42	1.57	0.52
3:51:3026:A:H2'	3:51:3027:A:C8	2.45	0.52
3:51:3426:U:OP1	42:T1:78:LYS:NZ	2.38	0.52
8:B1:322:HIS:O	8:B1:342:LYS:NZ	2.36	0.52
8:B1:378:ARG:HE	48:W1:32:LEU:HD21	1.74	0.52
13:D2:32:ASP:OD2	13:D2:65:ARG:NH2	2.43	0.52
16:F1:234:ARG:HB2	16:F1:237:GLN:HB2	1.92	0.52
20:H1:107:GLU:OE1	20:H1:127:ARG:NH2	2.42	0.52
56:a1:76:ASP:HB3	56:a1:115:GLY:HA3	1.92	0.52
67:g1:56:ILE:HG23	67:g1:72:LYS:HA	1.92	0.52
77:o1:6:LYS:HG2	77:o1:93:LEU:HG	1.92	0.52
2:22:979:U:OP2	31:N2:55:ARG:NH1	2.42	0.51
2:22:1536:U:O2	13:D2:9:ARG:NH2	2.42	0.51
3:51:2407:U:O2'	3:51:2419:A:N7	2.42	0.51
3:51:3386:C:O2'	24:J1:101:THR:OG1	2.28	0.51
18:G1:180:PRO:HG3	18:G1:219:VAL:HG13	1.91	0.51
2:22:1025:C:O2'	33:O2:150:ARG:O	2.27	0.51
2:22:1053:C:O2'	49:W2:2:VAL:N	2.40	0.51
2:22:1575:G:H22	2:22:1578:A:H5'	1.75	0.51
3:51:985:C:H2'	3:51:986:A:H8	1.74	0.51
3:51:1187:C:OP1	56:a1:7:LYS:N	2.41	0.51
3:51:3102:C:H1'	30:N1:125:SER:HB3	1.92	0.51
14:E1:259:MET:HB3	14:E1:264:LEU:HD11	1.93	0.51
20:H1:118:LEU:HD11	20:H1:167:VAL:HG22	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:Z1:25:ILE:HA	54:Z1:43:VAL:HG12	1.92	0.51
78:p1:7:LYS:O	78:p1:27:LYS:NZ	2.40	0.51
81:v2:650:TRP:NE1	81:v2:664:ASP:OD2	2.43	0.51
2:22:786:U:H5	25:J2:143:ASN:HB3	1.76	0.51
2:22:1086:C:H5"	9:B2:150:ILE:HG12	1.93	0.51
2:22:1791:A:H2	2:22:1794:G:H1	1.57	0.51
3:51:1392:U:H2'	3:51:1393:A:H8	1.74	0.51
3:51:2278:U:O4'	6:A1:187:HIS:HB3	2.10	0.51
3:51:3309:G:H5'	6:A1:233:ARG:HB2	1.92	0.51
3:51:3761:U:OP1	62:d1:39:ARG:NH1	2.40	0.51
9:B2:47:THR:OG1	9:B2:65:ARG:NH1	2.43	0.51
41:S2:113:ARG:HA	41:S2:116:LYS:HE3	1.92	0.51
63:d2:17:GLY:O	63:d2:27:ARG:NH1	2.43	0.51
3:51:726:G:OP1	16:F1:243:ARG:NH1	2.44	0.51
3:51:949:G:O2'	3:51:950:U:O5'	2.28	0.51
30:N1:143:ARG:O	30:N1:149:GLN:NE2	2.42	0.51
2:22:980:U:O2'	31:N2:86:GLU:OE2	2.28	0.51
3:51:196:A:N3	3:51:221:C:O2'	2.41	0.51
3:51:282:G:H2'	3:51:283:G:H8	1.75	0.51
6:A1:107:MET:HE1	6:A1:113:VAL:HG11	1.92	0.51
20:H1:128:MET:HE3	20:H1:157:SER:HB3	1.92	0.51
20:H1:137:SER:HB2	20:H1:145:ILE:HG13	1.91	0.51
28:L2:113:VAL:HG12	28:L2:142:PHE:HB2	1.92	0.51
34:P1:120:ASN:HB2	34:P1:145:HIS:HB2	1.91	0.51
59:b2:54:VAL:HG23	59:b2:63:LEU:HB2	1.93	0.51
2:22:1101:C:H5	2:22:1111:A:H62	1.57	0.51
3:51:2784:G:H22	3:51:2789:A:H1'	1.75	0.51
16:F1:114:GLN:H	16:F1:117:ASN:HD21	1.57	0.51
81:v2:594:LYS:HE2	81:v2:601:ARG:HD3	1.91	0.51
2:22:972:G:H2'	2:22:973:A:C8	2.45	0.51
2:22:1578:A:O2'	2:22:1582:U:OP2	2.23	0.51
2:22:1774:G:O2'	76:n1:20:MET:SD	2.69	0.51
3:51:216:C:H5	3:51:217:A:H62	1.59	0.51
16:F1:113:ARG:NH1	36:Q1:4:ASP:O	2.42	0.51
1:11:89:ASP:HB3	1:11:135:LEU:HD13	1.92	0.51
3:51:85:G:O2'	3:51:97:G:O6	2.27	0.51
3:51:955:G:H8	64:e1:17:THR:HB	1.76	0.51
3:51:1169:G:OP1	58:b1:44:ARG:NE	2.40	0.51
3:51:2804:U:H3	3:51:2814:A:H61	1.58	0.51
3:51:3391:G:O2'	3:51:3392:G:N2	2.44	0.51
25:J2:164:PRO:HB3	25:J2:170:PRO:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:O1:113:ARG:HG3	32:O1:127:LEU:HD11	1.93	0.51
33:O2:31:CYS:HB2	33:O2:93:LEU:HD13	1.93	0.51
2:22:418:C:O2'	19:G2:92:ARG:O	2.21	0.51
3:51:2974:G:OP2	3:51:2974:G:N2	2.34	0.51
9:B2:92:GLN:O	9:B2:95:ASN:ND2	2.43	0.51
29:M1:104:MET:HE2	29:M1:109:ARG:HG2	1.93	0.51
54:Z1:17:ARG:NH2	54:Z1:18:TYR:OH	2.30	0.51
58:b1:8:THR:HG22	58:b1:10:HIS:H	1.76	0.51
2:22:1276:U:H2'	26:K2:2:LEU:HD12	1.92	0.51
2:22:1402:U:OP2	37:Q2:15:ARG:NH1	2.44	0.51
2:22:1530:U:H2'	2:22:1531:G:C8	2.46	0.51
3:51:9:C:OP2	30:N1:40:PRO:HG3	2.11	0.51
3:51:2017:G:O2'	67:g1:62:LYS:NZ	2.40	0.51
3:51:2913:A:H5"	6:A1:243:THR:HB	1.93	0.51
8:B1:33:PRO:O	8:B1:186:ASN:ND2	2.44	0.51
8:B1:175:GLN:NE2	8:B1:177:LYS:O	2.44	0.51
12:D1:51:MET:N	12:D1:145:TYR:O	2.28	0.51
21:H2:51:ILE:HG21	21:H2:179:LYS:HG2	1.92	0.51
23:I2:69:SER:N	23:I2:191:GLU:OE2	2.43	0.51
68:g2:244:ASN:ND2	68:g2:294:ASP:O	2.44	0.51
73:k1:23:VAL:HA	73:k1:36:VAL:HA	1.91	0.51
3:51:1214:U:H2'	3:51:1215:G:C8	2.46	0.50
3:51:3073:A:H2	80:s1:107:ILE:O	1.94	0.50
13:D2:45:ARG:HH11	13:D2:85:GLU:HG3	1.77	0.50
14:E1:238:LEU:HA	14:E1:241:LYS:HE2	1.93	0.50
18:G1:146:LEU:HB3	18:G1:152:ALA:HB2	1.93	0.50
39:R2:57:LEU:HD13	39:R2:69:ILE:HD11	1.93	0.50
2:22:1290:G:N3	81:v2:670:GLN:NE2	2.60	0.50
3:51:68:U:OP1	30:N1:178:HIS:ND1	2.26	0.50
3:51:393:G:N2	3:51:396:G:OP2	2.37	0.50
12:D1:51:MET:HE3	12:D1:105:LEU:HD23	1.92	0.50
19:G2:198:ARG:HA	19:G2:201:LYS:HG2	1.94	0.50
22:I1:42:LYS:HE2	22:I1:192:PRO:HB2	1.92	0.50
48:W1:52:THR:HG23	48:W1:55:TYR:H	1.76	0.50
55:Z2:68:ILE:HB	55:Z2:109:TYR:HB2	1.92	0.50
2:22:28:U:H2'	2:22:29:G:H8	1.75	0.50
3:51:415:U:O2'	3:51:1810:G:N2	2.41	0.50
13:D2:31:GLU:O	13:D2:54:ARG:NH1	2.44	0.50
22:I1:35:ASP:HB3	22:I1:39:LYS:HG2	1.94	0.50
23:I2:119:LEU:HD12	23:I2:120:PRO:HD2	1.92	0.50
29:M1:123:ILE:HD13	32:O1:210:GLU:HG2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:W2:112:ASP:OD1	49:W2:112:ASP:N	2.42	0.50
68:g2:236:ILE:HD12	68:g2:250:ALA:HB1	1.93	0.50
69:h1:86:LYS:O	72:j1:73:ARG:NH2	2.43	0.50
2:22:551:G:H2'	25:J2:172:ARG:HH22	1.75	0.50
3:51:1151:G:O2'	3:51:1152:C:OP1	2.27	0.50
3:51:1228:G:H2'	3:51:1250:G:N2	2.26	0.50
3:51:1292:U:H2'	3:51:1293:G:H8	1.76	0.50
3:51:2167:U:OP1	44:U1:48:LYS:NZ	2.36	0.50
3:51:3512:C:OP2	3:51:3657:U:O2'	2.29	0.50
25:J2:176:LYS:HA	25:J2:179:LYS:HE2	1.94	0.50
26:K2:91:PRO:HG2	26:K2:94:LEU:HD13	1.93	0.50
36:Q1:67:ILE:HD12	36:Q1:92:ILE:HD12	1.94	0.50
40:S1:78:PHE:HE1	40:S1:102:THR:HG22	1.76	0.50
2:22:653:U:OP1	21:H2:116:ARG:NH2	2.29	0.50
3:51:506:G:O6	3:51:508:C:N4	2.45	0.50
3:51:1742:C:OP2	36:Q1:14:ARG:NH2	2.44	0.50
3:51:2427:G:HO2'	3:51:4079:A:HO2'	1.53	0.50
3:51:3641:G:OP2	8:B1:2:SER:N	2.44	0.50
8:B1:165:HIS:HB3	8:B1:180:LEU:HD23	1.93	0.50
13:D2:132:LYS:HB2	13:D2:189:MET:HG3	1.94	0.50
39:R2:98:VAL:HG21	39:R2:117:LEU:HD22	1.93	0.50
45:U2:26:SER:HB3	45:U2:32:LEU:HB2	1.93	0.50
49:W2:30:CYS:SG	49:W2:31:SER:N	2.85	0.50
2:22:1109:C:OP1	57:a2:6:ARG:NH2	2.44	0.50
3:51:126:C:OP1	69:h1:78:TYR:OH	2.24	0.50
3:51:296:U:O2'	30:N1:179:LYS:O	2.30	0.50
3:51:478:G:H2'	3:51:479:G:H8	1.77	0.50
3:51:4019:C:N4	3:51:4020:G:O6	2.44	0.50
10:C1:75:ARG:HH12	80:s1:97:LYS:HE3	1.75	0.50
37:Q2:97:GLN:HB2	37:Q2:105:LYS:HD2	1.94	0.50
2:22:110:U:H2'	2:22:111:A:C8	2.47	0.50
3:51:2865:C:O2'	3:51:2939:A:N3	2.41	0.50
3:51:3287:C:O2	18:G1:73:ARG:NH1	2.42	0.50
3:51:3368:C:OP2	3:51:3389:G:N1	2.37	0.50
5:81:15:G:HO2'	5:81:16:A:H8	1.59	0.50
5:81:79:A:N6	69:h1:42:SER:O	2.44	0.50
10:C1:35:PRO:HD2	10:C1:284:PRO:HG2	1.92	0.50
13:D2:107:TYR:HD1	13:D2:110:LEU:HD21	1.77	0.50
16:F1:152:ILE:HD12	16:F1:189:ILE:HG12	1.94	0.50
17:F2:33:SER:HA	61:c2:55:VAL:HB	1.94	0.50
81:v2:701:ARG:NE	81:v2:703:ASP:OD1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:1562:G:OP2	41:S2:38:ARG:NH1	2.44	0.50
3:51:28:C:OP1	30:N1:187:SER:OG	2.29	0.50
3:51:1392:U:H4'	3:51:3338:A:H5"	1.93	0.50
4:71:22:A:O2'	4:71:23:A:O5'	2.30	0.50
12:D1:38:ILE:HD11	42:T1:27:LEU:HD12	1.94	0.50
17:F2:141:SER:HB3	61:c2:50:VAL:HG22	1.93	0.50
61:c2:37:ASP:OD1	61:c2:38:SER:N	2.45	0.50
2:22:606:A:O2'	2:22:610:C:OP1	2.28	0.50
3:51:385:A:OP2	52:Y1:89:LYS:NZ	2.36	0.50
3:51:1194:A:H61	27:L1:19:GLN:HE22	1.59	0.50
3:51:3066:A:H8	3:51:3643:A:N1	2.09	0.50
8:B1:317:LEU:HB2	8:B1:372:SER:HB2	1.93	0.50
27:L1:80:GLU:OE2	27:L1:102:ARG:NH2	2.44	0.50
32:O1:65:ARG:HG3	32:O1:136:ILE:HG13	1.92	0.50
55:Z2:95:GLY:O	55:Z2:112:ASN:ND2	2.39	0.50
68:g2:119:GLN:HB3	68:g2:131:LEU:HD11	1.92	0.50
81:v2:690:GLY:N	81:v2:695:GLU:O	2.45	0.50
2:22:1146:G:OP1	76:n1:11:ARG:NH1	2.45	0.49
3:51:824:G:O6	14:E1:12:LYS:NZ	2.45	0.49
3:51:1200:A:H61	3:51:1327:G:H22	1.59	0.49
3:51:1293:G:H1'	3:51:2014:A:N6	2.27	0.49
3:51:1384:U:OP1	16:F1:129:ASN:ND2	2.41	0.49
3:51:4049:C:H2'	3:51:4050:G:O4'	2.12	0.49
9:B2:175:GLU:HG2	9:B2:193:ILE:HG12	1.94	0.49
15:E2:50:ASN:O	15:E2:53:LYS:NZ	2.44	0.49
23:I2:177:SER:OG	23:I2:182:CYS:SG	2.70	0.49
68:g2:34:SER:HB2	68:g2:69:VAL:HG23	1.94	0.49
1:11:134:ILE:HG23	1:11:152:ALA:HA	1.94	0.49
3:51:1410:G:H1	3:51:1434:C:H42	1.59	0.49
3:51:2855:U:O2'	3:51:2982:A:N3	2.38	0.49
3:51:3711:A:OP2	32:O1:102:ARG:NH1	2.45	0.49
6:A1:53:GLY:O	6:A1:192:LYS:NZ	2.33	0.49
22:I1:152:LEU:HB3	22:I1:165:ILE:HD12	1.94	0.49
35:P2:61:ARG:NH1	35:P2:88:GLU:OE2	2.41	0.49
14:E1:145:GLN:HE21	14:E1:149:GLY:HA2	1.77	0.49
22:I1:97:ASN:HD21	22:I1:126:VAL:HG13	1.76	0.49
40:S1:15:ARG:HD2	40:S1:25:PRO:HG2	1.93	0.49
54:Z1:76:ASN:OD1	54:Z1:77:TYR:N	2.44	0.49
2:22:1569:G:H21	41:S2:87:GLN:HE21	1.60	0.49
3:51:152:U:OP2	30:N1:49:ARG:NH1	2.33	0.49
3:51:228:G:H5"	52:Y1:11:ARG:HG3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:2004:G:N2	3:51:3212:G:O4'	2.45	0.49
3:51:3984:C:H5"	3:51:3985:C:H5'	1.93	0.49
13:D2:41:VAL:HG13	13:D2:46:THR:HG22	1.95	0.49
13:D2:45:ARG:NH1	13:D2:82:GLY:O	2.39	0.49
52:Y1:53:ASP:OD2	52:Y1:115:ARG:NH2	2.45	0.49
3:51:174:C:O2'	27:L1:129:ARG:HD3	2.13	0.49
3:51:991:G:H22	56:a1:25:HIS:CG	2.31	0.49
3:51:1476:G:O2'	12:D1:140:GLY:O	2.25	0.49
3:51:1819:G:OP2	64:e1:14:LYS:NZ	2.44	0.49
3:51:2818:A:N6	3:51:2856:G:O2'	2.42	0.49
3:51:3801:G:OP1	8:B1:281:ASN:ND2	2.44	0.49
8:B1:216:MET:HE2	8:B1:283:LYS:HE2	1.93	0.49
32:O1:82:TYR:OH	32:O1:101:PHE:O	2.30	0.49
45:U2:80:PHE:HB3	63:d2:52:PHE:HB3	1.95	0.49
60:c1:50:ASN:ND2	60:c1:75:SER:O	2.45	0.49
2:22:467:G:H4'	15:E2:62:LYS:HE3	1.95	0.49
2:22:881:A:OP2	31:N2:64:ARG:NH2	2.42	0.49
2:22:1303:C:OP2	2:22:1645:C:O2'	2.24	0.49
3:51:62:A:H5"	30:N1:174:LEU:HD13	1.95	0.49
10:C1:5:MET:HG3	10:C1:33:LYS:HB3	1.94	0.49
22:I1:33:ILE:HB	22:I1:69:ARG:HH12	1.78	0.49
26:K2:17:LYS:NZ	26:K2:18:GLU:OE2	2.36	0.49
27:L1:46:VAL:HB	27:L1:49:ARG:HB2	1.94	0.49
36:Q1:64:SER:OG	36:Q1:89:ASP:OD2	2.27	0.49
3:51:2832:C:H4'	6:A1:8:GLN:HA	1.94	0.49
3:51:3610:C:O2'	75:m1:114:LYS:NZ	2.46	0.49
6:A1:113:VAL:HG12	6:A1:166:VAL:HA	1.94	0.49
8:B1:29:VAL:HG22	8:B1:220:ILE:HD12	1.94	0.49
11:C2:152:ARG:HB3	11:C2:233:THR:HB	1.93	0.49
17:F2:203:ARG:HH21	61:c2:60:GLU:HB3	1.77	0.49
50:X1:124:ASN:HB2	50:X1:136:TYR:HB2	1.95	0.49
2:22:321:C:O2	2:22:321:C:H2'	2.12	0.49
2:22:441:A:N3	2:22:453:U:O2'	2.37	0.49
2:22:465:A:H3'	2:22:466:C:H6	1.77	0.49
2:22:1650:U:H2'	2:22:1651:G:C8	2.47	0.49
3:51:2231:G:H2'	3:51:2232:G:N2	2.28	0.49
3:51:3824:U:H1'	3:51:3825:A:H5"	1.94	0.49
7:A2:128:ARG:HE	7:A2:153:PRO:HD3	1.77	0.49
9:B2:110:MET:HE1	9:B2:140:VAL:HG11	1.94	0.49
14:E1:159:ILE:HG21	14:E1:249:LEU:HB2	1.94	0.49
16:F1:236:ASP:OD1	40:S1:37:HIS:NE2	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:L2:70:ILE:HG21	28:L2:145:LEU:HD11	1.94	0.49
34:P1:113:VAL:N	34:P1:151:THR:O	2.42	0.49
60:c1:96:ILE:HD13	60:c1:104:ILE:HD12	1.94	0.49
69:h1:55:ALA:O	69:h1:59:THR:OG1	2.30	0.49
78:p1:33:GLN:HG3	78:p1:49:ARG:HD3	1.95	0.49
81:v2:727:ARG:HH22	81:v2:856:ASP:HB2	1.77	0.49
2:22:1552:G:HO2'	2:22:1553:U:P	2.34	0.49
3:51:723:G:H4'	40:S1:8:ARG:HH12	1.77	0.49
3:51:2317:C:O2'	5:81:112:G:OP1	2.20	0.49
3:51:2349:G:N1	3:51:2352:C:OP2	2.38	0.49
5:81:141:C:H5'	30:N1:113:LEU:HD11	1.94	0.49
11:C2:195:VAL:HB	11:C2:196:PRO:HD3	1.94	0.49
11:C2:243:LYS:O	47:V2:16:LYS:NZ	2.35	0.49
15:E2:175:PHE:HE2	15:E2:198:ARG:HD2	1.78	0.49
21:H2:67:PRO:O	21:H2:68:GLN:HG2	2.13	0.49
28:L2:113:VAL:HG11	28:L2:130:VAL:HG11	1.93	0.49
51:X2:84:PHE:HB2	51:X2:118:VAL:HG11	1.95	0.49
69:h1:80:PRO:HD2	69:h1:83:LEU:HD12	1.94	0.49
2:22:65:C:C6	19:G2:174:PRO:HB3	2.47	0.49
2:22:152:G:H4'	19:G2:15:LEU:HD22	1.95	0.49
3:51:1493:G:O2'	42:T1:112:ASN:ND2	2.45	0.49
10:C1:64:HIS:NE2	10:C1:104:ARG:HD3	2.27	0.49
15:E2:36:HIS:CD2	15:E2:85:GLY:H	2.30	0.49
18:G1:229:ARG:NE	18:G1:232:GLU:OE2	2.40	0.49
30:N1:159:ARG:HB3	30:N1:164:LEU:HB2	1.95	0.49
31:N2:20:ARG:HH21	49:W2:56:HIS:HB3	1.77	0.49
35:P2:36:LEU:O	41:S2:88:LYS:NZ	2.45	0.49
2:22:1526:C:O2	2:22:1585:C:O2'	2.28	0.48
3:51:1048:G:O2'	3:51:3475:U:O4	2.31	0.48
3:51:1825:C:O2'	64:e1:98:GLU:OE1	2.30	0.48
3:51:2115:G:OP1	54:Z1:111:ARG:NH2	2.45	0.48
3:51:3920:G:C2	29:M1:94:LYS:HD2	2.48	0.48
12:D1:126:THR:HG23	12:D1:128:ASP:H	1.78	0.48
13:D2:175:VAL:HB	13:D2:182:LEU:HB2	1.95	0.48
16:F1:177:LEU:HB3	16:F1:182:LEU:HB2	1.94	0.48
36:Q1:41:SER:HB3	36:Q1:132:LYS:HD2	1.94	0.48
38:R1:81:ARG:HG2	38:R1:88:ARG:NH1	2.27	0.48
53:Y2:23:MET:HE3	53:Y2:44:LEU:HD21	1.95	0.48
60:c1:34:THR:HG21	60:c1:93:THR:HG22	1.95	0.48
2:22:553:G:N2	2:22:553:G:OP2	2.44	0.48
3:51:492:G:H1	3:51:573:G:H22	1.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:926:A:H8	16:F1:31:VAL:HG11	1.77	0.48
3:51:1223:A:N6	3:51:1257:G:O2'	2.45	0.48
3:51:2278:U:O2'	3:51:2280:G:N2	2.46	0.48
3:51:2773:A:OP2	38:R1:81:ARG:NH2	2.46	0.48
3:51:3250:G:H4'	67:g1:90:ARG:HG2	1.95	0.48
15:E2:11:ARG:HA	15:E2:28:ALA:HB2	1.94	0.48
15:E2:53:LYS:HB2	53:Y2:13:MET:HE1	1.95	0.48
42:T1:79:GLN:HB2	42:T1:84:ILE:HG12	1.94	0.48
45:U2:61:LEU:HB2	45:U2:82:MET:HB3	1.94	0.48
55:Z2:47:LEU:HB3	55:Z2:79:ILE:HG22	1.95	0.48
66:f1:4:ARG:NH1	66:f1:8:LYS:HE3	2.27	0.48
2:22:1545:G:C6	43:T2:68:ARG:HD3	2.48	0.48
3:51:278:A:OP1	30:N1:50:ARG:NH2	2.47	0.48
3:51:480:U:H3	3:51:584:G:H1	1.59	0.48
3:51:617:C:O2'	3:51:3988:A:N1	2.38	0.48
3:51:1705:G:O2'	3:51:1706:A:N7	2.41	0.48
4:71:55:U:O2'	24:J1:150:ILE:O	2.21	0.48
35:P2:81:ARG:NH2	35:P2:117:GLY:O	2.46	0.48
59:b2:45:THR:OG1	59:b2:81:ARG:NH1	2.46	0.48
2:22:148:C:O2'	19:G2:132:ARG:NH2	2.47	0.48
3:51:3850:C:H2'	3:51:3851:G:H8	1.79	0.48
15:E2:171:ASP:OD1	15:E2:172:PHE:N	2.43	0.48
35:P2:28:MET:HE2	35:P2:32:GLN:HB3	1.94	0.48
40:S1:6:THR:HA	40:S1:107:THR:HG21	1.95	0.48
41:S2:26:ILE:HD12	41:S2:59:LEU:HD21	1.95	0.48
81:v2:609:PHE:CD2	81:v2:699:GLY:HA2	2.49	0.48
2:22:926:A:N3	2:22:1016:G:O2'	2.40	0.48
3:51:194:C:H5'	52:Y1:122:LYS:HE2	1.96	0.48
3:51:587:C:H2'	3:51:588:G:C8	2.48	0.48
3:51:1555:A:P	16:F1:221:LYS:HZ1	2.36	0.48
3:51:1731:C:OP1	36:Q1:2:GLY:N	2.46	0.48
3:51:3600:G:OP2	20:H1:173:ARG:NH2	2.42	0.48
3:51:3829:C:H2'	3:51:3830:A:C8	2.48	0.48
10:C1:149:GLU:HG2	10:C1:150:GLU:HG3	1.95	0.48
26:K2:62:PHE:HA	26:K2:66:HIS:O	2.14	0.48
32:O1:141:ASP:OD1	32:O1:142:LYS:N	2.46	0.48
45:U2:35:VAL:HG21	45:U2:110:VAL:HG11	1.93	0.48
51:X2:90:CYS:HA	51:X2:93:PHE:HD2	1.78	0.48
3:51:68:U:H2'	3:51:69:A:O4'	2.13	0.48
3:51:869:G:H2'	3:51:870:A:H8	1.78	0.48
3:51:1175:C:OP1	36:Q1:150:ARG:NH2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:2325:A:N3	3:51:2325:A:H2'	2.29	0.48
4:71:95:C:OP1	40:S1:43:ARG:NH2	2.39	0.48
7:A2:81:ASN:HA	7:A2:84:GLN:HG3	1.95	0.48
10:C1:225:PHE:HB2	10:C1:233:LEU:HD21	1.96	0.48
18:G1:110:LYS:HE2	18:G1:114:LEU:HD11	1.94	0.48
38:R1:81:ARG:HG2	38:R1:88:ARG:HH11	1.78	0.48
46:V1:13:LYS:NZ	46:V1:14:PHE:O	2.32	0.48
2:22:969:C:O2'	31:N2:104:ARG:NH2	2.47	0.48
3:51:3517:G:N2	3:51:3520:U:O2	2.36	0.48
3:51:3690:C:OP1	32:O1:93:ASN:ND2	2.42	0.48
3:51:3886:G:OP2	32:O1:65:ARG:NH1	2.43	0.48
10:C1:11:LEU:HG	10:C1:25:ASN:HB3	1.96	0.48
10:C1:226:ARG:HD3	52:Y1:3:PHE:CZ	2.49	0.48
15:E2:175:PHE:HE1	15:E2:225:ILE:HG21	1.79	0.48
15:E2:191:ARG:HD2	15:E2:245:ARG:HD2	1.95	0.48
53:Y2:20:ARG:HH21	53:Y2:22:GLN:NE2	2.12	0.48
64:e1:124:ASN:OD1	64:e1:124:ASN:N	2.47	0.48
81:v2:649:ILE:HG22	81:v2:663:THR:HG22	1.93	0.48
2:22:86:C:O2'	2:22:168:A:N1	2.40	0.48
3:51:1900:G:O2'	3:51:2360:G:O2'	2.30	0.48
12:D1:83:LEU:HB3	12:D1:88:VAL:HB	1.95	0.48
23:I2:57:ALA:HB2	23:I2:183:GLY:HA2	1.95	0.48
28:L2:122:VAL:HG22	28:L2:147:VAL:HG11	1.94	0.48
34:P1:6:LEU:HD12	34:P1:116:HIS:CD2	2.48	0.48
40:S1:3:ALA:HA	40:S1:7:LEU:HD21	1.94	0.48
81:v2:820:LEU:HD23	81:v2:820:LEU:H	1.79	0.48
2:22:1154:U:OP2	51:X2:119:ARG:NH1	2.46	0.48
2:22:1555:C:H4'	2:22:1561:A:N6	2.28	0.48
2:22:1574:U:O4	35:P2:40:ARG:NH2	2.36	0.48
3:51:839:C:H42	3:51:912:G:H1	1.62	0.48
3:51:2021:C:H2'	3:51:2022:G:C8	2.49	0.48
3:51:2376:G:OP1	8:B1:248:LEU:N	2.40	0.48
3:51:3810:U:H2'	3:51:3811:G:C8	2.49	0.48
4:71:27:G:O6	12:D1:58:ARG:NH2	2.47	0.48
14:E1:15:CYS:SG	14:E1:16:SER:N	2.86	0.48
17:F2:39:ALA:HB1	17:F2:44:TYR:CG	2.49	0.48
22:I1:51:HIS:HB3	22:I1:134:VAL:HG13	1.96	0.48
32:O1:154:ILE:HG13	32:O1:155:VAL:HG23	1.95	0.48
57:a2:3:LYS:HE3	57:a2:8:ASN:HD21	1.79	0.48
67:g1:78:TYR:HB3	67:g1:82:MET:HB3	1.96	0.48
2:22:781:A:OP1	25:J2:80:ARG:NH1	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:40:G:N2	3:51:3505:A:N7	2.61	0.48
3:51:417:A:H62	5:81:15:G:H1'	1.79	0.48
3:51:496:C:H2'	3:51:497:G:C8	2.48	0.48
3:51:955:G:C8	64:e1:17:THR:HB	2.49	0.48
3:51:2175:G:N2	3:51:2235:A:N1	2.39	0.48
3:51:2211:G:H5"	3:51:2213:G:H1'	1.96	0.48
3:51:2382:A:O2'	3:51:3756:G:H4'	2.13	0.48
13:D2:211:VAL:O	39:R2:20:TYR:OH	2.28	0.48
19:G2:57:ASP:OD1	19:G2:61:PHE:N	2.47	0.48
20:H1:113:GLU:OE2	20:H1:125:ARG:NH1	2.47	0.48
34:P1:52:THR:O	34:P1:85:LYS:NZ	2.47	0.48
34:P1:108:ASP:N	34:P1:152:GLU:OE2	2.42	0.48
40:S1:1:MET:HG3	40:S1:39:VAL:HG11	1.96	0.48
2:22:1650:U:O3'	57:a2:92:ARG:NH2	2.47	0.47
3:51:29:G:OP2	30:N1:189:ARG:NH2	2.46	0.47
3:51:92:C:OP2	3:51:3466:C:O2'	2.26	0.47
3:51:279:G:OP2	30:N1:44:ARG:NH1	2.44	0.47
3:51:3313:U:H2'	3:51:3314:U:C6	2.49	0.47
20:H1:92:MET:HB3	20:H1:179:ILE:HG22	1.96	0.47
25:J2:21:GLU:HG3	25:J2:24:ARG:HB3	1.96	0.47
28:L2:70:ILE:HG13	28:L2:145:LEU:HD21	1.96	0.47
41:S2:10:GLN:NE2	41:S2:61:GLU:OE2	2.41	0.47
2:22:1481:C:H2'	2:22:1482:G:C8	2.49	0.47
3:51:738:C:O2'	3:51:739:G:H5'	2.13	0.47
3:51:3514:C:H2'	3:51:3515:A:C8	2.49	0.47
3:51:4039:G:H1	3:51:4102:G:H22	1.62	0.47
6:A1:5:ILE:H	6:A1:8:GLN:NE2	2.12	0.47
7:A2:127:PRO:HG2	7:A2:152:SER:HB3	1.96	0.47
10:C1:16:SER:OG	10:C1:20:GLU:OE1	2.32	0.47
30:N1:7:MET:HE1	30:N1:45:PRO:HD2	1.96	0.47
64:e1:35:TRP:CZ2	64:e1:56:PRO:HD2	2.49	0.47
3:51:1387:U:H1'	42:T1:101:SER:HB3	1.96	0.47
3:51:2826:G:N7	6:A1:152:SER:OG	2.43	0.47
3:51:3747:A:H4'	8:B1:13:SER:HB2	1.96	0.47
3:51:3943:G:N2	3:51:3970:U:O2	2.33	0.47
5:81:2:A:O2'	34:P1:61:ARG:HD2	2.14	0.47
12:D1:125:VAL:HG11	12:D1:199:ILE:HG21	1.96	0.47
81:v2:791:ASN:OD1	81:v2:792:GLU:N	2.47	0.47
3:51:88:A:N7	36:Q1:173:LYS:NZ	2.61	0.47
3:51:263:A:O2'	69:h1:108:GLN:OE1	2.32	0.47
3:51:2021:C:H2'	3:51:2022:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:R1:105:LEU:HD22	38:R1:135:LYS:HG3	1.95	0.47
48:W1:46:PRO:HB2	48:W1:54:LEU:HD12	1.96	0.47
72:j1:73:ARG:NH2	72:j1:80:GLU:OE2	2.48	0.47
81:v2:531:ASP:HB3	81:v2:534:VAL:HG12	1.96	0.47
2:22:109:U:OP1	2:22:772:A:O2'	2.23	0.47
3:51:33:A:N3	3:51:1203:A:O2'	2.42	0.47
3:51:3643:A:OP2	3:51:3643:A:H8	1.98	0.47
7:A2:58:LEU:HD21	7:A2:177:MET:HB3	1.95	0.47
8:B1:285:TYR:CE1	8:B1:363:ILE:HG12	2.49	0.47
11:C2:91:GLU:HB2	11:C2:202:MET:HE1	1.97	0.47
67:g1:5:LEU:HD23	67:g1:5:LEU:H	1.79	0.47
71:i2:203:ARG:HD3	71:i2:204:PRO:HD2	1.95	0.47
77:o1:45:GLN:HE22	77:o1:52:THR:H	1.63	0.47
2:22:1166:A:O2'	2:22:1658:C:OP2	2.31	0.47
3:51:222:G:O2'	3:51:224:G:OP2	2.29	0.47
3:51:432:A:C2	3:51:3032:A:H4'	2.49	0.47
3:51:1879:G:N2	3:51:1882:A:OP2	2.44	0.47
3:51:2890:G:N2	3:51:2893:A:OP2	2.42	0.47
7:A2:10:MET:HE3	7:A2:55:TRP:HB2	1.96	0.47
17:F2:59:ARG:HH21	61:c2:49:PRO:HA	1.80	0.47
31:N2:119:GLU:O	31:N2:123:HIS:ND1	2.36	0.47
60:c1:20:LEU:HB3	60:c1:102:SER:HB2	1.95	0.47
2:22:153:G:OP1	19:G2:2:LYS:NZ	2.47	0.47
3:51:180:C:O2	3:51:258:G:N2	2.48	0.47
3:51:506:G:H22	3:51:560:G:H22	1.63	0.47
3:51:728:C:H1'	10:C1:323:LEU:HB3	1.97	0.47
3:51:994:U:H5'	10:C1:113:ARG:HA	1.96	0.47
3:51:1001:C:H2'	3:51:1002:G:C8	2.50	0.47
3:51:1451:A:H5"	3:51:3339:A:H61	1.80	0.47
3:51:1537:G:OP2	58:b1:14:ARG:NH2	2.41	0.47
3:51:1769:A:OP2	79:r1:12:ARG:HD2	2.14	0.47
3:51:3719:U:H2'	3:51:3720:G:C8	2.49	0.47
4:71:77:A:H62	4:71:99:G:H21	1.62	0.47
5:81:153:C:H5'	18:G1:185:LYS:HD3	1.97	0.47
7:A2:143:PRO:HG3	47:V2:32:ILE:HB	1.96	0.47
8:B1:219:VAL:HG11	8:B1:337:VAL:HB	1.96	0.47
13:D2:106:ARG:HG3	13:D2:175:VAL:HG22	1.96	0.47
15:E2:151:ASP:HB3	15:E2:154:ILE:HG13	1.97	0.47
18:G1:66:GLN:HE21	30:N1:28:TRP:HZ2	1.61	0.47
19:G2:32:MET:O	19:G2:65:GLN:NE2	2.47	0.47
27:L1:77:SER:HB2	27:L1:80:GLU:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:M1:11:ARG:HG2	29:M1:57:LEU:HD22	1.97	0.47
34:P1:60:PHE:CE1	34:P1:82:ARG:HB2	2.49	0.47
37:Q2:21:ALA:HB2	37:Q2:72:VAL:HG13	1.96	0.47
38:R1:70:ARG:HG2	38:R1:75:HIS:HB2	1.97	0.47
40:S1:1:MET:HG2	40:S1:3:ALA:H	1.80	0.47
51:X2:49:GLY:HA2	51:X2:75:ILE:HG13	1.97	0.47
60:c1:103:ASP:N	60:c1:103:ASP:OD1	2.47	0.47
68:g2:78:ALA:O	68:g2:90:TRP:N	2.46	0.47
2:22:1552:G:O2'	2:22:1553:U:OP1	2.26	0.47
2:22:1822:C:O2	57:a2:92:ARG:HB3	2.14	0.47
3:51:223:C:HO2'	3:51:242:G:HO2'	1.55	0.47
3:51:1558:G:O2'	64:e1:57:ASN:OD1	2.31	0.47
3:51:1972:G:H21	50:X1:48:PRO:HD2	1.80	0.47
3:51:2194:U:H5"	54:Z1:38:TYR:HB3	1.96	0.47
3:51:2232:G:H3'	3:51:2232:G:OP2	2.15	0.47
13:D2:158:ILE:HG22	13:D2:164:VAL:HG12	1.97	0.47
24:J1:14:LEU:HD12	24:J1:164:TRP:HB2	1.97	0.47
38:R1:39:GLN:OE1	38:R1:42:ARG:NH2	2.42	0.47
2:22:1190:A:H2'	2:22:1191:G:C8	2.50	0.47
2:22:1356:C:OP1	37:Q2:126:ARG:NE	2.48	0.47
3:51:279:G:H5"	30:N1:14:LYS:HE2	1.97	0.47
3:51:386:G:O2'	3:51:411:G:O6	2.30	0.47
3:51:2029:G:H4'	3:51:2321:A:H4'	1.96	0.47
3:51:3662:C:H2'	3:51:3663:G:C8	2.50	0.47
6:A1:2:GLY:HA2	6:A1:207:VAL:HG23	1.97	0.47
7:A2:145:ILE:HG12	7:A2:159:ILE:HB	1.97	0.47
12:D1:64:ILE:HG13	12:D1:105:LEU:HD21	1.97	0.47
22:I1:51:HIS:CD2	22:I1:168:SER:HB2	2.50	0.47
33:O2:94:HIS:HD1	33:O2:128:ARG:HB2	1.80	0.47
40:S1:98:ARG:HG3	40:S1:142:ILE:HG23	1.97	0.47
81:v2:687:THR:HG22	81:v2:697:LEU:HD12	1.97	0.47
2:22:978:U:H5"	31:N2:14:SER:HB2	1.96	0.47
2:22:1275:A:H4'	2:22:1276:U:O5'	2.13	0.47
2:22:1651:G:H21	2:22:1791:A:H8	1.61	0.47
3:51:847:G:H2'	3:51:848:G:C8	2.50	0.47
3:51:906:G:O2'	3:51:908:G:OP2	2.23	0.47
3:51:1131:G:H2'	3:51:1132:C:C6	2.50	0.47
3:51:3109:G:H1	3:51:3197:U:H3	1.63	0.47
3:51:3750:C:OP1	8:B1:224:LYS:HG3	2.15	0.47
8:B1:22:CYS:SG	8:B1:276:HIS:HB2	2.55	0.47
11:C2:114:VAL:HG11	11:C2:141:ILE:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:C2:182:ILE:HB	11:C2:209:TYR:HB2	1.96	0.47
21:H2:153:LEU:HD11	21:H2:186:VAL:HG23	1.97	0.47
25:J2:33:GLY:HA3	65:e2:115:TYR:CG	2.50	0.47
81:v2:671:TYR:HB2	81:v2:709:LEU:HD12	1.97	0.47
2:22:617:U:H2'	2:22:618:A:C8	2.49	0.46
2:22:793:A:OP2	2:22:808:G:N2	2.47	0.46
2:22:1060:C:H2'	2:22:1061:G:C8	2.50	0.46
3:51:727:U:H5'	16:F1:145:LEU:HD23	1.97	0.46
3:51:1714:G:C4	32:O1:158:LYS:HD3	2.49	0.46
3:51:3927:C:H3'	3:51:3928:G:H21	1.81	0.46
12:D1:106:ALA:HB2	12:D1:166:ALA:HA	1.97	0.46
56:a1:35:ALA:O	56:a1:41:HIS:ND1	2.48	0.46
62:d1:35:GLY:O	62:d1:39:ARG:HG3	2.15	0.46
64:e1:99:ILE:HG22	64:e1:103:VAL:HG21	1.97	0.46
68:g2:70:VAL:HG21	68:g2:112:ALA:HA	1.97	0.46
2:22:67:C:H41	19:G2:164:LYS:H	1.62	0.46
2:22:89:C:H2'	2:22:90:G:H8	1.79	0.46
2:22:1447:A:H5'	2:22:1448:G:OP1	2.16	0.46
3:51:650:A:H61	3:51:706:C:H42	1.63	0.46
3:51:1359:U:H2'	3:51:1360:A:C8	2.50	0.46
3:51:1513:G:N2	3:51:3519:A:O4'	2.48	0.46
3:51:3819:G:H4'	20:H1:71:ARG:HH12	1.79	0.46
15:E2:166:THR:HG23	15:E2:168:LYS:H	1.80	0.46
22:I1:149:ILE:HD11	22:I1:167:ILE:HD11	1.98	0.46
22:I1:150:GLU:OE2	22:I1:153:ARG:NH1	2.38	0.46
24:J1:21:LEU:HD11	24:J1:81:ILE:HG21	1.98	0.46
28:L2:128:VAL:HG12	28:L2:147:VAL:HG22	1.97	0.46
68:g2:199:THR:HG21	68:g2:240:CYS:HA	1.97	0.46
2:22:1611:U:H2'	2:22:1612:G:C8	2.50	0.46
3:51:1026:G:H22	10:C1:243:ARG:NH2	2.13	0.46
7:A2:76:VAL:HG12	7:A2:123:VAL:HB	1.98	0.46
7:A2:89:LYS:NZ	39:R2:83:ASN:OD1	2.44	0.46
10:C1:41:VAL:HG13	10:C1:241:LEU:HD11	1.97	0.46
29:M1:29:ASP:OD1	29:M1:30:VAL:N	2.49	0.46
40:S1:94:TYR:O	40:S1:139:ARG:NH2	2.45	0.46
81:v2:656:GLY:H	81:v2:684:GLN:HE22	1.63	0.46
81:v2:742:GLU:OE2	81:v2:767:ARG:NH1	2.47	0.46
2:22:1564:G:N2	2:22:1590:G:H1'	2.31	0.46
2:22:1678:U:O2'	3:51:2961:U:O2'	2.26	0.46
3:51:1366:C:P	36:Q1:11:ARG:HH22	2.38	0.46
3:51:1531:G:O2'	3:51:3344:A:N3	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B2:87:ILE:HG22	9:B2:101:HIS:HB2	1.97	0.46
19:G2:2:LYS:HB3	19:G2:15:LEU:HD11	1.96	0.46
37:Q2:39:LEU:HD11	37:Q2:51:LEU:HB3	1.96	0.46
37:Q2:49:TYR:O	37:Q2:53:GLU:HG3	2.15	0.46
43:T2:41:ALA:HB3	43:T2:44:LYS:HG2	1.97	0.46
43:T2:117:ASP:N	43:T2:121:GLY:O	2.47	0.46
46:V1:91:LYS:HD3	46:V1:91:LYS:HA	1.75	0.46
2:22:337:U:O2'	28:L2:84:MET:SD	2.73	0.46
2:22:1041:C:O2'	2:22:1144:A:N1	2.49	0.46
2:22:1106:A:H2'	2:22:1107:A:C8	2.51	0.46
3:51:244:C:O2'	3:51:245:G:OP1	2.26	0.46
3:51:1839:C:O2	10:C1:249:HIS:NE2	2.40	0.46
3:51:2293:A:OP2	54:Z1:51:ARG:NH1	2.48	0.46
3:51:3256:A:O2'	18:G1:35:ARG:NH1	2.49	0.46
3:51:3649:G:C2	8:B1:252:ALA:HB1	2.51	0.46
5:81:100:C:O2'	72:j1:20:ARG:O	2.30	0.46
27:L1:47:ALA:HB3	27:L1:48:PRO:HD3	1.98	0.46
40:S1:98:ARG:HG3	40:S1:142:ILE:HD12	1.98	0.46
2:22:1221:A:O2'	2:22:1222:A:OP1	2.22	0.46
3:51:565:C:O2'	3:51:567:G:N7	2.47	0.46
3:51:943:G:H2'	3:51:944:G:C8	2.51	0.46
3:51:1483:G:H21	58:b1:50:ASN:HD21	1.63	0.46
9:B2:27:LYS:HA	9:B2:51:ARG:HE	1.81	0.46
17:F2:78:HIS:HB3	17:F2:80:ARG:HG2	1.97	0.46
67:g1:60:ARG:HB2	67:g1:63:VAL:HG23	1.98	0.46
2:22:286:G:H1	2:22:296:C:H42	1.64	0.46
2:22:775:A:H5'	15:E2:16:LYS:HD2	1.98	0.46
2:22:998:A:N3	2:22:1801:U:O2'	2.47	0.46
2:22:1183:G:H2'	2:22:1184:G:C8	2.50	0.46
3:51:54:G:OP1	72:j1:43:ARG:NH1	2.49	0.46
3:51:959:C:H2'	3:51:960:A:C8	2.51	0.46
11:C2:51:LYS:HD2	11:C2:259:LEU:HD13	1.96	0.46
15:E2:18:TRP:HH2	15:E2:31:PRO:HD3	1.80	0.46
20:H1:120:GLU:OE1	20:H1:124:ARG:NH2	2.49	0.46
39:R2:16:ILE:HG22	39:R2:24:LEU:HD11	1.98	0.46
51:X2:46:HIS:HB3	51:X2:101:LEU:HD11	1.98	0.46
2:22:57:U:OP1	2:22:469:G:O2'	2.29	0.46
3:51:623:C:O2	14:E1:108:LYS:NZ	2.48	0.46
3:51:649:C:H2'	3:51:650:A:C8	2.50	0.46
3:51:2788:C:O2	38:R1:82:LYS:NZ	2.35	0.46
3:51:3861:C:O2	3:51:4008:G:N2	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:81:29:U:OP1	27:L1:34:ARG:NH2	2.46	0.46
17:F2:109:GLN:HE21	17:F2:113:ASN:HD21	1.63	0.46
26:K2:58:VAL:HG11	26:K2:69:TRP:HB3	1.98	0.46
52:Y1:2:LYS:HD2	52:Y1:7:VAL:HB	1.98	0.46
53:Y2:86:GLU:OE2	53:Y2:90:ARG:HD2	2.16	0.46
56:a1:36:GLY:HA3	56:a1:40:HIS:CE1	2.51	0.46
56:a1:100:ILE:HG12	56:a1:123:ILE:HB	1.98	0.46
2:22:931:U:H4'	2:22:932:G:H4'	1.98	0.46
2:22:1486:G:O2'	2:22:1624:C:OP1	2.32	0.46
3:51:907:A:H3'	3:51:908:G:H5"	1.97	0.46
3:51:2276:C:O2'	3:51:2278:U:O2	2.31	0.46
3:51:3331:C:HO2'	3:51:3460:C:HO2'	1.63	0.46
5:81:66:U:H2'	5:81:67:G:H8	1.80	0.46
6:A1:48:ILE:HD13	78:p1:65:ALA:HB2	1.98	0.46
7:A2:66:VAL:HG11	7:A2:185:MET:HB2	1.96	0.46
25:J2:149:VAL:HG11	25:J2:157:ILE:HD11	1.97	0.46
42:T1:37:GLY:N	42:T1:64:VAL:O	2.47	0.46
44:U1:47:ILE:HD12	44:U1:63:ILE:HD11	1.98	0.46
44:U1:48:LYS:HE2	44:U1:53:VAL:HG22	1.98	0.46
68:g2:5:MET:HE1	68:g2:291:TRP:HH2	1.79	0.46
1:11:43:GLU:HB3	1:11:60:VAL:HB	1.97	0.46
2:22:1201:U:H5"	35:P2:124:LYS:HE2	1.98	0.46
2:22:1222:A:OP1	2:22:1224:C:N4	2.48	0.46
3:51:304:A:P	30:N1:15:GLN:HE22	2.39	0.46
3:51:2277:C:H4'	78:p1:52:VAL:HG21	1.98	0.46
13:D2:115:VAL:HG13	71:i2:216:TRP:HA	1.98	0.46
40:S1:15:ARG:HB3	40:S1:27:LEU:HD23	1.98	0.46
2:22:1017:A:N1	2:22:1025:C:N4	2.63	0.45
2:22:1215:A:H4'	2:22:1216:C:O5'	2.16	0.45
2:22:1822:C:OP2	57:a2:5:ARG:NH2	2.49	0.45
3:51:254:C:H2'	3:51:255:G:C8	2.51	0.45
3:51:3538:C:H5	3:51:3554:C:N4	2.13	0.45
9:B2:104:ASP:OD1	9:B2:105:LEU:N	2.49	0.45
10:C1:69:GLU:OE1	10:C1:70:SER:N	2.48	0.45
21:H2:80:VAL:HG13	21:H2:92:VAL:HG13	1.98	0.45
28:L2:37:ARG:NE	28:L2:55:GLY:O	2.49	0.45
30:N1:37:HIS:CE1	30:N1:63:ARG:HE	2.34	0.45
36:Q1:70:MET:HG3	36:Q1:98:LEU:HD22	1.98	0.45
63:d2:30:LEU:HA	63:d2:39:CYS:HA	1.98	0.45
68:g2:213:ASP:OD1	68:g2:213:ASP:N	2.49	0.45
2:22:1123:U:O4	51:X2:2:GLY:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:1412:A:OP2	39:R2:3:ARG:NH1	2.49	0.45
3:51:621:G:H21	14:E1:114:HIS:HE1	1.64	0.45
3:51:3345:A:H2'	3:51:3347:G:H5"	1.98	0.45
6:A1:49:ILE:HD13	6:A1:60:LYS:HD2	1.98	0.45
17:F2:111:LEU:HD13	17:F2:176:LEU:HD21	1.98	0.45
34:P1:50:ASP:HB3	34:P1:55:LYS:HB2	1.98	0.45
2:22:563:G:O2'	2:22:570:A:N1	2.47	0.45
3:51:1267:U:C5	3:51:3652:G:H5"	2.51	0.45
3:51:1940:G:H5'	3:51:2316:G:OP2	2.16	0.45
3:51:2786:A:O2'	3:51:3783:G:O2'	2.30	0.45
7:A2:154:LEU:O	47:V2:63:GLY:HA2	2.17	0.45
10:C1:234:LEU:HD11	10:C1:243:ARG:HB2	1.97	0.45
21:H2:53:VAL:HG11	21:H2:172:THR:HG22	1.98	0.45
52:Y1:19:PHE:O	52:Y1:26:ARG:NH2	2.49	0.45
55:Z2:92:LEU:HD22	55:Z2:109:TYR:HE2	1.81	0.45
2:22:1281:U:O3'	81:v2:633:ARG:NH2	2.49	0.45
2:22:1491:A:H8	2:22:1494:G:H1'	1.81	0.45
3:51:356:C:N4	3:51:359:A:OP2	2.35	0.45
3:51:742:G:N2	3:51:938:U:OP1	2.33	0.45
3:51:1164:G:OP1	27:L1:183:ARG:NE	2.42	0.45
3:51:1214:U:H2'	3:51:1215:G:H8	1.81	0.45
3:51:1775:C:H2'	3:51:1776:G:C8	2.51	0.45
3:51:2022:G:H5'	3:51:2177:G:H1'	1.98	0.45
3:51:2775:A:H2'	3:51:2776:A:C8	2.51	0.45
3:51:3353:G:H5"	3:51:3354:U:O4'	2.17	0.45
16:F1:50:LYS:HA	16:F1:53:GLU:HG2	1.99	0.45
25:J2:32:ILE:HD11	25:J2:40:LYS:HD3	1.98	0.45
32:O1:107:ILE:HG21	32:O1:166:LEU:HD11	1.98	0.45
43:T2:11:ASN:HD21	43:T2:13:GLN:HB2	1.81	0.45
54:Z1:50:PRO:HD3	54:Z1:68:ILE:HG12	1.98	0.45
81:v2:830:ARG:HB3	81:v2:831:PRO:HD3	1.97	0.45
3:51:233:U:H5'	10:C1:193:MET:HE1	1.99	0.45
3:51:363:G:O6	72:j1:52:LYS:HE3	2.17	0.45
3:51:1170:U:H2'	3:51:1171:G:H8	1.81	0.45
3:51:1548:U:O2'	3:51:1549:G:OP1	2.21	0.45
3:51:1958:G:OP1	30:N1:65:ARG:NH1	2.48	0.45
12:D1:151:THR:HB	12:D1:157:ASN:HD21	1.81	0.45
13:D2:42:THR:OG1	13:D2:45:ARG:O	2.25	0.45
19:G2:145:PHE:HB2	19:G2:147:LEU:HG	1.98	0.45
20:H1:128:MET:HE2	20:H1:134:CYS:HB2	1.99	0.45
31:N2:94:LYS:HG2	31:N2:118:ILE:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:5:U:H2'	2:22:6:G:H8	1.82	0.45
2:22:420:A:O2'	2:22:1693:A:N3	2.44	0.45
2:22:430:A:H4'	2:22:431:G:O5'	2.17	0.45
2:22:1558:G:C6	2:22:1560:U:H1'	2.51	0.45
2:22:1608:A:H5"	37:Q2:139:ALA:HB2	1.97	0.45
3:51:74:G:O6	27:L1:103:ARG:NH2	2.49	0.45
3:51:453:U:H4'	3:51:454:C:H5"	1.98	0.45
3:51:3577:U:OP2	3:51:3647:G:N1	2.37	0.45
3:51:3719:U:H2'	3:51:3720:G:H8	1.80	0.45
7:A2:184:ARG:HD3	7:A2:191:ARG:HG3	1.98	0.45
12:D1:119:TYR:OH	12:D1:139:PRO:O	2.33	0.45
15:E2:129:THR:HG22	15:E2:139:LEU:HD12	1.98	0.45
36:Q1:35:LEU:O	36:Q1:39:THR:OG1	2.29	0.45
56:a1:75:LEU:HG	56:a1:113:GLY:HA2	1.97	0.45
57:a2:60:ASP:OD1	57:a2:60:ASP:N	2.49	0.45
2:22:1447:A:H4'	2:22:1448:G:O5'	2.17	0.45
3:51:403:U:O3'	52:Y1:87:ARG:NH1	2.47	0.45
3:51:934:G:H5'	10:C1:327:ARG:HB2	1.98	0.45
3:51:1003:C:H2'	3:51:1004:G:C8	2.52	0.45
3:51:1321:C:H2'	3:51:1322:A:C8	2.51	0.45
3:51:1919:A:H5"	34:P1:125:MET:HE1	1.98	0.45
3:51:3984:C:H3'	14:E1:134:ARG:HH22	1.81	0.45
14:E1:69:THR:OG1	14:E1:85:VAL:O	2.24	0.45
30:N1:45:PRO:O	30:N1:49:ARG:HG2	2.17	0.45
31:N2:56:ASP:O	59:b2:46:VAL:HA	2.17	0.45
32:O1:109:TRP:HB2	32:O1:132:VAL:HG21	1.99	0.45
54:Z1:5:MET:O	54:Z1:28:ASN:ND2	2.49	0.45
81:v2:852:ASP:O	81:v2:857:LYS:NZ	2.49	0.45
2:22:115:U:O2'	2:22:346:C:O2	2.32	0.45
2:22:614:U:H2'	2:22:615:A:C8	2.52	0.45
2:22:875:A:N3	21:H2:66:VAL:HG11	2.32	0.45
2:22:903:C:H2'	2:22:904:G:C8	2.52	0.45
3:51:1012:G:O6	3:51:1182:G:H5"	2.17	0.45
3:51:1836:C:H2'	3:51:1837:G:H8	1.81	0.45
3:51:2164:C:OP2	44:U1:92:LYS:NZ	2.42	0.45
3:51:4039:G:HO2'	62:d1:53:LYS:HZ3	1.60	0.45
3:51:4046:U:H4'	8:B1:317:LEU:HB3	1.98	0.45
5:81:66:U:H2'	5:81:67:G:C8	2.52	0.45
9:B2:111:CYS:HB3	57:a2:68:TYR:HB2	1.99	0.45
11:C2:71:SER:OG	47:V2:25:GLY:O	2.28	0.45
12:D1:52:ILE:HB	12:D1:63:GLN:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D1:223:PHE:HB3	12:D1:226:TYR:HB2	1.98	0.45
16:F1:158:LEU:HD21	16:F1:167:MET:HE2	1.99	0.45
17:F2:135:ARG:HB2	17:F2:202:ASN:HD22	1.82	0.45
21:H2:138:GLU:OE2	31:N2:19:ARG:NH1	2.50	0.45
32:O1:217:ILE:HA	32:O1:220:TYR:HD2	1.82	0.45
68:g2:163:PRO:HB2	68:g2:179:LEU:HB2	1.98	0.45
2:22:487:A:H5"	25:J2:145:PRO:HD2	1.98	0.45
2:22:959:A:N1	2:22:994:C:O2'	2.47	0.45
2:22:1230:C:O2'	2:22:1231:G:H8	2.00	0.45
3:51:114:G:H22	3:51:158:A:H61	1.65	0.45
3:51:230:U:H4'	52:Y1:100:HIS:CD2	2.51	0.45
3:51:2410:C:H5"	76:n1:25:LYS:HE2	1.98	0.45
10:C1:337:LYS:HZ2	14:E1:25:ILE:HA	1.82	0.45
13:D2:123:LEU:HD21	13:D2:154:ASP:HB2	1.98	0.45
14:E1:260:TYR:HB2	14:E1:263:LYS:HG2	1.99	0.45
15:E2:185:GLY:HA3	15:E2:224:ASN:CG	2.42	0.45
16:F1:85:PRO:HG2	16:F1:142:TYR:CD2	2.52	0.45
52:Y1:54:GLU:HA	52:Y1:69:LYS:HA	1.99	0.45
2:22:1501:U:H5"	37:Q2:37:ARG:NH1	2.29	0.45
3:51:507:G:O2'	27:L1:163:LYS:HB2	2.16	0.45
15:E2:233:LYS:HD2	15:E2:234:PRO:HD2	1.99	0.45
17:F2:174:ASP:HA	17:F2:177:ILE:HG12	1.99	0.45
27:L1:60:ARG:HD2	27:L1:67:HIS:O	2.17	0.45
30:N1:94:PHE:CE2	30:N1:96:ARG:HB2	2.52	0.45
31:N2:22:VAL:HG13	31:N2:26:LEU:HD23	1.99	0.45
52:Y1:38:LEU:HD22	52:Y1:42:TYR:HE2	1.82	0.45
81:v2:751:CYS:SG	81:v2:755:VAL:HG23	2.57	0.45
2:22:68:A:OP2	19:G2:164:LYS:NZ	2.39	0.44
2:22:99:A:H61	2:22:398:A:H1'	1.82	0.44
2:22:1412:A:H2	2:22:1434:A:H1'	1.82	0.44
2:22:1547:A:N3	2:22:1611:U:O2'	2.45	0.44
3:51:450:C:H4'	3:51:451:G:H4'	1.99	0.44
3:51:1742:C:H4'	3:51:1743:C:OP2	2.17	0.44
3:51:2125:C:H5'	3:51:2126:C:H5"	1.98	0.44
3:51:3483:U:O3'	27:L1:197:LYS:NZ	2.40	0.44
3:51:3760:A:OP1	3:51:3761:U:O2'	2.31	0.44
6:A1:101:VAL:HG22	6:A1:165:ILE:HG12	2.00	0.44
8:B1:80:GLU:OE2	8:B1:328:ASN:ND2	2.39	0.44
10:C1:232:THR:OG1	10:C1:252:ARG:NH2	2.50	0.44
11:C2:56:VAL:HG21	11:C2:79:ILE:HG23	1.98	0.44
15:E2:246:LEU:H	15:E2:246:LEU:HD22	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:h1:104:THR:HG23	69:h1:107:GLN:H	1.82	0.44
2:22:559:A:C8	65:e2:106:THR:HG21	2.52	0.44
2:22:1822:C:O2'	57:a2:95:ARG:NH2	2.50	0.44
3:51:478:G:H2'	3:51:479:G:C8	2.52	0.44
3:51:1342:C:O2'	3:51:1364:G:OP1	2.29	0.44
3:51:1548:U:H3'	3:51:1549:G:C2	2.52	0.44
3:51:1960:G:N2	3:51:1963:C:OP2	2.45	0.44
3:51:1974:A:O2'	3:51:1975:G:OP1	2.30	0.44
3:51:2212:A:O4'	60:c1:56:ARG:NH1	2.41	0.44
3:51:3864:C:H2'	3:51:3865:G:H5"	2.00	0.44
5:81:91:U:H2'	5:81:92:C:O4'	2.17	0.44
6:A1:3:ARG:HD2	6:A1:208:GLU:HG2	1.99	0.44
8:B1:338:ILE:H	8:B1:338:ILE:HG13	1.56	0.44
27:L1:113:ASN:O	27:L1:117:LEU:N	2.47	0.44
29:M1:24:LEU:HD11	29:M1:86:TRP:CG	2.53	0.44
40:S1:82:LEU:HD13	40:S1:124:ILE:HG23	1.99	0.44
52:Y1:30:MET:HB3	52:Y1:101:PRO:HG2	1.99	0.44
78:p1:47:MET:SD	78:p1:57:CYS:HB2	2.57	0.44
79:r1:70:GLY:HA3	79:r1:77:SER:HA	1.97	0.44
81:v2:830:ARG:HD2	81:v2:833:GLN:HE21	1.82	0.44
2:22:10:G:O2'	11:C2:99:GLN:OE1	2.30	0.44
2:22:1133:G:O2'	2:22:1149:G:O6	2.31	0.44
2:22:1194:U:H2'	2:22:1195:G:C8	2.52	0.44
3:51:740:A:N6	3:51:936:G:H1'	2.32	0.44
3:51:1027:A:N1	5:81:27:C:O2'	2.43	0.44
3:51:1309:G:H5'	3:51:1310:A:OP1	2.17	0.44
3:51:3649:G:N3	8:B1:252:ALA:HB1	2.33	0.44
5:81:8:A:H2'	5:81:9:G:H8	1.82	0.44
16:F1:190:HIS:O	16:F1:194:THR:OG1	2.31	0.44
22:I1:54:SER:OG	22:I1:130:ASN:O	2.36	0.44
30:N1:193:LYS:O	30:N1:197:THR:OG1	2.32	0.44
41:S2:20:ILE:HD11	41:S2:33:ILE:HD11	1.98	0.44
1:11:41:ILE:HG21	1:11:44:MET:HE3	1.99	0.44
2:22:813:U:H5"	2:22:814:U:H5'	1.99	0.44
2:22:1101:C:H5	2:22:1111:A:N6	2.16	0.44
3:51:218:G:N7	10:C1:185:LYS:HD2	2.32	0.44
3:51:712:C:O2'	3:51:713:A:H8	2.00	0.44
3:51:951:C:H2'	3:51:952:G:C8	2.52	0.44
3:51:991:G:H22	56:a1:25:HIS:CD2	2.35	0.44
3:51:1605:G:O2'	3:51:1607:G:OP2	2.29	0.44
3:51:3875:G:H22	66:f1:66:ARG:HH22	1.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A2:141:ASN:ND2	11:C2:73:PRO:HD3	2.32	0.44
8:B1:382:VAL:HG12	8:B1:386:LYS:HE2	1.99	0.44
14:E1:187:PRO:HG2	14:E1:190:LEU:HG	2.00	0.44
35:P2:63:ALA:HB2	35:P2:76:ILE:HD11	1.98	0.44
38:R1:28:GLU:HG3	38:R1:31:GLU:HB3	1.98	0.44
63:d2:21:CYS:N	63:d2:26:ASN:O	2.44	0.44
2:22:621:G:H5'	2:22:627:G:N2	2.32	0.44
2:22:642:G:N1	2:22:989:A:OP2	2.29	0.44
2:22:946:C:O2'	33:O2:138:ASP:OD1	2.36	0.44
2:22:1520:C:H41	2:22:1531:G:H1	1.65	0.44
3:51:1178:G:H1	36:Q1:89:ASP:HA	1.82	0.44
3:51:1194:A:H61	27:L1:19:GLN:NE2	2.15	0.44
3:51:1974:A:C5	50:X1:46:ARG:HD3	2.53	0.44
3:51:3072:G:H2'	3:51:3572:C:O2'	2.18	0.44
3:51:3918:G:H5"	29:M1:91:TRP:CD2	2.52	0.44
13:D2:85:GLU:OE1	13:D2:87:TYR:OH	2.26	0.44
16:F1:153:TYR:OH	16:F1:186:GLU:OE2	2.36	0.44
62:d1:44:LEU:HD13	62:d1:70:VAL:HG21	1.99	0.44
62:d1:70:VAL:HG23	62:d1:71:TRP:CD1	2.52	0.44
2:22:594:A:O2'	2:22:596:U:OP1	2.35	0.44
3:51:92:C:C2	56:a1:55:LYS:HE2	2.52	0.44
3:51:1062:G:H2'	3:51:1063:C:H2'	2.00	0.44
3:51:1918:A:H61	3:51:1931:C:H1'	1.82	0.44
3:51:3867:G:H5'	3:51:3868:G:H8	1.83	0.44
9:B2:29:ASP:OD1	9:B2:51:ARG:HG2	2.17	0.44
35:P2:93:MET:SD	35:P2:104:GLN:NE2	2.90	0.44
61:c2:30:VAL:HG12	61:c2:32:VAL:HG22	2.00	0.44
2:22:162:G:H2'	2:22:163:A:H8	1.82	0.44
2:22:1348:A:OP2	13:D2:160:SER:OG	2.24	0.44
2:22:1778:U:H2'	2:22:1779:A:C8	2.52	0.44
3:51:74:G:H5'	27:L1:59:VAL:HB	2.00	0.44
3:51:114:G:N2	3:51:158:A:H61	2.15	0.44
3:51:196:A:N1	3:51:224:G:O2'	2.41	0.44
3:51:346:A:O2'	10:C1:54:GLN:NE2	2.50	0.44
3:51:1253:G:N7	6:A1:181:LYS:HB3	2.33	0.44
3:51:3362:C:H2'	3:51:3363:G:C8	2.52	0.44
3:51:3385:U:H2'	3:51:3386:C:C6	2.53	0.44
3:51:3888:U:C4	32:O1:154:ILE:HD13	2.52	0.44
6:A1:145:LYS:HD3	6:A1:159:SER:HA	1.99	0.44
13:D2:63:GLY:O	13:D2:67:ARG:NH2	2.50	0.44
18:G1:164:ILE:O	18:G1:168:VAL:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:O1:100:HIS:O	32:O1:102:ARG:NH1	2.48	0.44
75:m1:98:LYS:HD3	75:m1:115:CYS:HB2	2.00	0.44
2:22:1366:U:OP2	45:U2:21:ARG:NH1	2.51	0.44
3:51:1692:A:OP1	22:I1:162:ARG:NH1	2.51	0.44
3:51:2034:C:OP1	50:X1:138:ARG:NH1	2.50	0.44
3:51:2775:A:H2'	3:51:2776:A:H8	1.82	0.44
9:B2:224:GLU:OE1	9:B2:227:LYS:NZ	2.38	0.44
20:H1:93:ARG:HD3	75:m1:82:LEU:HD21	2.00	0.44
27:L1:80:GLU:HG2	27:L1:110:LEU:HD12	2.00	0.44
51:X2:84:PHE:CE2	51:X2:86:PRO:HA	2.53	0.44
55:Z2:90:GLU:HG3	55:Z2:94:LYS:HE3	2.00	0.44
2:22:1437:G:H5"	37:Q2:138:ARG:HH22	1.83	0.44
3:51:915:G:H2'	3:51:916:G:C8	2.53	0.44
3:51:1391:G:N2	3:51:1392:U:O4	2.40	0.44
23:I2:8:TRP:HA	23:I2:18:ARG:HD2	1.99	0.44
30:N1:11:TRP:O	30:N1:14:LYS:NZ	2.41	0.44
35:P2:59:ARG:HB3	35:P2:76:ILE:HD13	2.00	0.44
37:Q2:58:LEU:HD11	37:Q2:112:LEU:HD11	1.99	0.44
41:S2:46:ARG:HG2	43:T2:36:ASP:HB3	2.00	0.44
43:T2:34:TRP:HZ2	43:T2:103:LYS:HG3	1.83	0.44
51:X2:84:PHE:H	51:X2:121:LYS:HA	1.82	0.44
2:22:61:A:HO2'	2:22:281:C:HO2'	1.56	0.43
2:22:1141:G:N2	2:22:1144:A:OP2	2.46	0.43
2:22:1781:A:C5	2:22:1782:A:H1'	2.53	0.43
3:51:1687:C:H2'	3:51:1688:A:C8	2.53	0.43
3:51:2170:U:H5"	38:R1:61:ALA:HB2	2.00	0.43
3:51:3097:U:H2'	3:51:3098:G:C8	2.53	0.43
12:D1:41:LYS:HG3	42:T1:93:VAL:HG11	1.99	0.43
43:T2:117:ASP:OD2	43:T2:119:SER:OG	2.30	0.43
81:v2:644:THR:OG1	81:v2:645:GLU:OE1	2.29	0.43
1:11:127:LYS:HE3	1:11:134:ILE:HG12	1.99	0.43
2:22:1469:U:H2'	2:22:1470:C:C6	2.53	0.43
3:51:74:G:O3'	27:L1:71:ARG:NH2	2.46	0.43
3:51:292:G:N2	30:N1:178:HIS:O	2.44	0.43
3:51:493:G:H5"	10:C1:272:ARG:HD3	2.01	0.43
3:51:846:C:H2'	3:51:847:G:C8	2.53	0.43
3:51:1485:C:H2'	3:51:1486:G:H8	1.82	0.43
3:51:3993:C:H2'	3:51:3994:G:N2	2.33	0.43
5:81:141:C:H2'	5:81:142:U:C6	2.53	0.43
6:A1:80:GLU:HB2	6:A1:170:ALA:HA	1.99	0.43
7:A2:52:LYS:HD2	39:R2:109:LEU:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:C2:155:TYR:OH	11:C2:161:GLY:O	2.34	0.43
17:F2:67:ILE:H	17:F2:67:ILE:HG13	1.55	0.43
17:F2:100:HIS:HB2	17:F2:107:PRO:HG3	2.00	0.43
23:I2:81:VAL:HG12	23:I2:102:LEU:HB3	2.00	0.43
28:L2:73:ARG:H	28:L2:132:GLU:HB3	1.82	0.43
36:Q1:154:LYS:NZ	36:Q1:159:PRO:O	2.51	0.43
43:T2:105:LEU:HB3	43:T2:122:ARG:NH1	2.33	0.43
46:V1:48:ARG:HB3	46:V1:51:ARG:HB3	2.00	0.43
52:Y1:57:VAL:HA	52:Y1:104:VAL:HG12	2.01	0.43
63:d2:29:GLY:O	63:d2:40:ARG:N	2.46	0.43
1:11:33:VAL:HG23	1:11:83:PRO:HD3	1.99	0.43
2:22:1637:A:OP1	61:c2:20:ARG:NH2	2.48	0.43
3:51:639:U:H5”	16:F1:74:ARG:HD2	2.01	0.43
3:51:1371:G:O2’	3:51:1372:U:OP1	2.36	0.43
3:51:3073:A:N1	80:s1:107:ILE:O	2.51	0.43
3:51:3274:C:H5”	54:Z1:60:LYS:HE2	2.01	0.43
3:51:3583:C:H2’	3:51:3584:U:C6	2.54	0.43
6:A1:200:ARG:NH2	6:A1:217:GLN:HE22	2.16	0.43
11:C2:63:SER:OG	11:C2:66:GLU:OE1	2.25	0.43
21:H2:68:GLN:O	21:H2:71:SER:OG	2.27	0.43
35:P2:52:LYS:HE3	35:P2:80:LEU:HD21	1.99	0.43
36:Q1:66:LEU:HD21	36:Q1:100:VAL:HG11	2.00	0.43
49:W2:28:ARG:HB3	49:W2:29:PRO:HD3	2.00	0.43
53:Y2:12:PHE:HA	53:Y2:23:MET:HB3	2.00	0.43
54:Z1:58:GLY:O	54:Z1:62:ILE:HG12	2.19	0.43
62:d1:30:ARG:HD3	62:d1:46:GLU:HB3	2.00	0.43
67:g1:74:VAL:HG22	67:g1:79:GLY:HA3	2.00	0.43
2:22:64:A:OP1	19:G2:136:LYS:NZ	2.45	0.43
2:22:1355:U:HO2’	2:22:1356:C:H6	1.67	0.43
3:51:1459:A:O2’	42:T1:108:ARG:NH1	2.51	0.43
3:51:1875:A:H5’	62:d1:62:ILE:O	2.18	0.43
3:51:2113:G:OP1	54:Z1:48:ARG:NH2	2.51	0.43
3:51:2202:G:H4’	3:51:2215:G:H4’	2.01	0.43
3:51:2837:G:OP2	3:51:2837:G:N2	2.40	0.43
3:51:3649:G:OP1	3:51:3684:A:N6	2.45	0.43
3:51:3782:U:O2’	3:51:3784:G:OP2	2.37	0.43
10:C1:137:LEU:HD13	79:r1:7:GLN:HE21	1.83	0.43
16:F1:239:ASN:O	16:F1:243:ARG:HG2	2.17	0.43
21:H2:60:ILE:N	21:H2:91:HIS:O	2.42	0.43
2:22:892:C:H42	2:22:973:A:H62	1.66	0.43
2:22:1221:A:H61	2:22:1477:U:H5”	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:35:U:O4	3:51:46:U:O2'	2.34	0.43
3:51:707:C:C2	3:51:709:A:H4'	2.54	0.43
3:51:849:C:H2'	3:51:850:G:C8	2.53	0.43
3:51:1392:U:H2'	3:51:1393:A:C8	2.53	0.43
3:51:3102:C:O2'	30:N1:124:ASP:OD1	2.37	0.43
3:51:3928:G:H22	29:M1:116:LYS:HE3	1.84	0.43
4:71:11:A:H4'	4:71:13:A:C8	2.52	0.43
4:71:75:G:N2	4:71:99:G:H2'	2.33	0.43
6:A1:65:ASP:OD2	6:A1:68:ARG:N	2.51	0.43
8:B1:41:ILE:HA	8:B1:187:GLY:CA	2.49	0.43
8:B1:74:GLU:OE1	8:B1:285:TYR:OH	2.17	0.43
14:E1:156:PRO:HD2	14:E1:159:ILE:HD12	2.00	0.43
15:E2:34:GLY:HA3	15:E2:83:PRO:HG2	2.01	0.43
21:H2:30:LEU:O	21:H2:34:SER:OG	2.21	0.43
34:P1:94:MET:HE1	34:P1:146:ILE:HB	2.00	0.43
52:Y1:59:ARG:HB2	52:Y1:103:LYS:HD3	2.00	0.43
81:v2:650:TRP:HZ3	81:v2:679:VAL:HG11	1.82	0.43
1:11:51:5CT:H4	3:51:3509:U:OP1	2.19	0.43
2:22:576:G:H22	2:22:597:C:H5	1.65	0.43
2:22:1074:U:H2'	2:22:1075:A:C8	2.54	0.43
3:51:421:C:H2'	3:51:422:G:H8	1.83	0.43
3:51:3043:C:N4	3:51:3643:A:O4'	2.51	0.43
3:51:3082:A:H2'	3:51:3083:G:H8	1.83	0.43
6:A1:28:LYS:HD3	6:A1:123:ARG:HE	1.84	0.43
31:N2:130:LYS:NZ	31:N2:139:TRP:O	2.33	0.43
40:S1:161:ARG:HD2	40:S1:164:LYS:HB2	2.00	0.43
48:W1:12:LYS:HE3	48:W1:12:LYS:HB2	1.89	0.43
53:Y2:103:SER:O	53:Y2:106:GLN:N	2.42	0.43
64:e1:40:GLY:O	64:e1:46:ARG:NE	2.52	0.43
81:v2:609:PHE:HB3	81:v2:613:LEU:HB3	1.99	0.43
81:v2:698:ARG:HD3	81:v2:741:MET:SD	2.59	0.43
2:22:430:A:H5"	2:22:431:G:C4	2.54	0.43
2:22:902:U:H2'	2:22:903:C:C6	2.53	0.43
2:22:1661:C:H2'	2:22:1662:C:O4'	2.18	0.43
3:51:869:G:O2'	3:51:870:A:OP1	2.37	0.43
3:51:1459:A:H5"	3:51:1460:G:H5'	2.01	0.43
3:51:1956:G:H1'	3:51:1971:G:C4	2.54	0.43
3:51:2401:G:N2	38:R1:81:ARG:O	2.37	0.43
3:51:3278:C:H2'	3:51:3279:G:H8	1.84	0.43
3:51:3643:A:O5'	3:51:3645:G:H4'	2.17	0.43
12:D1:191:ASN:HD21	12:D1:193:GLU:HB3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:D2:142:LEU:HB3	71:i2:216:TRP:CE2	2.53	0.43
14:E1:93:TYR:CD1	79:r1:116:SER:HB3	2.53	0.43
14:E1:220:VAL:HG23	14:E1:224:ARG:HB2	2.01	0.43
36:Q1:80:ALA:HB3	36:Q1:100:VAL:HG12	2.01	0.43
49:W2:24:GLN:NE2	59:b2:7:LEU:H	2.17	0.43
3:51:423:U:OP1	34:P1:34:GLN:NE2	2.52	0.43
3:51:2196:G:N2	3:51:2214:A:OP2	2.43	0.43
3:51:2414:G:P	78:p1:6:LYS:H	2.42	0.43
3:51:3099:C:H2'	3:51:3100:A:C8	2.54	0.43
3:51:3363:G:H2'	3:51:3364:A:C8	2.54	0.43
3:51:3497:U:OP2	77:o1:61:LYS:HG2	2.19	0.43
4:71:7:G:O2'	12:D1:72:ASP:OD1	2.25	0.43
10:C1:163:GLU:HA	10:C1:221:ILE:HB	1.99	0.43
15:E2:186:GLY:C	15:E2:188:ASN:H	2.27	0.43
34:P1:30:ARG:NH2	34:P1:62:ARG:HH11	2.16	0.43
41:S2:66:ARG:O	41:S2:69:THR:OG1	2.36	0.43
60:c1:48:LEU:HD21	60:c1:60:ILE:HG21	2.01	0.43
2:22:922:U:O2'	2:22:924:A:N7	2.41	0.43
2:22:1651:G:P	57:a2:92:ARG:HH22	2.42	0.43
3:51:410:G:H4'	3:51:411:G:H5'	2.00	0.43
3:51:730:C:H2'	3:51:731:C:C6	2.54	0.43
3:51:912:G:H2'	3:51:913:G:H8	1.83	0.43
3:51:1177:U:OP2	36:Q1:68:ARG:NH2	2.42	0.43
3:51:1346:G:H2'	3:51:1514:G:H5"	2.00	0.43
3:51:1369:U:P	36:Q1:143:ARG:HH12	2.41	0.43
3:51:3383:C:H2'	3:51:3384:C:C6	2.54	0.43
8:B1:50:LYS:HB2	8:B1:345:LEU:HD11	2.00	0.43
9:B2:40:ASN:H	9:B2:75:GLN:HG3	1.84	0.43
14:E1:177:THR:HG21	29:M1:107:PHE:HB2	2.01	0.43
16:F1:94:ARG:HH21	16:F1:222:THR:HA	1.84	0.43
32:O1:43:LEU:HD12	32:O1:46:ARG:HG3	2.00	0.43
64:e1:85:LEU:HD22	64:e1:111:ILE:HG23	2.01	0.43
2:22:17:C:H2'	2:22:18:C:C6	2.54	0.43
2:22:924:A:N1	2:22:1017:A:O2'	2.52	0.43
2:22:1354:C:H41	2:22:1436:C:N4	2.16	0.43
3:51:1509:A:O2'	3:51:1784:G:O3'	2.36	0.43
3:51:3430:G:H2'	3:51:3430:G:N3	2.34	0.43
7:A2:10:MET:SD	7:A2:15:VAL:HG22	2.59	0.43
8:B1:160:ILE:HB	8:B1:193:LYS:HE2	2.01	0.43
14:E1:131:LEU:HD11	14:E1:173:ILE:HG13	2.00	0.43
14:E1:230:PHE:O	14:E1:234:GLN:NE2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:J1:73:VAL:HG21	24:J1:81:ILE:HD12	2.00	0.43
38:R1:159:ALA:O	38:R1:163:ARG:HG2	2.18	0.43
44:U1:28:PRO:HB2	44:U1:34:MET:HG2	2.01	0.43
68:g2:87:LEU:HD11	68:g2:122:SER:HB3	2.00	0.43
75:m1:104:HIS:CD2	75:m1:104:HIS:H	2.37	0.43
2:22:589:C:H41	51:X2:63:ASN:ND2	2.17	0.42
2:22:1059:G:H4'	7:A2:32:PHE:CG	2.54	0.42
2:22:1706:G:H2'	2:22:1707:G:C8	2.54	0.42
3:51:181:G:H3'	3:51:182:C:H5"	2.01	0.42
3:51:238:C:H2'	3:51:239:G:C8	2.54	0.42
3:51:300:G:H5"	30:N1:98:LEU:HD13	2.01	0.42
3:51:2114:C:H2'	3:51:2115:G:H8	1.84	0.42
3:51:2144:C:H2'	3:51:2145:G:C8	2.53	0.42
3:51:3577:U:N3	80:s1:108:GLN:HA	2.34	0.42
9:B2:133:TYR:HE1	9:B2:220:LYS:HE3	1.84	0.42
10:C1:193:MET:HG2	10:C1:199:LYS:HD3	2.00	0.42
18:G1:166:LEU:HD23	30:N1:7:MET:SD	2.59	0.42
27:L1:119:GLU:O	27:L1:122:SER:OG	2.31	0.42
30:N1:28:TRP:O	30:N1:32:GLN:HG2	2.19	0.42
36:Q1:178:ARG:N	56:a1:51:GLY:HA2	2.34	0.42
51:X2:87:ASN:HB2	51:X2:90:CYS:SG	2.59	0.42
68:g2:101:PHE:CD2	68:g2:136:GLY:HA2	2.54	0.42
74:l1:39:SER:HA	80:s1:86:ILE:HG12	2.01	0.42
3:51:41:C:O2'	3:51:42:A:H5'	2.19	0.42
3:51:417:A:H2	3:51:986:A:H4'	1.84	0.42
3:51:647:C:H2'	3:51:649:C:H4'	2.00	0.42
3:51:1277:A:OP2	72:j1:4:GLY:HA3	2.19	0.42
3:51:1727:C:OP1	66:f1:15:LYS:NZ	2.52	0.42
3:51:2412:U:O2'	3:51:2414:G:N7	2.49	0.42
3:51:4012:A:H2'	3:51:4013:A:C8	2.54	0.42
10:C1:196:GLY:H	10:C1:199:LYS:NZ	2.17	0.42
23:I2:192:GLY:HA3	28:L2:19:ASN:HD22	1.84	0.42
31:N2:4:MET:HG2	31:N2:5:HIS:CD2	2.53	0.42
34:P1:67:VAL:HG23	34:P1:80:GLN:HB3	2.02	0.42
39:R2:92:ASP:OD1	39:R2:92:ASP:N	2.51	0.42
40:S1:95:ARG:NH1	40:S1:113:MET:SD	2.92	0.42
46:V1:106:VAL:HG12	46:V1:112:MET:HA	2.00	0.42
74:l1:27:ILE:HG23	74:l1:30:LYS:HE2	2.01	0.42
77:o1:3:ASN:ND2	77:o1:95:GLY:HA3	2.34	0.42
2:22:1097:C:O2'	2:22:1098:U:OP1	2.37	0.42
3:51:371:A:O2'	72:j1:45:ARG:NH1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:1507:C:H2'	3:51:1508:U:O4'	2.19	0.42
3:51:1719:G:N2	40:S1:115:ALA:HB2	2.34	0.42
3:51:2847:A:H5"	6:A1:132:ASN:ND2	2.34	0.42
10:C1:334:PRO:HB2	16:F1:49:PHE:HD1	1.84	0.42
13:D2:134:CYS:SG	13:D2:135:GLU:N	2.93	0.42
15:E2:238:LEU:HB2	15:E2:242:LYS:HD2	2.01	0.42
18:G1:73:ARG:NH2	18:G1:241:ILE:O	2.51	0.42
37:Q2:116:ASP:HB3	37:Q2:119:LEU:HD13	2.01	0.42
44:U1:66:SER:OG	44:U1:67:LYS:N	2.52	0.42
45:U2:56:MET:HB2	45:U2:86:LYS:HB3	2.01	0.42
51:X2:27:TYR:O	51:X2:31:ASN:ND2	2.34	0.42
57:a2:22:ARG:NH2	57:a2:27:ALA:O	2.52	0.42
57:a2:73:TYR:HB3	57:a2:78:ALA:HB2	2.01	0.42
59:b2:36:LYS:HB2	59:b2:43:ILE:HG22	2.02	0.42
66:f1:36:ARG:HB2	66:f1:80:ASN:HA	2.01	0.42
68:g2:192:SER:O	68:g2:213:ASP:HB3	2.19	0.42
81:v2:592:LEU:HD11	81:v2:601:ARG:HB3	2.00	0.42
2:22:51:U:H2'	2:22:52:G:C8	2.54	0.42
2:22:486:A:H5'	2:22:788:C:H1'	2.01	0.42
2:22:583:C:H41	51:X2:67:ARG:NH1	2.17	0.42
2:22:1074:U:H2'	2:22:1075:A:H8	1.84	0.42
3:51:1807:G:H8	3:51:1807:G:OP2	2.02	0.42
3:51:2268:U:H2'	3:51:2269:C:C6	2.54	0.42
3:51:3402:G:H5"	42:T1:17:ARG:HG2	2.00	0.42
3:51:4009:C:O2'	3:51:4010:U:H5'	2.20	0.42
3:51:4023:G:H2'	3:51:4024:A:H5"	2.01	0.42
4:71:38:U:N3	4:71:41:G:OP2	2.36	0.42
5:81:77:G:O2'	5:81:79:A:N6	2.51	0.42
10:C1:325:ASN:ND2	10:C1:328:ILE:HG12	2.34	0.42
12:D1:261:VAL:HG23	12:D1:263:LYS:H	1.83	0.42
25:J2:150:ARG:H	25:J2:150:ARG:HG2	1.70	0.42
52:Y1:56:GLN:NE2	52:Y1:65:GLN:O	2.52	0.42
68:g2:133:ASN:HD21	68:g2:137:VAL:HG13	1.83	0.42
68:g2:152:SER:H	68:g2:169:GLY:HA2	1.83	0.42
68:g2:164:ILE:HD11	68:g2:221:LEU:HD23	2.02	0.42
76:n1:10:MET:O	76:n1:14:LYS:HG2	2.19	0.42
80:s1:107:ILE:HG23	80:s1:109:GLN:HE21	1.84	0.42
1:11:17:SER:H	1:11:84:ASN:HD22	1.67	0.42
2:22:819:U:H2'	2:22:820:A:C8	2.54	0.42
2:22:1194:U:H2'	2:22:1195:G:H8	1.84	0.42
3:51:986:A:H2'	3:51:987:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:1006:G:O2'	3:51:1008:G:O2'	2.34	0.42
3:51:1601:A:N3	3:51:3557:C:O2'	2.46	0.42
3:51:2036:G:H2'	3:51:2037:A:C8	2.54	0.42
3:51:3584:U:H5"	8:B1:10:ARG:NH2	2.35	0.42
18:G1:181:TYR:CZ	18:G1:226:TYR:HB3	2.54	0.42
29:M1:4:LYS:HE2	29:M1:4:LYS:HB2	1.92	0.42
33:O2:149:ARG:N	57:a2:26:CYS:HB2	2.34	0.42
45:U2:54:VAL:HB	45:U2:88:LEU:HG	2.01	0.42
60:c1:47:ILE:HD12	60:c1:94:LEU:HD11	2.01	0.42
61:c2:32:VAL:HG11	61:c2:56:LEU:HD12	2.01	0.42
64:e1:70:LEU:HD21	64:e1:76:LYS:HE3	2.01	0.42
81:v2:555:GLU:HG3	81:v2:559:LYS:HE2	2.00	0.42
81:v2:728:VAL:O	81:v2:732:CYS:N	2.49	0.42
81:v2:775:GLN:HG2	81:v2:777:ALA:H	1.84	0.42
2:22:340:U:H2'	2:22:341:A:C8	2.54	0.42
2:22:794:G:N7	53:Y2:11:LYS:NZ	2.55	0.42
2:22:1403:U:H1'	2:22:1538:A:N6	2.35	0.42
2:22:1561:A:H4'	41:S2:38:ARG:CZ	2.50	0.42
3:51:499:G:H22	3:51:567:G:H1'	1.85	0.42
3:51:563:C:N4	3:51:564:G:O6	2.53	0.42
3:51:645:G:H1	3:51:711:G:H22	1.65	0.42
3:51:743:G:N3	14:E1:101:ARG:NH2	2.68	0.42
3:51:3364:A:H2'	3:51:3365:G:C8	2.55	0.42
3:51:3583:C:OP1	8:B1:11:HIS:NE2	2.52	0.42
3:51:3712:G:O2'	8:B1:14:LEU:O	2.29	0.42
3:51:3927:C:H3'	3:51:3928:G:N2	2.35	0.42
5:81:93:G:C2	72:j1:84:PRO:HG3	2.54	0.42
12:D1:53:VAL:HG11	12:D1:159:VAL:HA	2.01	0.42
12:D1:179:ARG:HA	12:D1:179:ARG:HD3	1.86	0.42
15:E2:181:CYS:HB2	15:E2:225:ILE:HG23	2.02	0.42
27:L1:4:SER:O	56:a1:44:ASN:ND2	2.42	0.42
30:N1:114:ARG:HH12	30:N1:157:LYS:HG2	1.84	0.42
30:N1:137:THR:HG22	30:N1:151:ILE:HG23	2.01	0.42
32:O1:196:TYR:CE2	32:O1:200:LYS:HD2	2.54	0.42
41:S2:84:LEU:HD12	41:S2:95:TYR:HB3	2.01	0.42
46:V1:57:VAL:HG13	46:V1:84:GLN:HG2	2.02	0.42
51:X2:134:TYR:O	65:e2:90:ARG:NH2	2.43	0.42
81:v2:586:GLU:OE1	81:v2:587:SER:N	2.53	0.42
2:22:1276:U:H3'	2:22:1277:U:H5'	2.02	0.42
2:22:1354:C:P	45:U2:83:ARG:HH12	2.42	0.42
3:51:1154:C:H2'	3:51:1155:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:1601:A:OP2	3:51:1699:A:N6	2.45	0.42
3:51:3383:C:H2'	3:51:3384:C:H6	1.85	0.42
6:A1:196:TRP:HB3	6:A1:197:PRO:HD3	2.01	0.42
8:B1:85:VAL:HB	8:B1:165:HIS:CE1	2.55	0.42
10:C1:93:GLN:NE2	80:s1:94:THR:OG1	2.41	0.42
11:C2:200:LEU:HD23	11:C2:230:ILE:HD11	2.02	0.42
15:E2:112:HIS:NE2	15:E2:237:SER:O	2.53	0.42
19:G2:127:ASN:OD1	19:G2:128:THR:N	2.51	0.42
21:H2:113:LYS:HG2	21:H2:114:GLN:H	1.85	0.42
23:I2:194:GLU:HG2	28:L2:10:TYR:CE2	2.55	0.42
39:R2:71:ILE:HB	39:R2:74:GLN:HB2	2.00	0.42
42:T1:53:PRO:HB3	42:T1:91:VAL:HG11	2.00	0.42
47:V2:33:GLN:HE21	47:V2:52:THR:HG21	1.85	0.42
51:X2:105:PHE:HE2	51:X2:115:ILE:HD12	1.83	0.42
62:d1:44:LEU:HD12	62:d1:44:LEU:HA	1.79	0.42
78:p1:89:LEU:HA	78:p1:92:GLN:HE21	1.84	0.42
81:v2:686:ALA:HB2	81:v2:726:ARG:HD2	2.01	0.42
2:22:1520:C:H5	2:22:1531:G:H1	1.68	0.42
3:51:637:G:H5"	16:F1:67:VAL:HG11	2.01	0.42
3:51:1293:G:O3'	72:j1:12:ARG:NH2	2.53	0.42
3:51:1848:A:C4	64:e1:31:ILE:HD11	2.55	0.42
3:51:3086:U:OP1	6:A1:221:LYS:NZ	2.44	0.42
3:51:3092:U:H2'	3:51:3093:A:C8	2.55	0.42
3:51:3889:A:C2	20:H1:60:TRP:HD1	2.38	0.42
3:51:4091:U:OP1	62:d1:28:HIS:ND1	2.43	0.42
12:D1:205:ALA:HB2	12:D1:236:LEU:HD12	2.01	0.42
19:G2:137:ARG:HB3	19:G2:140:ARG:HG2	2.02	0.42
34:P1:14:SER:OG	34:P1:151:THR:HG22	2.20	0.42
37:Q2:123:ASP:OD1	37:Q2:123:ASP:N	2.53	0.42
68:g2:107:ASP:OD2	68:g2:125:ARG:NH1	2.53	0.42
81:v2:660:ASN:HD21	81:v2:697:LEU:HB2	1.84	0.42
2:22:905:U:OP2	9:B2:216:LYS:NZ	2.49	0.42
2:22:1136:U:H2'	2:22:1137:G:H8	1.84	0.42
3:51:621:G:H1	3:51:938:U:H3	1.67	0.42
3:51:627:C:H2'	3:51:628:U:C6	2.54	0.42
3:51:1506:C:H2'	3:51:1507:C:C6	2.55	0.42
3:51:1564:U:H3	3:51:1730:A:H61	1.68	0.42
3:51:1838:C:H4'	79:r1:20:LYS:HB2	2.01	0.42
3:51:2121:G:O6	67:g1:75:SER:OG	2.35	0.42
3:51:2888:A:H2'	3:51:2889:A:C8	2.55	0.42
5:81:35:G:C5	69:h1:89:ARG:HD3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:D1:40:ASP:HB2	12:D1:43:LYS:HG2	2.00	0.42
20:H1:82:LYS:O	20:H1:87:GLY:N	2.47	0.42
21:H2:78:ARG:HA	21:H2:81:ARG:HG2	2.01	0.42
45:U2:28:ASN:N	45:U2:28:ASN:OD1	2.52	0.42
51:X2:97:ASN:HB3	81:v2:521:VAL:HG11	2.02	0.42
66:f1:71:TRP:HD1	66:f1:89:ARG:HH12	1.67	0.42
77:o1:12:CYS:HB3	77:o1:15:CYS:HB2	2.01	0.42
79:r1:104:ARG:HH21	79:r1:107:LEU:HD11	1.85	0.42
2:22:96:C:H2'	2:22:97:U:C6	2.55	0.42
2:22:969:C:H2'	2:22:970:A:C8	2.55	0.42
2:22:1501:U:OP2	43:T2:63:ARG:NH2	2.52	0.42
2:22:1520:C:H5	2:22:1531:G:H22	1.68	0.42
3:51:203:U:H2'	3:51:204:C:C6	2.55	0.42
3:51:449:G:H4'	3:51:453:U:H5	1.85	0.42
3:51:1127:G:OP1	3:51:1373:C:N4	2.53	0.42
3:51:1224:G:O2'	3:51:2350:A:N3	2.41	0.42
3:51:1581:G:OP1	40:S1:160:ARG:NH1	2.41	0.42
3:51:1874:C:H5'	62:d1:44:LEU:HD23	2.02	0.42
3:51:3071:A:H5"	10:C1:73:THR:OG1	2.20	0.42
3:51:3861:C:H2'	3:51:3862:G:H8	1.85	0.42
18:G1:55:VAL:HG22	50:X1:43:PRO:HA	2.00	0.42
21:H2:46:THR:HG21	21:H2:97:GLN:HG2	2.02	0.42
26:K2:9:ILE:HG22	26:K2:82:PHE:HE2	1.85	0.42
27:L1:58:VAL:HG23	27:L1:116:ARG:HD2	2.01	0.42
27:L1:135:LYS:N	27:L1:138:ASP:OD2	2.52	0.42
34:P1:84:PRO:HB2	34:P1:87:SER:HB2	2.02	0.42
2:22:42:A:O2'	2:22:98:C:OP1	2.29	0.41
2:22:95:G:H21	2:22:439:G:H5'	1.85	0.41
2:22:1165:G:H1'	11:C2:101:GLN:HG3	2.02	0.41
2:22:1706:G:H2'	2:22:1707:G:H8	1.85	0.41
2:22:1802:A:H2'	2:22:1803:G:C8	2.54	0.41
3:51:1057:G:H2'	3:51:1058:G:C8	2.55	0.41
3:51:1276:A:H2	80:s1:99:ILE:HD12	1.85	0.41
3:51:1522:U:OP1	22:I1:15:LYS:HG3	2.19	0.41
3:51:1881:G:N2	3:51:1925:G:H5"	2.34	0.41
3:51:1912:C:H2'	3:51:1913:A:C8	2.55	0.41
3:51:2205:C:OP1	38:R1:100:ARG:NE	2.53	0.41
3:51:2401:G:O2'	38:R1:82:LYS:O	2.32	0.41
3:51:2427:G:O2'	3:51:4079:A:O2'	2.32	0.41
3:51:2872:U:H2'	3:51:2873:C:C6	2.55	0.41
3:51:3429:A:C2	56:a1:43:ILE:HG23	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:3929:C:C4	29:M1:113:MET:HG3	2.55	0.41
3:51:3983:A:H1'	14:E1:163:PRO:HG3	2.02	0.41
8:B1:60:VAL:HG12	8:B1:62:ARG:HG2	2.02	0.41
8:B1:89:ILE:HG13	8:B1:201:LEU:HD21	2.01	0.41
9:B2:180:ASP:OD1	9:B2:180:ASP:N	2.42	0.41
10:C1:66:THR:HG21	10:C1:95:ALA:HB1	2.02	0.41
10:C1:289:THR:HG21	36:Q1:125:GLN:NE2	2.35	0.41
11:C2:239:PRO:HA	11:C2:242:TRP:CD2	2.55	0.41
14:E1:179:VAL:HG23	14:E1:181:ILE:HG23	2.01	0.41
16:F1:93:ILE:O	16:F1:221:LYS:HD2	2.20	0.41
16:F1:149:ARG:HG2	16:F1:189:ILE:HD13	2.02	0.41
19:G2:7:PHE:HE2	19:G2:125:THR:HG23	1.85	0.41
21:H2:7:LYS:HG2	21:H2:8:ILE:H	1.85	0.41
31:N2:15:ALA:O	59:b2:28:PRO:HG3	2.19	0.41
36:Q1:176:ARG:HA	36:Q1:180:ARG:HG3	2.02	0.41
52:Y1:100:HIS:ND1	52:Y1:102:SER:OG	2.49	0.41
68:g2:34:SER:OG	68:g2:66:VAL:O	2.37	0.41
68:g2:67:SER:N	68:g2:81:GLY:O	2.41	0.41
68:g2:253:GLY:HA3	68:g2:254:PRO:HD3	1.87	0.41
73:k1:8:ILE:HG23	73:k1:56:LEU:HD13	2.02	0.41
80:s1:107:ILE:HG22	80:s1:109:GLN:HG3	2.02	0.41
81:v2:505:VAL:HG21	81:v2:550:GLY:HA2	2.02	0.41
81:v2:512:LYS:HB3	81:v2:568:ILE:HD11	2.01	0.41
81:v2:857:LYS:HB2	81:v2:857:LYS:HE2	1.84	0.41
2:22:61:A:O2'	2:22:281:C:O2'	2.31	0.41
2:22:344:U:OP1	23:I2:56:ARG:NH1	2.53	0.41
2:22:831:A:C4	2:22:877:G:H1'	2.54	0.41
2:22:1097:C:H2'	2:22:1098:U:C2	2.56	0.41
2:22:1422:C:O2'	39:R2:67:ARG:NH1	2.53	0.41
2:22:1506:G:H2'	2:22:1507:U:C6	2.56	0.41
3:51:30:C:H5'	30:N1:95:ALA:HB3	2.02	0.41
3:51:228:G:OP1	52:Y1:11:ARG:NH1	2.45	0.41
3:51:421:C:H2'	3:51:422:G:C8	2.55	0.41
3:51:1181:C:H2'	3:51:1182:G:C8	2.55	0.41
3:51:1948:U:O2'	3:51:2011:G:N1	2.53	0.41
3:51:2914:C:O2'	6:A1:220:GLY:O	2.37	0.41
3:51:2949:A:O2'	3:51:2950:A:H3'	2.21	0.41
13:D2:205:PRO:HA	39:R2:42:PRO:HB2	2.02	0.41
21:H2:73:GLN:HB3	21:H2:135:TYR:CZ	2.55	0.41
29:M1:25:VAL:HB	29:M1:38:VAL:HB	2.02	0.41
33:O2:108:PRO:HD2	57:a2:42:ARG:HH21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:S1:93:MET:HE1	40:S1:117:HIS:CE1	2.55	0.41
68:g2:5:MET:HE2	68:g2:312:VAL:HG12	2.01	0.41
72:j1:21:ARG:NH1	72:j1:41:ALA:O	2.46	0.41
78:p1:47:MET:HE2	78:p1:71:TYR:CE1	2.55	0.41
2:22:605:A:H2'	2:22:606:A:C8	2.55	0.41
3:51:318:A:H1'	3:51:2891:A:C8	2.48	0.41
3:51:661:G:H1'	3:51:698:A:C4	2.55	0.41
3:51:1862:G:C8	34:P1:27:LYS:HB2	2.55	0.41
3:51:2118:G:N3	3:51:2192:C:O2'	2.46	0.41
3:51:2297:G:O2'	3:51:2300:G:N1	2.53	0.41
3:51:2313:C:H2'	3:51:2314:G:C8	2.55	0.41
3:51:2807:A:O2'	72:j1:2:THR:OG1	2.37	0.41
3:51:3303:A:H2'	3:51:3304:G:C8	2.55	0.41
3:51:3598:A:H5"	75:m1:95:ILE:HD12	2.01	0.41
3:51:3771:U:H3	3:51:3776:A:H61	1.68	0.41
4:71:94:C:OP1	40:S1:46:TYR:OH	2.23	0.41
20:H1:41:ILE:HG22	20:H1:43:VAL:HG13	2.03	0.41
26:K2:11:ILE:HD13	26:K2:45:VAL:HA	2.02	0.41
30:N1:135:ILE:HD12	30:N1:151:ILE:HD13	2.01	0.41
36:Q1:144:LYS:HE3	36:Q1:144:LYS:HB3	1.95	0.41
56:a1:24:LYS:HD2	56:a1:24:LYS:H	1.85	0.41
61:c2:31:ARG:HA	61:c2:43:ILE:HA	2.03	0.41
2:22:465:A:H3'	2:22:466:C:C6	2.56	0.41
3:51:1548:U:O2'	3:51:1549:G:H5'	2.20	0.41
3:51:1601:A:H2'	3:51:1602:A:C8	2.56	0.41
3:51:1687:C:H2'	3:51:1688:A:H8	1.86	0.41
3:51:3278:C:H2'	3:51:3279:G:C8	2.55	0.41
3:51:3311:A:H2'	3:51:3312:G:C8	2.56	0.41
3:51:3333:U:OP2	42:T1:4:THR:OG1	2.35	0.41
3:51:3618:U:O2'	3:51:3619:G:H5'	2.20	0.41
5:81:140:C:H2'	5:81:141:C:C6	2.55	0.41
10:C1:223:LYS:HG2	10:C1:226:ARG:NH1	2.35	0.41
11:C2:84:LEU:O	11:C2:88:LEU:HB2	2.20	0.41
18:G1:138:ALA:HB2	18:G1:194:VAL:HG11	2.02	0.41
24:J1:22:ASN:HB3	24:J1:128:ASP:HB3	2.02	0.41
30:N1:158:HIS:HB3	30:N1:161:MET:HG2	2.02	0.41
31:N2:17:PRO:HG3	59:b2:28:PRO:HG2	2.02	0.41
61:c2:34:PHE:HZ	61:c2:61:SER:HB3	1.86	0.41
73:k1:32:VAL:HG11	73:k1:53:ALA:HB2	2.02	0.41
2:22:67:C:N4	19:G2:164:LYS:H	2.18	0.41
2:22:111:A:H2'	2:22:112:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:647:U:O2'	49:W2:4:MET:SD	2.70	0.41
2:22:1660:G:H2'	2:22:1661:C:O4'	2.21	0.41
3:51:151:G:OP2	30:N1:4:TYR:OH	2.26	0.41
3:51:302:C:OP2	30:N1:68:ARG:NH2	2.41	0.41
3:51:1003:C:OP1	36:Q1:20:SER:OG	2.22	0.41
3:51:1390:G:N3	3:51:3339:A:H2'	2.36	0.41
3:51:2773:A:H2'	3:51:2774:G:H8	1.85	0.41
3:51:3697:U:H4'	3:51:3698:G:OP2	2.21	0.41
3:51:4046:U:H2'	3:51:4047:U:O4'	2.21	0.41
5:81:59:G:O6	5:81:95:C:O2'	2.33	0.41
11:C2:67:ILE:HG23	11:C2:72:LEU:HB2	2.03	0.41
12:D1:37:VAL:HG12	12:D1:50:ARG:HD3	2.02	0.41
16:F1:84:GLU:HB2	42:T1:135:PRO:HB3	2.03	0.41
29:M1:62:ILE:HB	29:M1:76:ALA:HB1	2.03	0.41
35:P2:95:GLY:HA2	35:P2:104:GLN:HA	2.02	0.41
53:Y2:111:LYS:HE2	53:Y2:111:LYS:HB3	1.96	0.41
64:e1:100:ALA:O	64:e1:108:ARG:NH1	2.53	0.41
68:g2:37:ASP:OD1	68:g2:39:SER:OG	2.35	0.41
2:22:16:G:H2'	2:22:17:C:C6	2.56	0.41
2:22:43:U:OP2	2:22:450:A:N6	2.54	0.41
2:22:206:A:H4'	2:22:306:A:O4'	2.21	0.41
2:22:883:G:C6	49:W2:28:ARG:HG3	2.55	0.41
2:22:971:A:O2'	31:N2:114:ARG:HG2	2.19	0.41
2:22:1412:A:N6	2:22:1435:U:OP2	2.53	0.41
2:22:1508:G:O2'	2:22:1516:C:O2	2.26	0.41
3:51:68:U:O2'	3:51:100:G:O2'	2.24	0.41
3:51:439:U:H2'	3:51:440:G:C8	2.56	0.41
3:51:2231:G:C8	3:51:2232:G:H2'	2.56	0.41
3:51:4047:U:OP2	8:B1:385:LYS:NZ	2.49	0.41
4:71:23:A:H2'	4:71:24:A:C8	2.56	0.41
5:81:11:G:H21	34:P1:120:ASN:ND2	2.18	0.41
5:81:93:G:O2'	72:j1:82:THR:O	2.26	0.41
7:A2:31:ASP:OD1	7:A2:32:PHE:N	2.54	0.41
15:E2:100:ARG:NH2	15:E2:121:TYR:O	2.54	0.41
16:F1:228:GLY:HA3	40:S1:2:LYS:HD2	2.02	0.41
23:I2:23:LYS:HE2	23:I2:23:LYS:HB3	1.85	0.41
30:N1:108:ARG:HB2	30:N1:161:MET:HE1	2.02	0.41
32:O1:136:ILE:HD12	32:O1:188:ARG:CZ	2.50	0.41
34:P1:14:SER:O	34:P1:105:LYS:NZ	2.39	0.41
63:d2:33:LYS:HE2	63:d2:34:TYR:CZ	2.56	0.41
80:s1:78:ASP:C	80:s1:80:PRO:HD3	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:v2:801:ARG:O	81:v2:806:GLY:N	2.54	0.41
1:11:85:ILE:H	1:11:85:ILE:HG13	1.78	0.41
2:22:809:A:OP1	15:E2:108:ARG:NH2	2.54	0.41
2:22:1123:U:OP2	51:X2:4:CYS:HB3	2.21	0.41
3:51:1025:C:OP2	3:51:1026:G:O2'	2.24	0.41
3:51:1269:A:H5"	3:51:2377:U:H5"	2.02	0.41
3:51:1272:U:O2'	34:P1:135:ARG:NH2	2.34	0.41
3:51:3333:U:H2'	3:51:3334:G:H8	1.86	0.41
4:71:66:G:H5'	12:D1:10:LYS:HG3	2.03	0.41
9:B2:222:LYS:NZ	9:B2:224:GLU:OE2	2.48	0.41
11:C2:197:LYS:HG2	11:C2:201:MET:HE2	2.03	0.41
18:G1:209:PRO:HA	18:G1:212:LYS:HG3	2.03	0.41
20:H1:4:ILE:HG12	20:H1:61:TRP:CH2	2.56	0.41
33:O2:96:LYS:HD2	33:O2:132:VAL:HG11	2.02	0.41
48:W1:8:PHE:HZ	48:W1:49:ILE:HG13	1.85	0.41
51:X2:22:TRP:HE3	51:X2:28:LYS:HG3	1.86	0.41
60:c1:21:VAL:HG23	60:c1:99:PRO:HA	2.03	0.41
62:d1:70:VAL:HG23	62:d1:71:TRP:HD1	1.86	0.41
2:22:89:C:H2'	2:22:90:G:C8	2.54	0.41
2:22:398:A:H5"	23:I2:22:HIS:HB3	2.02	0.41
2:22:1754:U:H2'	2:22:1755:C:C6	2.56	0.41
3:51:28:C:OP1	30:N1:190:ALA:HB2	2.20	0.41
3:51:491:C:H2'	3:51:492:G:C8	2.56	0.41
3:51:1300:G:H2'	3:51:1319:A:H62	1.85	0.41
3:51:1368:C:H4'	36:Q1:143:ARG:NH2	2.34	0.41
3:51:1459:A:N3	42:T1:130:ARG:NH2	2.58	0.41
3:51:3446:U:H2'	3:51:3447:G:C8	2.56	0.41
3:51:3883:U:H6	3:51:3883:U:H2'	1.73	0.41
8:B1:83:PRO:O	8:B1:167:GLN:NE2	2.54	0.41
10:C1:5:MET:HE2	10:C1:5:MET:HA	2.02	0.41
16:F1:60:ARG:O	16:F1:64:ARG:HG2	2.21	0.41
17:F2:77:MET:HE1	17:F2:151:TRP:CD1	2.56	0.41
21:H2:109:ARG:HH11	21:H2:113:LYS:HD3	1.86	0.41
25:J2:109:ARG:NH1	25:J2:111:GLN:HE21	2.16	0.41
40:S1:159:LEU:HD22	40:S1:172:PRO:HG3	2.02	0.41
46:V1:21:PRO:HA	46:V1:54:ALA:HA	2.03	0.41
2:22:5:U:H2'	2:22:6:G:C8	2.56	0.41
2:22:283:C:OP2	19:G2:183:ARG:NH1	2.54	0.41
2:22:619:A:OP2	2:22:620:A:O2'	2.34	0.41
2:22:832:A:H62	2:22:878:A:H5'	1.86	0.41
2:22:1090:C:H2'	2:22:1091:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:1098:U:H2'	2:22:1099:U:C6	2.56	0.41
3:51:286:U:H2'	3:51:287:G:C8	2.56	0.41
3:51:439:U:H2'	3:51:440:G:H8	1.86	0.41
3:51:610:C:H2'	3:51:611:G:C8	2.51	0.41
3:51:970:U:H2'	3:51:971:C:C6	2.56	0.41
3:51:1798:G:H4'	10:C1:246:PRO:HB2	2.02	0.41
3:51:1905:A:O2'	72:j1:12:ARG:O	2.28	0.41
3:51:2034:C:OP2	50:X1:122:LYS:NZ	2.50	0.41
3:51:2212:A:N7	60:c1:78:ASN:ND2	2.65	0.41
3:51:3582:U:H1'	8:B1:252:ALA:HB3	2.02	0.41
3:51:3692:G:H5'	8:B1:20:LYS:HB3	2.02	0.41
3:51:3850:C:H2'	3:51:3851:G:C8	2.54	0.41
3:51:3853:U:H4'	3:51:4011:A:H1'	2.02	0.41
4:71:74:A:H8	4:71:74:A:OP1	2.04	0.41
4:71:112:C:H2'	4:71:113:G:H8	1.83	0.41
9:B2:35:ALA:HB2	9:B2:44:LEU:HD23	2.02	0.41
15:E2:183:VAL:HG11	15:E2:188:ASN:HB2	2.02	0.41
16:F1:87:LEU:HD11	16:F1:120:PHE:HB3	2.03	0.41
20:H1:43:VAL:HG12	20:H1:59:LYS:HD3	2.02	0.41
21:H2:8:ILE:HD13	21:H2:16:PRO:HG3	2.02	0.41
21:H2:84:GLU:HG3	21:H2:92:VAL:HG12	2.03	0.41
22:I1:33:ILE:HB	22:I1:69:ARG:NH1	2.36	0.41
24:J1:30:ASP:HA	24:J1:33:THR:HG22	2.02	0.41
31:N2:131:THR:OG1	31:N2:132:ARG:NH2	2.54	0.41
33:O2:149:ARG:H	57:a2:26:CYS:HB2	1.85	0.41
35:P2:68:PRO:HD2	35:P2:71:GLU:HB3	2.02	0.41
36:Q1:155:ALA:HB3	36:Q1:158:THR:HG23	2.03	0.41
37:Q2:131:LYS:HB2	37:Q2:140:ARG:HH12	1.85	0.41
40:S1:1:MET:HE3	40:S1:3:ALA:HB2	2.02	0.41
52:Y1:83:GLU:HG3	52:Y1:84:ARG:HG3	2.03	0.41
53:Y2:8:ARG:HB2	53:Y2:26:ASP:HB2	2.03	0.41
56:a1:104:VAL:HG23	56:a1:126:ALA:HA	2.02	0.41
68:g2:195:LEU:HA	68:g2:211:GLY:HA3	2.01	0.41
78:p1:38:THR:HA	78:p1:45:THR:HA	2.03	0.41
81:v2:827:ASN:O	81:v2:827:ASN:ND2	2.53	0.41
1:11:15:ALA:HB3	77:o1:63:THR:HA	2.03	0.41
2:22:60:A:N3	2:22:282:G:O2'	2.50	0.41
3:51:222:G:H4'	3:51:224:G:C8	2.56	0.41
3:51:310:G:H2'	3:51:311:G:H8	1.87	0.41
3:51:496:C:H2'	3:51:497:G:H8	1.84	0.41
3:51:958:C:OP1	5:81:6:U:O2'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:1354:C:O2'	3:51:3318:C:OP1	2.31	0.41
3:51:1610:G:O2'	40:S1:117:HIS:NE2	2.50	0.41
3:51:2287:C:H2'	3:51:2288:G:H8	1.86	0.41
9:B2:149:GLN:HE21	9:B2:151:ARG:HB2	1.86	0.41
11:C2:218:THR:HG22	11:C2:221:ASN:H	1.86	0.41
57:a2:42:ARG:HE	57:a2:67:LEU:HD12	1.86	0.41
69:h1:82:ASP:OD1	69:h1:82:ASP:N	2.48	0.41
2:22:787:C:C2	25:J2:144:ILE:HG13	2.56	0.40
2:22:1283:G:H1'	2:22:1284:G:P	2.61	0.40
2:22:1625:U:H2'	2:22:1626:C:C6	2.55	0.40
3:51:404:U:H1'	3:51:409:A:H61	1.86	0.40
3:51:417:A:N6	5:81:15:G:H1'	2.35	0.40
3:51:726:G:OP1	16:F1:144:ASN:ND2	2.49	0.40
3:51:1162:C:H2'	3:51:1163:G:C8	2.56	0.40
3:51:2037:A:H5"	73:k1:42:LEU:HD22	2.03	0.40
3:51:2148:A:H2'	3:51:2149:G:C8	2.56	0.40
3:51:3889:A:O2'	20:H1:43:VAL:O	2.33	0.40
3:51:3940:A:H2'	3:51:3941:C:H3'	2.02	0.40
4:71:46:C:OP1	12:D1:158:LYS:N	2.44	0.40
5:81:18:C:H2'	5:81:19:A:C8	2.56	0.40
7:A2:141:ASN:HD22	11:C2:73:PRO:HD3	1.86	0.40
10:C1:330:MET:HE2	10:C1:337:LYS:HB2	2.03	0.40
13:D2:17:PHE:HE2	13:D2:39:VAL:HG11	1.86	0.40
13:D2:169:ASP:OD1	13:D2:169:ASP:N	2.51	0.40
18:G1:137:ARG:HG3	18:G1:146:LEU:HD21	2.02	0.40
33:O2:86:LYS:NZ	33:O2:122:SER:O	2.53	0.40
34:P1:148:MET:HE2	34:P1:150:LEU:HD11	2.03	0.40
37:Q2:25:CYS:HB2	37:Q2:91:SER:HB2	2.02	0.40
39:R2:20:TYR:CD1	39:R2:38:ILE:HD12	2.56	0.40
41:S2:13:LEU:HD11	41:S2:57:GLY:HA2	2.03	0.40
52:Y1:89:LYS:HG2	52:Y1:90:ALA:H	1.86	0.40
60:c1:45:LEU:HD23	60:c1:96:ILE:HD12	2.02	0.40
2:22:371:U:H4'	2:22:372:A:C2	2.56	0.40
2:22:1493:U:O2'	17:F2:80:ARG:NH2	2.54	0.40
3:51:102:G:OP1	27:L1:71:ARG:NE	2.50	0.40
3:51:449:G:H4'	3:51:453:U:C5	2.57	0.40
3:51:452:G:H2'	3:51:452:G:N3	2.36	0.40
3:51:1024:G:N2	3:51:1024:G:OP2	2.55	0.40
3:51:1183:C:H2'	3:51:1184:G:C8	2.56	0.40
3:51:1337:C:H2'	3:51:1338:C:C6	2.55	0.40
3:51:1436:U:H2'	3:51:1437:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:1558:G:O2'	64:e1:58:ILE:O	2.40	0.40
3:51:3563:U:H2'	3:51:3564:U:O4'	2.20	0.40
3:51:3917:C:OP1	29:M1:90:SER:OG	2.31	0.40
3:51:3959:G:N3	3:51:3959:G:H2'	2.36	0.40
4:71:52:C:O2'	4:71:53:G:H5'	2.21	0.40
5:81:35:G:O2'	5:81:102:A:N1	2.49	0.40
5:81:89:C:H2'	5:81:90:A:C8	2.56	0.40
21:H2:63:PHE:CE1	21:H2:95:ILE:HD11	2.55	0.40
21:H2:127:ASP:O	21:H2:131:GLU:HG2	2.20	0.40
31:N2:37:ILE:HG12	31:N2:54:LEU:HD11	2.03	0.40
31:N2:108:ASP:OD1	31:N2:108:ASP:N	2.52	0.40
33:O2:151:LEU:H	33:O2:151:LEU:HD23	1.86	0.40
37:Q2:47:LEU:HB3	37:Q2:81:VAL:HG11	2.02	0.40
38:R1:13:SER:OG	38:R1:38:ARG:NH1	2.51	0.40
41:S2:132:ARG:HB2	41:S2:134:GLN:NE2	2.37	0.40
43:T2:43:HIS:NE2	43:T2:44:LYS:HE2	2.37	0.40
64:e1:35:TRP:CE2	64:e1:56:PRO:HD2	2.57	0.40
68:g2:87:LEU:HD21	68:g2:108:VAL:HG11	2.02	0.40
68:g2:165:ILE:HG23	68:g2:179:LEU:HD11	2.04	0.40
79:r1:20:LYS:HG2	79:r1:25:VAL:HG22	2.03	0.40
3:51:254:C:H2'	3:51:255:G:H8	1.86	0.40
3:51:384:A:N3	3:51:386:G:H5"	2.36	0.40
3:51:1688:A:H2'	3:51:1689:A:C8	2.57	0.40
3:51:2823:C:H2'	3:51:2824:G:C8	2.57	0.40
3:51:2865:C:H2'	3:51:2911:A:H61	1.87	0.40
3:51:3415:U:OP1	77:o1:9:ARG:HD3	2.21	0.40
5:81:45:G:O2'	5:81:60:A:N1	2.41	0.40
7:A2:69:GLU:HB2	11:C2:256:THR:HG21	2.03	0.40
15:E2:180:LEU:HG	15:E2:232:ASN:HA	2.02	0.40
18:G1:170:LEU:HD23	18:G1:170:LEU:HA	1.96	0.40
25:J2:91:LYS:HD2	25:J2:96:TYR:CZ	2.57	0.40
25:J2:109:ARG:HH12	25:J2:111:GLN:NE2	2.17	0.40
29:M1:20:HIS:CD2	29:M1:45:VAL:HG22	2.57	0.40
30:N1:96:ARG:HH12	30:N1:104:GLU:HB2	1.86	0.40
32:O1:38:ASP:OD2	32:O1:65:ARG:NH2	2.31	0.40
34:P1:40:HIS:HE2	34:P1:111:SER:HA	1.85	0.40
53:Y2:43:LYS:HE3	53:Y2:43:LYS:HB2	1.88	0.40
68:g2:207:CYS:HB3	68:g2:221:LEU:HD11	2.03	0.40
69:h1:10:ARG:HH12	69:h1:63:GLN:HE21	1.69	0.40
81:v2:641:TRP:CD1	81:v2:641:TRP:H	2.38	0.40
2:22:325:A:C2	2:22:327:C:H2'	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:620:A:H4'	2:22:621:G:H3'	2.03	0.40
2:22:910:U:H2'	2:22:911:G:H8	1.86	0.40
2:22:1136:U:H2'	2:22:1137:G:C8	2.56	0.40
2:22:1185:A:H2'	2:22:1186:G:O4'	2.22	0.40
2:22:1287:G:H2'	2:22:1287:G:N3	2.37	0.40
2:22:1336:C:H2'	2:22:1337:G:O4'	2.21	0.40
2:22:1571:G:OP2	35:P2:39:ALA:N	2.55	0.40
3:51:63:G:O2'	3:51:76:A:N3	2.48	0.40
3:51:1387:U:H4'	42:T1:100:LYS:HB2	2.04	0.40
3:51:1956:G:H1'	3:51:1971:G:C5	2.56	0.40
3:51:2040:C:H2'	3:51:2041:C:C6	2.56	0.40
3:51:2229:U:H2'	3:51:2230:U:C6	2.57	0.40
3:51:2294:G:O6	54:Z1:51:ARG:NH2	2.55	0.40
8:B1:77:THR:HG21	8:B1:337:VAL:HG22	2.04	0.40
8:B1:292:HIS:O	8:B1:299:VAL:HG22	2.22	0.40
9:B2:71:LEU:HG	9:B2:78:GLU:HB2	2.04	0.40
13:D2:48:ILE:HB	13:D2:86:LEU:HG	2.04	0.40
14:E1:28:TYR:HB3	14:E1:32:ALA:HB3	2.02	0.40
15:E2:45:ILE:HG13	15:E2:61:VAL:HG21	2.03	0.40
19:G2:85:ARG:HB3	19:G2:87:ARG:HH12	1.85	0.40
21:H2:163:GLN:O	21:H2:167:GLU:N	2.54	0.40
23:I2:165:GLN:HE22	23:I2:195:LEU:HD11	1.87	0.40
39:R2:95:ILE:HD11	39:R2:118:GLN:HB2	2.04	0.40
40:S1:127:MET:HA	42:T1:153:PRO:HD2	2.04	0.40
46:V1:48:ARG:HB3	46:V1:51:ARG:CB	2.52	0.40
56:a1:146:LEU:HD13	70:i1:7:MET:HG2	2.03	0.40
64:e1:101:HIS:HA	64:e1:108:ARG:HH12	1.87	0.40
68:g2:201:SER:O	68:g2:203:ASP:N	2.50	0.40
68:g2:300:ALA:HB3	68:g2:310:TRP:HZ3	1.86	0.40
1:11:124:ILE:HG12	1:11:150:LEU:HD13	2.03	0.40
2:22:28:U:H2'	2:22:29:G:C8	2.54	0.40
2:22:465:A:H5'	2:22:466:C:H5	1.87	0.40
2:22:1346:C:H5"	13:D2:158:ILE:HD13	2.03	0.40
2:22:1399:U:O2	2:22:1401:C:N4	2.53	0.40
2:22:1575:G:N1	2:22:1578:A:OP2	2.54	0.40
2:22:1605:A:N1	2:22:1633:A:H5"	2.36	0.40
2:22:1822:C:C2	57:a2:5:ARG:HG2	2.56	0.40
3:51:640:G:C6	16:F1:71:ARG:HD3	2.57	0.40
3:51:873:G:O2'	12:D1:286:SER:OG	2.27	0.40
3:51:1435:C:H2'	3:51:1436:U:C6	2.56	0.40
3:51:1485:C:H2'	3:51:1486:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:51:3021:A:H5"	34:P1:83:TRP:O	2.21	0.40
7:A2:119:PRO:HG2	7:A2:142:ILE:HD13	2.04	0.40
8:B1:86:ILE:HD12	8:B1:200:LYS:HB3	2.04	0.40
15:E2:220:THR:OG1	15:E2:221:ARG:N	2.54	0.40
23:I2:66:SER:HA	23:I2:73:THR:HA	2.04	0.40
25:J2:111:GLN:OE1	25:J2:127:ARG:HB2	2.22	0.40
46:V1:89:ARG:HB2	46:V1:95:PHE:CE2	2.57	0.40
57:a2:19:GLN:HA	57:a2:20:PRO:HD3	1.91	0.40
61:c2:32:VAL:N	61:c2:42:ILE:O	2.54	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	11	131/154 (85%)	123 (94%)	8 (6%)	0	100	100
6	A1	243/257 (95%)	233 (96%)	10 (4%)	0	100	100
7	A2	206/306 (67%)	202 (98%)	4 (2%)	0	100	100
8	B1	392/403 (97%)	378 (96%)	14 (4%)	0	100	100
9	B2	211/264 (80%)	203 (96%)	8 (4%)	0	100	100
10	C1	349/401 (87%)	339 (97%)	10 (3%)	0	100	100
11	C2	213/281 (76%)	211 (99%)	2 (1%)	0	100	100
12	D1	287/296 (97%)	283 (99%)	4 (1%)	0	100	100
13	D2	221/246 (90%)	214 (97%)	7 (3%)	0	100	100
14	E1	206/258 (80%)	202 (98%)	4 (2%)	0	100	100
15	E2	256/263 (97%)	242 (94%)	14 (6%)	0	100	100
16	F1	225/246 (92%)	217 (96%)	8 (4%)	0	100	100
17	F2	178/203 (88%)	170 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	G1	206/266 (77%)	205 (100%)	1 (0%)	0	100	100
19	G2	220/249 (88%)	217 (99%)	3 (1%)	0	100	100
20	H1	188/192 (98%)	184 (98%)	4 (2%)	0	100	100
21	H2	184/194 (95%)	170 (92%)	14 (8%)	0	100	100
22	I1	198/215 (92%)	192 (97%)	6 (3%)	0	100	100
23	I2	194/208 (93%)	190 (98%)	4 (2%)	0	100	100
24	J1	165/177 (93%)	163 (99%)	2 (1%)	0	100	100
25	J2	178/194 (92%)	175 (98%)	3 (2%)	0	100	100
26	K2	91/165 (55%)	86 (94%)	5 (6%)	0	100	100
27	L1	197/211 (93%)	191 (97%)	6 (3%)	0	100	100
28	L2	136/158 (86%)	132 (97%)	4 (3%)	0	100	100
29	M1	132/138 (96%)	130 (98%)	2 (2%)	0	100	100
30	N1	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
31	N2	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
32	O1	197/231 (85%)	194 (98%)	3 (2%)	0	100	100
33	O2	131/151 (87%)	125 (95%)	6 (5%)	0	100	100
34	P1	150/184 (82%)	144 (96%)	6 (4%)	0	100	100
35	P2	114/145 (79%)	114 (100%)	0	0	100	100
36	Q1	178/188 (95%)	171 (96%)	7 (4%)	0	100	100
37	Q2	132/146 (90%)	129 (98%)	3 (2%)	0	100	100
38	R1	164/197 (83%)	164 (100%)	0	0	100	100
39	R2	130/135 (96%)	129 (99%)	1 (1%)	0	100	100
40	S1	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
41	S2	134/152 (88%)	129 (96%)	5 (4%)	0	100	100
42	T1	155/160 (97%)	149 (96%)	6 (4%)	0	100	100
43	T2	135/146 (92%)	130 (96%)	5 (4%)	0	100	100
44	U1	95/128 (74%)	89 (94%)	6 (6%)	0	100	100
45	U2	81/119 (68%)	80 (99%)	1 (1%)	0	100	100
46	V1	127/140 (91%)	124 (98%)	3 (2%)	0	100	100
47	V2	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
48	W1	58/155 (37%)	58 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	W2	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
50	X1	117/155 (76%)	115 (98%)	2 (2%)	0	100	100
51	X2	137/143 (96%)	131 (96%)	6 (4%)	0	100	100
52	Y1	123/145 (85%)	122 (99%)	1 (1%)	0	100	100
53	Y2	121/132 (92%)	112 (93%)	9 (7%)	0	100	100
54	Z1	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
55	Z2	65/125 (52%)	64 (98%)	1 (2%)	0	100	100
56	a1	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
57	a2	96/115 (84%)	93 (97%)	3 (3%)	0	100	100
58	b1	61/75 (81%)	57 (93%)	4 (7%)	0	100	100
59	b2	79/84 (94%)	76 (96%)	3 (4%)	0	100	100
60	c1	92/116 (79%)	91 (99%)	1 (1%)	0	100	100
61	c2	57/69 (83%)	55 (96%)	2 (4%)	0	100	100
62	d1	104/125 (83%)	98 (94%)	6 (6%)	0	100	100
63	d2	53/86 (62%)	53 (100%)	0	0	100	100
64	e1	124/135 (92%)	123 (99%)	1 (1%)	0	100	100
65	e2	47/133 (35%)	46 (98%)	1 (2%)	0	100	100
66	f1	105/110 (96%)	104 (99%)	1 (1%)	0	100	100
67	g1	102/117 (87%)	99 (97%)	3 (3%)	0	100	100
68	g2	308/317 (97%)	287 (93%)	21 (7%)	0	100	100
69	h1	118/123 (96%)	115 (98%)	3 (2%)	0	100	100
70	i1	96/105 (91%)	96 (100%)	0	0	100	100
71	i2	47/378 (12%)	44 (94%)	3 (6%)	0	100	100
72	j1	84/97 (87%)	82 (98%)	2 (2%)	0	100	100
73	k1	66/70 (94%)	66 (100%)	0	0	100	100
74	l1	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
75	m1	48/128 (38%)	48 (100%)	0	0	100	100
76	n1	22/25 (88%)	22 (100%)	0	0	100	100
77	o1	100/106 (94%)	98 (98%)	2 (2%)	0	100	100
78	p1	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
79	r1	116/137 (85%)	115 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
80	s1	27/113 (24%)	24 (89%)	3 (11%)	0	100	100
81	v2	358/858 (42%)	339 (95%)	19 (5%)	0	100	100
All	All	11206/13815 (81%)	10880 (97%)	326 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	11	114/129 (88%)	112 (98%)	2 (2%)	51	73
6	A1	187/198 (94%)	187 (100%)	0	100	100
7	A2	175/252 (69%)	175 (100%)	0	100	100
8	B1	341/348 (98%)	338 (99%)	3 (1%)	70	85
9	B2	194/229 (85%)	192 (99%)	2 (1%)	68	84
10	C1	296/334 (89%)	294 (99%)	2 (1%)	76	88
11	C2	180/218 (83%)	180 (100%)	0	100	100
12	D1	243/248 (98%)	242 (100%)	1 (0%)	84	92
13	D2	186/204 (91%)	184 (99%)	2 (1%)	65	82
14	E1	192/230 (84%)	189 (98%)	3 (2%)	55	76
15	E2	221/225 (98%)	221 (100%)	0	100	100
16	F1	196/213 (92%)	196 (100%)	0	100	100
17	F2	154/171 (90%)	153 (99%)	1 (1%)	78	89
18	G1	182/223 (82%)	182 (100%)	0	100	100
19	G2	196/221 (89%)	196 (100%)	0	100	100
20	H1	170/172 (99%)	169 (99%)	1 (1%)	78	89
21	H2	165/174 (95%)	160 (97%)	5 (3%)	36	58
22	I1	174/181 (96%)	173 (99%)	1 (1%)	78	89
23	I2	171/178 (96%)	170 (99%)	1 (1%)	78	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
24	J1	140/149 (94%)	138 (99%)	2 (1%)	59 79
25	J2	160/168 (95%)	160 (100%)	0	100 100
26	K2	84/136 (62%)	83 (99%)	1 (1%)	63 81
27	L1	169/179 (94%)	167 (99%)	2 (1%)	63 81
28	L2	126/141 (89%)	126 (100%)	0	100 100
29	M1	115/118 (98%)	115 (100%)	0	100 100
30	N1	172/173 (99%)	172 (100%)	0	100 100
31	N2	130/131 (99%)	129 (99%)	1 (1%)	73 86
32	O1	171/194 (88%)	170 (99%)	1 (1%)	78 89
33	O2	104/119 (87%)	104 (100%)	0	100 100
34	P1	133/163 (82%)	132 (99%)	1 (1%)	73 86
35	P2	104/129 (81%)	103 (99%)	1 (1%)	68 84
36	Q1	157/163 (96%)	157 (100%)	0	100 100
37	Q2	109/119 (92%)	106 (97%)	3 (3%)	38 60
38	R1	147/175 (84%)	147 (100%)	0	100 100
39	R2	118/121 (98%)	118 (100%)	0	100 100
40	S1	155/155 (100%)	154 (99%)	1 (1%)	78 89
41	S2	118/132 (89%)	116 (98%)	2 (2%)	53 74
42	T1	137/139 (99%)	137 (100%)	0	100 100
43	T2	110/118 (93%)	110 (100%)	0	100 100
44	U1	88/117 (75%)	88 (100%)	0	100 100
45	U2	78/106 (74%)	76 (97%)	2 (3%)	40 63
46	V1	100/107 (94%)	100 (100%)	0	100 100
47	V2	69/69 (100%)	69 (100%)	0	100 100
48	W1	52/126 (41%)	51 (98%)	1 (2%)	50 71
49	W2	112/113 (99%)	111 (99%)	1 (1%)	70 85
50	X1	108/136 (79%)	108 (100%)	0	100 100
51	X2	110/114 (96%)	107 (97%)	3 (3%)	39 62
52	Y1	117/135 (87%)	115 (98%)	2 (2%)	53 74
53	Y2	107/114 (94%)	107 (100%)	0	100 100
54	Z1	116/117 (99%)	116 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	Z2	59/105 (56%)	59 (100%)	0	100	100
56	a1	120/121 (99%)	119 (99%)	1 (1%)	73	86
57	a2	85/99 (86%)	83 (98%)	2 (2%)	43	65
58	b1	56/62 (90%)	55 (98%)	1 (2%)	51	73
59	b2	73/76 (96%)	73 (100%)	0	100	100
60	c1	79/98 (81%)	78 (99%)	1 (1%)	61	80
61	c2	52/61 (85%)	51 (98%)	1 (2%)	50	71
62	d1	97/110 (88%)	96 (99%)	1 (1%)	68	84
63	d2	48/77 (62%)	48 (100%)	0	100	100
64	e1	114/121 (94%)	113 (99%)	1 (1%)	70	85
65	e2	42/113 (37%)	41 (98%)	1 (2%)	43	65
66	f1	87/89 (98%)	87 (100%)	0	100	100
67	g1	90/100 (90%)	88 (98%)	2 (2%)	45	67
68	g2	270/276 (98%)	268 (99%)	2 (1%)	76	88
69	h1	107/109 (98%)	106 (99%)	1 (1%)	70	85
70	i1	85/89 (96%)	84 (99%)	1 (1%)	63	81
71	i2	44/327 (14%)	44 (100%)	0	100	100
72	j1	73/80 (91%)	73 (100%)	0	100	100
73	k1	64/66 (97%)	62 (97%)	2 (3%)	35	57
74	l1	47/48 (98%)	47 (100%)	0	100	100
75	m1	46/116 (40%)	46 (100%)	0	100	100
76	n1	23/24 (96%)	23 (100%)	0	100	100
77	o1	90/94 (96%)	90 (100%)	0	100	100
78	p1	74/75 (99%)	73 (99%)	1 (1%)	59	79
79	r1	103/119 (87%)	101 (98%)	2 (2%)	50	71
80	s1	27/96 (28%)	27 (100%)	0	100	100
81	v2	307/735 (42%)	300 (98%)	7 (2%)	44	66
All	All	9815/11810 (83%)	9740 (99%)	75 (1%)	70	86

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	11	80	MET

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Mol	Chain	Res	Type
1	11	135	LEU
8	B1	338	ILE
8	B1	346	THR
8	B1	353	VAL
9	B2	127	VAL
9	B2	225	LEU
10	C1	69	GLU
10	C1	325	ASN
12	D1	93	THR
13	D2	72	VAL
13	D2	115	VAL
14	E1	84	VAL
14	E1	153	VAL
14	E1	220	VAL
17	F2	67	ILE
20	H1	104	VAL
21	H2	72	PHE
21	H2	82	GLU
21	H2	92	VAL
21	H2	133	LEU
21	H2	166	VAL
22	I1	191	ILE
23	I2	102	LEU
24	J1	72	THR
24	J1	167	GLN
26	K2	89	ILE
27	L1	67	HIS
27	L1	160	VAL
31	N2	63	VAL
32	O1	157	LEU
34	P1	24	VAL
35	P2	47	ARG
37	Q2	18	THR
37	Q2	72	VAL
37	Q2	100	VAL
40	S1	82	LEU
41	S2	26	ILE
41	S2	131	VAL
45	U2	65	THR
45	U2	68	THR
48	W1	3	VAL
49	W2	105	THR

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Mol	Chain	Res	Type
51	X2	82	THR
51	X2	105	PHE
51	X2	125	VAL
52	Y1	58	VAL
52	Y1	79	VAL
56	a1	56	VAL
57	a2	40	VAL
57	a2	83	VAL
58	b1	35	VAL
60	c1	104	ILE
61	c2	32	VAL
62	d1	84	VAL
64	e1	58	ILE
65	e2	95	LYS
67	g1	32	TYR
67	g1	73	HIS
68	g2	64	HIS
68	g2	137	VAL
69	h1	19	LYS
70	i1	44	ILE
73	k1	23	VAL
73	k1	32	VAL
78	p1	52	VAL
79	r1	24	GLN
79	r1	45	ILE
81	v2	552	LEU
81	v2	577	VAL
81	v2	582	THR
81	v2	665	VAL
81	v2	728	VAL
81	v2	756	VAL
81	v2	782	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (213) such sidechains are listed below:

Mol	Chain	Res	Type
1	11	29	ASN
1	11	58	HIS
1	11	91	GLN
6	A1	8	GLN
6	A1	22	HIS
6	A1	132	ASN

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Mol	Chain	Res	Type
6	A1	217	GLN
7	A2	132	GLN
7	A2	141	ASN
8	B1	55	HIS
8	B1	138	GLN
8	B1	167	GLN
8	B1	184	GLN
8	B1	354	GLN
9	B2	40	ASN
9	B2	43	ASN
9	B2	95	ASN
9	B2	124	HIS
9	B2	158	HIS
9	B2	159	GLN
9	B2	160	GLN
9	B2	163	GLN
9	B2	186	ASN
10	C1	54	GLN
10	C1	290	ASN
10	C1	325	ASN
10	C1	346	GLN
11	C2	122	HIS
11	C2	158	ASN
11	C2	164	HIS
11	C2	258	HIS
12	D1	175	HIS
12	D1	191	ASN
12	D1	198	HIS
12	D1	225	GLN
12	D1	229	ASN
12	D1	282	GLN
12	D1	291	GLN
13	D2	145	GLN
13	D2	179	GLN
14	E1	14	HIS
14	E1	244	GLN
15	E2	36	HIS
15	E2	188	ASN
15	E2	197	ASN
16	F1	22	GLN
16	F1	61	GLN
16	F1	163	GLN

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Mol	Chain	Res	Type
16	F1	219	ASN
16	F1	246	ASN
17	F2	100	HIS
17	F2	109	GLN
17	F2	117	ASN
18	G1	38	ASN
18	G1	66	GLN
18	G1	90	GLN
18	G1	149	ASN
19	G2	13	GLN
19	G2	81	HIS
19	G2	110	ASN
19	G2	197	GLN
19	G2	200	GLN
19	G2	202	ASN
20	H1	106	GLN
21	H2	162	GLN
22	I1	59	GLN
22	I1	97	ASN
22	I1	130	ASN
22	I1	166	HIS
23	I2	64	ASN
23	I2	84	ASN
23	I2	165	GLN
23	I2	168	GLN
23	I2	181	GLN
24	J1	9	ASN
24	J1	41	GLN
24	J1	64	ASN
24	J1	70	HIS
25	J2	111	GLN
25	J2	140	GLN
26	K2	28	HIS
26	K2	44	HIS
26	K2	66	HIS
27	L1	19	GLN
27	L1	115	GLN
28	L2	5	GLN
28	L2	11	GLN
28	L2	18	GLN
28	L2	19	ASN
28	L2	85	GLN

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Mol	Chain	Res	Type
29	M1	8	GLN
29	M1	20	HIS
29	M1	33	GLN
29	M1	66	HIS
30	N1	86	ASN
30	N1	181	HIS
31	N2	13	GLN
31	N2	69	ASN
31	N2	90	HIS
32	O1	33	GLN
32	O1	42	HIS
32	O1	74	ASN
32	O1	208	GLN
33	O2	113	GLN
34	P1	75	GLN
34	P1	97	ASN
34	P1	137	ASN
35	P2	24	GLN
35	P2	32	GLN
36	Q1	8	ASN
36	Q1	93	HIS
36	Q1	160	HIS
37	Q2	48	GLN
37	Q2	80	GLN
37	Q2	86	GLN
37	Q2	97	GLN
37	Q2	114	GLN
38	R1	34	ASN
39	R2	93	GLN
40	S1	66	GLN
40	S1	108	GLN
40	S1	122	HIS
40	S1	162	GLN
40	S1	163	HIS
41	S2	76	GLN
41	S2	87	GLN
41	S2	125	HIS
42	T1	112	ASN
42	T1	134	GLN
43	T2	11	ASN
43	T2	52	ASN
43	T2	138	GLN

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Mol	Chain	Res	Type
44	U1	94	ASN
44	U1	105	ASN
45	U2	81	GLN
46	V1	77	HIS
46	V1	84	GLN
47	V2	49	GLN
48	W1	17	HIS
49	W2	24	GLN
49	W2	56	HIS
49	W2	82	GLN
49	W2	113	HIS
50	X1	93	ASN
50	X1	106	HIS
50	X1	110	GLN
50	X1	124	ASN
51	X2	63	ASN
51	X2	110	HIS
51	X2	127	ASN
52	Y1	14	ASN
52	Y1	18	HIS
52	Y1	20	ASN
52	Y1	61	HIS
52	Y1	65	GLN
53	Y2	106	GLN
54	Z1	78	ASN
55	Z2	64	ASN
56	a1	40	HIS
56	a1	89	ASN
56	a1	120	GLN
57	a2	8	ASN
58	b1	50	ASN
58	b1	60	ASN
59	b2	26	GLN
60	c1	19	GLN
60	c1	33	GLN
62	d1	16	ASN
62	d1	32	HIS
62	d1	77	ASN
63	d2	45	GLN
64	e1	23	HIS
64	e1	34	ASN
64	e1	68	HIS

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Mol	Chain	Res	Type
65	e2	99	GLN
65	e2	114	GLN
65	e2	116	ASN
66	f1	21	GLN
68	g2	20	GLN
68	g2	56	GLN
68	g2	133	ASN
68	g2	143	GLN
68	g2	285	GLN
69	h1	63	GLN
69	h1	68	ASN
69	h1	98	HIS
70	i1	15	HIS
70	i1	26	HIS
70	i1	80	HIS
72	j1	76	ASN
74	l1	25	GLN
75	m1	84	GLN
75	m1	109	ASN
76	n1	22	GLN
77	o1	3	ASN
77	o1	25	GLN
77	o1	102	GLN
78	p1	56	HIS
79	r1	7	GLN
79	r1	22	ASN
79	r1	71	GLN
79	r1	96	HIS
80	s1	85	GLN
80	s1	89	GLN
81	v2	535	GLN
81	v2	553	HIS
81	v2	660	ASN
81	v2	684	GLN
81	v2	705	HIS
81	v2	710	HIS
81	v2	715	HIS
81	v2	737	GLN
81	v2	769	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	22	1477/1826 (80%)	245 (16%)	14 (0%)
3	51	3216/4115 (78%)	512 (15%)	34 (1%)
4	71	118/120 (98%)	10 (8%)	0
5	81	144/156 (92%)	19 (13%)	1 (0%)
All	All	4955/6217 (79%)	786 (15%)	49 (0%)

All (786) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	22	2	A
2	22	3	C
2	22	4	C
2	22	25	A
2	22	33	G
2	22	41	G
2	22	44	U
2	22	46	A
2	22	56	G
2	22	65	C
2	22	67	C
2	22	68	A
2	22	71	G
2	22	103	A
2	22	111	A
2	22	113	G
2	22	117	C
2	22	139	C
2	22	140	U
2	22	152	G
2	22	160	U
2	22	165	C
2	22	205	C
2	22	255	G
2	22	260	U
2	22	276	C
2	22	278	G
2	22	280	U
2	22	285	C
2	22	306	A
2	22	307	C
2	22	312	G
2	22	325	A
2	22	329	A

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Mol	Chain	Res	Type
2	22	335	G
2	22	347	U
2	22	350	G
2	22	351	C
2	22	365	C
2	22	374	C
2	22	403	G
2	22	413	A
2	22	415	C
2	22	429	A
2	22	430	A
2	22	431	G
2	22	435	G
2	22	436	G
2	22	437	C
2	22	438	A
2	22	447	G
2	22	452	U
2	22	457	C
2	22	458	A
2	22	465	A
2	22	473	A
2	22	482	C
2	22	490	A
2	22	495	U
2	22	524	G
2	22	525	A
2	22	532	A
2	22	548	A
2	22	553	G
2	22	555	A
2	22	556	U
2	22	558	U
2	22	569	A
2	22	571	G
2	22	572	U
2	22	573	C
2	22	579	C
2	22	591	G
2	22	592	U
2	22	593	A
2	22	594	A

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Mol	Chain	Res	Type
2	22	596	U
2	22	608	A
2	22	609	G
2	22	624	G
2	22	625	C
2	22	633	A
2	22	634	A
2	22	636	A
2	22	637	A
2	22	638	G
2	22	652	C
2	22	764	U
2	22	774	A
2	22	784	G
2	22	785	U
2	22	793	A
2	22	797	C
2	22	804	C
2	22	806	U
2	22	809	A
2	22	831	A
2	22	832	A
2	22	834	A
2	22	840	C
2	22	875	A
2	22	882	A
2	22	884	A
2	22	892	C
2	22	895	G
2	22	931	U
2	22	932	G
2	22	933	G
2	22	940	G
2	22	952	A
2	22	954	A
2	22	961	G
2	22	964	U
2	22	979	U
2	22	985	A
2	22	989	A
2	22	1007	U
2	22	1011	A

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Mol	Chain	Res	Type
2	22	1022	A
2	22	1023	U
2	22	1024	A
2	22	1026	C
2	22	1042	A
2	22	1045	A
2	22	1047	C
2	22	1070	G
2	22	1071	C
2	22	1098	U
2	22	1101	C
2	22	1110	A
2	22	1111	A
2	22	1115	C
2	22	1116	U
2	22	1117	U
2	22	1128	G
2	22	1132	A
2	22	1150	A
2	22	1157	A
2	22	1169	G
2	22	1170	A
2	22	1177	C
2	22	1178	C
2	22	1189	G
2	22	1202	A
2	22	1203	A
2	22	1204	U
2	22	1209	C
2	22	1213	A
2	22	1215	A
2	22	1216	C
2	22	1218	G
2	22	1219	G
2	22	1221	A
2	22	1222	A
2	22	1231	G
2	22	1236	G
2	22	1237	G
2	22	1252	G
2	22	1257	A
2	22	1276	U

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Mol	Chain	Res	Type
2	22	1277	U
2	22	1279	U
2	22	1282	G
2	22	1283	G
2	22	1284	G
2	22	1286	G
2	22	1287	G
2	22	1288	U
2	22	1289	G
2	22	1293	C
2	22	1304	U
2	22	1333	U
2	22	1340	A
2	22	1355	U
2	22	1356	C
2	22	1358	A
2	22	1359	U
2	22	1363	A
2	22	1367	A
2	22	1373	G
2	22	1375	G
2	22	1376	A
2	22	1386	G
2	22	1396	A
2	22	1399	U
2	22	1412	A
2	22	1420	U
2	22	1421	U
2	22	1422	C
2	22	1435	U
2	22	1436	C
2	22	1437	G
2	22	1447	A
2	22	1448	G
2	22	1452	U
2	22	1455	G
2	22	1456	A
2	22	1465	G
2	22	1468	G
2	22	1477	U
2	22	1479	C
2	22	1480	A

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Mol	Chain	Res	Type
2	22	1482	G
2	22	1491	A
2	22	1493	U
2	22	1494	G
2	22	1502	C
2	22	1533	G
2	22	1537	A
2	22	1538	A
2	22	1545	G
2	22	1546	A
2	22	1553	U
2	22	1554	U
2	22	1557	U
2	22	1558	G
2	22	1559	A
2	22	1561	A
2	22	1579	U
2	22	1581	A
2	22	1606	G
2	22	1623	G
2	22	1641	C
2	22	1645	C
2	22	1653	A
2	22	1654	C
2	22	1657	A
2	22	1673	A
2	22	1679	U
2	22	1680	G
2	22	1687	U
2	22	1705	C
2	22	1706	G
2	22	1761	U
2	22	1765	U
2	22	1783	G
2	22	1786	G
2	22	1788	A
2	22	1795	U
2	22	1806	G
2	22	1808	A
2	22	1818	G
2	22	1819	G
2	22	1820	A

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Mol	Chain	Res	Type
2	22	1822	C
3	51	2	C
3	51	3	A
3	51	21	G
3	51	25	A
3	51	33	A
3	51	39	A
3	51	42	A
3	51	48	C
3	51	49	U
3	51	59	A
3	51	64	A
3	51	65	A
3	51	66	A
3	51	71	C
3	51	72	C
3	51	76	A
3	51	91	G
3	51	109	G
3	51	119	G
3	51	140	G
3	51	159	C
3	51	170	A
3	51	173	C
3	51	179	G
3	51	181	G
3	51	182	C
3	51	199	U
3	51	200	C
3	51	208	U
3	51	209	C
3	51	215	C
3	51	216	C
3	51	217	A
3	51	218	G
3	51	219	C
3	51	232	U
3	51	234	A
3	51	244	C
3	51	245	G
3	51	263	A
3	51	265	C

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Mol	Chain	Res	Type
3	51	270	C
3	51	271	U
3	51	279	G
3	51	296	U
3	51	305	A
3	51	308	C
3	51	315	U
3	51	333	A
3	51	339	C
3	51	340	G
3	51	353	U
3	51	360	C
3	51	361	A
3	51	362	A
3	51	385	A
3	51	386	G
3	51	409	A
3	51	449	G
3	51	451	G
3	51	452	G
3	51	454	C
3	51	455	C
3	51	464	G
3	51	467	U
3	51	486	C
3	51	487	C
3	51	495	C
3	51	496	C
3	51	502	A
3	51	506	G
3	51	507	G
3	51	508	C
3	51	565	C
3	51	566	G
3	51	568	C
3	51	572	G
3	51	575	G
3	51	576	G
3	51	584	G
3	51	595	G
3	51	596	C
3	51	597	A

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Mol	Chain	Res	Type
3	51	603	U
3	51	606	G
3	51	607	C
3	51	613	U
3	51	615	C
3	51	618	C
3	51	640	G
3	51	641	G
3	51	644	A
3	51	648	C
3	51	649	C
3	51	653	G
3	51	657	C
3	51	659	G
3	51	660	G
3	51	694	U
3	51	696	A
3	51	698	A
3	51	703	C
3	51	705	C
3	51	707	C
3	51	708	C
3	51	709	A
3	51	712	C
3	51	713	A
3	51	715	C
3	51	716	A
3	51	722	C
3	51	728	C
3	51	729	G
3	51	730	C
3	51	732	C
3	51	739	G
3	51	740	A
3	51	743	G
3	51	759	C
3	51	764	U
3	51	830	A
3	51	834	G
3	51	840	C
3	51	870	A
3	51	879	A

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Mol	Chain	Res	Type
3	51	905	C
3	51	906	G
3	51	908	G
3	51	914	A
3	51	918	C
3	51	920	C
3	51	921	G
3	51	922	C
3	51	924	G
3	51	926	A
3	51	927	G
3	51	930	G
3	51	937	G
3	51	938	U
3	51	940	C
3	51	947	A
3	51	949	G
3	51	950	U
3	51	955	G
3	51	956	U
3	51	957	C
3	51	979	A
3	51	1007	A
3	51	1012	G
3	51	1013	A
3	51	1041	A
3	51	1048	G
3	51	1051	A
3	51	1062	G
3	51	1063	C
3	51	1064	C
3	51	1065	C
3	51	1070	U
3	51	1087	G
3	51	1129	G
3	51	1132	C
3	51	1133	G
3	51	1152	C
3	51	1153	C
3	51	1157	C
3	51	1158	C
3	51	1159	C

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Mol	Chain	Res	Type
3	51	1161	U
3	51	1165	G
3	51	1173	A
3	51	1174	G
3	51	1178	G
3	51	1194	A
3	51	1199	A
3	51	1210	A
3	51	1223	A
3	51	1230	A
3	51	1241	A
3	51	1254	U
3	51	1267	U
3	51	1272	U
3	51	1288	G
3	51	1289	A
3	51	1300	G
3	51	1307	A
3	51	1309	G
3	51	1310	A
3	51	1314	A
3	51	1316	C
3	51	1330	G
3	51	1337	C
3	51	1352	C
3	51	1353	U
3	51	1354	C
3	51	1355	A
3	51	1372	U
3	51	1373	C
3	51	1375	G
3	51	1398	G
3	51	1399	A
3	51	1407	G
3	51	1434	C
3	51	1435	C
3	51	1444	A
3	51	1445	A
3	51	1461	A
3	51	1472	G
3	51	1478	U
3	51	1480	G

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Mol	Chain	Res	Type
3	51	1490	G
3	51	1494	A
3	51	1499	G
3	51	1503	A
3	51	1504	C
3	51	1505	G
3	51	1514	G
3	51	1528	G
3	51	1529	C
3	51	1549	G
3	51	1550	A
3	51	1556	A
3	51	1577	U
3	51	1578	G
3	51	1579	C
3	51	1580	C
3	51	1581	G
3	51	1584	G
3	51	1590	C
3	51	1591	A
3	51	1599	G
3	51	1600	A
3	51	1607	G
3	51	1619	A
3	51	1620	G
3	51	1681	C
3	51	1684	A
3	51	1685	A
3	51	1705	G
3	51	1707	U
3	51	1711	G
3	51	1714	G
3	51	1715	G
3	51	1721	C
3	51	1728	A
3	51	1729	U
3	51	1743	C
3	51	1744	G
3	51	1767	C
3	51	1769	A
3	51	1790	C
3	51	1801	G

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Mol	Chain	Res	Type
3	51	1802	G
3	51	1807	G
3	51	1814	C
3	51	1817	G
3	51	1832	G
3	51	1834	G
3	51	1849	G
3	51	1851	U
3	51	1852	C
3	51	1861	A
3	51	1868	A
3	51	1896	A
3	51	1897	A
3	51	1898	G
3	51	1911	C
3	51	1918	A
3	51	1922	G
3	51	1926	U
3	51	1949	A
3	51	1951	G
3	51	1954	A
3	51	1969	U
3	51	1970	C
3	51	1971	G
3	51	1972	G
3	51	1974	A
3	51	1975	G
3	51	2003	G
3	51	2004	G
3	51	2006	C
3	51	2012	A
3	51	2014	A
3	51	2015	G
3	51	2044	A
3	51	2055	C
3	51	2056	G
3	51	2110	A
3	51	2120	C
3	51	2123	G
3	51	2124	A
3	51	2125	C
3	51	2155	G

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Mol	Chain	Res	Type
3	51	2164	C
3	51	2175	G
3	51	2189	C
3	51	2190	G
3	51	2191	C
3	51	2207	C
3	51	2212	A
3	51	2213	G
3	51	2224	G
3	51	2225	C
3	51	2232	G
3	51	2233	A
3	51	2234	A
3	51	2241	G
3	51	2250	G
3	51	2252	G
3	51	2259	G
3	51	2264	G
3	51	2280	G
3	51	2281	A
3	51	2300	G
3	51	2306	C
3	51	2307	U
3	51	2308	C
3	51	2325	A
3	51	2326	U
3	51	2332	C
3	51	2351	A
3	51	2352	C
3	51	2364	U
3	51	2365	G
3	51	2373	A
3	51	2393	G
3	51	2408	A
3	51	2415	G
3	51	2440	G
3	51	2769	A
3	51	2779	G
3	51	2783	C
3	51	2791	G
3	51	2800	A
3	51	2809	U

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Mol	Chain	Res	Type
3	51	2811	A
3	51	2813	A
3	51	2827	A
3	51	2845	U
3	51	2861	C
3	51	2874	U
3	51	2876	A
3	51	2913	A
3	51	2941	G
3	51	2942	G
3	51	2951	U
3	51	2976	G
3	51	2977	C
3	51	2979	U
3	51	2982	A
3	51	2983	U
3	51	2984	G
3	51	3005	U
3	51	3042	A
3	51	3043	C
3	51	3044	G
3	51	3046	G
3	51	3052	C
3	51	3062	G
3	51	3066	A
3	51	3070	A
3	51	3071	A
3	51	3072	G
3	51	3073	A
3	51	3080	U
3	51	3087	G
3	51	3204	U
3	51	3214	G
3	51	3247	C
3	51	3248	U
3	51	3255	A
3	51	3287	C
3	51	3288	U
3	51	3295	A
3	51	3296	C
3	51	3308	G
3	51	3309	G

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Mol	Chain	Res	Type
3	51	3316	G
3	51	3328	A
3	51	3347	G
3	51	3354	U
3	51	3358	A
3	51	3374	G
3	51	3379	G
3	51	3393	A
3	51	3398	A
3	51	3405	A
3	51	3406	A
3	51	3413	C
3	51	3416	G
3	51	3429	A
3	51	3430	G
3	51	3431	U
3	51	3455	G
3	51	3457	C
3	51	3462	C
3	51	3476	U
3	51	3479	U
3	51	3502	G
3	51	3503	A
3	51	3504	A
3	51	3507	G
3	51	3512	C
3	51	3516	G
3	51	3519	A
3	51	3546	C
3	51	3547	A
3	51	3549	A
3	51	3551	C
3	51	3563	U
3	51	3569	C
3	51	3573	G
3	51	3574	A
3	51	3577	U
3	51	3578	C
3	51	3589	A
3	51	3590	U
3	51	3601	C
3	51	3619	G

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Mol	Chain	Res	Type
3	51	3625	U
3	51	3626	U
3	51	3632	A
3	51	3637	U
3	51	3638	A
3	51	3643	A
3	51	3644	C
3	51	3645	G
3	51	3649	G
3	51	3650	C
3	51	3653	G
3	51	3674	G
3	51	3685	C
3	51	3692	G
3	51	3697	U
3	51	3698	G
3	51	3699	U
3	51	3714	A
3	51	3715	A
3	51	3725	G
3	51	3726	U
3	51	3761	U
3	51	3762	G
3	51	3781	A
3	51	3795	C
3	51	3796	C
3	51	3797	A
3	51	3825	A
3	51	3833	A
3	51	3834	U
3	51	3845	C
3	51	3865	G
3	51	3866	C
3	51	3867	G
3	51	3868	G
3	51	3875	G
3	51	3876	G
3	51	3879	G
3	51	3882	C
3	51	3883	U
3	51	3884	C
3	51	3886	G

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Mol	Chain	Res	Type
3	51	3890	G
3	51	3912	G
3	51	3918	G
3	51	3919	G
3	51	3920	G
3	51	3922	A
3	51	3923	G
3	51	3930	U
3	51	3931	C
3	51	3936	C
3	51	3938	G
3	51	3942	C
3	51	3943	G
3	51	3945	A
3	51	3947	C
3	51	3948	G
3	51	3956	A
3	51	3958	G
3	51	3964	C
3	51	3965	G
3	51	3968	U
3	51	3970	U
3	51	3971	C
3	51	3973	C
3	51	3980	C
3	51	3982	C
3	51	3988	A
3	51	3989	C
3	51	3994	G
3	51	4000	A
3	51	4001	A
3	51	4002	C
3	51	4003	C
3	51	4006	G
3	51	4010	U
3	51	4011	A
3	51	4021	U
3	51	4024	A
3	51	4030	U
3	51	4034	U
3	51	4035	C
3	51	4036	U

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Mol	Chain	Res	Type
3	51	4039	G
3	51	4059	A
3	51	4062	G
3	51	4079	A
3	51	4086	G
3	51	4095	C
3	51	4098	U
3	51	4099	U
3	51	4100	G
4	71	7	G
4	71	22	A
4	71	23	A
4	71	33	U
4	71	53	G
4	71	63	C
4	71	64	G
4	71	74	A
4	71	100	A
4	71	110	G
5	81	2	A
5	81	22	C
5	81	33	U
5	81	34	C
5	81	37	U
5	81	58	A
5	81	62	U
5	81	71	A
5	81	74	G
5	81	78	G
5	81	79	A
5	81	80	C
5	81	93	G
5	81	102	A
5	81	104	C
5	81	114	G
5	81	147	G
5	81	150	G
5	81	156	U

All (49) RNA pucker outliers are listed below:

Continued on next page...

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Mol	Chain	Res	Type
2	22	110	U
2	22	430	A
2	22	1097	C
2	22	1110	A
2	22	1215	A
2	22	1221	A
2	22	1256	G
2	22	1275	A
2	22	1283	G
2	22	1357	C
2	22	1447	A
2	22	1481	C
2	22	1552	G
2	22	1560	U
3	51	218	G
3	51	244	C
3	51	384	A
3	51	450	C
3	51	454	C
3	51	595	G
3	51	704	C
3	51	731	C
3	51	869	G
3	51	920	C
3	51	1064	C
3	51	1086	C
3	51	1131	G
3	51	1151	G
3	51	1309	G
3	51	1371	G
3	51	1434	C
3	51	1548	U
3	51	1680	G
3	51	1727	C
3	51	1742	C
3	51	1974	A
3	51	2232	G
3	51	2306	C
3	51	2875	G
3	51	3697	U
3	51	3724	A

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Mol	Chain	Res	Type
3	51	3725	G
3	51	3824	U
3	51	3865	G
3	51	3866	C
3	51	3946	G
3	51	3970	U
3	51	3972	U
5	81	77	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	5CT	11	51	1	13,14,15	0.70	0	8,15,17	1.15	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5CT	11	51	1	-	8/13/14/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	11	51	5CT	NZ-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
1	11	51	5CT	NZ-C1-C2-O1
1	11	51	5CT	C-CA-CB-CG
1	11	51	5CT	CD-CE-NZ-C1
1	11	51	5CT	CA-CB-CG-CD
1	11	51	5CT	CG-CD-CE-NZ
1	11	51	5CT	O1-C2-C3-C4
1	11	51	5CT	C1-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	11	51	5CT	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 141 ligands modelled in this entry, 141 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
2	22	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	22	1268:U	O3’	1269:U	P	4.01

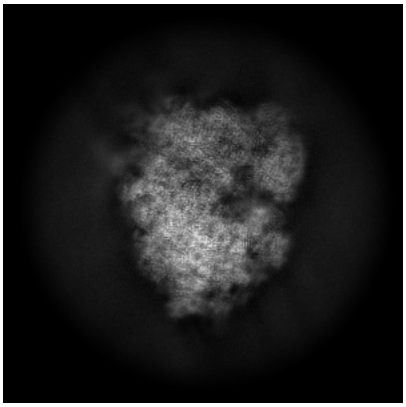
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13113. These allow visual inspection of the internal detail of the map and identification of artifacts.

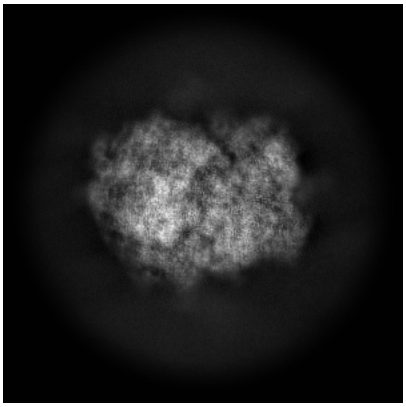
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

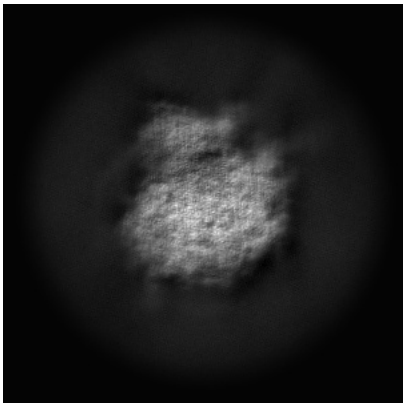
6.1.1 Primary map



X



Y

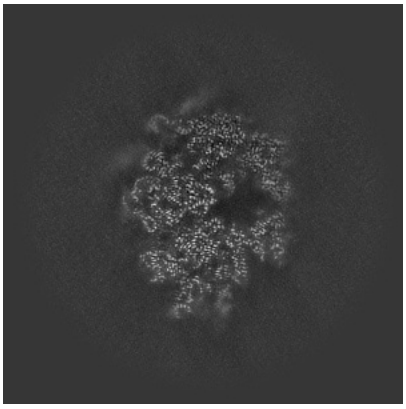


Z

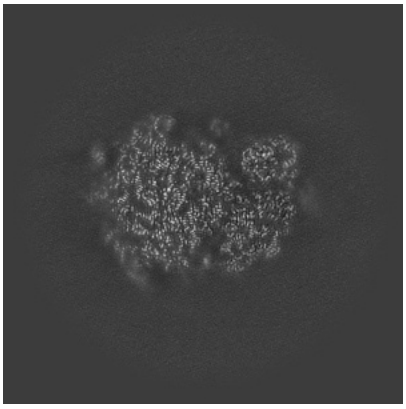
The images above show the map projected in three orthogonal directions.

6.2 Central slices

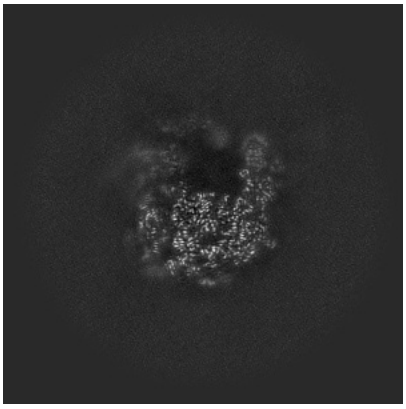
6.2.1 Primary map



X Index: 240



Y Index: 240

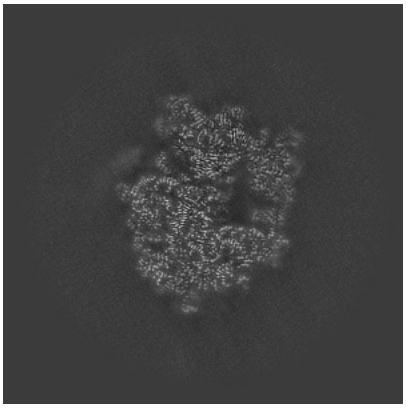


Z Index: 240

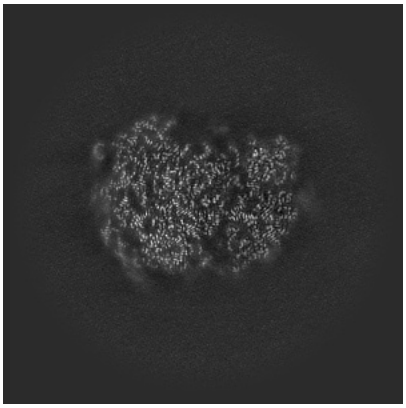
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

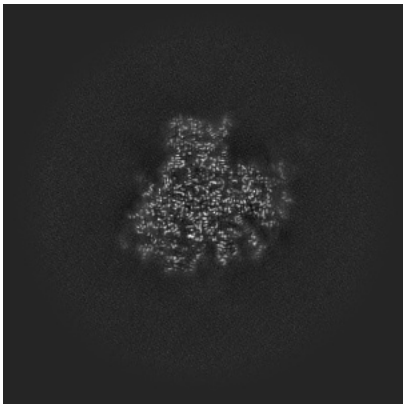
6.3.1 Primary map



X Index: 223



Y Index: 235

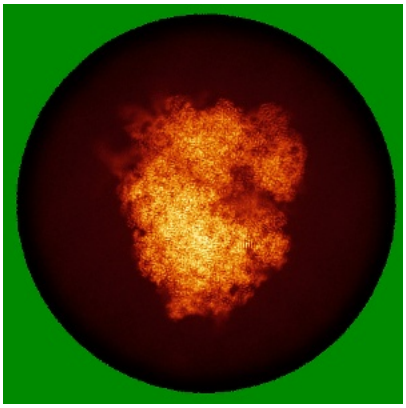


Z Index: 193

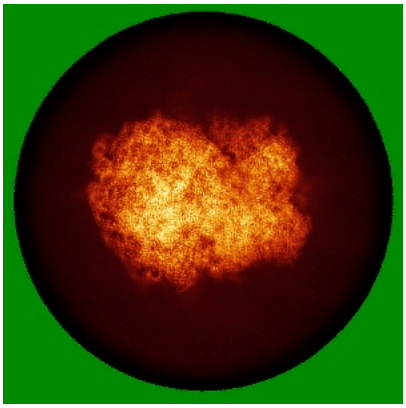
The images above show the largest variance slices of the map in three orthogonal directions.

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

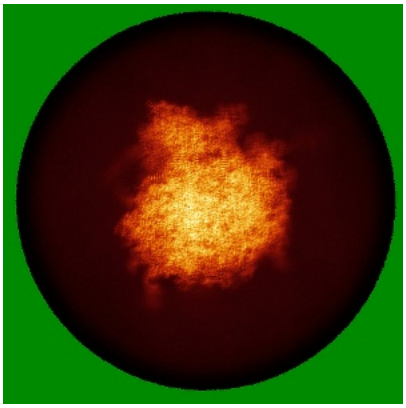
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.55. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

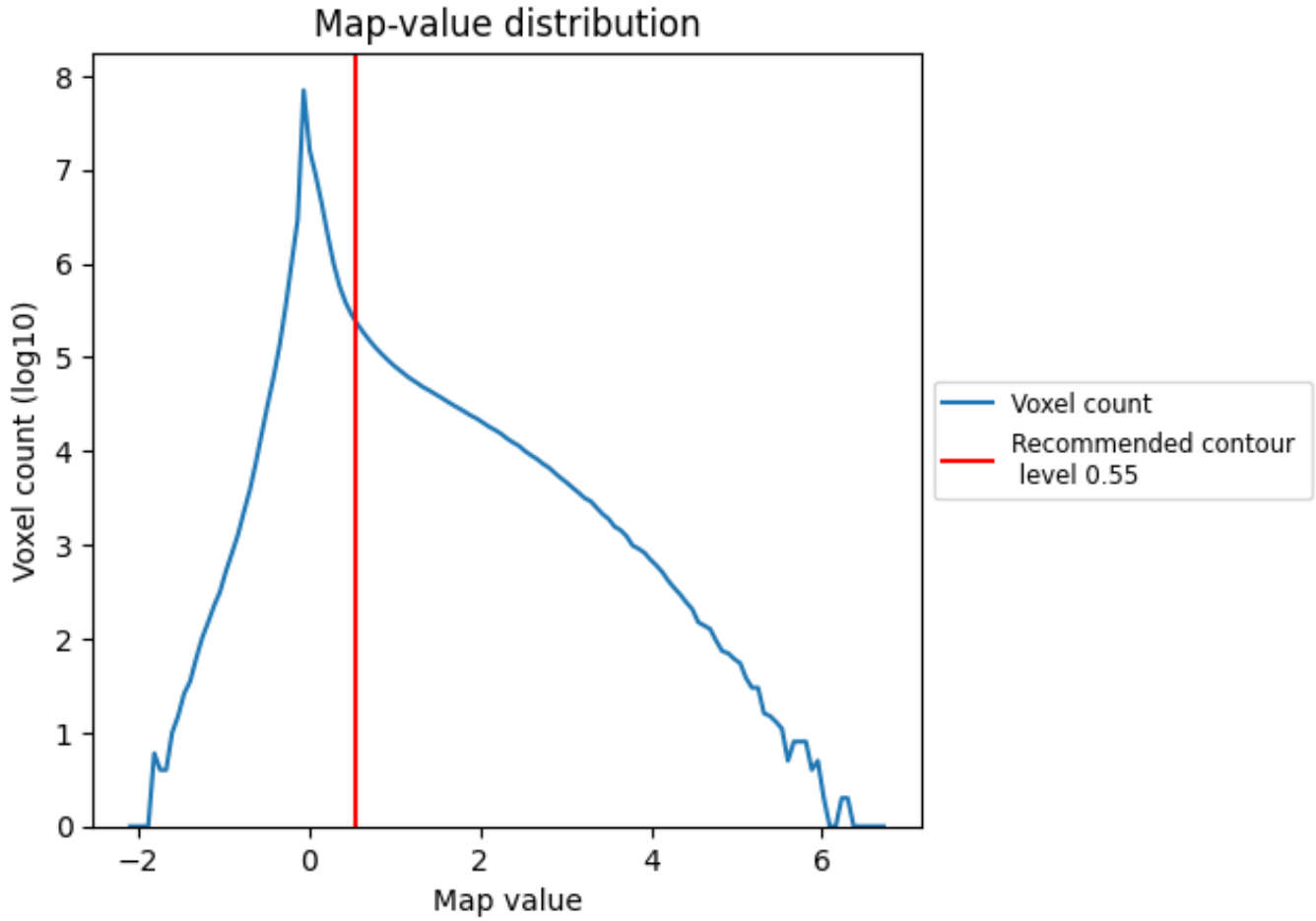
6.6 Mask visualisation (i)

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

7 Map analysis

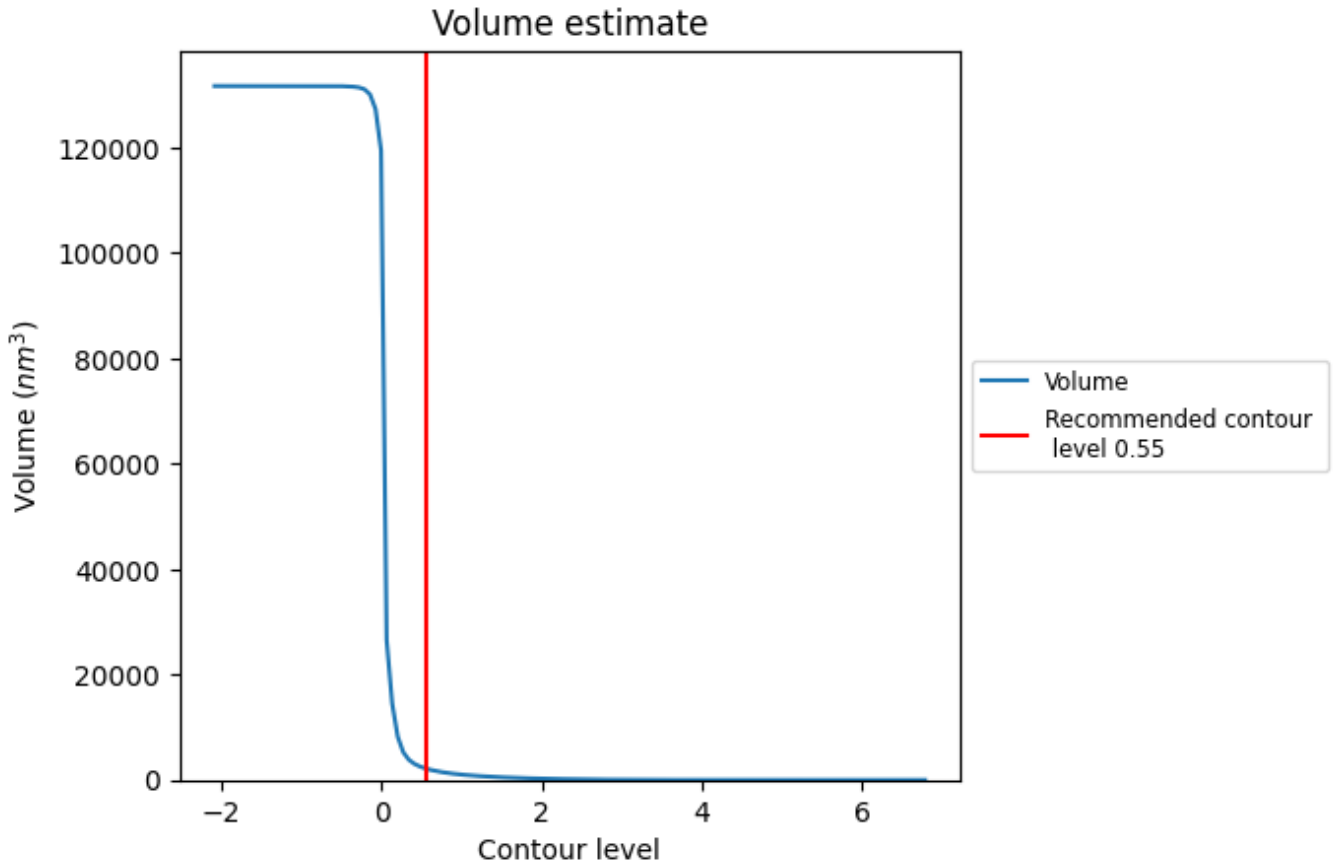
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

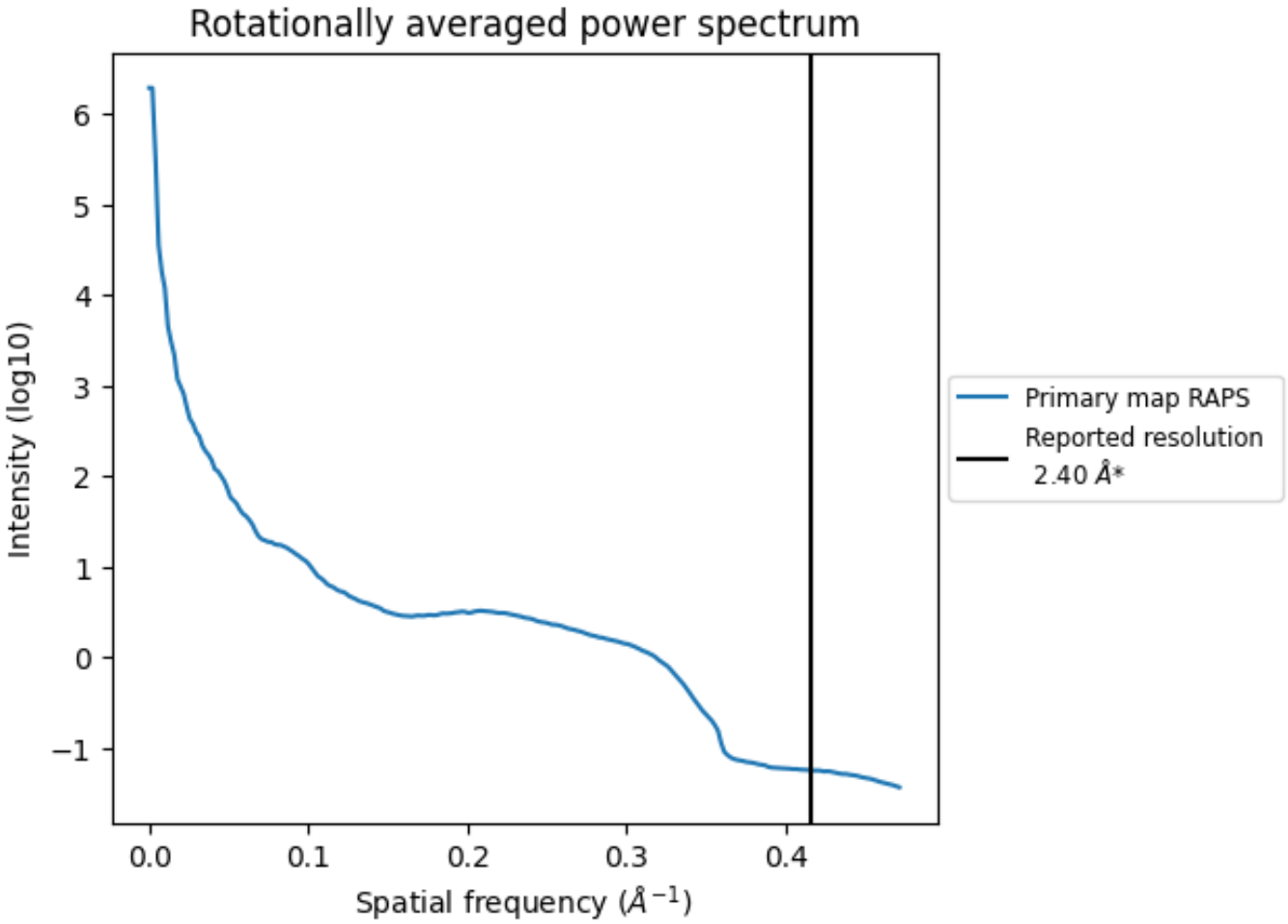
7.2 Volume estimate



The volume at the recommended contour level is 2175 nm^3; this corresponds to an approximate mass of 1964 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 0.417 $Å^{-1}$

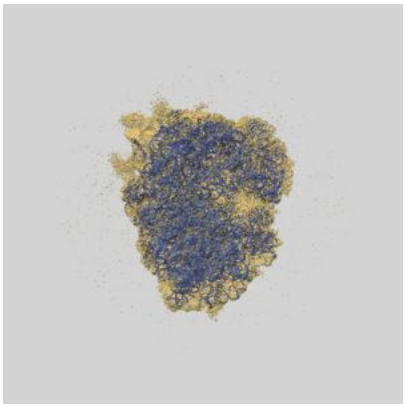
8 Fourier-Shell correlation

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

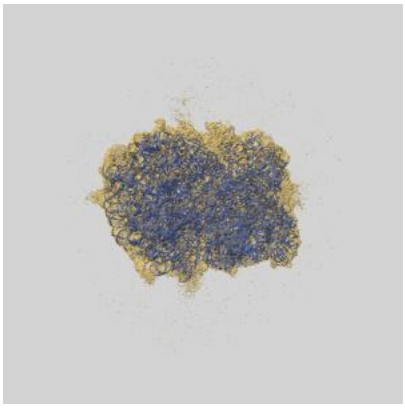
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13113 and PDB model 7OYC. Per-residue inclusion information can be found in section 3 on page 21.

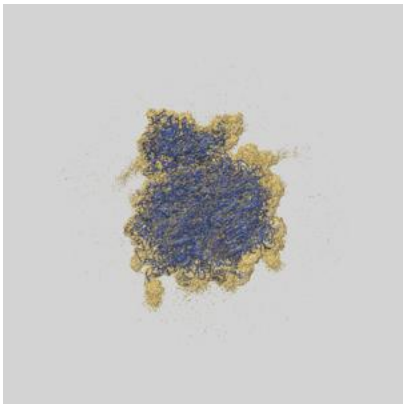
9.1 Map-model overlay



X



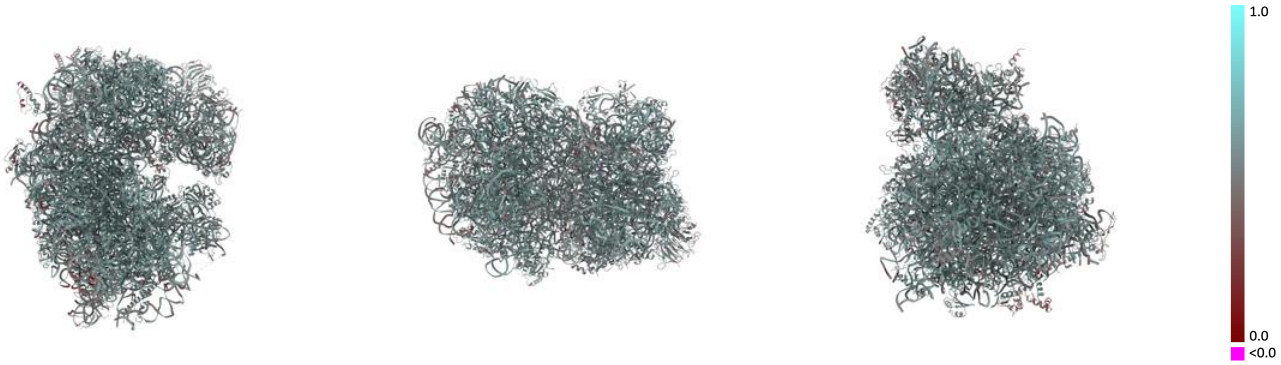
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.55 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.

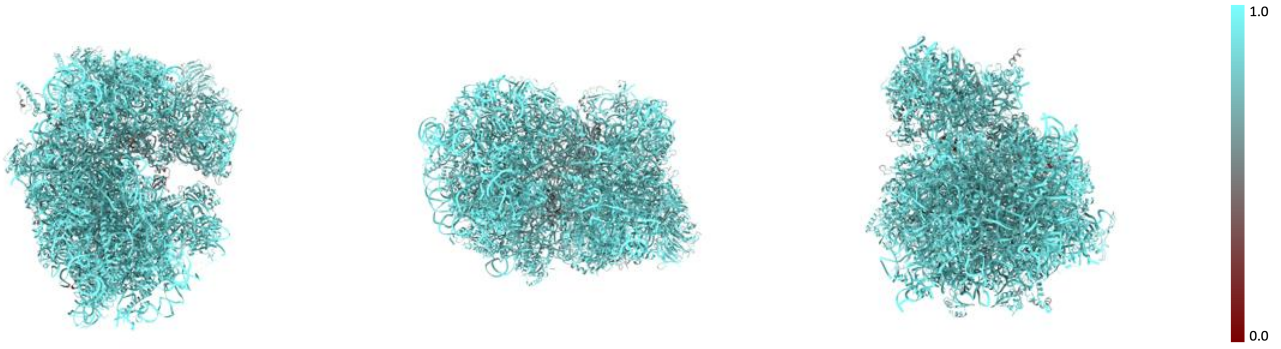
9.2 Q-score mapped to coordinate model (i)



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.

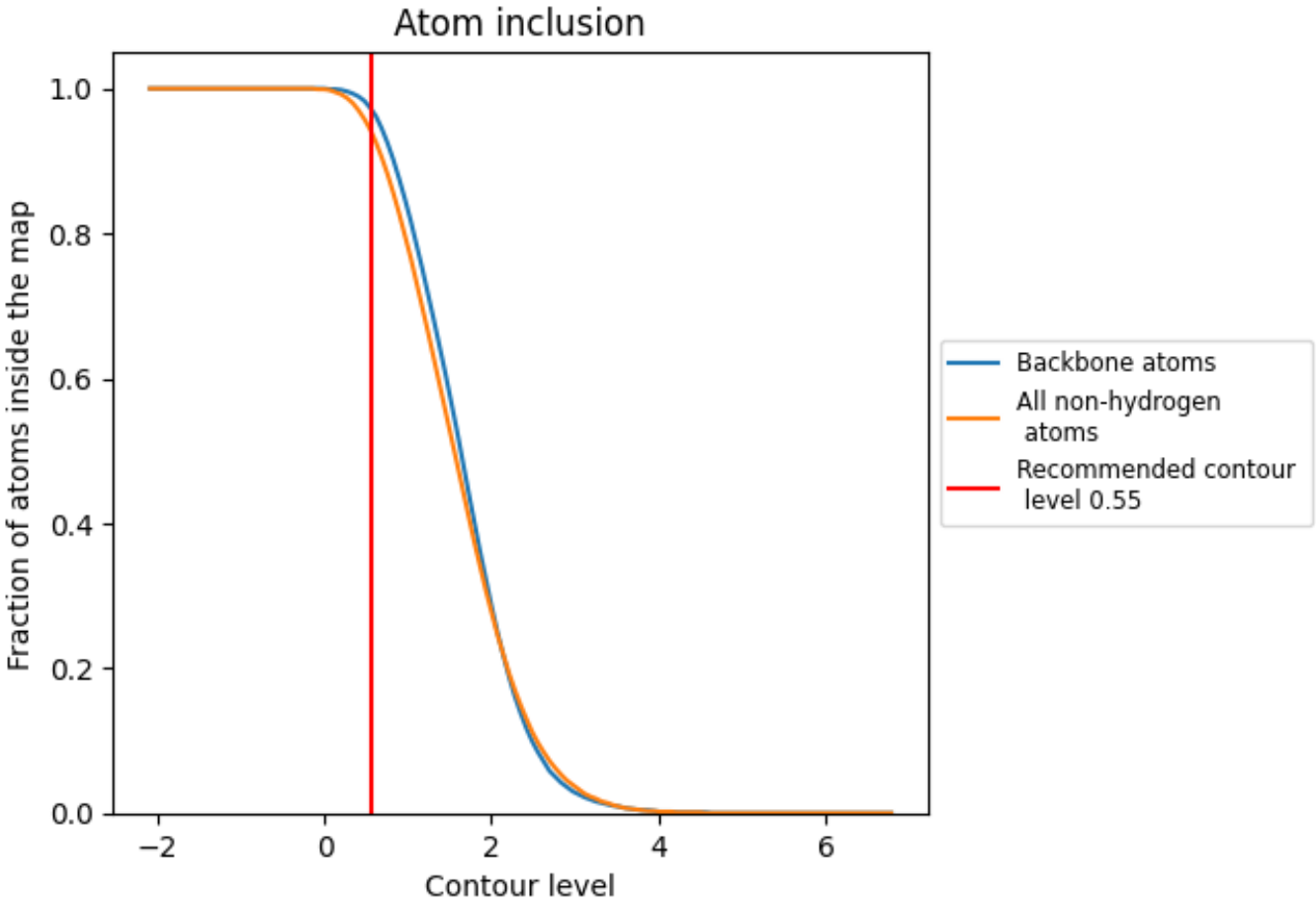
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.55).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9430	0.5570
11	0.4090	0.4890
22	0.9750	0.5620
51	0.9800	0.5630
71	0.9970	0.5760
81	0.9860	0.5640
A1	0.9420	0.5890
A2	0.9360	0.5690
B1	0.9360	0.5720
B2	0.8990	0.5410
C1	0.9550	0.5780
C2	0.9100	0.5690
D1	0.9470	0.5510
D2	0.8020	0.5210
E1	0.9430	0.5480
E2	0.9310	0.5610
F1	0.9380	0.5720
F2	0.8470	0.5130
G1	0.9380	0.5570
G2	0.8670	0.4930
H1	0.9220	0.5620
H2	0.8660	0.5030
I1	0.9330	0.5610
I2	0.8590	0.5200
J1	0.9000	0.5260
J2	0.9380	0.5630
K2	0.8970	0.5240
L1	0.9390	0.5630
L2	0.8880	0.5510
M1	0.9600	0.5670
N1	0.9740	0.6000
N2	0.9160	0.5610
O1	0.9650	0.5800
O2	0.9030	0.5480
P1	0.9600	0.5730

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Chain	Atom inclusion	Q-score
P2	0.8780	0.5190
Q1	0.9490	0.5810
Q2	0.9300	0.5570
R1	0.9060	0.5500
R2	0.8520	0.5280
S1	0.9590	0.5840
S2	0.8610	0.5120
T1	0.9270	0.5630
T2	0.9240	0.5460
U1	0.8750	0.4780
U2	0.8690	0.5220
V1	0.8980	0.5760
V2	0.9160	0.5580
W1	0.9110	0.5770
W2	0.9230	0.5770
X1	0.8950	0.5530
X2	0.8870	0.5600
Y1	0.9440	0.5620
Y2	0.9180	0.5320
Z1	0.9320	0.5490
Z2	0.8490	0.5020
a1	0.9780	0.5970
a2	0.9280	0.5680
b1	0.9220	0.5470
b2	0.9130	0.5190
c1	0.9300	0.5440
c2	0.7570	0.4720
d1	0.9190	0.5400
d2	0.9430	0.5740
e1	0.9400	0.5780
e2	0.8650	0.5310
f1	0.9580	0.5840
g1	0.9570	0.5810
g2	0.8570	0.4900
h1	0.9120	0.5490
i1	0.9280	0.5450
i2	0.6810	0.4760
j1	0.9610	0.5910
k1	0.8780	0.5280
l1	0.9340	0.5750
m1	0.9670	0.5830
n1	0.8090	0.5400

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Chain	Atom inclusion	Q-score
o1	0.9330	0.5650
p1	0.8830	0.5700
r1	0.9540	0.5730
s1	0.4730	0.4860
v2	0.6430	0.4830