Full wwPDB EM Validation Report

May 4, 2025 – 02:51 PM EDT

PDB ID	:	8ETJ / pdb_00008etj
EMDB ID	:	EMD-24396
Title	:	Fkbp39 associated 60S nascent ribosome State 2
Authors	:	Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on	:	2022-10-17
Resolution	:	3.20 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:

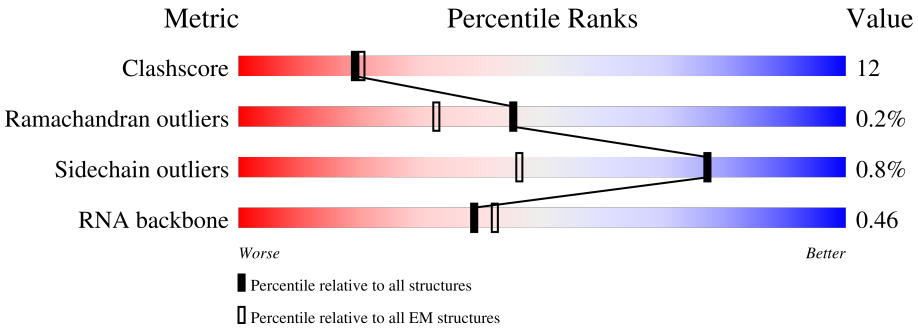
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	1	3497	27% 18% 7% 48%
2	2	165	55% 26% 6% 13%
3	3	302	28% 21% 20% 59%
4	B	388	59% 27% 14%
5	C	363	69% 20% 10%
6	E	195	13% 56% 28% 15%
7	F	250	64% 23% 13%

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Mol	Chain	Length	Quality of chain
8	G	259	15% 44% 20% 35%
9	H	190	8% 65% 30%
10	L	208	13% 61% 24% 13%
11	M	134	64% 29% 7%
12	N	201	54% 28% 17%
13	O	197	75% 25%
14	P	187	11% 59% 25% 17%
15	Q	187	56% 16% 29%
16	R	193	26% 29% 71%
17	S	176	13% 61% 34% 5%
18	V	139	9% 63% 35%
19	W	241	45% 85% 11%
20	Y	126	72% 26%
21	a	148	41% 22% 36%
22	b	642	23% 49% 15% 35%
23	d	113	18% 52% 34% 14%
24	e	127	69% 22% 7%
25	f	108	69% 28%
26	h	122	13% 59% 39%
27	i	99	24% 57% 37% 5%
28	j	91	56% 22% 22%
29	r	260	38% 52% 12% 36%
30	s	470	5% 94%
31	u	192	6% 41% 19% 41%
32	w	802	13% 12% 87%

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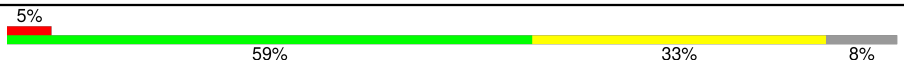
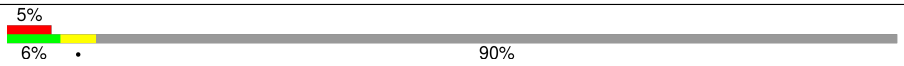
Mol	Chain	Length	Quality of chain
33	y	244	
34	z	117	
35	T	160	

2 Entry composition (i)

There are 36 unique types of molecules in this entry. The entry contains 79857 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 RNA (1758-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1817	38913	17383	7069	12644	1817	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	2930	U	C	conflict	GB 157310483
1	2948	A	G	conflict	GB 157310483
1	3196	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (144-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	144	3069	1373	551	1001	144	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	123	1042	657	199	180	6	0	0

- Molecule 4 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	B	335	2662	1687	492	474	9	0	0

- Molecule 5 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	325	2553	1620	483	447	3	0	0

- Molecule 6 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	165	Total	C	N	O	S	0	0
			1283	822	237	221	3		

- Molecule 7 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	217	Total	C	N	O	S	0	0
			1750	1128	322	297	3		

- Molecule 8 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	168	Total	C	N	O	S	2	0
			1307	837	229	239	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	183	Total	C	N	O	S	0	0
			1451	914	266	265	6		

- Molecule 10 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	180	Total	C	N	O	S	0	0
			1427	891	284	251	1		

- Molecule 11 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	125	Total	C	N	O	S	0	0
			1007	644	191	168	4		

- Molecule 12 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	166	Total	C	N	O	S	0	0
			1406	883	291	229	3		

- Molecule 13 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	196	Total	C	N	O	S	0	0
			1557	999	297	257	4		

- Molecule 14 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	156	Total	C	N	O	S	0	0
			1220	774	227	216	3		

- Molecule 15 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	133	Total	C	N	O	S	0	0
			1032	650	199	182	1		

- Molecule 16 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	R	56	Total	C	N	O	0	0
			278	166	56	56		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	168	Total	C	N	O	S	0	0
			1408	909	263	231	5		

- Molecule 18 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	137	Total	C	N	O	S	0	0
			1026	644	193	181	8		

- Molecule 19 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	W	215	Total	C	N	O	0	0
			1057	627	215	215		

- Molecule 20 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 21 is a protein called 60S ribosomal protein L28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	94	Total	C	N	O	0	0
			747	474	142	131		

- Molecule 22 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	415	Total	C	N	O	S	0	0
			2837	1765	535	534	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	97	Total	C	N	O	S	0	0
			810	512	159	136	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	118	Total	C	N	O	S	0	0
			944	591	191	157	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
26	h	121	Total	C	N	O	0	0
			999	629	194	176		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	94	Total	C	N	O	S	0	0
			748	466	155	126	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	71	Total	C	N	O	S	0	0
			563	346	121	90	6		

- Molecule 29 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	r	166	Total	C	N	O	S	0	0
			1086	656	224	205	1		

- Molecule 30 is a protein called GTPase grn1.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	s	30	Total	C	N	O	0	0
			257	155	61	41		

- Molecule 31 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	u	114	Total	C	N	O	S	0	0
			944	598	190	147	9		

- Molecule 32 is a protein called AdoMet-dependent rRNA methyltransferase spb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	w	104	Total	C	N	O	1	0
			521	311	105	105		

- Molecule 33 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	y	225	Total	C	N	O	S	0	0
			1697	1058	293	341	5		

- Molecule 34 is a protein called UPF0642 protein C32H8.05.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	z	35	Total 292	C 183	N 63	O 46	0	0

- Molecule 35 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	T	16	Total 126	C 79	N 22	O 25	0	0

- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

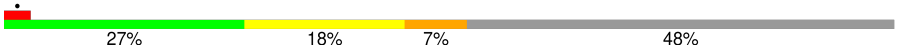
Mol	Chain	Residues	Atoms		AltConf
36	j	1	Total 1	Zn 1	0

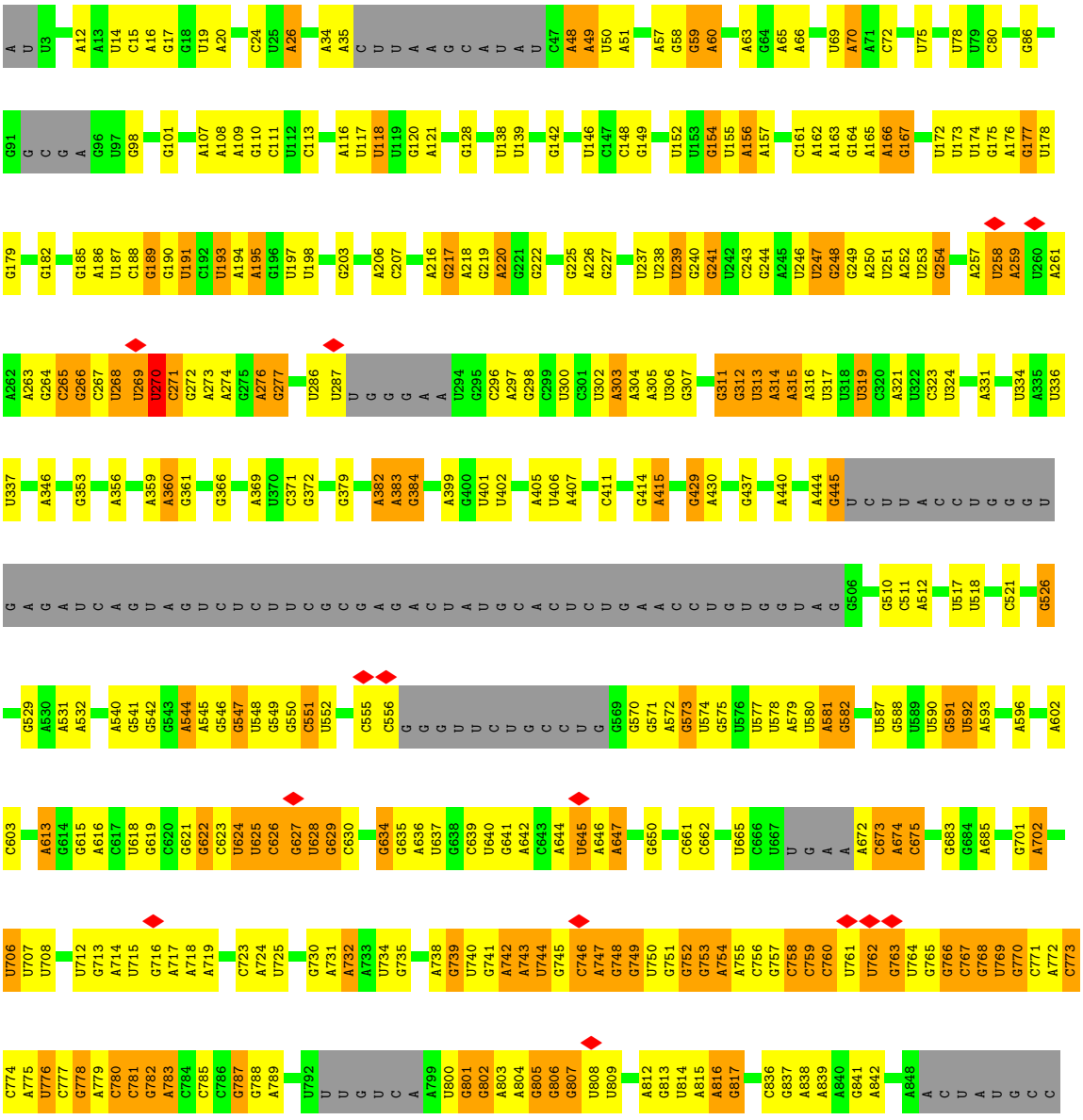
3 Residue-property plots (i)

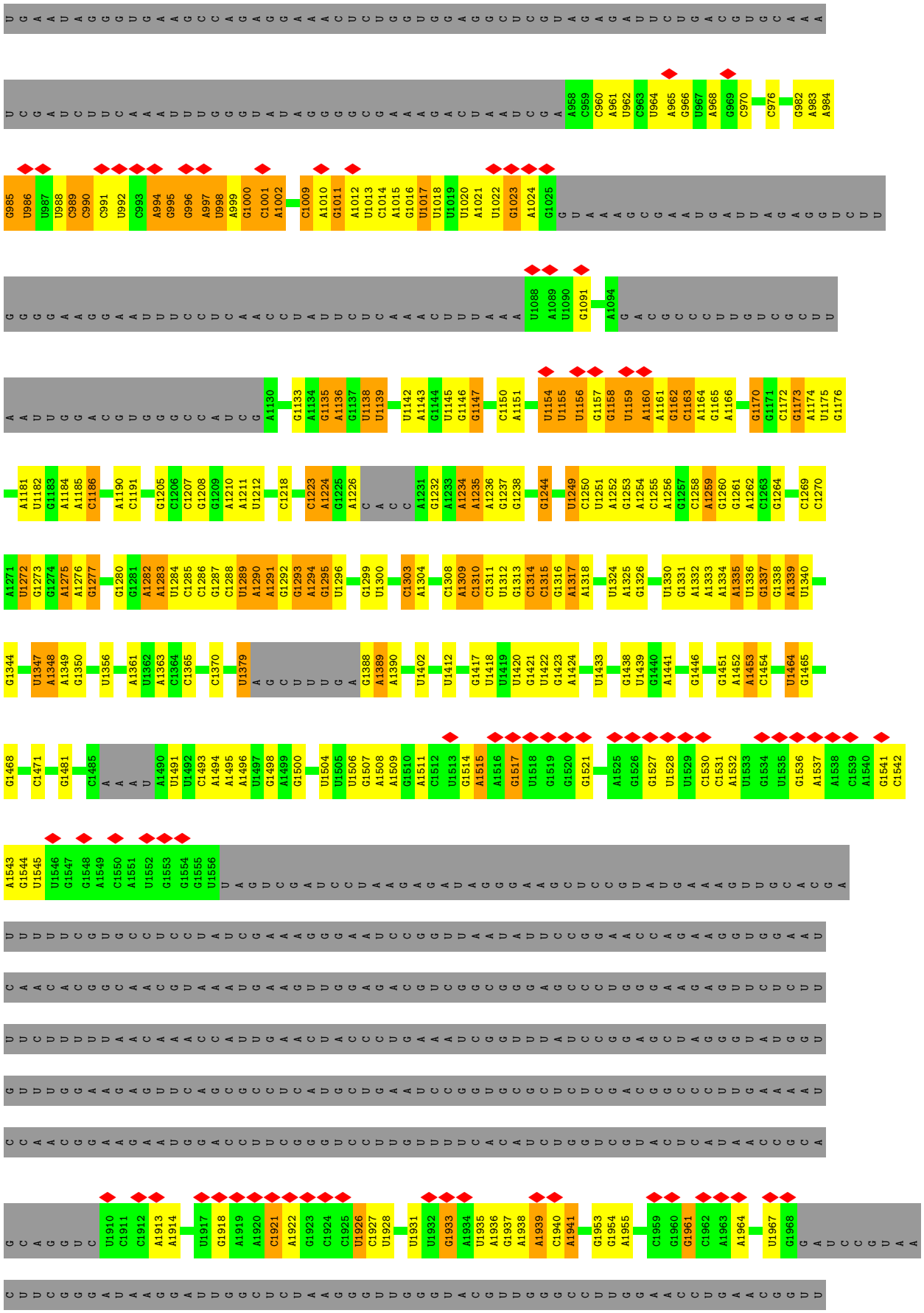
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

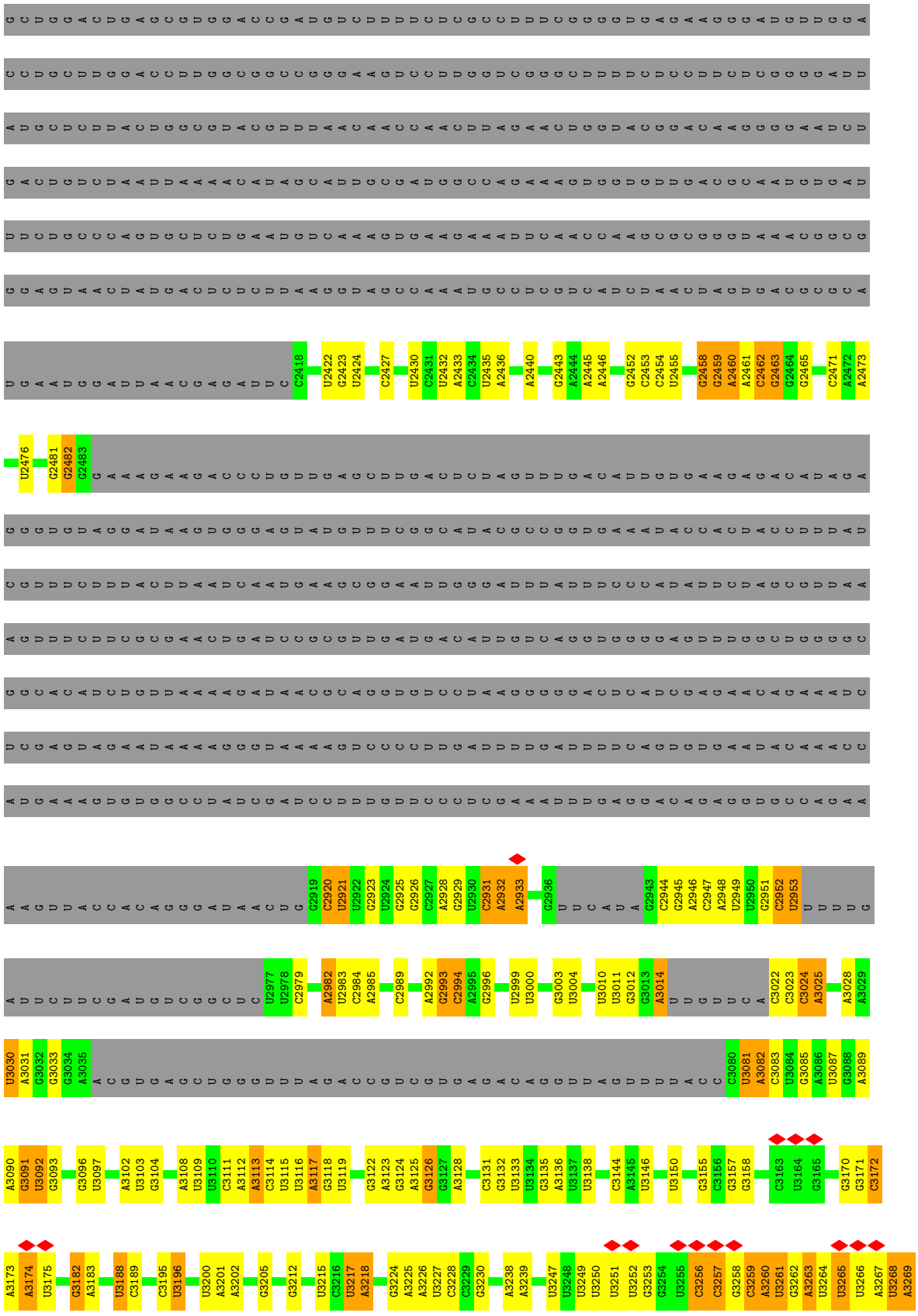
- Molecule 1: RNA (1758-MER)

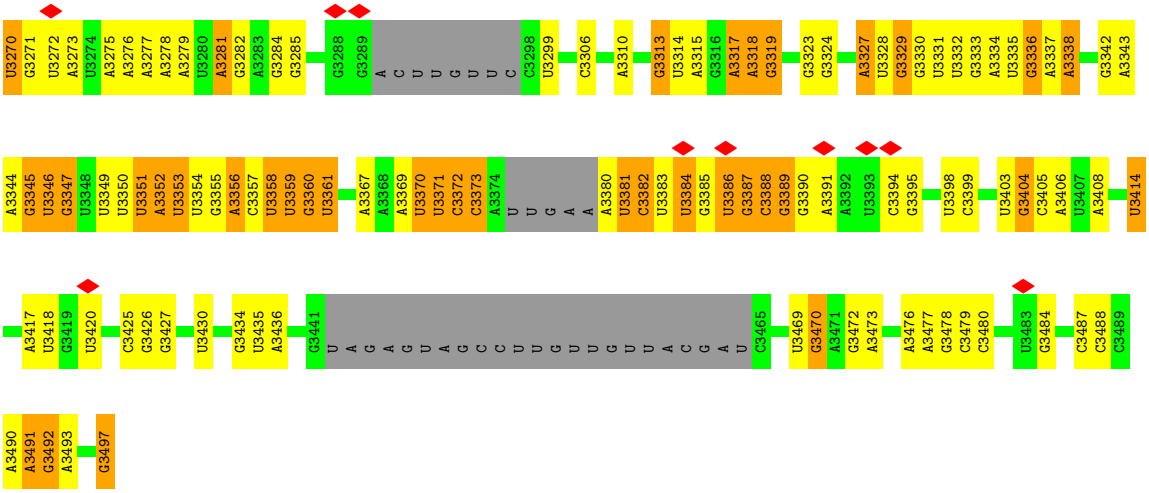
Chain 1:





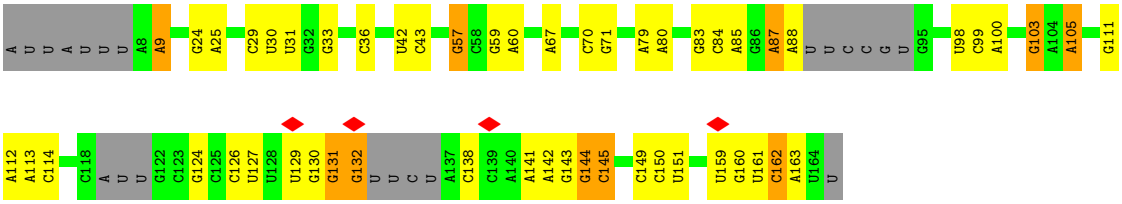






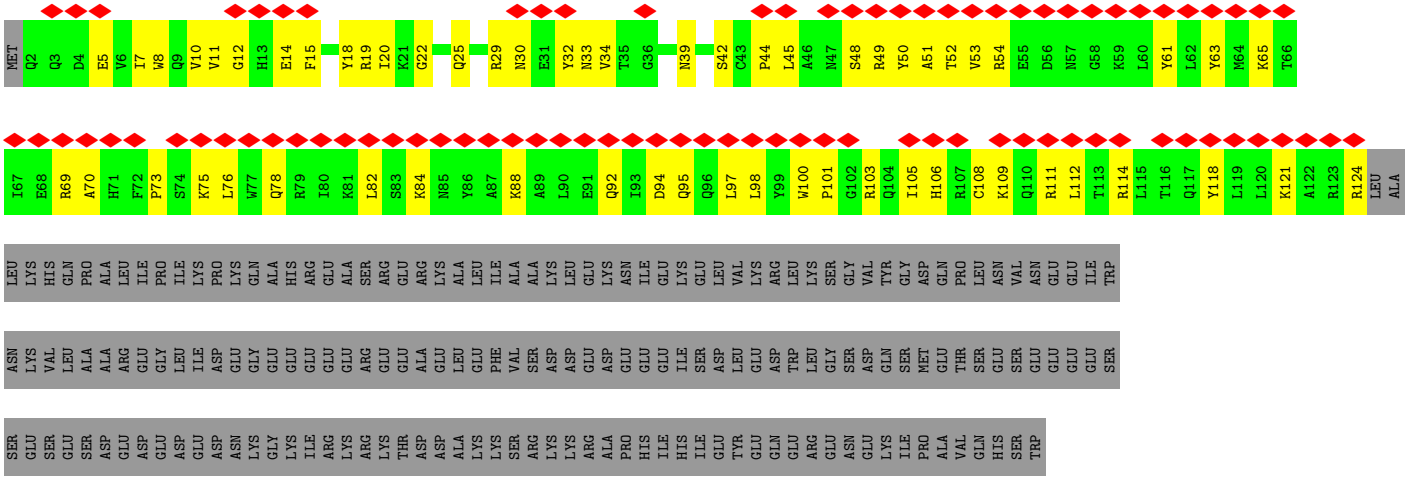
• Molecule 2: RNA (144-MER)

Chain 2:



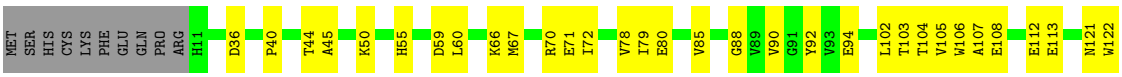
• Molecule 3: Protein mak16

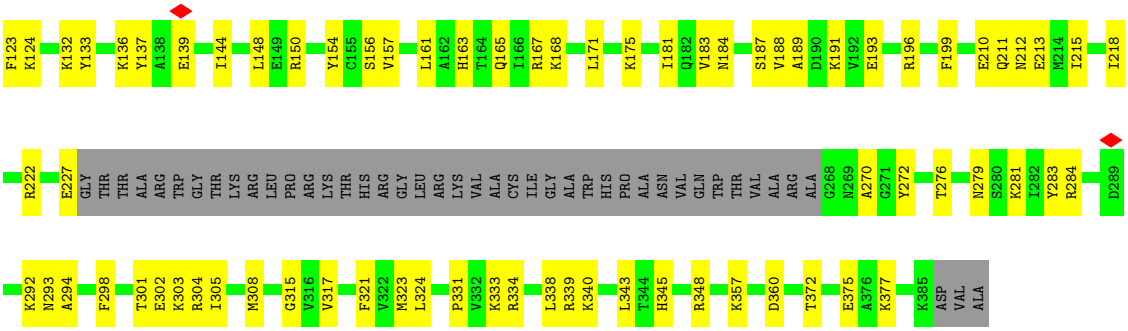
Chain 3:



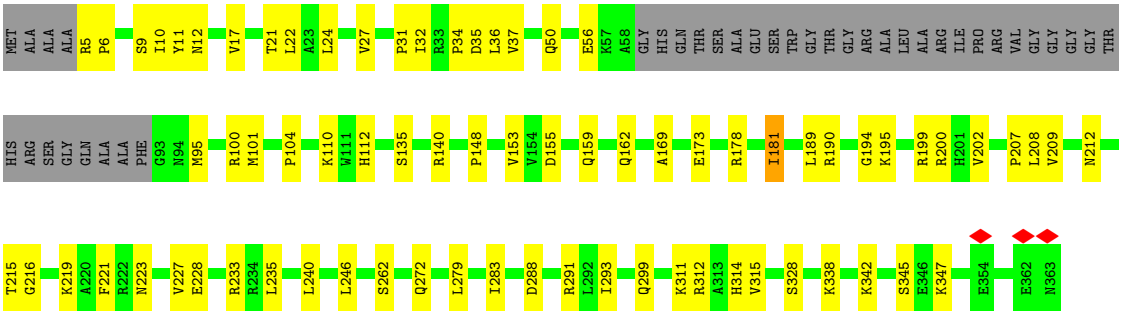
• Molecule 4: 60S ribosomal protein L3-A

Chain B:

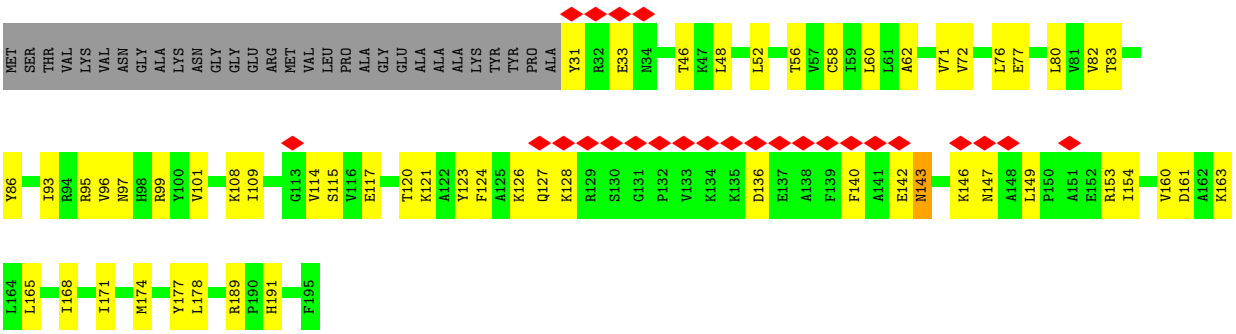




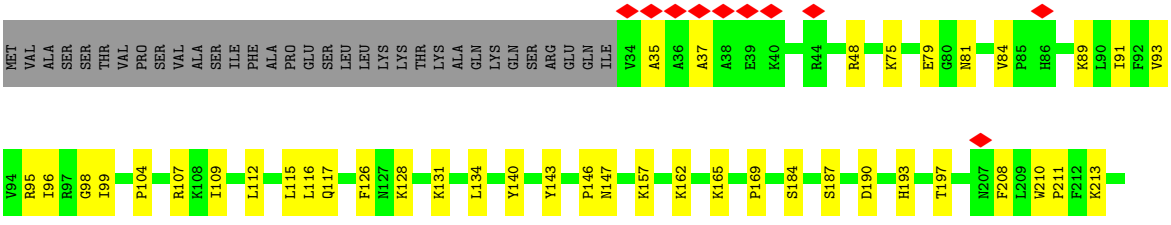
• Molecule 5: 60S ribosomal protein L4-B

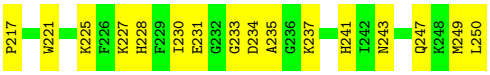


• Molecule 6: 60S ribosomal protein L6

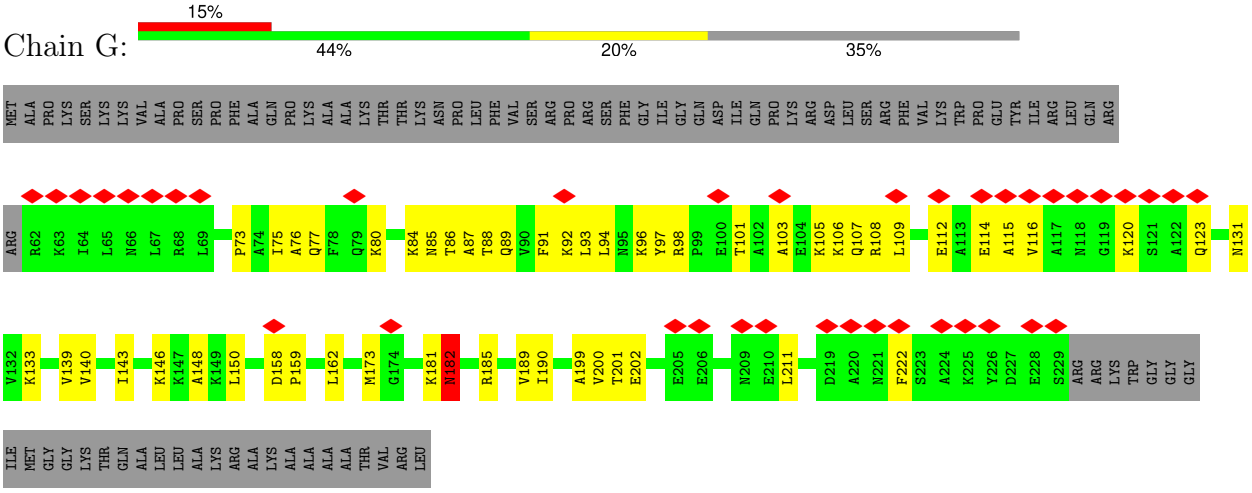


• Molecule 7: 60S ribosomal protein L7-B

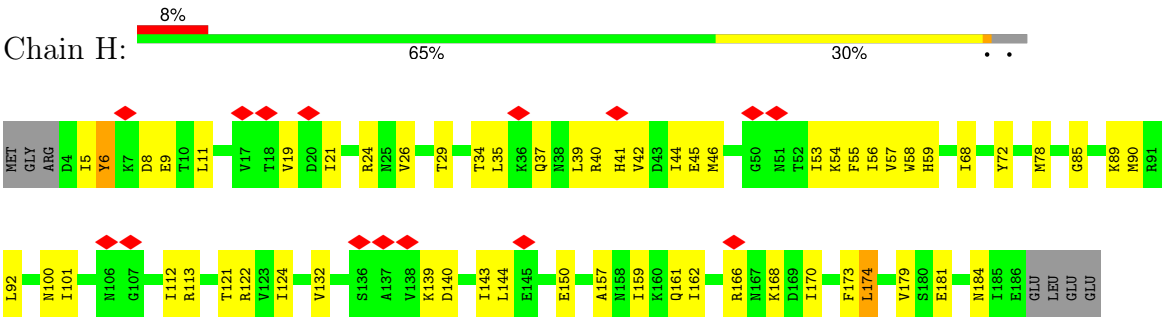




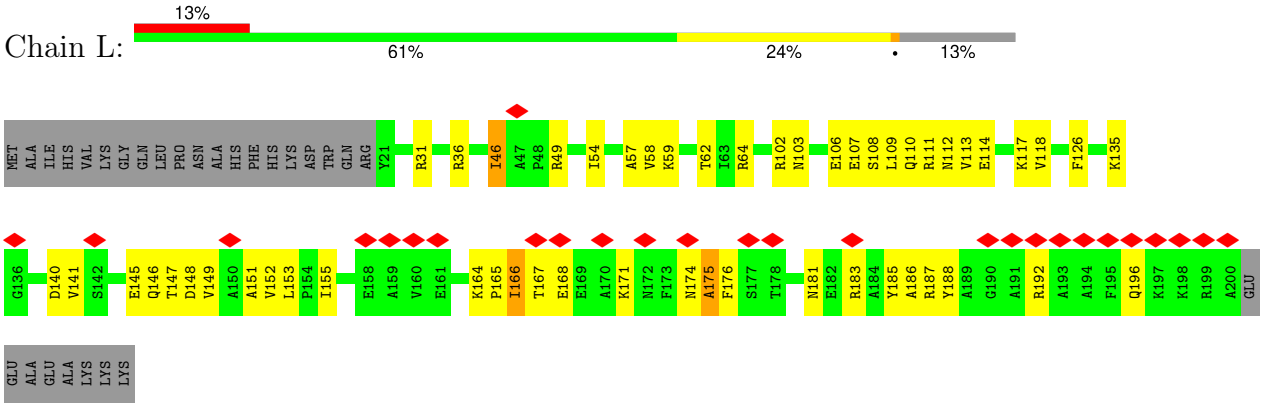
• Molecule 8: 60S ribosomal protein L8



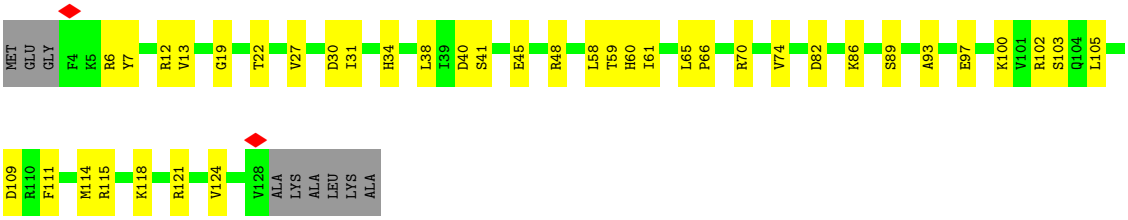
• Molecule 9: 60S ribosomal protein L9-A



• Molecule 10: 60S ribosomal protein L13

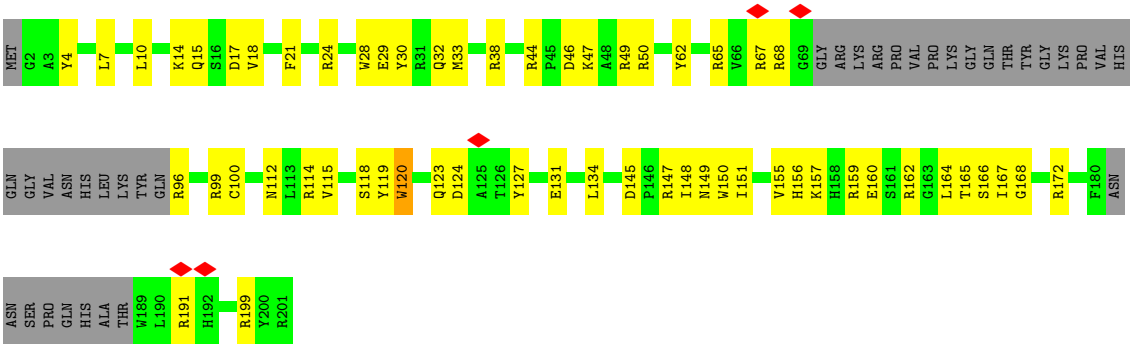


• Molecule 11: 60S ribosomal protein L14



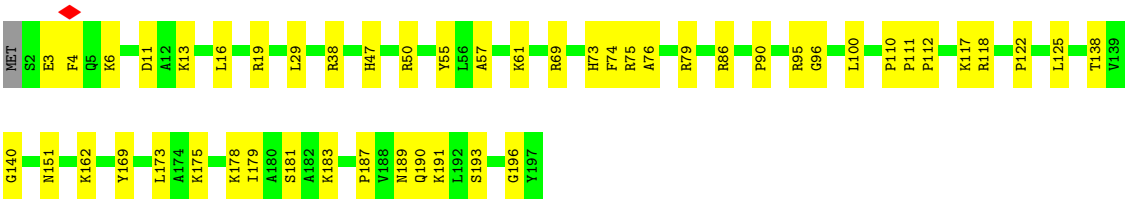
• Molecule 12: 60S ribosomal protein L15-A

Chain N:



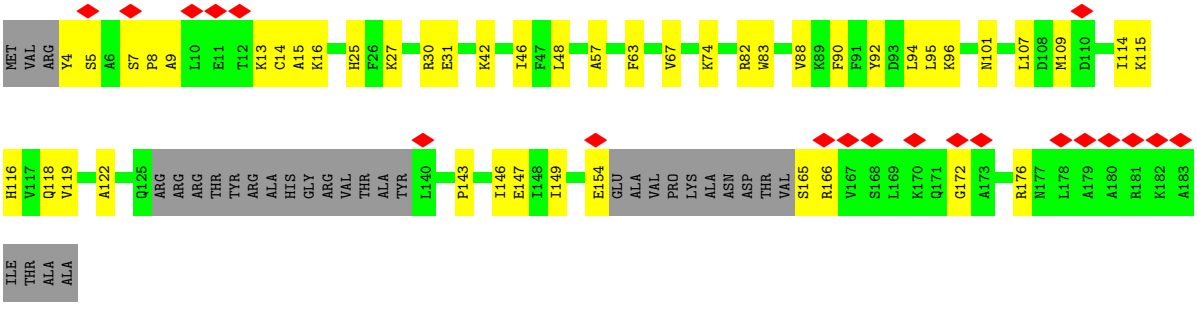
• Molecule 13: 60S ribosomal protein L16-B

Chain O:



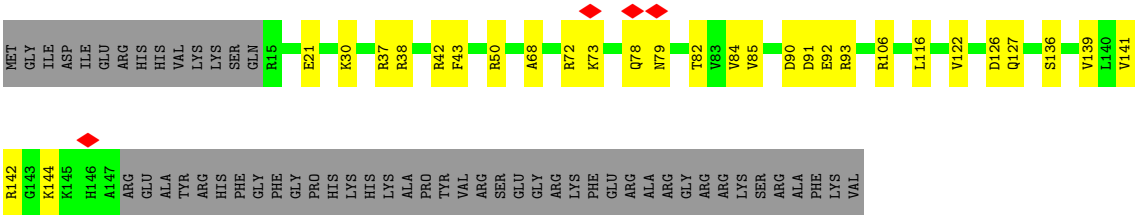
• Molecule 14: 60S ribosomal protein L17-A

Chain P:



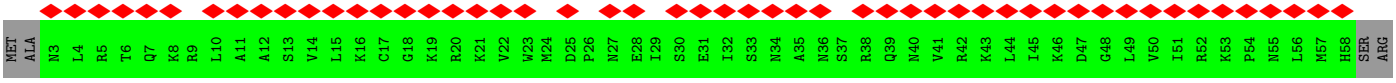
• Molecule 15: 60S ribosomal protein L18-A

Chain Q:



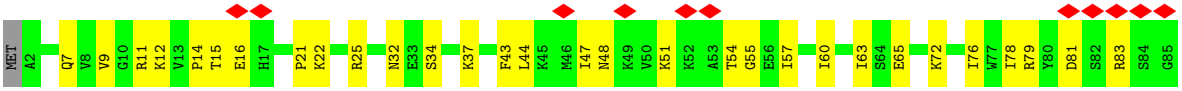
• Molecule 16: 60S ribosomal protein L19-A

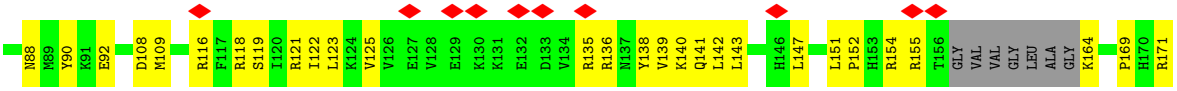
Chain R:



• Molecule 17: 60S ribosomal protein L20-A

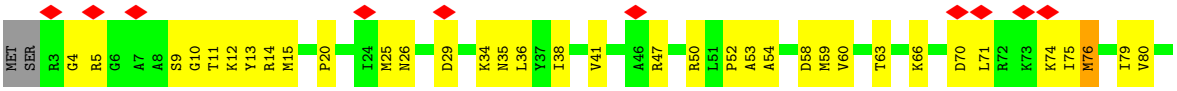
Chain S:

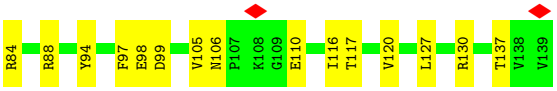




• Molecule 18: 60S ribosomal protein L23-A

Chain V:



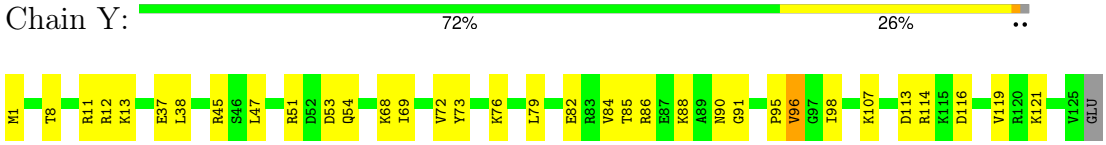


• Molecule 19: Ribosome assembly factor mrt4

Chain W:

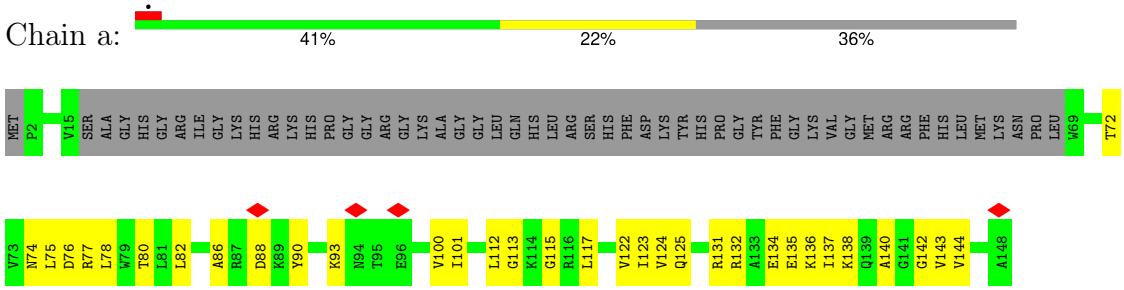
• Molecule 20: 60S ribosomal protein L26

Chain Y:



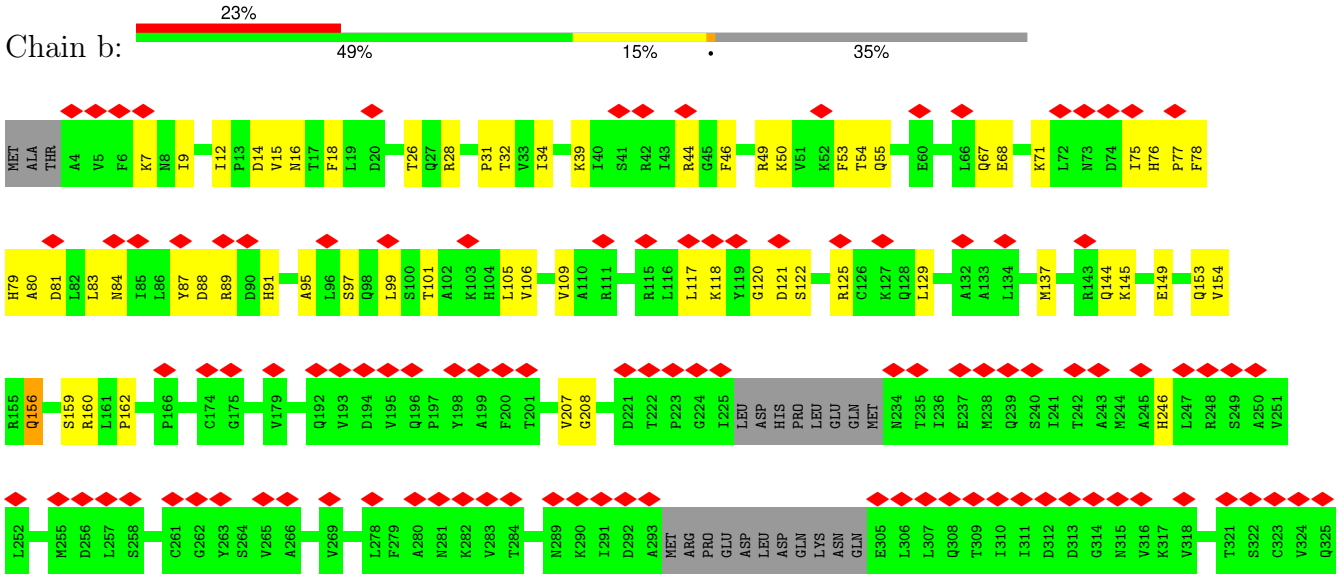
• Molecule 21: 60S ribosomal protein L28-A

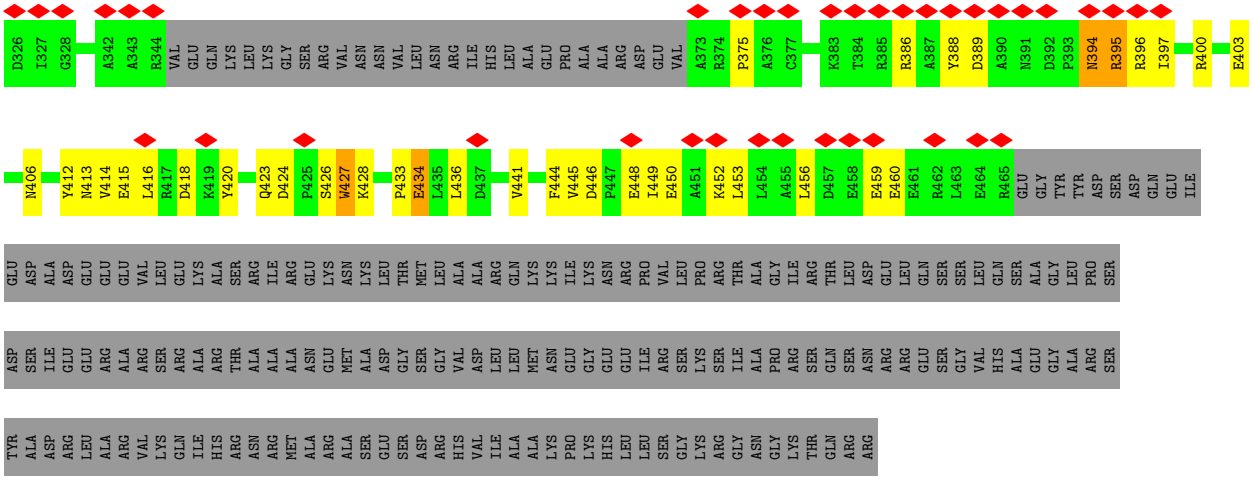
Chain a:



• Molecule 22: Probable nucleolar GTP-binding protein 1

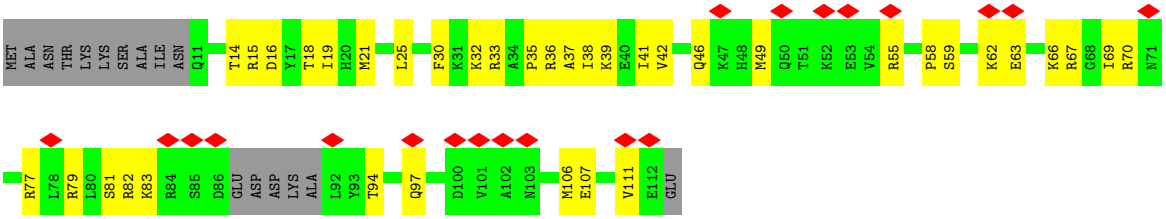
Chain b:





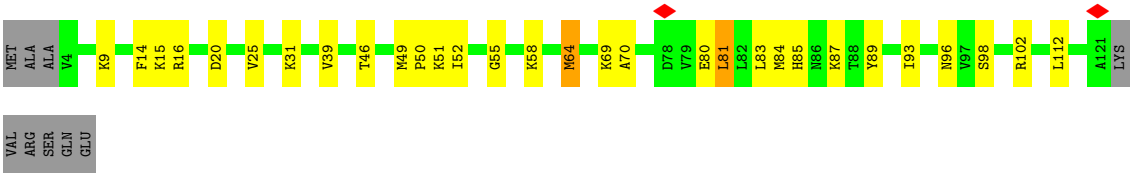
- Molecule 23: 60S ribosomal protein L31

Chain d:



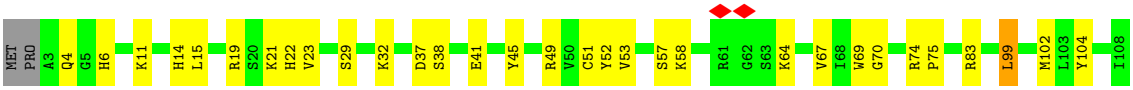
- Molecule 24: 60S ribosomal protein L32-A

Chain e:



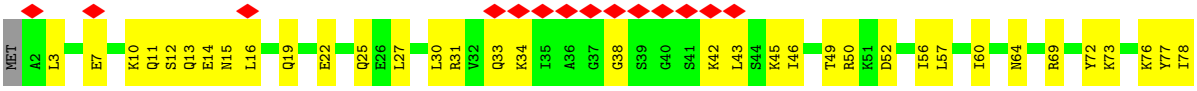
- Molecule 25: 60S ribosomal protein L33-B

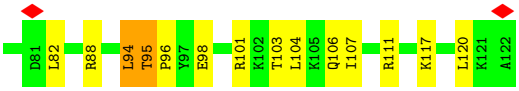
Chain f:



- Molecule 26: 60S ribosomal protein L35

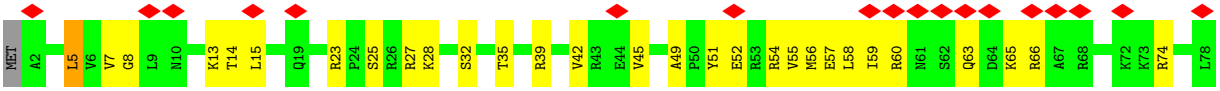
Chain h:

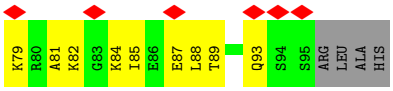




• Molecule 27: 60S ribosomal protein L36-B

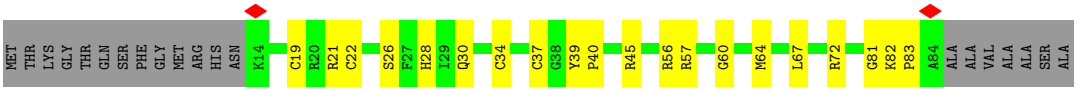
Chain i:





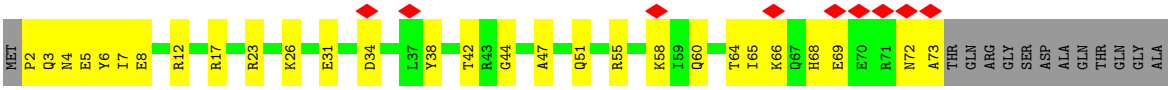
• Molecule 28: 60S ribosomal protein L37-B

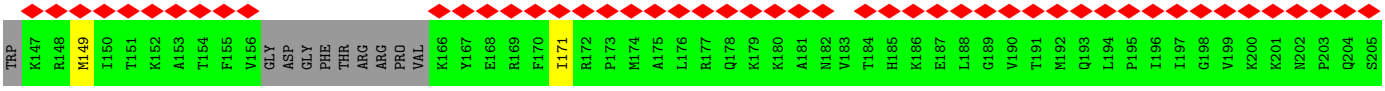
Chain j:

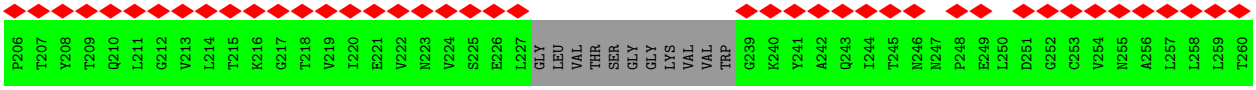


• Molecule 29: Ribosome biogenesis protein nsa2

Chain r:

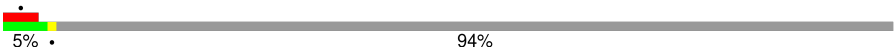


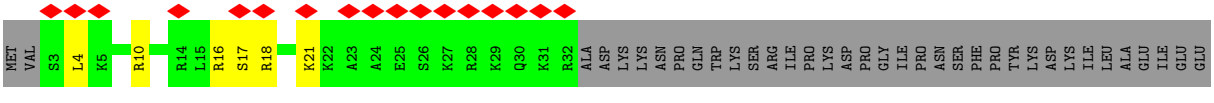


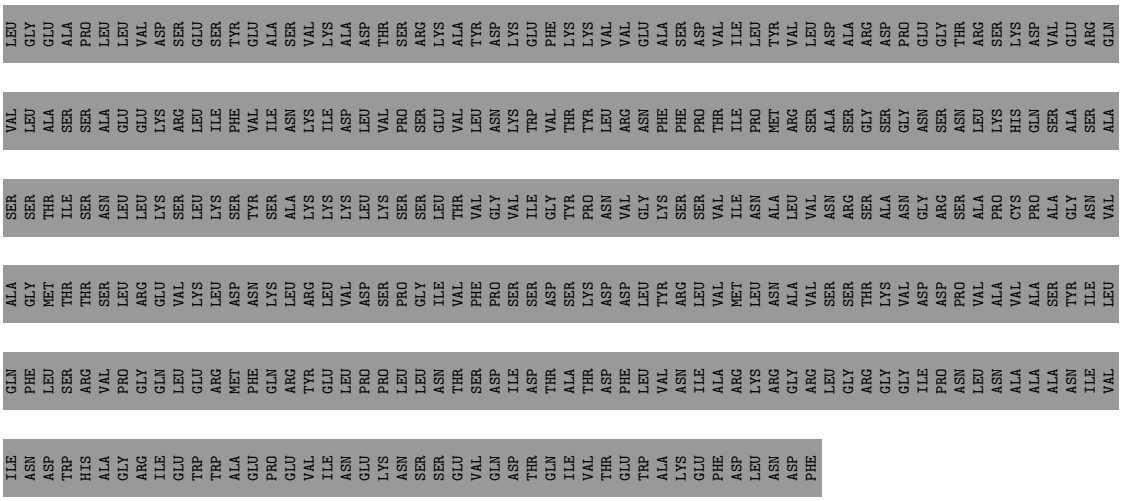


• Molecule 30: GTPase grn1

Chain s:

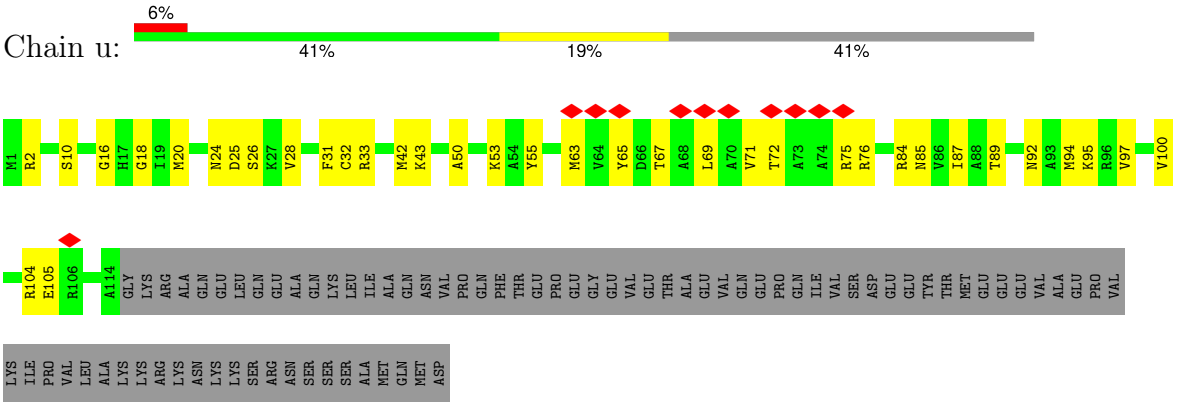






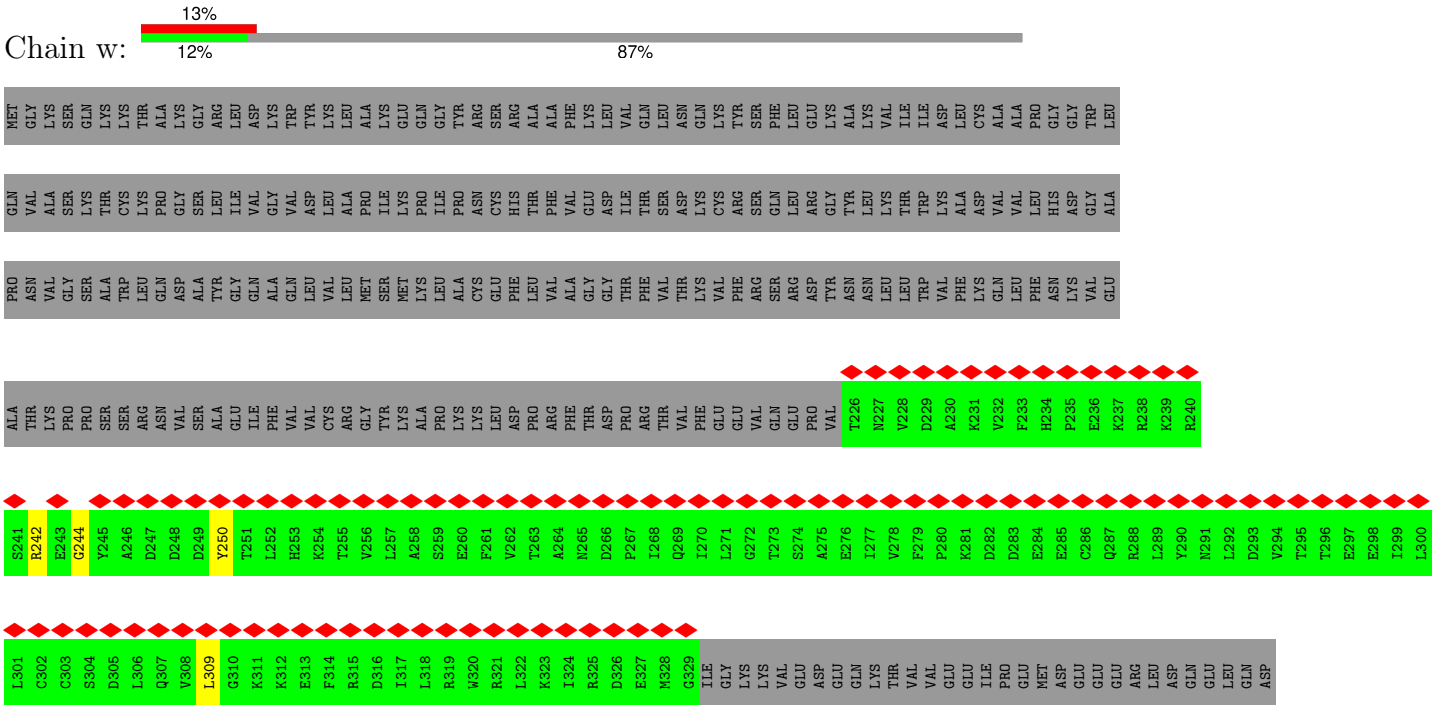
• Molecule 31: Ribosome biogenesis protein rlp24

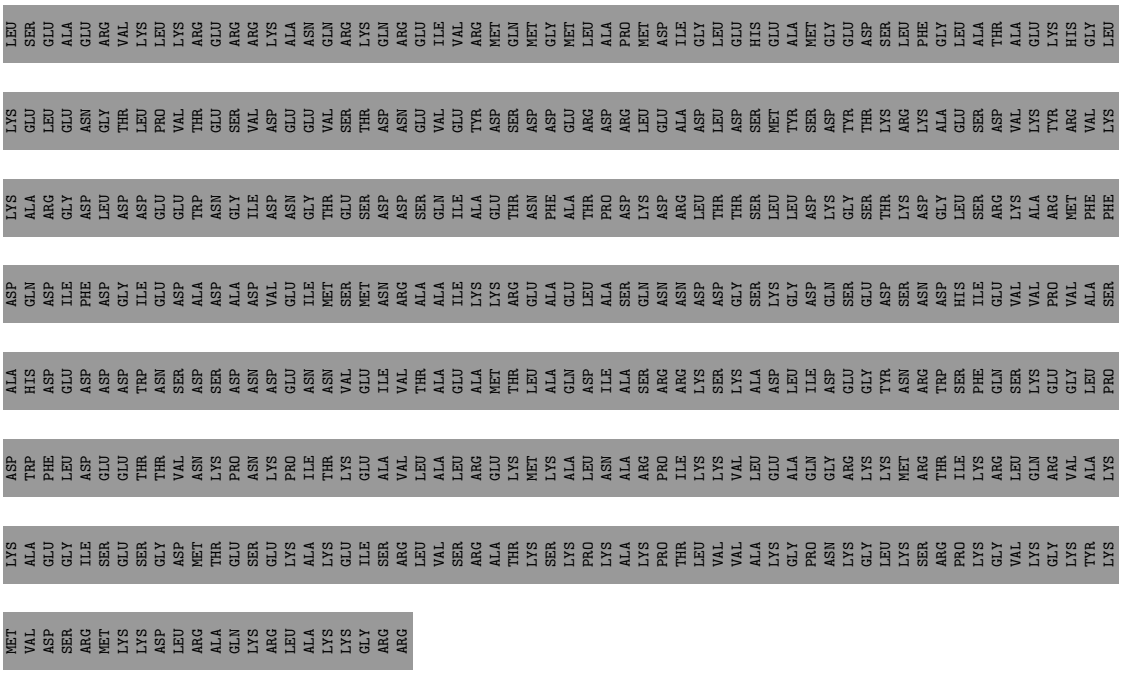
Chain u:



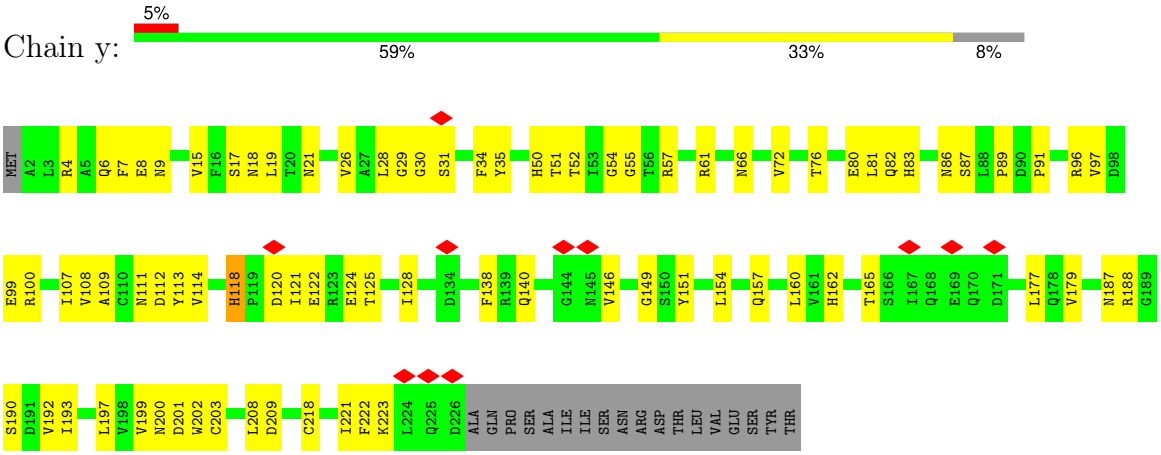
• Molecule 32: AdoMet-dependent rRNA methyltransferase spb1

Chain w:

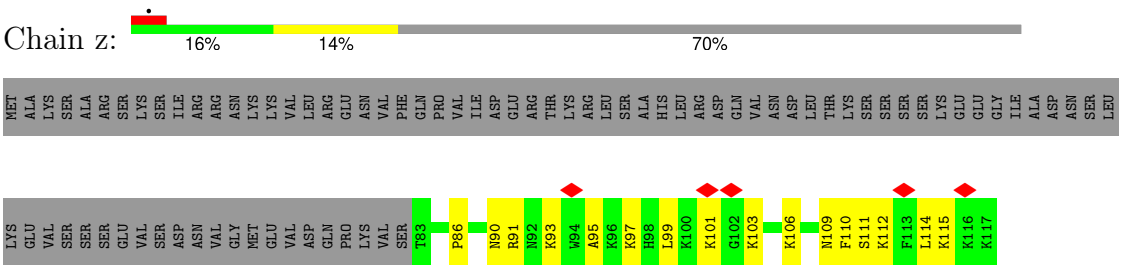




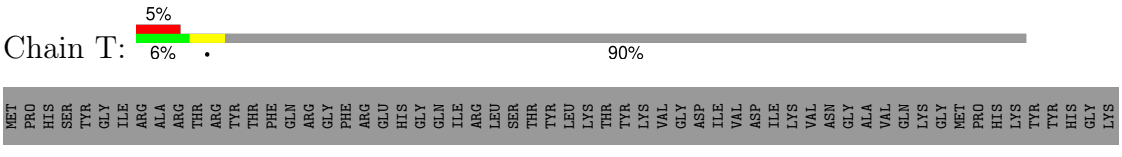
• Molecule 33: Eukaryotic translation initiation factor 6

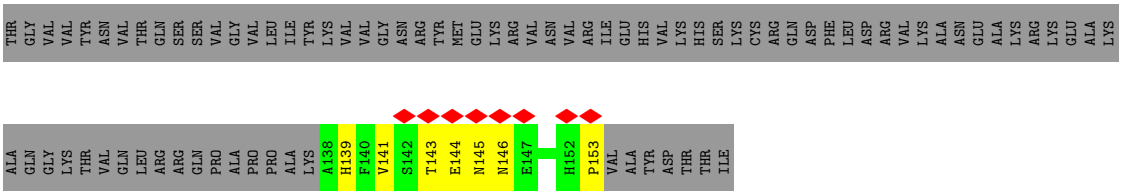


• Molecule 34: UPF0642 protein C32H8.05



• Molecule 35: 60S ribosomal protein L21-A




THR GLY VAL VAL TYR ASN VAL THR GLN SER SER VAL GLY VAL LEU ILE TYR LYS VAL VAL GLY ASN ARG TYR MET GLU LYS ARG VAL ASN VAL ARG ILE GLU HIS VAL LYS HIS SER LYS CYS ARG GLN ASP PHE LEU ASP ARG VAL LYS ALA ASN GLU ALA LYS ARG LYS GLU ALA LYS
ALA GLN GLY LYS THR VAL GLN LEU ARG ARG GLN PRO ALA PRO PRO ALA LYS A138 H139 F140 V141 S142 T143 E144 N145 N146 E147 H152 P153 VAL ALA TYR ASP THR THR ILE

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.402	Depositor
Minimum map value	-0.172	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.17	0/43553	0.26	1/67858 (0.0%)
2	2	0.15	0/3430	0.20	0/5335
3	3	0.18	0/1064	0.49	0/1431
4	B	0.20	0/2715	0.35	0/3647
5	C	0.22	0/2599	0.36	0/3505
6	E	0.20	0/1308	0.46	0/1763
7	F	0.21	0/1786	0.39	0/2399
8	G	0.18	0/1324	0.47	0/1790
9	H	0.18	0/1470	0.43	1/1982 (0.1%)
10	L	0.20	0/1452	0.45	0/1955
11	M	0.15	0/1024	0.36	0/1375
12	N	0.21	0/1436	0.42	0/1920
13	O	0.20	0/1588	0.36	0/2128
14	P	0.16	0/1240	0.37	0/1659
15	Q	0.16	0/1043	0.32	0/1401
16	R	0.05	0/277	0.18	0/385
17	S	0.17	0/1444	0.37	0/1939
18	V	0.18	0/1042	0.40	0/1402
19	W	0.08	0/1053	0.27	0/1457
20	Y	0.20	0/1008	0.42	0/1341
21	a	0.20	0/760	0.49	0/1026
22	b	0.21	0/2868	0.50	1/3902 (0.0%)
23	d	0.18	0/824	0.43	0/1106
24	e	0.21	0/958	0.35	0/1278
25	f	0.23	0/859	0.37	0/1152
26	h	0.20	0/1008	0.48	0/1340
27	i	0.18	0/755	0.54	0/1003
28	j	0.15	0/575	0.35	0/761
29	r	0.14	0/1091	0.36	0/1464
30	s	0.13	0/256	0.36	0/329
31	u	0.17	0/966	0.41	0/1292
32	w	0.06	0/520	0.23	0/724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
33	y	0.16	0/1720	0.39	0/2345
34	z	0.22	0/297	0.56	0/388
35	T	0.22	0/130	0.53	0/179
All	All	0.18	0/85443	0.33	3/124961 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	b	12	ILE	N-CA-C	7.75	115.30	108.63
9	H	6	TYR	N-CA-C	6.05	120.33	107.70
1	1	270	U	C4'-C3'-O3'	5.01	116.92	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	38913	0	19569	685	0
2	2	3069	0	1553	39	0
3	3	1042	0	1046	49	0
4	B	2662	0	2742	78	0
5	C	2553	0	2687	58	0
6	E	1283	0	1365	43	0
7	F	1750	0	1818	46	0
8	G	1307	0	1385	34	0
9	H	1451	0	1511	49	0
10	L	1427	0	1482	48	0
11	M	1007	0	1072	34	0
12	N	1406	0	1441	50	0
13	O	1557	0	1652	43	0
14	P	1220	0	1256	42	0
15	Q	1032	0	1129	25	0
16	R	278	0	120	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	S	1408	0	1462	54	0
18	V	1026	0	1076	50	0
19	W	1057	0	487	6	0
20	Y	998	0	1090	29	0
21	a	747	0	790	38	0
22	b	2837	0	2413	92	0
23	d	810	0	852	39	0
24	e	944	0	1005	25	0
25	f	839	0	866	26	0
26	h	999	0	1092	44	0
27	i	748	0	827	36	0
28	j	563	0	578	17	0
29	r	1086	0	842	39	0
30	s	257	0	304	5	0
31	u	944	0	983	34	0
32	w	521	0	224	4	0
33	y	1697	0	1679	64	0
34	z	292	0	317	16	0
35	T	126	0	113	11	0
36	j	1	0	0	0	0
All	All	79857	0	58828	1656	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 12.

All (1656) 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)
21:a:75:LEU:HA	21:a:78:LEU:HD23	1.48	0.95
22:b:456:LEU:HD13	31:u:69:LEU:HA	1.49	0.95
1:1:157:A:H5”	26:h:104:LEU:HD21	1.49	0.93
10:L:166:ILE:HG13	10:L:167:THR:H	1.34	0.93
1:1:3269:A:H4’	1:1:3270:U:H5’	1.49	0.92
20:Y:85:THR:HA	20:Y:95:PRO:HA	1.48	0.92
4:B:331:PRO:HD2	4:B:334:ARG:HE	1.35	0.91
1:1:3012:G:H1	1:1:3024:C:H5	1.14	0.89
1:1:982:G:H4’	1:1:1002:A:H4’	1.56	0.88
1:1:3333:G:H1	1:1:3354:U:H3	1.17	0.88
6:E:149:LEU:HD21	6:E:154:ILE:HD11	1.56	0.86
4:B:67:MET:HA	4:B:70:ARG:HE	1.41	0.86
21:a:135:GLU:HA	21:a:138:LYS:HG2	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:42:LYS:HZ1	14:P:46:ILE:HG23	1.43	0.84
1:1:3332:U:H3	1:1:3355:G:H1	1.26	0.84
10:L:175:ALA:HB3	21:a:131:ARG:HH22	1.44	0.82
1:1:749:G:H1	1:1:776:U:H3	1.28	0.81
1:1:277:G:H5"	12:N:14:LYS:HE3	1.61	0.80
1:1:1288:C:H42	1:1:1292:G:H22	1.29	0.80
1:1:164:G:H2'	1:1:165:A:C8	2.18	0.79
22:b:395:ARG:HH12	22:b:397:ILE:HA	1.46	0.79
14:P:95:LEU:HD11	14:P:114:ILE:HD11	1.64	0.78
1:1:552:U:H3	1:1:573:G:H1	1.32	0.77
3:3:32:TYR:HA	3:3:52:THR:HG21	1.66	0.77
23:d:63:GLU:HA	23:d:66:LYS:HG2	1.66	0.77
1:1:17:G:H4'	26:h:77:TYR:HE2	1.48	0.77
4:B:60:LEU:HD12	4:B:72:ILE:HD13	1.68	0.76
28:j:64:MET:HB3	28:j:67:LEU:HB2	1.67	0.76
26:h:30:LEU:HA	26:h:33:GLN:HE21	1.52	0.75
1:1:3014:A:H61	1:1:3022:C:H42	1.33	0.75
4:B:40:PRO:HG2	34:z:115:LYS:HD3	1.68	0.75
18:V:12:LYS:HE2	18:V:15:MET:HE3	1.69	0.75
22:b:106:VAL:HG23	22:b:137:MET:HG2	1.68	0.75
1:1:164:G:H2'	1:1:165:A:H8	1.49	0.74
22:b:445:VAL:O	31:u:76:ARG:NH1	2.20	0.74
15:Q:93:ARG:HG2	21:a:76:ASP:HB2	1.68	0.74
33:y:107:ILE:HG13	33:y:108:VAL:HG23	1.68	0.74
11:M:82:ASP:OD1	11:M:82:ASP:O	2.06	0.74
22:b:433:PRO:HB2	22:b:441:VAL:HG21	1.68	0.74
29:r:17:ARG:HD3	29:r:23:ARG:HH12	1.51	0.74
20:Y:54:GLN:HB3	20:Y:107:LYS:HB3	1.69	0.74
17:S:47:ILE:HD11	35:T:153:PRO:HA	1.70	0.73
1:1:756:C:H5'	15:Q:43:PHE:HB2	1.69	0.73
1:1:739:G:N2	1:1:783:A:OP1	2.21	0.73
1:1:1424:A:N6	1:1:1452:A:O2'	2.21	0.73
1:1:3352:A:H3'	1:1:3353:U:H5"	1.71	0.73
1:1:1379:U:OP1	15:Q:38:ARG:NH1	2.21	0.73
18:V:12:LYS:HB2	18:V:127:LEU:HD21	1.71	0.72
3:3:20:ILE:HD11	3:3:29:ARG:HB2	1.70	0.72
13:O:190:GLN:OE1	13:O:190:GLN:N	2.18	0.72
1:1:1146:G:N2	1:1:1146:G:OP2	2.20	0.72
9:H:170:ILE:HG13	29:r:17:ARG:HD2	1.71	0.72
22:b:144:GLN:OE1	22:b:144:GLN:N	2.21	0.72
11:M:40:ASP:OD1	11:M:41:SER:N	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:u:63:MET:HE1	31:u:104:ARG:HB3	1.70	0.72
35:T:144:GLU:OE2	35:T:144:GLU:N	2.17	0.72
22:b:456:LEU:HD11	22:b:460:GLU:HG2	1.72	0.72
1:1:3314:U:OP2	11:M:121:ARG:NH2	2.23	0.71
17:S:76:ILE:HG12	17:S:125:VAL:HG22	1.72	0.71
1:1:3490:A:H5"	1:1:3491:A:H5"	1.73	0.71
1:1:2993:G:H1	29:r:5:GLU:HA	1.55	0.71
33:y:109:ALA:HB2	33:y:149:GLY:HA2	1.73	0.71
1:1:626:C:H4'	1:1:627:G:OP1	1.90	0.71
1:1:1135:G:OP1	7:F:165:LYS:NZ	2.24	0.71
7:F:117:GLN:OE1	7:F:213:LYS:NZ	2.23	0.71
1:1:3131:C:OP1	34:z:91:ARG:NH2	2.23	0.71
1:1:3112:A:H5"	18:V:5:ARG:HH21	1.55	0.71
17:S:135:ARG:O	17:S:140:LYS:NZ	2.24	0.70
22:b:389:ASP:O	22:b:395:ARG:HG2	1.90	0.70
1:1:3173:A:OP1	23:d:70:ARG:NH1	2.25	0.70
1:1:3332:U:H2'	1:1:3333:G:C8	2.26	0.70
14:P:109:MET:H	14:P:109:MET:HE2	1.57	0.70
1:1:312:G:H1	1:1:319:U:H3	1.38	0.70
1:1:369:A:O3'	28:j:45:ARG:NH2	2.25	0.70
13:O:3:GLU:OE1	13:O:3:GLU:N	2.23	0.70
9:H:139:LYS:HD3	9:H:140:ASP:HB3	1.74	0.70
22:b:446:ASP:HB3	22:b:449:ILE:HB	1.74	0.70
9:H:6:TYR:CE1	9:H:56:ILE:HG23	2.27	0.70
1:1:3090:A:H2'	1:1:3091:G:H8	1.57	0.69
3:3:53:VAL:HG11	3:3:112:LEU:HD23	1.73	0.69
1:1:1270:C:H42	1:1:1280:G:H1	1.40	0.69
1:1:188:C:H2'	1:1:189:G:H8	1.54	0.69
26:h:19:GLN:HA	26:h:22:GLU:HG3	1.74	0.69
12:N:145:ASP:O	12:N:149:ASN:ND2	2.26	0.69
12:N:99:ARG:NH2	12:N:118:SER:O	2.25	0.69
22:b:84:ASN:HD22	22:b:89:ARG:HB3	1.58	0.69
14:P:5:SER:OG	14:P:118:GLN:NE2	2.25	0.69
1:1:277:G:O6	12:N:15:GLN:NE2	2.25	0.69
9:H:174:LEU:HA	29:r:17:ARG:NH1	2.08	0.69
18:V:63:THR:HG22	18:V:75:ILE:HG22	1.75	0.69
1:1:742:A:H2'	1:1:814:U:H1'	1.72	0.68
1:1:1284:U:H5"	1:1:1285:C:H5'	1.73	0.68
23:d:55:ARG:HH12	23:d:58:PRO:HD3	1.58	0.68
6:E:191:HIS:ND1	25:f:45:TYR:OH	2.24	0.68
2:2:36:C:H1'	5:C:50:GLN:HE21	1.56	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:9:ALA:HB1	14:P:16:LYS:HE2	1.74	0.68
1:1:1527:G:OP2	1:1:1527:G:N2	2.26	0.68
6:E:56:THR:HG22	6:E:108:LYS:HE3	1.74	0.68
2:2:132:G:N2	2:2:138:C:O2	2.26	0.68
10:L:107:GLU:OE2	10:L:107:GLU:N	2.24	0.68
11:M:38:LEU:HD21	11:M:48:ARG:HE	1.57	0.68
1:1:712:U:OP2	10:L:36:ARG:NH2	2.26	0.68
1:1:1308:C:O2'	1:1:1309:A:O5'	2.11	0.68
17:S:9:VAL:HG22	17:S:25:ARG:HB2	1.76	0.68
1:1:701:G:OP2	15:Q:106:ARG:NH2	2.26	0.67
31:u:69:LEU:HD21	31:u:100:VAL:HG21	1.75	0.67
1:1:311:G:H2'	1:1:312:G:C8	2.29	0.67
22:b:456:LEU:O	22:b:459:GLU:N	2.24	0.67
1:1:2459:G:OP1	1:1:2462:C:N4	2.23	0.67
17:S:12:LYS:HA	17:S:55:GLY:HA2	1.75	0.67
22:b:436:LEU:HB3	31:u:94:MET:SD	2.34	0.67
1:1:371:C:OP2	28:j:56:ARG:NH2	2.26	0.67
1:1:3277:A:O3'	13:O:162:LYS:NZ	2.28	0.67
10:L:186:ALA:HB2	27:i:8:GLY:HA2	1.77	0.67
33:y:15:VAL:HA	33:y:61:ARG:HG2	1.77	0.67
1:1:3398:U:O3'	14:P:74:LYS:NZ	2.26	0.67
18:V:47:ARG:HD3	18:V:50:ARG:HG2	1.76	0.67
23:d:69:ILE:HG23	23:d:70:ARG:HG3	1.76	0.67
27:i:57:GLU:HA	27:i:60:ARG:HB2	1.77	0.67
10:L:176:PHE:HB3	21:a:131:ARG:CZ	2.25	0.67
1:1:276:A:OP1	12:N:50:ARG:NH1	2.28	0.66
1:1:3136:A:H5"	18:V:14:ARG:HB2	1.76	0.66
1:1:1453:A:H5"	5:C:195:LYS:HE3	1.75	0.66
1:1:3257:C:H42	1:1:3389:G:H1	1.43	0.66
14:P:14:CYS:SG	14:P:15:ALA:N	2.68	0.66
1:1:128:G:OP2	26:h:76:LYS:NZ	2.28	0.66
1:1:742:A:OP2	21:a:132:ARG:NH1	2.28	0.66
1:1:1016:G:N2	1:1:1170:G:OP1	2.28	0.66
1:1:1022:U:H3	1:1:1091:G:H1	1.43	0.66
3:3:82:LEU:HD11	3:3:92:GLN:HG2	1.77	0.66
1:1:985:G:H2'	1:1:1147:G:C8	2.30	0.66
1:1:1235:A:H61	1:1:1331:G:H1'	1.60	0.66
1:1:3188:U:O2	18:V:14:ARG:NH2	2.29	0.66
22:b:426:SER:C	22:b:428:LYS:H	2.02	0.66
1:1:706:U:O2'	1:1:724:A:N6	2.28	0.66
1:1:1961:G:H21	1:1:1964:A:H61	1.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:54:ILE:HG22	10:L:149:VAL:HG11	1.78	0.66
1:1:238:U:H5'	1:1:240:G:H5'	1.78	0.66
1:1:753:G:N1	1:1:771:C:OP2	2.28	0.66
28:j:21:ARG:NH2	28:j:37:CYS:O	2.29	0.65
1:1:366:G:N2	1:1:369:A:OP2	2.29	0.65
5:C:189:LEU:HD11	5:C:200:ARG:HH11	1.59	0.65
12:N:96:ARG:NH2	12:N:100:CYS:SG	2.69	0.65
1:1:2985:A:O2'	1:1:3028:A:N3	2.28	0.65
21:a:75:LEU:HD23	21:a:113:GLY:HA2	1.77	0.65
1:1:762:U:H3'	1:1:763:G:H8	1.62	0.65
1:1:787:G:H21	1:1:804:A:H62	1.41	0.65
10:L:171:LYS:HZ3	21:a:143:VAL:HA	1.61	0.65
11:M:65:LEU:HD11	11:M:74:VAL:HG22	1.76	0.65
14:P:4:TYR:HE2	14:P:16:LYS:HB3	1.62	0.65
9:H:150:GLU:N	9:H:150:GLU:OE2	2.28	0.65
22:b:416:LEU:HD11	33:y:50:HIS:O	1.97	0.65
1:1:1423:G:H5"	24:e:98:SER:HB3	1.79	0.65
9:H:5:ILE:HD12	17:S:141:GLN:HE22	1.60	0.65
1:1:984:A:H1'	1:1:1145:U:H1'	1.79	0.65
7:F:93:VAL:HG22	7:F:143:TYR:HB3	1.78	0.65
18:V:106:ASN:HD21	18:V:110:GLU:HB2	1.61	0.64
22:b:156:GLN:HB3	22:b:160:ARG:HH21	1.62	0.64
1:1:714:A:H5'	1:1:717:A:H62	1.62	0.64
27:i:32:SER:HB2	27:i:35:THR:HG23	1.78	0.64
10:L:106:GLU:HA	10:L:109:LEU:HD23	1.79	0.64
29:r:5:GLU:OE1	29:r:5:GLU:N	2.30	0.64
1:1:2932:A:O2'	1:1:2945:G:N2	2.31	0.64
1:1:3090:A:H2'	1:1:3091:G:C8	2.33	0.64
22:b:76:HIS:ND1	22:b:77:PRO:HD2	2.12	0.64
1:1:526:G:O5'	5:C:342:LYS:NZ	2.30	0.64
1:1:756:C:OP2	15:Q:42:ARG:NH2	2.31	0.64
25:f:51:CYS:HB2	25:f:69:TRP:CZ3	2.33	0.64
1:1:996:G:N3	1:1:997:A:H1'	2.13	0.64
1:1:1259:A:H61	1:1:1312:U:H3	1.46	0.64
1:1:3122:G:H4'	29:r:2:PRO:HG3	1.80	0.64
8:G:146:LYS:NZ	8:G:173:MET:O	2.30	0.64
1:1:3196:U:H5'	4:B:343:LEU:HD22	1.79	0.63
14:P:48:LEU:HD22	14:P:88:VAL:HG13	1.80	0.63
33:y:76:THR:O	33:y:96:ARG:NH2	2.32	0.63
33:y:82:GLN:O	33:y:86:ASN:ND2	2.31	0.63
33:y:177:LEU:HB3	33:y:179:VAL:HG12	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:551:C:H1'	1:1:575:G:H22	1.62	0.63
10:L:103:ASN:ND2	10:L:109:LEU:HD22	2.13	0.63
20:Y:72:VAL:HG12	20:Y:79:LEU:HD22	1.80	0.63
23:d:18:THR:HB	23:d:77:ARG:HH11	1.62	0.63
33:y:17:SER:HB3	33:y:34:PHE:HE2	1.62	0.63
1:1:734:U:H3	1:1:739:G:H1	1.46	0.63
5:C:293:ILE:O	5:C:299:GLN:NE2	2.32	0.63
12:N:29:GLU:HG2	12:N:33:MET:HE1	1.80	0.63
25:f:52:TYR:HB2	25:f:99:LEU:HD23	1.79	0.63
34:z:101:LYS:HA	34:z:101:LYS:HE3	1.79	0.63
1:1:645:U:H2'	14:P:166:ARG:HH12	1.64	0.63
5:C:56:GLU:OE1	5:C:56:GLU:N	2.29	0.63
1:1:760:C:C5	1:1:762:U:H5'	2.33	0.63
3:3:32:TYR:OH	3:3:50:TYR:N	2.28	0.63
27:i:89:THR:O	27:i:93:GLN:NE2	2.31	0.63
1:1:20:A:OP2	26:h:88:ARG:NH2	2.32	0.63
21:a:122:VAL:H	21:a:142:GLY:HA3	1.64	0.63
17:S:78:ILE:HG22	17:S:122:ILE:HA	1.81	0.62
1:1:2952:C:H4'	1:1:2953:U:OP1	1.99	0.62
1:1:3247:U:OP1	4:B:132:LYS:NZ	2.32	0.62
10:L:109:LEU:O	10:L:113:VAL:HG23	2.00	0.62
1:1:836:C:H5'	5:C:95:MET:HE1	1.82	0.62
3:3:33:ASN:HB2	3:3:44:PRO:HG3	1.79	0.62
14:P:109:MET:HE2	14:P:109:MET:N	2.15	0.62
1:1:3091:G:H2'	1:1:3091:G:N3	2.14	0.62
13:O:117:LYS:NZ	17:S:169:PRO:O	2.33	0.62
1:1:203:G:N1	1:1:206:A:OP2	2.31	0.62
1:1:379:G:N1	1:1:382:A:OP2	2.31	0.62
17:S:7:GLN:HB3	17:S:63:ILE:HD11	1.81	0.62
1:1:591:G:H1'	1:1:592:U:H3'	1.82	0.62
1:1:743:A:H3'	1:1:744:U:H4'	1.80	0.62
1:1:3469:U:H4'	1:1:3470:G:H5'	1.81	0.62
5:C:328:SER:O	7:F:48:ARG:NH2	2.32	0.62
14:P:116:HIS:HB3	14:P:149:ILE:HB	1.81	0.62
25:f:57:SER:O	25:f:64:LYS:NZ	2.33	0.62
7:F:93:VAL:HG12	7:F:115:LEU:HD11	1.82	0.62
9:H:6:TYR:HB2	9:H:58:TRP:CZ3	2.35	0.62
1:1:3171:G:OP1	23:d:67:ARG:NH1	2.33	0.62
1:1:2933:A:N6	1:1:2945:G:O2'	2.33	0.62
15:Q:90:ASP:OD1	15:Q:91:ASP:N	2.33	0.62
1:1:3338:A:H61	1:1:3349:U:H3	1.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:105:A:OP1	26:h:69:ARG:NH2	2.33	0.62
1:1:529:G:OP2	1:1:529:G:N2	2.23	0.61
1:1:3215:U:H5"	29:r:26:LYS:HG2	1.82	0.61
25:f:51:CYS:HB2	25:f:69:TRP:HZ3	1.65	0.61
26:h:22:GLU:HA	26:h:25:GLN:OE1	2.00	0.61
27:i:49:ALA:N	27:i:52:GLU:OE2	2.32	0.61
29:r:60:GLN:O	29:r:64:THR:HG23	2.00	0.61
1:1:3089:A:O2'	2:2:9:A:N1	2.30	0.61
6:E:93:ILE:HG22	6:E:124:PHE:HZ	1.65	0.61
13:O:175:LYS:O	13:O:175:LYS:HD2	2.00	0.61
22:b:450:GLU:OE1	22:b:450:GLU:N	2.25	0.61
1:1:1312:U:H2'	1:1:1313:G:C8	2.36	0.61
8:G:75:ILE:HD11	12:N:18:VAL:HG13	1.81	0.61
4:B:213:GLU:HB3	34:z:110:PHE:CZ	2.34	0.61
10:L:103:ASN:HD21	10:L:109:LEU:HD13	1.66	0.61
1:1:740:U:H2'	1:1:741:G:O4'	1.99	0.61
1:1:1289:U:HO2'	1:1:1290:A:H8	1.48	0.61
1:1:3358:U:H3'	1:1:3359:U:H5"	1.81	0.61
4:B:55:HIS:NE2	4:B:360:ASP:OD2	2.32	0.61
22:b:207:VAL:O	29:r:3:GLN:NE2	2.34	0.61
1:1:249:G:H2'	1:1:250:A:H8	1.66	0.61
1:1:634:G:N7	5:C:311:LYS:NZ	2.44	0.61
1:1:781:C:H2'	1:1:782:G:H8	1.64	0.61
1:1:1941:A:H1'	1:1:3408:A:H5'	1.83	0.61
1:1:3314:U:C5	11:M:114:MET:HE1	2.34	0.61
3:3:52:THR:HG22	3:3:63:TYR:HB2	1.81	0.61
3:3:114:ARG:HH22	24:e:87:LYS:HE3	1.62	0.61
1:1:3324:G:H1	1:1:3361:U:H3	1.49	0.61
17:S:11:ARG:HH21	35:T:141:VAL:HG22	1.66	0.61
10:L:166:ILE:HG13	10:L:167:THR:N	2.11	0.61
13:O:86:ARG:HG3	13:O:100:LEU:HD11	1.82	0.61
9:H:21:ILE:HG22	9:H:26:VAL:HG12	1.84	0.60
1:1:755:A:H2'	1:1:756:C:O4'	2.01	0.60
1:1:1312:U:H2'	1:1:1313:G:H8	1.64	0.60
29:r:31:GLU:OE2	29:r:31:GLU:N	2.27	0.60
1:1:302:U:H5"	27:i:51:TYR:CE2	2.36	0.60
4:B:113:GLU:OE2	4:B:167:ARG:NH1	2.34	0.60
33:y:200:ASN:HD21	33:y:203:CYS:HB3	1.66	0.60
33:y:151:TYR:HE1	33:y:192:VAL:HG12	1.65	0.60
1:1:627:G:N3	1:1:627:G:H5"	2.17	0.60
18:V:41:VAL:HG22	18:V:60:VAL:HG12	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:j:39:TYR:CD1	28:j:40:PRO:HA	2.36	0.60
1:1:3491:A:O2'	1:1:3492:G:H8	1.84	0.60
5:C:190:ARG:O	5:C:195:LYS:NZ	2.32	0.60
1:1:772:A:H1'	15:Q:142:ARG:HH11	1.67	0.60
1:1:1154:U:H2'	1:1:1155:U:H5'	1.83	0.60
1:1:1446:G:OP1	24:e:102:ARG:NH1	2.34	0.60
22:b:77:PRO:HA	22:b:80:ALA:HB3	1.82	0.60
1:1:63:A:OP1	12:N:172:ARG:NH2	2.35	0.60
1:1:3268:U:H1'	1:1:3269:A:OP1	2.02	0.60
7:F:162:LYS:N	7:F:208:PHE:O	2.35	0.60
12:N:165:THR:HG23	12:N:168:GLY:H	1.67	0.60
4:B:107:ALA:HB2	4:B:199:PHE:HD1	1.66	0.60
17:S:65:GLU:OE2	17:S:72:LYS:NZ	2.34	0.60
18:V:98:GLU:OE2	18:V:98:GLU:N	2.25	0.60
1:1:2982:A:N7	22:b:32:THR:OG1	2.28	0.60
1:1:3024:C:O2'	1:1:3025:A:O5'	2.18	0.60
2:2:103:G:OP2	28:j:72:ARG:NH2	2.35	0.60
11:M:102:ARG:NH2	13:O:196:GLY:O	2.35	0.60
26:h:30:LEU:O	26:h:33:GLN:NE2	2.35	0.60
28:j:26:SER:OG	28:j:34:CYS:SG	2.60	0.60
5:C:10:ILE:HG23	5:C:153:VAL:HG12	1.84	0.59
9:H:8:ASP:OD1	9:H:9:GLU:N	2.35	0.59
21:a:88:ASP:O	21:a:93:LYS:NZ	2.30	0.59
22:b:9:ILE:HG12	22:b:68:GLU:HB3	1.84	0.59
31:u:2:ARG:HD3	31:u:75:ARG:HH22	1.66	0.59
1:1:2459:G:H21	30:s:17:SER:HB2	1.67	0.59
2:2:162:C:OP1	8:G:181:LYS:NZ	2.23	0.59
5:C:207:PRO:HG2	5:C:227:VAL:HG22	1.85	0.59
24:e:31:LYS:HE3	24:e:49:MET:HE3	1.85	0.59
34:z:106:LYS:HA	34:z:106:LYS:HE3	1.83	0.59
1:1:34:A:H3'	1:1:48:A:H61	1.66	0.59
1:1:324:U:O2'	27:i:28:LYS:NZ	2.31	0.59
4:B:102:LEU:HG	4:B:103:THR:HG23	1.84	0.59
18:V:29:ASP:HA	18:V:116:ILE:HA	1.84	0.59
1:1:24:C:OP1	28:j:57:ARG:NH1	2.32	0.59
1:1:219:G:OP2	20:Y:1:MET:N	2.32	0.59
7:F:95:ARG:HB2	7:F:115:LEU:HD13	1.84	0.59
11:M:12:ARG:NH1	11:M:59:THR:O	2.34	0.59
11:M:13:VAL:HG12	11:M:27:VAL:HB	1.84	0.59
33:y:157:GLN:HB3	33:y:223:LYS:HZ2	1.67	0.59
3:3:49:ARG:HA	3:3:65:LYS:HB2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:46:ASP:OD1	12:N:47:LYS:N	2.36	0.59
22:b:75:ILE:HD12	22:b:79:HIS:HB2	1.83	0.59
1:1:1936:A:H2'	1:1:1937:G:H8	1.67	0.59
1:1:3281:A:O2'	9:H:44:ILE:O	2.21	0.59
1:1:3315:A:OP2	11:M:118:LYS:NZ	2.34	0.59
25:f:14:HIS:HB2	25:f:99:LEU:HD11	1.84	0.59
28:j:22:CYS:HB3	28:j:37:CYS:SG	2.43	0.59
33:y:97:VAL:HG13	33:y:128:ILE:HD11	1.85	0.59
1:1:216:A:N3	5:C:223:ASN:ND2	2.49	0.59
1:1:323:C:OP1	10:L:102:ARG:NH2	2.24	0.59
1:1:998:U:H2'	1:1:999:A:H8	1.68	0.59
1:1:1417:G:H21	3:3:15:PHE:HE1	1.51	0.59
1:1:1422:U:O2'	24:e:96:ASN:O	2.20	0.59
1:1:3269:A:OP2	13:O:6:LYS:HD2	2.02	0.59
1:1:3323:G:H2'	1:1:3324:G:H8	1.67	0.59
3:3:30:ASN:HB3	3:3:44:PRO:HG2	1.83	0.59
9:H:89:LYS:HE2	9:H:181:GLU:HB2	1.84	0.59
23:d:19:ILE:HG23	23:d:21:MET:HG2	1.83	0.59
31:u:26:SER:HG	33:y:100:ARG:HH12	1.48	0.59
33:y:66:ASN:HD22	33:y:112:ASP:HA	1.65	0.59
1:1:3342:G:N2	1:1:3345:G:OP2	2.36	0.58
21:a:100:VAL:HG21	21:a:125:GLN:HE21	1.66	0.58
2:2:129:U:H2'	2:2:130:G:H8	1.68	0.58
13:O:110:PRO:HB2	13:O:112:PRO:HD2	1.85	0.58
1:1:1011:G:N2	1:1:1136:A:N3	2.50	0.58
1:1:3114:C:OP1	33:y:9:ASN:ND2	2.37	0.58
1:1:272:G:N7	27:i:27:ARG:NH2	2.50	0.58
26:h:103:THR:OG1	26:h:106:GLN:OE1	2.22	0.58
1:1:3387:G:O2'	1:1:3388:C:O5'	2.15	0.58
7:F:81:ASN:HA	35:T:143:THR:HG22	1.85	0.58
1:1:548:U:H2'	1:1:549:G:H8	1.68	0.58
9:H:5:ILE:HD11	11:M:34:HIS:CD2	2.39	0.58
33:y:100:ARG:HA	33:y:100:ARG:HH11	1.68	0.58
13:O:55:TYR:OH	13:O:74:PHE:O	2.20	0.58
17:S:11:ARG:HH12	17:S:14:PRO:HD3	1.67	0.58
1:1:401:U:O3'	20:Y:86:ARG:NH2	2.37	0.58
1:1:1299:G:H21	1:1:1304:A:H62	1.52	0.58
1:1:1438:G:N2	1:1:1441:A:OP2	2.30	0.58
1:1:3373:C:H4'	6:E:62:ALA:HB1	1.86	0.58
3:3:39:ASN:OD1	3:3:42:SER:N	2.37	0.58
12:N:28:TRP:CD1	12:N:32:GLN:HE22	2.22	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Q:84:VAL:HB	15:Q:141:VAL:HG23	1.86	0.58
18:V:4:GLY:O	18:V:5:ARG:HD3	2.04	0.58
1:1:735:G:N2	1:1:738:A:OP2	2.30	0.57
10:L:171:LYS:NZ	21:a:143:VAL:HA	2.19	0.57
18:V:29:ASP:HB3	18:V:116:ILE:HG22	1.85	0.57
1:1:3284:G:H2'	1:1:3285:G:H8	1.68	0.57
3:3:32:TYR:HD2	3:3:44:PRO:HB3	1.68	0.57
6:E:83:THR:HB	6:E:93:ILE:HA	1.85	0.57
18:V:58:ASP:OD2	18:V:59:MET:N	2.36	0.57
12:N:124:ASP:OD1	12:N:127:TYR:N	2.35	0.57
1:1:35:A:O2'	1:1:841:G:O2'	2.23	0.57
1:1:544:A:H2	1:1:582:G:H22	1.52	0.57
1:1:627:G:C5	1:1:628:U:H1'	2.40	0.57
1:1:1348:A:OP1	17:S:155:ARG:NH2	2.37	0.57
1:1:3259:C:C2	1:1:3260:A:H1'	2.38	0.57
12:N:120:TRP:NE1	12:N:123:GLN:OE1	2.38	0.57
26:h:12:SER:O	26:h:16:LEU:HD13	2.03	0.57
1:1:746:C:H5"	1:1:748:G:H5'	1.85	0.57
1:1:2929:G:H1	1:1:2949:U:H3	1.53	0.57
11:M:114:MET:HE2	11:M:114:MET:HA	1.86	0.57
1:1:760:C:C6	1:1:762:U:H5'	2.40	0.57
1:1:3259:C:H2'	1:1:3260:A:H4'	1.86	0.57
5:C:101:MET:SD	5:C:104:PRO:HA	2.44	0.57
10:L:110:GLN:O	10:L:113:VAL:N	2.37	0.57
17:S:123:LEU:HA	35:T:153:PRO:HD2	1.86	0.57
19:W:61:LYS:H	19:W:105:THR:HA	1.70	0.57
1:1:3263:A:H2	1:1:3384:U:H3	1.52	0.57
21:a:78:LEU:HB3	21:a:101:ILE:HD13	1.87	0.57
31:u:25:ASP:O	33:y:100:ARG:NH2	2.38	0.57
1:1:444:A:H61	1:1:647:A:H62	1.53	0.57
25:f:15:LEU:HD11	25:f:32:LYS:HB2	1.86	0.57
1:1:382:A:H1'	1:1:383:A:H5"	1.87	0.57
33:y:8:GLU:OE1	33:y:31:SER:OG	2.23	0.57
7:F:243:ASN:O	7:F:247:GLN:HG2	2.04	0.57
8:G:201:THR:OG1	8:G:202:GLU:OE1	2.21	0.57
9:H:122:ARG:NH1	9:H:162:ILE:O	2.37	0.57
23:d:107:GLU:OE1	23:d:107:GLU:N	2.36	0.57
24:e:9:LYS:NZ	24:e:55:GLY:O	2.38	0.56
1:1:70:A:N1	1:1:321:A:O2'	2.35	0.56
7:F:228:HIS:HB3	7:F:231:GLU:HG2	1.87	0.56
14:P:9:ALA:HA	14:P:14:CYS:SG	2.44	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3028:A:OP1	1:1:3111:C:H4'	2.05	0.56
12:N:17:ASP:OD2	12:N:18:VAL:N	2.38	0.56
20:Y:113:ASP:OD1	20:Y:114:ARG:N	2.37	0.56
20:Y:116:ASP:HA	20:Y:119:VAL:HG12	1.87	0.56
1:1:176:A:OP2	26:h:111:ARG:NH1	2.35	0.56
1:1:187:U:H2'	1:1:188:C:C6	2.41	0.56
1:1:3425:C:H4'	23:d:18:THR:HG23	1.87	0.56
1:1:702:A:N1	1:1:730:G:O2'	2.36	0.56
1:1:1514:G:O2'	1:1:1926:U:O4	2.22	0.56
1:1:3387:G:H2'	1:1:3388:C:C6	2.40	0.56
5:C:12:ASN:HA	5:C:155:ASP:OD2	2.05	0.56
15:Q:92:GLU:OE1	15:Q:92:GLU:N	2.27	0.56
29:r:31:GLU:HA	29:r:34:ASP:HB2	1.88	0.56
1:1:118:U:OP1	1:1:156:A:N6	2.36	0.56
21:a:76:ASP:OD1	21:a:76:ASP:N	2.39	0.56
26:h:104:LEU:HA	26:h:107:ILE:HB	1.86	0.56
1:1:1954:G:O2'	1:1:2422:U:O4	2.23	0.56
4:B:66:LYS:NZ	18:V:11:THR:O	2.33	0.56
18:V:79:ILE:HG12	18:V:105:VAL:HG11	1.87	0.56
1:1:175:G:O2'	1:1:177:G:OP2	2.24	0.56
1:1:998:U:H2'	1:1:999:A:C8	2.41	0.56
1:1:1218:C:H5	1:1:1350:G:H1	1.52	0.56
1:1:3004:U:O2'	1:1:3201:A:N3	2.33	0.56
4:B:165:GLN:OE1	4:B:168:LYS:NZ	2.39	0.56
1:1:627:G:C6	1:1:628:U:H1'	2.41	0.55
1:1:836:C:OP1	5:C:100:ARG:NH2	2.38	0.55
1:1:1223:C:H42	13:O:57:ALA:HB2	1.71	0.55
1:1:3261:U:H2'	1:1:3262:G:C8	2.42	0.55
10:L:62:THR:HG23	10:L:64:ARG:H	1.71	0.55
22:b:145:LYS:NZ	22:b:149:GLU:OE2	2.39	0.55
31:u:26:SER:OG	33:y:100:ARG:NH1	2.35	0.55
1:1:1324:U:O3'	17:S:83:ARG:NH2	2.40	0.55
1:1:3256:C:H2'	1:1:3257:C:C6	2.41	0.55
3:3:65:LYS:HG2	3:3:76:LEU:HD23	1.88	0.55
9:H:57:VAL:HG23	9:H:68:ILE:HD13	1.88	0.55
13:O:190:GLN:HA	13:O:193:SER:HB3	1.87	0.55
33:y:187:ASN:HB2	33:y:190:SER:HB3	1.88	0.55
1:1:739:G:OP1	10:L:183:ARG:NH2	2.39	0.55
1:1:1331:G:H5"	1:1:1332:A:H5'	1.86	0.55
33:y:118:HIS:CE1	33:y:146:VAL:HB	2.41	0.55
3:3:118:TYR:HD1	24:e:112:LEU:HD23	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:92:LEU:HD21	9:H:101:ILE:HD11	1.88	0.55
22:b:26:THR:HG21	22:b:54:THR:HB	1.89	0.55
1:1:172:U:H4'	10:L:135:LYS:HD3	1.89	0.55
12:N:28:TRP:NE1	12:N:32:GLN:HE22	2.04	0.55
18:V:4:GLY:C	18:V:5:ARG:HD3	2.32	0.55
23:d:79:ARG:HB3	23:d:97:GLN:HG2	1.89	0.55
26:h:104:LEU:HD23	26:h:104:LEU:H	1.71	0.55
1:1:1269:C:N3	1:1:1282:A:N6	2.55	0.55
1:1:1300:U:H1'	1:1:1303:C:H5	1.71	0.55
1:1:1339:A:N6	1:1:2455:U:O2	2.37	0.55
20:Y:84:VAL:HG12	20:Y:96:VAL:HG23	1.87	0.55
1:1:1379:U:OP2	15:Q:37:ARG:NH2	2.38	0.55
4:B:40:PRO:HG2	34:z:115:LYS:CD	2.37	0.55
1:1:270:U:H4'	1:1:271:C:OP1	2.06	0.55
1:1:1015:A:H2	7:F:112:LEU:HD11	1.72	0.55
21:a:82:LEU:HD21	21:a:101:ILE:HD11	1.88	0.55
1:1:188:C:H2'	1:1:189:G:C8	2.39	0.55
2:2:151:U:OP1	12:N:38:ARG:NH2	2.40	0.55
11:M:30:ASP:OD1	11:M:31:ILE:N	2.40	0.55
21:a:75:LEU:CD2	21:a:113:GLY:HA2	2.36	0.55
10:L:168:GLU:O	10:L:171:LYS:HB3	2.07	0.54
22:b:415:GLU:HB3	22:b:418:ASP:HB2	1.87	0.54
22:b:456:LEU:CD2	31:u:69:LEU:HD22	2.37	0.54
1:1:590:U:O5'	1:1:591:G:H5"	2.07	0.54
1:1:713:G:H2'	1:1:717:A:N7	2.22	0.54
1:1:764:U:H3'	1:1:765:G:H8	1.72	0.54
1:1:1344:G:O2'	1:1:1349:A:N1	2.35	0.54
1:1:3023:C:N4	1:1:3024:C:H42	2.05	0.54
1:1:3315:A:H62	11:M:118:LYS:HD2	1.72	0.54
4:B:215:ILE:HD12	4:B:338:LEU:HB3	1.89	0.54
12:N:99:ARG:HB3	12:N:167:ILE:HG12	1.88	0.54
18:V:120:VAL:HG23	18:V:137:THR:O	2.07	0.54
33:y:6:GLN:OE1	33:y:6:GLN:N	2.40	0.54
2:2:129:U:H2'	2:2:130:G:C8	2.42	0.54
18:V:9:SER:OG	18:V:10:GLY:N	2.41	0.54
1:1:263:A:H2'	1:1:264:G:C8	2.43	0.54
22:b:388:TYR:HD2	22:b:395:ARG:HB2	1.71	0.54
27:i:84:LYS:O	27:i:87:GLU:HG2	2.08	0.54
1:1:1272:U:H3	1:1:1275:A:H5"	1.72	0.54
1:1:3258:G:H1'	1:1:3389:G:H22	1.71	0.54
1:1:3306:C:O2	11:M:6:ARG:NH2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Y:37:GLU:CD	20:Y:37:GLU:H	2.16	0.54
23:d:49:MET:HE2	23:d:49:MET:HA	1.90	0.54
1:1:17:G:H4'	26:h:77:TYR:CE2	2.38	0.54
1:1:624:U:H2'	1:1:625:U:C2	2.43	0.54
1:1:674:A:O2'	1:1:675:C:OP1	2.26	0.54
4:B:105:VAL:HG21	4:B:148:LEU:HD12	1.90	0.54
10:L:114:GLU:O	10:L:118:VAL:HG22	2.08	0.54
21:a:78:LEU:HD12	21:a:101:ILE:HG21	1.89	0.54
22:b:39:LYS:HD2	22:b:39:LYS:H	1.72	0.54
26:h:27:LEU:O	26:h:31:ARG:HG2	2.08	0.54
1:1:1335:A:O2'	1:1:2979:C:O2	2.25	0.54
11:M:13:VAL:HA	11:M:27:VAL:HA	1.90	0.54
21:a:86:ALA:O	21:a:90:TYR:HB2	2.08	0.54
31:u:84:ARG:H	31:u:84:ARG:HD3	1.72	0.54
1:1:645:U:H3'	14:P:166:ARG:HH22	1.73	0.54
1:1:732:A:O4'	1:1:742:A:N6	2.41	0.54
4:B:196:ARG:HA	4:B:199:PHE:CD2	2.42	0.54
4:B:301:THR:O	4:B:301:THR:HG22	2.08	0.54
8:G:98:ARG:HG2	8:G:189:VAL:O	2.08	0.54
1:1:57:A:H5'	12:N:157:LYS:HE3	1.90	0.54
1:1:3318:A:C4	25:f:6:HIS:HE1	2.26	0.54
1:1:3384:U:H2'	1:1:3385:G:O4'	2.07	0.54
6:E:142:GLU:OE1	6:E:143:ASN:N	2.40	0.54
26:h:12:SER:HB3	26:h:15:ASN:OD1	2.08	0.54
1:1:731:A:O2'	1:1:817:G:N7	2.41	0.53
1:1:2931:C:H3'	1:1:2932:A:C8	2.42	0.53
1:1:3430:U:H4'	4:B:308:MET:HG2	1.90	0.53
7:F:157:LYS:HD3	7:F:250:LEU:HD21	1.90	0.53
22:b:31:PRO:HD2	22:b:49:ARG:HD3	1.90	0.53
33:y:118:HIS:O	33:y:121:ILE:HG23	2.08	0.53
1:1:3091:G:H5"	1:1:3092:U:H5	1.72	0.53
12:N:24:ARG:NH1	12:N:24:ARG:HB2	2.24	0.53
14:P:8:PRO:HG3	14:P:115:LYS:NZ	2.23	0.53
27:i:63:GLN:HE21	27:i:66:ARG:HG3	1.73	0.53
33:y:26:VAL:HG21	33:y:35:TYR:HD1	1.72	0.53
1:1:303:A:OP1	27:i:51:TYR:OH	2.22	0.53
1:1:985:G:O2'	1:1:1146:G:H4'	2.09	0.53
1:1:3388:C:H5"	1:1:3389:G:OP1	2.09	0.53
9:H:166:ARG:HH11	9:H:166:ARG:HG3	1.73	0.53
1:1:1022:U:H2'	1:1:1023:G:C8	2.43	0.53
1:1:2430:U:O2	1:1:3150:U:O2'	2.25	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2992:A:OP2	1:1:2994:C:N4	2.41	0.53
4:B:50:LYS:HA	4:B:79:ILE:HG22	1.90	0.53
18:V:34:LYS:HE2	32:w:244:GLY:HA3	1.90	0.53
22:b:81:ASP:HA	22:b:84:ASN:OD1	2.09	0.53
23:d:32:LYS:HE2	23:d:36:ARG:HE	1.72	0.53
1:1:2459:G:H3'	1:1:2460:A:C8	2.43	0.53
1:1:3010:U:H5"	1:1:3011:U:H5'	1.91	0.53
5:C:345:SER:HB2	5:C:347:LYS:HG2	1.90	0.53
7:F:91:ILE:HD13	7:F:126:PHE:HD1	1.72	0.53
1:1:3011:U:H2'	1:1:3012:G:C8	2.44	0.53
1:1:3480:C:H4'	4:B:315:GLY:HA2	1.91	0.53
10:L:102:ARG:HH21	27:i:23:ARG:CZ	2.22	0.53
13:O:13:LYS:HB2	13:O:38:ARG:HD2	1.91	0.53
17:S:51:LYS:HB2	17:S:54:THR:HG23	1.89	0.53
1:1:1290:A:O4'	19:W:68:GLY:HA2	2.08	0.53
1:1:1953:G:H1'	18:V:20:PRO:HG2	1.91	0.53
1:1:3317:A:H2	1:1:3319:G:H5"	1.74	0.53
3:3:32:TYR:CD2	3:3:44:PRO:HB3	2.44	0.53
7:F:116:LEU:HD23	7:F:116:LEU:H	1.74	0.53
8:G:133:LYS:HB2	8:G:199:ALA:HB3	1.91	0.53
33:y:100:ARG:HA	33:y:100:ARG:NH1	2.24	0.53
1:1:1347:U:H3'	17:S:155:ARG:HH21	1.74	0.53
29:r:66:LYS:HA	29:r:69:GLU:OE1	2.09	0.53
1:1:749:G:P	15:Q:72:ARG:HH22	2.31	0.53
1:1:772:A:H1'	15:Q:142:ARG:HD2	1.90	0.53
1:1:1337:G:O6	1:1:2454:C:O2'	2.26	0.53
1:1:3337:A:H61	1:1:3350:U:H3	1.57	0.53
4:B:211:GLN:HG2	4:B:284:ARG:HA	1.91	0.53
1:1:3492:G:H2'	1:1:3493:A:H8	1.73	0.52
9:H:5:ILE:O	9:H:58:TRP:HA	2.09	0.52
11:M:13:VAL:O	11:M:59:THR:OG1	2.24	0.52
13:O:122:PRO:HA	13:O:125:LEU:HD12	1.92	0.52
1:1:1288:C:N4	1:1:1292:G:H22	2.01	0.52
1:1:3083:C:OP2	13:O:69:ARG:NH2	2.42	0.52
3:3:94:ASP:OD1	3:3:95:GLN:N	2.42	0.52
5:C:200:ARG:HH21	20:Y:11:ARG:HD2	1.73	0.52
24:e:83:LEU:HB3	24:e:112:LEU:HD13	1.91	0.52
1:1:383:A:OP2	20:Y:88:LYS:NZ	2.40	0.52
1:1:3323:G:H2'	1:1:3324:G:C8	2.43	0.52
1:1:3345:G:N2	4:B:154:TYR:OH	2.41	0.52
14:P:122:ALA:HB3	14:P:143:PRO:HB2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:247:U:H3'	1:1:248:G:H21	1.74	0.52
1:1:787:G:N2	1:1:804:A:H62	2.08	0.52
1:1:2996:G:N2	1:1:3126:G:O2'	2.42	0.52
4:B:372:THR:HG23	4:B:375:GLU:H	1.74	0.52
10:L:166:ILE:CG1	10:L:167:THR:H	2.11	0.52
23:d:38:ILE:HA	23:d:41:ILE:HD12	1.91	0.52
1:1:155:U:OP2	12:N:49:ARG:NH2	2.43	0.52
1:1:3263:A:H2'	1:1:3264:U:H6	1.73	0.52
1:1:3370:U:P	14:P:176:ARG:HH22	2.32	0.52
3:3:100:TRP:CG	3:3:101:PRO:HD2	2.44	0.52
5:C:190:ARG:HD2	5:C:194:GLY:HA3	1.90	0.52
9:H:100:ASN:HB3	9:H:113:ARG:HB2	1.92	0.52
10:L:126:PHE:HB2	26:h:117:LYS:HB2	1.91	0.52
20:Y:82:GLU:OE1	20:Y:82:GLU:N	2.38	0.52
1:1:1277:G:O2'	1:1:1295:G:OP2	2.24	0.52
1:1:1284:U:O2'	1:1:1294:A:N3	2.36	0.52
1:1:3385:G:O5'	1:1:3385:G:H8	1.92	0.52
1:1:3492:G:H2'	1:1:3493:A:C8	2.45	0.52
7:F:147:ASN:OD1	7:F:243:ASN:ND2	2.42	0.52
11:M:19:GLY:O	11:M:22:THR:OG1	2.28	0.52
1:1:189:G:H2'	1:1:190:G:C8	2.45	0.52
1:1:276:A:N6	1:1:304:A:OP2	2.35	0.52
1:1:625:U:H4'	1:1:627:G:H1	1.75	0.52
1:1:719:A:OP1	12:N:199:ARG:NH2	2.43	0.52
1:1:723:C:H2'	1:1:724:A:C8	2.44	0.52
3:3:103:ARG:O	3:3:106:HIS:NE2	2.42	0.52
5:C:162:GLN:NE2	5:C:215:THR:O	2.36	0.52
11:M:6:ARG:HE	11:M:60:HIS:CD2	2.28	0.52
1:1:3112:A:HO2'	1:1:3113:A:H8	1.58	0.52
18:V:98:GLU:OE1	31:u:24:ASN:N	2.42	0.52
25:f:53:VAL:HG22	25:f:67:VAL:HG22	1.92	0.52
1:1:639:C:O3'	6:E:121:LYS:NZ	2.43	0.52
1:1:743:A:O2'	1:1:747:A:H1'	2.10	0.52
1:1:75:U:H5"	10:L:58:VAL:CG1	2.40	0.52
1:1:1454:C:OP2	5:C:195:LYS:NZ	2.41	0.52
1:1:3262:G:N2	1:1:3385:G:O2'	2.43	0.52
3:3:34:VAL:O	3:3:111:ARG:NH2	2.36	0.52
18:V:110:GLU:HG3	18:V:130:ARG:HD3	1.90	0.52
22:b:97:SER:O	22:b:101:THR:HG23	2.09	0.52
1:1:1260:G:H2'	1:1:1261:G:H8	1.76	0.51
22:b:67:GLN:O	22:b:71:LYS:NZ	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:742:A:O3'	1:1:780:C:O2'	2.28	0.51
1:1:3355:G:H2'	1:1:3356:A:O4'	2.11	0.51
4:B:70:ARG:HD3	33:y:55:GLY:HA2	1.92	0.51
7:F:227:LYS:HB2	7:F:233:GLY:HA3	1.93	0.51
6:E:31:TYR:HB2	24:e:87:LYS:HE2	1.91	0.51
13:O:179:ILE:O	13:O:183:LYS:N	2.41	0.51
14:P:119:VAL:HG22	14:P:146:ILE:HG12	1.93	0.51
18:V:35:ASN:HB2	18:V:66:LYS:HB2	1.92	0.51
33:y:99:GLU:HG3	33:y:125:THR:HG21	1.92	0.51
10:L:140:ASP:OD1	10:L:141:VAL:N	2.43	0.51
24:e:64:MET:HE3	24:e:70:ALA:HB2	1.93	0.51
26:h:78:ILE:HD12	26:h:82:LEU:HB2	1.93	0.51
27:i:55:VAL:O	27:i:58:LEU:HB2	2.10	0.51
28:j:82:LYS:HD3	28:j:83:PRO:HD2	1.91	0.51
1:1:764:U:H3'	1:1:765:G:C8	2.45	0.51
1:1:1508:A:H2'	1:1:1509:A:H8	1.75	0.51
31:u:43:LYS:HD3	32:w:309:LEU:H	1.76	0.51
1:1:138:U:H1'	26:h:73:LYS:HD3	1.93	0.51
1:1:271:C:H2'	1:1:272:G:O4'	2.11	0.51
1:1:3003:G:HO2'	1:1:3202:A:HO2'	1.55	0.51
5:C:27:VAL:HA	5:C:279:LEU:HD11	1.92	0.51
6:E:171:ILE:HD11	6:E:174:MET:HG2	1.92	0.51
20:Y:69:ILE:HG21	20:Y:72:VAL:HG13	1.92	0.51
27:i:5:LEU:HD23	27:i:7:VAL:H	1.76	0.51
1:1:1508:A:H2'	1:1:1509:A:C8	2.46	0.51
1:1:2443:G:OP2	14:P:25:HIS:NE2	2.35	0.51
1:1:3256:C:H2'	1:1:3257:C:H6	1.74	0.51
1:1:3260:A:H3'	1:1:3261:U:C6	2.45	0.51
9:H:19:VAL:O	9:H:21:ILE:HG23	2.11	0.51
22:b:46:PHE:CE1	22:b:50:LYS:HE2	2.46	0.51
23:d:42:VAL:O	23:d:46:GLN:HG3	2.10	0.51
31:u:65:TYR:HE2	31:u:67:THR:HG22	1.75	0.51
1:1:3281:A:N3	9:H:45:GLU:HB2	2.26	0.51
4:B:121:ASN:HB3	4:B:123:PHE:CE1	2.46	0.51
1:1:986:U:H3	1:1:1146:G:H1'	1.76	0.51
33:y:160:LEU:HB3	33:y:193:ILE:HG21	1.91	0.51
1:1:297:A:H2'	1:1:298:G:H8	1.76	0.51
1:1:3174:A:H5"	23:d:70:ARG:HH12	1.76	0.51
2:2:80:A:OP2	20:Y:51:ARG:NH1	2.43	0.51
17:S:44:LEU:HD12	17:S:48:ASN:HB3	1.93	0.51
1:1:101:G:OP2	1:1:101:G:N2	2.38	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:983:A:O2'	1:1:1001:C:H1'	2.11	0.50
1:1:3146:U:O2'	31:u:16:GLY:O	2.22	0.50
4:B:66:LYS:O	4:B:70:ARG:NH2	2.45	0.50
10:L:114:GLU:HA	10:L:117:LYS:HB2	1.94	0.50
22:b:46:PHE:HE1	22:b:50:LYS:HE2	1.75	0.50
29:r:69:GLU:H	29:r:69:GLU:CD	2.19	0.50
31:u:18:GLY:HA3	31:u:31:PHE:O	2.10	0.50
1:1:1494:A:H5"	23:d:55:ARG:HG2	1.92	0.50
1:1:3284:G:H2'	1:1:3285:G:C8	2.46	0.50
5:C:35:ASP:OD1	5:C:36:LEU:N	2.44	0.50
12:N:149:ASN:N	12:N:149:ASN:HD22	2.09	0.50
26:h:14:GLU:OE2	26:h:14:GLU:N	2.28	0.50
29:r:38:TYR:CE1	29:r:42:THR:HG21	2.46	0.50
29:r:69:GLU:O	29:r:73:ALA:N	2.33	0.50
31:u:63:MET:HE3	31:u:105:GLU:HA	1.93	0.50
9:H:124:ILE:HD13	9:H:162:ILE:HD11	1.94	0.50
12:N:67:ARG:HE	12:N:127:TYR:HE1	1.60	0.50
21:a:77:ARG:O	21:a:80:THR:OG1	2.30	0.50
34:z:103:LYS:HD3	34:z:103:LYS:N	2.26	0.50
1:1:545:A:N6	1:1:547:G:N3	2.58	0.50
1:1:1158:G:N1	1:1:1159:U:O4	2.45	0.50
18:V:117:THR:HG22	32:w:250:TYR:HA	1.93	0.50
1:1:551:C:H1'	1:1:575:G:N2	2.27	0.50
1:1:781:C:H2'	1:1:782:G:C8	2.46	0.50
1:1:3331:U:H2'	1:1:3332:U:C6	2.46	0.50
9:H:41:HIS:ND1	9:H:42:VAL:HG13	2.27	0.50
17:S:116:ARG:HB3	17:S:118:ARG:H	1.76	0.50
1:1:758:C:H2'	1:1:759:C:C6	2.46	0.50
1:1:1238:G:OP2	29:r:58:LYS:NZ	2.30	0.50
1:1:1517:G:H1	1:1:1928:U:H3	1.58	0.50
1:1:3278:A:H2'	1:1:3279:A:C8	2.47	0.50
3:3:49:ARG:O	3:3:100:TRP:HZ2	1.95	0.50
3:3:54:ARG:NH2	3:3:61:TYR:OH	2.34	0.50
22:b:71:LYS:O	22:b:75:ILE:HG23	2.11	0.50
31:u:69:LEU:CD2	31:u:100:VAL:HG21	2.40	0.50
1:1:619:G:N1	1:1:634:G:OP1	2.37	0.50
1:1:3263:A:H2'	1:1:3264:U:C6	2.46	0.50
3:3:18:TYR:O	3:3:29:ARG:N	2.39	0.50
6:E:127:GLN:HG2	6:E:128:LYS:H	1.77	0.50
7:F:221:TRP:HE3	7:F:234:ASP:OD1	1.95	0.50
10:L:57:ALA:HA	10:L:155:ILE:HD11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:V:70:ASP:OD1	18:V:70:ASP:N	2.45	0.50
18:V:70:ASP:OD1	18:V:71:LEU:HD12	2.11	0.50
1:1:624:U:O3'	1:1:629:G:N2	2.45	0.50
1:1:1262:A:H4'	1:1:1292:G:C8	2.47	0.50
1:1:3212:G:OP1	1:1:3212:G:N2	2.35	0.50
2:2:99:C:H2'	2:2:100:A:C8	2.47	0.50
11:M:7:TYR:O	11:M:12:ARG:NE	2.41	0.50
14:P:57:ALA:HB2	14:P:83:TRP:NE1	2.26	0.50
27:i:81:ALA:O	27:i:85:ILE:HG12	2.12	0.50
1:1:189:G:H2'	1:1:190:G:H8	1.77	0.50
1:1:253:U:H2'	1:1:254:G:C8	2.47	0.50
1:1:263:A:H2'	1:1:264:G:H8	1.76	0.50
1:1:445:G:OP2	1:1:445:G:H8	1.95	0.50
1:1:838:A:H2'	1:1:839:A:N3	2.26	0.50
1:1:3116:U:H3'	1:1:3117:A:C5'	2.42	0.50
3:3:10:VAL:HG22	5:C:34:PRO:HG3	1.94	0.50
5:C:37:VAL:HG21	5:C:246:LEU:HD21	1.93	0.50
14:P:147:GLU:OE2	14:P:149:ILE:HG13	2.12	0.50
21:a:74:ASN:OD1	21:a:112:LEU:HB2	2.12	0.50
22:b:71:LYS:N	22:b:71:LYS:HD2	2.26	0.50
22:b:105:LEU:O	22:b:109:VAL:HG23	2.11	0.50
1:1:334:U:OP1	10:L:31:ARG:NH1	2.44	0.49
1:1:1224:A:OP1	13:O:50:ARG:NH1	2.42	0.49
1:1:2482:G:H1	1:1:3081:U:H3	1.59	0.49
1:1:3318:A:O2'	1:1:3319:G:O5'	2.29	0.49
22:b:95:ALA:O	22:b:99:LEU:HD23	2.12	0.49
22:b:386:ARG:HB3	22:b:394:ASN:HD21	1.77	0.49
26:h:56:ILE:O	26:h:60:ILE:HG12	2.12	0.49
1:1:1289:U:H2'	1:1:1291:A:P	2.52	0.49
1:1:1541:G:OP1	1:1:1543:A:N6	2.44	0.49
1:1:2432:U:H2'	1:1:2433:A:H8	1.77	0.49
1:1:3123:A:H1'	22:b:208:GLY:HA2	1.94	0.49
6:E:76:LEU:HG	6:E:77:GLU:H	1.77	0.49
9:H:41:HIS:CE1	9:H:42:VAL:HG13	2.47	0.49
9:H:89:LYS:HG3	9:H:143:ILE:HG12	1.94	0.49
23:d:59:SER:O	23:d:62:LYS:HB2	2.12	0.49
27:i:79:LYS:HA	27:i:82:LYS:HE2	1.93	0.49
1:1:1017:U:O2'	7:F:109:ILE:HD11	2.11	0.49
1:1:1156:U:H2'	1:1:1157:G:H8	1.77	0.49
1:1:1207:C:H2'	1:1:1208:G:N2	2.26	0.49
6:E:72:VAL:HA	6:E:82:VAL:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:M:48:ARG:HH12	11:M:70:ARG:HA	1.77	0.49
24:e:93:ILE:HG21	24:e:102:ARG:HG2	1.94	0.49
33:y:157:GLN:HB3	33:y:223:LYS:NZ	2.28	0.49
1:1:315:A:H8	1:1:315:A:OP2	1.95	0.49
1:1:1288:C:H42	1:1:1292:G:N2	2.04	0.49
2:2:29:C:OP1	5:C:195:LYS:HE2	2.12	0.49
4:B:92:TYR:HB2	4:B:157:VAL:HB	1.93	0.49
1:1:1491:U:OP2	1:1:1933:G:N2	2.34	0.49
2:2:33:G:N7	20:Y:12:ARG:NH1	2.58	0.49
1:1:757:G:H3'	1:1:758:C:C6	2.47	0.49
1:1:1308:C:O2'	1:1:1309:A:H8	1.95	0.49
1:1:3262:G:H22	1:1:3385:G:H1'	1.77	0.49
10:L:59:LYS:HD2	10:L:111:ARG:HH22	1.77	0.49
10:L:106:GLU:O	10:L:109:LEU:HB2	2.13	0.49
14:P:14:CYS:SG	14:P:149:ILE:HG23	2.52	0.49
17:S:43:PHE:CE1	17:S:121:ARG:HG2	2.48	0.49
22:b:162:PRO:HB3	29:r:3:GLN:HG3	1.95	0.49
22:b:444:PHE:HE2	31:u:72:THR:O	1.95	0.49
1:1:550:G:C2'	1:1:551:C:H5'	2.43	0.49
1:1:996:G:H2'	1:1:997:A:H1'	1.95	0.49
1:1:3313:G:C6	1:1:3314:U:C5	3.01	0.49
1:1:3383:U:H2'	1:1:3384:U:C6	2.48	0.49
3:3:100:TRP:CD1	3:3:101:PRO:HD2	2.48	0.49
6:E:165:LEU:HA	6:E:168:ILE:HD12	1.95	0.49
18:V:74:LYS:O	18:V:76:MET:HG3	2.12	0.49
26:h:11:GLN:HB3	26:h:16:LEU:HD11	1.95	0.49
27:i:54:ARG:HA	27:i:57:GLU:OE1	2.13	0.49
1:1:634:G:O2'	5:C:315:VAL:HG22	2.13	0.49
1:1:743:A:C6	21:a:115:GLY:HA2	2.48	0.49
4:B:85:VAL:HB	4:B:163:HIS:CD2	2.48	0.49
5:C:110:LYS:HE2	5:C:112:HIS:O	2.13	0.49
7:F:157:LYS:HD3	7:F:250:LEU:CD2	2.43	0.49
13:O:13:LYS:O	17:S:171:ARG:NH1	2.43	0.49
22:b:125:ARG:O	22:b:129:LEU:HG	2.13	0.49
1:1:304:A:N3	1:1:307:G:O2'	2.44	0.49
1:1:549:G:C4	1:1:550:G:H1'	2.48	0.49
1:1:1150:C:H2'	1:1:1151:A:C8	2.48	0.49
1:1:1309:A:HO2'	1:1:1310:C:H6	1.60	0.49
1:1:3386:U:H2'	1:1:3387:G:C8	2.48	0.49
4:B:71:GLU:OE2	4:B:357:LYS:NZ	2.46	0.49
4:B:78:VAL:HG21	4:B:305:ILE:HD11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:b:118:LYS:O	22:b:118:LYS:HD3	2.13	0.49
27:i:57:GLU:H	27:i:57:GLU:CD	2.21	0.49
1:1:640:U:H2'	1:1:641:G:C8	2.48	0.49
1:1:754:A:C8	1:1:770:G:N2	2.80	0.49
1:1:1154:U:C6	1:1:1155:U:H5	2.31	0.49
1:1:1173:G:H5"	1:1:1174:A:H2'	1.95	0.49
1:1:1291:A:H4'	1:1:1310:C:O2'	2.13	0.49
1:1:3253:G:H21	1:1:3497:G:H1	1.60	0.49
1:1:3353:U:H2'	1:1:3354:U:C6	2.48	0.49
17:S:79:ARG:HG2	17:S:121:ARG:HH12	1.78	0.49
25:f:74:ARG:O	25:f:83:ARG:N	2.44	0.49
1:1:15:C:H2'	1:1:16:A:H8	1.78	0.48
1:1:222:G:H5"	20:Y:11:ARG:HG3	1.95	0.48
1:1:2432:U:H2'	1:1:2433:A:C8	2.48	0.48
4:B:106:TRP:HB2	4:B:133:TYR:CE1	2.48	0.48
5:C:312:ARG:CZ	5:C:315:VAL:HG12	2.42	0.48
6:E:93:ILE:HG22	6:E:124:PHE:CZ	2.47	0.48
14:P:16:LYS:O	14:P:101:ASN:ND2	2.37	0.48
23:d:49:MET:SD	23:d:82:ARG:HG3	2.53	0.48
33:y:162:HIS:O	33:y:165:THR:HG22	2.13	0.48
1:1:1262:A:O2'	1:1:1292:G:H1'	2.13	0.48
28:j:60:GLY:HA2	28:j:64:MET:HE3	1.95	0.48
31:u:10:SER:HB2	31:u:53:LYS:HB2	1.94	0.48
1:1:220:A:O4'	20:Y:1:MET:HA	2.13	0.48
1:1:985:G:H4'	1:1:986:U:C2	2.48	0.48
1:1:1163:C:H2'	1:1:1164:A:C8	2.47	0.48
4:B:193:GLU:OE1	4:B:196:ARG:NH1	2.23	0.48
6:E:31:TYR:CB	24:e:87:LYS:HE2	2.44	0.48
9:H:157:ALA:O	9:H:161:GLN:HG3	2.13	0.48
13:O:138:THR:HG22	13:O:140:GLY:H	1.77	0.48
28:j:28:HIS:CE1	28:j:30:GLN:HB2	2.47	0.48
33:y:111:ASN:HD22	33:y:154:LEU:HD21	1.76	0.48
33:y:188:ARG:NH2	33:y:209:ASP:OD2	2.47	0.48
1:1:63:A:N3	1:1:78:U:O2'	2.37	0.48
1:1:165:A:H2'	1:1:166:A:C8	2.48	0.48
1:1:772:A:C5	1:1:773:C:H1'	2.48	0.48
1:1:984:A:H4'	1:1:1000:G:H21	1.78	0.48
1:1:1494:A:H4'	23:d:55:ARG:CZ	2.43	0.48
6:E:52:LEU:HD22	6:E:80:LEU:HD21	1.93	0.48
9:H:29:THR:HG22	9:H:34:THR:HG23	1.95	0.48
27:i:52:GLU:HA	27:i:55:VAL:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:511:C:H4'	6:E:97:ASN:HD21	1.78	0.48
1:1:3202:A:H62	1:1:3224:G:H21	1.62	0.48
1:1:3257:C:N4	1:1:3389:G:H1	2.09	0.48
2:2:57:G:OP2	26:h:50:ARG:NH2	2.47	0.48
2:2:99:C:H2'	2:2:100:A:H8	1.78	0.48
3:3:97:LEU:HD22	3:3:100:TRP:CE3	2.48	0.48
10:L:187:ARG:HG2	10:L:188:TYR:CD1	2.48	0.48
13:O:111:PRO:N	13:O:112:PRO:HD2	2.28	0.48
13:O:175:LYS:HD2	13:O:175:LYS:C	2.38	0.48
15:Q:126:ASP:OD1	15:Q:127:GLN:N	2.47	0.48
17:S:164:LYS:HE2	25:f:37:ASP:O	2.14	0.48
21:a:132:ARG:HB2	21:a:135:GLU:OE1	2.14	0.48
1:1:314:A:H3'	1:1:315:A:C8	2.48	0.48
1:1:817:G:OP1	15:Q:144:LYS:NZ	2.46	0.48
1:1:1388:G:N3	1:1:1388:G:H2'	2.28	0.48
1:1:2423:G:N2	1:1:2427:C:O2'	2.46	0.48
6:E:177:TYR:HA	11:M:111:PHE:CE1	2.48	0.48
9:H:85:GLY:O	9:H:184:ASN:ND2	2.26	0.48
27:i:79:LYS:HA	27:i:82:LYS:HG2	1.96	0.48
1:1:113:C:OP1	12:N:147:ARG:NH2	2.47	0.48
1:1:640:U:H2'	1:1:641:G:H8	1.78	0.48
7:F:84:VAL:HG11	35:T:139:HIS:CD2	2.48	0.48
11:M:12:ARG:HD2	11:M:58:LEU:HD22	1.95	0.48
13:O:190:GLN:H	13:O:190:GLN:CD	2.18	0.48
17:S:11:ARG:HD2	17:S:21:PRO:HG2	1.95	0.48
22:b:456:LEU:HD22	31:u:69:LEU:HD22	1.95	0.48
1:1:50:U:H2'	1:1:51:A:H8	1.79	0.48
1:1:994:A:H2'	1:1:995:G:O4'	2.13	0.48
4:B:189:ALA:O	4:B:193:GLU:HG2	2.13	0.48
4:B:279:ASN:OD1	4:B:345:HIS:NE2	2.46	0.48
5:C:5:ARG:NH2	5:C:24:LEU:O	2.46	0.48
1:1:741:G:H1	21:a:72:THR:HG21	1.78	0.48
1:1:1500:G:N2	1:1:1544:G:H5"	2.29	0.48
1:1:1918:G:N1	1:1:1921:C:OP2	2.42	0.48
4:B:212:ASN:O	4:B:281:LYS:NZ	2.47	0.48
17:S:123:LEU:HD13	35:T:153:PRO:HD2	1.95	0.48
18:V:26:ASN:HD21	18:V:99:ASP:HB2	1.78	0.48
18:V:99:ASP:N	18:V:99:ASP:OD2	2.45	0.48
22:b:121:ASP:OD1	22:b:122:SER:N	2.46	0.48
22:b:388:TYR:CD2	22:b:395:ARG:HB2	2.47	0.48
33:y:89:PRO:HB2	33:y:91:PRO:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:z:90:ASN:OD1	34:z:93:LYS:HE3	2.14	0.48
1:1:1001:C:H2'	1:1:1002:A:C8	2.49	0.48
1:1:1250:C:O2'	1:1:1317:A:N7	2.47	0.48
11:M:111:PHE:O	11:M:114:MET:HB3	2.13	0.48
17:S:32:ASN:OD1	17:S:34:SER:N	2.46	0.48
1:1:765:G:H2'	1:1:766:G:O4'	2.13	0.47
1:1:1181:A:N1	30:s:10:ARG:NH2	2.62	0.47
4:B:59:ASP:OD1	4:B:59:ASP:N	2.42	0.47
4:B:215:ILE:HD11	4:B:324:LEU:HD21	1.95	0.47
5:C:31:PRO:C	5:C:32:ILE:HD13	2.39	0.47
6:E:93:ILE:HD11	6:E:160:VAL:HG21	1.96	0.47
10:L:108:SER:O	10:L:112:ASN:ND2	2.47	0.47
13:O:178:LYS:O	13:O:181:SER:OG	2.27	0.47
33:y:199:VAL:HG11	33:y:222:PHE:CE2	2.48	0.47
1:1:665:U:H3	1:1:674:A:H61	1.62	0.47
7:F:217:PRO:HD3	7:F:249:MET:HE3	1.96	0.47
8:G:88:THR:O	8:G:92:LYS:HG3	2.14	0.47
8:G:101:THR:HG22	8:G:103:ALA:H	1.79	0.47
12:N:62:TYR:HD2	12:N:134:LEU:HD13	1.79	0.47
12:N:119:TYR:OH	12:N:131:GLU:OE1	2.30	0.47
15:Q:21:GLU:HA	15:Q:21:GLU:OE2	2.14	0.47
17:S:79:ARG:NH1	17:S:88:ASN:HD22	2.13	0.47
26:h:7:GLU:HA	26:h:10:LYS:HB2	1.95	0.47
26:h:45:LYS:O	26:h:49:THR:HG23	2.14	0.47
27:i:55:VAL:HA	27:i:58:LEU:HD12	1.96	0.47
33:y:111:ASN:HD21	33:y:114:VAL:HB	1.79	0.47
1:1:48:A:H4'	1:1:49:A:H5'	1.96	0.47
1:1:645:U:OP2	14:P:166:ARG:NH2	2.47	0.47
1:1:646:A:H5'	14:P:166:ARG:CZ	2.44	0.47
1:1:3135:G:H1'	18:V:11:THR:HG21	1.95	0.47
1:1:3188:U:C2'	18:V:14:ARG:HH22	2.27	0.47
1:1:3262:G:C4	1:1:3263:A:H1'	2.50	0.47
1:1:3265:U:OP2	25:f:64:LYS:HE2	2.14	0.47
6:E:71:VAL:HG23	6:E:178:LEU:HD21	1.96	0.47
10:L:174:ASN:O	10:L:176:PHE:N	2.47	0.47
25:f:19:ARG:HB2	25:f:23:VAL:O	2.13	0.47
1:1:746:C:C4	15:Q:73:LYS:HA	2.49	0.47
1:1:998:U:C2	1:1:999:A:C8	3.02	0.47
1:1:3172:C:H2'	1:1:3173:A:C8	2.49	0.47
1:1:3269:A:C4'	1:1:3270:U:H5'	2.34	0.47
1:1:3315:A:H8	1:1:3315:A:O5'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:108:GLU:HB2	4:B:137:TYR:CD2	2.49	0.47
10:L:171:LYS:HB2	10:L:171:LYS:HE2	1.75	0.47
17:S:81:ASP:HB3	17:S:119:SER:HB3	1.95	0.47
31:u:32:CYS:SG	31:u:33:ARG:HG2	2.55	0.47
33:y:21:ASN:ND2	33:y:201:ASP:OD1	2.48	0.47
1:1:19:U:H2'	1:1:20:A:C8	2.50	0.47
1:1:34:A:H5"	1:1:48:A:N1	2.30	0.47
1:1:615:G:N2	1:1:637:U:OP1	2.34	0.47
1:1:718:A:N1	2:2:36:C:O2'	2.34	0.47
1:1:1260:G:H2'	1:1:1261:G:C8	2.50	0.47
1:1:3327:A:H2	1:1:3329:G:C5	2.32	0.47
2:2:149:C:O2	12:N:112:ASN:ND2	2.47	0.47
3:3:118:TYR:CD1	24:e:112:LEU:HD23	2.50	0.47
5:C:11:TYR:CZ	5:C:148:PRO:HB2	2.50	0.47
6:E:127:GLN:HG2	6:E:128:LYS:N	2.29	0.47
23:d:63:GLU:HA	23:d:66:LYS:CG	2.42	0.47
1:1:440:A:OP1	25:f:58:LYS:HB3	2.15	0.47
1:1:982:G:N1	1:1:1402:U:OP2	2.24	0.47
1:1:2925:G:H2'	1:1:2926:G:C8	2.50	0.47
1:1:3354:U:H2'	1:1:3355:G:C8	2.50	0.47
2:2:111:G:OP2	2:2:113:A:O2'	2.33	0.47
7:F:96:ILE:HB	7:F:225:LYS:HE2	1.96	0.47
13:O:76:ALA:HB3	13:O:79:ARG:HG2	1.96	0.47
33:y:202:TRP:CD1	33:y:202:TRP:C	2.92	0.47
1:1:240:G:O2'	1:1:241:G:H8	1.98	0.47
1:1:253:U:H2'	1:1:254:G:H8	1.80	0.47
1:1:548:U:H2'	1:1:549:G:C8	2.49	0.47
1:1:587:U:H2'	1:1:588:G:H8	1.80	0.47
1:1:645:U:H3'	1:1:645:U:OP2	2.15	0.47
1:1:1156:U:H2'	1:1:1157:G:C8	2.49	0.47
7:F:35:ALA:O	7:F:37:ALA:N	2.48	0.47
7:F:143:TYR:CE2	7:F:237:LYS:HB2	2.50	0.47
8:G:150:LEU:HB3	8:G:200:VAL:HB	1.97	0.47
11:M:65:LEU:HD23	11:M:66:PRO:O	2.15	0.47
12:N:21:PHE:CD1	12:N:21:PHE:C	2.93	0.47
14:P:13:LYS:HA	14:P:107:LEU:HD11	1.96	0.47
20:Y:38:LEU:H	20:Y:38:LEU:HD12	1.80	0.47
27:i:59:ILE:HG21	27:i:89:THR:HG22	1.97	0.47
28:j:19:CYS:HB3	28:j:22:CYS:SG	2.54	0.47
33:y:111:ASN:ND2	33:y:114:VAL:O	2.48	0.47
1:1:249:G:H2'	1:1:250:A:C8	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:591:G:O2'	1:1:592:U:H5"	2.15	0.47
1:1:623:C:H2'	1:1:624:U:O4'	2.15	0.47
1:1:985:G:N7	1:1:1173:G:N1	2.62	0.47
1:1:1936:A:H2'	1:1:1937:G:C8	2.48	0.47
1:1:2458:G:N1	1:1:2463:G:N7	2.60	0.47
1:1:3091:G:H5"	1:1:3092:U:C5	2.49	0.47
2:2:83:G:OP2	20:Y:73:TYR:OH	2.31	0.47
14:P:30:ARG:NH1	14:P:31:GLU:OE1	2.48	0.47
17:S:15:THR:OG1	17:S:16:GLU:N	2.47	0.47
19:W:134:THR:HA	19:W:189:THR:HA	1.96	0.47
22:b:67:GLN:OE1	22:b:67:GLN:HA	2.15	0.47
1:1:772:A:H5"	15:Q:144:LYS:HG2	1.97	0.47
1:1:989:C:H2'	1:1:990:C:C6	2.49	0.47
2:2:149:C:H1'	12:N:112:ASN:ND2	2.30	0.47
1:1:757:G:H3'	1:1:758:C:H6	1.80	0.47
1:1:802:G:H2'	1:1:803:A:C8	2.50	0.47
1:1:1439:U:H1'	24:e:51:LYS:O	2.14	0.47
1:1:1481:G:C8	14:P:27:LYS:HD2	2.50	0.47
7:F:75:LYS:O	7:F:79:GLU:HG3	2.14	0.47
8:G:108:ARG:O	8:G:112:GLU:HG2	2.15	0.47
14:P:82:ARG:HG3	14:P:83:TRP:H	1.80	0.47
1:1:548:U:H1'	1:1:581:A:C4	2.51	0.46
1:1:1138:U:N3	1:1:1139:U:O4	2.47	0.46
1:1:1234:A:H4'	1:1:1235:A:O5'	2.15	0.46
1:1:1515:A:OP2	1:1:1927:C:N4	2.45	0.46
1:1:3172:C:H2'	1:1:3173:A:H8	1.80	0.46
14:P:165:SER:OG	14:P:166:ARG:N	2.47	0.46
26:h:72:TYR:HB3	26:h:78:ILE:HG22	1.97	0.46
1:1:186:A:H2'	1:1:187:U:C6	2.50	0.46
5:C:11:TYR:CE2	5:C:17:VAL:HG22	2.50	0.46
5:C:190:ARG:HB2	5:C:202:VAL:HG13	1.98	0.46
17:S:79:ARG:HB2	17:S:123:LEU:HD21	1.97	0.46
18:V:71:LEU:HD12	18:V:71:LEU:H	1.79	0.46
18:V:110:GLU:N	18:V:110:GLU:OE1	2.48	0.46
1:1:414:G:H1'	2:2:24:G:N2	2.31	0.46
1:1:2931:C:N4	1:1:2947:C:H41	2.13	0.46
1:1:2933:A:OP1	29:r:66:LYS:NZ	2.47	0.46
12:N:10:LEU:HD23	27:i:42:VAL:HG23	1.97	0.46
13:O:16:LEU:HB2	13:O:19:ARG:HB2	1.96	0.46
21:a:131:ARG:NE	21:a:131:ARG:HA	2.30	0.46
22:b:46:PHE:CD1	22:b:46:PHE:C	2.93	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1335:A:N1	1:1:3033:G:O2'	2.39	0.46
1:1:2925:G:H2'	1:1:2926:G:H8	1.80	0.46
1:1:2993:G:H22	29:r:6:TYR:N	2.14	0.46
1:1:3367:A:H2'	6:E:86:TYR:OH	2.16	0.46
2:2:103:G:C8	28:j:83:PRO:HG3	2.50	0.46
8:G:93:LEU:HD21	8:G:211:LEU:HD12	1.98	0.46
8:G:116:VAL:HA	8:G:120:LYS:H	1.79	0.46
9:H:121:THR:HB	34:z:97:LYS:NZ	2.30	0.46
9:H:168:LYS:HB3	9:H:173:PHE:CD2	2.50	0.46
12:N:147:ARG:HE	26:h:103:THR:HG21	1.79	0.46
17:S:138:TYR:CD1	17:S:139:VAL:HG13	2.50	0.46
22:b:426:SER:C	22:b:428:LYS:N	2.67	0.46
1:1:258:U:H1'	1:1:259:A:H8	1.81	0.46
1:1:1185:A:H5"	1:1:1186:C:H5	1.80	0.46
1:1:3257:C:H3'	1:1:3258:G:C8	2.50	0.46
1:1:3269:A:H61	1:1:3380:A:H61	1.64	0.46
1:1:3388:C:H2'	1:1:3389:G:C4	2.51	0.46
6:E:108:LYS:C	6:E:109:ILE:HD13	2.40	0.46
9:H:55:PHE:HB3	9:H:68:ILE:HD11	1.96	0.46
11:M:45:GLU:OE1	11:M:45:GLU:N	2.39	0.46
22:b:412:TYR:HE1	22:b:414:VAL:HG22	1.79	0.46
1:1:286:U:H2'	1:1:287:U:C6	2.50	0.46
1:1:746:C:H2'	15:Q:72:ARG:HH11	1.81	0.46
1:1:2944:C:H2'	1:1:2945:G:O4'	2.16	0.46
1:1:3268:U:H1'	1:1:3269:A:P	2.56	0.46
3:3:32:TYR:CE2	3:3:50:TYR:HB2	2.50	0.46
5:C:178:ARG:HA	5:C:181:ILE:HD12	1.98	0.46
6:E:140:PHE:CE1	14:P:172:GLY:HA3	2.50	0.46
6:E:191:HIS:NE2	25:f:41:GLU:OE1	2.49	0.46
13:O:169:TYR:CZ	13:O:173:LEU:HD22	2.49	0.46
1:1:382:A:H4'	1:1:383:A:OP1	2.15	0.46
3:3:65:LYS:HE3	3:3:76:LEU:HD21	1.98	0.46
4:B:339:ARG:HG3	4:B:340:LYS:O	2.15	0.46
5:C:209:VAL:HG21	5:C:221:PHE:CD2	2.51	0.46
22:b:395:ARG:HH12	22:b:397:ILE:HD12	1.81	0.46
1:1:268:U:H3'	1:1:269:U:H3'	1.98	0.46
1:1:1531:C:H2'	1:1:1532:A:C8	2.51	0.46
1:1:3116:U:H3'	1:1:3117:A:H5'	1.97	0.46
4:B:292:LYS:HD3	4:B:302:GLU:CD	2.40	0.46
4:B:294:ALA:HB3	4:B:303:LYS:HG3	1.96	0.46
5:C:190:ARG:NE	5:C:199:ARG:HB3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:d:14:THR:HG22	23:d:111:VAL:HB	1.98	0.46
26:h:42:LYS:O	26:h:46:ILE:HG23	2.16	0.46
33:y:18:ASN:OD1	33:y:19:LEU:N	2.49	0.46
1:1:120:G:N2	8:G:123:GLN:O	2.48	0.46
1:1:2932:A:C2	1:1:2945:G:H2'	2.51	0.46
1:1:3359:U:O2'	1:1:3360:G:H3'	2.16	0.46
7:F:126:PHE:CZ	7:F:131:LYS:HD3	2.51	0.46
7:F:128:LYS:HA	7:F:128:LYS:HD3	1.83	0.46
17:S:37:LYS:HG2	17:S:57:ILE:HG13	1.98	0.46
20:Y:90:ASN:OD1	20:Y:91:GLY:N	2.49	0.46
23:d:33:ARG:HB2	23:d:70:ARG:HA	1.97	0.46
23:d:106:MET:HE2	23:d:106:MET:HB2	1.81	0.46
27:i:39:ARG:HA	27:i:42:VAL:HG12	1.97	0.46
1:1:999:A:H61	1:1:1145:U:H3	1.63	0.46
5:C:169:ALA:O	5:C:173:GLU:HG2	2.16	0.46
13:O:13:LYS:HB3	17:S:171:ARG:HH22	1.81	0.46
15:Q:68:ALA:O	15:Q:72:ARG:HB2	2.16	0.46
20:Y:73:TYR:CZ	20:Y:76:LYS:HD3	2.51	0.46
26:h:94:LEU:HD23	26:h:94:LEU:HA	1.78	0.46
29:r:7:ILE:HG13	29:r:8:GLU:OE1	2.16	0.46
1:1:1133:G:H1'	7:F:112:LEU:HD13	1.98	0.45
1:1:3104:G:OP2	13:O:75:ARG:NH1	2.33	0.45
2:2:57:G:H1'	26:h:43:LEU:HD11	1.97	0.45
13:O:4:PHE:CE2	25:f:11:LYS:HD2	2.50	0.45
18:V:35:ASN:C	18:V:36:LEU:HD12	2.41	0.45
23:d:30:PHE:HB3	23:d:70:ARG:HD3	1.98	0.45
1:1:673:C:H3'	1:1:674:A:H8	1.80	0.45
1:1:841:G:H2'	1:1:842:A:H8	1.81	0.45
1:1:1939:A:OP2	23:d:36:ARG:NH2	2.48	0.45
1:1:3331:U:H3	1:1:3356:A:H61	1.63	0.45
1:1:3096:G:H2'	1:1:3097:U:C6	2.52	0.45
1:1:3259:C:C2'	1:1:3260:A:H4'	2.45	0.45
4:B:108:GLU:HB2	4:B:137:TYR:CE2	2.51	0.45
13:O:74:PHE:HD2	13:O:79:ARG:HG3	1.81	0.45
18:V:41:VAL:HB	18:V:52:PRO:HB2	1.97	0.45
33:y:122:GLU:OE1	33:y:124:GLU:HB3	2.16	0.45
1:1:15:C:H2'	1:1:16:A:C8	2.51	0.45
1:1:80:C:H5"	12:N:191:ARG:HH21	1.81	0.45
1:1:999:A:H2'	1:1:1000:G:C8	2.51	0.45
1:1:1162:G:H2'	1:1:1163:C:H5'	1.98	0.45
1:1:1190:A:H2'	7:F:99:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1493:C:H2'	1:1:1494:A:C8	2.52	0.45
1:1:1922:A:H8	1:1:1922:A:OP2	1.99	0.45
1:1:2458:G:H5"	1:1:2459:G:H5'	1.99	0.45
1:1:3369:A:H4'	1:1:3370:U:H5'	1.98	0.45
5:C:21:THR:C	5:C:22:LEU:HD23	2.42	0.45
10:L:192:ARG:O	10:L:196:GLN:HG2	2.17	0.45
13:O:57:ALA:O	13:O:61:LYS:NZ	2.48	0.45
26:h:98:GLU:HA	26:h:101:ARG:HG2	1.97	0.45
27:i:84:LYS:O	27:i:88:LEU:HG	2.16	0.45
1:1:118:U:O2	1:1:121:A:H5"	2.17	0.45
1:1:1163:C:H2'	1:1:1164:A:H8	1.81	0.45
1:1:2928:A:H2'	1:1:2929:G:C8	2.52	0.45
1:1:3281:A:H3'	9:H:24:ARG:NH2	2.30	0.45
1:1:3336:G:H1	1:1:3351:U:H3	1.65	0.45
4:B:298:PHE:HB3	22:b:434:GLU:CD	2.41	0.45
5:C:262:SER:HA	5:C:272:GLN:OE1	2.16	0.45
1:1:382:A:N3	1:1:384:G:H5"	2.31	0.45
1:1:1218:C:H41	1:1:1350:G:H1	1.64	0.45
1:1:2440:A:OP1	14:P:82:ARG:HG3	2.16	0.45
9:H:166:ARG:HG3	9:H:166:ARG:NH1	2.31	0.45
18:V:20:PRO:HA	18:V:53:ALA:HA	1.98	0.45
29:r:47:ALA:O	29:r:51:GLN:HG2	2.17	0.45
33:y:7:PHE:CD2	33:y:8:GLU:HG2	2.52	0.45
33:y:28:LEU:O	33:y:30:GLY:N	2.49	0.45
1:1:300:U:OP2	12:N:68:ARG:NH2	2.49	0.45
1:1:672:A:H2'	1:1:673:C:O4'	2.16	0.45
1:1:3315:A:C6	11:M:115:ARG:HG2	2.52	0.45
3:3:84:LYS:HZ2	3:3:88:LYS:HG2	1.82	0.45
4:B:45:ALA:HB3	4:B:181:ILE:HG23	1.99	0.45
8:G:97:TYR:HB3	8:G:131:ASN:HA	1.99	0.45
17:S:154:ARG:HD3	17:S:154:ARG:H	1.81	0.45
27:i:58:LEU:O	27:i:63:GLN:N	2.45	0.45
31:u:84:ARG:HD3	31:u:84:ARG:N	2.31	0.45
1:1:624:U:H1'	1:1:629:G:N1	2.32	0.45
1:1:746:C:H4'	1:1:747:A:H5"	1.98	0.45
1:1:1255:C:H2'	1:1:1256:A:O4'	2.16	0.45
7:F:184:SER:O	7:F:184:SER:OG	2.28	0.45
12:N:4:TYR:HD1	12:N:7:LEU:HD12	1.79	0.45
12:N:160:GLU:OE1	12:N:160:GLU:N	2.48	0.45
13:O:187:PRO:C	13:O:191:LYS:HE3	2.42	0.45
22:b:7:LYS:HZ1	29:r:2:PRO:HD2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:e:80:GLU:HA	24:e:112:LEU:HD11	1.99	0.45
26:h:52:ASP:O	26:h:56:ILE:HG12	2.16	0.45
27:i:14:THR:O	27:i:15:LEU:HD22	2.17	0.45
33:y:118:HIS:CE1	33:y:120:ASP:HB2	2.51	0.45
34:z:111:SER:O	34:z:114:LEU:HG	2.17	0.45
1:1:2993:G:N1	29:r:5:GLU:HA	2.28	0.45
1:1:3336:G:H2'	1:1:3337:A:O4'	2.17	0.45
4:B:211:GLN:NE2	4:B:283:TYR:O	2.50	0.45
4:B:293:ASN:OD1	4:B:304:ARG:HA	2.17	0.45
5:C:209:VAL:HG21	5:C:221:PHE:HD2	1.82	0.45
14:P:176:ARG:HD2	14:P:176:ARG:C	2.42	0.45
22:b:423:GLN:NE2	22:b:424:ASP:HB2	2.32	0.45
1:1:276:A:N1	1:1:303:A:H5'	2.32	0.45
1:1:1244:G:H5'	17:S:136:ARG:NH2	2.32	0.45
1:1:3092:U:H5"	1:1:3093:G:H5"	1.99	0.45
1:1:3487:C:H2'	1:1:3488:C:H6	1.82	0.45
3:3:5:GLU:OE1	5:C:288:ASP:HA	2.17	0.45
3:3:105:ILE:O	3:3:109:LYS:HG2	2.16	0.45
5:C:235:LEU:HD12	5:C:240:LEU:HD11	1.98	0.45
10:L:181:ASN:O	10:L:185:TYR:N	2.40	0.45
17:S:175:PHE:CG	17:S:176:TYR:N	2.84	0.45
34:z:95:ALA:O	34:z:99:LEU:HG	2.17	0.45
1:1:1249:U:O2	1:1:1254:A:O2'	2.34	0.44
5:C:283:ILE:H	5:C:283:ILE:HD12	1.82	0.44
8:G:140:VAL:HA	8:G:143:ILE:HG22	1.97	0.44
9:H:6:TYR:CE1	9:H:56:ILE:HG12	2.52	0.44
10:L:145:GLU:HG3	10:L:147:THR:HG23	1.98	0.44
22:b:453:LEU:O	22:b:456:LEU:HB3	2.17	0.44
1:1:195:A:OP2	20:Y:45:ARG:NH2	2.50	0.44
1:1:1283:A:H5"	1:1:1284:U:C5	2.52	0.44
1:1:3331:U:H3	1:1:3356:A:N6	2.14	0.44
1:1:3349:U:H2'	1:1:3350:U:C6	2.52	0.44
4:B:44:THR:HG21	4:B:184:ASN:OD1	2.17	0.44
19:W:170:MET:O	19:W:172:THR:N	2.51	0.44
20:Y:53:ASP:O	20:Y:68:LYS:HA	2.17	0.44
29:r:2:PRO:HB2	29:r:6:TYR:CD2	2.53	0.44
33:y:28:LEU:C	33:y:30:GLY:H	2.24	0.44
14:P:67:VAL:HG22	14:P:82:ARG:NH2	2.32	0.44
18:V:25:MET:HE2	18:V:38:ILE:HG13	1.99	0.44
33:y:72:VAL:HG21	33:y:81:LEU:HD13	1.98	0.44
1:1:193:U:OP1	20:Y:121:LYS:HE3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:270:U:H1'	1:1:271:C:C6	2.52	0.44
1:1:756:C:H2'	1:1:757:G:C8	2.53	0.44
1:1:805:G:H2'	1:1:806:G:H8	1.82	0.44
1:1:3138:U:H5"	18:V:47:ARG:HG3	2.00	0.44
1:1:3337:A:N6	1:1:3350:U:H3	2.14	0.44
4:B:210:GLU:OE1	34:z:114:LEU:HD23	2.18	0.44
8:G:84:LYS:O	8:G:88:THR:HG23	2.17	0.44
12:N:114:ARG:CZ	12:N:157:LYS:HB3	2.47	0.44
12:N:155:VAL:O	12:N:162:ARG:NH2	2.43	0.44
14:P:5:SER:HG	14:P:118:GLN:HE22	1.63	0.44
17:S:164:LYS:HG2	25:f:37:ASP:HB3	1.99	0.44
22:b:87:TYR:CE1	22:b:154:VAL:HG13	2.52	0.44
23:d:37:ALA:O	23:d:41:ILE:HD12	2.18	0.44
1:1:265:C:O2'	1:1:266:G:O5'	2.29	0.44
1:1:1293:G:H21	19:W:13:ALA:HB2	1.82	0.44
3:3:84:LYS:NZ	3:3:88:LYS:HG2	2.33	0.44
6:E:120:THR:H	6:E:123:TYR:HB3	1.82	0.44
8:G:77:GLN:HA	8:G:80:LYS:NZ	2.33	0.44
11:M:6:ARG:HH21	11:M:60:HIS:CE1	2.35	0.44
22:b:7:LYS:NZ	29:r:2:PRO:HD2	2.33	0.44
22:b:120:GLY:HA2	22:b:125:ARG:NE	2.32	0.44
29:r:51:GLN:OE1	29:r:51:GLN:HA	2.17	0.44
1:1:257:A:H2	1:1:259:A:H62	1.64	0.44
1:1:757:G:C6	1:1:758:C:C2	3.05	0.44
1:1:3144:C:P	4:B:222:ARG:HH21	2.41	0.44
1:1:3261:U:H3	1:1:3385:G:N2	2.15	0.44
3:3:45:LEU:HB3	5:C:135:SER:OG	2.18	0.44
4:B:196:ARG:HA	4:B:199:PHE:CE2	2.53	0.44
8:G:158:ASP:HB3	8:G:159:PRO:HD3	1.99	0.44
10:L:46:ILE:HB	10:L:49:ARG:HH11	1.83	0.44
11:M:82:ASP:OD1	11:M:82:ASP:C	2.61	0.44
11:M:105:LEU:HD22	11:M:109:ASP:HB3	2.00	0.44
12:N:30:TYR:HA	12:N:33:MET:HE2	1.99	0.44
25:f:64:LYS:HA	25:f:64:LYS:HD2	1.42	0.44
26:h:30:LEU:CA	26:h:33:GLN:HE21	2.26	0.44
26:h:94:LEU:HD22	26:h:98:GLU:HB2	1.99	0.44
1:1:2920:C:H5"	1:1:2921:U:C5	2.52	0.44
1:1:3265:U:N3	1:1:3266:U:O4	2.51	0.44
1:1:3414:U:H5'	4:B:175:LYS:HD3	1.98	0.44
2:2:161:U:O2'	8:G:182[B]:ASN:ND2	2.51	0.44
4:B:188:VAL:HA	4:B:191:LYS:HD2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:146:LYS:HG3	6:E:147:ASN:OD1	2.17	0.44
8:G:139:VAL:HG23	8:G:199:ALA:HB2	2.00	0.44
10:L:145:GLU:OE2	10:L:146:GLN:N	2.51	0.44
22:b:400:ARG:O	22:b:403:GLU:HB3	2.18	0.44
22:b:448:GLU:OE2	22:b:452:LYS:HG3	2.17	0.44
23:d:83:LYS:HA	23:d:83:LYS:HD3	1.86	0.44
1:1:296:C:H2'	1:1:297:A:H8	1.83	0.44
1:1:415:A:C2	2:2:25:A:H1'	2.53	0.44
1:1:762:U:H3'	1:1:763:G:C8	2.46	0.44
1:1:836:C:H2'	1:1:837:G:C8	2.53	0.44
1:1:1236:A:H4'	29:r:55:ARG:HD2	1.99	0.44
1:1:1325:A:H5'	17:S:83:ARG:NH1	2.32	0.44
1:1:1370:C:OP1	24:e:58:LYS:HG3	2.17	0.44
1:1:3271:G:H5'	25:f:4:GLN:HA	2.00	0.44
1:1:3349:U:H2'	1:1:3350:U:H6	1.83	0.44
4:B:218:ILE:HG12	4:B:276:THR:HG23	2.00	0.44
5:C:338:LYS:HE2	5:C:338:LYS:HA	1.99	0.44
6:E:33:GLU:O	6:E:33:GLU:CD	2.60	0.44
6:E:123:TYR:OH	6:E:153:ARG:NE	2.51	0.44
9:H:24:ARG:HG3	9:H:40:ARG:HA	2.00	0.44
12:N:148:ILE:O	12:N:151:ILE:HG22	2.18	0.44
13:O:73:HIS:O	13:O:75:ARG:HD2	2.18	0.44
21:a:135:GLU:OE2	21:a:136:LYS:N	2.51	0.44
1:1:35:A:OP2	1:1:48:A:N6	2.44	0.44
1:1:216:A:H4'	1:1:218:A:C8	2.53	0.44
1:1:217:G:C4	1:1:237:U:H4'	2.53	0.44
1:1:801:G:O2'	1:1:802:G:OP1	2.33	0.44
1:1:1236:A:N1	1:1:1330:U:H5	2.15	0.44
1:1:3356:A:H2'	1:1:3357:C:O4'	2.17	0.44
3:3:70:ALA:HA	3:3:76:LEU:HG	2.00	0.44
15:Q:116:LEU:HD11	15:Q:122:VAL:HG22	1.99	0.44
25:f:38:SER:OG	25:f:41:GLU:HG3	2.18	0.44
33:y:51:THR:OG1	33:y:52:THR:N	2.51	0.44
1:1:1284:U:O2'	1:1:1294:A:H5"	2.18	0.43
1:1:3182:G:H3'	1:1:3183:A:H8	1.82	0.43
8:G:159:PRO:HG2	8:G:162:LEU:HD23	2.00	0.43
9:H:11:LEU:HB2	9:H:72:TYR:CE2	2.52	0.43
11:M:93:ALA:O	11:M:97:GLU:HG2	2.18	0.43
15:Q:50:ARG:HB3	15:Q:85:VAL:HG21	2.00	0.43
17:S:7:GLN:O	17:S:7:GLN:HG3	2.18	0.43
20:Y:8:THR:HG21	20:Y:13:LYS:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:a:137:ILE:HD12	21:a:140:ALA:HB3	2.00	0.43
33:y:28:LEU:HA	33:y:50:HIS:CD2	2.53	0.43
1:1:747:A:C5	1:1:816:A:H1'	2.53	0.43
1:1:1017:U:H2'	1:1:1018:U:C6	2.53	0.43
1:1:1332:A:O4'	29:r:44:GLY:HA2	2.18	0.43
1:1:1365:C:OP1	7:F:213:LYS:HE3	2.18	0.43
1:1:2931:C:H3'	1:1:2932:A:H8	1.82	0.43
2:2:103:G:O2'	28:j:81:GLY:O	2.29	0.43
7:F:140:TYR:N	7:F:140:TYR:CD1	2.84	0.43
8:G:94:LEU:HD23	8:G:189:VAL:HG11	1.99	0.43
13:O:11:ASP:HB2	13:O:118:ARG:HB3	2.01	0.43
17:S:142:LEU:O	17:S:147:LEU:HD22	2.18	0.43
22:b:424:ASP:HB3	22:b:427:TRP:CD1	2.53	0.43
29:r:65:ILE:HD12	29:r:65:ILE:HA	1.89	0.43
1:1:1299:G:N2	1:1:1304:A:H62	2.16	0.43
1:1:3477:A:H5'	1:1:3478:G:H5"	1.99	0.43
4:B:94:GLU:HG2	4:B:156:SER:OG	2.18	0.43
6:E:161:ASP:O	6:E:165:LEU:HD23	2.18	0.43
7:F:89:LYS:HD3	7:F:89:LYS:HA	1.73	0.43
8:G:91:PHE:CZ	8:G:185:ARG:HB3	2.54	0.43
8:G:190:ILE:O	8:G:190:ILE:HG13	2.18	0.43
10:L:152:VAL:HG11	26:h:120:LEU:HD13	2.00	0.43
11:M:86:LYS:O	11:M:89:SER:OG	2.33	0.43
13:O:90:PRO:O	13:O:96:GLY:HA3	2.18	0.43
22:b:207:VAL:H	29:r:3:GLN:HE21	1.65	0.43
23:d:79:ARG:HB3	23:d:97:GLN:CG	2.48	0.43
24:e:81:LEU:O	24:e:81:LEU:HG	2.17	0.43
33:y:197:LEU:HD21	33:y:222:PHE:HE2	1.82	0.43
1:1:712:U:H2'	1:1:713:G:C8	2.53	0.43
1:1:1000:G:C5	1:1:1001:C:C4	3.06	0.43
1:1:1155:U:H1'	1:1:1165:G:H22	1.84	0.43
1:1:1481:G:O2'	1:1:2443:G:O6	2.36	0.43
1:1:3113:A:H2'	1:1:3114:C:C6	2.53	0.43
3:3:14:GLU:O	3:3:19:ARG:NH2	2.51	0.43
4:B:123:PHE:CG	4:B:124:LYS:N	2.86	0.43
4:B:171:LEU:HD21	4:B:333:LYS:HB2	2.01	0.43
7:F:104:PRO:HA	7:F:107:ARG:HG2	2.01	0.43
15:Q:82:THR:HG23	15:Q:139:VAL:HG23	2.00	0.43
22:b:416:LEU:HG	33:y:83:HIS:CE1	2.53	0.43
23:d:16:ASP:OD1	23:d:77:ARG:NE	2.51	0.43
29:r:149:MET:HA	29:r:171:ILE:H	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:785:C:N3	1:1:807:G:N1	2.66	0.43
1:1:1020:U:H2'	1:1:1021:A:C8	2.54	0.43
1:1:2445:A:H2'	1:1:2446:A:C8	2.53	0.43
1:1:2993:G:H22	29:r:6:TYR:H	1.65	0.43
1:1:3426:G:H2'	1:1:3427:G:H8	1.84	0.43
2:2:143:G:C6	2:2:144:G:C5	3.07	0.43
3:3:95:GLN:HA	3:3:98:LEU:HD23	2.00	0.43
4:B:88:GLY:HA3	4:B:161:LEU:HD23	1.99	0.43
4:B:144:ILE:H	4:B:144:ILE:HD12	1.83	0.43
9:H:5:ILE:HG22	9:H:58:TRP:HE3	1.84	0.43
9:H:112:ILE:HB	9:H:122:ARG:HB2	2.00	0.43
21:a:123:ILE:HA	21:a:143:VAL:O	2.18	0.43
22:b:14:ASP:O	22:b:16:ASN:N	2.52	0.43
22:b:448:GLU:OE1	22:b:452:LYS:HE3	2.18	0.43
23:d:77:ARG:CZ	23:d:106:MET:HE2	2.47	0.43
27:i:65:LYS:HD2	27:i:66:ARG:HE	1.83	0.43
1:1:148:C:H2'	1:1:149:G:C8	2.54	0.43
1:1:1000:G:H2'	1:1:1001:C:O4'	2.19	0.43
1:1:3318:A:C4	25:f:6:HIS:CE1	3.07	0.43
1:1:3332:U:H2'	1:1:3333:G:H8	1.78	0.43
4:B:213:GLU:HB3	34:z:110:PHE:CE1	2.53	0.43
5:C:9:SER:HA	5:C:21:THR:HG22	2.01	0.43
8:G:86:THR:HA	8:G:89:GLN:NE2	2.34	0.43
13:O:29:LEU:HD22	13:O:95:ARG:NH1	2.34	0.43
14:P:7:SER:N	14:P:8:PRO:HD2	2.34	0.43
14:P:30:ARG:HD2	14:P:63:PHE:CE2	2.53	0.43
17:S:154:ARG:HG2	17:S:155:ARG:N	2.34	0.43
22:b:79:HIS:O	22:b:83:LEU:HG	2.17	0.43
22:b:418:ASP:HA	22:b:428:LYS:HE2	1.99	0.43
31:u:85:ASN:O	31:u:89:THR:HG23	2.17	0.43
1:1:550:G:H1	1:1:575:G:H1	1.66	0.43
1:1:625:U:O3'	1:1:627:G:N1	2.52	0.43
1:1:1160:A:C6	1:1:1161:A:C5	3.06	0.43
1:1:1237:G:H1'	29:r:51:GLN:OE1	2.18	0.43
4:B:36:ASP:OD1	4:B:36:ASP:N	2.51	0.43
5:C:208:LEU:HD12	5:C:228:GLU:O	2.18	0.43
6:E:114:VAL:HA	6:E:163:LYS:HD3	2.01	0.43
7:F:134:LEU:HD23	7:F:134:LEU:HA	1.85	0.43
8:G:115:ALA:O	8:G:120:LYS:N	2.51	0.43
22:b:88:ASP:O	22:b:91:HIS:N	2.51	0.43
33:y:107:ILE:HB	33:y:118:HIS:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:z:109:ASN:HA	34:z:112:LYS:HB2	2.01	0.43
1:1:541:G:H2'	1:1:542:G:H8	1.83	0.43
1:1:802:G:H2'	1:1:803:A:H8	1.84	0.43
1:1:1207:C:H4'	13:O:90:PRO:HD3	2.00	0.43
1:1:3259:C:H2'	1:1:3260:A:C4'	2.48	0.43
8:G:85:ASN:OD1	8:G:89:GLN:NE2	2.51	0.43
18:V:10:GLY:H	33:y:57:ARG:HH22	1.66	0.43
22:b:160:ARG:HB3	29:r:4:ASN:HA	2.00	0.43
25:f:14:HIS:NE2	25:f:29:SER:HB3	2.33	0.43
33:y:54:GLY:N	33:y:80:GLU:OE1	2.49	0.43
1:1:189:G:H22	1:1:243:C:H6	1.67	0.43
1:1:361:G:O2'	1:1:372:G:O6	2.25	0.43
1:1:517:U:H2'	1:1:518:U:O4'	2.19	0.43
1:1:3275:A:O2'	13:O:118:ARG:NH1	2.52	0.43
1:1:3314:U:C4	11:M:114:MET:HE1	2.54	0.43
1:1:3380:A:H2'	1:1:3381:U:H5'	2.00	0.43
1:1:3434:G:O2'	31:u:50:ALA:HB3	2.19	0.43
3:3:51:ALA:HA	3:3:63:TYR:O	2.19	0.43
6:E:189:ARG:HB3	6:E:191:HIS:CE1	2.54	0.43
17:S:90:TYR:OH	17:S:92:GLU:OE2	2.20	0.43
22:b:18:PHE:CD1	22:b:18:PHE:C	2.97	0.43
23:d:81:SER:O	23:d:94:THR:HA	2.18	0.43
24:e:15:LYS:HE3	24:e:15:LYS:HB3	1.92	0.43
28:j:82:LYS:HD3	28:j:83:PRO:CD	2.49	0.43
1:1:1418:U:OP1	5:C:140:ARG:NH2	2.46	0.43
1:1:1506:U:H2'	1:1:1507:G:C8	2.54	0.43
1:1:3196:U:H3	1:1:3230:G:H1	1.66	0.43
1:1:3346:U:H5'	1:1:3347:G:O4'	2.19	0.43
4:B:272:TYR:HE1	4:B:334:ARG:HH12	1.67	0.43
7:F:96:ILE:HD11	7:F:235:ALA:HB2	2.00	0.43
7:F:193:HIS:O	7:F:197:THR:OG1	2.35	0.43
18:V:106:ASN:ND2	18:V:110:GLU:O	2.52	0.43
20:Y:98:ILE:HD12	20:Y:98:ILE:N	2.33	0.43
21:a:113:GLY:H	21:a:132:ARG:NH1	2.17	0.43
21:a:134:GLU:OE1	21:a:134:GLU:N	2.42	0.43
22:b:34:ILE:HD12	22:b:46:PHE:HD2	1.83	0.43
22:b:444:PHE:HE1	31:u:94:MET:HE2	1.84	0.43
31:u:20:MET:HE2	31:u:28:VAL:HG21	2.01	0.43
1:1:624:U:O2'	1:1:628:U:O4	2.37	0.42
1:1:683:G:N2	5:C:95:MET:HB2	2.34	0.42
1:1:1506:U:H2'	1:1:1507:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1937:G:H2'	1:1:1938:A:C8	2.54	0.42
1:1:2435:U:H2'	1:1:2436:A:O4'	2.19	0.42
1:1:3258:G:H22	1:1:3387:G:H1	1.67	0.42
1:1:3279:A:OP2	13:O:13:LYS:NZ	2.46	0.42
2:2:131:G:O2'	2:2:132:G:OP1	2.27	0.42
3:3:69:ARG:HE	3:3:75:LYS:CG	2.32	0.42
4:B:187:SER:O	4:B:191:LYS:HG3	2.19	0.42
8:G:87:ALA:O	8:G:91:PHE:HD1	2.02	0.42
9:H:90:MET:HG2	9:H:179:VAL:HA	2.01	0.42
26:h:106:GLN:OE1	26:h:106:GLN:N	2.52	0.42
33:y:111:ASN:OD1	33:y:113:TYR:N	2.37	0.42
1:1:674:A:HO2'	1:1:675:C:P	2.42	0.42
1:1:756:C:C2	1:1:757:G:C8	3.06	0.42
1:1:2460:A:H2'	1:1:2460:A:OP2	2.18	0.42
1:1:3398:U:H2'	1:1:3399:C:H6	1.83	0.42
4:B:90:VAL:HG22	4:B:104:THR:HG23	2.00	0.42
4:B:150:ARG:HG2	4:B:154:TYR:HD2	1.84	0.42
10:L:166:ILE:CG1	10:L:167:THR:N	2.74	0.42
29:r:12:ARG:NH1	29:r:12:ARG:HB2	2.34	0.42
35:T:146:ASN:OD1	35:T:146:ASN:N	2.52	0.42
1:1:752:G:H1	1:1:773:C:H42	1.67	0.42
1:1:757:G:C2'	1:1:758:C:H5'	2.50	0.42
1:1:999:A:H2'	1:1:1000:G:O4'	2.18	0.42
1:1:1154:U:H3'	1:1:1155:U:C5	2.54	0.42
1:1:1309:A:O2'	1:1:1310:C:O5'	2.38	0.42
1:1:1325:A:H2'	1:1:1326:G:H8	1.85	0.42
1:1:2983:U:OP1	22:b:28:ARG:HD2	2.19	0.42
1:1:2999:U:H2'	1:1:3000:U:H6	1.83	0.42
4:B:66:LYS:HB2	18:V:13:TYR:CE2	2.54	0.42
7:F:210:TRP:CD1	7:F:211:PRO:HD2	2.54	0.42
27:i:28:LYS:HE3	27:i:28:LYS:HB2	1.91	0.42
1:1:107:A:H2'	1:1:108:A:O4'	2.20	0.42
1:1:189:G:H1	1:1:243:C:H5	1.65	0.42
1:1:742:A:P	21:a:132:ARG:CZ	3.08	0.42
1:1:1495:A:H2'	1:1:1496:A:H8	1.84	0.42
1:1:3113:A:H2'	1:1:3114:C:H6	1.84	0.42
3:3:48:SER:OG	3:3:49:ARG:N	2.52	0.42
15:Q:78:GLN:HB2	15:Q:79:ASN:H	1.55	0.42
23:d:21:MET:O	23:d:25:LEU:N	2.52	0.42
24:e:69:LYS:HB2	24:e:89:TYR:CD1	2.54	0.42
31:u:84:ARG:HA	31:u:87:ILE:HG22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:251:U:H2'	1:1:252:A:C8	2.55	0.42
1:1:621:G:H2'	1:1:622:G:C8	2.54	0.42
1:1:747:A:H8	1:1:815:A:H4'	1.84	0.42
1:1:772:A:N6	1:1:773:C:O2	2.52	0.42
1:1:997:A:H3'	1:1:998:U:H5"	2.02	0.42
1:1:1147:G:O6	1:1:1173:G:N2	2.46	0.42
1:1:2989:C:OP2	9:H:166:ARG:NH2	2.53	0.42
2:2:30:U:OP1	20:Y:11:ARG:NH2	2.47	0.42
4:B:377:LYS:NZ	31:u:105:GLU:OE1	2.50	0.42
12:N:44:ARG:NH1	12:N:120:TRP:HE3	2.17	0.42
18:V:130:ARG:HE	18:V:130:ARG:HB3	1.69	0.42
22:b:375:PRO:O	33:y:113:TYR:OH	2.35	0.42
25:f:74:ARG:HG3	25:f:75:PRO:HD2	2.02	0.42
26:h:14:GLU:H	26:h:14:GLU:CD	2.21	0.42
27:i:56:MET:HA	27:i:59:ILE:HG12	2.02	0.42
31:u:50:ALA:HA	31:u:55:TYR:CE2	2.55	0.42
1:1:59:G:H4'	1:1:60:A:H4'	2.02	0.42
1:1:324:U:C5	27:i:25:SER:HB3	2.54	0.42
1:1:1389:A:O2'	15:Q:30:LYS:HE2	2.20	0.42
1:1:1412:U:O2	1:1:1464:U:H1'	2.19	0.42
2:2:126:C:H2'	2:2:127:U:C6	2.55	0.42
2:2:143:G:H2'	2:2:144:G:O4'	2.20	0.42
5:C:216:GLY:O	5:C:219:LYS:HG2	2.18	0.42
12:N:99:ARG:HH11	12:N:167:ILE:HB	1.85	0.42
12:N:150:TRP:O	12:N:156:HIS:ND1	2.53	0.42
14:P:90:PHE:O	14:P:94:LEU:HD23	2.20	0.42
1:1:613:A:C6	1:1:635:G:H1'	2.55	0.42
1:1:1155:U:O2	1:1:1155:U:H2'	2.20	0.42
1:1:1543:A:O5'	1:1:1543:A:H8	2.02	0.42
1:1:3382:C:H2'	1:1:3383:U:C6	2.54	0.42
1:1:3385:G:N7	1:1:3386:U:N3	2.68	0.42
1:1:3398:U:H2'	1:1:3399:C:C6	2.55	0.42
1:1:3403:U:H1'	1:1:3414:U:O2	2.20	0.42
4:B:227:GLU:HG2	4:B:270:ALA:HB2	2.01	0.42
5:C:10:ILE:HD11	5:C:22:LEU:HG	2.01	0.42
21:a:137:ILE:HA	21:a:140:ALA:HB3	2.01	0.42
22:b:50:LYS:O	22:b:54:THR:HG22	2.19	0.42
23:d:39:LYS:O	23:d:42:VAL:HG22	2.19	0.42
1:1:191:U:H3	1:1:241:G:H1	1.68	0.42
1:1:757:G:H5'	15:Q:136:SER:HA	2.00	0.42
1:1:990:C:C2	1:1:996:G:N2	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:997:A:C5	1:1:998:U:C4	3.07	0.42
1:1:1314:C:O2'	1:1:1315:C:OP1	2.33	0.42
1:1:3109:U:OP2	34:z:86:PRO:HD2	2.20	0.42
1:1:3217:U:H1'	1:1:3218:A:H5"	2.01	0.42
1:1:3260:A:N6	1:1:3385:G:C2	2.85	0.42
1:1:3359:U:H3'	1:1:3359:U:O2	2.20	0.42
1:1:3472:G:H2'	1:1:3473:A:C8	2.54	0.42
4:B:213:GLU:HB3	34:z:110:PHE:HZ	1.81	0.42
6:E:46:THR:HG22	6:E:48:LEU:HD22	2.01	0.42
8:G:73:PRO:HA	8:G:76:ALA:HB3	2.01	0.42
14:P:92:TYR:O	14:P:96:LYS:HG2	2.20	0.42
21:a:124:VAL:HG13	21:a:144:VAL:HG23	2.02	0.42
33:y:160:LEU:HD11	33:y:221:ILE:HG21	2.00	0.42
1:1:178:U:O2	1:1:254:G:N2	2.48	0.42
1:1:1182:U:O4	30:s:16:ARG:NH1	2.53	0.42
1:1:2993:G:H22	29:r:5:GLU:HA	1.84	0.42
1:1:3138:U:OP1	18:V:47:ARG:HD2	2.19	0.42
1:1:3333:G:C6	1:1:3334:A:C6	3.07	0.42
7:F:241:HIS:NE2	17:S:32:ASN:HB2	2.34	0.42
17:S:11:ARG:HE	35:T:141:VAL:HG13	1.85	0.42
17:S:147:LEU:HD12	17:S:147:LEU:HA	1.72	0.42
18:V:84:ARG:HD3	18:V:98:GLU:O	2.19	0.42
22:b:44:ARG:O	22:b:117:LEU:HD21	2.20	0.42
24:e:52:ILE:HD12	24:e:52:ILE:HA	1.91	0.42
31:u:69:LEU:HD12	31:u:97:VAL:CG2	2.50	0.42
33:y:112:ASP:HB2	33:y:113:TYR:CE2	2.55	0.42
1:1:353:G:O2'	2:2:33:G:N3	2.52	0.42
1:1:723:C:H2'	1:1:724:A:H8	1.84	0.42
1:1:841:G:H2'	1:1:842:A:C8	2.55	0.42
1:1:1218:C:H5	1:1:1350:G:N1	2.16	0.42
1:1:3262:G:C6	1:1:3263:A:C4	3.07	0.42
1:1:3487:C:H4'	23:d:15:ARG:NH1	2.35	0.42
3:3:22:GLY:HA3	3:3:25:GLN:NE2	2.35	0.42
3:3:114:ARG:HH11	24:e:84:MET:HA	1.84	0.42
3:3:121:LYS:O	3:3:124:ARG:HG2	2.20	0.42
4:B:136:LYS:HA	4:B:139:GLU:HG3	2.02	0.42
6:E:154:ILE:N	6:E:154:ILE:HD13	2.34	0.42
8:G:105:LYS:O	8:G:109:LEU:HG	2.20	0.42
11:M:100:LYS:O	11:M:103:SER:OG	2.34	0.42
14:P:82:ARG:HG3	14:P:83:TRP:N	2.35	0.42
17:S:34:SER:HA	17:S:37:LYS:HE3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:b:78:PHE:HD2	22:b:246:HIS:O	2.03	0.42
30:s:18:ARG:HB2	30:s:21:LYS:HE3	2.02	0.42
33:y:138:PHE:HB3	33:y:140:GLN:HG3	2.02	0.42
1:1:152:U:OP1	1:1:154:G:H5'	2.19	0.41
1:1:304:A:O2'	1:1:305:A:H5'	2.20	0.41
1:1:741:G:N1	21:a:72:THR:HG21	2.33	0.41
1:1:1498:G:H1'	1:1:1545:U:O2	2.20	0.41
1:1:3082:A:H5'	13:O:69:ARG:NH2	2.34	0.41
1:1:3131:C:H2'	1:1:3132:G:C8	2.55	0.41
1:1:3171:G:H5"	23:d:67:ARG:HD2	2.02	0.41
1:1:3389:G:O2'	1:1:3390:G:H5"	2.21	0.41
4:B:79:ILE:HD11	4:B:338:LEU:HD11	2.02	0.41
7:F:95:ARG:NH2	7:F:98:GLY:O	2.43	0.41
14:P:154:GLU:N	14:P:154:GLU:OE1	2.52	0.41
24:e:14:PHE:CG	24:e:50:PRO:HG3	2.54	0.41
33:y:7:PHE:HD1	33:y:34:PHE:CG	2.37	0.41
1:1:238:U:H4'	1:1:239:U:H3'	2.03	0.41
1:1:276:A:O5'	12:N:47:LYS:NZ	2.52	0.41
1:1:551:C:H2'	1:1:552:U:C6	2.54	0.41
6:E:60:LEU:CD1	6:E:96:VAL:HG21	2.50	0.41
7:F:187:SER:OG	7:F:190:ASP:OD2	2.28	0.41
10:L:148:ASP:OD1	10:L:151:ALA:N	2.53	0.41
18:V:26:ASN:OD1	32:w:242:ARG:HA	2.21	0.41
24:e:39:VAL:HA	24:e:46:THR:HG21	2.02	0.41
1:1:646:A:O2'	1:1:647:A:C8	2.73	0.41
1:1:989:C:H2'	1:1:990:C:H6	1.85	0.41
1:1:3157:G:H2'	1:1:3158:G:H8	1.84	0.41
3:3:7:ILE:O	3:3:11:VAL:HG22	2.20	0.41
21:a:100:VAL:CG2	21:a:125:GLN:HE21	2.33	0.41
22:b:394:ASN:O	22:b:395:ARG:C	2.63	0.41
22:b:420:TYR:HA	33:y:87:SER:HA	2.01	0.41
22:b:426:SER:O	22:b:428:LYS:N	2.53	0.41
24:e:16:ARG:HD3	24:e:25:VAL:HG13	2.01	0.41
29:r:5:GLU:H	29:r:5:GLU:CD	2.24	0.41
1:1:641:G:H2'	1:1:642:A:C8	2.55	0.41
1:1:752:G:H1	1:1:773:C:N4	2.18	0.41
1:1:753:G:N7	1:1:770:G:C6	2.88	0.41
4:B:323:MET:HE3	4:B:323:MET:HB2	1.84	0.41
5:C:288:ASP:CG	5:C:291:ARG:HG3	2.45	0.41
7:F:91:ILE:HG23	7:F:126:PHE:HB2	2.01	0.41
9:H:90:MET:HE2	9:H:144:LEU:HD11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:V:26:ASN:ND2	18:V:99:ASP:HB2	2.36	0.41
22:b:412:TYR:CE1	22:b:414:VAL:HG22	2.55	0.41
1:1:166:A:H2'	1:1:167:G:H8	1.85	0.41
1:1:402:U:P	20:Y:86:ARG:HH22	2.44	0.41
1:1:3258:G:H2'	1:1:3259:C:C6	2.55	0.41
1:1:3265:U:C2	1:1:3266:U:C4	3.08	0.41
1:1:3371:U:C5	6:E:126:LYS:HD3	2.56	0.41
2:2:144:G:C6	2:2:145:C:C4	3.09	0.41
4:B:112:GLU:HG3	4:B:122:TRP:CZ2	2.54	0.41
7:F:146:PRO:HA	7:F:243:ASN:OD1	2.20	0.41
8:G:148:ALA:HA	8:G:201:THR:HG22	2.03	0.41
18:V:54:ALA:HB1	18:V:80:VAL:HG21	2.02	0.41
21:a:75:LEU:HG	21:a:117:LEU:HD21	2.03	0.41
22:b:121:ASP:H	22:b:125:ARG:HD3	1.84	0.41
25:f:21:LYS:HG3	25:f:22:HIS:CD2	2.54	0.41
27:i:14:THR:C	27:i:15:LEU:HD22	2.45	0.41
1:1:58:G:H4'	12:N:155:VAL:HG12	2.01	0.41
1:1:188:C:C2'	1:1:189:G:H5'	2.51	0.41
1:1:356:A:N3	1:1:360:A:O2'	2.54	0.41
1:1:511:C:H5"	6:E:99:ARG:HG3	2.00	0.41
1:1:512:A:H4'	6:E:46:THR:OG1	2.20	0.41
1:1:591:G:O3'	1:1:592:U:H2'	2.20	0.41
1:1:625:U:C2	1:1:626:C:C4	3.09	0.41
1:1:745:G:OP2	1:1:778:G:N2	2.53	0.41
1:1:3372:C:OP2	6:E:95:ARG:HB2	2.19	0.41
2:2:80:A:N6	2:2:87:A:H61	2.19	0.41
3:3:49:ARG:HG2	3:3:100:TRP:HE1	1.86	0.41
9:H:19:VAL:HG11	9:H:53:ILE:HD11	2.03	0.41
9:H:35:LEU:HD12	9:H:78:MET:HB2	2.02	0.41
13:O:47:HIS:CE1	13:O:50:ARG:HB2	2.55	0.41
13:O:189:ASN:OD1	13:O:189:ASN:C	2.63	0.41
17:S:139:VAL:O	17:S:143:LEU:HD23	2.20	0.41
21:a:137:ILE:HD11	21:a:142:GLY:HA3	2.01	0.41
22:b:397:ILE:HA	22:b:397:ILE:HD12	1.82	0.41
26:h:3:LEU:HB2	26:h:52:ASP:OD1	2.20	0.41
26:h:76:LYS:C	26:h:77:TYR:HD1	2.28	0.41
1:1:773:C:OP1	1:1:773:C:H4'	2.21	0.41
1:1:3081:U:H2'	1:1:3082:A:O4'	2.20	0.41
4:B:183:VAL:O	4:B:191:LYS:NZ	2.36	0.41
7:F:217:PRO:HB3	7:F:249:MET:HG2	2.01	0.41
9:H:39:LEU:HD22	9:H:46:MET:HE1	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:b:452:LYS:HD3	31:u:71:VAL:HG11	2.03	0.41
24:e:84:MET:HG2	24:e:85:HIS:CD2	2.54	0.41
25:f:102:MET:HB3	25:f:104:TYR:CE2	2.56	0.41
26:h:34:LYS:HE2	26:h:38:GLY:HA3	2.02	0.41
1:1:26:A:N3	1:1:336:U:O2'	2.47	0.41
1:1:571:G:H2'	1:1:572:A:O4'	2.20	0.41
1:1:714:A:H5'	1:1:717:A:N6	2.32	0.41
1:1:754:A:O4'	1:1:771:C:N4	2.52	0.41
1:1:767:C:C4	1:1:768:G:C8	3.08	0.41
1:1:1261:G:H4'	19:W:49:ARG:HA	2.02	0.41
1:1:3269:A:H1'	1:1:3270:U:C6	2.56	0.41
6:E:117:GLU:H	6:E:117:GLU:CD	2.24	0.41
8:G:93:LEU:HD12	8:G:96:LYS:HD2	2.03	0.41
8:G:101:THR:HG22	8:G:103:ALA:N	2.36	0.41
9:H:37:GLN:OE1	9:H:37:GLN:HA	2.21	0.41
17:S:43:PHE:HE1	17:S:121:ARG:HG2	1.86	0.41
20:Y:84:VAL:HG12	20:Y:96:VAL:CG2	2.50	0.41
21:a:77:ARG:NH1	21:a:80:THR:OG1	2.54	0.41
21:a:100:VAL:HA	21:a:123:ILE:O	2.20	0.41
22:b:118:LYS:HE2	22:b:118:LYS:HA	2.03	0.41
27:i:54:ARG:NH2	27:i:74:ARG:HH21	2.19	0.41
33:y:118:HIS:ND1	33:y:146:VAL:HB	2.36	0.41
1:1:273:A:H5"	1:1:274:A:OP2	2.21	0.41
1:1:713:G:H5"	1:1:714:A:OP2	2.20	0.41
1:1:747:A:C8	1:1:815:A:H4'	2.56	0.41
1:1:800:U:H2'	1:1:801:G:O4'	2.20	0.41
1:1:1259:A:N6	1:1:1312:U:H3	2.15	0.41
1:1:1294:A:N3	1:1:1294:A:H2'	2.36	0.41
1:1:3010:U:O2'	1:1:3030:U:H1'	2.20	0.41
1:1:3404:G:O2'	1:1:3406:A:N6	2.53	0.41
2:2:84:C:H2'	2:2:85:A:C8	2.56	0.41
2:2:142:A:H2'	2:2:143:G:C8	2.55	0.41
5:C:5:ARG:HA	5:C:6:PRO:HD3	1.91	0.41
6:E:58:CYS:HB2	6:E:101:VAL:HG13	2.03	0.41
10:L:126:PHE:HD2	26:h:117:LYS:HE3	1.84	0.41
12:N:115:VAL:HA	12:N:134:LEU:HA	2.03	0.41
17:S:22:LYS:HA	17:S:22:LYS:HD3	1.96	0.41
22:b:149:GLU:O	22:b:153:GLN:HG2	2.21	0.41
26:h:57:LEU:HD23	26:h:57:LEU:HA	1.78	0.41
31:u:42:MET:HE2	31:u:42:MET:HB2	2.01	0.41
33:y:28:LEU:HD23	33:y:29:GLY:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:y:157:GLN:OE1	33:y:157:GLN:HA	2.20	0.41
1:1:1226:A:H1'	1:1:1350:G:H4'	2.03	0.41
1:1:1938:A:OP1	23:d:39:LYS:NZ	2.54	0.41
4:B:80:GLU:HB2	4:B:317:VAL:HG13	2.03	0.41
14:P:30:ARG:HD2	14:P:63:PHE:HE2	1.86	0.41
17:S:108:ASP:OD1	17:S:109:MET:HE2	2.21	0.41
1:1:768:G:C5	1:1:769:U:C4	3.09	0.40
1:1:3096:G:H2'	1:1:3097:U:H6	1.86	0.40
5:C:32:ILE:HD13	5:C:32:ILE:N	2.36	0.40
5:C:212:ASN:OD1	5:C:233:ARG:NH2	2.55	0.40
7:F:228:HIS:ND1	7:F:230:ILE:HG12	2.37	0.40
9:H:8:ASP:OD2	9:H:54:LYS:NZ	2.44	0.40
17:S:22:LYS:HA	35:T:146:ASN:HD22	1.86	0.40
18:V:88:ARG:HB3	18:V:94:TYR:CE2	2.56	0.40
22:b:55:GLN:CD	22:b:55:GLN:C	2.90	0.40
22:b:406:ASN:HB3	22:b:412:TYR:HD2	1.86	0.40
26:h:95:THR:O	26:h:96:PRO:C	2.63	0.40
27:i:13:LYS:HE3	27:i:15:LEU:HD21	2.02	0.40
27:i:52:GLU:O	27:i:56:MET:HG2	2.21	0.40
29:r:60:GLN:OE1	29:r:60:GLN:HA	2.22	0.40
33:y:218:CYS:HA	33:y:221:ILE:HG22	2.03	0.40
1:1:1223:C:O2	30:s:4:LEU:HB3	2.21	0.40
1:1:2994:C:O2'	1:1:2996:G:OP2	2.39	0.40
1:1:3102:A:H2'	1:1:3103:U:O4'	2.21	0.40
1:1:3259:C:C3'	1:1:3260:A:H4'	2.51	0.40
1:1:3333:G:C6	1:1:3334:A:C5	3.09	0.40
9:H:5:ILE:HG12	9:H:59:HIS:NE2	2.37	0.40
10:L:185:TYR:HE2	10:L:192:ARG:HE	1.68	0.40
12:N:65:ARG:HD2	12:N:127:TYR:CD2	2.55	0.40
12:N:165:THR:OG1	12:N:166:SER:N	2.53	0.40
17:S:32:ASN:OD1	17:S:32:ASN:C	2.64	0.40
17:S:151:LEU:HD12	17:S:152:PRO:HD2	2.02	0.40
18:V:84:ARG:HD2	18:V:97:PHE:O	2.20	0.40
22:b:26:THR:HG22	22:b:53:PHE:HD1	1.87	0.40
23:d:16:ASP:OD1	23:d:16:ASP:C	2.63	0.40
27:i:42:VAL:HA	27:i:45:VAL:HG12	2.03	0.40
33:y:4:ARG:HB3	33:y:208:LEU:HD12	2.03	0.40
1:1:86:G:O2'	1:1:98:G:O6	2.35	0.40
1:1:146:U:OP1	8:G:106:LYS:NZ	2.51	0.40
1:1:312:G:C5	1:1:313:U:C2	3.10	0.40
1:1:960:C:H2'	1:1:961:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:73:PRO:HA	3:3:76:LEU:HB2	2.02	0.40
5:C:159:GLN:O	5:C:215:THR:OG1	2.32	0.40
13:O:151:ASN:OD1	13:O:151:ASN:C	2.64	0.40
25:f:49:ARG:HD3	25:f:70:GLY:O	2.21	0.40
28:j:67:LEU:HD23	28:j:67:LEU:HA	1.87	0.40
1:1:429:G:O6	1:1:2471:C:O2'	2.31	0.40
1:1:1914:A:H61	1:1:1926:U:H3	1.70	0.40
1:1:2932:A:H8	1:1:2932:A:OP2	2.05	0.40
1:1:3123:A:H2'	1:1:3124:G:O4'	2.22	0.40
1:1:3487:C:H2'	1:1:3488:C:C6	2.55	0.40
2:2:141:A:H2'	2:2:142:A:C8	2.57	0.40
2:2:162:C:H2'	2:2:163:A:C8	2.57	0.40
3:3:33:ASN:HB2	3:3:44:PRO:CG	2.49	0.40
3:3:34:VAL:HG11	3:3:108:CYS:SG	2.61	0.40
4:B:196:ARG:HA	4:B:199:PHE:HD2	1.86	0.40
4:B:293:ASN:HB2	4:B:321:PHE:HE1	1.86	0.40
9:H:5:ILE:HG22	9:H:58:TRP:CE3	2.55	0.40
10:L:164:LYS:HA	10:L:165:PRO:HD3	1.92	0.40
10:L:166:ILE:HD12	10:L:168:GLU:H	1.87	0.40
12:N:148:ILE:O	12:N:148:ILE:HG13	2.22	0.40
12:N:159:ARG:HB3	12:N:164:LEU:HB2	2.03	0.40
17:S:48:ASN:O	17:S:48:ASN:OD1	2.40	0.40
29:r:68:HIS:CE1	29:r:72:ASN:HD21	2.39	0.40
31:u:92:ASN:HA	31:u:95:LYS:HE3	2.04	0.40
1:1:182:G:H1	1:1:250:A:H61	1.69	0.40
1:1:444:A:N1	1:1:647:A:N6	2.69	0.40
1:1:994:A:C4	1:1:995:G:H1'	2.57	0.40
1:1:1009:C:N4	1:1:1135:G:H1	2.19	0.40
1:1:1494:A:H4'	23:d:55:ARG:NH1	2.36	0.40
1:1:3133:U:OP1	4:B:348:ARG:NH1	2.54	0.40
1:1:3268:U:H3'	1:1:3268:U:OP2	2.21	0.40
1:1:3318:A:H4'	1:1:3319:G:H5'	2.04	0.40
1:1:3333:G:C6	1:1:3355:G:N1	2.89	0.40
2:2:142:A:H2'	2:2:143:G:H8	1.86	0.40
3:3:8:TRP:CE3	3:3:12:GLY:HA3	2.57	0.40
5:C:314:HIS:CE1	7:F:169:PRO:HG2	2.56	0.40
6:E:76:LEU:HD12	6:E:76:LEU:HA	1.95	0.40
9:H:90:MET:HE1	9:H:159:ILE:HB	2.02	0.40
9:H:132:VAL:HG22	9:H:144:LEU:HG	2.03	0.40
10:L:118:VAL:CG2	10:L:153:LEU:HD11	2.51	0.40
22:b:149:GLU:OE1	22:b:149:GLU:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:b:413:ASN:OD1	22:b:413:ASN:C	2.65	0.40
23:d:32:LYS:C	23:d:35:PRO:HD2	2.47	0.40
35:T:144:GLU:HG2	35:T:145:ASN:H	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	121/302 (40%)	115 (95%)	6 (5%)	0	100	100
4	B	331/388 (85%)	320 (97%)	11 (3%)	0	100	100
5	C	321/363 (88%)	308 (96%)	13 (4%)	0	100	100
6	E	163/195 (84%)	144 (88%)	17 (10%)	2 (1%)	11	43
7	F	215/250 (86%)	202 (94%)	13 (6%)	0	100	100
8	G	168/259 (65%)	151 (90%)	14 (8%)	3 (2%)	7	35
9	H	181/190 (95%)	168 (93%)	13 (7%)	0	100	100
10	L	178/208 (86%)	161 (90%)	15 (8%)	2 (1%)	12	44
11	M	123/134 (92%)	115 (94%)	7 (6%)	1 (1%)	16	51
12	N	160/201 (80%)	156 (98%)	4 (2%)	0	100	100
13	O	194/197 (98%)	190 (98%)	4 (2%)	0	100	100
14	P	150/187 (80%)	144 (96%)	6 (4%)	0	100	100
15	Q	131/187 (70%)	127 (97%)	4 (3%)	0	100	100
16	R	54/193 (28%)	53 (98%)	1 (2%)	0	100	100
17	S	164/176 (93%)	153 (93%)	11 (7%)	0	100	100
18	V	135/139 (97%)	130 (96%)	5 (4%)	0	100	100
19	W	207/241 (86%)	195 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	Y	123/126 (98%)	115 (94%)	8 (6%)	0	100	100
21	a	90/148 (61%)	86 (96%)	4 (4%)	0	100	100
22	b	407/642 (63%)	388 (95%)	17 (4%)	2 (0%)	25	60
23	d	93/113 (82%)	90 (97%)	3 (3%)	0	100	100
24	e	116/127 (91%)	115 (99%)	1 (1%)	0	100	100
25	f	104/108 (96%)	95 (91%)	9 (9%)	0	100	100
26	h	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
27	i	92/99 (93%)	87 (95%)	5 (5%)	0	100	100
28	j	69/91 (76%)	64 (93%)	5 (7%)	0	100	100
29	r	158/260 (61%)	157 (99%)	1 (1%)	0	100	100
30	s	28/470 (6%)	27 (96%)	1 (4%)	0	100	100
31	u	112/192 (58%)	106 (95%)	6 (5%)	0	100	100
32	w	103/802 (13%)	100 (97%)	3 (3%)	0	100	100
33	y	223/244 (91%)	209 (94%)	14 (6%)	0	100	100
34	z	33/117 (28%)	30 (91%)	3 (9%)	0	100	100
35	T	14/160 (9%)	12 (86%)	2 (14%)	0	100	100
All	All	4880/7631 (64%)	4630 (95%)	240 (5%)	10 (0%)	45	75

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	L	175	ALA
6	E	143	ASN
22	b	427	TRP
6	E	136	ASP
8	G	222	PHE
10	L	166	ILE
8	G	182[A]	ASN
8	G	182[B]	ASN
22	b	15	VAL
11	M	124	VAL

5.3.2 Protein sidechains (i)

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	3	111/271 (41%)	110 (99%)	1 (1%)	75 89
4	B	284/326 (87%)	284 (100%)	0	100 100
5	C	275/297 (93%)	274 (100%)	1 (0%)	89 94
6	E	135/155 (87%)	134 (99%)	1 (1%)	81 92
7	F	178/210 (85%)	178 (100%)	0	100 100
8	G	139/212 (66%)	135 (97%)	4 (3%)	37 67
9	H	164/170 (96%)	163 (99%)	1 (1%)	84 92
10	L	144/167 (86%)	143 (99%)	1 (1%)	81 92
11	M	108/113 (96%)	107 (99%)	1 (1%)	75 89
12	N	146/176 (83%)	145 (99%)	1 (1%)	81 92
13	O	161/162 (99%)	161 (100%)	0	100 100
14	P	125/149 (84%)	125 (100%)	0	100 100
15	Q	114/159 (72%)	114 (100%)	0	100 100
17	S	150/154 (97%)	149 (99%)	1 (1%)	81 92
18	V	105/107 (98%)	104 (99%)	1 (1%)	73 87
20	Y	110/111 (99%)	108 (98%)	2 (2%)	54 77
21	a	81/122 (66%)	81 (100%)	0	100 100
22	b	214/556 (38%)	208 (97%)	6 (3%)	38 68
23	d	89/102 (87%)	89 (100%)	0	100 100
24	e	100/107 (94%)	97 (97%)	3 (3%)	36 66
25	f	89/91 (98%)	88 (99%)	1 (1%)	70 86
26	h	106/107 (99%)	102 (96%)	4 (4%)	28 60
27	i	80/84 (95%)	79 (99%)	1 (1%)	65 83
28	j	58/71 (82%)	58 (100%)	0	100 100
29	r	63/224 (28%)	63 (100%)	0	100 100
30	s	28/409 (7%)	28 (100%)	0	100 100
31	u	99/168 (59%)	99 (100%)	0	100 100
33	y	189/206 (92%)	188 (100%)	1 (0%)	86 93
34	z	31/107 (29%)	31 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
35	T	15/139 (11%)	15 (100%)	0	100 100
All	All	3691/5432 (68%)	3660 (99%)	31 (1%)	77 90

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	3	78	GLN
5	C	181	ILE
6	E	115	SER
8	G	107	GLN
8	G	114	GLU
8	G	182[A]	ASN
8	G	182[B]	ASN
9	H	174	LEU
10	L	46	ILE
11	M	61	ILE
12	N	120	TRP
17	S	60	ILE
18	V	76	MET
20	Y	47	LEU
20	Y	96	VAL
22	b	156	GLN
22	b	159	SER
22	b	394	ASN
22	b	395	ARG
22	b	396	ARG
22	b	434	GLU
24	e	20	ASP
24	e	64	MET
24	e	81	LEU
25	f	99	LEU
26	h	13	GLN
26	h	64	ASN
26	h	94	LEU
26	h	95	THR
27	i	5	LEU
33	y	118	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
3	3	25	GLN
4	B	182	GLN
4	B	184	ASN
4	B	269	ASN
5	C	41	HIS
5	C	50	GLN
5	C	361	HIS
6	E	157	GLN
7	F	45	GLN
8	G	89	GLN
9	H	77	ASN
10	L	112	ASN
12	N	32	GLN
12	N	149	ASN
12	N	153	ASN
14	P	72	GLN
14	P	116	HIS
14	P	145	HIS
15	Q	127	GLN
17	S	141	GLN
18	V	35	ASN
21	a	14	HIS
21	a	125	GLN
22	b	27	GLN
22	b	84	ASN
22	b	394	ASN
23	d	48	HIS
25	f	6	HIS
25	f	43	GLN
25	f	89	ASN
26	h	11	GLN
27	i	63	GLN
27	i	93	GLN
29	r	72	ASN
33	y	11	ASN
33	y	82	GLN
33	y	86	ASN
35	T	139	HIS

5.3.3 RNA (i)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1793/3497 (51%)	474 (26%)	28 (1%)
2	2	140/165 (84%)	26 (18%)	1 (0%)
All	All	1933/3662 (52%)	500 (25%)	29 (1%)

All (500) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	12	A
1	1	14	U
1	1	26	A
1	1	48	A
1	1	49	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	69	U
1	1	70	A
1	1	72	C
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	117	U
1	1	118	U
1	1	139	U
1	1	142	G
1	1	154	G
1	1	156	A
1	1	161	C
1	1	162	A
1	1	163	A
1	1	166	A
1	1	167	G
1	1	173	U
1	1	174	U
1	1	177	G
1	1	179	G
1	1	185	G
1	1	189	G
1	1	191	U

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Mol	Chain	Res	Type
1	1	193	U
1	1	194	A
1	1	195	A
1	1	197	U
1	1	198	U
1	1	207	C
1	1	217	G
1	1	220	A
1	1	225	G
1	1	226	A
1	1	227	G
1	1	239	U
1	1	241	G
1	1	244	G
1	1	246	U
1	1	247	U
1	1	248	G
1	1	254	G
1	1	258	U
1	1	259	A
1	1	261	A
1	1	265	C
1	1	266	G
1	1	267	C
1	1	268	U
1	1	269	U
1	1	270	U
1	1	271	C
1	1	276	A
1	1	277	G
1	1	303	A
1	1	306	U
1	1	311	G
1	1	312	G
1	1	313	U
1	1	314	A
1	1	315	A
1	1	316	A
1	1	317	U
1	1	319	U
1	1	331	A
1	1	337	U

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Mol	Chain	Res	Type
1	1	346	A
1	1	359	A
1	1	360	A
1	1	383	A
1	1	384	G
1	1	399	A
1	1	405	A
1	1	406	U
1	1	407	A
1	1	411	C
1	1	415	A
1	1	429	G
1	1	430	A
1	1	437	G
1	1	445	G
1	1	510	G
1	1	521	C
1	1	526	G
1	1	531	A
1	1	532	A
1	1	540	A
1	1	544	A
1	1	546	G
1	1	547	G
1	1	551	C
1	1	555	C
1	1	556	C
1	1	570	G
1	1	573	G
1	1	574	U
1	1	577	U
1	1	578	U
1	1	579	A
1	1	580	U
1	1	581	A
1	1	582	G
1	1	591	G
1	1	592	U
1	1	593	A
1	1	596	A
1	1	602	A
1	1	603	C

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Mol	Chain	Res	Type
1	1	613	A
1	1	616	A
1	1	618	U
1	1	622	G
1	1	624	U
1	1	625	U
1	1	626	C
1	1	627	G
1	1	628	U
1	1	629	G
1	1	630	C
1	1	634	G
1	1	636	A
1	1	645	U
1	1	647	A
1	1	650	G
1	1	661	C
1	1	662	C
1	1	673	C
1	1	675	C
1	1	685	A
1	1	702	A
1	1	706	U
1	1	707	U
1	1	708	U
1	1	715	U
1	1	716	G
1	1	725	U
1	1	732	A
1	1	739	G
1	1	742	A
1	1	743	A
1	1	744	U
1	1	746	C
1	1	747	A
1	1	748	G
1	1	749	G
1	1	750	U
1	1	751	G
1	1	752	G
1	1	753	G
1	1	754	A

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Mol	Chain	Res	Type
1	1	758	C
1	1	759	C
1	1	760	C
1	1	761	U
1	1	762	U
1	1	763	G
1	1	766	G
1	1	767	C
1	1	768	G
1	1	769	U
1	1	770	G
1	1	773	C
1	1	774	C
1	1	775	A
1	1	776	U
1	1	777	C
1	1	778	G
1	1	779	A
1	1	780	C
1	1	781	C
1	1	783	A
1	1	787	G
1	1	788	G
1	1	789	A
1	1	802	G
1	1	806	G
1	1	807	G
1	1	808	U
1	1	809	U
1	1	812	A
1	1	813	G
1	1	816	A
1	1	817	G
1	1	962	U
1	1	964	U
1	1	965	A
1	1	966	G
1	1	968	A
1	1	970	C
1	1	976	C
1	1	985	G
1	1	986	U

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Mol	Chain	Res	Type
1	1	988	U
1	1	989	C
1	1	990	C
1	1	991	C
1	1	992	U
1	1	994	A
1	1	995	G
1	1	996	G
1	1	997	A
1	1	998	U
1	1	1000	G
1	1	1001	C
1	1	1002	A
1	1	1009	C
1	1	1010	A
1	1	1011	G
1	1	1012	A
1	1	1013	U
1	1	1014	C
1	1	1017	U
1	1	1023	G
1	1	1024	A
1	1	1135	G
1	1	1136	A
1	1	1138	U
1	1	1139	U
1	1	1142	U
1	1	1143	A
1	1	1147	G
1	1	1154	U
1	1	1155	U
1	1	1156	U
1	1	1158	G
1	1	1159	U
1	1	1160	A
1	1	1162	G
1	1	1163	C
1	1	1166	A
1	1	1170	G
1	1	1172	C
1	1	1173	G
1	1	1175	U

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Mol	Chain	Res	Type
1	1	1176	G
1	1	1184	A
1	1	1186	C
1	1	1191	C
1	1	1205	G
1	1	1210	A
1	1	1211	A
1	1	1212	U
1	1	1223	C
1	1	1224	A
1	1	1232	G
1	1	1234	A
1	1	1235	A
1	1	1244	G
1	1	1249	U
1	1	1251	U
1	1	1252	A
1	1	1253	G
1	1	1258	C
1	1	1259	A
1	1	1264	G
1	1	1273	G
1	1	1275	A
1	1	1276	A
1	1	1277	G
1	1	1282	A
1	1	1283	A
1	1	1286	C
1	1	1287	G
1	1	1289	U
1	1	1290	A
1	1	1291	A
1	1	1293	G
1	1	1294	A
1	1	1295	G
1	1	1296	U
1	1	1303	C
1	1	1309	A
1	1	1310	C
1	1	1311	C
1	1	1315	C
1	1	1316	G

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Mol	Chain	Res	Type
1	1	1317	A
1	1	1318	A
1	1	1333	A
1	1	1334	A
1	1	1335	A
1	1	1336	U
1	1	1337	G
1	1	1338	G
1	1	1339	A
1	1	1340	U
1	1	1347	U
1	1	1348	A
1	1	1356	U
1	1	1361	A
1	1	1363	A
1	1	1379	U
1	1	1390	A
1	1	1420	U
1	1	1421	G
1	1	1433	U
1	1	1451	G
1	1	1453	A
1	1	1464	U
1	1	1465	G
1	1	1468	G
1	1	1471	C
1	1	1504	U
1	1	1511	A
1	1	1515	A
1	1	1517	G
1	1	1521	G
1	1	1528	U
1	1	1530	C
1	1	1536	G
1	1	1537	A
1	1	1542	C
1	1	1913	A
1	1	1921	C
1	1	1926	U
1	1	1931	U
1	1	1933	G
1	1	1935	U

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Mol	Chain	Res	Type
1	1	1939	A
1	1	1940	C
1	1	1941	A
1	1	1955	A
1	1	1961	G
1	1	1967	U
1	1	2424	U
1	1	2452	G
1	1	2453	C
1	1	2458	G
1	1	2459	G
1	1	2460	A
1	1	2461	A
1	1	2462	C
1	1	2463	G
1	1	2465	G
1	1	2473	A
1	1	2476	U
1	1	2481	G
1	1	2482	G
1	1	2920	C
1	1	2921	U
1	1	2923	G
1	1	2931	C
1	1	2932	A
1	1	2933	A
1	1	2946	A
1	1	2948	A
1	1	2951	G
1	1	2952	C
1	1	2953	U
1	1	2982	A
1	1	2984	C
1	1	2993	G
1	1	2994	C
1	1	3014	A
1	1	3024	C
1	1	3025	A
1	1	3030	U
1	1	3031	A
1	1	3082	A
1	1	3085	G

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Mol	Chain	Res	Type
1	1	3087	U
1	1	3091	G
1	1	3092	U
1	1	3108	A
1	1	3113	A
1	1	3115	U
1	1	3117	A
1	1	3118	G
1	1	3119	U
1	1	3125	A
1	1	3126	G
1	1	3128	A
1	1	3155	G
1	1	3170	G
1	1	3172	C
1	1	3174	A
1	1	3175	U
1	1	3182	G
1	1	3188	U
1	1	3189	C
1	1	3195	C
1	1	3196	U
1	1	3200	U
1	1	3205	G
1	1	3218	A
1	1	3225	A
1	1	3226	A
1	1	3227	U
1	1	3228	C
1	1	3238	A
1	1	3239	A
1	1	3249	U
1	1	3250	U
1	1	3251	U
1	1	3252	U
1	1	3257	C
1	1	3259	C
1	1	3260	A
1	1	3261	U
1	1	3263	A
1	1	3265	U
1	1	3267	A

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Mol	Chain	Res	Type
1	1	3268	U
1	1	3269	A
1	1	3270	U
1	1	3272	U
1	1	3273	A
1	1	3276	A
1	1	3281	A
1	1	3282	G
1	1	3299	U
1	1	3310	A
1	1	3313	G
1	1	3317	A
1	1	3318	A
1	1	3319	G
1	1	3327	A
1	1	3329	G
1	1	3330	G
1	1	3335	U
1	1	3336	G
1	1	3338	A
1	1	3343	A
1	1	3344	A
1	1	3345	G
1	1	3346	U
1	1	3347	G
1	1	3351	U
1	1	3352	A
1	1	3353	U
1	1	3356	A
1	1	3358	U
1	1	3359	U
1	1	3360	G
1	1	3361	U
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3373	C
1	1	3381	U
1	1	3382	C
1	1	3384	U
1	1	3386	U
1	1	3387	G

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Mol	Chain	Res	Type
1	1	3388	C
1	1	3389	G
1	1	3391	A
1	1	3394	C
1	1	3395	G
1	1	3404	G
1	1	3405	C
1	1	3414	U
1	1	3417	A
1	1	3418	U
1	1	3420	U
1	1	3435	U
1	1	3436	A
1	1	3470	G
1	1	3476	A
1	1	3479	C
1	1	3484	G
1	1	3491	A
1	1	3492	G
1	1	3497	G
2	2	9	A
2	2	31	U
2	2	42	U
2	2	43	C
2	2	57	G
2	2	59	G
2	2	60	A
2	2	67	A
2	2	70	C
2	2	71	G
2	2	79	A
2	2	87	A
2	2	88	A
2	2	98	U
2	2	103	G
2	2	105	A
2	2	112	A
2	2	114	C
2	2	124	G
2	2	132	G
2	2	144	G
2	2	145	C

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Mol	Chain	Res	Type
2	2	150	C
2	2	159	U
2	2	160	G
2	2	162	C

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	270	U
1	1	382	A
1	1	626	C
1	1	644	A
1	1	674	A
1	1	706	U
1	1	759	C
1	1	782	G
1	1	801	G
1	1	805	G
1	1	1013	U
1	1	1159	U
1	1	1223	C
1	1	1234	A
1	1	1272	U
1	1	1314	C
1	1	1333	A
1	1	1338	G
1	1	1389	A
1	1	2952	C
1	1	3081	U
1	1	3217	U
1	1	3256	C
1	1	3267	A
1	1	3268	U
1	1	3318	A
1	1	3328	U
1	1	3387	G
2	2	131	G

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 1 ligands modelled in this entry, 1 is 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)

There are no chain breaks in this entry.

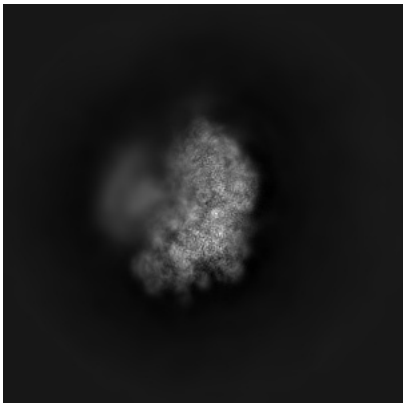
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24396. These allow visual inspection of the internal detail of the map and identification of artifacts.

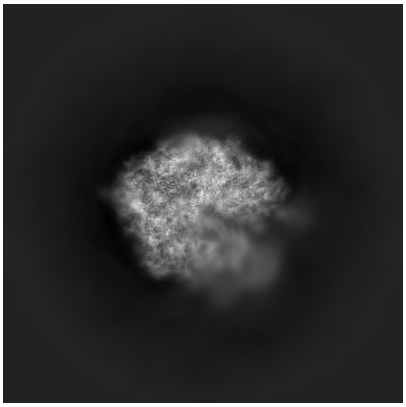
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

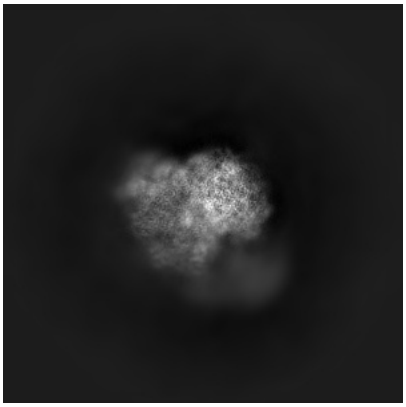
6.1.1 Primary map



X



Y

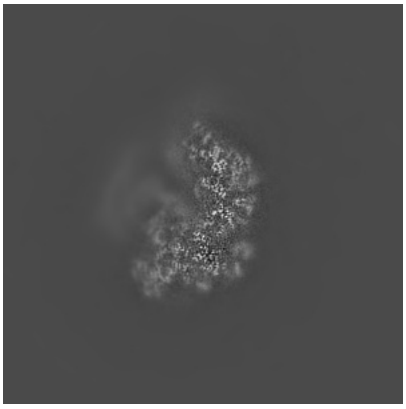


Z

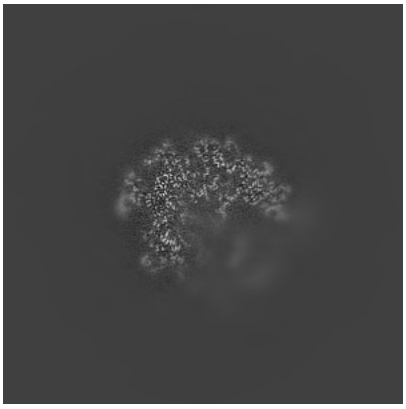
The images above show the map projected in three orthogonal directions.

6.2 Central slices

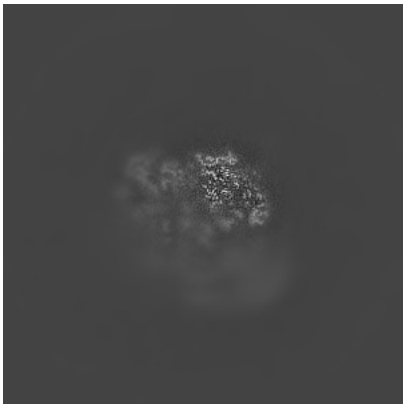
6.2.1 Primary map



X Index: 256



Y Index: 256

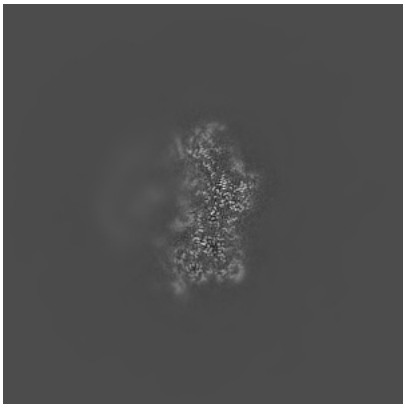


Z Index: 256

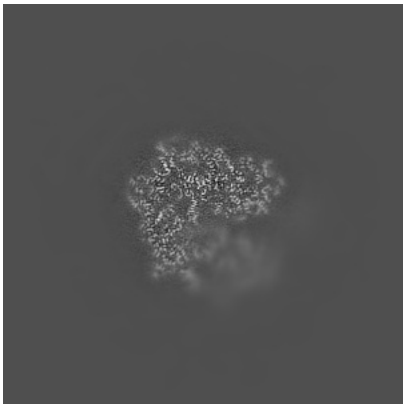
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

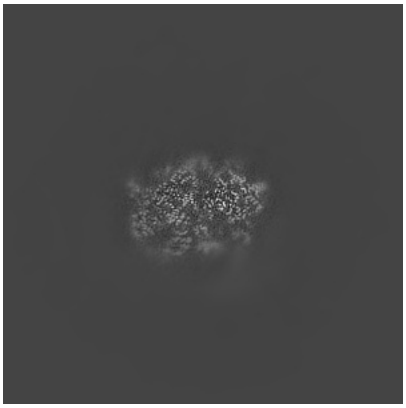
6.3.1 Primary map



X Index: 282



Y Index: 272

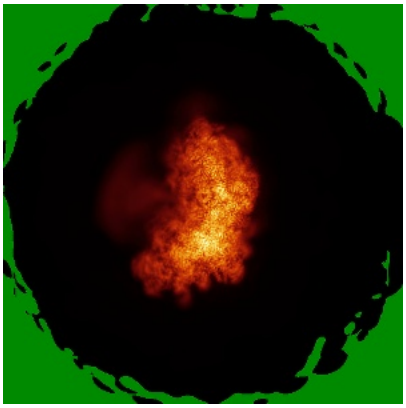


Z Index: 204

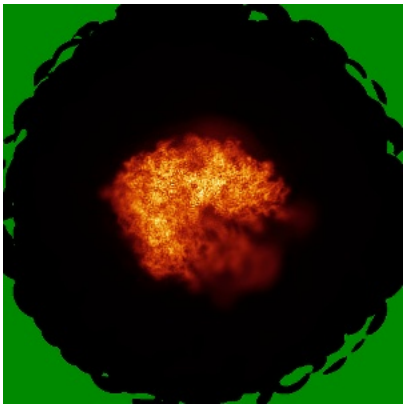
The images above show the largest variance slices of the map in three orthogonal directions.

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

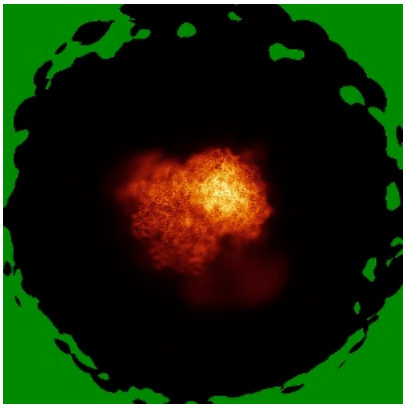
6.4.1 Primary map



X



Y

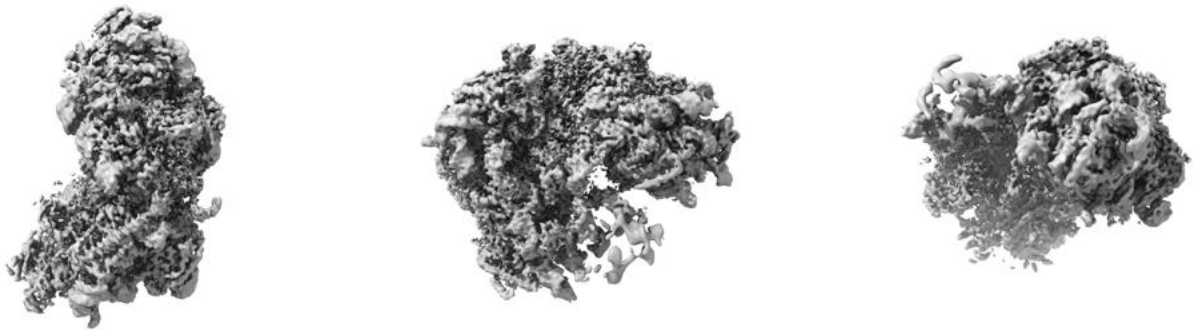


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

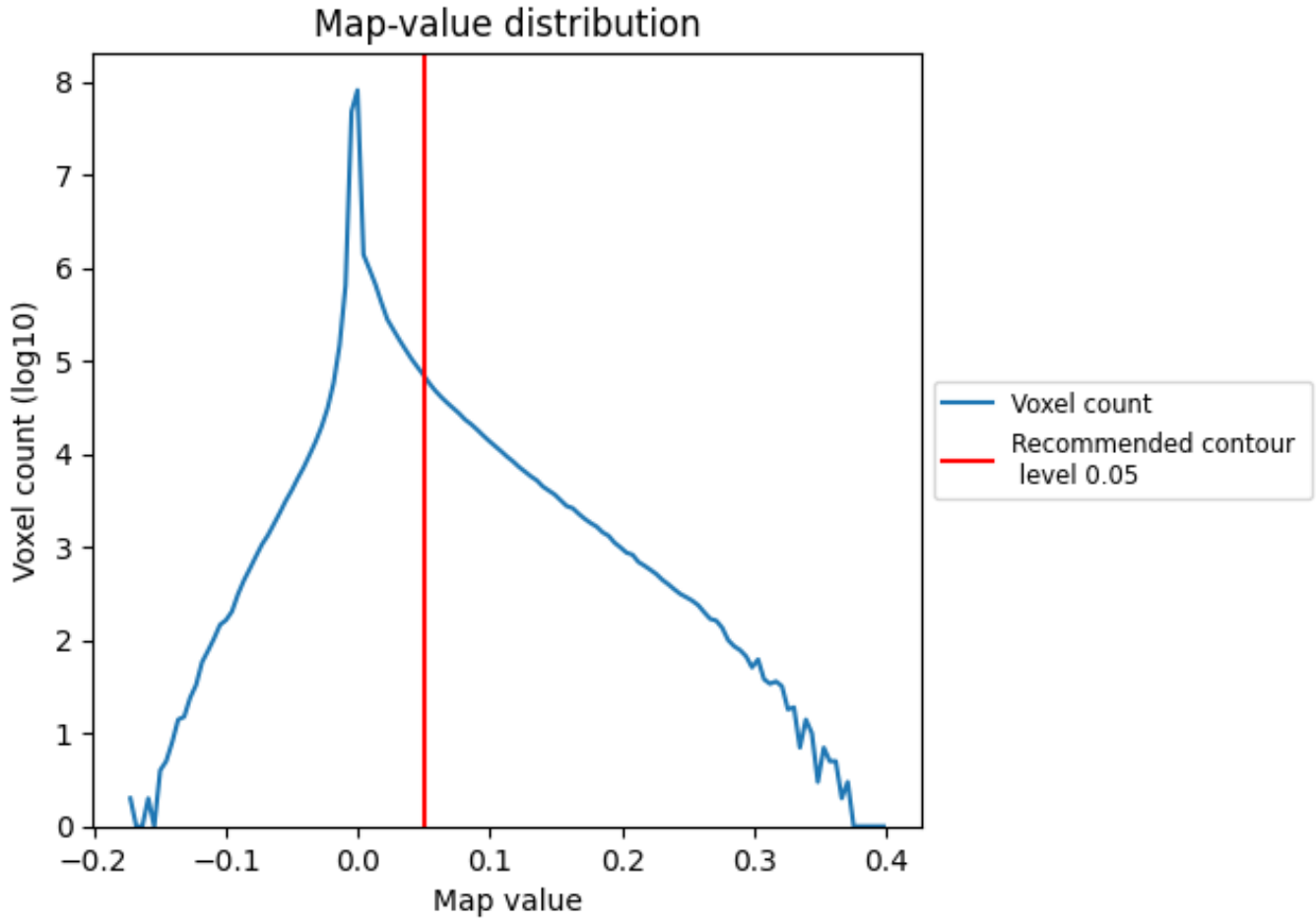
6.6 Mask visualisation (i)

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

7 Map analysis

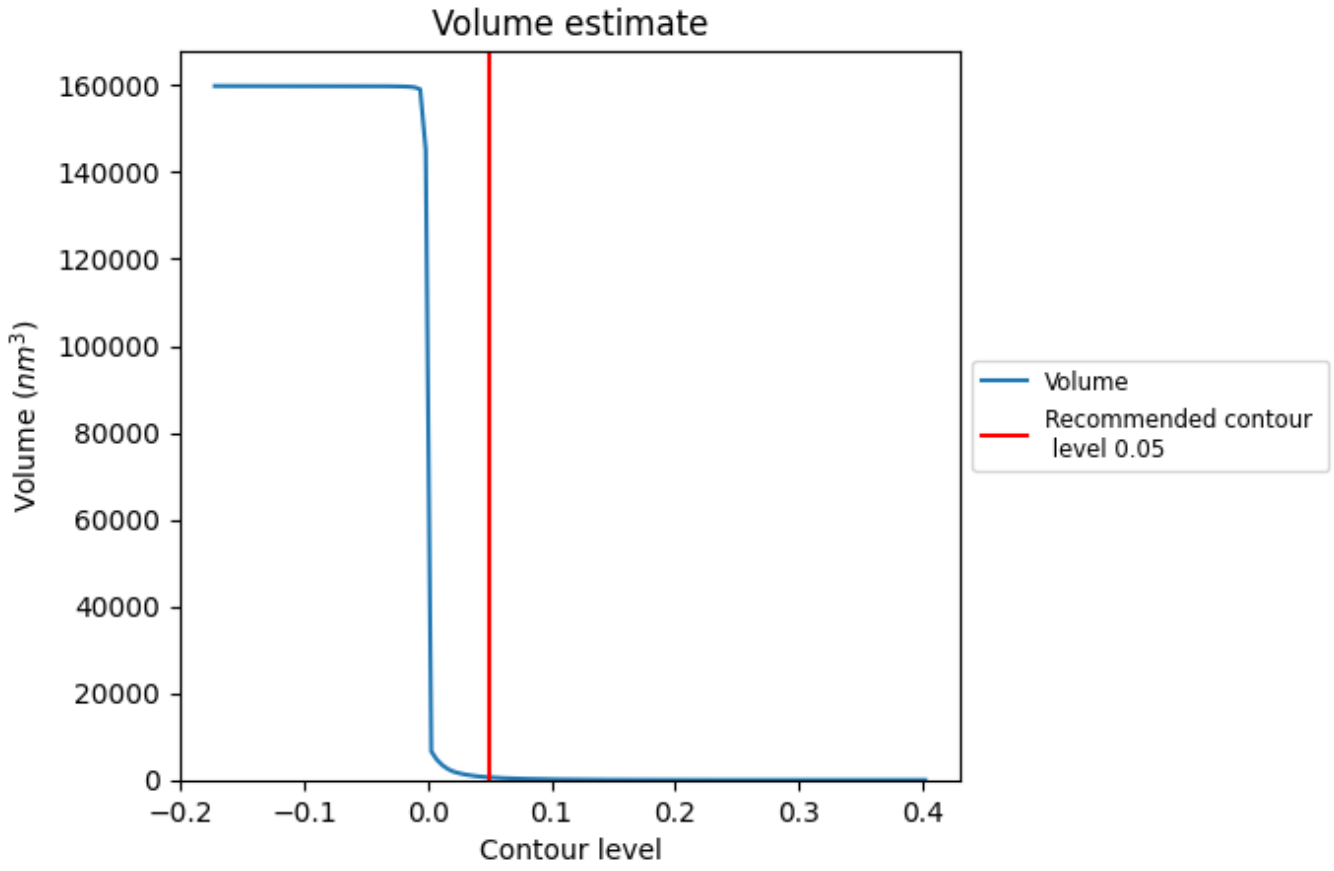
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

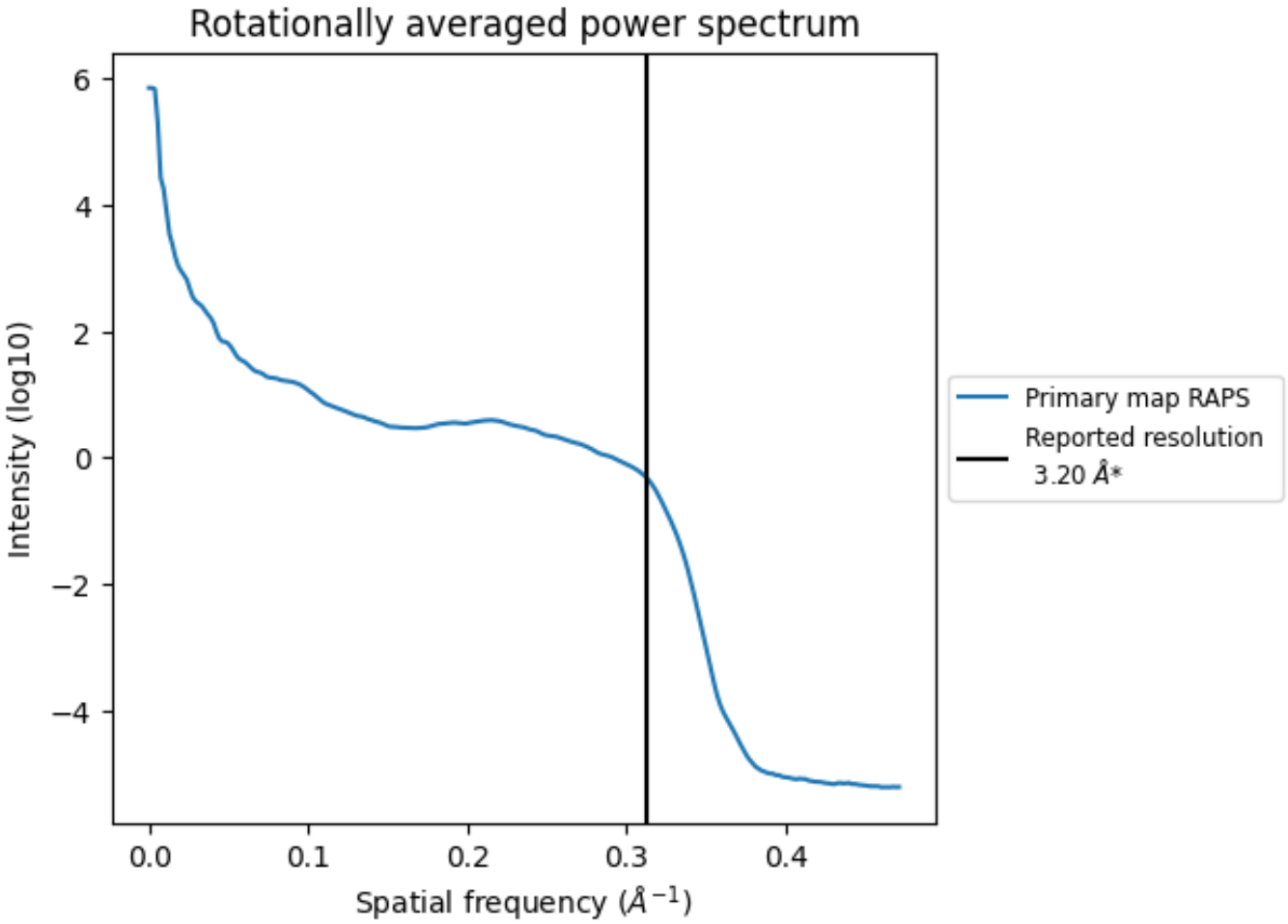
7.2 Volume estimate



The volume at the recommended contour level is 598 nm^3; this corresponds to an approximate mass of 540 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

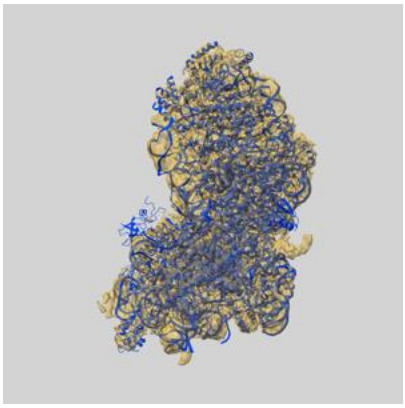
8 Fourier-Shell correlation

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

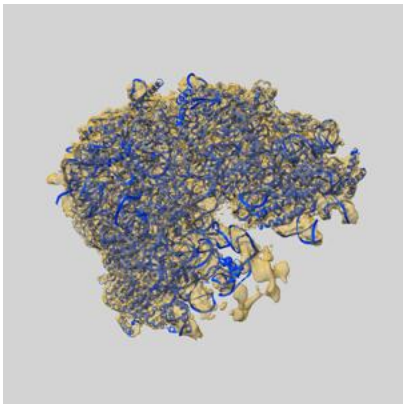
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-24396 and PDB model 8ETJ. Per-residue inclusion information can be found in section 3 on page 11.

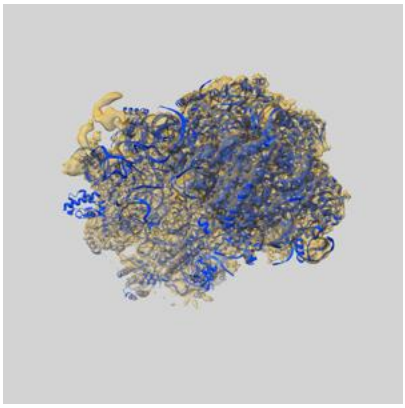
9.1 Map-model overlay



X



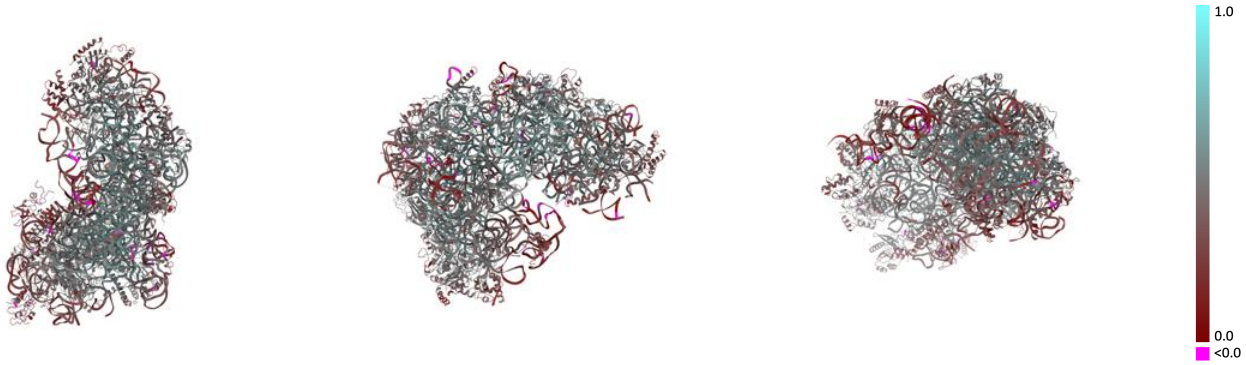
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

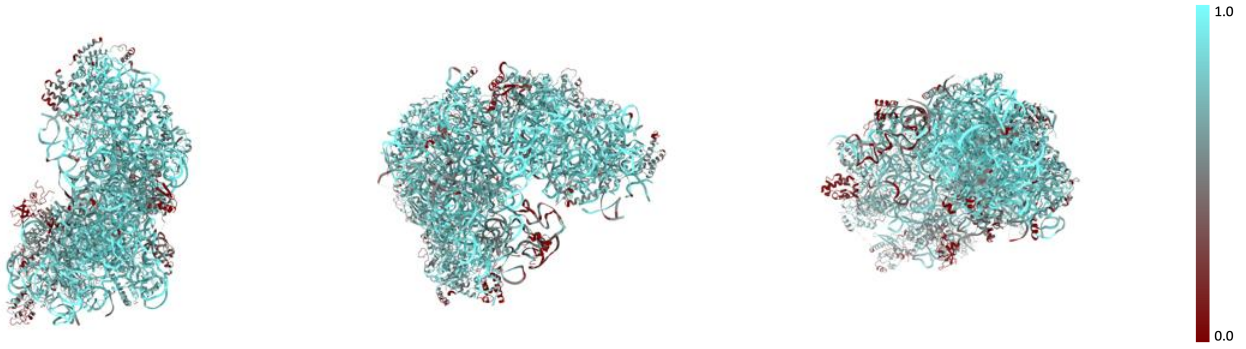
9.2 Q-score mapped to coordinate model



X Y Z

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

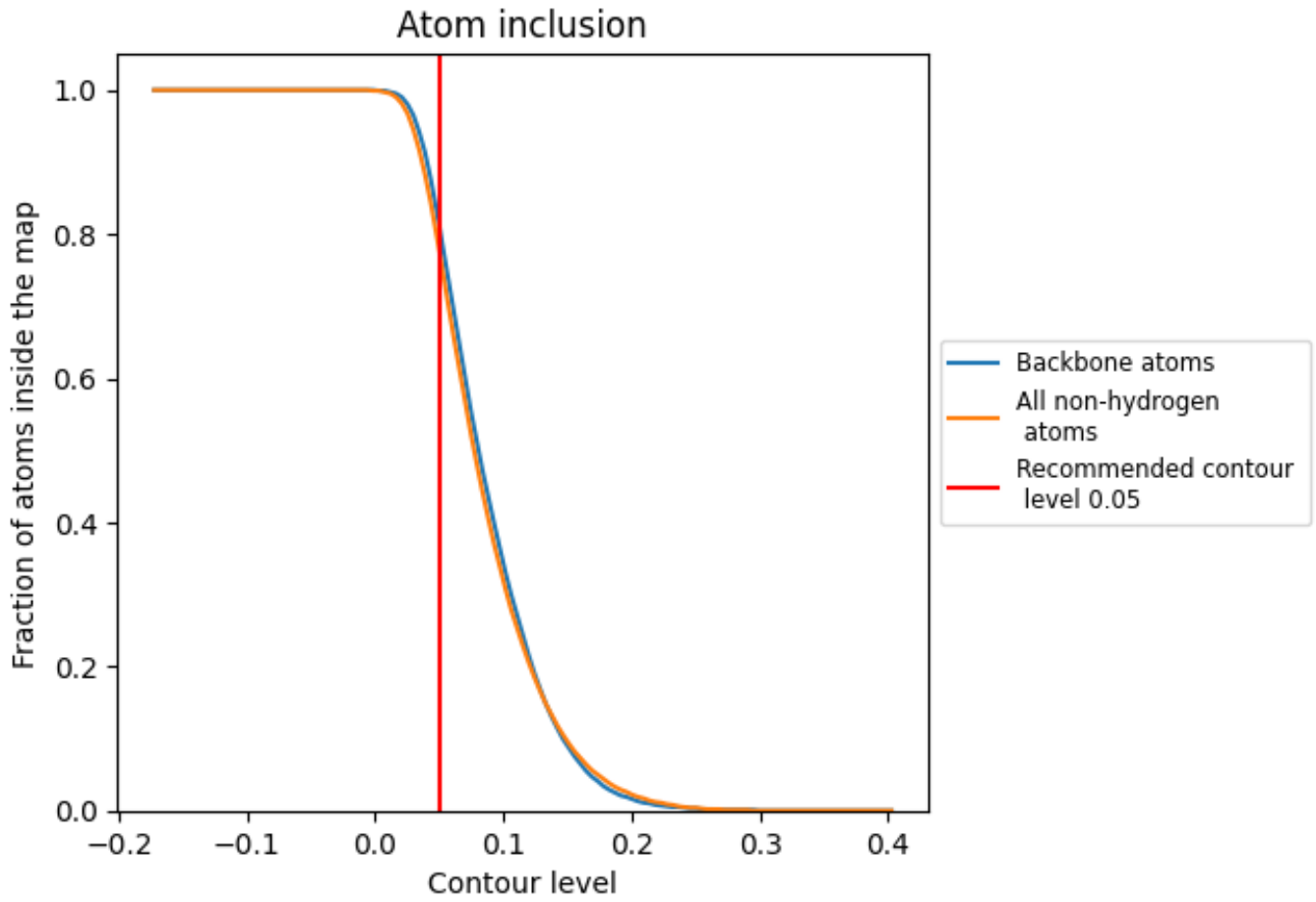
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7770	0.4360
1	0.8500	0.4230
2	0.8650	0.4220
3	0.2760	0.3470
B	0.8550	0.5270
C	0.8410	0.5250
E	0.7000	0.4480
F	0.8130	0.4970
G	0.5790	0.3520
H	0.6950	0.4620
L	0.7150	0.4550
M	0.8110	0.4750
N	0.8080	0.5040
O	0.8710	0.5360
P	0.7090	0.4850
Q	0.7850	0.4940
R	0.1330	0.2820
S	0.7030	0.4540
T	0.4360	0.3540
V	0.6890	0.4740
W	0.4590	0.3390
Y	0.8260	0.5090
a	0.7550	0.4620
b	0.5210	0.3430
d	0.6070	0.4240
e	0.8670	0.5460
f	0.9080	0.5570
h	0.6720	0.4160
i	0.5930	0.3440
j	0.8500	0.5350
r	0.3830	0.3640
s	0.3830	0.3580
u	0.7330	0.4260
w	0.0600	0.3310
y	0.7050	0.4300
z	0.6210	0.4330