



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:23 PM UTC

PDB ID : 8V87 / pdb_00008v87
EMDB ID : EMD-43027
Title : 60S ribosome biogenesis intermediate (Dbp10 post-catalytic structure - Overall map)
Authors : Cruz, V.E.; Weirich, C.S.; Peddada, N.; Erzberger, J.P.
Deposited on : 2023-12-04
Resolution : 2.66 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:

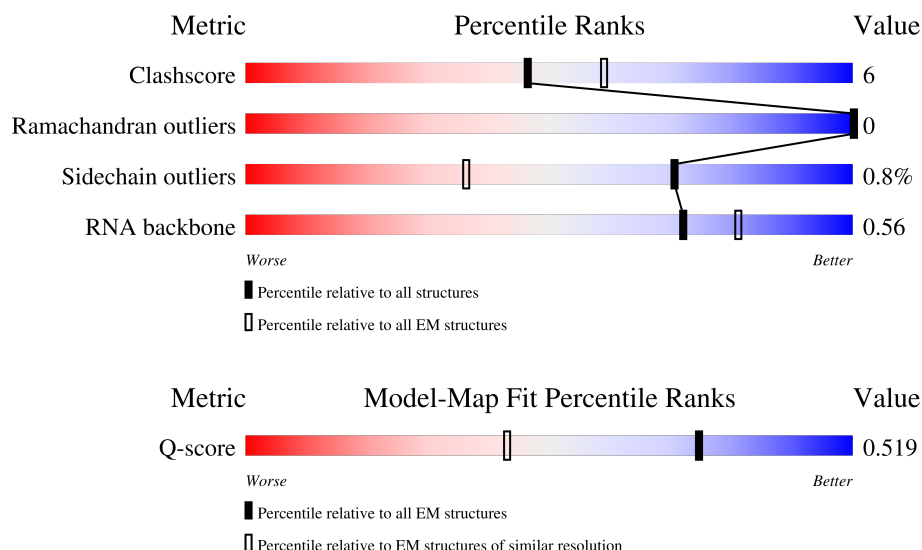
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.66 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	9119 (2.16 - 3.16)

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

Mol	Chain	Length	Quality of chain
1	1	3396	
2	2	158	
3	3	995	

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Mol	Chain	Length	Quality of chain
4	6	232	
5	7	204	
6	8	710	
7	A	291	
8	B	387	
9	C	362	
10	D	505	
11	E	176	
12	F	244	
13	G	256	
14	H	191	
15	I	663	
16	J	427	
17	K	376	
18	L	199	
19	M	138	
20	N	204	
21	O	199	
22	P	184	
23	Q	186	
24	R	189	
25	S	172	
26	U	121	
27	V	137	
28	W	236	

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Mol	Chain	Length	Quality of chain
29	X	142	
30	Y	127	
31	Z	136	
32	a	217	
33	b	647	
34	c	105	
35	d	113	
36	e	130	
37	f	107	
38	g	121	
39	h	120	
40	i	100	
41	j	88	
42	k	78	
43	l	181	
44	m	807	
45	n	605	
46	o	220	
47	p	460	
48	q	618	
49	r	261	
50	s	520	
51	t	322	
52	u	199	
53	v	231	

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Mol	Chain	Length	Quality of chain
54	w	841	20%29%67%
55	y	245	47%80%20%
56	z	106	35%47%5%48%

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 150186 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2489	Total	C	N	O	P	0	0
			53292	23794	9638	17371	2489		

- Molecule 2 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	155	Total	C	N	O	P	0	0
			3291	1472	577	1087	155		

- Molecule 3 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	656	Total	C	N	O	S	0	0
			5253	3347	925	960	21		

- Molecule 4 is a RNA chain called ITS2 RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	87	Total	C	N	O	P	0	0
			1838	823	309	619	87		

- Molecule 5 is a protein called 60S ribosomal subunit assembly/export protein LOC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	134	Total	C	N	O		0	0
			1093	679	211	203			

- Molecule 6 is a protein called Nucleolar complex protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	8	477	Total	C	N	O	S	0	0
			3868	2478	667	710	13		

- Molecule 7 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	248	Total	C	N	O	S	0	0
			2032	1294	359	373	6		

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	336	Total	C	N	O	S	0	0
			2670	1696	493	475	6		

- Molecule 9 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	358	Total	C	N	O	S	0	0
			2725	1717	517	488	3		

- Molecule 10 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	432	Total	C	N	O	S	0	0
			3451	2227	591	621	12		

- Molecule 11 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 12 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	215	Total	C	N	O	S	0	0
			1735	1122	316	296	1		

- Molecule 13 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	198	Total	C	N	O	S	0	0
			1549	998	271	277	3		

- Molecule 14 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	189	Total	C	N	O	S	0	0
			1502	953	272	273	4		

- Molecule 15 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	526	Total	C	N	O	S	0	0
			4201	2665	717	799	20		

- Molecule 16 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	145	Total	C	N	O	S	0	0
			1215	759	225	228	3		

- Molecule 17 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	280	Total	C	N	O	S	0	0
			2248	1448	368	428	4		

- Molecule 18 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	121	Total	C	N	O		0	0
			991	623	208	160			

- Molecule 19 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 20 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	189	Total	C	N	O	S	0	0
			1621	1015	343	262	1		

- Molecule 21 is a protein called Large ribosomal subunit protein uL13A.

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

- Molecule 22 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	164	Total	C	N	O		0	0
			1292	804	253	235			

- Molecule 23 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	127	Total	C	N	O	S	0	0
			973	625	180	167	1		

- Molecule 24 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	134	Total	C	N	O		0	0
			1082	679	220	183			

- Molecule 25 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	170	Total	C	N	O	S	0	0
			1432	922	265	242	3		

- Molecule 26 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	102	Total	C	N	O		0	0
			808	524	132	152			

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	V	127	Total	C	N	O	S	0	0
			939	593	173	166	7		

- Molecule 28 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	232	Total	C	N	O	S	0	0
			1870	1184	321	360	5		

- Molecule 29 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	137	Total	C	N	O	S	0	0
			1068	682	192	192	2		

- Molecule 30 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Y	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 32 is a protein called Large ribosomal subunit protein uL1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	214	Total	C	N	O	S	0	0
			1695	1083	295	308	9		

- Molecule 33 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	469	Total	C	N	O	S	0	0
			3806	2419	662	708	17		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 35 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	125	Total	C	N	O	S	0	0
			1009	641	203	164	1		

- Molecule 37 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 39 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	72	Total	C	N	O	S	0	0
			578	358	121	98	1		

- Molecule 41 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	73	Total	C	N	O	S	0	0
			580	353	126	96	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 43 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	176	Total	C	N	O	S	0	0
			1394	896	244	247	7		

- Molecule 44 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	666	Total	C	N	O	S	0	0
			5377	3421	936	1005	15		

- Molecule 45 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	425	Total	C	N	O	S	0	0
			3470	2241	600	615	14		

- Molecule 46 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 47 is a protein called YTM1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	307	Total	C	N	O	S	0	0
			2391	1492	422	471	6		

- Molecule 48 is a protein called 25S rRNA (cytosine(2870)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	371	Total	C	N	O	S	0	0
			2902	1842	504	543	13		

- Molecule 49 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	214	Total	C	N	O	S	0	0
			1738	1096	332	304	6		

- Molecule 50 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	36	Total	C	N	O	S	0	0
			301	184	69	46	2		

- Molecule 51 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	285	Total	C	N	O	S	0	0
			2293	1453	425	412	3		

- Molecule 52 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	114	Total	C	N	O	S	0	0
			959	602	196	152	9		

- Molecule 53 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	130	Total	C	N	O	S	0	0
			1087	678	211	195	3		

- Molecule 54 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w	280	Total	C	N	O	S	0	0
			2241	1395	419	417	10		

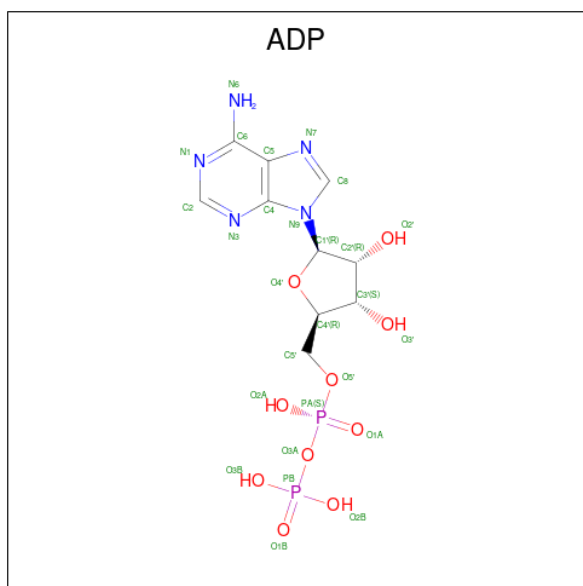
- Molecule 55 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	245	Total	C	N	O	S	0	0
			1855	1149	320	379	7		

- Molecule 56 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	z	55	Total	C	N	O	0	0
			444	273	88	83		

- Molecule 57 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

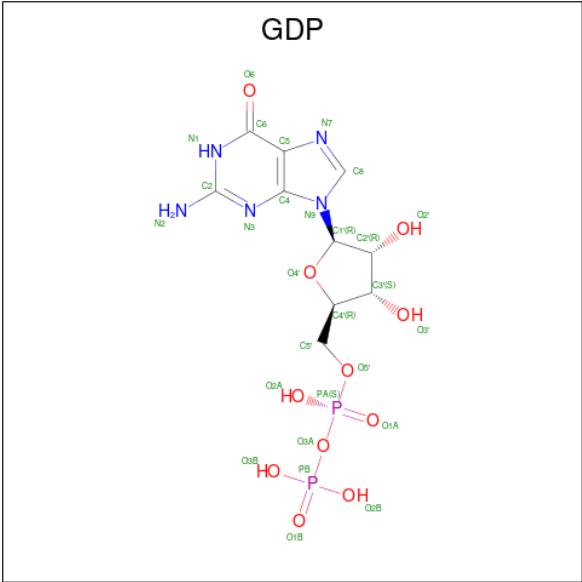


Mol	Chain	Residues	Atoms					AltConf
57	3	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	3	1	Total	Mg	0
			1	1	
58	b	1	Total	Mg	0
			1	1	

- Molecule 59 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



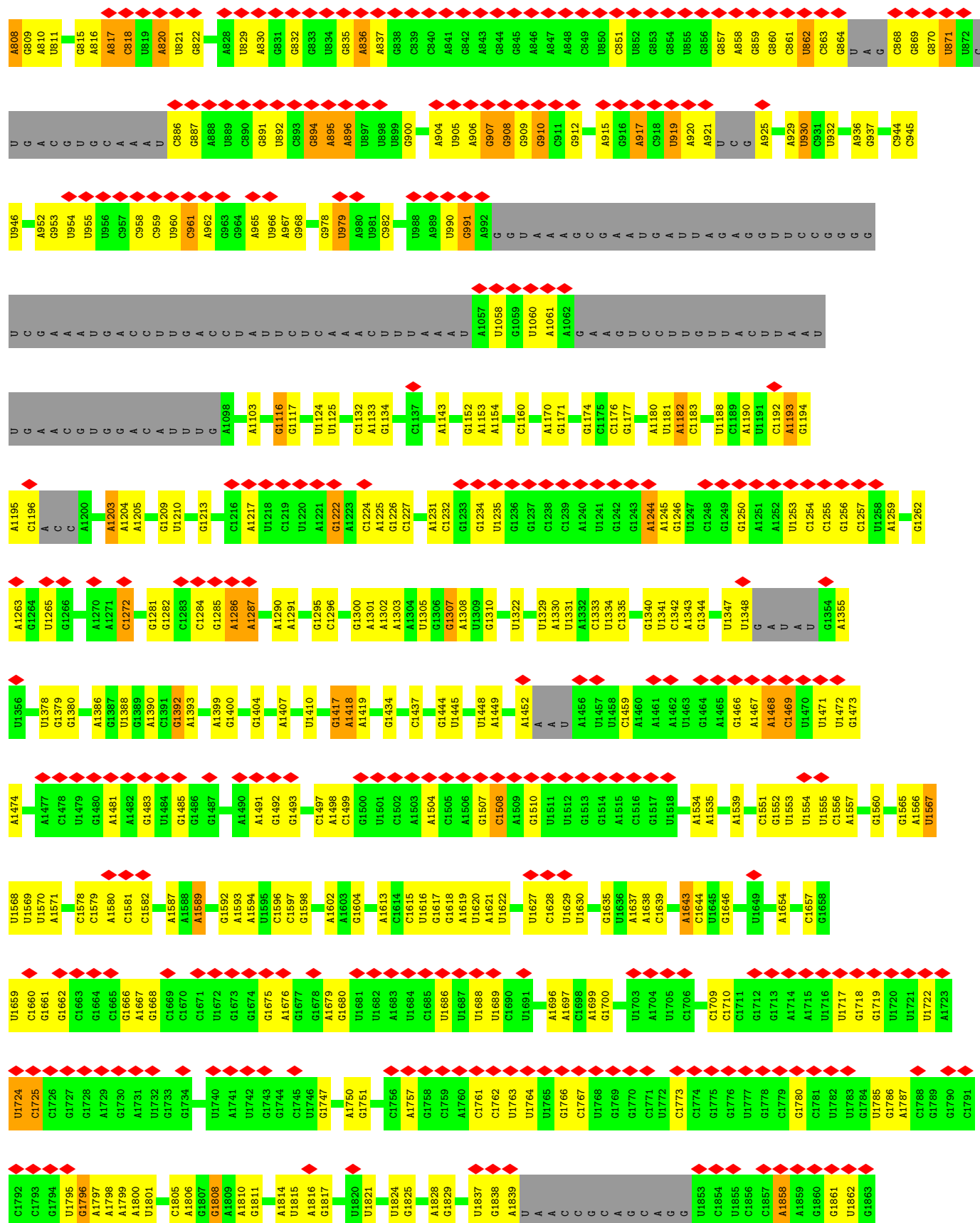
Mol	Chain	Residues	Atoms					AltConf
59	b	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 60 is POTASSIUM ION (CCD ID: K) (formula: K).

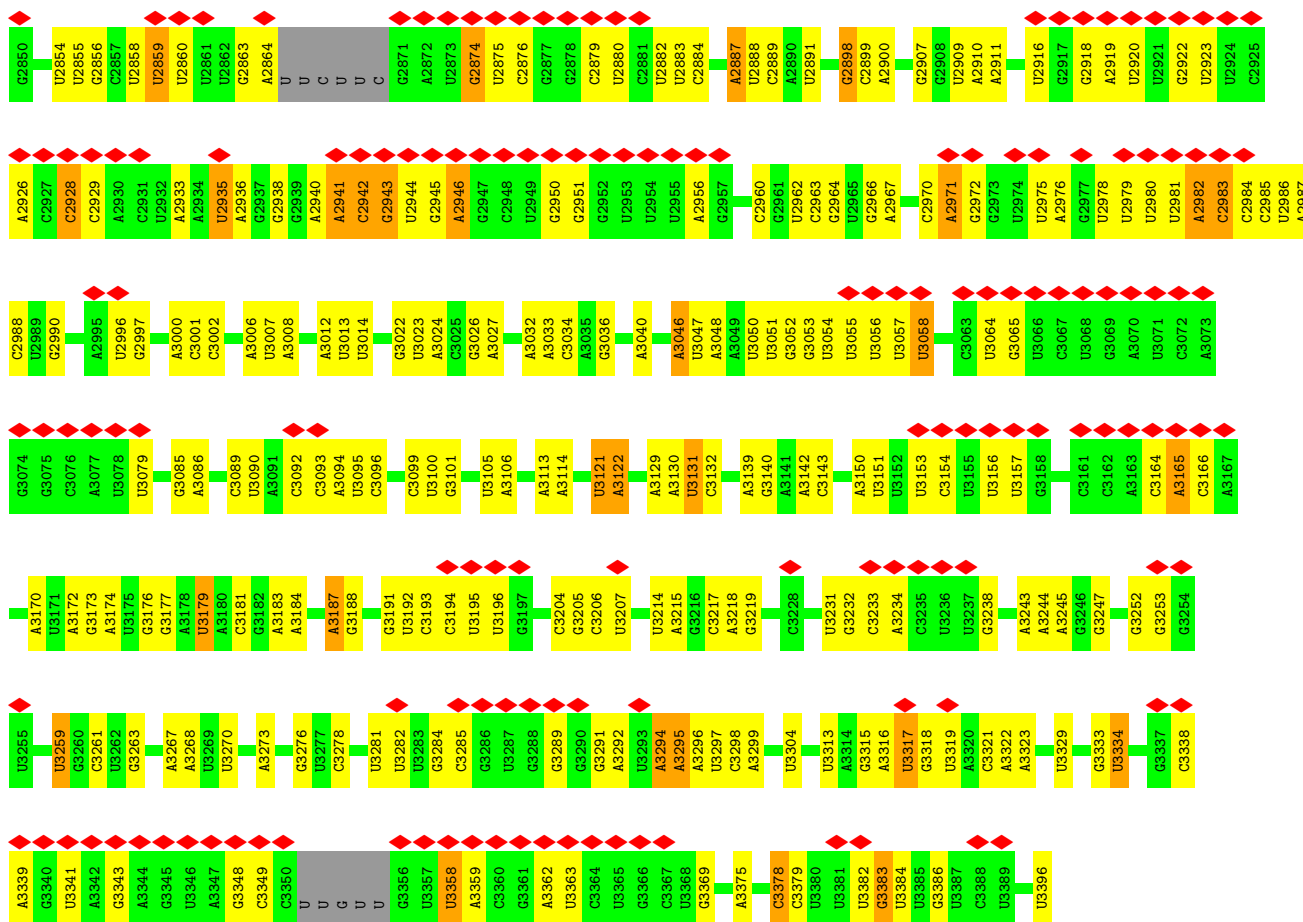
Mol	Chain	Residues	Atoms		AltConf
60	b	1	Total	K	0
			1	1	

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

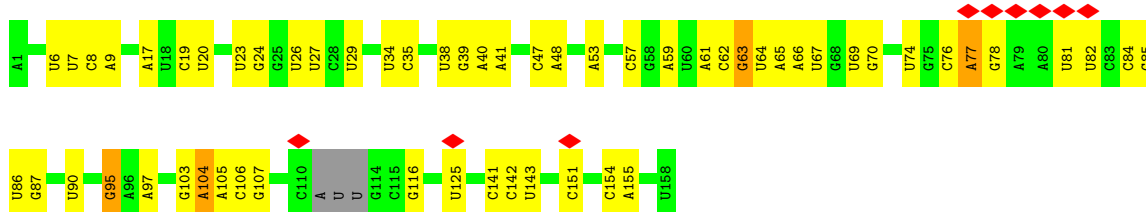
Mol	Chain	Residues	Atoms		AltConf
61	g	1	Total	Zn	0
			1	1	
61	j	1	Total	Zn	0
			1	1	



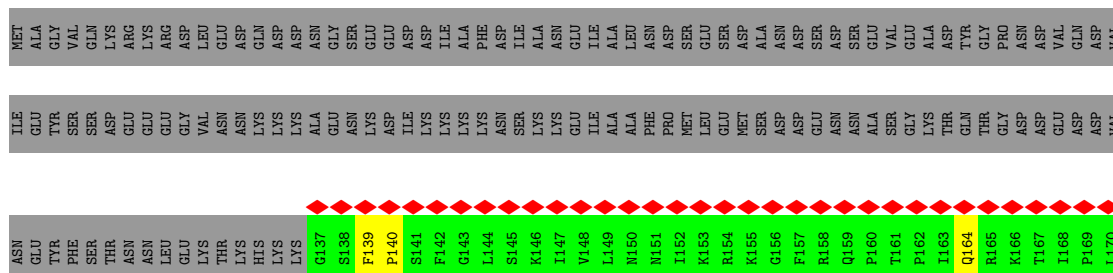




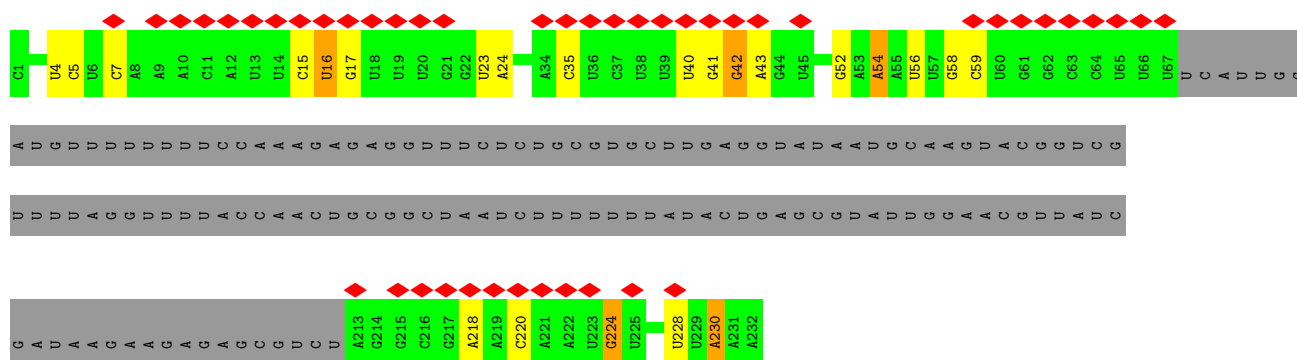
• Molecule 2: 5.8S ribosomal RNA



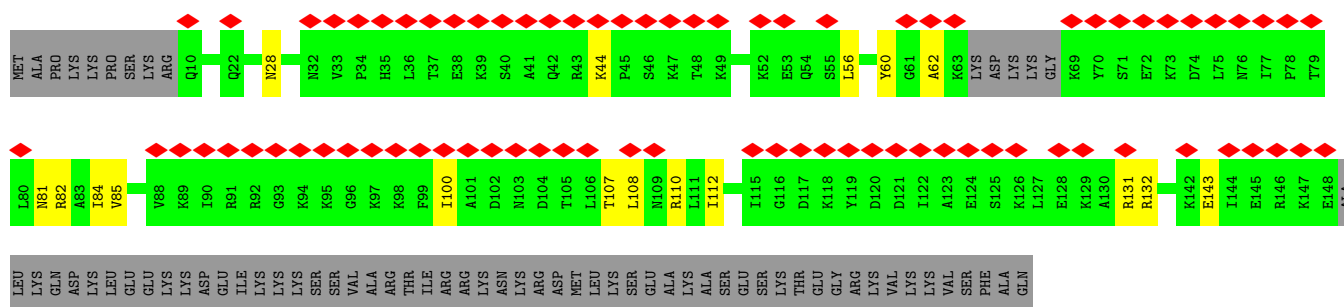
• Molecule 3: ATP-dependent RNA helicase DBP10



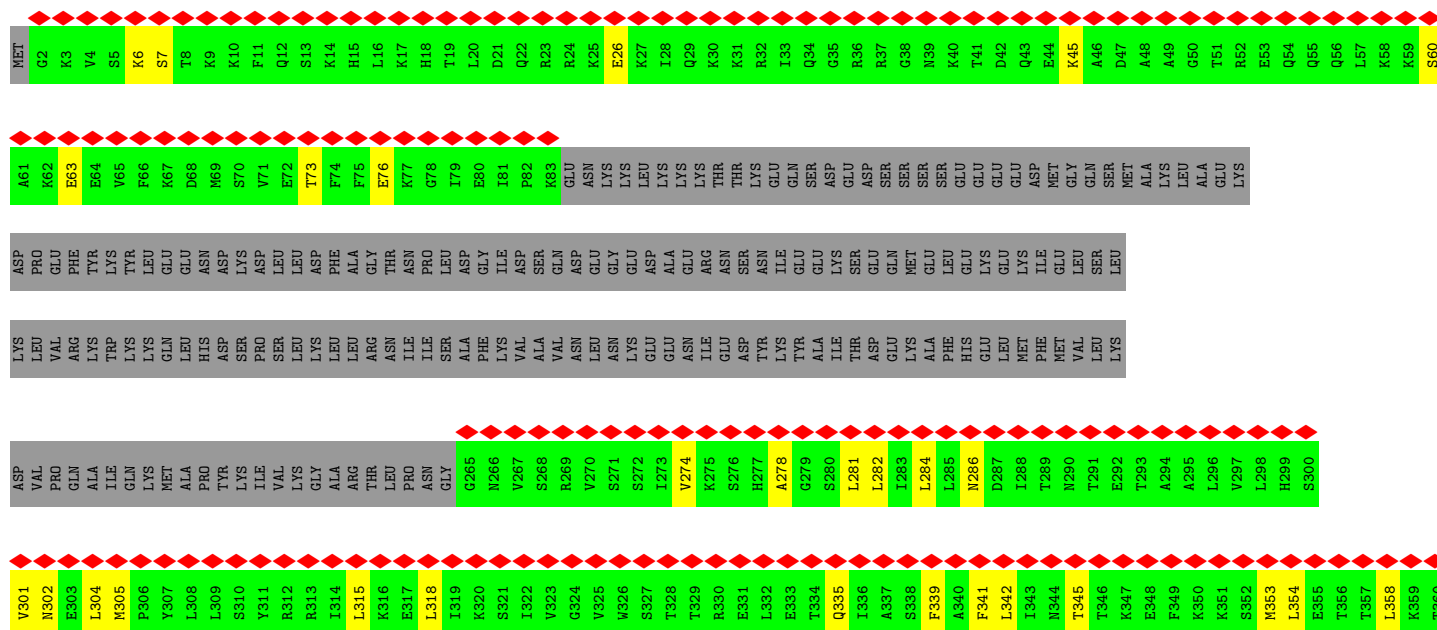
- Molecule 4: ITS2 RNA

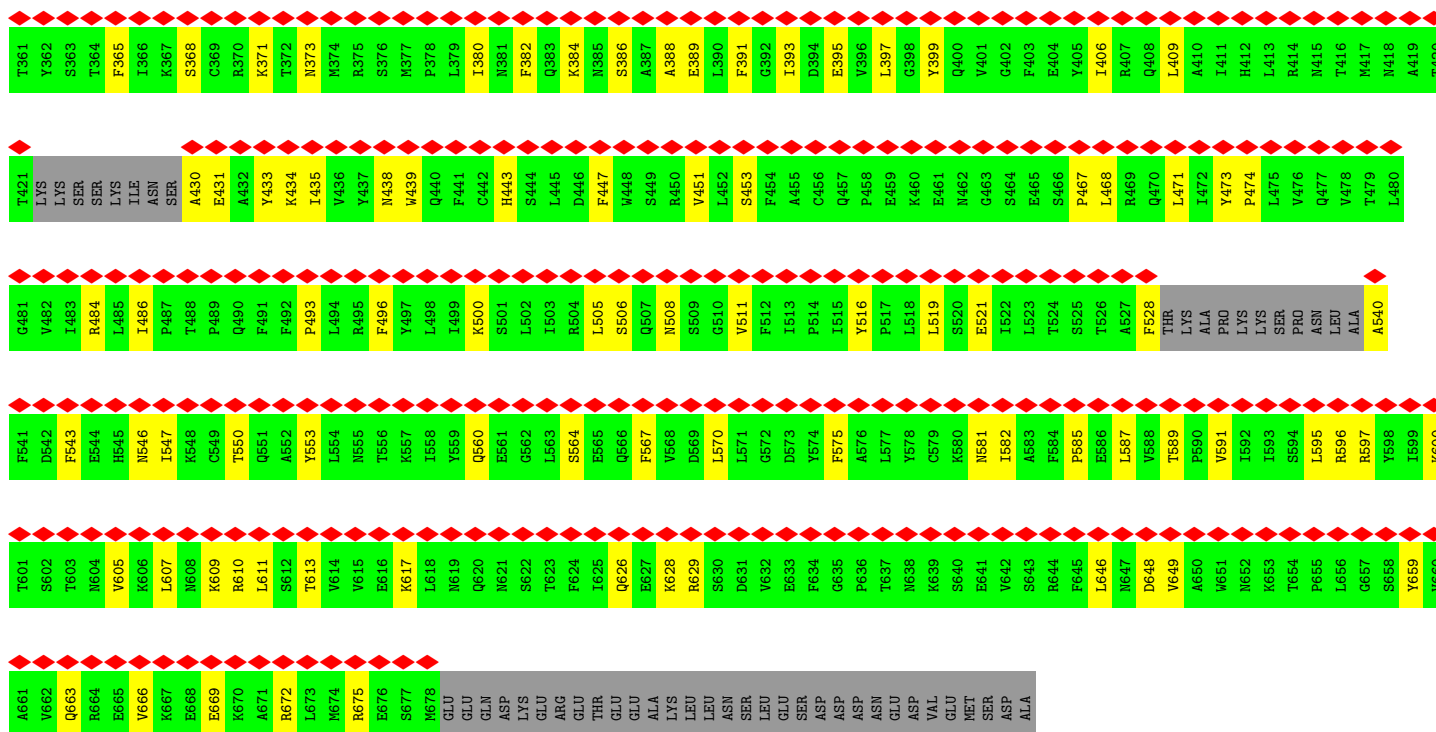


• Molecule 5: 60S ribosomal subunit assembly/export protein LOC1

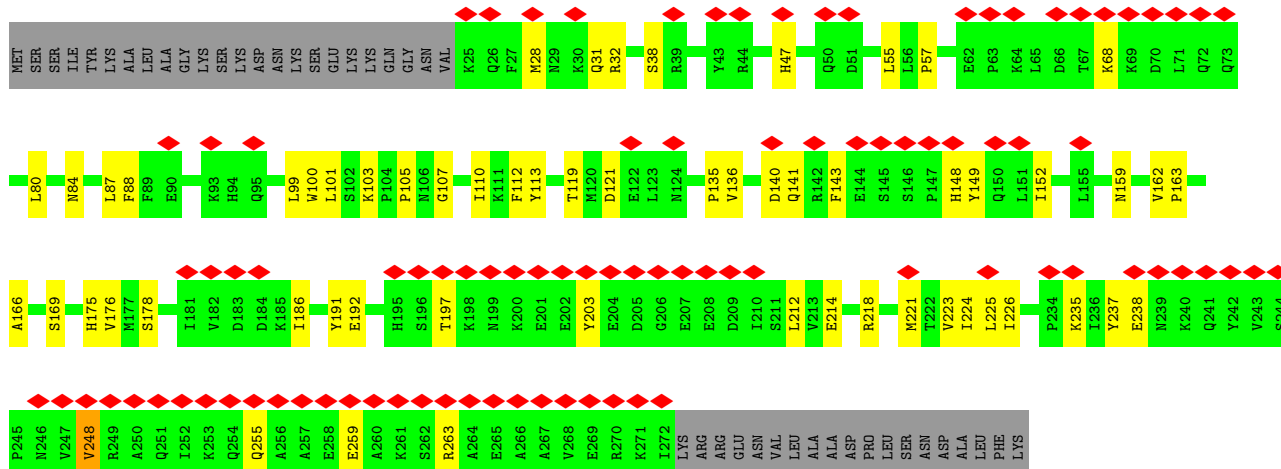


• Molecule 6: Nucleolar complex protein 2

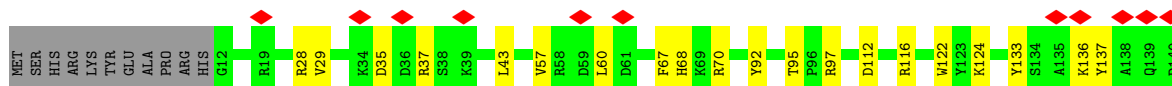


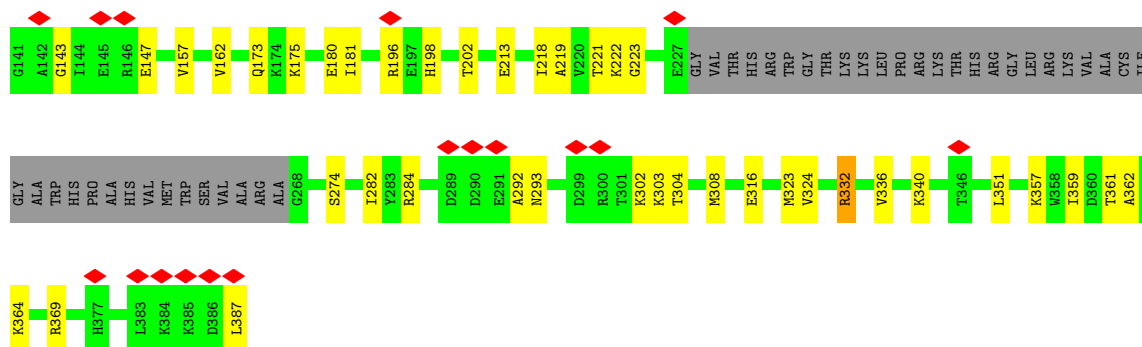


• Molecule 7: Ribosome biogenesis protein BRX1

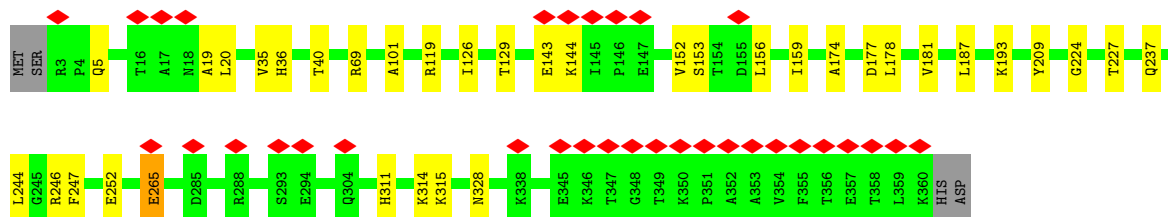
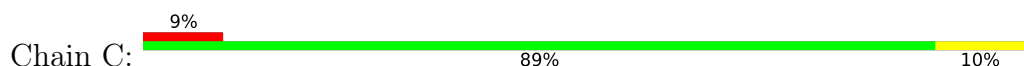


• Molecule 8: 60S ribosomal protein L3

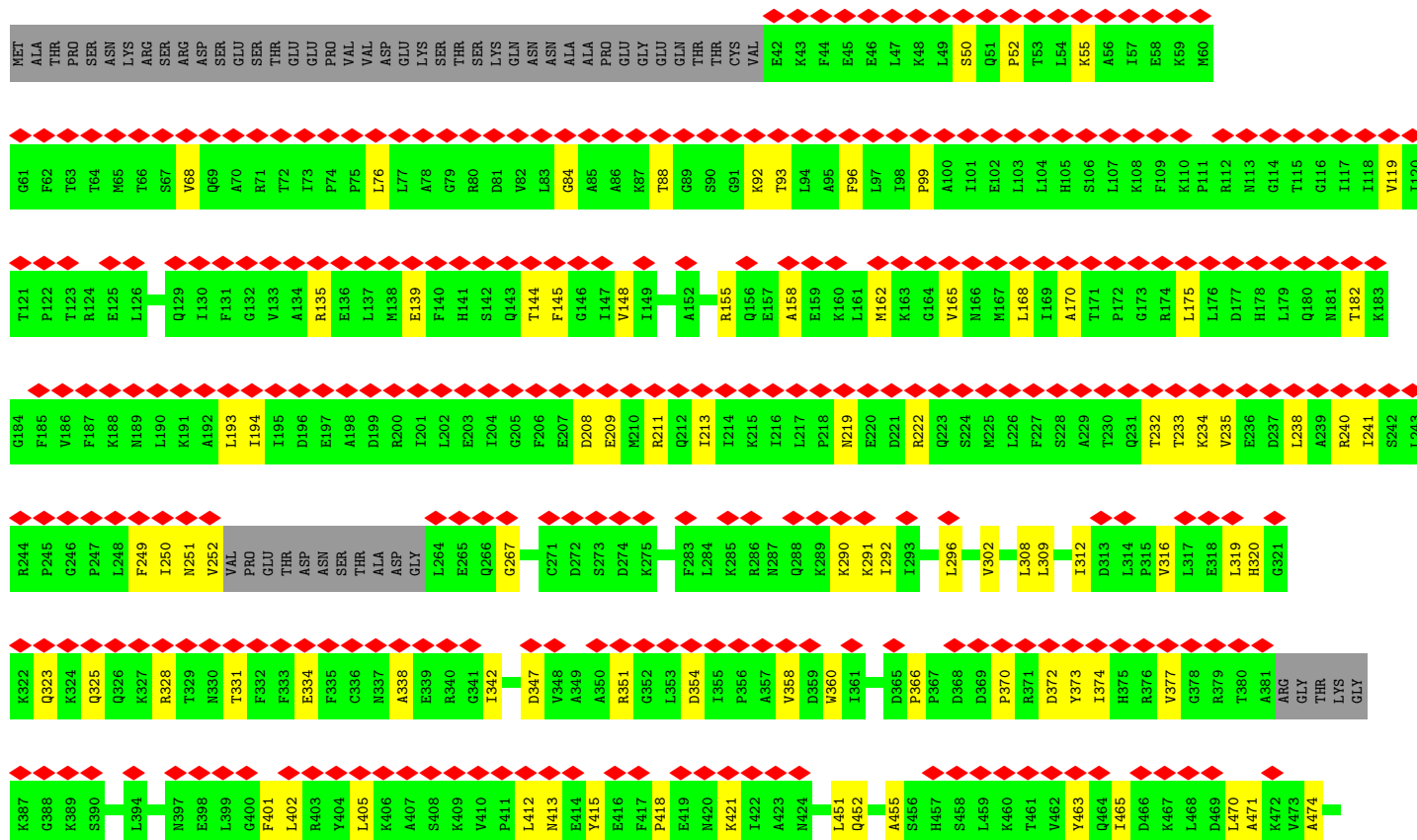


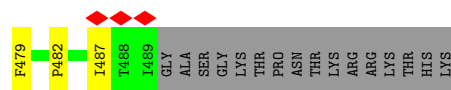


• Molecule 9: 60S ribosomal protein L4-A

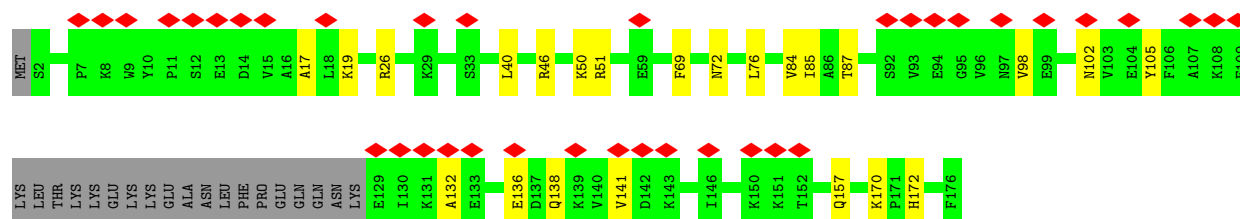
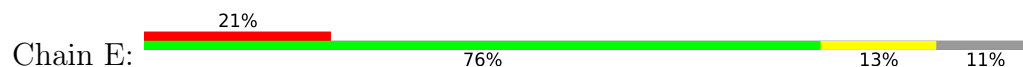


• Molecule 10: ATP-dependent RNA helicase HAS1

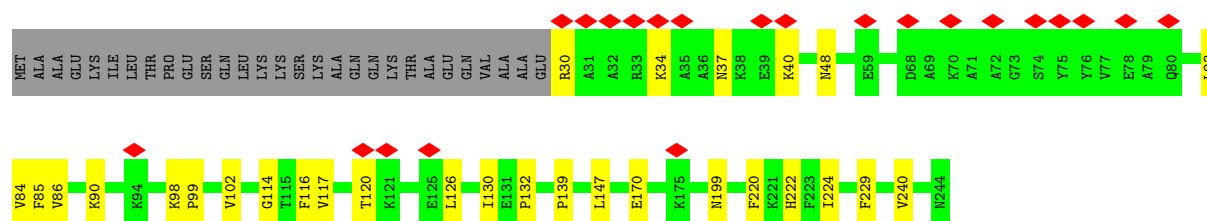
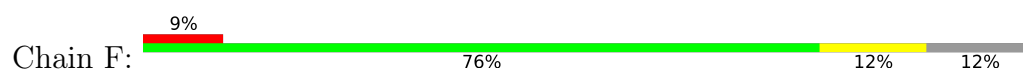




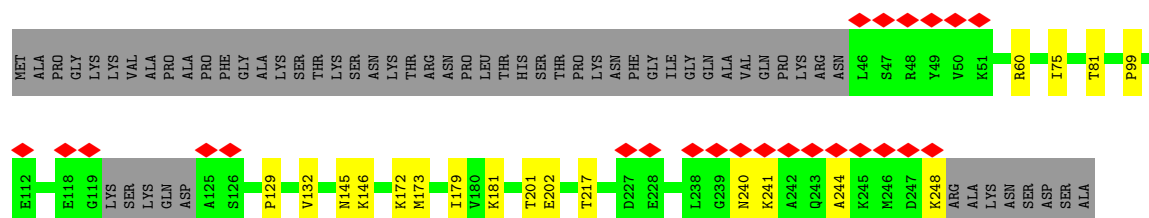
- Molecule 11: 60S ribosomal protein L6-A



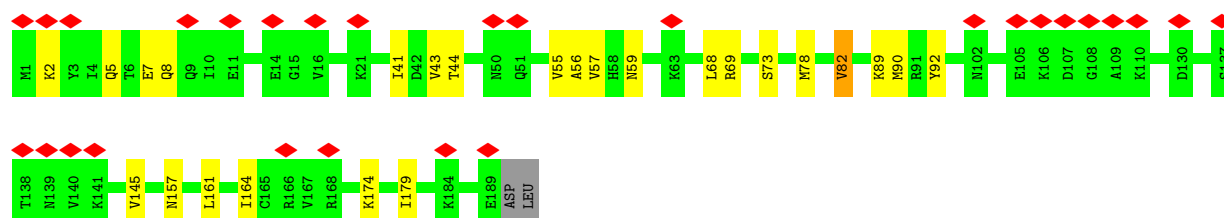
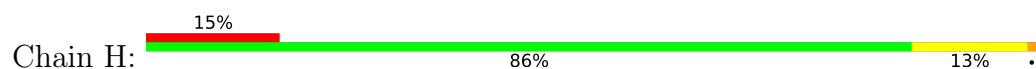
- Molecule 12: 60S ribosomal protein L7-A



- Molecule 13: Large ribosomal subunit protein eL8A



- Molecule 14: Large ribosomal subunit protein uL6A



- Molecule 15: Nucleolar complex-associated protein 3



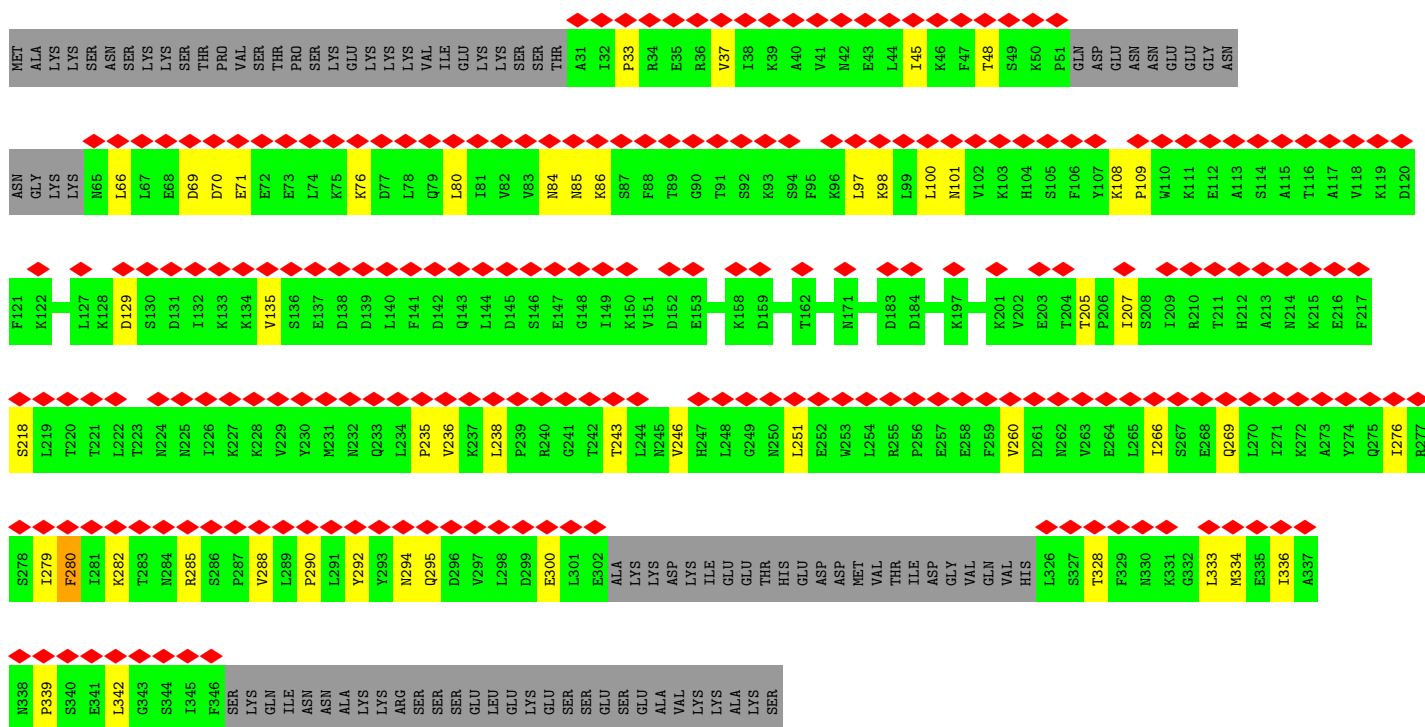
MET	ALA	LYS	ARG	ASN	ARG	GLN	PHE	ARG	ILE	GLN	GLU	ARG	THR	LYS	LYS	LYS	VAL	LYS	ASN	PHE	GLN	ASN	ALA	PRO	PRO	GLU	ASP	MET	ASP	GLU	GLU	ASN	THR	ILE	TYR	SER	SER	TRP	ASP	GLU	GLU	GLU	GLN	ASP	TYR	GLU	GLU	MET														
VAL	PRO	ALA	ARG	LYS	ASN	ARG	SER	THR	SER	ASN	LEU	VAL	GLU	GLY	ALA	PRO	LYS	ILE	VAL	VAL	GLN	GLY	LYS	LYS	LYS	LYS	ASP	ASP	ASP	GLU	GLU	ASP	GLU	ASP	SER	SER	GLU	ASP	ASP	GLU	GLU	PRO	GLN	ASN	GLU	GLU	GLN	GLU														
ALA	GLU	ALA	LYS	GLU	ASN	ARG	GLU	ASP	T130	E131	E132	K133	I134	G191	Y192	R193	I194	R195	P196	K138	E139	D140	I141	A142	D143	I144	V145	T146	K147	V148	M149	E150	E151	P152	E153	E154	M155	T156	A157	A158	L159	G160	R161	L162	C163	K164	M165	V166	E167	S168	K169	M170	P171	M172	T173	C174	K175	F176	S177	M178	L179	A180
L181	V182	P183	V184	F185	K186	S187	I188	I189	P190	G191	Y192	R193	I194	R195	P196	L197	T198	E199	T200	E201	K202	K203	E204	K205	V206	S207	K208	E209	V210	S211	K212	L213	R214	M215	F216	E217	Q218	A219	L220	V221	Y222	M223	Y224	K225	M226	Y227	V228	G229	R230	L231	Q232	S233	L234	S235	K236	T237	P238	N239	N240			
A241	A242	P243	T244	Q245	V246	S247	L248	G249	L250	L251	A252	T253	Q254	A255	A256	K257	E258	L259	T260	S261	T262	A263	S264	H265	F266	N267	F268	R269	T270	D271	T272	K273	T274	L275	L276	L277	R278	R279	T280	C281	K282	P283	R284	I285	S286	T287	D288	P289	T290	S291	T292	Q293	T294	I295	Q296	T297	F298	E299	T300			
L301	L302	N303	E304	D305	E306	E307	G308	S309	T310	S311	F312	E313	I314	L315	R316	I317	F318	N319	K320	I321	L322	K323	T324	R325	N326	F327	N328	I329	E330	E331	S332	V333	L334	N335	N336	L337	L338	S339	L340	D341	V342	L343	H344	D345	Y346	D347	F348	N349	T350	K351	L352	LYS	GLY	ASN	VAL	SER	ALA	PRO	K360			
L361	K362	K363	K364	D365	R366	V367	H368	L369	S370	K371	K372	Q373	R374	K375	A376	R377	K378	E379	M380	Q381	Q382	L383	T384	R385	E386	N387	R388	N389	A390	E391	Q392	A393	V394	S395	A396	E397	E398	R399	E400	R401	M402	Q403	S404	L405	K408	F411	T412	I413	M416	I417	L418	K419	M420	M421	A422	K423						
T424	L425	L426	G427	S428	V429	L430	E431	G432	L433	T434	K435	N438	M439	A440	D443	L444	G446	D447	F448	L449	E450	V451	E454	L455	L456	S457	D458	T459	E460	F461	D462	N463	L464	S465	S466	A467	E468	V469	R470	K471	A472	L473	L474	C475	I476	V477	S478	A479	F480	S481	L482	I483	S484	N485	T486							
Q487	Y488	M489	K490	V491	M492	V493	D494	L495	S496	K497	F498	V499	D500	G501	L502	Y503	A504	L505	L506	P507	Y508	I509	C510	L511	D512	A513	D514	E515	E516	L517	S518	Y519	R520	S521	L522	R523	L524	D525	P527	L528	N529	M530	E531	I532	I533	K534	P535	S536	V537	M538	V539	S540	T541	K542	A543	E544	L545	L546				
L547	K548	A549	L550	D551	H552	F555	R556	S557	K558	S559	G560	T561	K562	E563	R564	A565	F568	T569	K570	R571	L572	Y573	M574	C575	I576	S577	H578	T579	P580	E581	K582	T583	S584	L585	A586	L587	L588	K589	F590	I591	D592	K593	L594	M595	N596	R597	Y598	P599	E600	I601	S602	G603	L604	Y605	S606	S607	E608					
D609	R610	I611	G612	N613	G614	H615	F616	I617	M618	E619	A620	D621	N622	P623	S624	R625	S626	N627	P628	E629	A630	A631	T632	L633	W634	D635	M636	A637	L638	L639	E640	K641	H642	Y643	C644	P645	V646	V647	T648	K649	G650	L651	R652	S653	L654	S655	S656	R657	S658	K659	E660	C661	S662	LYS								

• Molecule 16: rRNA-processing protein EBP2

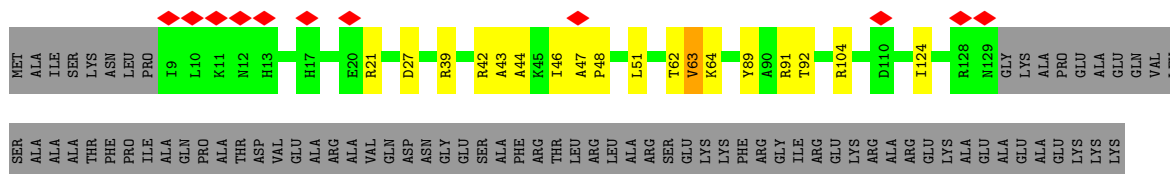


MET	ALA	GLY	PHE	LYS	LEU	LYS	GLU	LEU	LEU	TYR	SER	HIS	GLN	LYS	GLU	ILE	GLY	LYS	ALA	GLU	LYS	LEU	ASN	ASP	LEU	LYS	LYS	LYS	LYS	GLN	SER	GLN	GLY	GLU	PRO	THR	ILE	LYS	VAL	THR	ALA	SER	ASN	LEU	LYS	LYS	LEU	LYS	GLU	GLU	VAL			
LYS	LYS	GLU	VAL	ALA	ALA	ASP	THR	GLU	GLU	GLU	GLN	SER	GLN	ALA	LYS	SER	GLY	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	GLN	ASP	GLU	GLN	ALA	LYS	THR	VAL	THR	GLY	ASP	GLU	GLN	GLU	LYS	GLU	GLU	GLU	GLU	GLU	GLU	GLU		
GLU	GLU	GLU	GLU	GLY	ARG	LEU	ASP	ASP	GLU	LEU	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS	LYS

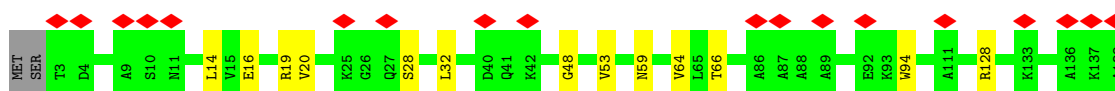
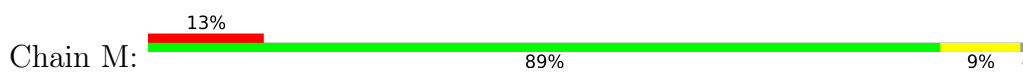
- Molecule 17: Proteasome-interacting protein CIC1



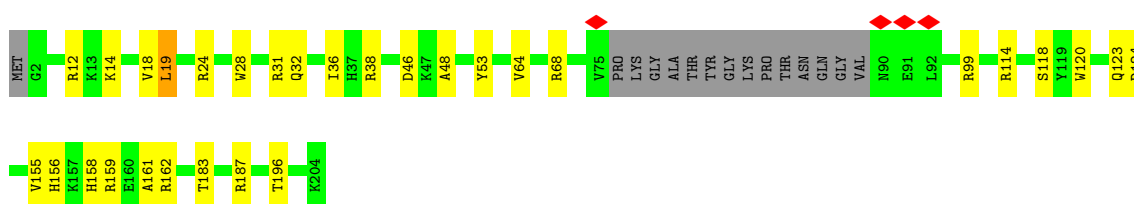
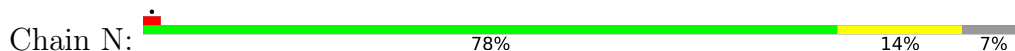
- Molecule 18: 60S ribosomal protein L13-A



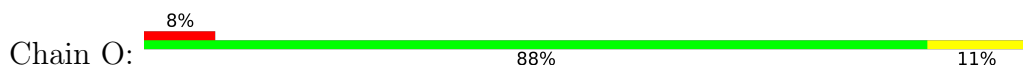
- Molecule 19: 60S ribosomal protein L14-A



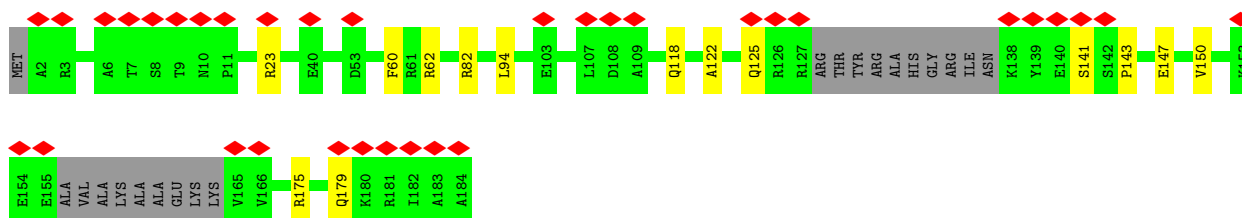
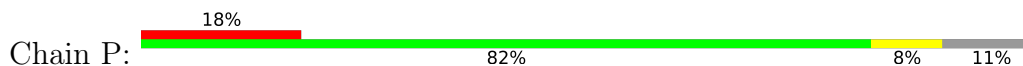
- Molecule 20: Large ribosomal subunit protein eL15A



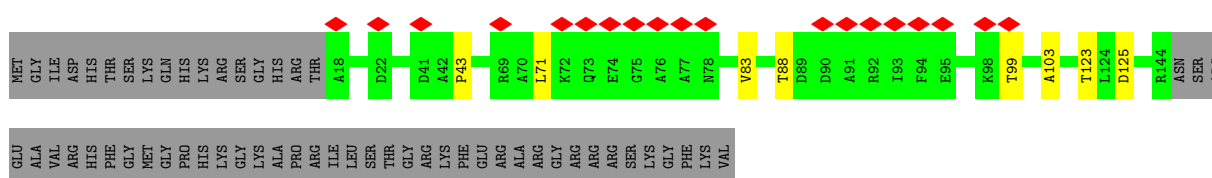
- Molecule 21: Large ribosomal subunit protein uL13A



- Molecule 22: 60S ribosomal protein L17-A

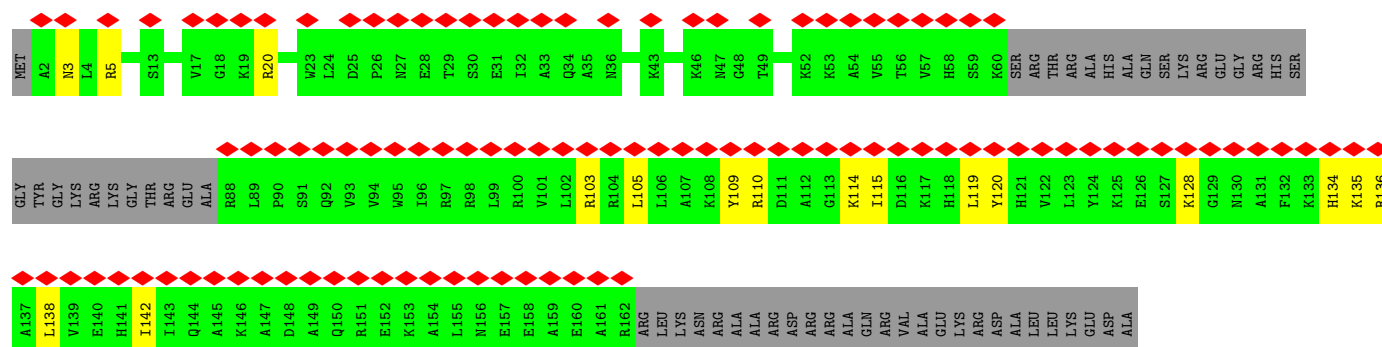


- Molecule 23: 60S ribosomal protein L18-A

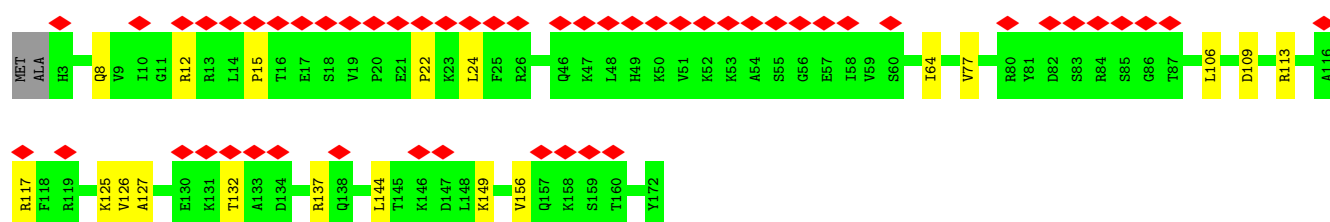
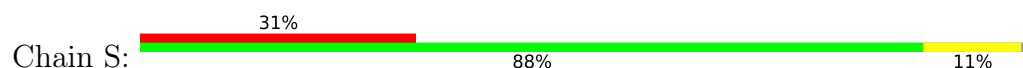


- Molecule 24: 60S ribosomal protein L19-A

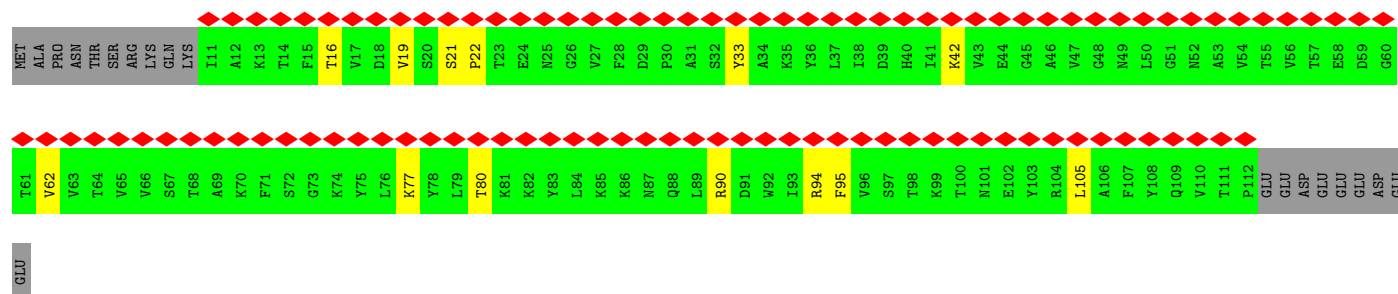
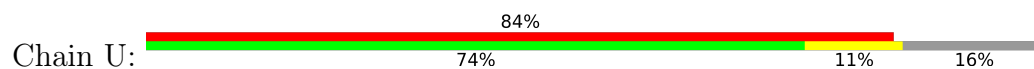




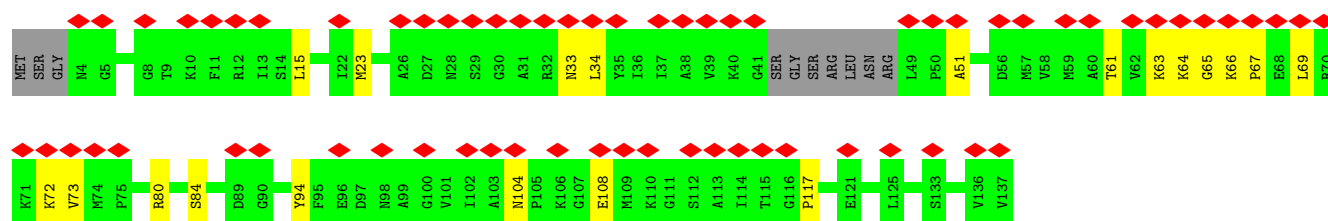
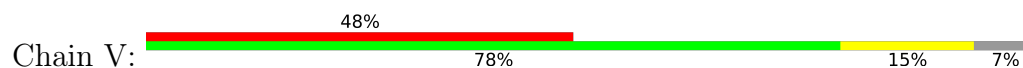
• Molecule 25: Large ribosomal subunit protein eL20A



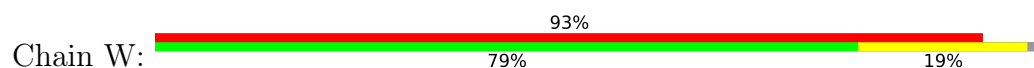
• Molecule 26: 60S ribosomal protein L22-A

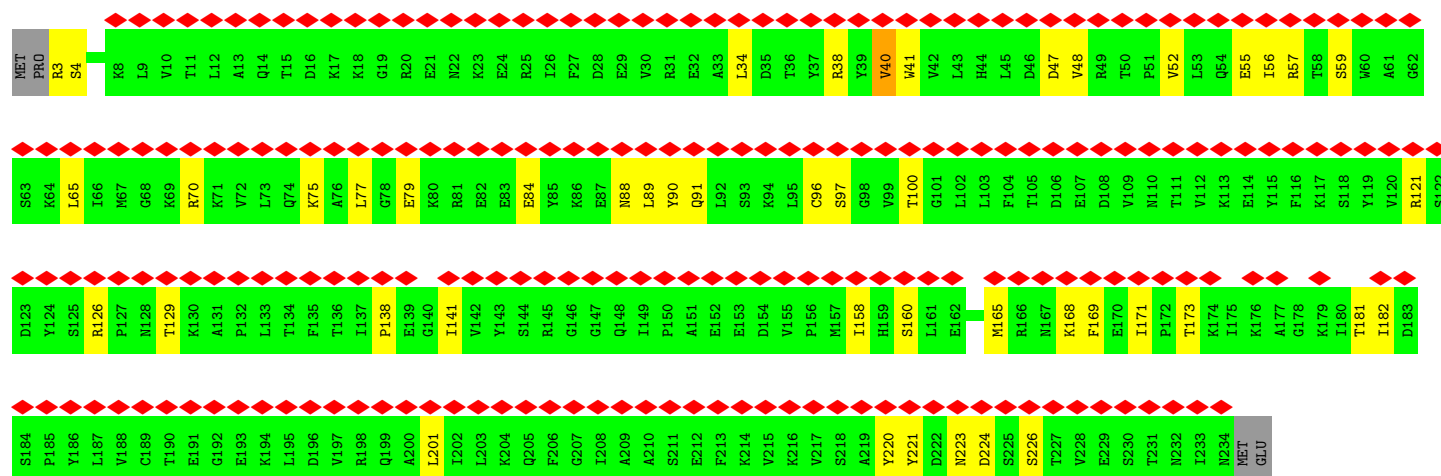


• Molecule 27: 60S ribosomal protein L23-A

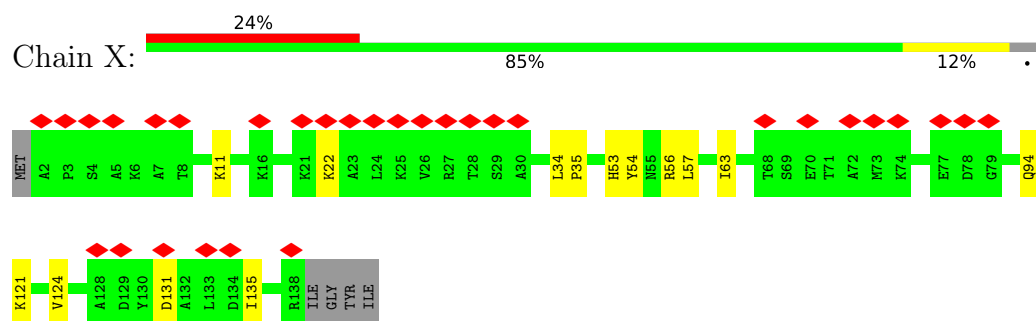


• Molecule 28: Ribosome assembly factor MRT4

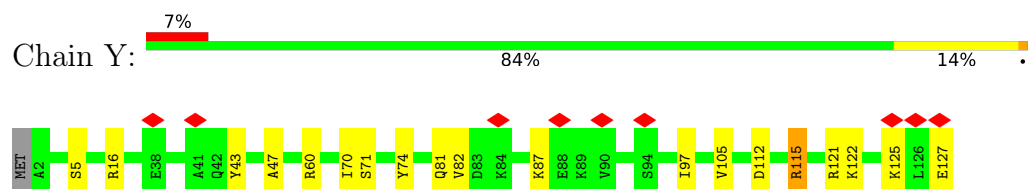




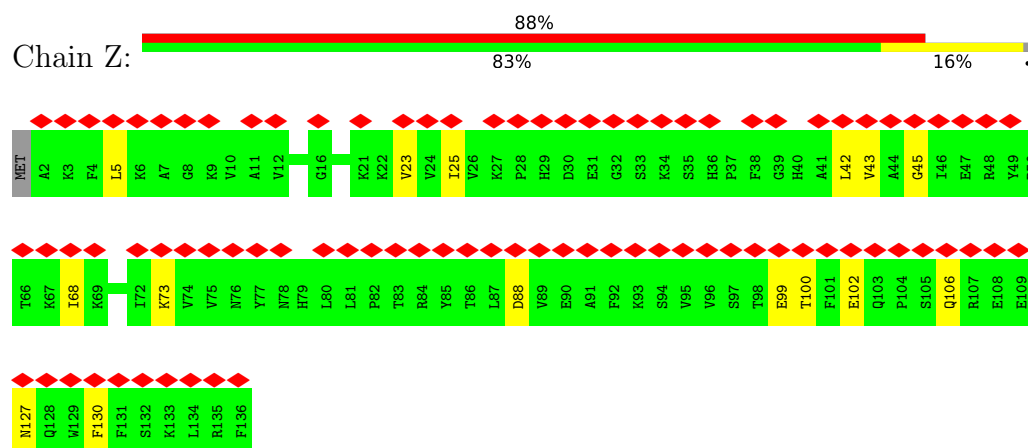
• Molecule 29: 60S ribosomal protein L25



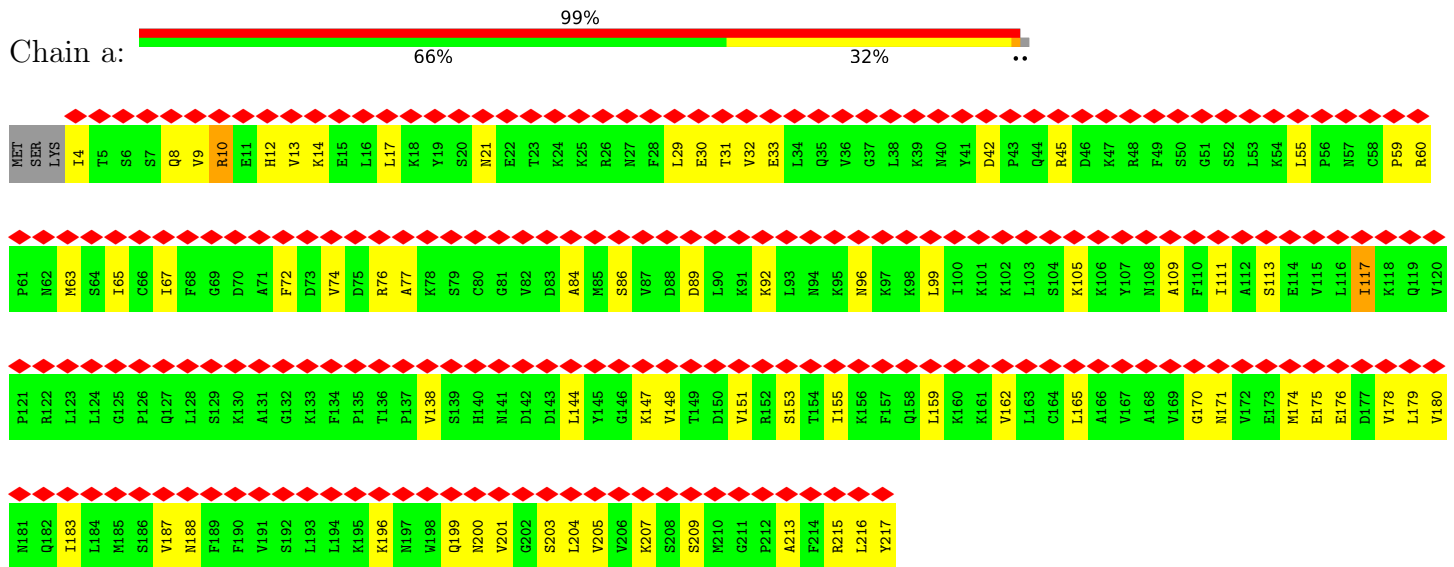
• Molecule 30: 60S ribosomal protein L26-A



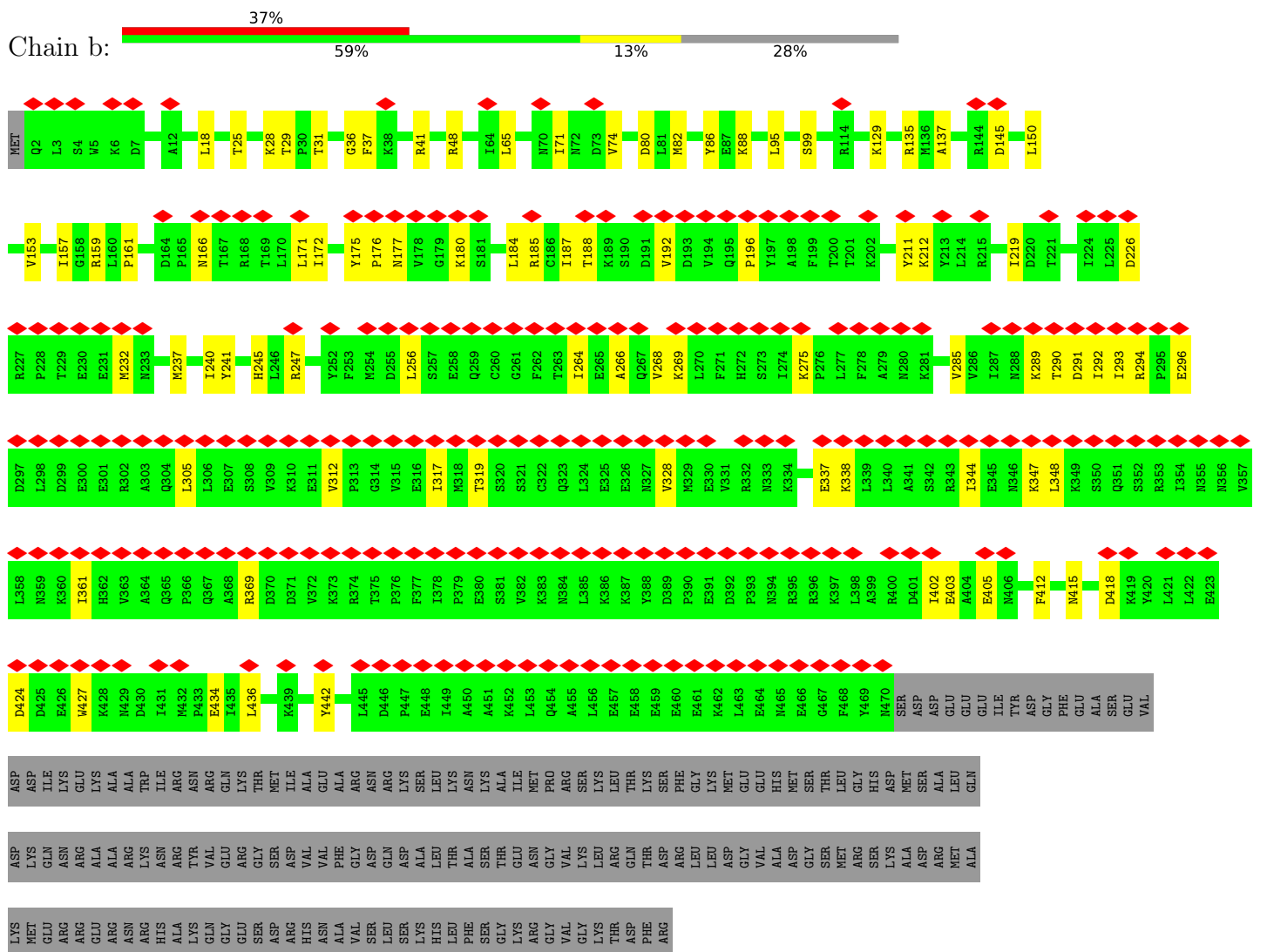
• Molecule 31: 60S ribosomal protein L27-A



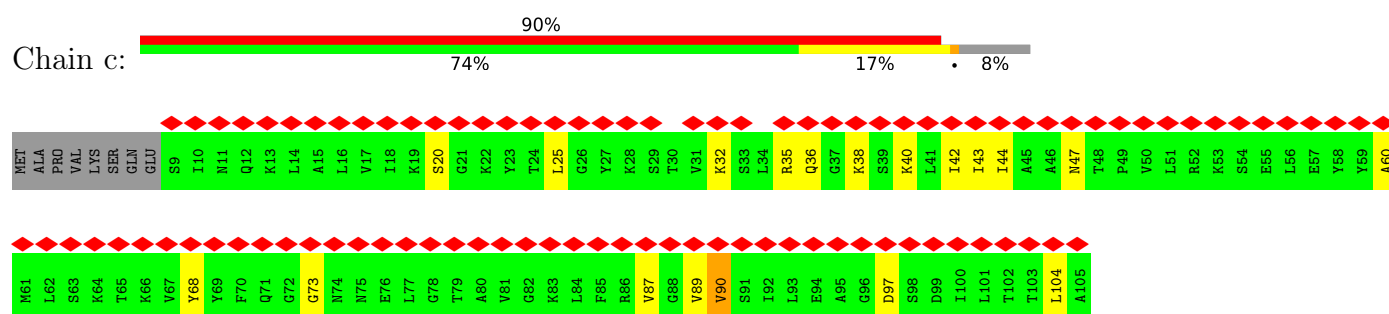
• Molecule 32: Large ribosomal subunit protein uL1A



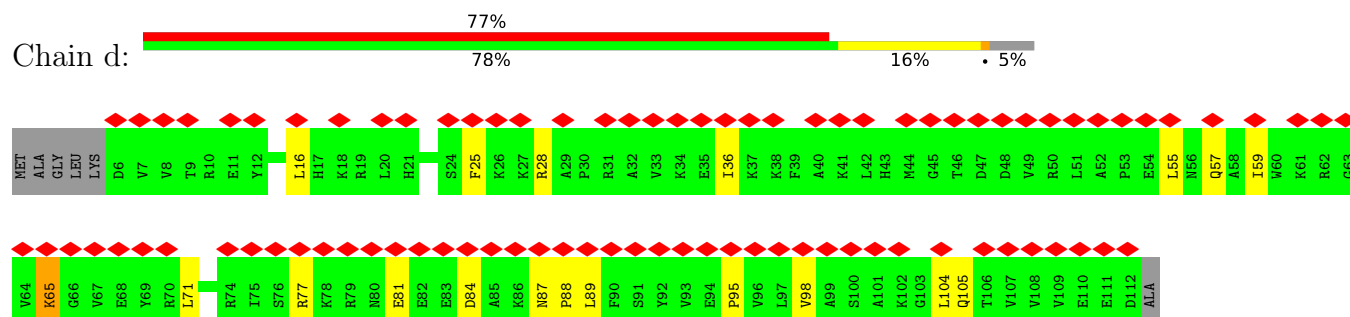
- Molecule 33: Nucleolar GTP-binding protein 1



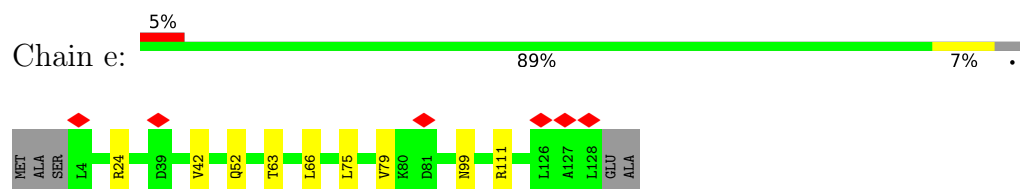
- Molecule 34: 60S ribosomal protein L30



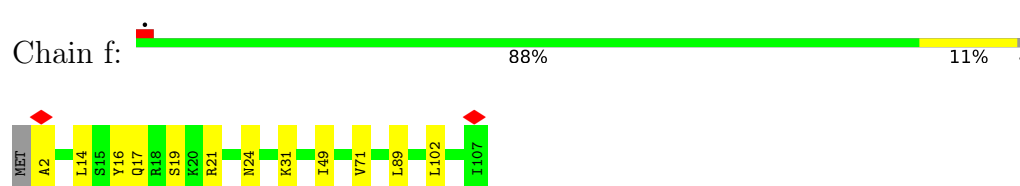
- Molecule 35: 60S ribosomal protein L31-A



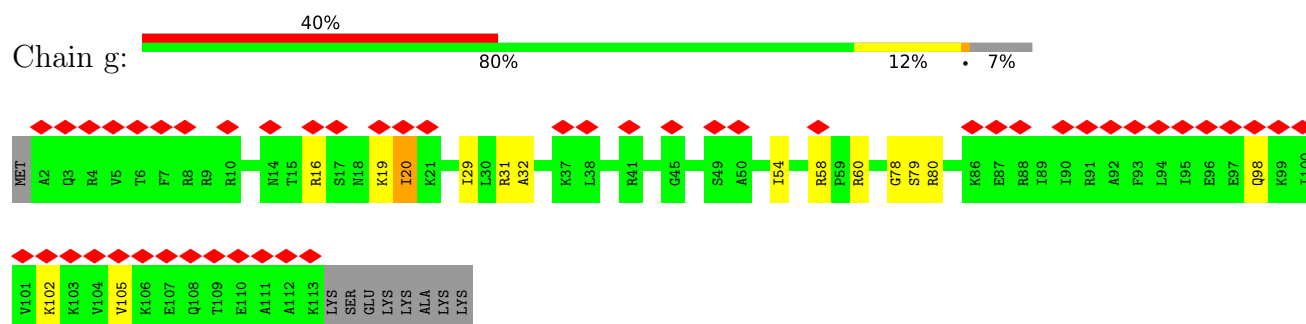
- Molecule 36: 60S ribosomal protein L32



- Molecule 37: 60S ribosomal protein L33-A

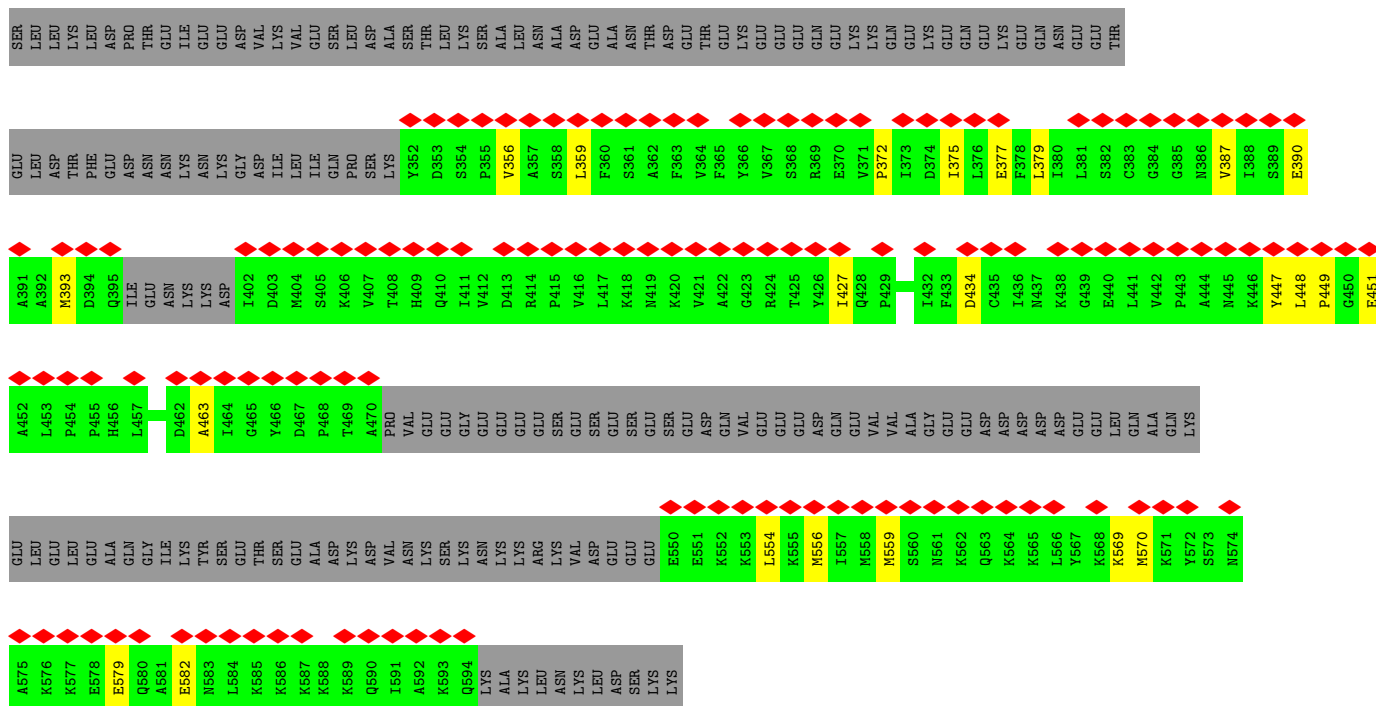


- Molecule 38: 60S ribosomal protein L34-A

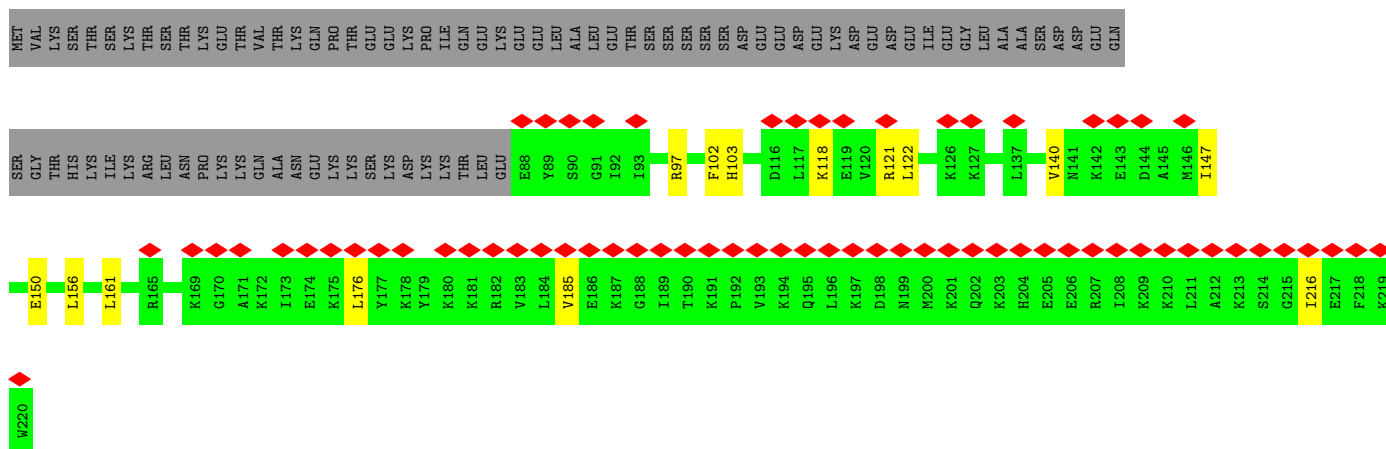


- Molecule 39: 60S ribosomal protein L35-A

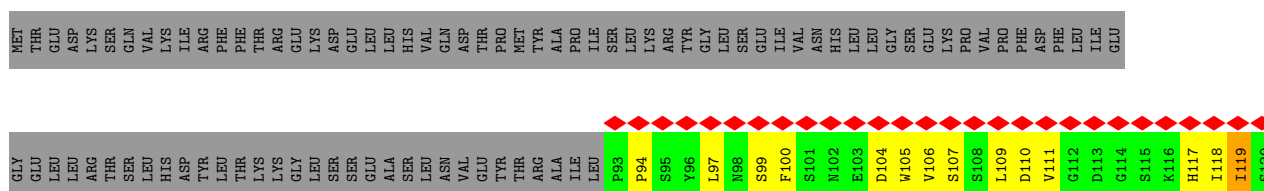
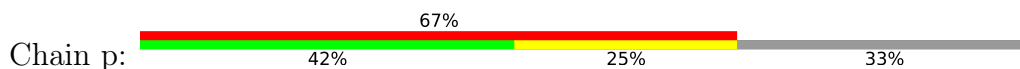


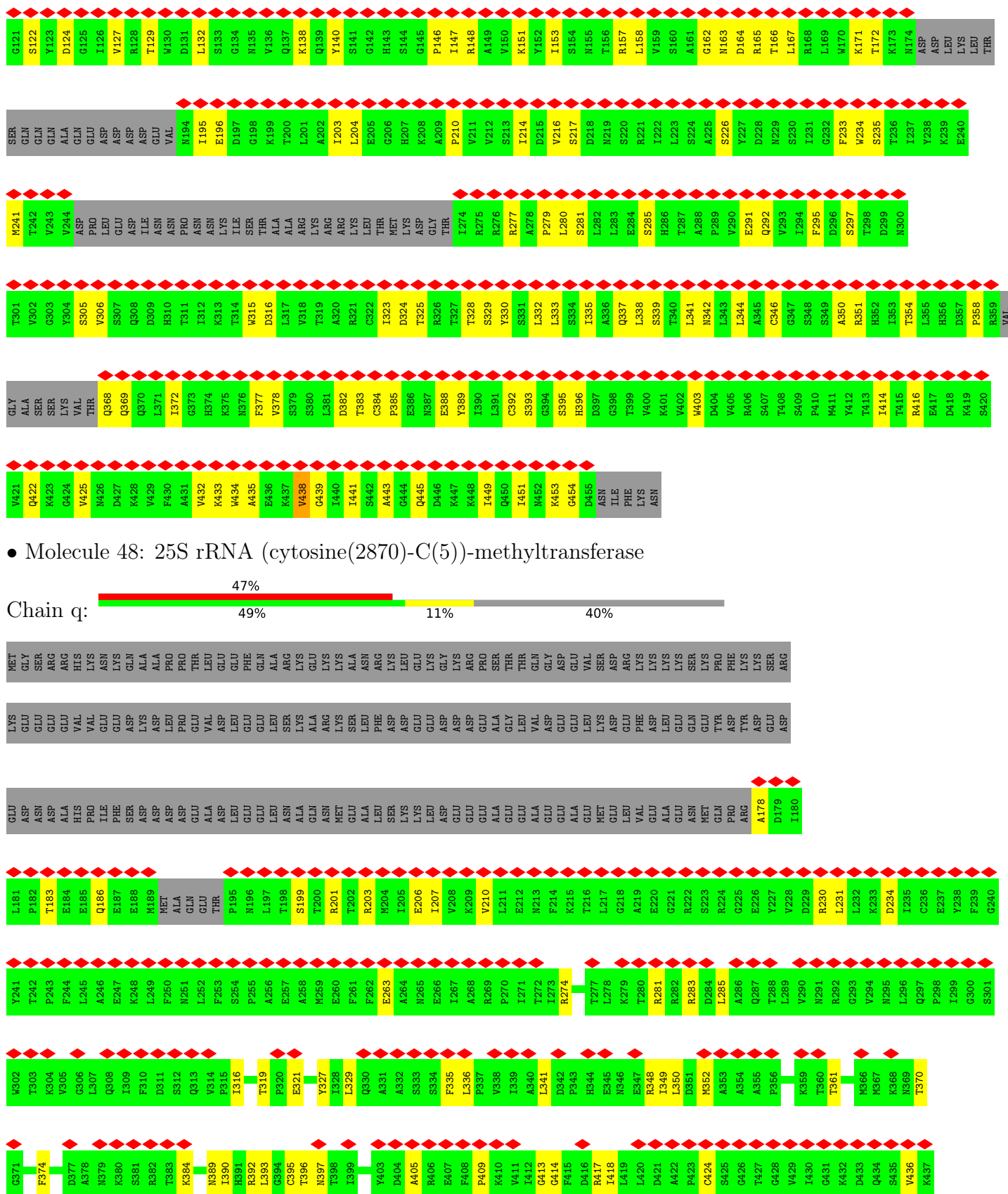


- Molecule 46: Ribosome biogenesis protein 15

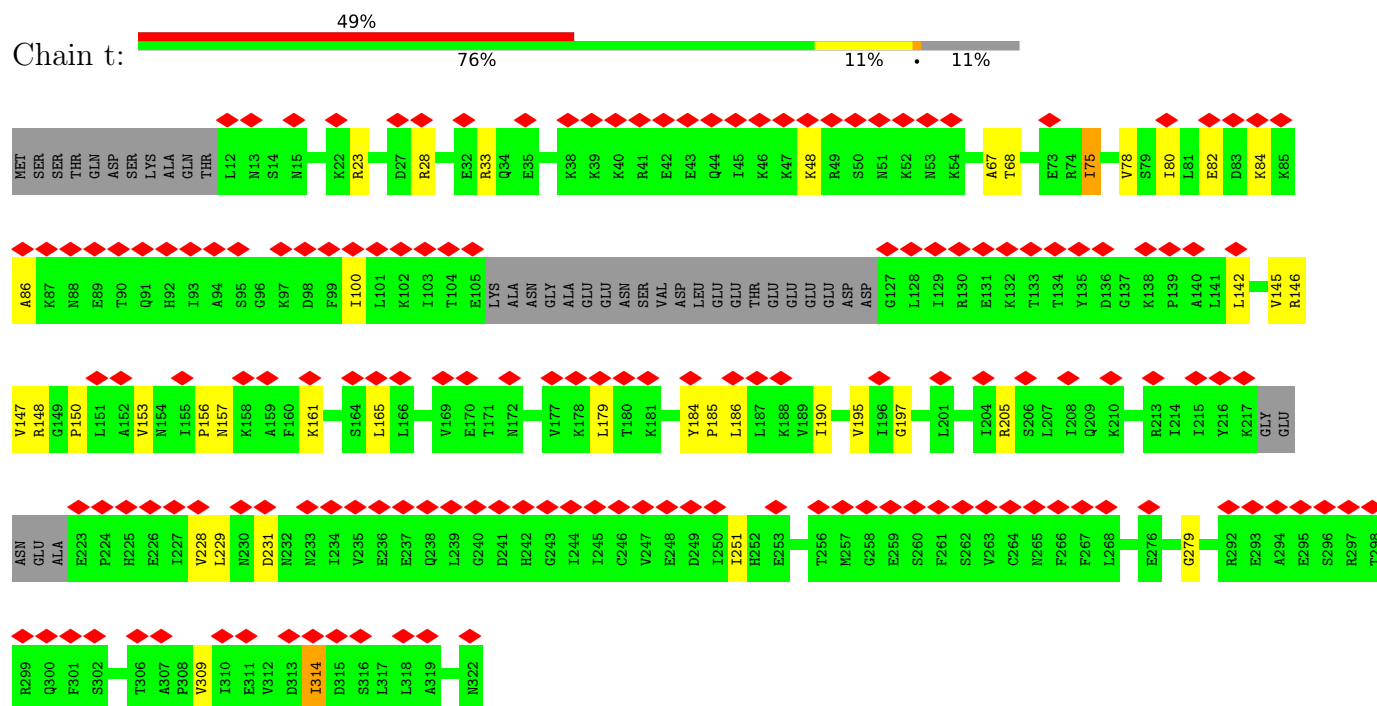


- Molecule 47: YTM1 isoform 1

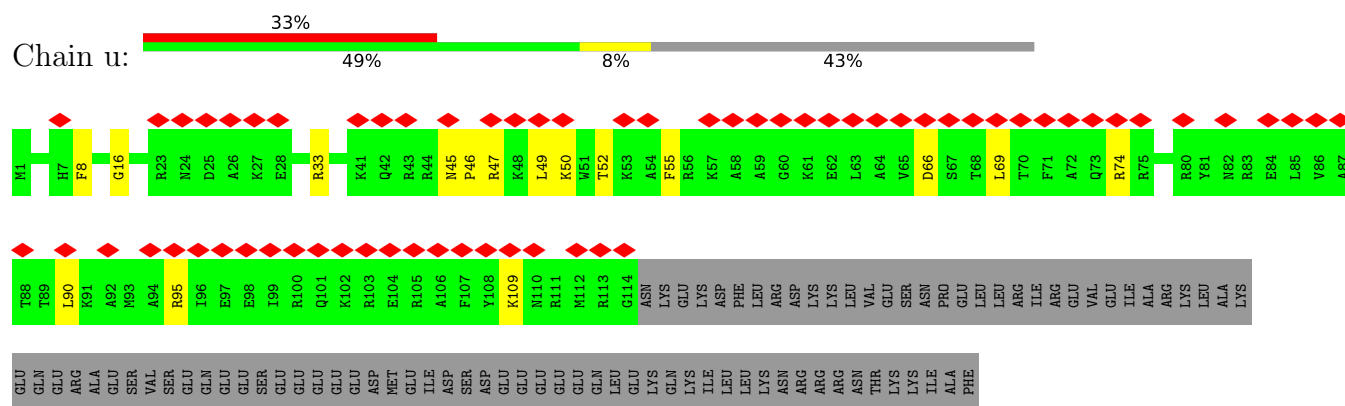




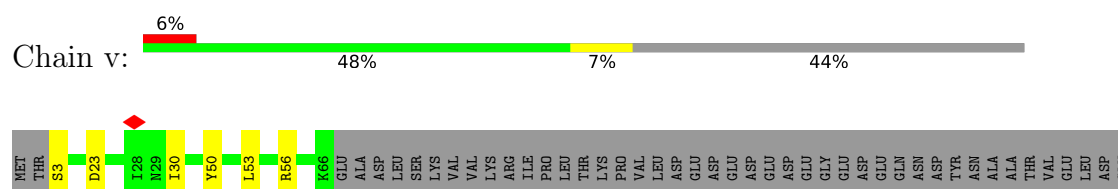
- Molecule 51: Ribosome biogenesis protein RLP7

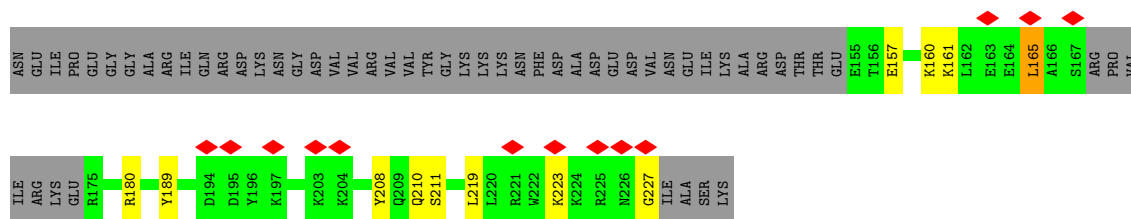


- Molecule 52: Ribosome biogenesis protein RLP24

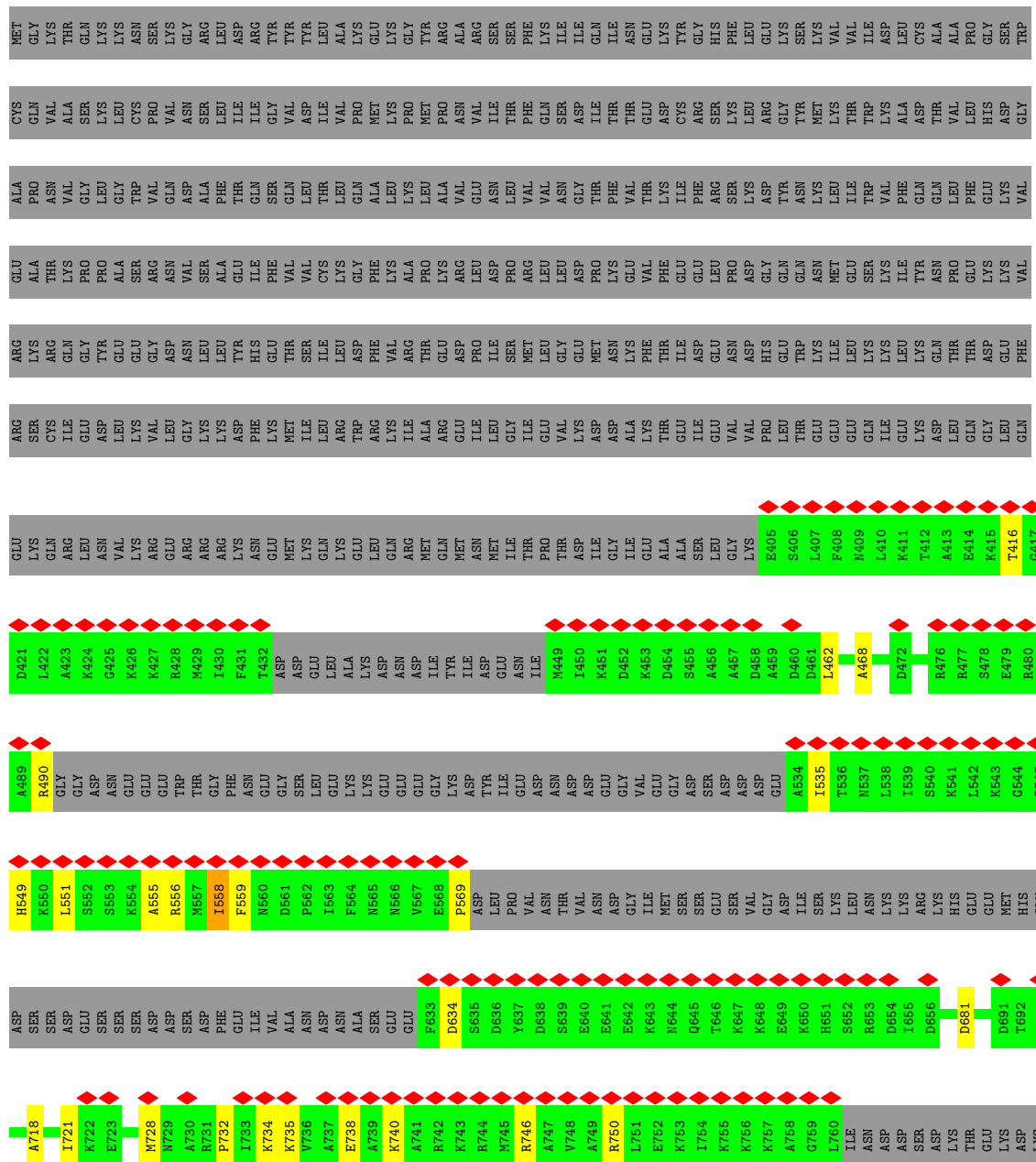


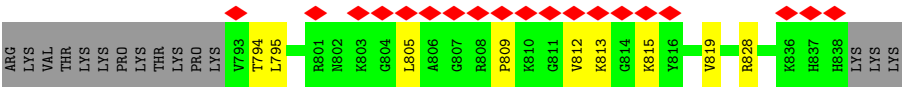
- Molecule 53: Nucleolar protein 16



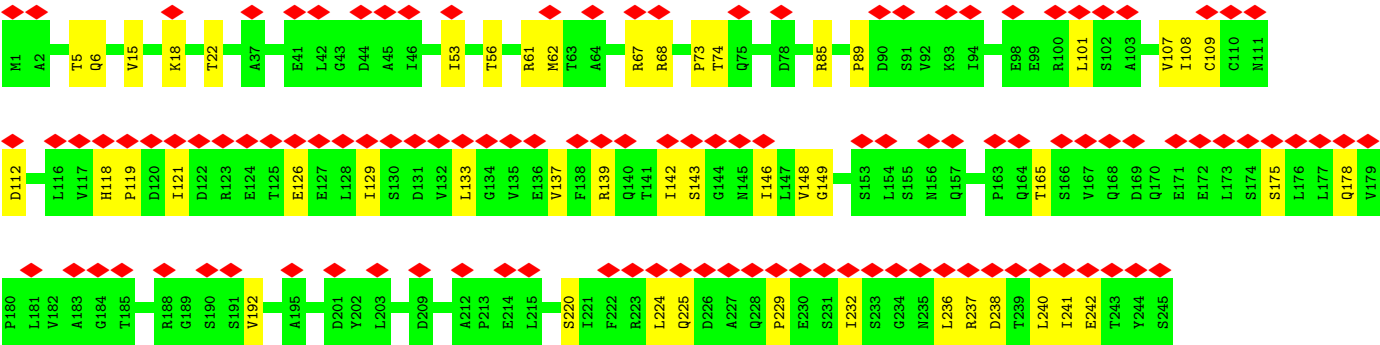
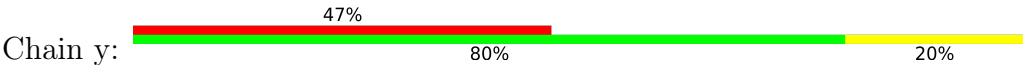


• Molecule 54: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase

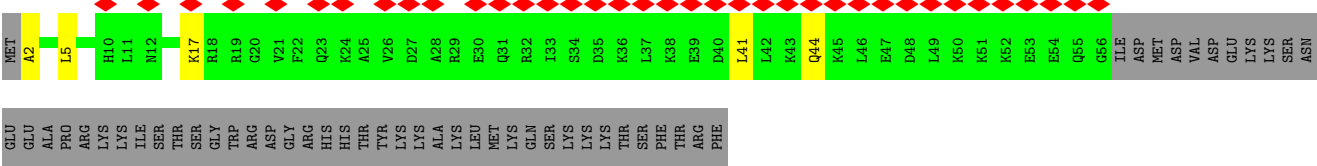




• Molecule 55: Eukaryotic translation initiation factor 6



• Molecule 56: UPF0642 protein YBL028C



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19700	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 ($e^-/\text{\AA}^2$)	39.3	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.348	Depositor
Minimum map value	-0.191	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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, K, GDP, ADP

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	1	0.10	0/59643	0.24	0/92963
2	2	0.11	0/3676	0.25	0/5721
3	3	0.09	0/5348	0.26	0/7191
4	6	0.09	0/2050	0.21	0/3186
5	7	0.08	0/1102	0.20	0/1468
6	8	0.09	0/3937	0.22	0/5301
7	A	0.10	0/2078	0.28	0/2803
8	B	0.10	0/2724	0.27	0/3659
9	C	0.10	0/2776	0.27	0/3758
10	D	0.10	0/3516	0.26	0/4741
11	E	0.09	0/1260	0.26	0/1694
12	F	0.10	0/1772	0.27	0/2384
13	G	0.10	0/1575	0.27	0/2125
14	H	0.10	0/1523	0.30	0/2051
15	I	0.10	0/4262	0.24	0/5740
16	J	0.11	0/1232	0.27	0/1642
17	K	0.09	0/2284	0.24	0/3082
18	L	0.11	0/1009	0.29	0/1355
19	M	0.11	0/1068	0.25	0/1438
20	N	0.10	0/1654	0.27	0/2212
21	O	0.12	0/1585	0.27	0/2128
22	P	0.11	0/1311	0.27	0/1760
23	Q	0.10	0/987	0.23	0/1335
24	R	0.08	0/1095	0.21	0/1465
25	S	0.10	0/1468	0.28	0/1973
26	U	0.08	0/825	0.22	0/1120
27	V	0.10	0/953	0.28	0/1282
28	W	0.10	0/1902	0.26	0/2564
29	X	0.09	0/1083	0.24	0/1458
30	Y	0.11	0/1004	0.32	0/1341
31	Z	0.08	0/1118	0.21	0/1497
32	a	0.10	0/1722	0.27	0/2313

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.10	0/3877	0.27	0/5232
34	c	0.07	0/751	0.20	0/1008
35	d	0.10	0/887	0.26	0/1191
36	e	0.09	0/1030	0.28	0/1379
37	f	0.11	0/868	0.28	0/1168
38	g	0.09	0/891	0.21	0/1191
39	h	0.10	0/978	0.24	0/1301
40	i	0.12	0/582	0.25	0/770
41	j	0.11	0/592	0.32	0/785
42	k	0.09	0/618	0.23	0/826
43	l	0.10	0/1425	0.26	0/1922
44	m	0.11	0/5511	0.28	0/7471
45	n	0.10	0/3544	0.23	0/4766
46	o	0.08	0/1129	0.25	0/1502
47	p	0.11	0/2434	0.32	0/3299
48	q	0.10	0/2958	0.25	0/4000
49	r	0.09	0/1765	0.24	0/2353
50	s	0.09	0/301	0.23	0/386
51	t	0.10	0/2319	0.24	0/3108
52	u	0.09	0/979	0.23	0/1302
53	v	0.09	0/1100	0.24	0/1456
54	w	0.08	0/2265	0.22	0/3009
55	y	0.10	0/1878	0.29	0/2556
56	z	0.09	0/445	0.19	0/585
All	All	0.10	0/158669	0.25	0/227316

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	53292	0	26784	570	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	2	3291	0	1665	35	0
3	3	5253	0	5380	86	0
4	6	1838	0	927	11	0
5	7	1093	0	1163	13	0
6	8	3868	0	3980	72	0
7	A	2032	0	2036	42	0
8	B	2670	0	2744	37	0
9	C	2725	0	2847	23	0
10	D	3451	0	3578	68	0
11	E	1239	0	1326	15	0
12	F	1735	0	1818	17	0
13	G	1549	0	1637	15	0
14	H	1502	0	1572	14	0
15	I	4201	0	4337	54	0
16	J	1215	0	1245	13	0
17	K	2248	0	2325	31	0
18	L	991	0	1044	16	0
19	M	1053	0	1149	8	0
20	N	1621	0	1678	20	0
21	O	1555	0	1659	17	0
22	P	1292	0	1322	10	0
23	Q	973	0	1058	5	0
24	R	1082	0	1160	15	0
25	S	1432	0	1470	14	0
26	U	808	0	822	10	0
27	V	939	0	983	13	0
28	W	1870	0	1902	32	0
29	X	1068	0	1153	11	0
30	Y	993	0	1081	11	0
31	Z	1092	0	1155	12	0
32	a	1695	0	1781	61	0
33	b	3806	0	3861	63	0
34	c	743	0	797	11	0
35	d	873	0	914	13	0
36	e	1009	0	1080	7	0
37	f	850	0	880	9	0
38	g	881	0	948	9	0
39	h	969	0	1078	5	0
40	i	578	0	629	11	0
41	j	580	0	584	8	0
42	k	612	0	682	7	0
43	l	1394	0	1426	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	m	5377	0	5363	76	0
45	n	3470	0	3586	31	0
46	o	1107	0	1159	8	0
47	p	2391	0	2366	77	0
48	q	2902	0	2927	44	0
49	r	1738	0	1837	14	0
50	s	301	0	359	4	0
51	t	2293	0	2449	28	0
52	u	959	0	992	12	0
53	v	1087	0	1133	15	0
54	w	2241	0	2318	26	0
55	y	1855	0	1841	33	0
56	z	444	0	478	5	0
57	3	27	0	12	0	0
58	3	1	0	0	0	0
58	b	1	0	0	0	0
59	b	28	0	12	1	0
60	b	1	0	0	0	0
61	g	1	0	0	0	0
61	j	1	0	0	0	0
All	All	150186	0	124492	1665	0

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

All (1665) 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)
10:D:162:MET:HE1	10:D:182:THR:CG2	1.53	1.36
32:a:67:ILE:HG22	32:a:111:ILE:HG23	1.25	1.19
10:D:162:MET:CE	10:D:182:THR:CG2	2.21	1.18
32:a:204:LEU:HD11	32:a:216:LEU:HB2	1.29	1.14
32:a:111:ILE:HD11	32:a:147:LYS:HB3	1.25	1.14
43:l:68:ILE:HD11	48:q:396:THR:HG22	1.22	1.10
28:W:141:ILE:HG13	28:W:181:THR:HG22	1.17	1.10
32:a:204:LEU:CD1	32:a:216:LEU:HB2	1.89	1.00
10:D:162:MET:CE	10:D:182:THR:HG22	1.91	0.94
28:W:141:ILE:HG13	28:W:181:THR:CG2	1.97	0.94
10:D:162:MET:HE1	10:D:182:THR:HG22	0.96	0.94
28:W:141:ILE:CG1	28:W:181:THR:HG22	2.03	0.89
10:D:162:MET:CE	10:D:182:THR:HG23	2.02	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:a:67:ILE:HA	32:a:111:ILE:O	1.75	0.86
32:a:67:ILE:HG22	32:a:111:ILE:CG2	2.05	0.85
43:l:68:ILE:CD1	48:q:396:THR:HG22	2.05	0.84
43:l:68:ILE:HD11	48:q:396:THR:CG2	2.06	0.84
55:y:5:THR:HG22	55:y:6:GLN:H	1.42	0.84
21:O:84:LEU:HD13	21:O:102:LEU:HD21	1.60	0.83
32:a:204:LEU:HD11	32:a:216:LEU:CB	2.09	0.83
55:y:5:THR:HG22	55:y:6:GLN:N	1.95	0.80
1:1:351:A:H1'	2:2:53:A:H1'	1.63	0.80
7:A:110:ILE:HD13	7:A:152:ILE:HG22	1.63	0.80
32:a:113:SER:O	32:a:117:ILE:HB	1.81	0.80
10:D:232:THR:HG22	10:D:233:THR:N	1.98	0.78
21:O:84:LEU:HD13	21:O:102:LEU:CD2	2.13	0.78
26:U:21:SER:OG	26:U:22:PRO:HD3	1.83	0.78
21:O:84:LEU:HD11	21:O:102:LEU:HD22	1.67	0.76
39:h:119:LYS:HB2	53:v:56:ARG:HG2	1.67	0.76
15:I:267:ASN:OD1	15:I:268:PHE:N	2.18	0.76
1:1:909:G:H5'	54:w:746:ARG:HD2	1.68	0.75
1:1:978:G:H5'	1:1:979:U:H5'	1.68	0.75
17:K:279:ILE:HB	17:K:292:TYR:HB3	1.69	0.75
47:p:235:SER:HB2	47:p:280:LEU:HD11	1.70	0.74
32:a:111:ILE:CD1	32:a:147:LYS:HB3	2.13	0.74
9:C:20:LEU:HD11	9:C:252:GLU:HG3	1.70	0.74
3:3:556:LEU:HB2	3:3:592:ARG:HE	1.53	0.74
1:1:2397:A:H61	1:1:2983:C:H42	1.33	0.74
10:D:232:THR:HG22	10:D:233:THR:H	1.52	0.74
3:3:459:ILE:HG22	3:3:485:ILE:HB	1.71	0.73
1:1:2450:G:N1	1:1:2497:U:N3	2.37	0.73
47:p:346:CYS:HG	47:p:354:THR:HG1	1.25	0.73
15:I:470:ARG:HB2	15:I:542:LYS:HE2	1.70	0.72
6:8:582:ILE:O	6:8:629:ARG:NH2	2.23	0.72
21:O:84:LEU:CD1	21:O:102:LEU:HD22	2.20	0.72
21:O:84:LEU:CD1	21:O:102:LEU:CD2	2.68	0.72
32:a:67:ILE:CD1	32:a:144:LEU:HD21	2.20	0.72
9:C:177:ASP:OD2	9:C:247:PHE:CD2	2.43	0.72
43:l:21:GLY:HA3	43:l:94:LYS:HD2	1.71	0.71
1:1:1310:G:HO2'	1:1:2380:U:HO2'	1.37	0.71
49:r:196:PRO:HG2	49:r:224:ASN:HB3	1.72	0.71
32:a:196:LYS:HB2	32:a:200:ASN:HB2	1.73	0.71
22:P:125:GLN:HG3	22:P:141:SER:HB3	1.72	0.71
47:p:328:THR:HG22	47:p:329:SER:N	2.06	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:V:61:THR:HG22	27:V:73:VAL:HG22	1.73	0.70
1:1:909:G:H2'	1:1:910:G:H8	1.56	0.70
1:1:2457:G:O2'	1:1:2481:G:N2	2.24	0.70
38:g:16:ARG:HA	38:g:19:LYS:HE2	1.73	0.70
7:A:197:THR:HG21	7:A:203:TYR:HB2	1.74	0.70
1:1:808:A:H2'	1:1:809:G:C8	2.25	0.70
1:1:685:G:OP1	18:L:39:ARG:NH2	2.24	0.69
3:3:685:LYS:O	3:3:707:ARG:NH2	2.26	0.69
55:y:68:ARG:NH2	55:y:112:ASP:O	2.25	0.69
6:8:540:ALA:N	6:8:553:TYR:HH	1.90	0.69
1:1:991:G:H1	1:1:1058:U:H3	1.41	0.68
43:l:20:ILE:HD11	43:l:24:ILE:HG23	1.75	0.68
6:8:433:TYR:HB3	6:8:486:ILE:HD11	1.75	0.68
1:1:959:C:O2'	16:J:309:ARG:NH2	2.26	0.68
52:u:74:ARG:HH22	55:y:74:THR:HG23	1.59	0.68
44:m:599:LYS:HB2	44:m:612:VAL:HB	1.75	0.68
14:H:57:VAL:HG23	14:H:68:LEU:HD13	1.76	0.68
1:1:358:G:N2	1:1:361:A:OP2	2.28	0.67
1:1:704:U:H3'	1:1:705:A:H5''	1.77	0.67
33:b:187:ILE:HG22	33:b:188:THR:HG23	1.75	0.67
7:A:113:TYR:HB2	7:A:224:ILE:HD11	1.75	0.67
24:R:105:LEU:HD23	24:R:138:LEU:HD23	1.76	0.67
1:1:1493:G:N2	1:1:1493:G:OP2	2.28	0.67
55:y:5:THR:CG2	55:y:6:GLN:H	2.08	0.67
1:1:1661:G:H2'	1:1:1662:G:C8	2.29	0.67
18:L:43:ALA:O	18:L:47:ALA:HA	1.94	0.67
1:1:2340:U:H2'	1:1:2341:A:H8	1.60	0.67
1:1:794:U:H2'	1:1:795:G:H8	1.60	0.66
1:1:2943:G:OP1	33:b:41:ARG:NH1	2.27	0.66
47:p:328:THR:HG22	47:p:329:SER:H	1.60	0.66
32:a:67:ILE:HD11	32:a:84:ALA:HB2	1.77	0.66
3:3:344:ALA:O	3:3:525:ARG:NH2	2.27	0.66
44:m:419:PRO:HA	44:m:422:LEU:HB2	1.76	0.66
1:1:895:A:H5''	1:1:896:A:H8	1.60	0.66
18:L:42:ARG:NH1	18:L:51:LEU:O	2.27	0.66
1:1:2393:G:N2	1:1:2394:G:O6	2.29	0.66
6:8:596:ARG:HG2	6:8:600:LYS:HE3	1.78	0.66
1:1:959:C:OP1	16:J:302:ARG:NH2	2.28	0.66
1:1:546:C:OP1	1:1:547:G:N2	2.29	0.66
10:D:162:MET:HE2	10:D:182:THR:CG2	2.25	0.66
18:L:62:THR:HG22	18:L:64:LYS:H	1.60	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:529:LYS:HE3	3:3:531:TRP:HE1	1.59	0.65
10:D:470:LEU:HD13	44:m:254:MET:HE3	1.77	0.65
52:u:66:ASP:HB3	52:u:69:LEU:HD13	1.78	0.65
1:1:3113:A:H4'	14:H:69:ARG:HG2	1.78	0.65
1:1:75:G:OP2	18:L:104:ARG:NH2	2.29	0.65
1:1:959:C:O2	1:1:961:C:N4	2.29	0.65
33:b:185:ARG:NH1	33:b:192:VAL:O	2.29	0.65
1:1:1467:A:O2'	1:1:1468:A:O2'	2.14	0.65
8:B:95:THR:HG22	8:B:97:ARG:H	1.60	0.65
31:Z:56:LYS:HD2	51:t:28:ARG:HD2	1.79	0.65
45:n:372:PRO:HB2	45:n:375:ILE:HG12	1.78	0.65
7:A:80:LEU:HD12	40:i:67:LYS:HG3	1.79	0.65
1:1:3014:U:H3	1:1:3040:A:H62	1.43	0.65
3:3:706:ARG:HD3	33:b:145:ASP:HB3	1.79	0.65
15:I:313:GLU:OE1	15:I:316:ARG:NH2	2.30	0.65
13:G:75:ILE:HD11	20:N:18:VAL:HG13	1.78	0.64
44:m:378:PRO:HB3	51:t:231:ASP:HB3	1.78	0.64
1:1:216:G:OP1	30:Y:16:ARG:NH1	2.29	0.64
48:q:352:MET:HE2	48:q:405:ALA:HB1	1.79	0.64
51:t:157:ASN:OD1	51:t:161:LYS:NZ	2.30	0.64
6:8:550:THR:HB	6:8:553:TYR:HB2	1.77	0.64
33:b:177:ASN:ND2	33:b:196:PRO:O	2.30	0.64
1:1:1654:A:OP2	15:I:371:LYS:NZ	2.26	0.64
6:8:605:VAL:HG12	6:8:609:LYS:HE3	1.78	0.64
10:D:471:ALA:HA	10:D:482:PRO:HG3	1.80	0.64
20:N:68:ARG:NH1	20:N:124:ASP:O	2.31	0.64
42:k:22:THR:HG22	42:k:74:LYS:HB3	1.78	0.64
44:m:518:PHE:O	47:p:165:ARG:NH1	2.31	0.64
1:1:2891:U:HO2'	56:z:2:ALA:N	1.96	0.64
1:1:3055:U:H3	1:1:3086:A:H62	1.46	0.64
3:3:693:ARG:HH22	33:b:159:ARG:HH22	1.45	0.64
1:1:2830:G:H2'	1:1:2831:G:C8	2.33	0.64
25:S:109:ASP:OD1	25:S:113:ARG:NH1	2.29	0.64
1:1:100:A:H3'	1:1:101:G:H21	1.61	0.64
1:1:733:G:N2	1:1:736:A:OP2	2.31	0.64
47:p:109:LEU:HD13	47:p:441:ILE:HG13	1.80	0.64
6:8:274:VAL:HG13	6:8:304:LEU:HD13	1.80	0.63
36:e:42:VAL:O	36:e:52:GLN:NE2	2.31	0.63
15:I:277:LEU:HD23	15:I:280:ILE:HD11	1.81	0.63
38:g:54:ILE:HD11	38:g:78:GLY:HA2	1.80	0.63
44:m:165:TYR:O	44:m:182:ARG:NH2	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:225:LEU:HD22	7:A:235:LYS:HD3	1.80	0.63
1:1:155:G:H1	10:D:155:ARG:HH22	1.46	0.63
1:1:3343:G:H21	1:1:3362:A:H2	1.45	0.63
32:a:207:LYS:HB3	32:a:213:ALA:HA	1.81	0.63
1:1:1210:U:H5	28:W:3:ARG:HG2	1.64	0.62
7:A:31:GLN:HB2	7:A:163:PRO:HG3	1.81	0.62
6:8:493:PRO:HG3	6:8:543:PHE:HD1	1.64	0.62
40:i:68:ARG:NH2	54:w:681:ASP:OD2	2.32	0.62
1:1:1504:A:OP1	22:P:23:ARG:NH1	2.32	0.62
7:A:226:ILE:HB	7:A:237:TYR:HB3	1.80	0.62
15:I:563:GLU:HG3	15:I:628:PRO:HG3	1.81	0.62
34:c:43:ILE:HB	34:c:90:VAL:HG22	1.80	0.62
44:m:285:GLU:OE1	44:m:287:ARG:NH1	2.32	0.62
45:n:127:ASP:OD1	45:n:130:ARG:NH1	2.32	0.62
45:n:556:MET:HB2	45:n:559:MET:HE2	1.82	0.62
55:y:118:HIS:HE2	55:y:146:ILE:HD12	1.64	0.62
1:1:728:G:H5'	23:Q:43:PRO:HB2	1.81	0.62
25:S:8:GLN:HB3	25:S:64:ILE:HD11	1.80	0.62
1:1:156:G:H22	18:L:91:ARG:HH12	1.46	0.62
4:6:228:U:O2'	51:t:48:LYS:NZ	2.32	0.62
20:N:183:THR:HG22	20:N:187:ARG:HB2	1.81	0.62
43:l:115:LYS:HD2	43:l:156:MET:HB3	1.81	0.62
44:m:277:MET:HE3	53:v:180:ARG:HH11	1.63	0.62
1:1:1469:C:H42	1:1:1508:C:H41	1.48	0.62
32:a:9:VAL:HG12	32:a:180:VAL:HG23	1.81	0.62
1:1:655:C:H2'	1:1:656:A:H8	1.65	0.61
17:K:101:ASN:H	17:K:269:GLN:HE22	1.48	0.61
46:o:121:ARG:HD3	46:o:176:LEU:HB2	1.82	0.61
7:A:84:ASN:OD1	7:A:103:LYS:NZ	2.29	0.61
1:1:714:G:H4'	1:1:753:C:H4'	1.82	0.61
30:Y:70:ILE:HD13	30:Y:82:VAL:HG22	1.80	0.61
3:3:612:ASN:ND2	55:y:242:GLU:O	2.34	0.61
1:1:1553:U:H4'	1:1:1554:U:H5'	1.82	0.61
47:p:127:VAL:HB	47:p:140:TYR:HB2	1.83	0.61
1:1:959:C:H1'	1:1:961:C:H41	1.66	0.61
20:N:99:ARG:NH2	20:N:118:SER:O	2.33	0.61
32:a:204:LEU:CD1	32:a:216:LEU:HD12	2.30	0.61
47:p:439:GLY:HA3	47:p:454:GLY:H	1.65	0.61
4:6:230:A:OP1	51:t:148:ARG:NH1	2.34	0.61
10:D:232:THR:CG2	10:D:233:THR:H	2.13	0.61
1:1:1154:A:OP2	1:1:2371:G:N1	2.29	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:232:THR:CG2	10:D:233:THR:N	2.64	0.60
24:R:109:TYR:HB3	24:R:115:ILE:HD13	1.82	0.60
27:V:15:LEU:HD13	27:V:51:ALA:HB3	1.83	0.60
1:1:3050:U:O2'	52:u:16:GLY:O	2.20	0.60
15:I:398:GLU:O	15:I:402:ASN:ND2	2.33	0.60
1:1:1459:C:OP2	1:1:1468:A:N6	2.34	0.60
38:g:98:GLN:HE21	38:g:102:LYS:HE3	1.66	0.60
2:2:103:G:OP2	2:2:105:A:O2'	2.19	0.60
1:1:531:G:H2'	1:1:532:A:C8	2.37	0.60
1:1:909:G:H2'	1:1:910:G:C8	2.36	0.60
1:1:1300:G:H5''	1:1:1301:A:H5'	1.83	0.60
1:1:2479:C:H2'	1:1:2480:A:H8	1.66	0.60
3:3:389:LEU:HD13	3:3:458:LEU:HD22	1.83	0.60
1:1:2880:U:H3	1:1:2946:A:H61	1.50	0.60
17:K:97:LEU:HD11	17:K:205:THR:HG23	1.84	0.60
1:1:2960:C:H5''	5:7:62:ALA:HB2	1.83	0.60
8:B:222:LYS:NZ	8:B:223:GLY:O	2.34	0.60
55:y:5:THR:CG2	55:y:6:GLN:N	2.64	0.60
17:K:100:LEU:HD13	17:K:266:ILE:HG23	1.83	0.60
32:a:204:LEU:HD12	32:a:204:LEU:O	2.01	0.60
1:1:664:U:H2'	1:1:665:A:H8	1.67	0.60
1:1:1231:A:H5''	1:1:1232:C:H5'	1.82	0.60
1:1:1244:A:N1	3:3:694:ASN:ND2	2.49	0.60
10:D:325:GLN:OE1	10:D:328:ARG:NH2	2.35	0.60
13:G:201:THR:HG22	13:G:202:GLU:HG2	1.84	0.60
48:q:178:ALA:HB1	48:q:206:GLU:HB3	1.84	0.60
1:1:297:G:O6	20:N:12:ARG:NH1	2.30	0.60
3:3:245:ASP:O	3:3:267:ARG:NH2	2.34	0.60
29:X:63:ILE:HD12	29:X:102:LEU:HD12	1.83	0.60
44:m:363:GLU:HG2	44:m:364:ARG:HG3	1.84	0.60
32:a:60:ARG:HD2	32:a:63:MET:HB3	1.84	0.59
33:b:266:ALA:HA	33:b:269:LYS:HE2	1.84	0.59
7:A:136:VAL:HB	7:A:176:VAL:HG22	1.82	0.59
32:a:67:ILE:HD13	32:a:144:LEU:HD21	1.84	0.59
33:b:184:LEU:HD23	33:b:192:VAL:HG21	1.84	0.59
47:p:129:THR:HB	47:p:138:LYS:HB2	1.83	0.59
1:1:394:G:N1	1:1:397:A:OP2	2.33	0.59
1:1:501:A:H2'	1:1:502:U:C6	2.38	0.59
1:1:1635:G:N2	1:1:1638:A:OP2	2.33	0.59
1:1:3204:C:H2'	1:1:3205:G:C8	2.37	0.59
1:1:3268:A:H5''	11:E:46:ARG:NH1	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:n:35:LEU:HB3	45:n:71:LEU:HD11	1.84	0.59
51:t:197:GLY:HA3	51:t:314:ILE:HB	1.84	0.59
1:1:820:A:O3'	1:1:894:G:O2'	2.19	0.59
1:1:868:C:H2'	1:1:869:G:C8	2.37	0.59
1:1:3233:C:H2'	1:1:3234:A:C8	2.38	0.59
20:N:24:ARG:NE	54:w:703:GLU:OE2	2.36	0.59
7:A:119:THR:OG1	7:A:121:ASP:OD1	2.20	0.59
15:I:257:LYS:HG3	15:I:297:THR:HG21	1.84	0.59
17:K:86:LYS:NZ	17:K:300:GLU:O	2.33	0.59
18:L:124:ILE:HG23	53:v:165:LEU:HD22	1.85	0.59
32:a:196:LYS:HB3	32:a:199:GLN:HB3	1.84	0.59
7:A:238:GLU:OE2	16:J:196:ASN:ND2	2.36	0.59
8:B:57:VAL:HG13	8:B:357:LYS:HB3	1.85	0.59
32:a:67:ILE:HD12	32:a:144:LEU:HD21	1.84	0.59
43:l:174:ARG:HB2	49:r:163:ARG:HG2	1.85	0.59
15:I:200:THR:HG22	54:w:468:ALA:HB1	1.85	0.59
17:K:333:LEU:HG	51:t:165:LEU:HD22	1.83	0.59
1:1:835:G:O2'	1:1:857:G:N2	2.36	0.59
1:1:2449:A:H2'	1:1:2450:G:C8	2.38	0.59
1:1:3329:U:H5''	8:B:308:MET:HE2	1.83	0.59
6:8:73:THR:HA	6:8:76:GLU:HG2	1.83	0.59
30:Y:5:SER:OG	53:v:23:ASP:OD2	2.20	0.59
1:1:689:U:H3	9:C:227:THR:HG23	1.68	0.58
1:1:2970:C:H3'	1:1:2971:A:H4'	1.84	0.58
1:1:3194:C:O2'	1:1:3195:U:O2	2.21	0.58
3:3:360:LYS:NZ	33:b:74:VAL:O	2.36	0.58
32:a:8:GLN:O	32:a:12:HIS:ND1	2.36	0.58
48:q:370:THR:O	48:q:397:ASN:ND2	2.36	0.58
1:1:656:A:H2'	1:1:657:A:C8	2.39	0.58
33:b:80:ASP:OD2	33:b:245:HIS:NE2	2.37	0.58
1:1:2942:C:O2	1:1:2942:C:H2'	2.02	0.58
10:D:219:ASN:OD1	10:D:222:ARG:NH2	2.37	0.58
29:X:11:LYS:HD2	46:o:147:ILE:HG23	1.85	0.58
32:a:17:LEU:O	32:a:21:ASN:ND2	2.30	0.58
48:q:409:PRO:HB3	48:q:462:SER:HB3	1.84	0.58
1:1:1786:G:H2'	1:1:1787:A:C8	2.38	0.58
1:1:2393:G:H22	1:1:2986:U:H3	1.50	0.58
1:1:3268:A:OP1	11:E:46:ARG:NH2	2.36	0.58
10:D:68:VAL:HG12	10:D:252:VAL:HG21	1.86	0.58
31:Z:25:ILE:HA	31:Z:43:VAL:HG12	1.84	0.58
32:a:138:VAL:HA	32:a:147:LYS:HE3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:275:LYS:HE3	33:b:312:VAL:HG13	1.86	0.58
48:q:348:ARG:NH1	48:q:413:GLY:O	2.36	0.58
1:1:870:G:N2	1:1:871:U:O4	2.36	0.58
3:3:474:GLN:HA	3:3:477:ASN:HD21	1.69	0.58
30:Y:47:ALA:O	30:Y:122:LYS:NZ	2.36	0.58
32:a:32:VAL:N	32:a:170:GLY:O	2.36	0.58
44:m:451:TRP:HZ3	44:m:465:GLU:HG2	1.68	0.58
47:p:111:VAL:HG21	47:p:435:ALA:HB2	1.85	0.58
3:3:601:LEU:O	33:b:347:LYS:NZ	2.36	0.58
10:D:291:LYS:HE3	10:D:358:VAL:HG12	1.84	0.58
28:W:48:VAL:HG23	28:W:52:VAL:HG23	1.84	0.58
47:p:119:ILE:HD12	47:p:158:LEU:HD13	1.85	0.58
1:1:39:A:N6	1:1:42:C:O2'	2.37	0.58
3:3:209:ARG:NH2	3:3:259:ASP:OD2	2.36	0.58
8:B:67:PHE:HA	8:B:70:ARG:HD2	1.85	0.58
32:a:204:LEU:HD13	32:a:216:LEU:HD12	1.86	0.58
44:m:806:THR:HG21	47:p:377:PHE:HZ	1.69	0.58
1:1:3295:A:H2'	1:1:3296:A:C8	2.39	0.58
3:3:790:LEU:O	48:q:537:ASN:ND2	2.37	0.58
24:R:3:ASN:HD21	24:R:5:ARG:HH21	1.52	0.58
25:S:77:VAL:HG11	25:S:106:LEU:HD22	1.84	0.58
44:m:691:ARG:HH22	44:m:756:ASP:HB3	1.69	0.58
1:1:2981:U:H3'	1:1:2982:A:H8	1.69	0.57
9:C:328:ASN:OD1	12:F:48:ASN:ND2	2.37	0.57
32:a:55:LEU:HD11	32:a:155:ILE:HG12	1.85	0.57
32:a:113:SER:HA	32:a:138:VAL:HB	1.85	0.57
37:f:17:GLN:O	37:f:24:ASN:N	2.36	0.57
1:1:428:A:H2'	1:1:429:U:C6	2.39	0.57
33:b:290:THR:HG21	33:b:319:THR:HB	1.85	0.57
48:q:341:LEU:HD11	48:q:417:ARG:HB3	1.86	0.57
1:1:155:G:H22	10:D:155:ARG:HH21	1.52	0.57
1:1:2943:G:H5'	33:b:37:PHE:HA	1.84	0.57
32:a:204:LEU:CD1	32:a:216:LEU:CB	2.75	0.57
1:1:1596:C:H2'	1:1:1597:C:C6	2.39	0.57
1:1:1757:A:OP1	26:U:94:ARG:NH2	2.29	0.57
2:2:29:U:H5''	18:L:27:ASP:HB3	1.85	0.57
1:1:94:G:H2'	1:1:95:A:C8	2.40	0.57
1:1:1805:C:H2'	1:1:1806:A:H8	1.69	0.57
1:1:2125:A:OP2	3:3:942:LYS:NZ	2.33	0.57
10:D:323:GLN:O	10:D:328:ARG:NH1	2.37	0.57
36:e:79:VAL:HG13	36:e:111:ARG:HG2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:p:316:ASP:HB2	47:p:323:ILE:HD11	1.86	0.57
1:1:1176:C:H2'	1:1:1177:G:N2	2.20	0.57
1:1:3291:G:H2'	1:1:3292:A:C8	2.40	0.57
6:8:567:PHE:HE2	6:8:611:LEU:HD21	1.69	0.57
14:H:5:GLN:NE2	14:H:7:GLU:OE2	2.37	0.57
15:I:449:LEU:HD11	15:I:483:ILE:HD11	1.86	0.57
39:h:118:ILE:HG22	39:h:119:LYS:H	1.68	0.57
1:1:905:U:H2'	1:1:906:A:C8	2.39	0.57
1:1:1613:A:OP2	42:k:46:ARG:NH1	2.36	0.57
20:N:158:HIS:HB3	20:N:161:ALA:HB3	1.86	0.57
1:1:713:U:O4	7:A:255:GLN:NE2	2.38	0.57
3:3:724:LEU:HB3	3:3:728:ARG:HH21	1.69	0.57
47:p:138:LYS:HG2	47:p:196:GLU:HB3	1.87	0.57
47:p:378:VAL:HA	47:p:395:SER:OG	2.04	0.57
47:p:443:ALA:HB2	47:p:449:ILE:HG23	1.87	0.57
1:1:116:A:N6	1:1:265:A:OP1	2.37	0.56
3:3:389:LEU:HA	3:3:482:LEU:HD23	1.87	0.56
8:B:202:THR:O	56:z:44:GLN:NE2	2.32	0.56
21:O:65:ASN:HB3	21:O:68:ARG:HD3	1.86	0.56
1:1:219:A:O2'	1:1:220:G:N2	2.32	0.56
1:1:633:C:O2'	37:f:21:ARG:O	2.19	0.56
31:Z:5:LEU:HD11	34:c:35:ARG:HD2	1.87	0.56
1:1:331:G:OP1	53:v:3:SER:OG	2.22	0.56
1:1:351:A:O2'	2:2:53:A:O2'	2.22	0.56
1:1:3058:U:H3	1:1:3085:G:H22	1.54	0.56
3:3:209:ARG:HA	3:3:282:VAL:HA	1.86	0.56
7:A:107:GLY:O	16:J:207:ARG:NH2	2.37	0.56
7:A:224:ILE:HG22	7:A:225:LEU:HG	1.88	0.56
8:B:68:HIS:O	8:B:70:ARG:NH1	2.39	0.56
10:D:88:THR:HA	10:D:92:LYS:HE2	1.88	0.56
24:R:115:ILE:HG12	24:R:142:ILE:HD11	1.85	0.56
31:Z:23:VAL:HG12	31:Z:45:GLY:HA3	1.86	0.56
54:w:734:LYS:NZ	54:w:738:GLU:OE2	2.39	0.56
1:1:1190:A:O2'	1:1:1193:A:OP2	2.22	0.56
1:1:1508:C:N3	1:1:1880:U:O2'	2.34	0.56
1:1:1643:A:H5''	1:1:1644:C:C4	2.41	0.56
1:1:498:A:O2'	1:1:3273:A:N1	2.36	0.56
13:G:244:ALA:HA	13:G:248:LYS:HE2	1.87	0.56
25:S:125:LYS:HE2	25:S:127:ALA:HB2	1.88	0.56
3:3:322:LEU:HB3	3:3:818:ALA:HA	1.87	0.56
27:V:104:ASN:HD21	27:V:108:GLU:HB2	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1675:G:H2'	1:1:1676:A:H8	1.71	0.56
3:3:347:LYS:O	3:3:525:ARG:NH2	2.36	0.56
17:K:282:LYS:HD2	17:K:288:VAL:HG12	1.87	0.56
48:q:230:ARG:NH1	48:q:234:ASP:OD1	2.38	0.56
1:1:1471:U:H5''	24:R:5:ARG:HG3	1.87	0.56
1:1:2367:A:H2'	1:1:2368:A:C8	2.40	0.56
3:3:680:GLN:OE1	33:b:241:TYR:OH	2.24	0.56
47:p:106:VAL:HB	47:p:443:ALA:HB1	1.88	0.56
55:y:142:ILE:HG12	55:y:148:VAL:HG12	1.88	0.56
1:1:1474:A:O2'	35:d:57:GLN:OE1	2.23	0.56
1:1:3164:C:O2'	1:1:3165:A:H8	1.88	0.56
31:Z:68:ILE:O	31:Z:115:LYS:NZ	2.38	0.56
1:1:3252:G:H2'	1:1:3253:G:C8	2.41	0.56
1:1:3343:G:O2'	1:1:3362:A:N6	2.39	0.56
3:3:687:THR:HG23	3:3:707:ARG:HH22	1.70	0.56
6:8:335:GLN:HE21	6:8:382:PHE:HD2	1.53	0.56
15:I:398:GLU:OE1	15:I:401:ARG:NH2	2.39	0.56
47:p:104:ASP:OD1	47:p:105:TRP:N	2.36	0.56
1:1:920:A:H2'	1:1:921:A:C8	2.40	0.55
1:1:2375:G:OP2	1:1:2375:G:N2	2.23	0.55
1:1:3165:A:H2'	1:1:3166:C:C6	2.41	0.55
1:1:1906:G:N2	27:V:65:GLY:O	2.35	0.55
20:N:31:ARG:NH1	20:N:124:ASP:OD2	2.37	0.55
47:p:110:ASP:HB3	47:p:119:ILE:HG23	1.88	0.55
47:p:163:ASN:HA	47:p:210:PRO:HB3	1.87	0.55
1:1:20:A:H2'	1:1:21:G:C8	2.42	0.55
1:1:921:A:OP1	5:7:44:LYS:NZ	2.39	0.55
3:3:462:ILE:HG22	3:3:492:ALA:HB1	1.88	0.55
4:6:16:U:H2'	4:6:17:G:H8	1.70	0.55
8:B:284:ARG:NH1	8:B:293:ASN:O	2.40	0.55
30:Y:87:LYS:HB2	30:Y:97:ILE:HD11	1.88	0.55
52:u:46:PRO:O	52:u:52:THR:OG1	2.20	0.55
33:b:71:ILE:HD13	33:b:88:LYS:HG3	1.89	0.55
54:w:795:LEU:HD13	54:w:819:VAL:HG11	1.89	0.55
3:3:330:VAL:HG13	3:3:334:LEU:HD22	1.87	0.55
15:I:466:SER:OG	15:I:542:LYS:NZ	2.36	0.55
47:p:97:LEU:HD11	47:p:453:LYS:HG3	1.88	0.55
1:1:12:A:H2'	1:1:13:A:C8	2.42	0.55
1:1:3002:C:O2'	8:B:180:GLU:OE2	2.23	0.55
47:p:122:SER:OG	47:p:124:ASP:OD1	2.23	0.55
54:w:549:HIS:HB2	54:w:556:ARG:HH21	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:q:207:ILE:HG21	48:q:231:LEU:HB2	1.89	0.55
48:q:350:LEU:HB3	48:q:418:ILE:HG12	1.88	0.55
55:y:220:SER:HB2	55:y:229:PRO:HA	1.89	0.55
9:C:177:ASP:OD2	9:C:247:PHE:HD2	1.86	0.55
14:H:89:LYS:HG2	14:H:145:VAL:HG22	1.88	0.55
44:m:363:GLU:OE2	44:m:364:ARG:NH1	2.40	0.55
1:1:815:G:H1	1:1:925:A:H62	1.55	0.55
1:1:966:U:H2'	1:1:967:A:H8	1.72	0.55
1:1:1498:A:H2'	1:1:1499:C:C6	2.42	0.55
3:3:289:GLU:HG2	3:3:292:ARG:HH11	1.71	0.55
3:3:493:ALA:HB1	3:3:498:ILE:HD11	1.88	0.55
5:7:28:ASN:ND2	44:m:159:ASN:OD1	2.40	0.55
8:B:213:GLU:OE2	8:B:340:LYS:NZ	2.39	0.55
1:1:908:G:H22	1:1:921:A:H1'	1.72	0.54
1:1:2855:U:H2'	1:1:2856:G:H8	1.72	0.54
8:B:323:MET:HE1	8:B:359:ILE:HD13	1.89	0.54
10:D:452:GLN:HG2	10:D:487:ILE:HD11	1.90	0.54
32:a:174:MET:HB3	32:a:179:LEU:HG	1.89	0.54
6:8:354:LEU:HG	6:8:397:LEU:HD23	1.89	0.54
31:Z:127:ASN:HB3	31:Z:130:PHE:HB3	1.90	0.54
34:c:32:LYS:NZ	34:c:36:GLN:OE1	2.41	0.54
1:1:745:C:H2'	1:1:746:A:H8	1.72	0.54
28:W:55:GLU:OE2	28:W:121:ARG:NH2	2.41	0.54
33:b:82:MET:HE2	33:b:157:ILE:HD11	1.90	0.54
1:1:1597:C:H5'	1:1:1696:A:H1'	1.90	0.54
47:p:338:LEU:O	47:p:342:ASN:N	2.41	0.54
47:p:338:LEU:HD13	47:p:341:LEU:HD12	1.87	0.54
55:y:175:SER:O	55:y:178:GLN:NE2	2.41	0.54
3:3:926:PRO:HG2	3:3:943:VAL:HG22	1.90	0.54
6:8:302:ASN:HA	6:8:305:MET:HG2	1.88	0.54
15:I:577:SER:HA	15:I:639:LEU:HD21	1.90	0.54
1:1:900:G:H1'	1:1:1589:A:N6	2.23	0.54
3:3:688:VAL:O	3:3:692:THR:OG1	2.20	0.54
6:8:45:LYS:HB3	15:I:349:ASN:HD22	1.72	0.54
8:B:303:LYS:HD2	8:B:361:THR:HG21	1.89	0.54
28:W:126:ARG:O	28:W:129:THR:OG1	2.26	0.54
32:a:10:ARG:HG2	32:a:180:VAL:HG21	1.89	0.54
34:c:44:ILE:HA	34:c:89:VAL:HG12	1.90	0.54
47:p:328:THR:CG2	47:p:329:SER:H	2.21	0.54
49:r:126:ARG:HE	49:r:160:GLY:HA3	1.72	0.54
55:y:15:VAL:HA	55:y:61:ARG:HG2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1322:U:OP1	25:S:117:ARG:NH1	2.39	0.54
44:m:393:ASP:OD1	51:t:23:ARG:NH1	2.37	0.54
1:1:549:U:O4	1:1:550:A:N6	2.40	0.54
1:1:1195:A:H5''	1:1:1196:C:H5''	1.90	0.54
15:I:644:CYS:HB3	15:I:647:VAL:HG12	1.89	0.54
34:c:43:ILE:HG13	34:c:68:TYR:HB3	1.88	0.54
1:1:1618:G:H2'	1:1:1619:A:C8	2.43	0.54
3:3:357:LEU:HD12	3:3:371:ILE:HD11	1.90	0.54
6:8:281:LEU:HD13	6:8:301:VAL:HG22	1.90	0.54
33:b:150:LEU:HA	33:b:153:VAL:HG12	1.90	0.54
1:1:117:U:O2'	1:1:119:U:OP2	2.16	0.54
1:1:817:A:H2'	1:1:818:C:C6	2.42	0.54
1:1:1799:A:H2'	1:1:1800:A:H8	1.72	0.54
14:H:2:LYS:HD3	14:H:59:ASN:HD21	1.73	0.54
32:a:205:VAL:HB	32:a:213:ALA:HB1	1.89	0.54
1:1:662:U:H2'	1:1:663:C:C6	2.43	0.53
1:1:1301:A:O2'	1:1:1302:A:O4'	2.23	0.53
1:1:1696:A:H2'	1:1:1697:A:C8	2.43	0.53
1:1:1719:G:OP1	24:R:110:ARG:NH1	2.41	0.53
9:C:126:ILE:O	9:C:129:THR:OG1	2.25	0.53
1:1:1281:G:H2'	1:1:1282:G:H8	1.73	0.53
17:K:328:THR:HG21	51:t:86:ALA:HB1	1.90	0.53
33:b:172:ILE:HG22	33:b:180:LYS:HB2	1.89	0.53
44:m:745:GLY:HA2	44:m:781:VAL:HG23	1.91	0.53
1:1:3291:G:H2'	1:1:3292:A:H8	1.73	0.53
5:7:84:ILE:HG13	5:7:85:VAL:HG23	1.90	0.53
28:W:158:ILE:HG12	28:W:160:SER:H	1.71	0.53
31:Z:100:THR:HG23	31:Z:106:GLN:HG3	1.91	0.53
33:b:294:ARG:HG2	33:b:296:GLU:H	1.73	0.53
1:1:3379:C:O2'	8:B:316:GLU:OE2	2.26	0.53
5:7:107:THR:HG23	5:7:110:ARG:HH12	1.73	0.53
44:m:547:LEU:HD13	44:m:566:ASN:HD22	1.74	0.53
45:n:390:GLU:HA	45:n:393:MET:HE2	1.89	0.53
1:1:3322:A:H2'	1:1:3323:A:C8	2.42	0.53
33:b:18:LEU:HD21	33:b:137:ALA:HA	1.91	0.53
44:m:229:ARG:HG3	44:m:231:GLU:HG3	1.91	0.53
1:1:528:U:H2'	1:1:529:A:C8	2.44	0.53
1:1:1209:G:H5'	28:W:4:SER:HB2	1.91	0.53
1:1:1657:C:O2'	1:1:1796:G:O2'	2.21	0.53
1:1:1875:G:N7	24:R:20:ARG:NH1	2.57	0.53
35:d:25:PHE:HB3	35:d:65:LYS:HD2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:155:G:H1	10:D:155:ARG:NH2	2.06	0.53
17:K:98:LYS:HD2	17:K:238:LEU:HD11	1.91	0.53
32:a:175:GLU:HB2	32:a:178:VAL:HG12	1.89	0.53
40:i:45:ARG:HD3	40:i:93:ILE:HD11	1.89	0.53
15:I:166:VAL:HG21	15:I:181:LEU:HD12	1.91	0.53
23:Q:71:LEU:HD11	23:Q:99:THR:HG21	1.91	0.53
28:W:168:LYS:HE3	28:W:201:LEU:HD13	1.91	0.53
1:1:953:G:H2'	1:1:1116:G:N7	2.23	0.53
1:1:958:C:H2'	1:1:959:C:O4'	2.09	0.53
20:N:14:LYS:HA	20:N:19:LEU:HD12	1.89	0.53
1:1:129:U:H2'	1:1:130:A:C8	2.44	0.52
1:1:1680:G:OP2	26:U:90:ARG:NH2	2.42	0.52
1:1:3317:U:O2	1:1:3318:G:N1	2.42	0.52
1:1:3375:A:O2'	1:1:3378:C:OP2	2.22	0.52
10:D:93:THR:HA	10:D:96:PHE:CE2	2.44	0.52
47:p:217:SER:HB3	47:p:295:PHE:CG	2.44	0.52
1:1:1404:G:N2	1:1:1407:A:OP2	2.33	0.52
1:1:1679:A:OP1	26:U:94:ARG:NE	2.42	0.52
1:1:3113:A:OP1	14:H:73:SER:OG	2.27	0.52
3:3:352:LEU:HD11	3:3:532:ALA:HB2	1.92	0.52
3:3:440:PRO:O	3:3:444:HIS:HB2	2.09	0.52
9:C:143:GLU:HG2	9:C:144:LYS:HD2	1.91	0.52
12:F:83:LEU:HD11	12:F:116:PHE:HB3	1.90	0.52
32:a:204:LEU:HD12	32:a:216:LEU:HB2	1.82	0.52
51:t:146:ARG:NH1	51:t:147:VAL:O	2.42	0.52
1:1:3064:U:H2'	1:1:3065:G:H8	1.73	0.52
17:K:85:ASN:OD1	17:K:85:ASN:N	2.43	0.52
55:y:53:ILE:O	55:y:56:THR:OG1	2.24	0.52
55:y:101:LEU:HB3	55:y:107:VAL:HG11	1.91	0.52
1:1:832:G:H1	1:1:862:U:H3	1.56	0.52
1:1:1593:A:N3	1:1:1615:C:O2'	2.42	0.52
1:1:2395:G:H2'	1:1:2396:G:C8	2.45	0.52
1:1:2928:C:H2'	1:1:2929:C:C6	2.43	0.52
15:I:532:ILE:HG13	15:I:533:ILE:HG13	1.91	0.52
34:c:38:LYS:O	34:c:40:LYS:NZ	2.42	0.52
48:q:207:ILE:HA	48:q:210:VAL:HG22	1.92	0.52
1:1:3193:C:H2'	1:1:3194:C:C6	2.44	0.52
1:1:3295:A:H2'	1:1:3296:A:H8	1.74	0.52
2:2:57:C:H4'	2:2:63:G:N7	2.25	0.52
8:B:35:ASP:OD2	8:B:37:ARG:NH1	2.42	0.52
15:I:338:LEU:O	15:I:435:LYS:NZ	2.36	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:n:255:ILE:HG22	45:n:256:ILE:HG12	1.91	0.52
45:n:448:LEU:HD12	45:n:449:PRO:HD2	1.91	0.52
1:1:22:G:H5''	41:j:43:LYS:HG2	1.92	0.52
1:1:1497:C:O2'	1:1:1602:A:N3	2.42	0.52
1:1:1798:A:H2'	1:1:1799:A:C8	2.44	0.52
43:l:156:MET:HE2	43:l:160:GLY:HA3	1.90	0.52
1:1:2981:U:H3'	1:1:2982:A:C8	2.45	0.52
8:B:92:TYR:HB2	8:B:157:VAL:HB	1.92	0.52
8:B:332:ARG:H	8:B:332:ARG:HD3	1.75	0.52
44:m:441:ARG:HA	44:m:782:LEU:HD11	1.91	0.52
44:m:644:ASP:OD1	44:m:645:ALA:N	2.42	0.52
45:n:356:VAL:HA	45:n:359:LEU:HG	1.91	0.52
55:y:85:ARG:NH2	55:y:89:PRO:O	2.43	0.52
1:1:675:C:O2'	1:1:679:U:OP1	2.27	0.52
1:1:1204:A:H2'	1:1:1205:A:O4'	2.10	0.52
6:8:435:ILE:O	6:8:438:ASN:ND2	2.43	0.52
21:O:121:PRO:HA	21:O:124:LEU:HD12	1.91	0.52
32:a:4:ILE:HG23	32:a:217:TYR:HB2	1.92	0.52
52:u:50:LYS:HG3	52:u:55:PHE:CE2	2.45	0.52
1:1:800:G:H22	9:C:101:ALA:HA	1.75	0.52
53:v:157:GLU:O	53:v:161:LYS:HG2	2.10	0.52
1:1:412:G:OP1	22:P:62:ARG:NH1	2.43	0.52
1:1:655:C:H2'	1:1:656:A:C8	2.44	0.52
1:1:1182:A:H2'	1:1:1183:C:C6	2.45	0.52
1:1:1592:G:OP1	38:g:58:ARG:NH2	2.43	0.52
1:1:2986:U:H2'	1:1:2987:A:H8	1.75	0.52
6:8:453:SER:HB2	6:8:508:ASN:HB2	1.91	0.52
15:I:281:CYS:O	15:I:325:ARG:NH1	2.42	0.52
44:m:207:ASP:OD1	44:m:208:LYS:N	2.43	0.52
45:n:50:LYS:HG2	45:n:55:GLY:HA2	1.90	0.52
1:1:2810:C:H2'	1:1:2811:A:H8	1.75	0.51
1:1:2858:U:H5''	1:1:2859:U:H2'	1.91	0.51
47:p:204:LEU:HD23	47:p:234:TRP:CG	2.44	0.51
51:t:67:ALA:HB1	51:t:153:VAL:HG22	1.91	0.51
2:2:63:G:H22	2:2:97:A:H2	1.59	0.51
3:3:139:PHE:CG	3:3:140:PRO:HD3	2.45	0.51
3:3:210:ALA:HB3	3:3:260:VAL:HG22	1.92	0.51
6:8:468:LEU:HA	6:8:471:LEU:HD13	1.91	0.51
10:D:402:LEU:HD22	10:D:412:LEU:HD13	1.93	0.51
12:F:40:LYS:NZ	12:F:170:GLU:OE2	2.43	0.51
1:1:895:A:H61	6:8:26:GLU:HA	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1290:A:H2'	1:1:1291:A:C8	2.45	0.51
1:1:1688:U:H2'	1:1:1689:U:C6	2.44	0.51
1:1:3140:G:N7	8:B:28:ARG:NH2	2.54	0.51
15:I:520:ARG:HE	15:I:540:SER:HB2	1.74	0.51
47:p:328:THR:CG2	47:p:329:SER:N	2.71	0.51
1:1:2401:A:O2'	1:1:2402:A:O4'	2.27	0.51
1:1:2964:G:N2	1:1:2967:A:O2'	2.43	0.51
17:K:236:VAL:HG21	17:K:246:VAL:HG22	1.93	0.51
19:M:19:ARG:NH1	19:M:66:THR:O	2.42	0.51
32:a:74:VAL:HG21	32:a:86:SER:HB2	1.93	0.51
1:1:8:C:H2'	1:1:9:U:C6	2.45	0.51
1:1:50:U:H2'	1:1:51:A:H8	1.76	0.51
1:1:571:U:H2'	1:1:572:A:H8	1.75	0.51
1:1:1534:A:H2'	1:1:1535:A:C8	2.45	0.51
1:1:1717:U:H2'	1:1:1718:G:H8	1.75	0.51
6:8:399:TYR:HB2	6:8:467:PRO:HB2	1.91	0.51
7:A:141:GLN:NE2	16:J:225:SER:O	2.40	0.51
48:q:319:THR:HG22	48:q:321:GLU:H	1.76	0.51
1:1:441:U:H3	1:1:493:G:H22	1.59	0.51
1:1:1660:C:H2'	1:1:1661:G:H8	1.75	0.51
3:3:679:LEU:HB3	33:b:237:MET:HE1	1.92	0.51
10:D:418:PRO:HG2	10:D:421:LYS:HB2	1.93	0.51
32:a:65:ILE:HD13	32:a:109:ALA:HB3	1.92	0.51
44:m:488:ILE:HG12	44:m:506:VAL:HG22	1.93	0.51
47:p:305:SER:HG	47:p:315:TRP:HE1	1.54	0.51
17:K:97:LEU:HD12	17:K:207:ILE:HG12	1.92	0.51
33:b:285:VAL:HB	33:b:317:ILE:HD13	1.91	0.51
47:p:97:LEU:HD21	47:p:453:LYS:HD2	1.93	0.51
47:p:350:ALA:O	47:p:351:ARG:HG2	2.11	0.51
54:w:732:PRO:HD2	54:w:735:LYS:HD2	1.93	0.51
55:y:22:THR:O	55:y:22:THR:HG22	2.10	0.51
1:1:829:U:OP1	6:8:7:SER:OG	2.28	0.51
6:8:672:ARG:HA	6:8:675:ARG:HG2	1.91	0.51
17:K:80:LEU:HD21	17:K:279:ILE:HG23	1.92	0.51
35:d:77:ARG:HD2	35:d:89:LEU:HD13	1.92	0.51
38:g:29:ILE:HD11	38:g:31:ARG:HH21	1.75	0.51
48:q:274:ARG:NH2	48:q:361:THR:OG1	2.43	0.51
1:1:72:C:H5'	18:L:63:VAL:HG22	1.93	0.51
2:2:26:U:H2'	2:2:27:U:C6	2.46	0.51
2:2:69:U:H2'	2:2:70:G:O4'	2.10	0.51
3:3:512:SER:HB3	3:3:515:ILE:HG13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:105:PRO:HD3	44:m:140:ILE:HG12	1.92	0.51
15:I:172:ASN:ND2	54:w:569:PRO:O	2.40	0.51
10:D:421:LYS:NZ	17:K:70:ASP:OD1	2.36	0.51
32:a:14:LYS:HE2	32:a:176:GLU:HG2	1.92	0.51
1:1:705:A:H62	7:A:263:ARG:HD2	1.74	0.50
11:E:85:ILE:HD11	37:f:102:LEU:HD23	1.93	0.50
1:1:595:G:OP2	12:F:30:ARG:NH1	2.44	0.50
13:G:217:THR:HG23	46:o:161:LEU:HD21	1.94	0.50
31:Z:51:LEU:HB2	31:Z:65:ARG:HB3	1.93	0.50
41:j:21:ARG:NH2	41:j:41:ALA:O	2.25	0.50
47:p:382:ASP:OD1	47:p:383:THR:N	2.44	0.50
48:q:390:ILE:HG23	48:q:395:CYS:HB2	1.92	0.50
48:q:486:GLU:HA	48:q:489:ILE:HG22	1.92	0.50
1:1:364:G:OP2	41:j:52:LYS:NZ	2.43	0.50
1:1:891:G:H2'	1:1:892:U:C6	2.47	0.50
1:1:3259:U:H5''	1:1:3261:C:H5	1.76	0.50
47:p:382:ASP:HB3	47:p:392:CYS:SG	2.50	0.50
1:1:1801:U:O2'	38:g:60:ARG:NH2	2.45	0.50
1:1:2882:U:H2'	1:1:2883:U:C6	2.46	0.50
6:8:60:SER:HB3	15:I:534:LYS:HG2	1.94	0.50
10:D:208:ASP:OD1	10:D:211:ARG:NH2	2.44	0.50
10:D:232:THR:H	10:D:235:VAL:HB	1.76	0.50
15:I:604:LEU:HB3	15:I:633:LEU:HG	1.94	0.50
32:a:30:GLU:OE1	32:a:209:SER:OG	2.29	0.50
43:l:50:HIS:O	43:l:54:LEU:HG	2.11	0.50
1:1:1194:G:H2'	1:1:1195:A:C8	2.46	0.50
17:K:71:GLU:OE2	17:K:285:ARG:NH1	2.44	0.50
20:N:156:HIS:HB3	20:N:159:ARG:HD2	1.93	0.50
28:W:40:VAL:HG13	28:W:221:TYR:HB3	1.91	0.50
41:j:48:ASN:OD1	41:j:54:LYS:NZ	2.41	0.50
49:r:22:GLU:OE2	49:r:25:ARG:NH2	2.43	0.50
1:1:162:G:OP1	53:v:211:SER:OG	2.30	0.50
1:1:407:A:C2	2:2:17:A:H1'	2.46	0.50
1:1:664:U:H2'	1:1:665:A:C8	2.45	0.50
1:1:3026:G:OP1	14:H:174:LYS:NZ	2.31	0.50
1:1:3296:A:H2'	1:1:3297:U:H6	1.76	0.50
2:2:154:C:H5''	13:G:181:LYS:HD3	1.94	0.50
15:I:160:GLY:O	15:I:164:LYS:HG2	2.12	0.50
7:A:214:GLU:OE2	7:A:218:ARG:NH2	2.43	0.50
26:U:19:VAL:HG12	26:U:105:LEU:HD12	1.93	0.50
44:m:698:SER:HB3	44:m:729:VAL:HG13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1661:G:H2'	1:1:1662:G:H8	1.77	0.50
6:8:315:LEU:HD21	6:8:353:MET:HG2	1.94	0.50
8:B:282:ILE:HA	8:B:324:VAL:HG12	1.93	0.50
32:a:148:VAL:HA	32:a:151:VAL:HG12	1.94	0.50
44:m:747:ILE:HD11	44:m:781:VAL:HG11	1.92	0.50
48:q:349:ILE:HD12	48:q:417:ARG:HB2	1.93	0.50
53:v:189:TYR:HB2	53:v:219:LEU:HD11	1.94	0.50
1:1:585:A:H2'	1:1:586:C:C6	2.47	0.50
1:1:783:A:H5''	1:1:784:A:H5''	1.94	0.50
1:1:817:A:H5''	1:1:818:C:C5	2.47	0.50
1:1:2129:U:H2'	1:1:2130:G:C8	2.47	0.50
4:6:42:G:H2'	4:6:43:A:H8	1.76	0.50
44:m:218:LYS:NZ	44:m:222:GLU:OE2	2.42	0.50
47:p:94:PRO:HG2	47:p:414:ILE:HD11	1.94	0.50
2:2:77:A:H2'	2:2:78:G:O4'	2.12	0.49
2:2:141:C:H2'	2:2:142:C:H6	1.77	0.49
33:b:415:ASN:ND2	33:b:418:ASP:OD1	2.44	0.49
54:w:794:THR:HG23	54:w:813:LYS:HE3	1.94	0.49
1:1:1620:U:H2'	1:1:1621:A:C8	2.47	0.49
1:1:3006:A:H2'	1:1:3007:U:O4'	2.12	0.49
1:1:3322:A:H2'	1:1:3323:A:H8	1.78	0.49
3:3:164:GLN:HG2	3:3:190:ALA:HB2	1.94	0.49
7:A:135:PRO:HB3	7:A:175:HIS:NE2	2.27	0.49
45:n:178:LYS:HB2	45:n:189:GLN:HB3	1.93	0.49
1:1:1810:A:H2'	1:1:1811:G:C8	2.48	0.49
1:1:3192:U:H2'	1:1:3193:C:C6	2.47	0.49
2:2:142:C:H2'	2:2:143:U:C6	2.47	0.49
3:3:682:ARG:HD2	33:b:232:MET:HB2	1.94	0.49
29:X:113:LEU:HD11	29:X:121:LYS:HE2	1.94	0.49
47:p:335:ILE:HD11	47:p:344:LEU:HD11	1.94	0.49
1:1:424:G:H21	36:e:24:ARG:HH12	1.59	0.49
1:1:2403:G:H4'	1:1:2403:G:OP1	2.12	0.49
1:1:2962:U:H2'	1:1:2963:C:C6	2.47	0.49
23:Q:123:THR:OG1	23:Q:125:ASP:OD1	2.28	0.49
28:W:38:ARG:HG3	28:W:223:ASN:OD1	2.11	0.49
1:1:689:U:O4	9:C:209:TYR:OH	2.27	0.49
3:3:287:PHE:HE2	3:3:302:LEU:HD22	1.78	0.49
5:7:108:LEU:O	5:7:112:ILE:HG12	2.13	0.49
6:8:439:TRP:HE3	6:8:443:HIS:HE1	1.61	0.49
26:U:33:TYR:HH	26:U:80:THR:HG1	1.57	0.49
27:V:80:ARG:HD3	27:V:117:PRO:HG2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:f:14:LEU:HD11	37:f:31:LYS:HB2	1.95	0.49
45:n:12:ALA:HB1	45:n:54:LYS:HE2	1.93	0.49
50:s:24:SER:OG	50:s:28:LYS:NZ	2.46	0.49
55:y:119:PRO:O	55:y:139:ARG:NH1	2.46	0.49
1:1:616:G:H2'	1:1:617:G:C8	2.48	0.49
1:1:3338:C:H2'	1:1:3339:A:H8	1.78	0.49
3:3:237:ARG:HD3	3:3:256:THR:HG22	1.94	0.49
4:6:16:U:H2'	4:6:17:G:C8	2.48	0.49
15:I:422:ALA:O	15:I:426:ILE:HG12	2.13	0.49
1:1:3183:A:H2	1:1:3188:G:H4'	1.77	0.49
18:L:42:ARG:O	18:L:46:ILE:HG12	2.13	0.49
28:W:84:GLU:OE2	28:W:89:LEU:N	2.46	0.49
1:1:1621:A:H2'	1:1:1622:U:C6	2.48	0.49
6:8:395:GLU:HB3	6:8:467:PRO:HD2	1.95	0.49
48:q:436:VAL:HG22	48:q:440:ARG:HG2	1.95	0.49
51:t:150:PRO:HB2	51:t:153:VAL:HG21	1.95	0.49
1:1:1666:G:H2'	1:1:1667:A:H8	1.78	0.49
12:F:85:PHE:HB2	12:F:139:PRO:HG3	1.95	0.49
43:l:174:ARG:HD2	49:r:165:PRO:HA	1.94	0.49
47:p:146:PRO:HD2	47:p:163:ASN:HB2	1.94	0.49
47:p:393:SER:OG	47:p:403:TRP:NE1	2.33	0.49
1:1:489:C:H2'	1:1:490:A:C8	2.48	0.48
1:1:1124:U:H2'	1:1:1125:U:C6	2.48	0.48
1:1:1620:U:H2'	1:1:1621:A:H8	1.77	0.48
1:1:393:U:H2'	1:1:394:G:O4'	2.12	0.48
1:1:412:G:H2'	1:1:413:U:C6	2.47	0.48
1:1:1340:G:H2'	1:1:1341:U:C6	2.47	0.48
15:I:175:LYS:HA	15:I:178:MET:HE2	1.95	0.48
48:q:510:LYS:O	48:q:530:ARG:N	2.42	0.48
1:1:293:C:H2'	1:1:294:U:O4'	2.13	0.48
1:1:1597:C:H2'	1:1:1598:G:C8	2.47	0.48
3:3:543:TYR:OH	3:3:639:THR:O	2.20	0.48
3:3:557:LEU:HD12	3:3:560:MET:HE3	1.96	0.48
6:8:453:SER:HB3	6:8:505:LEU:HA	1.95	0.48
52:u:45:ASN:OD1	52:u:47:ARG:NH1	2.46	0.48
1:1:118:U:O2	1:1:121:A:H5''	2.13	0.48
1:1:275:U:H2'	1:1:276:U:C6	2.49	0.48
1:1:2898:G:C8	33:b:159:ARG:HD3	2.48	0.48
6:8:575:PHE:CE2	6:8:591:VAL:HG11	2.49	0.48
33:b:187:ILE:HD11	33:b:328:VAL:HB	1.94	0.48
2:2:151:C:O2	29:X:22:LYS:NZ	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:474:GLN:HA	3:3:477:ASN:ND2	2.28	0.48
10:D:296:LEU:HD12	10:D:302:VAL:HA	1.94	0.48
14:H:41:ILE:HG22	14:H:43:VAL:HG13	1.94	0.48
25:S:12:ARG:HB3	25:S:24:LEU:HD23	1.94	0.48
44:m:751:HIS:NE2	44:m:753:THR:OG1	2.44	0.48
1:1:288:C:H2'	1:1:289:A:H8	1.77	0.48
1:1:1256:G:H2'	1:1:1257:C:C6	2.47	0.48
1:1:1660:C:H2'	1:1:1661:G:C8	2.49	0.48
7:A:178:SER:OG	16:J:250:SER:OG	2.26	0.48
1:1:806:A:H2'	1:1:807:A:C2	2.48	0.48
1:1:1567:U:OP1	44:m:395:TYR:OH	2.28	0.48
1:1:1828:A:H2'	1:1:1829:G:C8	2.49	0.48
14:H:90:MET:HE2	14:H:179:ILE:HG22	1.94	0.48
15:I:163:CYS:SG	15:I:223:ASN:HB3	2.53	0.48
19:M:48:GLY:HA3	19:M:53:VAL:HB	1.94	0.48
44:m:462:ARG:HG2	44:m:474:ARG:HG3	1.96	0.48
46:o:103:HIS:HA	46:o:122:LEU:HD22	1.96	0.48
54:w:809:PRO:HG2	54:w:812:VAL:HG21	1.96	0.48
1:1:3139:A:OP1	8:B:274:SER:OG	2.30	0.48
10:D:170:ALA:HB1	10:D:175:LEU:HB2	1.96	0.48
19:M:32:LEU:HD11	19:M:94:TRP:CG	2.49	0.48
32:a:67:ILE:HD11	32:a:77:ALA:CB	2.44	0.48
33:b:369:ARG:HG2	55:y:178:GLN:NE2	2.29	0.48
55:y:118:HIS:HB3	55:y:121:ILE:HG23	1.95	0.48
1:1:700:C:H2'	1:1:701:G:H8	1.79	0.48
1:1:909:G:H4'	54:w:750:ARG:HH12	1.78	0.48
1:1:2348:A:O2'	1:1:2349:U:H5'	2.14	0.48
1:1:3284:G:H2'	1:1:3285:C:C6	2.48	0.48
16:J:197:ASN:OD1	16:J:197:ASN:N	2.47	0.48
16:J:215:HIS:HB3	16:J:219:GLU:HG3	1.95	0.48
33:b:289:LYS:HE2	33:b:292:ILE:HD12	1.96	0.48
47:p:111:VAL:HG23	47:p:433:LYS:HG2	1.95	0.48
1:1:641:C:H2'	1:1:642:U:C6	2.49	0.48
4:6:224:G:C4	51:t:68:THR:HG21	2.48	0.48
10:D:84:GLY:HA2	10:D:250:ILE:HB	1.96	0.48
13:G:99:PRO:HD3	13:G:132:VAL:HG22	1.95	0.48
15:I:596:ASN:OD1	15:I:657:ARG:NH2	2.38	0.48
47:p:385:PRO:HD2	47:p:434:TRP:CD1	2.49	0.48
1:1:190:U:H2'	30:Y:60:ARG:HH22	1.79	0.47
1:1:656:A:H2'	1:1:657:A:H8	1.78	0.47
1:1:2916:U:C5	1:1:2935:U:H2'	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:369:ARG:HD2	52:u:33:ARG:HD3	1.96	0.47
9:C:181:VAL:HG11	9:C:224:GLY:HA3	1.96	0.47
37:f:49:ILE:HD11	37:f:71:VAL:HG22	1.96	0.47
42:k:11:PHE:CZ	42:k:43:PHE:HB3	2.49	0.47
47:p:328:THR:HG21	47:p:332:LEU:HD21	1.95	0.47
48:q:316:ILE:HG22	48:q:329:LEU:HD11	1.96	0.47
1:1:1686:U:OP1	26:U:42:LYS:NZ	2.43	0.47
6:8:506:SER:OG	6:8:511:VAL:O	2.21	0.47
1:1:952:A:H4'	1:1:968:G:N2	2.29	0.47
1:1:2863:G:C2	33:b:95:LEU:HD13	2.49	0.47
3:3:256:THR:HG22	3:3:256:THR:O	2.13	0.47
3:3:275:MET:HB2	3:3:277:LEU:HG	1.95	0.47
11:E:76:LEU:HD11	11:E:141:VAL:HG21	1.95	0.47
24:R:134:HIS:CD2	24:R:136:ARG:HB3	2.50	0.47
25:S:132:THR:HG23	25:S:144:LEU:HD13	1.96	0.47
34:c:25:LEU:HD22	34:c:87:VAL:HG11	1.96	0.47
47:p:416:ARG:HH22	47:p:443:ALA:HA	1.78	0.47
1:1:952:A:H2'	1:1:953:G:O4'	2.14	0.47
3:3:589:TYR:HD1	3:3:594:VAL:HG11	1.80	0.47
10:D:135:ARG:HG2	10:D:145:PHE:CE2	2.50	0.47
32:a:96:ASN:HB3	32:a:99:LEU:HB3	1.96	0.47
44:m:333:THR:HG21	45:n:463:ALA:HB2	1.96	0.47
48:q:443:LYS:HD3	48:q:446:ILE:HD11	1.95	0.47
1:1:608:A:OP1	9:C:315:LYS:NZ	2.47	0.47
1:1:2909:U:H2'	1:1:2910:A:O4'	2.14	0.47
2:2:143:U:OP1	20:N:38:ARG:NH2	2.47	0.47
6:8:500:LYS:HE3	6:8:570:LEU:HD21	1.95	0.47
8:B:133:TYR:O	8:B:136:LYS:HG2	2.14	0.47
47:p:241:MET:HE3	47:p:277:ARG:HG3	1.97	0.47
55:y:67:ARG:NH1	55:y:112:ASP:OD2	2.42	0.47
1:1:257:U:H2'	1:1:258:G:H8	1.80	0.47
1:1:1390:A:N6	1:1:1418:A:O2'	2.46	0.47
1:1:1616:U:H2'	1:1:1617:G:C8	2.50	0.47
1:1:3205:G:OP2	1:1:3206:C:N4	2.44	0.47
8:B:60:LEU:N	8:B:70:ARG:O	2.46	0.47
29:X:34:LEU:HD12	29:X:35:PRO:HD2	1.96	0.47
45:n:206:PRO:HB2	51:t:228:VAL:HB	1.97	0.47
48:q:389:ASN:OD1	48:q:392:ARG:NH1	2.47	0.47
1:1:40:A:H1'	1:1:41:G:N7	2.30	0.47
1:1:966:U:H2'	1:1:967:A:C8	2.50	0.47
1:1:1133:A:H2'	1:1:1134:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2411:U:H2'	1:1:2412:G:H8	1.80	0.47
3:3:357:LEU:HA	3:3:596:GLY:O	2.14	0.47
6:8:384:LYS:HG2	6:8:447:PHE:HB2	1.97	0.47
15:I:595:MET:HE3	15:I:602:SER:HB3	1.95	0.47
17:K:294:ASN:OD1	17:K:295:GLN:N	2.47	0.47
21:O:136:THR:HG22	21:O:137:THR:N	2.30	0.47
30:Y:112:ASP:H	30:Y:115:ARG:HB3	1.80	0.47
32:a:4:ILE:HD11	32:a:187:VAL:HG11	1.95	0.47
32:a:67:ILE:HD11	32:a:77:ALA:HB2	1.97	0.47
1:1:745:C:H2'	1:1:746:A:C8	2.50	0.47
1:1:816:A:OP2	41:j:28:HIS:NE2	2.38	0.47
1:1:953:G:H2'	1:1:1116:G:C8	2.50	0.47
1:1:2396:G:H2'	1:1:2397:A:C8	2.50	0.47
1:1:3296:A:H2'	1:1:3297:U:C6	2.50	0.47
3:3:468:GLN:O	3:3:472:LYS:HG2	2.14	0.47
10:D:320:HIS:CE1	10:D:323:GLN:HG3	2.50	0.47
35:d:55:LEU:HB2	35:d:95:PRO:HD3	1.97	0.47
40:i:57:LEU:HD21	40:i:73:ALA:HB2	1.96	0.47
1:1:424:G:H21	36:e:24:ARG:NH1	2.12	0.47
1:1:1596:C:O2'	1:1:1696:A:N3	2.43	0.47
6:8:516:TYR:CZ	6:8:591:VAL:HG13	2.50	0.47
7:A:143:PHE:HA	7:A:149:TYR:HB3	1.96	0.47
27:V:23:MET:HE3	27:V:34:LEU:HD12	1.96	0.47
28:W:48:VAL:CG2	28:W:52:VAL:HG23	2.44	0.47
42:k:3:ARG:NH2	42:k:52:TYR:OH	2.48	0.47
44:m:471:GLU:OE2	44:m:474:ARG:HB2	2.15	0.47
1:1:91:G:OP2	1:1:93:C:N4	2.48	0.47
1:1:385:A:H2'	1:1:386:A:C8	2.49	0.47
1:1:507:U:H2'	1:1:508:U:C6	2.50	0.47
1:1:1615:C:H2'	1:1:1616:U:C6	2.50	0.47
1:1:2393:G:N2	1:1:2986:U:H3	2.11	0.47
1:1:3150:A:H2'	1:1:3151:U:O4'	2.15	0.47
6:8:597:ARG:HH11	15:I:464:LEU:HD23	1.80	0.47
12:F:126:LEU:O	12:F:130:ILE:HG12	2.15	0.47
14:H:44:THR:HG23	14:H:56:ALA:HB3	1.97	0.47
18:L:21:ARG:HB3	20:N:196:THR:HG22	1.97	0.47
24:R:105:LEU:HD22	24:R:135:LYS:HG3	1.97	0.47
45:n:242:LEU:HD13	45:n:264:LEU:HD23	1.95	0.47
51:t:145:VAL:HB	51:t:195:VAL:HG23	1.97	0.47
1:1:66:A:N6	1:1:76:G:H1'	2.30	0.46
1:1:1637:A:OP1	31:Z:73:LYS:NZ	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3294:A:H2'	1:1:3295:A:O4'	2.14	0.46
3:3:608:ASP:OD2	33:b:247:ARG:NH2	2.33	0.46
6:8:406:ILE:HG21	6:8:474:PRO:HB2	1.97	0.46
6:8:564:SER:OG	6:8:610:ARG:NH1	2.48	0.46
7:A:38:SER:HB2	7:A:68:LYS:HD3	1.96	0.46
17:K:69:ASP:OD1	17:K:70:ASP:N	2.42	0.46
28:W:47:ASP:OD1	28:W:47:ASP:N	2.45	0.46
28:W:88:ASN:ND2	28:W:226:SER:O	2.49	0.46
44:m:127:LYS:HD2	44:m:131:GLY:HA2	1.96	0.46
1:1:127:G:H2'	1:1:128:G:H8	1.80	0.46
1:1:2984:C:H2'	1:1:2985:C:C6	2.50	0.46
10:D:373:TYR:O	10:D:377:VAL:HG13	2.15	0.46
15:I:550:LEU:HB3	15:I:590:PHE:CZ	2.50	0.46
27:V:33:ASN:OD1	27:V:64:LYS:N	2.42	0.46
34:c:47:ASN:HB2	34:c:73:GLY:HA2	1.97	0.46
35:d:36:ILE:HD12	35:d:59:ILE:HD11	1.96	0.46
44:m:134:ARG:NH1	44:m:136:ILE:HD11	2.30	0.46
44:m:766:PRO:HB2	45:n:554:LEU:HB3	1.96	0.46
47:p:306:VAL:HG13	47:p:335:ILE:HD12	1.96	0.46
1:1:339:C:OP1	1:1:1380:G:O2'	2.33	0.46
1:1:640:U:H2'	1:1:641:C:C6	2.51	0.46
7:A:47:HIS:NE2	7:A:121:ASP:HB3	2.30	0.46
10:D:354:ASP:OD1	10:D:354:ASP:N	2.46	0.46
48:q:460:ILE:HG21	48:q:496:ARG:HG3	1.97	0.46
53:v:157:GLU:HA	53:v:160:LYS:HD3	1.98	0.46
1:1:3036:G:H5''	56:z:17:LYS:HD3	1.97	0.46
1:1:314:U:H2'	1:1:315:C:C6	2.50	0.46
1:1:725:G:O6	1:1:746:A:N6	2.49	0.46
1:1:3013:U:H2'	1:1:3014:U:C6	2.51	0.46
1:1:3184:A:N3	1:1:3187:A:O2'	2.44	0.46
5:7:82:ARG:NH2	16:J:286:ASP:OD1	2.49	0.46
6:8:389:GLU:O	6:8:393:ILE:HG13	2.16	0.46
6:8:626:GLN:HA	6:8:629:ARG:HG2	1.96	0.46
6:8:646:LEU:HD22	6:8:649:VAL:HG11	1.97	0.46
9:C:265:GLU:CD	9:C:265:GLU:H	2.21	0.46
15:I:487:GLN:N	15:I:487:GLN:OE1	2.49	0.46
22:P:118:GLN:NE2	22:P:147:GLU:OE2	2.48	0.46
32:a:13:VAL:HG22	32:a:183:ILE:HD12	1.98	0.46
1:1:1578:C:H2'	1:1:1579:C:C6	2.51	0.46
1:1:2815:G:O3'	16:J:312:LYS:NZ	2.47	0.46
3:3:634:TYR:O	3:3:638:ARG:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:157:GLN:OE1	11:E:157:GLN:N	2.46	0.46
30:Y:71:SER:N	30:Y:81:GLN:O	2.45	0.46
1:1:80:G:H2'	1:1:81:C:H6	1.81	0.46
1:1:492:U:H2'	1:1:493:G:C8	2.51	0.46
1:1:2854:U:H2'	1:1:2855:U:C6	2.51	0.46
1:1:2887:A:N7	33:b:31:THR:OG1	2.44	0.46
2:2:154:C:H2'	2:2:155:A:H8	1.80	0.46
6:8:339:PHE:HA	6:8:342:LEU:HB2	1.97	0.46
13:G:172:LYS:HG2	40:i:39:PHE:CE2	2.49	0.46
55:y:143:SER:HB2	55:y:165:THR:HG23	1.97	0.46
55:y:224:LEU:O	55:y:225:GLN:HG3	2.16	0.46
1:1:226:C:H2'	1:1:227:G:O4'	2.16	0.46
1:1:314:U:H2'	1:1:315:C:H6	1.81	0.46
1:1:912:G:N2	1:1:915:A:OP2	2.48	0.46
2:2:76:C:N3	2:2:77:A:N6	2.64	0.46
3:3:572:TRP:CE2	3:3:582:PHE:HB2	2.51	0.46
8:B:29:VAL:HG22	8:B:218:ILE:HD12	1.97	0.46
33:b:361:ILE:HD12	55:y:240:LEU:HD22	1.98	0.46
49:r:207:PRO:O	49:r:211:GLN:HG2	2.16	0.46
55:y:232:ILE:O	55:y:236:LEU:N	2.45	0.46
1:1:121:A:C5	13:G:129:PRO:HG3	2.51	0.46
1:1:665:A:H2'	1:1:666:A:H8	1.80	0.46
1:1:738:A:H2'	1:1:739:G:H8	1.80	0.46
1:1:1347:U:H2'	1:1:1355:A:H61	1.80	0.46
1:1:1410:U:H4'	36:e:75:LEU:HD11	1.98	0.46
1:1:1646:G:H4'	45:n:57:THR:HG21	1.98	0.46
1:1:2424:A:H2'	1:1:2425:G:O4'	2.15	0.46
1:1:2447:A:N1	1:1:2500:A:N6	2.63	0.46
1:1:2943:G:H21	33:b:36:GLY:HA3	1.80	0.46
3:3:349:SER:OG	3:3:351:ASN:OD1	2.33	0.46
7:A:186:ILE:HB	7:A:221:MET:HG3	1.97	0.46
10:D:351:ARG:NH1	10:D:372:ASP:OD2	2.49	0.46
28:W:171:ILE:HG13	28:W:173:THR:HG23	1.96	0.46
32:a:204:LEU:HD12	32:a:204:LEU:C	2.41	0.46
47:p:132:LEU:HD13	47:p:438:VAL:HG21	1.96	0.46
47:p:441:ILE:HG22	47:p:451:ILE:HG13	1.96	0.46
48:q:199:SER:OG	48:q:203:ARG:NH1	2.49	0.46
1:1:185:C:H5'	30:Y:121:ARG:HG2	1.98	0.46
1:1:297:G:OP2	1:1:297:G:N2	2.30	0.46
1:1:2900:A:C5	49:r:2:PRO:HG3	2.50	0.46
1:1:3089:C:H2'	1:1:3090:U:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:193:LEU:HB2	10:D:222:ARG:HD2	1.98	0.46
13:G:217:THR:HG21	46:o:156:LEU:HB2	1.98	0.46
13:G:240:ASN:OD1	13:G:241:LYS:N	2.47	0.46
29:X:110:VAL:HG22	29:X:124:VAL:HG22	1.97	0.46
32:a:31:THR:OG1	32:a:33:GLU:OE2	2.34	0.46
48:q:361:THR:HB	48:q:393:LEU:HD22	1.98	0.46
49:r:25:ARG:O	49:r:28:GLU:HG3	2.16	0.46
1:1:573:C:H2'	1:1:574:U:C6	2.51	0.45
1:1:1188:U:OP1	1:1:1210:U:O2'	2.21	0.45
1:1:1254:C:H2'	1:1:1255:C:C6	2.51	0.45
1:1:1597:C:H2'	1:1:1598:G:H8	1.80	0.45
1:1:2879:C:H2'	1:1:2880:U:C6	2.51	0.45
1:1:2950:G:H2'	1:1:2951:G:C8	2.52	0.45
2:2:19:C:H2'	2:2:20:U:C6	2.51	0.45
8:B:173:GLN:HG2	8:B:175:LYS:H	1.81	0.45
33:b:171:LEU:HD23	33:b:219:ILE:HB	1.98	0.45
43:l:70:LEU:HA	43:l:85:SER:HB3	1.98	0.45
47:p:285:SER:HB3	47:p:315:TRP:CH2	2.51	0.45
47:p:422:GLN:HB2	47:p:425:VAL:HB	1.98	0.45
1:1:431:U:H2'	1:1:432:G:H8	1.80	0.45
1:1:1444:G:H2'	1:1:1445:U:O4'	2.16	0.45
1:1:2411:U:H2'	1:1:2412:G:C8	2.50	0.45
1:1:2486:A:OP1	32:a:105:LYS:NZ	2.48	0.45
5:7:100:ILE:HD11	43:l:6:GLU:HA	1.98	0.45
6:8:666:VAL:O	6:8:669:GLU:HG3	2.15	0.45
7:A:259:GLU:O	7:A:263:ARG:HG2	2.16	0.45
9:C:187:LEU:HG	9:C:193:LYS:HD3	1.97	0.45
10:D:290:LYS:NZ	10:D:360:TRP:HE1	2.14	0.45
25:S:12:ARG:HE	25:S:15:PRO:HG3	1.81	0.45
33:b:25:THR:O	33:b:29:THR:OG1	2.27	0.45
33:b:65:LEU:HD11	33:b:99:SER:HA	1.99	0.45
48:q:463:VAL:HG21	48:q:473:ILE:HG12	1.97	0.45
1:1:289:A:H2'	1:1:290:G:H8	1.80	0.45
1:1:567:G:H2'	1:1:568:G:C8	2.50	0.45
3:3:676:LEU:O	3:3:680:GLN:HG2	2.16	0.45
6:8:274:VAL:HG22	6:8:304:LEU:HD22	1.97	0.45
22:P:122:ALA:HB3	22:P:143:PRO:HB2	1.98	0.45
44:m:703:ARG:HH21	44:m:720:ARG:HH21	1.63	0.45
45:n:229:LEU:HD23	45:n:229:LEU:HA	1.75	0.45
47:p:111:VAL:HG13	47:p:118:ILE:HG22	1.97	0.45
47:p:346:CYS:SG	47:p:354:THR:OG1	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:u:95:ARG:HA	52:u:95:ARG:HD2	1.86	0.45
1:1:1234:G:H2'	1:1:1235:U:C5	2.51	0.45
1:1:2831:G:H2'	1:1:2832:C:C6	2.51	0.45
1:1:3121:U:H4'	1:1:3122:A:OP1	2.15	0.45
6:8:341:PHE:CZ	6:8:345:THR:HG21	2.51	0.45
10:D:455:ALA:HB2	10:D:465:ILE:HD12	1.98	0.45
17:K:108:LYS:HB3	17:K:109:PRO:HD3	1.97	0.45
42:k:9:LYS:HB2	44:m:711:LEU:HA	1.98	0.45
55:y:126:GLU:HG3	55:y:137:VAL:HG11	1.97	0.45
1:1:1152:G:OP2	1:1:1152:G:N2	2.31	0.45
1:1:3267:A:H2'	11:E:69:PHE:CZ	2.52	0.45
1:1:3338:C:H2'	1:1:3339:A:C8	2.52	0.45
17:K:84:ASN:HB3	17:K:276:ILE:HD13	1.97	0.45
19:M:16:GLU:HB3	25:S:149:LYS:HG2	1.99	0.45
32:a:205:VAL:HG12	32:a:215:ARG:HD3	1.97	0.45
42:k:7:ASP:HB2	42:k:10:GLN:HB3	1.99	0.45
45:n:25:LEU:HD23	45:n:72:MET:SD	2.57	0.45
47:p:151:LYS:HG2	47:p:214:ILE:HG13	1.98	0.45
47:p:153:ILE:HG12	47:p:216:VAL:HG21	1.98	0.45
48:q:414:GLY:HA2	48:q:464:ASP:HB2	1.99	0.45
1:1:665:A:H2'	1:1:666:A:C8	2.52	0.45
1:1:836:A:H2'	1:1:837:A:H8	1.81	0.45
1:1:863:C:H2'	1:1:864:G:C8	2.52	0.45
1:1:1295:G:H2'	1:1:1296:C:C6	2.51	0.45
1:1:1667:A:H2'	1:1:1668:G:H8	1.81	0.45
1:1:2933:A:C6	1:1:3014:U:H4'	2.51	0.45
1:1:3064:U:H2'	1:1:3065:G:C8	2.50	0.45
3:3:470:ALA:HB2	27:V:67:PRO:HB2	1.98	0.45
17:K:339:PRO:HA	17:K:342:LEU:HG	1.97	0.45
33:b:80:ASP:HB3	33:b:241:TYR:CD2	2.52	0.45
33:b:403:GLU:HG3	33:b:412:PHE:HB3	1.98	0.45
47:p:105:TRP:CE2	47:p:445:GLN:HG3	2.52	0.45
1:1:441:U:H3	1:1:493:G:N2	2.14	0.45
1:1:748:U:H2'	1:1:749:C:C6	2.51	0.45
1:1:3026:G:H4'	49:r:2:PRO:HG2	1.97	0.45
3:3:301:GLN:OE1	3:3:301:GLN:N	2.44	0.45
26:U:21:SER:HG	26:U:22:PRO:HD3	1.77	0.45
28:W:173:THR:HG22	28:W:182:ILE:HG22	1.99	0.45
44:m:196:ILE:HG12	54:w:728:MET:HE1	1.99	0.45
44:m:568:VAL:HG21	44:m:622:LEU:HD22	1.98	0.45
47:p:377:PHE:HB2	47:p:396:HIS:ND1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:t:142:LEU:HD11	51:t:179:LEU:HD22	1.99	0.45
1:1:628:A:H2'	1:1:629:U:O4'	2.17	0.45
1:1:1301:A:O4'	49:r:44:GLY:HA2	2.17	0.45
1:1:2874:G:H21	1:1:2951:G:H21	1.64	0.45
3:3:188:THR:HA	3:3:191:PHE:CE2	2.51	0.45
15:I:267:ASN:CG	15:I:268:PHE:CD1	2.95	0.45
15:I:434:THR:HG21	15:I:537:VAL:HG21	1.97	0.45
22:P:175:ARG:O	22:P:179:GLN:HG2	2.17	0.45
25:S:12:ARG:HD2	25:S:22:PRO:HD2	1.99	0.45
38:g:105:VAL:HG22	54:w:416:THR:HB	1.98	0.45
47:p:167:LEU:HB2	47:p:204:LEU:HB2	1.99	0.45
1:1:591:G:O2'	11:E:17:ALA:O	2.33	0.45
1:1:820:A:H61	1:1:905:U:H3	1.64	0.45
1:1:1393:A:N6	1:1:1417:G:H1'	2.32	0.45
1:1:2450:G:O6	1:1:2497:U:O4	2.35	0.45
3:3:364:ARG:HG2	3:3:507:TYR:CZ	2.51	0.45
10:D:238:LEU:HA	10:D:241:ILE:HG12	1.98	0.45
11:E:102:ASN:H	11:E:105:TYR:HB3	1.81	0.45
15:I:418:LEU:HG	15:I:429:VAL:HG11	1.99	0.45
15:I:655:SER:O	15:I:658:SER:OG	2.30	0.45
17:K:280:PHE:HD1	17:K:290:PRO:HA	1.81	0.45
47:p:234:TRP:CD1	47:p:279:PRO:HA	2.51	0.45
51:t:186:LEU:O	51:t:190:ILE:HG12	2.16	0.45
54:w:704:LYS:HE3	54:w:704:LYS:HB2	1.76	0.45
55:y:109:CYS:HB2	55:y:149:GLY:HA2	1.99	0.45
1:1:543:C:H2'	1:1:544:C:C5	2.52	0.45
1:1:600:G:N2	1:1:603:A:OP2	2.30	0.45
1:1:696:C:OP2	9:C:119:ARG:NH2	2.47	0.45
1:1:1378:U:H2'	1:1:1379:G:H8	1.82	0.45
1:1:1659:U:H2'	1:1:1660:C:C6	2.52	0.45
1:1:2493:U:H5'	32:a:203:SER:HB3	1.99	0.45
3:3:237:ARG:HB3	3:3:258:PRO:HA	1.99	0.45
6:8:63:GLU:OE2	15:I:548:LYS:NZ	2.37	0.45
9:C:36:HIS:O	9:C:40:THR:HG23	2.17	0.45
17:K:48:THR:HG21	17:K:76:LYS:HG2	1.98	0.45
27:V:84:SER:HA	27:V:94:TYR:HB3	1.98	0.45
33:b:291:ASP:OD1	33:b:291:ASP:N	2.50	0.45
35:d:84:ASP:O	35:d:87:ASN:ND2	2.34	0.45
45:n:579:GLU:O	45:n:582:GLU:HG3	2.17	0.45
53:v:223:LYS:O	53:v:227:GLY:N	2.48	0.45
1:1:503:C:H2'	1:1:504:A:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:738:A:H2'	1:1:739:G:C8	2.52	0.44
1:1:906:A:H2'	1:1:907:G:O4'	2.17	0.44
1:1:3281:U:H2'	1:1:3282:U:C6	2.52	0.44
4:6:230:A:H2'	4:6:230:A:N3	2.32	0.44
6:8:371:LYS:O	6:8:373:ASN:ND2	2.49	0.44
21:O:46:GLU:HG3	21:O:49:ARG:H	1.82	0.44
1:1:810:A:H2'	1:1:811:U:C6	2.52	0.44
1:1:1286:A:H8	1:1:1287:A:H1'	1.82	0.44
1:1:2412:G:H2'	1:1:2413:A:H8	1.82	0.44
1:1:3378:C:H2'	1:1:3379:C:H6	1.81	0.44
3:3:279:LEU:HB3	3:3:309:LEU:HD23	1.99	0.44
4:6:54:A:H5'	46:o:97:ARG:HG2	1.98	0.44
8:B:387:LEU:HD11	52:u:109:LYS:HG2	1.99	0.44
11:E:50:LYS:NZ	11:E:72:ASN:O	2.46	0.44
18:L:47:ALA:HB3	18:L:48:PRO:HD3	1.99	0.44
32:a:201:VAL:HG23	32:a:201:VAL:O	2.16	0.44
44:m:597:VAL:HA	44:m:613:GLN:HG3	1.99	0.44
1:1:67:A:O2'	1:1:315:C:O2	2.36	0.44
1:1:910:G:H1	1:1:917:A:N6	2.15	0.44
1:1:1699:A:H2'	1:1:1700:G:H8	1.82	0.44
10:D:308:LEU:O	10:D:312:ILE:HG12	2.17	0.44
17:K:334:MET:HG3	17:K:342:LEU:HD22	2.00	0.44
24:R:115:ILE:HG23	24:R:119:LEU:HD23	1.98	0.44
35:d:81:GLU:OE1	35:d:81:GLU:N	2.50	0.44
44:m:580:GLN:NE2	44:m:584:GLU:OE2	2.42	0.44
1:1:116:A:H5''	40:i:36:ARG:CZ	2.48	0.44
1:1:3191:G:H2'	1:1:3192:U:C6	2.51	0.44
2:2:47:C:H1'	2:2:61:A:H2'	2.00	0.44
3:3:436:ILE:HB	3:3:501:LEU:HD13	2.00	0.44
5:7:110:ARG:NH1	5:7:143:GLU:OE2	2.42	0.44
6:8:388:ALA:HA	6:8:451:VAL:HG23	1.99	0.44
10:D:165:VAL:HG21	10:D:168:LEU:HD13	1.99	0.44
33:b:256:LEU:HD22	33:b:264:ILE:HD12	2.00	0.44
45:n:570:MET:HE3	45:n:570:MET:HB2	1.86	0.44
47:p:388:GLU:HG3	47:p:389:TYR:HD1	1.82	0.44
48:q:274:ARG:HB2	48:q:335:PHE:CZ	2.52	0.44
55:y:237:ARG:O	55:y:241:ILE:HG13	2.17	0.44
1:1:868:C:H2'	1:1:869:G:H8	1.80	0.44
1:1:1182:A:H2'	1:1:1183:C:H6	1.81	0.44
1:1:2367:A:H2'	1:1:2368:A:H8	1.79	0.44
8:B:116:ARG:HG2	8:B:122:TRP:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:135:ARG:O	10:D:139:GLU:HG3	2.18	0.44
10:D:415:TYR:HB3	17:K:66:LEU:HG	1.99	0.44
12:F:98:LYS:O	12:F:102:VAL:HG23	2.17	0.44
16:J:258:ARG:O	16:J:262:LYS:HG2	2.17	0.44
33:b:436:LEU:HD22	52:u:90:LEU:HD22	1.98	0.44
34:c:42:ILE:HD11	34:c:60:ALA:HB2	2.00	0.44
1:1:500:C:H2'	1:1:501:A:H8	1.82	0.44
1:1:787:G:H2'	1:1:788:C:C6	2.53	0.44
1:1:1551:C:H2'	1:1:1552:G:O4'	2.18	0.44
1:1:1717:U:H2'	1:1:1718:G:C8	2.51	0.44
1:1:2421:U:H2'	1:1:2422:C:C6	2.53	0.44
7:A:140:ASP:OD1	7:A:141:GLN:N	2.50	0.44
10:D:233:THR:HG23	10:D:234:LYS:N	2.33	0.44
12:F:116:PHE:O	12:F:199:ASN:ND2	2.49	0.44
24:R:110:ARG:HD3	24:R:120:TYR:CG	2.53	0.44
28:W:96:CYS:HB2	28:W:100:THR:HG21	1.99	0.44
40:i:55:ARG:HH12	44:m:239:PRO:HA	1.83	0.44
54:w:486:ALA:O	54:w:490:ARG:NH1	2.51	0.44
1:1:794:U:H2'	1:1:795:G:C8	2.46	0.44
1:1:1472:U:H2'	1:1:1473:G:H8	1.83	0.44
1:1:1497:C:H2'	1:1:1498:A:H8	1.83	0.44
1:1:3051:U:C2	1:1:3052:G:C8	3.05	0.44
1:1:3095:U:H2'	1:1:3096:C:C6	2.53	0.44
3:3:490:ASP:OD1	3:3:519:ARG:NE	2.51	0.44
6:8:473:TYR:HB3	6:8:474:PRO:HD3	1.99	0.44
9:C:156:LEU:HD12	9:C:159:ILE:HD12	2.00	0.44
21:O:142:SER:HA	21:O:145:VAL:HG22	1.99	0.44
21:O:189:ASP:OD1	21:O:189:ASP:N	2.50	0.44
42:k:27:ILE:HD12	42:k:39:ARG:HE	1.83	0.44
47:p:337:GLN:HE22	47:p:358:PRO:HG3	1.82	0.44
1:1:2371:G:N7	50:s:17:GLU:HG3	2.33	0.44
1:1:2402:A:H3'	1:1:2403:G:H5''	1.98	0.44
1:1:3033:A:H2'	1:1:3034:C:H6	1.83	0.44
7:A:112:PHE:CE1	7:A:223:VAL:HG22	2.52	0.44
8:B:112:ASP:O	8:B:116:ARG:HG3	2.18	0.44
8:B:219:ALA:HB2	8:B:336:VAL:HG12	2.00	0.44
28:W:165:MET:HG2	28:W:169:PHE:HD2	1.83	0.44
29:X:131:ASP:O	29:X:135:ILE:HG12	2.18	0.44
44:m:155:ASN:ND2	44:m:208:LYS:O	2.49	0.44
44:m:572:VAL:HA	44:m:594:LYS:HB2	1.99	0.44
47:p:292:GLN:HB3	47:p:335:ILE:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1253:U:H5''	1:1:1254:C:H5'	1.98	0.44
1:1:1709:C:H2'	1:1:1710:C:H6	1.83	0.44
1:1:1814:A:N3	45:n:569:LYS:HA	2.33	0.44
1:1:2339:C:H2'	1:1:2340:U:C6	2.53	0.44
2:2:95:G:O2'	41:j:81:GLY:O	2.27	0.44
3:3:250:GLN:OE1	3:3:267:ARG:NE	2.41	0.44
6:8:659:TYR:O	6:8:663:GLN:HG2	2.17	0.44
10:D:374:ILE:O	10:D:377:VAL:HG22	2.18	0.44
15:I:411:PHE:HE2	15:I:440:ALA:HB2	1.83	0.44
21:O:127:LEU:HD22	25:S:156:VAL:HG13	1.99	0.44
28:W:34:LEU:HD11	28:W:77:LEU:HD23	2.00	0.44
33:b:212:LYS:NZ	55:y:238:ASP:OD2	2.51	0.44
44:m:616:SER:OG	44:m:619:THR:OG1	2.29	0.44
1:1:349:A:C4	2:2:24:G:H1'	2.53	0.43
1:1:786:A:H4'	1:1:787:G:H5'	2.00	0.43
1:1:869:G:H2'	1:1:870:G:O4'	2.18	0.43
1:1:1152:G:N7	50:s:13:THR:HG21	2.32	0.43
1:1:1858:A:OP2	6:8:6:LYS:NZ	2.51	0.43
1:1:2128:C:H2'	1:1:2129:U:C6	2.53	0.43
1:1:2938:G:OP1	33:b:48:ARG:NH1	2.48	0.43
10:D:144:THR:HB	10:D:165:VAL:HA	2.00	0.43
15:I:166:VAL:HG11	15:I:227:TYR:CD1	2.53	0.43
22:P:94:LEU:HD23	22:P:94:LEU:HA	1.87	0.43
24:R:134:HIS:HD2	24:R:136:ARG:HB3	1.82	0.43
35:d:98:VAL:HG11	35:d:104:LEU:HD11	1.99	0.43
44:m:123:ASN:OD1	44:m:123:ASN:N	2.51	0.43
44:m:491:ILE:HG22	44:m:504:VAL:HG13	2.00	0.43
44:m:702:LYS:HA	44:m:726:VAL:HG23	2.00	0.43
47:p:107:SER:H	47:p:122:SER:HA	1.83	0.43
1:1:127:G:H2'	1:1:128:G:C8	2.53	0.43
1:1:594:U:H5''	1:1:609:G:O6	2.17	0.43
1:1:1329:U:O3'	37:f:19:SER:HB3	2.18	0.43
1:1:1392:G:H1'	1:1:1418:A:N6	2.33	0.43
1:1:2338:C:H2'	1:1:2339:C:C6	2.52	0.43
1:1:2446:U:H2'	1:1:2447:A:C8	2.53	0.43
1:1:2466:G:H5''	32:a:60:ARG:NH2	2.34	0.43
1:1:2494:A:H2'	1:1:2495:C:C6	2.52	0.43
1:1:3298:C:C2	1:1:3299:A:C8	3.07	0.43
6:8:585:PRO:O	6:8:589:THR:OG1	2.33	0.43
17:K:97:LEU:HD13	17:K:235:PRO:HB2	2.00	0.43
19:M:14:LEU:O	19:M:19:ARG:NE	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:O:75:ALA:HB1	21:O:106:GLU:OE2	2.19	0.43
22:P:60:PHE:CE1	22:P:82:ARG:HB2	2.53	0.43
25:S:77:VAL:HG13	25:S:126:VAL:HG22	1.99	0.43
37:f:16:TYR:OH	37:f:89:LEU:O	2.25	0.43
47:p:100:PHE:HE1	47:p:449:ILE:HD12	1.84	0.43
47:p:111:VAL:HG22	47:p:118:ILE:HG22	1.99	0.43
48:q:536:TYR:HB2	48:q:538:VAL:HG22	2.00	0.43
55:y:129:ILE:HG23	55:y:133:LEU:HD12	1.99	0.43
1:1:1889:G:H2'	1:1:1890:U:H6	1.84	0.43
1:1:2988:C:OP1	21:O:65:ASN:ND2	2.45	0.43
3:3:139:PHE:CD1	3:3:140:PRO:HD3	2.54	0.43
3:3:556:LEU:HD22	3:3:592:ARG:HH21	1.83	0.43
12:F:98:LYS:HB3	12:F:99:PRO:HD3	1.99	0.43
28:W:56:ILE:O	28:W:59:SER:OG	2.27	0.43
31:Z:88:ASP:HB2	31:Z:121:ARG:HH12	1.83	0.43
33:b:180:LYS:NZ	59:b:701:GDP:O2B	2.40	0.43
43:l:54:LEU:HD13	48:q:374:PHE:HE1	1.83	0.43
1:1:646:A:H2'	1:1:647:A:O4'	2.19	0.43
1:1:668:G:H2'	1:1:669:U:H6	1.83	0.43
3:3:440:PRO:O	3:3:441:THR:OG1	2.30	0.43
7:A:191:TYR:CE1	7:A:214:GLU:HG2	2.53	0.43
18:L:47:ALA:O	53:v:50:TYR:OH	2.31	0.43
27:V:66:LYS:HB2	27:V:69:LEU:HD23	1.99	0.43
28:W:41:TRP:CD2	28:W:220:TYR:HB3	2.54	0.43
32:a:89:ASP:HA	32:a:92:LYS:HE3	2.01	0.43
33:b:232:MET:HE1	33:b:240:ILE:HG13	1.99	0.43
44:m:380:TYR:CE2	44:m:382:GLU:HB2	2.54	0.43
47:p:107:SER:OG	47:p:147:ILE:O	2.34	0.43
48:q:508:ILE:HG13	48:q:531:TYR:HE1	1.84	0.43
53:v:53:LEU:HD22	53:v:157:GLU:HG2	2.00	0.43
1:1:705:A:N6	7:A:263:ARG:HD2	2.33	0.43
1:1:1341:U:H2'	1:1:1342:C:C6	2.53	0.43
1:1:1646:G:O2'	1:1:1808:G:N2	2.50	0.43
1:1:1799:A:H2'	1:1:1800:A:C8	2.52	0.43
1:1:3046:A:H5'	8:B:221:THR:HG21	1.99	0.43
1:1:3131:U:H2'	1:1:3132:C:C6	2.54	0.43
10:D:292:ILE:HG12	10:D:360:TRP:HB2	2.00	0.43
10:D:366:PRO:HB3	10:D:463:TYR:CE1	2.54	0.43
32:a:67:ILE:CD1	32:a:77:ALA:HB2	2.48	0.43
33:b:434:GLU:HG2	33:b:442:TYR:HE2	1.83	0.43
44:m:277:MET:HE2	44:m:277:MET:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:m:648:HIS:ND1	44:m:649:PRO:O	2.52	0.43
47:p:171:LYS:NZ	47:p:172:THR:O	2.39	0.43
54:w:551:LEU:HB3	54:w:555:ALA:HB3	2.00	0.43
1:1:1785:U:H2'	1:1:1786:G:C8	2.53	0.43
1:1:2810:C:H2'	1:1:2811:A:C8	2.52	0.43
6:8:315:LEU:HA	6:8:318:LEU:HD12	2.00	0.43
6:8:528:PHE:HD2	6:8:560:GLN:HE21	1.65	0.43
6:8:581:ASN:ND2	15:I:638:LEU:HD13	2.33	0.43
6:8:587:LEU:HD12	15:I:578:HIS:CE1	2.53	0.43
7:A:87:LEU:HD22	7:A:99:LEU:HD11	2.01	0.43
16:J:251:LEU:HA	16:J:254:VAL:HG12	1.99	0.43
20:N:31:ARG:NE	54:w:702:ASP:OD2	2.44	0.43
33:b:266:ALA:HA	33:b:269:LYS:HG2	2.00	0.43
39:h:45:LYS:O	39:h:49:LYS:HG2	2.18	0.43
40:i:67:LYS:HG2	40:i:71:LYS:HE3	2.00	0.43
43:l:150:THR:O	43:l:154:ARG:HG3	2.19	0.43
45:n:64:TYR:CE1	45:n:66:LYS:HD3	2.54	0.43
47:p:305:SER:OG	47:p:315:TRP:NE1	2.32	0.43
1:1:413:U:H2'	1:1:414:U:C6	2.53	0.43
1:1:1699:A:C6	1:1:1747:G:C6	3.07	0.43
1:1:2357:A:H2'	1:1:2358:A:H8	1.84	0.43
1:1:2812:C:H2'	1:1:2813:A:H8	1.83	0.43
1:1:2975:U:H2'	1:1:2976:A:H8	1.84	0.43
2:2:6:U:H2'	2:2:7:U:H6	1.84	0.43
2:2:40:A:H2'	2:2:41:A:C8	2.53	0.43
6:8:365:PHE:HE1	6:8:380:ILE:HG23	1.82	0.43
7:A:32:ARG:O	7:A:84:ASN:N	2.52	0.43
7:A:88:PHE:HB3	7:A:100:TRP:HB2	1.99	0.43
8:B:198:HIS:CE1	56:z:41:LEU:HD22	2.54	0.43
14:H:92:TYR:HB3	14:H:179:ILE:HG12	2.01	0.43
28:W:90:TYR:CZ	28:W:91:GLN:HG2	2.54	0.43
28:W:223:ASN:OD1	28:W:224:ASP:N	2.52	0.43
32:a:31:THR:HA	32:a:171:ASN:HA	2.00	0.43
38:g:20:ILE:HG13	38:g:32:ALA:HB1	2.01	0.43
47:p:333:LEU:HD12	47:p:377:PHE:HB3	2.01	0.43
48:q:201:ARG:NH2	48:q:263:GLU:OE2	2.46	0.43
1:1:573:C:H2'	1:1:574:U:H6	1.84	0.43
1:1:1666:G:H2'	1:1:1667:A:C8	2.54	0.43
1:1:3215:A:H5''	37:f:2:ALA:HB2	2.01	0.43
4:6:42:G:H2'	4:6:43:A:C8	2.52	0.43
6:8:546:ASN:OD1	6:8:547:ILE:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:292:ALA:HB2	8:B:302:LYS:HG3	2.01	0.43
10:D:316:VAL:HG12	10:D:342:ILE:HB	2.01	0.43
12:F:90:LYS:HD3	12:F:220:PHE:CE1	2.54	0.43
34:c:20:SER:HB2	34:c:97:ASP:H	1.83	0.43
44:m:369:GLN:OE1	44:m:371:TYR:OH	2.26	0.43
47:p:291:GLU:HG3	47:p:333:LEU:HA	1.99	0.43
49:r:128:ILE:HG13	49:r:133:MET:HG2	2.01	0.43
54:w:813:LYS:NZ	54:w:815:LYS:HB2	2.34	0.43
1:1:648:C:O2	54:w:828:ARG:NH1	2.36	0.43
1:1:1222:G:H8	1:1:1222:G:OP2	2.02	0.43
1:1:1675:G:H2'	1:1:1676:A:C8	2.53	0.43
1:1:2393:G:H4'	1:1:2394:G:H5'	2.00	0.43
1:1:2812:C:H2'	1:1:2813:A:C8	2.54	0.43
1:1:2889:C:OP1	33:b:28:LYS:NZ	2.48	0.43
1:1:3047:U:O2'	1:1:3048:A:H5'	2.17	0.43
10:D:319:LEU:HD21	10:D:331:THR:HB	2.01	0.43
11:E:132:ALA:O	11:E:136:GLU:HG2	2.18	0.43
15:I:189:ILE:HD13	15:I:189:ILE:HA	1.89	0.43
31:Z:99:GLU:HA	31:Z:102:GLU:HG2	2.01	0.43
44:m:681:ARG:HB2	44:m:701:ASP:OD2	2.19	0.43
48:q:285:LEU:HD21	48:q:327:TYR:HB3	2.00	0.43
1:1:187:A:H2'	1:1:188:U:C6	2.54	0.43
1:1:1213:G:H5'	25:S:137:ARG:HH21	1.84	0.43
1:1:1388:U:O2'	36:e:99:ASN:O	2.34	0.43
1:1:1491:A:H2'	1:1:1492:G:H8	1.82	0.43
3:3:679:LEU:O	3:3:682:ARG:HG3	2.19	0.43
6:8:519:LEU:HG	6:8:567:PHE:HD1	1.84	0.43
7:A:84:ASN:ND2	44:m:140:ILE:O	2.52	0.43
17:K:37:VAL:HG12	17:K:260:VAL:HG12	2.01	0.43
33:b:338:LYS:HE3	33:b:338:LYS:HB2	1.87	0.43
43:l:68:ILE:HG23	43:l:84:THR:HG22	2.01	0.43
44:m:341:PRO:HB2	44:m:343:GLU:CD	2.44	0.43
47:p:210:PRO:C	47:p:226:SER:HG	2.27	0.43
47:p:368:GLN:HG3	47:p:369:GLN:HG2	2.00	0.43
1:1:1307:G:O2'	1:1:1308:A:N7	2.47	0.42
1:1:2482:U:H2'	1:1:2483:G:O4'	2.19	0.42
1:1:2830:G:N2	33:b:135:ARG:HE	2.17	0.42
1:1:2840:C:H2'	1:1:2841:G:O4'	2.19	0.42
1:1:3234:A:H2	1:1:3253:G:H22	1.67	0.42
3:3:462:ILE:HB	3:3:488:VAL:HG12	2.00	0.42
6:8:365:PHE:O	6:8:368:SER:OG	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:86:VAL:O	12:F:114:GLY:HA2	2.18	0.42
12:F:222:HIS:ND1	12:F:224:ILE:HG12	2.34	0.42
13:G:146:LYS:NZ	13:G:173:MET:O	2.52	0.42
26:U:77:LYS:NZ	26:U:95:PHE:O	2.52	0.42
33:b:161:PRO:HB3	49:r:3:GLN:HG3	2.01	0.42
44:m:696:ILE:HD12	44:m:729:VAL:HB	2.01	0.42
44:m:738:PHE:CE1	44:m:750:PHE:HB2	2.54	0.42
1:1:791:A:H2'	1:1:792:G:C8	2.55	0.42
1:1:1621:A:H2'	1:1:1622:U:H6	1.84	0.42
1:1:2966:G:O4'	43:l:80:ARG:NH1	2.51	0.42
5:7:131:ARG:HG3	5:7:132:ARG:N	2.34	0.42
6:8:595:LEU:HD12	6:8:595:LEU:HA	1.88	0.42
13:G:145:ASN:HA	44:m:255:PRO:HB3	2.01	0.42
20:N:36:ILE:HG12	20:N:64:VAL:HG23	2.01	0.42
28:W:75:LYS:NZ	28:W:79:GLU:OE2	2.44	0.42
44:m:461:VAL:HB	44:m:475:THR:HG23	2.02	0.42
47:p:99:SER:HA	47:p:449:ILE:O	2.19	0.42
47:p:148:ARG:H	47:p:162:GLY:HA2	1.83	0.42
51:t:229:LEU:HD23	51:t:229:LEU:HA	1.89	0.42
54:w:740:LYS:HE2	54:w:740:LYS:HB3	1.84	0.42
55:y:107:VAL:HG23	55:y:108:ILE:HG13	2.01	0.42
1:1:116:A:H5''	40:i:36:ARG:NH2	2.34	0.42
1:1:257:U:H2'	1:1:258:G:C8	2.54	0.42
1:1:1466:G:N2	1:1:1510:G:H5''	2.35	0.42
1:1:1491:A:H2'	1:1:1492:G:C8	2.54	0.42
1:1:2595:A:H5''	1:1:2596:U:H5	1.84	0.42
2:2:63:G:H2'	2:2:63:G:N3	2.35	0.42
6:8:278:ALA:HA	6:8:281:LEU:HD12	2.00	0.42
20:N:155:VAL:O	20:N:162:ARG:NH2	2.39	0.42
33:b:292:ILE:HG22	33:b:293:ILE:HG13	2.00	0.42
44:m:292:LYS:H	44:m:292:LYS:HD2	1.84	0.42
47:p:164:ASP:OD1	47:p:164:ASP:N	2.49	0.42
49:r:148:LYS:N	49:r:170:ARG:O	2.51	0.42
1:1:3000:A:H2'	1:1:3001:C:C6	2.54	0.42
3:3:357:LEU:HD13	3:3:598:CYS:SG	2.59	0.42
3:3:444:HIS:NE2	3:3:631:GLU:HB2	2.35	0.42
6:8:281:LEU:HD23	6:8:284:LEU:HD12	1.99	0.42
12:F:84:VAL:HG23	12:F:117:VAL:HB	2.01	0.42
19:M:20:VAL:O	19:M:66:THR:OG1	2.33	0.42
20:N:120:TRP:HE1	20:N:123:GLN:HB3	1.84	0.42
29:X:57:LEU:HD23	29:X:94:GLN:HE22	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:175:TYR:CD2	33:b:176:PRO:HD2	2.54	0.42
33:b:268:VAL:HG21	33:b:305:LEU:HD13	1.99	0.42
51:t:78:VAL:O	51:t:82:GLU:HG2	2.18	0.42
52:u:8:PHE:CE2	52:u:49:LEU:HD12	2.53	0.42
1:1:63:A:N3	1:1:78:U:O2'	2.47	0.42
1:1:1226:G:H2'	1:1:1227:C:C6	2.55	0.42
1:1:1340:G:H2'	1:1:1341:U:H6	1.84	0.42
1:1:3053:G:H2'	1:1:3054:U:C6	2.55	0.42
1:1:3315:G:P	8:B:116:ARG:HH22	2.43	0.42
1:1:3383:G:H2'	1:1:3384:U:C6	2.54	0.42
4:6:224:G:N3	51:t:68:THR:HG21	2.34	0.42
5:7:56:LEU:HD12	5:7:56:LEU:HA	1.94	0.42
11:E:170:LYS:HB3	11:E:172:HIS:CE1	2.54	0.42
14:H:8:GLN:HB2	14:H:55:VAL:HG23	2.01	0.42
41:j:63:ARG:HG3	41:j:65:ARG:HG3	2.01	0.42
44:m:304:GLU:HA	44:m:307:GLN:HG3	2.00	0.42
1:1:47:C:OP2	1:1:48:A:O2'	2.33	0.42
1:1:1272:C:H41	28:W:158:ILE:HD12	1.85	0.42
1:1:1565:G:OP2	45:n:18:ARG:NH2	2.46	0.42
1:1:1722:U:OP2	24:R:103:ARG:NH1	2.51	0.42
1:1:2344:U:H2'	1:1:2345:A:C8	2.54	0.42
1:1:2811:A:H2'	1:1:2812:C:C6	2.55	0.42
1:1:2883:U:H2'	1:1:2884:C:C6	2.54	0.42
1:1:3026:G:H5'	1:1:3027:A:OP2	2.19	0.42
1:1:3177:G:O2'	1:1:3179:U:OP1	2.31	0.42
7:A:192:GLU:O	7:A:212:LEU:HA	2.20	0.42
10:D:119:VAL:HG22	10:D:194:ILE:HD13	2.02	0.42
15:I:520:ARG:HH12	15:I:535:PRO:HG2	1.83	0.42
33:b:129:LYS:HB3	33:b:129:LYS:HE3	1.85	0.42
36:e:63:THR:HA	36:e:66:LEU:HD12	2.02	0.42
48:q:336:LEU:HD13	48:q:531:TYR:CZ	2.54	0.42
50:s:7:GLN:O	50:s:9:ARG:NH1	2.45	0.42
1:1:490:A:H2'	1:1:491:C:C6	2.54	0.42
1:1:2830:G:H2'	1:1:2831:G:H8	1.82	0.42
1:1:3164:C:HO2'	1:1:3165:A:P	2.43	0.42
6:8:613:THR:O	6:8:617:LYS:HG2	2.20	0.42
15:I:430:LEU:HD12	15:I:474:LEU:HB3	2.01	0.42
21:O:45:GLY:HA2	21:O:49:ARG:HH21	1.83	0.42
22:P:141:SER:O	22:P:143:PRO:HD3	2.19	0.42
33:b:226:ASP:OD2	33:b:269:LYS:HG3	2.19	0.42
44:m:484:PRO:O	44:m:487:HIS:NE2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:p:233:PHE:HB3	47:p:281:SER:HB3	2.00	0.42
1:1:353:G:N7	41:j:55:ARG:HD2	2.34	0.42
1:1:371:G:N1	1:1:374:A:OP2	2.39	0.42
1:1:1824:U:H2'	1:1:1825:G:H8	1.84	0.42
1:1:2411:U:C2	1:1:2412:G:C8	3.08	0.42
1:1:3105:U:H2'	1:1:3106:A:C8	2.55	0.42
1:1:3333:G:OP2	1:1:3333:G:H8	2.03	0.42
6:8:358:LEU:HD22	6:8:391:PHE:CD1	2.55	0.42
10:D:50:SER:OG	10:D:52:PRO:HD2	2.20	0.42
11:E:76:LEU:N	11:E:138:GLN:OE1	2.43	0.42
29:X:11:LYS:NZ	46:o:150:GLU:OE1	2.52	0.42
29:X:57:LEU:HD12	29:X:57:LEU:HA	1.88	0.42
32:a:32:VAL:H	32:a:171:ASN:HA	1.85	0.42
32:a:72:PHE:O	32:a:76:ARG:HD3	2.20	0.42
35:d:77:ARG:HG2	35:d:89:LEU:HD22	2.00	0.42
43:l:150:THR:HG23	43:l:151:SER:N	2.35	0.42
44:m:445:ILE:HG12	44:m:788:PRO:HD3	2.01	0.42
45:n:115:ASP:N	45:n:115:ASP:OD1	2.52	0.42
47:p:166:THR:HB	47:p:203:ILE:HG23	2.02	0.42
48:q:350:LEU:HD23	48:q:418:ILE:HD13	2.02	0.42
51:t:80:ILE:O	51:t:84:LYS:HG2	2.19	0.42
1:1:19:U:H2'	1:1:20:A:C8	2.55	0.42
1:1:417:A:H2'	1:1:418:A:C8	2.55	0.42
1:1:3023:U:H2'	1:1:3024:A:H8	1.84	0.42
2:2:64:U:C2	2:2:65:A:C8	3.08	0.42
3:3:608:ASP:OD1	33:b:166:ASN:HB3	2.20	0.42
6:8:406:ILE:HD13	6:8:409:LEU:HD12	2.01	0.42
7:A:101:LEU:HD21	7:A:159:ASN:ND2	2.35	0.42
10:D:209:GLU:O	10:D:213:ILE:HG12	2.20	0.42
10:D:249:PHE:CE2	10:D:251:ASN:HB2	2.55	0.42
13:G:172:LYS:HG2	40:i:39:PHE:HE2	1.85	0.42
15:I:472:ALA:HB3	15:I:505:LEU:HD11	2.01	0.42
15:I:622:ASN:OD1	15:I:624:SER:OG	2.28	0.42
18:L:124:ILE:HD11	39:h:120:ALA:HB3	2.02	0.42
19:M:28:SER:HB3	19:M:53:VAL:HG22	2.02	0.42
44:m:664:ILE:HD12	44:m:674:LYS:HB2	2.02	0.42
45:n:377:GLU:HA	45:n:387:VAL:HG21	2.02	0.42
48:q:186:GLN:HG2	48:q:230:ARG:HH21	1.84	0.42
1:1:1250:G:OP1	3:3:704:LYS:NZ	2.53	0.42
1:1:1593:A:H2'	1:1:1594:A:C8	2.55	0.42
1:1:2447:A:N6	1:1:2500:A:H61	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2505:U:H2'	1:1:2506:U:C6	2.55	0.42
2:2:7:U:H2'	2:2:8:C:H6	1.85	0.42
2:2:8:C:H2'	2:2:9:A:H8	1.85	0.42
3:3:929:PRO:HB2	3:3:936:TYR:CD1	2.54	0.42
9:C:311:HIS:CE1	9:C:314:LYS:HA	2.55	0.42
17:K:45:ILE:HG12	17:K:251:LEU:HD13	2.02	0.42
28:W:48:VAL:HG23	28:W:52:VAL:CG2	2.49	0.42
28:W:138:PRO:O	28:W:182:ILE:HD11	2.20	0.42
32:a:42:ASP:HB3	32:a:45:ARG:HE	1.84	0.42
47:p:157:ARG:O	47:p:158:LEU:HD23	2.20	0.42
54:w:634:ASP:OD1	54:w:634:ASP:N	2.48	0.42
55:y:118:HIS:CD2	55:y:146:ILE:HB	2.55	0.42
1:1:150:A:C4	1:1:151:A:C8	3.08	0.41
1:1:945:C:H2'	1:1:946:U:C6	2.55	0.41
1:1:2325:G:H2'	1:1:2326:A:H8	1.84	0.41
1:1:2408:U:H2'	1:1:2409:G:H8	1.85	0.41
1:1:2421:U:H2'	1:1:2422:C:H6	1.85	0.41
1:1:2450:G:N1	1:1:2497:U:C2	2.88	0.41
1:1:2811:A:H2'	1:1:2812:C:H6	1.84	0.41
1:1:2883:U:H2'	1:1:2884:C:H6	1.84	0.41
1:1:3231:U:H2'	1:1:3232:G:H8	1.84	0.41
3:3:341:ARG:NH1	3:3:817:ALA:HB2	2.34	0.41
6:8:431:GLU:O	6:8:435:ILE:HG13	2.19	0.41
8:B:362:ALA:O	8:B:364:LYS:NZ	2.48	0.41
10:D:267:GLY:HA2	10:D:413:ASN:O	2.20	0.41
15:I:419:LYS:HZ3	44:m:193:LEU:HD22	1.84	0.41
17:K:33:PRO:O	17:K:37:VAL:HG23	2.20	0.41
28:W:70:ARG:HH11	28:W:97:SER:HA	1.85	0.41
44:m:657:CYS:SG	44:m:683:LEU:HD23	2.60	0.41
44:m:732:HIS:HD2	44:m:786:TRP:CE3	2.38	0.41
1:1:377:A:H1'	1:1:392:G:N2	2.35	0.41
1:1:908:G:N3	1:1:908:G:H2'	2.34	0.41
1:1:953:G:H5''	1:1:954:U:O4'	2.20	0.41
1:1:1889:G:H2'	1:1:1890:U:C6	2.55	0.41
1:1:2595:A:H3'	1:1:2596:U:C6	2.54	0.41
1:1:3214:U:OP2	19:M:128:ARG:NH1	2.37	0.41
1:1:3334:U:C6	52:u:50:LYS:HD3	2.55	0.41
2:2:39:G:H1'	2:2:104:A:N6	2.34	0.41
10:D:158:ALA:O	10:D:162:MET:HG2	2.20	0.41
10:D:402:LEU:HD23	10:D:405:LEU:HD12	2.02	0.41
10:D:487:ILE:HD13	10:D:487:ILE:HA	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:N:48:ALA:HB1	20:N:53:TYR:HB3	2.02	0.41
39:h:79:ASP:OD1	39:h:79:ASP:N	2.53	0.41
45:n:179:VAL:HG21	45:n:379:LEU:HD11	2.01	0.41
48:q:440:ARG:HA	48:q:440:ARG:HD3	1.89	0.41
1:1:195:U:H2'	1:1:196:G:O4'	2.20	0.41
1:1:492:U:H2'	1:1:493:G:H8	1.85	0.41
1:1:954:U:H2'	1:1:955:U:H6	1.84	0.41
1:1:3008:A:OP2	21:O:74:ARG:NH1	2.50	0.41
2:2:6:U:C2	2:2:7:U:C5	3.08	0.41
3:3:596:GLY:HA3	3:3:661:ASN:HA	2.01	0.41
15:I:201:GLU:HA	15:I:204:GLU:HB3	2.02	0.41
17:K:129:ASP:N	17:K:129:ASP:OD1	2.52	0.41
26:U:16:THR:HG23	26:U:62:VAL:HG13	2.02	0.41
32:a:59:PRO:HD2	32:a:153:SER:HA	2.02	0.41
33:b:424:ASP:HB3	33:b:427:TRP:CE2	2.56	0.41
43:l:96:LYS:HG2	43:l:134:PHE:HE1	1.84	0.41
45:n:125:PHE:O	45:n:129:ILE:HG12	2.19	0.41
48:q:476:SER:HB3	48:q:541:PHE:CE2	2.55	0.41
1:1:49:A:N7	20:N:187:ARG:HD2	2.35	0.41
1:1:707:U:H2'	1:1:708:G:O4'	2.20	0.41
1:1:1060:U:H2'	1:1:1061:A:C8	2.55	0.41
1:1:1448:U:H2'	1:1:1449:A:H8	1.85	0.41
1:1:1508:C:C2	1:1:1880:U:H1'	2.56	0.41
1:1:2353:G:OP2	22:P:82:ARG:NH2	2.53	0.41
2:2:65:A:C4	2:2:66:A:C8	3.08	0.41
2:2:154:C:H2'	2:2:155:A:C8	2.54	0.41
3:3:870:ARG:NH2	3:3:875:ASP:OD1	2.54	0.41
8:B:43:LEU:HB3	8:B:181:ILE:HG21	2.02	0.41
9:C:35:VAL:HG21	9:C:244:LEU:HD21	2.02	0.41
10:D:370:PRO:HB3	10:D:401:PHE:HE1	1.85	0.41
12:F:34:LYS:HD3	12:F:34:LYS:HA	1.79	0.41
23:Q:83:VAL:O	23:Q:103:ALA:HA	2.19	0.41
27:V:69:LEU:HA	27:V:72:LYS:HD2	2.01	0.41
28:W:57:ARG:NH2	28:W:65:LEU:O	2.53	0.41
38:g:79:SER:HG	38:g:80:ARG:HH11	1.65	0.41
47:p:328:THR:HG22	47:p:330:TYR:H	1.86	0.41
1:1:129:U:H2'	1:1:130:A:H8	1.83	0.41
1:1:675:C:H2'	1:1:676:G:O4'	2.21	0.41
1:1:1334:U:H2'	1:1:1335:C:C6	2.55	0.41
1:1:1667:A:H2'	1:1:1668:G:C8	2.54	0.41
1:1:3099:C:H2'	56:z:5:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:241:LEU:HD13	3:3:271:LEU:HD12	2.02	0.41
6:8:282:LEU:O	6:8:286:ASN:ND2	2.36	0.41
10:D:52:PRO:O	10:D:55:LYS:HG2	2.19	0.41
14:H:78:MET:O	14:H:82:VAL:HG23	2.20	0.41
21:O:61:ALA:HA	21:O:70:PRO:HD2	2.02	0.41
27:V:104:ASN:OD1	27:V:108:GLU:N	2.51	0.41
28:W:89:LEU:HD12	28:W:89:LEU:HA	1.91	0.41
32:a:74:VAL:HG22	32:a:84:ALA:HB1	2.02	0.41
33:b:402:ILE:HA	33:b:405:GLU:HG2	2.01	0.41
51:t:100:ILE:HD13	51:t:309:VAL:HB	2.02	0.41
54:w:718:ALA:O	54:w:721:ILE:HG22	2.19	0.41
1:1:990:U:H2'	1:1:991:G:H5''	2.02	0.41
1:1:1170:A:H2'	1:1:1171:G:O4'	2.21	0.41
1:1:1333:C:C2	1:1:1334:U:C5	3.09	0.41
1:1:2374:C:O2'	1:1:2375:G:H5'	2.20	0.41
1:1:3321:C:H2'	1:1:3322:A:H8	1.86	0.41
15:I:186:LYS:NZ	15:I:262:THR:OG1	2.52	0.41
18:L:89:TYR:O	18:L:92:THR:OG1	2.35	0.41
35:d:25:PHE:HD1	35:d:28:ARG:HD2	1.85	0.41
44:m:443:LEU:HD12	44:m:452:LEU:HD11	2.01	0.41
48:q:384:LYS:HB3	48:q:384:LYS:HE2	1.83	0.41
49:r:195:LEU:HD13	49:r:225:VAL:HG12	2.02	0.41
55:y:18:LYS:HE2	55:y:18:LYS:HB2	1.91	0.41
55:y:62:MET:HE3	55:y:73:PRO:HG3	2.02	0.41
1:1:1224:C:C2	1:1:1225:A:C8	3.09	0.41
1:1:2324:A:H2'	1:1:2325:G:C8	2.55	0.41
1:1:2426:U:H3	1:1:2603:G:H1	1.67	0.41
6:8:430:ALA:O	6:8:434:LYS:HG2	2.21	0.41
18:L:44:ALA:HA	53:v:30:ILE:HD13	2.02	0.41
29:X:53:HIS:ND1	29:X:54:TYR:O	2.52	0.41
51:t:75:ILE:HD12	51:t:156:PRO:HG2	2.02	0.41
53:v:208:TYR:O	53:v:210:GLN:N	2.50	0.41
1:1:411:U:H2'	1:1:412:G:H8	1.84	0.41
1:1:528:U:H2'	1:1:529:A:H8	1.86	0.41
1:1:596:C:OP1	12:F:37:ASN:ND2	2.50	0.41
1:1:978:G:O2'	1:1:1103:A:N1	2.48	0.41
1:1:1203:A:C2	1:1:1300:G:H2'	2.56	0.41
1:1:1724:U:C5	24:R:128:LYS:HE3	2.56	0.41
7:A:152:ILE:HD12	7:A:186:ILE:HD11	2.01	0.41
10:D:76:LEU:HD23	10:D:99:PRO:HG2	2.03	0.41
10:D:334:GLU:O	10:D:338:ALA:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:I:607:SER:O	15:I:610:ARG:HG2	2.20	0.41
33:b:211:TYR:OH	33:b:337:GLU:OE1	2.33	0.41
44:m:358:GLU:O	44:m:362:ARG:HG3	2.21	0.41
44:m:785:ILE:HG22	44:m:794:PHE:HB2	2.03	0.41
1:1:616:G:H2'	1:1:617:G:H8	1.86	0.41
1:1:835:G:H1'	1:1:858:A:H61	1.86	0.41
1:1:1566:A:H5''	51:t:33:ARG:HH21	1.86	0.41
1:1:1724:U:H1'	1:1:1725:C:C6	2.55	0.41
1:1:2342:U:H2'	1:1:2343:C:H6	1.85	0.41
1:1:2422:C:H2'	1:1:2423:U:O4'	2.21	0.41
1:1:3358:U:H2'	1:1:3359:A:O4'	2.20	0.41
2:2:74:U:H2'	30:Y:74:TYR:OH	2.21	0.41
3:3:280:LYS:HA	3:3:310:PRO:HD3	2.02	0.41
4:6:35:C:O2	17:K:243:THR:OG1	2.39	0.41
6:8:496:PHE:O	6:8:500:LYS:HG3	2.21	0.41
9:C:5:GLN:HB3	9:C:19:ALA:HB1	2.03	0.41
9:C:152:VAL:HG12	9:C:153:SER:H	1.86	0.41
9:C:174:ALA:O	9:C:178:LEU:HG	2.20	0.41
9:C:237:GLN:O	9:C:246:ARG:NH1	2.52	0.41
10:D:309:LEU:HD23	10:D:316:VAL:HG11	2.03	0.41
10:D:474:ALA:HB1	10:D:479:PHE:HB2	2.03	0.41
12:F:132:PRO:HA	12:F:229:PHE:CD1	2.55	0.41
14:H:161:LEU:O	14:H:164:ILE:HG22	2.21	0.41
15:I:179:LEU:HD21	15:I:251:LEU:HD12	2.03	0.41
15:I:616:PHE:CD1	15:I:631:ALA:HB2	2.56	0.41
20:N:28:TRP:O	20:N:32:GLN:HG2	2.21	0.41
25:S:8:GLN:O	25:S:8:GLN:HG3	2.21	0.41
31:Z:53:VAL:HG13	31:Z:62:VAL:HG22	2.02	0.41
35:d:105:GLN:N	35:d:105:GLN:OE1	2.54	0.41
45:n:74:GLU:HG3	45:n:76:VAL:H	1.86	0.41
45:n:448:LEU:O	45:n:451:GLU:HG2	2.21	0.41
46:o:118:LYS:HE3	46:o:140:VAL:HA	2.03	0.41
1:1:29:C:H4'	1:1:62:A:H4'	2.03	0.41
1:1:144:A:H2'	1:1:145:G:O4'	2.21	0.41
1:1:543:C:H2'	1:1:544:C:C6	2.55	0.41
1:1:711:A:H4'	7:A:248:VAL:HG13	2.03	0.41
1:1:1343:A:H2'	1:1:1344:G:H8	1.85	0.41
1:1:1699:A:H2'	1:1:1700:G:C8	2.57	0.41
3:3:292:ARG:HH22	3:3:495:GLY:HA3	1.86	0.41
3:3:693:ARG:NH2	33:b:159:ARG:HH22	2.14	0.41
6:8:564:SER:HB2	6:8:607:LEU:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:240:ARG:HG3	10:D:241:ILE:N	2.36	0.41
11:E:40:LEU:HD13	11:E:84:VAL:HG21	2.02	0.41
12:F:147:LEU:HD11	12:F:240:VAL:HG11	2.03	0.41
24:R:114:LYS:HB2	24:R:115:ILE:HD12	2.03	0.41
44:m:351:LYS:HE3	44:m:351:LYS:HB2	1.90	0.41
44:m:534:PHE:CE1	44:m:577:LYS:HG2	2.56	0.41
44:m:777:ASN:O	44:m:779:LEU:HD23	2.21	0.41
44:m:787:HIS:CE1	44:m:789:ARG:HB3	2.56	0.41
47:p:297:SER:HB2	47:p:339:SER:HB3	2.02	0.41
1:1:506:U:H2'	1:1:507:U:O4'	2.21	0.40
1:1:673:U:H2'	1:1:674:G:C8	2.56	0.40
1:1:786:A:N6	23:Q:88:THR:OG1	2.54	0.40
1:1:886:C:H2'	1:1:887:G:H8	1.86	0.40
1:1:919:U:H2'	1:1:920:A:O4'	2.21	0.40
1:1:929:A:H2'	1:1:930:U:C6	2.57	0.40
1:1:937:G:O2'	5:7:60:TYR:OH	2.32	0.40
1:1:1498:A:H2'	1:1:1499:C:H6	1.85	0.40
1:1:1785:U:H2'	1:1:1786:G:H8	1.86	0.40
3:3:291:ASP:OD1	3:3:291:ASP:N	2.54	0.40
6:8:628:LYS:HD3	6:8:628:LYS:HA	1.87	0.40
6:8:648:ASP:OD1	6:8:648:ASP:N	2.54	0.40
7:A:28:MET:HE3	7:A:28:MET:HB3	1.94	0.40
13:G:60:ARG:HD3	54:w:462:LEU:HD11	2.03	0.40
17:K:336:ILE:HD13	51:t:186:LEU:HD13	2.02	0.40
44:m:225:SER:O	44:m:229:ARG:HG2	2.21	0.40
45:n:434:ASP:OD2	45:n:447:TYR:OH	2.26	0.40
47:p:324:ASP:OD1	47:p:325:THR:N	2.54	0.40
48:q:281:ARG:HH21	48:q:283:ARG:HE	1.69	0.40
51:t:184:TYR:HB3	51:t:185:PRO:HD3	2.03	0.40
1:1:261:U:H2'	1:1:262:U:C6	2.57	0.40
1:1:532:A:O2'	1:1:533:A:H5'	2.21	0.40
1:1:634:C:H5'	37:f:21:ARG:O	2.21	0.40
1:1:2423:U:O2'	1:1:2424:A:H8	2.04	0.40
1:1:2964:G:O2'	1:1:2967:A:N1	2.52	0.40
2:2:8:C:H2'	2:2:9:A:C8	2.56	0.40
3:3:298:PHE:O	3:3:302:LEU:HG	2.20	0.40
3:3:320:ALA:HB3	3:3:494:ARG:HD3	2.03	0.40
8:B:137:TYR:HE2	8:B:196:ARG:HH12	1.69	0.40
9:C:69:ARG:HD2	54:w:805:LEU:O	2.22	0.40
32:a:63:MET:N	32:a:63:MET:SD	2.94	0.40
34:c:36:GLN:HE21	34:c:36:GLN:HB2	1.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:252:U:N3	53:v:210:GLN:OE1	2.46	0.40
1:1:518:G:OP2	1:1:518:G:N2	2.38	0.40
1:1:659:G:H5''	1:1:660:A:OP1	2.21	0.40
1:1:858:A:H2'	1:1:859:G:C8	2.56	0.40
3:3:247:LEU:HB2	3:3:873:ARG:HH11	1.87	0.40
3:3:790:LEU:HB2	48:q:537:ASN:HB3	2.02	0.40
6:8:339:PHE:CE1	6:8:386:SER:HB2	2.56	0.40
7:A:57:PRO:HD2	7:A:162:VAL:HG22	2.03	0.40
10:D:451:LEU:HD23	10:D:451:LEU:HA	1.93	0.40
13:G:81:THR:HG22	13:G:179:ILE:HG22	2.02	0.40
15:I:520:ARG:NE	15:I:540:SER:HB2	2.36	0.40
15:I:659:LYS:HD3	15:I:659:LYS:HA	1.92	0.40
35:d:87:ASN:CG	35:d:88:PRO:HD3	2.46	0.40
45:n:30:ALA:O	45:n:34:ARG:HG3	2.22	0.40
48:q:424:CYS:HA	48:q:448:ILE:HG21	2.03	0.40
51:t:205:ARG:HG2	51:t:251:ILE:HG21	2.03	0.40
1:1:412:G:H2'	1:1:413:U:H6	1.87	0.40
1:1:548:G:H2'	1:1:549:U:O4'	2.22	0.40
1:1:591:G:H1'	11:E:19:LYS:HG3	2.04	0.40
1:1:1619:A:H2'	1:1:1620:U:O4'	2.21	0.40
1:1:1861:G:H2'	1:1:1862:U:C6	2.56	0.40
1:1:2342:U:H2'	1:1:2343:C:C6	2.56	0.40
1:1:2411:U:H5''	43:l:76:THR:HG21	2.03	0.40
1:1:2439:A:N6	1:1:2509:U:H3	2.20	0.40
1:1:2940:A:H3'	1:1:2941:A:H2'	2.04	0.40
1:1:3113:A:H2'	1:1:3114:A:O4'	2.21	0.40
1:1:3297:U:O4	8:B:124:LYS:NZ	2.54	0.40
3:3:275:MET:HE2	3:3:277:LEU:HD21	2.04	0.40
7:A:148:HIS:O	7:A:152:ILE:HG23	2.21	0.40
7:A:166:ALA:O	7:A:169:SER:OG	2.33	0.40
8:B:143:GLY:O	8:B:147:GLU:HG2	2.22	0.40
11:E:51:ARG:O	11:E:72:ASN:ND2	2.55	0.40
20:N:46:ASP:OD1	20:N:46:ASP:N	2.55	0.40
27:V:63:LYS:HE2	27:V:63:LYS:HB3	1.86	0.40
30:Y:43:TYR:O	30:Y:125:LYS:HG2	2.21	0.40
32:a:159:LEU:HB2	32:a:165:LEU:HD11	2.04	0.40
44:m:648:HIS:HB2	44:m:655:PHE:HE1	1.85	0.40
1:1:444:U:H2'	1:1:445:G:C8	2.57	0.40
1:1:500:C:H2'	1:1:501:A:C8	2.57	0.40
1:1:1570:U:H1'	51:t:279:GLY:HA2	2.04	0.40
1:1:1616:U:H2'	1:1:1617:G:H8	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2882:U:H2'	1:1:2883:U:H6	1.85	0.40
2:2:66:A:H2'	2:2:67:U:C6	2.56	0.40
2:2:142:C:H2'	2:2:143:U:H6	1.86	0.40
5:7:81:ASN:ND2	16:J:278:MET:HE1	2.37	0.40
6:8:484:ARG:NH2	6:8:521:GLU:OE1	2.55	0.40
7:A:149:TYR:HD1	7:A:149:TYR:HA	1.80	0.40
10:D:347:ASP:N	10:D:347:ASP:OD1	2.54	0.40
33:b:344:ILE:HA	33:b:348:LEU:HB2	2.03	0.40
35:d:16:LEU:HD11	35:d:71:LEU:HD12	2.03	0.40
40:i:60:LEU:HD13	40:i:68:ARG:HG3	2.02	0.40
44:m:444:SER:O	44:m:452:LEU:HD12	2.21	0.40
54:w:558:ILE:HG23	54:w:559:PHE:CD2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	644/995 (65%)	632 (98%)	12 (2%)	0	100	100
5	7	130/204 (64%)	129 (99%)	1 (1%)	0	100	100
6	8	469/710 (66%)	466 (99%)	3 (1%)	0	100	100
7	A	246/291 (84%)	245 (100%)	1 (0%)	0	100	100
8	B	332/387 (86%)	325 (98%)	7 (2%)	0	100	100
9	C	356/362 (98%)	350 (98%)	6 (2%)	0	100	100
10	D	426/505 (84%)	419 (98%)	7 (2%)	0	100	100
11	E	152/176 (86%)	147 (97%)	5 (3%)	0	100	100
12	F	213/244 (87%)	210 (99%)	3 (1%)	0	100	100
13	G	194/256 (76%)	193 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	H	187/191 (98%)	182 (97%)	5 (3%)	0	100	100
15	I	522/663 (79%)	515 (99%)	7 (1%)	0	100	100
16	J	143/427 (34%)	143 (100%)	0	0	100	100
17	K	274/376 (73%)	270 (98%)	4 (2%)	0	100	100
18	L	119/199 (60%)	116 (98%)	3 (2%)	0	100	100
19	M	134/138 (97%)	131 (98%)	3 (2%)	0	100	100
20	N	185/204 (91%)	183 (99%)	2 (1%)	0	100	100
21	O	195/199 (98%)	194 (100%)	1 (0%)	0	100	100
22	P	158/184 (86%)	153 (97%)	5 (3%)	0	100	100
23	Q	125/186 (67%)	125 (100%)	0	0	100	100
24	R	130/189 (69%)	126 (97%)	4 (3%)	0	100	100
25	S	168/172 (98%)	163 (97%)	5 (3%)	0	100	100
26	U	100/121 (83%)	97 (97%)	3 (3%)	0	100	100
27	V	123/137 (90%)	123 (100%)	0	0	100	100
28	W	230/236 (98%)	225 (98%)	5 (2%)	0	100	100
29	X	135/142 (95%)	133 (98%)	2 (2%)	0	100	100
30	Y	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
31	Z	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
32	a	212/217 (98%)	207 (98%)	5 (2%)	0	100	100
33	b	467/647 (72%)	458 (98%)	9 (2%)	0	100	100
34	c	95/105 (90%)	95 (100%)	0	0	100	100
35	d	105/113 (93%)	104 (99%)	1 (1%)	0	100	100
36	e	123/130 (95%)	119 (97%)	4 (3%)	0	100	100
37	f	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
38	g	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
39	h	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
40	i	70/100 (70%)	68 (97%)	2 (3%)	0	100	100
41	j	71/88 (81%)	70 (99%)	1 (1%)	0	100	100
42	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
43	l	174/181 (96%)	169 (97%)	5 (3%)	0	100	100
44	m	658/807 (82%)	636 (97%)	22 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	n	417/605 (69%)	409 (98%)	8 (2%)	0	100	100
46	o	131/220 (60%)	128 (98%)	3 (2%)	0	100	100
47	p	299/460 (65%)	291 (97%)	8 (3%)	0	100	100
48	q	367/618 (59%)	358 (98%)	9 (2%)	0	100	100
49	r	206/261 (79%)	205 (100%)	1 (0%)	0	100	100
50	s	34/520 (6%)	34 (100%)	0	0	100	100
51	t	279/322 (87%)	275 (99%)	4 (1%)	0	100	100
52	u	112/199 (56%)	112 (100%)	0	0	100	100
53	v	124/231 (54%)	122 (98%)	2 (2%)	0	100	100
54	w	270/841 (32%)	266 (98%)	4 (2%)	0	100	100
55	y	243/245 (99%)	236 (97%)	7 (3%)	0	100	100
56	z	53/106 (50%)	52 (98%)	1 (2%)	0	100	100
All	All	11263/15599 (72%)	11057 (98%)	206 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	3	573/870 (66%)	571 (100%)	2 (0%)	86	94
5	7	119/181 (66%)	119 (100%)	0	100	100
6	8	435/647 (67%)	435 (100%)	0	100	100
7	A	227/263 (86%)	225 (99%)	2 (1%)	70	82
8	B	282/323 (87%)	278 (99%)	4 (1%)	59	76
9	C	285/289 (99%)	284 (100%)	1 (0%)	84	93
10	D	378/440 (86%)	377 (100%)	1 (0%)	86	94
11	E	134/153 (88%)	131 (98%)	3 (2%)	45	67
12	F	182/205 (89%)	181 (100%)	1 (0%)	81	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	G	161/208 (77%)	161 (100%)	0	100	100
14	H	169/171 (99%)	167 (99%)	2 (1%)	63	79
15	I	479/602 (80%)	474 (99%)	5 (1%)	68	81
16	J	133/383 (35%)	133 (100%)	0	100	100
17	K	258/346 (75%)	255 (99%)	3 (1%)	63	79
18	L	100/159 (63%)	99 (99%)	1 (1%)	68	81
19	M	107/109 (98%)	105 (98%)	2 (2%)	50	71
20	N	165/176 (94%)	163 (99%)	2 (1%)	63	79
21	O	160/162 (99%)	159 (99%)	1 (1%)	78	88
22	P	132/146 (90%)	131 (99%)	1 (1%)	73	85
23	Q	103/151 (68%)	103 (100%)	0	100	100
24	R	112/154 (73%)	112 (100%)	0	100	100
25	S	155/156 (99%)	155 (100%)	0	100	100
26	U	89/107 (83%)	89 (100%)	0	100	100
27	V	97/105 (92%)	97 (100%)	0	100	100
28	W	209/213 (98%)	208 (100%)	1 (0%)	81	91
29	X	114/118 (97%)	113 (99%)	1 (1%)	70	82
30	Y	109/110 (99%)	106 (97%)	3 (3%)	38	60
31	Z	115/116 (99%)	114 (99%)	1 (1%)	70	82
32	a	195/198 (98%)	190 (97%)	5 (3%)	40	63
33	b	423/573 (74%)	422 (100%)	1 (0%)	87	95
34	c	81/88 (92%)	79 (98%)	2 (2%)	42	64
35	d	94/97 (97%)	93 (99%)	1 (1%)	65	80
36	e	108/111 (97%)	108 (100%)	0	100	100
37	f	90/91 (99%)	90 (100%)	0	100	100
38	g	95/103 (92%)	94 (99%)	1 (1%)	65	80
39	h	104/105 (99%)	104 (100%)	0	100	100
40	i	59/82 (72%)	59 (100%)	0	100	100
41	j	60/71 (84%)	60 (100%)	0	100	100
42	k	68/69 (99%)	68 (100%)	0	100	100
43	l	151/156 (97%)	150 (99%)	1 (1%)	76	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	m	599/723 (83%)	593 (99%)	6 (1%)	68	81
45	n	381/548 (70%)	378 (99%)	3 (1%)	73	85
46	o	118/199 (59%)	115 (98%)	3 (2%)	42	64
47	p	273/413 (66%)	266 (97%)	7 (3%)	40	63
48	q	316/535 (59%)	315 (100%)	1 (0%)	86	94
49	r	190/229 (83%)	189 (100%)	1 (0%)	81	91
50	s	32/445 (7%)	32 (100%)	0	100	100
51	t	256/287 (89%)	254 (99%)	2 (1%)	73	85
52	u	99/180 (55%)	99 (100%)	0	100	100
53	v	116/205 (57%)	115 (99%)	1 (1%)	70	82
54	w	237/745 (32%)	235 (99%)	2 (1%)	73	85
55	y	211/211 (100%)	210 (100%)	1 (0%)	81	91
56	z	48/95 (50%)	48 (100%)	0	100	100
All	All	9986/13622 (73%)	9911 (99%)	75 (1%)	70	85

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

Mol	Chain	Res	Type
3	3	494	ARG
3	3	594	VAL
7	A	55	LEU
7	A	248	VAL
8	B	162	VAL
8	B	304	THR
8	B	332	ARG
8	B	351	LEU
9	C	265	GLU
10	D	148	VAL
11	E	26	ARG
11	E	87	THR
11	E	98	VAL
12	F	120	THR
14	H	82	VAL
14	H	157	ASN
15	I	156	THR
15	I	320	LYS
15	I	493	VAL

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Mol	Chain	Res	Type
15	I	571	ARG
15	I	601	ILE
17	K	135	VAL
17	K	218	SER
17	K	280	PHE
18	L	63	VAL
19	M	59	ASN
19	M	64	VAL
20	N	19	LEU
20	N	114	ARG
21	O	101	ARG
22	P	150	VAL
28	W	40	VAL
29	X	56	ARG
30	Y	105	VAL
30	Y	115	ARG
30	Y	127	GLU
31	Z	42	LEU
32	a	10	ARG
32	a	29	LEU
32	a	117	ILE
32	a	162	VAL
32	a	188	ASN
33	b	86	TYR
34	c	90	VAL
34	c	104	LEU
35	d	65	LYS
38	g	20	ILE
43	l	24	ILE
44	m	123	ASN
44	m	475	THR
44	m	613	GLN
44	m	720	ARG
44	m	779	LEU
44	m	782	LEU
45	n	115	ASP
45	n	132	ILE
45	n	427	ILE
46	o	102	PHE
46	o	185	VAL
46	o	216	ILE
47	p	117	HIS

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Mol	Chain	Res	Type
47	p	119	ILE
47	p	195	ILE
47	p	372	ILE
47	p	384	CYS
47	p	432	VAL
47	p	438	VAL
48	q	183	THR
49	r	245	VAL
51	t	75	ILE
51	t	314	ILE
53	v	165	LEU
54	w	535	ILE
54	w	558	ILE
55	y	192	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) such sidechains are listed below:

Mol	Chain	Res	Type
3	3	151	ASN
3	3	367	ASN
3	3	503	ASN
3	3	694	ASN
3	3	882	ASN
5	7	42	GLN
5	7	109	ASN
6	8	335	GLN
6	8	560	GLN
7	A	73	GLN
7	A	148	HIS
8	B	139	GLN
8	B	182	GLN
9	C	221	ASN
9	C	311	HIS
10	D	143	GLN
10	D	180	GLN
10	D	287	ASN
10	D	320	HIS
10	D	330	ASN
10	D	441	GLN
12	F	93	ASN
12	F	244	ASN
14	H	9	GLN

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Mol	Chain	Res	Type
14	H	58	HIS
14	H	59	ASN
14	H	169	ASN
16	J	215	HIS
16	J	324	GLN
17	K	269	GLN
18	L	105	ASN
20	N	138	GLN
21	O	193	GLN
22	P	97	ASN
24	R	3	ASN
24	R	58	HIS
24	R	134	HIS
25	S	108	GLN
27	V	81	GLN
28	W	22	ASN
28	W	128	ASN
31	Z	122	HIS
31	Z	127	ASN
32	a	27	ASN
32	a	62	ASN
33	b	72	ASN
33	b	323	GLN
33	b	384	ASN
36	e	20	HIS
36	e	35	GLN
37	f	26	ASN
37	f	88	ASN
38	g	14	ASN
39	h	16	GLN
39	h	62	GLN
41	j	76	ASN
43	l	111	ASN
44	m	228	GLN
44	m	250	HIS
45	n	7	ASN
45	n	69	GLN
45	n	149	ASN
46	o	153	ASN
47	p	102	ASN
47	p	135	ASN
47	p	337	GLN

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Mol	Chain	Res	Type
48	q	391	HIS
48	q	402	ASN
48	q	450	HIS
48	q	466	ASN
48	q	537	ASN
49	r	10	HIS
49	r	14	HIS
51	t	88	ASN
51	t	92	HIS
52	u	24	ASN
52	u	82	ASN
53	v	29	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2469/3396 (72%)	407 (16%)	3 (0%)
2	2	153/158 (96%)	22 (14%)	0
4	6	85/232 (36%)	19 (22%)	0
All	All	2707/3786 (71%)	448 (16%)	3 (0%)

All (448) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	7	C
1	1	14	U
1	1	26	A
1	1	40	A
1	1	42	C
1	1	43	A
1	1	49	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A
1	1	74	G
1	1	77	A
1	1	92	G
1	1	96	G

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Mol	Chain	Res	Type
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	117	U
1	1	121	A
1	1	122	A
1	1	135	C
1	1	136	G
1	1	155	G
1	1	156	G
1	1	165	A
1	1	170	G
1	1	190	U
1	1	191	U
1	1	200	C
1	1	210	U
1	1	213	A
1	1	218	G
1	1	219	A
1	1	220	G
1	1	241	G
1	1	252	U
1	1	255	A
1	1	264	G
1	1	265	A
1	1	266	A
1	1	268	A
1	1	269	G
1	1	284	A
1	1	285	A
1	1	286	U
1	1	295	A
1	1	311	C
1	1	323	A
1	1	329	U
1	1	337	G
1	1	339	C
1	1	349	A
1	1	368	G
1	1	376	G
1	1	398	A

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Mol	Chain	Res	Type
1	1	401	U
1	1	402	A
1	1	403	C
1	1	421	G
1	1	422	A
1	1	439	C
1	1	440	A
1	1	521	A
1	1	533	A
1	1	535	G
1	1	543	C
1	1	544	C
1	1	545	U
1	1	547	G
1	1	550	A
1	1	551	A
1	1	557	A
1	1	559	A
1	1	579	G
1	1	582	G
1	1	589	A
1	1	604	G
1	1	611	A
1	1	612	U
1	1	620	U
1	1	621	A
1	1	629	U
1	1	636	C
1	1	660	A
1	1	677	A
1	1	681	U
1	1	690	A
1	1	691	A
1	1	705	A
1	1	706	A
1	1	719	U
1	1	721	G
1	1	734	C
1	1	742	G
1	1	785	G
1	1	800	G
1	1	808	A

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Mol	Chain	Res	Type
1	1	817	A
1	1	818	C
1	1	820	A
1	1	821	U
1	1	822	G
1	1	830	A
1	1	836	A
1	1	851	C
1	1	860	G
1	1	861	C
1	1	862	U
1	1	871	U
1	1	894	G
1	1	895	A
1	1	896	A
1	1	904	A
1	1	907	G
1	1	908	G
1	1	910	G
1	1	917	A
1	1	919	U
1	1	930	U
1	1	932	U
1	1	936	A
1	1	944	C
1	1	960	U
1	1	961	C
1	1	962	A
1	1	965	A
1	1	979	U
1	1	982	C
1	1	991	G
1	1	1116	G
1	1	1117	G
1	1	1132	C
1	1	1143	A
1	1	1153	A
1	1	1160	C
1	1	1174	G
1	1	1180	A
1	1	1181	U
1	1	1182	A

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Mol	Chain	Res	Type
1	1	1192	C
1	1	1193	A
1	1	1203	A
1	1	1217	A
1	1	1222	G
1	1	1244	A
1	1	1245	A
1	1	1246	G
1	1	1259	A
1	1	1262	G
1	1	1263	A
1	1	1265	U
1	1	1272	C
1	1	1284	C
1	1	1285	G
1	1	1286	A
1	1	1287	A
1	1	1303	A
1	1	1305	U
1	1	1307	G
1	1	1330	A
1	1	1331	U
1	1	1348	U
1	1	1386	A
1	1	1392	G
1	1	1399	A
1	1	1400	G
1	1	1417	G
1	1	1418	A
1	1	1419	A
1	1	1434	G
1	1	1437	C
1	1	1452	A
1	1	1468	A
1	1	1469	C
1	1	1481	A
1	1	1483	G
1	1	1485	G
1	1	1507	G
1	1	1508	C
1	1	1539	A
1	1	1555	U

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Mol	Chain	Res	Type
1	1	1556	C
1	1	1557	A
1	1	1560	G
1	1	1567	U
1	1	1568	U
1	1	1569	U
1	1	1571	A
1	1	1580	A
1	1	1581	C
1	1	1582	C
1	1	1587	A
1	1	1589	A
1	1	1604	G
1	1	1627	U
1	1	1628	C
1	1	1629	U
1	1	1630	U
1	1	1639	C
1	1	1643	A
1	1	1724	U
1	1	1725	C
1	1	1750	A
1	1	1751	G
1	1	1761	C
1	1	1762	C
1	1	1763	U
1	1	1764	U
1	1	1766	G
1	1	1767	C
1	1	1773	C
1	1	1780	G
1	1	1795	U
1	1	1796	G
1	1	1797	A
1	1	1808	G
1	1	1815	U
1	1	1816	A
1	1	1817	G
1	1	1821	U
1	1	1837	U
1	1	1838	G
1	1	1839	A

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Mol	Chain	Res	Type
1	1	1858	A
1	1	1864	A
1	1	1865	A
1	1	1866	C
1	1	1867	A
1	1	1878	G
1	1	1880	U
1	1	1882	G
1	1	1884	A
1	1	1886	A
1	1	1887	A
1	1	1897	G
1	1	1906	G
1	1	2332	A
1	1	2335	G
1	1	2348	A
1	1	2349	U
1	1	2370	G
1	1	2371	G
1	1	2374	C
1	1	2385	G
1	1	2388	U
1	1	2393	G
1	1	2394	G
1	1	2398	A
1	1	2400	G
1	1	2401	A
1	1	2403	G
1	1	2404	A
1	1	2405	C
1	1	2416	U
1	1	2419	A
1	1	2422	C
1	1	2423	U
1	1	2424	A
1	1	2431	C
1	1	2433	U
1	1	2434	U
1	1	2435	G
1	1	2436	U
1	1	2437	G
1	1	2438	A

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Mol	Chain	Res	Type
1	1	2440	G
1	1	2445	A
1	1	2447	A
1	1	2448	G
1	1	2453	U
1	1	2460	U
1	1	2463	G
1	1	2468	A
1	1	2469	G
1	1	2473	C
1	1	2474	G
1	1	2475	G
1	1	2476	C
1	1	2487	U
1	1	2495	C
1	1	2497	U
1	1	2502	A
1	1	2505	U
1	1	2596	U
1	1	2598	G
1	1	2599	U
1	1	2600	C
1	1	2602	G
1	1	2606	G
1	1	2803	A
1	1	2809	C
1	1	2818	U
1	1	2821	C
1	1	2822	U
1	1	2824	G
1	1	2836	C
1	1	2839	G
1	1	2848	G
1	1	2859	U
1	1	2860	U
1	1	2864	A
1	1	2874	G
1	1	2875	U
1	1	2876	C
1	1	2887	A
1	1	2888	U
1	1	2898	G

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Mol	Chain	Res	Type
1	1	2899	C
1	1	2907	G
1	1	2911	A
1	1	2918	G
1	1	2919	A
1	1	2920	U
1	1	2922	G
1	1	2923	U
1	1	2926	A
1	1	2928	C
1	1	2935	U
1	1	2936	A
1	1	2941	A
1	1	2942	C
1	1	2943	G
1	1	2944	U
1	1	2945	G
1	1	2946	A
1	1	2956	A
1	1	2971	A
1	1	2972	G
1	1	2978	U
1	1	2979	U
1	1	2980	U
1	1	2982	A
1	1	2983	C
1	1	2990	G
1	1	2996	U
1	1	2997	G
1	1	3012	A
1	1	3022	G
1	1	3032	A
1	1	3046	A
1	1	3056	U
1	1	3057	U
1	1	3058	U
1	1	3079	U
1	1	3092	C
1	1	3093	C
1	1	3094	A
1	1	3100	U
1	1	3101	G

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Mol	Chain	Res	Type
1	1	3122	A
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3153	U
1	1	3154	C
1	1	3156	U
1	1	3157	U
1	1	3165	A
1	1	3170	A
1	1	3172	A
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3179	U
1	1	3181	C
1	1	3187	A
1	1	3196	U
1	1	3207	U
1	1	3217	C
1	1	3218	A
1	1	3219	G
1	1	3238	G
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3247	G
1	1	3259	U
1	1	3263	G
1	1	3270	U
1	1	3276	G
1	1	3278	C
1	1	3289	G
1	1	3294	A
1	1	3295	A
1	1	3304	U
1	1	3313	U
1	1	3316	A
1	1	3317	U
1	1	3319	U

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Mol	Chain	Res	Type
1	1	3334	U
1	1	3341	U
1	1	3348	G
1	1	3349	C
1	1	3358	U
1	1	3363	U
1	1	3369	G
1	1	3378	C
1	1	3382	U
1	1	3383	G
1	1	3386	G
1	1	3396	U
2	2	23	U
2	2	34	U
2	2	35	C
2	2	38	U
2	2	48	A
2	2	59	A
2	2	62	C
2	2	63	G
2	2	77	A
2	2	81	U
2	2	82	U
2	2	84	C
2	2	85	G
2	2	86	U
2	2	87	G
2	2	90	U
2	2	95	G
2	2	104	A
2	2	106	C
2	2	107	G
2	2	116	G
2	2	125	U
4	6	4	U
4	6	5	C
4	6	7	C
4	6	15	C
4	6	16	U
4	6	23	U
4	6	24	A
4	6	40	U

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Mol	Chain	Res	Type
4	6	41	G
4	6	42	G
4	6	52	G
4	6	54	A
4	6	56	U
4	6	58	G
4	6	59	C
4	6	218	A
4	6	220	C
4	6	224	G
4	6	230	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	116	A
1	1	263	C
1	1	3121	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 for Mogul analysis.

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
59	GDP	b	701	58,60	29,30,30	1.16	2 (6%)	45,47,47	1.77	7 (15%)
57	ADP	3	1000	-	28,29,29	1.42	4 (14%)	43,45,45	1.82	9 (20%)

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
59	GDP	b	701	58,60	-	1/16/32/32	0/3/3/3
57	ADP	3	1000	-	-	2/16/32/32	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	3	1000	ADP	C5-C4	4.75	1.47	1.39
59	b	701	GDP	C5-C4	3.18	1.47	1.38
57	3	1000	ADP	C5-C6	2.76	1.48	1.41
59	b	701	GDP	C6-N1	-2.43	1.34	1.38
57	3	1000	ADP	C8-N7	2.36	1.36	1.31
57	3	1000	ADP	C5-N7	-2.23	1.35	1.39

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	b	701	GDP	C5-C4-N3	-6.17	118.56	128.39
57	3	1000	ADP	C5-C4-N3	-5.84	118.67	126.72
59	b	701	GDP	C2-N3-C4	5.06	121.01	112.30
57	3	1000	ADP	N3-C4-N9	4.63	135.04	127.17
59	b	701	GDP	N9-C4-N3	4.57	135.08	125.95
57	3	1000	ADP	C2-N3-C4	3.69	120.84	111.83
57	3	1000	ADP	C4-C5-N7	-3.47	106.62	110.58
59	b	701	GDP	C6-C5-N7	3.23	136.16	130.29
57	3	1000	ADP	N3-C2-N1	-3.17	123.78	128.58
57	3	1000	ADP	C4-N9-C8	2.62	108.49	105.74
59	b	701	GDP	C4-C5-N7	-2.59	106.56	110.67
57	3	1000	ADP	C5-N7-C8	2.54	107.44	103.45
57	3	1000	ADP	C3'-C2'-C1'	2.30	105.82	101.46
59	b	701	GDP	C3'-C2'-C1'	2.17	105.57	101.46
59	b	701	GDP	O6-C6-C5	-2.09	121.02	126.53
57	3	1000	ADP	C6-C5-N7	2.07	136.08	132.09

There are no chirality outliers.

All (3) torsion outliers are listed below:

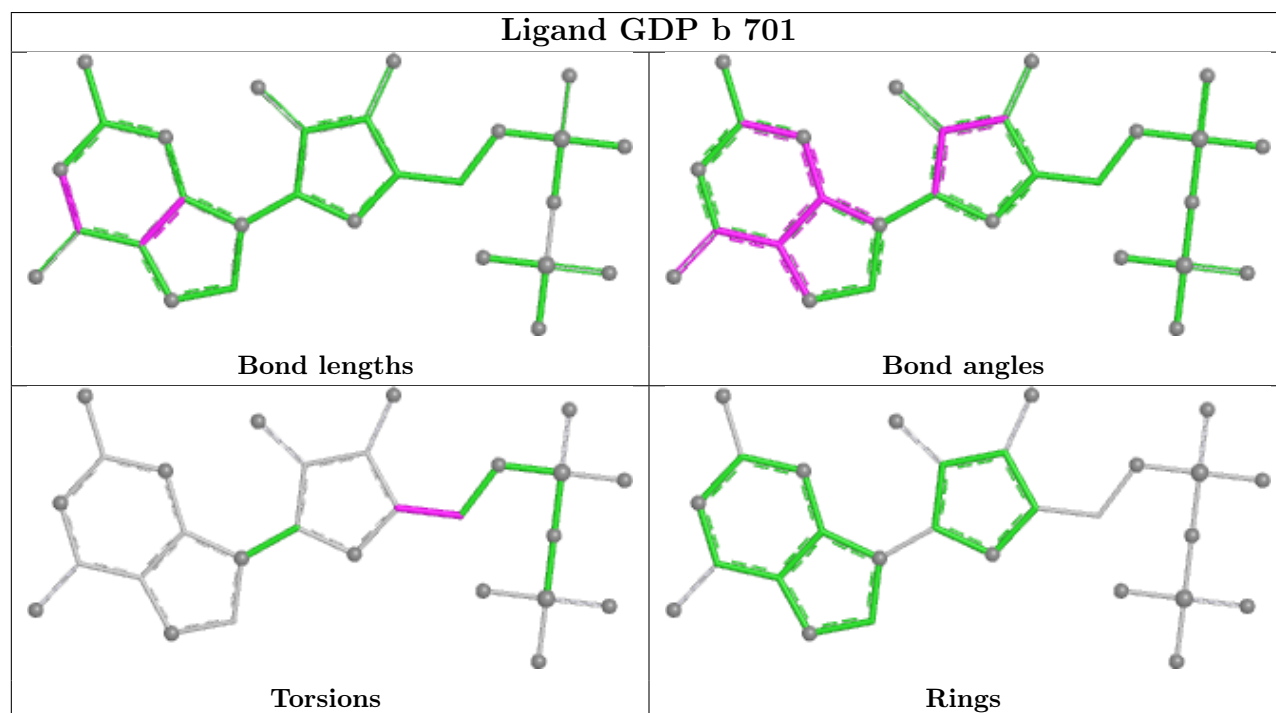
Mol	Chain	Res	Type	Atoms
57	3	1000	ADP	C3'-C4'-C5'-O5'
57	3	1000	ADP	O4'-C4'-C5'-O5'
59	b	701	GDP	C3'-C4'-C5'-O5'

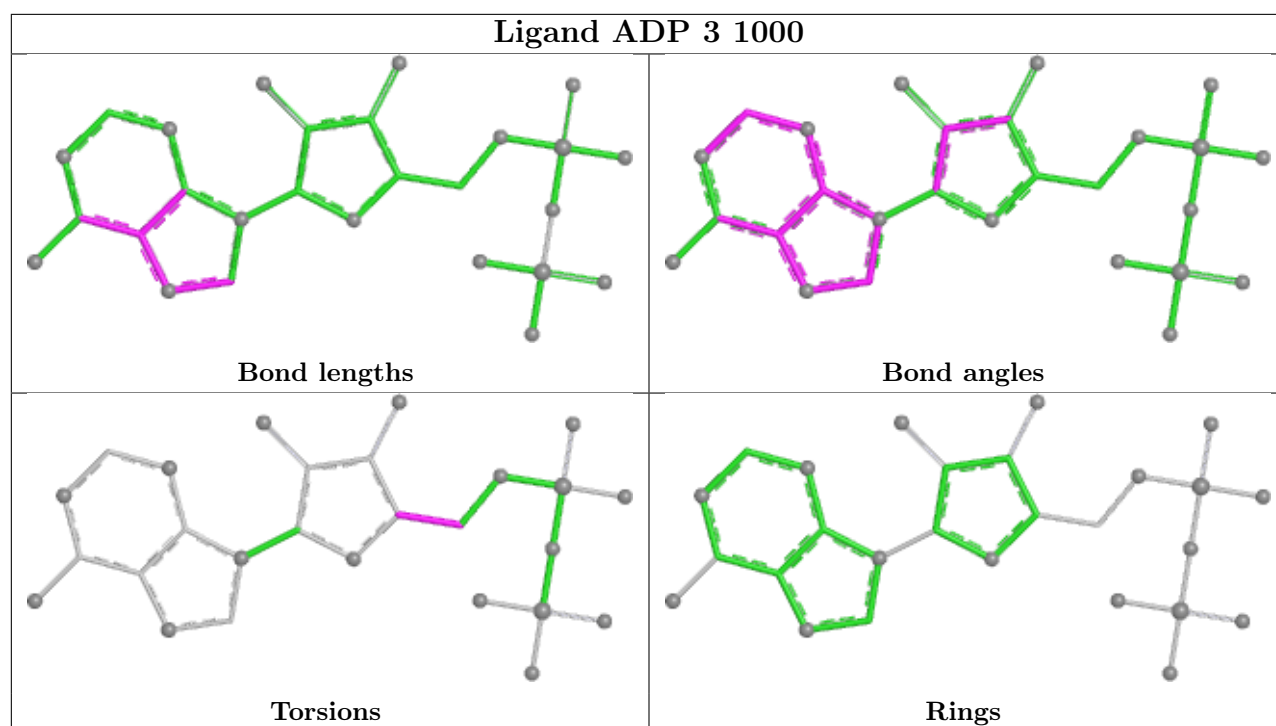
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	b	701	GDP	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

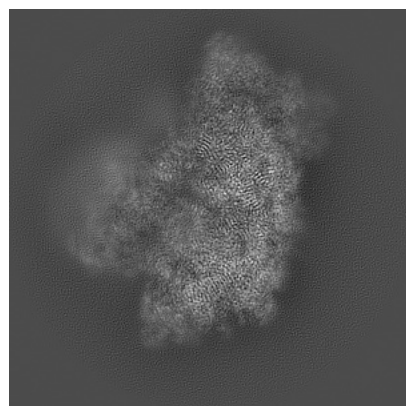
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43027. These allow visual inspection of the internal detail of the map and identification of artifacts.

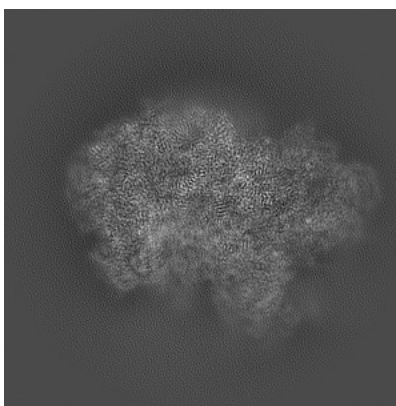
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

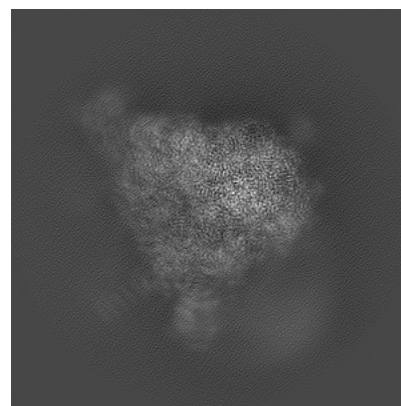
6.1.1 Primary map



X

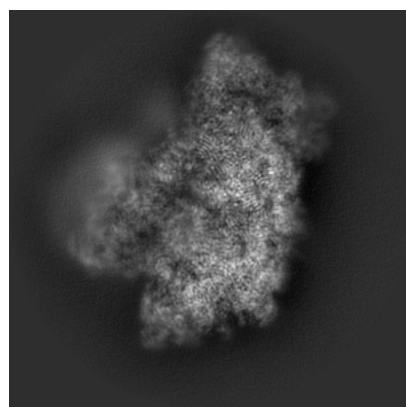


Y

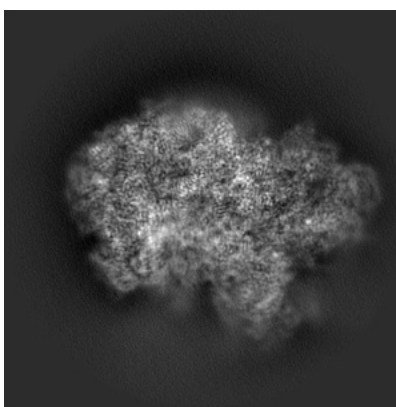


Z

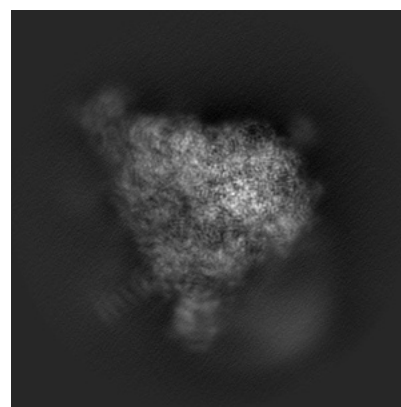
6.1.2 Raw map



X



Y

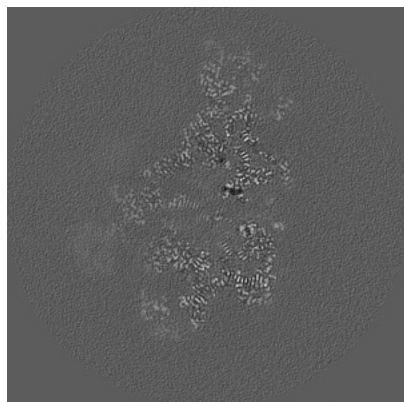


Z

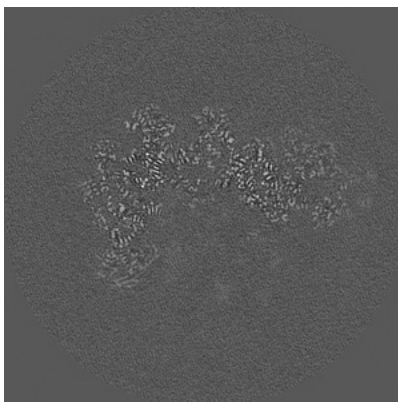
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

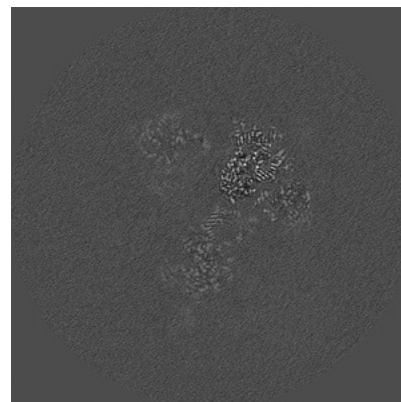
6.2.1 Primary map



X Index: 180

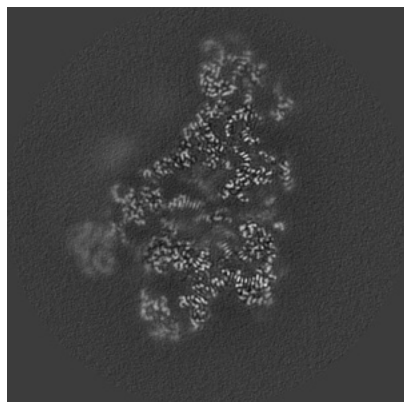


Y Index: 180

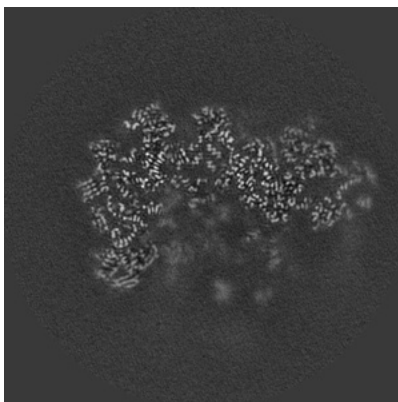


Z Index: 180

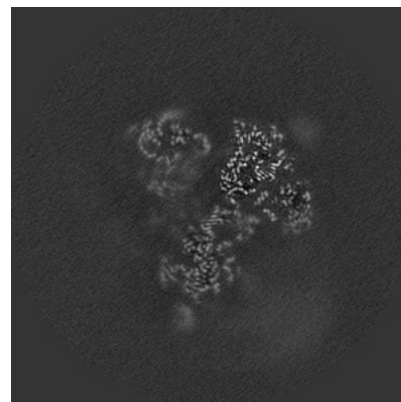
6.2.2 Raw map



X Index: 180



Y Index: 180

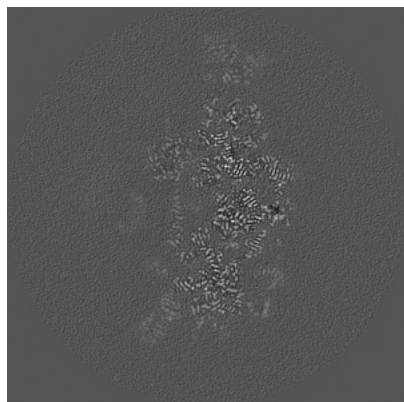


Z Index: 180

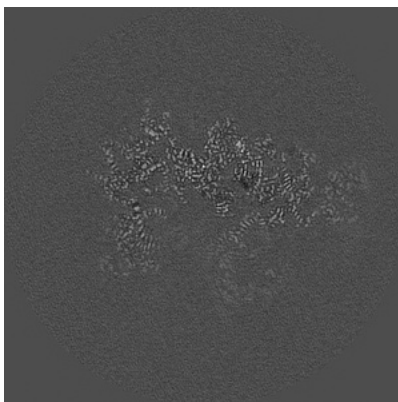
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

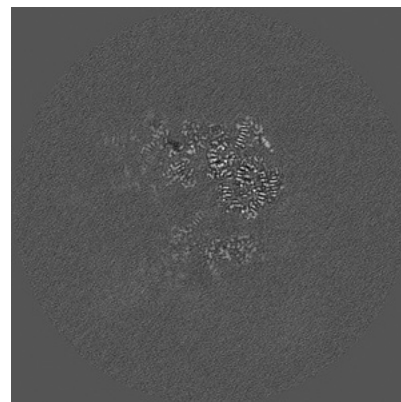
6.3.1 Primary map



X Index: 206

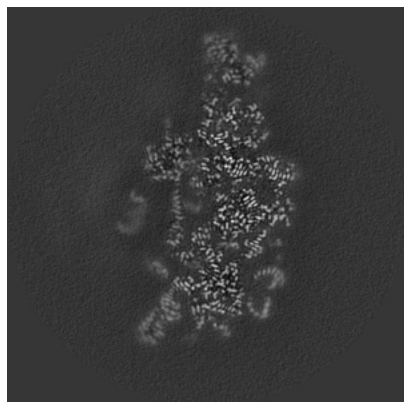


Y Index: 203

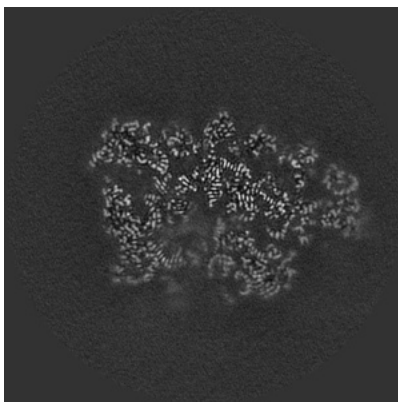


Z Index: 212

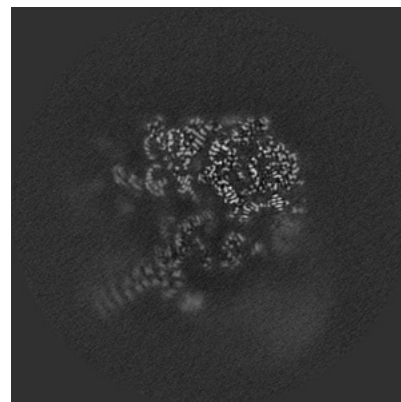
6.3.2 Raw map



X Index: 206



Y Index: 216

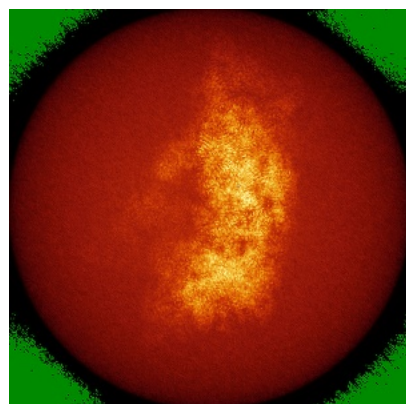


Z Index: 204

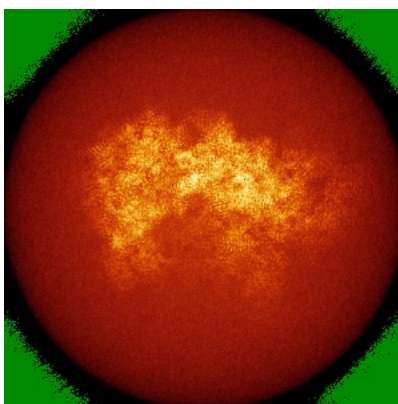
The images above show the largest variance slices of the map in three orthogonal directions.

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

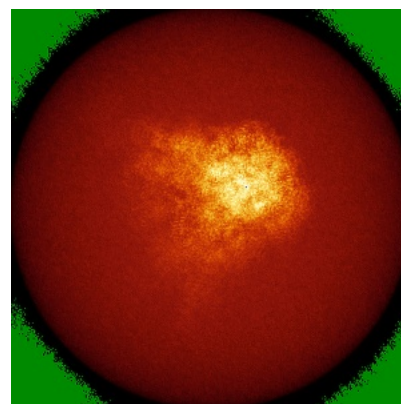
6.4.1 Primary map



X

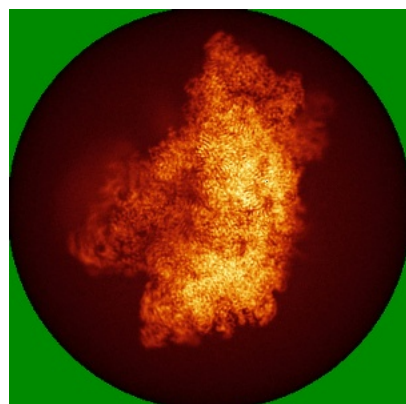


Y

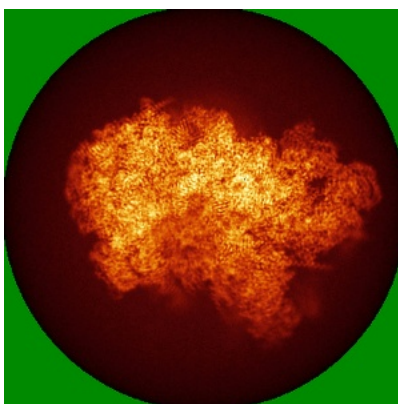


Z

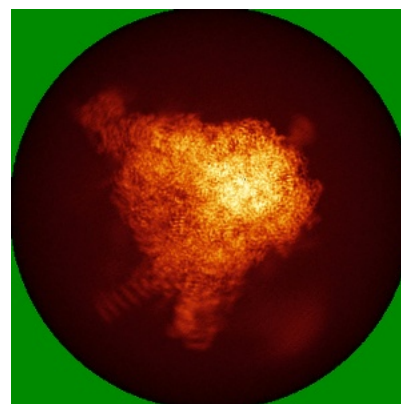
6.4.2 Raw map



X



Y

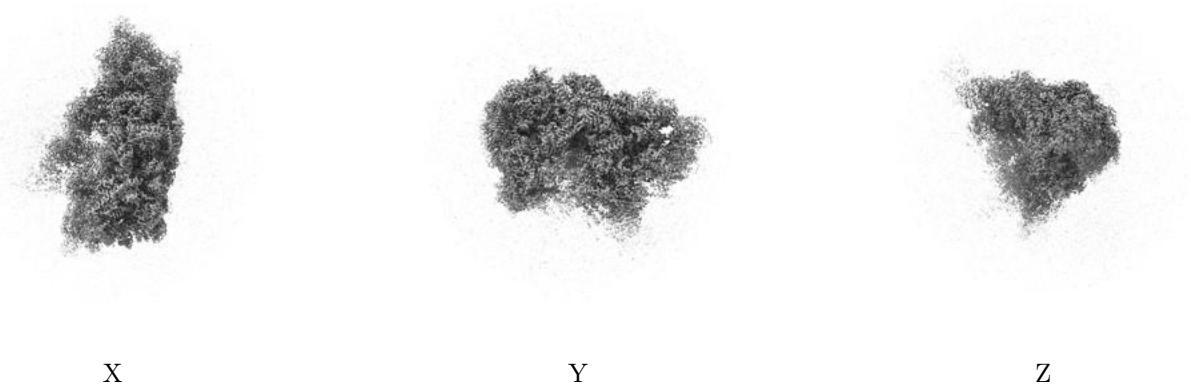


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

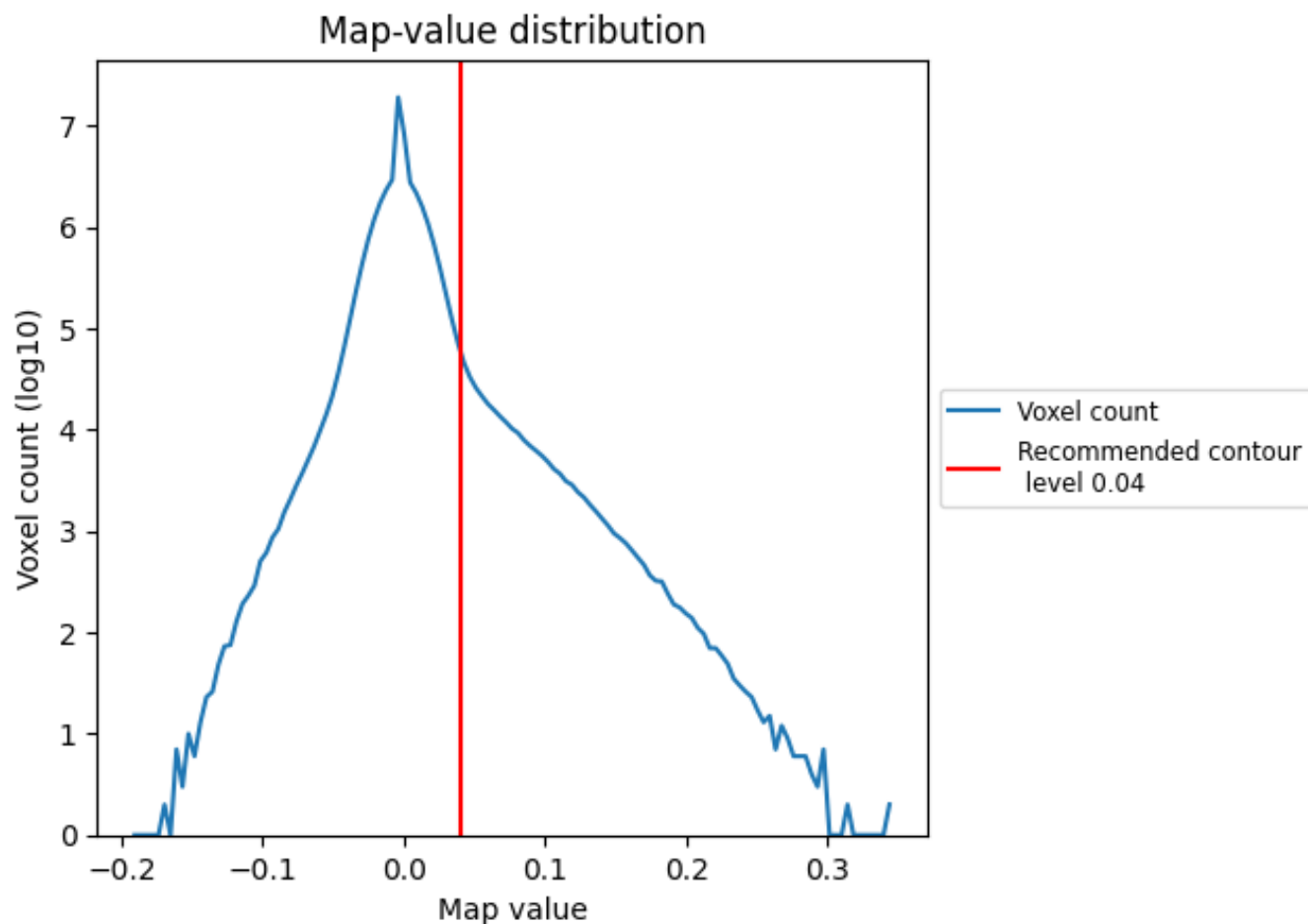
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

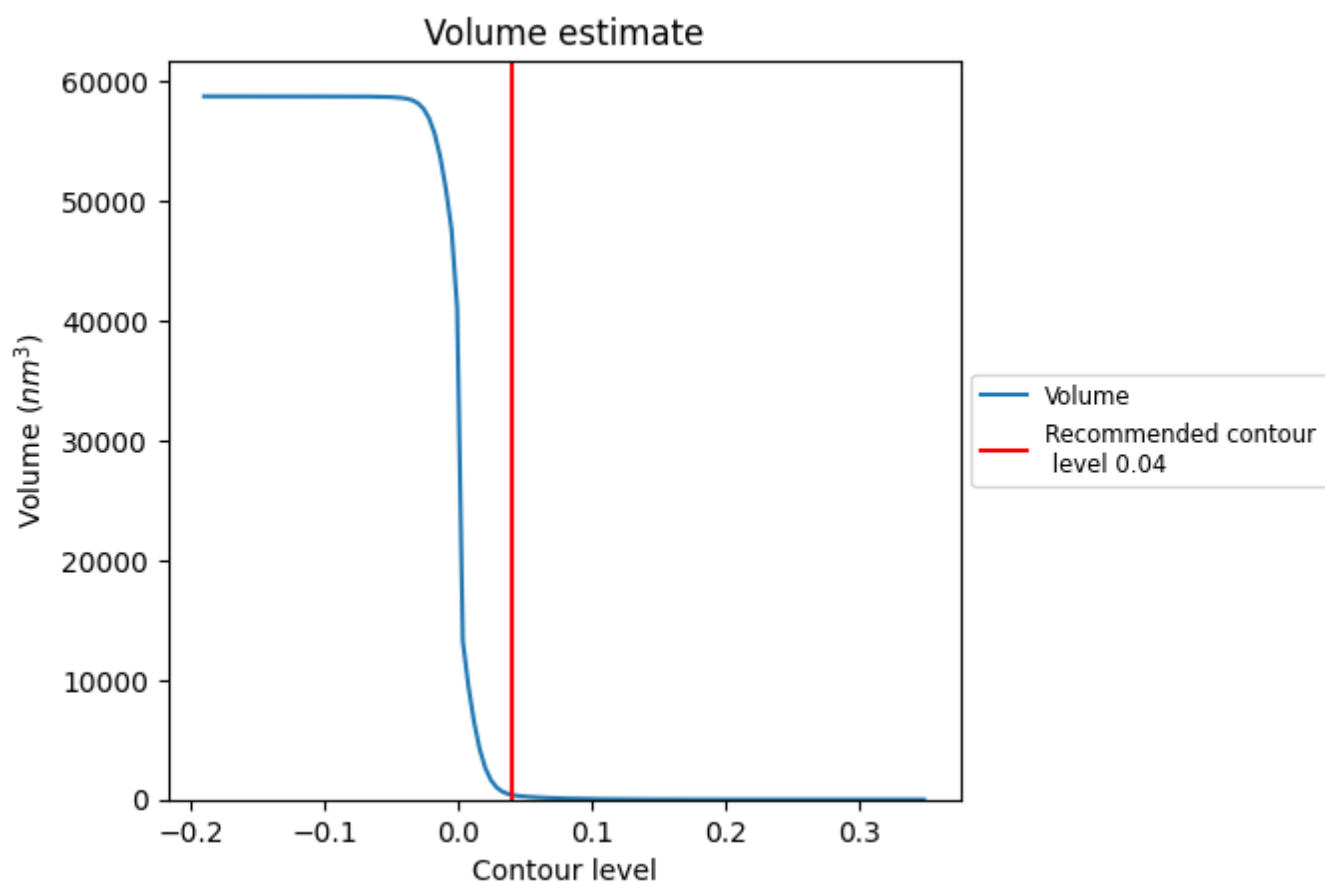
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

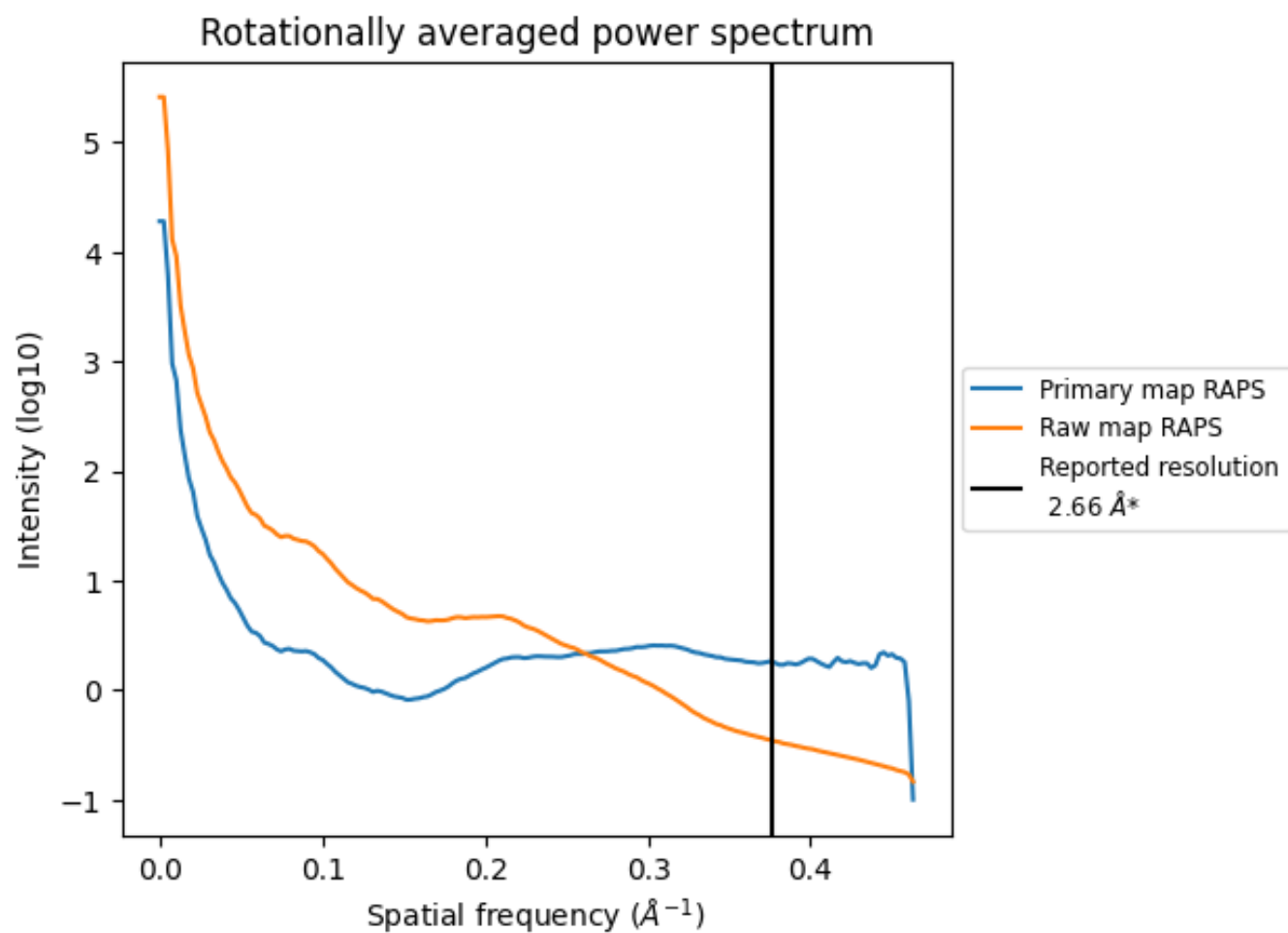
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 395 nm³; this corresponds to an approximate mass of 357 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

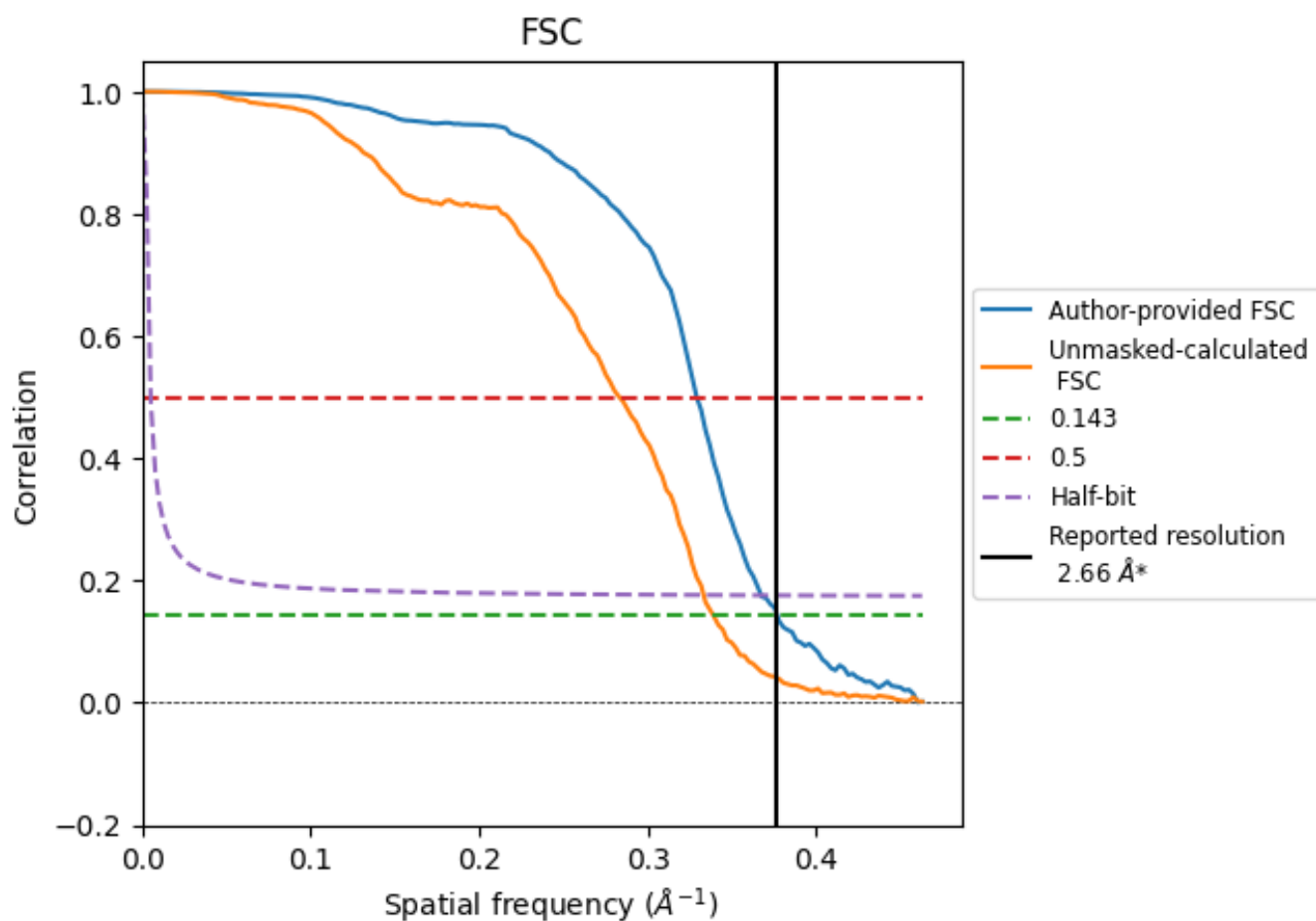


*Reported resolution corresponds to spatial frequency of 0.376 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.376 Å⁻¹

8.2 Resolution estimates [i](#)

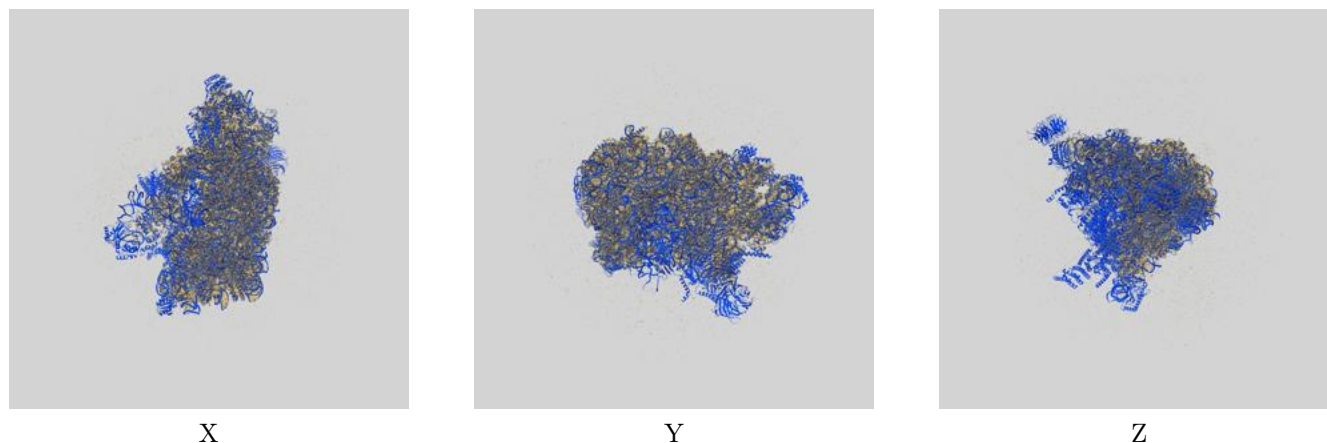
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.66	-	-
Author-provided FSC curve	2.65	3.04	2.72
Unmasked-calculated*	2.95	3.53	3.00

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.95 differs from the reported value 2.66 by more than 10 %

9 Map-model fit [i](#)

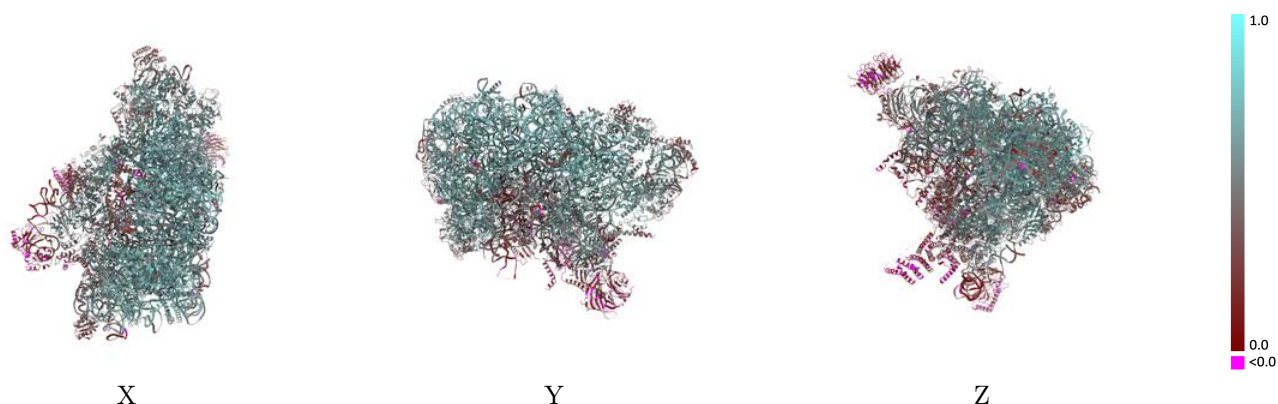
This section contains information regarding the fit between EMDB map EMD-43027 and PDB model 8V87. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



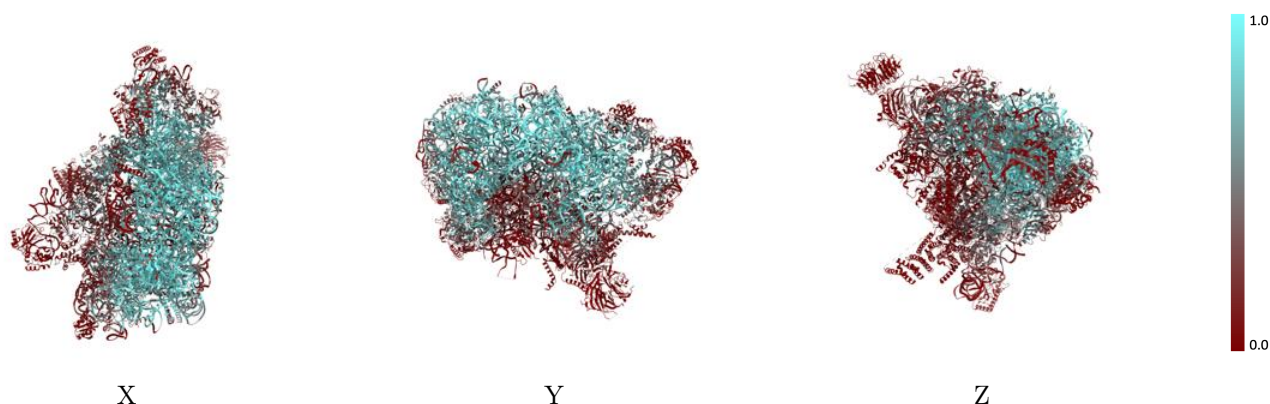
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



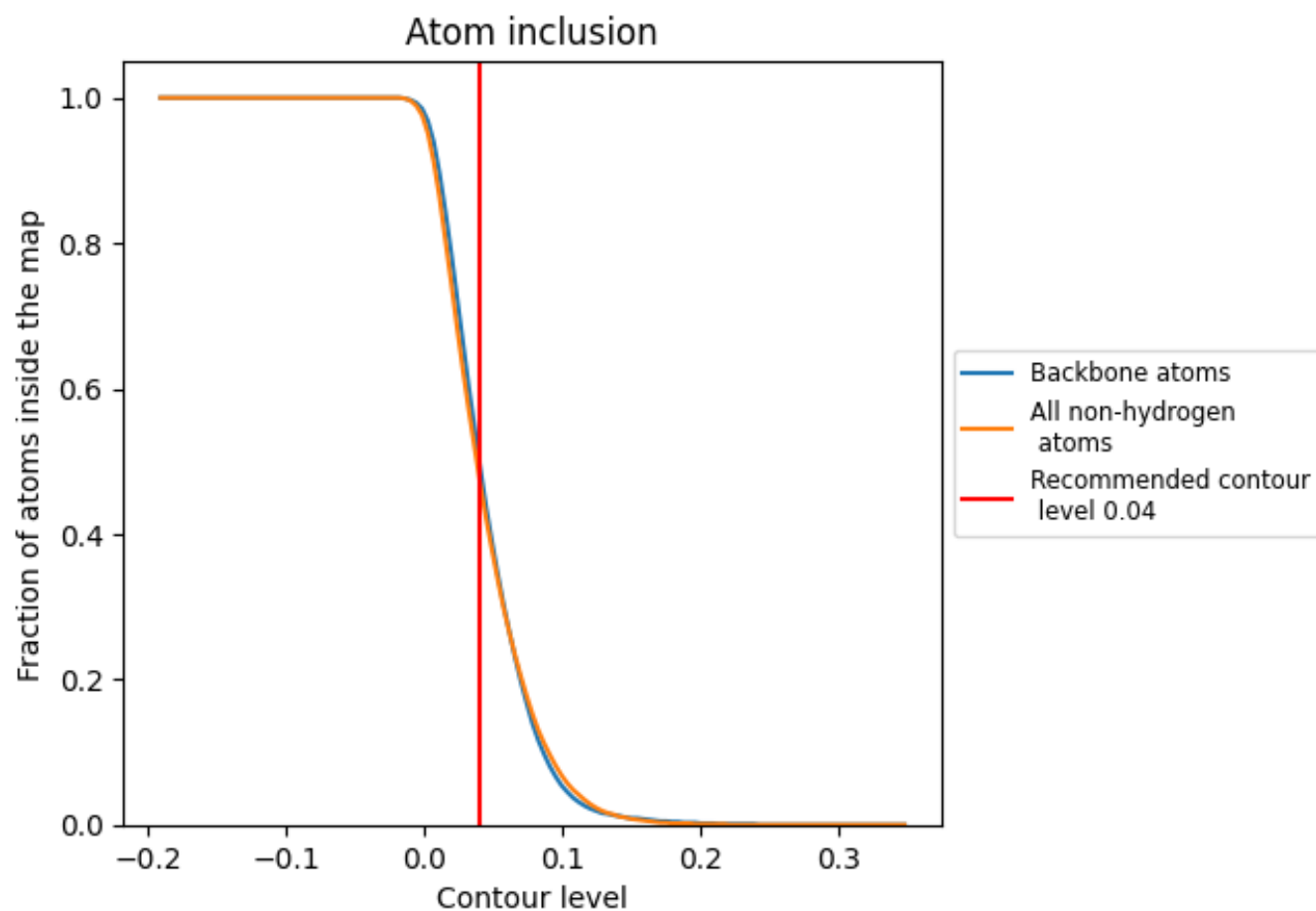
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 48% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4800	 0.5190
1	 0.6010	 0.5470
2	 0.8620	 0.6460
3	 0.0410	 0.3290
6	 0.3890	 0.5130
7	 0.3320	 0.4960
8	 0.0040	 0.1930
A	 0.4790	 0.5330
B	 0.7530	 0.6430
C	 0.7980	 0.6590
D	 0.2690	 0.4800
E	 0.6360	 0.6090
F	 0.7420	 0.6340
G	 0.7620	 0.6460
H	 0.6480	 0.6170
I	 0.1320	 0.4130
J	 0.3270	 0.4980
K	 0.2240	 0.4770
L	 0.7810	 0.6500
M	 0.7030	 0.6330
N	 0.9010	 0.6930
O	 0.8320	 0.6650
P	 0.7140	 0.6320
Q	 0.7030	 0.6270
R	 0.1710	 0.4040
S	 0.5580	 0.5790
U	 0.0470	 0.3510
V	 0.3910	 0.5580
W	 0.0940	 0.3840
X	 0.6470	 0.6070
Y	 0.7840	 0.6500
Z	 0.1770	 0.4600
a	 0.0010	 0.1180
b	 0.3920	 0.5160
c	 0.0290	 0.3270



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Chain	Atom inclusion	Q-score
d	 0.2670	 0.4980
e	 0.8200	 0.6660
f	 0.8960	 0.6940
g	 0.4230	 0.5410
h	 0.7430	 0.6430
i	 0.7080	 0.6380
j	 0.8850	 0.6940
k	 0.2440	 0.4690
l	 0.4130	 0.5590
m	 0.3060	 0.4860
n	 0.4800	 0.5660
o	 0.4040	 0.5080
p	 0.0030	 0.1780
q	 0.2190	 0.4680
r	 0.4000	 0.5310
s	 0.5920	 0.6200
t	 0.3810	 0.5380
u	 0.4050	 0.5380
v	 0.6860	 0.6080
w	 0.3340	 0.4460
y	 0.4060	 0.5270
z	 0.2930	 0.5090