Full wwPDB EM Validation Report

May 12, 2025 – 08:01 PM EDT

PDB ID	:	8EUY / pdb_00008euy
EMDB ID	:	EMD-24420
Title	:	Ytm1 associated nascent 60S ribosome (-fkbp39) State 1A
Authors	:	Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on	:	2022-10-19
Resolution	:	3.00 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:

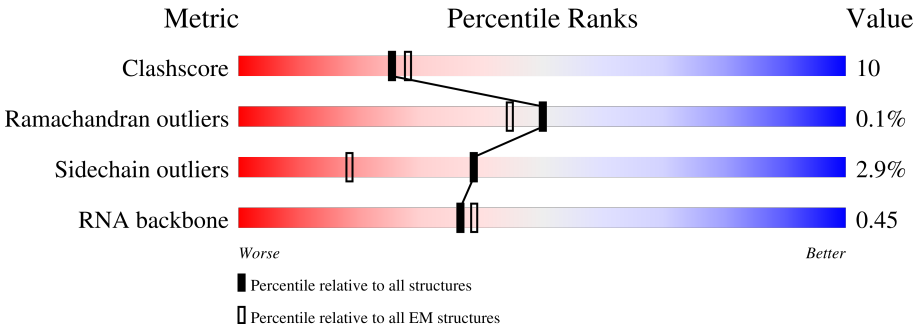
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (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 3.00 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	23% 14% 59%
2	2	165	53% 21% 5% 21%
3	3	302	52% 11% 36%
4	4	217	72% 23%
5	5	387	65% 22% 12%
6	6	300	8% 7% 12% 81%
7	A	295	12% 59% 27% 14%

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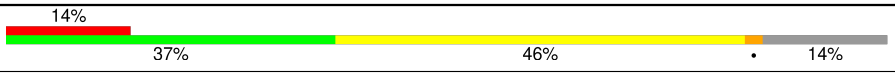
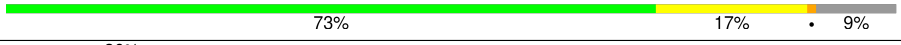
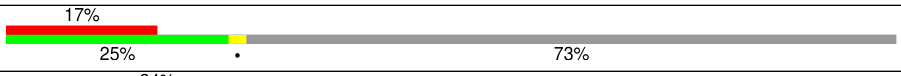
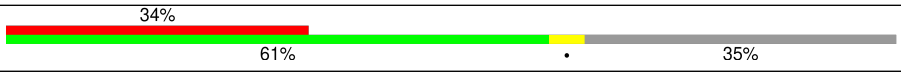
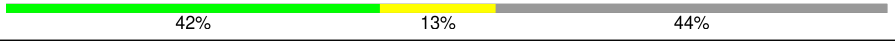
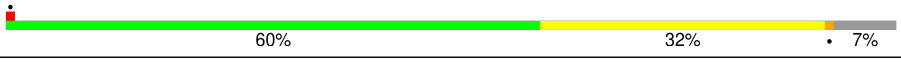
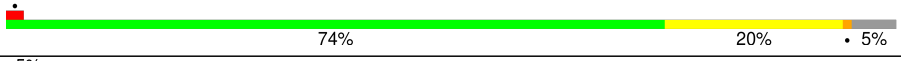
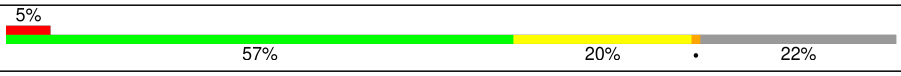
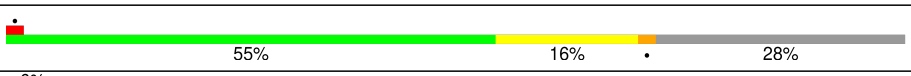
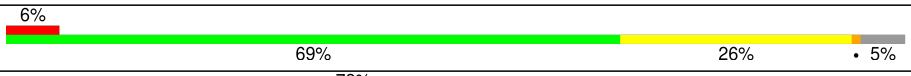
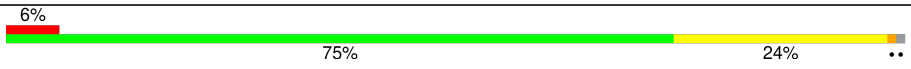
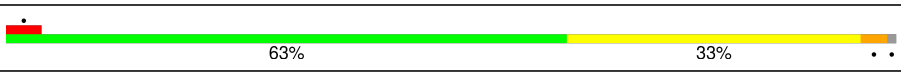
Mol	Chain	Length	Quality of chain
8	B	388	
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	J	333	
16	K	373	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	S	176	
24	V	139	
25	Y	126	
26	b	642	
27	e	127	
28	f	108	
29	h	122	
30	i	99	
31	j	91	
32	m	740	

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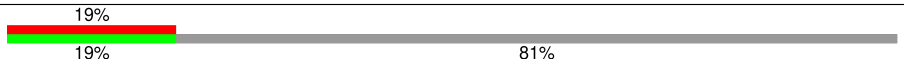
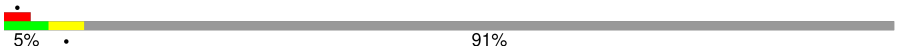
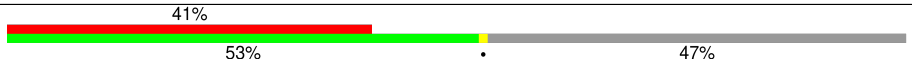
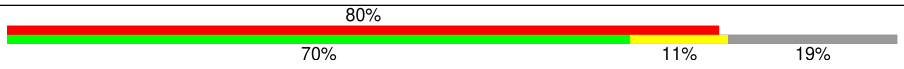
Mol	Chain	Length	Quality of chain
33	o	276	
34	r	260	
35	t	249	
36	u	192	
37	v	209	
38	x	306	
39	y	244	
40	T	160	

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 80249 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 (1095-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1433	30681	13703	5554	9991	1433	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	3196	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (148-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	130	2762	1236	487	909	130	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	192	1596	1010	304	276	6	0	0

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	210	1770	1153	302	307	8	0	0

- Molecule 5 is a protein called Ribosome biogenesis protein nsa1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	340	2686	1716	468	491	11	0	0

- Molecule 6 is a RNA chain called RNA (93-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	56	Total	C	N	O	P	0	0
			1160	522	171	411	56		

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	254	Total	C	N	O	S	0	0
			2057	1303	374	372	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	332	Total	C	N	O	S	0	0
			2641	1676	488	468	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	329	Total	C	N	O	S	0	0
			2572	1631	487	451	3		

- Molecule 10 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	406	Total	C	N	O	S	0	0
			3001	1931	519	542	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	170	Total	C	N	O	S	0	0
			1328	854	243	228	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	240	Total	C	N	O	S	0	0
			1944	1250	356	335	3		

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	164	Total	C	N	O	S	1	0
			1273	816	223	232	2		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	H	155	Total	C	N	O	0	0
			764	454	155	155		

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	J	89	Total	C	N	O	0	0
			444	266	89	89		

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	K	243	Total	C	N	O	0	0
			1205	719	243	243		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	116	Total	C	N	O	S	0	0
			942	592	198	151	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

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

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	187	Total	C	N	O	S	0	0
			1487	958	281	245	3		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	145	Total	C	N	O	S	0	0
			1139	725	207	204	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	135	Total	C	N	O	S	0	0
			1047	658	202	186	1		

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	168	Total	C	N	O	S	0	0
			1402	906	260	231	5		

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	113	Total	C	N	O	0	0
			554	327	113	114		

- Molecule 25 is a protein called 60S ribosomal protein L26.

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

- Molecule 26 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	b	120	Total	C	N	O	0	0
			594	354	120	120		

- Molecule 27 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	124	Total	C	N	O	S	0	0
			995	621	202	167	5		

- Molecule 28 is a protein called 60S ribosomal protein L33-B.

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

- Molecule 29 is a protein called 60S ribosomal protein L35.

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

- Molecule 30 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	98	Total	C	N	O	S	0	0
			768	478	159	130	1		

- Molecule 31 is a protein called 60S ribosomal protein L37-B.

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

- Molecule 32 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	m	92	Total	C	N	O	0	0
			725	447	128	150		

- Molecule 33 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	129	Total	C	N	O	S	0	0
			992	636	180	170	6		

- Molecule 34 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	r	50	Total	C	N	O	0	0
			249	149	50	50		

- Molecule 35 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	t	23	Total	C	N	O	0	0
			216	132	49	35		

- Molecule 36 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	u	102	Total	C	N	O	0	0
			506	302	102	102		

- Molecule 37 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	v	161	Total	C	N	O	S	0	0
			1299	818	243	235	3		

- Molecule 38 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	x	305	Total	C	N	O	S	0	0
			2516	1578	463	467	8		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	y	198	Total	C	N	O	0	0
			974	578	198	198		

- Molecule 40 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	T	19	Total	C	N	O	0	0
			147	93	26	28		

- Molecule 41 is ZINC ION (CCD ID: ZN) (formula: Zn).

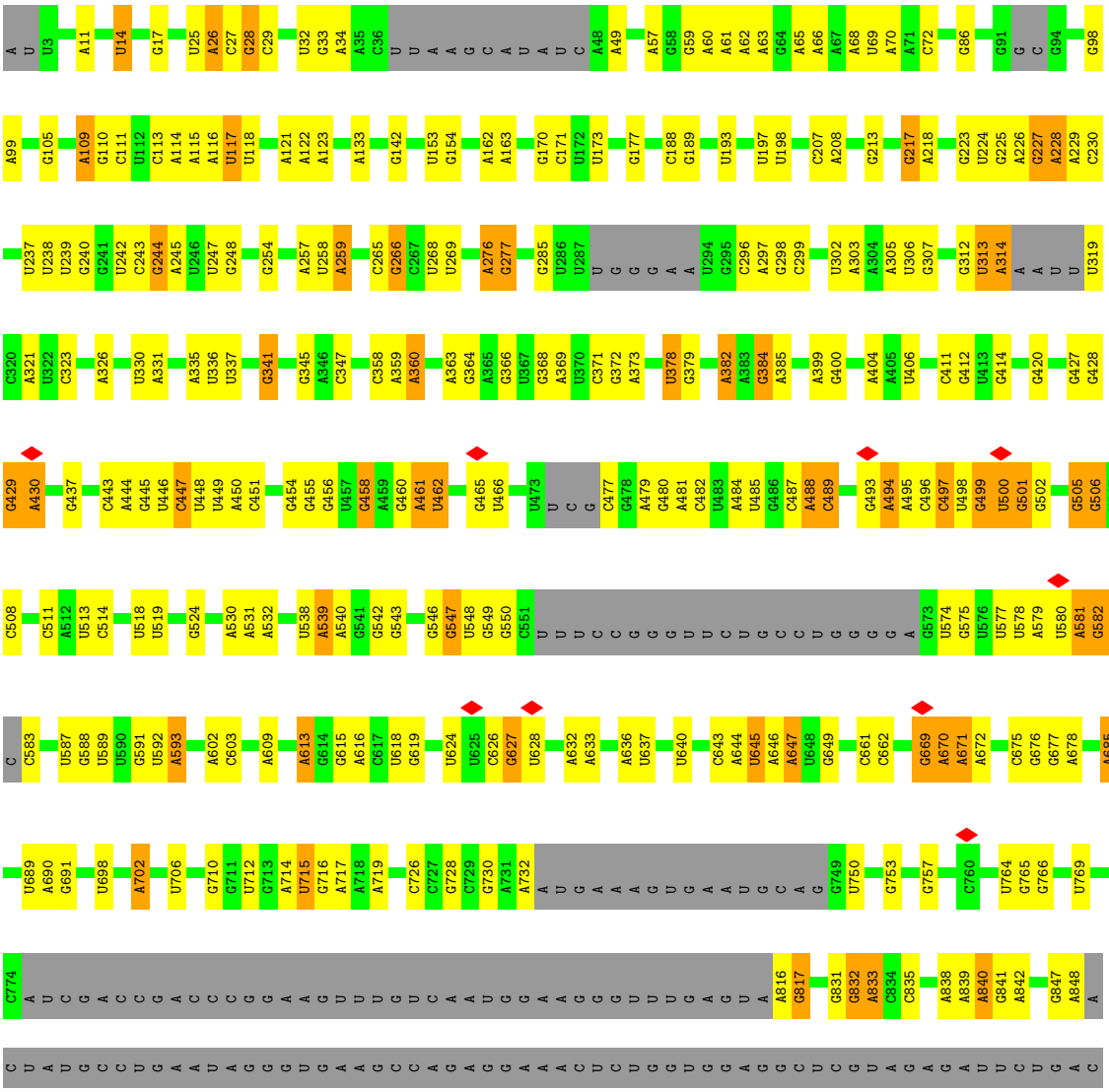
Mol	Chain	Residues	Atoms		AltConf
41	j	1	Total	Zn	0
			1	1	

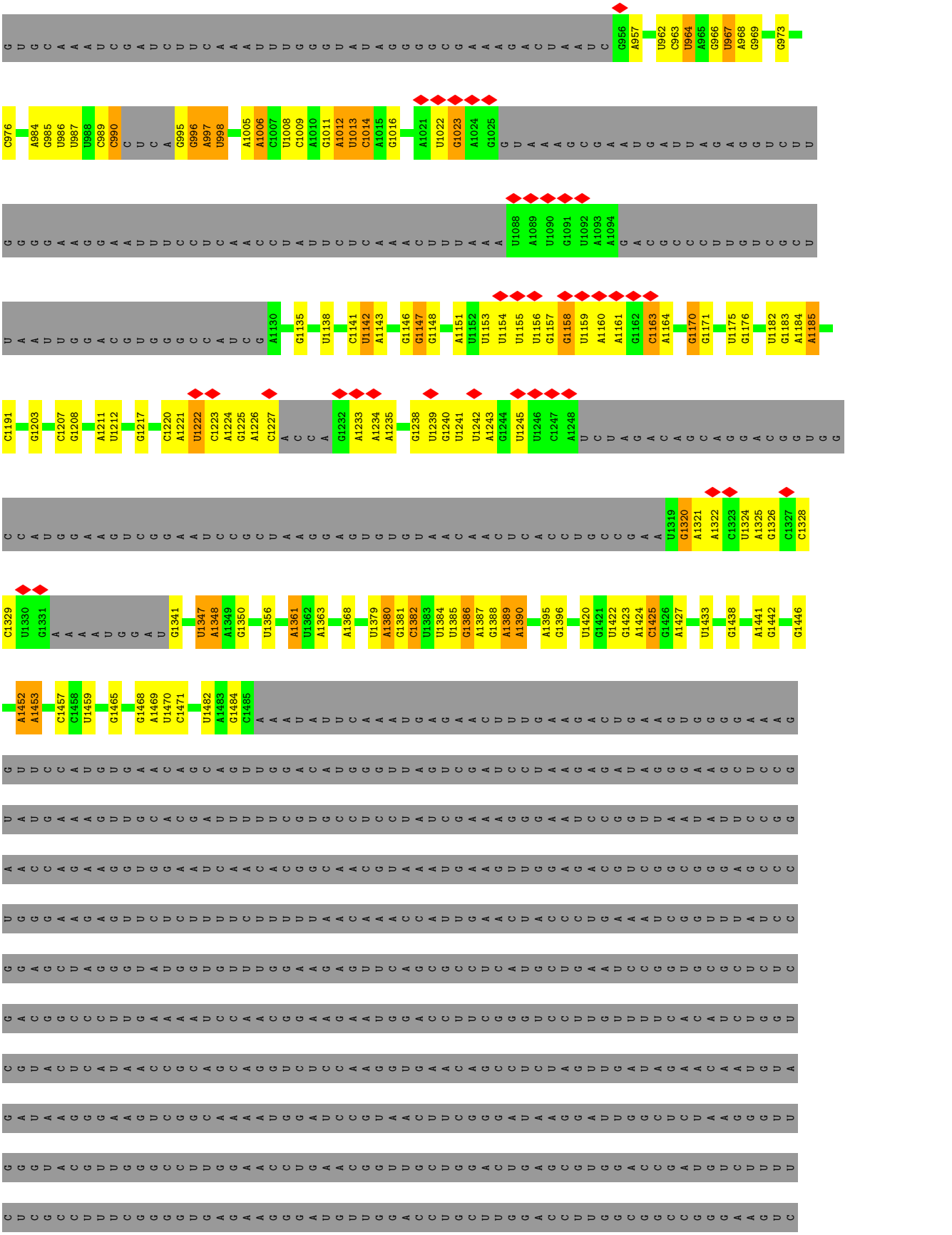
3 Residue-property plots (i)

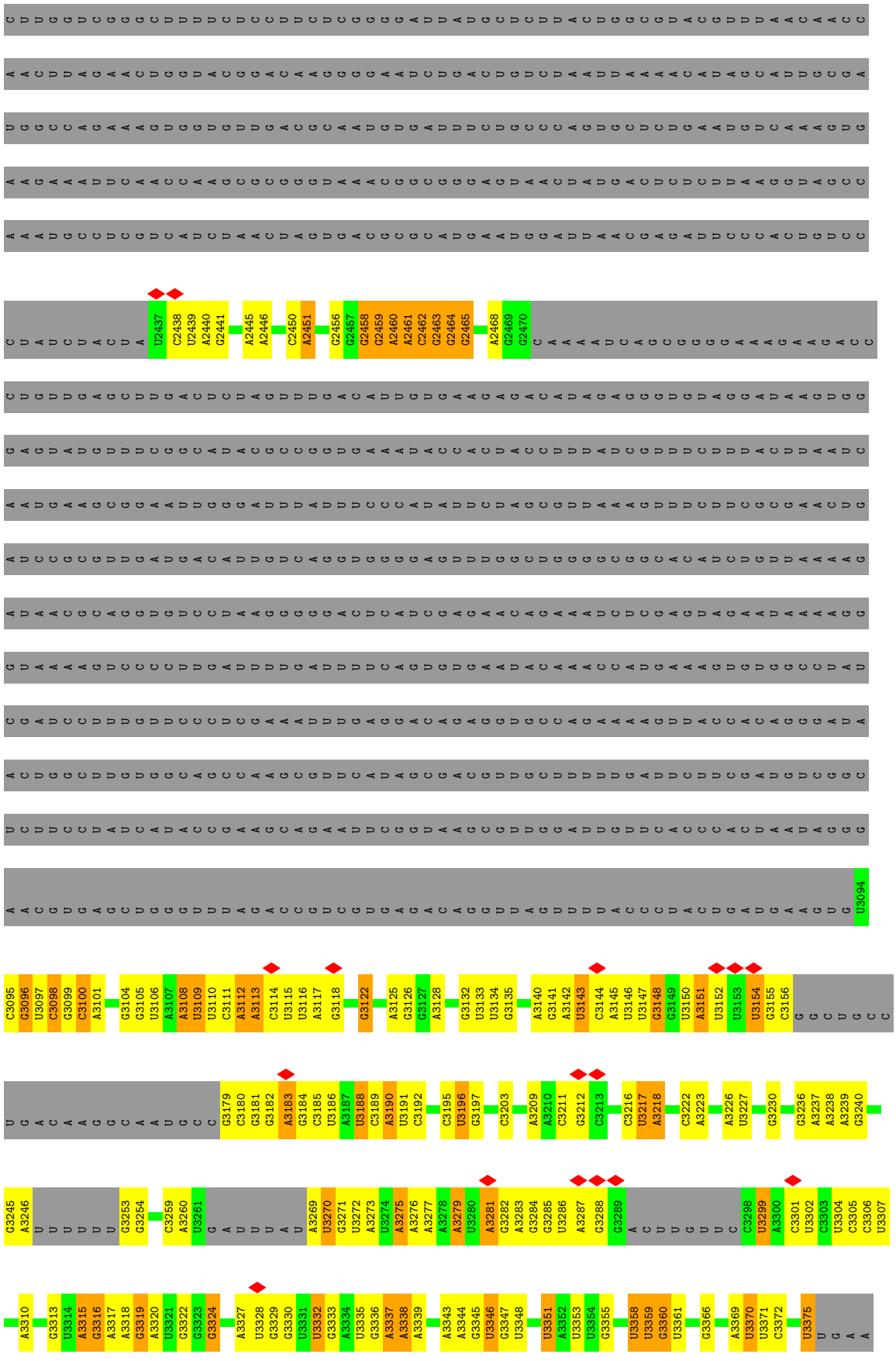
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

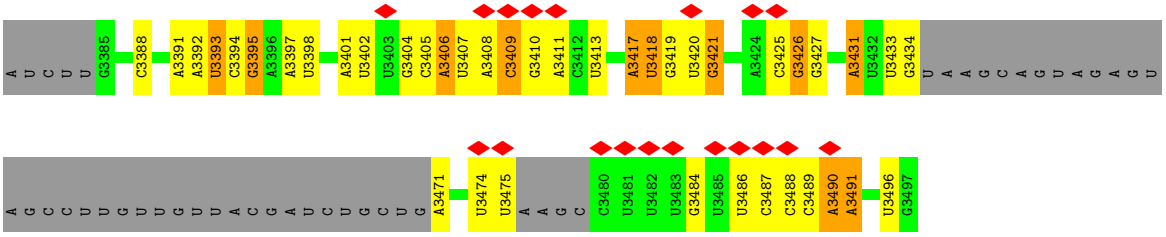
- Molecule 1: RNA (1095-MER)

Chain 1:



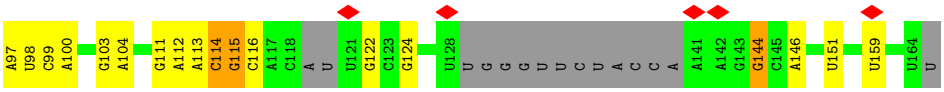






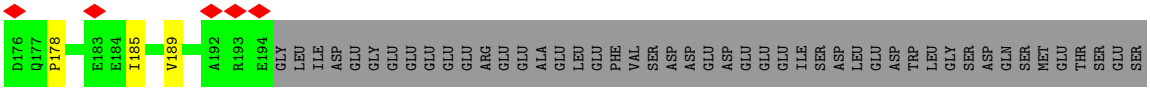
• Molecule 2: RNA (148-MER)

Chain 2:



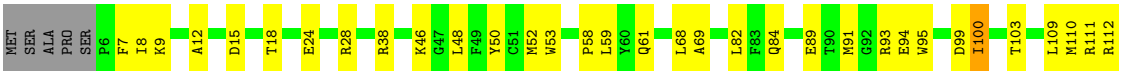
• Molecule 3: Protein mak16

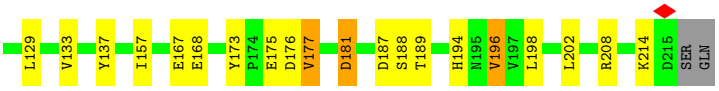
Chain 3:



• Molecule 4: Ribosomal RNA-processing protein 1 homolog

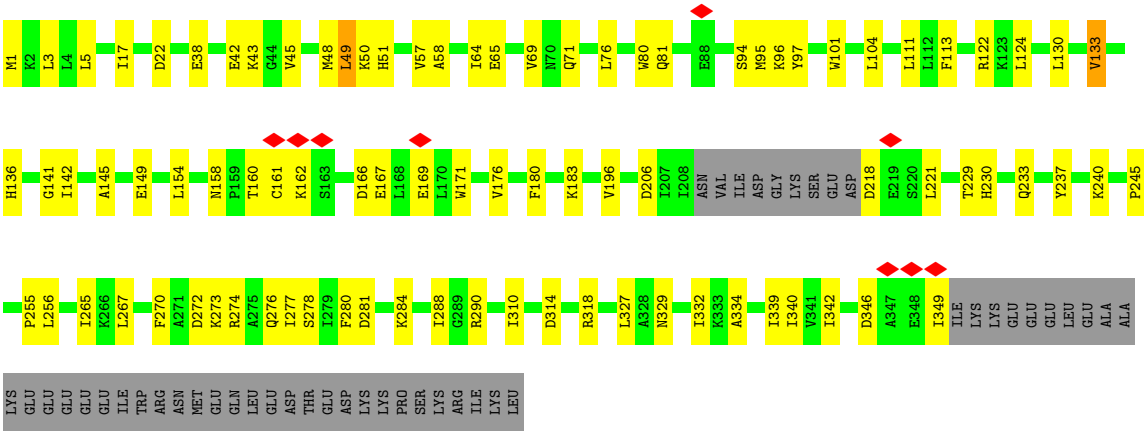
Chain 4:





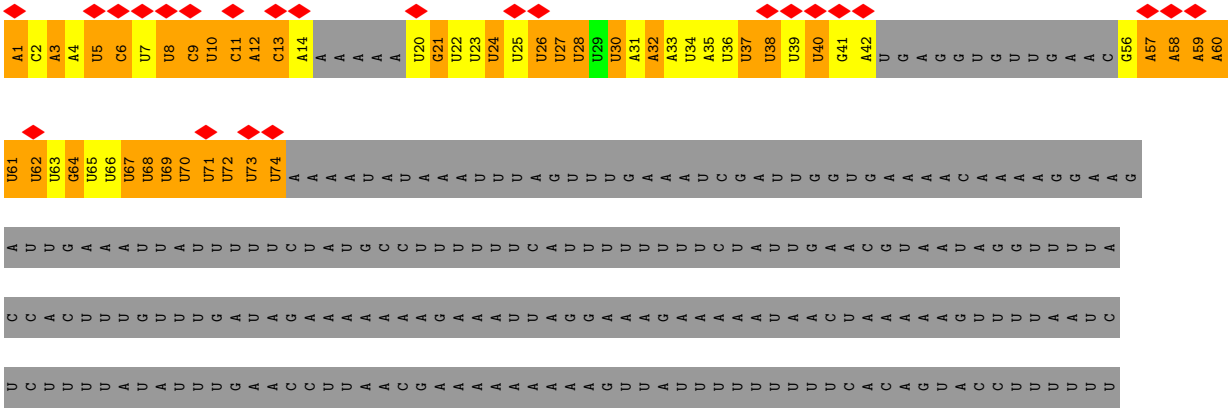
• Molecule 5: Ribosome biogenesis protein nsa1

Chain 5:



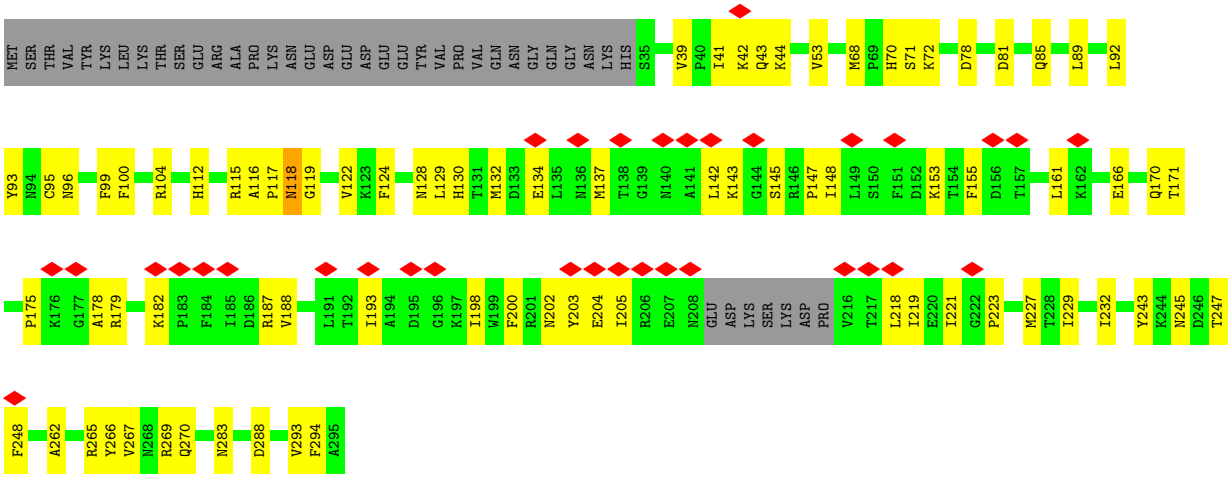
• Molecule 6: RNA (93-MER)

Chain 6:



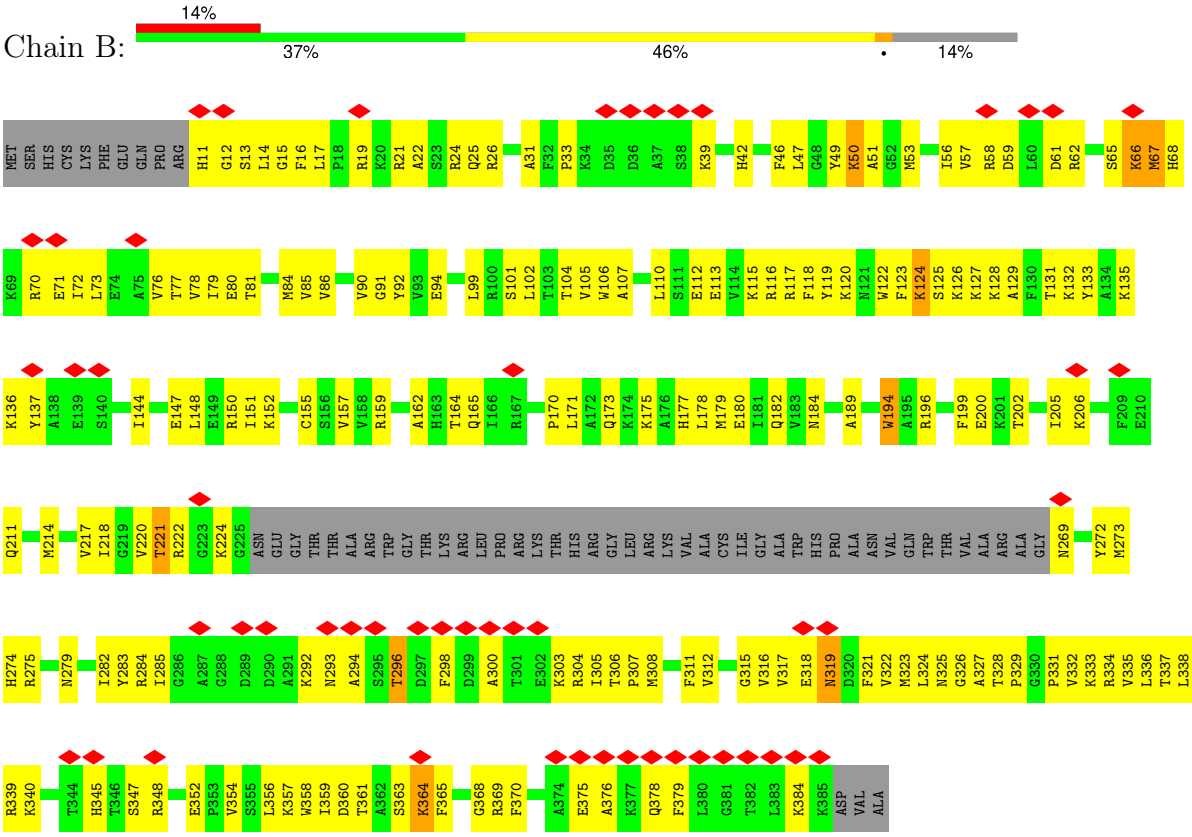
• Molecule 7: Ribosome biogenesis protein brx1

Chain A:



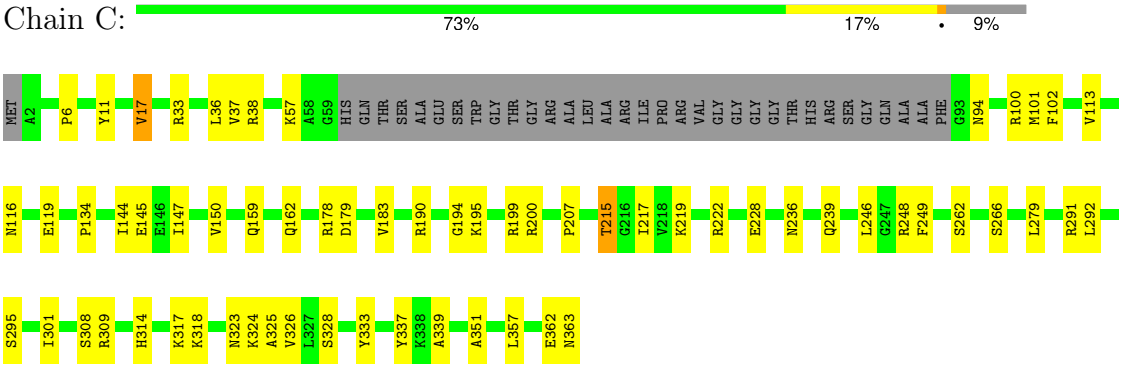
• Molecule 8: 60S ribosomal protein L3-A

Chain B:



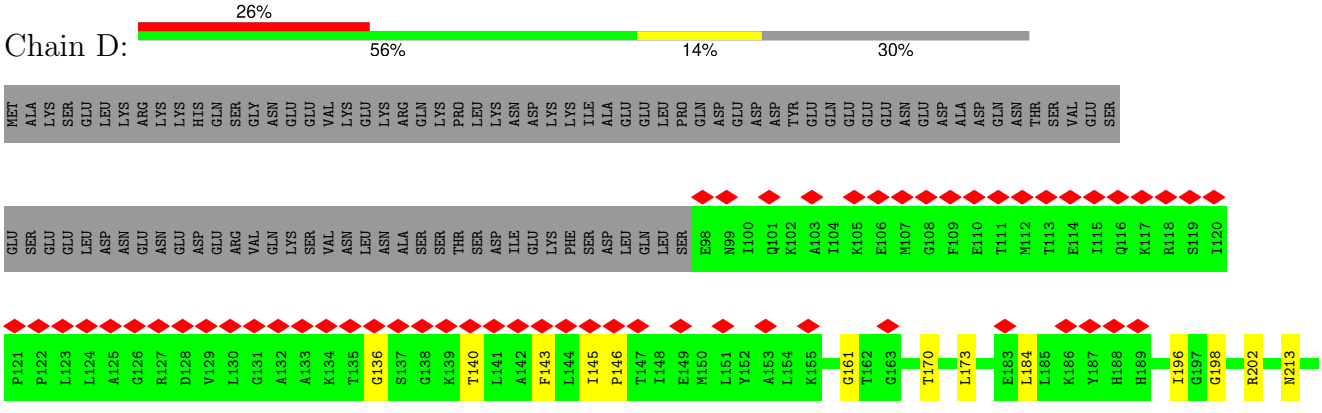
• Molecule 9: 60S ribosomal protein L4-B

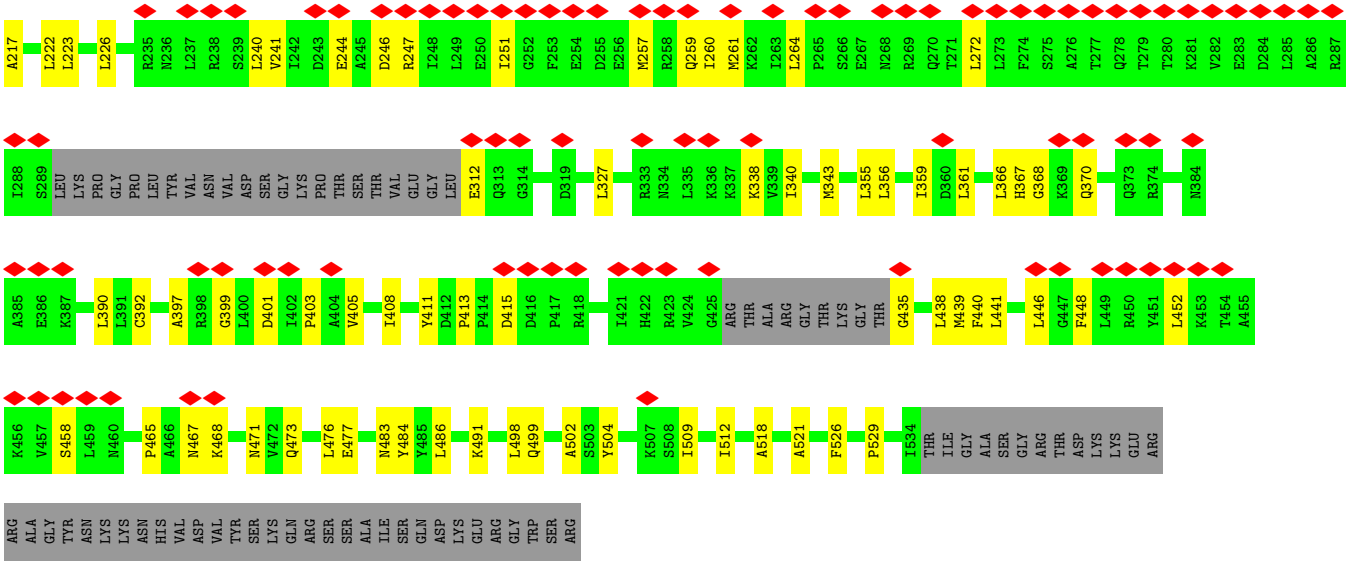
Chain C:



• Molecule 10: ATP-dependent RNA helicase has1

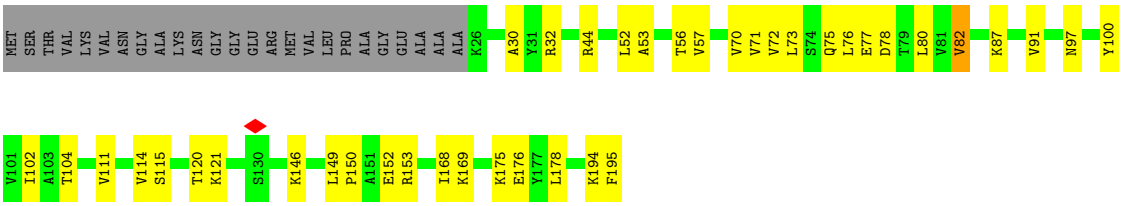
Chain D:





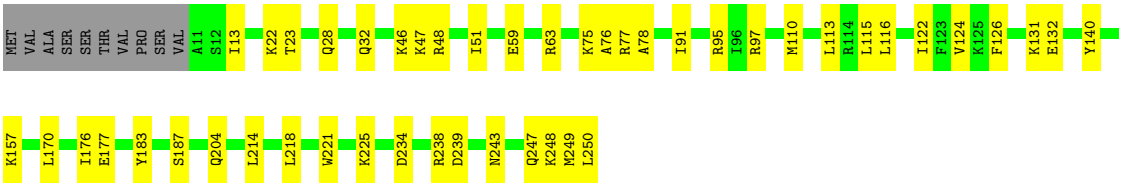
• Molecule 11: 60S ribosomal protein L6

Chain E:



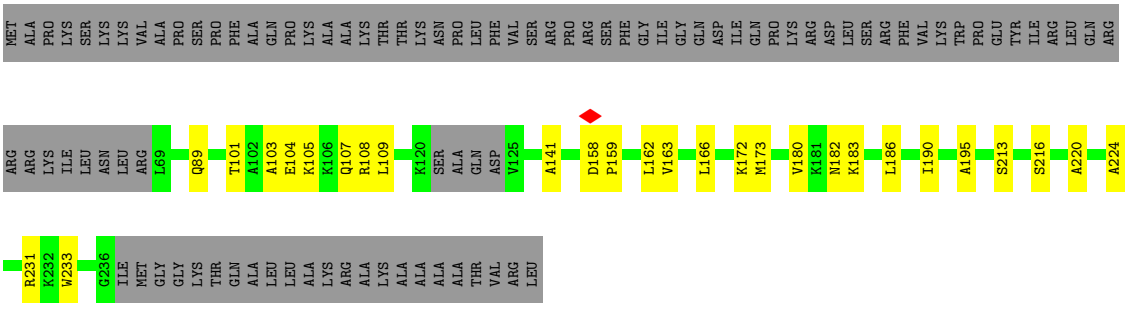
• Molecule 12: 60S ribosomal protein L7-B

Chain F:



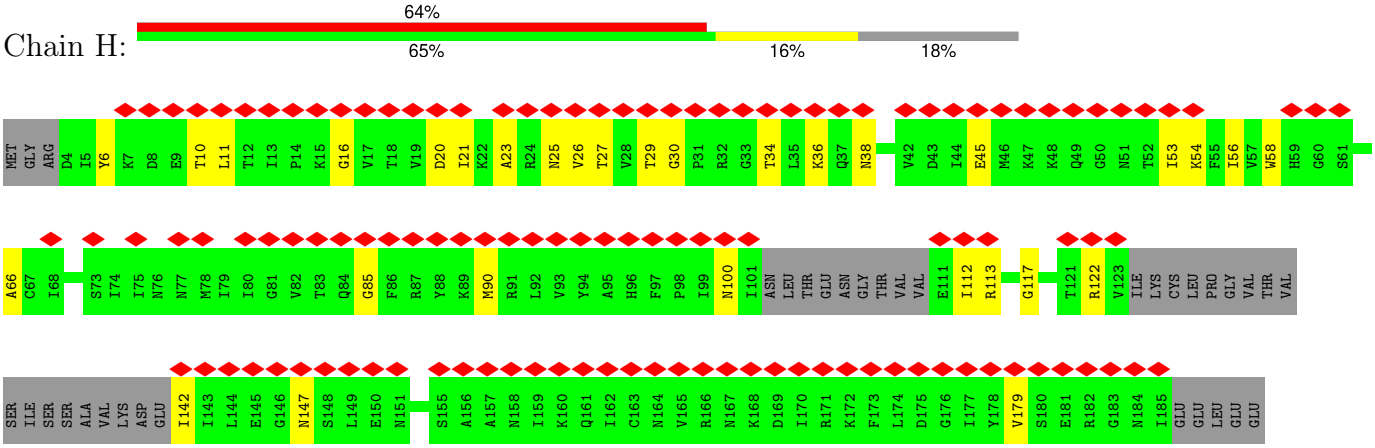
• Molecule 13: 60S ribosomal protein L8

Chain G:



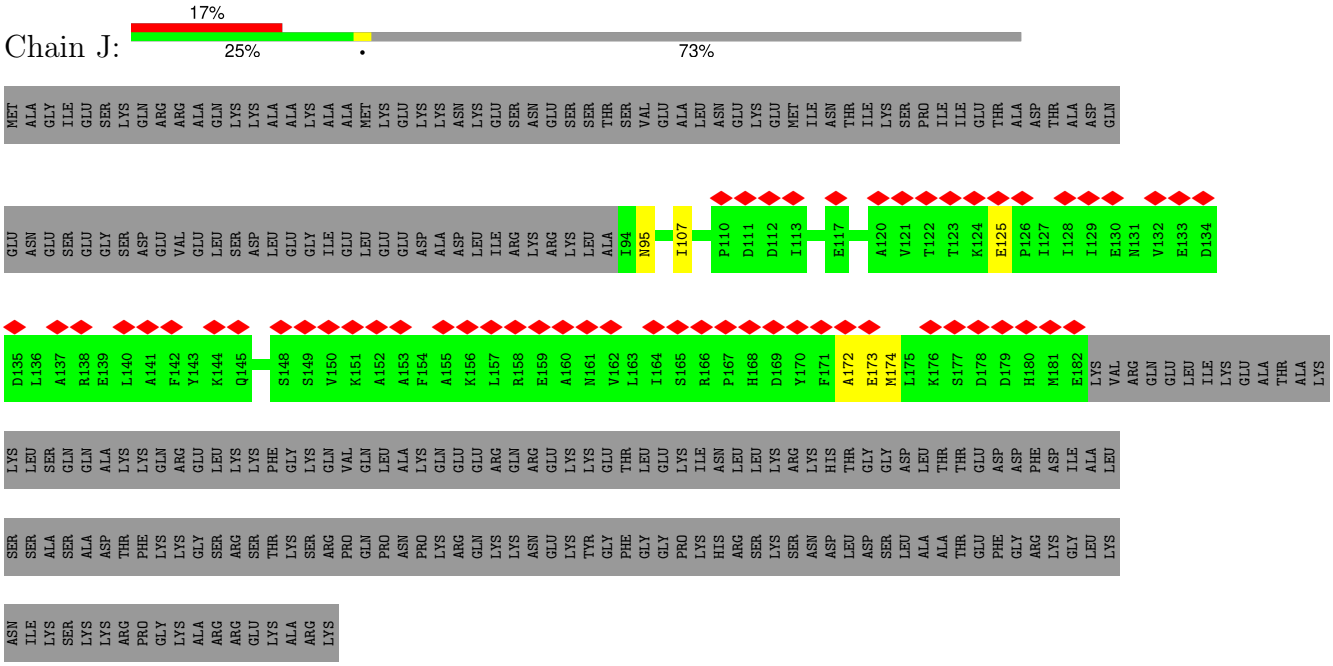
• Molecule 14: 60S ribosomal protein L9-A

Chain H:



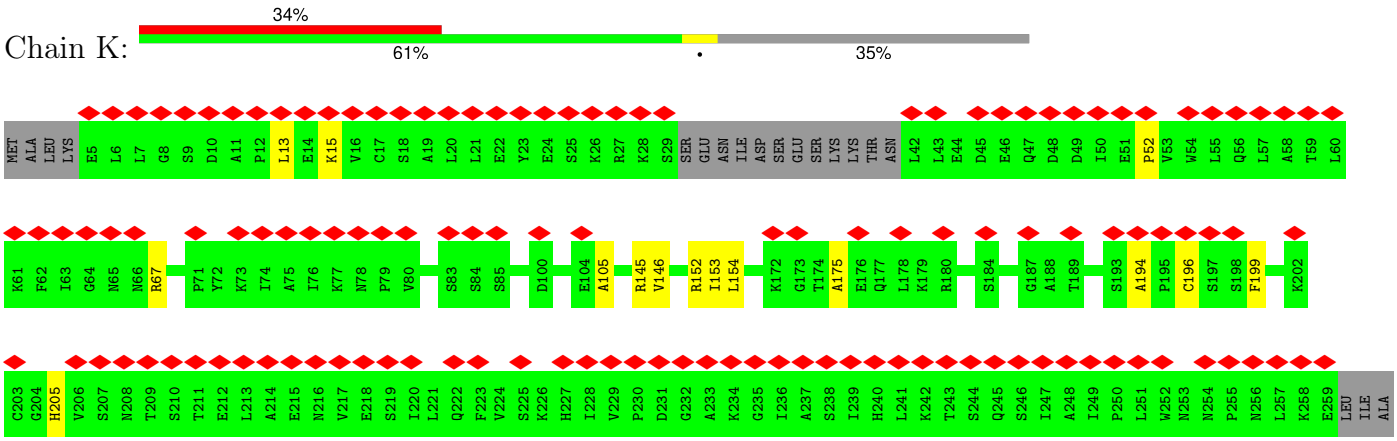
• Molecule 15: Probable rRNA-processing protein ebp2

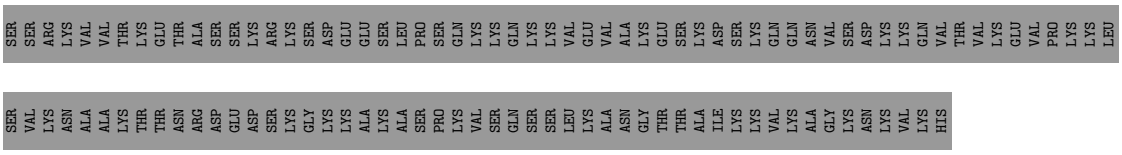
Chain J:



• Molecule 16: Putative ribosome biogenesis protein C8F11.04

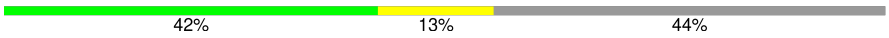
Chain K:

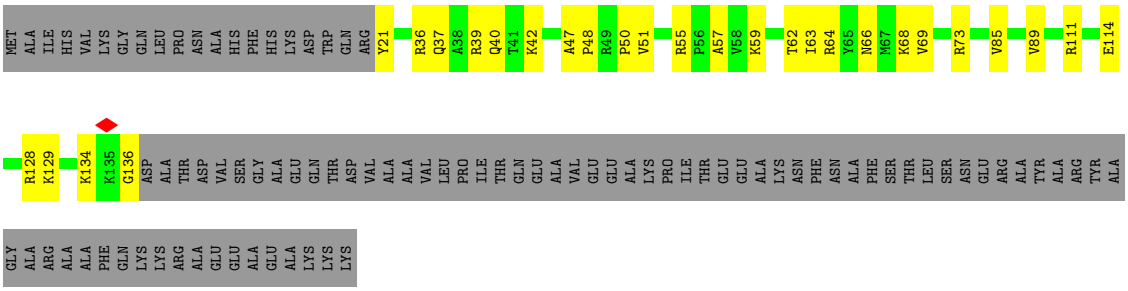




• Molecule 17: 60S ribosomal protein L13

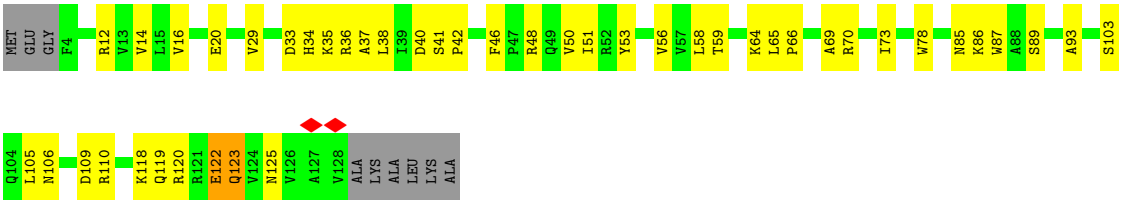
Chain L:





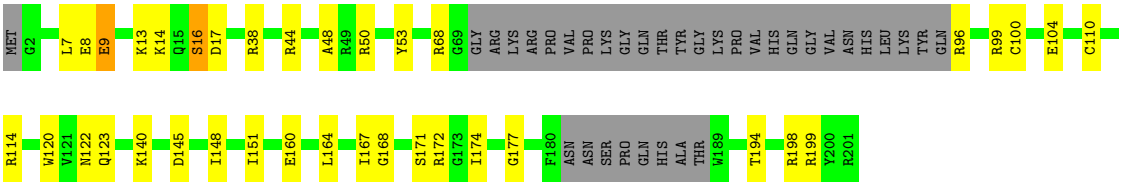
• Molecule 18: 60S ribosomal protein L14

Chain M:



• Molecule 19: 60S ribosomal protein L15-A

Chain N:

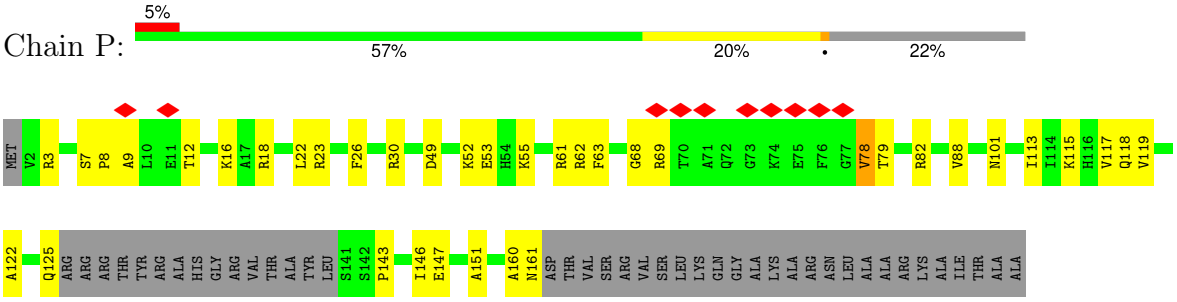


• Molecule 20: 60S ribosomal protein L16-B

Chain O:

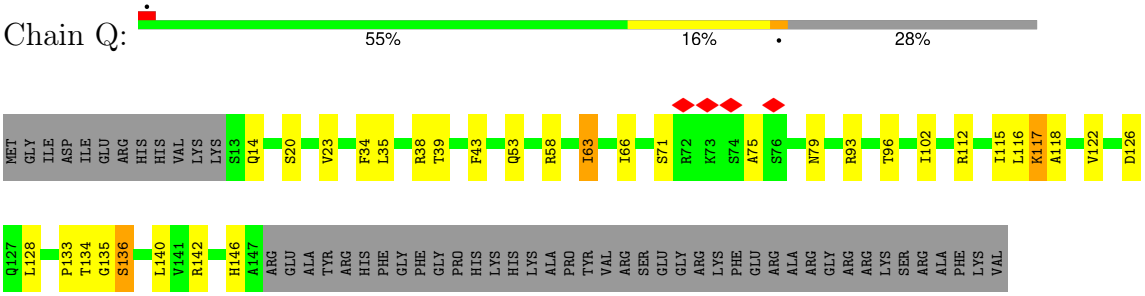
• Molecule 21: 60S ribosomal protein L17-A

Chain P:



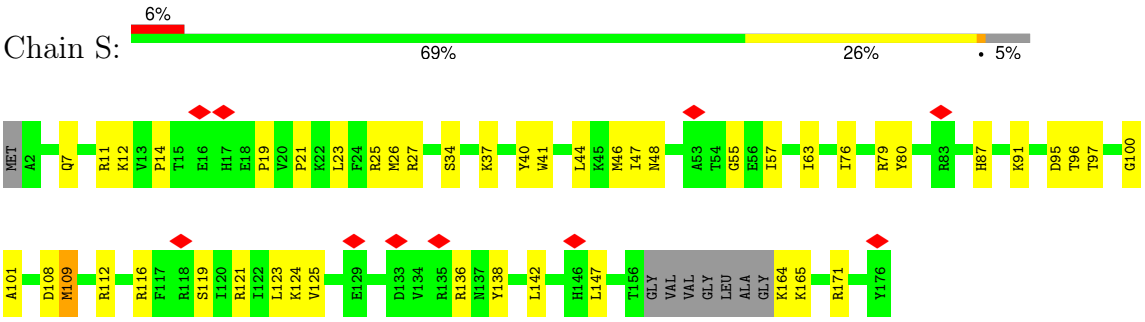
• Molecule 22: 60S ribosomal protein L18-A

Chain Q:



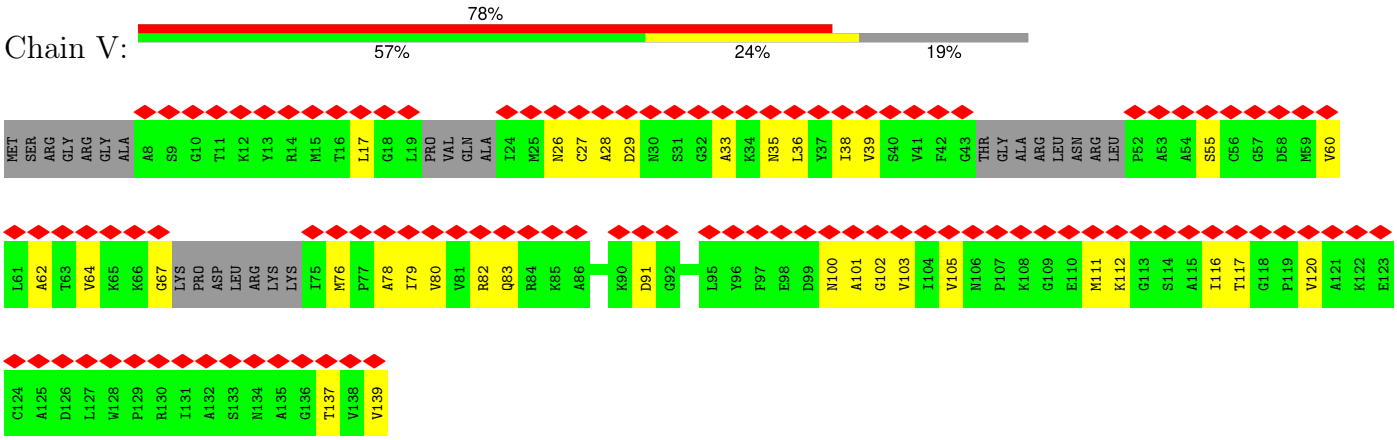
• Molecule 23: 60S ribosomal protein L20-A

Chain S:



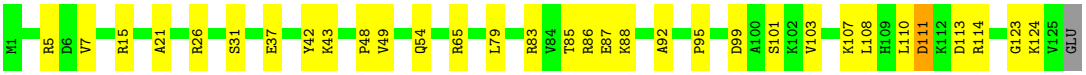
• Molecule 24: 60S ribosomal protein L23-A

Chain V:

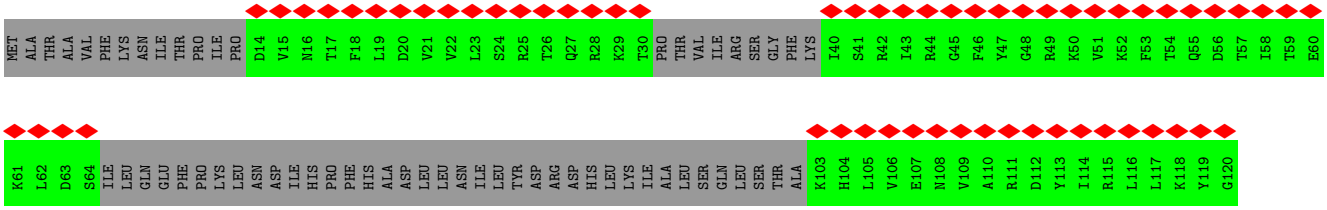


• Molecule 25: 60S ribosomal protein L26

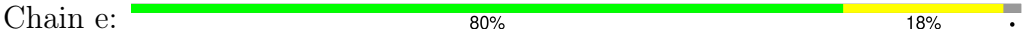
Chain Y:



• Molecule 26: Probable nucleolar GTP-binding protein 1



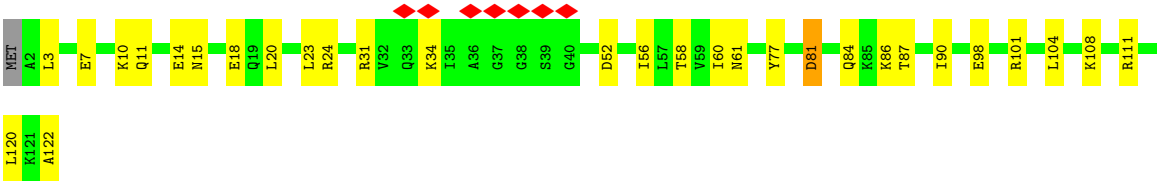
• Molecule 27: 60S ribosomal protein L32-A



• Molecule 28: 60S ribosomal protein L33-B

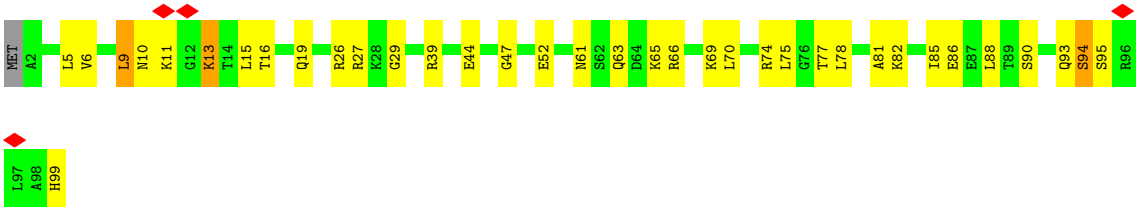
• Molecule 29: 60S ribosomal protein L35

Chain h:



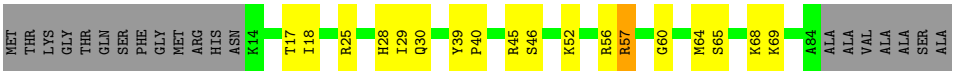
• Molecule 30: 60S ribosomal protein L36-B

Chain i:



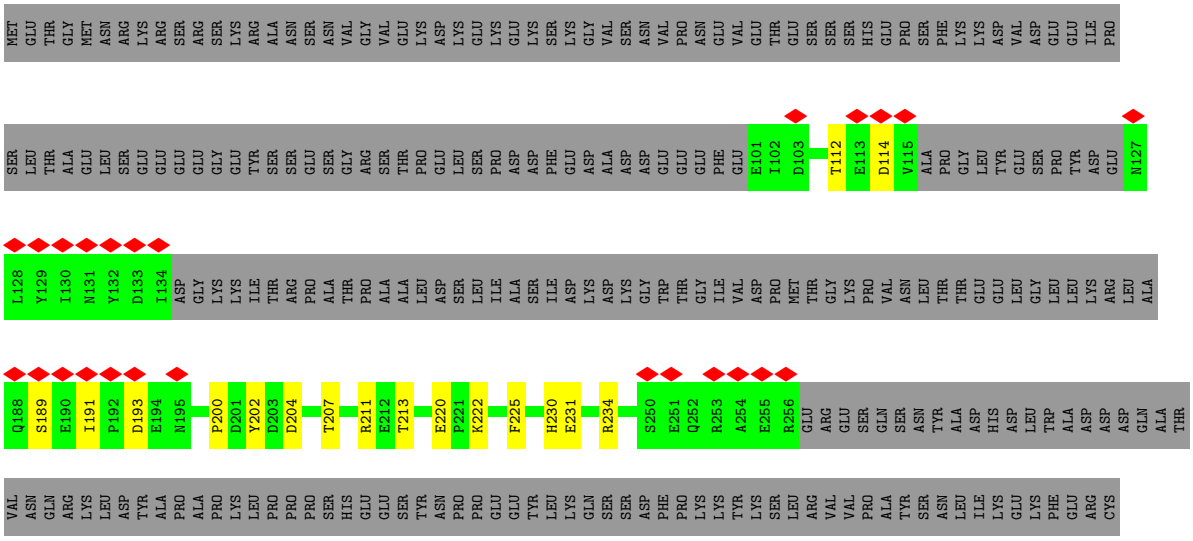
• Molecule 31: 60S ribosomal protein L37-B

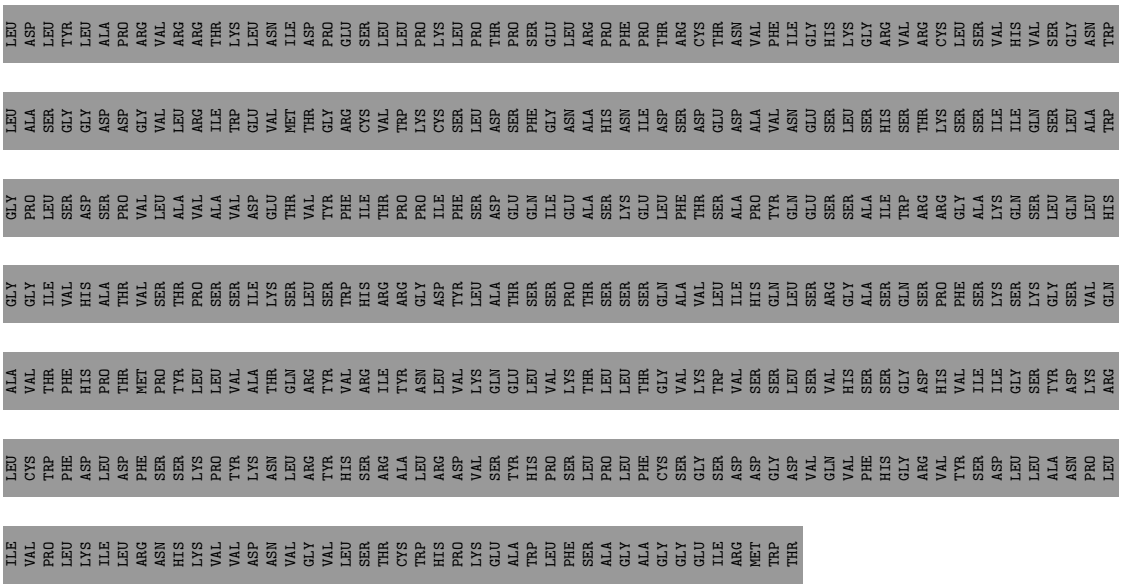
Chain j:



• Molecule 32: Ribosome biogenesis protein erb1

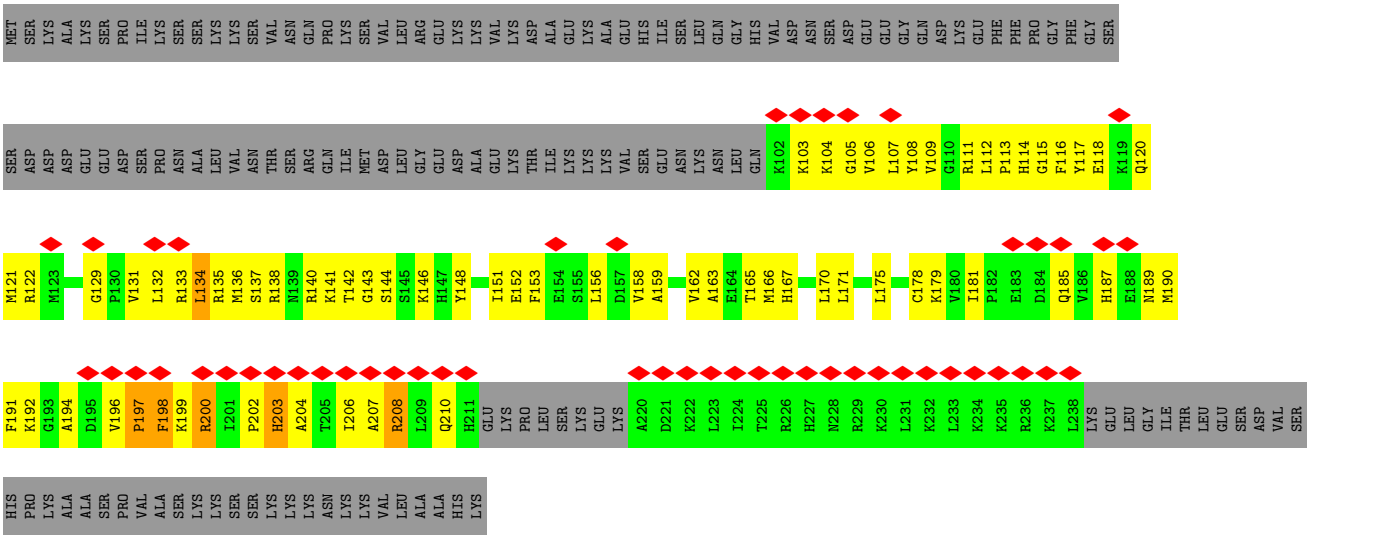
Chain m:





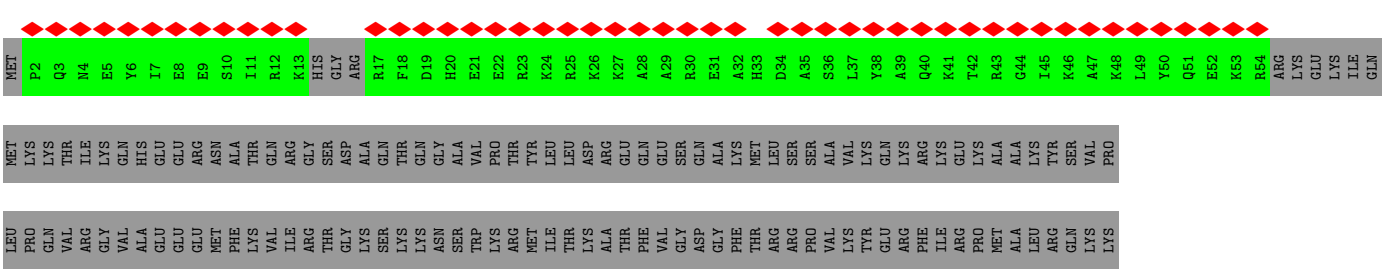
• Molecule 33: Uncharacterized RNA-binding protein C1827.05c

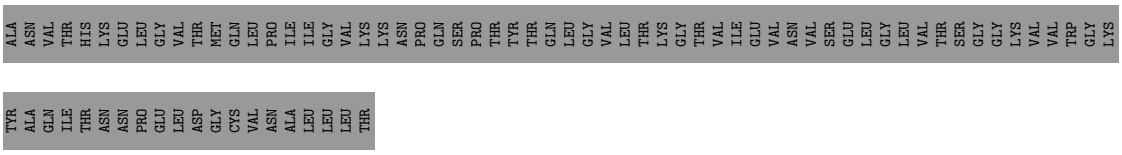
Chain o:



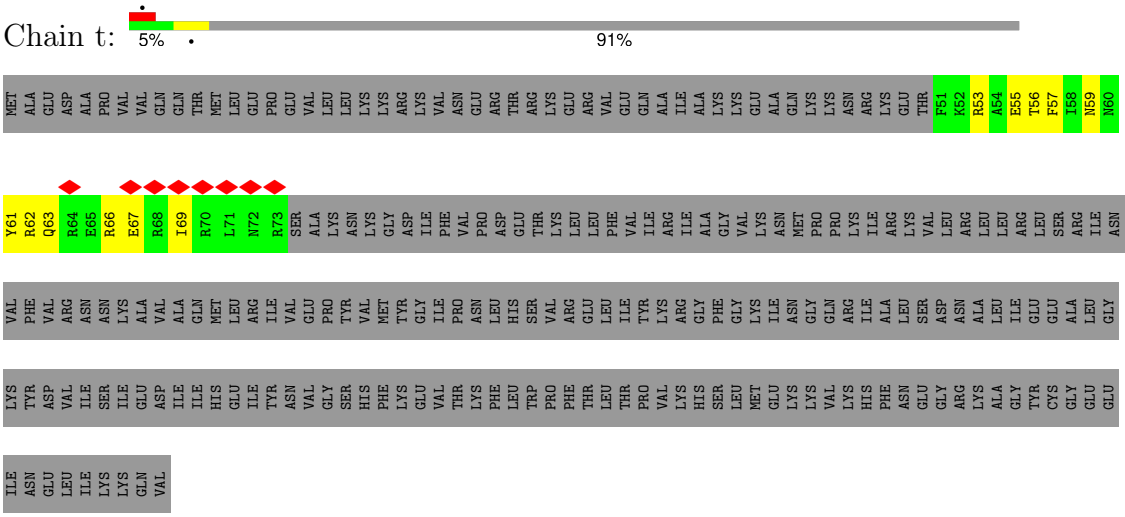
• Molecule 34: Ribosome biogenesis protein nsa2

Chain r:

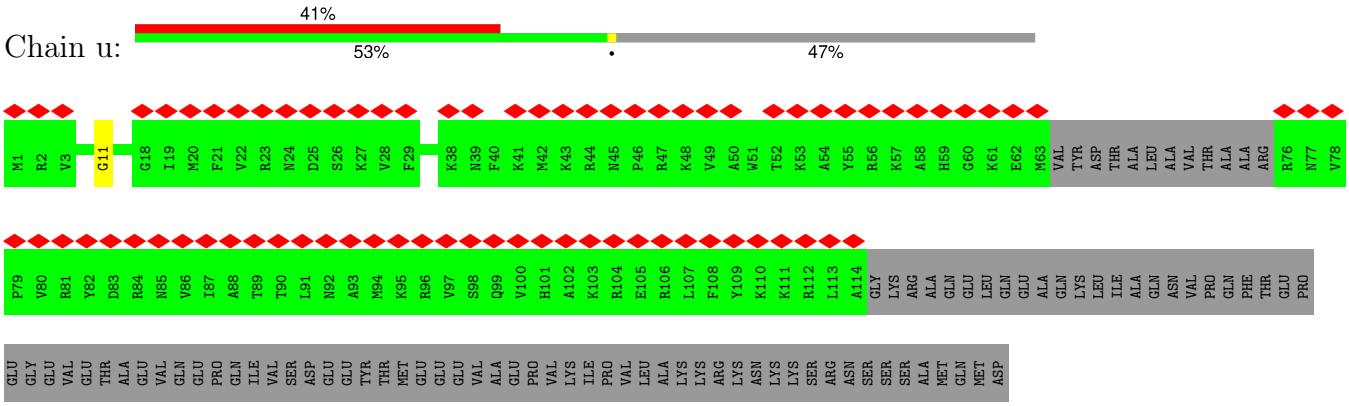




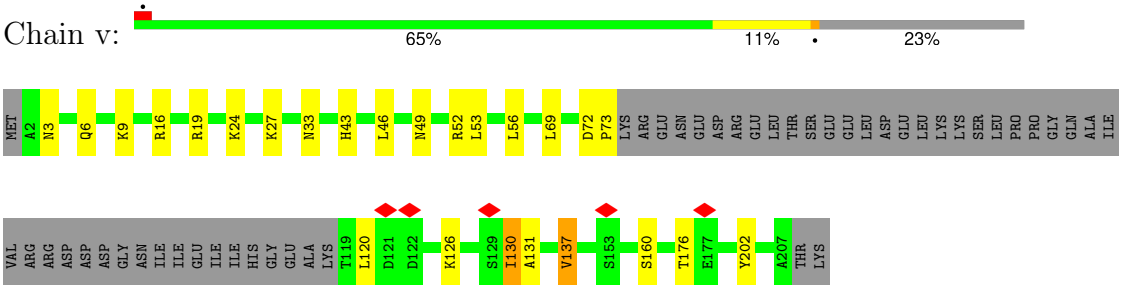
• Molecule 35: 60S ribosomal protein L7-A



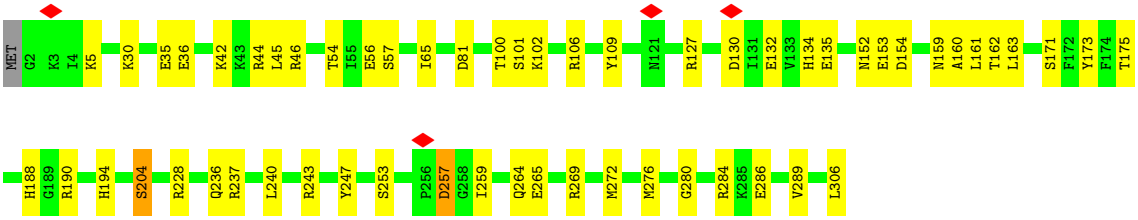
• Molecule 36: Ribosome biogenesis protein rlp24



• Molecule 37: Nucleolar protein 16



• Molecule 38: Brix domain-containing protein C4F8.04

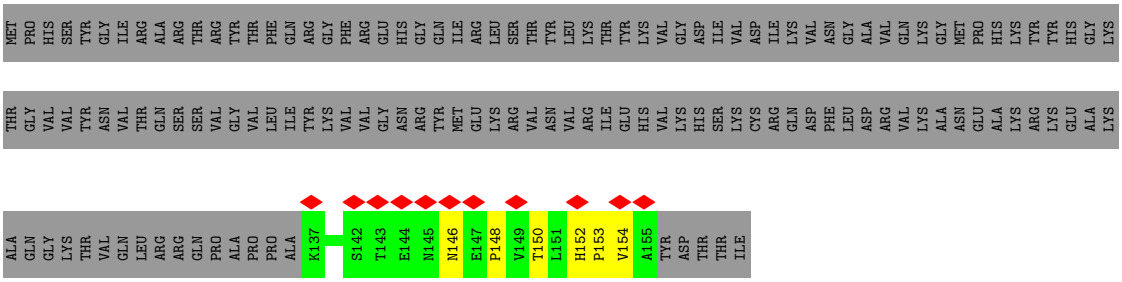


• Molecule 39: Eukaryotic translation initiation factor 6

Chain y:

• Molecule 40: 60S ribosomal protein L21-A

Chain T:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	220000	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	0.774	Depositor
Minimum map value	-0.343	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	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

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	1	0.17	0/34328	0.24	0/53470
2	2	0.16	0/3084	0.21	0/4794
3	3	0.23	0/1627	0.28	0/2188
4	4	0.16	0/1817	0.27	0/2454
5	5	0.14	0/2739	0.31	0/3702
6	6	0.35	0/1287	0.64	0/1990
7	A	0.12	0/2096	0.29	0/2826
8	B	0.21	0/2694	0.49	0/3619
9	C	0.20	0/2618	0.31	0/3531
10	D	0.10	0/3052	0.26	0/4138
11	E	0.15	0/1356	0.30	0/1829
12	F	0.15	0/1982	0.24	0/2658
13	G	0.17	0/1291	0.29	0/1742
14	H	0.09	0/761	0.23	0/1054
15	J	0.05	0/443	0.17	0/618
16	K	0.07	0/1203	0.22	0/1675
17	L	0.22	0/960	0.30	0/1288
18	M	0.15	0/1024	0.32	0/1375
19	N	0.19	0/1436	0.26	0/1920
20	O	0.15	0/1515	0.30	0/2028
21	P	0.13	0/1161	0.26	0/1559
22	Q	0.18	0/1058	0.28	0/1421
23	S	0.13	0/1438	0.30	1/1932 (0.1%)
24	V	0.07	0/550	0.22	0/755
25	Y	0.18	0/1008	0.35	0/1341
26	b	0.05	0/590	0.16	0/816
27	e	0.20	0/1009	0.26	0/1345
28	f	0.18	0/859	0.29	0/1152
29	h	0.17	0/1008	0.33	0/1340
30	i	0.15	0/775	0.27	0/1030
31	j	0.12	0/575	0.22	0/761
32	m	0.12	0/738	0.23	0/997

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
33	o	0.24	0/1014	0.56	0/1366
34	r	0.05	0/247	0.16	0/342
35	t	0.22	0/218	0.33	0/287
36	u	0.05	0/504	0.17	0/700
37	v	0.13	0/1319	0.25	0/1769
38	x	0.15	0/2562	0.27	0/3432
39	y	0.08	0/971	0.22	0/1345
40	T	0.08	0/151	0.20	0/207
All	All	0.17	0/85068	0.28	1/122796 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	S	19	PRO	CA-N-CD	-5.27	104.62	112.00

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	30681	0	15431	362	0
2	2	2762	0	1399	25	0
3	3	1596	0	1645	28	0
4	4	1770	0	1788	39	0
5	5	2686	0	2745	56	0
6	6	1160	0	586	118	0
7	A	2057	0	2088	61	0
8	B	2641	0	2727	202	0
9	C	2572	0	2705	50	0
10	D	3001	0	2897	56	0
11	E	1328	0	1408	27	0
12	F	1944	0	2035	30	0
13	G	1273	0	1348	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	H	764	0	330	19	0
15	J	444	0	202	6	0
16	K	1205	0	528	10	0
17	L	942	0	1012	23	0
18	M	1007	0	1072	30	0
19	N	1406	0	1441	27	0
20	O	1487	0	1585	34	0
21	P	1139	0	1158	28	0
22	Q	1047	0	1142	22	0
23	S	1402	0	1451	38	0
24	V	554	0	272	21	0
25	Y	998	0	1090	18	0
26	b	594	0	258	1	0
27	e	995	0	1059	20	0
28	f	839	0	866	16	0
29	h	999	0	1092	22	0
30	i	768	0	835	25	0
31	j	563	0	578	13	0
32	m	725	0	660	16	0
33	o	992	0	939	78	0
34	r	249	0	117	0	0
35	t	216	0	219	19	0
36	u	506	0	226	2	0
37	v	1299	0	1347	19	0
38	x	2516	0	2524	38	0
39	y	974	0	448	17	0
40	T	147	0	140	9	0
41	j	1	0	0	0	0
All	All	80249	0	61393	1383	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 10.

All (1383) 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)
8:B:331:PRO:HD2	8:B:334:ARG:HE	1.30	0.95
8:B:58:ARG:HB2	8:B:356:LEU:HD22	1.49	0.93
1:1:543:G:H1	1:1:582:G:H22	1.15	0.92
8:B:211:GLN:HB2	8:B:285:ILE:HG13	1.50	0.92
6:6:59:A:H3'	6:6:60:A:H8	1.32	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:311:PHE:HA	8:B:364:LYS:HG3	1.54	0.90
8:B:76:VAL:HA	8:B:325:ASN:HA	1.55	0.88
1:1:3133:U:H4'	8:B:65:SER:HA	1.56	0.87
6:6:70:U:H1'	6:6:71:U:H3	1.42	0.84
8:B:91:GLY:HA3	8:B:151:ILE:HD12	1.61	0.82
33:o:208:ARG:HE	33:o:208:ARG:HA	1.44	0.82
8:B:308:MET:HE2	8:B:363:SER:HB2	1.62	0.81
1:1:312:G:H1	1:1:319:U:H3	1.28	0.81
6:6:9:C:H5"	16:K:145:ARG:HA	1.63	0.80
8:B:56:ILE:HG22	8:B:360:ASP:H	1.47	0.80
3:3:158:GLU:HB2	21:P:12:THR:HG21	1.67	0.77
8:B:220:VAL:HA	8:B:274:HIS:HA	1.67	0.77
4:4:173:TYR:HB2	4:4:177:VAL:HG12	1.66	0.76
6:6:10:U:H3	6:6:24:U:H3	1.34	0.76
3:3:185:ILE:HG23	38:x:259:ILE:HD11	1.68	0.76
33:o:131:VAL:HG13	33:o:151:ILE:HG23	1.66	0.76
8:B:19:ARG:HB3	8:B:273:MET:HE1	1.67	0.75
33:o:120:GLN:OE1	33:o:120:GLN:N	2.18	0.75
8:B:59:ASP:HA	8:B:71:GLU:HA	1.67	0.75
33:o:121:MET:HE2	33:o:134:LEU:HD12	1.67	0.75
1:1:189:G:H22	1:1:243:C:H5	1.34	0.75
6:6:38:U:H2'	6:6:39:U:C6	2.21	0.75
7:A:245:ASN:ND2	7:A:247:THR:OG1	2.20	0.75
6:6:70:U:H1'	6:6:71:U:N3	2.01	0.74
6:6:74:U:C4	33:o:198:PHE:HA	2.22	0.74
16:K:67:ARG:HA	16:K:194:ALA:HA	1.68	0.74
33:o:104:LYS:HE2	33:o:132:LEU:HD21	1.68	0.74
6:6:61:U:H3'	6:6:62:U:H4'	1.69	0.74
7:A:179:ARG:HD2	32:m:114:ASP:HB3	1.70	0.73
8:B:57:VAL:HA	8:B:73:LEU:HA	1.70	0.73
6:6:3:A:H2'	6:6:4:A:C8	2.24	0.73
8:B:56:ILE:HD12	8:B:359:ILE:HD13	1.69	0.72
1:1:445:G:H1	1:1:647:A:H61	1.35	0.72
1:1:3140:A:H5"	8:B:12:GLY:H	1.54	0.72
1:1:3397:A:OP1	8:B:124:LYS:NZ	2.23	0.72
1:1:3417:A:OP1	1:1:3419:G:N2	2.22	0.72
1:1:531:A:OP2	12:F:77:ARG:NH1	2.23	0.72
6:6:20:U:H2'	6:6:21:G:C8	2.25	0.72
1:1:3133:U:H5"	8:B:62:ARG:HH11	1.53	0.71
1:1:305:A:H8	30:i:29:GLY:HA2	1.55	0.71
5:5:218:ASP:HB3	5:5:221:LEU:HD22	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:119:TYR:HE2	8:B:129:ALA:HB2	1.55	0.71
4:4:38:ARG:HG3	4:4:82:LEU:HD11	1.73	0.71
1:1:3182:G:N2	1:1:3475:U:O2'	2.23	0.71
26:b:420:TYR:HA	39:y:87:SER:HA	1.73	0.71
1:1:1222:U:OP2	20:O:50:ARG:NH1	2.23	0.71
9:C:363:ASN:OD1	23:S:124:LYS:NZ	2.23	0.71
39:y:39:GLU:HA	39:y:43:GLY:HA3	1.71	0.71
1:1:1221:A:H8	1:1:1328:C:H4'	1.55	0.71
6:6:13:C:H2'	6:6:14:A:C8	2.26	0.71
6:6:59:A:H3'	6:6:60:A:C8	2.21	0.70
1:1:265:C:H2'	1:1:266:G:H5"	1.72	0.70
1:1:835:C:H4'	9:C:94:ASN:HD21	1.57	0.70
4:4:46:LYS:HG2	7:A:293:VAL:HG11	1.73	0.70
23:S:80:TYR:HB3	23:S:87:HIS:HB2	1.72	0.70
13:G:173:MET:HE1	32:m:211:ARG:HD3	1.73	0.70
18:M:33:ASP:OD1	18:M:34:HIS:N	2.24	0.70
1:1:539:A:H1'	1:1:588:G:H22	1.57	0.69
8:B:14:LEU:HA	8:B:17:LEU:HB2	1.74	0.69
20:O:76:ALA:HB3	20:O:79:ARG:HG2	1.72	0.69
23:S:123:LEU:O	40:T:152:HIS:ND1	2.23	0.69
1:1:14:U:O4	2:2:144:G:N2	2.26	0.69
1:1:3315:A:OP2	18:M:118:LYS:NZ	2.25	0.69
29:h:98:GLU:HA	29:h:101:ARG:HG2	1.74	0.69
1:1:769:U:H3	22:Q:142:ARG:HH21	1.40	0.69
10:D:312:GLU:N	10:D:458:SER:HG	1.90	0.69
5:5:154:LEU:HB2	5:5:180:PHE:HB3	1.75	0.69
3:3:11:VAL:O	3:3:19:ARG:NH2	2.26	0.68
7:A:147:PRO:HB3	7:A:187:ARG:HG3	1.75	0.68
1:1:3254:G:H1	1:1:3392:A:H61	1.41	0.68
33:o:109:VAL:HG23	33:o:112:LEU:HD11	1.76	0.68
1:1:3409:C:H3'	1:1:3410:G:H21	1.58	0.68
9:C:162:GLN:OE1	9:C:219:LYS:NZ	2.27	0.68
8:B:307:PRO:HG2	8:B:364:LYS:HG2	1.75	0.68
1:1:505:G:H1	1:1:644:A:H61	1.41	0.68
6:6:39:U:C2	6:6:40:U:H1'	2.29	0.68
9:C:116:ASN:HB2	9:C:119:GLU:HG3	1.74	0.68
1:1:371:C:OP2	31:j:56:ARG:NH2	2.23	0.67
19:N:96:ARG:NH2	19:N:100:CYS:SG	2.67	0.67
6:6:38:U:H2'	6:6:39:U:H6	1.59	0.67
20:O:183:LYS:O	20:O:189:ASN:ND2	2.28	0.67
8:B:110:LEU:HB2	8:B:115:LYS:HE3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:124:LYS:N	25:Y:124:LYS:HE2	2.10	0.67
20:O:159:GLU:OE2	20:O:159:GLU:N	2.22	0.66
33:o:138:ARG:NH1	33:o:143:GLY:O	2.28	0.66
1:1:3146:U:H3	1:1:3190:A:H1'	1.60	0.66
4:4:111:ARG:NH1	4:4:167:GLU:OE2	2.26	0.66
8:B:126:LYS:HB2	8:B:128:LYS:HG2	1.78	0.66
1:1:1341:G:HO2'	1:1:2468:A:HO2'	1.44	0.66
5:5:22:ASP:OD1	5:5:329:ASN:ND2	2.28	0.66
1:1:609:A:O2'	28:f:85:ARG:NH2	2.29	0.66
1:1:3285:G:H22	1:1:3302:U:H3	1.43	0.66
2:2:11:A:O2'	21:P:61:ARG:NH2	2.28	0.66
23:S:76:ILE:HG23	23:S:125:VAL:HG22	1.76	0.66
3:3:20:ILE:HD11	3:3:29:ARG:HB3	1.78	0.65
6:6:61:U:H3'	6:6:62:U:C4'	2.26	0.65
6:6:74:U:O2	33:o:138:ARG:HD3	1.96	0.65
6:6:37:U:HO2'	6:6:38:U:H6	1.44	0.65
8:B:94:GLU:OE2	8:B:94:GLU:N	2.20	0.65
33:o:103:LYS:HB2	33:o:156:LEU:HD23	1.78	0.65
38:x:240:LEU:HD21	38:x:306:LEU:HD13	1.77	0.65
31:j:46:SER:OG	31:j:57:ARG:NH2	2.29	0.65
1:1:816:A:O2'	22:Q:93:ARG:NH2	2.30	0.65
1:1:997:A:H3'	1:1:998:U:H5"	1.77	0.65
7:A:68:MET:HE1	7:A:70:HIS:CE1	2.31	0.65
8:B:294:ALA:HA	8:B:359:ILE:HG13	1.78	0.65
1:1:358:C:H4'	38:x:5:LYS:HG3	1.79	0.65
33:o:143:GLY:HA3	33:o:198:PHE:CE1	2.32	0.65
6:6:71:U:H4'	6:6:72:U:C6	2.32	0.65
11:E:194:LYS:O	18:M:110:ARG:NH2	2.30	0.65
6:6:23:U:H2'	6:6:24:U:C6	2.32	0.65
1:1:753:G:N2	22:Q:140:LEU:O	2.30	0.64
24:V:80:VAL:HA	24:V:102:GLY:HA2	1.77	0.64
28:f:60:VAL:HG12	28:f:61:ARG:HD2	1.78	0.64
1:1:832:G:N2	1:1:835:C:OP1	2.30	0.64
8:B:312:VAL:HG23	8:B:364:LYS:HD3	1.78	0.64
39:y:197:LEU:HA	39:y:206:ALA:HA	1.78	0.64
8:B:77:THR:N	8:B:324:LEU:O	2.31	0.64
2:2:64:G:H21	2:2:70:C:H5'	1.62	0.64
9:C:94:ASN:HD22	9:C:102:PHE:HB2	1.61	0.64
33:o:208:ARG:HA	33:o:208:ARG:NE	2.12	0.64
1:1:3179:G:N2	1:1:3434:G:OP1	2.31	0.64
20:O:75:ARG:HD3	20:O:147:GLY:HA3	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:M:40:ASP:OD1	18:M:41:SER:N	2.31	0.64
23:S:12:LYS:HA	23:S:55:GLY:HA2	1.80	0.64
4:4:52:MET:HE1	4:4:61:GLN:HB2	1.79	0.64
7:A:283:ASN:OD1	22:Q:117:LYS:NZ	2.31	0.64
8:B:84:MET:HE3	8:B:84:MET:HA	1.78	0.64
1:1:1424:A:N6	1:1:1452:A:O2'	2.31	0.63
1:1:498:U:H3'	1:1:499:G:H5"	1.79	0.63
1:1:1386:G:OP1	11:E:32:ARG:NH1	2.31	0.63
23:S:11:ARG:HH12	23:S:14:PRO:HD3	1.63	0.63
24:V:26:ASN:HA	24:V:35:ASN:HA	1.80	0.63
1:1:25:U:O2'	1:1:27:C:N4	2.26	0.63
6:6:70:U:O4	33:o:179:LYS:HB3	1.99	0.63
1:1:3150:U:H2'	1:1:3151:A:C4	2.34	0.63
6:6:12:A:H61	6:6:22:U:H3	1.45	0.63
2:2:68:U:O4	29:h:61:ASN:ND2	2.32	0.63
6:6:8:U:H5"	16:K:146:VAL:HA	1.81	0.63
13:G:109:LEU:HD23	32:m:234:ARG:HG2	1.80	0.63
18:M:120:ARG:NH1	20:O:189:ASN:OD1	2.32	0.63
6:6:34:U:H2'	6:6:35:A:H8	1.64	0.62
1:1:715:U:O2	9:C:222:ARG:NH1	2.33	0.62
4:4:24:GLU:O	4:4:28:ARG:NH2	2.32	0.62
1:1:189:G:H1	1:1:243:C:H41	1.48	0.62
8:B:56:ILE:HG13	8:B:356:LEU:HD21	1.82	0.62
9:C:195:LYS:HB2	9:C:200:ARG:HD2	1.82	0.62
5:5:69:VAL:HG21	5:5:342:ILE:HD12	1.82	0.62
33:o:120:GLN:HE21	35:t:61:TYR:HB2	1.64	0.62
1:1:3434:G:H1'	1:1:3471:A:H61	1.64	0.62
24:V:137:THR:HA	39:y:103:ALA:H	1.64	0.62
33:o:109:VAL:HG12	33:o:178:CYS:SG	2.40	0.62
33:o:122:ARG:HH11	33:o:134:LEU:HD22	1.64	0.62
1:1:990:C:O2'	1:1:995:G:N1	2.32	0.62
8:B:66:LYS:HE3	8:B:67:MET:HG2	1.81	0.61
1:1:34:A:N3	1:1:842:A:O2'	2.31	0.61
2:2:57:G:H1	2:2:62:A:H61	1.48	0.61
7:A:96:ASN:HB2	7:A:115:ARG:HH21	1.65	0.61
7:A:96:ASN:HD22	7:A:115:ARG:NH2	1.98	0.61
1:1:276:A:OP1	19:N:50:ARG:NH1	2.33	0.61
8:B:102:LEU:HD21	8:B:150:ARG:HG2	1.81	0.61
25:Y:43:LYS:HB2	25:Y:123:GLY:HA2	1.82	0.61
1:1:461:A:H4'	1:1:462:U:OP1	1.99	0.61
3:3:43:CYS:O	3:3:47:ASN:ND2	2.26	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:116:ALA:HB3	7:A:117:PRO:HD3	1.81	0.61
8:B:26:ARG:HD2	8:B:179:MET:HB2	1.82	0.61
1:1:712:U:OP2	17:L:36:ARG:NH2	2.32	0.61
4:4:95:TRP:O	9:C:291:ARG:NH2	2.32	0.61
1:1:549:G:H1	1:1:575:G:H22	1.49	0.61
1:1:1459:U:H4'	9:C:38:ARG:HD2	1.83	0.61
3:3:129:HIS:ND1	38:x:132:GLU:OE2	2.34	0.61
33:o:112:LEU:HD13	33:o:148:TYR:HA	1.82	0.61
1:1:3147:U:H2'	1:1:3148:G:H8	1.65	0.61
1:1:3369:A:H4'	1:1:3370:U:H5'	1.81	0.61
8:B:72:ILE:HA	24:V:91:ASP:HA	1.81	0.61
1:1:3140:A:H4'	8:B:13:SER:H	1.64	0.60
6:6:74:U:N3	33:o:198:PHE:HA	2.16	0.60
18:M:34:HIS:HD1	23:S:138:TYR:HH	1.46	0.60
39:y:107:ILE:HA	39:y:147:LEU:HA	1.82	0.60
5:5:48:MET:HE2	5:5:57:VAL:HG22	1.83	0.60
9:C:215:THR:O	9:C:215:THR:OG1	2.19	0.60
1:1:671:A:C8	1:1:2460:A:H1'	2.36	0.60
6:6:35:A:C4	6:6:62:U:C2	2.89	0.60
23:S:11:ARG:HD2	23:S:21:PRO:HG2	1.82	0.60
1:1:3098:C:H5"	8:B:178:LEU:HD22	1.84	0.60
1:1:3360:G:H4'	18:M:122:GLU:HG2	1.82	0.60
6:6:20:U:H2'	6:6:21:G:H8	1.67	0.60
8:B:92:TYR:N	8:B:155:CYS:SG	2.75	0.60
1:1:341:G:OP2	37:v:9:LYS:NZ	2.32	0.60
1:1:669:G:H1'	1:1:1148:G:H21	1.66	0.60
1:1:3305:C:OP2	1:1:3306:C:N4	2.35	0.60
8:B:53:MET:HA	8:B:77:THR:HA	1.84	0.59
33:o:107:LEU:N	33:o:151:ILE:O	2.33	0.59
5:5:267:LEU:HD11	5:5:281:ASP:HA	1.83	0.59
7:A:202:ASN:HB3	7:A:221:ILE:HB	1.83	0.59
27:e:79:VAL:HG21	27:e:105:ILE:HG23	1.84	0.59
1:1:3122:G:N2	1:1:3125:A:OP2	2.35	0.59
9:C:328:SER:O	12:F:48:ARG:NH2	2.35	0.59
1:1:27:C:H2'	1:1:28:G:H5"	1.85	0.59
1:1:1380:A:H3'	12:F:22:LYS:HD2	1.85	0.59
1:1:3134:U:H4'	8:B:66:LYS:HD3	1.84	0.59
7:A:243:TYR:HA	15:J:95:ASN:H	1.67	0.59
1:1:840:A:H3'	1:1:841:G:H8	1.67	0.59
1:1:1006:A:OP1	22:Q:14:GLN:NE2	2.36	0.59
8:B:331:PRO:HD2	8:B:334:ARG:NE	2.11	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:59:GLU:OE2	12:F:63:ARG:NH2	2.36	0.59
7:A:44:LYS:HB3	7:A:95:CYS:HA	1.84	0.59
8:B:221:THR:HG22	8:B:272:TYR:N	2.18	0.59
6:6:34:U:H2'	6:6:35:A:C8	2.38	0.59
1:1:63:A:OP1	19:N:172:ARG:NH2	2.36	0.58
1:1:3192:C:H4'	8:B:326:GLY:HA2	1.85	0.58
7:A:41:ILE:HG12	7:A:178:ALA:HA	1.85	0.58
7:A:128:ASN:OD1	7:A:130:HIS:NE2	2.36	0.58
7:A:188:VAL:HG23	7:A:205:ILE:HD11	1.85	0.58
8:B:119:TYR:HA	8:B:124:LYS:HZ1	1.68	0.58
13:G:172:LYS:HB2	32:m:207:THR:HG22	1.84	0.58
8:B:294:ALA:HB2	8:B:305:ILE:HA	1.84	0.58
9:C:144:ILE:HA	9:C:147:ILE:HD13	1.85	0.58
11:E:152:GLU:OE1	11:E:152:GLU:N	2.20	0.58
23:S:7:GLN:HB3	23:S:63:ILE:HD11	1.85	0.58
38:x:171:SER:OG	38:x:280:GLY:O	2.20	0.58
4:4:187:ASP:OD2	4:4:208:ARG:NH1	2.36	0.58
1:1:366:G:N2	1:1:369:A:OP2	2.26	0.58
7:A:44:LYS:HA	7:A:70:HIS:HD2	1.68	0.58
10:D:143:PHE:HD2	10:D:241:VAL:HG11	1.68	0.58
10:D:355:LEU:HD21	10:D:476:LEU:HD11	1.84	0.58
1:1:359:A:H5"	2:2:59:G:H22	1.68	0.58
4:4:52:MET:HG2	4:4:109:LEU:HD22	1.86	0.58
38:x:228:ARG:NH1	38:x:247:TYR:O	2.34	0.58
21:P:18:ARG:NH1	21:P:147:GLU:OE1	2.37	0.58
33:o:146:LYS:NZ	33:o:148:TYR:OH	2.36	0.58
1:1:3106:U:H5'	8:B:14:LEU:HB2	1.86	0.58
1:1:3375:U:OP2	28:f:69:TRP:NE1	2.35	0.58
6:6:64:G:H3'	6:6:65:U:C6	2.39	0.58
1:1:458:G:H1	1:1:494:A:H2	1.51	0.58
6:6:3:A:H2'	6:6:4:A:H8	1.67	0.58
1:1:86:G:O2'	1:1:98:G:O6	2.22	0.57
19:N:114:ARG:NH1	19:N:151:ILE:O	2.37	0.57
21:P:160:ALA:HB3	38:x:228:ARG:HH21	1.69	0.57
25:Y:37:GLU:H	25:Y:37:GLU:CD	2.12	0.57
33:o:122:ARG:NH1	33:o:134:LEU:HD22	2.19	0.57
1:1:3156:C:O2'	1:1:3433:U:O2'	2.20	0.57
6:6:4:A:C2	35:t:63:GLN:HG2	2.38	0.57
18:M:20:GLU:CD	18:M:20:GLU:H	2.12	0.57
24:V:36:LEU:HA	24:V:64:VAL:HA	1.86	0.57
5:5:65:GLU:HB2	5:5:76:LEU:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:42:LYS:HG3	7:A:43:GLN:HE21	1.67	0.57
13:G:101:THR:HB	13:G:104:GLU:HG3	1.87	0.57
25:Y:111:ASP:HB2	25:Y:113:ASP:OD1	2.04	0.57
1:1:1220:C:N4	1:1:1347:U:OP2	2.35	0.57
1:1:3417:A:H1'	1:1:3490:A:H5"	1.86	0.57
9:C:351:ALA:HB1	12:F:78:ALA:HB2	1.87	0.57
21:P:119:VAL:HG22	21:P:146:ILE:HG12	1.85	0.57
38:x:36:GLU:OE1	38:x:46:ARG:NH1	2.38	0.57
1:1:498:U:H3'	1:1:499:G:C5'	2.33	0.57
1:1:615:G:N2	1:1:637:U:OP1	2.31	0.57
6:6:74:U:H4'	33:o:140:ARG:HA	1.87	0.57
18:M:41:SER:HB3	18:M:46:PHE:HB3	1.86	0.57
25:Y:65:ARG:NH2	25:Y:83:ARG:O	2.38	0.57
5:5:149:GLU:HA	5:5:196:VAL:HG23	1.86	0.57
7:A:78:ASP:OD1	7:A:78:ASP:N	2.36	0.57
10:D:136:GLY:HA3	10:D:399:GLY:HA3	1.86	0.57
18:M:50:VAL:HG21	23:S:96:THR:HG21	1.87	0.57
23:S:46:MET:HE1	23:S:121:ARG:HD2	1.86	0.57
33:o:108:TYR:HB2	33:o:181:ILE:HD11	1.86	0.57
1:1:28:G:O2'	1:1:61:A:N3	2.38	0.57
8:B:57:VAL:HG23	8:B:357:LYS:HB2	1.87	0.57
1:1:3145:A:O2'	8:B:364:LYS:HE3	2.05	0.56
17:L:21:TYR:HB3	19:N:194:THR:HG22	1.86	0.56
27:e:103:VAL:O	27:e:107:GLU:HG2	2.05	0.56
8:B:119:TYR:CE2	8:B:129:ALA:HB2	2.38	0.56
1:1:2438:C:H5"	21:P:68:GLY:HA3	1.87	0.56
1:1:3217:U:H1'	1:1:3218:A:H5"	1.88	0.56
1:1:3336:G:H1	1:1:3351:U:H3	1.52	0.56
6:6:41:G:H2'	6:6:42:A:O4'	2.05	0.56
5:5:38:GLU:HG2	5:5:43:LYS:HD3	1.87	0.56
8:B:285:ILE:HG12	8:B:322:VAL:HG12	1.86	0.56
6:6:10:U:H2'	6:6:11:C:C6	2.40	0.56
1:1:677:G:OP1	1:1:1470:U:O2'	2.21	0.56
8:B:58:ARG:HE	8:B:354:VAL:HA	1.71	0.56
8:B:131:THR:O	8:B:135:LYS:HG2	2.04	0.56
14:H:100:ASN:N	14:H:113:ARG:O	2.39	0.56
33:o:105:GLY:O	33:o:153:PHE:N	2.39	0.56
1:1:1385:U:OP2	1:1:1386:G:O2'	2.21	0.56
8:B:132:LYS:O	8:B:136:LYS:HG2	2.05	0.56
8:B:348:ARG:HD2	8:B:348:ARG:H	1.70	0.56
14:H:11:LEU:O	14:H:53:ILE:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:60:VAL:H	24:V:78:ALA:H	1.53	0.56
1:1:3150:U:OP2	1:1:3151:A:N6	2.35	0.56
7:A:262:ALA:HA	7:A:265:ARG:HG3	1.88	0.56
10:D:401:ASP:N	10:D:401:ASP:OD1	2.36	0.56
10:D:473:GLN:NE2	10:D:477:GLU:OE2	2.33	0.56
1:1:297:A:H2'	1:1:298:G:H8	1.71	0.56
1:1:3287:A:H62	1:1:3299:U:H3	1.54	0.56
6:6:25:U:H2'	6:6:26:U:H5'	1.87	0.56
1:1:1157:G:C4	1:1:1158:G:H1'	2.41	0.55
8:B:117:ARG:NH2	8:B:175:LYS:O	2.39	0.55
32:m:191:ILE:H	32:m:191:ILE:HD12	1.71	0.55
6:6:7:U:O4	6:6:28:U:H1'	2.06	0.55
8:B:206:LYS:NZ	8:B:285:ILE:O	2.38	0.55
10:D:246:ASP:N	10:D:246:ASP:OD1	2.39	0.55
17:L:68:LYS:HA	30:i:9:LEU:HA	1.88	0.55
25:Y:113:ASP:OD1	25:Y:113:ASP:N	2.35	0.55
29:h:7:GLU:HA	29:h:10:LYS:HD2	1.88	0.55
38:x:236:GLN:HG3	38:x:237:ARG:HD2	1.87	0.55
1:1:717:A:O2'	25:Y:5:ARG:NH2	2.39	0.55
8:B:171:LEU:HD22	8:B:333:LYS:HD2	1.88	0.55
1:1:3286:U:H3	1:1:3301:C:H42	1.52	0.55
1:1:3410:G:H1'	21:P:69:ARG:HH21	1.72	0.55
5:5:50:LYS:HB2	5:5:340:ILE:HD12	1.89	0.55
10:D:226:LEU:HD13	10:D:260:ILE:HD11	1.87	0.55
8:B:217:VAL:HB	8:B:338:LEU:HD23	1.88	0.55
14:H:112:ILE:O	14:H:122:ARG:N	2.39	0.55
24:V:28:ALA:HB1	24:V:117:THR:H	1.70	0.55
25:Y:49:VAL:HG21	25:Y:79:LEU:HD21	1.87	0.55
28:f:18:GLN:HB3	28:f:28:THR:HG23	1.88	0.55
1:1:3358:U:H3'	1:1:3359:U:H4'	1.89	0.55
8:B:57:VAL:HG22	8:B:358:TRP:HE3	1.71	0.55
9:C:363:ASN:HD21	40:T:152:HIS:CE1	2.24	0.55
21:P:122:ALA:HB3	21:P:143:PRO:HB2	1.88	0.55
23:S:91:LYS:NZ	23:S:108:ASP:OD2	2.40	0.55
24:V:82:ARG:O	24:V:101:ALA:N	2.40	0.55
4:4:100:ILE:HG23	9:C:291:ARG:HA	1.89	0.55
10:D:140:THR:HA	10:D:143:PHE:HE1	1.71	0.55
2:2:68:U:OP2	29:h:24:ARG:NH2	2.36	0.55
8:B:128:LYS:HE3	8:B:132:LYS:HZ2	1.72	0.55
8:B:159:ARG:HG2	8:B:182:GLN:HB2	1.88	0.55
19:N:104:GLU:HA	19:N:160:GLU:HG3	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:644:A:H4'	1:1:645:U:OP2	2.05	0.55
8:B:106:TRP:HH2	8:B:118:PHE:HZ	1.55	0.55
8:B:221:THR:OG1	8:B:329:PRO:HB3	2.06	0.55
13:G:108:ARG:NH2	32:m:231:GLU:OE2	2.38	0.55
18:M:123:GLN:O	18:M:125:ASN:ND2	2.40	0.55
19:N:145:ASP:HB3	19:N:148:ILE:HG22	1.88	0.54
5:5:278:SER:HB3	5:5:290:ARG:HG2	1.88	0.54
8:B:106:TRP:CH2	8:B:118:PHE:HZ	2.24	0.54
14:H:45:GLU:O	14:H:56:ILE:N	2.40	0.54
27:e:116:VAL:HB	27:e:119:ALA:HB2	1.90	0.54
1:1:1242:U:O2'	23:S:112:ARG:NH1	2.41	0.54
1:1:1382:C:O2'	1:1:1384:U:OP1	2.25	0.54
6:6:56:G:H1'	6:6:57:A:H5'	1.90	0.54
6:6:62:U:H4'	6:6:62:U:OP1	2.07	0.54
29:h:18:GLU:OE2	29:h:18:GLU:N	2.28	0.54
1:1:3147:U:H2'	1:1:3148:G:C8	2.43	0.54
5:5:314:ASP:OD2	5:5:318:ARG:NH1	2.40	0.54
1:1:581:A:C5	1:1:582:G:H1'	2.42	0.54
1:1:1170:G:H2'	1:1:1171:G:C8	2.42	0.54
11:E:52:LEU:O	11:E:75:GLN:NE2	2.37	0.54
33:o:129:GLY:HA3	33:o:158:VAL:HG11	1.89	0.54
1:1:3409:C:H2'	1:1:3410:G:O4'	2.07	0.54
3:3:31:GLU:CD	3:3:31:GLU:H	2.14	0.54
25:Y:123:GLY:C	25:Y:124:LYS:HE2	2.33	0.54
7:A:179:ARG:NH2	32:m:112:THR:O	2.41	0.54
11:E:57:VAL:O	11:E:104:THR:OG1	2.25	0.54
33:o:114:HIS:HD2	35:t:62:ARG:HE	1.56	0.54
5:5:276:GLN:HG3	5:5:290:ARG:HE	1.73	0.54
7:A:270:GLN:HG3	30:i:9:LEU:HD13	1.90	0.54
17:L:62:THR:HG23	17:L:64:ARG:H	1.73	0.54
1:1:323:C:OP2	30:i:26:ARG:NH2	2.37	0.54
1:1:1182:U:P	1:1:1183:G:H22	2.31	0.54
8:B:221:THR:HG22	8:B:272:TYR:H	1.72	0.54
1:1:998:U:H4'	1:1:998:U:OP1	2.07	0.53
2:2:111:G:OP2	2:2:113:A:O2'	2.24	0.53
5:5:124:LEU:HD11	5:5:176:VAL:HG21	1.89	0.53
10:D:356:LEU:HD23	10:D:359:ILE:HD11	1.90	0.53
10:D:413:PRO:HG2	10:D:504:TYR:HE2	1.73	0.53
33:o:117:TYR:CG	33:o:136:MET:HE1	2.43	0.53
37:v:27:LYS:NZ	37:v:43:HIS:O	2.36	0.53
38:x:35:GLU:HB3	38:x:42:LYS:HE3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1170:G:H2'	1:1:1171:G:H8	1.73	0.53
1:1:1183:G:OP2	1:1:1183:G:N2	2.25	0.53
8:B:304:ARG:HE	8:B:305:ILE:HG22	1.72	0.53
13:G:162:LEU:HD23	19:N:7:LEU:HD11	1.90	0.53
18:M:12:ARG:NH1	18:M:59:THR:O	2.41	0.53
29:h:23:LEU:HD21	29:h:52:ASP:HB3	1.90	0.53
33:o:133:ARG:HH21	33:o:152:GLU:CD	2.16	0.53
1:1:369:A:O3'	31:j:45:ARG:NH2	2.41	0.53
2:2:59:G:O2'	2:2:60:A:N3	2.35	0.53
5:5:270:PHE:HE1	5:5:280:PHE:HB2	1.73	0.53
9:C:100:ARG:NH1	9:C:101:MET:O	2.41	0.53
12:F:243:ASN:O	12:F:247:GLN:HG2	2.09	0.53
23:S:79:ARG:HG2	23:S:123:LEU:HD11	1.89	0.53
1:1:1182:U:O5'	1:1:1183:G:N2	2.42	0.53
18:M:38:LEU:HD21	18:M:48:ARG:HE	1.73	0.53
6:6:4:A:H2'	35:t:63:GLN:OE1	2.08	0.53
24:V:17:LEU:HA	24:V:55:SER:HA	1.90	0.53
29:h:84:GLN:OE1	29:h:86:LYS:NZ	2.40	0.53
33:o:120:GLN:HB3	35:t:57:PHE:HB3	1.91	0.53
38:x:152:ASN:HB3	38:x:160:ALA:HB3	1.89	0.53
1:1:719:A:OP1	19:N:199:ARG:NH2	2.34	0.53
1:1:3100:C:H4'	8:B:99:LEU:HB3	1.90	0.53
8:B:33:PRO:HG2	8:B:340:LYS:HB2	1.90	0.53
6:6:13:C:H2'	6:6:14:A:H8	1.71	0.53
8:B:51:ALA:HB3	8:B:78:VAL:HG13	1.91	0.53
11:E:75:GLN:HG2	11:E:80:LEU:HD23	1.91	0.53
1:1:646:A:O2'	1:1:647:A:H8	1.91	0.53
1:1:3203:C:H42	1:1:3223:A:H61	1.57	0.53
1:1:3269:A:HO2'	1:1:3270:U:H6	1.56	0.53
3:3:169:LEU:HD21	3:3:189:VAL:HG21	1.90	0.53
5:5:3:LEU:HD13	5:5:339:ILE:HD11	1.90	0.53
5:5:136:HIS:HB2	5:5:142:ILE:HB	1.89	0.53
6:6:61:U:C5	6:6:62:U:H1'	2.44	0.53
23:S:79:ARG:HB2	23:S:121:ARG:HG3	1.90	0.53
1:1:3417:A:H5"	1:1:3491:A:H62	1.74	0.53
8:B:152:LYS:HG2	8:B:189:ALA:HA	1.90	0.53
8:B:284:ARG:HH12	8:B:296:THR:HG22	1.74	0.53
10:D:343:MET:HG2	10:D:411:TYR:HB3	1.89	0.53
20:O:144:SER:HB3	20:O:151:ASN:HD22	1.73	0.53
1:1:372:G:OP2	31:j:52:LYS:NZ	2.33	0.53
5:5:94:SER:HB3	5:5:133:VAL:HG13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:996:G:H2'	1:1:997:A:C8	2.44	0.52
7:A:143:LYS:N	15:J:173:GLU:O	2.40	0.52
33:o:189:ASN:ND2	33:o:192:LYS:HD3	2.25	0.52
4:4:7:PHE:O	4:4:9:LYS:N	2.33	0.52
6:6:11:C:H2'	6:6:12:A:C8	2.43	0.52
7:A:72:LYS:HG2	7:A:93:TYR:HD2	1.72	0.52
17:L:69:VAL:HG21	30:i:11:LYS:HE2	1.91	0.52
3:3:31:GLU:OE1	3:3:31:GLU:N	2.42	0.52
4:4:48:LEU:HD22	4:4:68:LEU:HD21	1.90	0.52
6:6:5:U:H2'	35:t:66:ARG:HG2	1.92	0.52
10:D:198:GLY:O	10:D:499:GLN:NE2	2.42	0.52
10:D:338:LYS:HG2	10:D:405:VAL:HG12	1.91	0.52
10:D:521:ALA:HB1	10:D:526:PHE:HB2	1.92	0.52
33:o:189:ASN:HD21	33:o:192:LYS:HD3	1.73	0.52
1:1:121:A:OP2	32:m:230:HIS:NE2	2.42	0.52
1:1:963:C:H3'	1:1:964:U:H2'	1.91	0.52
1:1:3425:C:H2'	1:1:3426:G:H8	1.75	0.52
1:1:3112:A:HO2'	1:1:3113:A:H8	1.56	0.52
25:Y:54:GLN:HB3	25:Y:107:LYS:HB3	1.92	0.52
31:j:29:ILE:HG13	31:j:30:GLN:N	2.24	0.52
33:o:135:ARG:HB2	33:o:194:ALA:HA	1.91	0.52
6:6:40:U:H3'	6:6:41:G:C8	2.45	0.52
7:A:117:PRO:O	7:A:118:ASN:C	2.51	0.52
37:v:53:LEU:HD22	37:v:137:VAL:HG11	1.91	0.52
1:1:689:U:H2'	1:1:690:A:C8	2.45	0.52
7:A:142:LEU:HA	15:J:174:MET:HA	1.91	0.52
38:x:35:GLU:OE2	38:x:35:GLU:N	2.42	0.52
1:1:455:G:H2'	1:1:456:G:H8	1.75	0.52
5:5:277:ILE:HD13	5:5:310:ILE:HD13	1.92	0.52
6:6:6:C:C2	6:6:28:U:H4'	2.44	0.52
7:A:148:ILE:HB	7:A:188:VAL:HG22	1.91	0.52
8:B:47:LEU:HD22	8:B:335:VAL:HG12	1.90	0.52
8:B:68:HIS:O	8:B:70:ARG:HD3	2.10	0.52
11:E:77:GLU:OE1	11:E:121:LYS:NZ	2.36	0.52
19:N:44:ARG:NH1	19:N:120:TRP:O	2.39	0.52
39:y:24:ALA:N	39:y:47:PRO:O	2.42	0.52
1:1:242:U:H2'	1:1:243:C:O2	2.09	0.52
1:1:454:G:H2'	1:1:455:G:H8	1.74	0.52
1:1:1012:A:O2'	1:1:1013:U:O5'	2.28	0.52
8:B:57:VAL:HG12	8:B:73:LEU:HB2	1.90	0.52
11:E:104:THR:HG22	11:E:195:PHE:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:o:118:GLU:O	33:o:134:LEU:HD11	2.10	0.52
1:1:488:A:O2'	1:1:489:C:O5'	2.25	0.51
1:1:3182:G:H2'	1:1:3182:G:N3	2.25	0.51
20:O:122:PRO:HA	20:O:125:LEU:HD12	1.92	0.51
21:P:115:LYS:HG3	21:P:151:ALA:HB3	1.91	0.51
5:5:80:TRP:HE3	5:5:81:GLN:H	1.57	0.51
8:B:58:ARG:N	8:B:72:ILE:O	2.40	0.51
8:B:122:TRP:CH2	8:B:127:LYS:HD3	2.45	0.51
33:o:142:THR:HA	33:o:200:ARG:HG3	1.93	0.51
6:6:5:U:H2'	35:t:66:ARG:CG	2.40	0.51
6:6:41:G:O2'	6:6:57:A:H8	1.93	0.51
6:6:71:U:C2	33:o:190:MET:HE1	2.45	0.51
1:1:428:G:N3	1:1:429:G:N2	2.46	0.51
1:1:3281:A:H61	20:O:132:PRO:HB3	1.74	0.51
7:A:243:TYR:OH	7:A:245:ASN:OD1	2.20	0.51
1:1:685:A:N1	1:1:973:G:O2'	2.39	0.51
1:1:1217:G:OP2	18:M:35:LYS:NZ	2.44	0.51
1:1:1221:A:C8	1:1:1328:C:H4'	2.40	0.51
8:B:147:GLU:O	8:B:151:ILE:HG12	2.11	0.51
8:B:179:MET:HE1	8:B:337:THR:HG23	1.92	0.51
8:B:211:GLN:HE21	8:B:283:TYR:C	2.19	0.51
17:L:50:PRO:HG3	29:h:120:LEU:HD12	1.92	0.51
7:A:166:GLU:OE2	7:A:170:GLN:NE2	2.39	0.51
9:C:301:ILE:HD11	22:Q:133:PRO:HB2	1.91	0.51
12:F:47:LYS:NZ	12:F:177:GLU:OE2	2.30	0.51
1:1:3095:C:O2'	1:1:3397:A:H5'	2.11	0.51
1:1:3128:A:N6	14:H:117:GLY:O	2.33	0.51
6:6:23:U:H2'	6:6:24:U:H6	1.74	0.51
8:B:85:VAL:HG22	8:B:202:THR:HB	1.91	0.51
10:D:518:ALA:HA	10:D:529:PRO:HG3	1.92	0.51
1:1:1013:U:O2'	1:1:1014:C:O4'	2.28	0.51
21:P:23:ARG:NH1	21:P:125:GLN:OE1	2.44	0.51
8:B:104:THR:HG22	8:B:106:TRP:CD1	2.45	0.51
8:B:221:THR:O	8:B:272:TYR:HA	2.11	0.51
17:L:42:LYS:NZ	17:L:51:VAL:O	2.39	0.51
33:o:137:SER:OG	33:o:146:LYS:HD3	2.11	0.51
1:1:3133:U:H5"	8:B:62:ARG:HD2	1.92	0.51
8:B:211:GLN:HA	8:B:282:ILE:HB	1.94	0.51
10:D:370:GLN:HA	10:D:370:GLN:OE1	2.11	0.51
12:F:113:LEU:O	12:F:122:ILE:HD13	2.11	0.51
3:3:114:ARG:HG2	11:E:30:ALA:HB1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:166:ASP:OD1	5:5:169:GLU:HB2	2.10	0.50
8:B:49:TYR:O	8:B:80:GLU:N	2.43	0.50
2:2:57:G:H1	2:2:62:A:N6	2.08	0.50
2:2:60:A:O2'	2:2:61:A:H3'	2.11	0.50
1:1:644:A:H3'	1:1:645:U:C5	2.46	0.50
1:1:3275:A:O2'	20:O:118:ARG:NH2	2.44	0.50
4:4:91:MET:HE2	4:4:110:MET:HE2	1.94	0.50
1:1:430:A:N1	1:1:2465:G:N2	2.60	0.50
1:1:3183:A:H5"	8:B:365:PHE:HB2	1.93	0.50
2:2:29:C:OP1	9:C:195:LYS:NZ	2.45	0.50
5:5:230:HIS:NE2	38:x:286:GLU:OE1	2.37	0.50
13:G:233:TRP:NE1	32:m:200:PRO:O	2.44	0.50
6:6:41:G:H3'	6:6:42:A:C2	2.46	0.50
7:A:204:GLU:N	7:A:219:ILE:O	2.44	0.50
8:B:56:ILE:HG12	8:B:76:VAL:HG21	1.94	0.50
8:B:182:GLN:NE2	8:B:184:ASN:HD21	2.09	0.50
9:C:363:ASN:HD22	40:T:150:THR:HG21	1.77	0.50
10:D:244:GLU:HB3	10:D:247:ARG:HB3	1.94	0.50
18:M:37:ALA:HB2	18:M:53:TYR:CZ	2.47	0.50
33:o:133:ARG:HB3	33:o:191:PHE:CD2	2.47	0.50
38:x:132:GLU:OE1	38:x:134:HIS:NE2	2.43	0.50
1:1:244:G:H2'	1:1:245:A:O4'	2.12	0.50
6:6:35:A:H2'	6:6:35:A:N3	2.26	0.50
11:E:97:ASN:HB3	11:E:100:TYR:HD1	1.77	0.50
29:h:20:LEU:HB2	29:h:56:ILE:HG21	1.93	0.50
1:1:671:A:H3'	1:1:672:A:H8	1.76	0.50
4:4:9:LYS:NZ	7:A:294:PHE:O	2.32	0.50
4:4:15:ASP:OD1	4:4:18:THR:OG1	2.23	0.50
6:6:56:G:O2'	6:6:57:A:H5'	2.11	0.50
8:B:17:LEU:HD13	8:B:19:ARG:HG3	1.92	0.50
8:B:73:LEU:HB3	24:V:91:ASP:O	2.11	0.50
1:1:109:A:N1	1:1:330:U:O2'	2.43	0.50
1:1:454:G:H2'	1:1:455:G:C8	2.47	0.50
8:B:92:TYR:HB3	8:B:99:LEU:HD11	1.94	0.50
12:F:47:LYS:O	12:F:51:ILE:HG13	2.11	0.50
12:F:126:PHE:CE1	12:F:131:LYS:HG3	2.47	0.50
1:1:3489:C:H5"	1:1:3491:A:H5'	1.94	0.50
4:4:175:GLU:OE1	4:4:175:GLU:N	2.39	0.50
5:5:255:PRO:HG2	5:5:273:LYS:HD2	1.93	0.50
6:6:32:A:H61	6:6:64:G:H1	1.60	0.50
6:6:40:U:H2'	6:6:41:G:C8	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:57:A:H1'	6:6:58:A:H5'	1.93	0.50
10:D:415:ASP:OD1	10:D:415:ASP:N	2.45	0.50
13:G:163:VAL:HG12	13:G:166:LEU:HD12	1.94	0.50
18:M:16:VAL:HA	18:M:56:VAL:HG12	1.94	0.50
33:o:133:ARG:HB3	33:o:191:PHE:HD2	1.76	0.50
38:x:162:THR:HB	38:x:173:TYR:HD1	1.77	0.50
1:1:847:G:H1	1:1:957:A:H61	1.60	0.49
1:1:1156:U:H2'	1:1:1157:G:C8	2.46	0.49
1:1:1423:G:OP2	27:e:101:LYS:HE3	2.12	0.49
1:1:3143:U:H5'	8:B:222:ARG:HB3	1.94	0.49
5:5:48:MET:HG2	5:5:340:ILE:HG13	1.94	0.49
8:B:293:ASN:HD21	8:B:304:ARG:HE	1.60	0.49
9:C:362:GLU:OE2	40:T:150:THR:OG1	2.30	0.49
24:V:105:VAL:HA	24:V:111:MET:HA	1.94	0.49
29:h:31:ARG:HA	29:h:34:LYS:HG2	1.94	0.49
33:o:111:ARG:HD3	33:o:175:LEU:O	2.12	0.49
38:x:102:LYS:HE2	38:x:130:ASP:HA	1.94	0.49
1:1:3188:U:O2'	1:1:3191:U:OP2	2.30	0.49
5:5:42:GLU:N	5:5:42:GLU:OE1	2.45	0.49
6:6:12:A:N6	6:6:22:U:H3	2.10	0.49
25:Y:99:ASP:OD2	25:Y:101:SER:OG	2.29	0.49
28:f:15:LEU:HD11	28:f:32:LYS:HB2	1.94	0.49
38:x:265:GLU:OE1	38:x:269:ARG:NH2	2.45	0.49
7:A:92:LEU:O	30:i:65:LYS:NZ	2.42	0.49
21:P:22:LEU:HD12	21:P:146:ILE:HD12	1.94	0.49
1:1:68:A:O3'	19:N:177:GLY:HA2	2.12	0.49
5:5:49:LEU:HB3	5:5:95:MET:HE2	1.94	0.49
9:C:94:ASN:ND2	9:C:102:PHE:HB2	2.28	0.49
21:P:78:VAL:HG12	21:P:79:THR:H	1.78	0.49
29:h:120:LEU:HB3	37:v:56:LEU:HB2	1.93	0.49
1:1:314:A:OP1	7:A:104:ARG:NH1	2.45	0.49
6:6:7:U:H3	6:6:27:U:P	2.35	0.49
3:3:56:ASP:C	3:3:57:ASN:HD22	2.20	0.49
4:4:59:LEU:HG	12:F:13:ILE:HD11	1.93	0.49
5:5:256:LEU:HD23	5:5:272:ASP:HB3	1.95	0.49
6:6:24:U:H2'	6:6:25:U:O4'	2.13	0.49
1:1:341:G:H5'	37:v:16:ARG:HG2	1.94	0.49
1:1:632:A:OP1	11:E:44:ARG:NH2	2.44	0.49
1:1:1022:U:O2'	1:1:1023:G:H8	1.96	0.49
1:1:3408:A:H3'	1:1:3409:C:C6	2.48	0.49
1:1:123:A:OP1	13:G:105:LYS:NZ	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:530:A:H5”	12:F:77:ARG:HD3	1.94	0.49
8:B:46:PHE:CE1	8:B:205:ILE:HB	2.48	0.49
31:j:17:THR:OG1	31:j:18:ILE:N	2.45	0.49
1:1:117:U:H5’	13:G:141:ALA:HB2	1.94	0.49
8:B:11:HIS:HA	8:B:17:LEU:HD21	1.95	0.49
8:B:364:LYS:O	8:B:365:PHE:C	2.55	0.49
16:K:196:CYS:HA	33:o:208:ARG:HH12	1.78	0.49
1:1:385:A:H1’	1:1:400:G:N2	2.27	0.49
1:1:420:G:H5’	21:P:26:PHE:HZ	1.78	0.49
2:2:57:G:O4’	2:2:70:C:N4	2.45	0.49
6:6:74:U:C2	33:o:198:PHE:HD1	2.31	0.49
7:A:44:LYS:N	7:A:96:ASN:OD1	2.45	0.49
8:B:125:SER:OG	8:B:126:LYS:HG2	2.13	0.49
8:B:137:TYR:CE2	8:B:144:ILE:HG12	2.48	0.49
8:B:312:VAL:O	8:B:332:VAL:HG11	2.13	0.49
33:o:165:THR:C	33:o:166:MET:HE2	2.37	0.49
1:1:1012:A:O2’	1:1:1013:U:O4’	2.30	0.48
1:1:3182:G:H3’	1:1:3183:A:C8	2.47	0.48
1:1:3313:G:N2	28:f:4:GLN:OE1	2.31	0.48
4:4:175:GLU:HG2	4:4:176:ASP:H	1.77	0.48
5:5:274:ARG:HD3	38:x:289:VAL:HG21	1.95	0.48
9:C:145:GLU:OE1	9:C:178:ARG:NH1	2.39	0.48
13:G:103:ALA:O	13:G:107:GLN:HG3	2.13	0.48
24:V:120:VAL:H	24:V:139:VAL:H	1.61	0.48
28:f:57:SER:OG	28:f:58:LYS:NZ	2.46	0.48
38:x:56:GLU:OE2	38:x:236:GLN:NE2	2.46	0.48
1:1:582:G:H5’	18:M:73:ILE:HG21	1.95	0.48
1:1:1385:U:H5’	1:1:1386:G:H2’	1.96	0.48
7:A:124:PHE:HE1	7:A:229:ILE:HG12	1.78	0.48
9:C:333:TYR:OH	12:F:59:GLU:OE1	2.24	0.48
30:i:90:SER:O	30:i:94:SER:OG	2.30	0.48
38:x:54:THR:HG23	38:x:57:SER:H	1.78	0.48
1:1:238:U:H5’	1:1:240:G:H5’	1.95	0.48
1:1:3108:A:H2’	1:1:3109:U:C6	2.48	0.48
5:5:288:ILE:HD12	5:5:288:ILE:O	2.13	0.48
8:B:116:ARG:NH1	8:B:122:TRP:CD1	2.81	0.48
8:B:128:LYS:HE3	8:B:132:LYS:NZ	2.29	0.48
10:D:223:LEU:HD12	10:D:260:ILE:HB	1.96	0.48
22:Q:66:ILE:HD13	22:Q:102:ILE:HD13	1.95	0.48
24:V:105:VAL:HA	24:V:112:LYS:H	1.78	0.48
27:e:107:GLU:OE2	27:e:110:ARG:NH1	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:B:107:ALA:HB1	8:B:200:GLU:HG3	1.94	0.48
8:B:125:SER:HB2	8:B:126:LYS:HE3	1.94	0.48
8:B:170:PRO:HG3	8:B:316:VAL:O	2.13	0.48
8:B:369:ARG:HH21	36:u:11:GLY:HA3	1.78	0.48
9:C:292:LEU:O	9:C:295:SER:OG	2.28	0.48
30:i:93:GLN:OE1	30:i:93:GLN:HA	2.13	0.48
30:i:95:SER:O	30:i:99:HIS:N	2.40	0.48
1:1:368:G:OP1	31:j:25:ARG:NH1	2.45	0.48
8:B:21:ARG:HG2	8:B:269:ASN:HD21	1.78	0.48
8:B:307:PRO:HB3	8:B:361:THR:HA	1.95	0.48
1:1:1222:U:H4'	20:O:53:LEU:HD12	1.94	0.48
6:6:59:A:O2'	16:K:199:PHE:HA	2.14	0.48
8:B:194:TRP:CD1	8:B:194:TRP:C	2.92	0.48
10:D:145:ILE:HD13	10:D:184:LEU:HD22	1.95	0.48
8:B:49:TYR:N	8:B:80:GLU:O	2.38	0.48
8:B:205:ILE:HD13	8:B:322:VAL:HG11	1.95	0.48
14:H:6:TYR:HA	14:H:58:TRP:HA	1.95	0.48
23:S:47:ILE:HG22	23:S:48:ASN:OD1	2.13	0.48
5:5:111:LEU:HB2	5:5:124:LEU:O	2.13	0.48
6:6:41:G:O5'	6:6:41:G:H8	1.96	0.48
8:B:79:ILE:HD12	8:B:336:LEU:HD12	1.95	0.48
25:Y:87:GLU:OE2	25:Y:87:GLU:HA	2.14	0.48
1:1:549:G:O6	1:1:575:G:N1	2.42	0.48
1:1:1141:C:O2'	1:1:1142:U:H5'	2.14	0.48
1:1:1348:A:H4'	20:O:19:ARG:HH22	1.78	0.48
1:1:1422:U:OP1	27:e:101:LYS:NZ	2.35	0.48
8:B:78:VAL:HG23	8:B:321:PHE:CD1	2.48	0.48
8:B:348:ARG:HD2	8:B:348:ARG:N	2.29	0.48
9:C:239:GLN:O	9:C:248:ARG:HD3	2.14	0.48
21:P:118:GLN:NE2	21:P:147:GLU:OE2	2.47	0.48
28:f:55:LYS:HB3	28:f:65:ILE:HD13	1.95	0.48
33:o:122:ARG:NH2	33:o:132:LEU:O	2.39	0.48
39:y:61:ARG:O	39:y:106:ASN:N	2.47	0.48
1:1:305:A:C8	30:i:29:GLY:HA2	2.44	0.48
1:1:481:A:OP1	3:3:61:TYR:OH	2.26	0.48
9:C:11:TYR:CE2	9:C:17:VAL:HG22	2.48	0.48
1:1:372:G:O6	31:j:56:ARG:HD3	2.14	0.47
24:V:83:GLN:HA	24:V:100:ASN:HA	1.96	0.47
25:Y:85:THR:HG22	25:Y:95:PRO:HA	1.96	0.47
29:h:104:LEU:HG	29:h:108:LYS:HE3	1.96	0.47
33:o:142:THR:HG23	33:o:144:SER:H	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1226:A:H1'	1:1:1350:G:H4'	1.96	0.47
9:C:100:ARG:HH12	9:C:102:PHE:HA	1.78	0.47
13:G:231:ARG:HA	32:m:202:TYR:HB3	1.96	0.47
39:y:17:SER:HA	39:y:26:VAL:HA	1.95	0.47
1:1:312:G:C2	1:1:313:U:H2'	2.49	0.47
1:1:1438:G:N2	1:1:1441:A:OP2	2.40	0.47
4:4:58:PRO:HB2	12:F:13:ILE:HD12	1.97	0.47
6:6:9:C:H42	6:6:25:U:H3	1.62	0.47
8:B:173:GLN:HA	8:B:173:GLN:OE1	2.13	0.47
8:B:214:MET:SD	8:B:279:ASN:HA	2.54	0.47
8:B:311:PHE:HB2	8:B:315:GLY:O	2.15	0.47
10:D:223:LEU:HD11	10:D:259:GLN:HG2	1.95	0.47
11:E:71:VAL:HG23	11:E:178:LEU:HD21	1.96	0.47
12:F:157:LYS:HD3	12:F:250:LEU:HG	1.96	0.47
12:F:221:TRP:CE2	12:F:225:LYS:HE3	2.50	0.47
22:Q:116:LEU:HD21	22:Q:122:VAL:HG22	1.97	0.47
27:e:79:VAL:HG12	27:e:112:LEU:HD12	1.96	0.47
1:1:62:A:H5"	19:N:164:LEU:HD21	1.96	0.47
7:A:170:GLN:NE2	15:J:107:ILE:O	2.44	0.47
8:B:46:PHE:CD2	8:B:84:MET:HG2	2.48	0.47
8:B:159:ARG:HG2	8:B:182:GLN:CB	2.45	0.47
11:E:73:LEU:HA	11:E:111:VAL:HG11	1.96	0.47
33:o:202:PRO:HG2	33:o:206:ILE:HD13	1.97	0.47
39:y:108:VAL:HA	39:y:117:VAL:HA	1.95	0.47
39:y:109:ALA:N	39:y:116:LEU:O	2.39	0.47
1:1:840:A:H3'	1:1:841:G:C8	2.48	0.47
1:1:3487:C:H2'	1:1:3488:C:O4'	2.15	0.47
2:2:114:C:H4'	2:2:115:G:H5"	1.97	0.47
6:6:64:G:H3'	6:6:65:U:H6	1.77	0.47
8:B:116:ARG:HG2	8:B:175:LYS:HG2	1.95	0.47
14:H:90:MET:O	14:H:142:ILE:N	2.47	0.47
22:Q:53:GLN:O	22:Q:58:ARG:NH1	2.47	0.47
1:1:228:A:O2'	1:1:230:C:OP2	2.31	0.47
1:1:3182:G:H3'	1:1:3183:A:H8	1.78	0.47
8:B:105:VAL:HG22	8:B:147:GLU:HB3	1.96	0.47
9:C:33:ARG:HB3	9:C:36:LEU:HB3	1.95	0.47
17:L:114:GLU:OE2	17:L:114:GLU:HA	2.14	0.47
24:V:29:ASP:HA	24:V:116:ILE:HA	1.95	0.47
1:1:455:G:N2	1:1:498:U:H1'	2.29	0.47
1:1:1146:G:OP2	1:1:1146:G:N2	2.26	0.47
1:1:2458:G:N2	1:1:2463:G:N7	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:59:G:O2'	2:2:60:A:O5'	2.33	0.47
3:3:169:LEU:HA	3:3:174:TYR:HE2	1.80	0.47
5:5:346:ASP:H	5:5:349:ILE:HD12	1.79	0.47
6:6:32:A:H3'	6:6:33:A:H8	1.80	0.47
8:B:275:ARG:HB2	8:B:329:PRO:HG2	1.96	0.47
8:B:296:THR:HG21	8:B:356:LEU:HD12	1.97	0.47
8:B:304:ARG:NH2	8:B:317:VAL:HG12	2.29	0.47
14:H:21:ILE:HA	14:H:26:VAL:HA	1.96	0.47
16:K:13:LEU:O	16:K:15:LYS:N	2.45	0.47
23:S:37:LYS:HE3	23:S:57:ILE:HG13	1.96	0.47
38:x:30:LYS:HA	38:x:30:LYS:HD2	1.73	0.47
39:y:151:TYR:HA	39:y:192:VAL:HA	1.96	0.47
1:1:518:U:H2'	1:1:519:U:C6	2.50	0.47
1:1:2464:G:HO2'	1:1:2465:G:H8	1.62	0.47
1:1:3132:G:H5'	8:B:348:ARG:HE	1.80	0.47
1:1:3196:U:H3	1:1:3230:G:H1	1.63	0.47
1:1:3397:A:H2'	1:1:3398:U:C6	2.50	0.47
6:6:73:U:H1'	6:6:74:U:C2	2.50	0.47
10:D:448:PHE:HD1	10:D:509:ILE:HG21	1.80	0.47
29:h:11:GLN:OE1	29:h:15:ASN:ND2	2.45	0.47
33:o:115:GLY:HA2	35:t:61:TYR:CD2	2.50	0.47
37:v:176:THR:HG23	37:v:202:TYR:HE2	1.79	0.47
1:1:297:A:H2'	1:1:298:G:C8	2.50	0.47
1:1:3105:G:O2'	8:B:14:LEU:HB3	2.15	0.47
4:4:12:ALA:HB1	9:C:6:PRO:HG3	1.97	0.47
16:K:152:ARG:C	16:K:154:LEU:H	2.23	0.47
21:P:53:GLU:O	21:P:55:LYS:NZ	2.46	0.47
1:1:757:G:H1	1:1:764:U:H3	1.63	0.47
3:3:174:TYR:CE1	3:3:178:PRO:HG3	2.50	0.47
4:4:50:TYR:HA	4:4:53:TRP:HB3	1.97	0.47
4:4:93:ARG:HG3	4:4:94:GLU:HG2	1.96	0.47
6:6:4:A:H62	35:t:59:ASN:CG	2.22	0.47
1:1:698:U:OP1	22:Q:20:SER:OG	2.31	0.46
1:1:1182:U:H3'	1:1:1183:G:N2	2.30	0.46
13:G:190:ILE:HD11	13:G:195:ALA:HB2	1.97	0.46
20:O:51:ASN:HA	20:O:54:LYS:HD2	1.98	0.46
29:h:81:ASP:OD1	29:h:81:ASP:N	2.45	0.46
31:j:64:MET:HE2	31:j:68:LYS:HE3	1.97	0.46
38:x:188:HIS:O	38:x:264:GLN:NE2	2.39	0.46
1:1:728:G:O6	7:A:269:ARG:NH2	2.48	0.46
1:1:3101:A:O2'	1:1:3236:G:N2	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3140:A:H5”	8:B:12:GLY:N	2.25	0.46
1:1:3410:G:H3’	1:1:3411:A:H8	1.80	0.46
6:6:63:U:H3’	6:6:64:G:H8	1.81	0.46
8:B:92:TYR:HE1	8:B:101:SER:HB3	1.81	0.46
24:V:62:ALA:N	24:V:76:MET:O	2.48	0.46
33:o:187:HIS:H	33:o:190:MET:HB2	1.80	0.46
38:x:154:ASP:OD2	38:x:159:ASN:ND2	2.41	0.46
1:1:3283:A:OP1	14:H:23:ALA:N	2.47	0.46
8:B:369:ARG:NH2	36:u:11:GLY:HA3	2.29	0.46
14:H:20:ASP:O	14:H:27:THR:N	2.47	0.46
39:y:19:LEU:HA	39:y:24:ALA:HA	1.97	0.46
1:1:765:G:H2’	1:1:766:G:C8	2.50	0.46
1:1:3106:U:H1’	8:B:15:GLY:HA2	1.98	0.46
5:5:49:LEU:HD21	5:5:97:TYR:HB2	1.98	0.46
6:6:36:U:H2’	6:6:37:U:C2	2.51	0.46
7:A:85:GLN:OE1	30:i:82:LYS:NZ	2.43	0.46
9:C:236:ASN:HB3	9:C:239:GLN:HG3	1.98	0.46
13:G:180:VAL:HG21	13:G:186:LEU:HD21	1.97	0.46
37:v:176:THR:HG23	37:v:202:TYR:CE2	2.50	0.46
38:x:257:ASP:OD1	38:x:257:ASP:N	2.32	0.46
1:1:302:U:H4’	30:i:75:LEU:HD23	1.97	0.46
1:1:3431:A:O5’	8:B:308:MET:HE3	2.16	0.46
2:2:99:C:H2’	2:2:100:A:C8	2.51	0.46
6:6:41:G:C2	6:6:42:A:H1’	2.51	0.46
8:B:119:TYR:OH	8:B:128:LYS:N	2.49	0.46
17:L:55:ARG:NH1	17:L:73:ARG:O	2.37	0.46
18:M:42:PRO:HG3	18:M:78:TRP:CG	2.51	0.46
38:x:134:HIS:CE1	38:x:135:GLU:HG3	2.51	0.46
6:6:6:C:H5	35:t:69:ILE:HG21	1.81	0.46
6:6:22:U:H2’	6:6:23:U:C6	2.51	0.46
6:6:70:U:H4’	33:o:148:TYR:CE2	2.50	0.46
10:D:403:PRO:HG2	10:D:405:VAL:HG13	1.98	0.46
12:F:28:GLN:O	12:F:32:GLN:HG2	2.16	0.46
23:S:97:THR:HG23	23:S:100:GLY:H	1.80	0.46
37:v:49:ASN:OD1	37:v:52:ARG:NH2	2.44	0.46
37:v:130:ILE:HG22	37:v:131:ALA:H	1.78	0.46
1:1:1425:C:C2	27:e:100:ARG:HG3	2.51	0.46
1:1:3222:C:H2’	1:1:3223:A:H8	1.80	0.46
7:A:198:ILE:HB	7:A:227:MET:HB3	1.98	0.46
8:B:46:PHE:CE2	8:B:84:MET:HG2	2.51	0.46
8:B:164:THR:OG1	8:B:177:HIS:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:M:106:ASN:ND2	18:M:109:ASP:OD2	2.49	0.46
20:O:72:PHE:HB3	20:O:74:PHE:CE1	2.50	0.46
20:O:186:SER:HB2	20:O:189:ASN:HD22	1.80	0.46
22:Q:34:PHE:CE1	22:Q:38:ARG:HG3	2.51	0.46
33:o:118:GLU:OE2	33:o:136:MET:HB3	2.15	0.46
35:t:53:ARG:HB2	35:t:55:GLU:HG3	1.98	0.46
1:1:3145:A:H5"	8:B:312:VAL:HG11	1.98	0.46
1:1:3375:U:H5'	28:f:67:VAL:HG21	1.97	0.46
8:B:61:ASP:OD1	8:B:68:HIS:HE1	1.98	0.46
19:N:99:ARG:HB3	19:N:167:ILE:HG12	1.97	0.46
1:1:277:G:C6	19:N:14:LYS:HB3	2.51	0.46
1:1:3337:A:O2'	1:1:3338:A:OP1	2.32	0.46
4:4:69:ALA:HB2	4:4:112:ARG:HB3	1.97	0.46
6:6:9:C:H5'	6:6:10:U:OP2	2.15	0.46
6:6:57:A:OP1	33:o:203:HIS:HB3	2.15	0.46
6:6:58:A:C2'	6:6:59:A:H8	2.29	0.46
7:A:115:ARG:O	7:A:116:ALA:C	2.59	0.46
8:B:59:ASP:H	8:B:357:LYS:HG2	1.80	0.46
10:D:257:MET:HE3	10:D:257:MET:HA	1.97	0.46
18:M:12:ARG:HD3	18:M:58:LEU:HD12	1.98	0.46
18:M:119:GLN:O	18:M:122:GLU:HG3	2.15	0.46
21:P:16:LYS:O	21:P:101:ASN:ND2	2.43	0.46
38:x:44:ARG:C	38:x:44:ARG:HE	2.24	0.46
1:1:1242:U:O4	1:1:1243:A:N6	2.48	0.46
4:4:58:PRO:HA	4:4:61:GLN:HG2	1.98	0.46
6:6:71:U:H4'	6:6:72:U:H6	1.79	0.46
8:B:222:ARG:HB2	8:B:331:PRO:HD3	1.96	0.46
38:x:161:LEU:HD23	38:x:272:MET:HE3	1.98	0.46
1:1:70:A:N1	1:1:321:A:O2'	2.46	0.45
1:1:689:U:H2'	1:1:690:A:H8	1.81	0.45
1:1:1320:G:H2'	1:1:1321:A:C8	2.51	0.45
1:1:1457:C:H5"	3:3:21:LYS:HD2	1.97	0.45
6:6:58:A:H2'	6:6:59:A:H5"	1.98	0.45
10:D:405:VAL:O	10:D:435:GLY:N	2.49	0.45
11:E:150:PRO:HB2	11:E:152:GLU:OE1	2.16	0.45
17:L:48:PRO:HG3	37:v:33:ASN:HD22	1.80	0.45
18:M:85:ASN:OD1	18:M:85:ASN:C	2.58	0.45
22:Q:63:ILE:HD11	22:Q:115:ILE:HG13	1.97	0.45
25:Y:31:SER:HA	25:Y:48:PRO:HA	1.96	0.45
33:o:107:LEU:HB2	33:o:159:ALA:HB1	1.98	0.45
33:o:196:VAL:O	33:o:198:PHE:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:194:HIS:CG	22:Q:79:ASN:HD21	2.35	0.45
24:V:79:ILE:O	24:V:103:VAL:N	2.49	0.45
27:e:29:TRP:CZ2	27:e:50:PRO:HD2	2.52	0.45
33:o:190:MET:HG3	33:o:191:PHE:CD1	2.52	0.45
37:v:120:LEU:HD23	37:v:120:LEU:HA	1.83	0.45
1:1:451:C:OP2	3:3:124:ARG:NH2	2.49	0.45
2:2:12:C:P	21:P:61:ARG:HH12	2.39	0.45
5:5:64:ILE:HD12	5:5:64:ILE:H	1.80	0.45
8:B:284:ARG:N	8:B:323:MET:HB3	2.32	0.45
1:1:757:G:H22	1:1:764:U:H3	1.65	0.45
5:5:111:LEU:HD12	5:5:113:PHE:CZ	2.52	0.45
6:6:62:U:H2'	6:6:63:U:C6	2.51	0.45
7:A:203:TYR:HB3	7:A:218:LEU:HB3	1.98	0.45
8:B:58:ARG:HA	8:B:357:LYS:H	1.80	0.45
8:B:112:GLU:HG3	8:B:113:GLU:N	2.31	0.45
10:D:170:THR:HG23	10:D:173:LEU:H	1.81	0.45
10:D:202:ARG:HH21	30:i:27:ARG:NE	2.15	0.45
10:D:366:LEU:HG	10:D:390:LEU:HD21	1.97	0.45
25:Y:21:ALA:O	25:Y:26:ARG:NH1	2.49	0.45
30:i:63:GLN:HB3	30:i:66:ARG:HG3	1.97	0.45
37:v:3:ASN:HB2	37:v:6:GLN:HG2	1.98	0.45
1:1:1155:U:H2'	1:1:1156:U:C6	2.52	0.45
1:1:3097:U:H2'	1:1:3098:C:C6	2.52	0.45
3:3:39:ASN:HB2	3:3:42:SER:HB2	1.99	0.45
14:H:29:THR:HA	14:H:34:THR:HA	1.98	0.45
19:N:122:ASN:OD1	19:N:123:GLN:N	2.49	0.45
30:i:13:LYS:HD2	30:i:13:LYS:HA	1.71	0.45
1:1:257:A:H62	17:L:134:LYS:NZ	2.14	0.45
1:1:967:U:H2'	1:1:968:A:C8	2.52	0.45
1:1:3287:A:H3'	1:1:3288:G:H8	1.82	0.45
21:P:69:ARG:HB3	21:P:79:THR:HB	1.98	0.45
23:S:136:ARG:HA	23:S:136:ARG:HD3	1.74	0.45
33:o:106:VAL:HA	33:o:152:GLU:HA	1.98	0.45
33:o:135:ARG:HH21	33:o:192:LYS:H	1.65	0.45
1:1:243:C:H2'	1:1:244:G:H5"	1.99	0.45
5:5:332:ILE:O	5:5:334:ALA:N	2.47	0.45
6:6:57:A:HO2'	6:6:58:A:H8	1.63	0.45
6:6:64:G:N3	6:6:64:G:H2'	2.32	0.45
7:A:81:ASP:OD1	7:A:81:ASP:N	2.45	0.45
9:C:318:LYS:HB2	9:C:326:VAL:HG21	1.98	0.45
14:H:10:THR:HA	14:H:54:LYS:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:172:ARG:HG3	19:N:174:ILE:HG12	1.98	0.45
39:y:149:GLY:O	39:y:194:GLY:HA3	2.17	0.45
1:1:726:C:H5'	7:A:266:TYR:HE1	1.80	0.45
4:4:181:ASP:OD1	4:4:181:ASP:N	2.50	0.45
7:A:118:ASN:HB2	7:A:119:GLY:H	1.61	0.45
8:B:25:GLN:HG3	8:B:334:ARG:NH1	2.32	0.45
9:C:266:SER:HA	9:C:279:LEU:HD12	1.99	0.45
20:O:75:ARG:O	20:O:143:SER:OG	2.33	0.45
23:S:95:ASP:OD2	23:S:101:ALA:N	2.49	0.45
33:o:108:TYR:CE2	33:o:148:TYR:HB2	2.51	0.45
1:1:25:U:H5'	1:1:26:A:OP1	2.17	0.45
1:1:3246:A:OP1	8:B:132:LYS:HB2	2.17	0.45
2:2:76:G:O6	2:2:97:A:N6	2.50	0.45
6:6:30:U:C2	6:6:31:A:C8	3.05	0.45
6:6:58:A:OP1	33:o:204:ALA:HA	2.17	0.45
7:A:132:MET:HA	7:A:137:MET:HE1	1.99	0.45
8:B:122:TRP:H	8:B:124:LYS:HE3	1.81	0.45
9:C:308:SER:O	9:C:309:ARG:C	2.60	0.45
10:D:438:LEU:HD12	10:D:438:LEU:HA	1.85	0.45
31:j:60:GLY:HA2	31:j:64:MET:SD	2.57	0.45
1:1:2461:A:H2'	1:1:2462:C:H4'	1.99	0.45
1:1:3420:U:H3'	1:1:3421:G:H5'	1.98	0.45
1:1:3471:A:P	8:B:384:LYS:HD2	2.57	0.45
3:3:56:ASP:O	3:3:57:ASN:ND2	2.46	0.45
6:6:39:U:N1	6:6:40:U:H1'	2.32	0.45
8:B:292:LYS:NZ	8:B:300:ALA:O	2.43	0.45
12:F:46:LYS:HA	12:F:46:LYS:HD3	1.66	0.45
12:F:234:ASP:OD1	12:F:238:ARG:NH2	2.43	0.45
14:H:27:THR:HA	14:H:36:LYS:HA	1.99	0.45
33:o:112:LEU:HD23	33:o:116:PHE:O	2.17	0.45
5:5:101:TRP:NE1	5:5:167:GLU:O	2.48	0.44
6:6:11:C:H2'	6:6:12:A:C1'	2.47	0.44
7:A:142:LEU:HD22	15:J:172:ALA:HB3	1.99	0.44
10:D:529:PRO:HB2	32:m:213:THR:HG22	1.98	0.44
20:O:50:ARG:HG2	20:O:54:LYS:HZ2	1.82	0.44
24:V:33:ALA:HA	24:V:67:GLY:HA3	1.99	0.44
1:1:455:G:H2'	1:1:456:G:C8	2.51	0.44
1:1:1005:A:H5"	22:Q:14:GLN:NE2	2.33	0.44
3:3:114:ARG:NH2	27:e:112:LEU:O	2.43	0.44
8:B:62:ARG:HB2	8:B:352:GLU:OE1	2.17	0.44
8:B:363:SER:HB3	8:B:368:GLY:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:196:VAL:HG11	22:Q:136:SER:HB2	1.99	0.44
8:B:124:LYS:H	8:B:124:LYS:HG3	1.51	0.44
8:B:294:ALA:HB3	8:B:303:LYS:O	2.18	0.44
9:C:134:PRO:HG3	9:C:150:VAL:HB	1.98	0.44
10:D:261:MET:HE3	10:D:261:MET:HA	1.99	0.44
10:D:467:ASN:OD1	10:D:468:LYS:N	2.51	0.44
10:D:484:TYR:CE2	32:m:222:LYS:HD2	2.53	0.44
1:1:511:C:O2'	11:E:78:ASP:OD2	2.34	0.44
1:1:710:G:OP1	17:L:39:ARG:NH2	2.37	0.44
1:1:1006:A:P	22:Q:14:GLN:HE22	2.40	0.44
1:1:1157:G:N3	1:1:1158:G:H1'	2.33	0.44
1:1:3145:A:H1'	8:B:53:MET:H	1.81	0.44
6:6:4:A:N1	35:t:63:GLN:HG2	2.32	0.44
6:6:31:A:H2'	6:6:32:A:C1'	2.48	0.44
6:6:37:U:O2'	6:6:38:U:H6	1.99	0.44
6:6:57:A:O2'	6:6:58:A:H8	2.00	0.44
7:A:39:VAL:HG13	7:A:39:VAL:O	2.17	0.44
8:B:77:THR:OG1	8:B:326:GLY:O	2.32	0.44
8:B:179:MET:HE1	8:B:337:THR:CG2	2.47	0.44
8:B:298:PHE:CD2	8:B:357:LYS:HA	2.53	0.44
10:D:145:ILE:N	10:D:146:PRO:HD2	2.32	0.44
1:1:984:A:H2'	1:1:985:G:O4'	2.17	0.44
2:2:20:A:OP1	21:P:3:ARG:NH1	2.50	0.44
4:4:110:MET:HE1	4:4:157:ILE:HD13	1.99	0.44
9:C:159:GLN:HA	9:C:217:ILE:HB	2.00	0.44
13:G:89:GLN:HG3	33:o:170:LEU:HG	1.98	0.44
14:H:85:GLY:HA2	14:H:147:ASN:HA	1.99	0.44
20:O:111:PRO:N	20:O:112:PRO:HD2	2.32	0.44
25:Y:88:LYS:HB2	25:Y:92:ALA:O	2.16	0.44
28:f:53:VAL:HG22	28:f:67:VAL:HG22	2.00	0.44
1:1:27:C:O2'	1:1:335:A:N3	2.45	0.44
1:1:443:C:H2'	1:1:444:A:C8	2.52	0.44
1:1:1245:U:OP1	23:S:136:ARG:NH2	2.51	0.44
1:1:3245:G:H5"	8:B:133:TYR:HB2	1.99	0.44
3:3:134:ILE:O	27:e:124:ARG:N	2.43	0.44
5:5:141:GLY:HA2	5:5:171:TRP:CH2	2.53	0.44
5:5:221:LEU:HD23	5:5:240:LYS:HZ3	1.82	0.44
10:D:143:PHE:HD1	10:D:143:PHE:H	1.66	0.44
10:D:226:LEU:HD13	10:D:264:LEU:HD11	1.98	0.44
10:D:441:LEU:HD23	10:D:446:LEU:HD22	1.99	0.44
11:E:149:LEU:H	11:E:149:LEU:HD23	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:H:25:ASN:HA	14:H:38:ASN:HA	1.99	0.44
29:h:122:ALA:HA	37:v:56:LEU:HG	2.00	0.44
38:x:276:MET:HB2	38:x:276:MET:HE3	1.81	0.44
1:1:378:U:H4'	1:1:412:G:H5'	2.00	0.44
1:1:1163:C:H2'	1:1:1164:A:C8	2.53	0.44
1:1:1328:C:H2'	1:1:1329:C:C6	2.53	0.44
1:1:3406:A:H2	1:1:3411:A:H61	1.64	0.44
7:A:96:ASN:HD22	7:A:115:ARG:HH21	1.66	0.44
8:B:24:ARG:O	8:B:220:VAL:HG21	2.17	0.44
10:D:483:ASN:HB3	10:D:486:LEU:HB2	1.99	0.44
24:V:39:VAL:H	24:V:62:ALA:HA	1.83	0.44
39:y:14:GLY:HA3	39:y:194:GLY:O	2.18	0.44
1:1:259:A:O2'	17:L:136:GLY:O	2.32	0.44
1:1:702:A:N1	1:1:730:G:O2'	2.50	0.44
1:1:3395:G:H5'	8:B:125:SER:OG	2.17	0.44
3:3:25:GLN:HG2	3:3:37:LEU:HD22	1.99	0.44
8:B:116:ARG:HG3	8:B:122:TRP:HB2	1.99	0.44
13:G:158:ASP:HB3	13:G:159:PRO:HD3	1.99	0.44
1:1:547:G:H1'	1:1:581:A:C6	2.53	0.44
1:1:3338:A:H2'	1:1:3339:A:H8	1.83	0.44
21:P:113:ILE:HD11	21:P:115:LYS:HE2	2.00	0.44
1:1:299:C:OP1	19:N:68:ARG:HB3	2.18	0.43
2:2:115:G:H4'	2:2:146:A:H5'	2.00	0.43
7:A:155:PHE:HA	7:A:161:LEU:HB3	2.00	0.43
8:B:85:VAL:O	8:B:162:ALA:HA	2.17	0.43
20:O:28:LEU:HD11	20:O:103:LEU:HB2	1.99	0.43
32:m:189:SER:HB3	32:m:191:ILE:HD11	2.00	0.43
33:o:206:ILE:O	33:o:210:GLN:HG3	2.18	0.43
1:1:243:C:O2	1:1:243:C:O4'	2.35	0.43
1:1:633:A:H5'	9:C:325:ALA:HB3	2.00	0.43
1:1:3192:C:H1'	8:B:327:ALA:HB3	1.99	0.43
6:6:72:U:H4'	6:6:73:U:O5'	2.17	0.43
7:A:193:ILE:HG12	7:A:198:ILE:HG13	2.00	0.43
19:N:8:GLU:HB2	19:N:50:ARG:NH2	2.33	0.43
1:1:305:A:C8	1:1:307:G:H1'	2.53	0.43
5:5:160:THR:C	5:5:162:LYS:H	2.26	0.43
7:A:122:VAL:HG23	7:A:232:ILE:HG12	2.00	0.43
8:B:31:ALA:O	8:B:339:ARG:NH2	2.51	0.43
10:D:143:PHE:CD2	10:D:241:VAL:HG11	2.49	0.43
12:F:214:LEU:HB3	12:F:249:MET:HB3	1.99	0.43
18:M:29:VAL:HB	18:M:38:LEU:HD23	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:O:13:LYS:HG2	20:O:41:GLU:HB3	2.00	0.43
22:Q:112:ARG:HG3	22:Q:122:VAL:HG21	1.99	0.43
22:Q:117:LYS:HG3	22:Q:118:ALA:N	2.32	0.43
23:S:23:LEU:HD23	40:T:148:PRO:HG3	2.00	0.43
33:o:135:ARG:NH2	33:o:189:ASN:O	2.51	0.43
1:1:1207:C:H2'	1:1:1208:G:N2	2.33	0.43
1:1:3141:G:O2'	8:B:275:ARG:NE	2.51	0.43
8:B:16:PHE:HB3	8:B:275:ARG:HH21	1.82	0.43
9:C:248:ARG:HG3	9:C:249:PHE:N	2.34	0.43
10:D:367:HIS:ND1	10:D:368:GLY:O	2.52	0.43
12:F:122:ILE:HD12	12:F:124:VAL:HG23	2.00	0.43
20:O:151:ASN:C	20:O:151:ASN:OD1	2.61	0.43
27:e:98:SER:O	27:e:102:ARG:HG3	2.18	0.43
27:e:127:GLU:H	27:e:127:GLU:HG3	1.60	0.43
37:v:72:ASP:HA	37:v:73:PRO:HD3	1.85	0.43
1:1:17:G:H4'	29:h:77:TYR:CZ	2.53	0.43
1:1:1446:G:H5"	27:e:121:ALA:HB2	2.01	0.43
1:1:3332:U:H2'	1:1:3333:G:H8	1.82	0.43
1:1:3486:U:H2'	1:1:3487:C:C6	2.53	0.43
6:6:41:G:C6	6:6:42:A:C8	3.07	0.43
7:A:68:MET:HB3	7:A:71:SER:HB3	2.00	0.43
8:B:53:MET:HB2	8:B:77:THR:OG1	2.19	0.43
8:B:67:MET:HG3	8:B:72:ILE:HD11	2.00	0.43
11:E:102:ILE:HG23	28:f:108:ILE:HG23	2.00	0.43
17:L:136:GLY:HA3	37:v:160:SER:HB3	2.00	0.43
20:O:156:LYS:HE2	20:O:156:LYS:HB3	1.75	0.43
23:S:25:ARG:HH22	23:S:27:ARG:HD2	1.83	0.43
1:1:26:A:N3	1:1:336:U:O2'	2.46	0.43
1:1:3301:C:H2'	1:1:3302:U:C6	2.53	0.43
5:5:45:VAL:HG13	5:5:57:VAL:HG13	2.00	0.43
6:6:74:U:O4	33:o:196:VAL:HB	2.19	0.43
8:B:56:ILE:CD1	8:B:76:VAL:HG21	2.48	0.43
8:B:76:VAL:HB	8:B:323:MET:SD	2.58	0.43
8:B:162:ALA:O	8:B:178:LEU:HA	2.19	0.43
14:H:16:GLY:HA2	14:H:30:GLY:HA2	2.01	0.43
18:M:66:PRO:HG2	18:M:69:ALA:HB2	2.01	0.43
32:m:220:GLU:HG2	32:m:225:PHE:CE2	2.54	0.43
38:x:106:ARG:HA	38:x:109:TYR:HD2	1.81	0.43
1:1:592:U:H2'	1:1:593:A:O4'	2.19	0.43
1:1:835:C:H4'	9:C:94:ASN:ND2	2.28	0.43
1:1:1158:G:H2'	1:1:1158:G:N3	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3209:A:O2'	14:H:66:ALA:O	2.33	0.43
5:5:237:TYR:CZ	5:5:245:PRO:HG3	2.54	0.43
7:A:89:LEU:HG	30:i:78:LEU:HD22	2.00	0.43
12:F:75:LYS:HG3	12:F:76:ALA:N	2.33	0.43
18:M:64:LYS:O	18:M:65:LEU:HD23	2.18	0.43
22:Q:35:LEU:O	22:Q:39:THR:OG1	2.27	0.43
29:h:56:ILE:O	29:h:60:ILE:HG13	2.18	0.43
1:1:3283:A:H2'	1:1:3284:G:C8	2.53	0.43
1:1:3346:U:H4'	1:1:3347:G:O4'	2.19	0.43
8:B:196:ARG:HA	8:B:199:PHE:CD2	2.54	0.43
8:B:328:THR:HG21	8:B:336:LEU:HD13	2.00	0.43
17:L:47:ALA:HB3	17:L:48:PRO:HD3	2.01	0.43
24:V:38:ILE:HA	24:V:62:ALA:HA	2.01	0.43
33:o:202:PRO:HG2	33:o:206:ILE:CD1	2.49	0.43
1:1:547:G:H1'	1:1:581:A:C2	2.53	0.43
8:B:39:LYS:HD3	8:B:42:HIS:CD2	2.53	0.43
10:D:465:PRO:HG2	10:D:468:LYS:HG2	2.01	0.43
10:D:483:ASN:HD22	10:D:486:LEU:HD12	1.84	0.43
11:E:53:ALA:O	11:E:56:THR:HG23	2.19	0.43
11:E:169:LYS:HZ1	11:E:175:LYS:HE3	1.84	0.43
17:L:59:LYS:HD2	17:L:66:ASN:O	2.19	0.43
20:O:2:SER:HB2	23:S:165:LYS:HA	2.01	0.43
21:P:82:ARG:HE	21:P:82:ARG:HB3	1.55	0.43
33:o:113:PRO:HG3	33:o:171:LEU:HD22	2.01	0.43
1:1:848:A:OP2	31:j:28:HIS:NE2	2.35	0.43
1:1:3277:A:C2	1:1:3284:G:H4'	2.54	0.43
1:1:3431:A:OP2	1:1:3431:A:H8	2.02	0.43
2:2:151:U:OP1	19:N:38:ARG:NH2	2.49	0.43
5:5:130:LEU:HD11	5:5:145:ALA:HB1	1.99	0.43
6:6:4:A:H5"	35:t:66:ARG:NH1	2.33	0.43
7:A:70:HIS:CE1	7:A:175:PRO:HD2	2.53	0.43
10:D:491:LYS:HB2	10:D:491:LYS:HE2	1.81	0.43
17:L:111:ARG:HE	30:i:11:LYS:HG2	1.84	0.43
19:N:140:LYS:HD3	19:N:140:LYS:HA	1.80	0.43
30:i:44:GLU:OE2	32:m:204:ASP:HA	2.19	0.43
1:1:3155:G:O2'	1:1:3474:U:H1'	2.19	0.42
8:B:21:ARG:CB	8:B:272:TYR:HB3	2.48	0.42
8:B:46:PHE:CE1	8:B:81:THR:HB	2.54	0.42
8:B:85:VAL:HA	8:B:202:THR:HA	1.99	0.42
8:B:312:VAL:HG23	8:B:364:LYS:CD	2.46	0.42
10:D:502:ALA:HB2	10:D:512:ILE:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:H:90:MET:HA	14:H:179:VAL:HA	2.00	0.42
20:O:55:TYR:OH	20:O:74:PHE:O	2.34	0.42
32:m:193:ASP:OD1	32:m:193:ASP:N	2.51	0.42
33:o:158:VAL:O	33:o:162:VAL:HG23	2.19	0.42
1:1:1389:A:H4'	1:1:1390:A:O5'	2.18	0.42
11:E:72:VAL:HA	11:E:82:VAL:HG23	2.01	0.42
23:S:41:TRP:HA	23:S:41:TRP:CE3	2.54	0.42
23:S:47:ILE:HG13	40:T:154:VAL:HG23	2.01	0.42
35:t:63:GLN:HE21	35:t:67:GLU:HG2	1.84	0.42
38:x:106:ARG:HD2	38:x:109:TYR:HB2	2.02	0.42
39:y:69:GLY:HA2	39:y:93:LYS:N	2.34	0.42
1:1:447:C:H42	1:1:644:A:HO2'	1.63	0.42
1:1:451:C:P	3:3:124:ARG:HH22	2.42	0.42
1:1:546:G:N2	1:1:547:G:O6	2.29	0.42
6:6:6:C:H4'	6:6:7:U:C6	2.53	0.42
8:B:92:TYR:HB2	8:B:157:VAL:HB	2.00	0.42
8:B:106:TRP:O	8:B:137:TYR:HE2	2.01	0.42
8:B:170:PRO:HD3	8:B:318:GLU:OE1	2.19	0.42
8:B:307:PRO:CG	8:B:364:LYS:HG2	2.47	0.42
16:K:52:PRO:HA	16:K:205:HIS:HA	2.01	0.42
17:L:55:ARG:HA	17:L:55:ARG:HD3	1.84	0.42
39:y:200:ASN:H	39:y:204:ALA:HA	1.84	0.42
1:1:3417:A:H3'	8:B:123:PHE:HB3	2.00	0.42
5:5:95:MET:HG3	5:5:104:LEU:HD13	2.00	0.42
6:6:40:U:C6	6:6:58:A:H2	2.38	0.42
6:6:67:U:H5"	6:6:68:U:N3	2.34	0.42
8:B:224:LYS:HE3	8:B:224:LYS:HB3	1.87	0.42
10:D:340:ILE:HG22	10:D:408:ILE:HG22	2.01	0.42
12:F:115:LEU:HD21	12:F:122:ILE:HG12	2.02	0.42
17:L:57:ALA:HB2	30:i:5:LEU:HD11	2.02	0.42
33:o:135:ARG:HH21	33:o:192:LYS:N	2.18	0.42
1:1:227:G:O2'	1:1:228:A:H5"	2.20	0.42
1:1:359:A:O2'	1:1:360:A:H5'	2.19	0.42
1:1:485:U:OP2	5:5:183:LYS:NZ	2.50	0.42
1:1:1324:U:H2'	1:1:1325:A:C8	2.54	0.42
1:1:3369:A:N1	11:E:153:ARG:HG3	2.35	0.42
1:1:3409:C:O2'	21:P:69:ARG:O	2.36	0.42
5:5:265:ILE:HD12	5:5:267:LEU:HD23	2.02	0.42
7:A:145:SER:HA	7:A:182:LYS:HB2	2.02	0.42
8:B:22:ALA:N	8:B:272:TYR:O	2.50	0.42
8:B:376:ALA:HA	8:B:379:PHE:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:87:LYS:HE2	11:E:87:LYS:HB3	1.82	0.42
21:P:30:ARG:HD2	21:P:63:PHE:CE2	2.55	0.42
23:S:26:MET:HG3	23:S:40:TYR:CE1	2.55	0.42
35:t:53:ARG:NH2	35:t:55:GLU:OE2	2.47	0.42
38:x:65:ILE:HG23	38:x:204:SER:HB2	2.01	0.42
1:1:217:G:C4	1:1:237:U:H4'	2.54	0.42
1:1:1153:U:H2'	1:1:1154:U:C6	2.55	0.42
1:1:3425:C:H2'	1:1:3426:G:C8	2.54	0.42
2:2:99:C:H2'	2:2:100:A:H8	1.84	0.42
4:4:111:ARG:NH1	4:4:168:GLU:OE2	2.53	0.42
6:6:11:C:C2	6:6:24:U:C2	3.08	0.42
8:B:345:HIS:NE2	8:B:347:SER:HB2	2.34	0.42
9:C:324:LYS:HA	9:C:324:LYS:HD2	1.71	0.42
10:D:439:MET:HE1	10:D:448:PHE:CD2	2.55	0.42
11:E:70:VAL:HG11	11:E:91:VAL:HG11	2.01	0.42
18:M:36:ARG:HH12	23:S:95:ASP:HB2	1.85	0.42
33:o:104:LYS:CE	33:o:132:LEU:HD21	2.45	0.42
37:v:56:LEU:HD23	37:v:56:LEU:HA	1.86	0.42
1:1:547:G:H1'	1:1:581:A:N1	2.34	0.42
1:1:676:G:O2'	1:1:1469:A:OP1	2.38	0.42
1:1:1241:U:H3	1:1:1326:G:H1	1.67	0.42
1:1:3111:C:O2'	1:1:3112:A:H8	2.02	0.42
4:4:129:LEU:O	4:4:133:VAL:HG23	2.20	0.42
5:5:229:THR:OG1	5:5:233:GLN:HG2	2.19	0.42
6:6:25:U:C2'	6:6:26:U:H5'	2.50	0.42
6:6:74:U:H4'	33:o:140:ARG:O	2.19	0.42
12:F:97:ARG:HD3	12:F:140:TYR:CD1	2.55	0.42
33:o:181:ILE:HD13	33:o:190:MET:CE	2.49	0.42
1:1:363:A:H2'	1:1:364:G:O4'	2.20	0.42
1:1:379:G:N1	1:1:382:A:OP2	2.53	0.42
1:1:477:C:H6	1:1:477:C:H2'	1.66	0.42
1:1:505:G:H1	1:1:644:A:N6	2.11	0.42
1:1:671:A:H8	1:1:2460:A:H1'	1.83	0.42
1:1:1155:U:O2	1:1:1155:U:O4'	2.38	0.42
1:1:3148:G:H1	1:1:3186:U:H3	1.68	0.42
4:4:175:GLU:HG2	4:4:176:ASP:N	2.34	0.42
5:5:284:LYS:HE2	5:5:284:LYS:HB3	1.87	0.42
6:6:11:C:H42	6:6:23:U:H3	1.66	0.42
8:B:90:VAL:HG21	8:B:180:GLU:CD	2.44	0.42
8:B:102:LEU:HD23	8:B:151:ILE:HD13	2.01	0.42
8:B:218:ILE:HG12	8:B:337:THR:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:194:GLY:O	9:C:199:ARG:HB2	2.19	0.42
17:L:37:GLN:HE22	37:v:24:LYS:HD2	1.85	0.42
27:e:127:GLU:CD	38:x:127:ARG:HH12	2.28	0.42
37:v:126:LYS:HE3	37:v:126:LYS:HB2	1.66	0.42
38:x:106:ARG:HA	38:x:106:ARG:HD2	1.77	0.42
1:1:670:A:P	1:1:1147:G:H22	2.43	0.42
3:3:106:HIS:O	3:3:110:GLN:HG3	2.20	0.42
5:5:158:ASN:HB2	5:5:161:CYS:HB3	2.01	0.42
6:6:22:U:H2'	6:6:23:U:H6	1.85	0.42
8:B:50:LYS:HD3	8:B:336:LEU:HD11	2.01	0.42
9:C:190:ARG:NE	9:C:199:ARG:HB3	2.34	0.42
9:C:318:LYS:HD3	9:C:323:ASN:ND2	2.35	0.42
10:D:241:VAL:HG22	10:D:272:LEU:HD13	2.01	0.42
10:D:392:CYS:SG	10:D:397:ALA:HB2	2.60	0.42
12:F:51:ILE:HD13	12:F:187:SER:HB3	2.02	0.42
12:F:95:ARG:CZ	12:F:110:MET:HE3	2.49	0.42
18:M:86:LYS:O	18:M:89:SER:OG	2.37	0.42
27:e:118:ASN:OD1	27:e:118:ASN:N	2.52	0.42
1:1:153:U:O4	13:G:183:LYS:NZ	2.40	0.42
1:1:223:G:OP1	25:Y:15:ARG:NH1	2.52	0.42
1:1:360:A:N1	1:1:373:A:H5"	2.34	0.42
1:1:414:G:H1'	2:2:24:G:N2	2.35	0.42
1:1:587:U:H2'	1:1:588:G:C8	2.55	0.42
1:1:3111:C:O2'	1:1:3112:A:H5'	2.19	0.42
1:1:3113:A:O2'	1:1:3114:C:H5"	2.19	0.42
3:3:114:ARG:HD2	3:3:114:ARG:HA	1.74	0.42
6:6:33:A:N1	6:6:64:G:C6	2.88	0.42
6:6:58:A:H2'	6:6:59:A:H8	1.84	0.42
8:B:46:PHE:CD1	8:B:205:ILE:HD12	2.55	0.42
8:B:211:GLN:HE21	8:B:283:TYR:CA	2.33	0.42
9:C:228:GLU:OE2	9:C:239:GLN:NE2	2.52	0.42
12:F:183:TYR:CZ	12:F:204:GLN:HG2	2.55	0.42
17:L:62:THR:HG23	17:L:64:ARG:N	2.35	0.42
23:S:116:ARG:CZ	23:S:119:SER:HB3	2.50	0.42
23:S:123:LEU:HA	40:T:153:PRO:HD2	2.01	0.42
29:h:3:LEU:HB2	29:h:52:ASP:OD1	2.19	0.42
1:1:3128:A:H61	14:H:117:GLY:C	2.26	0.41
1:1:3217:U:H4'	1:1:3218:A:OP1	2.19	0.41
5:5:51:HIS:CD2	5:5:51:HIS:C	2.97	0.41
6:6:10:U:H2'	6:6:11:C:H6	1.83	0.41
8:B:221:THR:HB	8:B:273:MET:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:O:4:PHE:HE1	28:f:34:GLU:HG3	1.85	0.41
28:f:58:LYS:HA	28:f:58:LYS:HD3	1.91	0.41
29:h:20:LEU:HD11	29:h:24:ARG:HH11	1.85	0.41
38:x:100:THR:OG1	38:x:101:SER:N	2.53	0.41
1:1:1185:A:OP2	1:1:2459:G:N1	2.53	0.41
1:1:3254:G:H1	1:1:3392:A:N6	2.12	0.41
1:1:3259:C:OP1	38:x:190:ARG:N	2.52	0.41
2:2:56:A:O2'	2:2:57:G:H8	2.03	0.41
4:4:99:ASP:O	4:4:103:THR:HG23	2.20	0.41
5:5:265:ILE:HG13	5:5:267:LEU:HB3	2.02	0.41
5:5:274:ARG:NH2	38:x:284:ARG:O	2.53	0.41
6:6:33:A:H3'	6:6:34:U:C6	2.55	0.41
6:6:58:A:O2'	6:6:59:A:H8	2.02	0.41
8:B:375:GLU:HA	8:B:378:GLN:NE2	2.35	0.41
9:C:57:LYS:H	9:C:57:LYS:HG2	1.65	0.41
10:D:217:ALA:HB3	10:D:222:LEU:HD22	2.01	0.41
13:G:220:ALA:HA	13:G:224:ALA:HB3	2.02	0.41
20:O:152:ASP:OD1	20:O:152:ASP:N	2.51	0.41
29:h:14:GLU:N	29:h:14:GLU:OE2	2.53	0.41
1:1:646:A:O2'	1:1:647:A:P	2.79	0.41
1:1:1361:A:OP1	28:f:25:HIS:NE2	2.33	0.41
1:1:3096:G:H4'	8:B:120:LYS:HE2	2.02	0.41
1:1:3154:U:O2'	1:1:3155:G:N7	2.50	0.41
3:3:5:GLU:O	3:3:9:GLN:HG2	2.21	0.41
3:3:157:LEU:HD13	38:x:243:ARG:HG3	2.01	0.41
6:6:56:G:H2'	6:6:56:G:P	2.60	0.41
8:B:11:HIS:ND1	8:B:17:LEU:HD11	2.35	0.41
11:E:176:GLU:OE2	11:E:176:GLU:N	2.30	0.41
18:M:87:TRP:CE2	18:M:93:ALA:HB2	2.55	0.41
20:O:59:LEU:HA	20:O:73:HIS:CD2	2.54	0.41
28:f:91:PRO:HB2	28:f:93:LYS:HG2	2.03	0.41
1:1:382:A:N3	1:1:384:G:H5"	2.35	0.41
1:1:454:G:N2	1:1:498:U:O2	2.47	0.41
1:1:550:G:H1	1:1:574:U:H3	1.67	0.41
1:1:1386:G:H5'	11:E:32:ARG:HH12	1.85	0.41
1:1:2445:A:H2'	1:1:2446:A:C8	2.55	0.41
1:1:3180:C:H3'	1:1:3181:G:H8	1.84	0.41
4:4:8:ILE:HG21	7:A:293:VAL:HG22	2.03	0.41
5:5:49:LEU:HB3	5:5:95:MET:CE	2.49	0.41
5:5:327:LEU:HD23	5:5:327:LEU:HA	1.91	0.41
6:6:57:A:H4'	33:o:207:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:357:LEU:HD23	9:C:357:LEU:HA	1.90	0.41
11:E:146:LYS:HD2	11:E:146:LYS:HA	1.83	0.41
17:L:63:ILE:HD12	17:L:66:ASN:HD21	1.85	0.41
20:O:75:ARG:HG2	20:O:146:VAL:HG23	2.02	0.41
23:S:21:PRO:O	40:T:146:ASN:ND2	2.44	0.41
27:e:93:ILE:HG21	27:e:102:ARG:HG2	2.02	0.41
29:h:87:THR:HB	29:h:90:ILE:HD12	2.03	0.41
30:i:70:LEU:O	30:i:74:ARG:HG2	2.20	0.41
33:o:163:ALA:O	33:o:167:HIS:HB2	2.20	0.41
33:o:181:ILE:HD13	33:o:190:MET:HE2	2.02	0.41
1:1:591:G:H3'	1:1:591:G:N3	2.35	0.41
1:1:702:A:H8	1:1:817:G:C2	2.38	0.41
1:1:3104:G:OP1	20:O:73:HIS:ND1	2.50	0.41
1:1:3324:G:H1	1:1:3361:U:H3	1.69	0.41
9:C:37:VAL:HG21	9:C:246:LEU:HD21	2.02	0.41
12:F:239:ASP:OD2	23:S:34:SER:OG	2.25	0.41
21:P:30:ARG:NE	21:P:62:ARG:HH21	2.18	0.41
30:i:52:GLU:HG2	30:i:88:LEU:HD11	2.01	0.41
1:1:613:A:H1'	1:1:1368:A:H5"	2.02	0.41
4:4:82:LEU:HD12	4:4:82:LEU:HA	1.88	0.41
4:4:198:LEU:O	4:4:202:LEU:HB2	2.20	0.41
6:6:3:A:C6	6:6:4:A:C6	3.08	0.41
6:6:9:C:H5"	16:K:145:ARG:CA	2.42	0.41
6:6:73:U:O4	33:o:135:ARG:HA	2.20	0.41
10:D:161:GLY:O	10:D:213:ASN:ND2	2.52	0.41
10:D:327:LEU:HB2	10:D:440:PHE:HE2	1.84	0.41
19:N:13:LYS:HB3	19:N:16:SER:HB3	2.03	0.41
22:Q:126:ASP:OD1	22:Q:126:ASP:N	2.53	0.41
35:t:63:GLN:OE1	35:t:66:ARG:NH1	2.53	0.41
1:1:188:C:P	37:v:19:ARG:HH21	2.42	0.41
1:1:447:C:N4	1:1:644:A:O2'	2.37	0.41
1:1:500:U:O2'	1:1:501:G:OP1	2.31	0.41
1:1:583:C:OP1	18:M:70:ARG:N	2.52	0.41
4:4:202:LEU:HD12	4:4:202:LEU:HA	1.92	0.41
8:B:58:ARG:HD2	8:B:354:VAL:HG13	2.01	0.41
31:j:39:TYR:CD1	31:j:40:PRO:HA	2.55	0.41
33:o:114:HIS:O	35:t:62:ARG:NH2	2.54	0.41
1:1:538:U:N3	1:1:589:U:O2	2.54	0.41
7:A:99:PHE:HE1	7:A:171:THR:HG21	1.84	0.41
10:D:247:ARG:O	10:D:251:ILE:HG13	2.20	0.41
10:D:413:PRO:O	10:D:504:TYR:OH	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:N:168:GLY:O	19:N:172:ARG:HG2	2.21	0.41
24:V:27:CYS:H	24:V:35:ASN:HA	1.86	0.41
27:e:37:SER:O	27:e:41:ARG:HG3	2.21	0.41
33:o:106:VAL:HG12	33:o:181:ILE:HD12	2.02	0.41
33:o:141:LYS:O	33:o:200:ARG:HG3	2.21	0.41
35:t:53:ARG:O	35:t:56:THR:OG1	2.38	0.41
1:1:461:A:H2'	1:1:461:A:N3	2.36	0.41
1:1:542:G:H2'	1:1:543:G:C8	2.56	0.41
1:1:624:U:O2'	1:1:627:G:O6	2.38	0.41
1:1:3253:G:H1	1:1:3393:U:H3	1.68	0.41
1:1:3283:A:H2'	1:1:3284:G:H8	1.85	0.41
1:1:3486:U:H2'	1:1:3487:C:H6	1.86	0.41
4:4:173:TYR:CB	4:4:177:VAL:HG12	2.46	0.41
6:6:1:A:C8	6:6:3:A:C6	3.09	0.41
6:6:27:U:H1'	6:6:28:U:C6	2.56	0.41
6:6:31:A:H1'	6:6:69:U:N3	2.36	0.41
7:A:129:LEU:HD13	7:A:129:LEU:HA	1.92	0.41
7:A:200:PHE:HE2	7:A:223:PRO:HB2	1.86	0.41
8:B:49:TYR:CE1	8:B:335:VAL:HG22	2.56	0.41
8:B:222:ARG:CB	8:B:331:PRO:HD3	2.50	0.41
8:B:369:ARG:HG3	8:B:370:PHE:CD2	2.56	0.41
17:L:128:ARG:NH2	29:h:111:ARG:O	2.51	0.41
19:N:9:GLU:HG2	30:i:39:ARG:HG2	2.03	0.41
20:O:13:LYS:O	23:S:171:ARG:NH2	2.47	0.41
20:O:44:ILE:HD11	20:O:139:VAL:HG22	2.03	0.41
20:O:157:LEU:HD23	20:O:157:LEU:O	2.21	0.41
22:Q:71:SER:HA	22:Q:75:ALA:HA	2.03	0.41
23:S:109:MET:HE3	23:S:109:MET:HB3	1.79	0.41
27:e:29:TRP:CE2	27:e:50:PRO:HD2	2.56	0.41
33:o:196:VAL:HG13	33:o:197:PRO:HD2	2.03	0.41
1:1:114:A:H2'	1:1:115:A:O4'	2.21	0.41
1:1:832:G:N3	1:1:832:G:H2'	2.36	0.41
1:1:838:A:H2'	1:1:839:A:C4	2.56	0.41
1:1:1222:U:H5'	20:O:50:ARG:HA	2.02	0.41
1:1:3100:C:O2'	8:B:99:LEU:O	2.34	0.41
1:1:3316:G:H2'	1:1:3319:G:H1'	2.02	0.41
8:B:283:TYR:N	8:B:323:MET:O	2.39	0.41
11:E:76:LEU:HA	11:E:76:LEU:HD23	1.82	0.41
19:N:17:ASP:CG	30:i:47:GLY:HA3	2.45	0.41
19:N:48:ALA:O	19:N:53:TYR:HB3	2.21	0.41
21:P:7:SER:N	21:P:8:PRO:HD2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:497:C:H2'	1:1:498:U:O4'	2.20	0.40
1:1:832:G:H3'	1:1:833:A:C8	2.56	0.40
6:6:4:A:H62	35:t:59:ASN:ND2	2.19	0.40
7:A:134:GLU:HB2	7:A:137:MET:HE2	2.02	0.40
8:B:275:ARG:HD3	8:B:275:ARG:HA	1.76	0.40
9:C:314:HIS:CE1	9:C:317:LYS:HA	2.55	0.40
12:F:218:LEU:H	12:F:248:LYS:HB3	1.86	0.40
30:i:82:LYS:O	30:i:86:GLU:HG3	2.21	0.40
1:1:505:G:C6	1:1:506:G:C6	3.09	0.40
1:1:1325:A:H5'	23:S:87:HIS:CE1	2.56	0.40
1:1:3332:U:H2'	1:1:3333:G:C8	2.56	0.40
5:5:1:MET:HE3	5:5:17:ILE:HG23	2.02	0.40
6:6:21:G:H2'	6:6:22:U:O4'	2.21	0.40
8:B:125:SER:C	8:B:126:LYS:HD3	2.47	0.40
8:B:199:PHE:HD1	8:B:199:PHE:HA	1.80	0.40
9:C:337:TYR:CE2	9:C:339:ALA:HB2	2.56	0.40
10:D:498:LEU:HD23	10:D:498:LEU:HA	1.86	0.40
20:O:179:ILE:HD12	20:O:179:ILE:H	1.86	0.40
21:P:9:ALA:HB1	21:P:16:LYS:HE2	2.02	0.40
21:P:52:LYS:HE3	21:P:88:VAL:HG12	2.03	0.40
23:S:142:LEU:HA	23:S:147:LEU:HD11	2.02	0.40
28:f:56:SER:O	28:f:64:LYS:HD3	2.21	0.40
31:j:28:HIS:CE1	31:j:30:GLN:HB2	2.57	0.40
33:o:153:PHE:HB2	33:o:159:ALA:HB2	2.03	0.40
39:y:69:GLY:HA2	39:y:93:LYS:H	1.86	0.40
1:1:223:G:H2'	1:1:224:U:O4'	2.21	0.40
1:1:1427:A:N3	1:1:1453:A:O2'	2.50	0.40
1:1:3184:G:H2'	1:1:3185:C:C6	2.57	0.40
2:2:9:A:H3'	2:2:10:A:H8	1.85	0.40
6:6:9:C:C4	6:6:26:U:C4	3.10	0.40
6:6:36:U:H2'	6:6:37:U:C6	2.57	0.40
6:6:69:U:H4'	6:6:70:U:OP1	2.21	0.40
7:A:100:PHE:HB3	7:A:112:HIS:HB2	2.03	0.40
7:A:153:LYS:NZ	15:J:125:GLU:H	2.19	0.40
8:B:306:THR:HA	8:B:311:PHE:CE2	2.56	0.40
8:B:319:ASN:OD1	8:B:319:ASN:N	2.54	0.40
16:K:105:ALA:HB2	16:K:175:ALA:HB1	2.04	0.40
19:N:100:CYS:O	19:N:104:GLU:HG2	2.22	0.40
1:1:1442:G:OP2	27:e:28:SER:OG	2.32	0.40
1:1:2450:C:H2'	1:1:2451:A:C8	2.55	0.40
1:1:3259:C:H2'	1:1:3260:A:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3279:A:H2	1:1:3283:A:H1'	1.87	0.40
3:3:169:LEU:HD12	3:3:174:TYR:CE2	2.57	0.40
5:5:58:ALA:HB2	5:5:95:MET:SD	2.62	0.40
5:5:111:LEU:HB2	5:5:124:LEU:HB3	2.03	0.40
6:6:21:G:H2'	6:6:22:U:C6	2.57	0.40
9:C:179:ASP:O	9:C:183:VAL:HG23	2.21	0.40
10:D:471:ASN:O	10:D:471:ASN:CG	2.65	0.40
21:P:161:ASN:HB3	38:x:194:HIS:HE1	1.85	0.40
23:S:25:ARG:O	40:T:150:THR:HA	2.21	0.40
25:Y:42:TYR:OH	25:Y:110:LEU:HD11	2.22	0.40
30:i:81:ALA:O	30:i:85:ILE:HG12	2.21	0.40
1:1:28:G:H2'	1:1:29:C:O4'	2.22	0.40
1:1:296:C:H4'	19:N:171:SER:O	2.21	0.40
1:1:581:A:C4	1:1:582:G:H1'	2.56	0.40
1:1:1395:A:H2'	1:1:1396:G:C8	2.56	0.40
1:1:3418:U:O2	1:1:3490:A:H5'	2.22	0.40
3:3:57:ASN:O	3:3:57:ASN:CG	2.65	0.40
4:4:84:GLN:NE2	4:4:137:TYR:OH	2.55	0.40
4:4:214:LYS:H	4:4:214:LYS:HG2	1.56	0.40
8:B:91:GLY:O	8:B:102:LEU:N	2.46	0.40
9:C:179:ASP:HB3	9:C:207:PRO:HD3	2.04	0.40
12:F:170:LEU:HD22	12:F:176:ILE:HG12	2.03	0.40
18:M:105:LEU:HD22	18:M:109:ASP:HB3	2.02	0.40
22:Q:43:PHE:CD2	22:Q:135:GLY:HA3	2.57	0.40
23:S:164:LYS:HA	23:S:164:LYS:HD3	1.98	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	190/302 (63%)	183 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	4	208/217 (96%)	203 (98%)	5 (2%)	0	100	100
5	5	336/387 (87%)	314 (94%)	22 (6%)	0	100	100
7	A	250/295 (85%)	238 (95%)	10 (4%)	2 (1%)	16	51
8	B	328/388 (84%)	311 (95%)	16 (5%)	1 (0%)	37	70
9	C	325/363 (90%)	308 (95%)	17 (5%)	0	100	100
10	D	400/578 (69%)	391 (98%)	9 (2%)	0	100	100
11	E	168/195 (86%)	155 (92%)	13 (8%)	0	100	100
12	F	238/250 (95%)	231 (97%)	7 (3%)	0	100	100
13	G	161/259 (62%)	156 (97%)	5 (3%)	0	100	100
14	H	149/190 (78%)	141 (95%)	8 (5%)	0	100	100
15	J	87/333 (26%)	87 (100%)	0	0	100	100
16	K	239/373 (64%)	229 (96%)	9 (4%)	1 (0%)	30	66
17	L	114/208 (55%)	112 (98%)	2 (2%)	0	100	100
18	M	123/134 (92%)	120 (98%)	3 (2%)	0	100	100
19	N	160/201 (80%)	158 (99%)	2 (1%)	0	100	100
20	O	183/197 (93%)	180 (98%)	3 (2%)	0	100	100
21	P	141/187 (75%)	135 (96%)	6 (4%)	0	100	100
22	Q	133/187 (71%)	127 (96%)	6 (4%)	0	100	100
23	S	164/176 (93%)	154 (94%)	10 (6%)	0	100	100
24	V	105/139 (76%)	99 (94%)	6 (6%)	0	100	100
25	Y	123/126 (98%)	119 (97%)	4 (3%)	0	100	100
26	b	112/642 (17%)	112 (100%)	0	0	100	100
27	e	122/127 (96%)	120 (98%)	2 (2%)	0	100	100
28	f	104/108 (96%)	100 (96%)	4 (4%)	0	100	100
29	h	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
30	i	96/99 (97%)	92 (96%)	3 (3%)	1 (1%)	13	46
31	j	69/91 (76%)	67 (97%)	2 (3%)	0	100	100
32	m	86/740 (12%)	80 (93%)	6 (7%)	0	100	100
33	o	125/276 (45%)	116 (93%)	7 (6%)	2 (2%)	8	34
34	r	46/260 (18%)	46 (100%)	0	0	100	100
35	t	21/249 (8%)	21 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	u	98/192 (51%)	96 (98%)	2 (2%)	0	100	100
37	v	157/209 (75%)	151 (96%)	5 (3%)	1 (1%)	22	57
38	x	303/306 (99%)	300 (99%)	3 (1%)	0	100	100
39	y	192/244 (79%)	180 (94%)	12 (6%)	0	100	100
40	T	17/160 (11%)	17 (100%)	0	0	100	100
All	All	5992/9510 (63%)	5765 (96%)	219 (4%)	8 (0%)	50	81

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	K	153	ILE
7	A	118	ASN
7	A	248	PHE
33	o	197	PRO
37	v	130	ILE
8	B	124	LYS
33	o	198	PHE
30	i	10	ASN

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	169/271 (62%)	164 (97%)	5 (3%)	36	69
4	4	191/197 (97%)	184 (96%)	7 (4%)	29	63
5	5	301/345 (87%)	294 (98%)	7 (2%)	45	75
7	A	228/266 (86%)	225 (99%)	3 (1%)	65	85
8	B	282/326 (86%)	271 (96%)	11 (4%)	27	61
9	C	275/297 (93%)	271 (98%)	4 (2%)	60	83
10	D	288/505 (57%)	284 (99%)	4 (1%)	62	83
11	E	139/155 (90%)	134 (96%)	5 (4%)	30	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
12	F	201/210 (96%)	197 (98%)	4 (2%)	50 78
13	G	135/212 (64%)	132 (98%)	3 (2%)	47 76
17	L	97/167 (58%)	93 (96%)	4 (4%)	26 60
18	M	108/113 (96%)	103 (95%)	5 (5%)	23 56
19	N	146/176 (83%)	142 (97%)	4 (3%)	40 71
20	O	154/162 (95%)	152 (99%)	2 (1%)	65 85
21	P	118/149 (79%)	115 (98%)	3 (2%)	42 73
22	Q	116/159 (73%)	108 (93%)	8 (7%)	13 42
23	S	149/154 (97%)	147 (99%)	2 (1%)	65 85
25	Y	110/111 (99%)	104 (94%)	6 (6%)	18 50
27	e	106/107 (99%)	105 (99%)	1 (1%)	75 89
28	f	89/91 (98%)	87 (98%)	2 (2%)	47 76
29	h	106/107 (99%)	104 (98%)	2 (2%)	52 79
30	i	79/84 (94%)	69 (87%)	10 (13%)	3 17
31	j	58/71 (82%)	55 (95%)	3 (5%)	19 52
32	m	76/659 (12%)	76 (100%)	0	100 100
33	o	95/246 (39%)	89 (94%)	6 (6%)	15 45
35	t	22/223 (10%)	22 (100%)	0	100 100
37	v	138/181 (76%)	135 (98%)	3 (2%)	47 76
38	x	272/273 (100%)	264 (97%)	8 (3%)	37 70
40	T	17/139 (12%)	17 (100%)	0	100 100
All	All	4265/6156 (69%)	4143 (97%)	122 (3%)	39 70

All (122) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	3	34	VAL
3	3	57	ASN
3	3	80	ILE
3	3	120	LEU
3	3	130	GLN
4	4	89	GLU
4	4	100	ILE
4	4	177	VAL
4	4	181	ASP

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Mol	Chain	Res	Type
4	4	188	SER
4	4	189	THR
4	4	196	VAL
5	5	5	LEU
5	5	49	LEU
5	5	71	GLN
5	5	96	LYS
5	5	122	ARG
5	5	133	VAL
5	5	206	ASP
7	A	53	VAL
7	A	267	VAL
7	A	288	ASP
8	B	50	LYS
8	B	66	LYS
8	B	67	MET
8	B	86	VAL
8	B	148	LEU
8	B	165	GLN
8	B	194	TRP
8	B	221	THR
8	B	296	THR
8	B	319	ASN
8	B	364	LYS
9	C	17	VAL
9	C	113	VAL
9	C	215	THR
9	C	262	SER
10	D	196	ILE
10	D	240	LEU
10	D	361	LEU
10	D	452	LEU
11	E	82	VAL
11	E	114	VAL
11	E	115	SER
11	E	120	THR
11	E	168	ILE
12	F	23	THR
12	F	91	ILE
12	F	116	LEU
12	F	132	GLU
13	G	182	ASN

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Mol	Chain	Res	Type
13	G	213	SER
13	G	216	SER
17	L	40	GLN
17	L	85	VAL
17	L	89	VAL
17	L	129	LYS
18	M	14	VAL
18	M	51	ILE
18	M	103	SER
18	M	122	GLU
18	M	123	GLN
19	N	9	GLU
19	N	16	SER
19	N	110	CYS
19	N	198	ARG
20	O	75	ARG
20	O	100	LEU
21	P	49	ASP
21	P	78	VAL
21	P	117	VAL
22	Q	23	VAL
22	Q	63	ILE
22	Q	96	THR
22	Q	117	LYS
22	Q	128	LEU
22	Q	134	THR
22	Q	136	SER
22	Q	146	HIS
23	S	44	LEU
23	S	109	MET
25	Y	7	VAL
25	Y	86	ARG
25	Y	103	VAL
25	Y	108	LEU
25	Y	111	ASP
25	Y	114	ARG
27	e	4	VAL
28	f	10	VAL
28	f	28	THR
29	h	58	THR
29	h	81	ASP
30	i	6	VAL

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Mol	Chain	Res	Type
30	i	9	LEU
30	i	13	LYS
30	i	15	LEU
30	i	16	THR
30	i	19	GLN
30	i	61	ASN
30	i	69	LYS
30	i	77	THR
30	i	94	SER
31	j	57	ARG
31	j	65	SER
31	j	69	LYS
33	o	134	LEU
33	o	185	GLN
33	o	199	LYS
33	o	200	ARG
33	o	203	HIS
33	o	208	ARG
37	v	46	LEU
37	v	69	LEU
37	v	137	VAL
38	x	45	LEU
38	x	81	ASP
38	x	153	GLU
38	x	163	LEU
38	x	175	THR
38	x	204	SER
38	x	253	SER
38	x	257	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
5	5	71	GLN
5	5	258	HIS
7	A	70	HIS
7	A	245	ASN
7	A	277	GLN
8	B	121	ASN
8	B	184	ASN
8	B	211	GLN
8	B	269	ASN

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Mol	Chain	Res	Type
9	C	41	HIS
9	C	94	ASN
9	C	201	HIS
9	C	223	ASN
10	D	188	HIS
10	D	513	ASN
13	G	95	ASN
13	G	221	ASN
17	L	37	GLN
17	L	40	GLN
18	M	125	ASN
19	N	32	GLN
19	N	123	GLN
21	P	72	GLN
22	Q	14	GLN
22	Q	79	ASN
25	Y	90	ASN
27	e	126	GLN
29	h	19	GLN
33	o	189	ASN
37	v	21	ASN
38	x	13	GLN
40	T	139	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1408/3497 (40%)	354 (25%)	23 (1%)
2	2	126/165 (76%)	25 (19%)	0
6	6	54/300 (18%)	36 (66%)	3 (5%)
All	All	1588/3962 (40%)	415 (26%)	26 (1%)

All (415) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	11	A
1	1	14	U
1	1	26	A
1	1	28	G
1	1	32	U
1	1	33	G

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Mol	Chain	Res	Type
1	1	49	A
1	1	57	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	69	U
1	1	72	C
1	1	99	A
1	1	105	G
1	1	109	A
1	1	110	G
1	1	111	C
1	1	113	C
1	1	116	A
1	1	117	U
1	1	118	U
1	1	122	A
1	1	133	A
1	1	142	G
1	1	154	G
1	1	162	A
1	1	163	A
1	1	171	C
1	1	173	U
1	1	177	G
1	1	193	U
1	1	197	U
1	1	198	U
1	1	207	C
1	1	208	A
1	1	213	G
1	1	217	G
1	1	218	A
1	1	225	G
1	1	226	A
1	1	227	G
1	1	228	A
1	1	229	A
1	1	239	U
1	1	244	G
1	1	247	U

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Mol	Chain	Res	Type
1	1	248	G
1	1	254	G
1	1	258	U
1	1	259	A
1	1	266	G
1	1	268	U
1	1	269	U
1	1	276	A
1	1	277	G
1	1	285	G
1	1	303	A
1	1	306	U
1	1	313	U
1	1	314	A
1	1	326	A
1	1	331	A
1	1	337	U
1	1	341	G
1	1	345	G
1	1	347	C
1	1	360	A
1	1	378	U
1	1	382	A
1	1	384	G
1	1	399	A
1	1	404	A
1	1	406	U
1	1	411	C
1	1	427	G
1	1	429	G
1	1	430	A
1	1	437	G
1	1	446	U
1	1	448	U
1	1	449	U
1	1	450	A
1	1	458	G
1	1	460	G
1	1	461	A
1	1	462	U
1	1	465	G
1	1	466	U

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Mol	Chain	Res	Type
1	1	479	A
1	1	480	G
1	1	482	C
1	1	484	A
1	1	488	A
1	1	489	C
1	1	493	G
1	1	494	A
1	1	495	A
1	1	497	C
1	1	499	G
1	1	500	U
1	1	501	G
1	1	502	G
1	1	505	G
1	1	506	G
1	1	508	C
1	1	513	U
1	1	514	C
1	1	524	G
1	1	532	A
1	1	540	A
1	1	547	G
1	1	548	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	593	A
1	1	602	A
1	1	603	C
1	1	613	A
1	1	616	A
1	1	618	U
1	1	619	G
1	1	626	C
1	1	627	G
1	1	628	U
1	1	636	A
1	1	640	U

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Mol	Chain	Res	Type
1	1	643	C
1	1	645	U
1	1	647	A
1	1	649	G
1	1	661	C
1	1	662	C
1	1	669	G
1	1	670	A
1	1	671	A
1	1	675	C
1	1	678	A
1	1	685	A
1	1	691	G
1	1	702	A
1	1	706	U
1	1	714	A
1	1	715	U
1	1	716	G
1	1	732	A
1	1	750	U
1	1	817	G
1	1	831	G
1	1	833	A
1	1	840	A
1	1	962	U
1	1	964	U
1	1	966	G
1	1	967	U
1	1	969	G
1	1	976	C
1	1	986	U
1	1	987	U
1	1	989	C
1	1	990	C
1	1	997	A
1	1	998	U
1	1	1006	A
1	1	1008	U
1	1	1009	C
1	1	1011	G
1	1	1012	A
1	1	1013	U

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Mol	Chain	Res	Type
1	1	1014	C
1	1	1016	G
1	1	1023	G
1	1	1135	G
1	1	1138	U
1	1	1142	U
1	1	1143	A
1	1	1147	G
1	1	1151	A
1	1	1158	G
1	1	1159	U
1	1	1160	A
1	1	1161	A
1	1	1163	C
1	1	1170	G
1	1	1175	U
1	1	1176	G
1	1	1184	A
1	1	1185	A
1	1	1191	C
1	1	1203	G
1	1	1211	A
1	1	1212	U
1	1	1222	U
1	1	1223	C
1	1	1224	A
1	1	1225	G
1	1	1227	C
1	1	1233	A
1	1	1234	A
1	1	1235	A
1	1	1238	G
1	1	1239	U
1	1	1240	G
1	1	1320	G
1	1	1322	A
1	1	1347	U
1	1	1348	A
1	1	1356	U
1	1	1361	A
1	1	1363	A
1	1	1379	U

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Mol	Chain	Res	Type
1	1	1380	A
1	1	1381	G
1	1	1382	C
1	1	1386	G
1	1	1387	A
1	1	1388	G
1	1	1389	A
1	1	1390	A
1	1	1420	U
1	1	1425	C
1	1	1433	U
1	1	1452	A
1	1	1453	A
1	1	1465	G
1	1	1468	G
1	1	1471	C
1	1	1482	U
1	1	1484	G
1	1	2439	U
1	1	2440	A
1	1	2441	G
1	1	2451	A
1	1	2456	G
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	2464	G
1	1	2465	G
1	1	3096	G
1	1	3098	C
1	1	3099	G
1	1	3100	C
1	1	3108	A
1	1	3109	U
1	1	3110	U
1	1	3112	A
1	1	3113	A
1	1	3115	U
1	1	3116	U

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Mol	Chain	Res	Type
1	1	3117	A
1	1	3118	G
1	1	3122	G
1	1	3126	G
1	1	3135	G
1	1	3142	A
1	1	3143	U
1	1	3144	C
1	1	3148	G
1	1	3151	A
1	1	3152	U
1	1	3154	U
1	1	3183	A
1	1	3188	U
1	1	3189	C
1	1	3190	A
1	1	3195	C
1	1	3196	U
1	1	3197	G
1	1	3211	C
1	1	3212	G
1	1	3216	C
1	1	3218	A
1	1	3226	A
1	1	3227	U
1	1	3237	A
1	1	3238	A
1	1	3239	A
1	1	3240	G
1	1	3270	U
1	1	3271	G
1	1	3272	U
1	1	3273	A
1	1	3275	A
1	1	3276	A
1	1	3279	A
1	1	3281	A
1	1	3282	G
1	1	3299	U
1	1	3304	U
1	1	3307	U
1	1	3310	A

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Mol	Chain	Res	Type
1	1	3315	A
1	1	3316	G
1	1	3317	A
1	1	3318	A
1	1	3319	G
1	1	3320	A
1	1	3322	G
1	1	3324	G
1	1	3327	A
1	1	3328	U
1	1	3329	G
1	1	3330	G
1	1	3332	U
1	1	3335	U
1	1	3337	A
1	1	3338	A
1	1	3343	A
1	1	3344	A
1	1	3345	G
1	1	3346	U
1	1	3348	U
1	1	3351	U
1	1	3353	U
1	1	3355	G
1	1	3358	U
1	1	3359	U
1	1	3360	G
1	1	3366	G
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3375	U
1	1	3388	C
1	1	3391	A
1	1	3394	C
1	1	3395	G
1	1	3401	A
1	1	3402	U
1	1	3404	G
1	1	3405	C
1	1	3406	A
1	1	3407	U

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Mol	Chain	Res	Type
1	1	3409	C
1	1	3413	U
1	1	3417	A
1	1	3418	U
1	1	3421	G
1	1	3426	G
1	1	3427	G
1	1	3431	A
1	1	3484	G
1	1	3490	A
1	1	3491	A
1	1	3496	U
2	2	10	A
2	2	21	A
2	2	31	U
2	2	42	U
2	2	43	C
2	2	56	A
2	2	59	G
2	2	60	A
2	2	61	A
2	2	62	A
2	2	67	A
2	2	71	G
2	2	79	A
2	2	96	A
2	2	98	U
2	2	103	G
2	2	104	A
2	2	112	A
2	2	114	C
2	2	115	G
2	2	116	C
2	2	122	G
2	2	124	G
2	2	144	G
2	2	159	U
6	6	2	C
6	6	3	A
6	6	5	U
6	6	6	C
6	6	8	U

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Mol	Chain	Res	Type
6	6	9	C
6	6	10	U
6	6	11	C
6	6	12	A
6	6	13	C
6	6	21	G
6	6	24	U
6	6	26	U
6	6	27	U
6	6	28	U
6	6	30	U
6	6	32	A
6	6	37	U
6	6	38	U
6	6	40	U
6	6	57	A
6	6	58	A
6	6	59	A
6	6	60	A
6	6	61	U
6	6	62	U
6	6	64	G
6	6	66	U
6	6	67	U
6	6	68	U
6	6	69	U
6	6	70	U
6	6	71	U
6	6	72	U
6	6	73	U
6	6	74	U

All (26) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	170	G
1	1	447	C
1	1	449	U
1	1	461	A
1	1	487	C
1	1	488	A
1	1	493	G

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Mol	Chain	Res	Type
1	1	496	C
1	1	500	U
1	1	505	G
1	1	539	A
1	1	669	G
1	1	832	G
1	1	996	G
1	1	1159	U
1	1	1380	A
1	1	1389	A
1	1	3189	C
1	1	3217	U
1	1	3318	A
1	1	3329	G
1	1	3337	A
1	1	3393	U
6	6	1	A
6	6	71	U
6	6	72	U

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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.

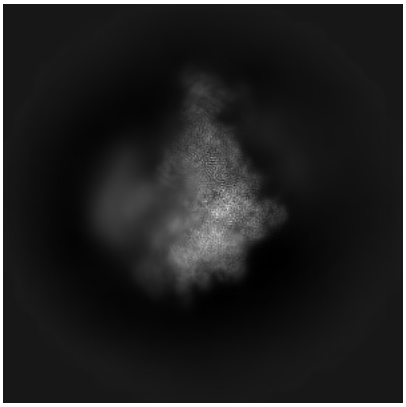
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24420. These allow visual inspection of the internal detail of the map and identification of artifacts.

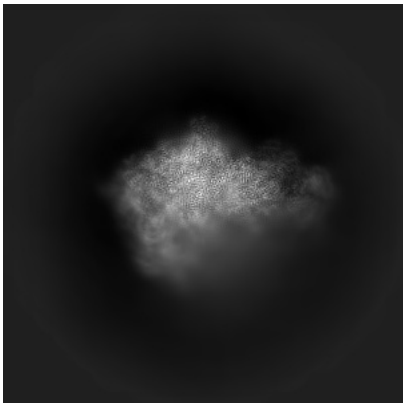
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

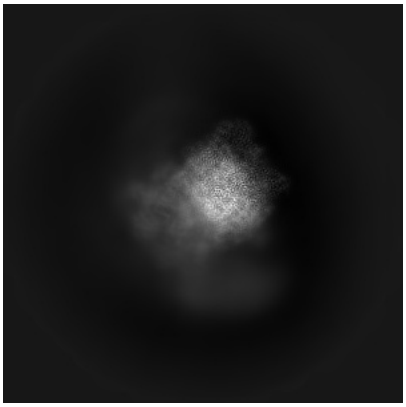
6.1.1 Primary map



X



Y

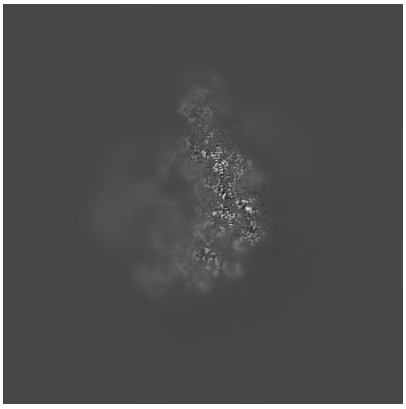


Z

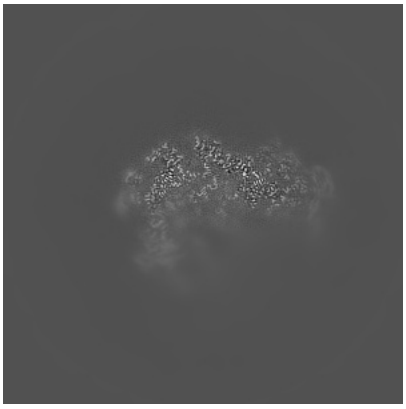
The images above show the map projected in three orthogonal directions.

6.2 Central slices

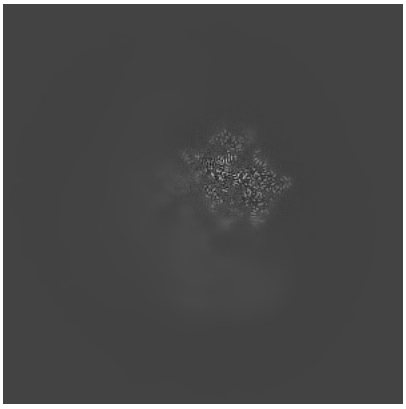
6.2.1 Primary map



X Index: 256



Y Index: 256

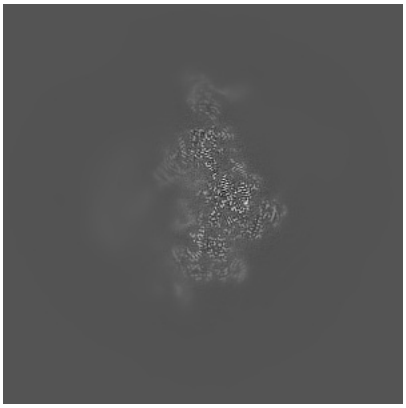


Z Index: 256

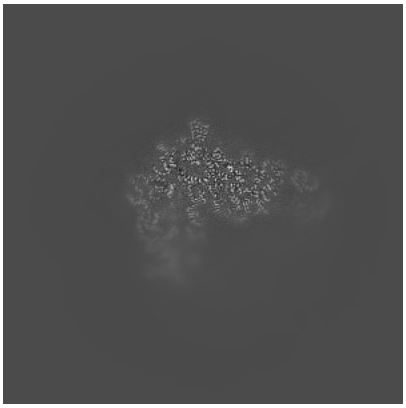
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

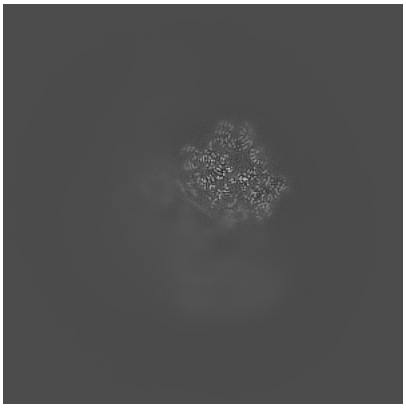
6.3.1 Primary map



X Index: 282



Y Index: 274

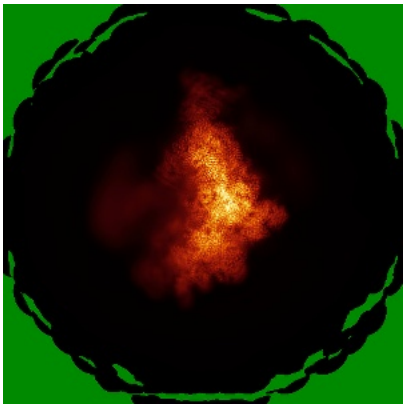


Z Index: 249

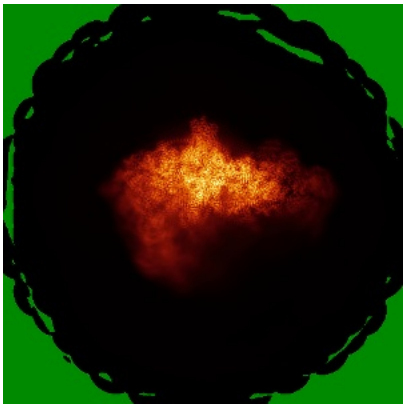
The images above show the largest variance slices of the map in three orthogonal directions.

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

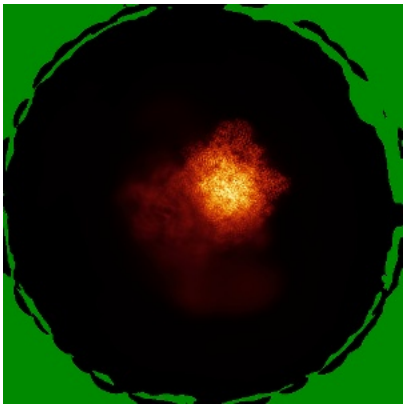
6.4.1 Primary map



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.

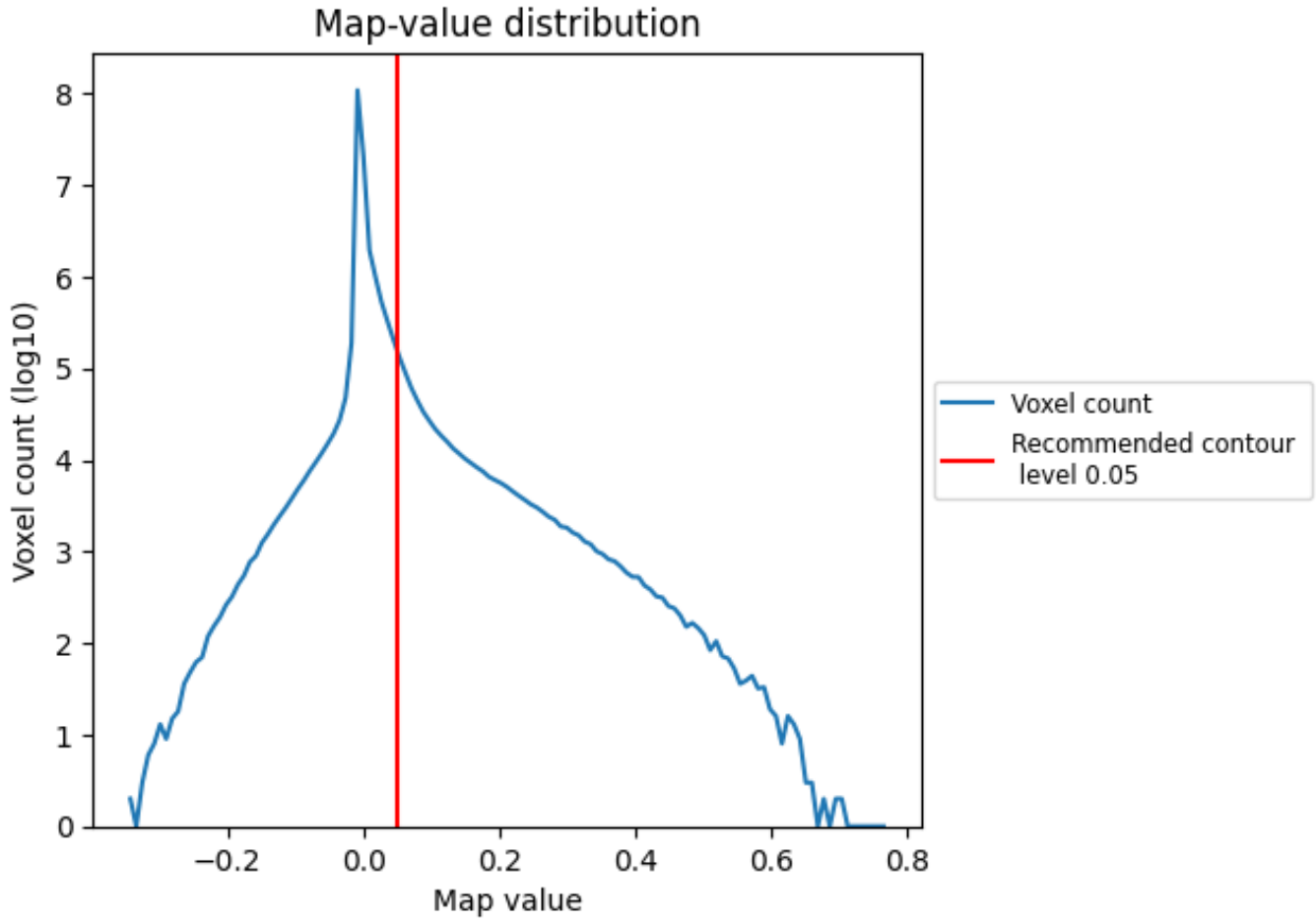
6.6 Mask visualisation (i)

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

7 Map analysis

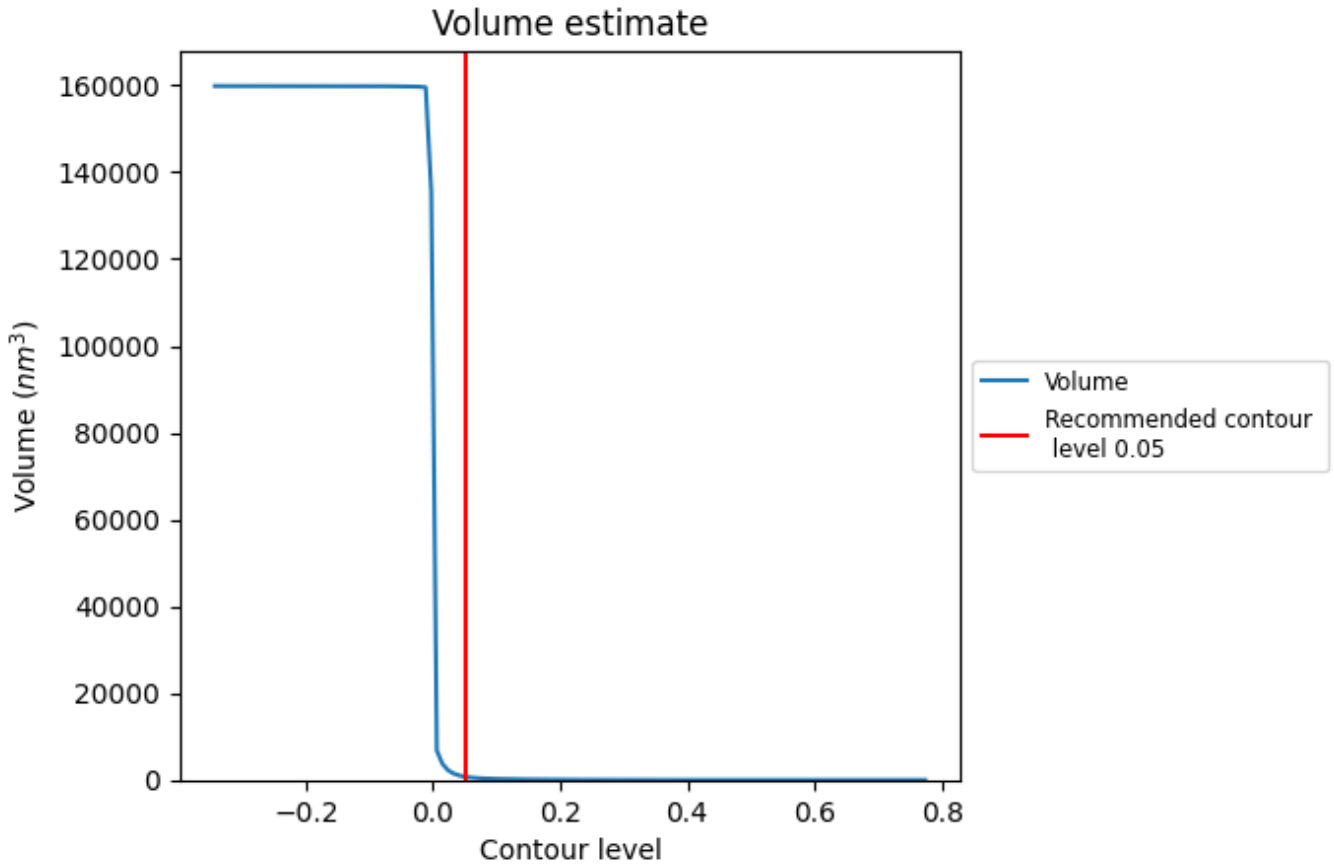
This section contains the results of statistical analysis of the map.

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.

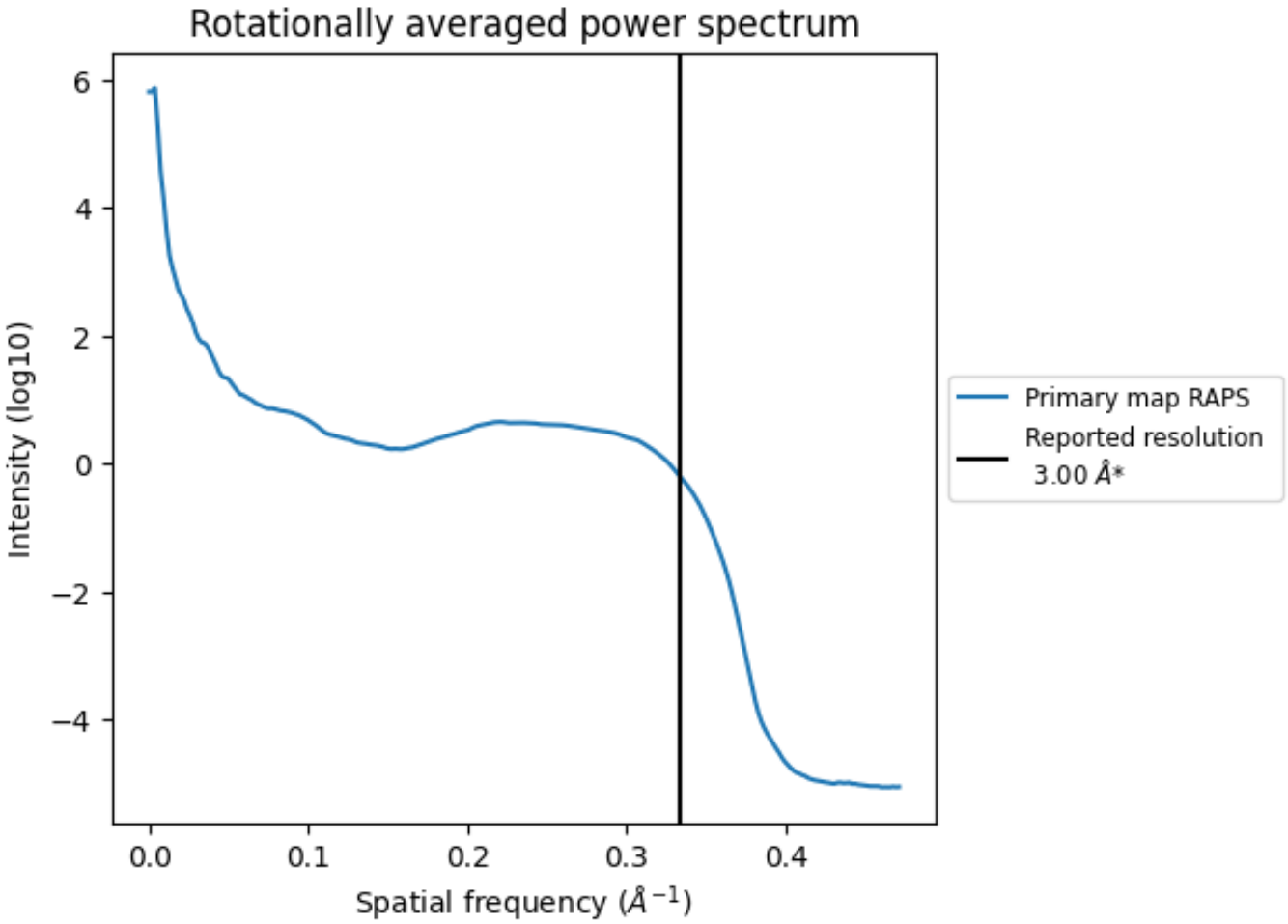
7.2 Volume estimate



The volume at the recommended contour level is 754 nm^3; this corresponds to an approximate mass of 681 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 0.333 Å^{-1}

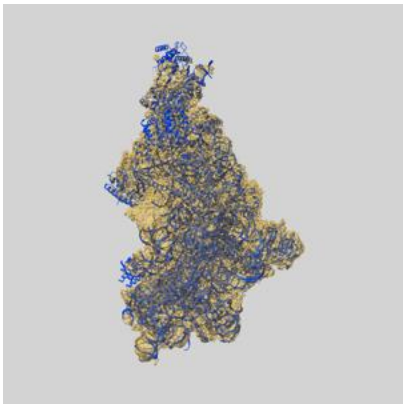
8 Fourier-Shell correlation

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

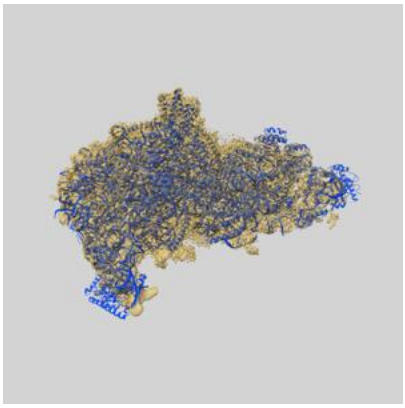
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-24420 and PDB model 8EUY. Per-residue inclusion information can be found in section 3 on page 12.

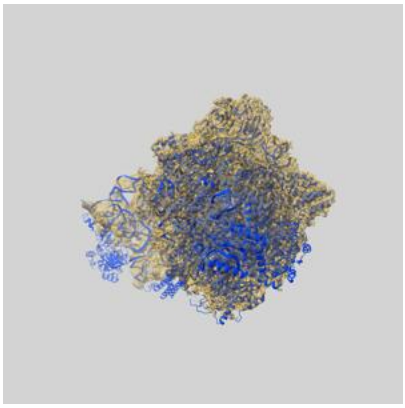
9.1 Map-model overlay



X



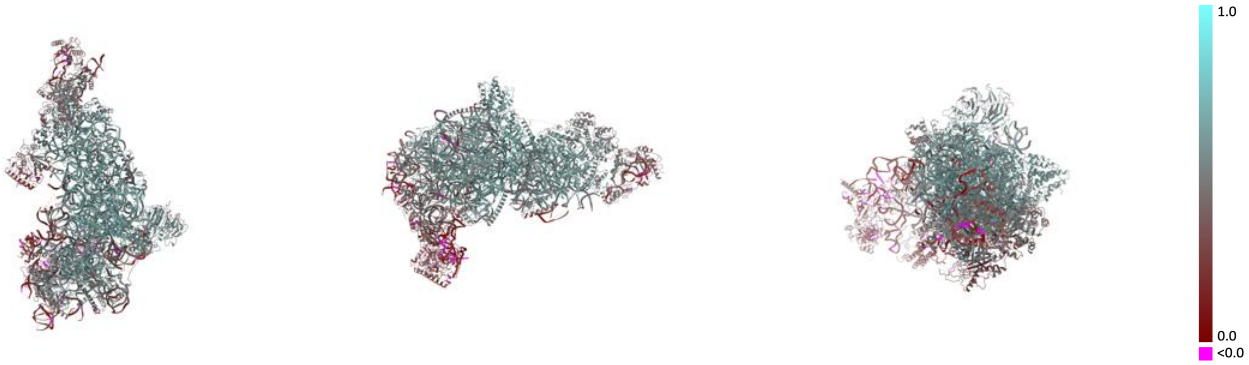
Y



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.

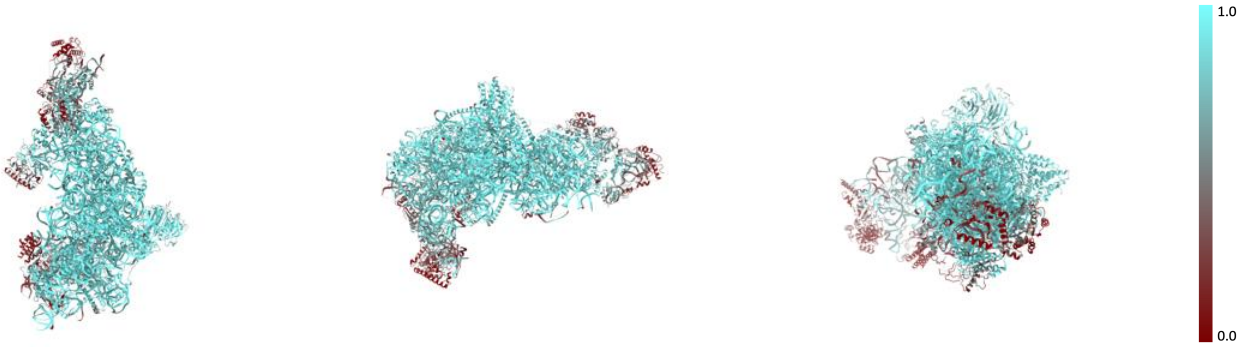
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

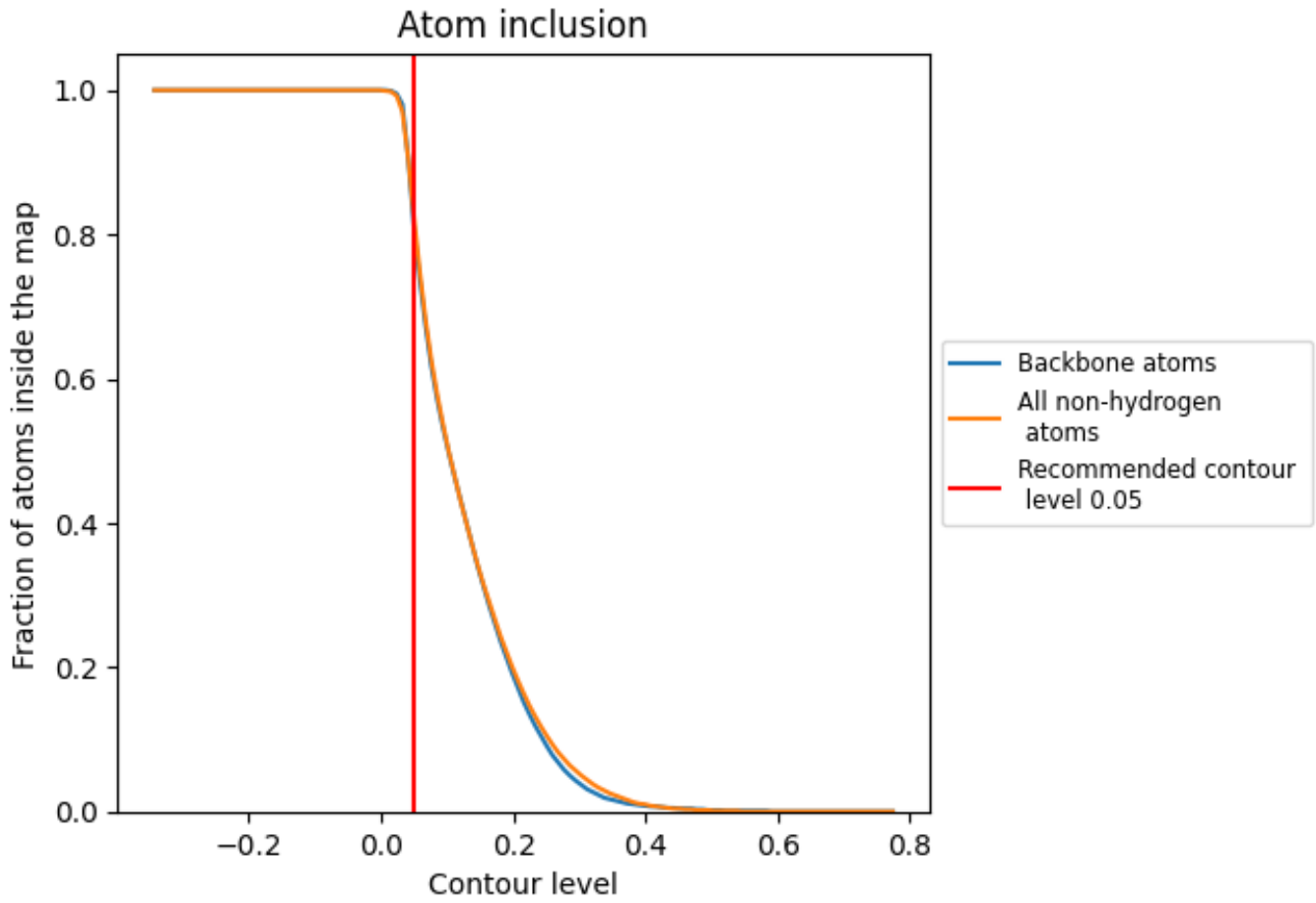
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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

9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 82% 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	0.8220	0.4810
1	0.8910	0.4590
2	0.9300	0.5240
3	0.9480	0.6070
4	0.9350	0.5900
5	0.8960	0.5460
6	0.4690	0.1990
A	0.7330	0.3900
B	0.6590	0.2860
C	0.9790	0.6230
D	0.5450	0.4790
E	0.9140	0.5420
F	0.9440	0.5790
G	0.9390	0.5790
H	0.2280	0.3100
J	0.3740	0.2880
K	0.4270	0.3990
L	0.9760	0.6280
M	0.9220	0.5050
N	0.9870	0.6140
O	0.9010	0.4930
P	0.8760	0.5360
Q	0.9590	0.5920
S	0.8350	0.4790
T	0.3740	0.3860
V	0.0670	0.1860
Y	0.9750	0.6070
b	0.0100	0.2360
e	0.9840	0.6280
f	0.9840	0.6140
h	0.8530	0.5270
i	0.9410	0.5740
j	0.9520	0.5980
m	0.7230	0.4810
o	0.4580	0.3660

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Chain	Atom inclusion	Q-score
r	0.0600	0.2490
t	0.5120	0.4230
u	0.2330	0.2230
v	0.8930	0.5610
x	0.9300	0.5810
y	0.0180	0.2290