



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 11:10 AM UTC

PDB ID : 6XIR / pdb_00006xir
EMDB ID : EMD-22198
Title : Cryo-EM Structure of K63 Ubiquitinated Yeast Translocating Ribosome under Oxidative Stress
Authors : Zhou, Y.; Bartesaghi, A.; Silva, G.M.
Deposited on : 2020-06-21
Resolution : 3.20 Å(reported)
Based on initial model : 6GQ1

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

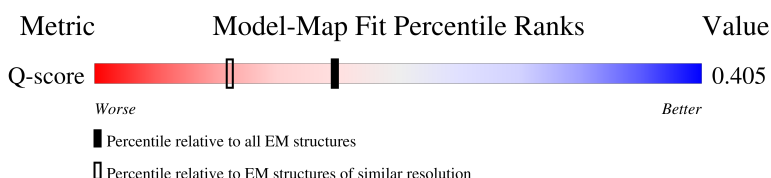
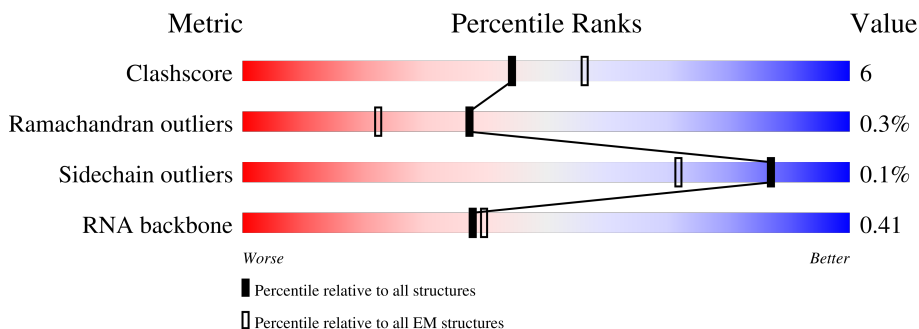
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



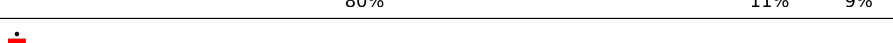
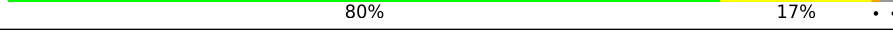
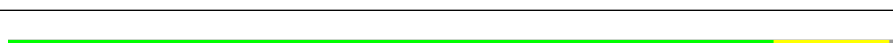
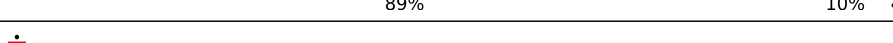
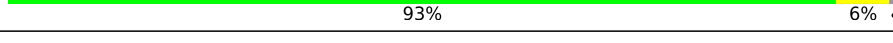
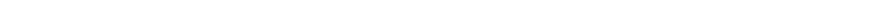
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	A	254	
2	B	387	
3	C	362	

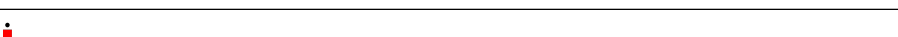
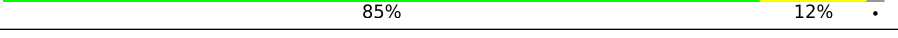
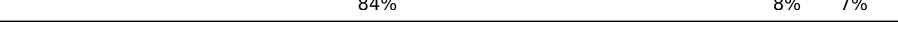
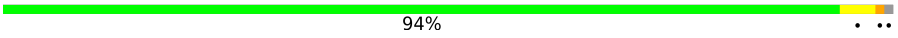
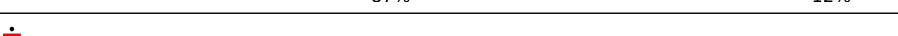
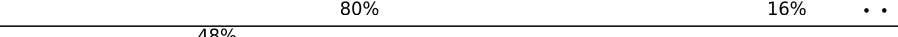
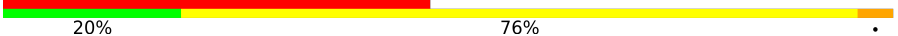
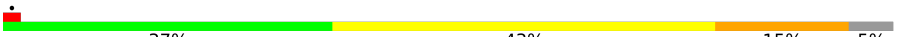
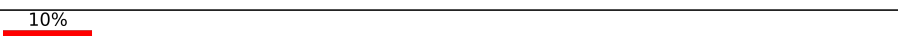
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Mol	Chain	Length	Quality of chain
4	D	297	
5	E	176	
6	F	244	
7	G	256	
8	H	191	
9	I	221	
10	J	174	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	R	189	
18	S	172	
19	T	160	
20	U	121	
21	V	137	
22	W	155	
23	X	142	
24	Y	127	
25	Z	136	
26	AA	105	
27	AB	156	
28	1	3395	

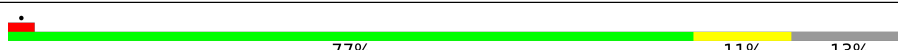
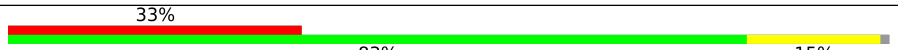
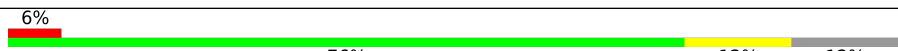
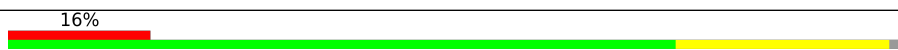
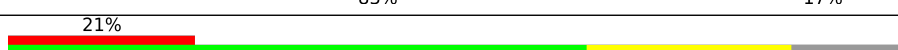
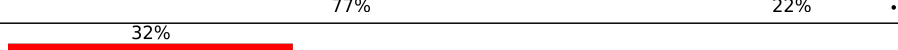
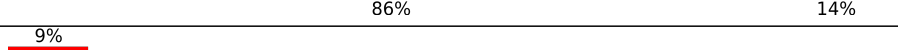
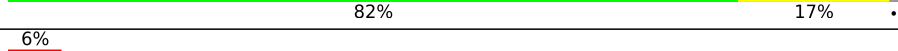
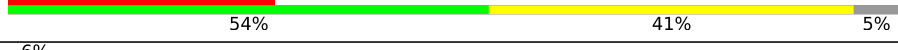
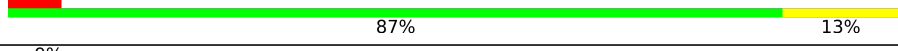
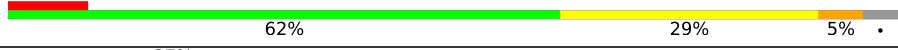
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Mol	Chain	Length	Quality of chain
29	3	121	
30	4	158	
31	a	149	
32	b	59	
33	c	105	
34	d	113	
35	e	130	
36	f	107	
37	g	121	
38	h	120	
39	i	100	
40	j	88	
41	k	78	
42	l	51	
43	n	25	
44	o	106	
45	p	92	
46	2	1800	
47	q	252	
48	r	255	
49	s	254	
50	t	240	
51	u	261	
52	v	225	
53	w	236	

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Mol	Chain	Length	Quality of chain
54	x	190	
55	y	200	
56	z	197	
57	AD	151	
58	AE	138	
59	AF	142	
60	AG	143	
61	AH	136	
62	AI	146	
63	AJ	144	
64	AK	121	
65	AL	87	
66	AM	130	
67	AN	145	
68	AO	135	
69	AP	108	
70	AQ	119	
71	AR	82	
72	AS	67	
73	AT	56	
74	AV	319	
75	AX	76	
75	AZ	76	

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 197132 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 2 is a protein called RPL3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 3 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 4 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 5 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 6 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 7 is a protein called RPL8A isoform 1.

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

- Molecule 8 is a protein called RPL9A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	211	Total	C	N	O	S	0	0
			1705	1083	322	294	6		

- Molecule 10 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 12 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 13 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 14 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	183	Total	C	N	O	S	0	0
			1420	882	281	257			

- Molecule 16 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	188	Total	C	N	O	S	0	0
			1521	935	326	260			

- Molecule 18 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 19 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 20 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 21 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 22 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 23 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 24 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L27-A.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AA	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

- Molecule 27 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AB	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

- Molecule 28 is a RNA chain called 35S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	3113	Total	C	N	O	P	0	0
			66567	29735	11981	21738	3113		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	G	deletion	GB 380294104

- Molecule 29 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 30 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 32 is a protein called RPL29 isoform 1.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 35 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 41 is a protein called RPL38 isoform 1.

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

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

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

- Molecule 43 is a protein called RPL41A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	25	Total	C	N	O	S	0	0
			227	139	60	27	1		

- Molecule 44 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 45 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2	1708	Total	C	N	O	P	0	0
			36409	16277	6464	11960	1708		

- Molecule 47 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 48 is a protein called RPS1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 49 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 50 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 51 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 52 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	v	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 53 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	223	Total	C	N	O	S	0	0
			1790	1123	346	318	3		

- Molecule 54 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	184	Total	C	N	O		0	0
			1481	951	265	265			

- Molecule 55 is a protein called RPS8A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 56 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 57 is a protein called 40S ribosomal protein S13.

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

- Molecule 58 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AE	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 59 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AF	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 60 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	AG	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 61 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AH	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 62 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AI	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 63 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 64 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AK	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 65 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AL	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 66 is a protein called RPS22A isoform 1.

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

- Molecule 67 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 68 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	AO	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 69 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
69	AP	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 70 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AQ	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 71 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AR	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 72 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	AS	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 73 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	AT	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 74 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	AV	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

- Molecule 75 is a RNA chain called Transfer RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AX	73	Total	C	N	O	P	0	0
			1564	697	282	512	73		
75	AZ	73	Total	C	N	O	P	0	0
			1564	697	282	512	73		

- Molecule 76 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by

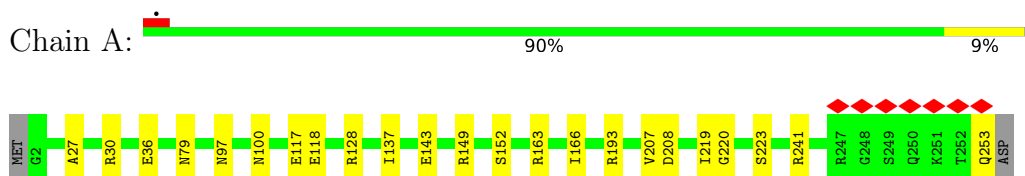
depositor).

Mol	Chain	Residues	Atoms		AltConf
76	j	1	Total 1	Zn 1	0
76	o	1	Total 1	Zn 1	0
76	p	1	Total 1	Zn 1	0
76	AQ	1	Total 1	Zn 1	0
76	AR	1	Total 1	Zn 1	0
76	AT	1	Total 1	Zn 1	0

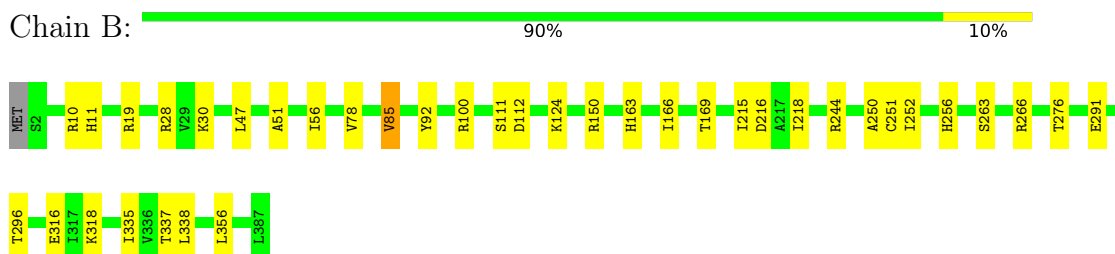
3 Residue-property plots [i](#)

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

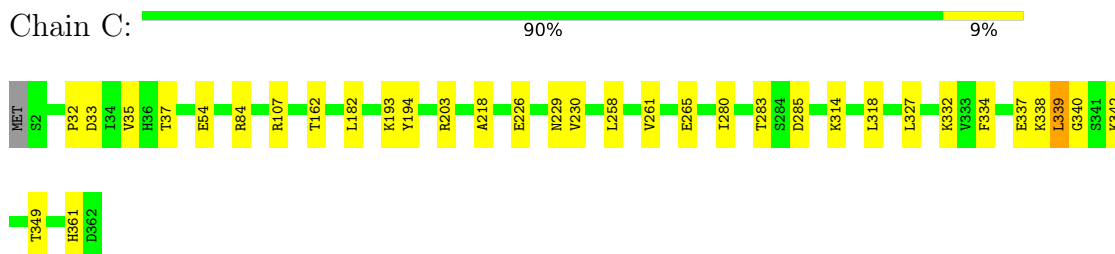
- Molecule 1: 60S ribosomal protein L2-A



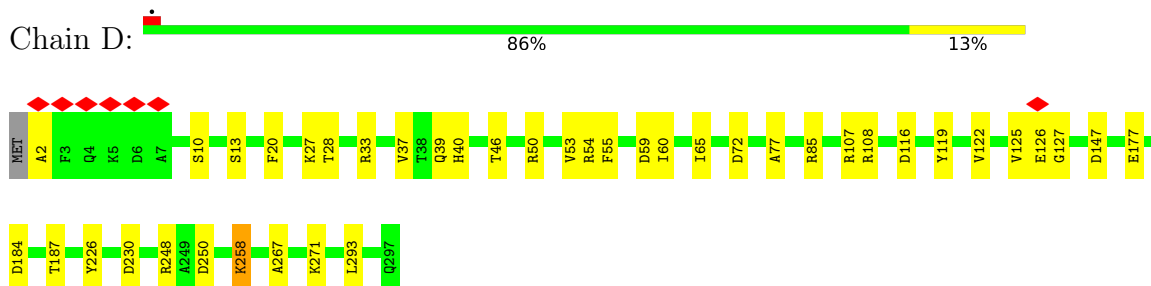
- Molecule 2: RPL3 isoform 1



- Molecule 3: RPL4A isoform 1

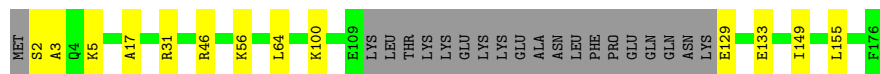


- Molecule 4: RPL5 isoform 1



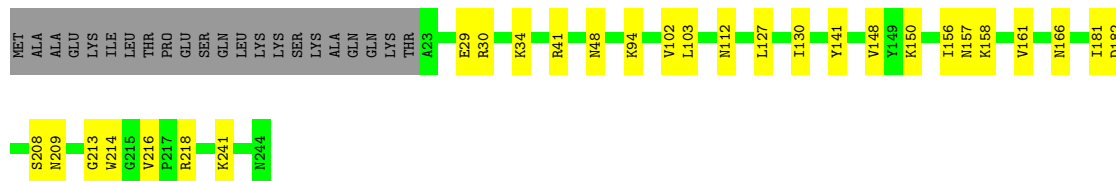
- Molecule 5: 60S ribosomal protein L6-A

Chain E:  81% 7% 11%



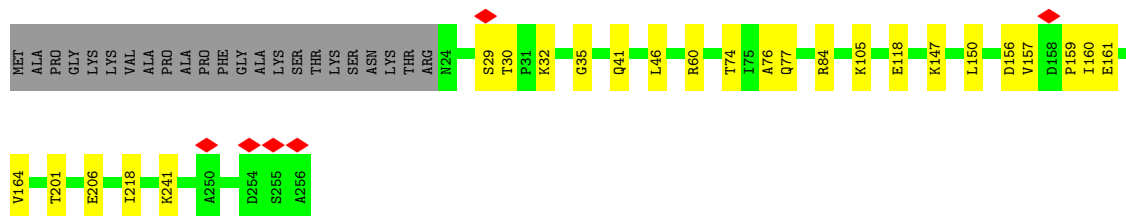
- Molecule 6: 60S ribosomal protein L7-A

Chain F:  80% 11% 9%



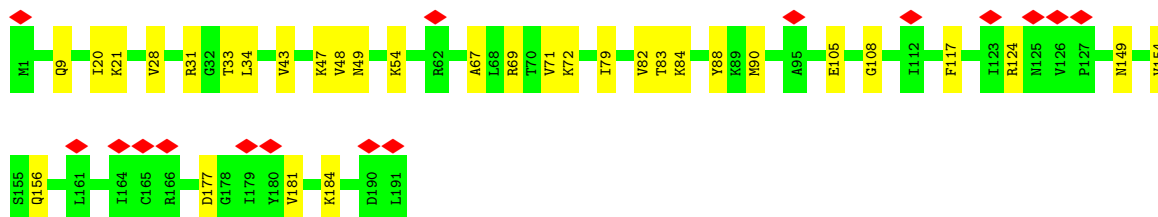
- Molecule 7: RPL8A isoform 1

Chain G:  81% 10% 9%



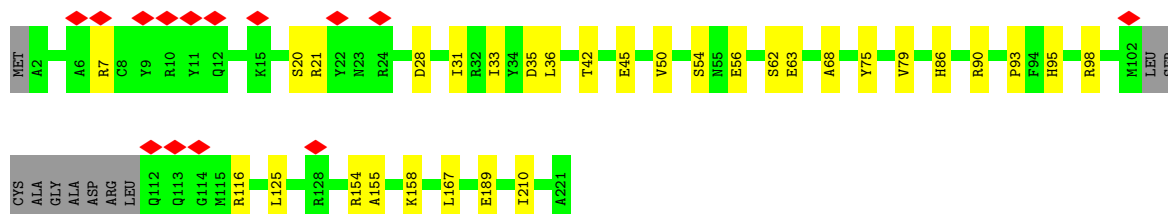
- Molecule 8: RPL9A isoform 1

Chain H:  8% 83% 17%

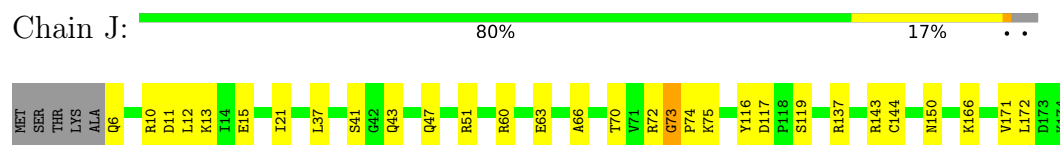


- Molecule 9: RPL10 isoform 1

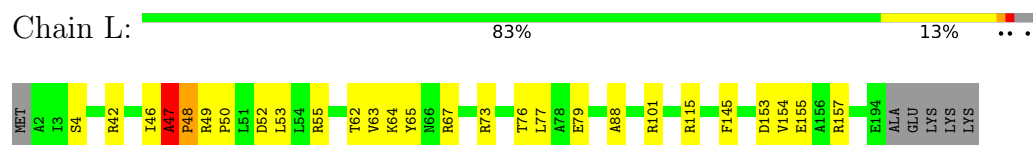
Chain I:  6% 81% 14% 5%



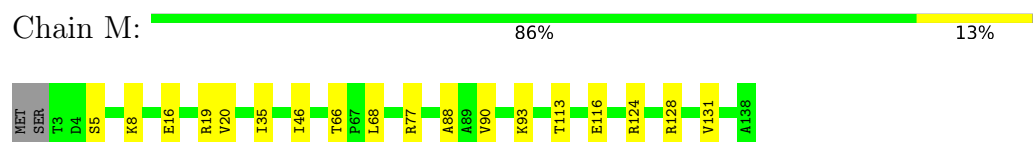
- Molecule 10: RPL11B isoform 1



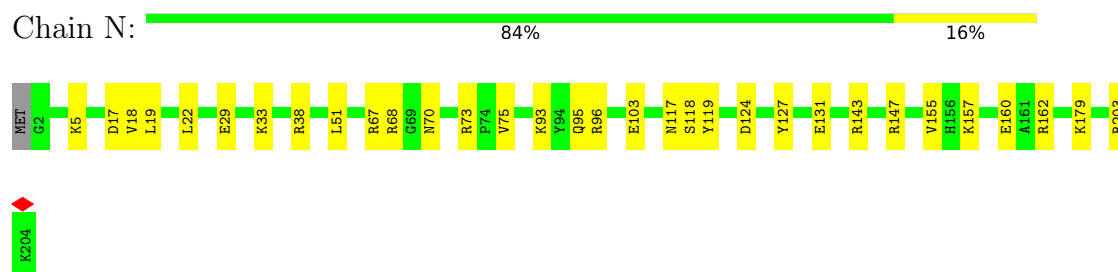
- Molecule 11: 60S ribosomal protein L13-A



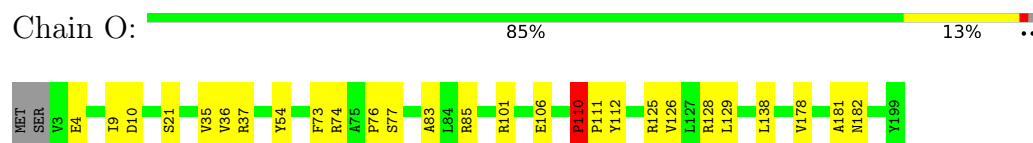
- Molecule 12: 60S ribosomal protein L14-A



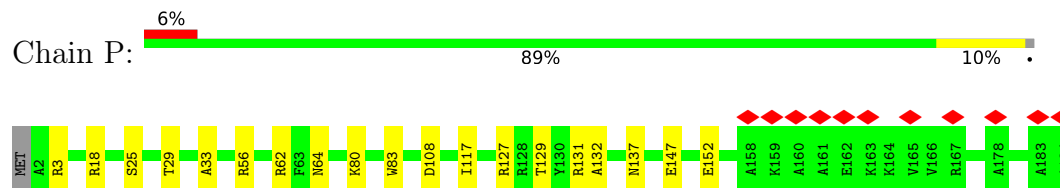
- Molecule 13: 60S ribosomal protein L15-A



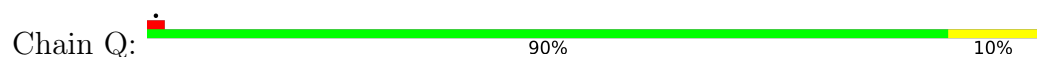
- Molecule 14: 60S ribosomal protein L16-A



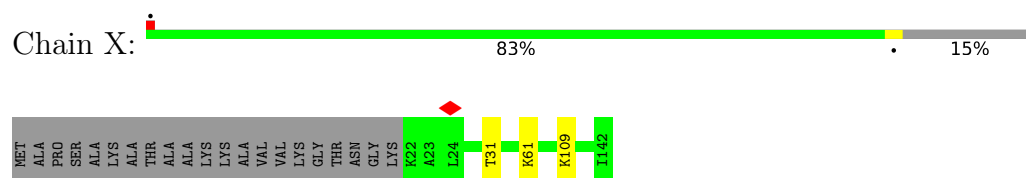
- Molecule 15: 60S ribosomal protein L17-A



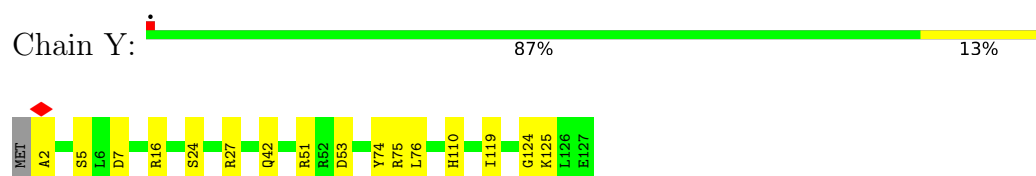
- Molecule 16: 60S ribosomal protein L18-A



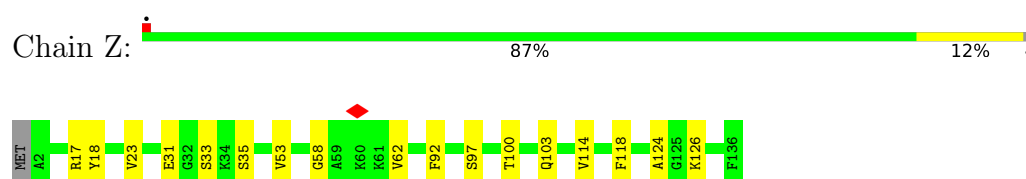
- Molecule 23: 60S ribosomal protein L25



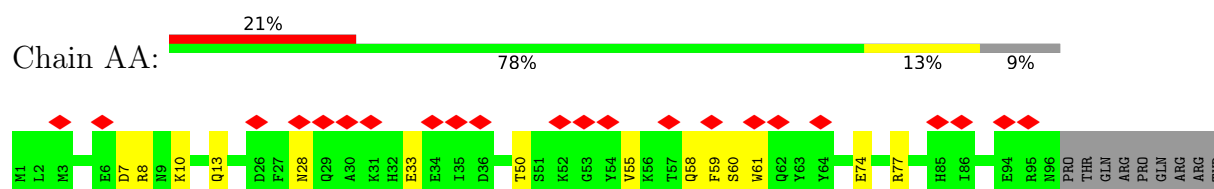
- Molecule 24: 60S ribosomal protein L26-A



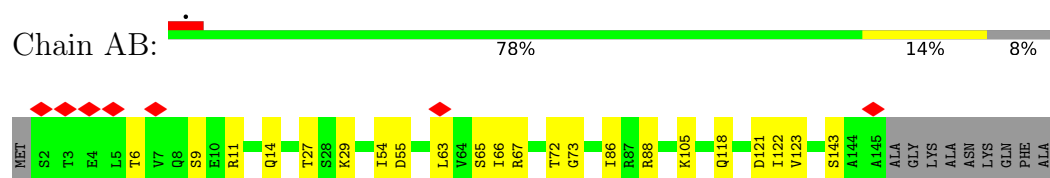
- Molecule 25: 60S ribosomal protein L27-A



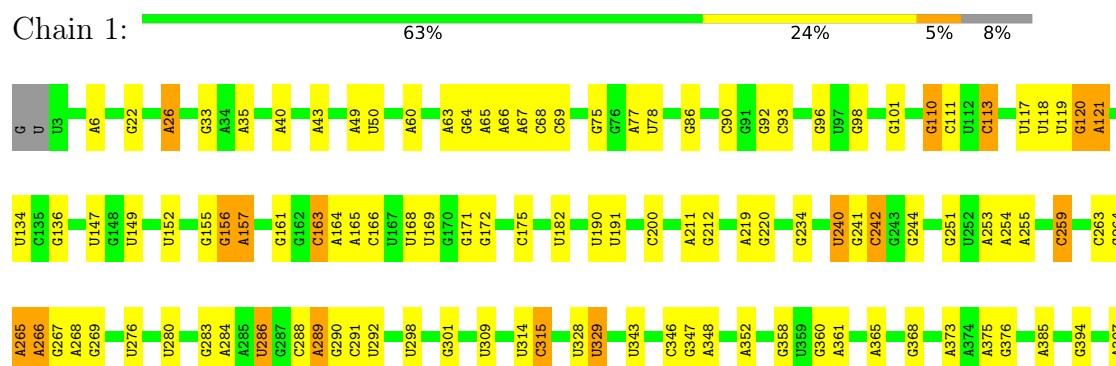
- Molecule 26: 40S ribosomal protein S10-A



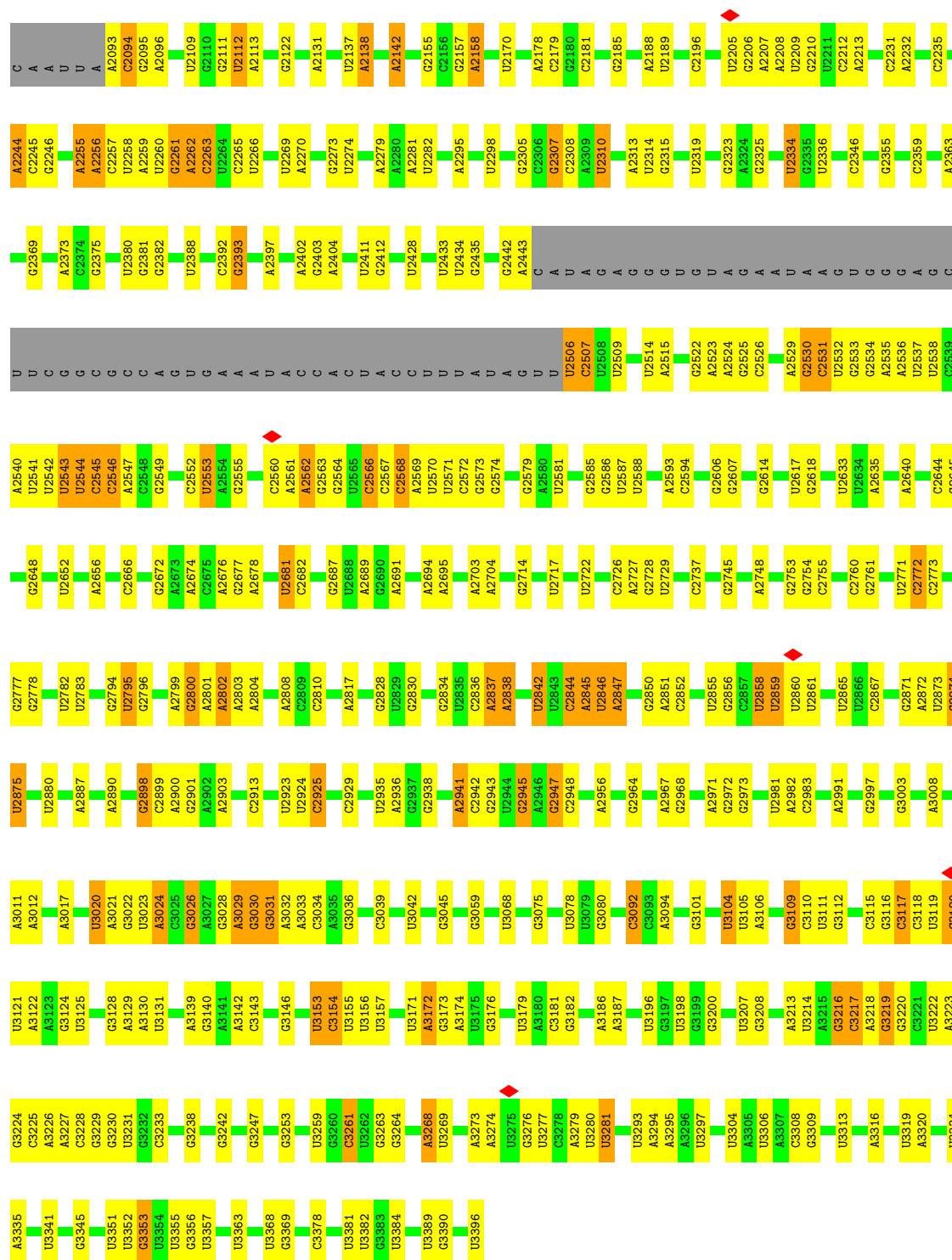
- Molecule 27: 40S ribosomal protein S11-A



- Molecule 28: 35S ribosomal RNA





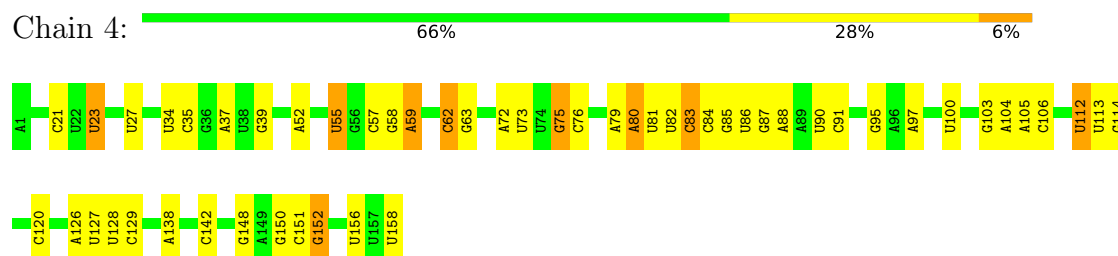


• Molecule 29: 5S ribosomal RNA

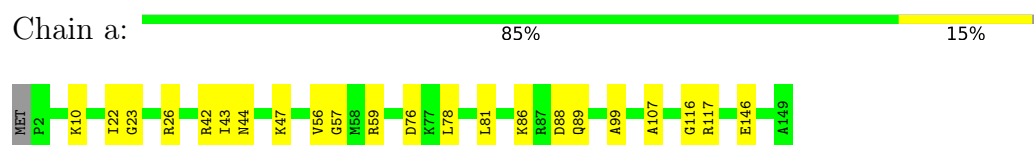
Chain 3: 73% 25%



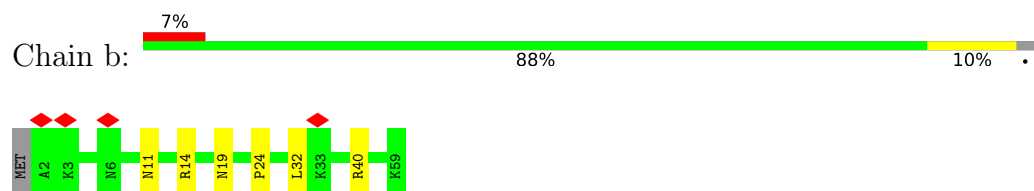
- Molecule 30: 5.8S ribosomal RNA



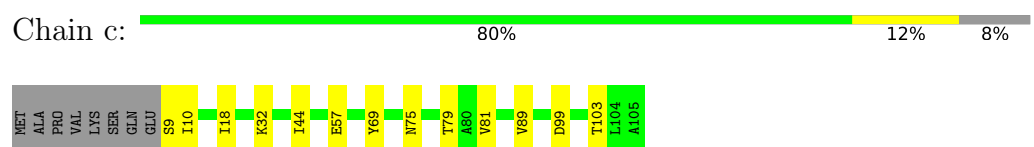
- Molecule 31: 60S ribosomal protein L28



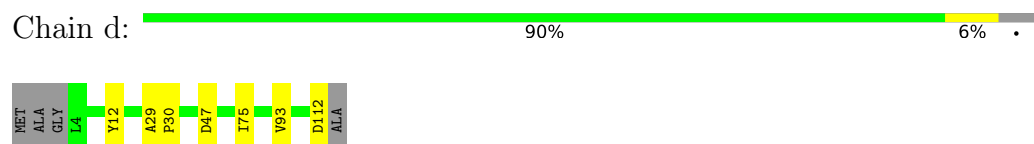
- Molecule 32: RPL29 isoform 1



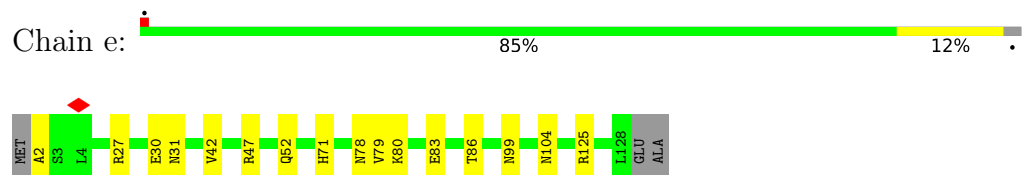
- Molecule 33: 60S ribosomal protein L30



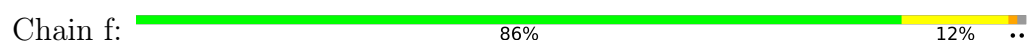
- Molecule 34: 60S ribosomal protein L31-A

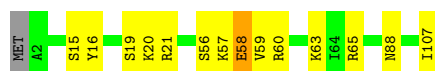


- Molecule 35: RPL32 isoform 1



- Molecule 36: 60S ribosomal protein L33-A





- Molecule 37: 60S ribosomal protein L34-A

Chain g: 84% 8% 7%



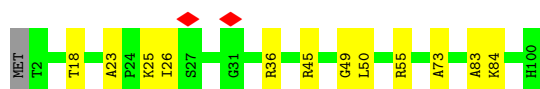
- Molecule 38: 60S ribosomal protein L35-A

Chain h: 94% . .



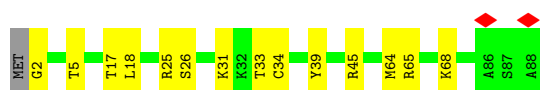
- Molecule 39: 60S ribosomal protein L36-A

Chain i: 87% 12% .



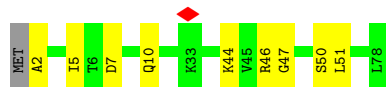
- Molecule 40: 60S ribosomal protein L37-A

Chain j: 83% 16% .



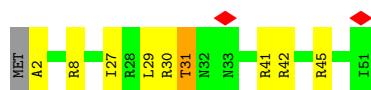
- Molecule 41: RPL38 isoform 1

Chain k: 87% 12% .

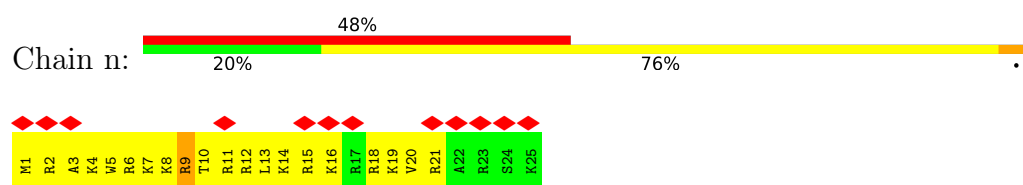


- Molecule 42: 60S ribosomal protein L39

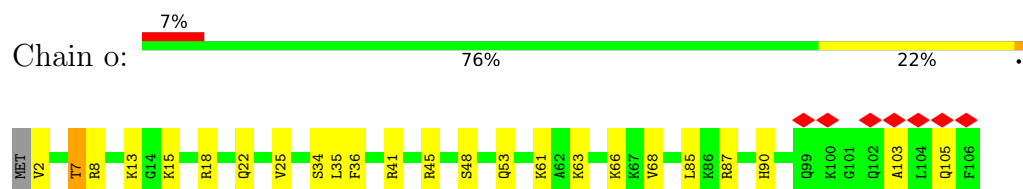
Chain l: 80% 16% . .



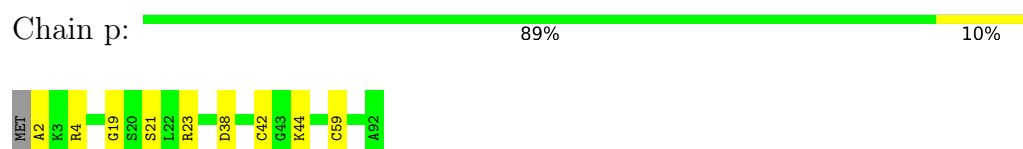
- Molecule 43: RPL41A isoform 1



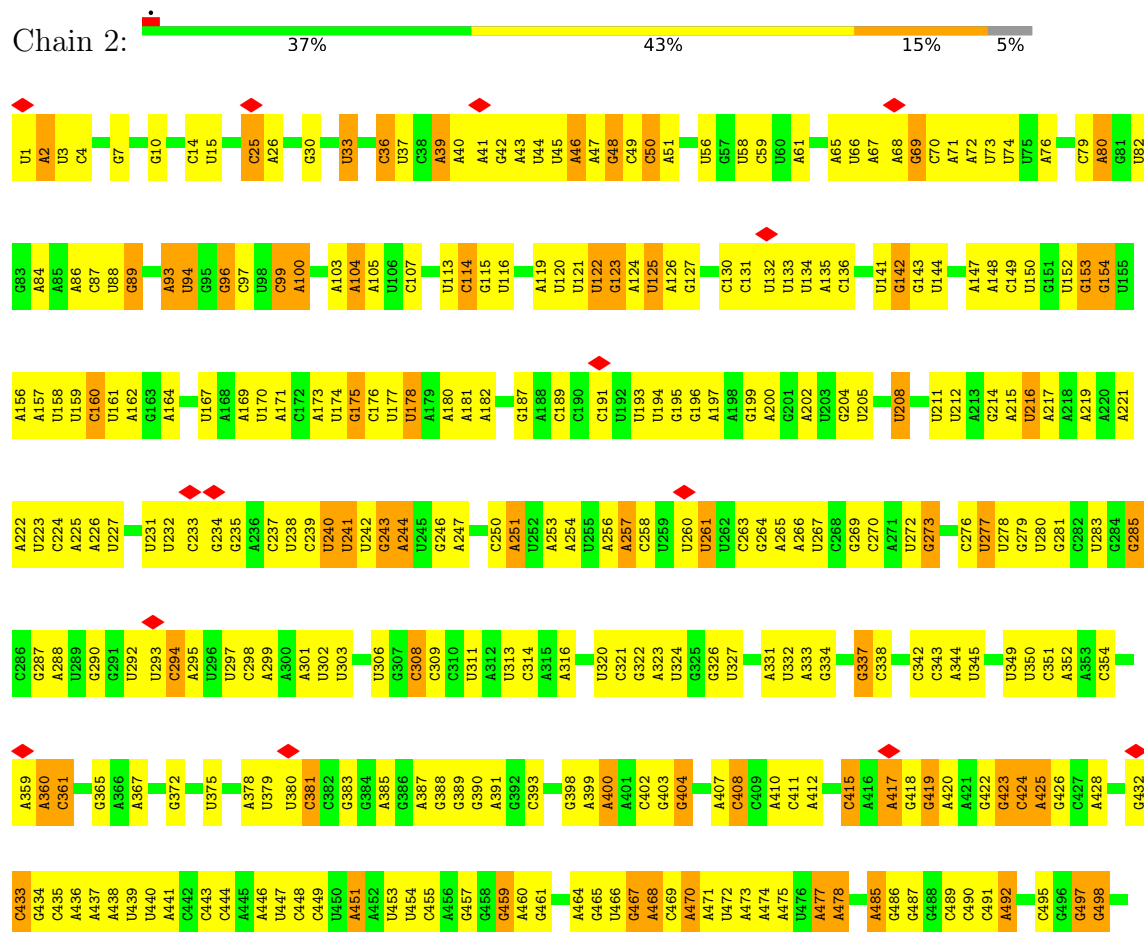
• Molecule 44: 60S ribosomal protein L42-A



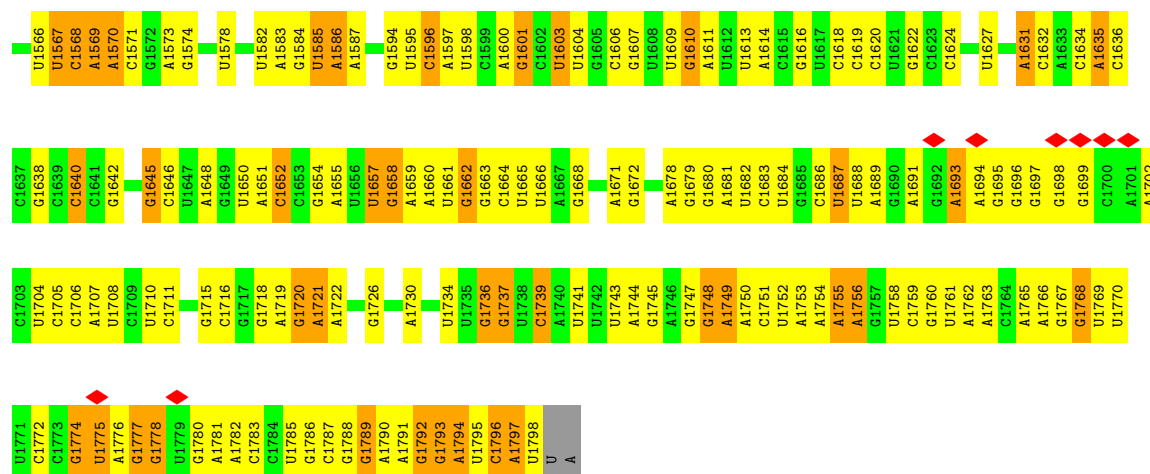
• Molecule 45: 60S ribosomal protein L43-A



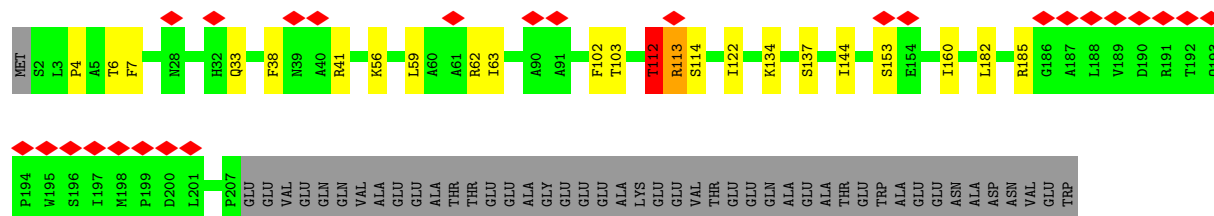
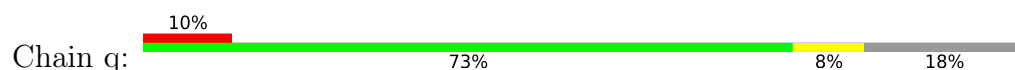
• Molecule 46: 18S ribosomal RNA



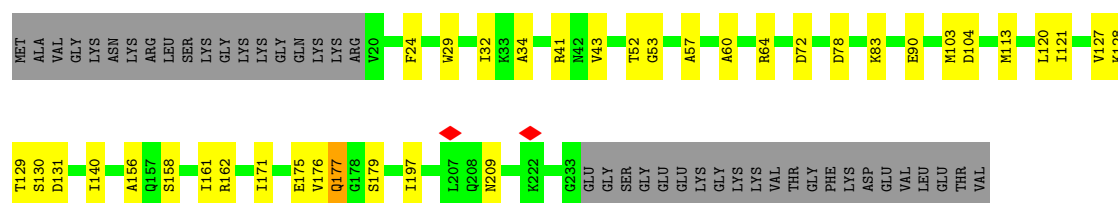
C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510	C1511	C1512	C1513	C1514	C1515	C1516	C1517	C1518	C1519	C1520	C1521	C1522	C1523	C1524	C1525	C1526	C1527	C1528	C1529	C1530	C1531	C1532	C1533	C1534	C1535	C1536	C1537	C1538	C1539	C1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551	C1552	C1553	C1554	C1555	C1556	C1557	C1558	C1559	C1560	C1561	C1562																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
U1285	U1286	U1287	U1288	U1289	U1290	U1291	U1292	U1293	U1294	U1295	U1296	U1297	U1298	U1299	U1300	U1301	U1302	U1303	U1304	U1305	U1306	U1307	U1308	U1309	U1310	U1311	U1312	U1313	U1314	U1315	U1316	U1317	U1318	U1319	U1320	U1321	U1322	U1323	U1324	U1325	U1326	U1327	U1328	U1329	U1330	U1331	U1332	U1333	U1334	U1335	U1336	U1337	U1338	U1339	U1340	U1341	U1342	U1343	U1344	U1345	U1346	U1347	U1348	U1349	U1350	U1351	U1352	U1353	U1354	U1355	U1356	U1357																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
C1222	C1223	C1224	U	A	A	G	G	U	U	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	U1175	C1176	U1181	U1182	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U



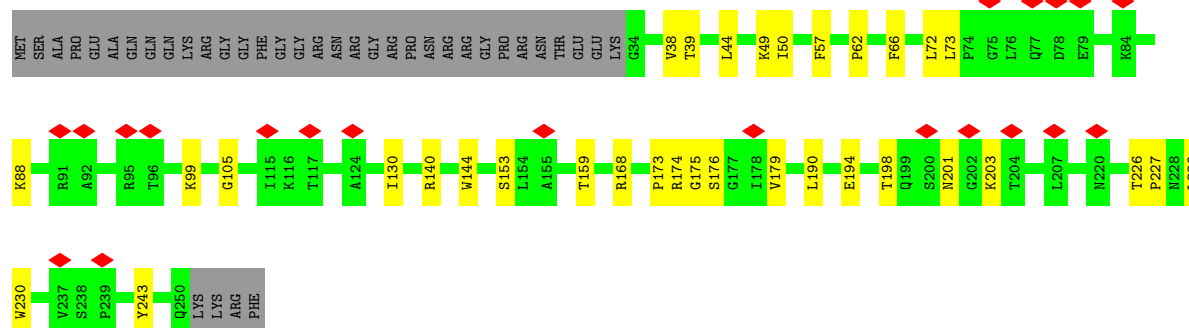
• Molecule 47: 40S ribosomal protein S0-A



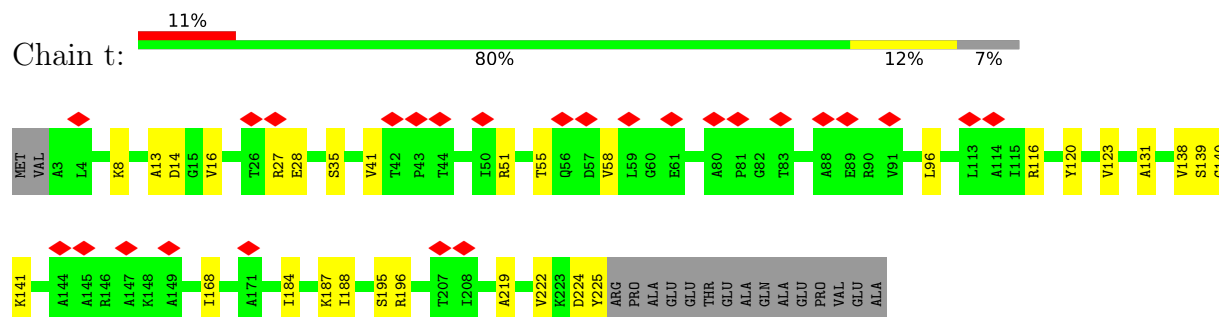
• Molecule 48: RPS1A isoform 1



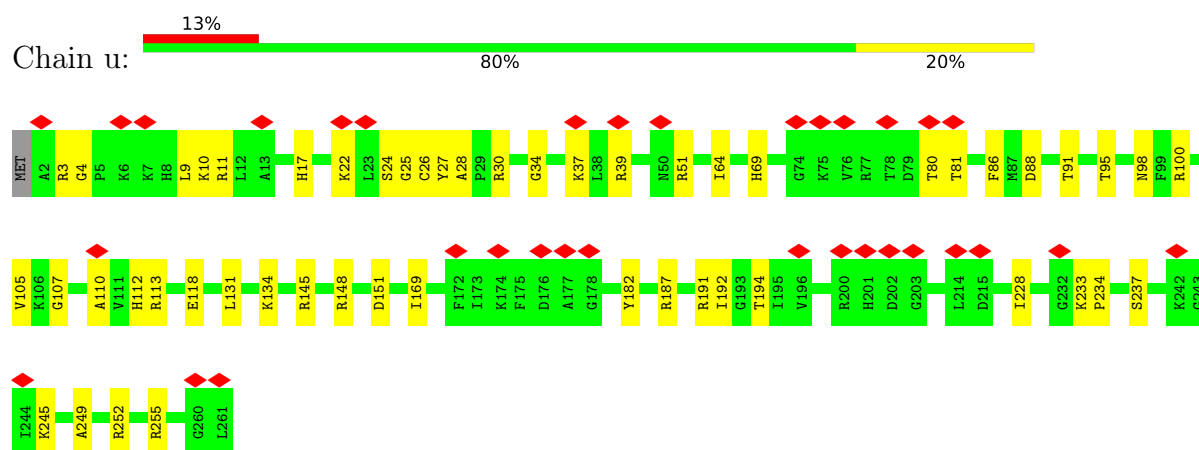
• Molecule 49: RPS2 isoform 1



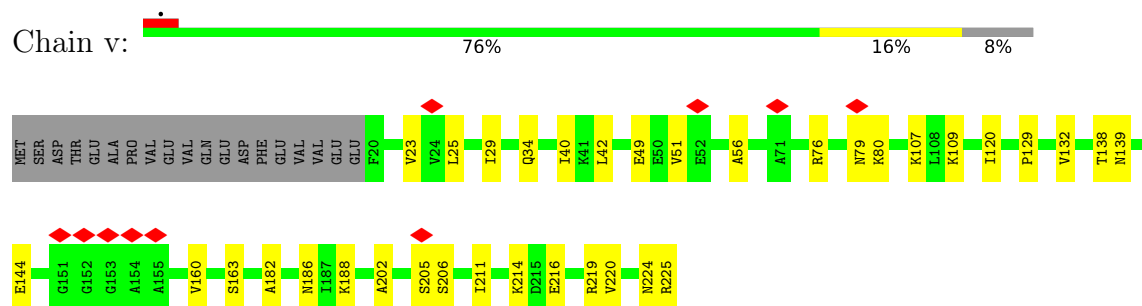
- Molecule 50: RPS3 isoform 1



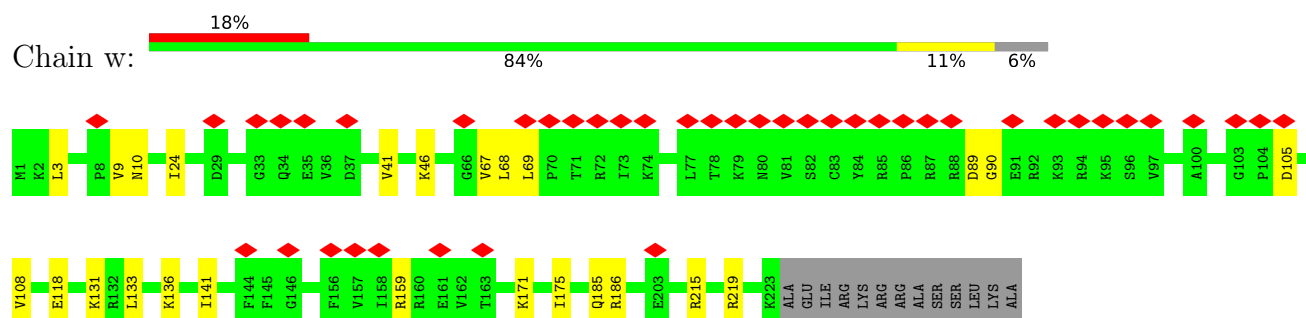
- Molecule 51: 40S ribosomal protein S4-A



- Molecule 52: Rps5p

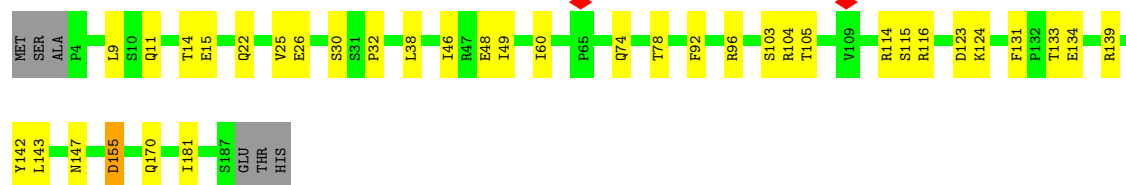


- Molecule 53: 40S ribosomal protein S6-A



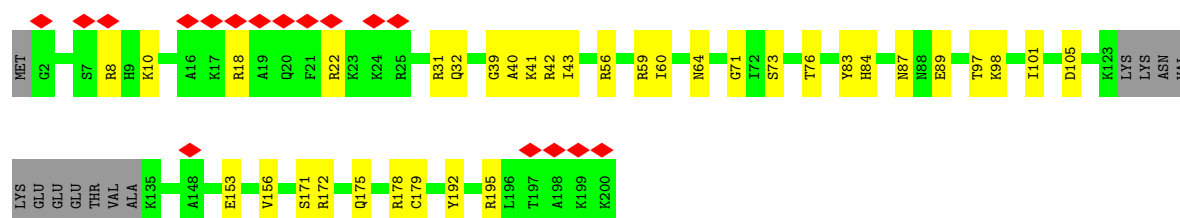
- Molecule 54: 40S ribosomal protein S7-A

Chain x:  78% 18% ..



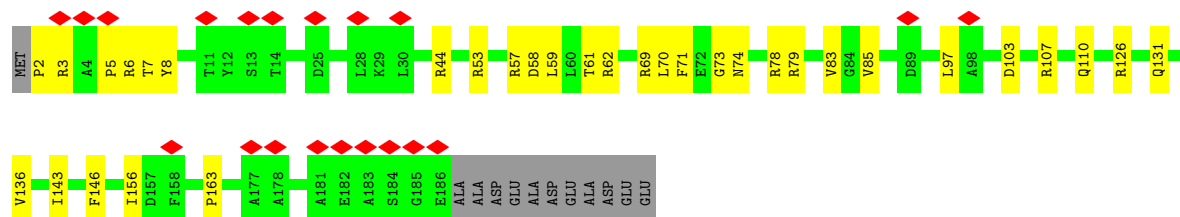
- Molecule 55: RPS8A isoform 1

Chain y:  8% 76% 18% 6%



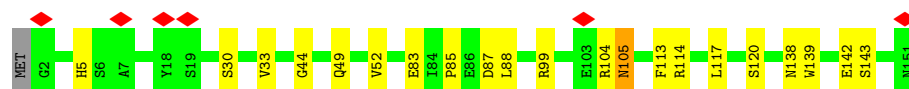
- Molecule 56: 40S ribosomal protein S9-A

Chain z:  10% 77% 17% 6%



- Molecule 57: 40S ribosomal protein S13

Chain AD:  85% 13% ..



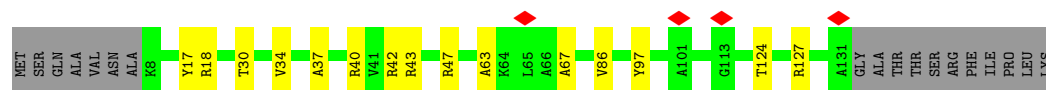
- Molecule 58: 40S ribosomal protein S14-B

Chain AE:  83% 9% 8%

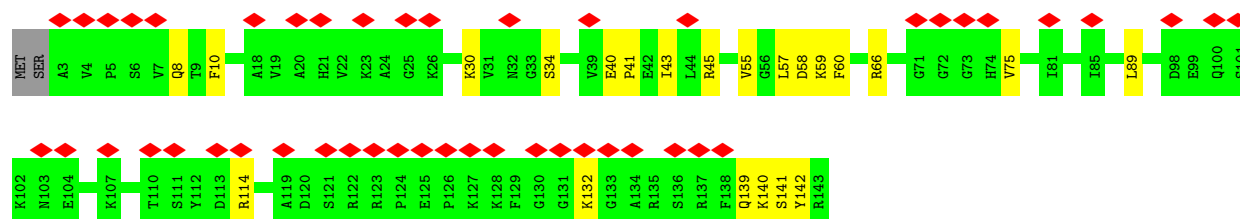
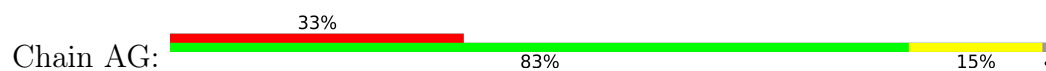


- Molecule 59: RPS15 isoform 1

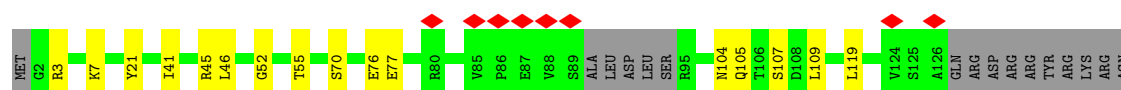
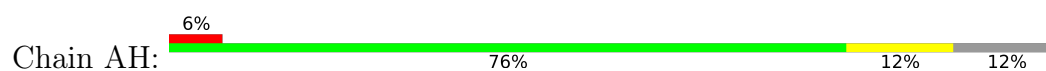
Chain AF:  77% 11% 13%



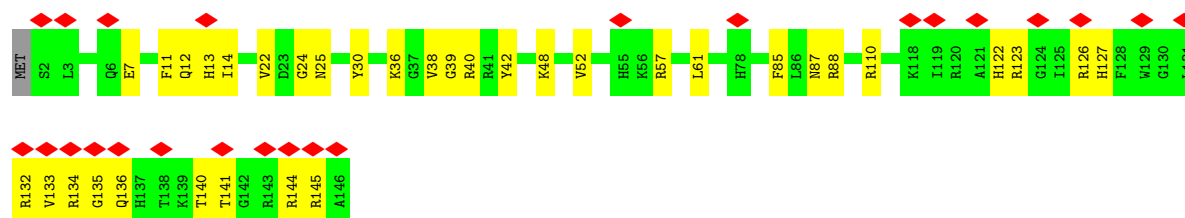
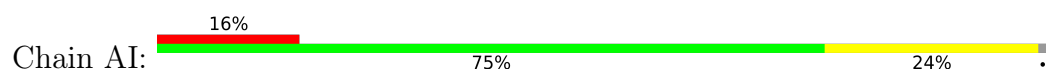
- Molecule 60: 40S ribosomal protein S16-A



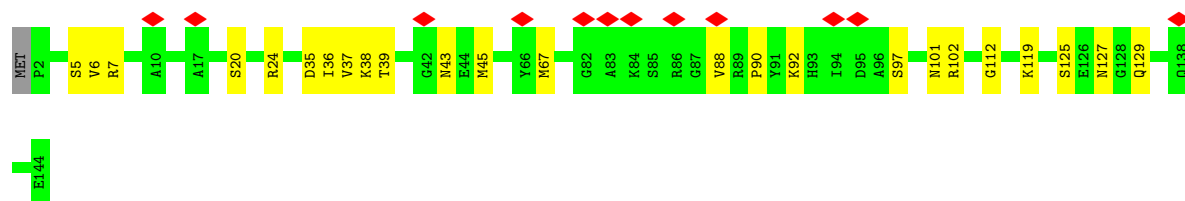
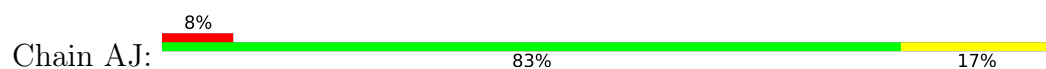
- Molecule 61: 40S ribosomal protein S17-B



- Molecule 62: 40S ribosomal protein S18-A

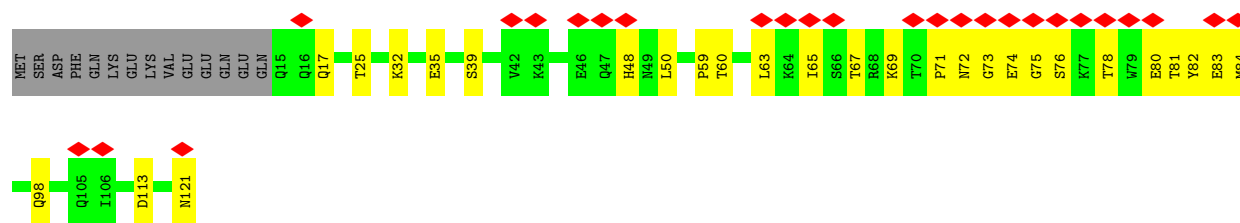


- Molecule 63: 40S ribosomal protein S19-A

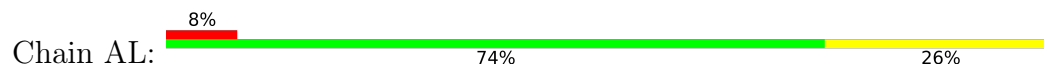


- Molecule 64: RPS20 isoform 1

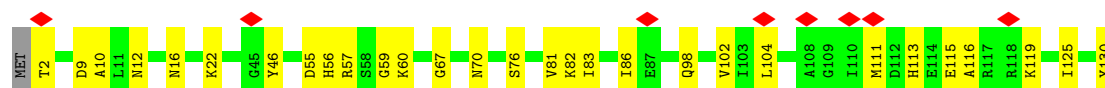
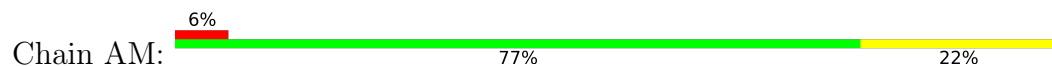




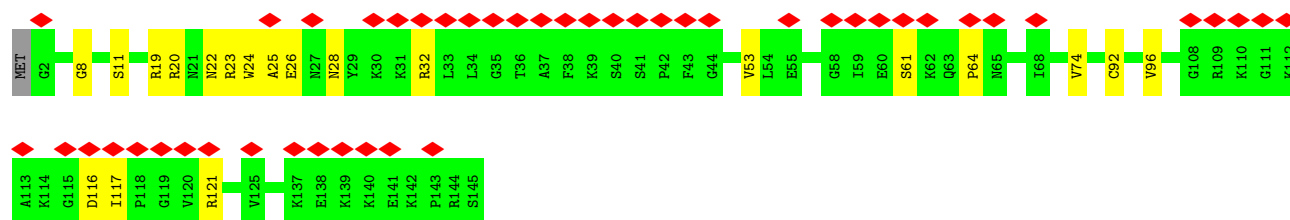
- Molecule 65: 40S ribosomal protein S21-A



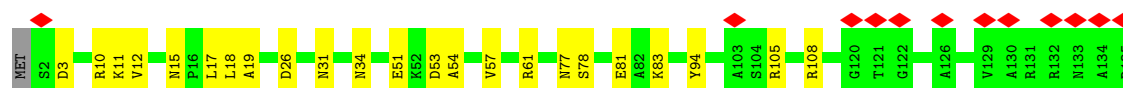
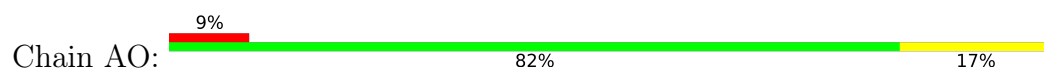
- Molecule 66: RPS22A isoform 1



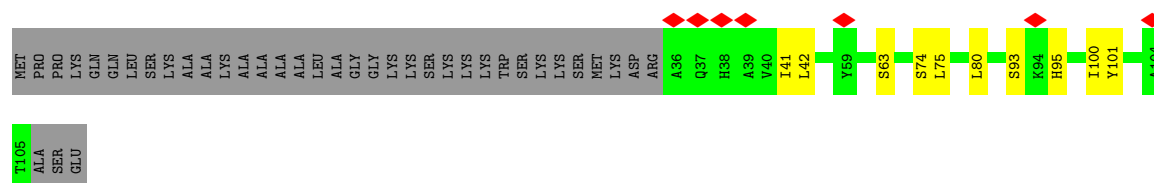
- Molecule 67: 40S ribosomal protein S23-A



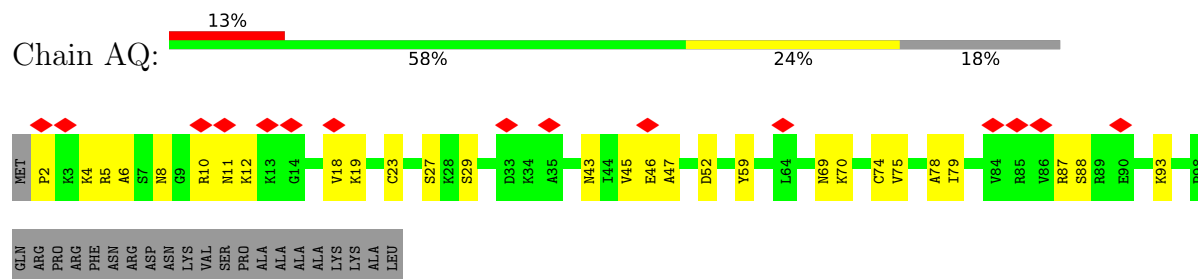
- Molecule 68: 40S ribosomal protein S24-A



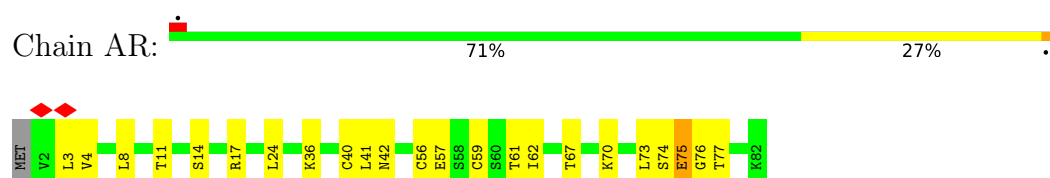
- Molecule 69: RPS25A isoform 1



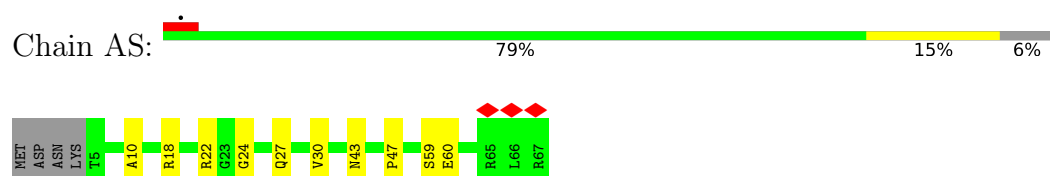
- Molecule 70: RPS26B isoform 1



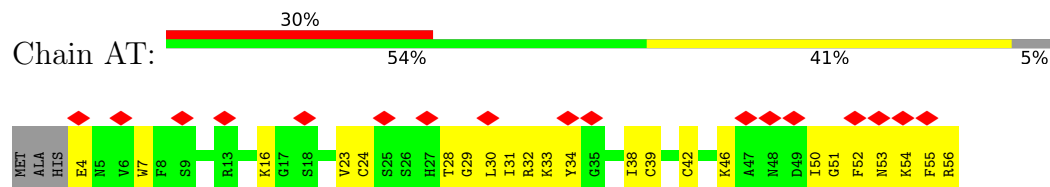
- Molecule 71: 40S ribosomal protein S27-A



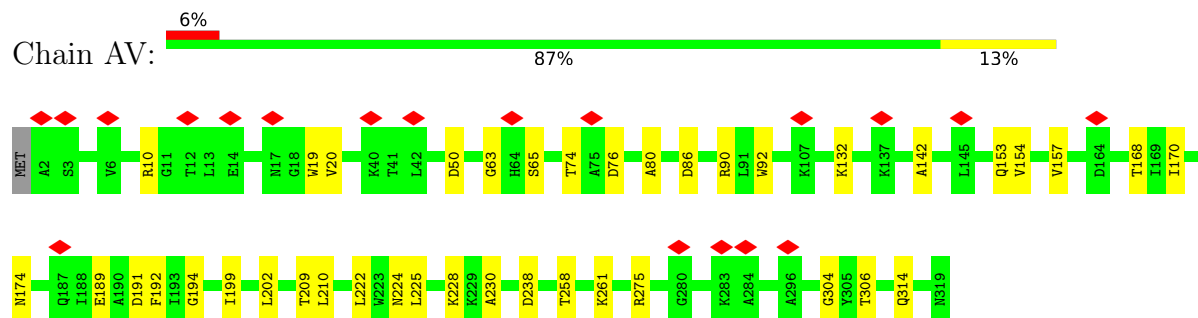
- Molecule 72: RPS28A isoform 1



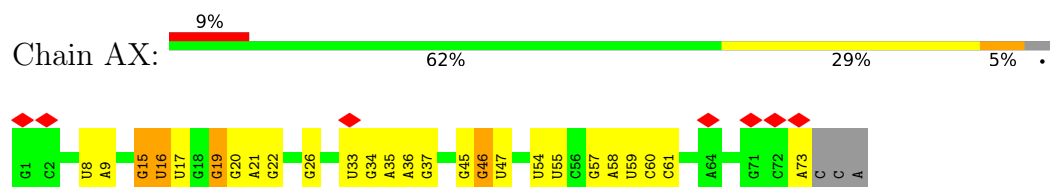
- Molecule 73: RPS29A isoform 1



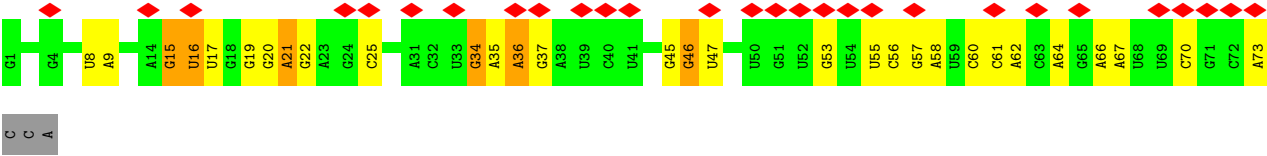
- Molecule 74: Guanine nucleotide-binding protein subunit beta-like protein



- Molecule 75: Transfer RNA



● Molecule 75: Transfer RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	87939	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	44.862	Depositor
Minimum map value	-22.382	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.6	Depositor
Map size ($\text{\AA}$)	652.8, 652.8, 652.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.36, 1.36, 1.36	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.49	0/1948	0.59	0/2617
2	B	0.48	0/3146	0.55	0/4228
3	C	0.46	0/2800	0.59	0/3790
4	D	0.33	0/2425	0.55	0/3271
5	E	0.36	0/1260	0.49	0/1694
6	F	0.49	0/1821	0.60	0/2451
7	G	0.36	0/1836	0.53	0/2481
8	H	0.27	0/1539	0.54	0/2073
9	I	0.26	0/1741	0.51	0/2335
10	J	0.27	0/1374	0.55	0/1842
11	L	0.43	0/1568	0.63	0/2106
12	M	0.37	0/1068	0.52	0/1438
13	N	0.48	0/1757	0.58	0/2354
14	O	0.50	0/1585	0.54	0/2128
15	P	0.45	0/1443	0.53	0/1944
16	Q	0.47	0/1465	0.55	0/1965
17	R	0.41	0/1538	0.53	0/2050
18	S	0.38	0/1481	0.53	0/1990
19	T	0.40	0/1300	0.52	0/1743
20	U	0.31	0/812	0.54	0/1099
21	V	0.44	0/1018	0.54	0/1369
22	W	0.43	0/533	0.50	0/707
23	X	0.41	0/979	0.48	0/1321
24	Y	0.41	0/1004	0.53	0/1341
25	Z	0.34	0/1118	0.52	0/1497
26	AA	0.27	0/789	0.53	0/1067
27	AB	0.25	0/1185	0.54	0/1598
28	1	0.35	0/74506	0.39	0/116154
29	3	0.30	0/2883	0.34	0/4491
30	4	0.35	0/3746	0.37	0/5832
31	a	0.47	0/1204	0.61	2/1612 (0.1%)
32	b	0.34	0/473	0.54	0/629

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.37	0/751	0.51	0/1008
34	d	0.44	0/897	0.50	0/1205
35	e	0.45	0/1041	0.53	0/1394
36	f	0.50	0/868	0.58	0/1168
37	g	0.42	0/890	0.58	1/1189 (0.1%)
38	h	0.38	0/978	0.54	0/1301
39	i	0.38	0/778	0.54	0/1034
40	j	0.46	0/696	0.61	0/923
41	k	0.33	0/618	0.48	0/826
42	l	0.42	0/443	0.62	0/588
43	n	0.41	0/228	0.83	0/293
44	o	0.34	0/860	0.59	0/1136
45	p	0.42	0/701	0.58	0/934
46	2	0.18	0/40725	0.36	0/63454
47	q	0.28	0/1617	0.58	0/2215
48	r	0.27	0/1735	0.59	0/2335
49	s	0.29	0/1665	0.57	0/2263
50	t	0.25	0/1759	0.60	0/2368
51	u	0.27	0/2109	0.56	0/2839
52	v	0.26	0/1629	0.61	0/2202
53	w	0.29	0/1814	0.61	0/2425
54	x	0.29	0/1506	0.60	0/2028
55	y	0.26	0/1514	0.63	0/2021
56	z	0.26	0/1519	0.58	0/2035
57	AD	0.29	0/1215	0.67	0/1638
58	AE	0.26	0/901	0.56	0/1217
59	AF	0.27	0/998	0.55	0/1341
60	AG	0.28	0/1125	0.55	0/1510
61	AH	0.27	0/935	0.61	0/1254
62	AI	0.26	0/1211	0.54	0/1628
63	AJ	0.26	0/1130	0.53	0/1517
64	AK	0.26	0/865	0.54	0/1169
65	AL	0.28	0/693	0.56	0/935
66	AM	0.26	0/1038	0.54	0/1395
67	AN	0.27	0/1139	0.61	0/1518
68	AO	0.26	0/1087	0.56	0/1449
69	AP	0.26	0/571	0.56	0/768
70	AQ	0.30	0/782	0.63	0/1047
71	AR	0.24	0/620	0.58	0/838
72	AS	0.26	0/499	0.50	0/670
73	AT	0.31	0/452	0.52	0/600
74	AV	0.22	0/2490	0.48	0/3389
75	AX	0.14	0/1749	0.31	0/2724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	AZ	0.13	0/1749	0.31	0/2724
All	All	0.33	0/211935	0.45	3/311732 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	C	0	2
4	D	0	1
6	F	0	1
7	G	0	2
10	J	0	3
11	L	0	1
14	O	0	2
16	Q	0	1
19	T	0	1
21	V	0	2
36	f	0	2
38	h	0	1
40	j	0	2
43	n	0	1
44	o	0	2
47	q	0	1
48	r	0	1
51	u	0	3
53	w	0	1
54	x	0	1
55	y	0	1
56	z	0	1
57	AD	0	2
58	AE	0	2
70	AQ	0	4
71	AR	0	1
All	All	0	43

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	g	81	CYS	CA-CB-SG	5.84	127.84	114.40
31	a	47	LYS	CA-C-N	5.20	131.47	121.54
31	a	47	LYS	C-N-CA	5.20	131.47	121.54

There are no chirality outliers.

All (43) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	143	GLU	Peptide
57	AD	138	ASN	Peptide
57	AD	44	GLY	Peptide
58	AE	122	PRO	Peptide
58	AE	123	SER	Peptide
70	AQ	10	ARG	Peptide
70	AQ	43	ASN	Peptide
70	AQ	47	ALA	Peptide
70	AQ	59	TYR	Peptide
71	AR	75	GLU	Peptide
3	C	182	LEU	Peptide
3	C	318	LEU	Peptide
4	D	258	LYS	Peptide
6	F	157	ASN	Peptide
7	G	156	ASP	Peptide
7	G	76	ALA	Peptide
10	J	166	LYS	Peptide
10	J	73	GLY	Peptide
10	J	74	PRO	Peptide
11	L	47	ALA	Peptide
14	O	110	PRO	Peptide
14	O	36	VAL	Peptide
16	Q	161	LYS	Peptide
19	T	17	ARG	Peptide
21	V	104	ASN	Peptide
21	V	92	PHE	Peptide
36	f	57	LYS	Peptide
36	f	58	GLU	Peptide
38	h	90	ARG	Peptide
40	j	5	THR	Peptide
40	j	64	MET	Peptide
43	n	9	ARG	Peptide
44	o	66	LYS	Peptide
44	o	7	THR	Peptide
47	q	112	THR	Peptide

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Mol	Chain	Res	Type	Group
48	r	177	GLN	Peptide
51	u	192	ILE	Peptide
51	u	194	THR	Peptide
51	u	233	LYS	Peptide
53	w	9	VAL	Peptide
54	x	155	ASP	Peptide
55	y	40	ALA	Peptide
56	z	163	PRO	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1914	0	1981	17	0
2	B	3075	0	3142	32	0
3	C	2748	0	2859	25	0
4	D	2375	0	2325	30	0
5	E	1239	0	1326	9	0
6	F	1784	0	1862	23	0
7	G	1804	0	1877	17	0
8	H	1518	0	1587	19	0
9	I	1705	0	1736	27	0
10	J	1353	0	1383	23	0
11	L	1543	0	1608	21	0
12	M	1053	0	1149	15	0
13	N	1720	0	1779	26	0
14	O	1555	0	1659	17	0
15	P	1420	0	1437	14	0
16	Q	1441	0	1543	14	0
17	R	1521	0	1617	16	0
18	S	1445	0	1487	14	0
19	T	1276	0	1323	8	0
20	U	796	0	812	4	0
21	V	1003	0	1048	10	0
22	W	521	0	551	4	0
23	X	964	0	1025	3	0
24	Y	993	0	1081	10	0
25	Z	1092	0	1155	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	AA	772	0	727	10	0
27	AB	1159	0	1225	20	0
28	1	66567	0	33454	383	0
29	3	2579	0	1304	15	0
30	4	3353	0	1695	21	0
31	a	1173	0	1215	17	0
32	b	462	0	491	6	0
33	c	743	0	797	8	0
34	d	883	0	918	5	0
35	e	1020	0	1090	11	0
36	f	850	0	880	9	0
37	g	880	0	941	7	0
38	h	969	0	1078	6	0
39	i	771	0	849	9	0
40	j	681	0	683	8	0
41	k	612	0	682	7	0
42	l	436	0	475	7	0
43	n	227	0	268	239	0
44	o	847	0	914	14	0
45	p	694	0	734	8	0
46	2	36409	0	18314	746	0
47	q	1577	0	1567	23	0
48	r	1709	0	1784	28	0
49	s	1635	0	1723	42	0
50	t	1734	0	1817	40	0
51	u	2068	0	2154	69	0
52	v	1609	0	1675	28	0
53	w	1790	0	1881	17	0
54	x	1481	0	1572	30	0
55	y	1489	0	1525	28	0
56	z	1494	0	1573	83	0
57	AD	1192	0	1255	12	0
58	AE	891	0	883	15	0
59	AF	977	0	1002	11	0
60	AG	1105	0	1166	42	0
61	AH	926	0	930	15	0
62	AI	1192	0	1221	98	0
63	AJ	1112	0	1124	49	0
64	AK	855	0	917	117	0
65	AL	684	0	672	22	0
66	AM	1021	0	1060	31	0
67	AN	1121	0	1196	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
68	AO	1073	0	1132	18	0
69	AP	563	0	603	26	0
70	AQ	769	0	817	39	0
71	AR	610	0	633	23	0
72	AS	497	0	535	23	0
73	AT	442	0	430	108	0
74	AV	2437	0	2386	31	0
75	AX	1564	0	787	5	0
75	AZ	1564	0	787	19	0
76	AQ	1	0	0	0	0
76	AR	1	0	0	0	0
76	AT	1	0	0	0	0
76	j	1	0	0	0	0
76	o	1	0	0	0	0
76	p	1	0	0	0	0
All	All	197132	0	144893	2043	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 (2043) 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)
43:n:9:ARG:HG3	46:2:1789:G:C6	1.13	1.64
43:n:10:THR:CB	46:2:1026:A:H2'	1.24	1.62
64:AK:80:GLU:HG3	73:AT:52:PHE:CE2	1.19	1.60
46:2:1543:A:C3'	62:AI:132:ARG:HH12	1.22	1.49
43:n:7:LYS:N	46:2:1027:A:C5'	1.70	1.48
46:2:1199:G:N2	64:AK:72:ASN:CB	1.77	1.46
43:n:9:ARG:HG3	46:2:1789:G:C5	1.18	1.45
43:n:2:ARG:CB	46:2:1029:U:H6	1.28	1.45
43:n:14:LYS:CE	46:2:979:A:O2'	1.65	1.42
43:n:11:ARG:HD2	46:2:1025:A:C4'	1.16	1.42
43:n:2:ARG:CB	46:2:1029:U:C6	2.03	1.41
43:n:5:TRP:HE1	70:AQ:12:LYS:NZ	1.14	1.40
43:n:7:LYS:N	46:2:1027:A:H5''	1.12	1.39
43:n:3:ALA:C	46:2:1028:C:C5'	1.96	1.39
46:2:1199:G:N2	64:AK:72:ASN:HB3	1.27	1.38
64:AK:67:THR:CB	73:AT:33:LYS:HE3	1.53	1.38
43:n:3:ALA:C	46:2:1028:C:H5''	1.51	1.35
43:n:9:ARG:CG	46:2:1789:G:C6	2.03	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:5:TRP:NE1	70:AQ:12:LYS:NZ	1.71	1.33
43:n:9:ARG:CG	46:2:1789:G:C5	1.91	1.33
43:n:11:ARG:CD	46:2:1025:A:H4'	1.30	1.32
46:2:1543:A:C3'	62:AI:132:ARG:NH1	1.88	1.32
64:AK:80:GLU:CG	73:AT:52:PHE:CE2	2.12	1.29
43:n:11:ARG:HD3	46:2:1025:A:O2'	1.31	1.29
43:n:10:THR:HB	46:2:1026:A:C2'	1.62	1.28
43:n:7:LYS:N	46:2:1027:A:C4'	1.94	1.28
43:n:5:TRP:HZ3	70:AQ:8:ASN:ND2	1.30	1.27
43:n:6:ARG:C	46:2:1027:A:H5''	1.58	1.27
46:2:1419:G:O2'	73:AT:54:LYS:HE2	1.24	1.27
46:2:772:G:OP1	56:z:6:ARG:NH1	1.63	1.27
43:n:14:LYS:HE2	46:2:979:A:O2'	1.09	1.27
43:n:15:ARG:CD	46:2:978:A:H61	1.47	1.26
64:AK:82:TYR:HA	73:AT:50:ILE:O	1.19	1.25
43:n:4:LYS:N	46:2:1028:C:C5'	2.00	1.25
43:n:10:THR:CB	46:2:1026:A:C2'	2.14	1.24
43:n:5:TRP:HE1	70:AQ:12:LYS:CE	1.51	1.23
43:n:1:MET:SD	46:2:1033:C:OP2	1.96	1.22
43:n:9:ARG:HA	46:2:1789:G:C2	1.74	1.21
43:n:8:LYS:NZ	46:2:942:G:OP1	1.74	1.20
46:2:1199:G:H22	64:AK:72:ASN:CB	1.39	1.20
46:2:1281:G:OP1	64:AK:76:SER:CB	1.89	1.20
51:u:26:CYS:HA	56:z:2:PRO:CB	1.72	1.18
64:AK:82:TYR:CE2	73:AT:50:ILE:HA	1.77	1.18
43:n:7:LYS:N	46:2:1027:A:C3'	2.06	1.18
43:n:14:LYS:HE2	46:2:979:A:C2'	1.73	1.18
46:2:1281:G:OP1	64:AK:76:SER:HB2	1.00	1.18
43:n:8:LYS:HG3	46:2:1789:G:H1'	1.25	1.16
46:2:1171:A:H4'	62:AI:144:ARG:NE	1.59	1.16
46:2:1334:U:O4'	73:AT:55:PHE:CE2	2.00	1.15
46:2:1199:G:N2	64:AK:72:ASN:HB2	1.58	1.15
64:AK:82:TYR:CE2	73:AT:50:ILE:HG23	1.82	1.15
49:s:174:ARG:O	56:z:53:ARG:NH2	1.76	1.14
64:AK:69:LYS:NZ	73:AT:33:LYS:HB2	1.62	1.14
43:n:7:LYS:N	46:2:1027:A:H3'	1.64	1.13
43:n:3:ALA:CA	46:2:1028:C:C5'	2.25	1.13
64:AK:67:THR:HB	73:AT:33:LYS:CE	1.78	1.13
64:AK:80:GLU:HG3	73:AT:52:PHE:CD2	1.84	1.13
43:n:3:ALA:CA	46:2:1028:C:H5'	1.79	1.12
43:n:6:ARG:NH2	46:2:1792:G:C2	2.18	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:AG:142:TYR:CE2	64:AK:75:GLY:CA	2.33	1.12
9:I:28:ASP:OD2	75:AZ:64:A:O4'	1.66	1.11
43:n:5:TRP:HB2	46:2:1028:C:H3'	1.30	1.11
43:n:4:LYS:N	46:2:1028:C:H5''	1.16	1.10
43:n:9:ARG:HB3	46:2:1027:A:OP1	1.47	1.10
46:2:1543:A:H3'	62:AI:132:ARG:NH1	1.52	1.10
43:n:13:LEU:HD22	46:2:977:A:N1	1.68	1.09
43:n:13:LEU:HD12	46:2:1788:G:N2	1.68	1.08
43:n:15:ARG:HD2	46:2:978:A:H61	1.11	1.08
64:AK:67:THR:HB	73:AT:33:LYS:HE3	1.10	1.08
43:n:3:ALA:HA	46:2:1028:C:H5'	1.33	1.08
46:2:772:G:P	56:z:6:ARG:NH1	2.27	1.08
43:n:5:TRP:NE1	70:AQ:12:LYS:HZ1	1.34	1.08
43:n:11:ARG:HB3	46:2:1025:A:C2'	1.47	1.07
46:2:1419:G:N3	73:AT:54:LYS:NZ	2.01	1.07
67:AN:64:PRO:HG3	75:AZ:36:A:O3'	1.43	1.07
64:AK:67:THR:HG21	73:AT:33:LYS:HG3	1.22	1.07
43:n:2:ARG:N	46:2:1031:U:H5''	1.70	1.07
43:n:5:TRP:CZ3	70:AQ:8:ASN:ND2	2.09	1.07
43:n:8:LYS:CG	46:2:1789:G:H1'	1.84	1.07
46:2:1543:A:O3'	62:AI:132:ARG:NH1	1.85	1.07
64:AK:67:THR:CG2	73:AT:33:LYS:HG3	1.85	1.06
46:2:1419:G:O2'	73:AT:54:LYS:CE	2.03	1.06
43:n:10:THR:OG1	46:2:1026:A:O2'	1.74	1.06
46:2:763:G:OP1	51:u:255:ARG:NH2	1.89	1.05
51:u:26:CYS:HA	56:z:2:PRO:CA	1.86	1.05
43:n:11:ARG:CD	46:2:1025:A:C4'	2.02	1.05
62:AI:48:LYS:HE3	63:AJ:35:ASP:O	1.53	1.04
43:n:11:ARG:CD	46:2:1025:A:O2'	2.05	1.04
64:AK:82:TYR:CA	73:AT:50:ILE:O	2.06	1.04
43:n:10:THR:OG1	46:2:1026:A:H2'	1.58	1.04
64:AK:67:THR:CG2	73:AT:33:LYS:HE3	1.87	1.03
43:n:3:ALA:C	46:2:1028:C:H5'	1.74	1.03
43:n:10:THR:OG1	46:2:1026:A:C2'	2.06	1.03
50:t:41:VAL:HG21	64:AK:32:LYS:HE2	1.40	1.03
64:AK:67:THR:HG21	73:AT:33:LYS:CG	1.88	1.03
46:2:1558:U:O4'	62:AI:122:HIS:CE1	2.12	1.03
60:AG:142:TYR:CE2	64:AK:75:GLY:HA3	1.91	1.03
43:n:5:TRP:CD1	46:2:1029:U:OP1	2.11	1.02
43:n:10:THR:H	46:2:1026:A:H3'	1.23	1.02
43:n:3:ALA:HA	46:2:1028:C:C5'	1.84	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AI:24:GLY:O	69:AP:41:ILE:CD1	2.08	1.01
64:AK:69:LYS:HZ1	73:AT:33:LYS:HB2	0.86	1.01
46:2:1030:A:N6	70:AQ:5:ARG:O	1.94	1.01
46:2:1334:U:C1'	73:AT:55:PHE:HE2	1.74	1.01
46:2:1794:A:OP2	70:AQ:4:LYS:NZ	1.94	1.01
46:2:1419:G:H2'	73:AT:54:LYS:HZ1	1.21	1.00
64:AK:82:TYR:CD2	73:AT:50:ILE:O	2.15	1.00
46:2:1604:U:O2	60:AG:132:LYS:NZ	1.94	0.99
64:AK:82:TYR:HE2	73:AT:50:ILE:HG23	1.19	0.99
43:n:11:ARG:HD3	46:2:1025:A:HO2'	1.03	0.99
46:2:1280:C:OP1	64:AK:78:THR:HG21	1.62	0.99
53:w:3:LEU:HD21	53:w:24:ILE:HD11	1.44	0.99
46:2:1419:G:H2'	73:AT:54:LYS:NZ	1.78	0.99
50:t:219:ALA:HB2	74:AV:194:GLY:HA2	1.45	0.98
43:n:2:ARG:CB	46:2:1029:U:C5	2.45	0.98
43:n:9:ARG:HA	46:2:1789:G:N3	1.79	0.98
51:u:22:LYS:NZ	56:z:6:ARG:HA	1.80	0.97
46:2:1544:U:P	62:AI:132:ARG:NH1	2.37	0.97
62:AI:48:LYS:CE	63:AJ:35:ASP:O	2.13	0.97
46:2:1171:A:O3'	62:AI:144:ARG:HD3	1.63	0.95
52:v:76:ARG:O	60:AG:114:ARG:NH1	1.98	0.95
64:AK:69:LYS:HZ1	73:AT:33:LYS:CB	1.80	0.95
64:AK:81:THR:OG1	73:AT:53:ASN:OD1	1.83	0.95
64:AK:83:GLU:H	73:AT:51:GLY:HA3	1.28	0.95
46:2:1367:G:O3'	63:AJ:119:LYS:NZ	2.00	0.94
43:n:14:LYS:HE3	46:2:979:A:O2'	1.66	0.94
43:n:15:ARG:CD	46:2:978:A:N6	2.31	0.94
64:AK:80:GLU:CG	73:AT:52:PHE:CD2	2.49	0.94
62:AI:24:GLY:C	69:AP:41:ILE:HD12	1.92	0.93
46:2:772:G:P	56:z:6:ARG:HH12	1.86	0.93
43:n:1:MET:N	46:2:1032:G:OP2	1.88	0.92
46:2:1501:C:OP2	63:AJ:102:ARG:NE	2.02	0.92
46:2:1558:U:H5'	62:AI:122:HIS:ND1	1.84	0.92
43:n:7:LYS:HD2	46:2:624:G:H4'	1.51	0.92
46:2:1559:A:H5''	62:AI:135:GLY:HA3	1.49	0.92
62:AI:40:ARG:HB3	63:AJ:45:MET:CE	1.98	0.92
43:n:4:LYS:H	46:2:1028:C:H5''	1.13	0.92
43:n:8:LYS:NZ	46:2:942:G:P	2.41	0.92
46:2:1280:C:OP1	64:AK:78:THR:CG2	2.16	0.92
64:AK:81:THR:OG1	73:AT:53:ASN:O	1.87	0.91
46:2:1570:A:H5''	62:AI:144:ARG:HH12	1.32	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:1794:A:N3	70:AQ:79:ILE:HD11	1.86	0.91
46:2:1171:A:H4'	62:AI:144:ARG:CZ	2.01	0.90
43:n:9:ARG:HG3	46:2:1789:G:C4	2.05	0.90
43:n:15:ARG:NE	46:2:978:A:H61	1.70	0.90
62:AI:24:GLY:O	69:AP:41:ILE:HD12	1.69	0.90
46:2:123:G:N3	51:u:148:ARG:NH1	2.20	0.90
64:AK:80:GLU:HG3	73:AT:52:PHE:HE2	1.07	0.90
46:2:1171:A:H4'	62:AI:144:ARG:CD	2.02	0.89
43:n:6:ARG:NH2	46:2:1792:G:N1	2.19	0.89
46:2:1367:G:C5'	63:AJ:119:LYS:HZ2	1.86	0.89
43:n:6:ARG:CA	46:2:1027:A:H5'	2.01	0.89
46:2:1559:A:C4	62:AI:134:ARG:O	2.26	0.89
64:AK:69:LYS:HE3	73:AT:31:ILE:CG2	2.03	0.89
46:2:1162:C:C5'	72:AS:22:ARG:HD3	2.03	0.88
64:AK:82:TYR:CE2	73:AT:50:ILE:CG2	2.55	0.88
43:n:8:LYS:HD2	46:2:977:A:N3	1.88	0.88
46:2:1567:U:O4'	62:AI:36:LYS:HD3	1.73	0.88
46:2:1658:G:O6	46:2:1743:U:C2	2.26	0.88
43:n:13:LEU:HD12	46:2:1788:G:C2	2.07	0.88
60:AG:142:TYR:CD1	64:AK:74:GLU:HG3	2.08	0.88
64:AK:69:LYS:HE3	73:AT:31:ILE:HG21	1.53	0.88
43:n:5:TRP:O	46:2:1027:A:H5'	1.73	0.87
46:2:1569:A:H2	62:AI:145:ARG:HH12	1.22	0.87
51:u:26:CYS:CA	56:z:2:PRO:CB	2.53	0.87
46:2:1334:U:O2'	73:AT:56:ARG:NH2	2.07	0.87
43:n:15:ARG:NE	46:2:978:A:N6	2.23	0.87
62:AI:57:ARG:HH21	69:AP:75:LEU:HD11	1.39	0.86
43:n:8:LYS:HZ1	46:2:942:G:P	1.98	0.86
46:2:1545:A:OP1	62:AI:133:VAL:HG22	1.75	0.86
66:AM:22:LYS:NZ	71:AR:4:VAL:HG12	1.91	0.86
43:n:15:ARG:H	46:2:979:A:H2	1.20	0.85
62:AI:40:ARG:HB3	63:AJ:45:MET:HE2	1.57	0.85
18:S:22:PRO:O	19:T:146:ASN:ND2	2.09	0.85
43:n:5:TRP:HE1	70:AQ:12:LYS:HE3	1.40	0.85
43:n:14:LYS:HA	46:2:979:A:N3	1.91	0.85
46:2:404:G:O2'	53:w:89:ASP:O	1.93	0.85
51:u:26:CYS:HA	56:z:2:PRO:HB2	1.55	0.85
50:t:219:ALA:CB	74:AV:194:GLY:HA2	2.06	0.85
46:2:1609:U:O2'	52:v:107:LYS:NZ	2.09	0.84
49:s:173:PRO:HG2	56:z:57:ARG:NE	1.91	0.84
43:n:10:THR:C	46:2:1026:A:H5'	2.03	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:6:ARG:C	46:2:1027:A:C5'	2.30	0.84
46:2:1274:C:N4	75:AZ:34:G:OP2	2.08	0.84
46:2:1199:G:H21	64:AK:72:ASN:CB	1.89	0.84
46:2:1601:G:OP1	63:AJ:90:PRO:HD2	1.77	0.84
49:s:174:ARG:HB2	56:z:97:LEU:HG	1.58	0.84
60:AG:142:TYR:CE2	64:AK:75:GLY:HA2	2.09	0.84
46:2:1199:G:O6	64:AK:71:PRO:HD2	1.77	0.84
66:AM:22:LYS:NZ	71:AR:4:VAL:CG1	2.40	0.84
47:q:6:THR:HG21	65:AL:41:GLU:OE1	1.77	0.84
43:n:10:THR:HB	46:2:1026:A:H2'	0.85	0.83
46:2:1419:G:C2'	73:AT:54:LYS:NZ	2.41	0.83
60:AG:142:TYR:HE2	64:AK:75:GLY:CA	1.87	0.83
43:n:3:ALA:CA	46:2:1028:C:H5''	2.01	0.83
46:2:771:A:O3'	56:z:6:ARG:NH1	2.11	0.83
64:AK:82:TYR:CD2	73:AT:50:ILE:CG2	2.61	0.83
43:n:15:ARG:HH21	46:2:979:A:H61	1.27	0.82
43:n:5:TRP:CB	46:2:1028:C:H3'	2.09	0.82
71:AR:11:THR:HG1	71:AR:14:SER:HG	1.22	0.82
64:AK:82:TYR:CE2	73:AT:50:ILE:CA	2.60	0.82
43:n:13:LEU:HD13	46:2:1788:G:N3	1.95	0.82
46:2:1334:U:C1'	73:AT:55:PHE:CE2	2.58	0.82
43:n:13:LEU:HD12	46:2:1788:G:H21	1.41	0.82
46:2:1569:A:C2	62:AI:145:ARG:NH1	2.48	0.82
60:AG:140:LYS:O	64:AK:73:GLY:HA2	1.79	0.82
60:AG:142:TYR:CD1	64:AK:74:GLU:CG	2.63	0.82
43:n:9:ARG:CG	46:2:1789:G:C4	2.63	0.81
46:2:1545:A:H5''	62:AI:133:VAL:CG2	2.09	0.81
43:n:15:ARG:HD2	46:2:978:A:N6	1.92	0.81
46:2:1334:U:O4'	73:AT:55:PHE:CD2	2.33	0.81
6:F:156:ILE:HD11	6:F:161:VAL:HG21	1.63	0.81
46:2:1543:A:H3'	62:AI:132:ARG:HH12	0.66	0.81
46:2:285:G:N7	53:w:186:ARG:NH1	2.27	0.81
46:2:1558:U:OP1	62:AI:122:HIS:HB3	1.80	0.81
43:n:6:ARG:HA	46:2:1027:A:H5'	1.63	0.81
46:2:1162:C:O5'	72:AS:22:ARG:HD3	1.81	0.81
51:u:22:LYS:HZ1	56:z:6:ARG:HA	1.41	0.81
43:n:5:TRP:NE1	70:AQ:12:LYS:HZ2	1.65	0.81
46:2:1559:A:N3	62:AI:134:ARG:O	2.14	0.80
46:2:1567:U:O4'	62:AI:36:LYS:CD	2.29	0.80
43:n:9:ARG:CB	46:2:1789:G:C4	2.64	0.80
46:2:333:A:OP2	55:y:31:ARG:NH2	2.15	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:444:C:N4	46:2:460:A:H62	1.79	0.80
28:1:1566:A:N6	28:1:1572:U:O4	2.12	0.80
50:t:222:VAL:HG13	74:AV:191:ASP:O	1.80	0.80
28:1:1565:G:H2'	28:1:1566:A:C8	2.17	0.80
43:n:5:TRP:HB2	46:2:1028:C:C3'	2.10	0.79
22:W:48:ARG:NH2	28:1:2112:U:OP1	2.15	0.79
46:2:1543:A:C2'	62:AI:132:ARG:NH1	2.45	0.79
43:n:12:ARG:N	46:2:1025:A:O2'	2.15	0.79
43:n:6:ARG:CA	46:2:1027:A:C5'	2.61	0.79
46:2:1334:U:H1'	73:AT:55:PHE:HE2	1.46	0.79
43:n:5:TRP:CE2	46:2:1029:U:OP2	2.35	0.79
46:2:404:G:O2'	53:w:90:GLY:O	2.00	0.78
50:t:225:TYR:CD2	74:AV:191:ASP:OD2	2.36	0.78
2:B:10:ARG:NH2	2:B:263:SER:O	2.16	0.78
43:n:7:LYS:HZ2	46:2:624:G:H5''	1.48	0.78
43:n:5:TRP:CE2	70:AQ:12:LYS:NZ	2.42	0.78
43:n:13:LEU:CD1	46:2:1788:G:N3	2.47	0.78
43:n:14:LYS:HE2	46:2:979:A:H2'	1.64	0.77
46:2:1:U:H5''	49:s:179:VAL:HG21	1.65	0.77
62:AI:85:PHE:CZ	63:AJ:36:ILE:O	2.37	0.77
46:2:1559:A:C2	62:AI:134:ARG:O	2.37	0.77
64:AK:82:TYR:CD2	73:AT:50:ILE:HA	2.19	0.77
66:AM:60:LYS:NZ	71:AR:24:LEU:O	2.16	0.77
43:n:13:LEU:CD2	46:2:977:A:N1	2.47	0.77
46:2:389:G:N2	46:2:408:C:O2	2.18	0.77
46:2:1671:A:N6	46:2:1730:A:O2'	2.17	0.77
50:t:222:VAL:HG11	74:AV:192:PHE:HD1	1.48	0.77
51:u:27:TYR:CE2	56:z:2:PRO:HD3	2.19	0.77
64:AK:81:THR:OG1	73:AT:53:ASN:N	2.18	0.77
43:n:5:TRP:NE1	70:AQ:12:LYS:CE	2.35	0.77
46:2:1098:U:OP1	49:s:159:THR:OG1	2.02	0.77
62:AI:24:GLY:O	69:AP:41:ILE:HD13	1.83	0.77
28:1:3092:C:O2'	28:1:3094:A:OP2	2.04	0.76
43:n:10:THR:HG21	46:2:1772:C:N3	1.99	0.76
2:B:266:ARG:NH2	28:1:2392:C:O2'	2.19	0.76
43:n:9:ARG:CA	46:2:1789:G:C2	2.64	0.76
49:s:173:PRO:HD2	56:z:57:ARG:CZ	2.15	0.76
49:s:173:PRO:HD3	56:z:57:ARG:NH2	1.99	0.76
64:AK:67:THR:HG21	73:AT:33:LYS:HE3	1.67	0.76
43:n:9:ARG:HG3	46:2:1789:G:N1	1.97	0.76
43:n:5:TRP:C	46:2:1027:A:H5'	2.10	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:s:173:PRO:CD	56:z:57:ARG:CZ	2.64	0.76
46:2:1215:C:O2	46:2:1217:A:N6	2.19	0.75
10:J:51:ARG:NH2	28:1:2681:U:OP2	2.19	0.75
16:Q:111:ARG:NH1	16:Q:121:CYS:SG	2.60	0.75
43:n:9:ARG:CB	46:2:1027:A:OP1	2.29	0.75
9:I:68:ALA:HB1	9:I:155:ALA:HB1	1.69	0.75
28:1:970:A:OP2	32:b:19:ASN:ND2	2.19	0.75
46:2:1199:G:C6	64:AK:71:PRO:HD2	2.21	0.75
60:AG:142:TYR:HE2	64:AK:75:GLY:HA2	1.47	0.75
43:n:7:LYS:NZ	46:2:624:G:H5''	2.00	0.75
43:n:9:ARG:CB	46:2:1789:G:C5	2.70	0.75
51:u:27:TYR:N	56:z:2:PRO:HB3	2.02	0.75
28:1:3110:C:O2	28:1:3124:G:N2	2.20	0.75
43:n:13:LEU:O	46:2:979:A:H1'	1.87	0.75
46:2:1597:A:OP1	73:AT:32:ARG:NH2	2.19	0.75
43:n:16:LYS:O	43:n:20:VAL:HA	1.87	0.75
46:2:415:C:O2'	46:2:419:G:N2	2.20	0.75
43:n:7:LYS:CA	46:2:1027:A:H5''	2.16	0.75
46:2:1603:U:O2'	60:AG:139:GLN:OE1	2.04	0.75
46:2:258:C:O2	55:y:178:ARG:NH2	2.18	0.75
46:2:1171:A:O3'	62:AI:144:ARG:CD	2.35	0.75
46:2:105:A:N7	46:2:308:C:N3	2.35	0.74
46:2:1652:C:O2	46:2:1749:A:N6	2.20	0.74
24:Y:74:TYR:OH	30:4:75:G:OP2	2.03	0.74
43:n:11:ARG:HB3	46:2:1025:A:H2'	1.64	0.74
46:2:1199:G:H22	64:AK:72:ASN:HB3	0.59	0.74
62:AI:40:ARG:HB3	63:AJ:45:MET:HE1	1.69	0.74
46:2:767:U:O2	56:z:143:ILE:HG22	1.87	0.74
46:2:1114:G:O2'	46:2:1130:G:O6	2.04	0.74
12:M:8:LYS:NZ	28:1:3200:G:OP2	2.15	0.74
28:1:2138:A:HO2'	40:j:2:GLY:N	1.85	0.74
9:I:7:ARG:NH1	28:1:2856:G:N7	2.35	0.74
28:1:1592:G:OP1	37:g:58:ARG:NH2	2.21	0.74
46:2:772:G:OP1	56:z:6:ARG:CZ	2.34	0.74
46:2:444:C:H42	46:2:460:A:H62	1.36	0.74
46:2:1203:A:H61	46:2:1553:G:H21	1.35	0.74
50:t:219:ALA:CB	74:AV:194:GLY:CA	2.65	0.74
46:2:125:U:O2	46:2:205:U:O2'	2.06	0.74
50:t:225:TYR:HD2	74:AV:191:ASP:OD2	1.71	0.74
27:AB:11:ARG:NH1	55:y:83:TYR:OH	2.20	0.74
28:1:3112:G:O6	28:1:3120:C:O2'	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:11:ARG:CD	46:2:1025:A:C2'	2.52	0.74
47:q:33:GLN:NE2	65:AL:63:GLY:O	2.21	0.74
13:N:5:LYS:NZ	28:1:266:A:OP1	2.21	0.74
64:AK:82:TYR:HD2	73:AT:50:ILE:HG22	1.52	0.74
43:n:11:ARG:CB	46:2:1025:A:C2'	2.36	0.73
2:B:244:ARG:NH2	28:1:2948:C:OP1	2.21	0.73
39:i:23:ALA:O	39:i:25:LYS:NZ	2.21	0.73
64:AK:82:TYR:CD2	73:AT:50:ILE:HG23	2.22	0.73
49:s:175:GLY:O	56:z:53:ARG:NE	2.21	0.73
8:H:9:GLN:O	8:H:72:LYS:NZ	2.22	0.73
8:H:69:ARG:NH2	28:1:3117:C:OP2	2.22	0.73
13:N:93:LYS:O	28:1:289:A:O2'	2.07	0.73
43:n:11:ARG:C	46:2:1025:A:O2'	2.32	0.73
43:n:13:LEU:CD1	46:2:1788:G:C2	2.71	0.73
46:2:977:A:N7	46:2:1025:A:N6	2.37	0.73
46:2:1537:C:O2'	46:2:1540:G:O6	2.07	0.73
13:N:68:ARG:NH1	13:N:124:ASP:O	2.22	0.73
54:x:26:GLU:O	54:x:30:SER:OG	2.07	0.73
28:1:1003:A:N1	28:1:1049:C:O2'	2.20	0.73
28:1:3280:U:O2'	28:1:3281:U:O4'	2.07	0.73
64:AK:67:THR:HB	73:AT:33:LYS:NZ	2.03	0.73
43:n:15:ARG:CZ	46:2:978:A:N6	2.51	0.73
46:2:1359:C:P	63:AJ:129:GLN:HE21	2.12	0.73
64:AK:69:LYS:NZ	73:AT:33:LYS:CB	2.43	0.73
64:AK:69:LYS:CE	73:AT:31:ILE:HG21	2.18	0.73
28:1:762:U:O4	28:1:769:G:O2'	2.06	0.73
28:1:1147:G:OP1	35:e:47:ARG:NH1	2.22	0.73
51:u:22:LYS:HZ1	56:z:5:PRO:C	1.96	0.73
59:AF:37:ALA:O	59:AF:42:ARG:NH1	2.21	0.72
1:A:220:GLY:O	28:1:2245:C:O2'	2.07	0.72
46:2:1533:C:O2'	62:AI:30:TYR:CE2	2.41	0.72
66:AM:22:LYS:NZ	71:AR:3:LEU:O	2.23	0.72
46:2:486:G:O6	46:2:501:U:O4	2.08	0.72
46:2:873:U:O2'	46:2:1047:G:OP1	2.07	0.72
46:2:1571:C:O2'	46:2:1574:G:N2	2.22	0.72
55:y:76:THR:OG1	55:y:105:ASP:OD2	2.08	0.72
43:n:11:ARG:NE	46:2:1025:A:H4'	2.01	0.72
47:q:41:ARG:NH1	61:AH:105:GLN:HG3	2.04	0.72
1:A:30:ARG:O	1:A:163:ARG:NH2	2.22	0.72
4:D:27:LYS:NZ	10:J:144:CYS:SG	2.62	0.72
21:V:81:GLN:O	21:V:98:ASN:ND2	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:1544:U:O5'	62:AI:132:ARG:NH1	2.23	0.72
13:N:96:ARG:NH2	13:N:160:GLU:O	2.22	0.72
28:1:3106:A:N6	28:1:3128:G:H21	1.87	0.72
6:F:241:LYS:NZ	28:1:576:C:OP1	2.22	0.72
28:1:877:C:O2'	28:1:880:G:O2'	2.08	0.72
12:M:113:THR:OG1	12:M:116:GLU:OE1	2.07	0.71
28:1:2212:C:N4	28:1:2232:A:OP2	2.23	0.71
43:n:11:ARG:CD	46:2:1025:A:HO2'	1.89	0.71
46:2:1331:A:OP2	61:AH:45:ARG:NH2	2.23	0.71
49:s:173:PRO:CD	56:z:57:ARG:NH2	2.53	0.71
10:J:47:GLN:NE2	10:J:66:ALA:O	2.23	0.71
18:S:90:MET:SD	18:S:92:LYS:NZ	2.62	0.71
43:n:5:TRP:CD2	46:2:1029:U:OP2	2.43	0.71
46:2:1658:G:O6	46:2:1743:U:O2	2.07	0.71
1:A:241:ARG:NH1	28:1:2155:G:OP1	2.23	0.71
28:1:3106:A:N6	28:1:3128:G:N2	2.38	0.71
46:2:752:A:N6	46:2:793:A:O2'	2.22	0.71
46:2:1377:U:O2'	46:2:1379:C:OP2	2.09	0.71
46:2:1794:A:P	70:AQ:4:LYS:HZ1	2.12	0.71
28:1:1646:G:O2'	28:1:1809:A:N6	2.24	0.71
28:1:3020:U:O2	28:1:3034:C:N4	2.21	0.71
46:2:123:G:O2'	51:u:148:ARG:NH2	2.24	0.71
46:2:1502:G:N2	46:2:1505:A:OP2	2.24	0.71
46:2:1796:C:OP1	70:AQ:87:ARG:NH2	2.21	0.71
50:t:222:VAL:HG23	74:AV:230:ALA:HB2	1.71	0.71
74:AV:10:ARG:NH2	74:AV:50:ASP:O	2.24	0.71
3:C:162:THR:OG1	3:C:218:ALA:O	2.08	0.71
46:2:1108:G:N2	67:AN:22:ASN:OD1	2.22	0.71
52:v:182:ALA:O	52:v:186:ASN:ND2	2.24	0.71
7:G:84:ARG:NH2	30:4:156:U:OP2	2.23	0.70
43:n:9:ARG:HB2	46:2:1789:G:C4	2.26	0.70
46:2:813:U:O2'	46:2:815:G:O6	2.09	0.70
46:2:1367:G:H5''	63:AJ:119:LYS:CE	2.20	0.70
30:4:55:U:O4	30:4:62:C:N3	2.25	0.70
43:n:10:THR:N	46:2:1026:A:H3'	2.03	0.70
46:2:856:A:O2'	46:2:858:G:OP1	2.10	0.70
51:u:91:THR:OG1	51:u:98:ASN:ND2	2.24	0.70
10:J:51:ARG:NH1	28:1:2682:C:OP2	2.24	0.70
43:n:11:ARG:NH1	46:2:1024:U:C2	2.59	0.70
46:2:1546:G:N7	62:AI:134:ARG:NH2	2.39	0.70
48:r:158:SER:O	48:r:162:ARG:NH1	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:AR:67:THR:OG1	71:AR:70:LYS:O	2.10	0.70
25:Z:33:SER:OG	25:Z:35:SER:O	2.08	0.70
46:2:584:C:N4	46:2:586:G:O6	2.24	0.70
46:2:1203:A:H61	46:2:1553:G:N2	1.88	0.70
67:AN:117:ILE:O	67:AN:121:ARG:NH2	2.24	0.70
75:AX:16:U:OP1	75:AX:60:C:N4	2.25	0.70
28:1:2298:U:O4	28:1:2925:C:N4	2.24	0.70
46:2:580:A:O2'	46:2:582:U:OP2	2.09	0.70
3:C:193:LYS:NZ	28:1:1420:C:OP2	2.23	0.70
28:1:2945:G:O2'	28:1:2948:C:OP2	2.10	0.70
4:D:107:ARG:NH1	4:D:116:ASP:OD1	2.25	0.70
11:L:4:SER:O	31:a:44:ASN:ND2	2.24	0.70
24:Y:16:ARG:NE	30:4:23:U:OP2	2.24	0.70
51:u:37:LYS:O	51:u:39:ARG:NH2	2.25	0.70
46:2:648:G:O6	46:2:688:G:N2	2.25	0.70
46:2:1055:U:O2	46:2:1064:G:O6	2.10	0.70
10:J:11:ASP:OD1	10:J:13:LYS:NZ	2.24	0.70
17:R:13:SER:OG	17:R:38:ARG:NH2	2.25	0.70
43:n:10:THR:HB	46:2:1026:A:C3'	2.20	0.70
46:2:7:G:O2'	46:2:1138:A:OP2	2.10	0.70
46:2:1662:G:N7	46:2:1739:C:N4	2.39	0.70
1:A:30:ARG:NH1	1:A:36:GLU:OE1	2.25	0.69
1:A:193:ARG:NH1	28:1:2181:C:OP1	2.24	0.69
60:AG:142:TYR:CE1	64:AK:74:GLU:HB2	2.27	0.69
64:AK:81:THR:CG2	73:AT:53:ASN:O	2.40	0.69
28:1:1636:U:O2'	28:1:1637:A:O4'	2.10	0.69
46:2:1558:U:O4'	62:AI:122:HIS:HE1	1.72	0.69
53:w:131:LYS:NZ	53:w:133:LEU:O	2.24	0.69
64:AK:67:THR:CB	73:AT:33:LYS:CE	2.46	0.69
28:1:2295:A:N3	28:1:2929:C:O2'	2.23	0.69
46:2:107:C:OP1	46:2:383:G:O2'	2.10	0.69
43:n:10:THR:O	46:2:1026:A:H5'	1.91	0.69
46:2:992:A:O2'	46:2:1785:U:O2	2.07	0.69
46:2:1367:G:C4'	63:AJ:119:LYS:NZ	2.55	0.69
56:z:70:LEU:O	56:z:74:ASN:ND2	2.24	0.69
12:M:19:ARG:NH2	12:M:66:THR:O	2.24	0.69
28:1:2213:A:OP2	28:1:2231:C:N4	2.26	0.69
28:1:3153:U:OP2	28:1:3293:U:O2'	2.10	0.69
46:2:105:A:N6	46:2:308:C:O2	2.26	0.69
47:q:182:LEU:O	47:q:185:ARG:C	2.36	0.69
60:AG:30:LYS:O	60:AG:66:ARG:NH1	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:622:A:OP1	36:f:60:ARG:NH1	2.26	0.69
46:2:1162:C:C4	72:AS:24:GLY:CA	2.76	0.69
59:AF:17:TYR:O	59:AF:18:ARG:NH1	2.26	0.69
27:AB:65:SER:O	27:AB:67:ARG:NH1	2.25	0.69
28:1:2530:G:O2'	28:1:2531:C:OP1	2.11	0.69
46:2:1533:C:O2'	62:AI:30:TYR:HE2	1.75	0.69
46:2:1569:A:N3	62:AI:145:ARG:NH1	2.41	0.69
53:w:159:ARG:NH1	53:w:171:LYS:O	2.26	0.69
2:B:150:ARG:NH1	28:1:3242:G:N7	2.40	0.69
43:n:9:ARG:CZ	46:2:1790:A:N7	2.56	0.69
46:2:399:A:O2'	46:2:400:A:O5'	2.10	0.69
46:2:1681:A:N6	46:2:1720:G:O2'	2.26	0.69
47:q:182:LEU:O	47:q:185:ARG:O	2.11	0.69
2:B:251:CYS:SG	28:1:2943:G:N2	2.66	0.68
43:n:7:LYS:HD2	46:2:624:G:C4'	2.21	0.68
43:n:8:LYS:HZ2	46:2:942:G:P	2.12	0.68
46:2:562:G:O2'	46:2:563:U:O4'	2.11	0.68
46:2:1594:G:OP2	46:2:1596:C:N4	2.26	0.68
1:A:253:GLN:N	46:2:989:U:OP2	2.27	0.68
13:N:155:VAL:O	13:N:162:ARG:NH2	2.26	0.68
27:AB:11:ARG:NH2	55:y:84:HIS:O	2.27	0.68
28:1:3106:A:H62	28:1:3128:G:N2	1.90	0.68
60:AG:40:GLU:OE1	60:AG:45:ARG:NH1	2.26	0.68
28:1:1565:G:OP2	28:1:1571:A:N6	2.25	0.68
62:AI:57:ARG:NH2	69:AP:75:LEU:HD11	2.07	0.68
68:AO:57:VAL:O	68:AO:94:TYR:OH	2.10	0.68
1:A:118:GLU:OE2	28:1:2158:A:O2'	2.12	0.68
13:N:93:LYS:NZ	28:1:276:U:O2	2.27	0.68
51:u:249:ALA:HA	56:z:71:PHE:CE1	2.28	0.68
13:N:73:ARG:NH1	28:1:33:G:OP1	2.27	0.68
25:Z:17:ARG:NH2	25:Z:18:TYR:OH	2.27	0.68
46:2:14:C:OP2	49:s:203:LYS:NZ	2.26	0.68
74:AV:153:GLN:NE2	74:AV:154:VAL:O	2.26	0.68
75:AX:8:U:O2'	75:AX:46:G:N2	2.27	0.68
14:O:178:VAL:O	14:O:182:ASN:ND2	2.26	0.68
28:1:451:U:O2'	28:1:487:U:OP2	2.12	0.68
28:1:2761:G:OP2	44:o:87:ARG:NH2	2.27	0.68
46:2:621:A:O2'	46:2:622:A:OP1	2.11	0.68
46:2:1755:A:O2'	46:2:1756:A:OP2	2.12	0.68
51:u:22:LYS:HZ1	56:z:6:ARG:CA	2.05	0.68
28:1:999:G:N3	28:1:1002:A:N6	2.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:1120:U:O2	46:2:1127:G:O6	2.11	0.68
64:AK:82:TYR:CD2	73:AT:50:ILE:CA	2.77	0.68
28:1:767:U:O2'	28:1:768:C:O4'	2.10	0.68
43:n:3:ALA:HA	46:2:1028:C:C4'	2.22	0.68
43:n:5:TRP:HZ3	70:AQ:8:ASN:CG	1.98	0.68
46:2:1419:G:C2'	73:AT:54:LYS:CE	2.72	0.68
4:D:28:THR:O	28:1:2703:A:N6	2.26	0.68
28:1:2530:G:N2	28:1:2546:C:OP2	2.26	0.68
30:4:57:C:OP2	40:j:68:LYS:NZ	2.27	0.68
46:2:767:U:C2	56:z:143:ILE:HG22	2.29	0.68
50:t:222:VAL:HG11	74:AV:192:PHE:CD1	2.29	0.68
63:AJ:125:SER:OG	63:AJ:127:ASN:OD1	2.12	0.68
8:H:31:ARG:NH2	8:H:84:LYS:O	2.27	0.68
46:2:1218:G:N2	46:2:1259:U:OP2	2.26	0.68
13:N:147:ARG:NE	28:1:113:C:OP1	2.27	0.67
28:1:760:G:H21	28:1:771:A:H62	1.41	0.67
43:n:15:ARG:HH21	46:2:979:A:N6	1.91	0.67
4:D:226:TYR:O	4:D:230:ASP:N	2.27	0.67
28:1:2189:U:O3'	45:p:21:SER:OG	2.12	0.67
28:1:2545:C:O2'	28:1:2547:A:O2'	2.11	0.67
6:F:41:ARG:NH2	28:1:597:G:O5'	2.28	0.67
28:1:618:C:O2'	28:1:620:U:O2	2.11	0.67
46:2:58:U:O2	46:2:89:G:O6	2.12	0.67
46:2:1632:C:O2	46:2:1635:A:O2'	2.11	0.67
28:1:727:G:OP2	28:1:742:G:N2	2.26	0.67
28:1:2531:C:N4	28:1:2547:A:OP1	2.27	0.67
46:2:1555:A:OP1	59:AF:47:ARG:NH2	2.27	0.67
46:2:97:C:O2	46:2:425:A:O2'	2.12	0.67
16:Q:8:LYS:NZ	28:1:949:C:O2'	2.28	0.67
17:R:176:ARG:NH1	46:2:853:G:OP2	2.28	0.67
28:1:1566:A:H2'	28:1:1567:U:C6	2.29	0.67
44:o:2:VAL:N	44:o:90:HIS:O	2.27	0.67
52:v:29:ILE:HG21	60:AG:57:LEU:HD21	1.76	0.67
2:B:316:GLU:OE1	2:B:318:LYS:NZ	2.28	0.67
4:D:50:ARG:NH1	4:D:147:ASP:OD1	2.27	0.67
26:AA:74:GLU:OE1	26:AA:77:ARG:NH1	2.27	0.67
28:1:2257:C:H41	46:2:1755:A:H61	1.42	0.67
63:AJ:97:SER:O	63:AJ:101:ASN:ND2	2.28	0.67
43:n:7:LYS:NZ	46:2:624:G:C5'	2.57	0.67
46:2:1157:A:O2'	46:2:1285:U:O2	2.13	0.67
74:AV:170:ILE:HG23	74:AV:202:LEU:HD21	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:96:G:O6	46:2:387:A:N1	2.28	0.67
46:2:105:A:N6	46:2:308:C:C2	2.63	0.67
64:AK:82:TYR:HE2	73:AT:50:ILE:CG2	1.98	0.67
6:F:48:ASN:ND2	6:F:182:ASP:OD2	2.28	0.66
28:1:1626:U:O4	28:1:1816:A:N6	2.28	0.66
46:2:1199:G:C5	64:AK:71:PRO:HG2	2.30	0.66
24:Y:42:GLN:O	24:Y:125:LYS:NZ	2.25	0.66
43:n:18:ARG:HE	46:2:1023:A:C5'	2.08	0.66
66:AM:22:LYS:HZ1	71:AR:4:VAL:HG12	1.60	0.66
2:B:215:ILE:HD12	2:B:338:LEU:HD12	1.77	0.66
10:J:43:GLN:NE2	29:3:39:C:O2	2.29	0.66
28:1:734:C:O2'	28:1:735:A:OP1	2.10	0.66
28:1:1055:A:N3	29:3:81:U:O2'	2.28	0.66
45:p:44:LYS:NZ	45:p:59:CYS:SG	2.66	0.66
64:AK:80:GLU:CG	73:AT:52:PHE:HE2	1.75	0.66
46:2:773:C:O2	46:2:787:G:N2	2.28	0.66
5:E:17:ALA:O	28:1:591:G:O2'	2.14	0.66
62:AI:11:PHE:CE2	69:AP:41:ILE:HG21	2.31	0.66
46:2:39:A:O5'	56:z:8:TYR:OH	2.11	0.66
46:2:1545:A:H5''	62:AI:133:VAL:HG21	1.76	0.66
46:2:1601:G:OP1	63:AJ:90:PRO:CD	2.44	0.66
28:1:1157:G:O2'	28:1:1169:A:N3	2.26	0.66
46:2:1203:A:N6	46:2:1553:G:H21	1.93	0.66
46:2:1409:G:O2'	46:2:1411:A:OP2	2.08	0.66
51:u:22:LYS:HZ2	56:z:6:ARG:HA	1.57	0.66
28:1:1517:G:OP2	42:l:41:ARG:NH2	2.29	0.66
46:2:434:G:N2	46:2:437:A:OP2	2.29	0.66
46:2:1542:G:N2	46:2:1568:C:O2'	2.26	0.66
64:AK:80:GLU:HB3	73:AT:52:PHE:CD2	2.31	0.66
10:J:6:GLN:O	10:J:10:ARG:NH2	2.29	0.65
52:v:188:LYS:NZ	69:AP:63:SER:HA	2.11	0.65
28:1:2717:U:O3'	44:o:13:LYS:NZ	2.29	0.65
46:2:125:U:OP1	46:2:126:A:O2'	2.07	0.65
51:u:17:HIS:ND1	51:u:107:GLY:O	2.29	0.65
51:u:27:TYR:CE2	56:z:2:PRO:HG3	2.30	0.65
11:L:157:ARG:O	31:a:99:ALA:N	2.29	0.65
46:2:537:G:O2'	46:2:538:A:OP1	2.14	0.65
44:o:7:THR:O	44:o:22:GLN:NE2	2.29	0.65
46:2:1367:G:C5'	63:AJ:119:LYS:NZ	2.59	0.65
3:C:314:LYS:NZ	6:F:150:LYS:O	2.30	0.65
10:J:43:GLN:NE2	10:J:70:THR:O	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:2185:G:O2'	28:1:2314:U:OP2	2.15	0.65
46:2:444:C:H42	46:2:460:A:N6	1.94	0.65
46:2:1264:G:O2'	46:2:1443:U:O4	2.11	0.65
47:q:41:ARG:HH11	61:AH:105:GLN:HG3	1.61	0.65
1:A:79:ASN:ND2	1:A:166:ILE:O	2.29	0.65
6:F:103:LEU:HD23	6:F:130:ILE:HD11	1.79	0.65
7:G:241:LYS:NZ	28:1:2588:U:OP1	2.30	0.65
14:O:54:TYR:OH	14:O:73:PHE:O	2.15	0.65
27:AB:67:ARG:NE	46:2:114:C:O2'	2.30	0.65
28:1:1605:A:O2'	28:1:1607:U:OP2	2.14	0.65
46:2:1679:G:N2	46:2:1721:A:OP2	2.26	0.65
54:x:96:ARG:NH1	54:x:115:SER:O	2.29	0.65
28:1:3353:G:O2'	28:1:3355:U:OP2	2.09	0.65
46:2:1216:C:N4	46:2:1446:A:OP2	2.29	0.65
62:AI:123:ARG:O	62:AI:127:HIS:ND1	2.30	0.65
51:u:26:CYS:HA	56:z:2:PRO:HA	1.73	0.65
28:1:733:G:N2	28:1:736:A:OP2	2.29	0.65
43:n:7:LYS:CD	46:2:1027:A:N7	2.60	0.65
64:AK:80:GLU:CB	73:AT:52:PHE:CD2	2.79	0.65
28:1:348:A:N3	28:1:352:A:O2'	2.30	0.64
28:1:953:G:OP2	32:b:11:ASN:ND2	2.29	0.64
46:2:913:G:OP1	46:2:913:G:N2	2.25	0.64
49:s:174:ARG:HB2	56:z:97:LEU:CG	2.25	0.64
47:q:6:THR:CG2	65:AL:41:GLU:OE1	2.45	0.64
64:AK:83:GLU:H	73:AT:51:GLY:CA	2.06	0.64
66:AM:22:LYS:NZ	71:AR:4:VAL:HG13	2.11	0.64
43:n:3:ALA:HA	46:2:1028:C:O4'	1.98	0.64
51:u:100:ARG:NH2	51:u:118:GLU:O	2.29	0.64
54:x:170:GLN:NE2	54:x:181:ILE:O	2.29	0.64
74:AV:174:ASN:ND2	74:AV:199:ILE:O	2.30	0.64
13:N:157:LYS:O	13:N:162:ARG:NH1	2.31	0.64
16:Q:151:ARG:NH1	28:1:781:G:OP1	2.29	0.64
30:4:58:G:O2'	30:4:100:U:O2	2.15	0.64
46:2:326:G:O6	46:2:337:G:O6	2.16	0.64
60:AG:140:LYS:O	64:AK:74:GLU:N	2.30	0.64
62:AI:40:ARG:HD2	63:AJ:45:MET:HE2	1.77	0.64
28:1:2678:A:C2	75:AZ:56:C:C4	2.85	0.64
28:1:2771:U:OP2	28:1:2772:C:N4	2.30	0.64
28:1:3024:A:N6	28:1:3031:G:O2'	2.28	0.64
70:AQ:23:CYS:O	70:AQ:27:SER:HA	1.98	0.64
28:1:837:A:OP2	45:p:4:ARG:NE	2.26	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:3024:A:OP2	28:1:3031:G:N2	2.31	0.64
28:1:3109:G:O6	28:1:3125:U:O2	2.16	0.64
40:j:26:SER:OG	40:j:34:CYS:SG	2.55	0.64
43:n:11:ARG:HB3	46:2:1025:A:O2'	1.97	0.64
68:AO:19:ALA:O	68:AO:77:ASN:ND2	2.30	0.64
28:1:2543:U:O2'	28:1:2544:U:OP1	2.13	0.64
41:k:2:ALA:N	41:k:51:LEU:O	2.30	0.64
28:1:1574:C:H2'	28:1:1575:A:H8	1.63	0.64
46:2:142:G:C6	46:2:173:A:N6	2.65	0.64
43:n:11:ARG:HD2	46:2:1025:A:H4'	0.64	0.64
46:2:779:U:O2'	46:2:782:U:OP2	2.16	0.64
46:2:1211:A:H1'	59:AF:97:TYR:OH	1.98	0.64
4:D:72:ASP:O	29:3:115:G:N2	2.31	0.63
15:P:64:ASN:O	15:P:80:LYS:NZ	2.28	0.63
44:o:61:LYS:NZ	44:o:63:LYS:O	2.30	0.63
46:2:825:U:O4'	46:2:848:C:N4	2.27	0.63
46:2:1162:C:C5	72:AS:24:GLY:CA	2.81	0.63
46:2:1544:U:P	62:AI:132:ARG:HH11	2.11	0.63
54:x:32:PRO:HB2	54:x:38:LEU:HD11	1.80	0.63
74:AV:209:THR:OG1	74:AV:224:ASN:OD1	2.16	0.63
75:AZ:8:U:O2'	75:AZ:46:G:N2	2.30	0.63
9:I:158:LYS:NZ	28:1:2852:C:N3	2.45	0.63
17:R:135:LYS:NZ	28:1:1949:G:OP2	2.29	0.63
30:4:103:G:OP2	30:4:105:A:O2'	2.16	0.63
47:q:134:LYS:O	47:q:137:SER:OG	2.09	0.63
51:u:252:ARG:NH1	56:z:78:ARG:CZ	2.61	0.63
28:1:2305:G:OP2	28:1:2305:G:N2	2.28	0.63
43:n:10:THR:HG1	46:2:1026:A:C2'	2.01	0.63
64:AK:69:LYS:CE	73:AT:31:ILE:CG2	2.75	0.63
64:AK:82:TYR:CD2	73:AT:50:ILE:HG22	2.30	0.63
28:1:937:G:N2	28:1:961:C:OP1	2.31	0.63
46:2:825:U:OP2	46:2:842:C:N4	2.32	0.63
46:2:1301:U:O5'	49:s:88:LYS:HE3	1.99	0.63
64:AK:80:GLU:CD	73:AT:52:PHE:CE2	2.77	0.63
2:B:124:LYS:NZ	28:1:3297:U:O4	2.31	0.63
28:1:2137:U:OP2	28:1:2142:A:N6	2.31	0.63
28:1:3110:C:N3	28:1:3124:G:N1	2.47	0.63
46:2:1482:C:N4	46:2:1607:G:O2'	2.32	0.63
21:V:63:LYS:NZ	28:1:2295:A:OP1	2.32	0.63
28:1:2196:C:O2'	28:1:2270:A:N3	2.27	0.63
66:AM:12:ASN:OD1	66:AM:16:ASN:ND2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:490:C:OP2	46:2:492:A:N6	2.30	0.63
46:2:1334:U:H1'	73:AT:56:ARG:HE	1.64	0.63
46:2:1543:A:O2'	62:AI:136:GLN:HG2	1.98	0.63
46:2:1638:G:O6	46:2:1767:G:N2	2.31	0.63
64:AK:69:LYS:CE	73:AT:33:LYS:CB	2.76	0.63
24:Y:27:ARG:NH1	24:Y:76:LEU:O	2.32	0.62
43:n:5:TRP:CD1	70:AQ:12:LYS:HZ1	2.14	0.62
61:AH:52:GLY:O	61:AH:55:THR:OG1	2.11	0.62
46:2:65:A:OP1	53:w:136:LYS:NZ	2.32	0.62
51:u:249:ALA:HA	56:z:71:PHE:CD1	2.33	0.62
7:G:30:THR:OG1	28:1:2562:A:O3'	2.15	0.62
43:n:11:ARG:HD2	46:2:1025:A:O4'	1.95	0.62
46:2:468:A:OP1	46:2:470:A:N6	2.32	0.62
46:2:541:A:O2'	46:2:542:A:N3	2.31	0.62
13:N:119:TYR:OH	13:N:131:GLU:OE2	2.12	0.62
14:O:101:ARG:NH2	28:1:3172:A:O2'	2.32	0.62
28:1:2800:G:O6	31:a:42:ARG:NH2	2.32	0.62
43:n:11:ARG:CB	46:2:1025:A:O2'	2.46	0.62
46:2:646:C:O2'	46:2:650:U:O4	2.14	0.62
1:A:97:ASN:OD1	1:A:100:ASN:ND2	2.33	0.62
28:1:1310:G:HO2'	28:1:2380:U:HO2'	1.45	0.62
46:2:1215:C:H4'	73:AT:7:TRP:HZ2	1.65	0.62
28:1:523:A:N6	28:1:569:A:C2	2.66	0.62
46:2:444:C:OP2	68:AO:105:ARG:NH1	2.33	0.62
49:s:176:SER:HB3	56:z:57:ARG:HH11	1.63	0.62
62:AI:57:ARG:NH2	69:AP:75:LEU:CD1	2.61	0.62
14:O:83:ALA:O	28:1:1312:C:O2'	2.17	0.62
28:1:1750:A:OP1	41:k:44:LYS:NZ	2.23	0.62
43:n:7:LYS:HG2	46:2:1027:A:H3'	1.82	0.62
28:1:3216:G:O6	28:1:3261:C:N4	2.32	0.62
43:n:5:TRP:CH2	46:2:1791:A:OP1	2.53	0.62
50:t:16:VAL:HG23	73:AT:46:LYS:HE3	1.80	0.62
28:1:2109:U:HO2'	28:1:3363:U:HO2'	1.45	0.62
46:2:1585:U:O2'	46:2:1586:A:OP1	2.12	0.62
49:s:49:LYS:NZ	49:s:243:TYR:O	2.33	0.62
64:AK:82:TYR:CD2	73:AT:50:ILE:C	2.78	0.62
28:1:1567:U:C5	28:1:1568:U:H1'	2.34	0.62
46:2:610:G:O2'	46:2:613:G:O3'	2.17	0.62
46:2:748:U:OP1	66:AM:82:LYS:NZ	2.28	0.62
46:2:762:A:O4'	56:z:79:ARG:NH1	2.33	0.62
46:2:886:U:O2'	58:AE:121:VAL:O	2.18	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:244:ARG:NH1	28:1:2981:U:OP2	2.33	0.61
7:G:105:LYS:NZ	28:1:121:A:O2'	2.33	0.61
13:N:143:ARG:NH2	38:h:90:ARG:O	2.33	0.61
28:1:1630:U:O4	28:1:1812:G:O2'	2.15	0.61
28:1:2323:G:O2'	28:1:2325:G:OP2	2.19	0.61
35:e:42:VAL:O	35:e:52:GLN:NE2	2.32	0.61
3:C:361:HIS:O	18:S:26:ARG:NH2	2.34	0.61
12:M:20:VAL:O	12:M:66:THR:OG1	2.18	0.61
43:n:5:TRP:CZ3	70:AQ:8:ASN:CG	2.74	0.61
43:n:6:ARG:N	46:2:1027:A:C3'	2.57	0.61
10:J:37:LEU:O	10:J:41:SER:OG	2.12	0.61
28:1:2678:A:C2	75:AZ:56:C:C2	2.88	0.61
46:2:50:C:OP1	46:2:423:G:N2	2.33	0.61
46:2:1418:G:H21	73:AT:56:ARG:HB2	1.64	0.61
51:u:26:CYS:CA	56:z:2:PRO:CA	2.72	0.61
63:AJ:90:PRO:O	63:AJ:92:LYS:NZ	2.34	0.61
64:AK:82:TYR:CG	73:AT:50:ILE:O	2.53	0.61
46:2:1367:G:H5''	63:AJ:119:LYS:HZ2	1.65	0.61
49:s:174:ARG:HH11	56:z:97:LEU:HD23	1.64	0.61
28:1:2255:A:N6	28:1:2261:G:O3'	2.34	0.61
2:B:10:ARG:NH1	2:B:11:HIS:O	2.33	0.61
46:2:96:G:N1	46:2:387:A:C2	2.69	0.61
46:2:372:G:O2'	46:2:611:U:O4	2.17	0.61
46:2:1175:U:O4	62:AI:140:THR:HG21	2.01	0.61
61:AH:21:TYR:OH	61:AH:70:SER:O	2.12	0.61
9:I:50:VAL:HG12	9:I:167:LEU:HA	1.82	0.61
28:1:2844:C:O2'	28:1:2846:U:O2'	2.17	0.61
43:n:9:ARG:HG2	46:2:1789:G:C6	2.29	0.61
46:2:1471:A:N6	46:2:1535:U:OP1	2.33	0.61
28:1:2874:G:O2'	28:1:2875:U:OP1	2.12	0.61
68:AO:15:ASN:O	68:AO:19:ALA:N	2.33	0.61
4:D:2:ALA:N	10:J:150:ASN:OD1	2.34	0.61
28:1:2506:U:HO2'	28:1:2507:C:P	2.24	0.61
43:n:7:LYS:CA	46:2:1027:A:C3'	2.78	0.61
50:t:35:SER:OG	50:t:51:ARG:NH2	2.33	0.61
46:2:208:U:O2'	55:y:171:SER:OG	2.10	0.60
50:t:14:ASP:OD1	64:AK:84:MET:HE1	1.99	0.60
16:Q:8:LYS:O	16:Q:11:LYS:NZ	2.29	0.60
43:n:6:ARG:HH22	46:2:1792:G:N2	1.99	0.60
6:F:141:TYR:OH	28:1:578:A:N6	2.35	0.60
43:n:9:ARG:NH1	46:2:1790:A:N7	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:251:A:O2'	51:u:131:LEU:O	2.16	0.60
46:2:1217:A:H5''	73:AT:4:GLU:OE1	2.01	0.60
46:2:1540:G:O2'	46:2:1541:G:O4'	2.12	0.60
46:2:1736:G:O2'	46:2:1737:G:O5'	2.18	0.60
74:AV:74:THR:OG1	74:AV:76:ASP:OD1	2.13	0.60
6:F:30:ARG:NH2	28:1:595:G:OP2	2.35	0.60
28:1:1763:U:O2'	28:1:1764:U:OP1	2.18	0.60
28:1:855:U:O4	45:p:4:ARG:NH1	2.34	0.60
46:2:221:A:N7	46:2:832:U:N3	2.49	0.60
62:AI:52:VAL:HG11	62:AI:61:LEU:HD11	1.84	0.60
20:U:94:ARG:NH1	28:1:1679:A:OP1	2.35	0.60
46:2:240:U:H3	46:2:830:U:HO2'	1.50	0.60
46:2:497:G:O2'	46:2:498:G:N7	2.31	0.60
46:2:1276:U:OP1	50:t:141:LYS:NZ	2.35	0.60
67:AN:23:ARG:NH1	67:AN:26:GLU:OE2	2.35	0.60
67:AN:92:CYS:O	67:AN:96:VAL:HG22	2.02	0.60
75:AZ:16:U:OP1	75:AZ:60:C:N4	2.34	0.60
5:E:149:ILE:HG23	5:E:155:LEU:HD22	1.84	0.60
9:I:33:ILE:HD12	9:I:36:LEU:HD21	1.84	0.60
13:N:103:GLU:OE2	13:N:118:SER:OG	2.17	0.60
18:S:109:ASP:OD2	18:S:113:ARG:NH1	2.34	0.60
28:1:1492:G:O6	42:l:2:ALA:N	2.35	0.60
31:a:56:VAL:HG12	31:a:57:GLY:H	1.67	0.60
46:2:1367:G:C4'	63:AJ:119:LYS:HZ2	2.13	0.60
2:B:291:GLU:OE1	2:B:291:GLU:N	2.35	0.59
21:V:48:ARG:NH1	28:1:3042:U:OP1	2.35	0.59
28:1:2858:U:O2'	28:1:2860:U:O4	2.19	0.59
43:n:8:LYS:HG2	46:2:1789:G:H1'	1.76	0.59
46:2:332:U:OP2	55:y:175:GLN:NE2	2.34	0.59
46:2:856:A:N6	54:x:116:ARG:HG2	2.18	0.59
70:AQ:74:CYS:O	70:AQ:78:ALA:N	2.36	0.59
3:C:107:ARG:O	13:N:203:ARG:NH2	2.35	0.59
28:1:2802:A:N6	44:o:53:GLN:O	2.36	0.59
28:1:166:C:N3	28:1:255:A:N6	2.50	0.59
46:2:740:A:N1	54:x:104:ARG:HD3	2.16	0.59
18:S:43:TYR:OH	29:3:96:U:OP1	2.16	0.59
46:2:331:A:OP2	55:y:172:ARG:NH1	2.35	0.59
46:2:1162:C:C5	72:AS:24:GLY:HA2	2.37	0.59
51:u:22:LYS:NZ	56:z:6:ARG:CA	2.60	0.59
51:u:26:CYS:CA	56:z:2:PRO:HB3	2.33	0.59
15:P:132:ALA:N	28:1:880:G:OP2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:1171:A:C4'	62:AI:144:ARG:CZ	2.78	0.59
46:2:1567:U:C6	62:AI:36:LYS:HE2	2.37	0.59
49:s:174:ARG:HB2	56:z:97:LEU:CD2	2.32	0.59
52:v:188:LYS:HZ2	69:AP:63:SER:HA	1.66	0.59
2:B:111:SER:OG	2:B:112:ASP:N	2.36	0.59
3:C:84:ARG:NH1	28:1:365:A:OP1	2.35	0.59
11:L:62:THR:O	11:L:65:TYR:N	2.35	0.59
15:P:25:SER:O	15:P:29:THR:OG1	2.10	0.59
46:2:154:G:O6	46:2:160:C:O2'	2.20	0.59
46:2:622:A:OP1	46:2:1106:U:O2'	2.20	0.59
46:2:1553:G:O6	59:AF:43:ARG:NH1	2.35	0.59
68:AO:78:SER:OG	68:AO:81:GLU:OE2	2.20	0.59
26:AA:50:THR:HG22	26:AA:55:VAL:HG11	1.84	0.59
46:2:294:C:O2'	46:2:295:A:O4'	2.18	0.59
60:AG:34:SER:OG	63:AJ:7:ARG:NH2	2.36	0.59
64:AK:35:GLU:O	64:AK:39:SER:OG	2.12	0.59
65:AL:17:CYS:SG	65:AL:18:SER:N	2.76	0.59
67:AN:53:VAL:HG22	67:AN:74:VAL:HG22	1.85	0.59
18:S:77:VAL:HG11	18:S:106:LEU:HD22	1.84	0.59
43:n:1:MET:C	46:2:1031:U:C4'	2.71	0.59
46:2:258:C:O4'	55:y:64:ASN:ND2	2.35	0.59
48:r:128:LYS:NZ	48:r:131:ASP:O	2.36	0.59
52:v:216:GLU:OE1	52:v:219:ARG:NH2	2.36	0.59
17:R:68:GLN:OE1	17:R:71:ARG:NH1	2.36	0.58
28:1:1071:U:O2'	28:1:1072:G:O5'	2.15	0.58
43:n:5:TRP:NE1	70:AQ:12:LYS:HE3	2.09	0.58
27:AB:6:THR:O	27:AB:9:SER:OG	2.17	0.58
46:2:1171:A:C3'	62:AI:144:ARG:HD3	2.32	0.58
48:r:113:MET:HE1	48:r:209:ASN:HB2	1.84	0.58
52:v:49:GLU:HG3	52:v:51:VAL:HG13	1.86	0.58
28:1:2830:G:O6	28:1:2859:U:C4	2.56	0.58
46:2:93:A:OP1	51:u:3:ARG:NH1	2.37	0.58
46:2:1272:U:O2	46:2:1274:C:O2'	2.22	0.58
46:2:1335:U:HO2'	46:2:1416:G:H1	1.52	0.58
28:1:240:U:O2'	28:1:242:C:N4	2.35	0.58
52:v:129:PRO:HA	52:v:132:VAL:HG12	1.85	0.58
64:AK:69:LYS:HE2	73:AT:33:LYS:HD2	1.85	0.58
66:AM:102:VAL:O	66:AM:113:HIS:ND1	2.35	0.58
27:AB:88:ARG:NH2	46:2:306:U:OP1	2.37	0.58
46:2:1334:U:C4'	73:AT:55:PHE:CE2	2.87	0.58
64:AK:69:LYS:CE	73:AT:33:LYS:HB2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:8:LYS:H	46:2:1027:A:C5'	2.17	0.58
43:n:9:ARG:HH21	46:2:1789:G:H3'	1.69	0.58
46:2:1553:G:N1	46:2:1556:A:OP2	2.37	0.58
2:B:19:ARG:NH2	28:1:3045:G:OP1	2.37	0.58
28:1:1712:G:OP2	33:c:32:LYS:NZ	2.37	0.58
46:2:1545:A:C5'	62:AI:133:VAL:CG2	2.80	0.58
6:F:208:SER:OG	6:F:209:ASN:N	2.35	0.58
10:J:137:ARG:NH1	29:3:28:C:OP1	2.36	0.58
31:a:76:ASP:OD1	31:a:116:GLY:N	2.36	0.58
46:2:1390:U:O4'	61:AH:3:ARG:NH1	2.37	0.58
51:u:27:TYR:CE2	56:z:2:PRO:CD	2.86	0.58
44:o:34:SER:OG	44:o:35:LEU:N	2.34	0.58
10:J:116:TYR:OH	62:AI:110:ARG:NH1	2.37	0.57
14:O:126:VAL:O	18:S:154:HIS:NE2	2.37	0.57
28:1:240:U:O2	28:1:242:C:N4	2.36	0.57
28:1:939:U:OP2	31:a:26:ARG:NH2	2.37	0.57
46:2:785:U:O4	68:AO:11:LYS:HE3	2.03	0.57
48:r:29:TRP:CZ3	58:AE:13:VAL:HG21	2.39	0.57
48:r:32:ILE:HD12	48:r:43:VAL:HG23	1.86	0.57
9:I:28:ASP:OD2	75:AZ:64:A:C1'	2.50	0.57
28:1:90:C:OP1	31:a:59:ARG:NH1	2.36	0.57
28:1:3109:G:C6	28:1:3125:U:O2	2.57	0.57
46:2:1162:C:C5	72:AS:24:GLY:HA3	2.39	0.57
75:AZ:66:A:N6	75:AZ:67:A:N6	2.52	0.57
46:2:609:U:O4	67:AN:25:ALA:HB3	2.04	0.57
28:1:3216:G:N2	28:1:3264:G:O6	2.37	0.57
43:n:15:ARG:NE	46:2:979:A:N1	2.47	0.57
46:2:100:A:N6	46:2:385:A:N3	2.53	0.57
46:2:777:C:H41	68:AO:10:ARG:HG3	1.68	0.57
50:t:224:ASP:OD2	74:AV:228:LYS:HD2	2.04	0.57
7:G:35:GLY:O	7:G:41:GLN:NE2	2.38	0.57
9:I:56:GLU:OE1	9:I:56:GLU:N	2.37	0.57
28:1:86:G:O2'	28:1:98:G:O6	2.17	0.57
43:n:7:LYS:HZ2	46:2:624:G:C5'	2.14	0.57
46:2:94:U:OP1	51:u:4:GLY:CA	2.52	0.57
46:2:1645:G:O2'	46:2:1646:C:O4'	2.18	0.57
51:u:26:CYS:CA	56:z:2:PRO:HA	2.33	0.57
62:AI:7:GLU:N	62:AI:7:GLU:OE1	2.38	0.57
9:I:42:THR:OG1	9:I:45:GLU:OE1	2.12	0.57
48:r:90:GLU:OE1	48:r:90:GLU:N	2.38	0.57
28:1:69:C:O2'	28:1:101:G:O2'	2.23	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:1359:C:OP1	63:AJ:129:GLN:HB3	2.05	0.57
64:AK:80:GLU:CD	73:AT:52:PHE:HE2	2.11	0.57
64:AK:83:GLU:N	73:AT:51:GLY:HA3	2.09	0.57
28:1:1574:C:H2'	28:1:1575:A:C8	2.39	0.57
51:u:27:TYR:H	56:z:2:PRO:HB3	1.67	0.57
64:AK:67:THR:HG21	73:AT:33:LYS:CE	2.35	0.57
15:P:131:ARG:NH1	15:P:137:ASN:OD1	2.37	0.57
43:n:15:ARG:HH11	46:2:1025:A:H2	1.53	0.57
46:2:1035:G:O2'	66:AM:2:THR:O	2.17	0.57
46:2:1367:G:H4'	63:AJ:119:LYS:NZ	2.20	0.57
47:q:62:ARG:HH21	65:AL:37:ALA:C	2.12	0.57
52:v:56:ALA:HB3	52:v:138:THR:HG21	1.86	0.57
27:AB:11:ARG:O	55:y:195:ARG:NH2	2.37	0.57
46:2:1160:A:O2'	46:2:1620:C:N3	2.33	0.57
46:2:1218:G:N2	46:2:1444:A:N7	2.53	0.57
57:AD:99:ARG:NH2	57:AD:143:SER:OG	2.36	0.57
60:AG:59:LYS:HD3	60:AG:89:LEU:HD13	1.86	0.57
40:j:33:THR:OG1	40:j:39:TYR:O	2.15	0.56
46:2:1000:C:N4	46:2:1005:A:N7	2.52	0.56
46:2:1367:G:C3'	63:AJ:119:LYS:NZ	2.66	0.56
48:r:121:ILE:HD12	48:r:161:ILE:HG23	1.87	0.56
71:AR:42:ASN:ND2	71:AR:57:GLU:OE1	2.38	0.56
28:1:1566:A:O5'	28:1:1566:A:H8	1.86	0.56
43:n:4:LYS:HZ3	46:2:940:A:H5'	1.70	0.56
43:n:18:ARG:HE	46:2:1023:A:H5'	1.70	0.56
46:2:767:U:O2	56:z:143:ILE:CG2	2.53	0.56
46:2:1353:U:O2'	46:2:1373:C:O2	2.22	0.56
63:AJ:43:ASN:ND2	63:AJ:45:MET:O	2.38	0.56
4:D:184:ASP:OD2	4:D:187:THR:OG1	2.22	0.56
46:2:1334:U:H1'	73:AT:55:PHE:CE2	2.31	0.56
51:u:26:CYS:C	56:z:2:PRO:HB3	2.29	0.56
66:AM:83:ILE:HA	66:AM:86:ILE:HD12	1.86	0.56
71:AR:59:CYS:O	71:AR:61:THR:HG23	2.05	0.56
5:E:129:GLU:OE1	5:E:129:GLU:N	2.38	0.56
11:L:46:ILE:HD11	11:L:49:ARG:CZ	2.36	0.56
17:R:181:ARG:NH1	17:R:182:ASP:OD1	2.37	0.56
26:AA:59:PHE:HE1	46:2:1434:U:O2	1.89	0.56
28:1:1523:U:OP2	28:1:1604:G:O2'	2.24	0.56
62:AI:12:GLN:NE2	62:AI:13:HIS:O	2.38	0.56
66:AM:111:MET:HE1	66:AM:119:LYS:HD2	1.87	0.56
28:1:2307:G:O2'	28:1:2310:U:OP2	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:688:G:OP2	46:2:693:U:N3	2.38	0.56
46:2:277:U:OP1	46:2:281:G:N2	2.39	0.56
47:q:62:ARG:NH2	65:AL:37:ALA:O	2.38	0.56
71:AR:40:CYS:SG	71:AR:41:LEU:N	2.78	0.56
28:1:439:C:OP2	28:1:441:U:N3	2.39	0.56
43:n:5:TRP:O	46:2:1027:A:C5'	2.51	0.56
46:2:130:C:N4	46:2:178:U:O2'	2.38	0.56
46:2:792:U:OP2	51:u:187:ARG:NH2	2.38	0.56
4:D:107:ARG:NH2	4:D:119:TYR:O	2.38	0.56
28:1:1576:G:H2'	28:1:1577:G:H5''	1.88	0.56
46:2:771:A:H5''	56:z:6:ARG:CD	2.35	0.56
46:2:828:U:O4	46:2:844:A:N6	2.36	0.56
47:q:56:LYS:HB3	47:q:160:ILE:HG22	1.87	0.56
21:V:32:ARG:NH1	46:2:1734:U:O3'	2.39	0.56
27:AB:121:ASP:O	27:AB:123:VAL:HG13	2.04	0.56
46:2:1367:G:H5''	63:AJ:119:LYS:NZ	2.21	0.56
55:y:8:ARG:O	55:y:18:ARG:NH2	2.39	0.56
2:B:56:ILE:HD11	2:B:356:LEU:HD22	1.87	0.56
46:2:1543:A:H2'	62:AI:132:ARG:NH1	2.21	0.56
54:x:14:THR:OG1	54:x:15:GLU:OE2	2.23	0.56
24:Y:24:SER:OG	24:Y:75:ARG:NH1	2.38	0.55
28:1:1482:A:OP2	28:1:1858:A:O2'	2.24	0.55
43:n:10:THR:CB	46:2:1026:A:C3'	2.82	0.55
1:A:137:ILE:HD11	1:A:149:ARG:HB2	1.88	0.55
28:1:1952:G:O4'	28:1:2095:G:N2	2.39	0.55
43:n:19:LYS:HD2	46:2:1022:C:O2'	2.06	0.55
46:2:1162:C:C6	72:AS:24:GLY:HA3	2.41	0.55
74:AV:314:GLN:OE1	74:AV:314:GLN:N	2.38	0.55
28:1:831:G:O2'	28:1:1864:A:N3	2.33	0.55
46:2:1375:A:C2	60:AG:8:GLN:HB2	2.41	0.55
46:2:1570:A:H5''	62:AI:144:ARG:NH1	2.14	0.55
66:AM:22:LYS:HZ3	71:AR:4:VAL:CG1	2.20	0.55
46:2:609:U:O3'	67:AN:19:ARG:NH2	2.39	0.55
73:AT:28:THR:OG1	73:AT:29:GLY:N	2.39	0.55
27:AB:105:LYS:NZ	46:2:306:U:OP2	2.26	0.55
43:n:5:TRP:CG	46:2:1029:U:OP1	2.57	0.55
47:q:7:PHE:HE2	65:AL:40:ASP:HA	1.71	0.55
49:s:144:TRP:CH2	56:z:61:THR:HG22	2.41	0.55
55:y:41:LYS:N	55:y:59:ARG:O	2.40	0.55
69:AP:93:SER:HB2	69:AP:100:ILE:HD11	1.89	0.55
48:r:32:ILE:CD1	48:r:43:VAL:HG23	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:w:41:VAL:HG21	53:w:46:LYS:HA	1.88	0.55
2:B:218:ILE:HG23	2:B:337:THR:OG1	2.07	0.55
28:1:431:U:OP1	36:f:65:ARG:NH1	2.39	0.55
46:2:1349:G:N2	46:2:1350:U:O4	2.40	0.55
51:u:105:VAL:HG21	51:u:245:LYS:H	1.72	0.55
62:AI:24:GLY:C	69:AP:41:ILE:CD1	2.67	0.55
63:AJ:5:SER:OG	63:AJ:6:VAL:N	2.40	0.55
28:1:2282:U:OP1	28:1:2973:G:O2'	2.22	0.55
34:d:12:TYR:CD2	34:d:75:ILE:HD12	2.42	0.55
60:AG:142:TYR:CD2	64:AK:75:GLY:HA3	2.41	0.55
46:2:99:C:OP2	46:2:378:A:O2'	2.12	0.55
46:2:765:G:N2	56:z:146:PHE:O	2.37	0.55
46:2:1367:G:C3'	63:AJ:119:LYS:HZ1	2.19	0.55
16:Q:2:GLY:N	28:1:1333:C:OP1	2.40	0.55
28:1:68:C:OP2	28:1:301:G:N2	2.40	0.55
28:1:1223:A:OP2	28:1:1225:A:N6	2.27	0.55
28:1:1568:U:HO2'	28:1:1570:U:HO2'	1.51	0.55
43:n:2:ARG:N	46:2:1031:U:C5'	2.60	0.55
43:n:10:THR:CG2	46:2:1026:A:H2'	2.26	0.55
48:r:72:ASP:HB3	58:AE:114:ARG:NH2	2.22	0.55
49:s:57:PHE:HB3	65:AL:12:TYR:OH	2.07	0.55
11:L:76:THR:OG1	11:L:101:ARG:NH2	2.41	0.54
66:AM:22:LYS:CE	71:AR:3:LEU:O	2.54	0.54
67:AN:8:GLY:O	67:AN:11:SER:OG	2.23	0.54
4:D:293:LEU:HD22	9:I:210:ILE:HG23	1.88	0.54
17:R:68:GLN:NE2	17:R:72:GLU:OE2	2.40	0.54
28:1:775:A:O2'	28:1:777:U:OP2	2.22	0.54
28:1:3106:A:C5	28:1:3128:G:N2	2.75	0.54
46:2:817:A:N3	46:2:855:A:N6	2.55	0.54
60:AG:34:SER:OG	63:AJ:7:ARG:CZ	2.56	0.54
28:1:3104:U:N3	28:1:3128:G:O6	2.40	0.54
30:4:37:A:OP1	38:h:89:ARG:NH2	2.37	0.54
45:p:38:ASP:OD1	45:p:38:ASP:N	2.39	0.54
49:s:173:PRO:HG2	56:z:57:ARG:CD	2.37	0.54
49:s:173:PRO:CG	56:z:57:ARG:NE	2.69	0.54
64:AK:67:THR:CG2	73:AT:33:LYS:CG	2.66	0.54
64:AK:67:THR:HG22	73:AT:33:LYS:HG3	1.83	0.54
28:1:2842:U:O4	28:1:2898:G:N2	2.40	0.54
46:2:311:U:OP2	67:AN:20:ARG:NH1	2.41	0.54
46:2:641:G:O6	46:2:693:U:O2'	2.24	0.54
50:t:16:VAL:HG23	73:AT:46:LYS:CE	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:v:163:SER:OG	72:AS:47:PRO:O	2.11	0.54
7:G:157:VAL:HG23	7:G:159:PRO:HD2	1.89	0.54
46:2:1055:U:C2	46:2:1064:G:O6	2.60	0.54
50:t:8:LYS:HB3	64:AK:65:ILE:HD11	1.88	0.54
52:v:40:ILE:HG23	52:v:42:LEU:CD2	2.37	0.54
19:T:88:ARG:O	28:1:2722:U:O2'	2.24	0.54
28:1:1374:G:N7	31:a:10:LYS:NZ	2.56	0.54
34:d:75:ILE:HG12	34:d:93:VAL:HG12	1.90	0.54
43:n:10:THR:CG2	46:2:1772:C:N3	2.69	0.54
46:2:51:A:OP2	46:2:424:C:N4	2.41	0.54
46:2:142:G:N1	46:2:173:A:N6	2.56	0.54
47:q:122:ILE:HG22	47:q:144:ILE:CG2	2.37	0.54
28:1:1000:C:O2	28:1:1046:A:N6	2.41	0.54
43:n:7:LYS:HD2	46:2:1027:A:N7	2.22	0.54
24:Y:2:ALA:N	28:1:212:G:OP2	2.41	0.54
28:1:1574:C:C2	28:1:1575:A:C8	2.96	0.54
28:1:2256:A:N6	28:1:2261:G:C2	2.75	0.54
46:2:1512:G:N3	46:2:1518:C:O2'	2.39	0.54
51:u:27:TYR:CD2	56:z:2:PRO:HG3	2.42	0.54
64:AK:69:LYS:HD2	73:AT:31:ILE:HG21	1.89	0.54
66:AM:22:LYS:HE2	71:AR:3:LEU:O	2.07	0.54
4:D:10:SER:OG	29:3:66:A:O2'	2.20	0.54
28:1:733:G:O3'	28:1:735:A:N6	2.41	0.54
46:2:214:G:H21	46:2:251:A:H62	1.55	0.54
46:2:1780:G:O2'	46:2:1781:A:O4'	2.24	0.54
62:AI:25:ASN:N	69:AP:41:ILE:HD12	2.23	0.54
1:A:223:SER:OG	28:1:2244:A:O2'	2.26	0.54
4:D:77:ALA:O	4:D:108:ARG:NH1	2.41	0.54
9:I:28:ASP:CG	75:AZ:64:A:O4'	2.48	0.54
14:O:77:SER:OG	14:O:106:GLU:OE2	2.20	0.54
28:1:1575:A:N1	28:1:1576:G:C5	2.76	0.54
43:n:5:TRP:CG	46:2:1028:C:H3'	2.43	0.54
43:n:7:LYS:CD	46:2:624:G:H4'	2.32	0.54
46:2:1545:A:C5'	62:AI:133:VAL:HG21	2.38	0.54
50:t:8:LYS:CB	64:AK:65:ILE:HD11	2.38	0.54
64:AK:67:THR:CG2	73:AT:33:LYS:CE	2.73	0.54
5:E:100:LYS:NZ	5:E:133:GLU:OE1	2.31	0.53
16:Q:36:LEU:O	16:Q:40:THR:HG22	2.08	0.53
33:c:18:ILE:HD13	33:c:81:VAL:O	2.08	0.53
46:2:864:U:OP2	66:AM:57:ARG:NH1	2.41	0.53
46:2:872:G:N2	46:2:1047:G:O2'	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:v:144:GLU:OE1	52:v:225:ARG:NH2	2.41	0.53
69:AP:80:LEU:HD11	69:AP:101:TYR:CE2	2.43	0.53
14:O:125:ARG:HG3	14:O:129:LEU:HD12	1.90	0.53
18:S:169:SER:OG	18:S:170:THR:N	2.41	0.53
21:V:61:THR:OG1	21:V:72:LYS:O	2.21	0.53
28:1:26:A:N3	28:1:328:U:O2'	2.40	0.53
46:2:1162:C:C4	72:AS:24:GLY:HA3	2.43	0.53
66:AM:55:ASP:OD2	66:AM:59:GLY:N	2.40	0.53
3:C:33:ASP:O	3:C:37:THR:HG23	2.08	0.53
8:H:117:PHE:O	8:H:124:ARG:NH2	2.41	0.53
29:3:35:C:N3	29:3:45:A:O2'	2.33	0.53
43:n:18:ARG:HE	46:2:1023:A:H5''	1.74	0.53
46:2:748:U:C2	46:2:802:G:N1	2.76	0.53
14:O:21:SER:OG	28:1:1181:U:O4	2.16	0.53
28:1:3106:A:C6	28:1:3128:G:N2	2.77	0.53
47:q:112:THR:O	47:q:114:SER:N	2.41	0.53
74:AV:157:VAL:O	74:AV:168:THR:OG1	2.24	0.53
28:1:2901:G:N2	28:1:3030:G:N3	2.56	0.53
43:n:8:LYS:CD	46:2:977:A:N3	2.68	0.53
43:n:11:ARG:HD2	46:2:1025:A:C1'	2.39	0.53
46:2:46:A:N6	46:2:433:C:O2'	2.42	0.53
46:2:96:G:C6	46:2:387:A:N1	2.77	0.53
66:AM:81:VAL:HG22	66:AM:125:ILE:HD11	1.91	0.53
10:J:171:VAL:HG13	10:J:172:LEU:HD12	1.89	0.53
15:P:25:SER:OG	28:1:1447:G:N7	2.41	0.53
15:P:127:ARG:NH1	28:1:1508:C:OP1	2.42	0.53
26:AA:58:GLN:CG	50:t:28:GLU:OE2	2.57	0.53
46:2:518:A:O2'	46:2:519:C:O5'	2.27	0.53
46:2:761:G:O2'	46:2:763:G:N2	2.41	0.53
46:2:918:U:O2'	58:AE:18:ARG:NH1	2.41	0.53
46:2:918:U:O3'	58:AE:18:ARG:NH1	2.41	0.53
46:2:1299:G:O2'	49:s:99:LYS:NZ	2.37	0.53
49:s:57:PHE:CB	65:AL:12:TYR:OH	2.56	0.53
51:u:9:LEU:HG	51:u:28:ALA:HB3	1.89	0.53
65:AL:7:GLN:NE2	65:AL:8:LEU:O	2.42	0.53
28:1:1841:A:N3	42:l:45:ARG:NH2	2.56	0.53
43:n:9:ARG:HA	46:2:1789:G:C4	2.43	0.53
43:n:9:ARG:CA	46:2:1789:G:N3	2.63	0.53
46:2:1378:U:O4'	60:AG:10:PHE:CZ	2.62	0.53
57:AD:83:GLU:OE1	57:AD:83:GLU:N	2.41	0.53
64:AK:82:TYR:HD2	73:AT:50:ILE:O	1.80	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:AZ:22:G:N7	75:AZ:46:G:O6	2.41	0.53
26:AA:33:GLU:OE1	26:AA:33:GLU:N	2.41	0.53
28:1:3306:U:O2'	28:1:3308:C:OP2	2.18	0.53
46:2:1120:U:C2	46:2:1127:G:O6	2.62	0.53
46:2:1171:A:H4'	62:AI:144:ARG:HD3	1.88	0.53
62:AI:11:PHE:CE2	69:AP:41:ILE:CG2	2.92	0.53
8:H:90:MET:HE2	8:H:181:VAL:HG22	1.91	0.53
28:1:821:U:O2'	28:1:912:G:OP1	2.25	0.53
36:f:19:SER:OG	36:f:20:LYS:N	2.41	0.53
39:i:45:ARG:NH2	39:i:49:GLY:O	2.42	0.53
43:n:8:LYS:NZ	46:2:977:A:H1'	2.24	0.53
46:2:1409:G:N2	46:2:1412:G:OP2	2.41	0.53
46:2:1610:G:H21	46:2:1611:A:H61	1.56	0.53
55:y:87:ASN:ND2	55:y:89:GLU:OE1	2.42	0.53
10:J:60:ARG:HE	44:o:103:ALA:HB1	1.74	0.52
15:P:129:THR:OG1	28:1:1507:G:N7	2.35	0.52
43:n:5:TRP:C	46:2:1027:A:C4'	2.80	0.52
46:2:273:G:O6	46:2:283:U:O2	2.27	0.52
46:2:1181:U:O2'	46:2:1182:U:OP1	2.19	0.52
46:2:1775:U:O2'	46:2:1777:G:OP2	2.16	0.52
60:AG:140:LYS:O	64:AK:73:GLY:CA	2.54	0.52
14:O:110:PRO:O	14:O:112:TYR:N	2.42	0.52
28:1:156:G:O2'	28:1:157:A:O4'	2.23	0.52
28:1:1027:A:O3'	28:1:1030:A:N6	2.43	0.52
43:n:6:ARG:N	46:2:1027:A:H5'	2.23	0.52
49:s:176:SER:HB3	56:z:57:ARG:NH1	2.24	0.52
51:u:95:THR:O	51:u:113:ARG:NH2	2.41	0.52
15:P:18:ARG:NH2	15:P:147:GLU:OE1	2.42	0.52
19:T:137:GLU:N	19:T:137:GLU:OE1	2.41	0.52
28:1:1203:A:OP2	28:1:1301:A:N6	2.35	0.52
28:1:2899:C:H4'	28:1:2903:A:H62	1.74	0.52
46:2:444:C:N4	46:2:459:G:OP2	2.36	0.52
46:2:1070:C:O2'	71:AR:17:ARG:O	2.26	0.52
46:2:1748:G:O2'	46:2:1749:A:O5'	2.15	0.52
50:t:222:VAL:HG13	74:AV:191:ASP:C	2.33	0.52
6:F:34:LYS:NZ	28:1:596:C:OP2	2.29	0.52
28:1:1565:G:C6	28:1:1575:A:C6	2.98	0.52
46:2:1349:G:O2'	46:2:1350:U:O4'	2.15	0.52
75:AX:22:G:N7	75:AX:46:G:O6	2.42	0.52
8:H:28:VAL:HG12	8:H:33:THR:HG22	1.91	0.52
22:W:6:ASP:OD1	22:W:7:SER:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:c:44:ILE:HG22	33:c:89:VAL:HG12	1.91	0.52
46:2:562:G:O2'	46:2:563:U:O5'	2.25	0.52
46:2:565:C:N4	46:2:577:G:O4'	2.42	0.52
46:2:746:A:N1	46:2:804:A:N6	2.58	0.52
49:s:194:GLU:OE1	49:s:194:GLU:N	2.42	0.52
59:AF:30:THR:O	59:AF:34:VAL:HG23	2.10	0.52
5:E:46:ARG:NH2	28:1:3268:A:OP1	2.42	0.52
19:T:35:LYS:NZ	28:1:1084:A:OP1	2.41	0.52
28:1:1198:C:OP2	28:1:1199:C:O2'	2.19	0.52
46:2:1162:C:H5''	72:AS:22:ARG:HD3	1.89	0.52
48:r:78:ASP:OD1	48:r:78:ASP:N	2.43	0.52
65:AL:66:ASP:O	65:AL:70:ASN:ND2	2.42	0.52
16:Q:155:MET:HE2	16:Q:163:PRO:HB3	1.92	0.52
19:T:40:VAL:HG21	19:T:96:ILE:HD11	1.91	0.52
27:AB:122:ILE:O	27:AB:143:SER:OG	2.28	0.52
28:1:266:A:H61	39:i:26:ILE:HG12	1.75	0.52
6:F:214:TRP:O	6:F:216:VAL:HG12	2.10	0.52
11:L:50:PRO:HG3	38:h:118:ILE:HD12	1.92	0.52
18:S:167:ARG:NH2	28:1:3182:G:N7	2.57	0.52
46:2:533:U:OP1	68:AO:31:ASN:ND2	2.42	0.52
46:2:772:G:OP1	56:z:6:ARG:NH2	2.43	0.52
46:2:782:U:H4'	68:AO:12:VAL:HG21	1.91	0.52
46:2:1367:G:H5''	63:AJ:119:LYS:HD2	1.92	0.52
8:H:88:TYR:CE2	8:H:154:VAL:HG12	2.44	0.52
10:J:117:ASP:OD1	10:J:119:SER:OG	2.27	0.52
28:1:1017:C:OP1	28:1:1034:U:N3	2.43	0.52
43:n:8:LYS:CG	46:2:1789:G:C1'	2.75	0.52
46:2:153:G:O2'	53:w:108:VAL:HG22	2.10	0.52
46:2:1570:A:H5'	62:AI:144:ARG:HH22	1.74	0.52
16:Q:144:ARG:NH1	28:1:975:C:O2'	2.43	0.52
28:1:2553:U:O2'	37:g:91:ARG:NH1	2.43	0.52
43:n:5:TRP:C	46:2:1027:A:C5'	2.81	0.52
46:2:879:G:O2'	57:AD:105:ASN:ND2	2.41	0.52
14:O:128:ARG:NH2	28:1:1318:A:OP1	2.44	0.51
28:1:1452:A:N3	28:1:2346:C:O2'	2.36	0.51
28:1:1812:G:N3	28:1:1817:G:O2'	2.42	0.51
54:x:134:GLU:OE2	54:x:155:ASP:N	2.40	0.51
62:AI:25:ASN:HA	69:AP:41:ILE:HB	1.92	0.51
67:AN:28:ASN:OD1	67:AN:32:ARG:NH2	2.42	0.51
43:n:15:ARG:NH2	46:2:979:A:N6	2.58	0.51
46:2:771:A:C5'	56:z:6:ARG:HD3	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:1205:C:OP1	73:AT:16:LYS:NZ	2.44	0.51
46:2:1681:A:N6	46:2:1719:A:N1	2.58	0.51
60:AG:142:TYR:CD1	64:AK:74:GLU:HG2	2.44	0.51
10:J:12:LEU:O	10:J:13:LYS:NZ	2.28	0.51
27:AB:72:THR:HG22	27:AB:122:ILE:HD11	1.92	0.51
33:c:99:ASP:O	33:c:103:THR:OG1	2.25	0.51
11:L:64:LYS:O	11:L:67:ARG:NH1	2.43	0.51
28:1:1523:U:OP1	28:1:1607:U:N3	2.42	0.51
28:1:1566:A:H2'	28:1:1567:U:H6	1.73	0.51
43:n:5:TRP:CH2	70:AQ:8:ASN:OD1	2.63	0.51
46:2:311:U:OP1	67:AN:24:TRP:NE1	2.43	0.51
46:2:1595:U:C5'	73:AT:31:ILE:HD11	2.40	0.51
48:r:52:THR:OG1	48:r:53:GLY:N	2.44	0.51
54:x:46:ILE:HG23	54:x:60:ILE:HG22	1.91	0.51
56:z:85:VAL:HG22	56:z:103:ASP:OD2	2.11	0.51
2:B:256:HIS:NE2	28:1:2941:A:N7	2.59	0.51
4:D:293:LEU:HD22	9:I:210:ILE:HD12	1.91	0.51
28:1:1718:G:OP1	31:a:117:ARG:NH2	2.42	0.51
28:1:2830:G:O6	28:1:2859:U:C5	2.63	0.51
46:2:283:U:C5	53:w:185:GLN:NE2	2.78	0.51
46:2:1170:G:N2	46:2:1571:C:O2'	2.44	0.51
46:2:1199:G:H21	64:AK:72:ASN:HB2	1.58	0.51
51:u:25:GLY:O	56:z:2:PRO:C	2.53	0.51
64:AK:81:THR:HG21	73:AT:53:ASN:O	2.11	0.51
1:A:207:VAL:HG11	28:1:916:G:C6	2.46	0.51
5:E:31:ARG:NE	36:f:107:ILE:O	2.44	0.51
6:F:112:ASN:ND2	6:F:209:ASN:OD1	2.42	0.51
7:G:160:ILE:O	7:G:164:VAL:HG23	2.11	0.51
28:1:1920:U:O2'	28:1:1932:A:N7	2.38	0.51
46:2:415:C:N4	46:2:417:A:O4'	2.42	0.51
46:2:1663:G:O6	46:2:1739:C:N4	2.44	0.51
54:x:143:LEU:HD13	54:x:147:ASN:ND2	2.26	0.51
58:AE:132:ARG:O	70:AQ:29:SER:N	2.43	0.51
2:B:218:ILE:HD12	2:B:276:THR:OG1	2.10	0.51
9:I:95:HIS:O	9:I:125:LEU:HD13	2.10	0.51
11:L:46:ILE:HD11	11:L:49:ARG:NH2	2.25	0.51
28:1:1390:A:N6	28:1:1418:A:O2'	2.44	0.51
28:1:2262:A:N1	46:2:1758:U:O2'	2.42	0.51
46:2:771:A:O3'	56:z:6:ARG:CZ	2.59	0.51
46:2:1686:C:O2'	46:2:1687:U:O5'	2.29	0.51
50:t:219:ALA:CB	74:AV:194:GLY:HA3	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AI:40:ARG:CB	63:AJ:45:MET:HE2	2.35	0.51
10:J:21:ILE:HD12	10:J:37:LEU:HD11	1.91	0.51
13:N:51:LEU:O	13:N:117:ASN:ND2	2.44	0.51
49:s:105:GLY:C	49:s:190:LEU:HD22	2.36	0.51
8:H:20:ILE:HG22	8:H:21:LYS:O	2.11	0.51
28:1:853:G:O6	45:p:2:ALA:N	2.44	0.51
46:2:799:A:O2'	46:2:800:U:O4'	2.11	0.51
46:2:1601:G:N1	63:AJ:88:VAL:HG22	2.26	0.51
46:2:1788:G:N7	58:AE:132:ARG:NE	2.59	0.51
47:q:59:LEU:HD11	65:AL:79:LEU:HD21	1.92	0.51
64:AK:69:LYS:CD	73:AT:31:ILE:HG21	2.41	0.51
66:AM:104:LEU:HD23	66:AM:116:ALA:HB1	1.93	0.51
9:I:116:ARG:NH2	28:1:2617:U:O2'	2.43	0.51
28:1:2666:C:OP2	28:1:2687:G:N1	2.44	0.51
43:n:7:LYS:CB	46:2:1027:A:C3'	2.88	0.51
43:n:12:ARG:CB	46:2:1025:A:O2'	2.59	0.51
8:H:105:GLU:OE2	8:H:108:GLY:N	2.44	0.50
15:P:62:ARG:NH1	28:1:412:G:OP1	2.40	0.50
28:1:152:U:OP1	38:h:106:LYS:NZ	2.34	0.50
28:1:815:G:OP2	40:j:31:LYS:NZ	2.32	0.50
28:1:2678:A:C2	75:AZ:56:C:N3	2.79	0.50
43:n:10:THR:HG1	46:2:1026:A:H2'	1.64	0.50
45:p:19:GLY:O	45:p:23:ARG:NE	2.44	0.50
46:2:1603:U:O2	60:AG:139:GLN:NE2	2.35	0.50
48:r:128:LYS:NZ	48:r:129:THR:O	2.43	0.50
59:AF:124:THR:OG1	59:AF:127:ARG:NH2	2.43	0.50
28:1:438:A:O2'	28:1:494:G:N3	2.41	0.50
28:1:1566:A:N6	28:1:1571:A:C4	2.79	0.50
43:n:8:LYS:N	46:2:1027:A:C5'	2.73	0.50
46:2:1596:C:OP2	73:AT:30:LEU:HD23	2.11	0.50
46:2:1657:U:O2'	46:2:1658:G:N7	2.41	0.50
66:AM:98:GLN:OE1	66:AM:98:GLN:N	2.43	0.50
44:o:45:ARG:O	44:o:48:SER:OG	2.24	0.50
46:2:326:G:O6	46:2:337:G:C6	2.64	0.50
59:AF:63:ALA:O	59:AF:67:ALA:HA	2.11	0.50
43:n:1:MET:C	46:2:1031:U:H5''	2.34	0.50
43:n:8:LYS:CD	46:2:977:A:C4	2.95	0.50
44:o:15:LYS:O	44:o:18:ARG:NH1	2.45	0.50
68:AO:53:ASP:O	68:AO:83:LYS:NZ	2.43	0.50
50:t:16:VAL:CG2	73:AT:46:LYS:NZ	2.74	0.50
52:v:120:ILE:HG22	69:AP:100:ILE:HG22	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:z:59:LEU:O	56:z:69:ARG:NE	2.41	0.50
62:AI:40:ARG:CD	63:AJ:45:MET:HE2	2.42	0.50
3:C:334:PHE:HA	3:C:339:LEU:HD12	1.94	0.50
28:1:1802:C:O2'	37:g:59:PRO:O	2.21	0.50
28:1:1899:G:O2'	28:1:2334:U:O4	2.26	0.50
46:2:551:G:OP2	46:2:581:U:O2'	2.09	0.50
46:2:1570:A:C5'	62:AI:144:ARG:HH12	2.16	0.50
48:r:156:ALA:CB	48:r:161:ILE:HD11	2.41	0.50
66:AM:22:LYS:HZ2	71:AR:4:VAL:CG1	2.22	0.50
11:L:76:THR:O	11:L:79:GLU:N	2.45	0.50
28:1:1389:G:OP1	35:e:104:ASN:ND2	2.42	0.50
30:4:80:A:O2'	30:4:83:C:N4	2.44	0.50
46:2:2:A:OP1	49:s:179:VAL:HB	2.12	0.50
46:2:771:A:H5''	56:z:6:ARG:HD3	1.93	0.50
46:2:1375:A:H2	60:AG:8:GLN:HB2	1.75	0.50
46:2:1627:U:O2'	70:AQ:88:SER:HA	2.11	0.50
55:y:42:ARG:O	55:y:43:ILE:HD13	2.11	0.50
43:n:9:ARG:CA	46:2:1789:G:C4	2.95	0.50
46:2:215:A:N6	46:2:241:U:OP2	2.45	0.50
46:2:390:G:OP2	46:2:390:G:N2	2.44	0.50
46:2:809:A:N1	54:x:114:ARG:NH2	2.60	0.50
46:2:1640:C:N4	46:2:1761:U:O4	2.44	0.50
48:r:156:ALA:HB3	48:r:161:ILE:HD11	1.92	0.50
49:s:176:SER:CB	56:z:57:ARG:NH1	2.75	0.50
51:u:26:CYS:HA	56:z:2:PRO:C	2.36	0.50
7:G:147:LYS:O	7:G:201:THR:OG1	2.13	0.50
9:I:20:SER:OG	9:I:21:ARG:N	2.43	0.50
28:1:264:G:OP1	39:i:36:ARG:NH1	2.44	0.50
46:2:94:U:OP1	51:u:4:GLY:HA3	2.12	0.50
46:2:214:G:N2	46:2:251:A:H62	2.10	0.50
46:2:773:C:O2'	46:2:787:G:N2	2.38	0.50
46:2:811:A:N7	46:2:858:G:O2'	2.43	0.50
46:2:1171:A:C4'	62:AI:144:ARG:CD	2.84	0.50
10:J:60:ARG:NH1	10:J:63:GLU:OE2	2.45	0.49
46:2:1333:C:H1'	73:AT:55:PHE:HB2	1.94	0.49
48:r:120:LEU:HD11	48:r:140:ILE:HD11	1.94	0.49
2:B:250:ALA:HB1	28:1:2947:G:N3	2.26	0.49
3:C:32:PRO:HA	3:C:35:VAL:HG12	1.93	0.49
13:N:67:ARG:NH2	13:N:127:TYR:OH	2.45	0.49
28:1:633:C:O2'	36:f:21:ARG:O	2.30	0.49
28:1:1567:U:O4	28:1:1571:A:H1'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:1636:U:O2'	28:1:1637:A:O5'	2.30	0.49
43:n:6:ARG:C	46:2:1027:A:H3'	2.31	0.49
43:n:12:ARG:O	43:n:13:LEU:HD23	2.12	0.49
46:2:1099:U:O4	49:s:168:ARG:NH1	2.45	0.49
48:r:129:THR:OG1	48:r:130:SER:N	2.45	0.49
60:AG:142:TYR:CE2	64:AK:75:GLY:N	2.80	0.49
16:Q:39:ARG:NH1	28:1:1348:U:OP1	2.46	0.49
28:1:1477:A:OP1	28:1:3075:G:O2'	2.30	0.49
48:r:24:PHE:CG	58:AE:74:VAL:HG22	2.47	0.49
50:t:55:THR:HA	50:t:58:VAL:HG12	1.95	0.49
66:AM:22:LYS:HZ3	71:AR:4:VAL:HG13	1.75	0.49
66:AM:70:ASN:HD21	66:AM:130:TYR:HE2	1.61	0.49
3:C:258:LEU:HA	3:C:261:VAL:HG12	1.94	0.49
8:H:47:LYS:NZ	12:M:5:SER:O	2.43	0.49
11:L:52:ASP:OD1	11:L:53:LEU:N	2.44	0.49
28:1:1565:G:H2'	28:1:1566:A:N7	2.27	0.49
30:4:128:U:P	30:4:129:C:H41	2.35	0.49
43:n:7:LYS:CB	46:2:1027:A:H3'	2.43	0.49
46:2:87:C:O2'	46:2:169:A:N1	2.39	0.49
46:2:687:G:O2'	46:2:688:G:O5'	2.30	0.49
46:2:690:G:OP2	46:2:696:C:N4	2.45	0.49
18:S:99:ARG:NH2	18:S:126:VAL:O	2.45	0.49
28:1:63:A:N3	28:1:78:U:O2'	2.39	0.49
28:1:1565:G:C6	28:1:1575:A:N1	2.80	0.49
43:n:6:ARG:N	46:2:1027:A:H3'	2.27	0.49
4:D:177:GLU:OE1	4:D:177:GLU:N	2.46	0.49
28:1:1388:U:O2'	35:e:99:ASN:O	2.30	0.49
28:1:1648:A:H62	28:1:1807:G:H21	1.61	0.49
46:2:1162:C:C4'	72:AS:22:ARG:CD	2.91	0.49
51:u:27:TYR:CE2	56:z:2:PRO:CG	2.95	0.49
35:e:30:GLU:OE1	35:e:30:GLU:N	2.44	0.49
39:i:50:LEU:O	39:i:55:ARG:NH2	2.45	0.49
43:n:15:ARG:CZ	46:2:978:A:H62	2.24	0.49
46:2:243:G:N2	46:2:244:A:N7	2.61	0.49
46:2:257:A:O2'	55:y:73:SER:O	2.27	0.49
48:r:176:VAL:HG12	48:r:177:GLN:H	1.78	0.49
50:t:41:VAL:HG21	64:AK:32:LYS:CE	2.27	0.49
4:D:33:ARG:NH1	4:D:72:ASP:OD2	2.44	0.49
6:F:103:LEU:CD2	6:F:130:ILE:HD11	2.42	0.49
27:AB:66:ILE:O	46:2:246:G:N2	2.45	0.49
28:1:1218:U:O2	28:1:1286:A:N6	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:773:C:N4	46:2:788:A:O2'	2.45	0.49
50:t:120:TYR:HA	50:t:123:VAL:HG22	1.95	0.49
51:u:26:CYS:CA	56:z:2:PRO:HB2	2.31	0.49
53:w:118:GLU:OE1	53:w:118:GLU:N	2.45	0.49
61:AH:104:ASN:OD1	61:AH:105:GLN:N	2.45	0.49
68:AO:3:ASP:N	68:AO:3:ASP:OD1	2.46	0.49
28:1:1064:A:N7	28:1:1097:G:O6	2.46	0.49
28:1:1926:C:OP1	45:p:23:ARG:NH1	2.44	0.49
43:n:5:TRP:CD1	46:2:1028:C:OP2	2.66	0.49
46:2:697:C:H5	54:x:105:THR:HG23	1.78	0.49
46:2:856:A:C2	54:x:96:ARG:NH2	2.81	0.49
46:2:1533:C:HO2'	62:AI:30:TYR:HH	1.61	0.49
60:AG:140:LYS:N	64:AK:73:GLY:HA2	2.28	0.49
68:AO:26:ASP:OD1	68:AO:26:ASP:N	2.46	0.49
2:B:30:LYS:NZ	28:1:3139:A:OP2	2.23	0.49
10:J:73:GLY:O	10:J:75:LYS:N	2.42	0.49
46:2:485:A:OP2	46:2:503:G:N2	2.45	0.49
46:2:1419:G:C2'	73:AT:54:LYS:HZ3	2.25	0.49
6:F:156:ILE:HD11	6:F:161:VAL:CG2	2.40	0.48
11:L:55:ARG:O	11:L:115:ARG:NH2	2.44	0.48
27:AB:118:GLN:OE1	27:AB:118:GLN:N	2.46	0.48
28:1:1570:U:O2'	28:1:1571:A:H4'	2.13	0.48
44:o:103:ALA:HB3	44:o:105:GLN:NE2	2.28	0.48
46:2:1147:A:O2'	46:2:1636:C:OP2	2.30	0.48
46:2:1467:C:H1'	46:2:1601:G:H21	1.78	0.48
48:r:103:MET:SD	48:r:104:ASP:N	2.86	0.48
64:AK:81:THR:CB	73:AT:53:ASN:O	2.61	0.48
74:AV:19:TRP:NE1	74:AV:306:THR:O	2.46	0.48
2:B:252:ILE:HD12	28:1:2393:G:H4'	1.94	0.48
4:D:122:VAL:O	4:D:248:ARG:NH2	2.46	0.48
9:I:63:GLU:N	9:I:63:GLU:OE2	2.43	0.48
12:M:77:ARG:NH2	28:1:525:C:OP2	2.45	0.48
28:1:1047:A:N3	28:1:2633:U:O2'	2.46	0.48
46:2:104:A:O4'	46:2:308:C:N4	2.46	0.48
65:AL:15:ARG:NH1	65:AL:33:GLN:OE1	2.45	0.48
4:D:13:SER:O	29:3:11:A:N6	2.47	0.48
7:G:118:GLU:N	7:G:118:GLU:OE1	2.46	0.48
14:O:10:ASP:OD1	14:O:37:ARG:NH1	2.46	0.48
16:Q:21:SER:OG	16:Q:22:ASP:N	2.44	0.48
18:S:57:GLU:OE1	19:T:139:ARG:NH2	2.46	0.48
47:q:62:ARG:NH2	65:AL:37:ALA:C	2.71	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:AE:70:LYS:O	58:AE:74:VAL:HG23	2.13	0.48
28:1:2846:U:O2'	28:1:2847:A:OP1	2.23	0.48
46:2:1039:A:O4'	65:AL:62:ARG:NH1	2.43	0.48
46:2:1391:A:H62	46:2:1393:C:H42	1.59	0.48
52:v:34:GLN:HA	60:AG:57:LEU:HD11	1.95	0.48
55:y:39:GLY:O	55:y:59:ARG:NH2	2.47	0.48
3:C:349:THR:OG1	28:1:520:U:O4	2.30	0.48
8:H:79:ILE:O	8:H:83:THR:HG22	2.14	0.48
22:W:49:ILE:O	22:W:52:THR:HG22	2.13	0.48
34:d:29:ALA:HB3	34:d:30:PRO:HD3	1.95	0.48
43:n:7:LYS:HZ3	46:2:624:G:C5'	2.27	0.48
43:n:7:LYS:CG	46:2:1027:A:H3'	2.44	0.48
43:n:8:LYS:HD2	46:2:977:A:C4	2.46	0.48
46:2:58:U:O2'	46:2:451:A:N3	2.45	0.48
46:2:514:G:OP1	56:z:131:GLN:OE1	2.31	0.48
3:C:194:TYR:OH	30:4:21:C:OP2	2.17	0.48
11:L:47:ALA:O	11:L:49:ARG:N	2.47	0.48
21:V:47:ASN:ND2	28:1:2880:U:OP1	2.47	0.48
46:2:46:A:O2'	46:2:48:G:N7	2.35	0.48
46:2:1030:A:N7	70:AQ:6:ALA:O	2.46	0.48
62:AI:11:PHE:CZ	69:AP:41:ILE:HG21	2.49	0.48
65:AL:14:PRO:HB2	65:AL:23:ILE:HD11	1.95	0.48
2:B:28:ARG:NH2	28:1:3140:G:N7	2.62	0.48
24:Y:53:ASP:OD1	24:Y:110:HIS:ND1	2.47	0.48
28:1:1139:G:N7	32:b:14:ARG:NH2	2.61	0.48
43:n:11:ARG:CG	46:2:1025:A:O2'	2.60	0.48
46:2:1136:U:O2'	46:2:1137:A:O5'	2.30	0.48
51:u:105:VAL:HG22	51:u:191:ARG:HE	1.79	0.48
74:AV:132:LYS:HA	74:AV:142:ALA:HB3	1.95	0.48
11:L:153:ASP:OD1	11:L:154:VAL:N	2.47	0.48
12:M:16:GLU:O	12:M:35:ILE:HD11	2.14	0.48
20:U:18:ASP:OD1	20:U:20:SER:OG	2.31	0.48
28:1:1228:C:N3	28:1:1282:G:N2	2.62	0.48
43:n:2:ARG:CA	46:2:1029:U:C5	2.97	0.48
46:2:1288:G:N1	46:2:1328:G:N7	2.62	0.48
49:s:44:LEU:HD12	49:s:50:ILE:HD12	1.95	0.48
2:B:296:THR:OG1	2:B:356:LEU:O	2.31	0.48
13:N:95:GLN:NE2	28:1:288:C:O2	2.43	0.48
28:1:1433:A:N3	35:e:27:ARG:NH1	2.62	0.48
37:g:46:ASP:N	37:g:46:ASP:OD2	2.46	0.48
46:2:1419:G:H2'	73:AT:54:LYS:CE	2.42	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AD:30:SER:HA	57:AD:33:VAL:HG22	1.95	0.48
64:AK:17:GLN:NE2	64:AK:98:GLN:OE1	2.46	0.48
8:H:184:LYS:NZ	28:1:3111:U:OP1	2.26	0.48
25:Z:58:GLY:O	25:Z:62:VAL:HG23	2.13	0.48
35:e:78:ASN:O	35:e:80:LYS:N	2.46	0.48
43:n:7:LYS:CA	46:2:1027:A:H3'	2.42	0.48
50:t:16:VAL:HG22	73:AT:46:LYS:NZ	2.29	0.48
3:C:229:ASN:OD1	3:C:230:VAL:N	2.47	0.47
13:N:68:ARG:NH2	28:1:292:U:OP2	2.47	0.47
18:S:34:GLU:OE1	18:S:34:GLU:N	2.45	0.47
20:U:86:LYS:NZ	28:1:1684:U:OP1	2.47	0.47
28:1:2838:A:OP2	28:1:2845:A:N6	2.47	0.47
28:1:2991:A:O2'	28:1:3309:G:N7	2.47	0.47
46:2:459:G:OP1	68:AO:105:ARG:NH2	2.47	0.47
46:2:523:G:N3	68:AO:61:ARG:NH1	2.61	0.47
50:t:41:VAL:CG2	64:AK:32:LYS:HE2	2.28	0.47
12:M:16:GLU:C	12:M:35:ILE:HD11	2.38	0.47
28:1:2568:C:O2'	28:1:2573:G:N2	2.45	0.47
43:n:13:LEU:HB3	46:2:978:A:C2	2.49	0.47
46:2:1367:G:H5''	63:AJ:119:LYS:CD	2.43	0.47
66:AM:111:MET:HE3	66:AM:115:GLU:C	2.39	0.47
19:T:84:TYR:O	32:b:24:PRO:HB3	2.14	0.47
28:1:1952:G:H22	28:1:2094:C:H42	1.61	0.47
46:2:733:A:N6	46:2:737:A:N7	2.62	0.47
46:2:769:A:N7	46:2:770:A:N6	2.61	0.47
50:t:195:SER:OG	50:t:196:ARG:N	2.46	0.47
61:AH:41:ILE:HG23	61:AH:46:LEU:HD23	1.96	0.47
28:1:1567:U:C4	28:1:1568:U:H1'	2.50	0.47
43:n:7:LYS:CD	46:2:1027:A:C8	2.58	0.47
50:t:116:ARG:O	50:t:116:ARG:NH1	2.48	0.47
11:L:157:ARG:NH2	31:a:146:GLU:OE2	2.47	0.47
24:Y:51:ARG:NH2	30:4:83:C:O2'	2.47	0.47
28:1:1114:U:OP1	31:a:23:GLY:N	2.48	0.47
28:1:1225:A:O2'	28:1:3118:C:N3	2.47	0.47
28:1:1573:G:H3'	28:1:1574:C:H6	1.78	0.47
46:2:1556:A:OP2	59:AF:40:ARG:NH1	2.48	0.47
51:u:252:ARG:HH11	56:z:78:ARG:NH1	2.13	0.47
54:x:139:ARG:NH2	71:AR:8:LEU:O	2.26	0.47
62:AI:38:VAL:HG23	62:AI:42:TYR:HD2	1.79	0.47
15:P:33:ALA:HB1	15:P:117:ILE:HD12	1.95	0.47
28:1:2964:G:N2	28:1:2967:A:OP2	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:548:G:O6	46:2:591:A:N6	2.47	0.47
46:2:1597:A:P	73:AT:32:ARG:NH2	2.88	0.47
49:s:66:PHE:CZ	49:s:130:ILE:HD12	2.48	0.47
4:D:267:ALA:O	4:D:271:LYS:NZ	2.48	0.47
9:I:28:ASP:HB2	75:AZ:64:A:H4'	1.96	0.47
10:J:41:SER:O	10:J:75:LYS:NZ	2.37	0.47
11:L:115:ARG:NH1	11:L:145:PHE:O	2.42	0.47
16:Q:8:LYS:NZ	28:1:971:G:OP1	2.47	0.47
23:X:61:LYS:NZ	30:4:59:A:O3'	2.48	0.47
27:AB:73:GLY:O	27:AB:122:ILE:HD12	2.15	0.47
30:4:150:G:O2'	30:4:152:G:OP1	2.32	0.47
36:f:15:SER:OG	36:f:16:TYR:N	2.48	0.47
43:n:5:TRP:CZ3	46:2:1791:A:OP1	2.68	0.47
43:n:10:THR:HB	46:2:1026:A:H5'	1.97	0.47
46:2:381:C:OP2	51:u:10:LYS:NZ	2.45	0.47
47:q:153:SER:OG	47:q:153:SER:O	2.30	0.47
50:t:224:ASP:CG	74:AV:189:GLU:O	2.58	0.47
51:u:22:LYS:HZ1	56:z:6:ARG:N	2.12	0.47
61:AH:76:GLU:OE1	61:AH:76:GLU:N	2.46	0.47
72:AS:27:GLN:NE2	72:AS:43:ASN:OD1	2.46	0.47
9:I:189:GLU:OE1	9:I:189:GLU:N	2.46	0.47
12:M:68:LEU:HD23	12:M:90:VAL:HG23	1.95	0.47
28:1:358:G:N2	28:1:361:A:OP2	2.46	0.47
28:1:1504:A:N1	28:1:1515:A:O2'	2.41	0.47
30:4:126:A:O2'	30:4:128:U:OP2	2.33	0.47
35:e:83:GLU:O	35:e:86:THR:HG23	2.15	0.47
40:j:17:THR:OG1	40:j:18:LEU:N	2.46	0.47
43:n:4:LYS:HE3	46:2:940:A:O2'	2.15	0.47
46:2:1023:A:HO2'	46:2:1024:U:P	2.38	0.47
46:2:1482:C:H1'	60:AG:75:VAL:HG22	1.97	0.47
47:q:102:PHE:O	47:q:103:THR:OG1	2.33	0.47
50:t:168:ILE:HD12	50:t:187:LYS:HE3	1.96	0.47
52:v:49:GLU:CG	52:v:51:VAL:HG13	2.44	0.47
63:AJ:38:LYS:O	63:AJ:39:THR:OG1	2.27	0.47
74:AV:210:LEU:HD12	74:AV:222:LEU:HD12	1.97	0.47
3:C:337:GLU:N	3:C:337:GLU:OE2	2.48	0.47
11:L:88:ALA:O	38:h:111:PHE:CD1	2.68	0.47
13:N:68:ARG:NE	28:1:291:C:OP1	2.48	0.47
41:k:7:ASP:OD1	41:k:7:ASP:N	2.42	0.47
43:n:21:ARG:NE	46:2:1126:G:OP1	2.48	0.47
46:2:1350:U:C4	60:AG:8:GLN:OE1	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:u:182:TYR:HB2	51:u:228:ILE:HD11	1.96	0.47
54:x:9:LEU:HD12	54:x:11:GLN:H	1.80	0.47
17:R:104:ARG:NH2	28:1:1949:G:OP1	2.46	0.47
25:Z:124:ALA:O	25:Z:126:LYS:NZ	2.46	0.47
27:AB:73:GLY:C	27:AB:86:ILE:HD11	2.40	0.47
28:1:2678:A:C2	75:AZ:56:C:C5	3.03	0.47
46:2:120:U:O4	46:2:298:C:N4	2.48	0.47
46:2:1358:G:O3'	63:AJ:129:GLN:NE2	2.47	0.47
46:2:1631:A:N6	46:2:1763:A:O2'	2.47	0.47
51:u:112:HIS:NE2	51:u:237:SER:OG	2.25	0.47
71:AR:61:THR:OG1	71:AR:62:ILE:N	2.48	0.47
8:H:31:ARG:NH1	8:H:149:ASN:OD1	2.47	0.46
17:R:15:VAL:HG23	17:R:17:VAL:HG22	1.97	0.46
28:1:3154:C:O2'	28:1:3155:U:O4'	2.33	0.46
46:2:772:G:P	56:z:6:ARG:CZ	3.01	0.46
46:2:811:A:O2'	46:2:858:G:N2	2.45	0.46
46:2:1215:C:H4'	73:AT:7:TRP:CZ2	2.47	0.46
54:x:131:PHE:CD2	54:x:133:THR:HG23	2.50	0.46
59:AF:30:THR:HG21	59:AF:86:VAL:HG23	1.97	0.46
7:G:161:GLU:OE1	13:N:22:LEU:HD13	2.15	0.46
9:I:75:TYR:O	9:I:79:VAL:HG12	2.15	0.46
11:L:48:PRO:HB2	38:h:117:ALA:HB2	1.96	0.46
13:N:19:LEU:HA	13:N:22:LEU:HD12	1.97	0.46
43:n:7:LYS:HD2	46:2:624:G:C5'	2.45	0.46
43:n:13:LEU:HB3	46:2:978:A:N3	2.30	0.46
46:2:885:G:H21	58:AE:123:SER:CB	2.26	0.46
52:v:40:ILE:HG23	52:v:42:LEU:HD22	1.98	0.46
52:v:139:ASN:O	52:v:214:LYS:NZ	2.35	0.46
62:AI:25:ASN:HA	69:AP:41:ILE:HD12	1.97	0.46
74:AV:20:VAL:HG23	74:AV:304:GLY:HA3	1.97	0.46
28:1:1953:G:O6	28:1:2093:A:N6	2.47	0.46
30:4:52:A:H62	42:l:27:ILE:HD13	1.81	0.46
43:n:2:ARG:CB	46:2:1029:U:H5	2.22	0.46
46:2:1199:G:C6	64:AK:71:PRO:CD	2.96	0.46
46:2:1338:C:O2'	46:2:1339:C:OP2	2.24	0.46
52:v:25:LEU:HD13	60:AG:60:PHE:HB2	1.97	0.46
54:x:48:GLU:OE2	54:x:49:ILE:N	2.48	0.46
74:AV:63:GLY:O	74:AV:90:ARG:NH2	2.48	0.46
28:1:865:U:OP2	28:1:893:C:N4	2.43	0.46
28:1:1712:G:O2'	28:1:1713:G:O4'	2.33	0.46
43:n:8:LYS:HD2	46:2:977:A:C2	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:15:ARG:NE	46:2:979:A:C6	2.81	0.46
46:2:1284:C:N4	46:2:1422:A:N7	2.64	0.46
46:2:1796:C:C5	70:AQ:93:LYS:CD	2.99	0.46
54:x:142:TYR:C	54:x:143:LEU:HD12	2.41	0.46
62:AI:24:GLY:O	69:AP:41:ILE:HB	2.15	0.46
15:P:131:ARG:NH2	28:1:879:U:O2'	2.48	0.46
28:1:1408:G:OP2	35:e:31:ASN:ND2	2.48	0.46
28:1:2433:U:OP2	28:1:2434:U:O2'	2.29	0.46
46:2:524:U:O2'	46:2:527:A:N7	2.40	0.46
54:x:15:GLU:OE2	54:x:15:GLU:N	2.46	0.46
6:F:218:ARG:NH2	29:3:85:G:O3'	2.45	0.46
7:G:157:VAL:HG22	28:1:147:U:O4	2.15	0.46
17:R:83:GLY:N	28:1:1864:A:OP1	2.48	0.46
39:i:18:THR:O	39:i:18:THR:OG1	2.34	0.46
46:2:25:C:N4	46:2:367:A:OP1	2.48	0.46
46:2:1595:U:H5'	73:AT:31:ILE:HD11	1.97	0.46
49:s:226:THR:HG22	49:s:227:PRO:HD2	1.98	0.46
73:AT:38:ILE:HG22	73:AT:42:CYS:HB2	1.97	0.46
5:E:56:LYS:HB3	5:E:64:LEU:HD12	1.97	0.46
8:H:34:LEU:HD12	8:H:82:VAL:HB	1.98	0.46
28:1:679:U:O2'	28:1:788:C:O2	2.33	0.46
28:1:1494:U:OP1	42:l:42:ARG:NH2	2.44	0.46
46:2:122:U:O2'	51:u:145:ARG:NH1	2.48	0.46
46:2:240:U:N3	46:2:830:U:O2'	2.41	0.46
46:2:912:U:OP1	46:2:913:G:O2'	2.25	0.46
46:2:1691:A:OP2	46:2:1693:A:N6	2.49	0.46
62:AI:25:ASN:CA	69:AP:41:ILE:HD12	2.45	0.46
15:P:108:ASP:N	15:P:152:GLU:OE2	2.46	0.46
21:V:23:MET:HE3	21:V:34:LEU:HD12	1.98	0.46
24:Y:119:ILE:O	24:Y:124:GLY:N	2.46	0.46
28:1:1348:U:O4'	28:1:1355:A:N6	2.49	0.46
28:1:1646:G:O2'	28:1:1808:G:N2	2.48	0.46
43:n:4:LYS:HZ3	46:2:940:A:C5'	2.17	0.46
46:2:381:C:OP1	56:z:3:ARG:O	2.34	0.46
46:2:757:A:O2'	56:z:7:THR:HG21	2.15	0.46
46:2:811:A:HO2'	46:2:858:G:N2	2.13	0.46
2:B:85:VAL:HG13	2:B:163:HIS:CE1	2.51	0.46
7:G:29:SER:O	7:G:32:LYS:NZ	2.48	0.46
14:O:85:ARG:NH2	28:1:2382:G:OP1	2.49	0.46
24:Y:5:SER:OG	24:Y:7:ASP:OD2	2.33	0.46
46:2:216:U:OP2	53:w:219:ARG:NH2	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:818:C:H41	46:2:853:G:H21	1.64	0.46
28:1:1712:G:N2	28:1:1733:G:O6	2.49	0.46
33:c:9:SER:OG	33:c:10:ILE:N	2.48	0.46
46:2:582:U:OP1	46:2:583:C:N4	2.49	0.46
46:2:861:U:O2'	66:AM:56:HIS:O	2.29	0.46
46:2:1274:C:H41	75:AZ:34:G:P	2.38	0.46
46:2:1482:C:H1'	60:AG:75:VAL:CG2	2.46	0.46
48:r:64:ARG:CZ	58:AE:34:SER:CB	2.94	0.46
51:u:80:THR:OG1	51:u:81:THR:N	2.49	0.46
64:AK:48:HIS:HE1	64:AK:50:LEU:HD13	1.81	0.46
28:1:1693:C:O2'	28:1:1772:U:O2'	2.12	0.45
28:1:2506:U:O2'	28:1:2507:C:O5'	2.15	0.45
46:2:457:G:OP1	68:AO:108:ARG:NH1	2.48	0.45
46:2:505:A:N6	46:2:508:U:O4	2.49	0.45
46:2:1528:U:OP2	52:v:109:LYS:NZ	2.43	0.45
55:y:97:THR:HG22	55:y:98:LYS:H	1.80	0.45
56:z:58:ASP:OD1	56:z:62:ARG:NH1	2.49	0.45
60:AG:142:TYR:CG	64:AK:74:GLU:HG2	2.51	0.45
62:AI:126:ARG:HG3	62:AI:133:VAL:HG12	1.98	0.45
64:AK:82:TYR:CE2	73:AT:50:ILE:CB	2.98	0.45
28:1:1226:G:O2'	28:1:3117:C:N4	2.50	0.45
28:1:2678:A:H2	75:AZ:56:C:C4	2.34	0.45
46:2:478:A:N6	46:2:511:A:N3	2.61	0.45
56:z:83:VAL:O	56:z:107:ARG:NE	2.50	0.45
9:I:54:SER:OG	9:I:56:GLU:O	2.32	0.45
11:L:73:ARG:NH1	28:1:110:G:OP2	2.48	0.45
28:1:2393:G:O2'	28:1:2982:A:N6	2.48	0.45
46:2:792:U:P	51:u:187:ARG:HH22	2.39	0.45
47:q:38:PHE:CZ	61:AH:109:LEU:HD11	2.51	0.45
47:q:112:THR:OG1	47:q:113:ARG:N	2.49	0.45
50:t:139:SER:OG	50:t:140:GLY:N	2.49	0.45
51:u:51:ARG:NE	51:u:110:ALA:O	2.47	0.45
52:v:205:SER:O	52:v:206:SER:OG	2.28	0.45
4:D:59:ASP:OD1	4:D:60:ILE:N	2.50	0.45
46:2:486:G:C6	46:2:501:U:O4	2.68	0.45
46:2:1172:G:H3'	62:AI:141:THR:HG21	1.89	0.45
46:2:1512:G:O4'	46:2:1518:C:O2'	2.35	0.45
54:x:103:SER:OG	54:x:104:ARG:N	2.49	0.45
2:B:216:ASP:OD1	2:B:216:ASP:N	2.50	0.45
3:C:342:LYS:O	28:1:515:C:O2'	2.33	0.45
28:1:824:C:O2'	28:1:1534:A:N3	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:g:71:THR:OG1	37:g:72:VAL:N	2.49	0.45
46:2:338:C:H5''	55:y:10:LYS:HG3	1.98	0.45
46:2:1367:G:H5''	63:AJ:119:LYS:HE3	1.98	0.45
46:2:1566:U:OP1	62:AI:39:GLY:HA3	2.16	0.45
64:AK:69:LYS:CE	73:AT:33:LYS:HB3	2.46	0.45
3:C:338:LYS:O	3:C:340:GLY:N	2.50	0.45
11:L:155:GLU:OE2	31:a:86:LYS:NZ	2.49	0.45
12:M:128:ARG:NH1	28:1:3214:U:OP2	2.46	0.45
13:N:38:ARG:NH1	30:4:142:C:OP1	2.49	0.45
13:N:179:LYS:O	28:1:286:U:O2'	2.34	0.45
28:1:1310:G:N2	28:1:2381:G:OP1	2.50	0.45
28:1:1575:A:C6	28:1:1576:G:C5	3.04	0.45
28:1:2257:C:H42	46:2:1646:C:H2'	1.81	0.45
46:2:599:A:N6	46:2:600:U:O2	2.50	0.45
46:2:1162:C:H4'	72:AS:22:ARG:CD	2.47	0.45
46:2:1794:A:C2	70:AQ:79:ILE:HD11	2.49	0.45
49:s:140:ARG:NH1	65:AL:10:GLU:HG3	2.31	0.45
51:u:151:ASP:OD1	53:w:215:ARG:NH2	2.48	0.45
11:L:42:ARG:O	11:L:46:ILE:HG22	2.16	0.45
28:1:1706:C:N4	28:1:1738:C:H42	2.15	0.45
43:n:8:LYS:NZ	46:2:941:A:O3'	2.38	0.45
43:n:13:LEU:CB	46:2:978:A:C2	2.87	0.45
44:o:68:VAL:HG13	44:o:85:LEU:HD12	1.98	0.45
46:2:324:U:OP2	55:y:10:LYS:NZ	2.44	0.45
46:2:697:C:H5	54:x:105:THR:CG2	2.30	0.45
46:2:1208:A:H61	46:2:1456:C:H1'	1.82	0.45
46:2:1263:G:O6	46:2:1264:G:N2	2.50	0.45
48:r:83:LYS:HZ1	58:AE:114:ARG:HB3	1.81	0.45
50:t:13:ALA:HB2	73:AT:34:TYR:HE2	1.82	0.45
60:AG:142:TYR:CZ	64:AK:75:GLY:CA	2.95	0.45
63:AJ:20:SER:OG	63:AJ:24:ARG:NH2	2.50	0.45
74:AV:238:ASP:OD2	74:AV:261:LYS:NZ	2.48	0.45
1:A:207:VAL:HG13	1:A:208:ASP:OD1	2.17	0.45
4:D:55:PHE:CE1	4:D:60:ILE:HG23	2.52	0.45
7:G:206:GLU:OE1	7:G:206:GLU:N	2.47	0.45
28:1:1022:U:O4	28:1:1027:A:O2'	2.26	0.45
46:2:1150:G:O2'	46:2:1768:G:N3	2.45	0.45
46:2:1303:U:O2'	46:2:1322:A:OP2	2.34	0.45
51:u:151:ASP:CB	51:u:169:ILE:HG21	2.47	0.45
56:z:59:LEU:HD11	56:z:73:GLY:CA	2.47	0.45
60:AG:142:TYR:CZ	64:AK:75:GLY:N	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:126:GLU:N	4:D:126:GLU:OE2	2.50	0.45
6:F:127:LEU:HA	6:F:130:ILE:HG22	1.98	0.45
8:H:48:VAL:HG22	8:H:54:LYS:NZ	2.32	0.45
26:AA:10:LYS:O	26:AA:13:GLN:NE2	2.49	0.45
28:1:1565:G:C6	28:1:1566:A:N6	2.85	0.45
34:d:47:ASP:OD1	34:d:47:ASP:N	2.48	0.45
34:d:112:ASP:OD1	34:d:112:ASP:N	2.49	0.45
46:2:58:U:O2	46:2:89:G:C6	2.70	0.45
46:2:261:U:H1'	46:2:263:C:H41	1.82	0.45
46:2:1162:C:C4'	72:AS:22:ARG:HD3	2.44	0.45
46:2:1555:A:P	59:AF:47:ARG:NH2	2.90	0.45
46:2:1558:U:C5'	62:AI:122:HIS:ND1	2.67	0.45
72:AS:10:ALA:HB1	72:AS:30:VAL:HG22	1.99	0.45
2:B:166:ILE:O	2:B:169:THR:OG1	2.28	0.44
4:D:33:ARG:NH2	29:3:7:G:O3'	2.50	0.44
28:1:895:A:O2'	28:1:896:A:OP2	2.29	0.44
43:n:5:TRP:CG	46:2:1029:U:P	3.10	0.44
43:n:8:LYS:HG2	46:2:1789:G:O2'	2.16	0.44
43:n:12:ARG:N	46:2:1025:A:C2'	2.79	0.44
43:n:15:ARG:N	46:2:979:A:H2	2.00	0.44
47:q:63:ILE:HD11	65:AL:35:ASN:O	2.17	0.44
52:v:79:ASN:OD1	52:v:80:LYS:N	2.47	0.44
54:x:9:LEU:O	54:x:11:GLN:NE2	2.50	0.44
55:y:101:ILE:HD11	55:y:192:TYR:CE1	2.52	0.44
9:I:93:PRO:O	9:I:125:LEU:HD12	2.17	0.44
28:1:1149:G:OP1	36:f:20:LYS:NZ	2.51	0.44
43:n:5:TRP:HD1	46:2:1028:C:OP2	2.00	0.44
46:2:1441:C:O2	46:2:1447:C:N4	2.50	0.44
46:2:1559:A:C5	62:AI:134:ARG:O	2.70	0.44
56:z:110:GLN:OE1	56:z:126:ARG:NH2	2.51	0.44
62:AI:14:ILE:HG23	62:AI:22:VAL:O	2.17	0.44
62:AI:40:ARG:CB	63:AJ:45:MET:CE	2.82	0.44
4:D:65:ILE:HD13	29:3:6:C:O2'	2.18	0.44
7:G:46:LEU:HD23	7:G:46:LEU:H	1.82	0.44
28:1:1571:A:H2'	28:1:1572:U:C6	2.53	0.44
28:1:2255:A:H61	28:1:2262:A:P	2.40	0.44
46:2:256:A:O2'	55:y:71:GLY:O	2.27	0.44
46:2:407:A:O2'	46:2:1671:A:N3	2.44	0.44
46:2:449:C:OP1	51:u:30:ARG:HB3	2.17	0.44
46:2:1354:G:N2	46:2:1369:U:OP2	2.50	0.44
48:r:175:GLU:O	48:r:179:SER:OG	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:u:27:TYR:HE2	56:z:2:PRO:HG3	1.77	0.44
1:A:152:SER:OG	28:1:2157:G:N7	2.48	0.44
2:B:92:TYR:HH	28:1:3003:G:HO2'	1.63	0.44
3:C:285:ASP:OD1	3:C:285:ASP:N	2.47	0.44
7:G:74:THR:O	7:G:77:GLN:NE2	2.49	0.44
16:Q:135:GLN:OE1	16:Q:135:GLN:N	2.50	0.44
17:R:124:TYR:OH	28:1:1721:U:OP2	2.18	0.44
46:2:444:C:C4	46:2:460:A:N6	2.84	0.44
46:2:446:A:N1	46:2:461:G:O2'	2.41	0.44
46:2:1376:C:OP1	64:AK:121:ASN:C	2.61	0.44
69:AP:80:LEU:HD11	69:AP:101:TYR:HE2	1.79	0.44
71:AR:36:LYS:O	71:AR:77:THR:HG21	2.17	0.44
74:AV:65:SER:OG	74:AV:86:ASP:OD2	2.31	0.44
75:AZ:15:G:N2	75:AZ:21:A:N3	2.65	0.44
3:C:280:ILE:HD11	16:Q:25:TYR:HB2	1.99	0.44
6:F:213:GLY:N	28:1:1168:U:OP1	2.50	0.44
28:1:1203:A:N3	28:1:2855:U:O2'	2.36	0.44
30:4:39:G:O2'	30:4:105:A:N1	2.49	0.44
43:n:21:ARG:HG3	46:2:1125:A:H5''	1.98	0.44
46:2:628:G:OP1	57:AD:5:HIS:NE2	2.49	0.44
46:2:1042:G:H22	46:2:1076:A:H2	1.64	0.44
60:AG:141:SER:HA	64:AK:74:GLU:OE1	2.17	0.44
3:C:283:THR:OG1	3:C:285:ASP:OD1	2.26	0.44
5:E:5:LYS:HE2	28:1:1422:G:H21	1.83	0.44
9:I:90:ARG:NH1	28:1:1044:U:OP1	2.51	0.44
22:W:13:ILE:HG22	22:W:32:GLN:HG2	1.99	0.44
27:AB:14:GLN:OE1	46:2:327:U:O2'	2.29	0.44
28:1:1573:G:C6	28:1:1574:C:H1'	2.52	0.44
46:2:1142:A:OP1	70:AQ:2:PRO:HB3	2.17	0.44
46:2:1202:A:N6	46:2:1456:C:O2	2.51	0.44
46:2:1542:G:H22	46:2:1568:C:HO2'	1.59	0.44
54:x:147:ASN:OD1	54:x:147:ASN:N	2.51	0.44
55:y:60:ILE:HD11	55:y:179:CYS:HB2	2.00	0.44
57:AD:87:ASP:OD1	57:AD:88:LEU:N	2.50	0.44
9:I:98:ARG:NH2	28:1:1126:G:OP1	2.51	0.44
28:1:163:C:N3	28:1:259:C:N4	2.65	0.44
43:n:5:TRP:HE1	70:AQ:12:LYS:HZ1	1.00	0.44
43:n:9:ARG:HA	43:n:13:LEU:HD21	1.99	0.44
46:2:253:A:OP1	51:u:134:LYS:HD3	2.17	0.44
46:2:439:U:O2	46:2:465:G:N1	2.50	0.44
46:2:1162:C:C4'	72:AS:22:ARG:HD2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:t:224:ASP:OD1	50:t:225:TYR:N	2.51	0.44
62:AI:48:LYS:HE2	63:AJ:35:ASP:O	2.08	0.44
70:AQ:18:VAL:HG13	70:AQ:19:LYS:H	1.83	0.44
2:B:51:ALA:HB3	2:B:78:VAL:HG23	2.00	0.44
9:I:31:ILE:HD11	9:I:62:SER:O	2.18	0.44
28:1:2794:G:O2'	28:1:2795:U:O5'	2.33	0.44
50:t:8:LYS:NZ	64:AK:63:LEU:HD12	2.33	0.44
52:v:220:VAL:O	52:v:224:ASN:ND2	2.51	0.44
6:F:216:VAL:O	6:F:216:VAL:HG13	2.18	0.43
12:M:88:ALA:O	12:M:93:LYS:NZ	2.49	0.43
14:O:76:PRO:HB2	14:O:138:LEU:HD23	1.99	0.43
43:n:8:LYS:HB3	46:2:1789:G:O2'	2.18	0.43
43:n:16:LYS:O	43:n:20:VAL:CA	2.62	0.43
46:2:338:C:OP2	55:y:10:LYS:HE3	2.18	0.43
46:2:1172:G:N1	46:2:1468:U:O4	2.51	0.43
46:2:1181:U:O2	46:2:1458:G:O6	2.35	0.43
51:u:11:ARG:NH2	51:u:24:SER:OG	2.51	0.43
54:x:22:GLN:HA	54:x:25:VAL:HG22	1.99	0.43
55:y:32:GLN:O	55:y:56:ARG:NH1	2.51	0.43
10:J:15:GLU:OE1	10:J:15:GLU:N	2.51	0.43
28:1:119:U:O2'	28:1:120:G:OP2	2.27	0.43
28:1:523:A:N6	28:1:569:A:H2	2.16	0.43
43:n:5:TRP:HH2	70:AQ:8:ASN:OD1	2.01	0.43
43:n:14:LYS:NZ	46:2:979:A:O2'	2.39	0.43
46:2:1055:U:O2	46:2:1064:G:C6	2.70	0.43
46:2:1172:G:H5'	62:AI:141:THR:HB	2.00	0.43
46:2:1616:G:O4'	72:AS:18:ARG:NH1	2.51	0.43
52:v:23:VAL:HG21	60:AG:58:ASP:OD2	2.17	0.43
54:x:60:ILE:HD11	54:x:92:PHE:CD1	2.53	0.43
17:R:38:ARG:NH1	28:1:1603:A:OP1	2.51	0.43
44:o:8:ARG:HG3	44:o:25:VAL:HG11	2.00	0.43
66:AM:9:ASP:OD2	66:AM:10:ALA:N	2.51	0.43
2:B:56:ILE:CD1	2:B:356:LEU:HD22	2.47	0.43
3:C:332:LYS:NZ	28:1:599:C:OP1	2.52	0.43
18:S:119:ARG:NH2	29:3:87:G:O2'	2.49	0.43
28:1:642:U:P	31:a:22:ILE:HG22	2.58	0.43
46:2:2:A:O2'	49:s:198:THR:O	2.36	0.43
62:AI:48:LYS:HE2	63:AJ:36:ILE:HD13	2.00	0.43
73:AT:23:VAL:HG21	73:AT:39:CYS:SG	2.58	0.43
1:A:27:ALA:O	1:A:128:ARG:NH1	2.51	0.43
9:I:35:ASP:O	9:I:36:LEU:HD23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:X:31:THR:HG22	28:1:2523:A:OP1	2.19	0.43
28:1:1414:G:OP2	35:e:125:ARG:NH1	2.52	0.43
28:1:1751:G:O6	41:k:44:LYS:NZ	2.46	0.43
46:2:444:C:N4	46:2:460:A:N6	2.53	0.43
46:2:1795:U:O2'	46:2:1797:A:N7	2.51	0.43
53:w:67:VAL:HG22	53:w:68:LEU:HG	2.00	0.43
62:AI:127:HIS:CE1	62:AI:133:VAL:HG11	2.54	0.43
4:D:39:GLN:OE1	4:D:40:HIS:N	2.50	0.43
9:I:35:ASP:OD1	9:I:86:HIS:NE2	2.51	0.43
10:J:143:ARG:NH2	29:3:5:G:OP1	2.50	0.43
17:R:176:ARG:NH1	46:2:852:C:OP1	2.52	0.43
25:Z:53:VAL:HG11	25:Z:62:VAL:HG22	2.01	0.43
26:AA:58:GLN:HG3	50:t:28:GLU:OE2	2.18	0.43
28:1:67:A:O2'	28:1:315:C:O2	2.34	0.43
28:1:1570:U:H1'	28:1:1571:A:O3'	2.19	0.43
43:n:7:LYS:HD2	46:2:624:G:H5'	2.00	0.43
46:2:1100:G:O2'	66:AM:76:SER:N	2.51	0.43
46:2:1378:U:C1'	60:AG:10:PHE:CE2	3.02	0.43
51:u:69:HIS:HB3	68:AO:17:LEU:HD12	1.99	0.43
62:AI:11:PHE:HB2	69:AP:42:LEU:HD12	2.00	0.43
14:O:74:ARG:NH1	28:1:3008:A:OP2	2.52	0.43
28:1:1574:C:O2'	28:1:1575:A:H5'	2.18	0.43
46:2:952:A:O2'	57:AD:114:ARG:NH1	2.52	0.43
46:2:1199:G:C6	64:AK:71:PRO:HG2	2.54	0.43
48:r:57:ALA:HA	48:r:60:ALA:HB3	2.00	0.43
52:v:160:VAL:HG13	72:AS:43:ASN:HB2	1.99	0.43
54:x:74:GLN:O	54:x:78:THR:OG1	2.16	0.43
63:AJ:67:MET:HE2	63:AJ:67:MET:HA	2.00	0.43
2:B:100:ARG:NH1	28:1:3146:G:O2'	2.51	0.43
13:N:17:ASP:OD1	13:N:18:VAL:N	2.51	0.43
28:1:1575:A:N1	28:1:1576:G:C6	2.87	0.43
30:4:112:U:OP1	42:l:8:ARG:NH1	2.52	0.43
46:2:372:G:O2'	46:2:612:U:O2	2.37	0.43
51:u:64:ILE:CD1	68:AO:18:LEU:HD21	2.49	0.43
55:y:83:TYR:HD2	55:y:101:ILE:HD12	1.82	0.43
73:AT:23:VAL:HG23	73:AT:24:CYS:H	1.84	0.43
9:I:154:ARG:NH2	28:1:2837:A:O3'	2.51	0.43
13:N:70:ASN:OD1	28:1:290:G:O2'	2.20	0.43
18:S:155:ARG:NH1	18:S:171:PHE:O	2.52	0.43
19:T:10:ARG:NH2	28:1:2640:A:OP2	2.46	0.43
28:1:360:G:OP1	40:j:25:ARG:NH1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:1794:G:O2'	28:1:1796:G:N2	2.51	0.43
28:1:3217:C:OP2	28:1:3219:G:N2	2.52	0.43
43:n:12:ARG:CG	46:2:1025:A:HO2'	2.32	0.43
46:2:696:C:OP1	54:x:103:SER:OG	2.36	0.43
51:u:86:PHE:N	51:u:88:ASP:OD1	2.52	0.43
62:AI:24:GLY:O	69:AP:41:ILE:CB	2.67	0.43
64:AK:25:THR:OG1	64:AK:113:ASP:O	2.33	0.43
25:Z:17:ARG:NH1	28:1:1634:G:N7	2.65	0.43
28:1:309:U:OP1	39:i:84:LYS:NZ	2.31	0.43
28:1:1565:G:C6	28:1:1566:A:C6	3.07	0.43
46:2:477:A:N6	46:2:511:A:N1	2.66	0.43
46:2:837:G:N1	46:2:838:G:O6	2.52	0.43
46:2:1381:U:O2'	64:AK:60:THR:O	2.37	0.43
46:2:1387:G:O2'	46:2:1411:A:N6	2.52	0.43
46:2:1796:C:C4	70:AQ:93:LYS:CE	3.02	0.43
3:C:265:GLU:OE1	3:C:265:GLU:N	2.47	0.42
8:H:43:VAL:O	28:1:3186:A:O2'	2.26	0.42
28:1:2566:C:N4	28:1:2573:G:O6	2.47	0.42
32:b:32:LEU:O	32:b:40:ARG:NH1	2.48	0.42
36:f:56:SER:O	36:f:63:LYS:NZ	2.51	0.42
41:k:46:ARG:NE	41:k:47:GLY:O	2.47	0.42
43:n:5:TRP:CD1	46:2:1029:U:P	3.10	0.42
28:1:969:C:P	32:b:19:ASN:HD22	2.39	0.42
28:1:1488:G:O2'	37:g:10:ARG:O	2.36	0.42
43:n:9:ARG:CG	46:2:1789:G:O6	2.54	0.42
46:2:562:G:OP2	46:2:579:A:O2'	2.29	0.42
49:s:230:TRP:CE3	66:AM:46:TYR:CD1	3.07	0.42
50:t:138:VAL:HG23	50:t:184:ILE:CD1	2.48	0.42
52:v:132:VAL:HG23	52:v:202:ALA:HB2	2.01	0.42
4:D:53:VAL:O	4:D:54:ARG:NH1	2.46	0.42
12:M:35:ILE:HG22	12:M:46:ILE:HG22	2.00	0.42
28:1:429:U:O2'	36:f:88:ASN:O	2.35	0.42
46:2:33:U:O5'	46:2:594:A:N6	2.52	0.42
46:2:67:A:H61	46:2:69:G:N2	2.16	0.42
53:w:68:LEU:HB2	53:w:69:LEU:HD12	2.01	0.42
6:F:102:VAL:HG12	6:F:130:ILE:HD12	2.01	0.42
14:O:9:ILE:HG23	14:O:35:VAL:HA	2.01	0.42
28:1:1572:U:O2'	28:1:1573:G:O4'	2.19	0.42
28:1:1900:A:O2'	28:1:1906:G:N7	2.39	0.42
44:o:36:PHE:O	44:o:41:ARG:NH1	2.50	0.42
46:2:1752:U:O4	46:2:1753:A:N6	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:v:23:VAL:O	52:v:34:GLN:NE2	2.44	0.42
57:AD:117:LEU:O	57:AD:120:SER:OG	2.32	0.42
63:AJ:88:VAL:HG13	63:AJ:88:VAL:O	2.19	0.42
71:AR:73:LEU:O	71:AR:74:SER:OG	2.30	0.42
72:AS:59:SER:OG	72:AS:60:GLU:N	2.52	0.42
75:AX:19:G:OP1	75:AX:59:U:N3	2.52	0.42
3:C:280:ILE:HG22	16:Q:104:LEU:O	2.19	0.42
13:N:75:VAL:HG13	13:N:75:VAL:O	2.19	0.42
26:AA:7:ASP:OD1	26:AA:8:ARG:N	2.53	0.42
27:AB:73:GLY:O	27:AB:86:ILE:HD11	2.20	0.42
28:1:2618:G:O2'	28:1:2865:U:OP1	2.25	0.42
42:l:29:LEU:O	42:l:31:THR:N	2.52	0.42
46:2:104:A:O5'	46:2:308:C:N4	2.52	0.42
46:2:1382:A:O3'	64:AK:59:PRO:HB3	2.19	0.42
46:2:1775:U:O2'	46:2:1778:G:N7	2.53	0.42
51:u:34:GLY:O	51:u:39:ARG:NH2	2.52	0.42
53:w:105:ASP:OD1	53:w:105:ASP:N	2.52	0.42
57:AD:113:PHE:CE2	57:AD:117:LEU:HD11	2.55	0.42
70:AQ:69:ASN:OD1	70:AQ:70:LYS:N	2.52	0.42
3:C:327:LEU:HD13	6:F:166:ASN:ND2	2.35	0.42
6:F:94:LYS:NZ	28:1:1155:C:OP2	2.36	0.42
28:1:155:G:N1	28:1:265:A:OP2	2.47	0.42
28:1:373:A:N6	28:1:394:G:O2'	2.53	0.42
28:1:1016:C:O2'	28:1:1020:G:O6	2.33	0.42
41:k:46:ARG:NH2	41:k:50:SER:O	2.52	0.42
46:2:514:G:P	56:z:131:GLN:OE1	2.77	0.42
46:2:1419:G:C2	73:AT:54:LYS:NZ	2.82	0.42
46:2:1558:U:OP1	62:AI:122:HIS:CB	2.60	0.42
46:2:1796:C:C4	70:AQ:93:LYS:HD3	2.55	0.42
46:2:1796:C:C4	70:AQ:93:LYS:HE3	2.54	0.42
47:q:41:ARG:NH1	61:AH:105:GLN:HE21	2.16	0.42
48:r:121:ILE:CD1	48:r:161:ILE:HD12	2.49	0.42
53:w:141:ILE:CD1	53:w:175:ILE:HG22	2.50	0.42
74:AV:258:THR:OG1	74:AV:275:ARG:NH2	2.53	0.42
12:M:131:VAL:HG23	14:O:181:ALA:O	2.19	0.42
20:U:90:ARG:NH1	28:1:1682:U:O4	2.53	0.42
25:Z:31:GLU:OE1	25:Z:31:GLU:N	2.48	0.42
25:Z:97:SER:O	25:Z:100:THR:HG22	2.20	0.42
28:1:3042:U:OP2	28:1:3092:C:N4	2.40	0.42
46:2:175:G:H21	46:2:176:C:H41	1.66	0.42
46:2:226:A:N6	46:2:834:G:N7	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:2:301:A:O2'	46:2:334:G:N1	2.49	0.42
46:2:1173:C:O5'	62:AI:140:THR:OG1	2.37	0.42
46:2:1796:C:C4	70:AQ:93:LYS:CD	3.02	0.42
49:s:229:LEU:HD22	65:AL:13:VAL:HG23	2.02	0.42
60:AG:41:PRO:O	60:AG:43:ILE:HD12	2.20	0.42
62:AI:87:ASN:OD1	62:AI:88:ARG:N	2.52	0.42
6:F:29:GLU:OE1	6:F:29:GLU:N	2.50	0.42
6:F:148:VAL:HG12	6:F:181:ILE:HD11	2.01	0.42
25:Z:114:VAL:HG22	25:Z:118:PHE:CE2	2.55	0.42
28:1:1150:A:N6	28:1:2369:G:O2'	2.46	0.42
28:1:1481:A:O2'	28:1:1859:A:OP2	2.32	0.42
46:2:1367:G:H4'	63:AJ:119:LYS:HE3	2.02	0.42
61:AH:77:GLU:OE2	61:AH:77:GLU:N	2.51	0.42
1:A:117:GLU:OE1	1:A:163:ARG:NH1	2.52	0.42
3:C:203:ARG:NH1	3:C:226:GLU:OE1	2.53	0.42
8:H:156:GLN:NE2	28:1:3125:U:O2'	2.49	0.42
46:2:1162:C:C4	72:AS:24:GLY:HA2	2.50	0.42
60:AG:55:VAL:HG11	60:AG:89:LEU:HD11	2.02	0.42
64:AK:80:GLU:CD	73:AT:52:PHE:CD2	2.97	0.42
69:AP:95:HIS:HE1	69:AP:100:ILE:HG23	1.83	0.42
11:L:46:ILE:HG23	11:L:46:ILE:O	2.20	0.42
17:R:20:ARG:NH1	28:1:1875:G:N7	2.62	0.42
21:V:10:LYS:O	28:1:3039:C:O2'	2.36	0.42
28:1:361:A:O3'	40:j:45:ARG:NH2	2.53	0.42
28:1:1349:G:N2	28:1:1355:A:H62	2.18	0.42
33:c:99:ASP:N	33:c:99:ASP:OD1	2.53	0.42
46:2:80:A:H61	46:2:270:C:H5''	1.85	0.42
46:2:385:A:OP1	55:y:22:ARG:NE	2.53	0.42
46:2:1011:G:N2	46:2:1012:U:O4	2.53	0.42
50:t:96:LEU:O	50:t:96:LEU:HD23	2.19	0.42
57:AD:114:ARG:HA	57:AD:117:LEU:HD12	2.01	0.42
58:AE:103:ARG:NH1	70:AQ:52:ASP:OD2	2.53	0.42
10:J:72:ARG:NH1	29:3:40:C:O2	2.53	0.41
28:1:965:A:C2	31:a:43:ILE:HD11	2.55	0.41
46:2:697:C:C5	54:x:105:THR:CG2	3.03	0.41
46:2:747:C:N4	46:2:803:A:N1	2.68	0.41
46:2:1162:C:H4'	72:AS:22:ARG:HD2	2.02	0.41
46:2:1399:C:O2'	46:2:1401:A:OP2	2.38	0.41
72:AS:10:ALA:HB1	72:AS:30:VAL:CG2	2.50	0.41
15:P:3:ARG:NH1	28:1:398:A:N7	2.67	0.41
17:R:59:SER:OG	17:R:60:LYS:N	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:R:123:LEU:HD12	17:R:138:LEU:HD11	2.02	0.41
43:n:12:ARG:H	46:2:1025:A:H2'	1.84	0.41
46:2:365:G:H4'	46:2:757:A:H61	1.85	0.41
46:2:1367:G:C4'	63:AJ:119:LYS:HZ1	2.30	0.41
47:q:4:PRO:HG3	65:AL:40:ASP:CG	2.45	0.41
55:y:153:GLU:HB3	55:y:156:VAL:HG22	2.03	0.41
13:N:29:GLU:OE1	13:N:33:LYS:NZ	2.50	0.41
28:1:1566:A:C4	28:1:1567:U:C5	3.08	0.41
39:i:73:ALA:HB3	39:i:83:ALA:HB1	2.01	0.41
43:n:8:LYS:HG2	46:2:1789:G:C1'	2.45	0.41
46:2:360:A:O2'	46:2:361:C:O3'	2.33	0.41
46:2:1543:A:O2'	62:AI:136:GLN:NE2	2.53	0.41
49:s:62:PRO:HB3	65:AL:29:HIS:CE1	2.55	0.41
63:AJ:112:GLY:O	63:AJ:125:SER:OG	2.38	0.41
65:AL:39:VAL:HG13	65:AL:43:GLY:HA2	2.01	0.41
28:1:1903:U:O2'	28:1:1905:G:N7	2.48	0.41
31:a:81:LEU:HD22	31:a:107:ALA:CB	2.50	0.41
43:n:8:LYS:CB	46:2:1789:G:O2'	2.69	0.41
43:n:14:LYS:HB3	46:2:1774:G:O2'	2.21	0.41
46:2:748:U:P	66:AM:82:LYS:HZ2	2.40	0.41
46:2:1793:G:N1	70:AQ:75:VAL:CG2	2.83	0.41
52:v:206:SER:H	52:v:211:ILE:HD11	1.84	0.41
4:D:46:THR:O	4:D:46:THR:OG1	2.28	0.41
5:E:2:SER:OG	5:E:3:ALA:N	2.53	0.41
12:M:124:ARG:NH2	28:1:3213:A:N7	2.68	0.41
25:Z:92:PHE:CE1	25:Z:114:VAL:HG23	2.55	0.41
28:1:64:G:O2'	28:1:77:A:N3	2.47	0.41
28:1:280:U:N3	28:1:283:G:OP1	2.48	0.41
28:1:642:U:O2'	28:1:644:G:N7	2.46	0.41
43:n:1:MET:C	46:2:1031:U:C5'	2.94	0.41
46:2:36:C:N4	46:2:472:U:O2'	2.53	0.41
46:2:465:G:N7	46:2:467:G:N2	2.69	0.41
46:2:769:A:N3	56:z:44:ARG:NH1	2.67	0.41
48:r:171:ILE:HD13	48:r:197:ILE:HD13	2.02	0.41
49:s:230:TRP:HZ3	66:AM:46:TYR:CD2	2.37	0.41
69:AP:74:SER:O	69:AP:75:LEU:HD12	2.20	0.41
4:D:85:ARG:NH2	4:D:250:ASP:OD2	2.54	0.41
15:P:56:ARG:O	15:P:83:TRP:NE1	2.54	0.41
28:1:394:G:N1	28:1:397:A:OP2	2.49	0.41
28:1:1568:U:H5'	28:1:1569:U:O5'	2.20	0.41
28:1:2754:G:O2'	28:1:2755:C:OP1	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:3106:A:N6	28:1:3128:G:C2	2.84	0.41
43:n:11:ARG:NH1	46:2:1024:U:N3	2.68	0.41
43:n:12:ARG:HB2	46:2:1025:A:O2'	2.20	0.41
46:2:1338:C:OP2	46:2:1410:A:O2'	2.17	0.41
51:u:252:ARG:NH1	56:z:78:ARG:NH1	2.68	0.41
67:AN:23:ARG:O	67:AN:25:ALA:N	2.53	0.41
71:AR:75:GLU:O	71:AR:77:THR:N	2.52	0.41
74:AV:80:ALA:HB3	74:AV:92:TRP:HB2	2.03	0.41
1:A:219:ILE:HD11	28:1:2245:C:H5''	2.03	0.41
2:B:250:ALA:HB3	28:1:2880:U:O2	2.21	0.41
4:D:125:VAL:HG22	4:D:127:GLY:H	1.86	0.41
28:1:2263:C:P	46:2:1780:G:H21	2.44	0.41
28:1:2890:A:H61	28:1:2913:C:H42	1.68	0.41
58:AE:134:GLY:O	58:AE:136:ARG:NH1	2.54	0.41
60:AG:140:LYS:H	64:AK:73:GLY:HA2	1.86	0.41
62:AI:40:ARG:CB	63:AJ:45:MET:HE1	2.45	0.41
7:G:150:LEU:HD11	7:G:218:ILE:HD11	2.02	0.41
21:V:2:SER:OG	21:V:3:GLY:N	2.54	0.41
28:1:1646:G:N2	28:1:1808:G:O2'	2.48	0.41
28:1:3280:U:HO2'	28:1:3281:U:H6	1.69	0.41
37:g:44:CYS:N	37:g:49:SER:O	2.49	0.41
43:n:15:ARG:CZ	46:2:978:A:H61	2.22	0.41
46:2:94:U:OP1	51:u:4:GLY:C	2.64	0.41
48:r:83:LYS:HZ1	58:AE:114:ARG:CG	2.34	0.41
49:s:72:LEU:C	49:s:73:LEU:HD12	2.46	0.41
51:u:22:LYS:NZ	56:z:5:PRO:O	2.49	0.41
70:AQ:45:VAL:HG12	70:AQ:46:GLU:O	2.20	0.41
3:C:54:GLU:OE1	28:1:329:U:N3	2.53	0.41
8:H:67:ALA:O	8:H:71:VAL:HG23	2.21	0.41
8:H:177:ASP:OD1	8:H:177:ASP:N	2.53	0.41
23:X:109:LYS:NZ	28:1:1609:C:OP2	2.54	0.41
27:AB:27:THR:HG23	27:AB:29:LYS:H	1.85	0.41
27:AB:54:ILE:HG23	27:AB:55:ASP:H	1.85	0.41
28:1:2745:G:N2	28:1:2748:A:OP2	2.53	0.41
35:e:2:ALA:O	35:e:71:HIS:NE2	2.47	0.41
41:k:5:ILE:HG23	41:k:10:GLN:NE2	2.36	0.41
46:2:419:G:O2'	46:2:420:A:O4'	2.33	0.41
46:2:512:A:N6	46:2:538:A:O2'	2.54	0.41
46:2:792:U:P	51:u:187:ARG:NH2	2.94	0.41
46:2:967:A:O4'	66:AM:2:THR:HG21	2.21	0.41
50:t:131:ALA:HB1	50:t:188:ILE:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:x:123:ASP:OD2	54:x:124:LYS:N	2.53	0.41
57:AD:49:GLN:HA	57:AD:52:VAL:HG12	2.02	0.41
57:AD:142:GLU:OE1	57:AD:143:SER:N	2.54	0.41
74:AV:157:VAL:HG11	74:AV:225:LEU:HD13	2.02	0.41
75:AX:15:G:O2'	75:AX:60:C:N4	2.51	0.41
4:D:33:ARG:O	4:D:37:VAL:HG12	2.21	0.41
28:1:1019:G:O6	28:1:1033:U:C4	2.74	0.41
46:2:1162:C:C4	72:AS:24:GLY:C	2.99	0.41
46:2:1595:U:H5''	73:AT:31:ILE:HD11	2.01	0.41
49:s:38:VAL:HG13	49:s:39:THR:HG22	2.02	0.41
51:u:25:GLY:O	56:z:2:PRO:O	2.38	0.41
61:AH:105:GLN:N	61:AH:105:GLN:OE1	2.51	0.41
67:AN:61:SER:OG	67:AN:116:ASP:O	2.35	0.41
12:M:20:VAL:HG13	12:M:66:THR:OG1	2.21	0.40
14:O:4:GLU:OE1	14:O:4:GLU:N	2.54	0.40
27:AB:63:LEU:HD12	27:AB:63:LEU:O	2.21	0.40
28:1:761:A:H61	28:1:770:G:H1'	1.85	0.40
30:4:55:U:O4	30:4:62:C:C4	2.74	0.40
46:2:511:A:N6	46:2:538:A:O2'	2.53	0.40
46:2:1316:G:OP1	61:AH:7:LYS:N	2.54	0.40
46:2:1521:G:O2'	46:2:1522:U:OP1	2.37	0.40
48:r:127:VAL:HG21	48:r:176:VAL:HB	2.02	0.40
61:AH:107:SER:HB2	61:AH:119:LEU:HD13	2.03	0.40
4:D:258:LYS:NZ	29:3:119:U:OP2	2.47	0.40
26:AA:61:TRP:CZ3	73:AT:23:VAL:HA	2.56	0.40
28:1:266:A:H61	39:i:26:ILE:CG1	2.35	0.40
28:1:1447:G:O2'	28:1:2355:G:O6	2.33	0.40
31:a:88:ASP:OD1	31:a:89:GLN:N	2.54	0.40
33:c:57:GLU:OE1	33:c:69:TYR:OH	2.39	0.40
49:s:173:PRO:HD2	56:z:57:ARG:NH2	2.30	0.40
56:z:136:VAL:HG23	56:z:156:ILE:HB	2.03	0.40
68:AO:51:GLU:HG2	68:AO:54:ALA:HB2	2.03	0.40
2:B:47:LEU:HD22	2:B:335:ILE:HD11	2.03	0.40
7:G:60:ARG:NH2	30:4:151:C:OP1	2.54	0.40
17:R:62:ARG:NH2	28:1:3068:U:OP2	2.53	0.40
26:AA:60:SER:HB2	50:t:27:ARG:NH2	2.36	0.40
46:2:222:A:N7	46:2:833:U:N3	2.68	0.40
46:2:697:C:C5	54:x:105:THR:HG23	2.56	0.40
46:2:1503:A:H4'	63:AJ:37:VAL:HG13	2.04	0.40
71:AR:56:CYS:SG	71:AR:57:GLU:N	2.95	0.40
2:B:47:LEU:HD23	2:B:337:THR:HG22	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:1:68:C:N4	28:1:314:U:O2'	2.50	0.40
28:1:1219:C:N4	28:1:1220:U:O4	2.54	0.40
28:1:2678:A:N1	75:AZ:56:C:C2	2.89	0.40
43:n:9:ARG:HB2	46:2:1789:G:N9	2.37	0.40
46:2:1171:A:C4'	62:AI:144:ARG:HD3	2.48	0.40
75:AZ:66:A:N6	75:AZ:67:A:H62	2.20	0.40
21:V:37:ILE:HD11	21:V:61:THR:HG22	2.03	0.40
28:1:642:U:OP2	31:a:22:ILE:HG22	2.22	0.40
28:1:3026:G:H4'	28:1:3029:A:H62	1.86	0.40
33:c:75:ASN:O	33:c:79:THR:HG23	2.21	0.40
46:2:774:A:N6	46:2:786:C:O2	2.54	0.40
46:2:1354:G:H1	46:2:1368:G:HO2'	1.66	0.40
48:r:34:ALA:HB3	48:r:41:ARG:HB2	2.03	0.40
49:s:144:TRP:N	49:s:153:SER:OG	2.54	0.40
51:u:249:ALA:CB	56:z:71:PHE:HD1	2.34	0.40
55:y:105:ASP:OD1	55:y:105:ASP:N	2.54	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	
1	A	250/254 (98%)	238 (95%)	12 (5%)	0	100	100
2	B	384/387 (99%)	357 (93%)	27 (7%)	0	100	100
3	C	359/362 (99%)	320 (89%)	38 (11%)	1 (0%)	36	68
4	D	294/297 (99%)	267 (91%)	26 (9%)	1 (0%)	36	68
5	E	152/176 (86%)	142 (93%)	10 (7%)	0	100	100
6	F	220/244 (90%)	201 (91%)	18 (8%)	1 (0%)	24	59
7	G	231/256 (90%)	211 (91%)	20 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	H	189/191 (99%)	164 (87%)	25 (13%)	0	100	100
9	I	207/221 (94%)	192 (93%)	15 (7%)	0	100	100
10	J	167/174 (96%)	144 (86%)	23 (14%)	0	100	100
11	L	191/199 (96%)	162 (85%)	25 (13%)	4 (2%)	5	31
12	M	134/138 (97%)	122 (91%)	12 (9%)	0	100	100
13	N	201/204 (98%)	183 (91%)	18 (9%)	0	100	100
14	O	195/199 (98%)	177 (91%)	16 (8%)	2 (1%)	12	45
15	P	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
16	Q	183/186 (98%)	173 (94%)	10 (6%)	0	100	100
17	R	186/189 (98%)	174 (94%)	12 (6%)	0	100	100
18	S	170/172 (99%)	158 (93%)	12 (7%)	0	100	100
19	T	157/160 (98%)	142 (90%)	15 (10%)	0	100	100
20	U	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
21	V	134/137 (98%)	122 (91%)	11 (8%)	1 (1%)	18	52
22	W	61/155 (39%)	58 (95%)	3 (5%)	0	100	100
23	X	119/142 (84%)	115 (97%)	4 (3%)	0	100	100
24	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
25	Z	133/136 (98%)	118 (89%)	15 (11%)	0	100	100
26	AA	94/105 (90%)	79 (84%)	15 (16%)	0	100	100
27	AB	142/156 (91%)	123 (87%)	19 (13%)	0	100	100
31	a	146/149 (98%)	125 (86%)	20 (14%)	1 (1%)	18	52
32	b	56/59 (95%)	47 (84%)	9 (16%)	0	100	100
33	c	95/105 (90%)	86 (90%)	9 (10%)	0	100	100
34	d	107/113 (95%)	101 (94%)	6 (6%)	0	100	100
35	e	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	50
36	f	104/107 (97%)	97 (93%)	5 (5%)	2 (2%)	6	33
37	g	110/121 (91%)	101 (92%)	9 (8%)	0	100	100
38	h	117/120 (98%)	105 (90%)	12 (10%)	0	100	100
39	i	97/100 (97%)	81 (84%)	16 (16%)	0	100	100
40	j	85/88 (97%)	73 (86%)	11 (13%)	1 (1%)	10	42
41	k	75/78 (96%)	69 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	l	48/51 (94%)	40 (83%)	6 (12%)	2 (4%)	2	16
43	n	23/25 (92%)	16 (70%)	7 (30%)	0	100	100
44	o	103/106 (97%)	83 (81%)	20 (19%)	0	100	100
45	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
47	q	204/252 (81%)	166 (81%)	36 (18%)	2 (1%)	12	45
48	r	212/255 (83%)	184 (87%)	28 (13%)	0	100	100
49	s	215/254 (85%)	195 (91%)	20 (9%)	0	100	100
50	t	221/240 (92%)	198 (90%)	23 (10%)	0	100	100
51	u	258/261 (99%)	204 (79%)	53 (20%)	1 (0%)	30	62
52	v	204/225 (91%)	178 (87%)	26 (13%)	0	100	100
53	w	221/236 (94%)	173 (78%)	47 (21%)	1 (0%)	24	59
54	x	182/190 (96%)	160 (88%)	22 (12%)	0	100	100
55	y	184/200 (92%)	159 (86%)	25 (14%)	0	100	100
56	z	183/197 (93%)	166 (91%)	17 (9%)	0	100	100
57	AD	148/151 (98%)	130 (88%)	14 (10%)	4 (3%)	4	25
58	AE	125/138 (91%)	114 (91%)	11 (9%)	0	100	100
59	AF	122/142 (86%)	107 (88%)	15 (12%)	0	100	100
60	AG	139/143 (97%)	122 (88%)	17 (12%)	0	100	100
61	AH	116/136 (85%)	102 (88%)	14 (12%)	0	100	100
62	AI	143/146 (98%)	125 (87%)	18 (13%)	0	100	100
63	AJ	141/144 (98%)	131 (93%)	10 (7%)	0	100	100
64	AK	105/121 (87%)	95 (90%)	10 (10%)	0	100	100
65	AL	85/87 (98%)	71 (84%)	14 (16%)	0	100	100
66	AM	127/130 (98%)	115 (91%)	11 (9%)	1 (1%)	16	50
67	AN	142/145 (98%)	119 (84%)	23 (16%)	0	100	100
68	AO	132/135 (98%)	109 (83%)	23 (17%)	0	100	100
69	AP	68/108 (63%)	60 (88%)	8 (12%)	0	100	100
70	AQ	95/119 (80%)	62 (65%)	32 (34%)	1 (1%)	11	43
71	AR	79/82 (96%)	64 (81%)	14 (18%)	1 (1%)	9	40
72	AS	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
73	AT	51/56 (91%)	43 (84%)	8 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	AV	316/319 (99%)	287 (91%)	29 (9%)	0	100	100
All	All	10615/11395 (93%)	9433 (89%)	1154 (11%)	28 (0%)	37	68

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	339	LEU
14	O	111	PRO
36	f	58	GLU
47	q	113	ARG
11	L	48	PRO
35	e	79	VAL
36	f	59	VAL
40	j	65	ARG
11	L	77	LEU
14	O	110	PRO
21	V	105	PRO
47	q	112	THR
57	AD	85	PRO
57	AD	105	ASN
71	AR	76	GLY
4	D	20	PHE
31	a	78	LEU
53	w	10	ASN
57	AD	139	TRP
70	AQ	11	ASN
11	L	63	VAL
42	l	30	ARG
57	AD	104	ARG
6	F	158	LYS
42	l	31	THR
11	L	47	ALA
51	u	234	PRO
66	AM	67	GLY

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	
1	A	193/196 (98%)	193 (100%)	0	100	100
2	B	321/323 (99%)	320 (100%)	1 (0%)	86	88
3	C	288/289 (100%)	288 (100%)	0	100	100
4	D	244/245 (100%)	244 (100%)	0	100	100
5	E	134/153 (88%)	134 (100%)	0	100	100
6	F	186/205 (91%)	186 (100%)	0	100	100
7	G	187/208 (90%)	187 (100%)	0	100	100
8	H	171/171 (100%)	170 (99%)	1 (1%)	78	84
9	I	177/187 (95%)	177 (100%)	0	100	100
10	J	147/151 (97%)	147 (100%)	0	100	100
11	L	154/159 (97%)	154 (100%)	0	100	100
12	M	107/109 (98%)	107 (100%)	0	100	100
13	N	175/176 (99%)	175 (100%)	0	100	100
14	O	160/162 (99%)	160 (100%)	0	100	100
15	P	140/146 (96%)	140 (100%)	0	100	100
16	Q	150/151 (99%)	150 (100%)	0	100	100
17	R	153/154 (99%)	153 (100%)	0	100	100
18	S	156/156 (100%)	156 (100%)	0	100	100
19	T	136/137 (99%)	136 (100%)	0	100	100
20	U	87/107 (81%)	87 (100%)	0	100	100
21	V	104/105 (99%)	104 (100%)	0	100	100
22	W	55/129 (43%)	55 (100%)	0	100	100
23	X	104/118 (88%)	104 (100%)	0	100	100
24	Y	109/110 (99%)	109 (100%)	0	100	100
25	Z	115/116 (99%)	113 (98%)	2 (2%)	53	75
26	AA	77/98 (79%)	76 (99%)	1 (1%)	61	78
27	AB	129/137 (94%)	129 (100%)	0	100	100
31	a	118/119 (99%)	118 (100%)	0	100	100
32	b	46/47 (98%)	46 (100%)	0	100	100
33	c	81/88 (92%)	81 (100%)	0	100	100
34	d	94/97 (97%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	e	109/111 (98%)	109 (100%)	0	100	100
36	f	90/91 (99%)	90 (100%)	0	100	100
37	g	95/103 (92%)	95 (100%)	0	100	100
38	h	104/105 (99%)	104 (100%)	0	100	100
39	i	81/82 (99%)	81 (100%)	0	100	100
40	j	70/71 (99%)	70 (100%)	0	100	100
41	k	68/69 (99%)	68 (100%)	0	100	100
42	l	45/46 (98%)	45 (100%)	0	100	100
43	n	22/23 (96%)	22 (100%)	0	100	100
44	o	90/91 (99%)	90 (100%)	0	100	100
45	p	71/72 (99%)	70 (99%)	1 (1%)	59	77
47	q	164/210 (78%)	164 (100%)	0	100	100
48	r	191/224 (85%)	191 (100%)	0	100	100
49	s	176/205 (86%)	175 (99%)	1 (1%)	78	84
50	t	182/195 (93%)	182 (100%)	0	100	100
51	u	221/222 (100%)	221 (100%)	0	100	100
52	v	173/191 (91%)	173 (100%)	0	100	100
53	w	189/201 (94%)	189 (100%)	0	100	100
54	x	165/170 (97%)	165 (100%)	0	100	100
55	y	150/161 (93%)	150 (100%)	0	100	100
56	z	158/166 (95%)	158 (100%)	0	100	100
57	AD	127/128 (99%)	127 (100%)	0	100	100
58	AE	81/105 (77%)	81 (100%)	0	100	100
59	AF	101/118 (86%)	101 (100%)	0	100	100
60	AG	117/119 (98%)	117 (100%)	0	100	100
61	AH	94/124 (76%)	94 (100%)	0	100	100
62	AI	128/129 (99%)	128 (100%)	0	100	100
63	AJ	115/116 (99%)	115 (100%)	0	100	100
64	AK	100/114 (88%)	100 (100%)	0	100	100
65	AL	74/74 (100%)	74 (100%)	0	100	100
66	AM	110/111 (99%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	AN	119/120 (99%)	119 (100%)	0	100	100
68	AO	112/113 (99%)	111 (99%)	1 (1%)	70	81
69	AP	61/89 (68%)	61 (100%)	0	100	100
70	AQ	83/100 (83%)	83 (100%)	0	100	100
71	AR	70/71 (99%)	70 (100%)	0	100	100
72	AS	56/60 (93%)	56 (100%)	0	100	100
73	AT	47/49 (96%)	47 (100%)	0	100	100
74	AV	259/262 (99%)	259 (100%)	0	100	100
All	All	8966/9560 (94%)	8958 (100%)	8 (0%)	87	91

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	85	VAL
8	H	49	ASN
25	Z	23	VAL
25	Z	103	GLN
26	AA	28	ASN
45	p	42	CYS
49	s	201	ASN
68	AO	34	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
2	B	319	ASN
3	C	196	ASN
6	F	244	ASN
8	H	8	GLN
16	Q	158	HIS
17	R	166	ASN
19	T	49	GLN
20	U	40	HIS
21	V	98	ASN
24	Y	42	GLN
35	e	78	ASN
40	j	69	HIS

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Mol	Chain	Res	Type
41	k	40	GLN
42	l	19	GLN
44	o	82	GLN
47	q	21	ASN
48	r	79	HIS
49	s	201	ASN
49	s	209	ASN
51	u	98	ASN
52	v	35	GLN
52	v	86	GLN
54	x	74	GLN
56	z	123	HIS
57	AD	36	GLN
57	AD	58	HIS
60	AG	94	GLN
62	AI	12	GLN
63	AJ	48	GLN
63	AJ	129	GLN
65	AL	70	ASN
67	AN	27	ASN
68	AO	77	ASN
68	AO	110	GLN
74	AV	52	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	1	3109/3395 (91%)	680 (21%)	7 (0%)
29	3	120/121 (99%)	20 (16%)	0
30	4	157/158 (99%)	37 (23%)	0
46	2	1703/1800 (94%)	807 (47%)	13 (0%)
75	AX	72/76 (94%)	22 (30%)	0
75	AZ	72/76 (94%)	23 (31%)	0
All	All	5233/5626 (93%)	1589 (30%)	20 (0%)

All (1589) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	1	6	A
28	1	22	G
28	1	26	A

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Mol	Chain	Res	Type
28	1	35	A
28	1	40	A
28	1	43	A
28	1	49	A
28	1	50	U
28	1	60	A
28	1	65	A
28	1	66	A
28	1	75	G
28	1	92	G
28	1	93	C
28	1	96	G
28	1	110	G
28	1	111	C
28	1	113	C
28	1	117	U
28	1	118	U
28	1	120	G
28	1	121	A
28	1	134	U
28	1	136	G
28	1	149	U
28	1	156	G
28	1	157	A
28	1	161	G
28	1	163	C
28	1	164	A
28	1	165	A
28	1	168	U
28	1	169	U
28	1	171	G
28	1	172	G
28	1	175	C
28	1	182	U
28	1	190	U
28	1	191	U
28	1	200	C
28	1	211	A
28	1	219	A
28	1	220	G
28	1	234	G
28	1	240	U

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Mol	Chain	Res	Type
28	1	241	G
28	1	242	C
28	1	244	G
28	1	251	G
28	1	253	A
28	1	254	A
28	1	259	C
28	1	263	C
28	1	265	A
28	1	266	A
28	1	267	G
28	1	268	A
28	1	269	G
28	1	284	A
28	1	286	U
28	1	289	A
28	1	298	U
28	1	315	C
28	1	329	U
28	1	343	U
28	1	346	C
28	1	347	G
28	1	368	G
28	1	375	A
28	1	376	G
28	1	385	A
28	1	398	A
28	1	399	A
28	1	403	C
28	1	404	G
28	1	411	U
28	1	421	G
28	1	422	A
28	1	438	A
28	1	439	C
28	1	440	A
28	1	441	U
28	1	442	G
28	1	447	U
28	1	448	U
28	1	451	U
28	1	487	U

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Mol	Chain	Res	Type
28	1	488	U
28	1	490	C
28	1	492	C
28	1	494	G
28	1	495	G
28	1	498	A
28	1	512	U
28	1	520	U
28	1	521	A
28	1	523	A
28	1	533	A
28	1	534	U
28	1	535	G
28	1	540	U
28	1	541	U
28	1	542	G
28	1	543	C
28	1	544	C
28	1	552	G
28	1	553	U
28	1	554	A
28	1	555	U
28	1	557	A
28	1	558	U
28	1	559	A
28	1	560	G
28	1	582	G
28	1	597	G
28	1	604	G
28	1	607	A
28	1	611	A
28	1	619	A
28	1	620	U
28	1	621	A
28	1	645	A
28	1	649	A
28	1	662	U
28	1	677	A
28	1	678	G
28	1	681	U
28	1	691	A
28	1	705	A

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Mol	Chain	Res	Type
28	1	712	G
28	1	715	A
28	1	719	U
28	1	723	U
28	1	733	G
28	1	734	C
28	1	735	A
28	1	737	G
28	1	761	A
28	1	763	G
28	1	764	U
28	1	765	C
28	1	766	U
28	1	767	U
28	1	768	C
28	1	770	G
28	1	771	A
28	1	773	G
28	1	776	U
28	1	777	U
28	1	780	A
28	1	781	G
28	1	785	G
28	1	786	A
28	1	799	G
28	1	800	G
28	1	801	A
28	1	808	A
28	1	815	G
28	1	817	A
28	1	821	U
28	1	825	U
28	1	826	G
28	1	830	A
28	1	847	A
28	1	861	C
28	1	864	G
28	1	874	U
28	1	879	U
28	1	880	G
28	1	896	A
28	1	907	G

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Mol	Chain	Res	Type
28	1	908	G
28	1	914	A
28	1	916	G
28	1	923	C
28	1	937	G
28	1	944	C
28	1	953	G
28	1	959	C
28	1	960	U
28	1	974	G
28	1	978	G
28	1	979	U
28	1	980	A
28	1	984	G
28	1	985	U
28	1	994	G
28	1	1001	G
28	1	1002	A
28	1	1010	G
28	1	1011	A
28	1	1014	U
28	1	1015	U
28	1	1017	C
28	1	1018	G
28	1	1020	G
28	1	1024	G
28	1	1026	A
28	1	1027	A
28	1	1028	U
28	1	1029	G
28	1	1030	A
28	1	1031	C
28	1	1035	G
28	1	1036	A
28	1	1044	U
28	1	1047	A
28	1	1049	C
28	1	1063	G
28	1	1064	A
28	1	1066	G
28	1	1072	G
28	1	1075	A

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Mol	Chain	Res	Type
28	1	1081	U
28	1	1093	A
28	1	1094	U
28	1	1095	U
28	1	1097	G
28	1	1098	A
28	1	1103	A
28	1	1108	U
28	1	1116	G
28	1	1117	G
28	1	1122	U
28	1	1124	U
28	1	1131	G
28	1	1135	A
28	1	1153	A
28	1	1155	C
28	1	1157	G
28	1	1159	A
28	1	1163	A
28	1	1168	U
28	1	1177	G
28	1	1178	G
28	1	1180	A
28	1	1181	U
28	1	1190	A
28	1	1192	C
28	1	1196	C
28	1	1201	C
28	1	1203	A
28	1	1208	U
28	1	1215	U
28	1	1216	C
28	1	1217	A
28	1	1219	C
28	1	1220	U
28	1	1222	G
28	1	1223	A
28	1	1224	C
28	1	1226	G
28	1	1227	C
28	1	1228	C
28	1	1280	C

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Mol	Chain	Res	Type
28	1	1281	G
28	1	1282	G
28	1	1283	C
28	1	1285	G
28	1	1287	A
28	1	1288	U
28	1	1289	G
28	1	1294	A
28	1	1305	U
28	1	1307	G
28	1	1309	U
28	1	1313	G
28	1	1317	A
28	1	1330	A
28	1	1348	U
28	1	1350	A
28	1	1351	U
28	1	1352	A
28	1	1353	U
28	1	1356	U
28	1	1357	G
28	1	1366	A
28	1	1386	A
28	1	1399	A
28	1	1400	G
28	1	1408	G
28	1	1421	G
28	1	1434	G
28	1	1437	C
28	1	1443	G
28	1	1446	A
28	1	1458	U
28	1	1482	A
28	1	1483	G
28	1	1508	C
28	1	1511	U
28	1	1523	U
28	1	1527	C
28	1	1539	A
28	1	1555	U
28	1	1556	C
28	1	1561	G

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Mol	Chain	Res	Type
28	1	1562	C
28	1	1563	C
28	1	1566	A
28	1	1567	U
28	1	1568	U
28	1	1569	U
28	1	1570	U
28	1	1571	A
28	1	1572	U
28	1	1573	G
28	1	1575	A
28	1	1576	G
28	1	1577	G
28	1	1580	A
28	1	1581	C
28	1	1582	C
28	1	1583	A
28	1	1588	A
28	1	1589	A
28	1	1593	A
28	1	1605	A
28	1	1606	U
28	1	1613	A
28	1	1620	U
28	1	1627	U
28	1	1628	C
28	1	1629	U
28	1	1630	U
28	1	1636	U
28	1	1637	A
28	1	1642	A
28	1	1643	A
28	1	1645	U
28	1	1647	A
28	1	1657	C
28	1	1677	G
28	1	1694	U
28	1	1715	A
28	1	1717	U
28	1	1724	U
28	1	1741	A
28	1	1742	U

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Mol	Chain	Res	Type
28	1	1750	A
28	1	1751	G
28	1	1756	C
28	1	1761	C
28	1	1763	U
28	1	1764	U
28	1	1765	U
28	1	1770	G
28	1	1773	C
28	1	1775	G
28	1	1780	G
28	1	1795	U
28	1	1797	A
28	1	1808	G
28	1	1809	A
28	1	1812	G
28	1	1813	A
28	1	1814	A
28	1	1815	U
28	1	1817	G
28	1	1821	U
28	1	1822	C
28	1	1840	U
28	1	1842	A
28	1	1850	A
28	1	1855	U
28	1	1878	G
28	1	1879	A
28	1	1880	U
28	1	1886	A
28	1	1893	A
28	1	1906	G
28	1	1908	A
28	1	1926	C
28	1	1928	G
28	1	1948	G
28	1	1950	U
28	1	1952	G
28	1	1953	G
28	1	1954	G
28	1	1955	U
28	1	2094	C

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Mol	Chain	Res	Type
28	1	2096	A
28	1	2111	G
28	1	2112	U
28	1	2113	A
28	1	2122	G
28	1	2131	A
28	1	2138	A
28	1	2142	A
28	1	2158	A
28	1	2170	U
28	1	2178	A
28	1	2179	C
28	1	2188	A
28	1	2205	U
28	1	2206	G
28	1	2207	A
28	1	2208	A
28	1	2209	U
28	1	2210	G
28	1	2235	C
28	1	2244	A
28	1	2246	G
28	1	2255	A
28	1	2256	A
28	1	2258	U
28	1	2259	A
28	1	2260	U
28	1	2261	G
28	1	2262	A
28	1	2263	C
28	1	2265	C
28	1	2266	U
28	1	2269	U
28	1	2273	G
28	1	2274	U
28	1	2279	A
28	1	2281	A
28	1	2307	G
28	1	2308	C
28	1	2310	U
28	1	2313	A
28	1	2315	G

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Mol	Chain	Res	Type
28	1	2319	U
28	1	2334	U
28	1	2336	U
28	1	2359	C
28	1	2363	A
28	1	2373	A
28	1	2375	G
28	1	2388	U
28	1	2393	G
28	1	2397	A
28	1	2402	A
28	1	2403	G
28	1	2404	A
28	1	2411	U
28	1	2412	G
28	1	2428	U
28	1	2435	G
28	1	2442	G
28	1	2443	A
28	1	2507	C
28	1	2509	U
28	1	2514	U
28	1	2515	A
28	1	2522	G
28	1	2524	A
28	1	2525	G
28	1	2526	C
28	1	2529	A
28	1	2530	G
28	1	2531	C
28	1	2532	U
28	1	2533	G
28	1	2534	G
28	1	2535	A
28	1	2536	A
28	1	2537	U
28	1	2538	U
28	1	2540	A
28	1	2541	U
28	1	2542	U
28	1	2544	U
28	1	2545	C

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Mol	Chain	Res	Type
28	1	2546	C
28	1	2549	G
28	1	2552	C
28	1	2553	U
28	1	2555	G
28	1	2560	C
28	1	2561	A
28	1	2562	A
28	1	2563	G
28	1	2564	G
28	1	2566	C
28	1	2567	C
28	1	2568	C
28	1	2569	A
28	1	2570	U
28	1	2571	U
28	1	2572	C
28	1	2574	G
28	1	2579	G
28	1	2581	U
28	1	2585	G
28	1	2586	G
28	1	2587	U
28	1	2593	A
28	1	2594	C
28	1	2606	G
28	1	2607	G
28	1	2614	G
28	1	2635	A
28	1	2644	C
28	1	2645	G
28	1	2648	G
28	1	2652	U
28	1	2656	A
28	1	2672	G
28	1	2674	A
28	1	2676	A
28	1	2677	G
28	1	2681	U
28	1	2689	A
28	1	2691	A
28	1	2694	A

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Mol	Chain	Res	Type
28	1	2695	A
28	1	2704	A
28	1	2714	G
28	1	2726	C
28	1	2727	A
28	1	2728	G
28	1	2729	U
28	1	2737	C
28	1	2753	G
28	1	2760	C
28	1	2772	C
28	1	2773	C
28	1	2777	G
28	1	2778	G
28	1	2782	U
28	1	2783	U
28	1	2795	U
28	1	2796	G
28	1	2799	A
28	1	2800	G
28	1	2801	A
28	1	2802	A
28	1	2803	A
28	1	2804	A
28	1	2808	A
28	1	2810	C
28	1	2817	A
28	1	2828	G
28	1	2834	G
28	1	2836	C
28	1	2837	A
28	1	2838	A
28	1	2842	U
28	1	2844	C
28	1	2845	A
28	1	2846	U
28	1	2847	A
28	1	2850	G
28	1	2851	A
28	1	2858	U
28	1	2859	U
28	1	2861	U

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Mol	Chain	Res	Type
28	1	2867	C
28	1	2871	G
28	1	2872	A
28	1	2873	U
28	1	2875	U
28	1	2887	A
28	1	2898	G
28	1	2900	A
28	1	2923	U
28	1	2924	U
28	1	2925	C
28	1	2935	U
28	1	2936	A
28	1	2938	G
28	1	2941	A
28	1	2942	C
28	1	2945	G
28	1	2947	G
28	1	2956	A
28	1	2968	G
28	1	2971	A
28	1	2972	G
28	1	2983	C
28	1	2997	G
28	1	3011	A
28	1	3012	A
28	1	3017	A
28	1	3020	U
28	1	3021	A
28	1	3022	G
28	1	3023	U
28	1	3024	A
28	1	3026	G
28	1	3028	G
28	1	3029	A
28	1	3030	G
28	1	3031	G
28	1	3032	A
28	1	3033	A
28	1	3036	G
28	1	3059	G
28	1	3078	U

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Mol	Chain	Res	Type
28	1	3080	G
28	1	3092	C
28	1	3101	G
28	1	3104	U
28	1	3105	U
28	1	3109	G
28	1	3115	C
28	1	3116	G
28	1	3117	C
28	1	3119	U
28	1	3120	C
28	1	3121	U
28	1	3122	A
28	1	3129	A
28	1	3130	A
28	1	3131	U
28	1	3142	A
28	1	3143	C
28	1	3153	U
28	1	3154	C
28	1	3156	U
28	1	3157	U
28	1	3171	U
28	1	3172	A
28	1	3173	G
28	1	3174	A
28	1	3176	G
28	1	3179	U
28	1	3181	C
28	1	3187	A
28	1	3196	U
28	1	3198	U
28	1	3207	U
28	1	3208	G
28	1	3216	G
28	1	3217	C
28	1	3218	A
28	1	3219	G
28	1	3220	G
28	1	3222	U
28	1	3223	A
28	1	3224	G

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Mol	Chain	Res	Type
28	1	3225	C
28	1	3226	A
28	1	3227	A
28	1	3228	C
28	1	3229	G
28	1	3230	G
28	1	3231	U
28	1	3233	C
28	1	3238	G
28	1	3247	G
28	1	3253	G
28	1	3259	U
28	1	3261	C
28	1	3263	G
28	1	3268	A
28	1	3269	U
28	1	3273	A
28	1	3274	A
28	1	3276	G
28	1	3277	U
28	1	3279	A
28	1	3281	U
28	1	3294	A
28	1	3295	A
28	1	3304	U
28	1	3313	U
28	1	3316	A
28	1	3319	U
28	1	3320	A
28	1	3334	U
28	1	3335	A
28	1	3341	U
28	1	3345	G
28	1	3351	U
28	1	3352	U
28	1	3353	G
28	1	3356	G
28	1	3357	U
28	1	3368	U
28	1	3369	G
28	1	3378	C
28	1	3381	U

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Mol	Chain	Res	Type
28	1	3382	U
28	1	3384	U
28	1	3389	U
28	1	3390	G
28	1	3396	U
29	3	7	G
29	3	10	C
29	3	11	A
29	3	22	A
29	3	33	C
29	3	35	C
29	3	42	A
29	3	49	G
29	3	50	U
29	3	51	A
29	3	55	A
29	3	65	G
29	3	67	G
29	3	71	G
29	3	72	A
29	3	73	C
29	3	74	C
29	3	93	C
29	3	112	G
29	3	121	U
30	4	23	U
30	4	27	U
30	4	34	U
30	4	35	C
30	4	55	U
30	4	59	A
30	4	62	C
30	4	63	G
30	4	72	A
30	4	73	U
30	4	75	G
30	4	76	C
30	4	79	A
30	4	80	A
30	4	81	U
30	4	82	U
30	4	83	C

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Mol	Chain	Res	Type
30	4	84	C
30	4	85	G
30	4	86	U
30	4	87	G
30	4	88	A
30	4	90	U
30	4	91	C
30	4	95	G
30	4	97	A
30	4	104	A
30	4	106	C
30	4	112	U
30	4	113	U
30	4	114	G
30	4	120	C
30	4	127	U
30	4	138	A
30	4	148	G
30	4	152	G
30	4	158	U
46	2	2	A
46	2	3	U
46	2	4	C
46	2	10	G
46	2	15	U
46	2	25	C
46	2	26	A
46	2	30	G
46	2	33	U
46	2	36	C
46	2	37	U
46	2	39	A
46	2	40	A
46	2	41	A
46	2	42	G
46	2	43	A
46	2	44	U
46	2	45	U
46	2	46	A
46	2	47	A
46	2	48	G
46	2	49	C

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Mol	Chain	Res	Type
46	2	50	C
46	2	56	U
46	2	59	C
46	2	61	A
46	2	66	U
46	2	68	A
46	2	69	G
46	2	70	C
46	2	71	A
46	2	72	A
46	2	73	U
46	2	74	U
46	2	76	A
46	2	79	C
46	2	80	A
46	2	82	U
46	2	84	A
46	2	86	A
46	2	88	U
46	2	89	G
46	2	93	A
46	2	94	U
46	2	96	G
46	2	99	C
46	2	100	A
46	2	103	A
46	2	104	A
46	2	113	U
46	2	114	C
46	2	115	G
46	2	116	U
46	2	119	A
46	2	121	U
46	2	122	U
46	2	123	G
46	2	124	A
46	2	125	U
46	2	127	G
46	2	131	C
46	2	132	U
46	2	133	U
46	2	134	U

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Mol	Chain	Res	Type
46	2	135	A
46	2	136	C
46	2	141	U
46	2	142	G
46	2	143	G
46	2	144	U
46	2	147	A
46	2	148	A
46	2	149	C
46	2	150	U
46	2	152	U
46	2	153	G
46	2	154	G
46	2	156	A
46	2	157	A
46	2	158	U
46	2	159	U
46	2	160	C
46	2	161	U
46	2	162	A
46	2	164	A
46	2	167	U
46	2	170	U
46	2	171	A
46	2	174	U
46	2	175	G
46	2	177	U
46	2	178	U
46	2	180	A
46	2	181	A
46	2	182	A
46	2	187	G
46	2	189	C
46	2	191	C
46	2	193	U
46	2	194	U
46	2	195	G
46	2	196	G
46	2	197	A
46	2	199	G
46	2	200	A
46	2	202	A

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Mol	Chain	Res	Type
46	2	204	G
46	2	208	U
46	2	211	U
46	2	212	U
46	2	216	U
46	2	217	A
46	2	219	A
46	2	223	U
46	2	224	C
46	2	225	A
46	2	227	U
46	2	231	U
46	2	232	U
46	2	233	C
46	2	234	G
46	2	235	G
46	2	237	C
46	2	238	U
46	2	239	C
46	2	240	U
46	2	241	U
46	2	242	U
46	2	243	G
46	2	244	A
46	2	247	A
46	2	250	C
46	2	251	A
46	2	254	A
46	2	257	A
46	2	260	U
46	2	261	U
46	2	264	G
46	2	265	A
46	2	266	A
46	2	267	U
46	2	269	G
46	2	272	U
46	2	273	G
46	2	276	C
46	2	277	U
46	2	278	U
46	2	279	G

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Mol	Chain	Res	Type
46	2	280	U
46	2	285	G
46	2	287	G
46	2	288	A
46	2	290	G
46	2	292	U
46	2	293	U
46	2	294	C
46	2	297	U
46	2	299	A
46	2	302	U
46	2	303	U
46	2	308	C
46	2	309	C
46	2	313	U
46	2	314	C
46	2	316	A
46	2	320	U
46	2	321	C
46	2	322	G
46	2	323	A
46	2	337	G
46	2	342	C
46	2	343	C
46	2	344	A
46	2	345	U
46	2	349	U
46	2	350	U
46	2	351	C
46	2	352	A
46	2	354	C
46	2	359	A
46	2	360	A
46	2	361	C
46	2	375	U
46	2	379	U
46	2	380	U
46	2	381	C
46	2	388	G
46	2	391	A
46	2	393	C
46	2	398	G

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Mol	Chain	Res	Type
46	2	400	A
46	2	402	C
46	2	403	G
46	2	404	G
46	2	408	C
46	2	410	A
46	2	411	C
46	2	412	A
46	2	415	C
46	2	417	A
46	2	418	G
46	2	419	G
46	2	422	G
46	2	423	G
46	2	424	C
46	2	425	A
46	2	426	G
46	2	428	A
46	2	432	G
46	2	433	C
46	2	435	C
46	2	436	A
46	2	438	A
46	2	440	U
46	2	441	A
46	2	443	C
46	2	447	U
46	2	448	C
46	2	451	A
46	2	453	U
46	2	454	U
46	2	455	C
46	2	459	G
46	2	464	A
46	2	466	U
46	2	467	G
46	2	468	A
46	2	469	C
46	2	470	A
46	2	471	A
46	2	473	A
46	2	474	A

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Mol	Chain	Res	Type
46	2	475	A
46	2	477	A
46	2	478	A
46	2	485	A
46	2	487	G
46	2	489	C
46	2	491	C
46	2	492	A
46	2	495	C
46	2	497	G
46	2	498	G
46	2	502	U
46	2	503	G
46	2	504	U
46	2	505	A
46	2	507	U
46	2	508	U
46	2	509	G
46	2	511	A
46	2	513	U
46	2	514	G
46	2	515	A
46	2	518	A
46	2	519	C
46	2	525	A
46	2	526	A
46	2	533	U
46	2	534	A
46	2	538	A
46	2	539	G
46	2	540	G
46	2	541	A
46	2	542	A
46	2	543	C
46	2	544	A
46	2	545	A
46	2	546	U
46	2	551	G
46	2	553	G
46	2	557	G
46	2	558	U
46	2	561	G

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Mol	Chain	Res	Type
46	2	563	U
46	2	564	G
46	2	565	C
46	2	567	A
46	2	568	G
46	2	569	C
46	2	570	A
46	2	571	G
46	2	572	C
46	2	574	G
46	2	577	G
46	2	578	U
46	2	579	A
46	2	580	A
46	2	581	U
46	2	583	C
46	2	585	A
46	2	586	G
46	2	589	C
46	2	593	U
46	2	594	A
46	2	598	U
46	2	600	U
46	2	601	A
46	2	603	U
46	2	605	A
46	2	606	A
46	2	607	G
46	2	608	U
46	2	609	U
46	2	611	U
46	2	612	U
46	2	613	G
46	2	615	A
46	2	617	U
46	2	619	A
46	2	620	A
46	2	622	A
46	2	623	A
46	2	624	G
46	2	628	G
46	2	629	U

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Mol	Chain	Res	Type
46	2	638	U
46	2	639	U
46	2	640	U
46	2	643	G
46	2	645	C
46	2	646	C
46	2	647	G
46	2	648	G
46	2	649	U
46	2	650	U
46	2	651	G
46	2	652	G
46	2	686	C
46	2	687	G
46	2	688	G
46	2	689	G
46	2	690	G
46	2	691	C
46	2	692	C
46	2	693	U
46	2	694	U
46	2	695	U
46	2	696	C
46	2	698	U
46	2	699	U
46	2	700	C
46	2	702	G
46	2	703	G
46	2	704	C
46	2	705	U
46	2	706	A
46	2	707	A
46	2	731	C
46	2	732	G
46	2	733	A
46	2	734	A
46	2	735	C
46	2	736	C
46	2	737	A
46	2	738	G
46	2	739	G
46	2	740	A

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Mol	Chain	Res	Type
46	2	741	C
46	2	742	U
46	2	743	U
46	2	747	C
46	2	748	U
46	2	750	U
46	2	751	G
46	2	753	A
46	2	756	A
46	2	759	U
46	2	761	G
46	2	763	G
46	2	766	U
46	2	768	C
46	2	769	A
46	2	770	A
46	2	772	G
46	2	774	A
46	2	778	G
46	2	779	U
46	2	780	A
46	2	781	U
46	2	783	G
46	2	785	U
46	2	786	C
46	2	790	U
46	2	791	A
46	2	794	U
46	2	796	A
46	2	797	G
46	2	798	C
46	2	799	A
46	2	801	G
46	2	802	G
46	2	803	A
46	2	809	A
46	2	810	G
46	2	811	A
46	2	812	A
46	2	813	U
46	2	814	A
46	2	815	G

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Mol	Chain	Res	Type
46	2	816	G
46	2	817	A
46	2	819	G
46	2	820	U
46	2	821	U
46	2	824	G
46	2	825	U
46	2	827	C
46	2	828	U
46	2	830	U
46	2	831	U
46	2	833	U
46	2	834	G
46	2	835	U
46	2	837	G
46	2	841	U
46	2	842	C
46	2	848	C
46	2	849	C
46	2	850	A
46	2	853	G
46	2	855	A
46	2	856	A
46	2	857	U
46	2	858	G
46	2	859	A
46	2	863	A
46	2	864	U
46	2	865	A
46	2	869	A
46	2	873	U
46	2	888	U
46	2	894	U
46	2	897	C
46	2	898	A
46	2	902	G
46	2	905	A
46	2	906	A
46	2	907	A
46	2	913	G
46	2	920	U
46	2	932	U

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Mol	Chain	Res	Type
46	2	933	A
46	2	934	C
46	2	935	U
46	2	942	G
46	2	951	A
46	2	960	U
46	2	963	A
46	2	964	U
46	2	966	A
46	2	988	A
46	2	990	C
46	2	992	A
46	2	993	A
46	2	1004	U
46	2	1005	A
46	2	1024	U
46	2	1025	A
46	2	1026	A
46	2	1027	A
46	2	1028	C
46	2	1029	U
46	2	1030	A
46	2	1031	U
46	2	1032	G
46	2	1038	U
46	2	1039	A
46	2	1053	G
46	2	1055	U
46	2	1063	U
46	2	1064	G
46	2	1065	A
46	2	1066	C
46	2	1076	A
46	2	1081	A
46	2	1089	U
46	2	1092	A
46	2	1096	C
46	2	1097	U
46	2	1098	U
46	2	1099	U
46	2	1100	G
46	2	1113	A

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Mol	Chain	Res	Type
46	2	1124	A
46	2	1125	A
46	2	1128	C
46	2	1136	U
46	2	1137	A
46	2	1138	A
46	2	1150	G
46	2	1151	A
46	2	1156	C
46	2	1158	C
46	2	1159	C
46	2	1162	C
46	2	1163	A
46	2	1164	G
46	2	1166	A
46	2	1167	G
46	2	1168	U
46	2	1171	A
46	2	1172	G
46	2	1173	C
46	2	1175	U
46	2	1176	G
46	2	1181	U
46	2	1182	U
46	2	1185	U
46	2	1190	C
46	2	1191	U
46	2	1192	C
46	2	1194	A
46	2	1196	A
46	2	1199	G
46	2	1200	G
46	2	1201	G
46	2	1202	A
46	2	1203	A
46	2	1205	C
46	2	1207	C
46	2	1208	A
46	2	1209	C
46	2	1213	G
46	2	1214	U
46	2	1217	A

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Mol	Chain	Res	Type
46	2	1218	G
46	2	1219	A
46	2	1222	C
46	2	1224	A
46	2	1258	U
46	2	1261	G
46	2	1264	G
46	2	1265	G
46	2	1266	U
46	2	1269	U
46	2	1270	G
46	2	1273	G
46	2	1275	A
46	2	1276	U
46	2	1277	G
46	2	1280	C
46	2	1285	U
46	2	1286	U
46	2	1287	A
46	2	1295	G
46	2	1298	U
46	2	1299	G
46	2	1301	U
46	2	1307	U
46	2	1309	C
46	2	1310	U
46	2	1311	U
46	2	1312	A
46	2	1314	U
46	2	1315	U
46	2	1319	A
46	2	1320	U
46	2	1321	A
46	2	1327	C
46	2	1328	G
46	2	1329	A
46	2	1331	A
46	2	1332	C
46	2	1335	U
46	2	1336	A
46	2	1337	A
46	2	1338	C

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Mol	Chain	Res	Type
46	2	1339	C
46	2	1340	U
46	2	1341	A
46	2	1343	U
46	2	1344	A
46	2	1345	A
46	2	1347	U
46	2	1348	A
46	2	1349	G
46	2	1350	U
46	2	1353	U
46	2	1354	G
46	2	1355	C
46	2	1356	U
46	2	1357	A
46	2	1360	A
46	2	1361	U
46	2	1362	U
46	2	1363	U
46	2	1367	G
46	2	1368	G
46	2	1369	U
46	2	1370	U
46	2	1371	A
46	2	1372	U
46	2	1373	C
46	2	1374	C
46	2	1380	U
46	2	1381	U
46	2	1383	G
46	2	1386	G
46	2	1387	G
46	2	1388	A
46	2	1390	U
46	2	1392	U
46	2	1397	U
46	2	1399	C
46	2	1402	G
46	2	1403	C
46	2	1406	A
46	2	1407	U
46	2	1408	G

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Mol	Chain	Res	Type
46	2	1409	G
46	2	1411	A
46	2	1413	U
46	2	1414	U
46	2	1416	G
46	2	1418	G
46	2	1420	C
46	2	1421	A
46	2	1422	A
46	2	1424	A
46	2	1425	A
46	2	1427	A
46	2	1429	G
46	2	1431	C
46	2	1432	U
46	2	1433	G
46	2	1434	U
46	2	1435	G
46	2	1436	A
46	2	1438	G
46	2	1440	C
46	2	1441	C
46	2	1443	U
46	2	1444	A
46	2	1445	G
46	2	1446	A
46	2	1452	U
46	2	1455	G
46	2	1457	C
46	2	1458	G
46	2	1460	A
46	2	1467	C
46	2	1468	U
46	2	1469	A
46	2	1471	A
46	2	1472	C
46	2	1473	U
46	2	1474	G
46	2	1477	G
46	2	1478	G
46	2	1479	A
46	2	1480	G

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Mol	Chain	Res	Type
46	2	1481	C
46	2	1484	G
46	2	1486	G
46	2	1489	U
46	2	1490	C
46	2	1492	A
46	2	1493	A
46	2	1495	C
46	2	1496	U
46	2	1498	G
46	2	1508	U
46	2	1509	C
46	2	1511	U
46	2	1513	G
46	2	1514	U
46	2	1517	U
46	2	1518	C
46	2	1519	U
46	2	1520	U
46	2	1522	U
46	2	1523	G
46	2	1524	A
46	2	1526	A
46	2	1528	U
46	2	1530	C
46	2	1533	C
46	2	1534	G
46	2	1535	U
46	2	1536	G
46	2	1537	C
46	2	1538	U
46	2	1539	G
46	2	1540	G
46	2	1543	A
46	2	1544	U
46	2	1545	A
46	2	1554	U
46	2	1557	U
46	2	1559	A
46	2	1561	U
46	2	1562	G
46	2	1567	U

Continued on next page...

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Mol	Chain	Res	Type
46	2	1568	C
46	2	1569	A
46	2	1570	A
46	2	1573	A
46	2	1578	U
46	2	1582	U
46	2	1583	A
46	2	1584	G
46	2	1585	U
46	2	1586	A
46	2	1587	A
46	2	1596	C
46	2	1598	U
46	2	1600	A
46	2	1601	G
46	2	1603	U
46	2	1606	C
46	2	1610	G
46	2	1613	U
46	2	1614	A
46	2	1618	C
46	2	1619	C
46	2	1622	G
46	2	1624	C
46	2	1631	A
46	2	1634	C
46	2	1635	A
46	2	1640	C
46	2	1642	G
46	2	1645	G
46	2	1648	A
46	2	1650	U
46	2	1651	A
46	2	1652	C
46	2	1654	G
46	2	1655	A
46	2	1657	U
46	2	1658	G
46	2	1659	A
46	2	1660	A
46	2	1661	U
46	2	1662	G

Continued on next page...

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Mol	Chain	Res	Type
46	2	1664	C
46	2	1665	U
46	2	1666	U
46	2	1668	G
46	2	1672	G
46	2	1678	A
46	2	1680	G
46	2	1682	U
46	2	1683	C
46	2	1684	U
46	2	1687	U
46	2	1688	U
46	2	1689	A
46	2	1693	A
46	2	1694	A
46	2	1695	G
46	2	1696	G
46	2	1697	G
46	2	1698	G
46	2	1699	G
46	2	1702	A
46	2	1704	U
46	2	1705	C
46	2	1706	C
46	2	1707	A
46	2	1708	U
46	2	1710	U
46	2	1711	C
46	2	1715	G
46	2	1716	C
46	2	1718	G
46	2	1720	G
46	2	1721	A
46	2	1722	A
46	2	1726	G
46	2	1736	G
46	2	1737	G
46	2	1739	C
46	2	1741	U
46	2	1744	A
46	2	1745	G
46	2	1747	G

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Mol	Chain	Res	Type
46	2	1749	A
46	2	1750	A
46	2	1751	C
46	2	1754	A
46	2	1756	A
46	2	1759	C
46	2	1760	G
46	2	1762	A
46	2	1765	A
46	2	1766	A
46	2	1768	G
46	2	1769	U
46	2	1770	U
46	2	1774	G
46	2	1775	U
46	2	1776	A
46	2	1777	G
46	2	1778	G
46	2	1782	A
46	2	1783	C
46	2	1786	G
46	2	1787	C
46	2	1789	G
46	2	1792	G
46	2	1793	G
46	2	1794	A
46	2	1796	C
46	2	1797	A
46	2	1798	U
75	AX	9	A
75	AX	15	G
75	AX	16	U
75	AX	17	U
75	AX	19	G
75	AX	20	G
75	AX	21	A
75	AX	26	G
75	AX	33	U
75	AX	34	G
75	AX	35	A
75	AX	36	A
75	AX	37	G

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Mol	Chain	Res	Type
75	AX	45	G
75	AX	46	G
75	AX	47	U
75	AX	54	U
75	AX	55	U
75	AX	57	G
75	AX	58	A
75	AX	61	C
75	AX	73	A
75	AZ	9	A
75	AZ	15	G
75	AZ	16	U
75	AZ	17	U
75	AZ	19	G
75	AZ	20	G
75	AZ	21	A
75	AZ	25	C
75	AZ	34	G
75	AZ	35	A
75	AZ	36	A
75	AZ	37	G
75	AZ	45	G
75	AZ	46	G
75	AZ	47	U
75	AZ	53	G
75	AZ	55	U
75	AZ	57	G
75	AZ	58	A
75	AZ	61	C
75	AZ	62	A
75	AZ	70	C
75	AZ	73	A

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
28	1	619	A
28	1	734	C
28	1	1763	U
28	1	2506	U
28	1	2530	G
28	1	2543	U

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Mol	Chain	Res	Type
28	1	2874	G
46	2	243	G
46	2	518	A
46	2	537	G
46	2	621	A
46	2	687	G
46	2	904	G
46	2	1181	U
46	2	1366	U
46	2	1406	A
46	2	1585	U
46	2	1665	U
46	2	1748	G
46	2	1755	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

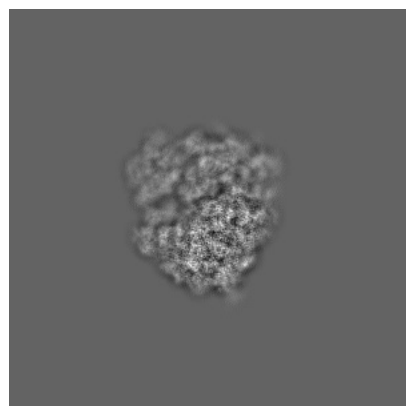
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22198. These allow visual inspection of the internal detail of the map and identification of artifacts.

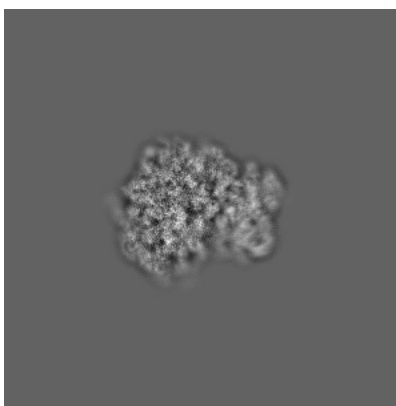
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

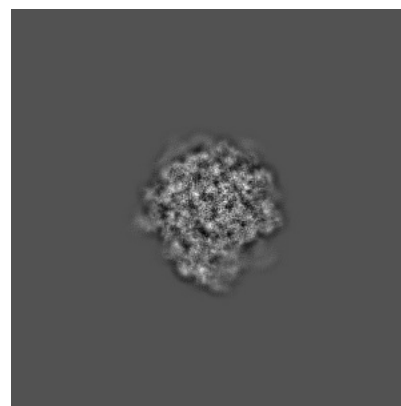
6.1.1 Primary map



X

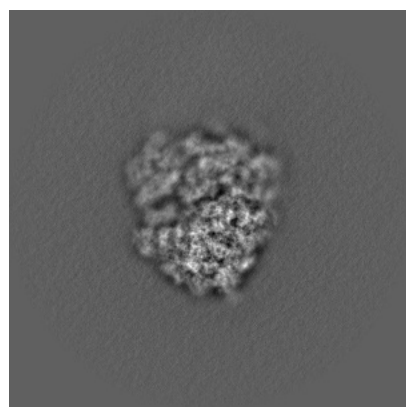


Y

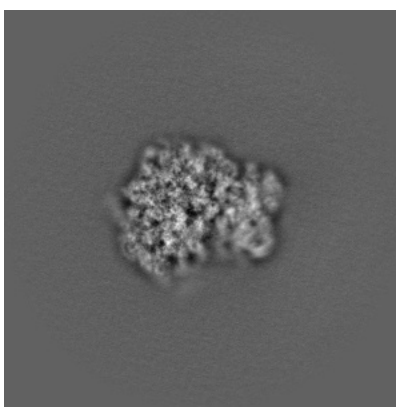


Z

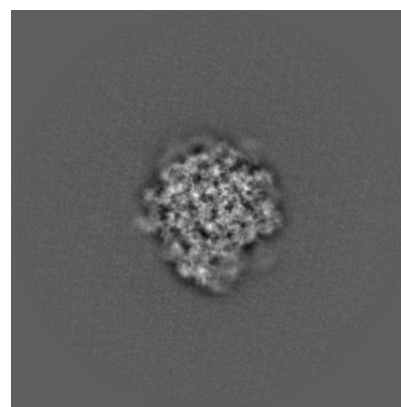
6.1.2 Raw map



X



Y

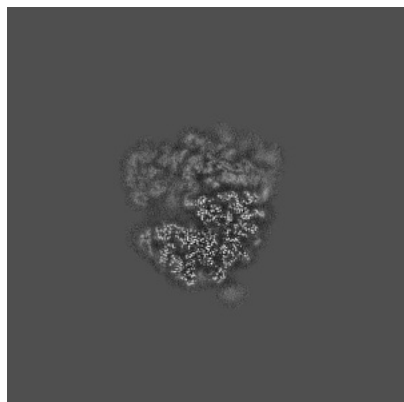


Z

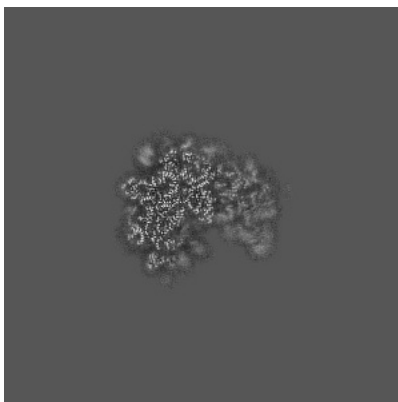
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

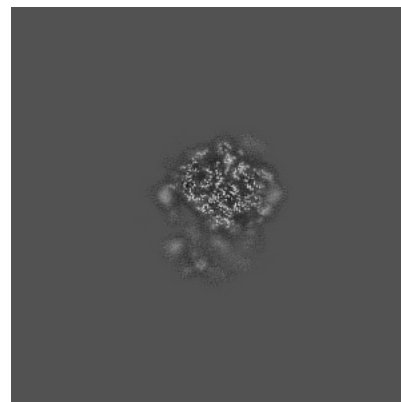
6.2.1 Primary map



X Index: 240

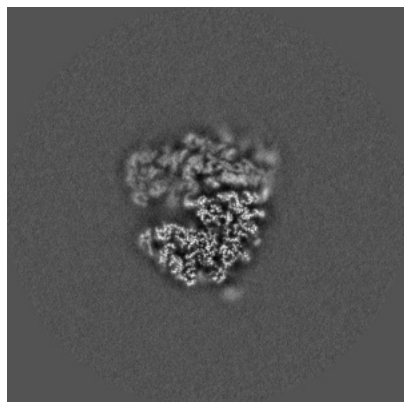


Y Index: 240

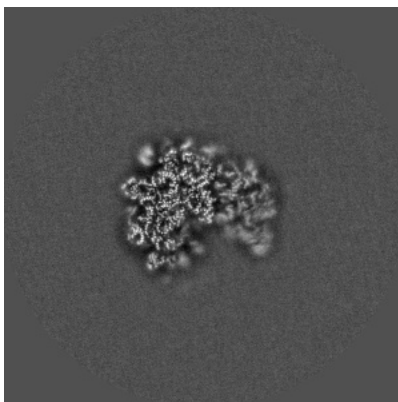


Z Index: 240

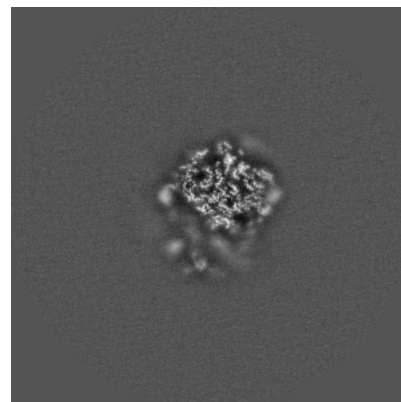
6.2.2 Raw map



X Index: 240



Y Index: 240

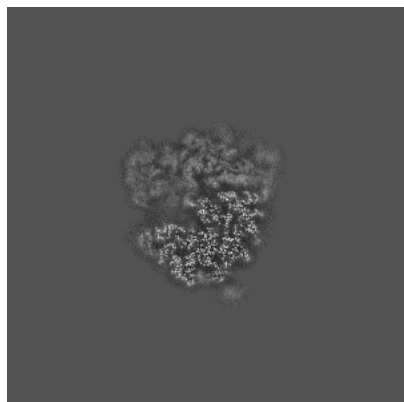


Z Index: 240

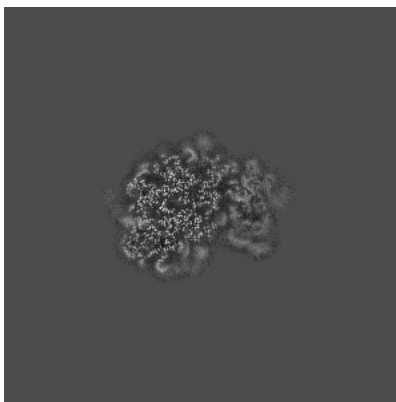
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

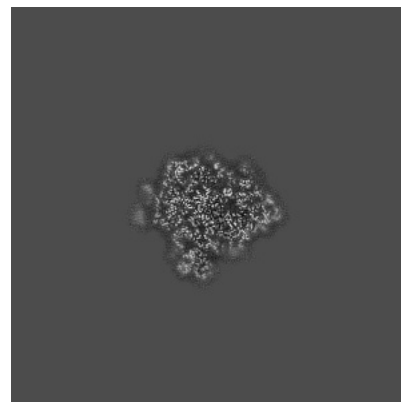
6.3.1 Primary map



X Index: 239

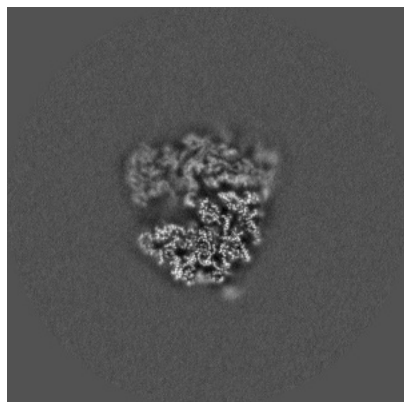


Y Index: 257

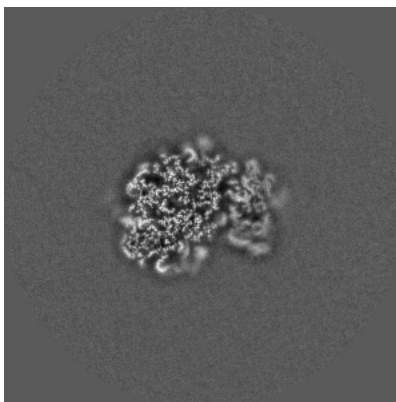


Z Index: 195

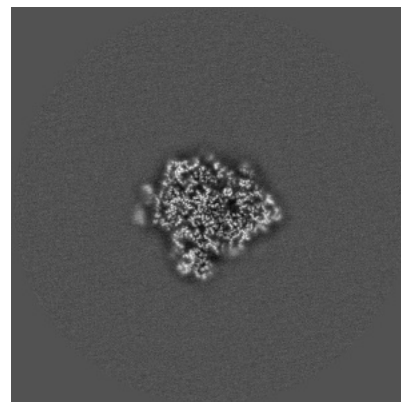
6.3.2 Raw map



X Index: 238



Y Index: 257

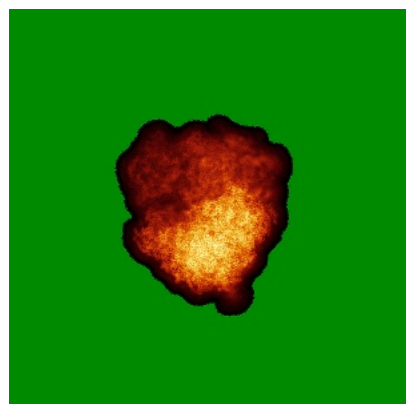


Z Index: 195

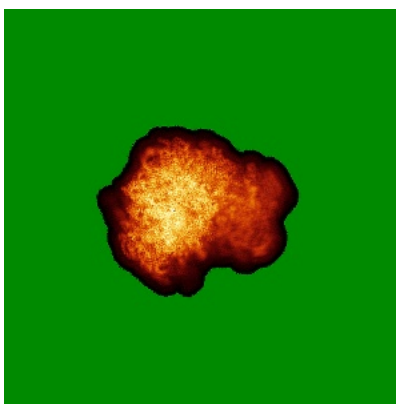
The images above show the largest variance slices of the map in three orthogonal directions.

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

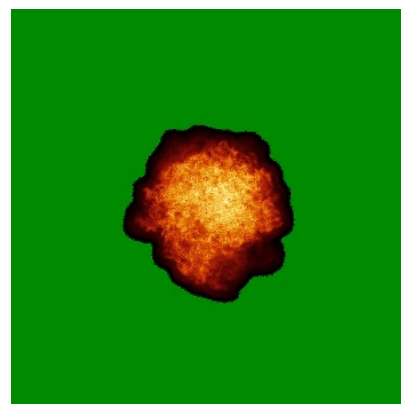
6.4.1 Primary map



X

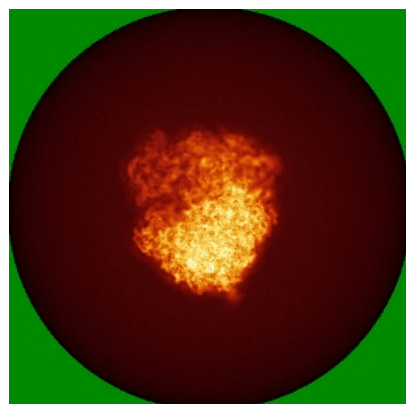


Y

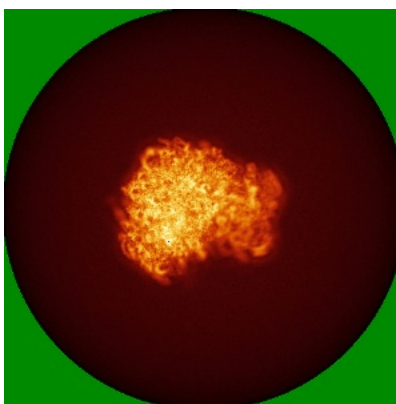


Z

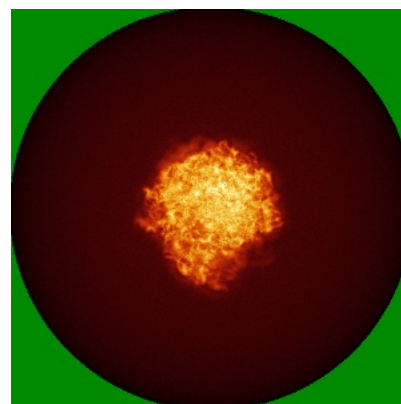
6.4.2 Raw map



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](#)

This section was not generated.

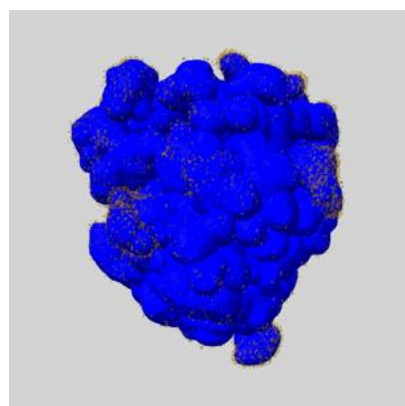
6.6 Mask visualisation [i](#)

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

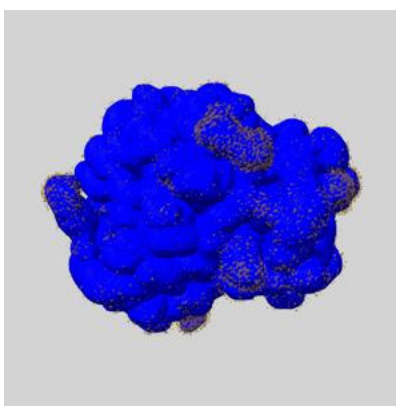
A mask typically either:

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

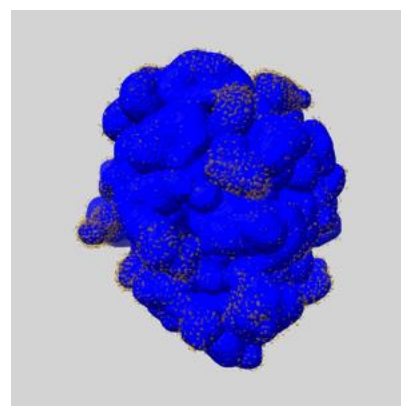
6.6.1 emd_22198_msk_1.map [i](#)



X



Y

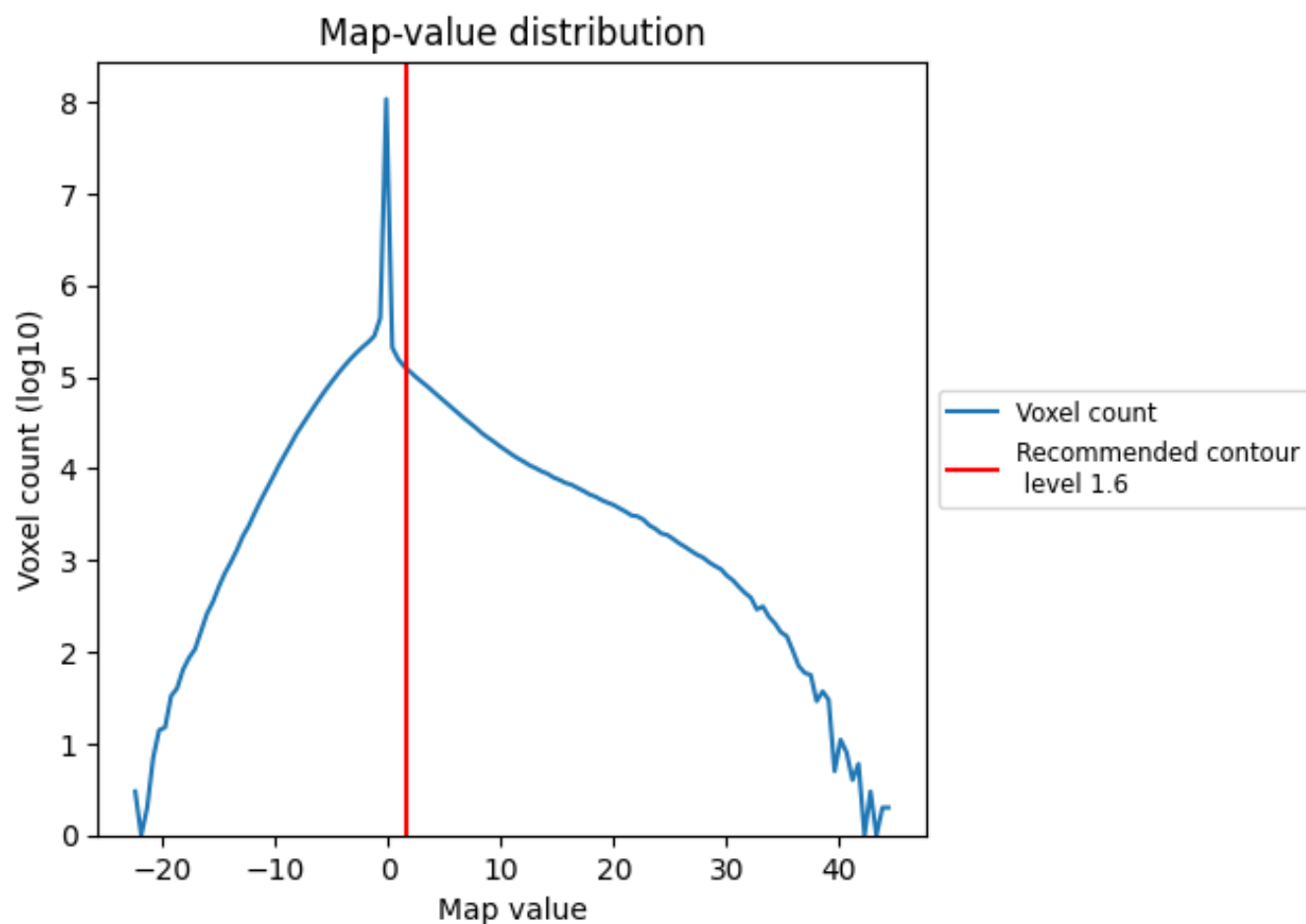


Z

7 Map analysis [i](#)

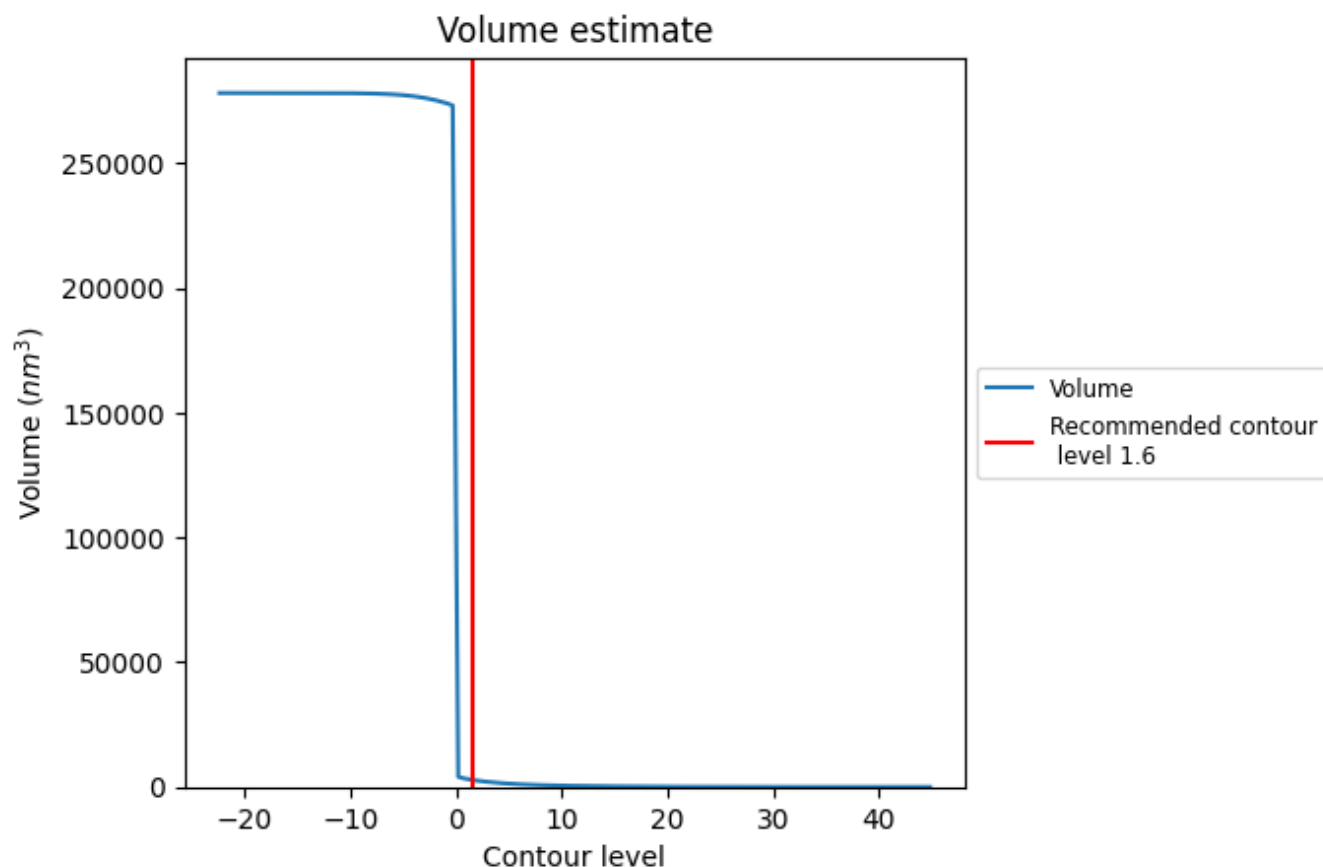
This section contains the results of statistical analysis of the map.

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.

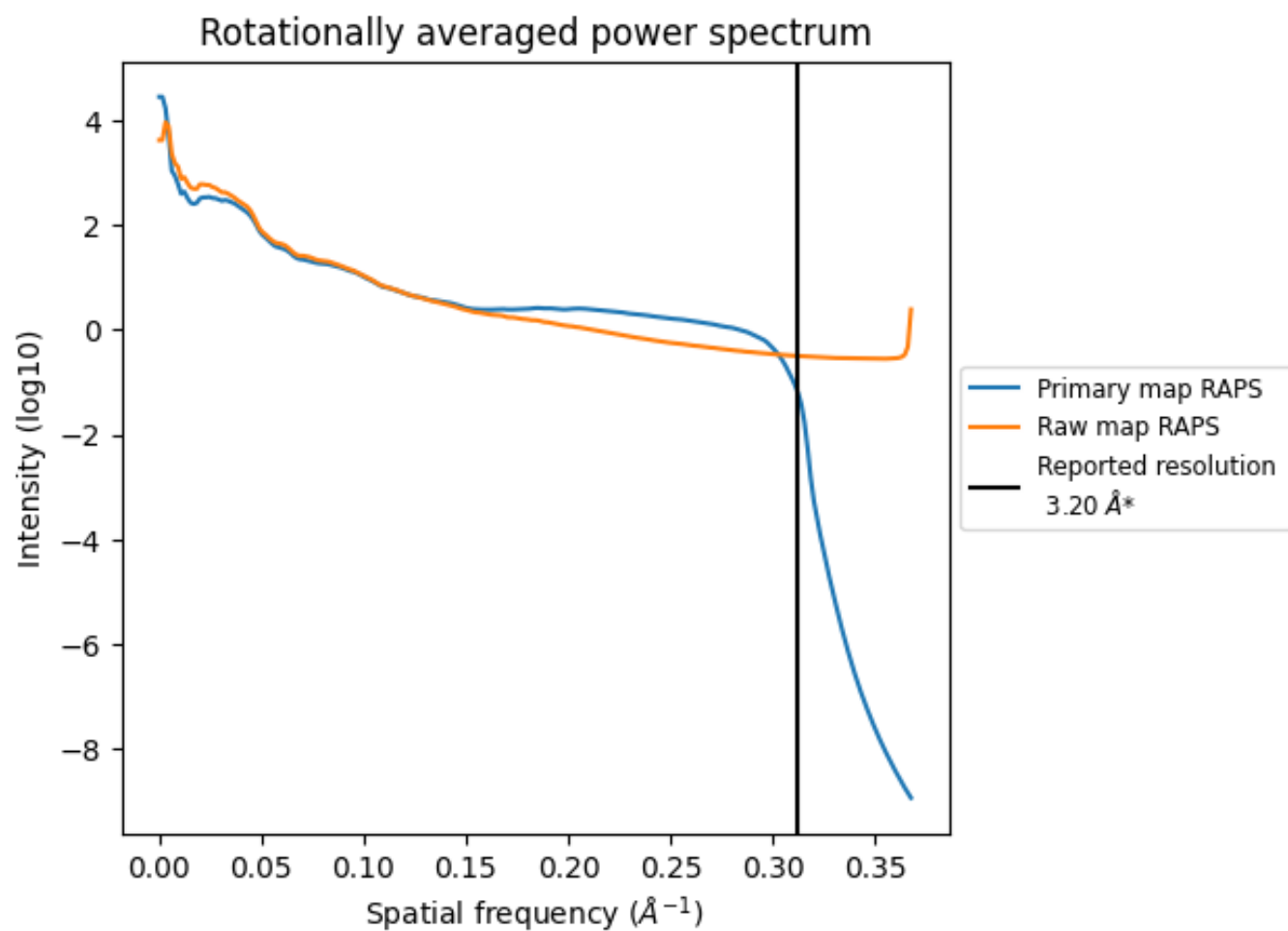
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2788 nm^3 ; this corresponds to an approximate mass of 2518 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 ⓘ

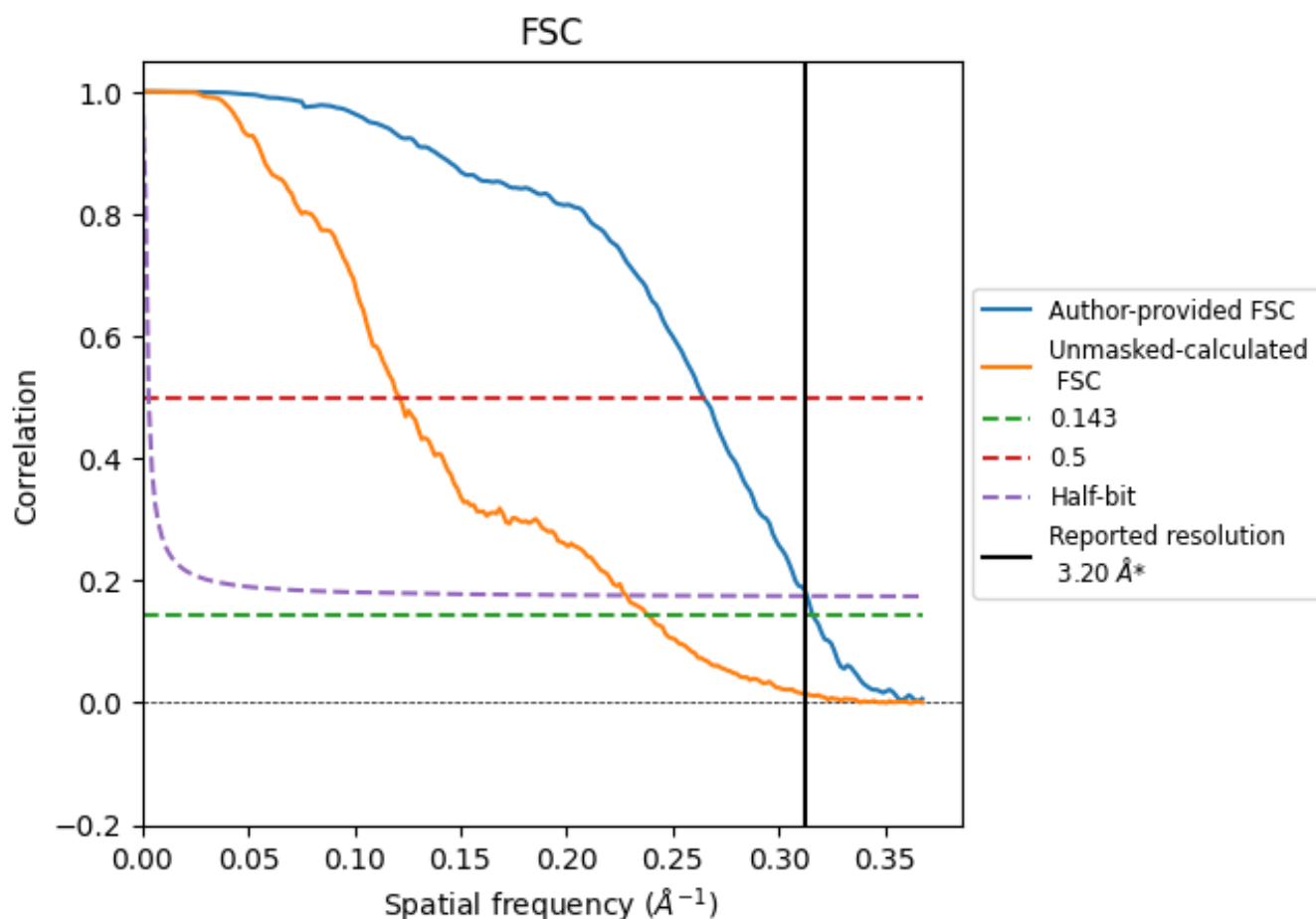


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

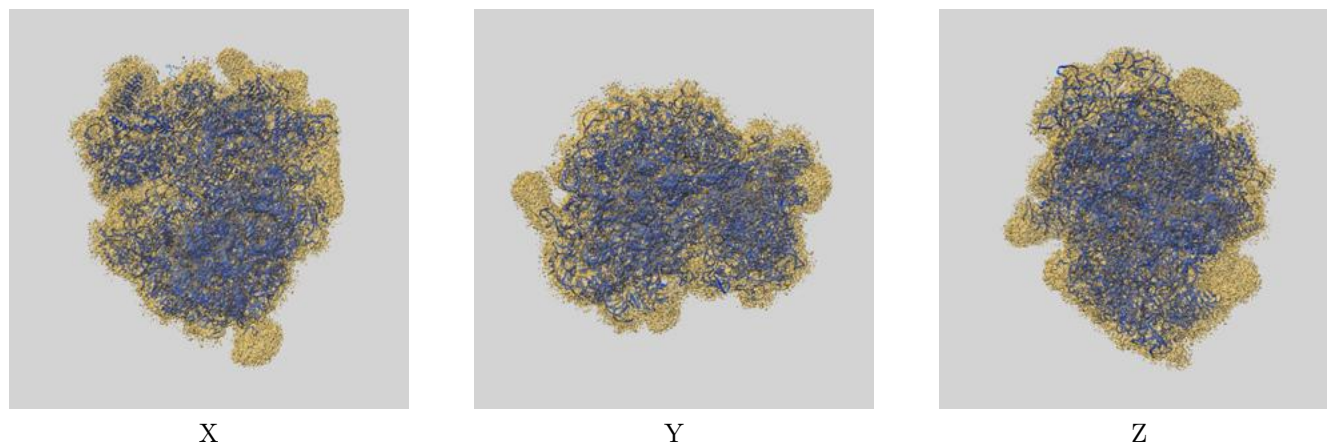
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.16	3.78	3.19
Unmasked-calculated*	4.19	8.25	4.38

*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 4.19 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

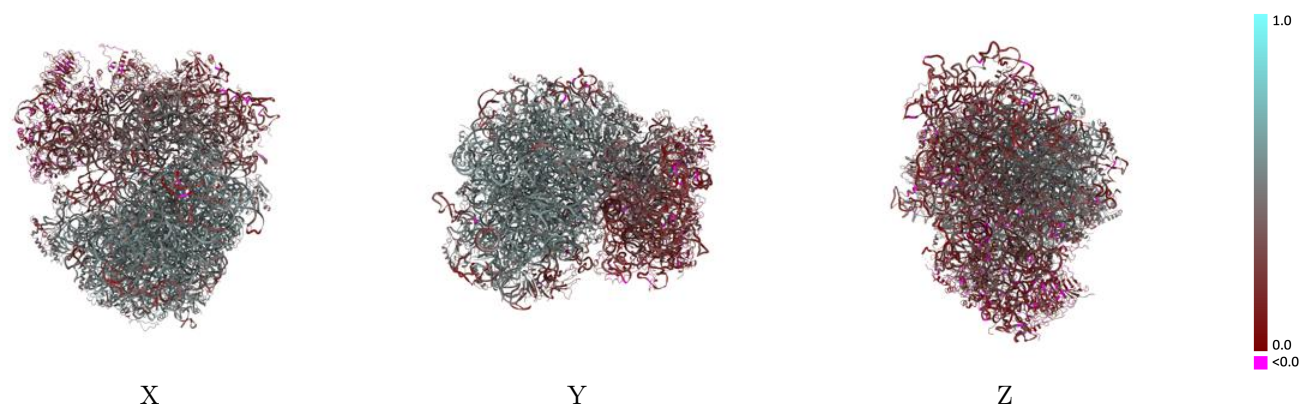
This section contains information regarding the fit between EMDB map EMD-22198 and PDB model 6XIR. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 1.6 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](#)

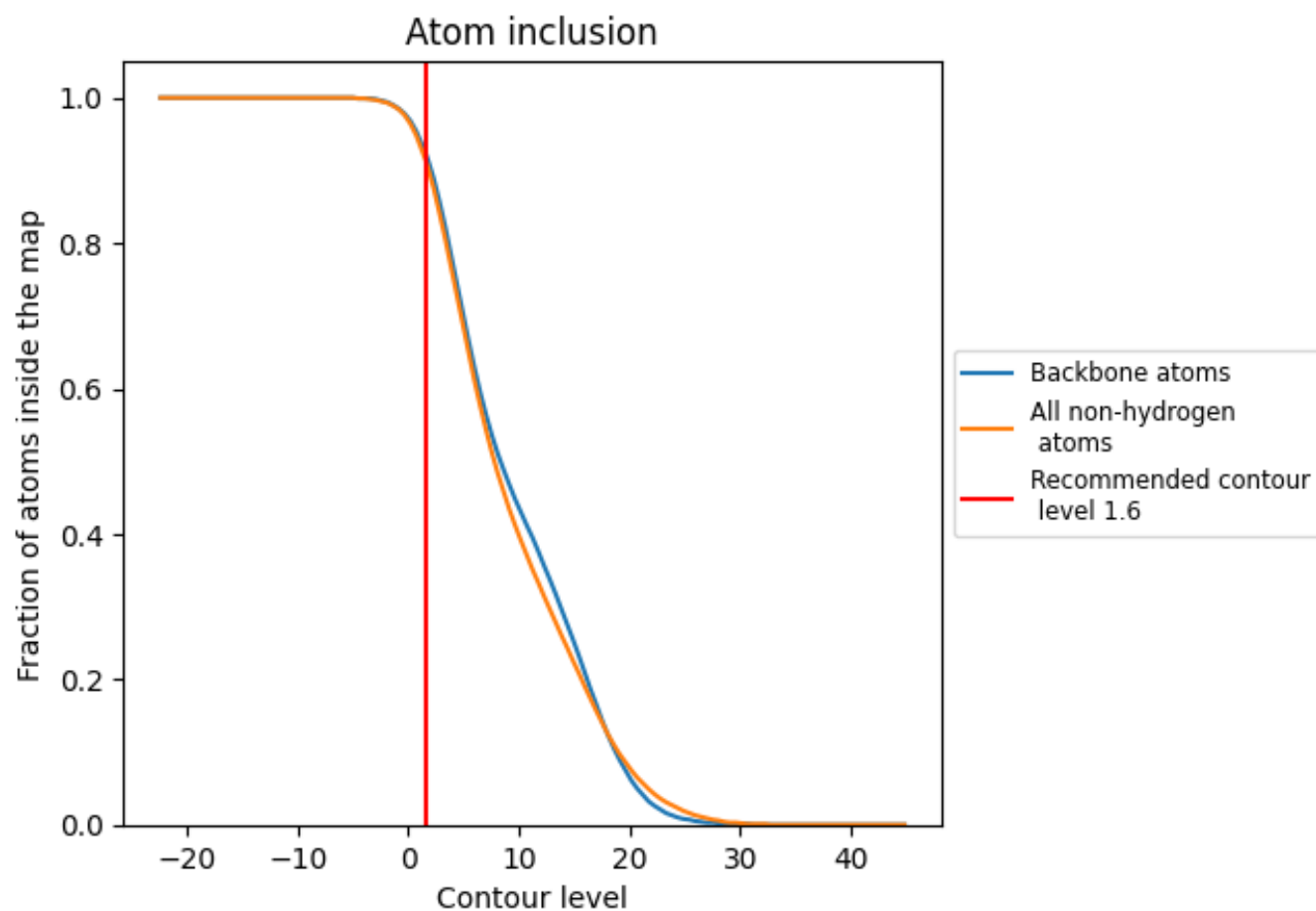


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 91% 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 (1.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9130	 0.4050
1	 0.9840	 0.4910
2	 0.8980	 0.2740
3	 0.9990	 0.5000
4	 0.9860	 0.5060
A	 0.9030	 0.5470
AA	 0.6560	 0.1760
AB	 0.8470	 0.3740
AD	 0.8620	 0.3890
AE	 0.9050	 0.4360
AF	 0.8630	 0.2210
AG	 0.5970	 0.1940
AH	 0.8430	 0.2600
AI	 0.7090	 0.1080
AJ	 0.8060	 0.2200
AK	 0.6540	 0.1760
AL	 0.8390	 0.3140
AM	 0.7980	 0.3400
AN	 0.5990	 0.2360
AO	 0.8530	 0.2020
AP	 0.8260	 0.2530
AQ	 0.6920	 0.3610
AR	 0.9190	 0.3470
AS	 0.8830	 0.3040
AT	 0.5380	 0.1300
AV	 0.8500	 0.2030
AX	 0.7230	 0.2110
AZ	 0.4880	 0.0760
B	 0.9580	 0.5460
C	 0.9580	 0.5360
D	 0.9340	 0.4330
E	 0.9600	 0.4980
F	 0.9500	 0.5220
G	 0.9290	 0.4670
H	 0.8330	 0.3160



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Chain	Atom inclusion	Q-score
I	 0.8260	 0.4120
J	 0.9490	 0.3660
L	 0.9590	 0.5110
M	 0.9510	 0.4900
N	 0.8970	 0.5520
O	 0.9480	 0.5300
P	 0.8950	 0.5140
Q	 0.9350	 0.5400
R	 0.9490	 0.4830
S	 0.9240	 0.5190
T	 0.9170	 0.5200
U	 0.9800	 0.4540
V	 0.9220	 0.5210
W	 0.9430	 0.5250
X	 0.9400	 0.5310
Y	 0.9660	 0.5190
Z	 0.9530	 0.4440
a	 0.9450	 0.5470
b	 0.8430	 0.4850
c	 0.9630	 0.4700
d	 0.9510	 0.5220
e	 0.9080	 0.5410
f	 0.9510	 0.5560
g	 0.9120	 0.5240
h	 0.9400	 0.4850
i	 0.9210	 0.4660
j	 0.9050	 0.5460
k	 0.9500	 0.4810
l	 0.8460	 0.5280
n	 0.4470	 0.0030
o	 0.8430	 0.5010
p	 0.9420	 0.5170
q	 0.8170	 0.2390
r	 0.9050	 0.3870
s	 0.7770	 0.2580
t	 0.7410	 0.2330
u	 0.7800	 0.2230
v	 0.8290	 0.3060
w	 0.6810	 0.2230
x	 0.9070	 0.2580
y	 0.8230	 0.2900
z	 0.7790	 0.2110