



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:29 PM UTC

PDB ID : 7R7A / pdb_00007r7a
EMDB ID : EMD-24296
Title : State E1 nucleolar 60S ribosome biogenesis intermediate - Composite model
Authors : Cruz, V.E.; Sekulski, K.; Peddada, N.; Erzberger, J.P.
Deposited on : 2021-06-24
Resolution : 3.04 Å (reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

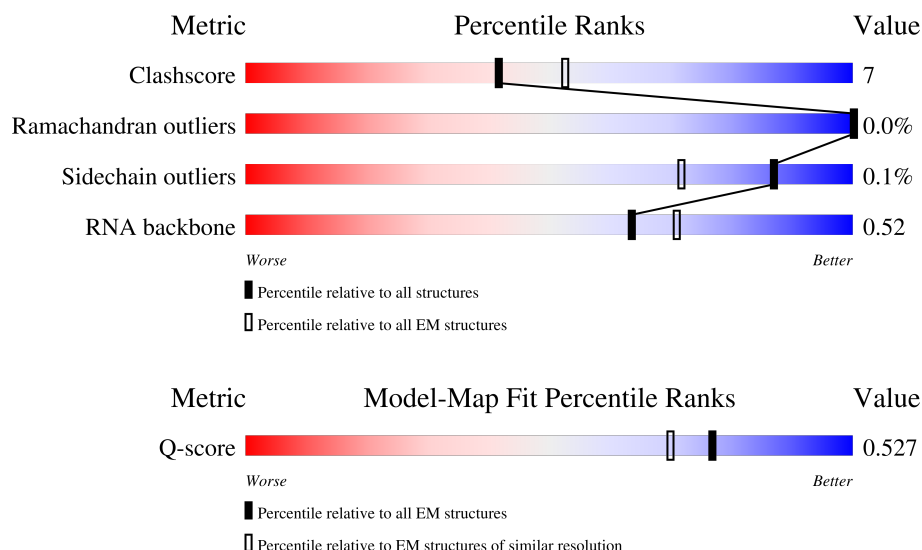
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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

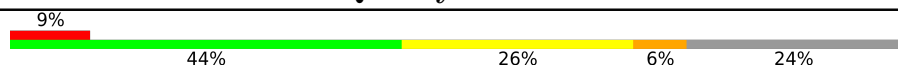
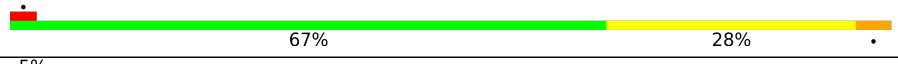
The reported resolution of this entry is 3.04 Å.

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	13952 (2.54 - 3.54)

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

Mol	Chain	Length	Quality of chain
1	1	3396	
2	2	158	
3	7	204	

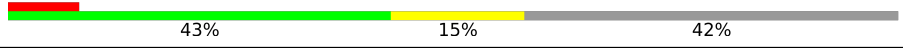
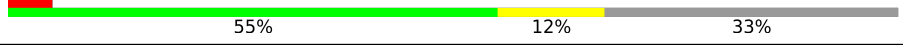
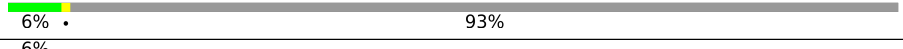
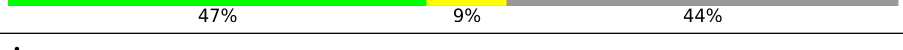
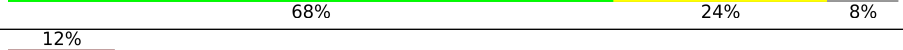
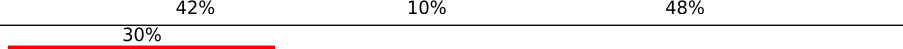
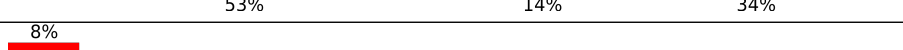
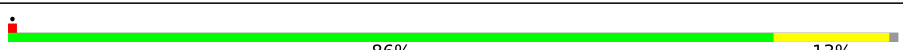
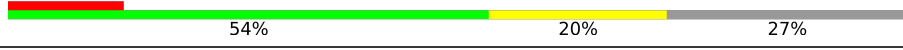
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Mol	Chain	Length	Quality of chain
4	A	291	
5	B	387	
6	C	362	
7	E	175	
8	F	244	
9	H	191	
10	J	427	
11	L	199	
12	M	138	
13	N	204	
14	O	199	
15	P	184	
16	Q	186	
17	S	172	
18	T	160	
19	W	236	
20	X	142	
21	Y	127	
22	b	647	
23	d	113	
24	e	130	
25	f	107	
26	h	120	
27	i	100	
28	j	88	

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Mol	Chain	Length	Quality of chain
29	l	181	
30	m	807	
31	q	618	
32	r	261	
33	s	520	
34	u	199	
35	v	231	
36	y	245	
37	z	106	
38	8	710	
39	I	663	
40	K	376	
41	V	137	
42	R	189	
43	G	256	
44	Z	136	
45	U	121	
46	c	105	
47	g	121	
48	k	78	
49	n	605	
50	p	460	
51	t	322	
52	6	87	
53	D	505	

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Mol	Chain	Length	Quality of chain
54	o	220	5% 50% 11% 40%
55	w	841	21% 43% 7% 50%
56	a	217	95% 63% 35% ..
57	x	606	65% 70% 18% • 11%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 153087 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2571	Total	C	N	O	P	0	0
			55024	24568	9931	17955	2570		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 3 is a protein called 60S ribosomal subunit assembly/export protein LOC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	7	129	Total	C	N	O	0	0
			1048	650	204	194		

- Molecule 4 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	266	Total	C	N	O	S	0	0
			2174	1382	386	400	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	335	Total	C	N	O	S	0	0
			2661	1691	492	472	6		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	359	Total	C	N	O	S	0	0
			2731	1720	518	490	3		

- Molecule 7 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	164	Total	C	N	O	S	0	0
			1309	843	235	230	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	LEU	deletion	UNP Q02326

- Molecule 8 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 10 is a protein called rRNA-processing protein EBP2.

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

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

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

- 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	189	Total	C	N	O	S	0	0
			1621	1015	343	262	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
			1442	896	287	259			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	134	Total	C	N	O	S	0	0
			1035	659	196	179	1		

- Molecule 17 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	52	Total	C	N	O	S	0	0
			401	244	82	74	1		

- Molecule 19 is a protein called Ribosome assembly factor MRT4.

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

- Molecule 20 is a protein called 60S ribosomal protein L25.

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

- Molecule 21 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 22 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	502	Total	C	N	O	S	0	0
			4066	2581	710	754	21		

- Molecule 23 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L32.

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

- Molecule 25 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	79	Total	C	N	O	S	0	0
			628	388	130	108	2		

- Molecule 28 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 29 is a protein called 60S ribosome subunit biogenesis protein NIP7.

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

- Molecule 30 is a protein called Ribosome biogenesis protein ERB1.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	551	ALA	GLU	conflict	UNP Q04660

- Molecule 31 is a protein called 25S rRNA (cytosine(2870)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	q	358	Total	C	N	O	S	0	0
			2799	1779	490	518	12		

- Molecule 32 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	r	176	Total	C	N	O	S	0	0
			1438	906	279	248	5		

- Molecule 33 is a protein called Nuclear GTP-binding protein NUG1.

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

- Molecule 34 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	u	140	Total	C	N	O	S	0	0
			1183	742	237	195	9		

- Molecule 35 is a protein called Nucleolar protein 16.

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

- Molecule 36 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	y	225	Total	C	N	O	S	0	0
			1701	1056	295	343	7		

- Molecule 37 is a protein called UPF0642 protein YBL028C.

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

- Molecule 38 is a protein called Nucleolar complex protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	8	470	Total	C	N	O	S	0	0
			3567	2269	632	655	11		

- Molecule 39 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	I	533	Total	C	N	O	S	0	0
			4247	2693	726	808	20		

- Molecule 40 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	K	284	Total	C	N	O	S	0	0
			2274	1462	375	433	4		

- Molecule 41 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	V	134	Total	C	N	O	S	0	0
			993	623	187	176	7		

- Molecule 42 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L30.

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

- Molecule 47 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L38.

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

- Molecule 49 is a protein called Pescadillo homolog.

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

- Molecule 50 is a protein called YTM1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	337	Total	C	N	O	S	0	0
			2628	1633	470	518	7		

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

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

- Molecule 52 is a RNA chain called 5.8S ribosomal RNA gene and internal transcribed spacer 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	6	87	Total	C	N	O	P	0	0
			1838	823	309	619	87		

- Molecule 53 is a protein called ATP-dependent RNA helicase HAS1.

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

- Molecule 54 is a protein called Ribosome biogenesis protein 15.

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

- Molecule 55 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	422	Total	C	N	O	S	0	0
			3446	2146	633	649	18		

- Molecule 56 is a protein called Ribosomal protein.

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

- Molecule 57 is a protein called ATP-dependent rRNA helicase SPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	x	539	Total	C	N	O	S	0	0
			4340	2781	744	795	20		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	405	ALA	THR	conflict	UNP A7A237

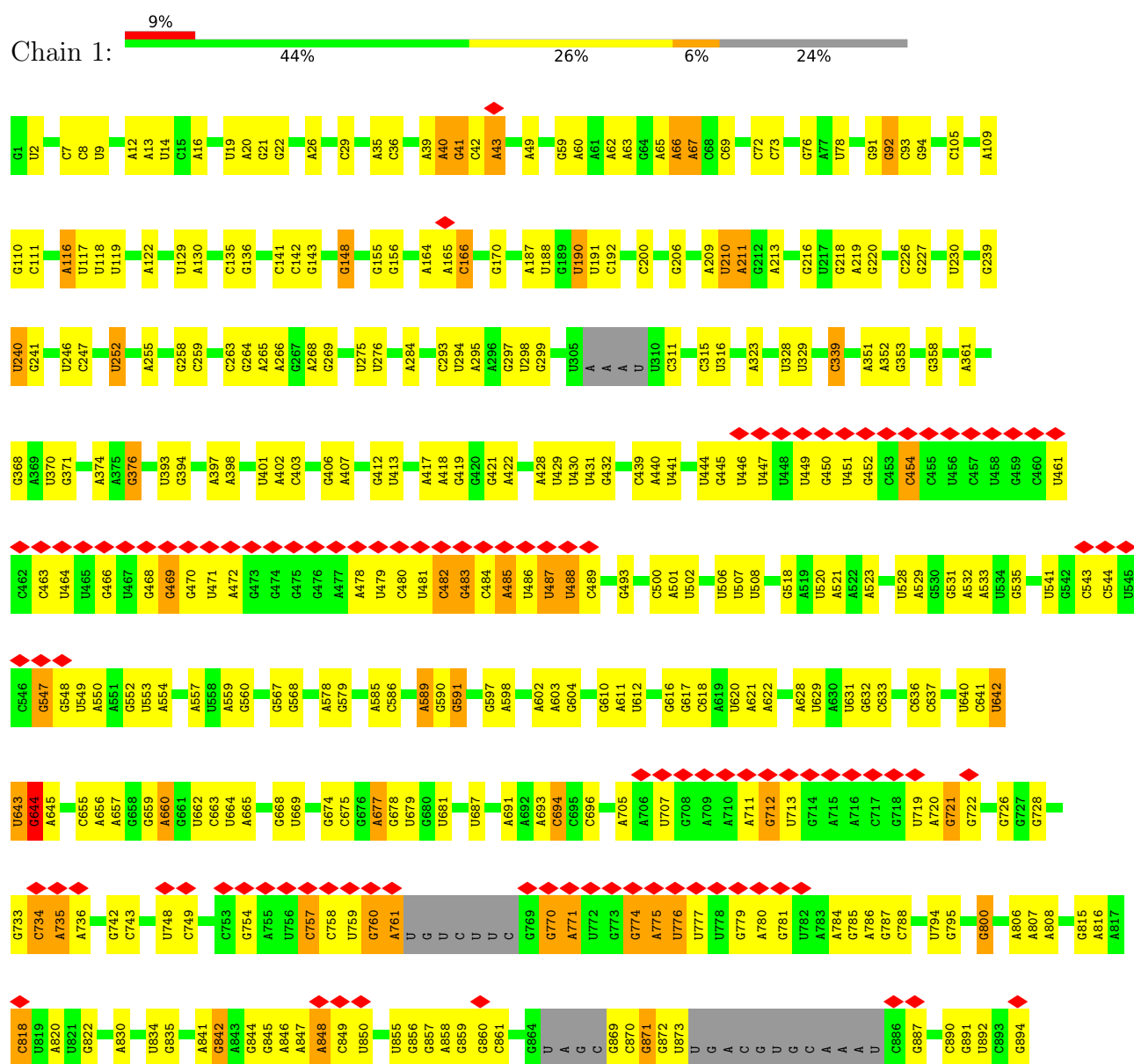
- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

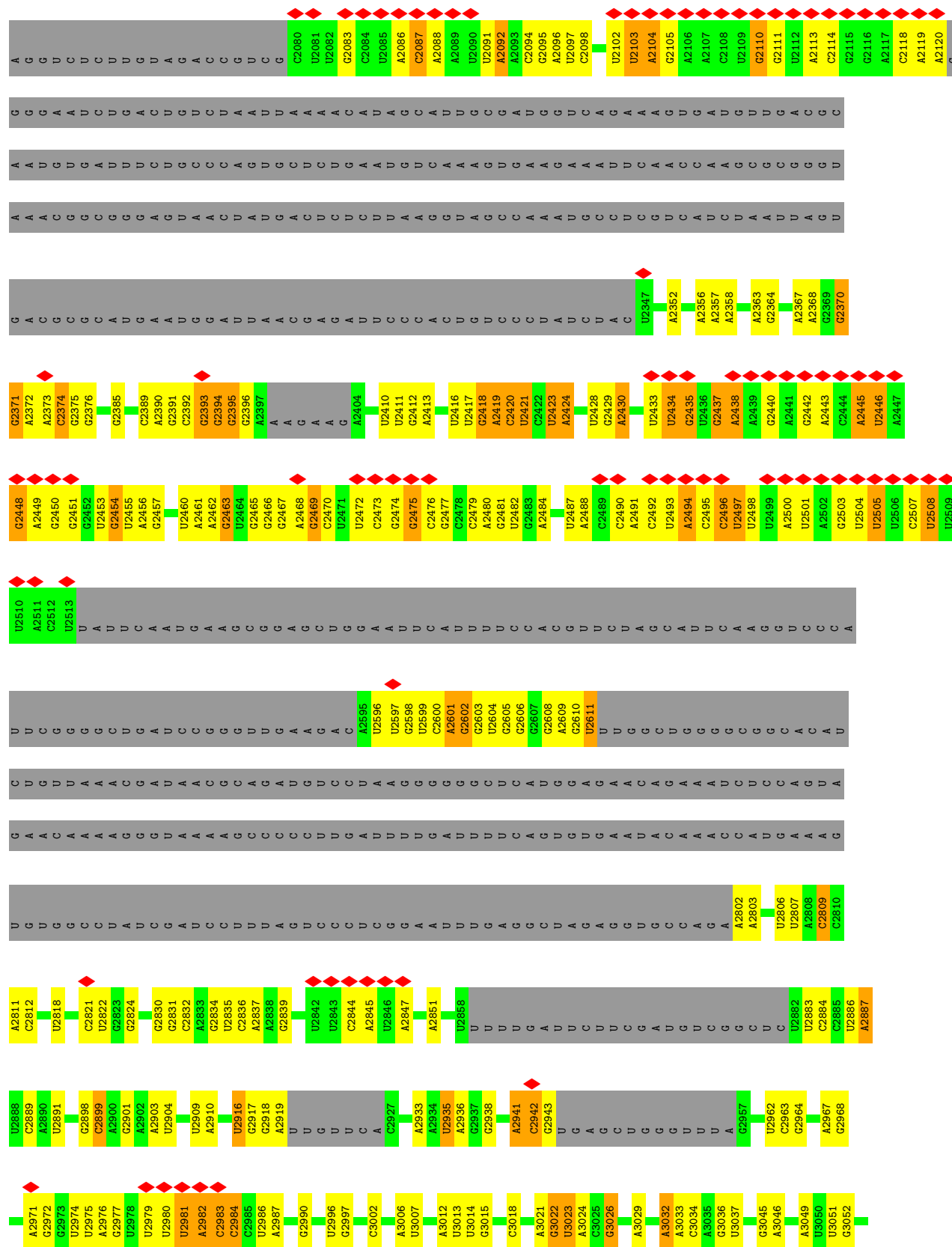
3 Residue-property plots

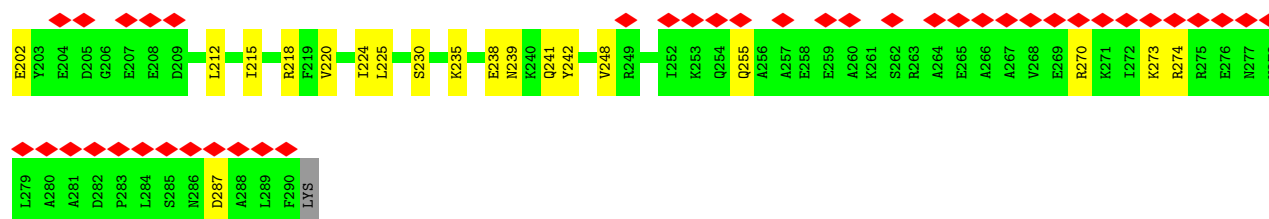
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 25S rRNA



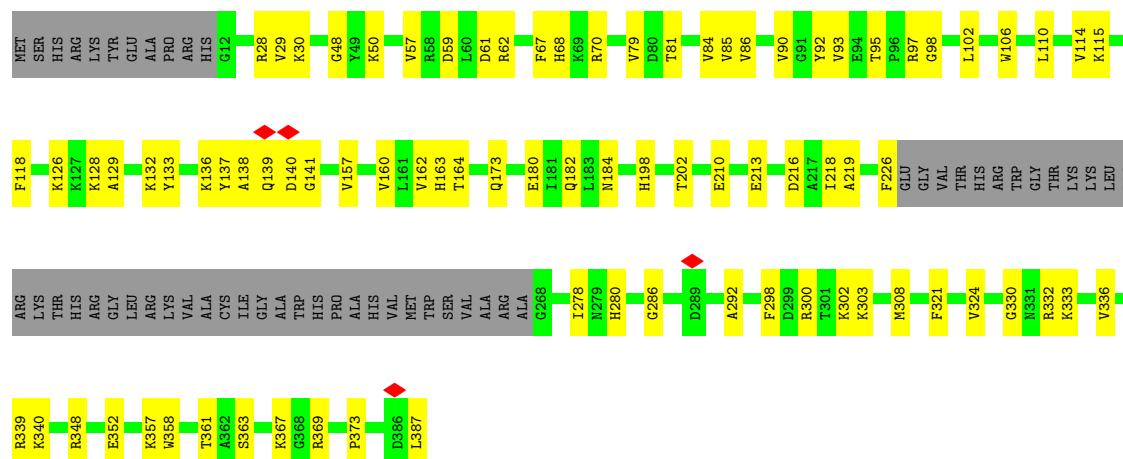






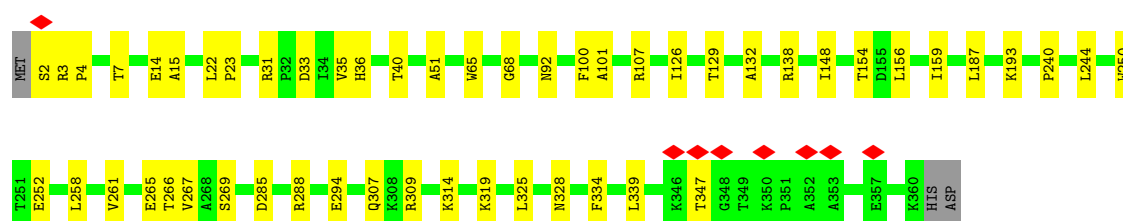
• Molecule 5: 60S ribosomal protein L3

Chain B: 65% 22% 13%



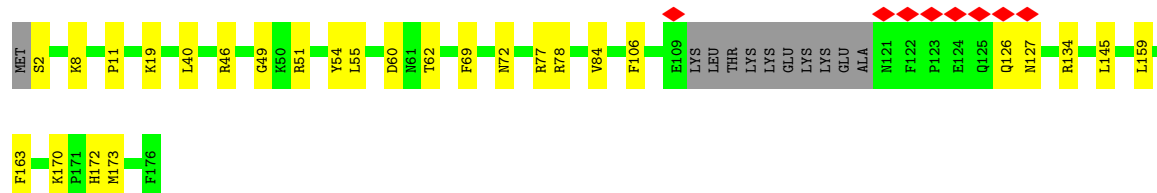
• Molecule 6: 60S ribosomal protein L4-A

Chain C: 85% 14%



• Molecule 7: 60S ribosomal protein L6-A

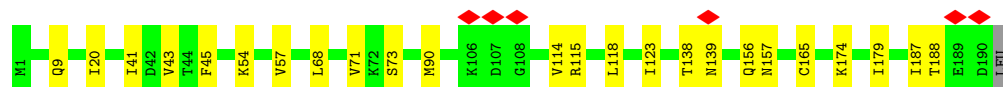
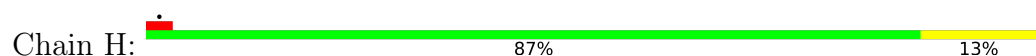
Chain E: 5% 78% 15% 6%



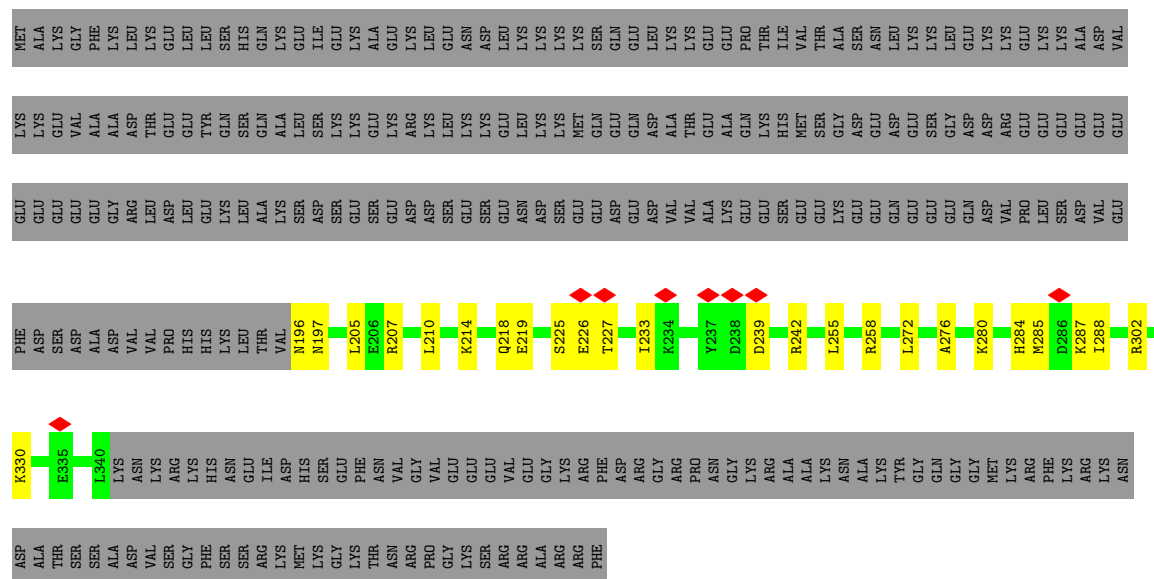
• Molecule 8: 60S ribosomal protein L7-A

Chain F: 77% 14% 9%

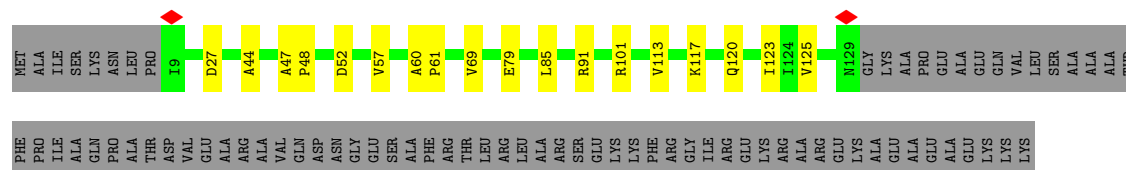
- Molecule 9: 60S ribosomal protein L9-A



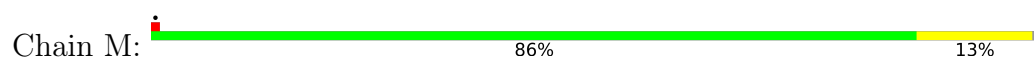
- Molecule 10: rRNA-processing protein EBP2

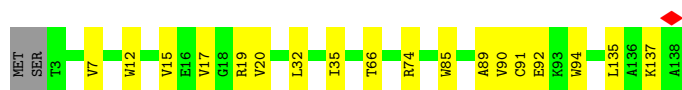


- Molecule 11: 60S ribosomal protein L13-A



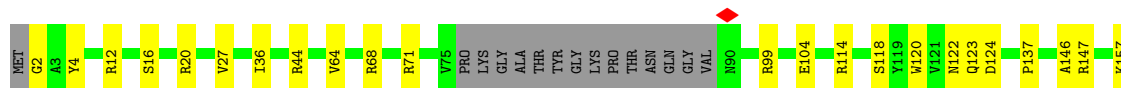
- Molecule 12: 60S ribosomal protein L14-A





- Molecule 13: 60S ribosomal protein L15-A

Chain N: 75% 17% 7%



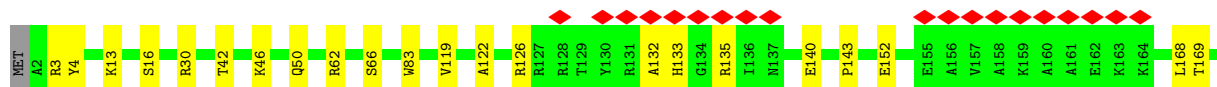
- Molecule 14: 60S ribosomal protein L16-A

Chain O: 96% ..



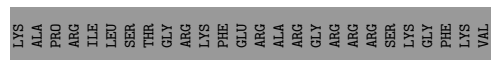
- Molecule 15: 60S ribosomal protein L17-A

Chain P: 11% 86% 14%



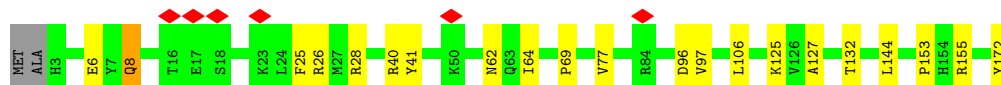
- Molecule 16: 60S ribosomal protein L18-A

Chain Q: 65% 8% 28%

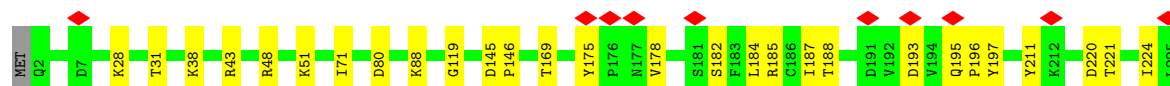
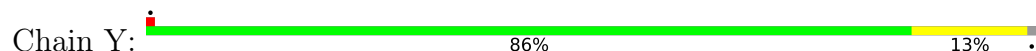
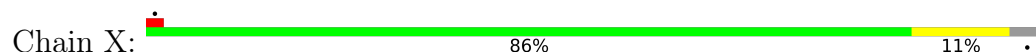
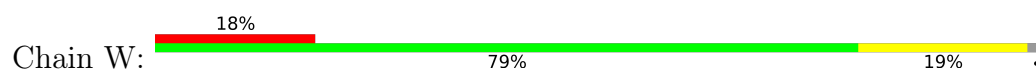


- Molecule 17: 60S ribosomal protein L20-A

Chain S: 87% 12% ..



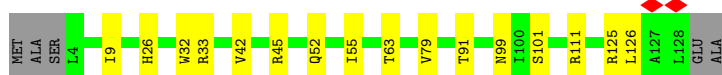
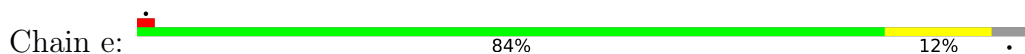
Chain T: 32% 29% 68%



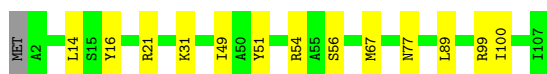
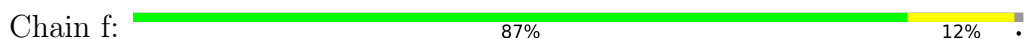
- Molecule 23: 60S ribosomal protein L31-A



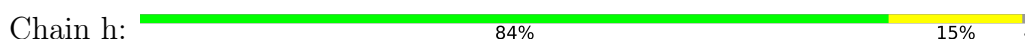
- Molecule 24: 60S ribosomal protein L32



- Molecule 25: 60S ribosomal protein L33-A



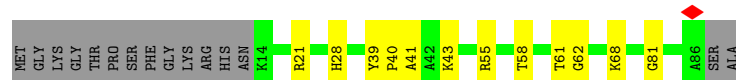
- Molecule 26: 60S ribosomal protein L35-A



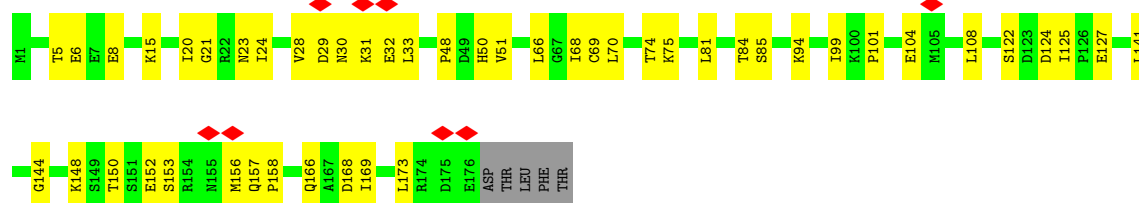
- Molecule 27: 60S ribosomal protein L36-A



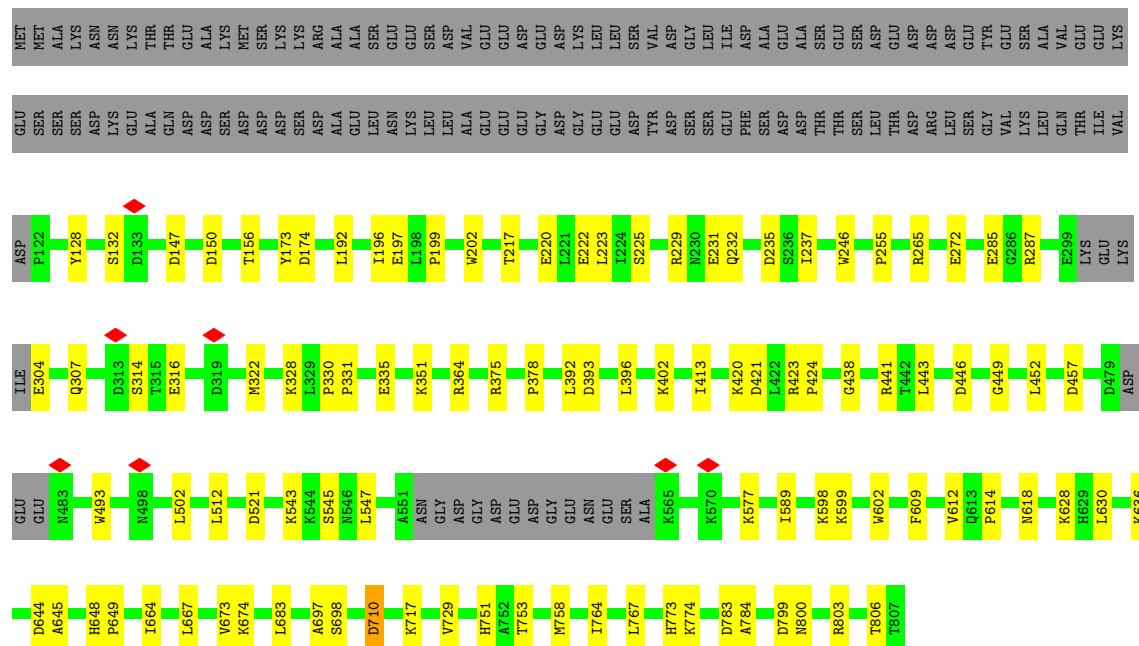
Chain j: 69% 14% 17%

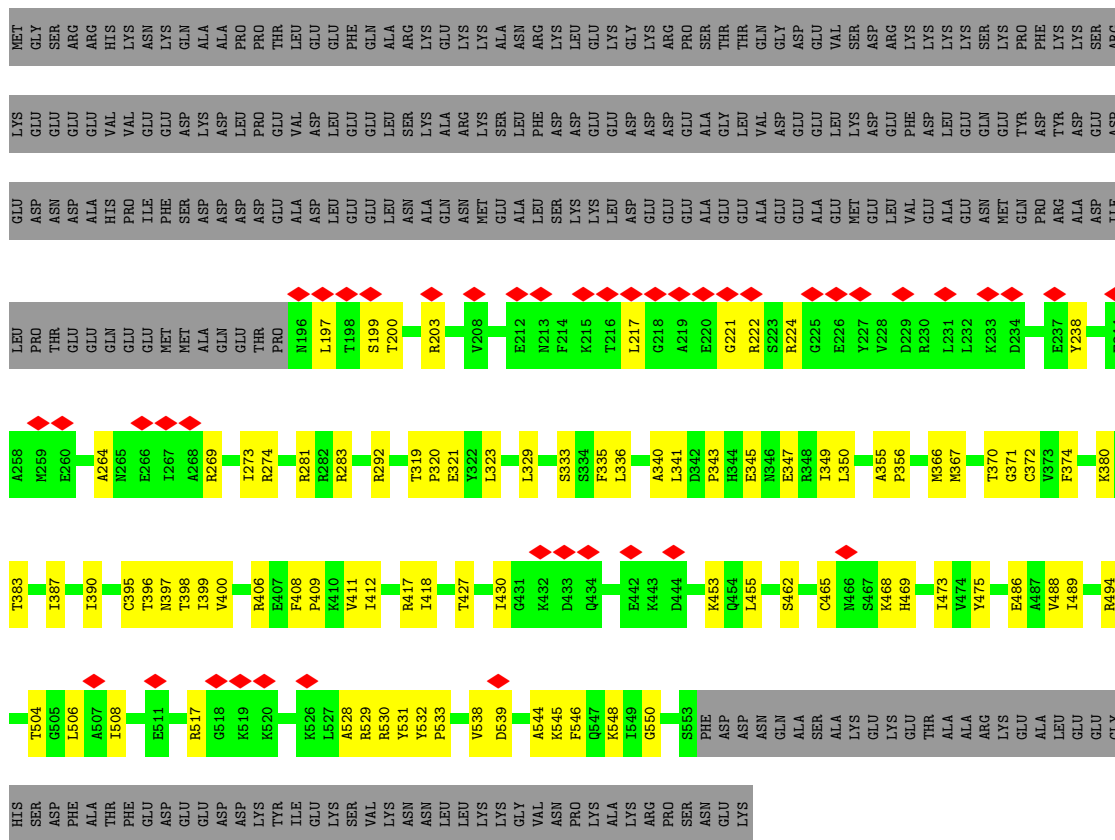


Chain 1: 71% 27%



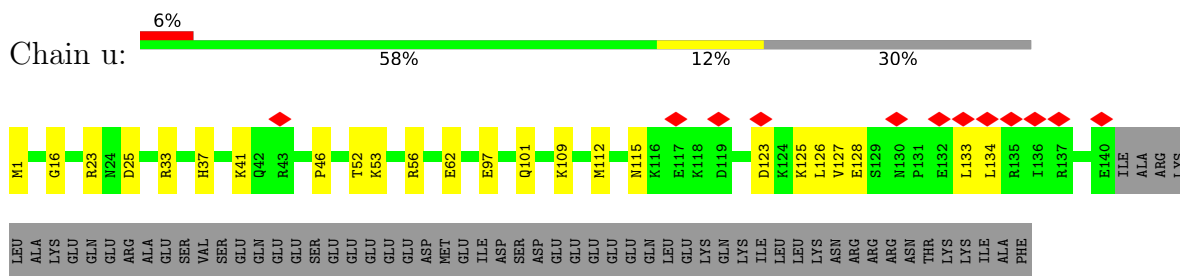
Chain m:



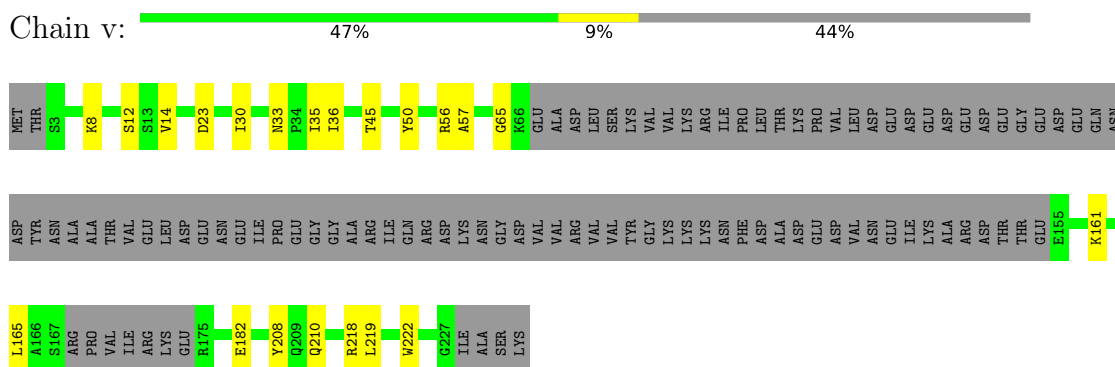
[illegible][illegible]

[illegible]

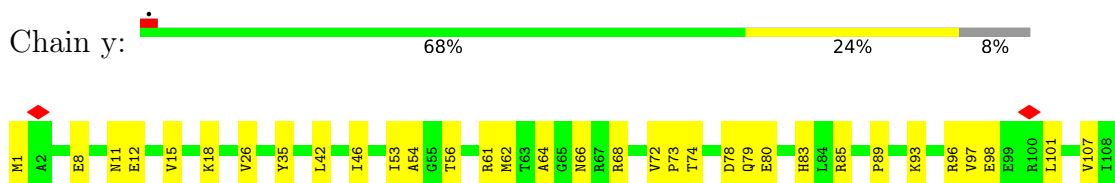
- Molecule 34: Ribosome biogenesis protein RLP24

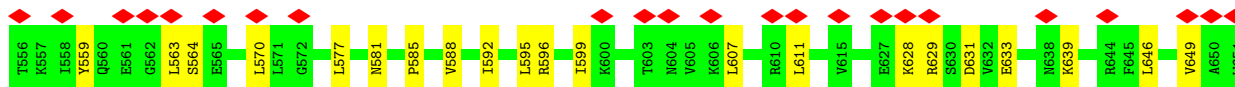


- Molecule 35: Nucleolar protein 16

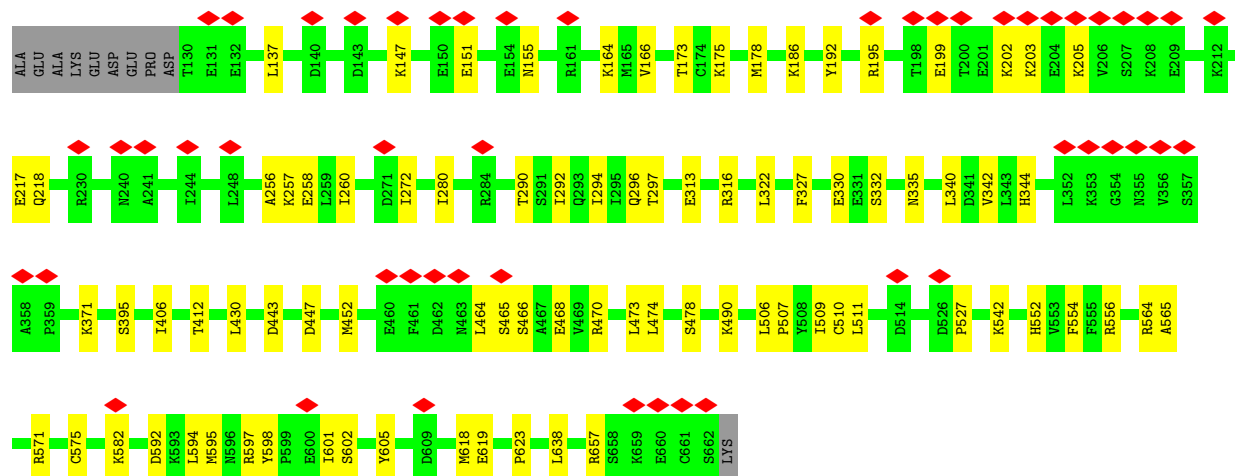
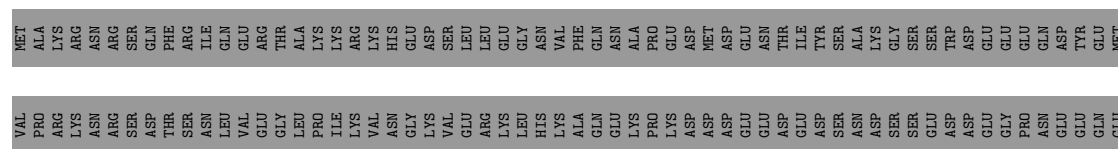


- Molecule 36: Eukaryotic translation initiation factor 6

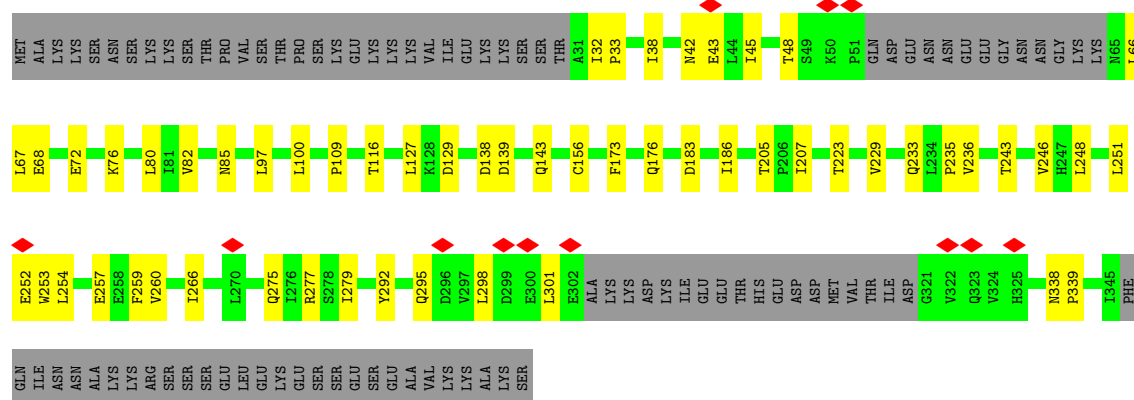




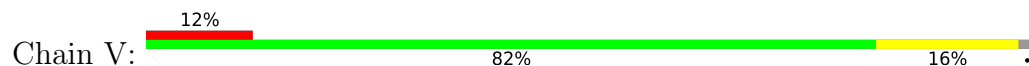
- Molecule 39: Nucleolar complex-associated protein 3

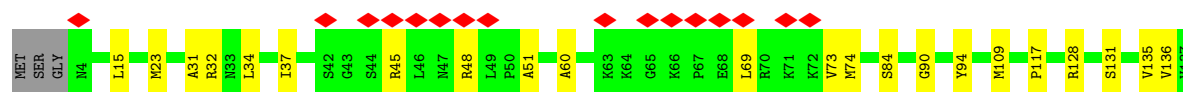


- Molecule 40: Proteasome-interacting protein CIC1

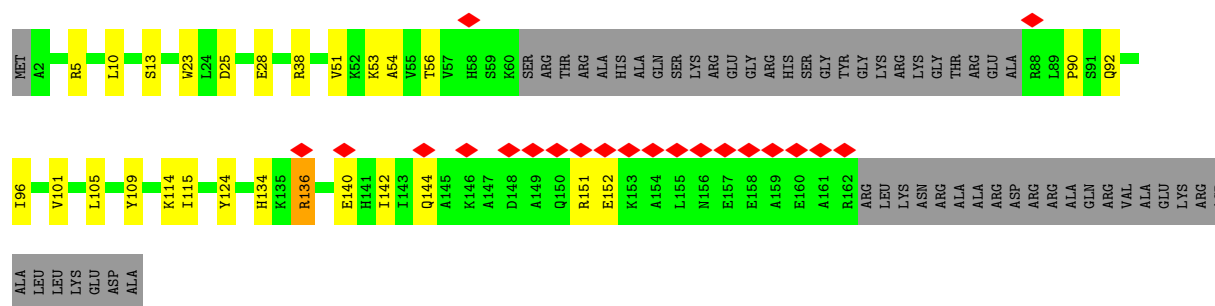


- Molecule 41: 60S ribosomal protein L23-A

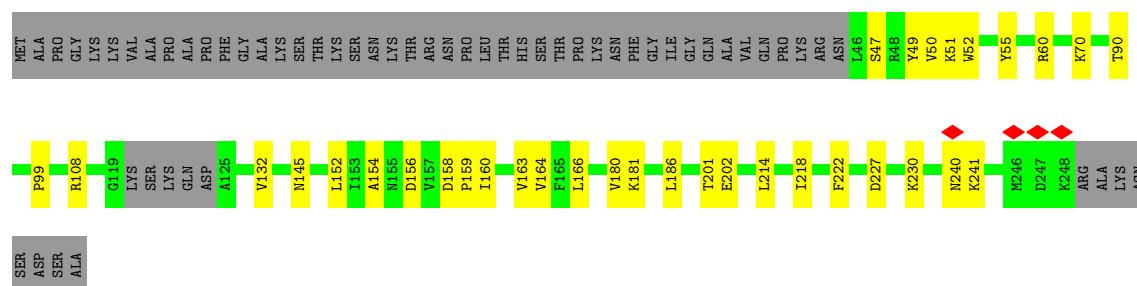




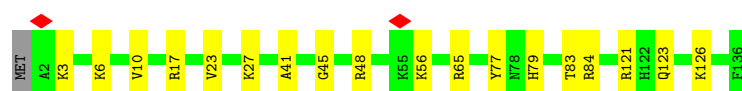
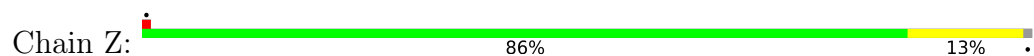
- Molecule 42: 60S ribosomal protein L19-A



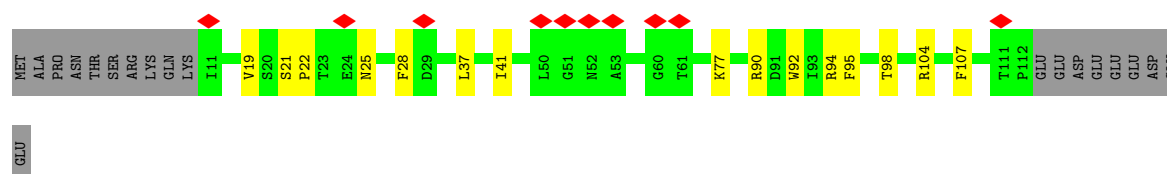
- Molecule 43: 60S ribosomal protein L8-A



- Molecule 44: 60S ribosomal protein L27-A

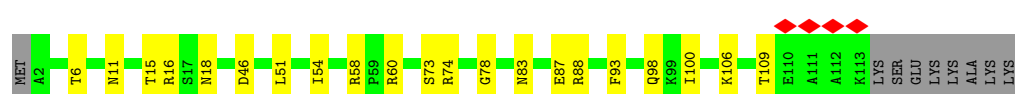


- Molecule 45: 60S ribosomal protein L22-A

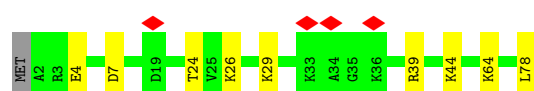


- Molecule 46: 60S ribosomal protein L30

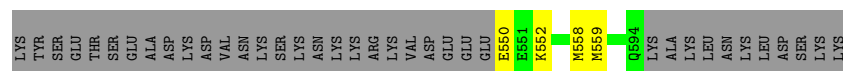
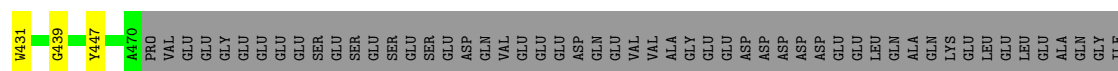
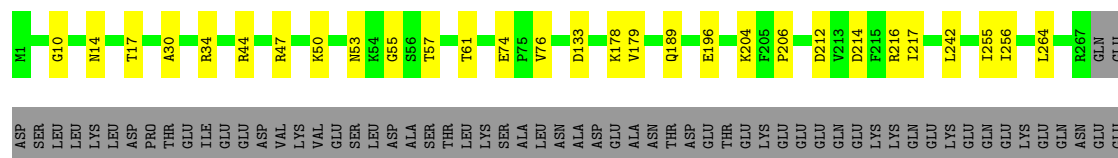
Chain g: 75% 17% 7%



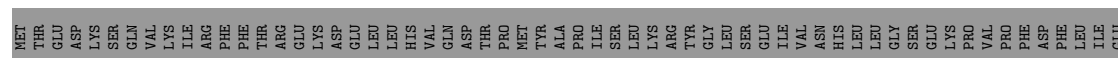
Chain k:

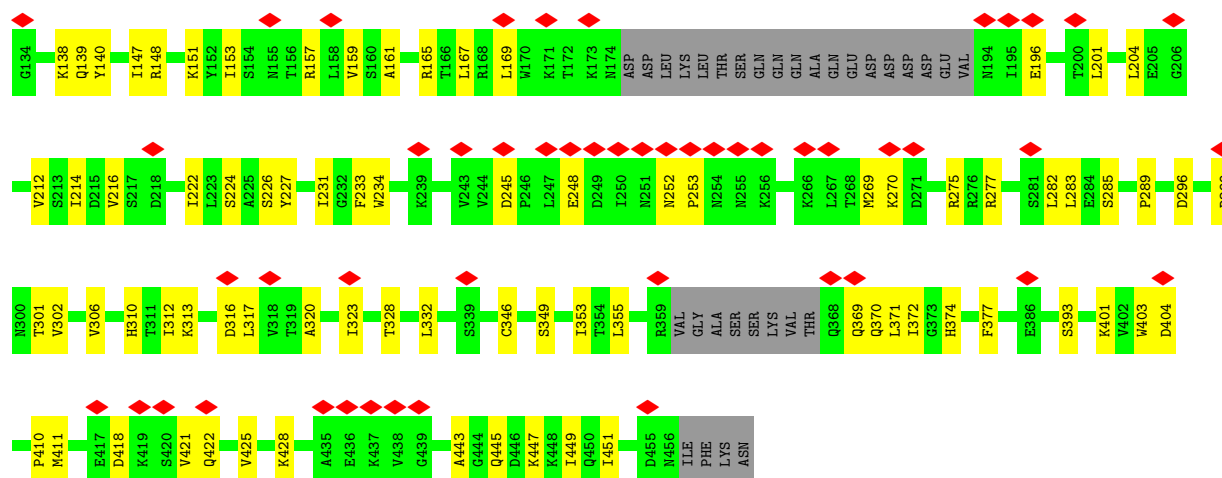


Chain n: 62% 8% 30%



Chain p:





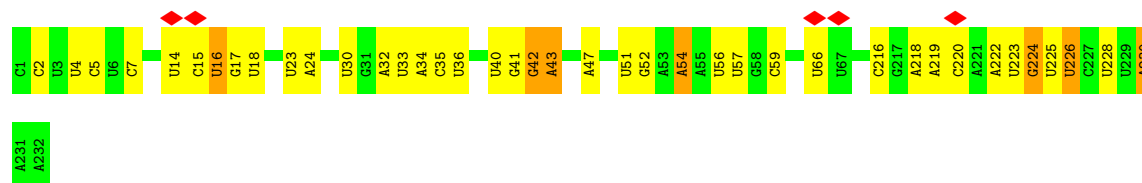
• Molecule 51: Ribosome biogenesis protein RLP7

Chain t: 74% 14% 11%



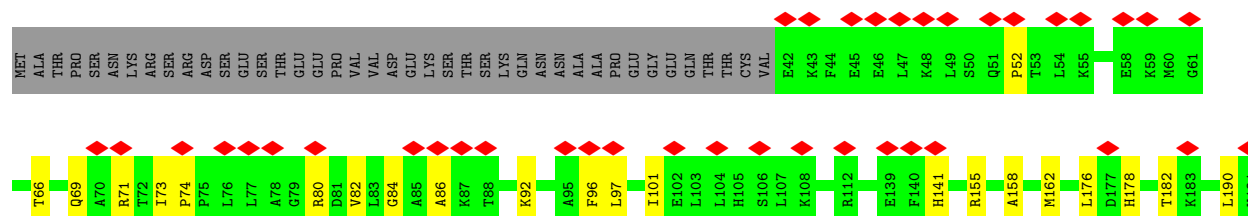
• Molecule 52: 5.8S ribosomal RNA gene and internal transcribed spacer 2

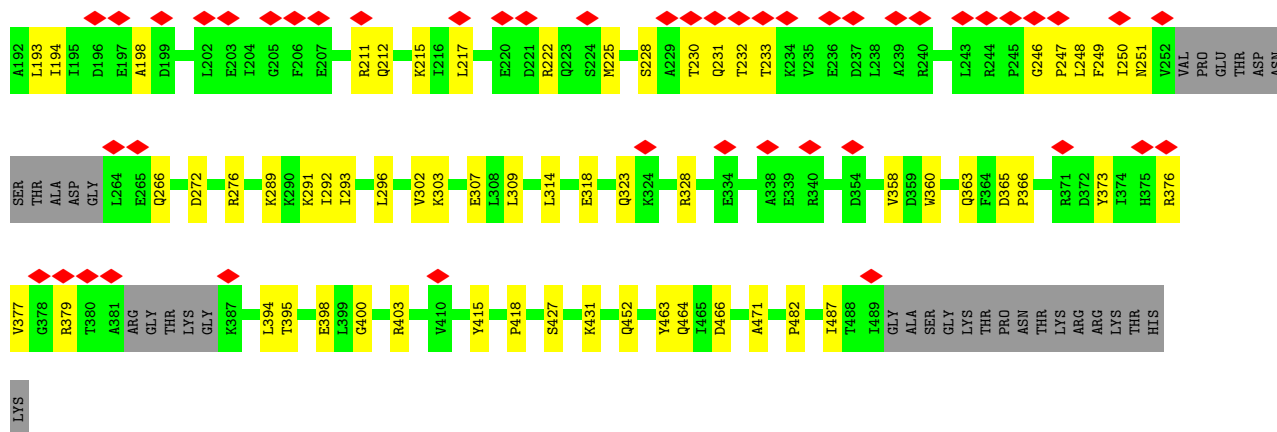
Chain 6: 6% 54% 38% 8%



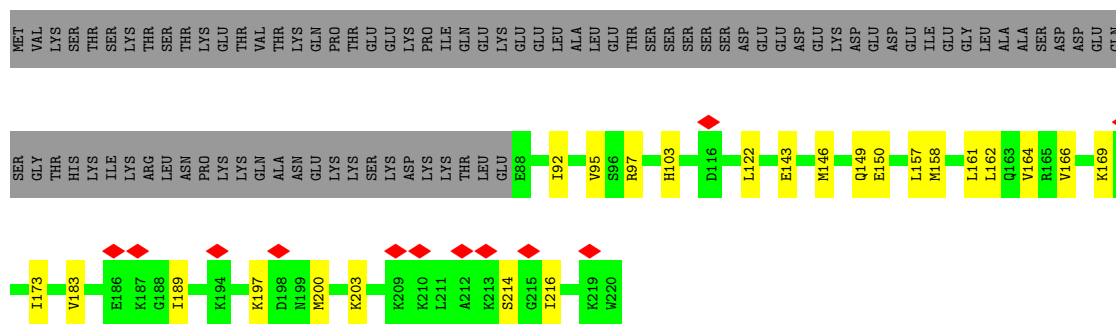
• Molecule 53: ATP-dependent RNA helicase HAS1

Chain D: 17% 69% 16% 14%

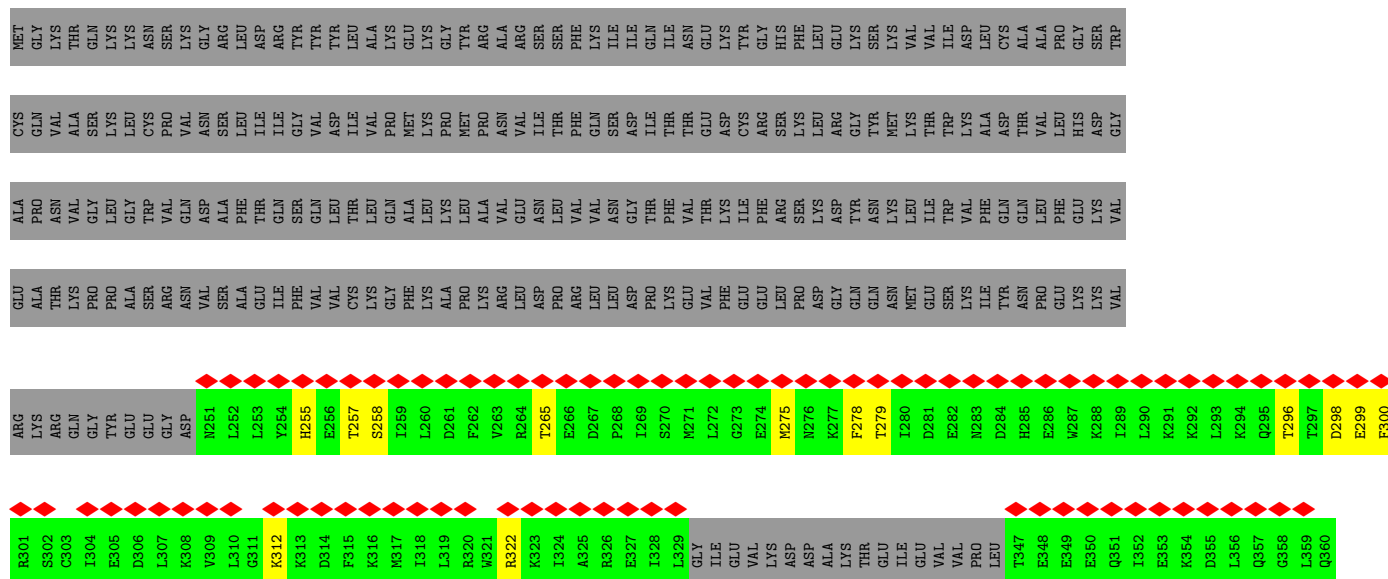
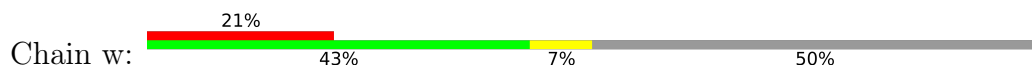


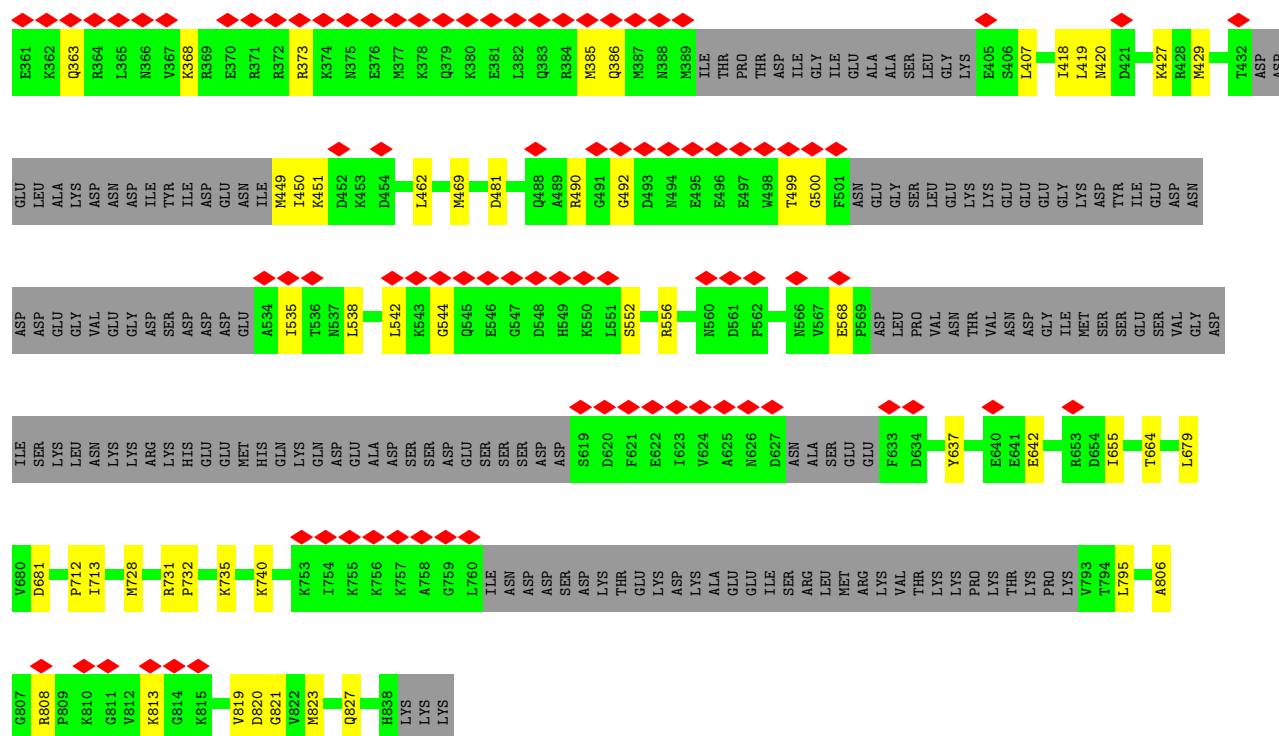


• Molecule 54: Ribosome biogenesis protein 15

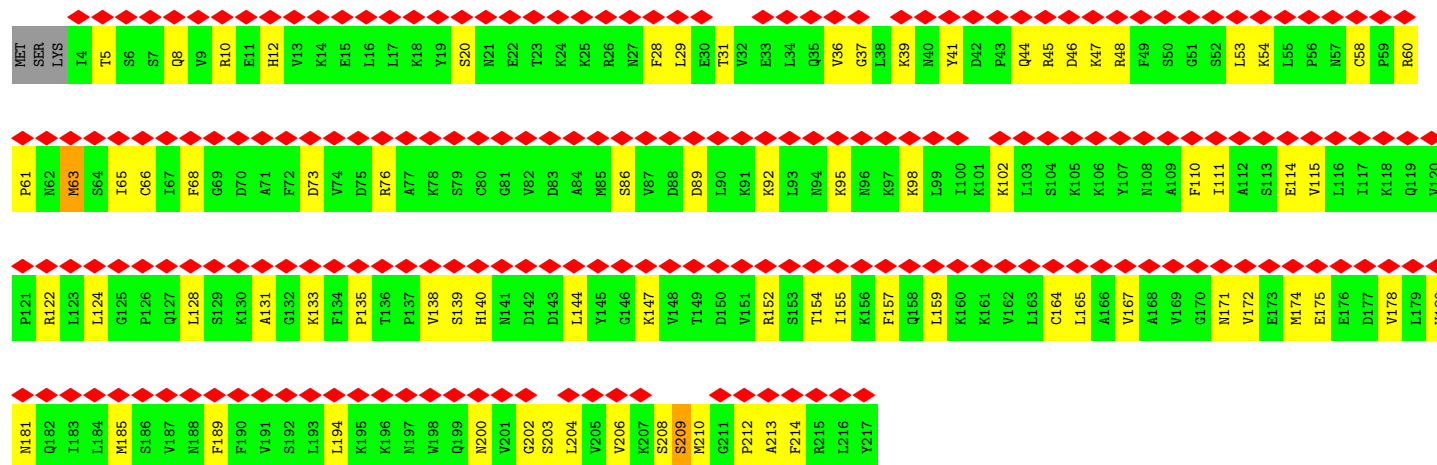


• Molecule 55: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase

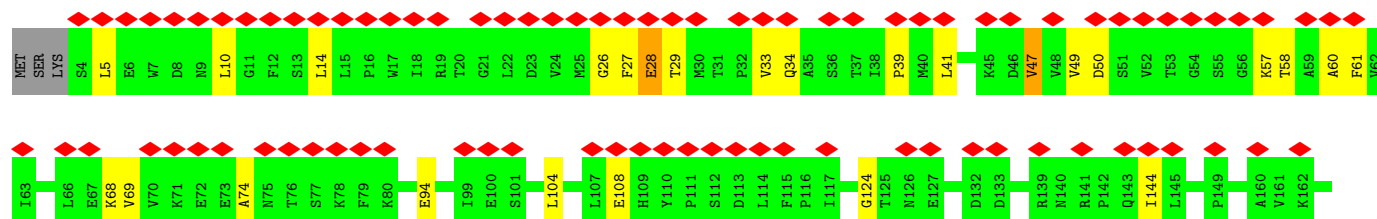




• Molecule 56: Ribosomal protein



• Molecule 57: ATP-dependent rRNA helicase SPB4



ASP LEU	R545	K546	L547	E548	R549	K550	E551	K552	M553	S554	L555	K556	R557	K558	A559	I560	GLU	GLU	GLU	LEU	LYS	ALA	GLU	GLU	LEU	ASP	ASN	ALA	GLU	T512	GLU	ARG	K514	N515	L516	ASP	TRP	LYS	GLU	ILE	N520	VAL	LEU	GLN	ASN	LYS	ARG	LYS	LYS	VAL	VAL	SER	SER	LYS	ALA	ILE	GLY	ASN	PHE	L534	A535	M536	S537	D538	K539	T540	L541	T542	K543	E544
	GLY	M486	M487	L488	M489	D490	P491	P492	M493	M494	M495	D496	E497	Y498	K499	Y500	K501	D502	K503	K504	R505	E506	K507	E508	R509	Q510	E511	T512	L513	K514	N515	L516	S517	L518	L518	L519	I519	N520	L461	F462	R463	L464	P465	R466	M467	P468	E469	T470	T471	K472	Y473	L474	ALA	THR	GLU	LYS	GLN	GLY	ILE	PHE	PRO									
		G425	V426	K427	A428	Y429	A431	F432	I433	K434	Y435	Y436	S437	M438	H439	S440	A441	T442	S443	I444	F445	R446	L447	Q448	S449	L450	D451	Y452	V453	G454	I455	A456	K457	L458	Y459	G460	L461	F462	R463	L464	P465	R466	M467	P468	E469	T470	T471	K472	Y473	L474	ALA	THR	GLU	LYS	GLN	GLY	ILE	PHE	PRO											
		N365	R366	V367	G368	K369	A370	I371	T372	F373	L374	N375	E376	G377	R378	E379	E380	D381	F382	I383	P384	F385	M386	Q387	V388	K389	N390	V391	E392	L393	E394	E395	L396	D397	L398	E399	V400	K401	G402	I403	T404	A405	M406	F407	Y408	E409	D410	F411	R412	M413	M414	I415	L416	E417	D418	R419	D420	R421	F422	D423	K424									
		G301	K302	L303	R308	T309	K310	T311	L312	T313	A314	F315	T316	D317	SER	LEU	S320	N321	S322	V323	L324	F325	T326	T327	D328	V329	A330	A331	I334	D335	I336	P337	D338	V339	D340	L341	V342	L345	D346	F347	P348	T349	N350	T351	M353	F354	M355	H356	R357	C358	G359	R360	T361	G362	R363	A364														
		L238	N239	Y240	C241	V242	V243	N244	P245	A246	E247	K248	L249	Q250	L251	L252	V253	S254	I255	L256	N257	N258	Y259	K260	F261	K262	T205	K263	C264	I265	V266	Y267	T270	D212	C271	V272	S273	V274	S275	Y276	F277	Y278	S279	F280	I281	Q282	Y283	L284	G285	K286	R287	N288	I289	L290	V291	N292	E293	V294	E295	I296	F297	S298								
		S167	M168	V169	D172	E173	A174	D175	D179	M180	K184	L190	R191	K196	R197	R198	T199	G200	L201	F202	S203	A204	T205	M206	R207	S208	A209	G210	S211	D212	I213	F214	K215	T216	G217	L218	R219	N220	P221	V222	R223	I224	T225	V226	N227	S228	LYS	ASN	GLN	ALA	PRO	S234	S235	L236	K237															

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	211000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.2	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	900	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.169	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.017	Depositor
Map size ($\text{\AA}$)	453.6, 453.6, 453.6	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	1	0.15	0/61575	0.28	4/95973 (0.0%)
2	2	0.18	0/3746	0.31	0/5832
3	7	0.12	0/1056	0.31	0/1408
4	A	0.13	0/2222	0.29	0/2998
5	B	0.15	0/2715	0.32	0/3647
6	C	0.15	0/2782	0.28	0/3766
7	E	0.13	0/1332	0.29	0/1791
8	F	0.14	0/1821	0.28	0/2451
9	H	0.13	0/1531	0.29	0/2062
10	J	0.12	0/1232	0.27	0/1642
11	L	0.15	0/1009	0.34	0/1355
12	M	0.13	0/1068	0.29	0/1438
13	N	0.16	0/1654	0.28	0/2212
14	O	0.15	0/1585	0.26	0/2128
15	P	0.13	0/1465	0.28	0/1968
16	Q	0.13	0/1050	0.25	0/1419
17	S	0.13	0/1468	0.26	0/1973
18	T	0.12	0/404	0.28	0/542
19	W	0.12	0/1902	0.32	0/2564
20	X	0.14	0/1083	0.29	0/1458
21	Y	0.17	0/1004	0.30	0/1341
22	b	0.11	0/4141	0.28	0/5575
23	d	0.12	0/887	0.30	0/1191
24	e	0.14	0/1030	0.27	0/1379
25	f	0.17	0/868	0.29	0/1168
26	h	0.14	0/978	0.29	0/1301
27	i	0.13	0/633	0.27	0/839
28	j	0.15	0/592	0.30	0/785
29	l	0.14	0/1425	0.34	0/1922
30	m	0.13	0/5511	0.30	0/7471
31	q	0.13	0/2854	0.34	0/3860
32	r	0.12	0/1462	0.28	0/1952

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	s	0.12	0/301	0.21	0/386
34	u	0.10	0/1205	0.25	0/1603
35	v	0.14	0/1100	0.25	0/1456
36	y	0.12	0/1722	0.29	0/2343
37	z	0.11	0/445	0.25	0/585
38	8	0.12	0/3624	0.30	1/4891 (0.0%)
39	I	0.11	0/4310	0.26	0/5807
40	K	0.13	0/2310	0.30	0/3118
41	V	0.12	0/1008	0.31	0/1356
42	R	0.13	0/1095	0.29	0/1465
43	G	0.16	0/1575	0.29	0/2125
44	Z	0.12	0/1118	0.22	0/1497
45	U	0.11	0/825	0.26	0/1120
46	c	0.10	0/751	0.21	0/1008
47	g	0.13	0/891	0.26	0/1191
48	k	0.13	0/618	0.26	0/826
49	n	0.14	0/3544	0.26	0/4766
50	p	0.10	0/2674	0.29	0/3623
51	t	0.12	0/2319	0.24	0/3108
52	6	0.12	0/2050	0.27	0/3186
53	D	0.12	0/3516	0.30	0/4741
54	o	0.12	0/1129	0.28	0/1502
55	w	0.11	0/3483	0.26	0/4628
56	a	0.11	0/1722	0.32	0/2313
57	x	0.15	0/4419	0.33	0/5958
All	All	0.14	0/161839	0.28	5/232013 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	644	G	C2'-C3'-O3'	8.84	126.95	113.70
1	1	906	A	C2'-C3'-O3'	7.19	124.49	113.70
1	1	908	G	C4'-C3'-O3'	6.88	119.71	109.40
1	1	906	A	C3'-C2'-O2'	6.67	120.71	110.70
38	8	306	PRO	N-CA-CB	5.84	109.98	103.44

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	55024	0	27662	641	0
2	2	3353	0	1695	29	0
3	7	1048	0	1117	23	0
4	A	2174	0	2179	54	0
5	B	2661	0	2738	61	0
6	C	2731	0	2852	37	0
7	E	1309	0	1389	19	0
8	F	1784	0	1862	23	0
9	H	1510	0	1576	18	0
10	J	1215	0	1245	21	0
11	L	991	0	1044	15	0
12	M	1053	0	1149	11	0
13	N	1621	0	1678	24	0
14	O	1555	0	1659	5	0
15	P	1442	0	1485	17	0
16	Q	1035	0	1115	9	0
17	S	1432	0	1470	14	0
18	T	401	0	418	5	0
19	W	1870	0	1902	31	0
20	X	1068	0	1153	12	0
21	Y	993	0	1081	12	0
22	b	4066	0	4111	55	0
23	d	873	0	914	19	0
24	e	1009	0	1080	12	0
25	f	850	0	880	10	0
26	h	969	0	1078	14	0
27	i	628	0	675	12	0
28	j	580	0	584	10	0
29	l	1394	0	1426	35	0
30	m	5377	0	5366	71	0
31	q	2799	0	2834	66	0
32	r	1438	0	1515	21	0
33	s	301	0	359	7	0
34	u	1183	0	1227	20	0
35	v	1087	0	1133	18	0
36	y	1701	0	1697	38	0
37	z	444	0	478	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	8	3567	0	3408	71	0
39	I	4247	0	4386	56	0
40	K	2274	0	2352	41	0
41	V	993	0	1040	14	0
42	R	1082	0	1160	30	0
43	G	1549	0	1637	23	0
44	Z	1092	0	1155	16	0
45	U	808	0	822	12	0
46	c	743	0	797	12	0
47	g	881	0	945	15	0
48	k	612	0	682	8	0
49	n	3470	0	3586	34	0
50	p	2628	0	2612	56	0
51	t	2293	0	2449	35	0
52	6	1838	0	927	22	0
53	D	3451	0	3578	53	0
54	o	1107	0	1159	20	0
55	w	3446	0	3521	53	0
56	a	1695	0	1781	60	0
57	x	4340	0	4468	92	0
58	g	1	0	0	0	0
58	j	1	0	0	0	0
All	All	153087	0	126291	1869	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (1869) 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)
1:1:890:C:H5	38:8:37:ARG:NE	1.20	1.39
1:1:890:C:N4	38:8:37:ARG:HH21	1.30	1.25
57:x:190:LEU:HD22	57:x:197:ARG:NH2	1.57	1.17
1:1:2103:U:O2	57:x:526:LYS:HD3	1.42	1.15
1:1:890:C:H41	38:8:37:ARG:NH2	1.42	1.15
57:x:190:LEU:HD22	57:x:197:ARG:HH21	0.95	1.12
57:x:190:LEU:CD2	57:x:197:ARG:HH21	1.74	1.01
1:1:890:C:OP2	38:8:37:ARG:HD2	1.65	0.96
1:1:1943:C:H5''	57:x:329:VAL:HB	1.49	0.91
57:x:169:VAL:CG2	57:x:197:ARG:HD2	2.01	0.91
1:1:890:C:C5	38:8:37:ARG:NE	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:818:C:N4	1:1:907:G:H22	1.73	0.87
1:1:3350:C:N4	57:x:552:LYS:CE	2.39	0.86
1:1:3350:C:N4	57:x:552:LYS:HE2	1.90	0.85
1:1:441:U:H3	1:1:493:G:H22	1.24	0.85
42:R:134:HIS:CD2	42:R:136:ARG:HB2	2.12	0.85
42:R:151:ARG:NH1	57:x:442:THR:HB	1.91	0.84
40:K:338:ASN:OD1	40:K:339:PRO:HD3	1.76	0.84
1:1:2442:G:H1	1:1:2505:U:H3	1.24	0.83
1:1:890:C:N4	38:8:37:ARG:NH2	2.12	0.82
1:1:890:C:H41	38:8:37:ARG:HH21	0.82	0.81
1:1:818:C:H42	1:1:907:G:N2	1.77	0.81
57:x:190:LEU:CD2	57:x:197:ARG:NH2	2.38	0.80
30:m:378:PRO:HB3	51:t:231:ASP:HB3	1.62	0.80
57:x:169:VAL:HG23	57:x:197:ARG:HD2	1.61	0.80
31:q:336:LEU:HD12	31:q:506:LEU:HD23	1.65	0.79
1:1:818:C:N4	1:1:907:G:N2	2.30	0.79
1:1:2451:G:N2	1:1:2496:C:C2	2.52	0.78
31:q:343:PRO:HG2	31:q:366:MET:HB2	1.67	0.77
57:x:263:LYS:HB2	57:x:339:VAL:HA	1.66	0.75
32:r:175:SER:HA	32:r:178:ARG:HD2	1.68	0.74
5:B:358:TRP:HB2	34:u:1:MET:HE1	1.69	0.74
21:Y:3:LYS:HD2	21:Y:8:VAL:HG13	1.69	0.74
57:x:247:GLU:OE1	57:x:403:ILE:HD13	1.85	0.74
1:1:2465:G:H1	1:1:2490:C:H42	1.31	0.74
9:H:9:GLN:HE22	9:H:54:LYS:HE3	1.51	0.74
57:x:169:VAL:HG21	57:x:197:ARG:HD2	1.69	0.74
1:1:2392:C:H42	1:1:2987:A:H61	1.36	0.73
1:1:156:G:H22	11:L:91:ARG:HH12	1.36	0.73
23:d:88:PRO:HB2	23:d:89:LEU:HD12	1.71	0.73
1:1:351:A:H1'	2:2:53:A:H1'	1.68	0.73
43:G:227:ASP:HA	43:G:230:LYS:HE3	1.71	0.73
51:t:197:GLY:HA2	51:t:311:GLU:HG3	1.71	0.73
1:1:2428:U:O2	1:1:2602:G:N2	2.22	0.73
55:w:808:ARG:NH2	55:w:813:LYS:O	2.21	0.73
1:1:3350:C:H41	57:x:552:LYS:HE3	1.53	0.73
1:1:3350:C:H41	57:x:552:LYS:CE	2.02	0.73
26:h:119:LYS:HB2	35:v:56:ARG:HG2	1.71	0.73
1:1:2429:G:H2'	1:1:2430:A:H8	1.54	0.72
1:1:1661:G:H2'	1:1:1662:G:C8	2.24	0.72
1:1:712:G:N2	1:1:754:G:O2'	2.23	0.72
40:K:109:PRO:HB2	40:K:253:TRP:HB3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:u:112:MET:HE3	34:u:115:ASN:HD21	1.52	0.72
6:C:3:ARG:HD2	6:C:22:LEU:HB2	1.72	0.72
50:p:306:VAL:HG12	50:p:312:ILE:HG12	1.72	0.72
36:y:1:MET:H2	36:y:224:LEU:HD13	1.53	0.72
57:x:57:LYS:HD3	57:x:202:PHE:HB3	1.71	0.72
56:a:29:LEU:HD21	56:a:61:PRO:HD2	1.72	0.71
1:1:3268:A:OP1	7:E:46:ARG:NH2	2.22	0.71
23:d:80:ASN:ND2	23:d:84:ASP:OD2	2.23	0.71
31:q:292:ARG:HH21	31:q:320:PRO:HG2	1.55	0.71
1:1:674:G:OP1	6:C:31:ARG:NH1	2.23	0.71
36:y:12:GLU:OE2	41:V:128:ARG:NH1	2.24	0.71
38:8:494:LEU:HB2	38:8:547:ILE:HG23	1.71	0.71
22:b:450:ALA:O	22:b:454:GLN:NE2	2.23	0.71
1:1:991:G:H1	1:1:1058:U:H3	1.37	0.70
1:1:890:C:H5	38:8:37:ARG:CD	2.03	0.70
39:I:175:LYS:NZ	55:w:568:GLU:O	2.25	0.70
39:I:554:PHE:O	39:I:597:ARG:NH2	2.23	0.70
1:1:2482:U:OP1	56:a:98:LYS:NZ	2.25	0.69
5:B:85:VAL:HG12	5:B:202:THR:HG22	1.74	0.69
40:K:48:THR:HG21	40:K:76:LYS:HG2	1.73	0.69
1:1:2457:G:O2'	1:1:2481:G:N2	2.24	0.69
32:r:4:ASN:O	32:r:9:ARG:NH1	2.26	0.69
1:1:1124:U:H5	1:1:1134:G:H1	1.41	0.69
1:1:655:C:H2'	1:1:656:A:H8	1.58	0.69
1:1:3056:U:H4'	1:1:3057:U:H5'	1.75	0.69
36:y:68:ARG:NH2	36:y:112:ASP:O	2.26	0.69
50:p:222:ILE:HB	50:p:234:TRP:HB2	1.75	0.69
57:x:418:ASP:HB3	57:x:421:ARG:HG3	1.75	0.69
1:1:1553:U:H4'	1:1:1554:U:H5'	1.75	0.69
28:j:21:ARG:NH2	28:j:41:ALA:O	2.22	0.69
39:I:335:ASN:HD22	39:I:527:PRO:HG3	1.59	0.68
13:N:99:ARG:NH2	13:N:118:SER:O	2.25	0.68
38:8:524:THR:HG23	39:I:465:SER:HB2	1.74	0.68
1:1:870:C:H2'	1:1:871:G:C8	2.29	0.68
42:R:134:HIS:HD2	42:R:136:ARG:HB2	1.59	0.68
5:B:115:LYS:NZ	5:B:129:ALA:O	2.26	0.68
2:2:83:C:OP1	2:2:85:G:N2	2.27	0.68
1:1:40:A:O2'	1:1:41:G:N7	2.26	0.67
1:1:1634:G:N7	44:Z:17:ARG:NH2	2.40	0.67
5:B:213:GLU:OE2	5:B:340:LYS:NZ	2.25	0.67
22:b:169:THR:HB	22:b:248:SER:HB3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:I:470:ARG:HB2	39:I:542:LYS:HE2	1.76	0.67
5:B:50:LYS:NZ	5:B:330:GLY:O	2.25	0.67
31:q:486:GLU:OE2	31:q:530:ARG:NH2	2.28	0.67
4:A:167:ARG:NH1	30:m:150:ASP:O	2.27	0.67
31:q:538:VAL:HG23	31:q:539:ASP:H	1.60	0.67
34:u:97:GLU:O	34:u:101:GLN:NE2	2.27	0.67
9:H:57:VAL:HG23	9:H:68:LEU:HD13	1.77	0.67
50:p:285:SER:OG	50:p:313:LYS:NZ	2.25	0.67
4:A:128:ASN:HB2	10:J:285:MET:HE1	1.76	0.67
22:b:227:ARG:HH12	22:b:232:MET:HA	1.59	0.67
43:G:201:THR:HG22	43:G:202:GLU:HG2	1.76	0.66
39:I:443:ASP:OD1	55:w:731:ARG:NH1	2.29	0.66
5:B:29:VAL:HG22	5:B:218:ILE:HD12	1.78	0.66
43:G:158:ASP:HB3	43:G:159:PRO:HD3	1.77	0.66
57:x:430:VAL:HG22	57:x:467:MET:HE2	1.75	0.66
38:8:500:LYS:HG2	38:8:570:LEU:HD21	1.77	0.66
40:K:143:GLN:HG3	40:K:223:THR:HG21	1.78	0.66
1:1:696:C:H1'	35:v:65:GLY:H	1.61	0.66
1:1:713:U:O4	4:A:255:GLN:NE2	2.29	0.66
1:1:1924:U:H1'	1:1:2110:G:N2	2.11	0.66
1:1:873:U:H3'	39:I:490:LYS:HE2	1.78	0.66
38:8:489:PRO:HB3	38:8:527:ALA:HB2	1.78	0.66
42:R:109:TYR:HB3	42:R:115:ILE:HD13	1.78	0.66
4:A:28:MET:HE1	10:J:210:LEU:HB3	1.78	0.66
52:6:42:G:H2'	52:6:43:A:H8	1.61	0.66
1:1:92:G:H5'	1:1:93:C:H5''	1.78	0.65
31:q:370:THR:O	31:q:397:ASN:ND2	2.28	0.65
49:n:189:GLN:NE2	49:n:196:GLU:OE2	2.29	0.65
23:d:47:ASP:H	23:d:86:LYS:HZ2	1.44	0.65
40:K:76:LYS:HB3	40:K:251:LEU:HB2	1.79	0.65
4:A:44:ARG:NH2	4:A:117:LEU:O	2.29	0.65
29:l:127:GLU:HG3	29:l:148:LYS:HA	1.78	0.65
38:8:585:PRO:HB2	39:I:618:MET:HE1	1.78	0.65
4:A:134:ARG:NH1	10:J:218:GLN:O	2.25	0.65
29:l:157:GLN:HG3	29:l:158:PRO:HD2	1.78	0.65
1:1:2830:G:H2'	1:1:2831:G:C8	2.32	0.65
44:Z:121:ARG:HG3	44:Z:126:LYS:HE3	1.77	0.65
4:A:113:TYR:HB2	4:A:224:ILE:HD11	1.79	0.65
39:I:313:GLU:OE1	39:I:316:ARG:NH2	2.30	0.65
56:a:73:ASP:OD1	56:a:76:ARG:NH2	2.29	0.65
6:C:328:ASN:OD1	8:F:48:ASN:ND2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:68:ARG:NH1	13:N:124:ASP:O	2.29	0.65
1:1:394:G:N1	1:1:397:A:OP2	2.26	0.64
3:7:86:PRO:HG2	10:J:272:LEU:HA	1.79	0.64
1:1:2454:G:N2	31:q:251:ASN:O	2.30	0.64
4:A:27:PHE:O	4:A:30:LYS:NZ	2.30	0.64
1:1:2469:G:N2	1:1:2477:G:H1'	2.13	0.64
1:1:2491:A:H4'	56:a:213:ALA:HB2	1.79	0.64
1:1:2891:U:HO2'	37:z:2:ALA:N	1.95	0.64
38:8:465:GLU:HG3	38:8:466:SER:H	1.61	0.64
47:g:54:ILE:HD11	47:g:78:GLY:HA2	1.79	0.64
57:x:506:GLU:OE2	57:x:509:ARG:NH2	2.30	0.64
1:1:1635:G:N2	1:1:1638:A:OP2	2.31	0.64
56:a:10:ARG:HD3	56:a:180:VAL:HG11	1.79	0.64
1:1:870:C:H2'	1:1:871:G:H8	1.62	0.64
1:1:1429:G:OP2	6:C:107:ARG:NH2	2.31	0.64
19:W:96:CYS:HB2	19:W:100:THR:HG21	1.78	0.64
1:1:610:G:O6	6:C:309:ARG:NH2	2.31	0.64
13:N:146:ALA:HB3	26:h:101:THR:HG23	1.80	0.63
31:q:341:LEU:O	31:q:417:ARG:NE	2.28	0.63
42:R:136:ARG:HB3	42:R:136:ARG:CZ	2.28	0.63
1:1:1863:G:N2	1:1:1867:A:OP2	2.32	0.63
5:B:95:THR:HG22	5:B:97:ARG:H	1.62	0.63
31:q:475:TYR:HB3	31:q:544:ALA:HB3	1.79	0.63
36:y:219:GLU:HA	36:y:224:LEU:HD12	1.81	0.63
49:n:212:ASP:OD2	51:t:34:GLN:NE2	2.32	0.63
46:c:19:LYS:O	57:x:220:ASN:HB2	1.97	0.63
1:1:1639:C:OP2	47:g:74:ARG:NH1	2.30	0.63
1:1:2802:A:O3'	3:7:92:ARG:NH2	2.32	0.63
17:S:6:GLU:OE2	17:S:28:ARG:NH1	2.32	0.63
19:W:158:ILE:HG22	19:W:160:SER:H	1.64	0.63
6:C:2:SER:OG	6:C:3:ARG:N	2.28	0.63
6:C:68:GLY:HA2	55:w:820:ASP:HB2	1.81	0.63
1:1:3350:C:H42	57:x:552:LYS:HE2	1.62	0.63
36:y:11:ASN:ND2	36:y:209:ASP:OD2	2.32	0.63
41:V:15:LEU:HD23	41:V:51:ALA:HB3	1.80	0.63
50:p:418:ASP:HB3	50:p:421:VAL:HG22	1.80	0.63
56:a:41:TYR:HB2	56:a:200:ASN:HD21	1.64	0.63
1:1:3313:U:H4'	5:B:173:GLN:HG3	1.81	0.62
1:1:1680:G:OP2	45:U:90:ARG:NH2	2.32	0.62
31:q:273:ILE:HA	31:q:329:LEU:HA	1.81	0.62
55:w:535:ILE:HD12	55:w:538:LEU:HD21	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1385:C:HO2'	7:E:2:SER:N	1.98	0.62
53:D:471:ALA:HA	53:D:482:PRO:HG3	1.81	0.62
30:m:285:GLU:OE1	30:m:287:ARG:NH1	2.33	0.62
34:u:97:GLU:HG3	34:u:101:GLN:HE22	1.65	0.62
1:1:2442:G:H2'	1:1:2443:A:H8	1.64	0.62
19:W:38:ARG:NE	19:W:224:ASP:OD2	2.33	0.62
23:d:55:LEU:HB2	23:d:95:PRO:HD3	1.80	0.62
1:1:216:G:OP1	21:Y:16:ARG:NH1	2.32	0.62
14:O:59:ARG:NH1	33:s:3:VAL:O	2.33	0.62
19:W:221:TYR:HD1	19:W:228:VAL:HG22	1.65	0.62
44:Z:3:LYS:O	44:Z:6:LYS:NZ	2.33	0.62
49:n:179:VAL:HG21	49:n:379:LEU:HD11	1.81	0.61
46:c:19:LYS:HB2	57:x:220:ASN:HB2	1.82	0.61
1:1:761:A:N6	1:1:770:G:OP1	2.32	0.61
4:A:140:ASP:HB2	4:A:180:SER:HA	1.82	0.61
11:L:57:VAL:HG22	11:L:69:VAL:HG12	1.82	0.61
39:I:452:MET:SD	39:I:478:SER:OG	2.57	0.61
31:q:530:ARG:NH1	31:q:532:TYR:OH	2.33	0.61
42:R:151:ARG:NH1	57:x:442:THR:CB	2.63	0.61
56:a:10:ARG:HG2	56:a:180:VAL:HG21	1.82	0.61
1:1:815:G:H1	1:1:925:A:H61	1.47	0.61
1:1:2428:U:O2	1:1:2602:G:C2	2.53	0.61
1:1:3367:C:H5''	34:u:112:MET:HE1	1.82	0.61
56:a:54:LYS:HA	56:a:154:THR:HA	1.82	0.61
51:t:70:ARG:NH2	52:6:2:C:O2	2.28	0.61
1:1:2434:U:H5''	1:1:2435:G:H8	1.65	0.61
38:8:514:PRO:O	38:8:517:PRO:HD2	2.01	0.61
1:1:371:G:N1	1:1:374:A:OP2	2.30	0.61
1:1:3329:U:H5''	5:B:308:MET:HE2	1.83	0.61
39:I:552:HIS:HA	39:I:556:ARG:HB2	1.81	0.61
1:1:1105:A:H2'	1:1:1106:G:H8	1.66	0.60
13:N:36:ILE:HG12	13:N:64:VAL:HG23	1.83	0.60
31:q:498:ASN:ND2	31:q:550:GLY:O	2.30	0.60
53:D:71:ARG:NH1	53:D:251:ASN:O	2.34	0.60
1:1:316:U:O2'	27:i:29:LYS:NZ	2.31	0.60
1:1:1620:U:H5'	49:n:47:ARG:HD2	1.84	0.60
23:d:58:ALA:HA	23:d:61:LYS:HE2	1.82	0.60
5:B:198:HIS:CE1	37:z:41:LEU:HD12	2.37	0.60
30:m:443:LEU:HD12	30:m:452:LEU:HD11	1.82	0.60
39:I:592:ASP:OD1	39:I:657:ARG:NH1	2.34	0.60
1:1:890:C:H41	38:8:37:ARG:CZ	2.11	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:V:45:ARG:HD2	41:V:48:ARG:HD3	1.83	0.60
1:1:845:G:N2	1:1:848:A:OP2	2.34	0.60
5:B:57:VAL:HG13	5:B:357:LYS:HB3	1.81	0.60
57:x:169:VAL:HG21	57:x:197:ARG:CD	2.30	0.60
1:1:844:G:H2'	1:1:845:G:C8	2.37	0.60
5:B:216:ASP:OD1	5:B:339:ARG:HB3	2.01	0.60
50:p:231:ILE:HB	50:p:283:LEU:HB2	1.83	0.60
1:1:728:G:H5'	16:Q:43:PRO:HB2	1.84	0.60
2:2:154:C:H5''	43:G:181:LYS:HD3	1.83	0.60
4:A:102:SER:HB3	4:A:109:THR:HG23	1.84	0.60
22:b:43:ARG:NH1	22:b:119:GLY:O	2.35	0.60
31:q:528:ALA:O	31:q:529:ARG:NH1	2.32	0.60
49:n:402:ILE:HG13	49:n:403:ASP:H	1.66	0.60
1:1:164:A:O2'	1:1:166:C:O5'	2.20	0.59
1:1:3194:C:O2'	1:1:3195:U:O2	2.20	0.59
4:A:86:VAL:HG23	4:A:104:PRO:HG3	1.83	0.59
56:a:36:VAL:HG23	56:a:204:LEU:HB3	1.84	0.59
13:N:27:VAL:HB	13:N:122:ASN:ND2	2.16	0.59
15:P:42:THR:HG22	15:P:46:LYS:HE3	1.84	0.59
27:i:68:ARG:NH2	55:w:681:ASP:OD2	2.34	0.59
1:1:1596:C:H2'	1:1:1597:C:C6	2.37	0.59
1:1:3205:G:OP2	1:1:3206:C:N4	2.34	0.59
30:m:393:ASP:OD1	51:t:23:ARG:NH1	2.36	0.59
1:1:1721:U:OP2	42:R:124:TYR:OH	2.20	0.59
1:1:3277:U:O4	15:P:172:GLN:NE2	2.31	0.59
5:B:369:ARG:HH11	34:u:33:ARG:HD3	1.67	0.59
1:1:1157:G:O2'	1:1:1169:A:N3	2.36	0.59
9:H:90:MET:HE2	9:H:179:ILE:HG22	1.85	0.59
22:b:182:SER:OG	22:b:185:ARG:NH2	2.36	0.59
38:8:628:LYS:HG3	38:8:629:ARG:HG3	1.84	0.59
53:D:363:GLN:NE2	53:D:365:ASP:O	2.30	0.59
56:a:124:LEU:HD22	56:a:128:LEU:HB2	1.83	0.59
23:d:47:ASP:H	23:d:86:LYS:NZ	2.01	0.59
51:t:77:ARG:NH2	51:t:303:ASN:O	2.35	0.59
1:1:675:C:O2'	1:1:679:U:OP1	2.21	0.59
38:8:12:GLN:HA	38:8:16:LEU:HB2	1.85	0.59
1:1:1300:G:H5''	1:1:1301:A:H5'	1.84	0.59
1:1:1679:A:H4'	22:b:520:PRO:HB3	1.83	0.59
1:1:2437:G:H2'	1:1:2438:A:C8	2.38	0.59
17:S:77:VAL:HG11	17:S:106:LEU:HD22	1.84	0.59
38:8:12:GLN:HG2	38:8:16:LEU:HD22	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:8:515:ILE:HG13	38:8:518:LEU:HD12	1.85	0.59
1:1:2449:A:H2'	1:1:2450:G:C8	2.38	0.58
36:y:85:ARG:NH2	36:y:89:PRO:O	2.36	0.58
1:1:1299:U:O2'	32:r:42:LEU:O	2.21	0.58
12:M:17:VAL:HG11	12:M:74:ARG:HA	1.84	0.58
56:a:114:GLU:HG2	56:a:115:VAL:HG13	1.85	0.58
1:1:655:C:H2'	1:1:656:A:C8	2.38	0.58
6:C:31:ARG:NH2	6:C:33:ASP:OD2	2.26	0.58
17:S:125:LYS:HE2	17:S:127:ALA:HB2	1.86	0.58
39:I:137:LEU:HD21	39:I:173:THR:HG22	1.85	0.58
52:6:51:U:O2'	52:6:54:A:N7	2.34	0.58
1:1:412:G:OP1	15:P:62:ARG:NH1	2.36	0.58
4:A:287:ASP:OD2	6:C:3:ARG:NH2	2.36	0.58
21:Y:126:LEU:HD12	21:Y:127:GLU:HG2	1.86	0.58
41:V:117:PRO:HA	41:V:135:VAL:HB	1.86	0.58
53:D:292:ILE:HG12	53:D:360:TRP:HB2	1.86	0.58
57:x:420:ASP:OD2	57:x:505:ARG:NH2	2.37	0.58
1:1:784:A:N7	16:Q:69:ARG:NH2	2.52	0.58
50:p:299:ASP:OD1	50:p:301:THR:OG1	2.21	0.58
1:1:119:U:H5'	30:m:265:ARG:HG2	1.86	0.58
1:1:1195:A:H5''	1:1:1196:C:H5''	1.85	0.58
1:1:1757:A:OP1	45:U:94:ARG:NH2	2.30	0.58
1:1:1863:G:O2'	1:1:1867:A:N6	2.37	0.58
30:m:644:ASP:OD1	30:m:645:ALA:N	2.37	0.58
50:p:122:SER:OG	50:p:124:ASP:OD1	2.22	0.58
5:B:292:ALA:HB2	5:B:302:LYS:HG3	1.86	0.58
12:M:135:LEU:HD21	14:O:178:VAL:HG22	1.86	0.58
1:1:937:G:N2	1:1:962:A:O4'	2.36	0.58
30:m:441:ARG:NH1	30:m:457:ASP:OD1	2.36	0.58
45:U:98:THR:OG1	45:U:104:ARG:NH1	2.37	0.58
53:D:190:LEU:HD22	53:D:217:LEU:HD23	1.85	0.58
56:a:95:LYS:NZ	56:a:122:ARG:O	2.36	0.58
56:a:209:SER:OG	56:a:210:MET:N	2.37	0.58
1:1:2887:A:N7	22:b:31:THR:OG1	2.34	0.58
10:J:285:MET:HG2	10:J:288:ILE:HD12	1.85	0.58
17:S:8:GLN:HB3	17:S:64:ILE:HD11	1.85	0.58
36:y:18:LYS:HE2	36:y:64:ALA:HA	1.86	0.58
40:K:85:ASN:HB2	40:K:301:LEU:HD21	1.85	0.58
1:1:644:G:H4'	1:1:1116:G:N2	2.19	0.57
1:1:1448:U:H5''	15:P:66:SER:HB3	1.86	0.57
1:1:2356:A:H61	1:1:2983:C:H42	1.50	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:68:HIS:O	5:B:70:ARG:NH1	2.38	0.57
7:E:40:LEU:HD13	7:E:84:VAL:HG11	1.85	0.57
22:b:178:VAL:HG23	22:b:255:ASP:HB2	1.85	0.57
30:m:222:GLU:HG2	55:w:655:ILE:HG21	1.86	0.57
31:q:355:ALA:HB3	31:q:356:PRO:HD3	1.86	0.57
43:G:240:ASN:OD1	43:G:241:LYS:N	2.37	0.57
1:1:252:U:O2'	35:v:218:ARG:NH1	2.37	0.57
3:7:138:GLU:HG3	3:7:142:LYS:HE2	1.85	0.57
11:L:113:VAL:HG12	11:L:117:LYS:HE2	1.86	0.57
30:m:698:SER:HB3	30:m:729:VAL:HG13	1.86	0.57
6:C:266:THR:HG23	6:C:267:VAL:HG13	1.85	0.57
56:a:194:LEU:HD23	56:a:200:ASN:HB3	1.87	0.57
1:1:1353:U:O2'	7:E:8:LYS:O	2.21	0.57
1:1:2095:G:H2'	1:1:2096:A:H8	1.69	0.57
4:A:142:ARG:HB2	4:A:181:ILE:HD13	1.86	0.57
13:N:114:ARG:NH2	13:N:157:LYS:HG2	2.20	0.57
1:1:2428:U:H2'	1:1:2429:G:C8	2.39	0.57
1:1:3278:C:H3'	1:1:3279:A:H5'	1.85	0.57
10:J:239:ASP:OD1	10:J:242:ARG:NH2	2.33	0.57
19:W:188:VAL:HG21	19:W:202:ILE:HG21	1.86	0.57
22:b:80:ASP:OD2	22:b:245:HIS:NE2	2.37	0.57
39:I:564:ARG:HG2	39:I:623:PRO:HG2	1.86	0.57
42:R:105:LEU:HD21	42:R:109:TYR:CE2	2.39	0.57
42:R:115:ILE:HG12	42:R:142:ILE:HD11	1.86	0.57
1:1:358:G:N2	1:1:361:A:OP2	2.32	0.57
50:p:227:TYR:HA	50:p:289:PRO:HB3	1.87	0.57
52:6:16:U:H2'	52:6:17:G:H8	1.70	0.57
1:1:759:U:H2'	1:1:771:A:H61	1.68	0.57
1:1:2419:A:O2'	1:1:2420:C:OP1	2.23	0.57
19:W:84:GLU:OE2	19:W:89:LEU:N	2.37	0.57
22:b:184:LEU:HD22	22:b:220:ASP:HB2	1.86	0.57
30:m:335:GLU:OE1	30:m:364:ARG:NH1	2.37	0.57
39:I:166:VAL:HG13	39:I:178:MET:HB2	1.87	0.57
39:I:203:LYS:HA	39:I:205:LYS:HE3	1.87	0.57
40:K:301:LEU:HB3	54:o:189:ILE:HD13	1.85	0.57
44:Z:56:LYS:HD2	51:t:28:ARG:HD2	1.87	0.57
51:t:48:LYS:NZ	52:6:228:U:O2'	2.29	0.57
1:1:1062:A:O2'	1:1:1098:A:OP1	2.23	0.57
2:2:29:U:H5''	11:L:27:ASP:HB3	1.87	0.57
4:A:143:PHE:HA	4:A:149:TYR:HB3	1.87	0.57
31:q:264:ALA:O	31:q:269:ARG:NH2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:c:22:LYS:HB2	46:c:93:LEU:HB2	1.87	0.57
50:p:296:ASP:HB2	50:p:302:VAL:HB	1.85	0.57
30:m:446:ASP:OD1	30:m:449:GLY:N	2.33	0.56
31:q:390:ILE:HG23	31:q:395:CYS:HB2	1.85	0.56
1:1:869:G:H22	1:1:892:U:H3	1.52	0.56
1:1:2493:U:H2'	1:1:2494:A:C8	2.41	0.56
51:t:232:ASN:HB3	51:t:246:CYS:HA	1.86	0.56
53:D:82:VAL:HG22	53:D:225:MET:HG3	1.86	0.56
56:a:39:LYS:HG2	56:a:202:GLY:HA2	1.87	0.56
1:1:449:U:N3	1:1:450:G:O6	2.39	0.56
1:1:2476:C:H2'	1:1:2477:G:O4'	2.06	0.56
1:1:3388:C:H5''	1:1:3389:U:H5'	1.87	0.56
6:C:156:LEU:HD12	6:C:159:ILE:HD12	1.86	0.56
29:l:99:ILE:HD11	29:l:141:LEU:HD12	1.87	0.56
30:m:304:GLU:HA	30:m:307:GLN:HG3	1.88	0.56
30:m:751:HIS:NE2	30:m:753:THR:OG1	2.38	0.56
36:y:116:LEU:HD11	36:y:177:LEU:HD21	1.86	0.56
38:8:499:ILE:HD13	38:8:519:LEU:HB3	1.87	0.56
52:6:42:G:H2'	52:6:43:A:C8	2.40	0.56
56:a:47:LYS:NZ	56:a:48:ARG:O	2.38	0.56
57:x:68:LYS:NZ	57:x:198:ARG:HG3	2.20	0.56
1:1:633:C:O2'	25:f:21:ARG:O	2.21	0.56
1:1:1366:A:O2'	24:e:45:ARG:NH2	2.38	0.56
1:1:2372:A:N7	1:1:2374:C:N4	2.53	0.56
1:1:2496:C:O2'	1:1:2497:U:OP1	2.21	0.56
49:n:255:ILE:HG22	49:n:256:ILE:HG12	1.86	0.56
1:1:733:G:N2	1:1:736:A:OP2	2.39	0.56
1:1:815:G:H2'	1:1:816:A:O4'	2.06	0.56
1:1:1947:G:OP2	1:1:1947:G:N2	2.37	0.56
1:1:2411:U:H2'	1:1:2412:G:C8	2.41	0.56
3:7:47:LYS:HG3	3:7:51:LYS:HE2	1.86	0.56
5:B:61:ASP:OD2	22:b:413:ASN:ND2	2.35	0.56
5:B:182:GLN:NE2	5:B:184:ASN:OD1	2.36	0.56
1:1:953:G:H2'	1:1:1116:G:N7	2.20	0.56
31:q:319:THR:HG22	31:q:321:GLU:H	1.70	0.56
1:1:806:A:H2'	1:1:807:A:C2	2.41	0.56
1:1:1448:U:O2'	1:1:2983:C:O2	2.24	0.56
19:W:169:PHE:O	19:W:198:ARG:NH1	2.39	0.56
29:l:69:CYS:O	29:l:84:THR:OG1	2.22	0.56
39:I:602:SER:HA	39:I:605:TYR:HD2	1.70	0.56
40:K:243:THR:OG1	52:6:35:C:O2	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1345:G:N2	6:C:307:GLN:OE1	2.39	0.56
1:1:1603:A:OP1	42:R:38:ARG:NH1	2.38	0.56
23:d:44:MET:O	23:d:77:ARG:NH1	2.38	0.56
51:t:236:GLU:HG3	51:t:245:ILE:HG22	1.88	0.56
1:1:1971:C:N4	1:1:2052:G:O6	2.39	0.55
27:i:51:SER:HB2	27:i:54:GLU:HG2	1.87	0.55
35:v:35:ILE:HB	35:v:161:LYS:HZ1	1.70	0.55
16:Q:123:THR:OG1	16:Q:125:ASP:OD1	2.22	0.55
23:d:16:LEU:HD12	23:d:71:LEU:HD13	1.87	0.55
55:w:258:SER:HA	55:w:279:THR:HB	1.87	0.55
1:1:1188:U:OP1	1:1:1210:U:O2'	2.24	0.55
1:1:3217:C:O2'	1:1:3218:A:OP1	2.24	0.55
5:B:93:VAL:HG13	5:B:102:LEU:HD22	1.88	0.55
19:W:49:ARG:HB3	19:W:51:PRO:HD2	1.89	0.55
22:b:268:VAL:HG21	22:b:305:LEU:HD13	1.88	0.55
38:8:517:PRO:HA	38:8:520:SER:HB3	1.88	0.55
49:n:242:LEU:HD13	49:n:264:LEU:HD23	1.89	0.55
53:D:178:HIS:O	53:D:182:THR:OG1	2.24	0.55
1:1:1209:G:H5'	19:W:4:SER:HB2	1.89	0.55
1:1:1210:U:H5	19:W:3:ARG:HG2	1.72	0.55
5:B:210:GLU:OE2	37:z:32:ARG:NH2	2.39	0.55
13:N:44:ARG:NH1	13:N:120:TRP:O	2.38	0.55
38:8:564:SER:HB2	38:8:607:LEU:HD13	1.89	0.55
1:1:520:U:H3	6:C:347:THR:HG1	1.55	0.55
1:1:1643:A:H5''	1:1:1644:C:C4	2.41	0.55
55:w:820:ASP:OD1	55:w:821:GLY:N	2.39	0.55
29:l:68:ILE:HD11	31:q:396:THR:HG22	1.88	0.55
29:l:144:GLY:HA2	29:l:166:GLN:HG3	1.88	0.55
53:D:194:ILE:HG13	53:D:225:MET:HE2	1.89	0.55
57:x:47:VAL:HG13	57:x:49:VAL:HG23	1.87	0.55
1:1:275:U:H2'	1:1:276:U:C6	2.42	0.55
1:1:2493:U:OP1	56:a:203:SER:OG	2.24	0.55
1:1:3006:A:H2'	1:1:3007:U:O4'	2.07	0.55
29:l:20:ILE:HG13	29:l:21:GLY:H	1.71	0.55
36:y:78:ASP:OD1	36:y:96:ARG:NH2	2.40	0.55
1:1:351:A:O2'	2:2:53:A:O2'	2.24	0.55
5:B:367:LYS:O	5:B:369:ARG:NH1	2.40	0.55
1:1:3165:A:H2'	1:1:3166:C:C6	2.42	0.54
1:1:3343:G:HO2'	1:1:3362:A:H61	1.54	0.54
31:q:343:PRO:HG2	31:q:366:MET:CB	2.36	0.54
46:c:24:THR:HB	46:c:29:SER:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:759:U:H3'	1:1:760:G:H5''	1.89	0.54
1:1:849:C:H2'	1:1:850:U:C6	2.42	0.54
1:1:2933:A:C6	1:1:3014:U:H4'	2.43	0.54
17:S:132:THR:HG23	17:S:144:LEU:HD13	1.89	0.54
38:8:433:TYR:HB3	38:8:486:ILE:HD11	1.90	0.54
57:x:426:VAL:HA	57:x:461:LEU:HD11	1.89	0.54
1:1:1350:A:H8	1:1:1351:U:H3'	1.71	0.54
6:C:325:LEU:O	8:F:41:ARG:NH2	2.34	0.54
38:8:649:VAL:HB	38:8:653:LYS:HD2	1.89	0.54
1:1:1152:G:OP2	1:1:1152:G:N2	2.32	0.54
1:1:1312:C:O2'	14:O:83:ALA:O	2.25	0.54
1:1:3252:G:H2'	1:1:3253:G:C8	2.43	0.54
7:E:170:LYS:HD2	7:E:173:MET:HE2	1.88	0.54
40:K:32:ILE:HD12	40:K:33:PRO:HD2	1.88	0.54
1:1:1660:C:H2'	1:1:1661:G:H8	1.72	0.54
40:K:42:ASN:HA	40:K:45:ILE:HD12	1.88	0.54
49:n:390:GLU:HA	49:n:393:MET:HE2	1.89	0.54
50:p:422:GLN:HB2	50:p:425:VAL:HB	1.89	0.54
1:1:116:A:N1	1:1:264:G:O2'	2.36	0.54
1:1:444:U:H2'	1:1:445:G:C8	2.43	0.54
56:a:20:SER:HB3	56:a:172:VAL:HG21	1.88	0.54
1:1:1329:U:O2'	1:1:1330:A:OP1	2.19	0.54
28:j:62:GLY:O	35:v:8:LYS:NZ	2.38	0.54
53:D:190:LEU:HD23	53:D:222:ARG:HD3	1.90	0.54
1:1:890:C:OP2	38:8:37:ARG:CD	2.48	0.54
1:1:1198:C:C2	33:s:27:ARG:HD3	2.42	0.54
1:1:1943:C:OP1	57:x:327:THR:OG1	2.20	0.54
1:1:1954:G:O2'	1:1:1955:U:OP1	2.22	0.54
1:1:2469:G:H4'	56:a:28:PHE:HE1	1.73	0.54
6:C:314:LYS:HD2	8:F:162:PRO:HB3	1.90	0.54
15:P:122:ALA:HB3	15:P:143:PRO:HB2	1.90	0.54
42:R:92:GLN:O	42:R:96:ILE:HG12	2.07	0.54
50:p:125:GLY:HA2	50:p:147:ILE:HG12	1.91	0.54
1:1:3113:A:OP1	9:H:73:SER:OG	2.24	0.53
7:E:51:ARG:HB3	7:E:159:LEU:HD23	1.89	0.53
42:R:114:LYS:HB2	42:R:115:ILE:HD12	1.90	0.53
56:a:131:ALA:HB1	56:a:133:LYS:HE3	1.88	0.53
1:1:662:U:H2'	1:1:663:C:C6	2.43	0.53
1:1:3166:C:H2'	1:1:3167:A:H8	1.72	0.53
10:J:330:LYS:NZ	32:r:205:GLN:OE1	2.42	0.53
22:b:256:LEU:HA	22:b:264:ILE:HD11	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:m:521:ASP:N	30:m:521:ASP:OD1	2.41	0.53
1:1:1551:C:O2'	1:1:1552:G:OP1	2.26	0.53
1:1:1688:U:H2'	1:1:1689:U:C6	2.43	0.53
6:C:285:ASP:OD2	6:C:288:ARG:NH1	2.41	0.53
7:E:49:GLY:O	7:E:163:PHE:N	2.34	0.53
30:m:545:SER:HB3	30:m:630:LEU:HD23	1.90	0.53
48:k:29:LYS:HZ3	48:k:39:ARG:HE	1.55	0.53
1:1:1615:C:H2'	1:1:1616:U:C6	2.43	0.53
1:1:1616:U:H2'	1:1:1617:G:C8	2.44	0.53
1:1:1920:U:H3'	1:1:1921:A:H8	1.73	0.53
1:1:2429:G:H2'	1:1:2430:A:C8	2.39	0.53
1:1:2469:G:H2'	1:1:2470:C:C6	2.43	0.53
1:1:2982:A:O2'	1:1:2984:C:OP2	2.21	0.53
1:1:240:U:H4'	1:1:241:G:H5'	1.91	0.53
1:1:1740:U:H4'	1:1:1741:A:H5'	1.90	0.53
21:Y:35:LEU:HD23	21:Y:106:ILE:HB	1.91	0.53
30:m:758:MET:HE2	48:k:64:LYS:HG2	1.89	0.53
40:K:80:LEU:HB2	40:K:248:LEU:HD11	1.89	0.53
45:U:25:ASN:HD22	45:U:107:PHE:HE2	1.55	0.53
1:1:1786:G:H2'	1:1:1787:A:C8	2.43	0.53
1:1:3233:C:H2'	1:1:3234:A:C8	2.44	0.53
8:F:121:LYS:HB2	18:T:133:ALA:HB3	1.90	0.53
10:J:226:GLU:HG2	10:J:227:THR:HG23	1.90	0.53
12:M:19:ARG:NH1	12:M:66:THR:O	2.41	0.53
13:N:163:GLY:O	13:N:172:ARG:NH1	2.33	0.53
22:b:187:ILE:HG23	22:b:188:THR:HG23	1.90	0.53
31:q:197:LEU:HD12	31:q:238:TYR:HD1	1.72	0.53
56:a:208:SER:O	56:a:210:MET:N	2.41	0.53
57:x:10:LEU:HD11	57:x:39:PRO:HG3	1.90	0.53
1:1:2442:G:H2'	1:1:2443:A:C8	2.42	0.53
5:B:57:VAL:HG12	5:B:358:TRP:HB3	1.91	0.53
22:b:506:GLU:HB2	23:d:97:LEU:HD21	1.91	0.53
23:d:10:ARG:NE	23:d:12:TYR:OH	2.39	0.53
38:8:493:PRO:HG3	38:8:543:PHE:HD1	1.74	0.53
40:K:254:LEU:HB2	40:K:259:PHE:CE1	2.44	0.53
41:V:34:LEU:HB3	41:V:60:ALA:HB1	1.90	0.53
1:1:1498:A:H2'	1:1:1499:C:C6	2.44	0.53
1:1:1597:C:H5'	1:1:1696:A:H1'	1.91	0.53
30:m:197:GLU:OE1	39:I:412:THR:OG1	2.26	0.53
38:8:449:SER:OG	38:8:504:ARG:NH2	2.41	0.53
57:x:409:GLU:OE1	57:x:412:ARG:NH2	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:891:G:H2'	1:1:892:U:C6	2.43	0.53
1:1:1799:A:H2'	1:1:1800:A:H8	1.74	0.53
9:H:138:THR:O	9:H:139:ASN:ND2	2.42	0.53
54:o:149:GLN:HG3	54:o:166:VAL:HG23	1.91	0.53
56:a:159:LEU:HB2	56:a:165:LEU:HD11	1.91	0.53
57:x:426:VAL:HG23	57:x:465:PRO:HG3	1.90	0.53
1:1:2418:G:H5'	1:1:2419:A:H5''	1.91	0.52
5:B:160:VAL:HG12	5:B:162:VAL:HG13	1.91	0.52
5:B:219:ALA:HB2	5:B:336:VAL:HG23	1.91	0.52
15:P:175:ARG:O	15:P:179:GLN:HG2	2.09	0.52
23:d:25:PHE:HD1	23:d:28:ARG:HD2	1.74	0.52
30:m:598:LYS:HD3	30:m:614:PRO:HG2	1.90	0.52
31:q:269:ARG:HH21	31:q:533:PRO:HB2	1.73	0.52
1:1:417:A:H2'	1:1:418:A:C8	2.43	0.52
1:1:1178:G:N3	1:1:1328:C:O2'	2.42	0.52
7:E:11:PRO:HG2	24:e:91:THR:HG21	1.90	0.52
17:S:155:ARG:HB2	17:S:172:TYR:HB2	1.91	0.52
19:W:108:ASP:O	19:W:111:THR:OG1	2.28	0.52
27:i:46:GLU:HB3	30:m:246:TRP:CE2	2.44	0.52
38:8:492:PHE:HD2	38:8:563:LEU:HD11	1.74	0.52
42:R:25:ASP:HB3	42:R:28:GLU:HB2	1.90	0.52
44:Z:84:ARG:NH2	55:w:427:LYS:O	2.35	0.52
49:n:206:PRO:HB2	51:t:228:VAL:HB	1.90	0.52
1:1:707:U:O2	1:1:712:G:N2	2.27	0.52
1:1:1097:G:H4'	18:T:129:LYS:HE2	1.92	0.52
1:1:2982:A:H2'	1:1:2984:C:C6	2.43	0.52
2:2:57:C:H4'	2:2:63:G:N7	2.24	0.52
50:p:374:HIS:NE2	50:p:393:SER:OG	2.35	0.52
57:x:303:LEU:HB2	57:x:308:ARG:HG3	1.90	0.52
1:1:678:G:H5'	4:A:274:ARG:HH21	1.74	0.52
2:2:127:U:O2	49:n:14:ASN:ND2	2.34	0.52
8:F:85:PHE:HB2	8:F:139:PRO:HG3	1.91	0.52
31:q:530:ARG:HG2	31:q:532:TYR:CZ	2.45	0.52
51:t:103:ILE:HG12	51:t:130:ARG:HG2	1.91	0.52
1:1:585:A:H2'	1:1:586:C:C6	2.45	0.52
1:1:1877:U:H4'	1:1:1878:G:C5	2.45	0.52
38:8:506:SER:OG	38:8:511:VAL:O	2.21	0.52
1:1:41:G:H22	3:7:42:GLN:HG2	1.75	0.52
1:1:1390:A:N6	1:1:1418:A:O2'	2.42	0.52
1:1:2481:G:OP2	56:a:102:LYS:NZ	2.29	0.52
5:B:286:GLY:HA3	5:B:321:PHE:CE1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:m:751:HIS:HB2	30:m:767:LEU:HD11	1.92	0.52
38:8:388:ALA:HA	38:8:451:VAL:HG22	1.91	0.52
1:1:1259:A:N3	1:1:1280:C:O2'	2.30	0.52
1:1:1534:A:H2'	1:1:1535:A:C8	2.45	0.52
1:1:3307:A:H5''	5:B:226:PHE:HD1	1.75	0.52
50:p:159:VAL:HG13	50:p:214:ILE:HD12	1.91	0.52
57:x:249:LEU:HD11	57:x:281:ILE:HD11	1.92	0.52
1:1:428:A:H2'	1:1:429:U:C6	2.45	0.52
1:1:1388:U:O2'	24:e:99:ASN:O	2.27	0.52
19:W:38:ARG:NH1	19:W:39:TYR:OH	2.42	0.52
29:l:148:LYS:HD3	29:l:152:GLU:HG2	1.92	0.52
31:q:221:GLY:O	31:q:222:ARG:HG2	2.10	0.52
36:y:26:VAL:HG21	36:y:35:TYR:HD2	1.75	0.52
36:y:109:CYS:HB2	36:y:149:GLY:HA2	1.90	0.52
37:z:23:GLN:HA	37:z:26:VAL:HG22	1.92	0.52
38:8:380:ILE:O	38:8:383:GLN:HG2	2.10	0.52
41:V:69:LEU:HD22	41:V:74:MET:HE1	1.92	0.52
50:p:204:LEU:HD13	50:p:277:ARG:HB2	1.90	0.52
53:D:69:GLN:HB2	53:D:73:ILE:HG13	1.91	0.52
53:D:176:LEU:HD13	53:D:212:GLN:OE1	2.10	0.52
56:a:144:LEU:HG	56:a:147:LYS:HE3	1.92	0.52
1:1:1336:U:H2'	1:1:1337:A:H8	1.75	0.52
1:1:1621:A:H2'	1:1:1622:U:C6	2.45	0.52
1:1:1765:U:O2'	1:1:1766:G:O4'	2.26	0.52
1:1:1949:G:H5''	30:m:577:LYS:HD2	1.90	0.52
8:F:239:LEU:O	8:F:243:MET:HG3	2.10	0.52
31:q:292:ARG:NH2	31:q:321:GLU:OE1	2.43	0.52
40:K:38:ILE:HA	40:K:260:VAL:HG11	1.90	0.52
50:p:169:LEU:O	50:p:201:LEU:N	2.38	0.52
1:1:628:A:H2'	1:1:629:U:O4'	2.10	0.52
1:1:1566:A:H5''	51:t:33:ARG:HH21	1.75	0.52
1:1:2434:U:H5''	1:1:2435:G:C8	2.45	0.52
1:1:3325:G:OP2	23:d:70:ARG:NH2	2.43	0.52
38:8:672:ARG:HA	38:8:675:ARG:HE	1.75	0.52
55:w:449:MET:HB3	55:w:451:LYS:HE3	1.92	0.52
1:1:129:U:H2'	1:1:130:A:C8	2.45	0.51
1:1:961:C:H42	3:7:61:GLY:HA3	1.74	0.51
1:1:2412:G:H2'	1:1:2413:A:H8	1.75	0.51
38:8:406:ILE:HD13	38:8:471:LEU:HD13	1.92	0.51
39:I:322:LEU:HD22	39:I:327:PHE:HA	1.91	0.51
41:V:23:MET:HE3	41:V:34:LEU:HD12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:835:G:O2'	1:1:857:G:N2	2.30	0.51
1:1:1194:G:H2'	1:1:1195:A:C8	2.45	0.51
1:1:1497:C:O2'	1:1:1602:A:N3	2.39	0.51
4:A:199:ASN:OD1	4:A:200:LYS:N	2.43	0.51
5:B:95:THR:HB	5:B:98:GLY:O	2.09	0.51
11:L:85:LEU:HD22	11:L:120:GLN:HE22	1.74	0.51
23:d:50:ARG:HG3	23:d:92:TYR:HD1	1.74	0.51
38:8:377:MET:HE1	38:8:545:HIS:HD2	1.76	0.51
50:p:275:ARG:HD2	50:p:277:ARG:HH21	1.75	0.51
53:D:318:GLU:HG3	53:D:323:GLN:HE22	1.74	0.51
57:x:462:PHE:HB2	57:x:489:VAL:HG12	1.92	0.51
1:1:3295:A:H2'	1:1:3296:A:C8	2.46	0.51
1:1:3343:G:O2'	1:1:3362:A:N6	2.36	0.51
5:B:140:ASP:OD1	5:B:141:GLY:N	2.44	0.51
15:P:133:HIS:O	15:P:135:ARG:NH1	2.44	0.51
29:l:124:ASP:H	29:l:150:THR:HG21	1.74	0.51
31:q:508:ILE:HG13	31:q:531:TYR:HE1	1.75	0.51
40:K:116:THR:HG21	53:D:289:LYS:HE2	1.93	0.51
1:1:2356:A:H61	1:1:2983:C:N4	2.08	0.51
1:1:2411:U:H2'	1:1:2412:G:H8	1.74	0.51
13:N:114:ARG:HD3	13:N:137:PRO:HG3	1.93	0.51
34:u:37:HIS:CE1	34:u:41:LYS:HE2	2.45	0.51
39:I:506:LEU:HD23	39:I:509:ILE:HD12	1.93	0.51
55:w:499:THR:OG1	55:w:500:GLY:N	2.42	0.51
55:w:542:LEU:HG	55:w:544:GLY:H	1.76	0.51
22:b:195:GLN:NE2	22:b:196:PRO:HD2	2.26	0.51
34:u:56:ARG:HE	34:u:62:GLU:HG2	1.76	0.51
44:Z:10:VAL:O	44:Z:83:THR:OG1	2.27	0.51
46:c:16:LEU:HB3	46:c:98:SER:HB2	1.91	0.51
55:w:420:ASN:HD21	55:w:535:ILE:H	1.59	0.51
57:x:169:VAL:HG21	57:x:197:ARG:NE	2.25	0.51
57:x:175:ASP:OD1	57:x:203:SER:OG	2.26	0.51
1:1:63:A:N3	1:1:78:U:O2'	2.31	0.51
1:1:501:A:H2'	1:1:502:U:C6	2.46	0.51
1:1:820:A:H61	1:1:905:U:H3	1.59	0.51
1:1:3033:A:H2'	1:1:3034:C:H6	1.75	0.51
6:C:3:ARG:HD3	6:C:4:PRO:HD2	1.91	0.51
30:m:543:LYS:HD2	30:m:630:LEU:HD13	1.91	0.51
45:U:22:PRO:HB2	45:U:28:PHE:HB2	1.92	0.51
1:1:441:U:H3	1:1:493:G:N2	2.02	0.51
1:1:787:G:H2'	1:1:788:C:C6	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:952:A:H2'	1:1:953:G:O4'	2.11	0.51
1:1:1828:A:H2'	1:1:1829:G:C8	2.46	0.51
1:1:3343:G:HO2'	1:1:3362:A:N6	2.09	0.51
2:2:69:U:H2'	2:2:70:G:O4'	2.09	0.51
40:K:127:LEU:HA	40:K:183:ASP:HB2	1.92	0.51
44:Z:23:VAL:HG12	44:Z:45:GLY:HA3	1.92	0.51
50:p:204:LEU:HD12	50:p:234:TRP:CE3	2.45	0.51
1:1:1176:C:H2'	1:1:1177:G:N2	2.26	0.51
1:1:1567:U:O2'	49:n:216:ARG:NH1	2.44	0.51
1:1:3026:G:N2	1:1:3029:A:OP2	2.41	0.51
1:1:3051:U:H2'	1:1:3052:G:H8	1.75	0.51
3:7:121:ASP:HA	3:7:124:GLU:HG3	1.93	0.51
4:A:135:PRO:HB3	4:A:175:HIS:NE2	2.26	0.51
30:m:512:LEU:HB2	30:m:589:ILE:HG22	1.92	0.51
36:y:72:VAL:HG23	36:y:96:ARG:HG2	1.93	0.51
1:1:339:C:OP1	1:1:1380:G:O2'	2.27	0.51
1:1:678:G:OP1	4:A:273:LYS:NZ	2.31	0.51
7:E:106:PHE:HA	7:E:134:ARG:NH2	2.26	0.51
22:b:523:LYS:HD3	42:R:51:VAL:HG13	1.93	0.51
31:q:222:ARG:HA	56:a:98:LYS:HE3	1.93	0.51
40:K:43:GLU:OE2	54:o:216:ILE:HG13	2.10	0.51
40:K:100:LEU:HD13	40:K:266:ILE:HG23	1.91	0.51
1:1:2393:G:N2	1:1:2394:G:O6	2.44	0.51
5:B:86:VAL:HA	5:B:162:VAL:HG12	1.92	0.51
19:W:182:ILE:HG22	19:W:184:SER:H	1.76	0.51
31:q:347:GLU:OE1	31:q:349:ILE:HD11	2.10	0.51
1:1:1927:G:N3	1:1:2104:A:H2	2.09	0.50
9:H:41:ILE:HG22	9:H:43:VAL:HG13	1.92	0.50
37:z:41:LEU:HD21	37:z:45:LYS:HE2	1.93	0.50
38:8:275:LYS:O	38:8:279:GLY:N	2.44	0.50
40:K:97:LEU:HD13	40:K:235:PRO:HB2	1.92	0.50
40:K:97:LEU:HD11	40:K:205:THR:HG23	1.92	0.50
1:1:618:C:H5'	15:P:169:THR:HG22	1.93	0.50
1:1:655:C:H5''	24:e:26:HIS:HB3	1.93	0.50
1:1:1696:A:H2'	1:1:1697:A:C8	2.46	0.50
1:1:2889:C:OP1	22:b:28:LYS:NZ	2.38	0.50
2:2:149:A:N3	43:G:55:TYR:OH	2.42	0.50
48:k:26:LYS:HD2	48:k:78:LEU:HD13	1.93	0.50
53:D:84:GLY:HA2	53:D:250:ILE:HB	1.92	0.50
1:1:22:G:H5''	28:j:43:LYS:HG2	1.92	0.50
1:1:148:G:OP2	13:N:4:TYR:OH	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1657:C:O2'	1:1:1796:G:O2'	2.29	0.50
1:1:2916:U:C5	1:1:2935:U:H2'	2.46	0.50
4:A:116:ASN:HB2	4:A:220:VAL:HG12	1.94	0.50
6:C:35:VAL:HG21	6:C:244:LEU:HD21	1.93	0.50
21:Y:5:SER:OG	35:v:23:ASP:OD2	2.27	0.50
30:m:683:LEU:HD11	30:m:697:ALA:HB1	1.94	0.50
37:z:40:ASP:O	37:z:44:GLN:HG2	2.11	0.50
46:c:17:VAL:HG11	46:c:92:ILE:HD12	1.93	0.50
50:p:443:ALA:HB2	50:p:449:ILE:HG12	1.93	0.50
51:t:90:THR:HG23	51:t:93:ILE:HD11	1.93	0.50
1:1:759:U:H2'	1:1:771:A:N6	2.27	0.50
5:B:308:MET:HE3	5:B:373:PRO:HA	1.92	0.50
6:C:36:HIS:O	6:C:40:THR:HG23	2.12	0.50
10:J:233:ILE:HD13	10:J:242:ARG:HG3	1.92	0.50
22:b:442:TYR:CD2	36:y:78:ASP:HB3	2.47	0.50
36:y:53:ILE:O	36:y:56:THR:OG1	2.22	0.50
36:y:125:THR:HG22	36:y:125:THR:O	2.10	0.50
56:a:144:LEU:HA	56:a:147:LYS:HE3	1.94	0.50
57:x:420:ASP:OD1	57:x:505:ARG:NH1	2.40	0.50
1:1:2479:C:C2	1:1:2480:A:C8	2.99	0.50
4:A:151:LEU:HA	10:J:205:LEU:HD13	1.92	0.50
5:B:84:VAL:HG12	5:B:162:VAL:HB	1.94	0.50
17:S:8:GLN:OE1	17:S:62:ASN:ND2	2.33	0.50
22:b:497:ARG:NH2	34:u:123:ASP:OD1	2.45	0.50
35:v:208:TYR:O	35:v:210:GLN:N	2.43	0.50
38:8:522:ILE:HG22	38:8:528:PHE:HE2	1.77	0.50
50:p:102:ASN:N	50:p:447:LYS:O	2.39	0.50
1:1:3002:C:O2'	5:B:180:GLU:OE2	2.29	0.50
2:2:95:G:O2'	28:j:81:GLY:O	2.27	0.50
4:A:270:ARG:HH11	4:A:273:LYS:HZ3	1.60	0.50
11:L:47:ALA:HB3	11:L:48:PRO:HD3	1.92	0.50
13:N:99:ARG:HD3	13:N:167:THR:HG21	1.93	0.50
29:l:122:SER:HB3	29:l:125:ILE:HD11	1.93	0.50
32:r:182:ALA:HB2	32:r:197:ILE:HD11	1.94	0.50
42:R:151:ARG:CZ	57:x:442:THR:HB	2.41	0.50
56:a:31:THR:HA	56:a:171:ASN:HA	1.93	0.50
57:x:381:ASP:HB3	57:x:444:ILE:HG12	1.93	0.50
1:1:8:C:H2'	1:1:9:U:C6	2.45	0.50
1:1:470:G:H2'	1:1:471:U:C6	2.46	0.50
1:1:907:G:H8	1:1:907:G:O5'	1.94	0.50
1:1:1159:A:H8	8:F:92:ILE:HG13	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1544:G:O2'	3:7:12:LEU:O	2.28	0.50
5:B:84:VAL:HG13	5:B:163:HIS:O	2.12	0.50
22:b:282:SER:OG	22:b:338:LYS:HD3	2.12	0.50
40:K:183:ASP:HB3	40:K:186:ILE:HG22	1.92	0.50
40:K:298:LEU:HA	40:K:301:LEU:HD23	1.94	0.50
55:w:257:THR:O	55:w:279:THR:N	2.38	0.50
56:a:210:MET:HA	56:a:210:MET:HE3	1.94	0.50
57:x:5:LEU:O	57:x:29:THR:OG1	2.30	0.50
1:1:406:G:H1'	2:2:16:G:N2	2.27	0.50
1:1:417:A:H2'	1:1:418:A:H8	1.77	0.50
1:1:2909:U:H2'	1:1:2910:A:O4'	2.12	0.50
1:1:3294:A:H2'	1:1:3295:A:O4'	2.11	0.50
10:J:284:HIS:O	10:J:287:LYS:HG2	2.12	0.50
23:d:75:ILE:HG23	23:d:93:VAL:HG22	1.94	0.50
27:i:34:SER:HG	27:i:37:THR:HG1	1.59	0.50
36:y:42:LEU:HD22	36:y:46:ILE:HG12	1.93	0.50
50:p:127:VAL:HB	50:p:140:TYR:HB2	1.94	0.50
1:1:26:A:N3	1:1:328:U:O2'	2.42	0.50
1:1:952:A:H4'	1:1:968:G:N2	2.27	0.50
1:1:1393:A:N6	1:1:1417:G:H1'	2.27	0.50
1:1:1667:A:H2'	1:1:1668:G:H8	1.76	0.50
1:1:2420:C:H2'	1:1:2421:U:C6	2.47	0.50
1:1:2901:G:O2'	1:1:3024:A:N1	2.43	0.50
5:B:79:VAL:HG12	5:B:81:THR:HG23	1.92	0.50
6:C:126:ILE:O	6:C:129:THR:OG1	2.30	0.50
17:S:26:ARG:O	18:T:151:LEU:N	2.43	0.50
56:a:157:PHE:HD1	56:a:165:LEU:HD13	1.76	0.50
57:x:33:VAL:HG22	57:x:226:VAL:HG21	1.93	0.50
1:1:959:C:H2'	1:1:960:U:H4'	1.94	0.49
5:B:303:LYS:HD2	5:B:361:THR:HG21	1.94	0.49
22:b:518:ILE:HB	42:R:54:ALA:HB3	1.93	0.49
31:q:269:ARG:HG2	31:q:538:VAL:O	2.12	0.49
38:8:446:ASP:OD1	38:8:504:ARG:NH2	2.43	0.49
43:G:160:ILE:O	43:G:164:VAL:HG13	2.12	0.49
44:Z:41:ALA:HB2	44:Z:77:TYR:HE1	1.76	0.49
54:o:103:HIS:HA	54:o:122:LEU:HD22	1.94	0.49
1:1:1528:G:O2'	1:1:1588:A:N3	2.40	0.49
1:1:2831:G:H2'	1:1:2832:C:C6	2.47	0.49
1:1:3251:U:H2'	1:1:3252:G:C8	2.47	0.49
1:1:3275:U:O2'	25:f:99:ARG:NH1	2.45	0.49
19:W:137:ILE:HG21	19:W:182:ILE:HD12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:c:75:ASN:HD22	55:w:385:MET:HE1	1.77	0.49
51:t:148:ARG:NH1	52:6:230:A:OP1	2.45	0.49
53:D:80:ARG:HH12	53:D:248:LEU:N	2.10	0.49
55:w:265:THR:O	55:w:322:ARG:NH1	2.40	0.49
57:x:405:ALA:O	57:x:406:ASN:HB2	2.11	0.49
1:1:3164:C:O2'	1:1:3165:A:H8	1.94	0.49
12:M:89:ALA:HB1	12:M:92:GLU:OE2	2.12	0.49
30:m:328:LYS:NZ	49:n:133:ASP:OD2	2.40	0.49
38:8:577:LEU:HD23	38:8:577:LEU:H	1.77	0.49
49:n:50:LYS:HE2	49:n:57:THR:HG22	1.94	0.49
50:p:153:ILE:HD11	50:p:159:VAL:HG12	1.95	0.49
57:x:34:GLN:HG2	57:x:60:ALA:HB2	1.94	0.49
1:1:1958:U:H3	1:1:2083:G:H1	1.59	0.49
3:7:81:ASN:HB3	4:A:128:ASN:HB3	1.93	0.49
6:C:334:PHE:HA	6:C:339:LEU:HD12	1.94	0.49
24:e:32:TRP:O	24:e:33:ARG:NH1	2.44	0.49
27:i:45:ARG:NH1	27:i:89:GLU:OE2	2.40	0.49
32:r:181:LYS:HG2	32:r:196:PRO:HA	1.94	0.49
39:I:199:GLU:HA	39:I:202:LYS:HB2	1.94	0.49
40:K:295:GLN:NE2	54:o:197:LYS:O	2.45	0.49
50:p:128:ARG:HG2	50:p:139:GLN:HG2	1.94	0.49
1:1:461:U:H3	1:1:469:G:H22	1.59	0.49
1:1:3192:U:H2'	1:1:3193:C:C6	2.48	0.49
9:H:115:ARG:HG2	9:H:123:ILE:HG12	1.93	0.49
10:J:255:LEU:HD22	10:J:258:ARG:HH21	1.77	0.49
30:m:599:LYS:HB2	30:m:612:VAL:HB	1.94	0.49
43:G:152:LEU:HD13	43:G:180:VAL:HG21	1.95	0.49
45:U:37:LEU:O	45:U:41:ILE:HG12	2.12	0.49
49:n:374:ASP:OD1	49:n:375:ILE:HG23	2.12	0.49
49:n:402:ILE:HG13	49:n:403:ASP:N	2.27	0.49
1:1:3121:U:H1'	1:1:3122:A:H5''	1.93	0.49
2:2:63:G:H22	2:2:97:A:H2	1.60	0.49
3:7:108:LEU:O	3:7:112:ILE:HG13	2.13	0.49
5:B:138:ALA:O	5:B:139:GLN:HG3	2.13	0.49
17:S:69:PRO:O	17:S:97:VAL:HG22	2.13	0.49
30:m:648:HIS:ND1	30:m:649:PRO:O	2.44	0.49
31:q:504:THR:HB	31:q:506:LEU:HD13	1.94	0.49
40:K:82:VAL:HG22	40:K:279:ILE:HG12	1.94	0.49
42:R:152:GLU:OE2	55:w:363:GLN:NE2	2.45	0.49
1:1:1618:G:H2'	1:1:1619:A:C8	2.48	0.49
1:1:1798:A:H2'	1:1:1799:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:103:LYS:HB2	4:A:107:GLY:HA3	1.94	0.49
11:L:44:ALA:HA	35:v:30:ILE:HD13	1.95	0.49
31:q:333:SER:HB3	31:q:539:ASP:OD1	2.12	0.49
38:8:592:ILE:HG22	38:8:596:ARG:HH12	1.76	0.49
1:1:1159:A:O2'	1:1:1333:C:OP1	2.20	0.49
1:1:1290:A:H2'	1:1:1291:A:C8	2.48	0.49
1:1:1436:U:N3	55:w:820:ASP:OD2	2.43	0.49
1:1:2469:G:H4'	56:a:28:PHE:CE1	2.47	0.49
7:E:55:LEU:HD21	7:E:145:LEU:HD11	1.94	0.49
19:W:70:ARG:HD2	19:W:97:SER:HA	1.94	0.49
29:l:173:LEU:HD21	32:r:162:THR:HB	1.94	0.49
51:t:231:ASP:OD1	51:t:231:ASP:N	2.45	0.49
1:1:2465:G:H2'	1:1:2466:G:C8	2.48	0.49
13:N:192:LYS:O	13:N:196:THR:HG23	2.12	0.49
1:1:528:U:H2'	1:1:529:A:C8	2.48	0.49
38:8:52:ARG:O	38:8:56:GLN:HG3	2.12	0.49
1:1:1956:A:H2'	1:1:1957:G:C8	2.48	0.48
2:2:26:U:O2'	6:C:51:ALA:O	2.31	0.48
22:b:271:PHE:HE2	22:b:309:VAL:HG13	1.77	0.48
22:b:420:TYR:OH	36:y:83:HIS:ND1	2.36	0.48
29:l:33:LEU:HD12	29:l:33:LEU:O	2.13	0.48
32:r:245:VAL:HA	32:r:257:ALA:HA	1.95	0.48
50:p:404:ASP:HB2	50:p:411:MET:HE3	1.93	0.48
57:x:262:LYS:N	57:x:340:ASP:OD2	2.38	0.48
1:1:531:G:H2'	1:1:532:A:C8	2.48	0.48
1:1:3066:U:H2'	1:1:3067:C:C6	2.48	0.48
12:M:85:TRP:NE1	12:M:91:CYS:SG	2.81	0.48
29:l:51:VAL:HG23	31:q:372:CYS:SG	2.53	0.48
30:m:806:THR:HG21	50:p:377:PHE:HZ	1.78	0.48
34:u:46:PRO:O	34:u:52:THR:OG1	2.22	0.48
36:y:142:ILE:HG12	36:y:148:VAL:HG12	1.95	0.48
50:p:96:TYR:HE1	50:p:99:SER:HB3	1.78	0.48
53:D:291:LYS:HD3	53:D:358:VAL:HG12	1.94	0.48
57:x:94:GLU:HG2	57:x:312:LEU:HD22	1.95	0.48
1:1:1227:C:O2'	1:1:1228:C:OP1	2.29	0.48
1:1:1631:C:H5	44:Z:48:ARG:NH2	2.12	0.48
7:E:51:ARG:O	7:E:72:ASN:ND2	2.45	0.48
31:q:333:SER:HA	31:q:336:LEU:HD23	1.95	0.48
38:8:516:TYR:CE2	39:I:511:LEU:HD11	2.48	0.48
56:a:206:VAL:HG13	56:a:214:PHE:HB2	1.96	0.48
1:1:487:U:H3'	1:1:488:U:H5''	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:138:ARG:HH21	6:C:240:PRO:HB2	1.78	0.48
30:m:229:ARG:HG3	30:m:231:GLU:HG3	1.95	0.48
43:G:99:PRO:HD3	43:G:132:VAL:HG22	1.94	0.48
1:1:29:C:H4'	1:1:62:A:H4'	1.96	0.48
1:1:815:G:H1	1:1:925:A:N6	2.10	0.48
1:1:2465:G:H2'	1:1:2466:G:H8	1.77	0.48
1:1:3333:G:OP2	1:1:3333:G:H8	1.96	0.48
8:F:98:LYS:HB3	8:F:99:PRO:HD3	1.94	0.48
24:e:9:ILE:HD13	24:e:63:THR:HB	1.96	0.48
30:m:773:HIS:CE1	30:m:803:ARG:HD2	2.49	0.48
36:y:126:GLU:HG3	36:y:137:VAL:HG11	1.96	0.48
45:U:77:LYS:NZ	45:U:95:PHE:O	2.47	0.48
50:p:98:ASN:HB3	50:p:451:ILE:HD13	1.95	0.48
50:p:151:LYS:HG2	50:p:216:VAL:HG23	1.96	0.48
51:t:142:LEU:HD11	51:t:179:LEU:HD22	1.96	0.48
1:1:842:G:OP2	55:w:373:ARG:NH1	2.47	0.48
1:1:1192:C:N4	14:O:56:ASP:OD1	2.33	0.48
1:1:1714:A:OP2	57:x:195:LYS:HD3	2.14	0.48
1:1:2942:C:C4	22:b:38:LYS:HG3	2.49	0.48
3:7:138:GLU:OE1	3:7:141:ARG:NH1	2.46	0.48
16:Q:76:ALA:HA	16:Q:79:LYS:HG3	1.95	0.48
29:l:20:ILE:O	29:l:94:LYS:HB2	2.13	0.48
30:m:413:ILE:HA	49:n:559:MET:HE3	1.95	0.48
30:m:664:ILE:HD12	30:m:674:LYS:HB2	1.95	0.48
40:K:236:VAL:HG21	40:K:246:VAL:HG22	1.96	0.48
53:D:464:GLN:HG3	53:D:466:ASP:H	1.77	0.48
1:1:591:G:OP2	1:1:591:G:H8	1.97	0.48
1:1:1105:A:H2'	1:1:1106:G:C8	2.47	0.48
1:1:1667:A:H2'	1:1:1668:G:C8	2.49	0.48
1:1:3022:G:N2	1:1:3032:A:OP2	2.40	0.48
1:1:3109:G:N2	9:H:156:GLN:OE1	2.46	0.48
20:X:31:THR:HG23	43:G:50:VAL:HG12	1.95	0.48
36:y:54:ALA:N	36:y:80:GLU:OE1	2.46	0.48
39:I:330:GLU:OE1	39:I:332:SER:OG	2.22	0.48
1:1:1283:C:O2'	1:1:1284:C:OP1	2.27	0.48
1:1:2981:U:H2'	1:1:2982:A:H4'	1.94	0.48
1:1:3151:U:OP2	5:B:132:LYS:NZ	2.47	0.48
26:h:5:LYS:HB2	26:h:8:GLU:OE1	2.14	0.48
31:q:343:PRO:HB2	31:q:367:MET:HG3	1.96	0.48
39:I:510:CYS:HB3	39:I:575:CYS:SG	2.53	0.48
47:g:98:GLN:NE2	55:w:407:LEU:O	2.35	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:a:175:GLU:OE1	56:a:175:GLU:N	2.41	0.48
1:1:567:G:H2'	1:1:568:G:C8	2.49	0.48
1:1:1616:U:H2'	1:1:1617:G:H8	1.77	0.48
1:1:1666:G:H2'	1:1:1667:A:H8	1.79	0.48
1:1:2367:A:H2'	1:1:2368:A:C8	2.49	0.48
1:1:2445:A:H4'	1:1:2446:U:OP1	2.14	0.48
19:W:50:THR:N	19:W:51:PRO:HD2	2.28	0.48
22:b:519:MET:HG3	22:b:524:LEU:HD11	1.95	0.48
54:o:157:LEU:HB3	54:o:162:LEU:HD13	1.95	0.48
57:x:58:THR:HA	57:x:61:PHE:CE2	2.48	0.48
1:1:544:C:N4	1:1:547:G:O6	2.47	0.48
1:1:720:A:H1'	1:1:721:G:OP2	2.14	0.48
1:1:1203:A:C2	1:1:1300:G:H2'	2.49	0.48
1:1:1810:A:H2'	1:1:1811:G:C8	2.49	0.48
1:1:2097:U:H2'	1:1:2098:C:H6	1.79	0.48
22:b:389:ASP:HB3	22:b:392:ASP:HB2	1.96	0.48
30:m:423:ARG:HB3	30:m:424:PRO:HA	1.96	0.48
31:q:539:ASP:OD1	31:q:539:ASP:N	2.47	0.48
38:8:553:TYR:HD1	38:8:559:TYR:HB2	1.79	0.48
56:a:37:GLY:O	56:a:202:GLY:N	2.42	0.48
56:a:58:CYS:SG	56:a:152:ARG:HB3	2.53	0.48
57:x:169:VAL:CG2	57:x:197:ARG:CD	2.83	0.48
57:x:331:ALA:HB3	57:x:353:MET:HE2	1.96	0.48
1:1:393:U:H2'	1:1:394:G:O4'	2.13	0.47
1:1:845:G:H1	1:1:849:C:N4	2.12	0.47
1:1:1378:U:H2'	1:1:1379:G:H8	1.79	0.47
1:1:1725:C:H2'	1:1:1726:C:C6	2.49	0.47
1:1:2097:U:H2'	1:1:2098:C:C6	2.49	0.47
1:1:2419:A:H2'	1:1:2420:C:C6	2.49	0.47
1:1:3165:A:H2'	1:1:3166:C:H6	1.79	0.47
5:B:216:ASP:HB3	5:B:278:ILE:HA	1.96	0.47
8:F:165:ASP:OD1	8:F:166:ASN:N	2.47	0.47
8:F:173:LEU:HB3	8:F:178:ILE:HB	1.96	0.47
19:W:30:VAL:HG22	19:W:66:ILE:HG21	1.95	0.47
20:X:59:SER:OG	20:X:101:GLU:OE1	2.32	0.47
25:f:49:ILE:HG12	25:f:100:ILE:HG13	1.96	0.47
38:8:33:ILE:HA	38:8:36:ARG:HD2	1.95	0.47
39:I:597:ARG:NH2	39:I:598:TYR:OH	2.47	0.47
40:K:277:ARG:NH2	54:o:200:MET:SD	2.86	0.47
43:G:218:ILE:HG23	43:G:222:PHE:HB3	1.96	0.47
56:a:89:ASP:OD1	56:a:92:LYS:NZ	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:445:G:H2'	1:1:446:U:C6	2.49	0.47
4:A:36:ILE:HD11	4:A:65:LEU:HD13	1.97	0.47
22:b:417:LYS:HD3	22:b:429:ASN:HA	1.96	0.47
30:m:545:SER:HB2	30:m:628:LYS:HD2	1.96	0.47
40:K:173:PHE:O	40:K:176:GLN:HG2	2.14	0.47
43:G:60:ARG:HG2	55:w:462:LEU:HD11	1.97	0.47
56:a:53:LEU:HD13	56:a:189:PHE:HB2	1.96	0.47
1:1:774:G:H2'	1:1:775:A:C8	2.48	0.47
1:1:1942:U:O2'	57:x:328:ASP:HB2	2.14	0.47
1:1:3231:U:H2'	1:1:3232:G:H8	1.78	0.47
20:X:50:ALA:O	26:h:66:VAL:HG21	2.14	0.47
22:b:184:LEU:HA	22:b:187:ILE:HG22	1.96	0.47
22:b:497:ARG:HE	34:u:126:LEU:HD22	1.78	0.47
29:l:70:LEU:HA	29:l:85:SER:HB3	1.95	0.47
34:u:112:MET:HE3	34:u:115:ASN:ND2	2.25	0.47
38:8:633:GLU:HG3	38:8:639:LYS:HE2	1.96	0.47
41:V:128:ARG:O	41:V:131:SER:OG	2.24	0.47
45:U:21:SER:HB3	45:U:22:PRO:HD3	1.95	0.47
57:x:69:VAL:HG21	57:x:144:ILE:HD11	1.95	0.47
57:x:524:LYS:O	57:x:528:GLU:HG2	2.14	0.47
1:1:1631:C:H5	44:Z:48:ARG:HH22	1.62	0.47
1:1:2095:G:H2'	1:1:2096:A:C8	2.47	0.47
2:2:12:A:OP1	15:P:3:ARG:NH1	2.47	0.47
19:W:91:GLN:HB2	19:W:228:VAL:HG21	1.96	0.47
27:i:46:GLU:HB3	30:m:246:TRP:CZ2	2.50	0.47
28:j:39:TYR:CD1	28:j:40:PRO:HA	2.49	0.47
51:t:132:LYS:HE3	51:t:308:PRO:HG3	1.96	0.47
53:D:80:ARG:NH2	53:D:246:GLY:O	2.47	0.47
56:a:124:LEU:HD13	56:a:128:LEU:HD22	1.97	0.47
56:a:155:ILE:HG23	56:a:167:VAL:HG21	1.97	0.47
57:x:543:LYS:HE2	57:x:547:LEU:HG	1.96	0.47
1:1:1953:G:O4'	1:1:2092:A:N6	2.44	0.47
1:1:2053:C:OP1	50:p:157:ARG:NH1	2.38	0.47
23:d:51:LEU:HB3	23:d:55:LEU:HD23	1.95	0.47
56:a:138:VAL:HG21	56:a:147:LYS:HD2	1.96	0.47
56:a:212:PRO:HG2	56:a:214:PHE:HE1	1.78	0.47
1:1:2608:G:H2'	1:1:2609:A:C8	2.49	0.47
4:A:160:PHE:CD2	4:A:177:MET:HE1	2.49	0.47
4:A:238:GLU:OE1	10:J:196:ASN:ND2	2.47	0.47
7:E:170:LYS:HB3	7:E:172:HIS:CE1	2.49	0.47
26:h:45:LYS:O	26:h:49:LYS:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:r:24:LYS:O	32:r:28:GLU:HG3	2.15	0.47
34:u:127:VAL:HG13	34:u:134:LEU:HD11	1.96	0.47
40:K:279:ILE:HB	40:K:292:TYR:HB3	1.97	0.47
52:6:216:C:H2'	54:o:183:VAL:HG11	1.95	0.47
1:1:69:C:OP1	13:N:178:HIS:ND1	2.40	0.47
1:1:116:A:OP1	27:i:36:ARG:NH2	2.48	0.47
1:1:800:G:H22	6:C:101:ALA:HA	1.79	0.47
1:1:918:C:O2	1:1:918:C:H2'	2.14	0.47
1:1:1293:U:H2'	1:1:1294:A:H8	1.80	0.47
1:1:1355:A:H4'	1:1:1356:U:O5'	2.15	0.47
1:1:1940:G:N3	57:x:434:LYS:HB2	2.30	0.47
1:1:1951:C:H2'	1:1:1952:G:H8	1.80	0.47
1:1:2469:G:H2'	1:1:2470:C:H6	1.78	0.47
1:1:3026:G:OP1	9:H:174:LYS:NZ	2.42	0.47
1:1:3193:C:H2'	1:1:3194:C:C6	2.49	0.47
4:A:57:PRO:HD2	4:A:162:VAL:HG22	1.96	0.47
4:A:141:GLN:NE2	10:J:225:SER:O	2.48	0.47
5:B:67:PHE:HA	5:B:70:ARG:HD2	1.96	0.47
8:F:73:GLY:O	18:T:143:THR:OG1	2.33	0.47
11:L:85:LEU:HD22	11:L:120:GLN:NE2	2.30	0.47
22:b:193:ASP:OD1	22:b:193:ASP:N	2.48	0.47
24:e:79:VAL:HG13	24:e:111:ARG:HG2	1.96	0.47
29:l:153:SER:HA	29:l:156:MET:HE3	1.97	0.47
31:q:504:THR:HA	31:q:545:LYS:HD3	1.97	0.47
32:r:164:ARG:HD2	32:r:169:GLU:HA	1.97	0.47
36:y:62:MET:HE3	36:y:73:PRO:HG3	1.97	0.47
43:G:47:SER:HB2	43:G:49:TYR:HE1	1.80	0.47
50:p:224:SER:OG	50:p:234:TRP:NE1	2.30	0.47
50:p:252:ASN:HB3	50:p:253:PRO:HD3	1.96	0.47
53:D:293:ILE:HD11	53:D:358:VAL:HG11	1.97	0.47
1:1:1142:G:OP1	1:1:1144:U:O2'	2.22	0.47
1:1:1513:G:OP1	42:R:5:ARG:NH2	2.45	0.47
1:1:1659:U:H2'	1:1:1660:C:C6	2.49	0.47
1:1:3014:U:H2'	1:1:3015:G:C8	2.49	0.47
4:A:107:GLY:HA2	10:J:207:ARG:HH21	1.79	0.47
11:L:125:VAL:O	35:v:165:LEU:HD13	2.15	0.47
29:l:48:PRO:HB2	29:l:51:VAL:HG12	1.96	0.47
30:m:232:GLN:HE21	30:m:237:ILE:HB	1.80	0.47
30:m:375:ARG:O	51:t:232:ASN:ND2	2.32	0.47
51:t:205:ARG:O	51:t:209:GLN:HG2	2.15	0.47
55:w:418:ILE:HG13	55:w:418:ILE:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:656:A:H2'	1:1:657:A:C8	2.50	0.47
1:1:1392:G:H3'	24:e:125:ARG:HH12	1.80	0.47
15:P:126:ARG:HG3	15:P:140:GLU:HG2	1.96	0.47
20:X:26:VAL:HG22	55:w:450:ILE:HG12	1.96	0.47
39:I:464:LEU:HD23	39:I:468:GLU:HB3	1.97	0.47
44:Z:17:ARG:HD3	47:g:73:SER:HB3	1.96	0.47
52:6:230:A:H2'	52:6:230:A:N3	2.30	0.47
1:1:776:U:H2'	1:1:777:U:H6	1.80	0.47
1:1:794:U:H2'	1:1:795:G:H8	1.79	0.47
1:1:1126:G:O6	33:s:32:LYS:NZ	2.47	0.47
1:1:1926:C:H5'	42:R:101:VAL:HG21	1.96	0.47
38:8:445:LEU:HD11	38:8:482:VAL:HG21	1.97	0.47
40:K:67:LEU:HB2	53:D:418:PRO:HD2	1.96	0.47
40:K:257:GLU:OE1	40:K:257:GLU:N	2.48	0.47
52:6:17:G:H2'	52:6:18:U:C6	2.50	0.47
1:1:1964:C:H3'	1:1:1965:C:H5''	1.97	0.46
1:1:3228:C:H4'	1:1:3229:G:O5'	2.16	0.46
5:B:48:GLY:HA3	5:B:81:THR:HG22	1.98	0.46
23:d:82:GLU:HG2	23:d:83:GLU:H	1.80	0.46
30:m:235:ASP:OD1	30:m:235:ASP:N	2.45	0.46
32:r:203:ASN:ND2	32:r:209:TYR:HB3	2.30	0.46
36:y:97:VAL:HG12	36:y:128:LEU:HD13	1.98	0.46
38:8:453:SER:HB2	38:8:508:ASN:HB2	1.97	0.46
1:1:12:A:H2'	1:1:13:A:C8	2.50	0.46
1:1:297:G:O6	13:N:12:ARG:NH1	2.42	0.46
1:1:429:U:H2'	1:1:430:U:H6	1.79	0.46
1:1:500:C:H2'	1:1:501:A:H8	1.80	0.46
1:1:846:A:H2'	1:1:847:A:C4	2.51	0.46
1:1:1350:A:C8	1:1:1351:U:H3'	2.49	0.46
8:F:221:LYS:HB3	8:F:227:GLY:HA3	1.97	0.46
13:N:27:VAL:HG21	13:N:124:ASP:OD1	2.15	0.46
30:m:673:VAL:HG12	30:m:674:LYS:HG3	1.97	0.46
38:8:629:ARG:HD2	38:8:646:LEU:HD12	1.96	0.46
50:p:355:LEU:HD12	50:p:369:GLN:HB2	1.97	0.46
53:D:376:ARG:HE	53:D:379:ARG:HB2	1.80	0.46
57:x:419:ARG:NH1	57:x:498:TYR:HB3	2.30	0.46
1:1:1448:U:H2'	1:1:1449:A:H8	1.81	0.46
1:1:1744:G:H2'	1:1:1745:C:C6	2.50	0.46
1:1:2463:G:N2	56:a:164:CYS:SG	2.89	0.46
31:q:473:ILE:HB	31:q:546:PHE:HB2	1.97	0.46
31:q:486:GLU:HA	31:q:489:ILE:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:y:118:HIS:NE2	36:y:146:ILE:HD12	2.29	0.46
53:D:80:ARG:HH12	53:D:248:LEU:H	1.63	0.46
55:w:732:PRO:HD2	55:w:735:LYS:HD2	1.96	0.46
1:1:1480:G:O2'	1:1:1871:U:O4	2.24	0.46
8:F:176:TYR:CZ	8:F:197:GLN:HG2	2.51	0.46
26:h:57:VAL:HA	26:h:60:GLU:HG2	1.98	0.46
30:m:255:PRO:HB3	43:G:145:ASN:HA	1.97	0.46
36:y:163:PRO:HG3	36:y:185:THR:HG22	1.98	0.46
39:I:395:SER:OG	55:w:490:ARG:NH2	2.48	0.46
56:a:45:ARG:HG3	56:a:46:ASP:N	2.31	0.46
57:x:423:ASP:OD2	57:x:500:TYR:OH	2.22	0.46
1:1:947:G:H5''	24:e:55:ILE:HB	1.97	0.46
3:7:98:LYS:NZ	4:A:202:GLU:OE2	2.49	0.46
19:W:162:GLU:HG3	19:W:175:ILE:CG2	2.45	0.46
22:b:71:ILE:HD13	22:b:88:LYS:HG3	1.98	0.46
22:b:434:GLU:OE1	36:y:79:GLN:NE2	2.49	0.46
45:U:19:VAL:O	45:U:19:VAL:HG12	2.16	0.46
55:w:795:LEU:HB3	55:w:819:VAL:HG21	1.98	0.46
57:x:69:VAL:HG13	57:x:74:ALA:HB3	1.97	0.46
1:1:1746:U:H2'	1:1:1747:G:H8	1.80	0.46
1:1:2604:U:H2'	1:1:2605:G:O4'	2.14	0.46
4:A:130:LEU:HB3	4:A:170:LYS:HD2	1.97	0.46
6:C:7:THR:HG21	6:C:15:ALA:HB1	1.97	0.46
13:N:122:ASN:OD1	13:N:123:GLN:N	2.44	0.46
13:N:193:ARG:NH1	13:N:194:GLN:OE1	2.48	0.46
20:X:2:ALA:N	54:o:143:GLU:OE1	2.49	0.46
33:s:20:LYS:HB3	33:s:20:LYS:HE3	1.73	0.46
49:n:550:GLU:HG3	49:n:552:LYS:H	1.80	0.46
51:t:241:ASP:N	51:t:241:ASP:OD1	2.48	0.46
1:1:1214:U:H2'	1:1:1215:U:C6	2.51	0.46
1:1:1666:G:H2'	1:1:1667:A:C8	2.51	0.46
1:1:2974:U:O2'	3:7:58:ARG:NH2	2.48	0.46
22:b:400:ARG:HA	22:b:403:GLU:HB3	1.98	0.46
27:i:34:SER:OG	27:i:37:THR:OG1	2.30	0.46
31:q:217:LEU:O	31:q:217:LEU:HD23	2.16	0.46
39:I:294:ILE:O	39:I:297:THR:OG1	2.27	0.46
47:g:106:LYS:HA	47:g:109:THR:HG22	1.97	0.46
50:p:316:ASP:HB2	50:p:323:ILE:HD11	1.98	0.46
53:D:366:PRO:HB3	53:D:463:TYR:CE1	2.50	0.46
21:Y:51:ARG:HG2	21:Y:52:ARG:H	1.81	0.46
30:m:774:LYS:HB2	30:m:799:ASP:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:R:140:GLU:O	42:R:144:GLN:OE1	2.33	0.46
1:1:616:G:H2'	1:1:617:G:C8	2.51	0.46
1:1:2836:C:H5	1:1:2851:A:H62	1.62	0.46
4:A:31:GLN:HB2	4:A:163:PRO:HG3	1.97	0.46
31:q:380:LYS:O	31:q:383:THR:HG22	2.16	0.46
31:q:409:PRO:HA	31:q:462:SER:HB3	1.98	0.46
43:G:156:ASP:N	43:G:156:ASP:OD1	2.48	0.46
50:p:109:LEU:HD21	50:p:449:ILE:HD13	1.98	0.46
50:p:138:LYS:HG3	50:p:196:GLU:HB3	1.98	0.46
50:p:428:LYS:HB2	50:p:445:GLN:HB2	1.98	0.46
1:1:20:A:H2'	1:1:21:G:C8	2.51	0.46
1:1:155:G:N2	53:D:155:ARG:HH22	2.13	0.46
1:1:2475:G:H2'	1:1:2476:C:C6	2.51	0.46
3:7:22:GLN:HE21	3:7:27:ARG:HE	1.64	0.46
19:W:14:GLN:HA	32:r:72:LYS:HE2	1.98	0.46
30:m:547:LEU:HD21	30:m:667:LEU:HD22	1.96	0.46
30:m:783:ASP:OD1	30:m:784:ALA:N	2.46	0.46
34:u:23:ARG:NH2	34:u:25:ASP:OD2	2.46	0.46
37:z:46:LEU:O	37:z:50:LYS:HG2	2.16	0.46
38:8:374:MET:HG3	38:8:375:ARG:HG2	1.98	0.46
38:8:473:TYR:HB3	38:8:474:PRO:HD3	1.98	0.46
39:I:256:ALA:HB1	39:I:272:ILE:HG23	1.98	0.46
44:Z:123:GLN:OE1	44:Z:123:GLN:N	2.49	0.46
1:1:117:U:OP2	13:N:2:GLY:N	2.48	0.45
1:1:1204:A:H2'	1:1:1205:A:O4'	2.15	0.45
1:1:1936:A:N3	1:1:1936:A:H2'	2.31	0.45
1:1:2367:A:H2'	1:1:2368:A:H8	1.81	0.45
1:1:2507:C:H2'	1:1:2508:U:C6	2.51	0.45
1:1:2886:U:OP2	33:s:2:ARG:NH2	2.44	0.45
11:L:79:GLU:OE2	11:L:101:ARG:NH2	2.49	0.45
22:b:221:THR:HG21	22:b:224:ILE:HD11	1.98	0.45
31:q:468:LYS:HG2	31:q:469:HIS:ND1	2.31	0.45
42:R:23:TRP:HB2	42:R:53:LYS:HE3	1.98	0.45
50:p:270:LYS:HD3	50:p:270:LYS:HA	1.79	0.45
1:1:1799:A:H2'	1:1:1800:A:C8	2.50	0.45
8:F:189:ILE:HG23	8:F:190:THR:HG23	1.97	0.45
12:M:137:LYS:HB3	12:M:137:LYS:HE2	1.71	0.45
25:f:51:TYR:HD2	25:f:67:MET:HE3	1.81	0.45
43:G:51:LYS:HG3	43:G:52:TRP:CD1	2.51	0.45
54:o:143:GLU:HA	54:o:146:MET:HE2	1.99	0.45
57:x:351:THR:HG21	57:x:385:PHE:HE2	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1104:G:H2'	1:1:1105:A:C8	2.52	0.45
1:1:1245:A:H2'	1:1:1272:C:OP1	2.16	0.45
1:1:1297:C:C2	1:1:1298:C:C5	3.05	0.45
1:1:3170:A:C8	25:f:56:SER:HB2	2.51	0.45
2:2:52:A:H2'	2:2:53:A:C8	2.51	0.45
3:7:112:ILE:HG23	29:l:24:ILE:HG13	1.96	0.45
38:8:336:ILE:O	38:8:340:ALA:N	2.41	0.45
42:R:136:ARG:HB3	42:R:136:ARG:NH1	2.32	0.45
53:D:246:GLY:N	53:D:247:PRO:HD3	2.32	0.45
57:x:403:ILE:HG23	57:x:403:ILE:O	2.16	0.45
57:x:415:ILE:O	57:x:498:TYR:OH	2.35	0.45
1:1:845:G:H1	1:1:849:C:H42	1.65	0.45
1:1:1654:A:OP2	39:l:371:LYS:NZ	2.50	0.45
4:A:287:ASP:HB2	6:C:265:GLU:HB2	1.98	0.45
15:P:168:LEU:HB3	15:P:172:GLN:HB2	1.97	0.45
39:I:218:GLN:NE2	55:w:499:THR:OG1	2.50	0.45
53:D:276:ARG:NH2	53:D:365:ASP:OD1	2.50	0.45
54:o:203:LYS:HE2	54:o:203:LYS:HB2	1.73	0.45
1:1:687:U:OP1	35:v:45:THR:OG1	2.28	0.45
5:B:387:LEU:HD11	34:u:109:LYS:HG2	1.98	0.45
6:C:154:THR:OG1	6:C:252:GLU:HB3	2.17	0.45
43:G:49:TYR:HA	55:w:469:MET:HE3	1.98	0.45
53:D:97:LEU:O	53:D:101:ILE:HD12	2.16	0.45
55:w:296:THR:HA	55:w:300:PHE:CD2	2.51	0.45
1:1:374:A:O2'	1:1:376:G:H5'	2.17	0.45
1:1:909:G:H2'	1:1:910:G:H8	1.82	0.45
1:1:1493:G:OP2	1:1:1493:G:N2	2.33	0.45
1:1:1809:A:P	44:Z:65:ARG:HH12	2.38	0.45
1:1:2964:G:N2	1:1:2967:A:O2'	2.50	0.45
1:1:3169:U:H2'	1:1:3170:A:C8	2.51	0.45
38:8:631:ASP:OD1	38:8:631:ASP:N	2.49	0.45
43:G:163:VAL:HG12	43:G:166:LEU:HD12	1.97	0.45
51:t:85:LYS:NZ	51:t:98:ASP:OD1	2.45	0.45
1:1:870:C:O2'	1:1:871:G:OP1	2.28	0.45
1:1:1102:A:O2'	1:1:1103:A:OP1	2.31	0.45
1:1:1597:C:H2'	1:1:1598:G:C8	2.51	0.45
1:1:1622:U:H2'	1:1:1623:G:C8	2.52	0.45
1:1:1724:U:H1'	1:1:1725:C:C6	2.51	0.45
1:1:1954:G:HO2'	1:1:1955:U:P	2.39	0.45
4:A:239:ASN:HD22	4:A:242:TYR:HB2	1.81	0.45
4:A:241:GLN:O	4:A:241:GLN:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:106:TRP:O	5:B:137:TYR:OH	2.33	0.45
5:B:133:TYR:O	5:B:136:LYS:HG2	2.16	0.45
7:E:126:GLN:HG3	7:E:127:ASN:H	1.82	0.45
30:m:223:LEU:HD21	55:w:679:LEU:HB2	1.98	0.45
32:r:22:GLU:OE2	32:r:25:ARG:NH2	2.42	0.45
52:6:42:G:HO2'	52:6:43:A:P	2.38	0.45
53:D:309:LEU:HD23	53:D:314:LEU:HD22	1.98	0.45
1:1:2938:G:OP1	22:b:48:ARG:NH1	2.42	0.45
1:1:3166:C:H2'	1:1:3167:A:C8	2.51	0.45
4:A:119:THR:OG1	4:A:121:ASP:OD1	2.21	0.45
22:b:250:VAL:HG13	22:b:283:VAL:HG13	1.97	0.45
38:8:381:ASN:O	38:8:385:ASN:ND2	2.50	0.45
38:8:513:ILE:HG22	38:8:515:ILE:H	1.82	0.45
39:I:619:GLU:OE1	39:I:619:GLU:N	2.50	0.45
55:w:275:MET:HG2	55:w:278:PHE:CE1	2.51	0.45
56:a:29:LEU:O	56:a:29:LEU:HD23	2.16	0.45
1:1:67:A:O2'	1:1:315:C:O2	2.33	0.45
1:1:2352:A:H5''	15:P:83:TRP:O	2.17	0.45
2:2:123:G:H2'	2:2:124:G:C8	2.52	0.45
5:B:369:ARG:NH1	34:u:33:ARG:HD3	2.31	0.45
29:l:5:THR:OG1	29:l:8:GLU:HG3	2.17	0.45
30:m:392:LEU:O	30:m:396:LEU:HB2	2.17	0.45
31:q:427:THR:HA	31:q:430:ILE:HD11	1.98	0.45
39:I:186:LYS:NZ	39:I:258:GLU:O	2.33	0.45
39:I:292:ILE:O	39:I:296:GLN:HG3	2.17	0.45
42:R:105:LEU:CD2	42:R:109:TYR:CE2	2.99	0.45
1:1:1104:G:O2'	1:1:1105:A:OP1	2.32	0.45
1:1:1466:G:N2	1:1:1510:G:H5''	2.32	0.45
1:1:2356:A:N6	1:1:2983:C:H42	2.15	0.45
4:A:71:LEU:HD23	4:A:71:LEU:O	2.17	0.45
4:A:88:PHE:HB3	4:A:100:TRP:HB2	1.99	0.45
6:C:319:LYS:HB2	6:C:319:LYS:HE2	1.76	0.45
16:Q:19:PRO:HD3	16:Q:53:PHE:HE1	1.81	0.45
19:W:48:VAL:HG11	19:W:213:PHE:CZ	2.51	0.45
21:Y:17:LYS:O	21:Y:21:THR:OG1	2.25	0.45
22:b:211:TYR:HD2	22:b:336:CYS:SG	2.40	0.45
51:t:154:ASN:OD1	52:6:224:G:N2	2.33	0.45
1:1:816:A:OP2	28:j:28:HIS:NE2	2.49	0.44
1:1:1448:U:H2'	1:1:1449:A:C8	2.51	0.44
1:1:2941:A:O2'	1:1:2942:C:O4'	2.27	0.44
1:1:2974:U:H2'	1:1:2975:U:O4'	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:65:TRP:CE2	55:w:806:ALA:HB2	2.52	0.44
27:i:57:LEU:HD21	27:i:73:ALA:HB2	1.99	0.44
29:l:29:ASP:C	29:l:31:LYS:H	2.26	0.44
53:D:52:PRO:HB2	53:D:141:HIS:CE1	2.52	0.44
55:w:255:HIS:HB2	55:w:275:MET:HE3	1.99	0.44
1:1:597:G:H2'	1:1:598:A:H8	1.82	0.44
1:1:1231:A:H5''	1:1:1232:C:H5'	1.98	0.44
1:1:1404:G:N2	1:1:1407:A:OP2	2.40	0.44
1:1:1454:A:H2'	1:1:1879:A:C2	2.52	0.44
1:1:1694:U:O2'	1:1:1695:U:H5'	2.17	0.44
19:W:70:ARG:O	19:W:74:GLN:HG2	2.18	0.44
30:m:438:GLY:N	30:m:800:ASN:OD1	2.50	0.44
38:8:595:LEU:O	38:8:599:ILE:HG12	2.16	0.44
39:I:340:LEU:O	39:I:344:HIS:ND1	2.49	0.44
1:1:293:C:H2'	1:1:294:U:O4'	2.17	0.44
1:1:761:A:C6	1:1:770:G:H5'	2.53	0.44
1:1:1389:G:H5''	24:e:101:SER:HB3	1.99	0.44
1:1:3296:A:H2'	1:1:3297:U:C6	2.53	0.44
2:2:40:A:H2'	2:2:41:A:C8	2.53	0.44
7:E:60:ASP:OD1	7:E:62:THR:OG1	2.28	0.44
9:H:20:ILE:HD13	9:H:45:PHE:CD2	2.52	0.44
26:h:9:LEU:HD23	26:h:12:LYS:HE2	1.98	0.44
39:I:465:SER:OG	39:I:466:SER:N	2.51	0.44
40:K:295:GLN:HE21	54:o:197:LYS:HB3	1.82	0.44
50:p:148:ARG:HE	50:p:212:VAL:HG12	1.83	0.44
51:t:144:ILE:HG23	51:t:194:VAL:HB	1.99	0.44
57:x:383:ILE:HB	57:x:384:PRO:HD3	2.00	0.44
1:1:774:G:O2'	1:1:775:A:O4'	2.22	0.44
1:1:870:C:HO2'	1:1:871:G:P	2.39	0.44
26:h:118:ILE:HG22	26:h:119:LYS:H	1.81	0.44
31:q:350:LEU:HB3	31:q:418:ILE:HG12	1.99	0.44
1:1:263:C:H2'	1:1:264:G:O4'	2.17	0.44
1:1:786:A:H4'	1:1:787:G:H5'	1.99	0.44
1:1:1295:G:H2'	1:1:1296:C:H6	1.82	0.44
1:1:1618:G:O3'	49:n:10:GLY:HA3	2.17	0.44
1:1:1750:A:OP1	48:k:44:LYS:NZ	2.30	0.44
1:1:2396:G:H1	1:1:2984:C:H42	1.64	0.44
2:2:56:G:OP1	28:j:68:LYS:HE2	2.18	0.44
10:J:196:ASN:HB3	10:J:197:ASN:H	1.55	0.44
17:S:96:ASP:OD1	17:S:97:VAL:N	2.39	0.44
20:X:131:ASP:O	20:X:135:ILE:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:q:387:ILE:HG12	31:q:400:VAL:HG21	2.00	0.44
39:I:466:SER:O	39:I:542:LYS:NZ	2.50	0.44
53:D:323:GLN:O	53:D:328:ARG:NH1	2.50	0.44
54:o:169:LYS:HB2	54:o:169:LYS:HE3	1.74	0.44
55:w:823:MET:O	55:w:827:GLN:HG2	2.17	0.44
1:1:659:G:H5''	1:1:660:A:OP1	2.18	0.44
1:1:3338:C:H2'	1:1:3339:A:H8	1.83	0.44
2:2:39:G:H1'	2:2:104:A:N6	2.32	0.44
3:7:124:GLU:HA	3:7:128:GLU:OE2	2.18	0.44
13:N:183:THR:HG22	13:N:187:ARG:HB2	1.99	0.44
16:Q:83:VAL:O	16:Q:103:ALA:HA	2.17	0.44
22:b:328:VAL:HG23	22:b:329:MET:SD	2.57	0.44
55:w:552:SER:O	55:w:556:ARG:HG3	2.18	0.44
1:1:210:U:C2	1:1:230:U:H4'	2.53	0.44
1:1:1679:A:OP1	45:U:94:ARG:NE	2.45	0.44
1:1:2389:C:H2'	1:1:2390:A:H8	1.82	0.44
1:1:2806:U:H2'	1:1:2807:U:C6	2.53	0.44
1:1:2811:A:H2'	1:1:2812:C:C6	2.52	0.44
6:C:250:TRP:CZ3	6:C:258:LEU:HD11	2.53	0.44
10:J:214:LYS:HE3	10:J:214:LYS:HB3	1.75	0.44
19:W:55:GLU:OE1	19:W:119:TYR:OH	2.31	0.44
29:l:101:PRO:HA	29:l:104:GLU:HG3	2.00	0.44
31:q:274:ARG:HB2	31:q:335:PHE:CZ	2.53	0.44
40:K:138:ASP:OD1	40:K:139:ASP:N	2.51	0.44
41:V:31:ALA:O	41:V:32:ARG:NH1	2.51	0.44
46:c:17:VAL:HG11	46:c:92:ILE:HG23	1.99	0.44
46:c:61:MET:HE2	46:c:61:MET:HB3	1.92	0.44
1:1:518:G:OP2	1:1:518:G:N2	2.31	0.44
1:1:1566:A:H5''	51:t:33:ARG:NH2	2.31	0.44
1:1:1763:U:H3'	1:1:1765:U:H5	1.83	0.44
1:1:3252:G:H2'	1:1:3253:G:H8	1.81	0.44
4:A:97:LEU:HB3	4:A:114:ILE:HB	1.99	0.44
5:B:115:LYS:HA	5:B:118:PHE:CD2	2.53	0.44
9:H:43:VAL:HG12	9:H:57:VAL:HG22	2.00	0.44
18:T:126:VAL:HG22	18:T:128:LEU:HB3	1.99	0.44
25:f:14:LEU:HD11	25:f:31:LYS:HB2	2.00	0.44
56:a:171:ASN:OD1	56:a:174:MET:HG3	2.18	0.44
57:x:335:ASP:OD1	57:x:335:ASP:N	2.49	0.44
1:1:591:G:H4'	7:E:19:LYS:HE3	2.00	0.44
1:1:1392:G:H1'	1:1:1418:A:N6	2.33	0.44
1:1:3267:A:H2'	7:E:69:PHE:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:300:ARG:HE	22:b:433:PRO:HG3	1.82	0.44
9:H:41:ILE:HG21	9:H:71:VAL:HG21	2.00	0.44
30:m:192:LEU:HD13	39:I:447:ASP:HB3	1.99	0.44
36:y:15:VAL:HA	36:y:61:ARG:HG2	2.00	0.44
40:K:207:ILE:HD11	40:K:235:PRO:HG3	2.00	0.44
49:n:53:ASN:O	49:n:55:GLY:N	2.50	0.44
49:n:365:PHE:CD2	49:n:411:ILE:HD11	2.53	0.44
53:D:232:THR:OG1	53:D:233:THR:N	2.50	0.44
53:D:266:GLN:HG3	53:D:377:VAL:HG11	1.99	0.44
55:w:385:MET:SD	55:w:386:GLN:HG3	2.58	0.44
1:1:13:A:H4'	20:X:39:LYS:HD3	2.00	0.43
1:1:815:G:C2	1:1:926:A:C2	3.06	0.43
1:1:834:U:H2'	1:1:835:G:O4'	2.18	0.43
1:1:1222:G:H21	1:1:1286:A:H2	1.65	0.43
1:1:1460:A:H2'	1:1:1461:A:H8	1.83	0.43
1:1:1930:A:H3'	1:1:1931:U:C6	2.53	0.43
1:1:2610:G:N2	1:1:2611:U:O2'	2.51	0.43
1:1:3170:A:H8	25:f:56:SER:HB2	1.83	0.43
12:M:20:VAL:HG21	12:M:90:VAL:HG21	2.00	0.43
39:I:151:GLU:O	39:I:155:ASN:ND2	2.47	0.43
41:V:37:ILE:HD11	41:V:73:VAL:HG21	2.00	0.43
54:o:97:ARG:HD3	54:o:161:LEU:O	2.18	0.43
54:o:214:SER:O	54:o:214:SER:OG	2.30	0.43
1:1:297:G:OP2	1:1:297:G:N2	2.26	0.43
1:1:488:U:H2'	1:1:489:C:O4'	2.18	0.43
1:1:844:G:C6	1:1:845:G:C6	3.06	0.43
1:1:912:G:N2	1:1:915:A:OP2	2.50	0.43
1:1:1646:G:H4'	49:n:57:THR:HG21	2.00	0.43
1:1:2357:A:H2'	1:1:2358:A:H8	1.84	0.43
1:1:2371:G:N7	33:s:17:GLU:HG3	2.33	0.43
1:1:3018:C:H5''	36:y:8:GLU:HB3	2.00	0.43
4:A:36:ILE:HG23	4:A:88:PHE:HD1	1.82	0.43
9:H:114:VAL:HG11	9:H:165:CYS:SG	2.58	0.43
15:P:4:TYR:CZ	15:P:16:SER:HB3	2.53	0.43
23:d:77:ARG:HG2	23:d:89:LEU:HD23	1.99	0.43
29:l:74:THR:HG22	29:l:75:LYS:N	2.34	0.43
30:m:322:MET:O	49:n:44:ARG:NH1	2.45	0.43
31:q:355:ALA:HB1	31:q:382:ARG:HD3	1.99	0.43
31:q:374:PHE:CE1	31:q:399:ILE:HD12	2.53	0.43
35:v:219:LEU:HD12	35:v:219:LEU:HA	1.84	0.43
39:I:290:THR:O	39:I:294:ILE:HG13	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:K:129:ASP:HA	40:K:156:CYS:SG	2.58	0.43
44:Z:83:THR:HG22	47:g:93:PHE:CZ	2.53	0.43
46:c:74:ASN:HB3	46:c:86:ARG:HB3	1.99	0.43
50:p:353:ILE:HD12	50:p:371:LEU:HD12	2.00	0.43
53:D:211:ARG:O	53:D:215:LYS:HG3	2.18	0.43
56:a:128:LEU:HD21	56:a:135:PRO:HD3	1.99	0.43
1:1:640:U:H2'	1:1:641:C:C6	2.54	0.43
1:1:858:A:H2'	1:1:859:G:C8	2.53	0.43
1:1:1513:G:P	42:R:5:ARG:HH22	2.41	0.43
1:1:2423:U:O2'	1:1:2424:A:H8	2.01	0.43
1:1:3371:G:H2'	1:1:3372:A:H8	1.82	0.43
29:l:28:VAL:HG23	29:l:29:ASP:H	1.82	0.43
57:x:242:VAL:HG22	57:x:374:LEU:HD12	2.00	0.43
1:1:216:G:H4'	21:Y:19:TYR:CE2	2.54	0.43
1:1:246:U:H2'	1:1:247:C:C6	2.54	0.43
1:1:523:A:O2'	17:S:69:PRO:HD2	2.18	0.43
1:1:726:G:N1	1:1:743:C:OP2	2.39	0.43
1:1:1192:C:C5	33:s:6:ARG:HB2	2.53	0.43
22:b:175:TYR:H	22:b:178:VAL:HG11	1.82	0.43
36:y:66:ASN:HD21	36:y:133:LEU:HB3	1.84	0.43
38:8:599:ILE:HD11	38:8:611:LEU:HB2	2.00	0.43
39:I:257:LYS:HG3	39:I:297:THR:HG21	2.00	0.43
40:K:68:GLU:HB3	40:K:72:GLU:HB3	2.00	0.43
50:p:245:ASP:OD2	50:p:248:GLU:N	2.52	0.43
56:a:181:ASN:O	56:a:185:MET:HG3	2.17	0.43
57:x:10:LEU:HD23	57:x:14:LEU:HD11	2.00	0.43
1:1:258:G:H2'	1:1:259:C:C6	2.53	0.43
1:1:841:A:P	55:w:373:ARG:HH22	2.42	0.43
1:1:1272:C:N4	19:W:158:ILE:HG12	2.34	0.43
1:1:2056:U:H2'	1:1:2057:G:C8	2.54	0.43
1:1:2374:C:H2'	1:1:2375:G:N3	2.32	0.43
1:1:3133:C:H2'	1:1:3134:A:O4'	2.18	0.43
5:B:280:HIS:HB3	5:B:324:VAL:HG13	2.00	0.43
25:f:16:TYR:OH	25:f:89:LEU:O	2.24	0.43
34:u:125:LYS:HA	34:u:128:GLU:HG2	2.00	0.43
43:G:90:THR:HA	43:G:214:LEU:HD21	2.01	0.43
49:n:30:ALA:O	49:n:34:ARG:HG3	2.19	0.43
50:p:161:ALA:HB2	50:p:167:LEU:HG	1.99	0.43
57:x:50:ASP:HA	57:x:203:SER:O	2.18	0.43
1:1:693:A:C2'	1:1:694:C:H5'	2.49	0.43
1:1:845:G:OP2	55:w:368:LYS:HE2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2903:A:H2'	1:1:2904:U:O4'	2.18	0.43
12:M:12:TRP:CZ2	17:S:153:PRO:HB3	2.54	0.43
30:m:402:LYS:HD2	51:t:19:LEU:HD22	2.00	0.43
34:u:16:GLY:N	41:V:90:GLY:O	2.50	0.43
36:y:93:LYS:HG3	36:y:132:VAL:HG13	1.99	0.43
48:k:24:THR:HB	48:k:44:LYS:HB2	2.01	0.43
50:p:167:LEU:HB2	50:p:204:LEU:HB2	2.01	0.43
1:1:631:U:H2'	1:1:632:G:C8	2.53	0.43
1:1:748:U:H2'	1:1:749:C:C6	2.54	0.43
1:1:1259:A:OP1	19:W:57:ARG:NH2	2.51	0.43
8:F:130:ILE:HD12	8:F:134:VAL:HG11	2.01	0.43
24:e:126:LEU:HD23	24:e:126:LEU:HA	1.90	0.43
35:v:50:TYR:CG	35:v:57:ALA:HB2	2.54	0.43
43:G:70:LYS:HA	43:G:70:LYS:HD2	1.82	0.43
53:D:158:ALA:O	53:D:162:MET:HG2	2.18	0.43
1:1:407:A:C2	2:2:17:A:H1'	2.54	0.43
1:1:589:A:H8	1:1:590:G:C8	2.37	0.43
1:1:1286:A:H8	1:1:1287:A:H1'	1.84	0.43
1:1:2497:U:H2'	1:1:2498:U:C6	2.53	0.43
6:C:132:ALA:HB2	6:C:148:ILE:HG21	1.99	0.43
6:C:261:VAL:O	6:C:269:SER:OG	2.24	0.43
22:b:211:TYR:HB2	22:b:332:ARG:HH12	1.84	0.43
22:b:285:VAL:HB	22:b:317:ILE:HD13	2.00	0.43
28:j:68:LYS:HD3	35:v:14:VAL:HG21	2.01	0.43
39:I:192:TYR:OH	39:I:217:GLU:OE2	2.24	0.43
51:t:143:PHE:CZ	51:t:207:LEU:HD21	2.53	0.43
54:o:95:VAL:HG12	54:o:164:VAL:HG22	2.00	0.43
1:1:66:A:N6	1:1:76:G:H1'	2.34	0.43
1:1:190:U:H2'	21:Y:60:ARG:HH22	1.84	0.43
1:1:656:A:H2'	1:1:657:A:H8	1.84	0.43
1:1:1250:G:H2'	1:1:1251:A:C8	2.53	0.43
1:1:1580:A:N1	20:X:33:ARG:NH1	2.66	0.43
1:1:1856:C:H2'	1:1:1857:C:H6	1.83	0.43
11:L:48:PRO:HG2	35:v:33:ASN:HD22	1.84	0.43
29:l:66:LEU:HD12	31:q:399:ILE:HG12	2.00	0.43
31:q:408:PHE:CD1	31:q:411:VAL:HB	2.54	0.43
32:r:186:HIS:ND1	32:r:189:LEU:HD23	2.33	0.43
36:y:74:THR:OG1	36:y:98:GLU:HA	2.19	0.43
38:8:73:THR:HA	38:8:76:GLU:HG2	2.01	0.43
40:K:277:ARG:NH1	52:6:36:U:O3'	2.52	0.43
43:G:154:ALA:HB2	43:G:186:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:6:2:C:C5	54:o:158:MET:HE1	2.54	0.43
57:x:94:GLU:OE1	57:x:94:GLU:N	2.46	0.43
1:1:482:C:H2'	1:1:483:G:N7	2.34	0.43
1:1:757:C:H42	1:1:775:A:H61	1.66	0.43
1:1:1969:G:O6	1:1:2054:C:N4	2.52	0.43
1:1:3329:U:O2'	5:B:363:SER:OG	2.36	0.43
1:1:3371:G:H2'	1:1:3372:A:C8	2.54	0.43
19:W:136:THR:OG1	19:W:186:TYR:O	2.28	0.43
20:X:23:ALA:HB1	55:w:451:LYS:HZ2	1.84	0.43
20:X:63:ILE:HD13	20:X:86:VAL:HG12	2.00	0.43
30:m:351:LYS:HB2	30:m:351:LYS:HE3	1.67	0.43
31:q:199:SER:OG	31:q:203:ARG:NH2	2.52	0.43
31:q:390:ILE:HD12	31:q:398:THR:HG21	2.01	0.43
43:G:47:SER:HB2	43:G:49:TYR:CE1	2.54	0.43
49:n:74:GLU:HG3	49:n:76:VAL:H	1.82	0.43
49:n:558:MET:HE3	49:n:558:MET:HB3	1.95	0.43
53:D:231:GLN:HE22	53:D:249:PHE:HE1	1.67	0.43
53:D:373:TYR:O	53:D:377:VAL:HG13	2.19	0.43
56:a:68:PHE:HE2	56:a:110:PHE:CG	2.37	0.43
57:x:427:LYS:HE3	57:x:427:LYS:HB2	1.63	0.43
1:1:226:C:H2'	1:1:227:G:O4'	2.19	0.42
1:1:591:G:N2	1:1:612:U:OP1	2.46	0.42
1:1:3033:A:H2'	1:1:3034:C:C6	2.53	0.42
1:1:3393:U:H2'	1:1:3394:U:C6	2.54	0.42
9:H:157:ASN:O	9:H:157:ASN:ND2	2.50	0.42
15:P:13:LYS:HB3	15:P:152:GLU:HB3	2.00	0.42
16:Q:64:VAL:HG13	16:Q:93:ILE:HD11	2.01	0.42
19:W:107:GLU:OE1	19:W:111:THR:OG1	2.26	0.42
22:b:275:LYS:HA	22:b:278:PHE:CE1	2.54	0.42
26:h:64:GLU:OE2	26:h:68:GLN:NE2	2.50	0.42
52:6:225:U:H4'	52:6:226:U:H5''	2.01	0.42
53:D:96:PHE:HB2	53:D:194:ILE:HG12	2.01	0.42
55:w:419:LEU:HD13	55:w:538:LEU:HD23	2.01	0.42
1:1:35:A:H2'	1:1:36:C:H6	1.84	0.42
1:1:164:A:HO2'	1:1:166:C:P	2.42	0.42
1:1:239:G:H2'	1:1:240:U:C6	2.54	0.42
1:1:1124:U:H2'	1:1:1125:U:C6	2.54	0.42
1:1:2086:A:H2'	1:1:2087:C:C6	2.53	0.42
1:1:2410:U:H2'	1:1:2411:U:O4'	2.19	0.42
1:1:2899:C:O2'	1:1:2901:G:OP2	2.38	0.42
1:1:3096:C:H2'	1:1:3097:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3305:A:H2'	1:1:3306:U:O4'	2.19	0.42
2:2:110:C:H1'	2:2:112:U:H5	1.84	0.42
5:B:28:ARG:H	5:B:28:ARG:HG2	1.67	0.42
5:B:216:ASP:CB	5:B:278:ILE:HA	2.49	0.42
31:q:251:ASN:HB3	31:q:517:ARG:HH21	1.83	0.42
52:6:16:U:H2'	52:6:17:G:C8	2.53	0.42
1:1:641:C:H2'	1:1:642:U:C6	2.54	0.42
1:1:668:G:H2'	1:1:669:U:H6	1.84	0.42
1:1:1283:C:HO2'	1:1:1284:C:P	2.42	0.42
1:1:2370:G:H5''	1:1:2371:G:H5'	2.00	0.42
1:1:2417:U:O2'	1:1:2418:G:OP1	2.32	0.42
1:1:3084:C:O2'	1:1:3332:U:OP1	2.27	0.42
1:1:3278:C:OP1	25:f:54:ARG:NH2	2.39	0.42
29:l:168:ASP:OD1	29:l:168:ASP:N	2.52	0.42
38:8:588:VAL:HG12	38:8:592:ILE:HG13	2.00	0.42
39:I:147:LYS:O	39:I:155:ASN:ND2	2.52	0.42
53:D:228:SER:OG	53:D:230:THR:O	2.34	0.42
1:1:164:A:N6	1:1:258:G:O6	2.52	0.42
1:1:664:U:H2'	1:1:665:A:H8	1.84	0.42
1:1:787:G:H2'	1:1:788:C:H6	1.83	0.42
1:1:906:A:H2'	1:1:907:G:C8	2.55	0.42
1:1:950:G:H4'	1:1:970:A:H4'	2.01	0.42
1:1:1347:U:H2'	1:1:1355:A:H61	1.85	0.42
1:1:1660:C:H2'	1:1:1661:G:C8	2.53	0.42
1:1:1936:A:N1	57:x:523:LYS:HD2	2.35	0.42
1:1:1956:A:H2'	1:1:1957:G:H8	1.84	0.42
1:1:3295:A:H2'	1:1:3296:A:H8	1.83	0.42
16:Q:16:ARG:HG2	16:Q:53:PHE:HB3	2.01	0.42
17:S:25:PHE:O	17:S:41:TYR:OH	2.34	0.42
38:8:457:GLN:O	38:8:462:ASN:HB3	2.19	0.42
39:I:164:LYS:HD2	39:I:164:LYS:HA	1.92	0.42
39:I:473:LEU:HD21	39:I:509:ILE:HD11	2.01	0.42
40:K:43:GLU:CD	54:o:216:ILE:HG13	2.44	0.42
40:K:66:LEU:HD23	40:K:66:LEU:HA	1.94	0.42
53:D:198:ALA:HB3	53:D:228:SER:HB2	2.02	0.42
56:a:63:MET:HE2	56:a:152:ARG:HG2	2.01	0.42
56:a:138:VAL:HG11	56:a:147:LYS:HD3	2.01	0.42
56:a:174:MET:HB3	56:a:178:VAL:HG13	2.00	0.42
1:1:406:G:N3	2:2:16:G:C2	2.87	0.42
1:1:461:U:H3	1:1:469:G:H1	1.66	0.42
1:1:677:A:H4'	1:1:678:G:O5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1486:G:H21	47:g:6:THR:HB	1.85	0.42
3:7:110:ARG:NH2	29:l:6:GLU:OE2	2.51	0.42
5:B:59:ASP:OD1	5:B:59:ASP:N	2.53	0.42
9:H:20:ILE:HD12	12:M:7:VAL:HG22	2.01	0.42
17:S:40:ARG:HA	17:S:40:ARG:HD2	1.77	0.42
29:l:50:HIS:NE2	31:q:371:GLY:O	2.37	0.42
30:m:128:TYR:HD2	30:m:132:SER:HB2	1.85	0.42
30:m:598:LYS:HE3	30:m:598:LYS:HB3	1.86	0.42
40:K:229:VAL:HA	40:K:233:GLN:HB2	2.01	0.42
41:V:109:MET:HE1	41:V:128:ARG:C	2.45	0.42
50:p:370:GLN:HG3	50:p:372:ILE:HD11	2.01	0.42
51:t:81:LEU:O	51:t:85:LYS:HG3	2.20	0.42
53:D:394:LEU:HD23	53:D:394:LEU:HA	1.90	0.42
57:x:198:ARG:NE	57:x:198:ARG:HA	2.35	0.42
1:1:62:A:H5''	13:N:164:LEU:HD21	2.01	0.42
1:1:720:A:H4'	1:1:721:G:O5'	2.20	0.42
1:1:1234:G:H2'	1:1:1235:U:C5	2.55	0.42
1:1:1326:A:O2'	25:f:77:ASN:OD1	2.28	0.42
1:1:1643:A:H2'	1:1:1644:C:C2	2.55	0.42
3:7:117:ASP:OD1	29:l:94:LYS:NZ	2.52	0.42
7:E:40:LEU:HD11	7:E:54:TYR:HB2	2.00	0.42
13:N:104:GLU:HA	13:N:160:GLU:HG3	2.00	0.42
22:b:372:VAL:HB	22:b:374:ARG:CZ	2.49	0.42
26:h:77:PRO:HD2	26:h:80:LEU:HD12	2.02	0.42
32:r:186:HIS:HE1	32:r:188:GLU:HB2	1.84	0.42
49:n:214:ASP:HB3	49:n:217:ILE:HD12	2.01	0.42
50:p:269:MET:HE2	50:p:269:MET:HB3	1.94	0.42
51:t:30:ARG:O	51:t:34:GLN:HG2	2.20	0.42
1:1:553:U:H2'	1:1:554:A:O4'	2.19	0.42
1:1:1116:G:H2'	1:1:1117:G:O4'	2.19	0.42
1:1:1498:A:H2'	1:1:1499:C:H6	1.83	0.42
1:1:1596:C:H2'	1:1:1597:C:H6	1.83	0.42
1:1:1681:U:OP2	22:b:521:ARG:NH1	2.37	0.42
1:1:1717:U:H2'	1:1:1718:G:C8	2.54	0.42
1:1:1930:A:H3'	1:1:1931:U:H6	1.83	0.42
4:A:39:ARG:HD3	4:A:64:LYS:HD3	2.02	0.42
4:A:215:ILE:O	10:J:280:LYS:NZ	2.41	0.42
30:m:225:SER:O	30:m:229:ARG:HG2	2.20	0.42
36:y:42:LEU:HD13	36:y:46:ILE:HD11	2.00	0.42
39:I:342:VAL:HG11	39:I:406:ILE:HD13	2.01	0.42
42:R:13:SER:OG	42:R:38:ARG:NH2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:n:377:GLU:HA	49:n:387:VAL:HG21	2.02	0.42
53:D:86:ALA:HB3	53:D:92:LYS:HD3	2.01	0.42
57:x:68:LYS:HZ2	57:x:198:ARG:HG3	1.85	0.42
1:1:506:U:H2'	1:1:507:U:O4'	2.20	0.42
1:1:549:U:N3	1:1:550:A:N7	2.67	0.42
1:1:1254:C:H2'	1:1:1255:C:H6	1.85	0.42
1:1:1636:U:O2'	44:Z:79:HIS:ND1	2.46	0.42
1:1:1746:U:O2'	48:k:4:GLU:OE1	2.36	0.42
1:1:1950:U:H2'	1:1:1951:C:C6	2.55	0.42
2:2:63:G:O2'	26:h:49:LYS:NZ	2.50	0.42
4:A:45:HIS:CE1	4:A:97:LEU:HB2	2.55	0.42
13:N:147:ARG:HG3	26:h:101:THR:HG21	2.01	0.42
40:K:76:LYS:HD2	40:K:252:GLU:OE2	2.20	0.42
51:t:187:LEU:HD22	51:t:196:ILE:HD13	2.00	0.42
54:o:146:MET:O	54:o:150:GLU:HG3	2.20	0.42
56:a:86:SER:H	56:a:89:ASP:HB3	1.84	0.42
57:x:351:THR:HG21	57:x:385:PHE:CE2	2.55	0.42
1:1:91:G:O2'	1:1:94:G:O6	2.27	0.42
1:1:155:G:H4'	1:1:156:G:H2'	2.02	0.42
1:1:500:C:H2'	1:1:501:A:C8	2.55	0.42
1:1:1281:G:H2'	1:1:1282:G:H8	1.84	0.42
1:1:2428:U:H5'	31:q:412:ILE:HD11	2.02	0.42
1:1:2448:G:H2'	1:1:2449:A:C8	2.55	0.42
1:1:2455:U:O4	1:1:2456:A:N6	2.53	0.42
1:1:2482:U:H5''	31:q:224:ARG:HG2	2.02	0.42
1:1:2883:U:H2'	1:1:2884:C:C6	2.55	0.42
1:1:3036:G:OP1	37:z:17:LYS:HD2	2.18	0.42
1:1:3138:U:OP2	5:B:30:LYS:HD2	2.19	0.42
1:1:3383:G:H2'	1:1:3384:U:C6	2.55	0.42
35:v:182:GLU:HG2	35:v:222:TRP:HD1	1.85	0.42
36:y:156:ASN:HB2	36:y:201:ASP:OD1	2.20	0.42
57:x:104:LEU:O	57:x:108:GLU:HG2	2.20	0.42
57:x:237:LYS:NZ	57:x:367:VAL:HG13	2.34	0.42
57:x:290:LEU:H	57:x:290:LEU:HD23	1.85	0.42
1:1:353:G:O6	28:j:55:ARG:NH2	2.53	0.42
1:1:484:C:H4'	1:1:485:A:OP1	2.20	0.42
1:1:1615:C:H2'	1:1:1616:U:H6	1.83	0.42
1:1:1779:C:C2	42:R:90:PRO:HD3	2.55	0.42
4:A:130:LEU:HD22	10:J:276:ALA:HB3	2.01	0.42
30:m:232:GLN:NE2	30:m:237:ILE:HB	2.34	0.42
30:m:314:SER:HB2	30:m:316:GLU:OE1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:m:717:LYS:HG3	30:m:764:ILE:HD12	2.01	0.42
39:I:507:PRO:HD3	39:I:571:ARG:HH11	1.85	0.42
39:I:595:MET:HG2	39:I:601:ILE:HB	2.02	0.42
42:R:151:ARG:HG3	42:R:151:ARG:HH11	1.84	0.42
49:n:204:LYS:HD2	49:n:374:ASP:OD2	2.20	0.42
49:n:431:TRP:HD1	49:n:447:TYR:CD2	2.38	0.42
50:p:401:LYS:HD3	50:p:410:PRO:HG3	2.02	0.42
57:x:201:LEU:HD21	57:x:216:THR:HG21	2.02	0.42
1:1:41:G:O6	1:1:43:A:C6	2.73	0.41
1:1:711:A:H5'	4:A:248:VAL:HG13	2.02	0.41
1:1:844:G:OP2	55:w:368:LYS:HE3	2.19	0.41
1:1:1129:A:OP2	32:r:251:ARG:NH2	2.53	0.41
1:1:1196:C:H4'	1:1:1197:A:N7	2.35	0.41
1:1:1260:A:H1'	1:1:1280:C:H1'	2.02	0.41
1:1:1878:G:H2'	1:1:1879:A:C4	2.54	0.41
1:1:1962:G:H5'	50:p:275:ARG:HH11	1.84	0.41
9:H:187:ILE:HG22	9:H:188:THR:HG23	2.02	0.41
31:q:406:ARG:HB3	31:q:455:LEU:HD23	2.01	0.41
32:r:186:HIS:CE1	32:r:188:GLU:HB2	2.55	0.41
36:y:129:ILE:HG23	36:y:133:LEU:HD12	2.01	0.41
38:8:374:MET:O	38:8:375:ARG:NE	2.53	0.41
44:Z:27:LYS:HE3	44:Z:27:LYS:HB2	1.90	0.41
49:n:359:LEU:HD11	49:n:439:GLY:HA2	2.02	0.41
50:p:233:PHE:CZ	50:p:317:LEU:HD23	2.55	0.41
50:p:316:ASP:O	50:p:320:ALA:N	2.52	0.41
53:D:193:LEU:HB2	53:D:222:ARG:HD2	2.02	0.41
1:1:209:A:H4'	1:1:211:A:C8	2.55	0.41
1:1:1228:C:H2'	1:1:1229:G:H8	1.84	0.41
1:1:1532:C:H2'	1:1:1533:U:C6	2.54	0.41
1:1:2357:A:H2'	1:1:2358:A:C8	2.55	0.41
1:1:2364:G:O2'	1:1:2986:U:H5'	2.20	0.41
1:1:2395:G:H2'	1:1:2396:G:C8	2.55	0.41
1:1:3045:G:H2'	1:1:3046:A:O4'	2.19	0.41
1:1:3298:C:C2	1:1:3299:A:C8	3.08	0.41
4:A:135:PRO:HB3	4:A:175:HIS:CE1	2.54	0.41
30:m:272:GLU:OE2	43:G:108:ARG:NH2	2.53	0.41
31:q:281:ARG:HE	31:q:283:ARG:HH11	1.67	0.41
39:I:280:ILE:HD11	39:I:294:ILE:HG22	2.01	0.41
52:6:17:G:H2'	52:6:18:U:H6	1.85	0.41
52:6:32:A:C6	52:6:47:A:C8	3.08	0.41
52:6:42:G:O2'	52:6:43:A:OP1	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:x:27:PHE:C	57:x:29:THR:H	2.27	0.41
1:1:1221:A:C8	19:W:75:LYS:HD2	2.55	0.41
1:1:2363:A:H2'	1:1:2364:G:O4'	2.21	0.41
1:1:2469:G:C2	1:1:2477:G:H1'	2.54	0.41
1:1:3269:U:H4'	1:1:3270:U:O5'	2.19	0.41
2:2:56:G:OP1	35:v:12:SER:HB2	2.20	0.41
3:7:127:LEU:HD13	39:I:447:ASP:OD2	2.20	0.41
8:F:84:VAL:HA	8:F:139:PRO:HD3	2.01	0.41
28:j:58:THR:O	28:j:61:THR:OG1	2.33	0.41
30:m:199:PRO:HD2	30:m:202:TRP:CD1	2.55	0.41
30:m:217:THR:OG1	30:m:220:GLU:HG3	2.19	0.41
31:q:340:ALA:O	31:q:545:LYS:NZ	2.35	0.41
36:y:107:VAL:HB	36:y:118:HIS:HB2	2.02	0.41
38:8:483:ILE:H	38:8:483:ILE:HD12	1.85	0.41
47:g:100:ILE:HG12	55:w:429:MET:HE2	2.02	0.41
57:x:10:LEU:HD12	57:x:10:LEU:HA	1.85	0.41
57:x:448:GLN:H	57:x:448:GLN:CD	2.29	0.41
1:1:2390:A:H2'	1:1:2391:G:H8	1.86	0.41
1:1:2467:G:OP2	56:a:60:ARG:NH2	2.53	0.41
1:1:2883:U:H2'	1:1:2884:C:H6	1.86	0.41
1:1:3037:U:H5''	5:B:348:ARG:HE	1.86	0.41
1:1:3095:U:H2'	1:1:3096:C:C6	2.56	0.41
15:P:46:LYS:O	15:P:50:GLN:HG3	2.21	0.41
20:X:67:ILE:HD11	20:X:85:GLN:HB2	2.02	0.41
22:b:145:ASP:HB2	22:b:146:PRO:HD3	2.02	0.41
22:b:254:MET:HB2	22:b:287:ILE:HG13	2.01	0.41
27:i:68:ARG:HD3	30:m:147:ASP:OD2	2.20	0.41
31:q:453:LYS:HG3	31:q:488:VAL:HG12	2.02	0.41
31:q:494:ARG:NE	56:a:44:GLN:OE1	2.53	0.41
47:g:11:ASN:HB3	47:g:18:ASN:HD22	1.86	0.41
48:k:29:LYS:NZ	48:k:39:ARG:HE	2.19	0.41
55:w:298:ASP:O	55:w:299:GLU:HG2	2.21	0.41
57:x:227:ASN:OD1	57:x:227:ASN:N	2.53	0.41
1:1:602:A:H2'	1:1:603:A:C8	2.55	0.41
1:1:1355:A:H4'	1:1:1356:U:C5'	2.50	0.41
1:1:1392:G:H1'	1:1:1418:A:H61	1.84	0.41
1:1:1393:A:N3	1:1:1419:A:O2'	2.51	0.41
1:1:1566:A:O2'	49:n:217:ILE:HD11	2.20	0.41
1:1:1961:G:H2'	1:1:1962:G:H8	1.85	0.41
1:1:2429:G:N1	1:1:2601:A:C2	2.89	0.41
2:2:83:C:H42	21:Y:52:ARG:NH2	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:90:VAL:HG21	5:B:180:GLU:OE2	2.20	0.41
8:F:86:VAL:O	8:F:114:GLY:HA2	2.21	0.41
8:F:232:ARG:HB2	8:F:235:PHE:HB2	2.02	0.41
12:M:32:LEU:HD11	12:M:94:TRP:CG	2.55	0.41
22:b:51:LYS:HE3	22:b:51:LYS:HB3	1.82	0.41
29:l:21:GLY:C	29:l:23:ASN:H	2.28	0.41
30:m:330:PRO:HA	30:m:331:PRO:HD3	1.94	0.41
31:q:200:THR:N	31:q:203:ARG:HH21	2.18	0.41
45:U:90:ARG:HA	45:U:90:ARG:HD2	1.98	0.41
1:1:1286:A:C8	1:1:1287:A:H1'	2.56	0.41
1:1:1460:A:H2'	1:1:1461:A:C8	2.55	0.41
1:1:2103:U:O2	57:x:526:LYS:CD	2.36	0.41
1:1:2962:U:H2'	1:1:2963:C:C6	2.56	0.41
1:1:3251:U:H2'	1:1:3252:G:H8	1.86	0.41
9:H:90:MET:HE2	9:H:90:MET:HB3	1.90	0.41
10:J:302:ARG:HE	10:J:302:ARG:HB3	1.68	0.41
22:b:531:MET:SD	45:U:92:TRP:NE1	2.92	0.41
24:e:42:VAL:O	24:e:52:GLN:NE2	2.51	0.41
29:l:30:ASN:C	29:l:32:GLU:H	2.29	0.41
51:t:136:ASP:OD1	51:t:136:ASP:N	2.52	0.41
53:D:296:LEU:HD12	53:D:302:VAL:HA	2.02	0.41
1:1:1334:U:OP1	8:F:206:LYS:HE3	2.21	0.41
2:2:9:A:H2'	2:2:10:A:C8	2.55	0.41
4:A:192:GLU:O	4:A:212:LEU:HA	2.20	0.41
5:B:62:ARG:NH2	5:B:352:GLU:OE2	2.40	0.41
5:B:163:HIS:ND1	5:B:164:THR:O	2.50	0.41
11:L:47:ALA:HB1	35:v:36:ILE:HG21	2.03	0.41
21:Y:59:VAL:HG12	21:Y:60:ARG:HG2	2.02	0.41
30:m:156:THR:OG1	30:m:173:TYR:O	2.37	0.41
30:m:710:ASP:C	48:k:7:ASP:HB3	2.45	0.41
47:g:58:ARG:HA	47:g:58:ARG:HD2	1.93	0.41
47:g:83:ASN:O	47:g:87:GLU:HG3	2.20	0.41
53:D:400:GLY:O	53:D:403:ARG:HG2	2.20	0.41
56:a:66:CYS:O	56:a:111:ILE:HG22	2.21	0.41
56:a:139:SER:OG	56:a:140:HIS:N	2.53	0.41
57:x:511:GLU:OE2	57:x:515:ASN:ND2	2.53	0.41
1:1:187:A:H2'	1:1:188:U:C6	2.56	0.41
1:1:855:U:H2'	1:1:856:G:O4'	2.20	0.41
1:1:1925:U:OP1	42:R:134:HIS:CB	2.69	0.41
1:1:3295:A:OP2	5:B:126:LYS:N	2.45	0.41
2:2:26:U:H2'	2:2:27:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:189:ARG:NH1	4:A:218:ARG:HG3	2.35	0.41
6:C:187:LEU:HG	6:C:193:LYS:HD3	2.03	0.41
12:M:15:VAL:HG23	12:M:35:ILE:HD13	2.03	0.41
19:W:81:ARG:HG2	19:W:90:TYR:CE1	2.56	0.41
22:b:495:TRP:HZ3	34:u:133:LEU:HG	1.85	0.41
29:l:15:LYS:HG3	29:l:81:LEU:HD23	2.02	0.41
32:r:243:ALA:HB2	32:r:259:LEU:HD12	2.01	0.41
36:y:62:MET:HE1	41:V:136:VAL:HG21	2.03	0.41
50:p:153:ILE:HG13	50:p:216:VAL:HG21	2.03	0.41
50:p:310:HIS:HB3	50:p:328:THR:O	2.19	0.41
53:D:66:THR:H	53:D:69:GLN:NE2	2.18	0.41
57:x:351:THR:OG1	57:x:389:LYS:NZ	2.52	0.41
1:1:141:C:H2'	1:1:142:C:C6	2.56	0.41
1:1:734:C:O2'	1:1:735:A:OP1	2.30	0.41
1:1:1239:C:H2'	1:1:1240:A:O4'	2.21	0.41
1:1:1263:A:N3	1:1:1263:A:H2'	2.35	0.41
1:1:1281:G:O5'	19:W:69:LYS:NZ	2.53	0.41
1:1:1315:U:O2'	14:O:133:ARG:HD2	2.21	0.41
1:1:1593:A:N3	1:1:1615:C:O2'	2.54	0.41
1:1:1643:A:H5''	1:1:1644:C:C5	2.56	0.41
1:1:1881:A:H2'	1:1:1882:G:H8	1.86	0.41
1:1:1940:G:H1'	57:x:434:LYS:HD2	2.03	0.41
1:1:2491:A:H2'	1:1:2492:C:C6	2.55	0.41
1:1:2834:G:H2'	1:1:2835:U:C6	2.55	0.41
1:1:3216:G:H3'	1:1:3219:G:N3	2.36	0.41
3:7:14:ARG:HA	13:N:71:ARG:O	2.21	0.41
4:A:89:PHE:CE1	4:A:99:LEU:HD13	2.56	0.41
5:B:92:TYR:HB2	5:B:157:VAL:HB	2.02	0.41
6:C:92:ASN:HD22	6:C:100:PHE:HB2	1.86	0.41
7:E:126:GLN:HG3	7:E:127:ASN:N	2.35	0.41
13:N:16:SER:O	13:N:20:ARG:HB2	2.21	0.41
19:W:48:VAL:HG11	19:W:213:PHE:CE2	2.56	0.41
21:Y:39:LEU:HD22	21:Y:43:TYR:CE2	2.56	0.41
22:b:392:ASP:O	22:b:395:ARG:NH1	2.50	0.41
22:b:516:LYS:C	42:R:56:THR:HG22	2.46	0.41
23:d:97:LEU:HD12	23:d:97:LEU:HA	1.89	0.41
26:h:86:ARG:O	26:h:90:ARG:HD3	2.21	0.41
29:l:108:LEU:HD11	29:l:169:ILE:HG13	2.02	0.41
29:l:156:MET:HG2	29:l:157:GLN:N	2.36	0.41
30:m:196:ILE:HG12	55:w:728:MET:HE1	2.03	0.41
30:m:420:LYS:HG3	30:m:421:ASP:OD1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:m:493:TRP:CZ3	30:m:502:LEU:HB2	2.55	0.41
30:m:618:ASN:HB3	30:m:636:LYS:O	2.21	0.41
31:q:465:CYS:HB3	31:q:548:LYS:HE2	2.03	0.41
31:q:538:VAL:HG23	31:q:539:ASP:N	2.31	0.41
38:8:452:LEU:HD23	38:8:452:LEU:HA	1.89	0.41
38:8:490:GLN:HG3	38:8:491:PHE:N	2.36	0.41
38:8:542:ASP:OD2	38:8:545:HIS:ND1	2.20	0.41
46:c:16:LEU:HD23	46:c:98:SER:HA	2.01	0.41
47:g:46:ASP:OD2	47:g:88:ARG:NH1	2.52	0.41
47:g:51:LEU:HB3	47:g:54:ILE:HD12	2.03	0.41
50:p:93:PRO:HA	50:p:94:PRO:HD3	1.96	0.41
50:p:282:LEU:HD23	50:p:282:LEU:HA	1.82	0.41
51:t:150:PRO:HB2	51:t:153:VAL:HG21	2.02	0.41
51:t:157:ASN:N	52:6:224:G:H5'	2.36	0.41
51:t:157:ASN:H	52:6:224:G:H5'	1.86	0.41
53:D:427:SER:O	53:D:431:LYS:HG3	2.20	0.41
55:w:664:THR:HG21	55:w:713:ILE:HA	2.02	0.41
56:a:5:THR:HG23	56:a:8:GLN:H	1.86	0.41
57:x:536:TRP:O	57:x:540:THR:HG23	2.21	0.41
1:1:841:A:OP1	55:w:373:ARG:NH2	2.54	0.41
1:1:1460:A:H5'	23:d:51:LEU:O	2.21	0.41
1:1:1951:C:H2'	1:1:1952:G:C8	2.56	0.41
3:7:45:PRO:HB2	3:7:50:VAL:HG13	2.03	0.41
3:7:110:ARG:HD3	3:7:143:GLU:OE2	2.21	0.41
4:A:66:ASP:OD1	4:A:66:ASP:N	2.52	0.41
5:B:110:LEU:HD23	5:B:114:VAL:HG11	2.03	0.41
5:B:332:ARG:HG2	5:B:333:LYS:HG3	2.02	0.41
15:P:132:ALA:O	15:P:135:ARG:HG2	2.21	0.41
27:i:43:LEU:O	27:i:47:ILE:HG12	2.20	0.41
29:l:173:LEU:HB2	31:q:323:LEU:HD21	2.02	0.41
30:m:774:LYS:HA	30:m:774:LYS:HD3	1.94	0.41
32:r:225:VAL:HG12	32:r:225:VAL:O	2.21	0.41
36:y:202:TYR:O	36:y:203:LEU:HD23	2.19	0.41
38:8:581:ASN:ND2	39:I:638:LEU:HD13	2.36	0.41
49:n:178:LYS:HB2	49:n:189:GLN:HB3	2.03	0.41
50:p:371:LEU:HB3	50:p:403:TRP:CE3	2.56	0.41
55:w:481:ASP:OD1	55:w:481:ASP:N	2.50	0.41
55:w:740:LYS:HE3	55:w:740:LYS:HB3	1.80	0.41
57:x:328:ASP:HB3	57:x:353:MET:HE1	2.02	0.41
1:1:2:U:H4'	20:X:23:ALA:HB2	2.03	0.40
1:1:209:A:H4'	1:1:211:A:N7	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:431:U:H2'	1:1:432:G:H8	1.85	0.40
1:1:2417:U:H2'	1:1:2418:G:O4'	2.21	0.40
1:1:3013:U:H2'	1:1:3014:U:C6	2.56	0.40
1:1:3021:A:H5'	1:1:3023:U:H1'	2.03	0.40
1:1:3159:C:H2'	1:1:3160:U:C6	2.56	0.40
1:1:3177:G:O2'	1:1:3179:U:OP1	2.32	0.40
4:A:164:PRO:HG3	10:J:219:GLU:HA	2.02	0.40
38:8:75:PHE:HA	39:I:582:LYS:HD3	2.02	0.40
38:8:639:LYS:HD2	38:8:639:LYS:HA	1.86	0.40
38:8:675:ARG:O	38:8:678:MET:HG2	2.21	0.40
40:K:85:ASN:ND2	40:K:275:GLN:OE1	2.42	0.40
53:D:272:ASP:O	53:D:276:ARG:HG3	2.21	0.40
57:x:41:LEU:HD13	57:x:47:VAL:HB	2.03	0.40
1:1:507:U:H2'	1:1:508:U:C6	2.57	0.40
1:1:696:C:H1'	35:v:65:GLY:N	2.34	0.40
1:1:1659:U:H2'	1:1:1660:C:H6	1.85	0.40
1:1:1801:U:O2'	47:g:60:ARG:NH2	2.54	0.40
1:1:1945:A:OP1	57:x:124:GLY:N	2.51	0.40
1:1:2393:G:H1'	1:1:2394:G:C8	2.57	0.40
1:1:2809:C:O2	32:r:167:LYS:NZ	2.52	0.40
1:1:3051:U:H2'	1:1:3052:G:C8	2.54	0.40
2:2:37:A:OP2	26:h:86:ARG:HD2	2.21	0.40
2:2:106:C:H4'	2:2:107:G:H5''	2.02	0.40
6:C:22:LEU:HA	6:C:23:PRO:HD3	1.94	0.40
8:F:190:THR:O	8:F:190:THR:OG1	2.37	0.40
8:F:214:TRP:CE2	8:F:219:LYS:HD2	2.55	0.40
11:L:52:ASP:OD1	11:L:52:ASP:N	2.53	0.40
31:q:489:ILE:HG13	31:q:546:PHE:CZ	2.56	0.40
32:r:224:ASN:OD1	32:r:226:SER:N	2.52	0.40
34:u:53:LYS:HD2	34:u:53:LYS:HA	1.91	0.40
39:I:565:ALA:HB1	39:I:594:LEU:HD21	2.03	0.40
42:R:10:LEU:HD22	42:R:38:ARG:HG2	2.03	0.40
50:p:332:LEU:HD22	50:p:346:CYS:HB2	2.03	0.40
53:D:73:ILE:HB	53:D:74:PRO:HD3	2.03	0.40
53:D:452:GLN:HG2	53:D:487:ILE:HD11	2.02	0.40
54:o:92:ILE:HD13	54:o:173:ILE:HG23	2.03	0.40
55:w:637:TYR:OH	55:w:642:GLU:OE1	2.26	0.40
1:1:1452:A:N6	1:1:1507:G:O2'	2.51	0.40
1:1:2442:G:N2	1:1:2505:U:O2	2.34	0.40
4:A:225:LEU:HG	4:A:235:LYS:HG2	2.02	0.40
6:C:14:GLU:H	6:C:14:GLU:HG2	1.72	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:118:LEU:HD23	9:H:118:LEU:HA	1.87	0.40
11:L:60:ALA:HA	11:L:61:PRO:HD3	1.93	0.40
22:b:519:MET:CG	22:b:524:LEU:HD11	2.52	0.40
41:V:84:SER:HA	41:V:94:TYR:HB3	2.02	0.40
47:g:15:THR:HG22	47:g:16:ARG:N	2.37	0.40
49:n:371:VAL:HG11	49:n:411:ILE:HG22	2.03	0.40
50:p:226:SER:OG	50:p:227:TYR:N	2.54	0.40
51:t:78:VAL:O	51:t:82:GLU:HG2	2.21	0.40
53:D:303:LYS:O	53:D:307:GLU:HG3	2.22	0.40
53:D:395:THR:OG1	53:D:398:GLU:HG2	2.21	0.40
56:a:60:ARG:HD2	56:a:63:MET:SD	2.61	0.40
57:x:412:ARG:O	57:x:416:LEU:HG	2.20	0.40
1:1:19:U:H2'	1:1:20:A:C8	2.57	0.40
1:1:129:U:H2'	1:1:130:A:H8	1.87	0.40
1:1:412:G:H2'	1:1:413:U:C6	2.56	0.40
1:1:452:G:N2	1:1:454:C:H5'	2.36	0.40
1:1:643:U:H2'	1:1:644:G:H3'	2.03	0.40
1:1:2451:G:C2	1:1:2496:C:O2	2.73	0.40
1:1:3089:C:H2'	1:1:3090:U:O4'	2.20	0.40
1:1:3293:U:H5''	5:B:128:LYS:NZ	2.37	0.40
3:7:21:PHE:HE1	55:w:712:PRO:HB3	1.86	0.40
8:F:40:LYS:NZ	8:F:170:GLU:OE2	2.55	0.40
11:L:123:ILE:HD12	11:L:123:ILE:HA	1.93	0.40
22:b:195:GLN:O	22:b:197:TYR:N	2.51	0.40
30:m:602:TRP:CE3	30:m:609:PHE:HB3	2.56	0.40
31:q:349:ILE:HD12	31:q:417:ARG:HB2	2.04	0.40
39:I:260:ILE:HD13	39:I:272:ILE:HB	2.02	0.40
39:I:430:LEU:HD13	39:I:474:LEU:HB3	2.03	0.40
40:K:66:LEU:HG	53:D:415:TYR:HB3	2.02	0.40
46:c:42:ILE:HD11	46:c:67:VAL:HG22	2.03	0.40
53:D:190:LEU:CD2	53:D:217:LEU:HD23	2.52	0.40
55:w:312:LYS:HE3	55:w:312:LYS:HB2	1.95	0.40
56:a:12:HIS:ND1	56:a:214:PHE:HB3	2.36	0.40
56:a:45:ARG:HG3	56:a:46:ASP:H	1.86	0.40
57:x:429:TYR:HE2	57:x:465:PRO:HD2	1.87	0.40
1:1:1334:U:H5''	8:F:206:LYS:HB3	2.02	0.40
4:A:109:THR:OG1	4:A:230:SER:HA	2.22	0.40
4:A:171:PRO:HG3	30:m:174:ASP:O	2.21	0.40
5:B:298:PHE:CG	5:B:357:LYS:HG3	2.57	0.40
6:C:294:GLU:HG2	16:Q:129:VAL:O	2.21	0.40
7:E:77:ARG:NH1	7:E:78:ARG:O	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:P:30:ARG:HA	15:P:119:VAL:HG11	2.03	0.40
29:l:74:THR:HG22	29:l:75:LYS:H	1.85	0.40
36:y:101:LEU:HD13	36:y:107:VAL:HG11	2.04	0.40
36:y:185:THR:OG1	36:y:214:GLU:OE2	2.29	0.40
38:8:483:ILE:HG23	38:8:495:ARG:HG3	2.04	0.40
38:8:519:LEU:HD23	38:8:519:LEU:H	1.85	0.40
38:8:551:GLN:O	38:8:551:GLN:NE2	2.54	0.40
39:l:195:ARG:HH12	55:w:492:GLY:HA3	1.87	0.40
49:n:17:THR:HA	49:n:61:THR:O	2.21	0.40
50:p:165:ARG:N	50:p:165:ARG:HD3	2.37	0.40
50:p:349:SER:HB2	50:p:377:PHE:CE1	2.56	0.40
56:a:53:LEU:O	56:a:155:ILE:N	2.55	0.40
57:x:26:GLY:C	57:x:28:GLU:H	2.29	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	7	125/204 (61%)	120 (96%)	5 (4%)	0	100	100
4	A	264/291 (91%)	249 (94%)	15 (6%)	0	100	100
5	B	331/387 (86%)	321 (97%)	10 (3%)	0	100	100
6	C	357/362 (99%)	346 (97%)	11 (3%)	0	100	100
7	E	160/175 (91%)	149 (93%)	11 (7%)	0	100	100
8	F	220/244 (90%)	216 (98%)	4 (2%)	0	100	100
9	H	188/191 (98%)	177 (94%)	11 (6%)	0	100	100
10	J	143/427 (34%)	138 (96%)	5 (4%)	0	100	100
11	L	119/199 (60%)	115 (97%)	4 (3%)	0	100	100
12	M	134/138 (97%)	126 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	N	185/204 (91%)	181 (98%)	4 (2%)	0	100	100
14	O	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
15	P	181/184 (98%)	173 (96%)	8 (4%)	0	100	100
16	Q	132/186 (71%)	132 (100%)	0	0	100	100
17	S	168/172 (98%)	162 (96%)	6 (4%)	0	100	100
18	T	50/160 (31%)	48 (96%)	2 (4%)	0	100	100
19	W	230/236 (98%)	220 (96%)	10 (4%)	0	100	100
20	X	135/142 (95%)	128 (95%)	7 (5%)	0	100	100
21	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
22	b	494/647 (76%)	474 (96%)	20 (4%)	0	100	100
23	d	105/113 (93%)	101 (96%)	4 (4%)	0	100	100
24	e	123/130 (95%)	121 (98%)	2 (2%)	0	100	100
25	f	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
26	h	117/120 (98%)	114 (97%)	3 (3%)	0	100	100
27	i	75/100 (75%)	68 (91%)	7 (9%)	0	100	100
28	j	71/88 (81%)	69 (97%)	2 (3%)	0	100	100
29	l	174/181 (96%)	160 (92%)	14 (8%)	0	100	100
30	m	658/807 (82%)	633 (96%)	24 (4%)	1 (0%)	43	73
31	q	356/618 (58%)	323 (91%)	33 (9%)	0	100	100
32	r	170/261 (65%)	166 (98%)	4 (2%)	0	100	100
33	s	34/520 (6%)	34 (100%)	0	0	100	100
34	u	138/199 (69%)	135 (98%)	3 (2%)	0	100	100
35	v	124/231 (54%)	122 (98%)	2 (2%)	0	100	100
36	y	223/245 (91%)	214 (96%)	9 (4%)	0	100	100
37	z	53/106 (50%)	53 (100%)	0	0	100	100
38	8	456/710 (64%)	431 (94%)	25 (6%)	0	100	100
39	I	531/663 (80%)	509 (96%)	22 (4%)	0	100	100
40	K	278/376 (74%)	266 (96%)	12 (4%)	0	100	100
41	V	132/137 (96%)	129 (98%)	3 (2%)	0	100	100
42	R	130/189 (69%)	129 (99%)	1 (1%)	0	100	100
43	G	194/256 (76%)	191 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	Z	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
45	U	100/121 (83%)	92 (92%)	8 (8%)	0	100	100
46	c	95/105 (90%)	95 (100%)	0	0	100	100
47	g	110/121 (91%)	107 (97%)	3 (3%)	0	100	100
48	k	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
49	n	417/605 (69%)	402 (96%)	15 (4%)	0	100	100
50	p	331/460 (72%)	305 (92%)	26 (8%)	0	100	100
51	t	279/322 (87%)	272 (98%)	7 (2%)	0	100	100
53	D	426/505 (84%)	415 (97%)	11 (3%)	0	100	100
54	o	131/220 (60%)	126 (96%)	5 (4%)	0	100	100
55	w	406/841 (48%)	390 (96%)	16 (4%)	0	100	100
56	a	212/217 (98%)	195 (92%)	14 (7%)	3 (1%)	9	33
57	x	531/606 (88%)	509 (96%)	21 (4%)	1 (0%)	43	73
All	All	11427/15369 (74%)	10966 (96%)	456 (4%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	m	710	ASP
56	a	209	SER
57	x	406	ASN
56	a	63	MET
56	a	65	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	7	114/181 (63%)	114 (100%)	0	100	100
4	A	242/263 (92%)	241 (100%)	1 (0%)	84	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	281/323 (87%)	281 (100%)	0	100	100
6	C	286/289 (99%)	286 (100%)	0	100	100
7	E	142/152 (93%)	142 (100%)	0	100	100
8	F	186/205 (91%)	186 (100%)	0	100	100
9	H	170/171 (99%)	170 (100%)	0	100	100
10	J	133/383 (35%)	133 (100%)	0	100	100
11	L	100/159 (63%)	100 (100%)	0	100	100
12	M	107/109 (98%)	107 (100%)	0	100	100
13	N	165/176 (94%)	165 (100%)	0	100	100
14	O	160/162 (99%)	160 (100%)	0	100	100
15	P	145/146 (99%)	145 (100%)	0	100	100
16	Q	110/151 (73%)	110 (100%)	0	100	100
17	S	155/156 (99%)	154 (99%)	1 (1%)	78	85
18	T	41/137 (30%)	41 (100%)	0	100	100
19	W	209/213 (98%)	209 (100%)	0	100	100
20	X	114/118 (97%)	114 (100%)	0	100	100
21	Y	109/110 (99%)	109 (100%)	0	100	100
22	b	447/573 (78%)	447 (100%)	0	100	100
23	d	94/97 (97%)	94 (100%)	0	100	100
24	e	108/111 (97%)	108 (100%)	0	100	100
25	f	90/91 (99%)	90 (100%)	0	100	100
26	h	104/105 (99%)	104 (100%)	0	100	100
27	i	65/82 (79%)	65 (100%)	0	100	100
28	j	60/71 (84%)	60 (100%)	0	100	100
29	l	151/156 (97%)	151 (100%)	0	100	100
30	m	599/722 (83%)	599 (100%)	0	100	100
31	q	304/535 (57%)	303 (100%)	1 (0%)	86	88
32	r	156/229 (68%)	156 (100%)	0	100	100
33	s	32/445 (7%)	32 (100%)	0	100	100
34	u	125/180 (69%)	125 (100%)	0	100	100
35	v	116/205 (57%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	y	193/211 (92%)	193 (100%)	0	100	100
37	z	48/95 (50%)	48 (100%)	0	100	100
38	8	351/647 (54%)	351 (100%)	0	100	100
39	I	484/602 (80%)	484 (100%)	0	100	100
40	K	261/346 (75%)	261 (100%)	0	100	100
41	V	103/105 (98%)	103 (100%)	0	100	100
42	R	112/154 (73%)	111 (99%)	1 (1%)	70	82
43	G	161/208 (77%)	161 (100%)	0	100	100
44	Z	115/116 (99%)	115 (100%)	0	100	100
45	U	89/107 (83%)	89 (100%)	0	100	100
46	c	81/88 (92%)	81 (100%)	0	100	100
47	g	95/103 (92%)	95 (100%)	0	100	100
48	k	68/69 (99%)	68 (100%)	0	100	100
49	n	381/548 (70%)	381 (100%)	0	100	100
50	p	300/413 (73%)	300 (100%)	0	100	100
51	t	256/287 (89%)	256 (100%)	0	100	100
53	D	378/440 (86%)	378 (100%)	0	100	100
54	o	118/199 (59%)	118 (100%)	0	100	100
55	w	371/745 (50%)	371 (100%)	0	100	100
56	a	195/198 (98%)	195 (100%)	0	100	100
57	x	489/548 (89%)	481 (98%)	8 (2%)	55	76
All	All	10069/13435 (75%)	10057 (100%)	12 (0%)	87	91

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	84	ASN
17	S	8	GLN
31	q	345	GLU
42	R	136	ARG
57	x	28	GLU
57	x	47	VAL
57	x	291	VAL
57	x	292	ASN
57	x	400	VAL

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Mol	Chain	Res	Type
57	x	435	TYR
57	x	500	TYR
57	x	538	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (98) such sidechains are listed below:

Mol	Chain	Res	Type
3	7	32	ASN
4	A	95	GLN
4	A	118	HIS
4	A	141	GLN
4	A	195	HIS
4	A	239	ASN
4	A	255	GLN
5	B	121	ASN
5	B	198	HIS
5	B	345	ASN
6	C	322	GLN
7	E	126	GLN
8	F	93	ASN
8	F	231	ASN
9	H	96	HIS
9	H	125	ASN
9	H	157	ASN
10	J	215	HIS
10	J	327	GLN
11	L	102	GLN
11	L	120	GLN
12	M	41	GLN
12	M	56	GLN
13	N	11	GLN
13	N	156	HIS
14	O	31	GLN
15	P	97	ASN
17	S	74	ASN
22	b	195	GLN
22	b	208	HIS
22	b	333	ASN
23	d	57	GLN
24	e	49	ASN
24	e	104	ASN
25	f	5	HIS

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Mol	Chain	Res	Type
25	f	87	ASN
27	i	92	ASN
28	j	57	HIS
29	l	102	ASN
30	m	191	GLN
30	m	209	ASN
30	m	232	GLN
30	m	318	ASN
30	m	483	ASN
31	q	287	GLN
31	q	297	GLN
31	q	313	GLN
32	r	10	HIS
34	u	7	HIS
34	u	17	HIS
34	u	24	ASN
34	u	101	GLN
34	u	115	ASN
35	v	25	GLN
35	v	31	GLN
35	v	33	ASN
35	v	39	ASN
35	v	210	GLN
36	y	9	ASN
36	y	170	GLN
38	8	383	GLN
38	8	462	ASN
38	8	470	GLN
38	8	555	ASN
39	I	172	ASN
39	I	218	GLN
39	I	530	ASN
40	K	143	GLN
40	K	214	ASN
40	K	225	ASN
40	K	247	HIS
40	K	295	GLN
43	G	221	ASN
44	Z	122	HIS
45	U	87	ASN
45	U	101	ASN
49	n	11	ASN

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Mol	Chain	Res	Type
49	n	189	GLN
49	n	428	GLN
49	n	445	ASN
50	p	135	ASN
50	p	292	GLN
50	p	337	GLN
53	D	287	ASN
53	D	323	GLN
53	D	325	GLN
54	o	100	HIS
54	o	154	ASN
55	w	420	ASN
55	w	467	ASN
55	w	645	GLN
56	a	96	ASN
56	a	182	GLN
56	a	200	ASN
57	x	98	GLN
57	x	356	HIS
57	x	375	ASN
57	x	486	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2551/3396 (75%)	504 (19%)	21 (0%)
2	2	157/158 (99%)	26 (16%)	0
52	6	85/87 (97%)	27 (31%)	3 (3%)
All	All	2793/3641 (76%)	557 (19%)	24 (0%)

All (557) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	7	C
1	1	14	U
1	1	16	A
1	1	39	A
1	1	40	A
1	1	41	G
1	1	42	C
1	1	43	A

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Mol	Chain	Res	Type
1	1	49	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A
1	1	72	C
1	1	73	C
1	1	92	G
1	1	105	C
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	118	U
1	1	122	A
1	1	135	C
1	1	136	G
1	1	143	G
1	1	148	G
1	1	165	A
1	1	166	C
1	1	170	G
1	1	190	U
1	1	191	U
1	1	192	C
1	1	200	C
1	1	206	G
1	1	210	U
1	1	211	A
1	1	213	A
1	1	218	G
1	1	219	A
1	1	220	G
1	1	240	U
1	1	252	U
1	1	255	A
1	1	265	A
1	1	266	A
1	1	268	A
1	1	269	G
1	1	284	A

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Mol	Chain	Res	Type
1	1	295	A
1	1	298	U
1	1	299	G
1	1	311	C
1	1	323	A
1	1	329	U
1	1	339	C
1	1	352	A
1	1	368	G
1	1	370	U
1	1	376	G
1	1	398	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	421	G
1	1	422	A
1	1	439	C
1	1	440	A
1	1	447	U
1	1	451	U
1	1	454	C
1	1	463	C
1	1	464	U
1	1	466	G
1	1	468	G
1	1	469	G
1	1	472	A
1	1	478	A
1	1	479	U
1	1	480	C
1	1	481	U
1	1	482	C
1	1	483	G
1	1	485	A
1	1	486	U
1	1	487	U
1	1	488	U
1	1	521	A
1	1	533	A
1	1	535	G
1	1	541	U

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Mol	Chain	Res	Type
1	1	543	C
1	1	547	G
1	1	548	G
1	1	552	G
1	1	557	A
1	1	559	A
1	1	560	G
1	1	578	A
1	1	579	G
1	1	589	A
1	1	591	G
1	1	604	G
1	1	611	A
1	1	620	U
1	1	621	A
1	1	622	A
1	1	636	C
1	1	637	C
1	1	642	U
1	1	643	U
1	1	644	G
1	1	645	A
1	1	660	A
1	1	677	A
1	1	681	U
1	1	691	A
1	1	694	C
1	1	705	A
1	1	712	G
1	1	719	U
1	1	721	G
1	1	722	G
1	1	734	C
1	1	735	A
1	1	742	G
1	1	757	C
1	1	758	C
1	1	760	G
1	1	761	A
1	1	770	G
1	1	771	A
1	1	774	G

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Mol	Chain	Res	Type
1	1	776	U
1	1	779	G
1	1	780	A
1	1	781	G
1	1	785	G
1	1	800	G
1	1	808	A
1	1	818	C
1	1	822	G
1	1	830	A
1	1	842	G
1	1	848	A
1	1	860	G
1	1	861	C
1	1	871	G
1	1	872	G
1	1	887	G
1	1	894	G
1	1	895	A
1	1	896	A
1	1	906	A
1	1	907	G
1	1	908	G
1	1	909	G
1	1	917	A
1	1	936	A
1	1	944	C
1	1	959	C
1	1	960	U
1	1	961	C
1	1	962	A
1	1	963	G
1	1	964	G
1	1	966	U
1	1	978	G
1	1	979	U
1	1	980	A
1	1	982	C
1	1	985	U
1	1	991	G
1	1	1098	A
1	1	1103	A

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Mol	Chain	Res	Type
1	1	1104	G
1	1	1105	A
1	1	1116	G
1	1	1117	G
1	1	1129	A
1	1	1132	C
1	1	1143	A
1	1	1145	G
1	1	1153	A
1	1	1159	A
1	1	1160	C
1	1	1174	G
1	1	1180	A
1	1	1181	U
1	1	1191	U
1	1	1192	C
1	1	1193	A
1	1	1197	A
1	1	1198	C
1	1	1199	C
1	1	1200	A
1	1	1204	A
1	1	1217	A
1	1	1222	G
1	1	1228	C
1	1	1235	U
1	1	1239	C
1	1	1241	U
1	1	1242	G
1	1	1245	A
1	1	1251	A
1	1	1252	A
1	1	1259	A
1	1	1262	G
1	1	1263	A
1	1	1272	C
1	1	1280	C
1	1	1284	C
1	1	1286	A
1	1	1287	A
1	1	1303	A
1	1	1304	A

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Mol	Chain	Res	Type
1	1	1305	U
1	1	1307	G
1	1	1308	A
1	1	1330	A
1	1	1332	A
1	1	1348	U
1	1	1349	G
1	1	1350	A
1	1	1351	U
1	1	1352	A
1	1	1353	U
1	1	1354	G
1	1	1356	U
1	1	1357	G
1	1	1386	A
1	1	1392	G
1	1	1399	A
1	1	1400	G
1	1	1418	A
1	1	1419	A
1	1	1421	G
1	1	1431	G
1	1	1434	G
1	1	1437	C
1	1	1452	A
1	1	1454	A
1	1	1455	U
1	1	1469	C
1	1	1481	A
1	1	1483	G
1	1	1484	U
1	1	1485	G
1	1	1496	C
1	1	1552	G
1	1	1555	U
1	1	1556	C
1	1	1560	G
1	1	1567	U
1	1	1568	U
1	1	1569	U
1	1	1571	A
1	1	1580	A

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Mol	Chain	Res	Type
1	1	1581	C
1	1	1582	C
1	1	1587	A
1	1	1589	A
1	1	1593	A
1	1	1604	G
1	1	1605	A
1	1	1627	U
1	1	1628	C
1	1	1629	U
1	1	1630	U
1	1	1639	C
1	1	1643	A
1	1	1688	U
1	1	1694	U
1	1	1724	U
1	1	1725	C
1	1	1728	G
1	1	1741	A
1	1	1750	A
1	1	1751	G
1	1	1761	C
1	1	1762	C
1	1	1763	U
1	1	1764	U
1	1	1766	G
1	1	1767	C
1	1	1773	C
1	1	1780	G
1	1	1795	U
1	1	1797	A
1	1	1808	G
1	1	1815	U
1	1	1816	A
1	1	1817	G
1	1	1821	U
1	1	1858	A
1	1	1864	A
1	1	1865	A
1	1	1866	C
1	1	1867	A
1	1	1868	G

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Mol	Chain	Res	Type
1	1	1876	U
1	1	1878	G
1	1	1918	C
1	1	1921	A
1	1	1922	A
1	1	1923	C
1	1	1927	G
1	1	1929	G
1	1	1930	A
1	1	1932	A
1	1	1935	G
1	1	1939	G
1	1	1940	G
1	1	1954	G
1	1	1955	U
1	1	1965	C
1	1	1971	C
1	1	2057	G
1	1	2087	C
1	1	2088	A
1	1	2091	U
1	1	2092	A
1	1	2094	C
1	1	2102	U
1	1	2103	U
1	1	2104	A
1	1	2105	G
1	1	2110	G
1	1	2111	G
1	1	2113	A
1	1	2114	C
1	1	2118	C
1	1	2119	A
1	1	2120	A
1	1	2370	G
1	1	2371	G
1	1	2373	A
1	1	2374	C
1	1	2376	G
1	1	2385	G
1	1	2393	G
1	1	2394	G

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Mol	Chain	Res	Type
1	1	2395	G
1	1	2416	U
1	1	2418	G
1	1	2419	A
1	1	2420	C
1	1	2421	U
1	1	2423	U
1	1	2424	A
1	1	2430	A
1	1	2433	U
1	1	2434	U
1	1	2435	G
1	1	2437	G
1	1	2438	A
1	1	2440	G
1	1	2446	U
1	1	2448	G
1	1	2453	U
1	1	2454	G
1	1	2460	U
1	1	2461	A
1	1	2462	A
1	1	2463	G
1	1	2468	A
1	1	2469	G
1	1	2472	U
1	1	2473	C
1	1	2474	G
1	1	2475	G
1	1	2484	A
1	1	2487	U
1	1	2488	A
1	1	2494	A
1	1	2495	C
1	1	2497	U
1	1	2501	U
1	1	2503	G
1	1	2504	U
1	1	2505	U
1	1	2596	U
1	1	2598	G
1	1	2599	U

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Mol	Chain	Res	Type
1	1	2601	A
1	1	2602	G
1	1	2603	G
1	1	2606	G
1	1	2611	U
1	1	2803	A
1	1	2809	C
1	1	2818	U
1	1	2821	C
1	1	2822	U
1	1	2824	G
1	1	2837	A
1	1	2839	G
1	1	2844	C
1	1	2845	A
1	1	2847	A
1	1	2887	A
1	1	2898	G
1	1	2899	C
1	1	2916	U
1	1	2917	G
1	1	2918	G
1	1	2919	A
1	1	2935	U
1	1	2936	A
1	1	2941	A
1	1	2942	C
1	1	2943	G
1	1	2968	G
1	1	2971	A
1	1	2972	G
1	1	2976	A
1	1	2977	G
1	1	2979	U
1	1	2980	U
1	1	2981	U
1	1	2982	A
1	1	2983	C
1	1	2984	C
1	1	2990	G
1	1	2996	U
1	1	2997	G

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Mol	Chain	Res	Type
1	1	3012	A
1	1	3022	G
1	1	3023	U
1	1	3026	G
1	1	3032	A
1	1	3049	A
1	1	3057	U
1	1	3058	U
1	1	3059	G
1	1	3078	U
1	1	3079	U
1	1	3092	C
1	1	3100	U
1	1	3102	G
1	1	3109	G
1	1	3122	A
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3153	U
1	1	3154	C
1	1	3155	U
1	1	3156	U
1	1	3157	U
1	1	3165	A
1	1	3167	A
1	1	3172	A
1	1	3173	G
1	1	3174	A
1	1	3176	G
1	1	3179	U
1	1	3180	A
1	1	3181	C
1	1	3187	A
1	1	3196	U
1	1	3207	U
1	1	3210	A
1	1	3217	C
1	1	3218	A
1	1	3219	G

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Mol	Chain	Res	Type
1	1	3227	A
1	1	3229	G
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3247	G
1	1	3259	U
1	1	3263	G
1	1	3270	U
1	1	3276	G
1	1	3278	C
1	1	3279	A
1	1	3289	G
1	1	3290	G
1	1	3294	A
1	1	3295	A
1	1	3304	U
1	1	3313	U
1	1	3316	A
1	1	3317	U
1	1	3319	U
1	1	3334	U
1	1	3341	U
1	1	3346	U
1	1	3347	A
1	1	3350	C
1	1	3358	U
1	1	3369	G
1	1	3375	A
1	1	3378	C
1	1	3382	U
1	1	3383	G
1	1	3386	G
1	1	3396	U
2	2	23	U
2	2	34	U
2	2	35	C
2	2	48	A
2	2	59	A
2	2	62	C
2	2	63	G
2	2	79	A

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Mol	Chain	Res	Type
2	2	81	U
2	2	82	U
2	2	84	C
2	2	85	G
2	2	86	U
2	2	87	G
2	2	90	U
2	2	95	G
2	2	104	A
2	2	105	A
2	2	106	C
2	2	107	G
2	2	111	A
2	2	113	U
2	2	116	G
2	2	124	G
2	2	125	U
2	2	148	G
52	6	4	U
52	6	5	C
52	6	7	C
52	6	14	U
52	6	15	C
52	6	16	U
52	6	23	U
52	6	24	A
52	6	30	U
52	6	33	U
52	6	34	A
52	6	40	U
52	6	41	G
52	6	43	A
52	6	52	G
52	6	54	A
52	6	56	U
52	6	57	U
52	6	59	C
52	6	66	U
52	6	218	A
52	6	219	A
52	6	220	C
52	6	223	U

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Mol	Chain	Res	Type
52	6	224	G
52	6	226	U
52	6	230	A

All (24) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	419	G
1	1	734	C
1	1	775	A
1	1	1105	A
1	1	1196	C
1	1	1241	U
1	1	1283	C
1	1	1302	A
1	1	1307	G
1	1	1329	U
1	1	1355	A
1	1	1497	C
1	1	1551	C
1	1	1954	G
1	1	2445	A
1	1	2496	C
1	1	2500	A
1	1	2508	U
1	1	2597	U
1	1	2600	C
1	1	2602	G
52	6	42	G
52	6	56	U
52	6	222	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 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
52	6	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	6	67:U	O3'	213:A	P	14.70

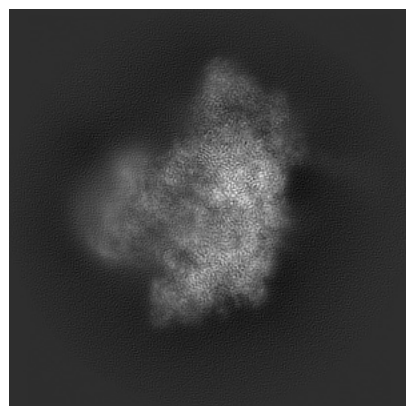
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24296. These allow visual inspection of the internal detail of the map and identification of artifacts.

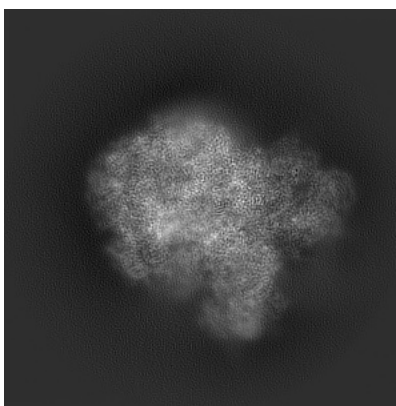
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

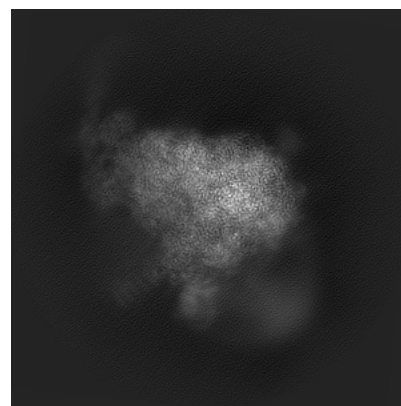
6.1.1 Primary map



X

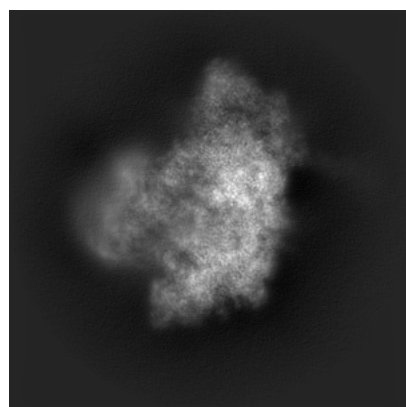


Y

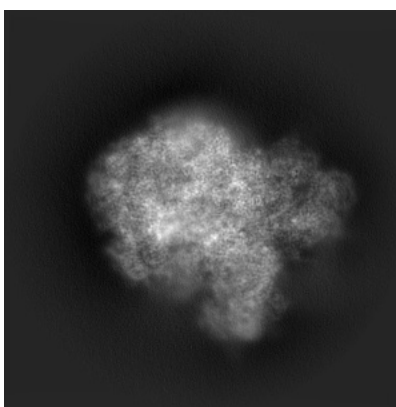


Z

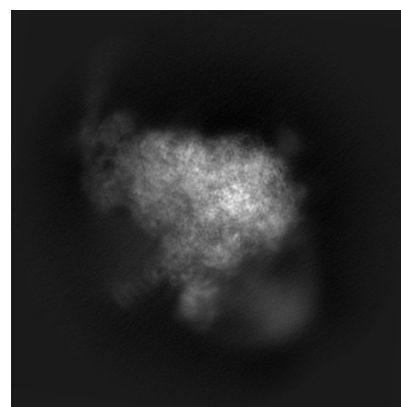
6.1.2 Raw map



X



Y

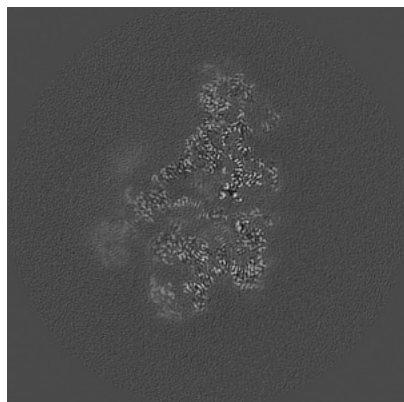


Z

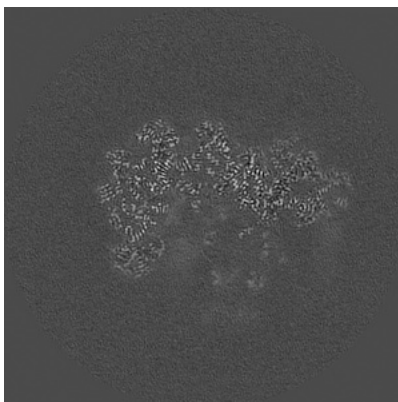
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

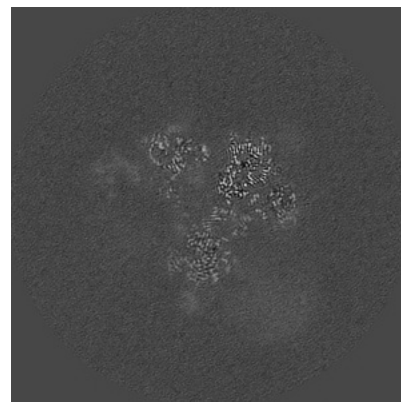
6.2.1 Primary map



X Index: 210

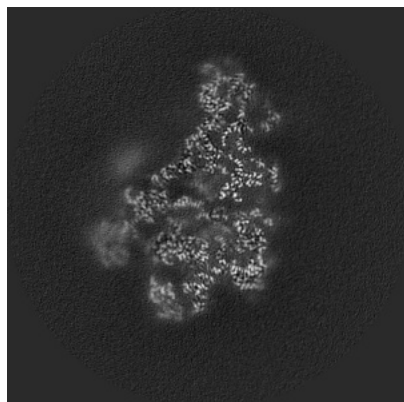


Y Index: 210

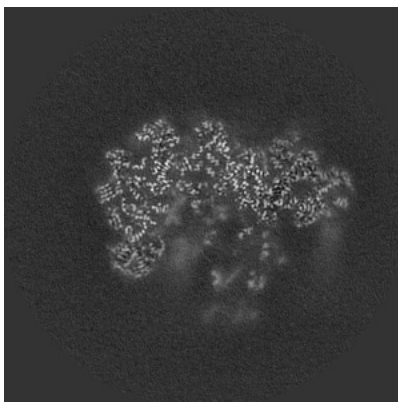


Z Index: 210

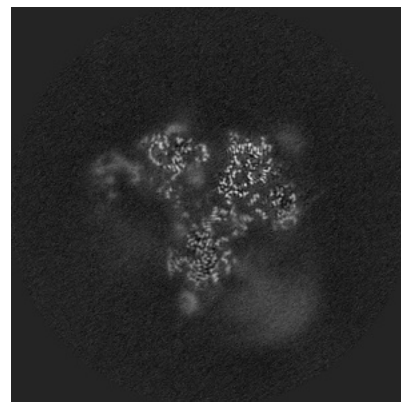
6.2.2 Raw map



X Index: 210



Y Index: 210

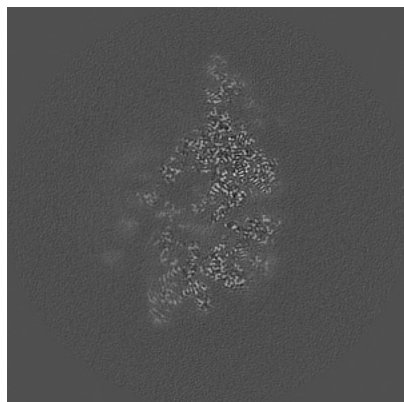


Z Index: 210

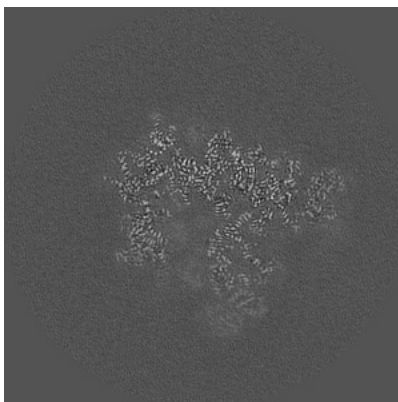
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

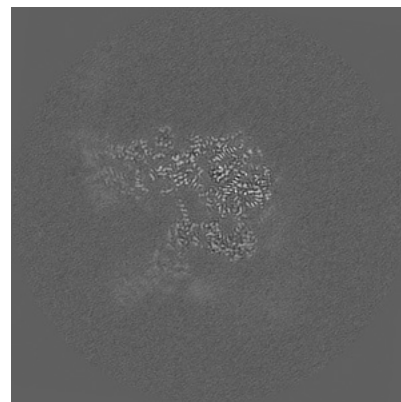
6.3.1 Primary map



X Index: 219

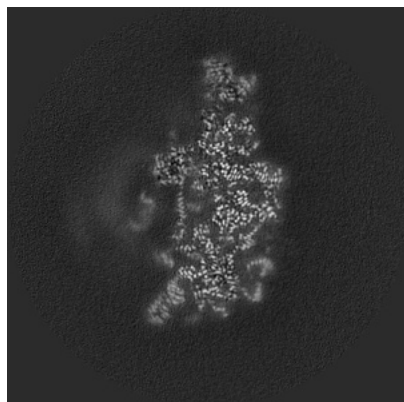


Y Index: 233

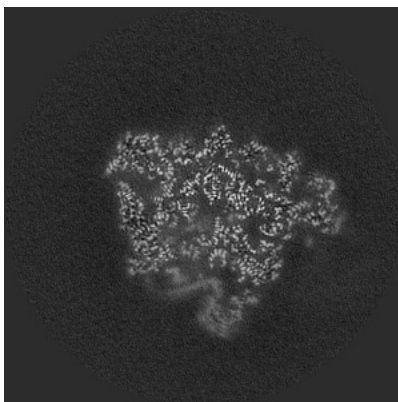


Z Index: 247

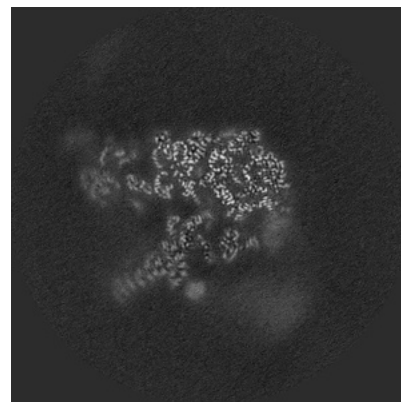
6.3.2 Raw map



X Index: 236



Y Index: 247

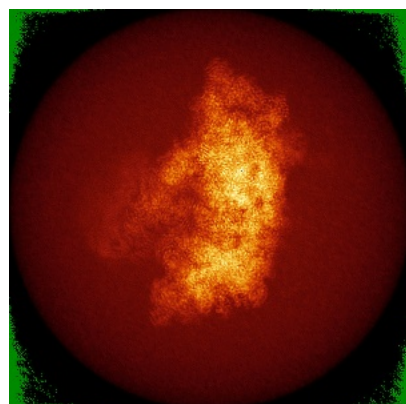


Z Index: 235

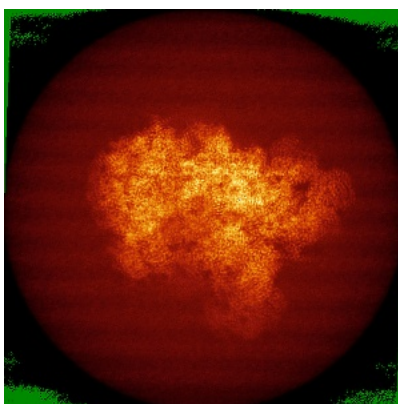
The images above show the largest variance slices of the map in three orthogonal directions.

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

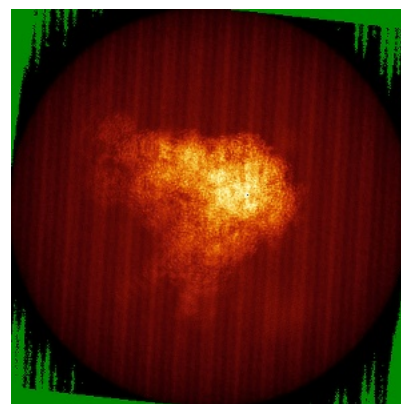
6.4.1 Primary map



X



Y

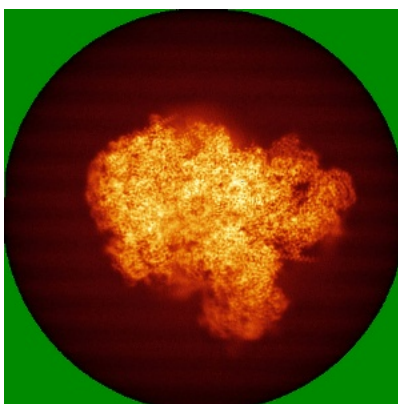


Z

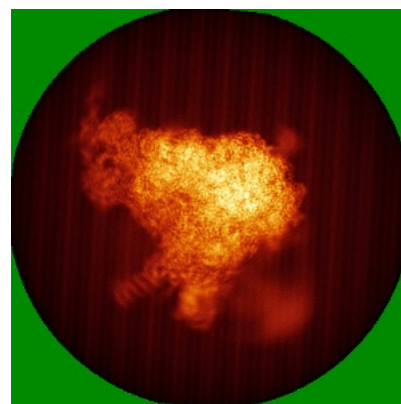
6.4.2 Raw map



X



Y

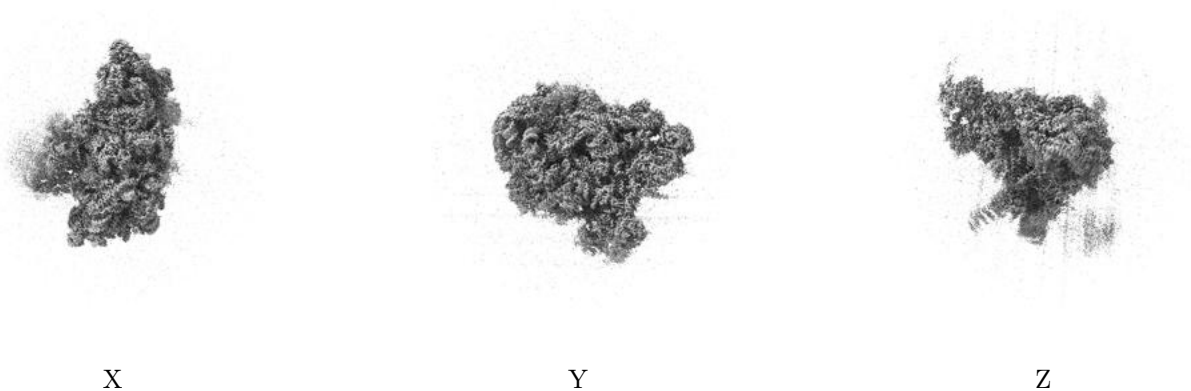


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

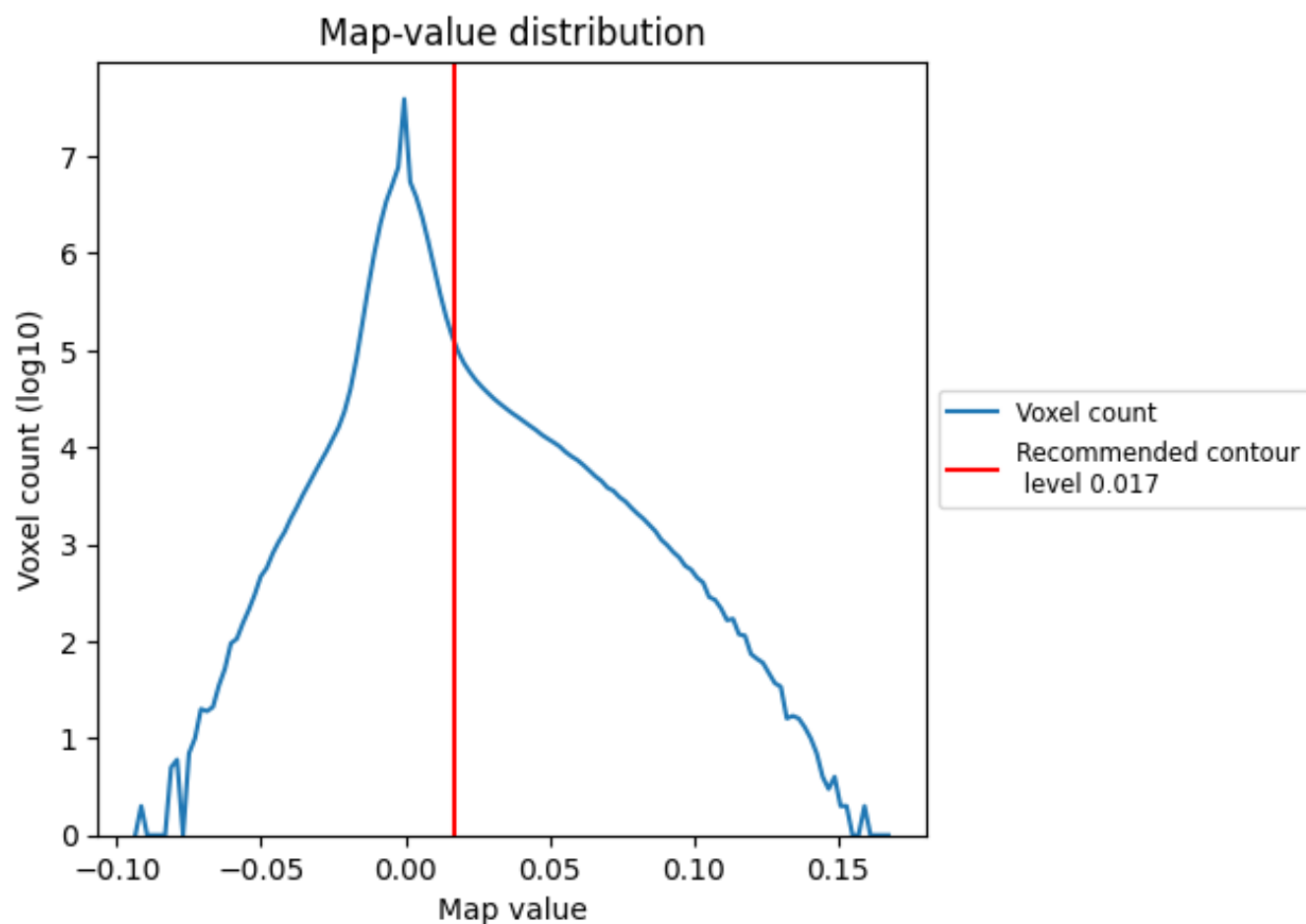
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

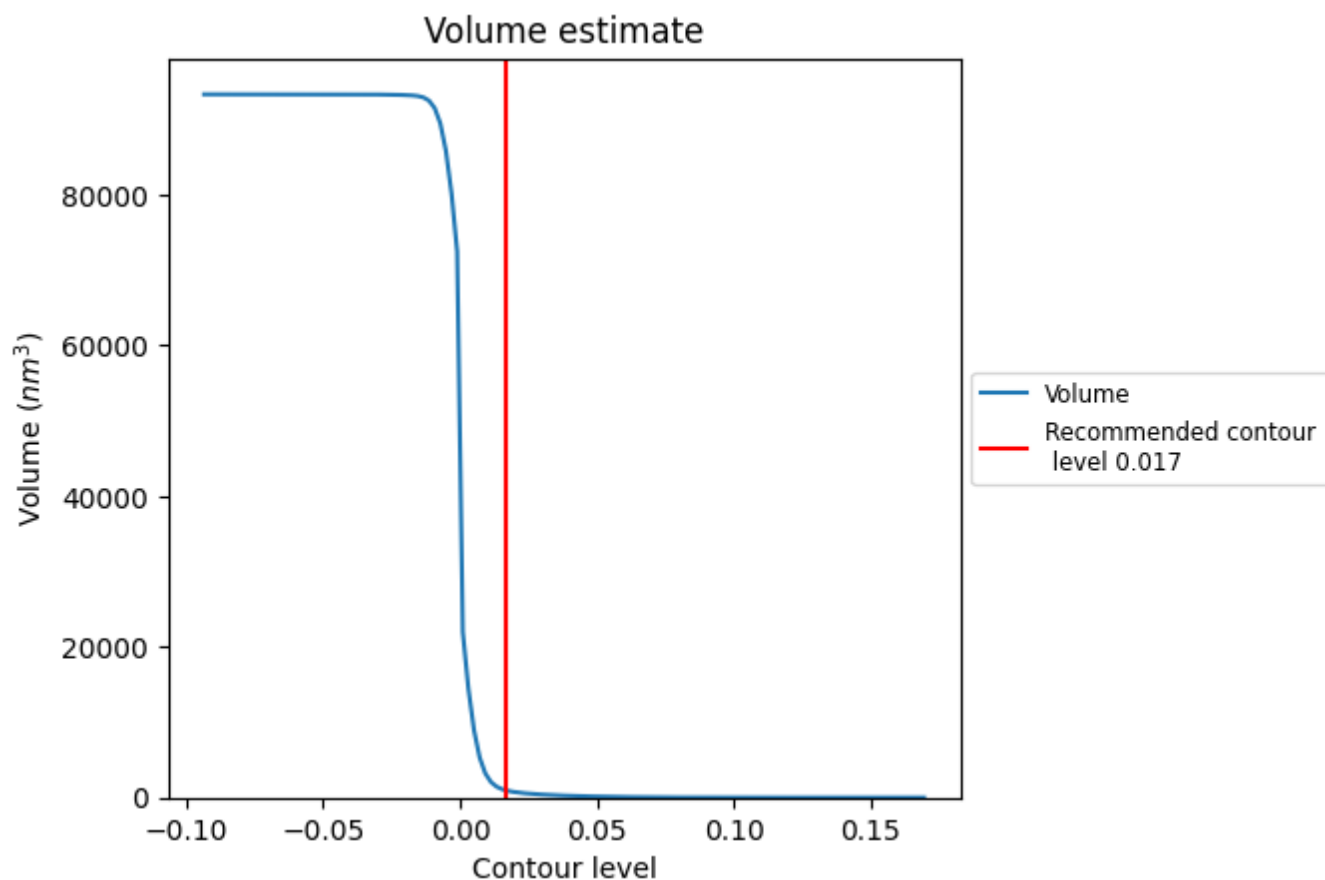
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

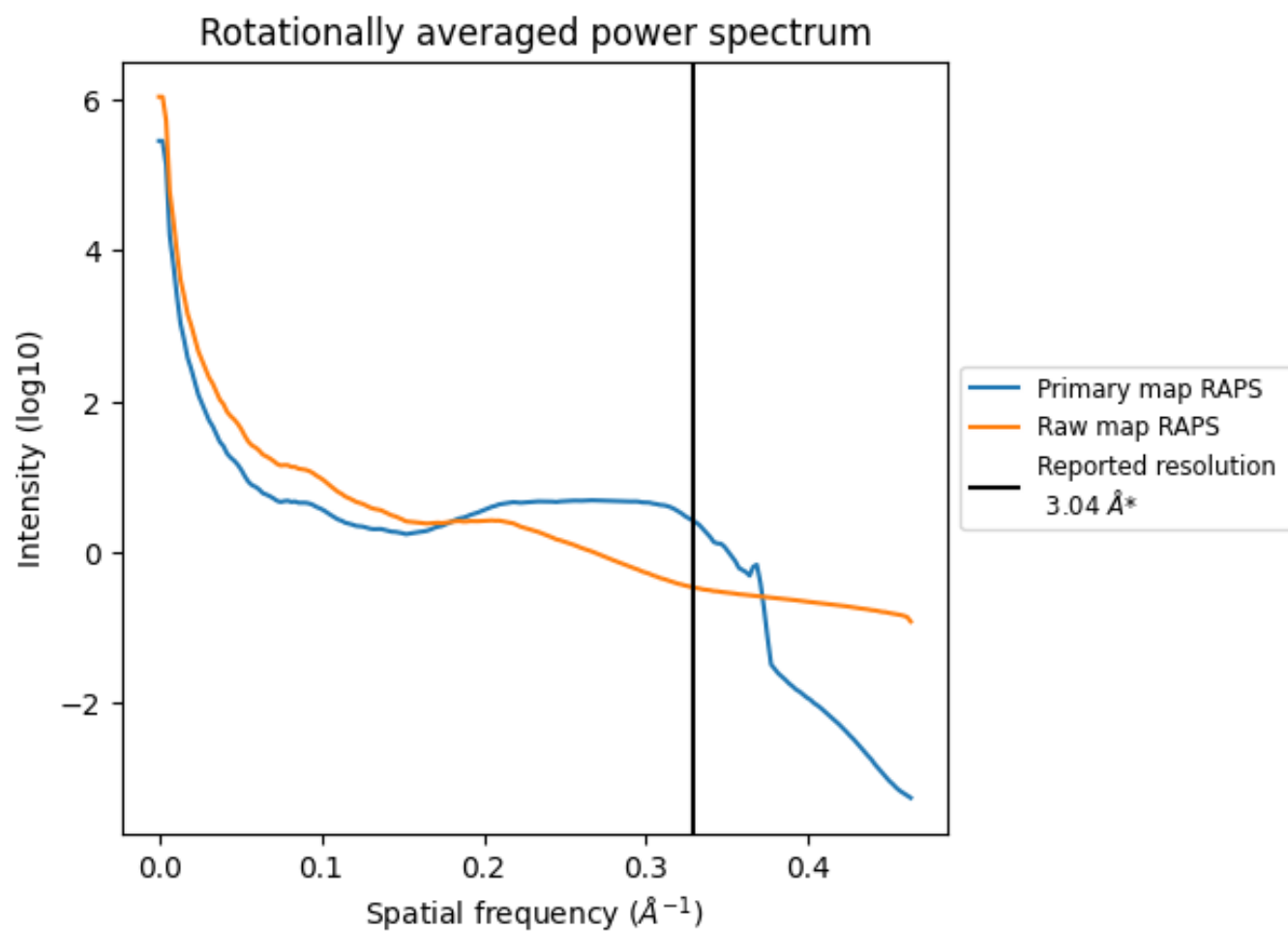
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 937 nm³; this corresponds to an approximate mass of 846 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 ⓘ

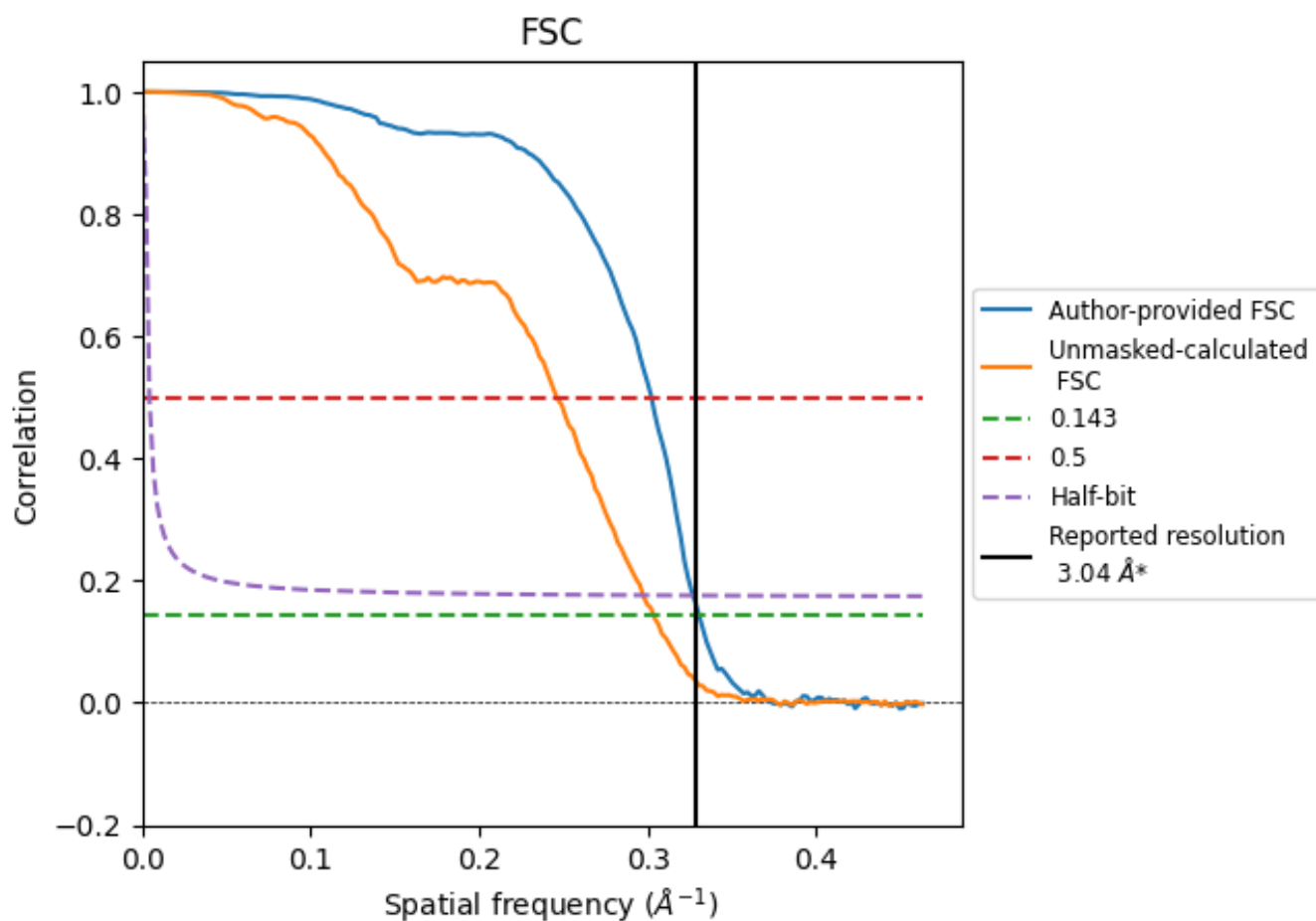


*Reported resolution corresponds to spatial frequency of $0.329 \text{ \AA}^{-1}$

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 0.329 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

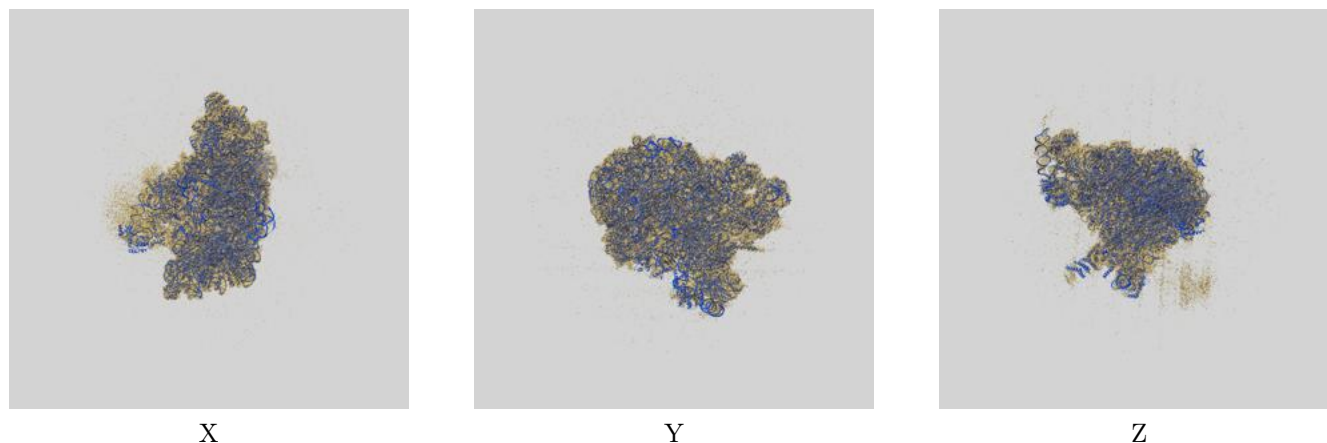
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.04	-	-
Author-provided FSC curve	3.02	3.31	3.06
Unmasked-calculated*	3.29	4.06	3.36

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

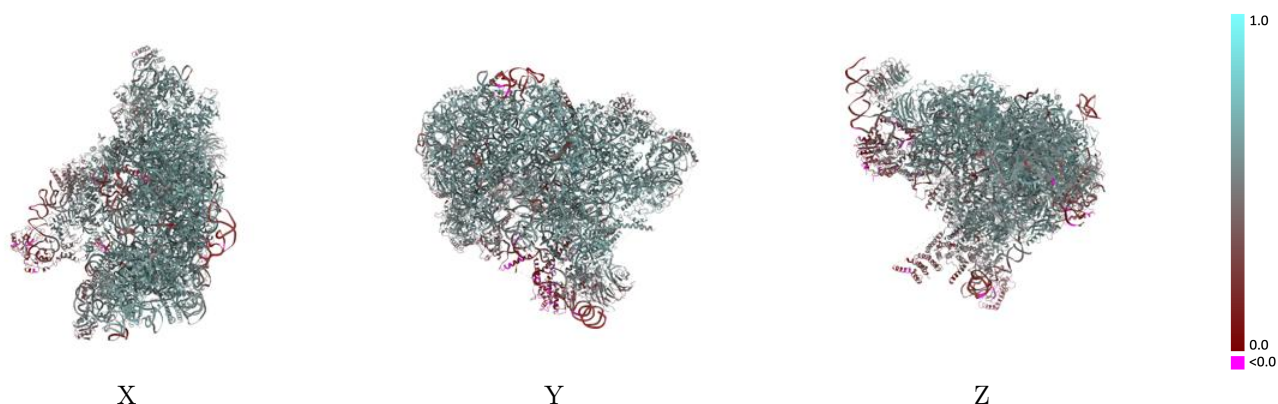
This section contains information regarding the fit between EMDB map EMD-24296 and PDB model 7R7A. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



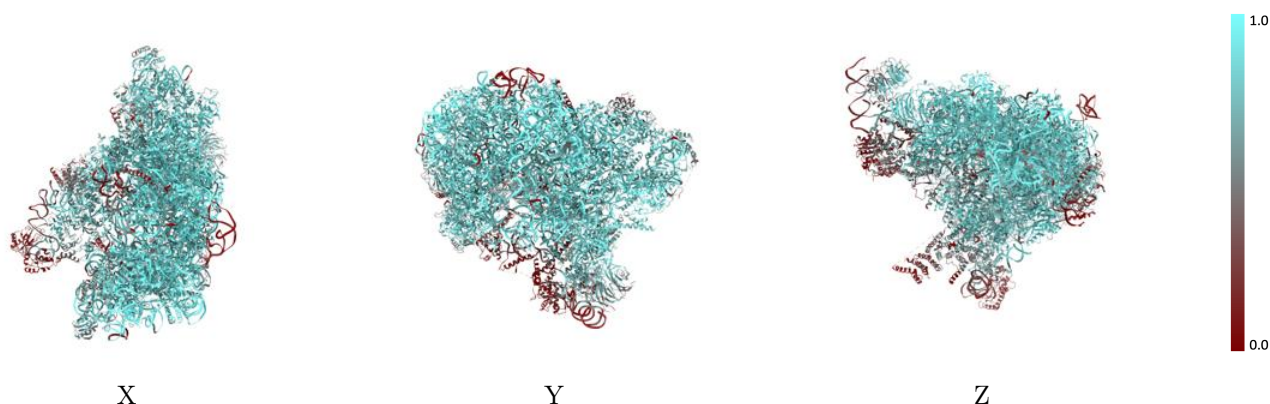
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



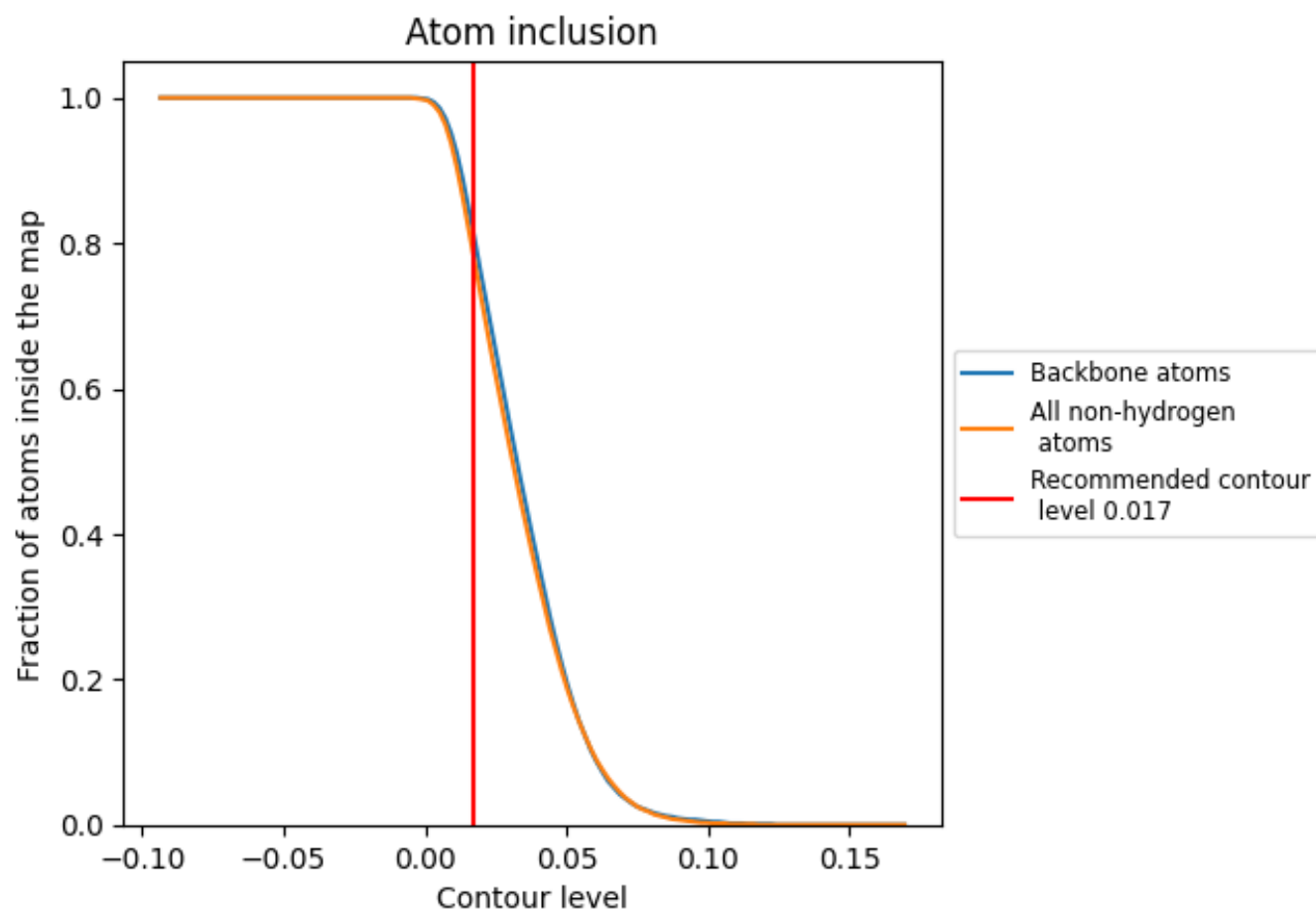
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.017).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7840	 0.5270
1	 0.8410	 0.5280
2	 0.9490	 0.5970
6	 0.8540	 0.5320
7	 0.7410	 0.5380
8	 0.4630	 0.4010
A	 0.7540	 0.5180
B	 0.9070	 0.5800
C	 0.9130	 0.6090
D	 0.6570	 0.5010
E	 0.8420	 0.5610
F	 0.8940	 0.5950
G	 0.8940	 0.5980
H	 0.8730	 0.5790
I	 0.7410	 0.5150
J	 0.7500	 0.5300
K	 0.7660	 0.5280
L	 0.9210	 0.6040
M	 0.9120	 0.6000
N	 0.9640	 0.6310
O	 0.9350	 0.6110
P	 0.8230	 0.5610
Q	 0.8660	 0.5820
R	 0.7540	 0.5340
S	 0.8500	 0.5750
T	 0.0570	 0.2370
U	 0.7290	 0.5110
V	 0.7190	 0.5190
W	 0.6300	 0.4540
X	 0.8980	 0.6020
Y	 0.9260	 0.6000
Z	 0.8610	 0.5920
a	 0.0980	 0.2300
b	 0.6770	 0.4900
c	 0.7770	 0.5480



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Chain	Atom inclusion	Q-score
d	 0.7820	 0.5440
e	 0.9400	 0.6160
f	 0.9720	 0.6300
g	 0.8930	 0.6010
h	 0.9230	 0.6070
i	 0.8560	 0.5630
j	 0.9550	 0.6340
k	 0.8130	 0.5620
l	 0.8220	 0.5640
m	 0.8540	 0.5820
n	 0.8880	 0.5950
o	 0.7780	 0.5270
p	 0.6230	 0.4630
q	 0.6830	 0.4860
r	 0.7870	 0.5570
s	 0.8790	 0.6070
t	 0.8500	 0.5830
u	 0.7780	 0.5280
v	 0.8940	 0.5890
w	 0.4960	 0.4480
x	 0.2630	 0.2640
y	 0.8130	 0.5240
z	 0.5550	 0.4810