Full wwPDB EM Validation Report ⓘ

May 4, 2025 – 12:39 PM EDT

PDB ID	:	8EUP / pdb_00008eup
EMDB ID	:	EMD-24410
Title	:	Ytm1 associated 60S nascent ribosome State 1A
Authors	:	Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on	:	2022-10-19
Resolution	:	3.10 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:

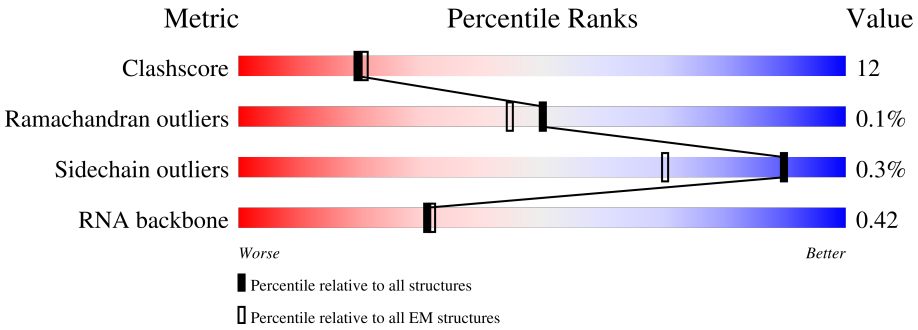
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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	18% 16% 6% 59%
2	2	165	12% 44% 38% 7% 12%
3	3	302	43% 21% 36%
4	4	217	71% 24% 5%
5	5	387	58% 29% 13%
6	6	300	11% 11% 5% 82%
7	A	295	14% 54% 32% 14%

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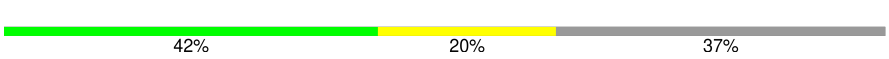
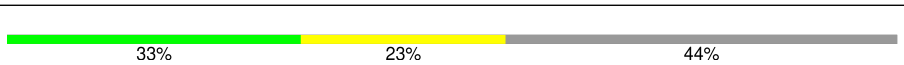
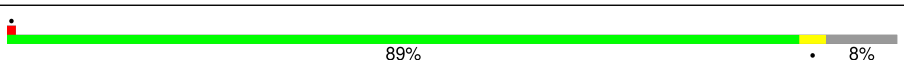
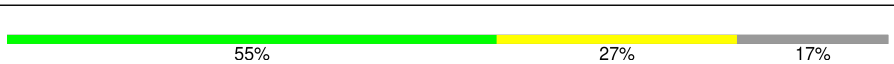
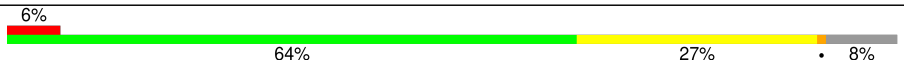
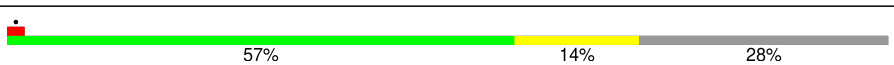
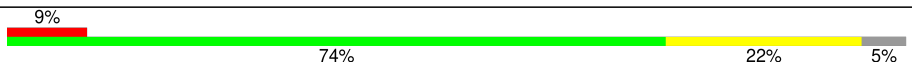
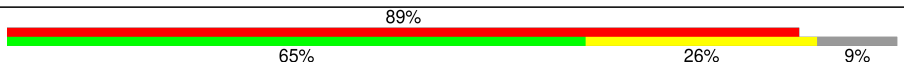
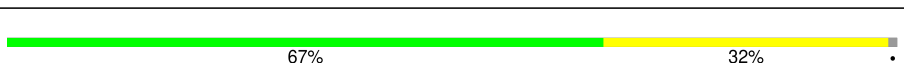
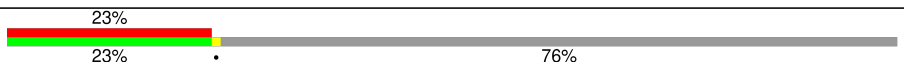
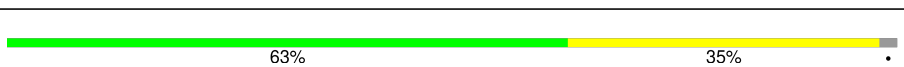
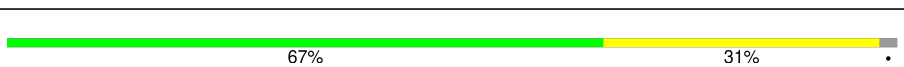
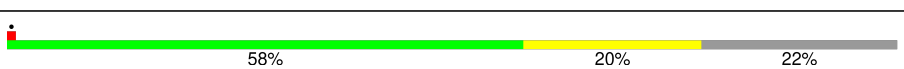
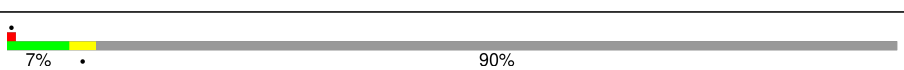
Mol	Chain	Length	Quality of chain
8	B	388	
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	J	333	
16	K	373	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	S	176	
24	V	139	
25	Y	126	
26	b	642	
27	e	127	
28	f	108	
29	h	122	
30	i	99	
31	j	91	
32	m	740	

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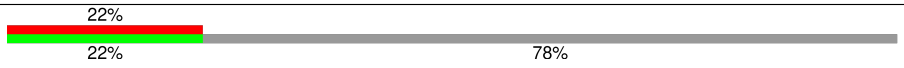
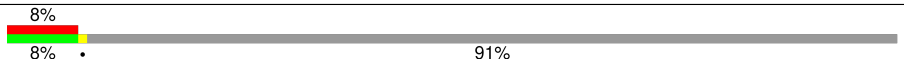
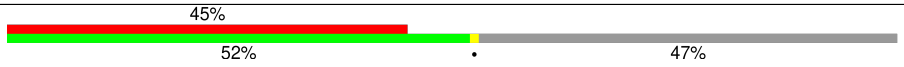
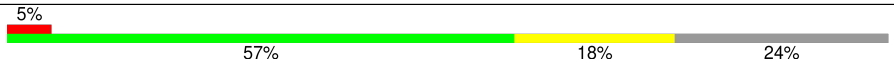
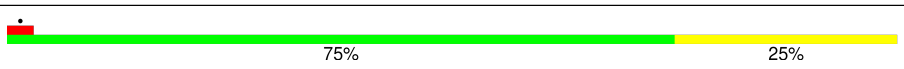
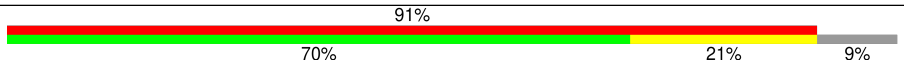
Mol	Chain	Length	Quality of chain
33	o	276	
34	r	260	
35	t	249	
36	u	192	
37	v	209	
38	x	306	
39	y	244	
40	T	160	

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 78722 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 (1422-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1422	30438	13596	5508	9912	1422	0	0

- Molecule 2 is a RNA chain called RNA (146-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	146	3109	1391	555	1017	146	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	194	1613	1020	307	279	7	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	207	1746	1138	298	302	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	338	2669	1705	466	487	11	0	0

- Molecule 6 is a RNA chain called RNA (55-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	6	55	1167	524	204	384	55	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	253	Total	C	N	O	S	0	0
			2049	1299	372	370	8		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
8	B	315	Total	C	N	O	0	0
			1552	922	315	315		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	328	Total	C	N	O	S	0	0
			2568	1629	486	450	3		

- Molecule 10 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	400	Total	C	N	O	S	0	0
			3055	1966	532	548	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	239	Total	C	N	O	S	0	0
			1939	1247	355	334	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	163	Total	C	N	O	S	2	0
			1277	818	224	233	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
14	H	175	Total 862	C 512	N 175	O 175	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
15	J	94	Total 469	C 281	N 94	O 94	0	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
16	K	247	Total 1225	C 731	N 247	O 247	0	0

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
18	M	123	Total 609	C 363	N 123	O 123	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	181	Total 1437	C 925	N 271	O 238	S 3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	130	Total	C	N	O	S	0	0
			1037	663	187	184	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	134	Total	C	N	O	S	0	0
			1041	655	201	184	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
			1408	909	263	231	5		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	126	Total	C	N	O	0	0
			619	366	126	127		

- Molecule 25 is a protein called 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	151	Total	C	N	O	0	0
			749	447	151	151		

- 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	120	Total	C	N	O	0	0
			993	626	193	174		

- 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
			783	487	164	131	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	73	Total	C	N	O	0	0
			595	368	107	120		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
33	o	136	Total	C	N	O	0	0
			673	401	136	136		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
34	r	56	Total	C	N	O	0	0
			278	166	56	56		

- 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
			167	105	32	30		

- 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	158	Total	C	N	O	S	0	0
			1276	804	240	229	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	x	306	Total	C	N	O	S	0	0
			2524	1583	464	468	9		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
39	y	222	Total	C	N	O	0	0
			1092	648	222	222		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
40	T	18	Total	C	N	O	0	0
			125	80	23	22		

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

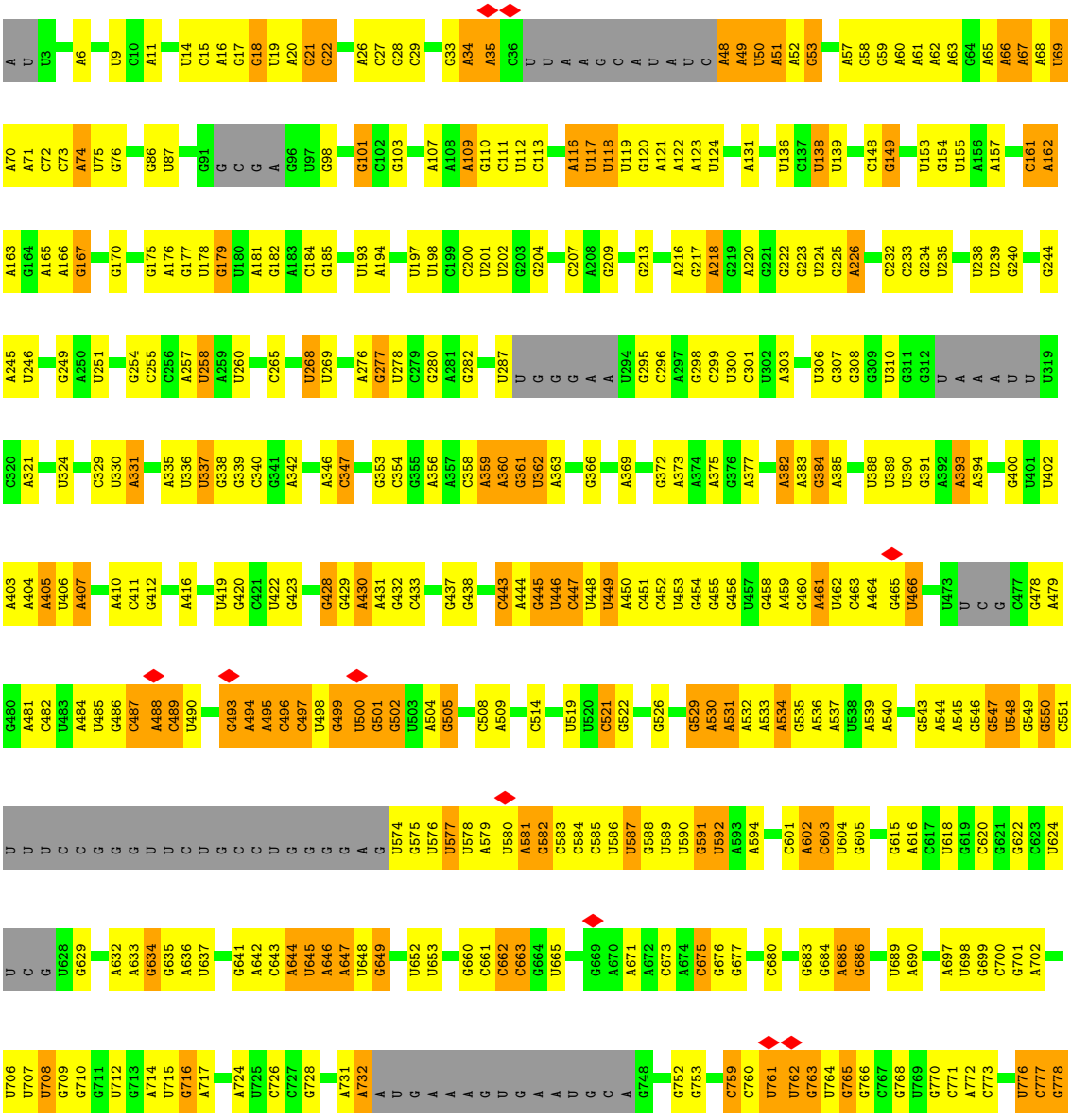
Mol	Chain	Residues	Atoms		AltConf
41	j	1	Total	Zn	0
			1	1	

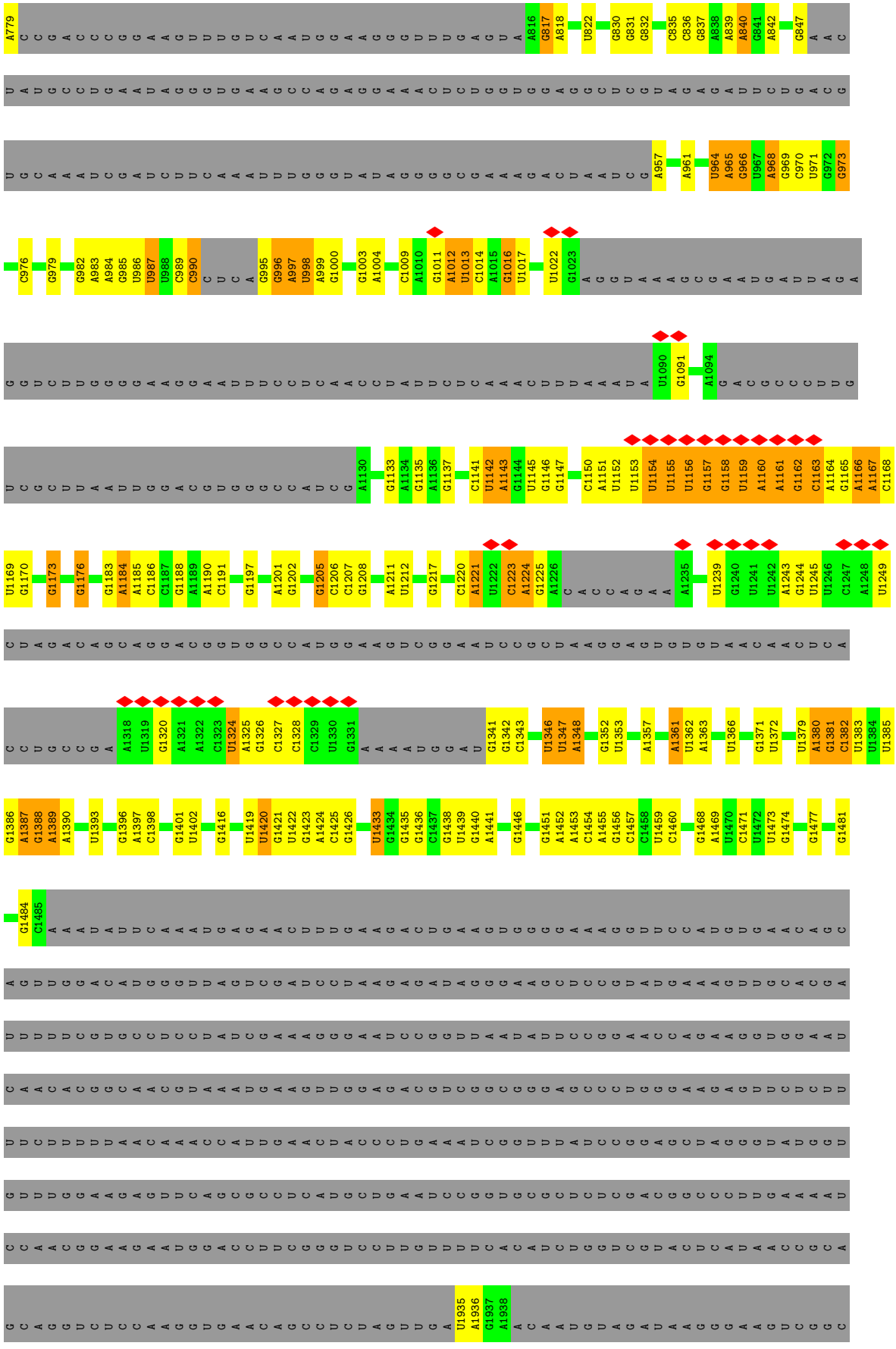
3 Residue-property plots (i)

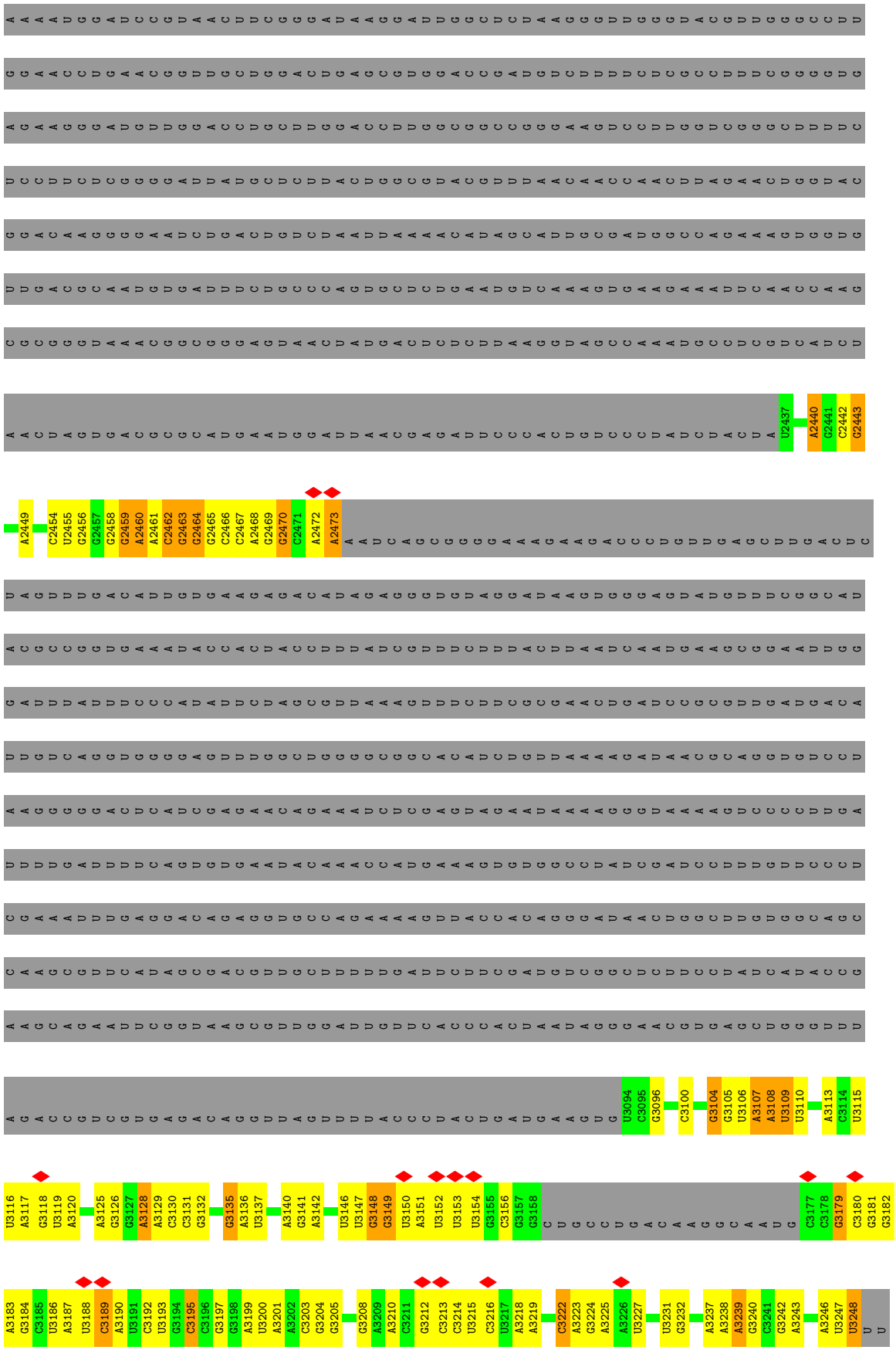
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

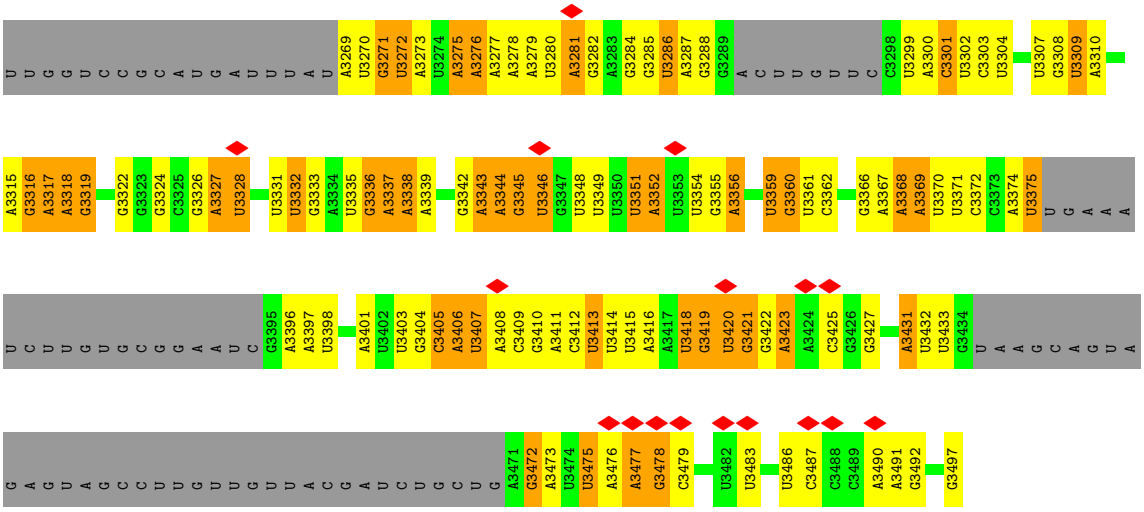
- Molecule 1: RNA (1422-MER)

Chain 1:



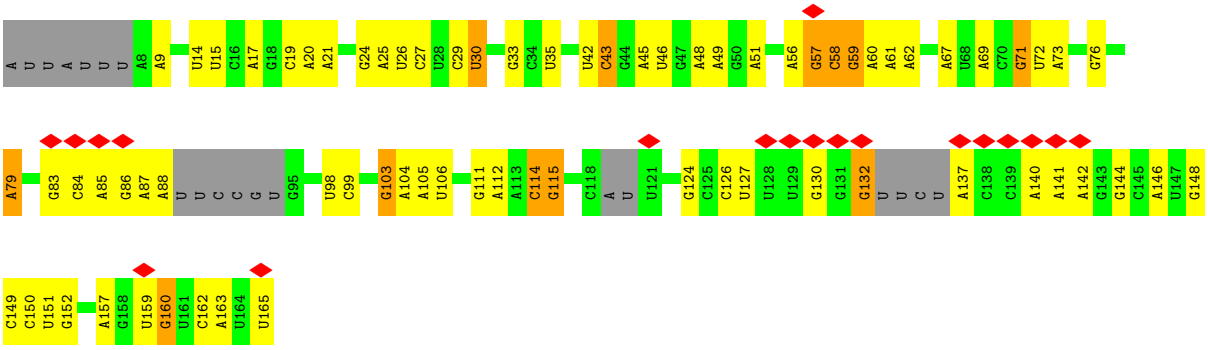






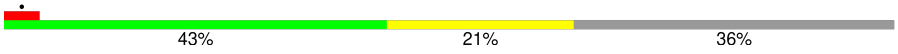
• Molecule 2: RNA (146-MER)

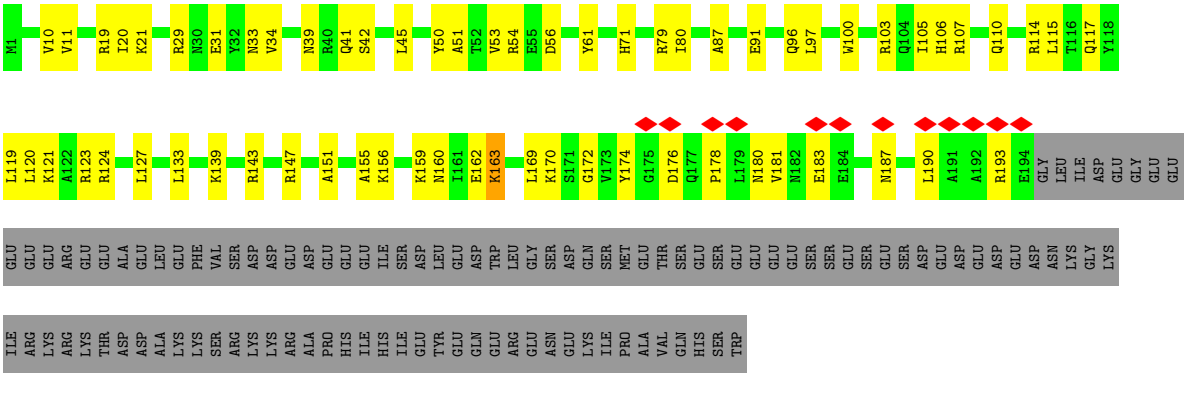
Chain 2:



• Molecule 3: Protein mak16

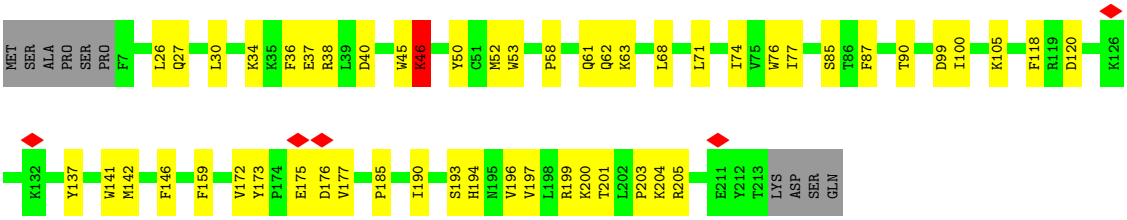
Chain 3:





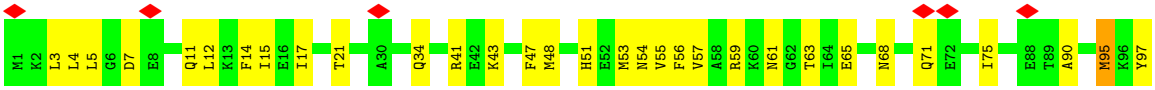
• Molecule 4: Ribosomal RNA-processing protein 1 homolog

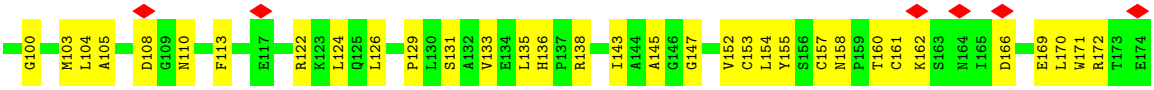
Chain 4:

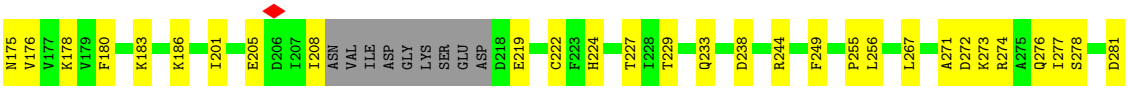


• Molecule 5: Ribosome biogenesis protein nsa1

Chain 5:

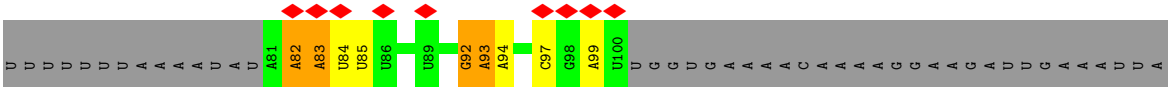


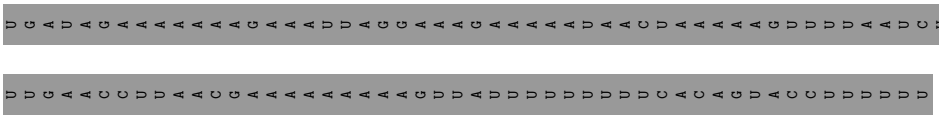




• Molecule 6: RNA (55-MER)

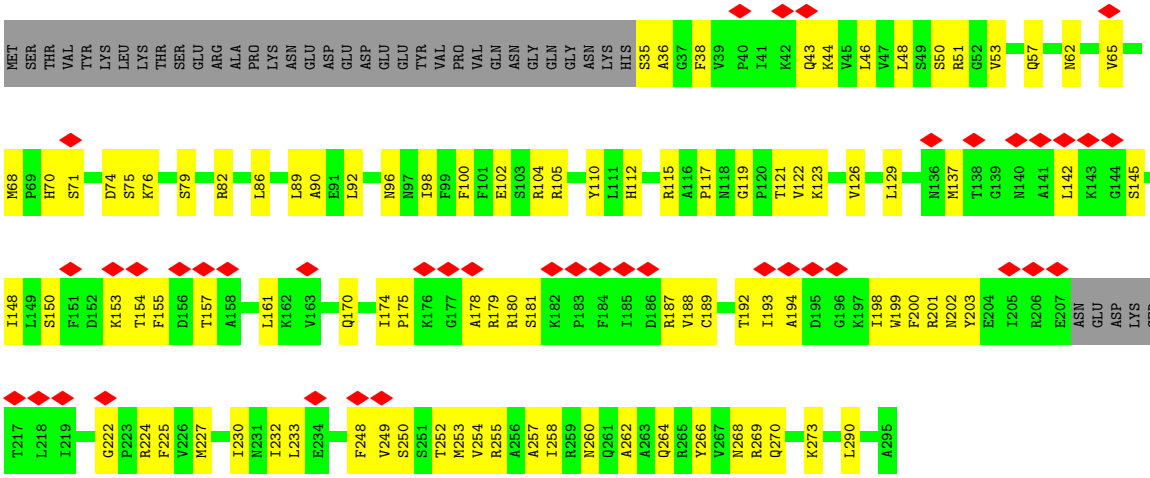
Chain 6:





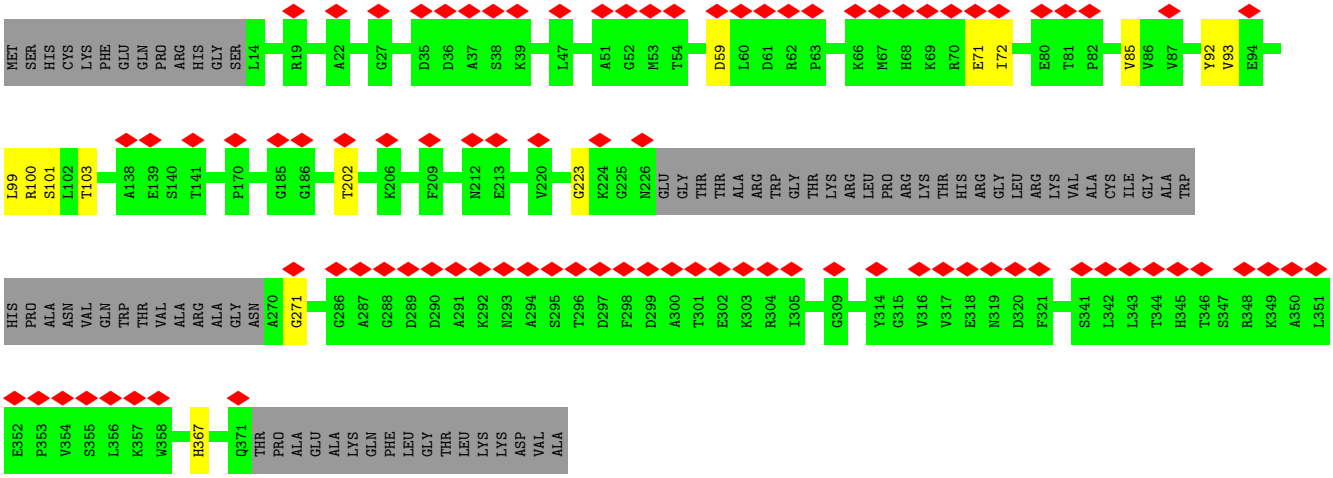
• Molecule 7: Ribosome biogenesis protein brx1

Chain A:



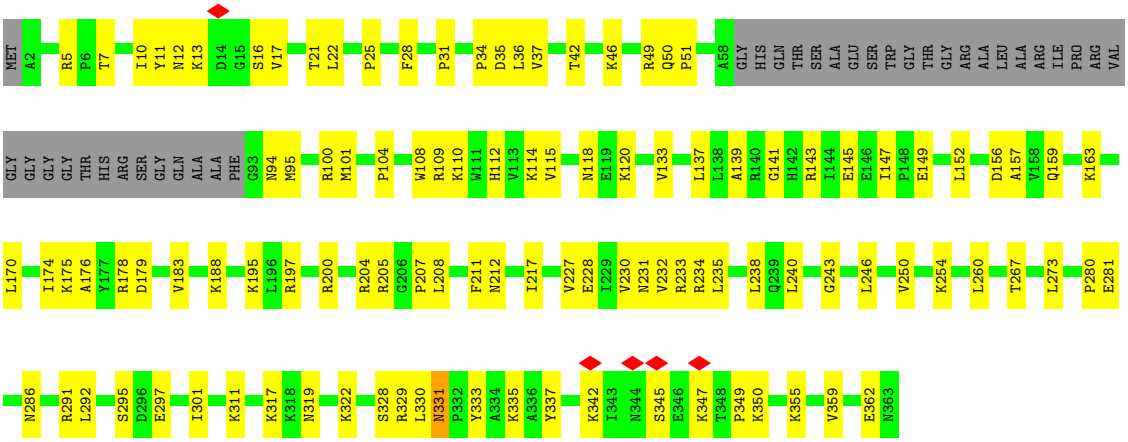
• Molecule 8: 60S ribosomal protein L3-A

Chain B:



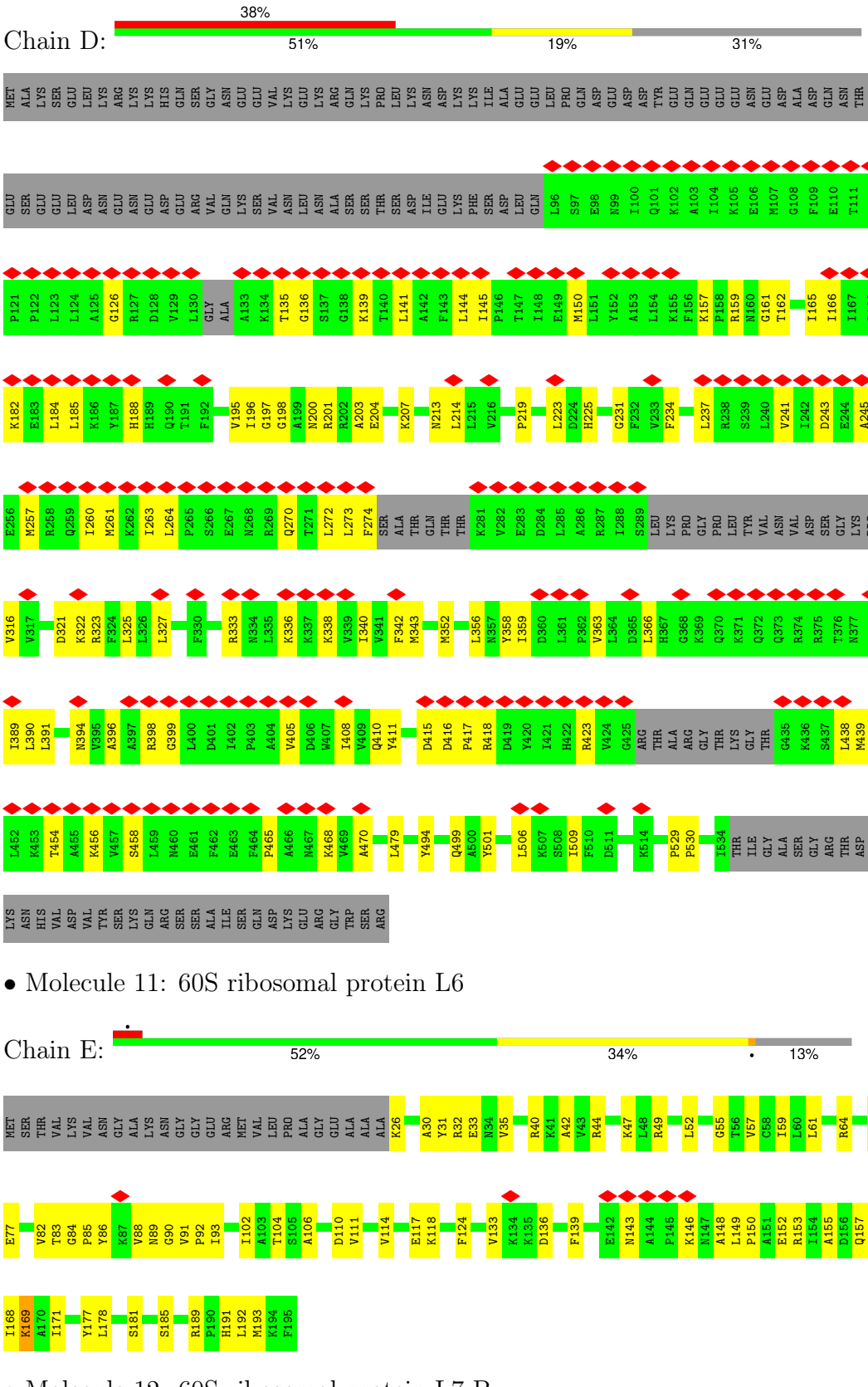
• Molecule 9: 60S ribosomal protein L4-B

Chain C:



• Molecule 10: RNA helicase

Chain D:

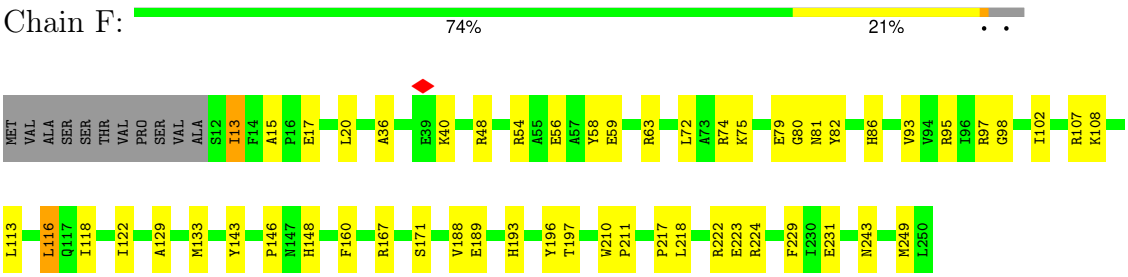


• Molecule 11: 60S ribosomal protein L6

Chain E:

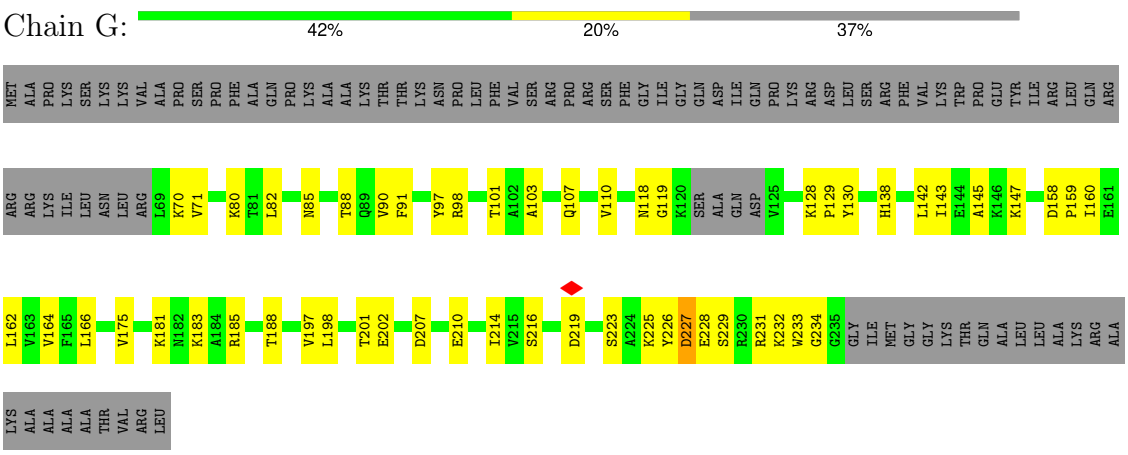
• Molecule 12: 60S ribosomal protein L7-B

Chain F:



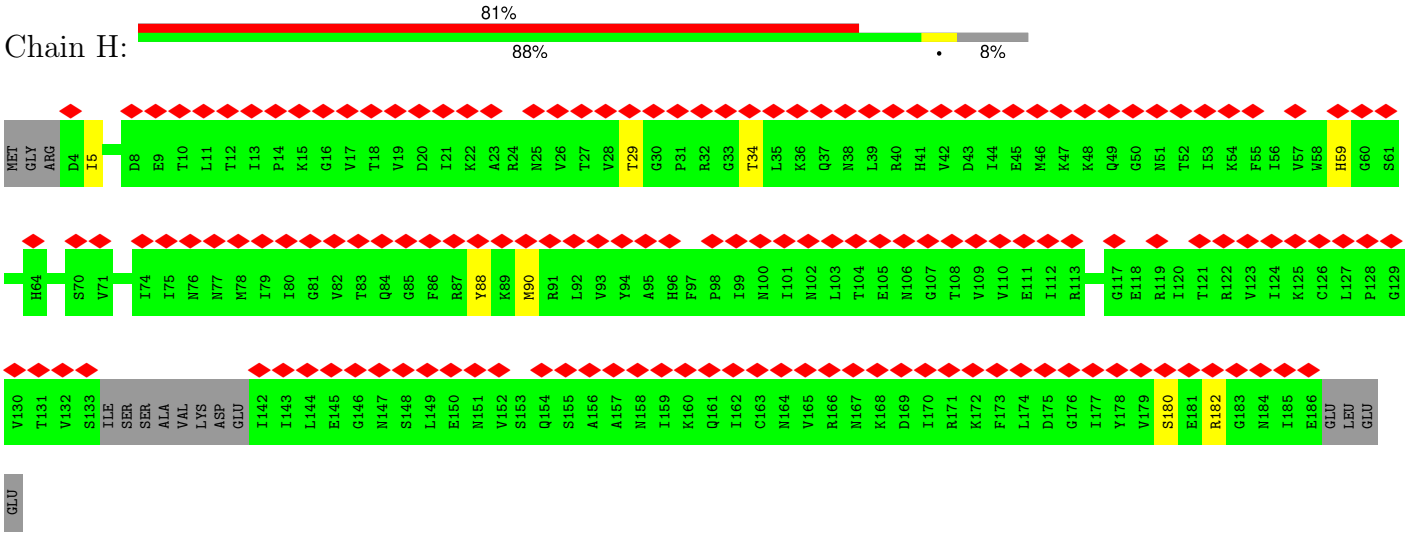
• Molecule 13: 60S ribosomal protein L8

Chain G:



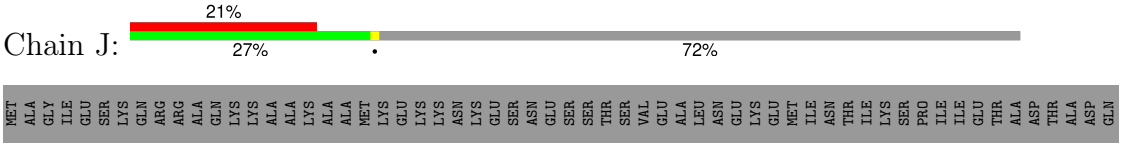
• Molecule 14: 60S ribosomal protein L9-A

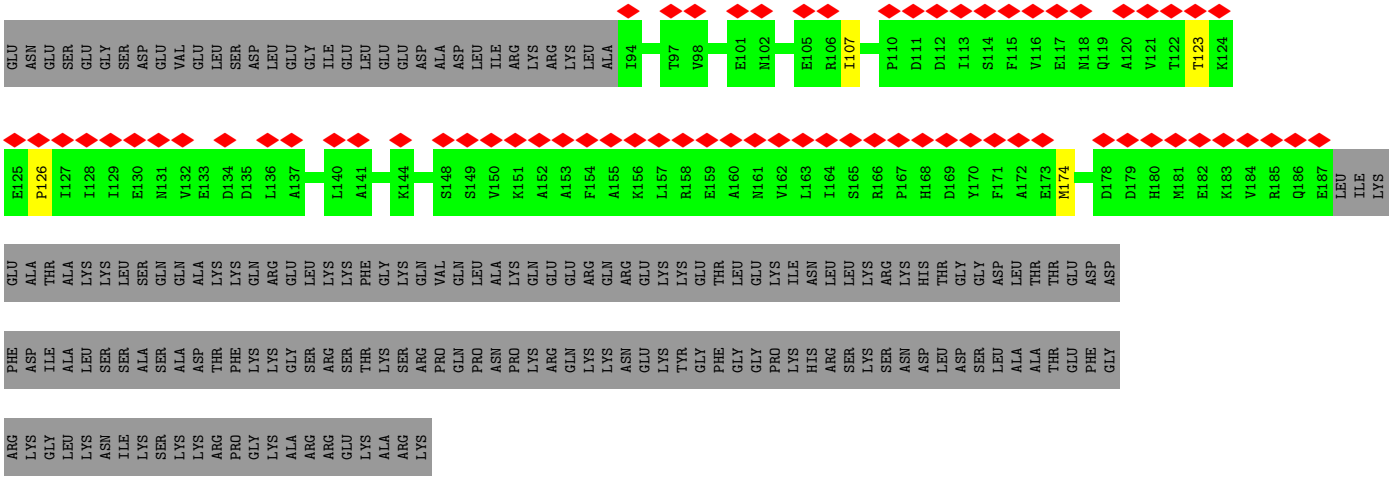
Chain H:



• Molecule 15: Probable rRNA-processing protein ebp2

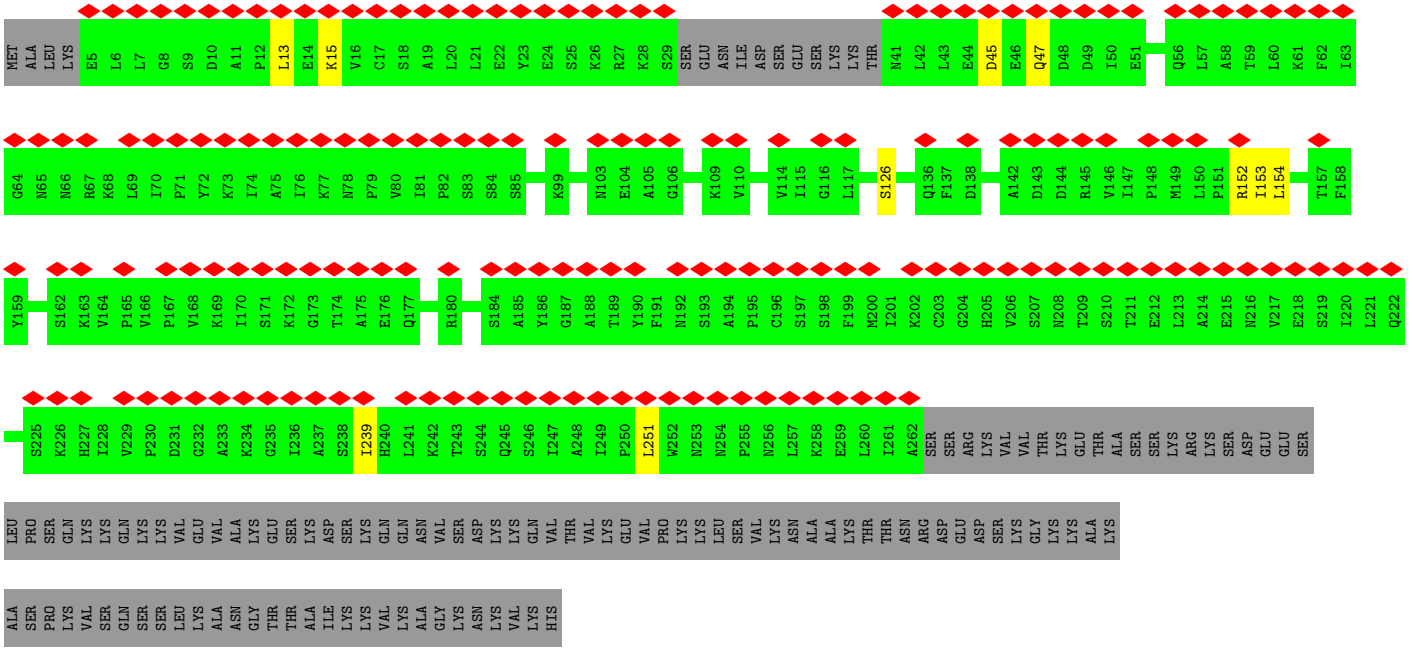
Chain J:





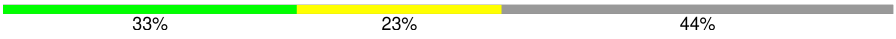
• Molecule 16: Putative ribosome biogenesis protein C8F11.04

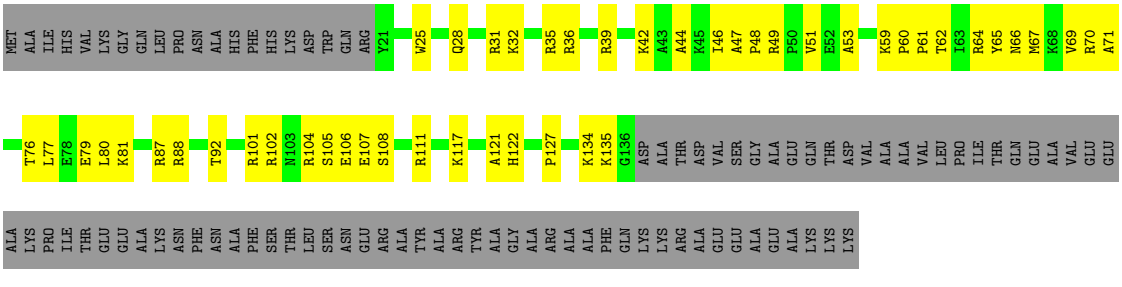
Chain K:



• Molecule 17: 60S ribosomal protein L13

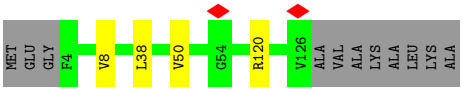
Chain L:





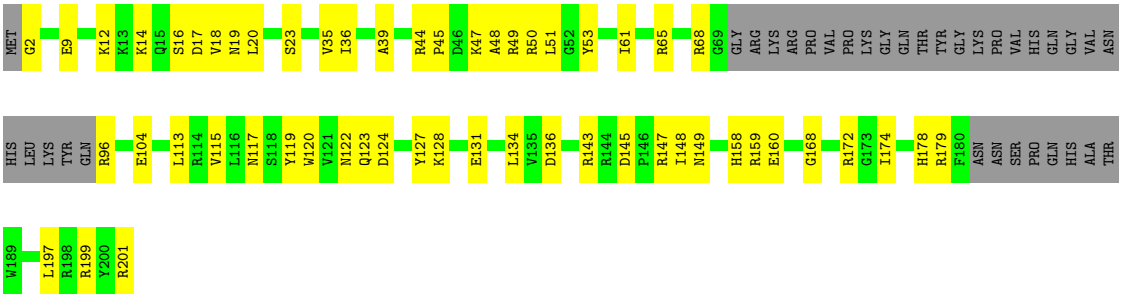
• Molecule 18: 60S ribosomal protein L14

Chain M:



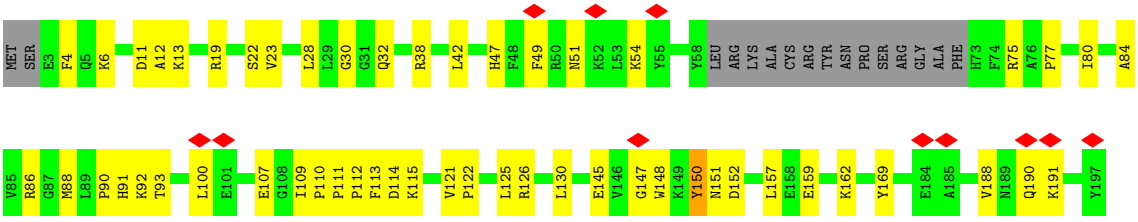
• Molecule 19: 60S ribosomal protein L15-A

Chain N:



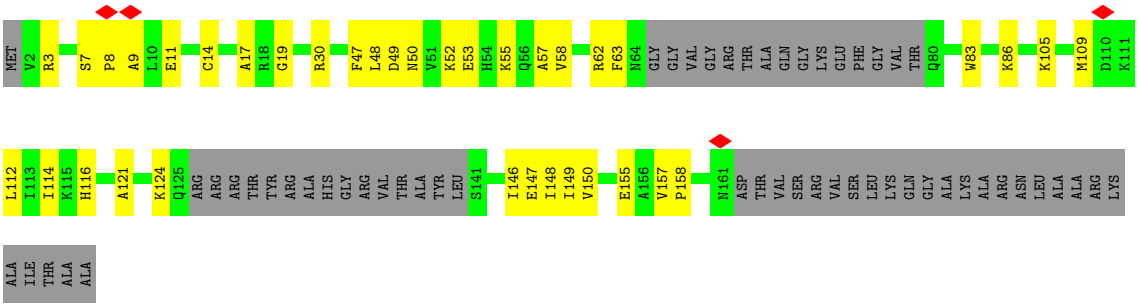
• Molecule 20: 60S ribosomal protein L16-B

Chain O:



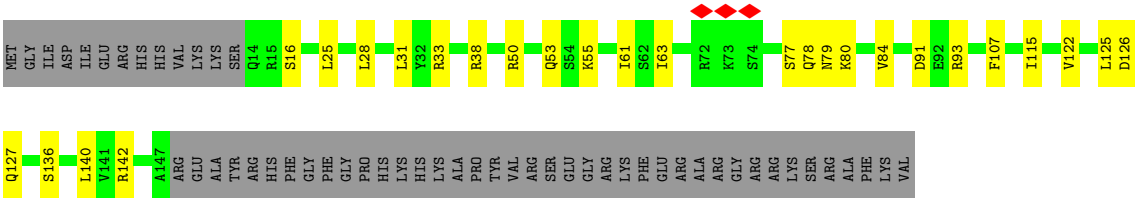
• Molecule 21: 60S ribosomal protein L17-A

Chain P:



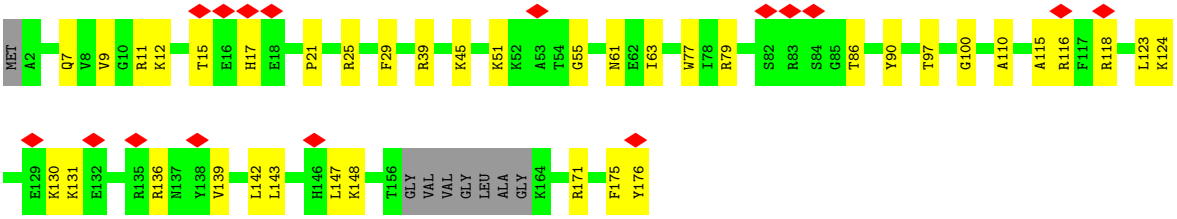
• Molecule 22: 60S ribosomal protein L18-A

Chain Q:



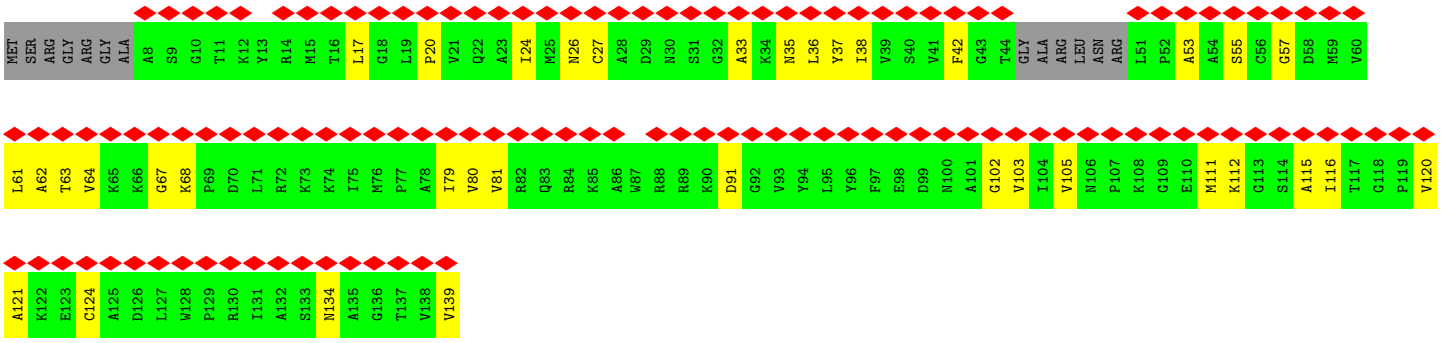
• Molecule 23: 60S ribosomal protein L20-A

Chain S:



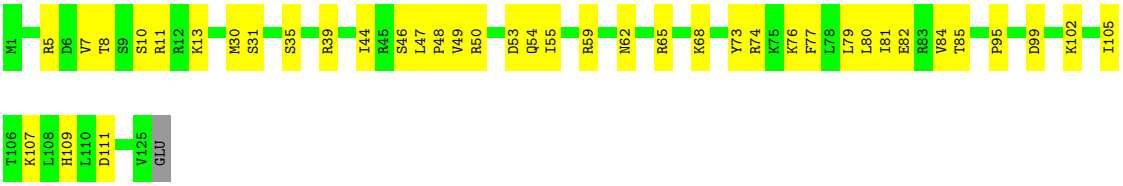
• Molecule 24: 60S ribosomal protein L23-A

Chain V:



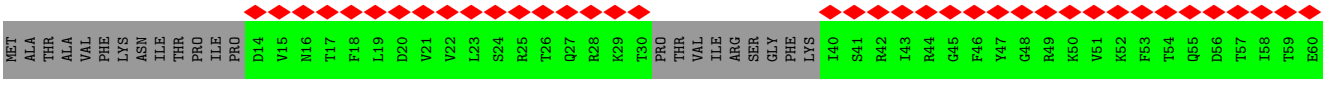
• Molecule 25: Ribosomal protein L26

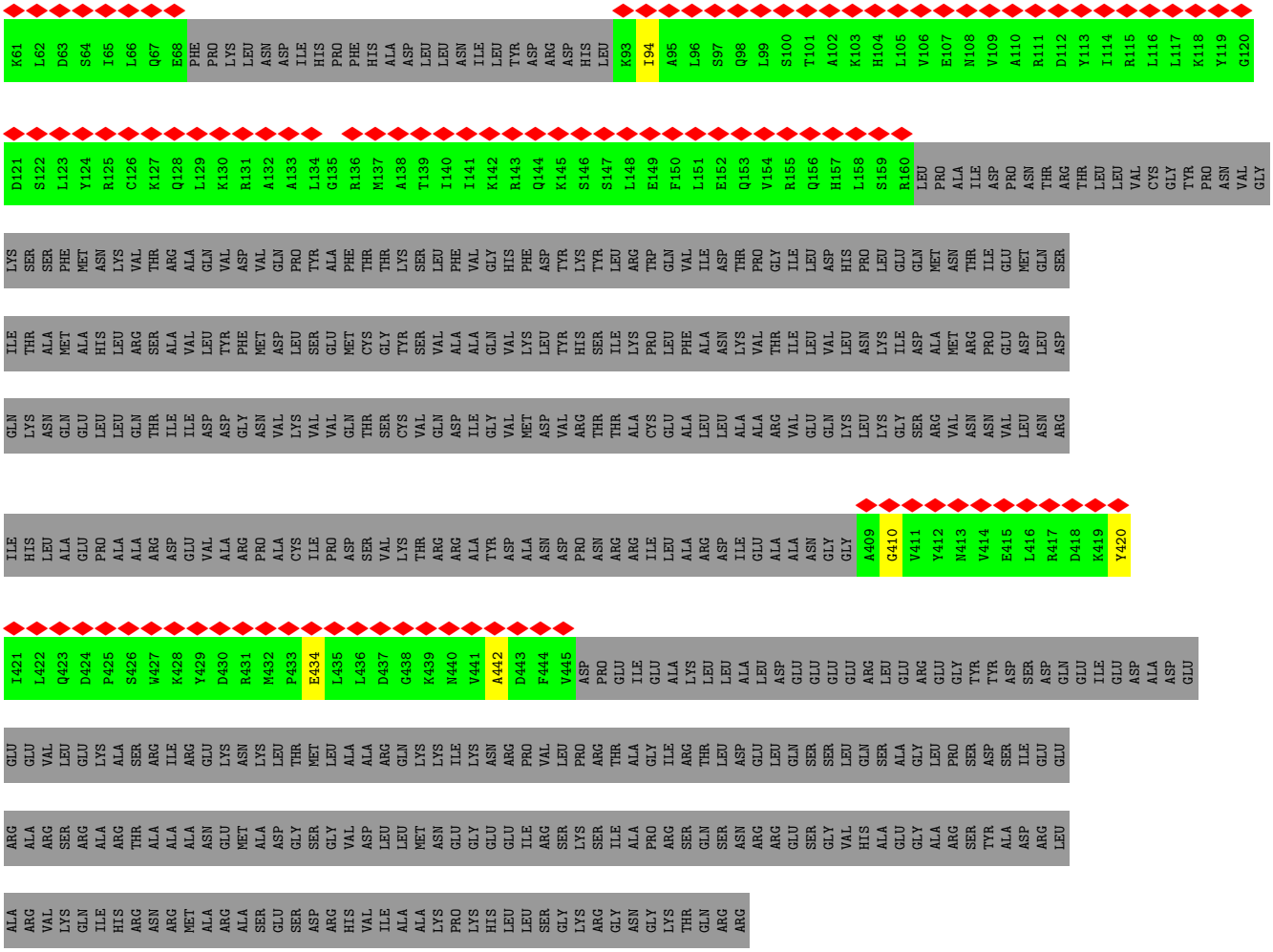
Chain Y:



• Molecule 26: Probable nucleolar GTP-binding protein 1

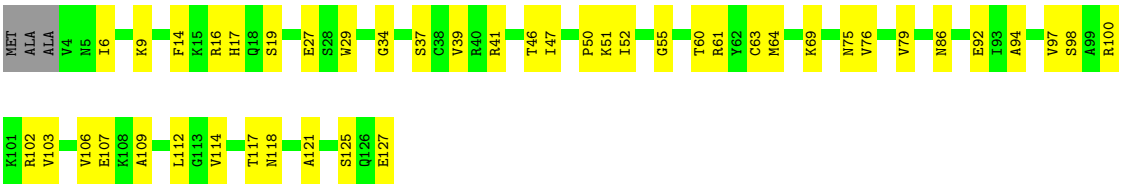
Chain b:





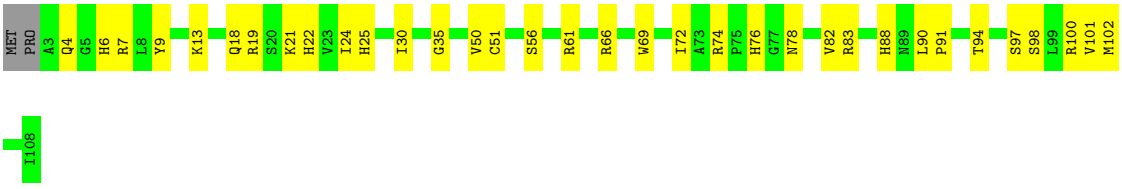
• Molecule 27: 60S ribosomal protein L32-A

Chain e:



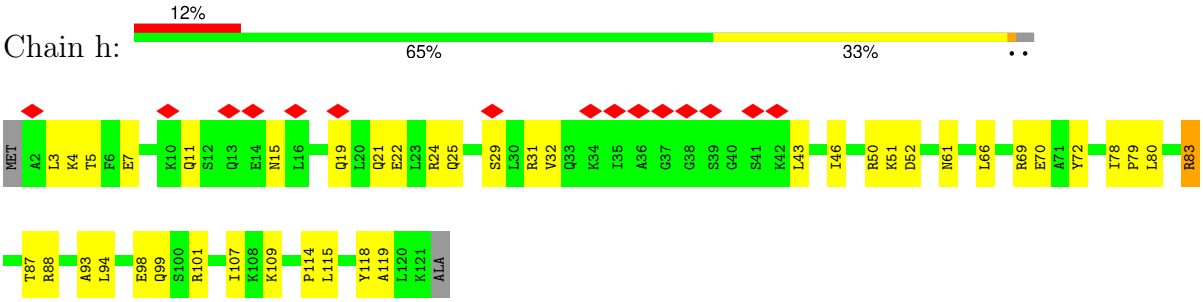
• Molecule 28: 60S ribosomal protein L33-B

Chain f:



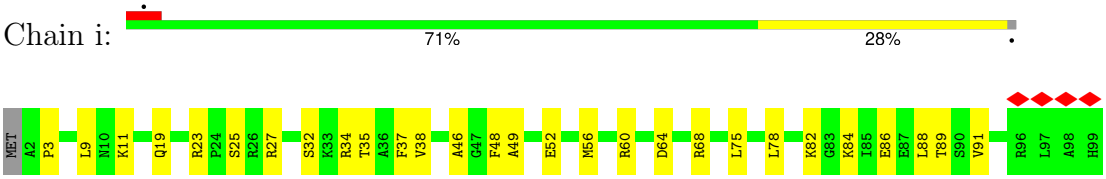
• Molecule 29: 60S ribosomal protein L35

Chain h:



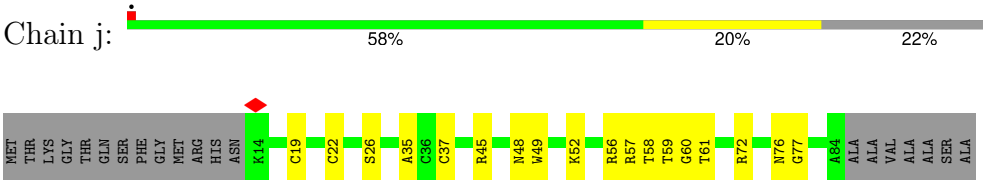
• Molecule 30: 60S ribosomal protein L36-B

Chain i:



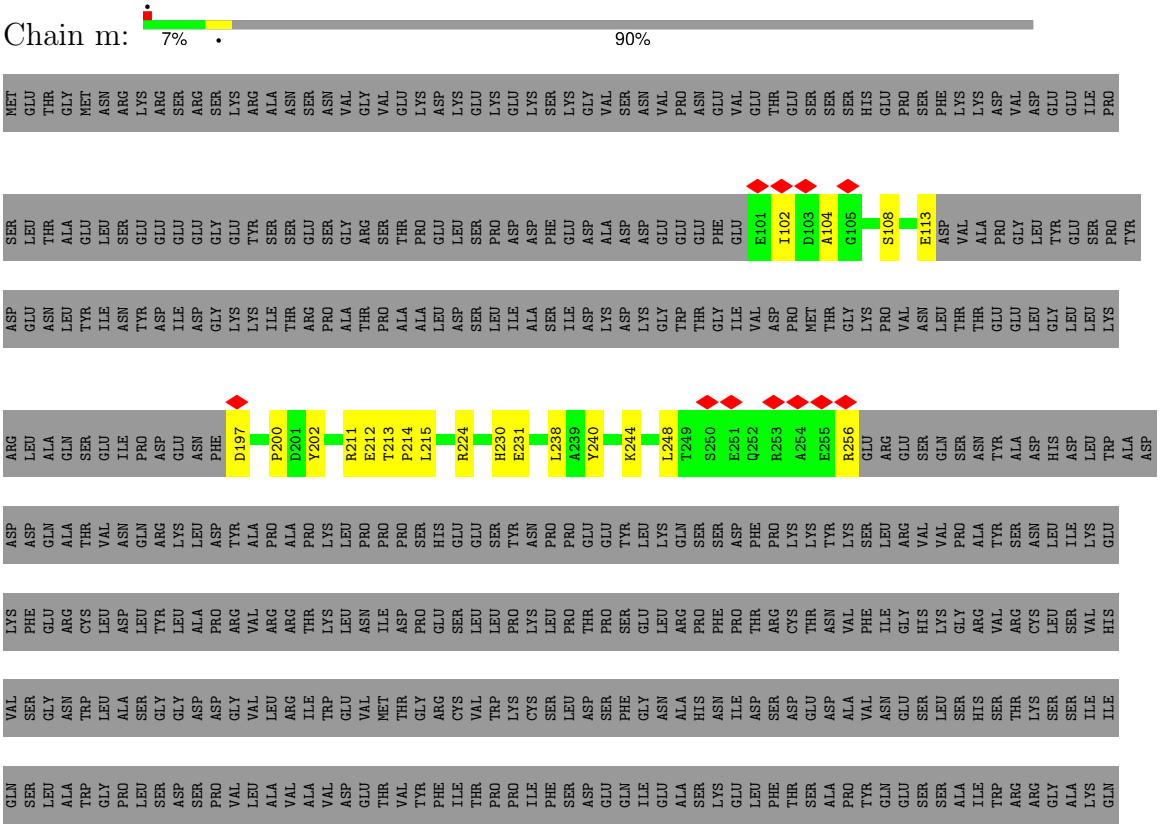
• Molecule 31: 60S ribosomal protein L37-B

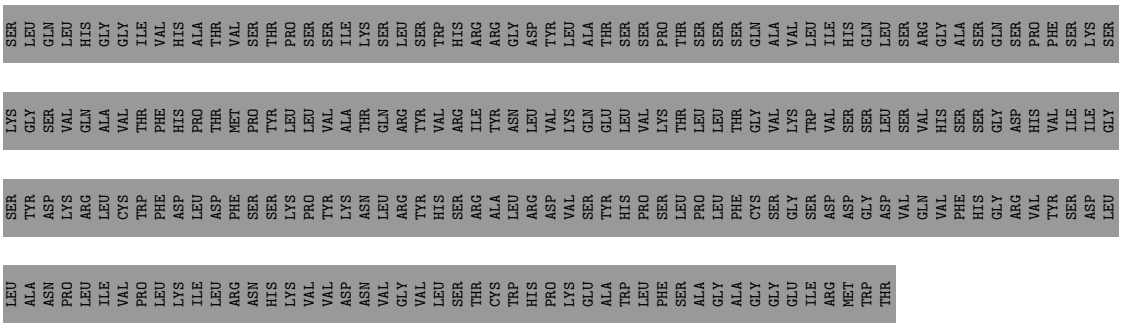
Chain j:



• Molecule 32: Ribosome biogenesis protein erb1

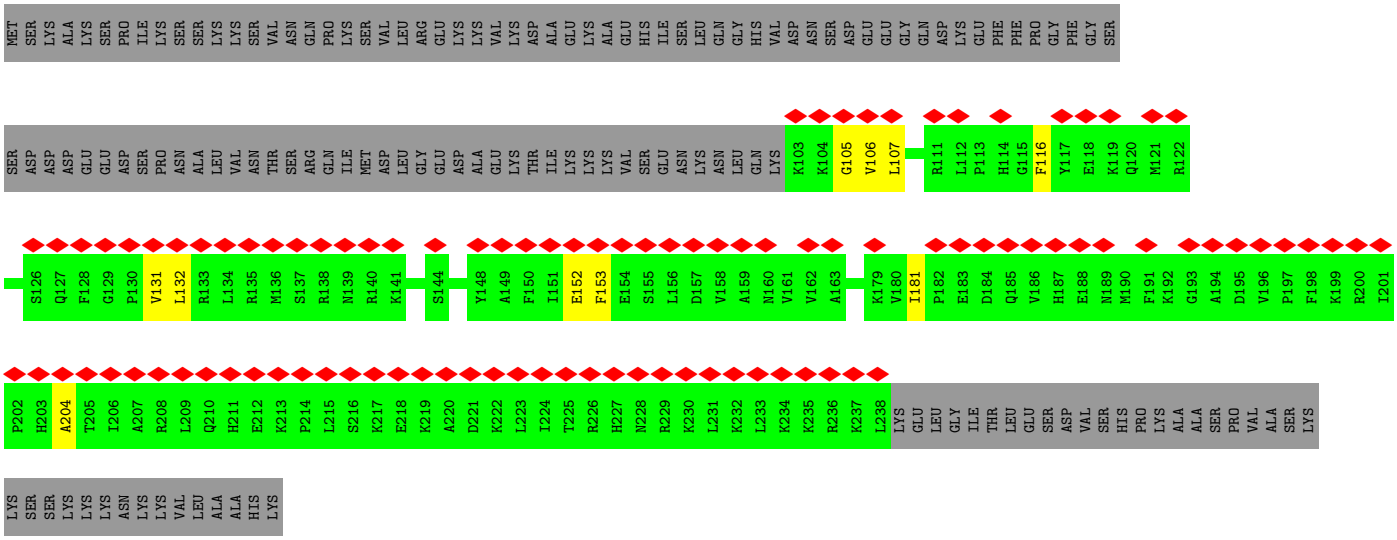
Chain m:





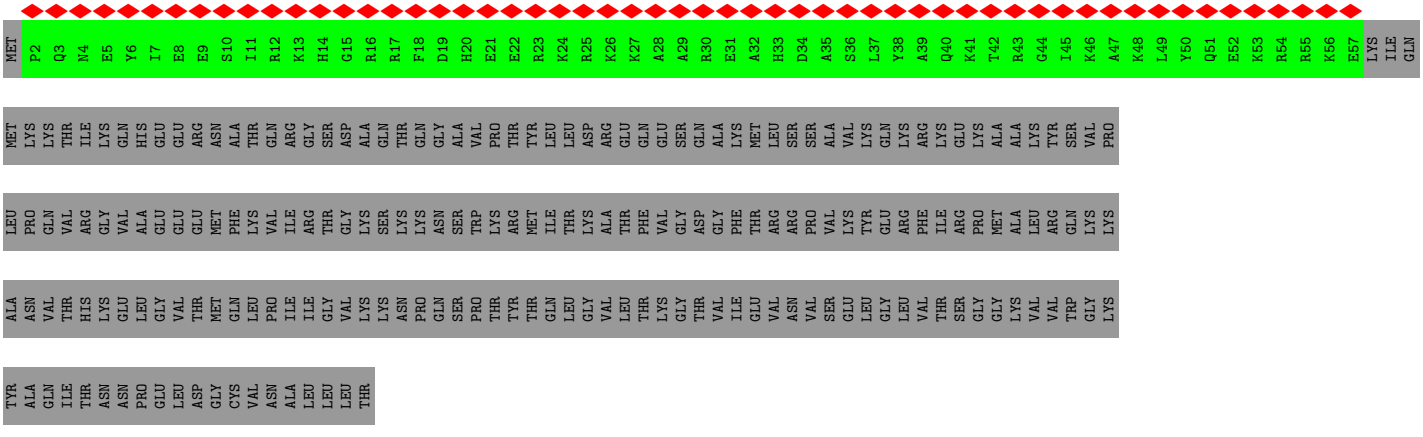
• Molecule 33: Uncharacterized RNA-binding protein C1827.05c

Chain o:



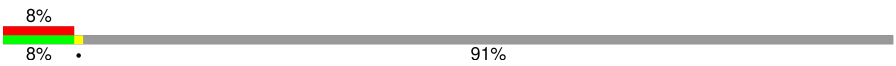
• Molecule 34: Ribosome biogenesis protein nsa2

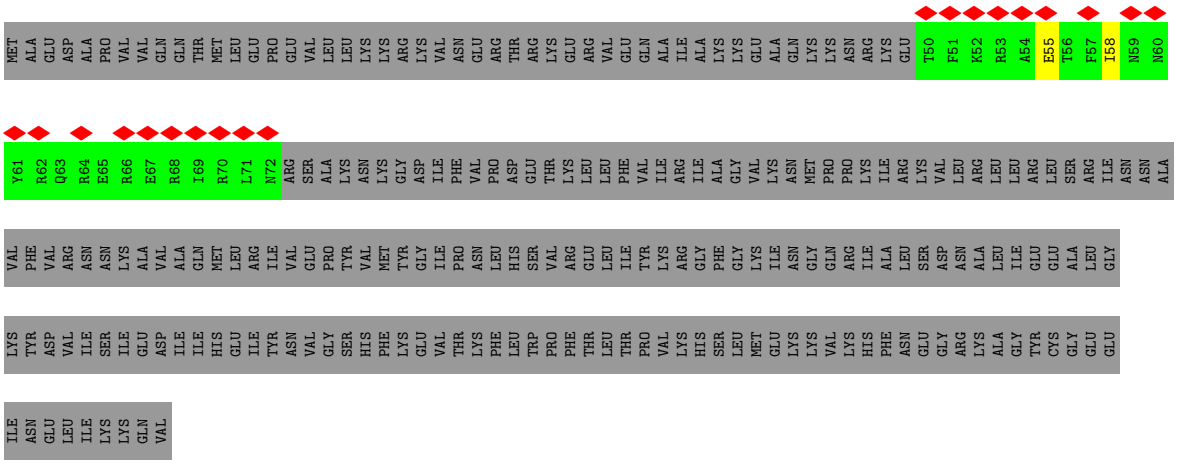
Chain r:



• Molecule 35: 60S ribosomal protein L7-A

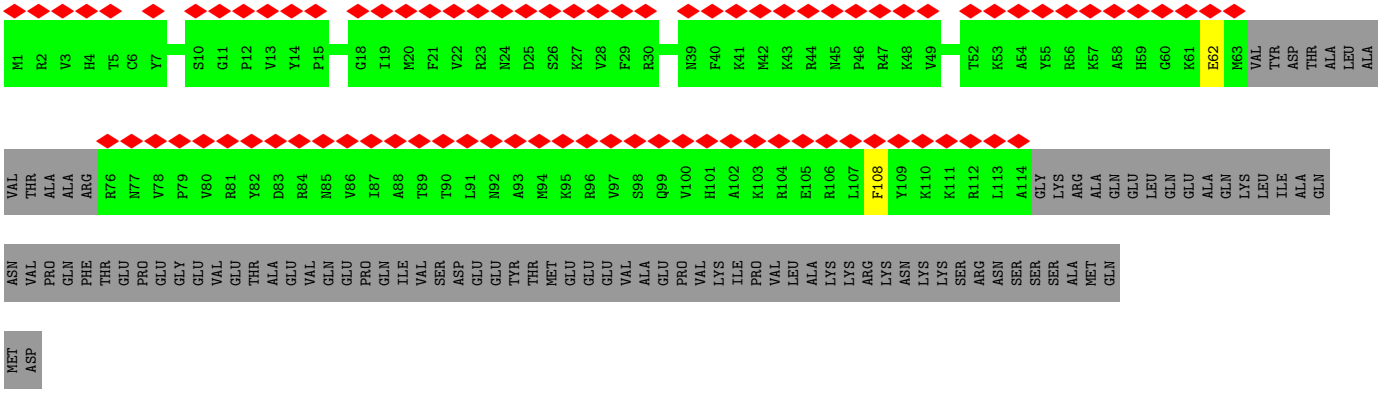
Chain t:





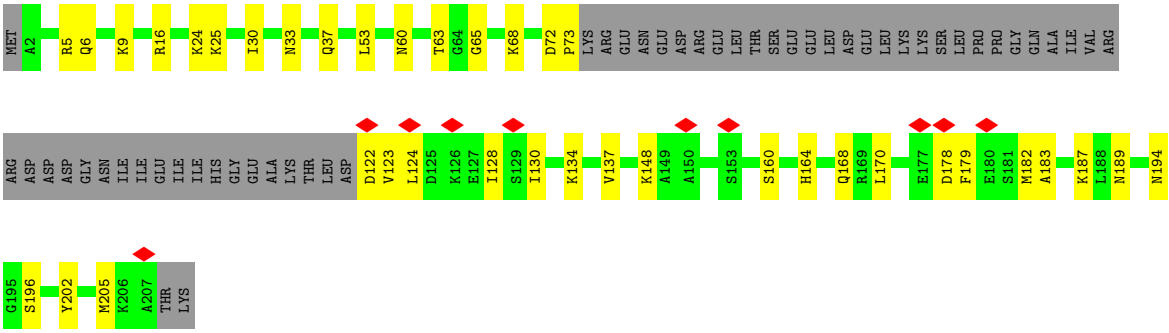
• Molecule 36: Ribosome biogenesis protein rlp24

Chain u:



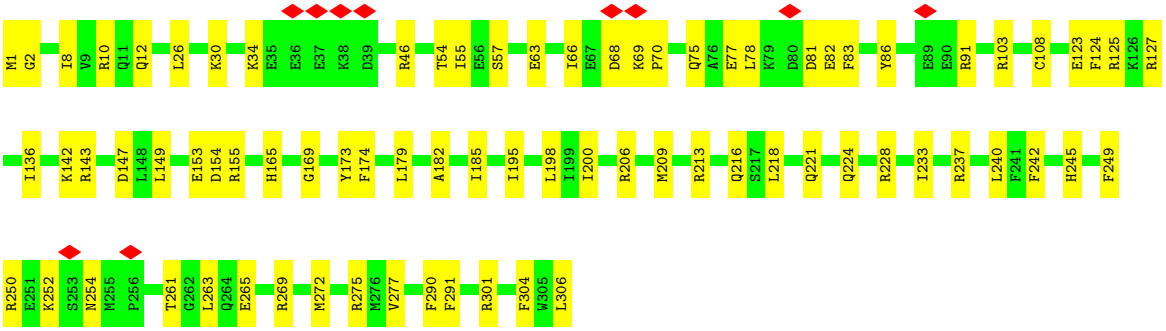
• Molecule 37: Nucleolar protein 16

Chain v:

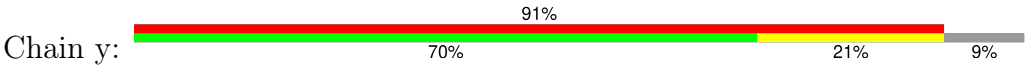


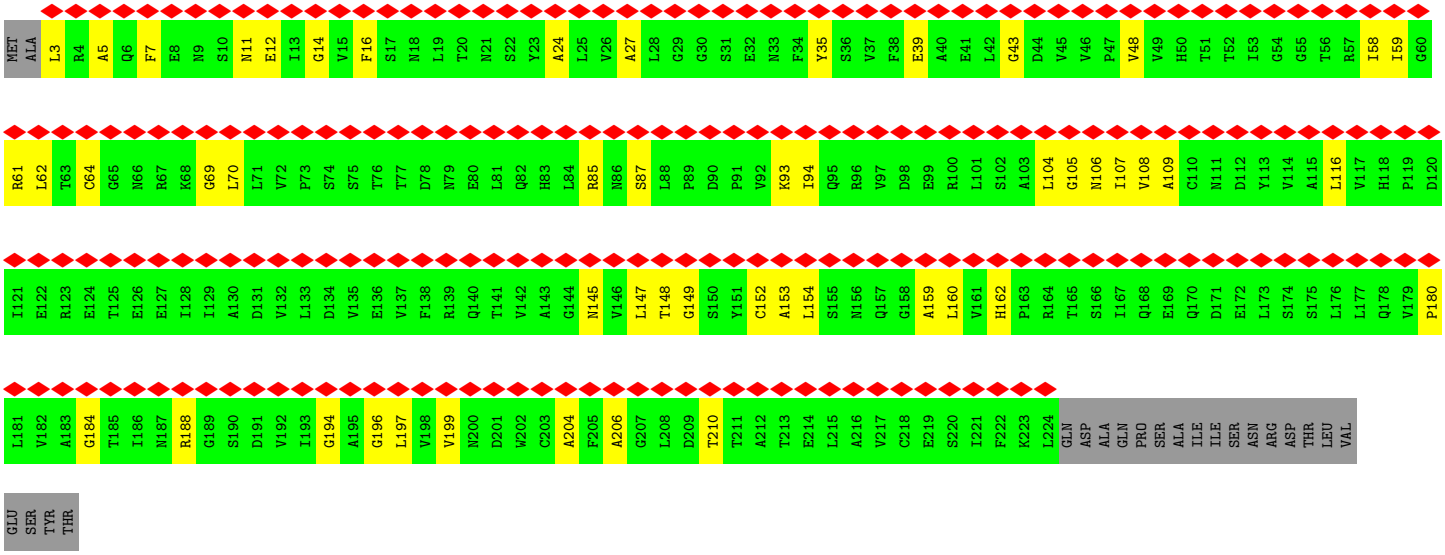
• Molecule 38: Brix domain-containing protein C4F8.04

Chain x:

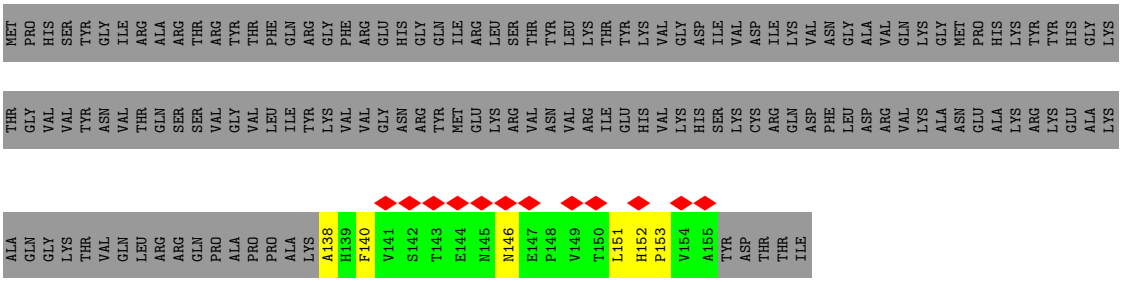


• Molecule 39: Eukaryotic translation initiation factor 6





• Molecule 40: 60S ribosomal protein L21-A



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	71000	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	0.590	Depositor
Minimum map value	-0.339	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	1	0.24	0/34054	0.28	0/53038
2	2	0.23	0/3474	0.25	0/5403
3	3	0.32	0/1644	0.35	0/2210
4	4	0.23	0/1792	0.37	1/2421 (0.0%)
5	5	0.18	0/2722	0.34	0/3679
6	6	0.07	0/1303	0.13	0/2021
7	A	0.13	0/2088	0.31	0/2815
8	B	0.06	0/1550	0.20	0/2153
9	C	0.32	0/2614	0.41	1/3526 (0.0%)
10	D	0.14	0/3108	0.30	0/4197
11	E	0.20	0/1356	0.42	0/1829
12	F	0.20	0/1977	0.28	0/2651
13	G	0.22	0/1295	0.33	0/1748
14	H	0.06	0/860	0.21	0/1193
15	J	0.10	0/468	0.26	0/653
16	K	0.06	0/1223	0.20	0/1703
17	L	0.35	0/960	0.39	0/1288
18	M	0.09	0/608	0.28	0/846
19	N	0.32	0/1436	0.36	0/1920
20	O	0.11	0/1464	0.25	0/1961
21	P	0.16	0/1057	0.30	0/1419
22	Q	0.28	0/1052	0.36	0/1413
23	S	0.12	0/1444	0.31	0/1939
24	V	0.14	0/617	0.34	0/852
25	Y	0.23	0/1008	0.35	0/1341
26	b	0.09	0/745	0.26	0/1033
27	e	0.31	0/1009	0.36	0/1345
28	f	0.21	0/859	0.31	0/1152
29	h	0.23	0/1002	0.40	0/1333
30	i	0.21	0/791	0.33	0/1050
31	j	0.19	0/575	0.35	0/761
32	m	0.18	0/607	0.31	0/818

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	o	0.09	0/672	0.23	0/935
34	r	0.07	0/277	0.20	0/385
35	t	0.10	0/169	0.23	0/228
36	u	0.06	0/504	0.19	0/700
37	v	0.22	0/1296	0.36	0/1737
38	x	0.19	0/2570	0.34	0/3442
39	y	0.14	0/1091	0.42	0/1515
40	T	0.11	0/129	0.32	0/179
All	All	0.22	0/83470	0.30	2/120832 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	C	331	ASN	CB-CA-C	-5.81	104.61	110.65
4	4	46	LYS	N-CA-C	-5.50	105.19	111.07

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	30438	0	15314	545	0
2	2	3109	0	1573	49	0
3	3	1613	0	1665	57	0
4	4	1746	0	1763	41	0
5	5	2669	0	2728	84	0
6	6	1167	0	589	10	0
7	A	2049	0	2082	71	0
8	B	1552	0	708	11	0
9	C	2568	0	2702	103	0
10	D	3055	0	3009	75	0
11	E	1328	0	1408	56	0
12	F	1939	0	2030	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	G	1277	0	1350	47	0
14	H	862	0	372	4	0
15	J	469	0	212	3	0
16	K	1225	0	539	6	0
17	L	942	0	1012	57	0
18	M	609	0	278	3	0
19	N	1406	0	1441	48	0
20	O	1437	0	1529	48	0
21	P	1037	0	1056	32	0
22	Q	1041	0	1137	24	0
23	S	1408	0	1462	35	0
24	V	619	0	300	26	0
25	Y	998	0	1090	33	0
26	b	749	0	326	4	0
27	e	995	0	1059	34	0
28	f	839	0	866	26	0
29	h	993	0	1087	38	0
30	i	783	0	863	30	0
31	j	563	0	578	19	0
32	m	595	0	570	19	0
33	o	673	0	293	7	0
34	r	278	0	131	0	0
35	t	167	0	133	2	0
36	u	506	0	226	1	0
37	v	1276	0	1325	37	0
38	x	2524	0	2536	58	0
39	y	1092	0	505	30	0
40	T	125	0	108	6	0
41	j	1	0	0	0	0
All	All	78722	0	57955	1513	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (1513) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:3285:G:H1	1:1:3302:U:H3	1.14	0.95
1:1:1155:U:H3	1:1:1165:G:H1	1.11	0.94
31:j:22:CYS:HB3	31:j:37:CYS:SG	2.11	0.91
19:N:115:VAL:HG11	19:N:160:GLU:HB3	1.54	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:710:G:H21	37:v:65:GLY:H	1.24	0.86
17:L:67:MET:HE3	17:L:67:MET:H	1.39	0.85
24:V:80:VAL:HA	24:V:102:GLY:HA2	1.59	0.85
1:1:3148:G:H1	1:1:3186:U:H3	1.21	0.84
1:1:3367:A:OP2	1:1:3368:A:N6	2.11	0.84
17:L:62:THR:HG22	17:L:64:ARG:H	1.41	0.84
1:1:1160:A:H3'	1:1:1161:A:H8	1.43	0.83
39:y:39:GLU:HA	39:y:43:GLY:HA3	1.61	0.82
31:j:52:LYS:HB3	31:j:56:ARG:HH21	1.45	0.80
1:1:277:G:H5"	19:N:14:LYS:HE2	1.62	0.80
10:D:253:PHE:HB3	10:D:257:MET:HE3	1.63	0.78
25:Y:30:MET:HE1	25:Y:74:ARG:HG2	1.66	0.78
17:L:111:ARG:HE	30:i:11:LYS:HD2	1.47	0.77
1:1:550:G:H22	1:1:576:U:H1'	1.49	0.77
7:A:115:ARG:HG3	7:A:117:PRO:HD2	1.66	0.77
1:1:1386:G:N7	11:E:32:ARG:NH2	2.32	0.77
19:N:68:ARG:HH12	19:N:123:GLN:HB2	1.50	0.77
5:5:278:SER:HB3	5:5:290:ARG:HG3	1.66	0.76
31:j:19:CYS:HB3	31:j:22:CYS:SG	2.26	0.76
1:1:1160:A:H3'	1:1:1161:A:C8	2.20	0.76
13:G:162:LEU:HD11	19:N:45:PRO:HG3	1.68	0.76
21:P:112:LEU:HD12	21:P:150:VAL:HB	1.68	0.76
11:E:72:VAL:HA	11:E:82:VAL:HG12	1.68	0.75
1:1:449:U:H1'	1:1:450:A:C8	2.21	0.75
1:1:3150:U:H3	1:1:3184:G:H1	1.35	0.74
7:A:122:VAL:HG13	7:A:232:ILE:HG12	1.69	0.74
3:3:110:GLN:NE2	11:E:30:ALA:O	2.20	0.74
19:N:145:ASP:HB3	19:N:148:ILE:HG22	1.70	0.74
4:4:196:VAL:HG22	22:Q:136:SER:HB2	1.70	0.73
1:1:1416:G:N2	9:C:243:GLY:O	2.20	0.73
3:3:31:GLU:OE1	3:3:54:ARG:NH1	2.21	0.73
9:C:292:LEU:HD11	22:Q:126:ASP:HB2	1.69	0.73
33:o:107:LEU:HA	33:o:181:ILE:H	1.53	0.73
1:1:1146:G:N2	1:1:1146:G:OP2	2.21	0.73
17:L:117:LYS:NZ	37:v:124:LEU:O	2.21	0.73
11:E:165:LEU:HD12	11:E:168:ILE:HD11	1.71	0.73
3:3:114:ARG:NH2	27:e:112:LEU:O	2.22	0.72
4:4:62:GLN:HE22	12:F:13:ILE:H	1.36	0.72
1:1:715:U:OP2	37:v:25:LYS:NZ	2.22	0.72
1:1:53:G:OP1	31:j:48:ASN:ND2	2.23	0.72
1:1:402:U:OP2	38:x:301:ARG:NH1	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1158:G:H2'	1:1:1158:G:N3	2.02	0.71
33:o:131:VAL:HA	33:o:153:PHE:HA	1.72	0.71
1:1:644:A:H5'	1:1:645:U:H3'	1.72	0.71
10:D:179:GLY:HA2	10:D:182:LYS:HE3	1.71	0.71
23:S:7:GLN:HB3	23:S:63:ILE:HD11	1.72	0.71
1:1:404:A:OP1	3:3:147:ARG:NH1	2.23	0.71
1:1:116:A:OP2	19:N:2:GLY:N	2.23	0.71
10:D:231:GLY:H	30:i:19:GLN:HG3	1.55	0.71
1:1:277:G:N2	1:1:278:U:O4	2.23	0.70
1:1:1379:U:OP1	22:Q:38:ARG:NH1	2.23	0.70
27:e:39:VAL:HG13	27:e:46:THR:HB	1.73	0.70
1:1:1161:A:H3'	1:1:1162:G:H8	1.56	0.70
7:A:145:SER:O	7:A:187:ARG:NH2	2.24	0.70
20:O:148:TRP:CD1	20:O:150:TYR:H	2.10	0.70
24:V:36:LEU:HA	24:V:64:VAL:HA	1.74	0.69
2:2:79:A:OP2	25:Y:50:ARG:NH1	2.26	0.69
12:F:95:ARG:NH2	12:F:98:GLY:O	2.25	0.69
17:L:42:LYS:NZ	17:L:51:VAL:O	2.22	0.69
19:N:123:GLN:OE1	19:N:128:LYS:NZ	2.25	0.69
1:1:777:C:H3'	1:1:778:G:H5"	1.73	0.69
10:D:136:GLY:HA3	10:D:399:GLY:HA3	1.73	0.69
10:D:219:PRO:HB3	10:D:257:MET:HE1	1.75	0.69
1:1:216:A:OP1	9:C:163:LYS:NZ	2.26	0.69
1:1:107:A:OP1	17:L:39:ARG:NH1	2.27	0.68
7:A:170:GLN:NE2	15:J:107:ILE:O	2.26	0.68
9:C:5:ARG:NH2	9:C:149:GLU:OE2	2.21	0.68
38:x:245:HIS:HB3	38:x:263:LEU:HD12	1.76	0.68
1:1:34:A:N3	1:1:842:A:O2'	2.26	0.68
27:e:102:ARG:NH2	27:e:118:ASN:O	2.22	0.68
39:y:154:LEU:HA	39:y:159:ALA:HA	1.75	0.68
1:1:1157:G:H1	1:1:1163:C:H42	1.42	0.68
1:1:3104:G:OP2	20:O:75:ARG:NH1	2.26	0.68
7:A:122:VAL:HG22	7:A:232:ILE:HG23	1.76	0.68
2:2:162:C:OP1	13:G:181:LYS:NZ	2.21	0.67
1:1:76:G:O6	17:L:102:ARG:NH1	2.27	0.67
1:1:447:C:C4	38:x:103:ARG:HD3	2.29	0.67
4:4:196:VAL:HG12	4:4:199:ARG:HH21	1.58	0.67
24:V:33:ALA:HA	24:V:67:GLY:HA3	1.75	0.67
1:1:3151:A:H1'	1:1:3183:A:H61	1.59	0.67
20:O:30:GLY:O	28:f:13:LYS:NZ	2.24	0.67
38:x:250:ARG:HB2	38:x:252:LYS:HE3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:43:LYS:HB3	5:5:59:ARG:HD3	1.77	0.67
23:S:77:TRP:HB2	23:S:124:LYS:HB3	1.76	0.67
1:1:466:U:H3	1:1:484:A:H61	1.42	0.67
23:S:123:LEU:O	40:T:152:HIS:ND1	2.27	0.67
1:1:486:G:H21	1:1:488:A:H62	1.42	0.67
1:1:1361:A:OP1	28:f:25:HIS:NE2	2.22	0.67
1:1:1387:A:OP1	3:3:103:ARG:NH2	2.25	0.67
39:y:109:ALA:HA	39:y:149:GLY:HA2	1.77	0.67
1:1:526:G:OP1	9:C:342:LYS:NZ	2.26	0.66
12:F:231:GLU:HB3	23:S:118:ARG:HH21	1.60	0.66
1:1:166:A:H61	1:1:268:U:H3	1.41	0.66
1:1:117:U:O4	13:G:147:LYS:NZ	2.25	0.66
1:1:817:G:N2	22:Q:91:ASP:OD1	2.27	0.66
7:A:115:ARG:HB3	7:A:119:GLY:HA3	1.76	0.66
21:P:14:CYS:O	21:P:105:LYS:NZ	2.29	0.66
5:5:61:ASN:ND2	5:5:63:THR:OG1	2.28	0.66
7:A:270:GLN:OE1	7:A:273:LYS:NZ	2.26	0.66
13:G:145:ALA:HA	32:m:214:PRO:HB3	1.78	0.66
9:C:207:PRO:HG2	9:C:227:VAL:HG22	1.78	0.66
4:4:53:TRP:O	4:4:105:LYS:NZ	2.28	0.66
5:5:154:LEU:HB2	5:5:180:PHE:HB3	1.76	0.66
39:y:109:ALA:N	39:y:116:LEU:O	2.29	0.66
1:1:257:A:N7	17:L:134:LYS:NZ	2.42	0.66
1:1:1245:U:OP1	23:S:136:ARG:NH1	2.29	0.66
10:D:529:PRO:HB2	32:m:213:THR:HG22	1.77	0.66
1:1:1176:G:OP1	27:e:41:ARG:NH1	2.28	0.66
1:1:35:A:N6	1:1:48:A:OP2	2.30	0.65
1:1:377:A:OP1	38:x:10:ARG:NH2	2.29	0.65
38:x:182:ALA:HA	38:x:185:ILE:HD12	1.78	0.65
39:y:197:LEU:HA	39:y:206:ALA:HA	1.79	0.65
8:B:72:ILE:HA	24:V:91:ASP:HA	1.77	0.65
1:1:6:A:N6	2:2:160:G:O6	2.30	0.65
5:5:153:CYS:SG	5:5:178:LYS:NZ	2.69	0.65
7:A:100:PHE:HB3	7:A:112:HIS:HB2	1.79	0.65
7:A:142:LEU:O	7:A:187:ARG:NH1	2.29	0.65
38:x:149:LEU:HD11	38:x:218:LEU:HD11	1.77	0.65
4:4:87:PHE:HA	4:4:90:THR:HG22	1.77	0.65
5:5:3:LEU:HD13	5:5:339:ILE:HD11	1.77	0.65
9:C:292:LEU:HD13	22:Q:31:LEU:HD22	1.79	0.65
19:N:51:LEU:HB3	19:N:117:ASN:HD22	1.62	0.65
21:P:17:ALA:HB3	21:P:148:ILE:HG22	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:P:157:VAL:O	38:x:228:ARG:NH2	2.30	0.65
22:Q:61:ILE:HG21	22:Q:84:VAL:HG21	1.79	0.65
24:V:17:LEU:HA	24:V:55:SER:HA	1.79	0.65
3:3:41:GLN:OE1	3:3:107:ARG:NH2	2.30	0.65
17:L:44:ALA:HA	37:v:30:ILE:HD13	1.79	0.65
1:1:487:C:H4'	1:1:488:A:O5'	1.97	0.64
1:1:602:A:C6	9:C:337:TYR:HE2	2.15	0.64
1:1:615:G:N2	1:1:637:U:OP1	2.28	0.64
1:1:1438:G:N2	1:1:1441:A:OP2	2.30	0.64
1:1:1396:G:H2'	1:1:1397:A:C8	2.31	0.64
9:C:333:TYR:HE1	12:F:56:GLU:HG2	1.63	0.64
11:E:104:THR:HG22	11:E:106:ALA:H	1.62	0.64
25:Y:55:ILE:HD11	25:Y:81:ILE:HD12	1.79	0.64
39:y:188:ARG:H	39:y:210:THR:HA	1.63	0.64
7:A:148:ILE:HB	7:A:188:VAL:HG22	1.80	0.64
13:G:98:ARG:NH2	13:G:188:THR:O	2.30	0.64
38:x:123:GLU:OE1	38:x:125:ARG:NH2	2.31	0.64
1:1:519:U:H5"	12:F:218:LEU:HD21	1.79	0.64
1:1:964:U:H4'	1:1:965:A:H3'	1.80	0.64
7:A:199:TRP:O	7:A:201:ARG:NH1	2.31	0.64
32:m:248:LEU:HD11	32:m:256:ARG:HH21	1.62	0.64
3:3:11:VAL:O	3:3:19:ARG:NH2	2.27	0.64
5:5:59:ARG:NH2	5:5:65:GLU:OE2	2.31	0.64
5:5:138:ARG:NH1	5:5:205:GLU:OE2	2.31	0.64
1:1:369:A:O3'	31:j:45:ARG:NH2	2.31	0.63
20:O:11:ASP:OD2	23:S:171:ARG:NH2	2.29	0.63
26:b:420:TYR:HA	39:y:87:SER:HA	1.79	0.63
5:5:274:ARG:O	5:5:274:ARG:NH1	2.22	0.63
10:D:340:ILE:HG22	10:D:405:VAL:HG11	1.80	0.63
1:1:590:U:O2'	1:1:591:G:N3	2.31	0.63
1:1:3117:A:N6	1:1:3129:A:OP2	2.32	0.63
10:D:366:LEU:HD23	10:D:396:ALA:HB1	1.79	0.63
1:1:73:C:H5	17:L:66:ASN:ND2	1.97	0.63
2:2:103:G:OP1	31:j:76:ASN:ND2	2.29	0.63
9:C:115:VAL:HB	9:C:120:LYS:HE3	1.80	0.63
1:1:712:U:OP2	17:L:36:ARG:NH2	2.32	0.63
1:1:1157:G:N3	1:1:1158:G:H1'	2.13	0.63
1:1:3288:G:H1	1:1:3299:U:H3	1.47	0.63
24:V:26:ASN:HA	24:V:35:ASN:HA	1.79	0.63
1:1:182:G:N2	1:1:251:U:O2	2.31	0.63
7:A:68:MET:HG3	7:A:71:SER:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Q:78:GLN:NE2	22:Q:79:ASN:OD1	2.32	0.63
10:D:159:ARG:NH2	17:L:106:GLU:OE1	2.31	0.63
10:D:261:MET:HA	10:D:264:LEU:HD12	1.80	0.63
19:N:143:ARG:NH2	29:h:93:ALA:O	2.31	0.63
1:1:75:U:H1'	17:L:61:PRO:HG3	1.81	0.62
1:1:113:C:OP1	19:N:147:ARG:NH2	2.31	0.62
1:1:839:A:H2'	1:1:840:A:H4'	1.81	0.62
3:3:170:LYS:HE3	3:3:170:LYS:HA	1.81	0.62
11:E:85:PRO:HB2	11:E:88:VAL:HB	1.80	0.62
28:f:90:LEU:HD12	28:f:94:THR:HG21	1.81	0.62
9:C:317:LYS:HE2	12:F:160:PHE:HE1	1.65	0.62
10:D:201:ARG:HA	10:D:204:GLU:HB2	1.81	0.62
20:O:188:VAL:HA	20:O:191:LYS:HE2	1.81	0.62
1:1:817:G:OP2	22:Q:93:ARG:NH2	2.32	0.62
7:A:192:THR:HB	7:A:199:TRP:HD1	1.64	0.62
21:P:155:GLU:O	38:x:250:ARG:NH2	2.32	0.62
1:1:109:A:O2'	1:1:331:A:N6	2.32	0.62
1:1:498:U:H3'	1:1:499:G:H5"	1.80	0.62
13:G:158:ASP:HB3	13:G:159:PRO:HD3	1.81	0.62
7:A:153:LYS:NZ	15:J:123:THR:O	2.33	0.62
1:1:647:A:OP1	28:f:61:ARG:NH1	2.32	0.62
4:4:46:LYS:HZ1	7:A:290:LEU:HB3	1.64	0.62
10:D:144:LEU:HD22	10:D:184:LEU:HD12	1.82	0.62
25:Y:10:SER:HB3	25:Y:13:LYS:HB2	1.80	0.62
1:1:984:A:H4'	1:1:1000:G:H21	1.64	0.62
1:1:3278:A:H2'	1:1:3279:A:C8	2.35	0.62
13:G:231:ARG:HG2	32:m:202:TYR:HD2	1.64	0.62
3:3:159:LYS:NZ	21:P:105:LYS:O	2.28	0.62
10:D:439:MET:HE2	10:D:439:MET:HA	1.81	0.62
3:3:174:TYR:CG	3:3:178:PRO:HG3	2.34	0.61
10:D:456:LYS:HD3	10:D:456:LYS:N	2.15	0.61
11:E:57:VAL:HG11	11:E:177:TYR:HE2	1.64	0.61
38:x:147:ASP:OD1	38:x:165:HIS:ND1	2.33	0.61
25:Y:55:ILE:HG22	25:Y:105:ILE:HA	1.82	0.61
1:1:1477:G:OP2	21:P:124:LYS:NZ	2.28	0.61
9:C:108:TRP:O	19:N:201:ARG:NH2	2.32	0.61
20:O:122:PRO:HA	20:O:125:LEU:HD12	1.81	0.61
1:1:3477:A:H3'	1:1:3478:G:H3'	1.80	0.61
3:3:39:ASN:HB2	3:3:42:SER:HB3	1.82	0.61
13:G:101:THR:HG22	13:G:103:ALA:H	1.64	0.61
20:O:159:GLU:HA	20:O:162:LYS:HG2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:P:158:PRO:O	38:x:228:ARG:NH1	2.32	0.61
1:1:18:G:OP1	29:h:83:ARG:NH2	2.25	0.61
3:3:151:ALA:O	3:3:155:ALA:N	2.33	0.61
7:A:53:VAL:HG23	7:A:57:GLN:HB2	1.83	0.61
11:E:86:TYR:HA	11:E:90:GLY:HA2	1.82	0.61
1:1:832:G:H22	9:C:104:PRO:HD2	1.65	0.61
1:1:73:C:H5	17:L:66:ASN:HD22	1.49	0.61
1:1:707:U:H5"	1:1:708:U:H5	1.65	0.61
23:S:21:PRO:O	40:T:146:ASN:ND2	2.32	0.61
39:y:7:PHE:H	39:y:11:ASN:HA	1.66	0.61
1:1:1371:G:H2'	1:1:1372:U:H6	1.65	0.61
5:5:332:ILE:O	5:5:334:ALA:N	2.31	0.61
10:D:358:TYR:OH	37:v:187:LYS:NZ	2.28	0.61
1:1:201:U:OP1	5:5:290:ARG:NH2	2.33	0.61
1:1:3149:G:H1'	1:1:3189:C:H42	1.66	0.61
10:D:139:LYS:HD2	10:D:398:ARG:HH12	1.65	0.61
10:D:506:LEU:HD13	10:D:509:ILE:HD13	1.82	0.61
10:D:468:LYS:HE2	16:K:45:ASP:HA	1.83	0.60
28:f:9:TYR:CZ	28:f:100:ARG:HD2	2.36	0.60
1:1:698:U:O4	22:Q:55:LYS:NZ	2.32	0.60
1:1:1348:A:H4'	20:O:19:ARG:HH22	1.65	0.60
7:A:123:LYS:HB3	7:A:230:ILE:HB	1.83	0.60
1:1:461:A:O2'	1:1:463:C:N4	2.34	0.60
1:1:3287:A:H2'	1:1:3288:G:H8	1.65	0.60
39:y:153:ALA:N	39:y:160:LEU:O	2.34	0.60
11:E:136:ASP:OD1	11:E:136:ASP:N	2.33	0.60
38:x:78:LEU:HD21	38:x:206:ARG:HH22	1.66	0.60
1:1:161:C:H5"	1:1:162:A:H2'	1.83	0.60
1:1:1153:U:H2'	1:1:1154:U:C6	2.37	0.60
39:y:61:ARG:O	39:y:106:ASN:N	2.30	0.60
2:2:132:G:H1	2:2:137:A:H61	1.49	0.60
11:E:73:LEU:HA	11:E:111:VAL:HG21	1.82	0.60
4:4:99:ASP:OD1	4:4:99:ASP:N	2.32	0.60
20:O:152:ASP:OD1	20:O:152:ASP:N	2.33	0.60
21:P:116:HIS:HB3	21:P:149:ILE:HB	1.82	0.60
29:h:22:GLU:HA	29:h:25:GLN:OE1	2.02	0.60
1:1:3278:A:H2'	1:1:3279:A:H8	1.67	0.60
3:3:117:GLN:HE21	11:E:26:LYS:HD2	1.66	0.60
22:Q:63:ILE:HD11	22:Q:115:ILE:HD11	1.84	0.60
1:1:984:A:N3	1:1:1145:U:O2'	2.31	0.59
9:C:355:LYS:HE2	12:F:80:GLY:HA3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:115:ALA:HB2	39:y:145:ASN:HA	1.84	0.59
1:1:73:C:C5	17:L:66:ASN:ND2	2.70	0.59
1:1:544:A:H61	1:1:582:G:H1	1.50	0.59
1:1:1183:G:OP2	1:1:1183:G:N2	2.30	0.59
9:C:328:SER:O	12:F:48:ARG:NH2	2.35	0.59
38:x:91:ARG:HG3	38:x:221:GLN:HE21	1.67	0.59
1:1:86:G:N2	1:1:98:G:H2'	2.17	0.59
1:1:1457:C:H5"	3:3:21:LYS:HD2	1.84	0.59
10:D:323:ARG:HG2	10:D:411:TYR:HE1	1.67	0.59
1:1:1176:G:N1	1:1:1190:A:O2'	2.31	0.59
9:C:319:ASN:HB3	9:C:322:LYS:HB3	1.84	0.59
29:h:80:LEU:HA	29:h:83:ARG:HD3	1.83	0.59
38:x:173:TYR:HD2	38:x:275:ARG:HB2	1.67	0.59
1:1:488:A:C4	1:1:489:C:H5	2.21	0.59
7:A:253:MET:HE2	7:A:253:MET:HA	1.84	0.59
7:A:264:GLN:O	7:A:268:ASN:ND2	2.36	0.59
12:F:54:ARG:NH2	12:F:58:TYR:OH	2.30	0.59
19:N:158:HIS:ND1	19:N:160:GLU:OE2	2.36	0.59
32:m:212:GLU:HG2	32:m:213:THR:HG23	1.85	0.59
1:1:63:A:OP1	19:N:172:ARG:NH2	2.36	0.59
1:1:2458:G:H5'	1:1:2459:G:H8	1.68	0.59
4:4:71:LEU:HA	4:4:74:ILE:HD11	1.83	0.59
1:1:155:U:OP2	19:N:49:ARG:NH1	2.29	0.59
9:C:267:THR:OG1	9:C:281:GLU:OE1	2.20	0.59
24:V:38:ILE:HA	24:V:62:ALA:HA	1.84	0.59
37:v:178:ASP:OD1	37:v:178:ASP:N	2.34	0.59
2:2:73:A:H5"	29:h:5:THR:HG21	1.85	0.59
7:A:250:SER:H	7:A:253:MET:HB2	1.67	0.59
27:e:63:CYS:SG	27:e:69:LYS:NZ	2.70	0.59
1:1:1440:G:H5'	27:e:14:PHE:HD2	1.68	0.59
1:1:683:G:N2	9:C:95:MET:HB2	2.18	0.58
1:1:1208:G:N7	28:f:21:LYS:NZ	2.51	0.58
5:5:7:ASP:OD2	5:5:11:GLN:NE2	2.36	0.58
24:V:81:VAL:O	24:V:121:ALA:N	2.33	0.58
1:1:461:A:HO2'	1:1:463:C:N4	2.01	0.58
3:3:160:ASN:OD1	3:3:163:LYS:NZ	2.33	0.58
20:O:77:PRO:HA	20:O:80:ILE:HB	1.84	0.58
10:D:157:LYS:O	10:D:213:ASN:ND2	2.37	0.58
13:G:214:ILE:HD12	13:G:214:ILE:H	1.67	0.58
4:4:201:THR:HA	4:4:204:LYS:HE2	1.86	0.58
1:1:3431:A:H4'	8:B:367:HIS:H	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:86:TYR:CD1	11:E:157:GLN:HG2	2.36	0.58
11:E:110:ASP:OD2	11:E:110:ASP:N	2.34	0.58
1:1:1207:C:H4'	20:O:90:PRO:HD3	1.85	0.58
39:y:16:PHE:HA	39:y:58:ILE:HA	1.84	0.58
1:1:347:C:OP1	9:C:197:ARG:NH1	2.35	0.58
1:1:530:A:OP1	23:S:61:ASN:ND2	2.36	0.58
1:1:961:A:O2'	31:j:49:TRP:O	2.22	0.58
2:2:105:A:OP1	29:h:69:ARG:NH2	2.36	0.58
1:1:222:G:H5"	25:Y:11:ARG:HG3	1.85	0.58
1:1:3375:U:OP2	28:f:69:TRP:NE1	2.37	0.58
5:5:131:SER:HB2	5:5:147:GLY:HA2	1.85	0.58
38:x:265:GLU:OE1	38:x:269:ARG:NH2	2.30	0.58
1:1:372:G:O6	31:j:56:ARG:NH1	2.36	0.58
1:1:634:G:N7	9:C:311:LYS:NZ	2.43	0.58
1:1:836:C:H5'	9:C:95:MET:HE1	1.86	0.58
1:1:968:A:O2'	1:1:970:C:N4	2.37	0.58
2:2:58:C:N4	2:2:83:G:H1	2.02	0.58
7:A:35:SER:OG	7:A:36:ALA:N	2.36	0.58
23:S:110:ALA:HA	23:S:115:ALA:H	1.68	0.58
1:1:591:G:H1'	1:1:592:U:H3'	1.85	0.57
3:3:41:GLN:OE1	3:3:103:ARG:NH1	2.37	0.57
23:S:29:PHE:O	23:S:39:ARG:NH1	2.37	0.57
1:1:3317:A:H1'	1:1:3367:A:H1'	1.87	0.57
39:y:107:ILE:HA	39:y:147:LEU:HA	1.86	0.57
17:L:111:ARG:HH21	30:i:11:LYS:HB3	1.68	0.57
1:1:464:A:H1'	1:1:488:A:N6	2.19	0.57
10:D:394:ASN:OD1	10:D:410:GLN:NE2	2.38	0.57
1:1:1353:U:OP1	23:S:116:ARG:NH1	2.30	0.57
2:2:103:G:OP2	31:j:72:ARG:NH1	2.37	0.57
11:E:189:ARG:H	11:E:193:MET:HE3	1.68	0.57
17:L:53:ALA:O	37:v:60:ASN:ND2	2.37	0.57
30:i:32:SER:HB3	30:i:35:THR:HG22	1.86	0.57
5:5:5:LEU:HD11	5:5:336:PRO:HB3	1.86	0.57
5:5:48:MET:HE1	5:5:57:VAL:HG22	1.87	0.57
5:5:68:ASN:HB3	5:5:71:GLN:HE22	1.68	0.57
5:5:222:CYS:HB3	5:5:224:HIS:HE1	1.70	0.57
19:N:172:ARG:HE	19:N:174:ILE:HG13	1.68	0.57
37:v:170:LEU:HD12	37:v:182:MET:HB2	1.86	0.57
1:1:665:U:O2'	1:1:973:G:OP2	2.21	0.57
10:D:241:VAL:HG22	10:D:272:LEU:HD23	1.86	0.57
23:S:11:ARG:HD2	23:S:21:PRO:HG2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:20:A:OP1	21:P:3:ARG:NE	2.38	0.57
5:5:108:ASP:OD2	5:5:110:ASN:ND2	2.37	0.57
5:5:249:PHE:HZ	5:5:285:LYS:HD3	1.68	0.57
1:1:622:G:O3'	9:C:335:LYS:NZ	2.37	0.57
1:1:689:U:H2'	1:1:690:A:C8	2.40	0.57
1:1:1022:U:H3	1:1:1091:G:H22	1.52	0.57
1:1:438:G:OP1	28:f:88:HIS:ND1	2.38	0.57
1:1:204:G:N7	3:3:139:LYS:NZ	2.51	0.56
1:1:1325:A:H2'	1:1:1326:G:C8	2.40	0.56
1:1:1385:U:H5'	1:1:1386:G:H2'	1.86	0.56
1:1:3201:A:OP2	1:1:3224:G:N1	2.37	0.56
3:3:71:HIS:CG	9:C:5:ARG:HD2	2.40	0.56
8:B:92:TYR:HA	8:B:101:SER:HA	1.87	0.56
10:D:465:PRO:HD2	10:D:468:LYS:HE3	1.87	0.56
21:P:53:GLU:O	21:P:55:LYS:NZ	2.32	0.56
27:e:103:VAL:HA	27:e:106:VAL:HG12	1.87	0.56
1:1:715:U:P	37:v:25:LYS:HZ3	2.29	0.56
1:1:3153:U:H3	1:1:3181:G:H21	1.53	0.56
5:5:201:ILE:HG23	5:5:227:THR:HG22	1.87	0.56
12:F:72:LEU:HD22	40:T:140:PHE:HE1	1.70	0.56
12:F:222:ARG:HH21	12:F:229:PHE:HE1	1.53	0.56
17:L:46:ILE:HB	17:L:49:ARG:HG3	1.86	0.56
7:A:179:ARG:NH1	32:m:113:GLU:OE2	2.38	0.56
17:L:87:ARG:HD3	17:L:88:ARG:NH1	2.20	0.56
28:f:97:SER:OG	28:f:98:SER:N	2.38	0.56
38:x:165:HIS:HB3	38:x:169:GLY:HA3	1.86	0.56
9:C:330:LEU:HD23	12:F:188:VAL:HG21	1.86	0.56
20:O:145:GLU:N	20:O:145:GLU:OE1	2.37	0.56
1:1:360:A:H4'	1:1:361:G:OP1	2.04	0.56
1:1:1016:G:N1	1:1:1170:G:OP1	2.39	0.56
27:e:6:ILE:HD12	27:e:60:THR:HG23	1.87	0.56
2:2:56:A:N6	2:2:59:G:H2'	2.21	0.56
25:Y:54:GLN:HB3	25:Y:107:LYS:HB3	1.86	0.56
39:y:3:LEU:O	39:y:206:ALA:N	2.35	0.56
1:1:181:A:H2'	1:1:182:G:C8	2.41	0.56
1:1:223:G:H2'	1:1:224:U:O4'	2.06	0.56
1:1:1153:U:H2'	1:1:1154:U:H6	1.70	0.56
11:E:146:LYS:HG3	11:E:148:ALA:H	1.71	0.56
1:1:310:U:OP2	7:A:51:ARG:NH1	2.38	0.55
1:1:360:A:H61	1:1:373:A:H5"	1.70	0.55
1:1:498:U:H3'	1:1:499:G:C5'	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:299:C:OP1	19:N:68:ARG:HB3	2.05	0.55
1:1:1380:A:O2'	1:1:1381:G:OP2	2.23	0.55
1:1:3326:G:H1'	1:1:3360:G:N2	2.20	0.55
1:1:3332:U:H2'	1:1:3333:G:H8	1.71	0.55
3:3:80:ILE:HD13	3:3:96:GLN:HG3	1.89	0.55
7:A:121:THR:HB	7:A:233:LEU:HB2	1.88	0.55
9:C:12:ASN:ND2	9:C:16:SER:O	2.39	0.55
23:S:15:THR:HG23	23:S:17:HIS:H	1.69	0.55
38:x:81:ASP:OD1	38:x:83:PHE:N	2.40	0.55
39:y:85:ARG:HA	39:y:94:ILE:H	1.70	0.55
4:4:142:MET:HE1	4:4:185:PRO:HA	1.88	0.55
19:N:197:LEU:HB3	19:N:201:ARG:HD3	1.89	0.55
23:S:97:THR:HG22	23:S:100:GLY:H	1.70	0.55
7:A:154:THR:O	7:A:157:THR:OG1	2.23	0.55
28:f:91:PRO:O	28:f:94:THR:HG22	2.06	0.55
12:F:231:GLU:OE1	23:S:118:ARG:NE	2.39	0.55
17:L:135:LYS:HB3	37:v:160:SER:HB2	1.88	0.55
20:O:13:LYS:HB3	23:S:171:ARG:HH22	1.72	0.55
1:1:1012:A:O2'	1:1:1013:U:O4'	2.20	0.55
1:1:3288:G:H22	1:1:3299:U:H3	1.54	0.55
2:2:49:A:N6	2:2:111:G:O2'	2.38	0.55
5:5:53:MET:HE3	5:5:53:MET:HA	1.89	0.55
7:A:46:LEU:HD21	7:A:89:LEU:HD22	1.87	0.55
10:D:338:LYS:HG2	10:D:405:VAL:HG22	1.87	0.55
24:V:105:VAL:HA	24:V:112:LYS:H	1.72	0.55
28:f:19:ARG:HB3	28:f:24:ILE:HG12	1.89	0.55
1:1:496:C:H2'	1:1:497:C:C6	2.42	0.55
3:3:33:ASN:OD1	3:3:42:SER:OG	2.24	0.55
2:2:56:A:N6	2:2:62:A:H61	2.05	0.55
13:G:128:LYS:HD2	13:G:129:PRO:HD2	1.89	0.55
17:L:70:ARG:NH1	17:L:71:ALA:O	2.39	0.55
23:S:12:LYS:HA	23:S:55:GLY:HA2	1.89	0.55
38:x:69:LYS:HD2	38:x:69:LYS:C	2.31	0.55
12:F:17:GLU:CD	12:F:17:GLU:H	2.15	0.55
13:G:143:ILE:HG23	13:G:175:VAL:HG21	1.88	0.55
13:G:97:TYR:OH	13:G:207:ASP:OD2	2.23	0.54
37:v:187:LYS:H	37:v:187:LYS:HD2	1.72	0.54
21:P:9:ALA:HA	21:P:14:CYS:HB2	1.89	0.54
30:i:52:GLU:HG3	30:i:88:LEU:HD21	1.89	0.54
1:1:422:U:H2'	1:1:423:G:H8	1.71	0.54
1:1:447:C:C3'	1:1:449:U:OP1	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:752:G:N2	1:1:773:C:O2	2.31	0.54
3:3:147:ARG:NH1	38:x:301:ARG:HE	2.05	0.54
21:P:109:MET:HA	21:P:112:LEU:HD23	1.88	0.54
1:1:686:G:N2	1:1:686:G:OP2	2.40	0.54
2:2:162:C:H2'	2:2:163:A:O4'	2.06	0.54
5:5:103:MET:HB2	5:5:135:LEU:HD11	1.88	0.54
11:E:42:ALA:O	11:E:44:ARG:NH1	2.41	0.54
11:E:191:HIS:CD2	11:E:192:LEU:HG	2.42	0.54
12:F:113:LEU:O	12:F:122:ILE:HD13	2.08	0.54
18:M:120:ARG:HA	20:O:188:VAL:HG11	1.90	0.54
27:e:34:GLY:O	27:e:37:SER:OG	2.20	0.54
1:1:446:U:H3'	1:1:447:C:C5	2.43	0.54
1:1:455:G:H2'	1:1:456:G:H8	1.72	0.54
7:A:180:ARG:NH1	32:m:113:GLU:O	2.41	0.54
10:D:243:ASP:HA	10:D:274:PHE:HB2	1.89	0.54
11:E:73:LEU:HD21	11:E:83:THR:HG22	1.89	0.54
11:E:117:GLU:N	11:E:117:GLU:OE1	2.36	0.54
21:P:116:HIS:NE2	21:P:147:GLU:OE2	2.37	0.54
25:Y:62:ASN:OD1	25:Y:65:ARG:NH2	2.40	0.54
11:E:152:GLU:HA	11:E:155:ALA:HB3	1.88	0.54
1:1:675:C:N4	1:1:676:G:O6	2.41	0.54
1:1:771:C:O2	22:Q:142:ARG:NH1	2.39	0.54
7:A:257:ALA:HA	7:A:260:ASN:ND2	2.23	0.54
11:E:89:ASN:ND2	11:E:178:LEU:O	2.40	0.54
1:1:353:G:O2'	2:2:33:G:N3	2.38	0.54
1:1:3156:C:O2'	1:1:3433:U:O2	2.25	0.54
6:6:46:G:O2'	6:6:48:G:N2	2.41	0.54
13:G:226:TYR:O	13:G:228:GLU:N	2.41	0.54
1:1:1197:G:OP1	28:f:74:ARG:NH1	2.33	0.54
7:A:44:LYS:HA	7:A:70:HIS:HD2	1.72	0.54
38:x:277:VAL:HG23	38:x:291:PHE:HD2	1.72	0.54
1:1:817:G:C6	22:Q:93:ARG:HD3	2.43	0.53
20:O:190:GLN:OE1	20:O:190:GLN:N	2.26	0.53
24:V:20:PRO:HA	24:V:53:ALA:HA	1.90	0.53
29:h:24:ARG:O	29:h:24:ARG:NH1	2.31	0.53
1:1:760:C:C2	1:1:762:U:H4'	2.43	0.53
1:1:990:C:O2'	1:1:995:G:N2	2.31	0.53
19:N:14:LYS:HD3	19:N:120:TRP:CZ3	2.42	0.53
24:V:116:ILE:N	24:V:134:ASN:O	2.38	0.53
25:Y:44:ILE:HD12	25:Y:47:LEU:HD13	1.90	0.53
33:o:116:PHE:HA	35:t:58:ILE:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:y:12:GLU:HA	39:y:196:GLY:HA2	1.90	0.53
1:1:35:A:OP2	1:1:48:A:N6	2.42	0.53
1:1:342:A:P	37:v:16:ARG:HD3	2.48	0.53
3:3:61:TYR:CD2	3:3:79:ARG:HD2	2.43	0.53
27:e:86:ASN:OD1	27:e:86:ASN:N	2.42	0.53
3:3:97:LEU:HB3	3:3:105:ILE:HG12	1.89	0.53
5:5:166:ASP:HB3	5:5:169:GLU:CD	2.34	0.53
21:P:57:ALA:HB2	21:P:83:TRP:CE2	2.43	0.53
1:1:633:A:N7	11:E:40:ARG:HD3	2.24	0.53
1:1:1224:A:N6	1:1:1346:U:O2	2.41	0.53
1:1:1224:A:H3'	1:1:1225:G:C8	2.44	0.53
9:C:179:ASP:HB3	9:C:207:PRO:HD3	1.89	0.53
20:O:148:TRP:HE1	20:O:151:ASN:N	2.06	0.53
29:h:15:ASN:O	29:h:19:GLN:N	2.31	0.53
1:1:445:G:H1'	1:1:446:U:O4'	2.09	0.53
1:1:488:A:H8	1:1:488:A:OP2	1.91	0.53
2:2:35:U:O2'	9:C:51:PRO:O	2.24	0.53
9:C:11:TYR:CE2	9:C:17:VAL:HG22	2.44	0.53
10:D:260:ILE:HA	10:D:263:ILE:HD12	1.91	0.53
17:L:102:ARG:HH21	30:i:23:ARG:CZ	2.20	0.53
1:1:455:G:H2'	1:1:456:G:C8	2.43	0.53
1:1:1325:A:H2'	1:1:1326:G:H8	1.73	0.53
2:2:57:G:OP2	29:h:50:ARG:NH2	2.40	0.53
9:C:141:GLY:O	9:C:143:ARG:NH1	2.42	0.53
19:N:35:VAL:HG12	19:N:36:ILE:HG13	1.90	0.53
24:V:42:PHE:H	24:V:61:LEU:H	1.57	0.53
39:y:148:THR:O	39:y:152:CYS:N	2.41	0.53
1:1:454:G:H2'	1:1:455:G:C8	2.44	0.53
5:5:224:HIS:NE2	5:5:238:ASP:OD2	2.41	0.53
12:F:17:GLU:HA	12:F:20:LEU:HG	1.91	0.53
17:L:48:PRO:HB2	29:h:118:TYR:O	2.09	0.53
27:e:17:HIS:NE2	27:e:39:VAL:HG21	2.23	0.53
27:e:79:VAL:HG21	27:e:109:ALA:HB2	1.91	0.53
38:x:198:LEU:HD21	38:x:200:ILE:HG13	1.90	0.53
1:1:69:U:O2'	1:1:101:G:O2'	2.26	0.52
1:1:1371:G:H2'	1:1:1372:U:C6	2.44	0.52
1:1:3269:A:H4'	1:1:3272:U:N3	2.24	0.52
9:C:37:VAL:HG21	9:C:246:LEU:HD21	1.91	0.52
11:E:111:VAL:HG23	11:E:164:LEU:HD11	1.90	0.52
12:F:97:ARG:HG2	12:F:102:ILE:HD11	1.91	0.52
29:h:11:GLN:HB2	29:h:15:ASN:HD21	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:i:37:PHE:CD2	32:m:215:LEU:HD11	2.44	0.52
1:1:3406:A:H5"	8:B:223:GLY:HA3	1.90	0.52
2:2:49:A:O2'	31:j:59:THR:HG22	2.09	0.52
3:3:20:ILE:HD11	3:3:29:ARG:HG3	1.90	0.52
13:G:70:LYS:HD2	13:G:233:TRP:HB3	1.91	0.52
4:4:46:LYS:NZ	7:A:290:LEU:HB3	2.23	0.52
5:5:47:PHE:HB2	5:5:95:MET:CE	2.40	0.52
19:N:44:ARG:NH1	19:N:120:TRP:O	2.37	0.52
32:m:211:ARG:NH2	32:m:213:THR:OG1	2.42	0.52
1:1:602:A:C5	9:C:337:TYR:HE2	2.27	0.52
1:1:3410:G:OP2	1:1:3410:G:N2	2.31	0.52
10:D:343:MET:HE1	10:D:391:LEU:HB3	1.91	0.52
1:1:298:G:C6	1:1:299:C:C4	2.98	0.52
11:E:31:TYR:HB2	11:E:33:GLU:HG3	1.91	0.52
38:x:68:ASP:N	38:x:68:ASP:OD1	2.42	0.52
1:1:496:C:H2'	1:1:497:C:H6	1.75	0.52
1:1:521:C:H42	1:1:605:G:H1	1.57	0.52
1:1:709:G:H5"	17:L:35:ARG:HH12	1.75	0.52
1:1:1157:G:C4	1:1:1158:G:H1'	2.43	0.52
1:1:1341:G:H2'	1:1:1342:G:H8	1.74	0.52
1:1:3179:G:N2	1:1:3433:U:O2'	2.42	0.52
2:2:21:A:O2'	21:P:121:ALA:O	2.26	0.52
3:3:169:LEU:HA	3:3:174:TYR:HE2	1.75	0.52
1:1:112:U:OP1	29:h:109:LYS:NZ	2.43	0.52
1:1:822:U:H5"	9:C:114:LYS:HE3	1.91	0.52
1:1:1176:G:N2	1:1:1362:U:O2'	2.43	0.52
1:1:3475:U:H4'	1:1:3477:A:H61	1.74	0.52
5:5:103:MET:HG3	5:5:135:LEU:HD21	1.92	0.52
7:A:70:HIS:HE1	7:A:174:ILE:HG23	1.75	0.52
12:F:86:HIS:HB3	40:T:138:ALA:HB2	1.92	0.52
20:O:47:HIS:NE2	20:O:49:PHE:HB2	2.24	0.52
24:V:57:GLY:N	24:V:80:VAL:O	2.43	0.52
37:v:164:HIS:O	37:v:168:GLN:HG2	2.10	0.52
1:1:103:G:HO2'	1:1:726:C:HO2'	1.58	0.52
1:1:547:G:N2	1:1:576:U:O2'	2.43	0.52
5:5:160:THR:C	5:5:162:LYS:H	2.18	0.52
10:D:416:ASP:OD1	10:D:416:ASP:N	2.43	0.52
24:V:120:VAL:O	24:V:139:VAL:N	2.43	0.52
9:C:25:PRO:HD2	9:C:28:PHE:HD2	1.75	0.52
9:C:329:ARG:NH1	12:F:171:SER:O	2.42	0.52
23:S:79:ARG:HH22	23:S:86:THR:HG23	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:65:ARG:HE	25:Y:84:VAL:HG22	1.75	0.52
10:D:246:ASP:N	10:D:246:ASP:OD1	2.43	0.52
22:Q:16:SER:O	22:Q:33:ARG:NH2	2.43	0.52
24:V:27:CYS:H	24:V:35:ASN:HA	1.74	0.52
1:1:3368:A:C5	11:E:86:TYR:HE2	2.27	0.51
2:2:24:G:O2'	2:2:25:A:OP2	2.27	0.51
4:4:175:GLU:HG2	4:4:176:ASP:N	2.25	0.51
7:A:48:LEU:HD12	7:A:74:ASP:HB3	1.92	0.51
8:B:93:VAL:N	8:B:100:ARG:O	2.41	0.51
9:C:156:ASP:OD1	9:C:254:LYS:HB3	2.10	0.51
38:x:249:PHE:HA	38:x:261:THR:HA	1.92	0.51
5:5:323:ASP:OD1	5:5:323:ASP:N	2.36	0.51
1:1:29:C:H4'	1:1:62:A:H4'	1.92	0.51
1:1:339:G:P	37:v:6:GLN:HE21	2.33	0.51
1:1:3181:G:O2'	1:1:3432:U:O2'	2.28	0.51
7:A:70:HIS:CE1	7:A:175:PRO:HD2	2.45	0.51
9:C:273:LEU:HA	37:v:68:LYS:HD3	1.93	0.51
20:O:110:PRO:HG2	20:O:113:PHE:HD2	1.75	0.51
7:A:102:GLU:HB3	7:A:110:TYR:HB2	1.92	0.51
11:E:59:ILE:HB	11:E:102:ILE:HB	1.92	0.51
11:E:76:LEU:HG	11:E:77:GLU:H	1.75	0.51
17:L:69:VAL:HG11	30:i:11:LYS:HE2	1.93	0.51
25:Y:53:ASP:OD1	25:Y:109:HIS:N	2.42	0.51
38:x:55:ILE:HB	38:x:237:ARG:HH21	1.76	0.51
1:1:3104:G:H2'	1:1:3105:G:C8	2.45	0.51
1:1:3276:A:H1'	20:O:169:TYR:HB2	1.92	0.51
23:S:123:LEU:HA	40:T:153:PRO:HD2	1.93	0.51
1:1:257:A:H4'	1:1:258:U:N3	2.26	0.51
1:1:1184:A:N6	1:1:2460:A:O4'	2.43	0.51
1:1:3318:A:H61	28:f:6:HIS:H	1.59	0.51
4:4:173:TYR:HB2	4:4:177:VAL:HG12	1.92	0.51
5:5:256:LEU:HD23	5:5:272:ASP:HB3	1.93	0.51
1:1:277:G:OP2	19:N:44:ARG:NH1	2.40	0.51
1:1:633:A:C5	11:E:40:ARG:HD3	2.46	0.51
1:1:3280:U:H5"	1:1:3281:A:H2'	1.92	0.51
7:A:225:PHE:HE1	7:A:227:MET:HB2	1.76	0.51
11:E:133:VAL:HG21	11:E:143:ASN:HD22	1.75	0.51
21:P:9:ALA:HA	21:P:14:CYS:CB	2.40	0.51
27:e:92:GLU:OE1	27:e:117:THR:HB	2.11	0.51
1:1:70:A:N1	1:1:321:A:O2'	2.34	0.51
1:1:226:A:H8	1:1:1424:A:C5	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:158:ASN:HB2	5:5:161:CYS:HB3	1.91	0.51
5:5:162:LYS:HA	5:5:219:GLU:HG3	1.93	0.51
14:H:29:THR:HA	14:H:34:THR:HA	1.92	0.51
38:x:277:VAL:HB	38:x:290:PHE:HB3	1.92	0.51
1:1:422:U:H2'	1:1:423:G:C8	2.45	0.51
1:1:1158:G:C2	1:1:1163:C:C2	2.98	0.51
7:A:193:ILE:HG12	7:A:198:ILE:HG13	1.93	0.51
1:1:49:A:C6	1:1:287:U:H4'	2.46	0.50
1:1:369:A:OP1	31:j:26:SER:OG	2.22	0.50
1:1:2470:G:OP2	20:O:91:HIS:NE2	2.44	0.50
2:2:29:C:OP1	9:C:195:LYS:HE2	2.11	0.50
5:5:105:ALA:HB3	5:5:133:VAL:HG11	1.93	0.50
7:A:129:LEU:HD13	7:A:225:PHE:HB3	1.92	0.50
10:D:342:PHE:O	10:D:411:TYR:N	2.36	0.50
10:D:454:THR:O	10:D:456:LYS:NZ	2.31	0.50
39:y:199:VAL:HA	39:y:204:ALA:HA	1.92	0.50
1:1:340:C:OP1	37:v:9:LYS:NZ	2.27	0.50
5:5:314:ASP:OD1	5:5:314:ASP:N	2.38	0.50
11:E:166:PRO:O	11:E:169:LYS:NZ	2.33	0.50
17:L:47:ALA:HB3	17:L:48:PRO:HD3	1.94	0.50
30:i:49:ALA:HB3	30:i:52:GLU:HB3	1.92	0.50
1:1:1154:U:C2	1:1:1167:A:C2	2.99	0.50
17:L:42:LYS:O	17:L:46:ILE:HG12	2.10	0.50
27:e:75:ASN:OD1	27:e:75:ASN:N	2.43	0.50
1:1:544:A:H2'	1:1:545:A:C8	2.47	0.50
1:1:3231:U:H2'	1:1:3232:G:C8	2.46	0.50
4:4:196:VAL:HG12	4:4:199:ARG:NH2	2.25	0.50
4:4:200:LYS:O	4:4:204:LYS:NZ	2.42	0.50
9:C:147:ILE:HG23	9:C:152:LEU:HD22	1.93	0.50
1:1:3286:U:H2'	1:1:3287:A:C8	2.47	0.50
7:A:257:ALA:HA	7:A:260:ASN:HD21	1.76	0.50
12:F:95:ARG:HG2	12:F:118:ILE:HA	1.94	0.50
28:f:51:CYS:SG	28:f:102:MET:HE3	2.51	0.50
1:1:777:C:H3'	1:1:778:G:C5'	2.41	0.50
1:1:1220:C:N4	1:1:1347:U:OP2	2.45	0.50
1:1:3366:G:H2'	1:1:3367:A:C8	2.46	0.50
4:4:38:ARG:NH2	4:4:85:SER:OG	2.38	0.50
14:H:5:ILE:O	14:H:59:HIS:N	2.45	0.50
1:1:162:A:P	30:i:25:SER:HB3	2.52	0.50
1:1:405:A:H5"	1:1:407:A:OP1	2.11	0.50
1:1:3271:G:H5'	28:f:4:GLN:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:93:A:H2	16:K:126:SER:HA	1.76	0.50
10:D:162:THR:HA	10:D:213:ASN:HA	1.92	0.50
21:P:48:LEU:HB3	21:P:52:LYS:HZ1	1.76	0.50
1:1:494:A:H5"	3:3:123:ARG:NH1	2.27	0.50
1:1:996:G:O2'	1:1:997:A:OP1	2.27	0.50
1:1:1207:C:H2'	1:1:1208:G:N2	2.26	0.50
3:3:87:ALA:O	3:3:91:GLU:HG2	2.11	0.50
7:A:142:LEU:HA	15:J:174:MET:HA	1.94	0.50
28:f:50:VAL:HG23	28:f:101:VAL:HG22	1.94	0.50
30:i:78:LEU:O	30:i:82:LYS:N	2.36	0.50
1:1:201:U:H2'	1:1:202:U:C6	2.47	0.50
1:1:508:C:H4'	1:1:648:U:H4'	1.94	0.50
1:1:581:A:C5	1:1:582:G:H1'	2.47	0.50
1:1:615:G:O2'	11:E:35:VAL:O	2.25	0.50
1:1:984:A:H2'	1:1:985:G:O4'	2.12	0.50
1:1:3319:G:N1	11:E:181:SER:OG	2.44	0.50
4:4:52:MET:HE3	4:4:105:LYS:HB2	1.94	0.50
4:4:159:PHE:HB3	4:4:205:ARG:HE	1.77	0.50
12:F:54:ARG:HH21	12:F:58:TYR:HH	1.59	0.50
13:G:142:LEU:HD13	13:G:201:THR:HG21	1.94	0.50
31:j:58:THR:O	31:j:61:THR:OG1	2.27	0.50
37:v:170:LEU:HB3	37:v:182:MET:HE2	1.94	0.50
1:1:1343:C:O2'	20:O:84:ALA:O	2.29	0.49
1:1:3359:U:H5"	1:1:3361:U:H5	1.76	0.49
1:1:3410:G:H3'	1:1:3411:A:H8	1.77	0.49
4:4:45:TRP:HB3	4:4:90:THR:HG21	1.94	0.49
19:N:178:HIS:CD2	19:N:179:ARG:HD3	2.47	0.49
20:O:22:SER:HA	20:O:88:MET:HE2	1.92	0.49
1:1:67:A:N1	1:1:308:G:O2'	2.38	0.49
3:3:143:ARG:HD2	3:3:147:ARG:HH21	1.77	0.49
6:6:57:A:O2'	6:6:58:A:H5"	2.12	0.49
29:h:29:SER:HA	29:h:32:VAL:HG22	1.94	0.49
1:1:762:U:H3'	1:1:763:G:H8	1.77	0.49
1:1:3331:U:H3	1:1:3356:A:H61	1.61	0.49
1:1:489:C:H2'	1:1:490:U:C6	2.47	0.49
1:1:3242:G:O2'	8:B:101:SER:O	2.28	0.49
1:1:3413:U:H2'	1:1:3414:U:C6	2.47	0.49
3:3:120:LEU:O	3:3:124:ARG:HG2	2.12	0.49
8:B:85:VAL:HA	8:B:202:THR:HA	1.94	0.49
10:D:135:THR:OG1	10:D:398:ARG:NE	2.46	0.49
10:D:257:MET:N	10:D:257:MET:HE2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:75:LYS:O	12:F:79:GLU:HG3	2.12	0.49
38:x:179:LEU:HD23	38:x:179:LEU:H	1.77	0.49
1:1:493:G:H4'	1:1:494:A:OP2	2.13	0.49
1:1:728:G:O6	7:A:269:ARG:NH2	2.41	0.49
1:1:3343:A:H2	20:O:157:LEU:HD22	1.76	0.49
4:4:193:SER:O	4:4:199:ARG:NH1	2.45	0.49
5:5:41:ARG:NH2	38:x:77:GLU:O	2.46	0.49
17:L:79:GLU:CD	17:L:101:ARG:HH22	2.19	0.49
27:e:6:ILE:HA	27:e:60:THR:HG21	1.94	0.49
29:h:22:GLU:O	29:h:25:GLN:HB2	2.11	0.49
1:1:1156:U:H2'	1:1:1157:G:C8	2.46	0.49
5:5:51:HIS:ND1	5:5:56:PHE:HE1	2.11	0.49
5:5:249:PHE:CZ	5:5:285:LYS:HD3	2.46	0.49
1:1:1158:G:H3'	1:1:1159:U:H6	1.76	0.49
1:1:2442:C:OP1	21:P:86:LYS:NZ	2.39	0.49
1:1:3203:C:H2'	1:1:3204:G:C8	2.48	0.49
1:1:136:U:N3	31:j:77:GLY:O	2.46	0.49
1:1:1154:U:H3	1:1:1166:A:H61	1.60	0.49
5:5:157:CYS:HG	5:5:171:TRP:CD1	2.31	0.49
7:A:44:LYS:N	7:A:96:ASN:OD1	2.46	0.49
8:B:59:ASP:HA	8:B:71:GLU:HA	1.95	0.49
12:F:129:ALA:O	12:F:133:MET:HB2	2.13	0.49
25:Y:85:THR:HA	25:Y:95:PRO:HA	1.95	0.49
1:1:446:U:H3	1:1:644:A:HO2'	1.61	0.49
1:1:709:G:OP2	17:L:28:GLN:NE2	2.28	0.49
3:3:176:ASP:OD1	3:3:176:ASP:N	2.45	0.49
1:1:366:G:N2	1:1:369:A:OP2	2.44	0.49
1:1:644:A:N3	1:1:644:A:H2'	2.28	0.49
1:1:699:G:O2'	9:C:118:ASN:OD1	2.27	0.49
9:C:205:ARG:NH2	9:C:238:LEU:O	2.46	0.49
13:G:219:ASP:O	13:G:223:SER:OG	2.29	0.49
17:L:105:SER:OG	17:L:107:GLU:HG3	2.12	0.49
1:1:1438:G:H5"	27:e:61:ARG:HG2	1.95	0.48
9:C:10:ILE:HD11	9:C:22:LEU:HG	1.94	0.48
9:C:110:LYS:HE3	19:N:201:ARG:HG3	1.94	0.48
9:C:145:GLU:HB2	9:C:178:ARG:HH12	1.78	0.48
20:O:126:ARG:HG3	20:O:130:LEU:HD13	1.95	0.48
28:f:72:ILE:HD12	28:f:82:VAL:HG21	1.93	0.48
39:y:5:ALA:N	39:y:206:ALA:O	2.46	0.48
39:y:104:LEU:O	39:y:108:VAL:N	2.37	0.48
1:1:21:G:H22	2:2:146:A:H2	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:184:C:O2	1:1:249:G:N2	2.46	0.48
1:1:449:U:H1'	1:1:450:A:N9	2.28	0.48
1:1:1361:A:P	28:f:25:HIS:HE2	2.36	0.48
3:3:143:ARG:HD2	3:3:147:ARG:NH2	2.27	0.48
4:4:197:VAL:O	4:4:201:THR:HG22	2.13	0.48
6:6:82:A:HO2'	6:6:83:A:H8	1.60	0.48
7:A:92:LEU:HD13	30:i:78:LEU:HD11	1.95	0.48
31:j:35:ALA:O	31:j:45:ARG:NE	2.45	0.48
1:1:50:U:H2'	1:1:51:A:C8	2.49	0.48
1:1:446:U:H5"	1:1:447:C:N4	2.28	0.48
1:1:495:A:H5"	3:3:127:LEU:HD11	1.95	0.48
1:1:1150:C:H2'	1:1:1151:A:C8	2.48	0.48
1:1:3354:U:H2'	1:1:3355:G:H8	1.77	0.48
2:2:43:C:H5"	29:h:87:THR:HG22	1.95	0.48
2:2:114:C:H4'	2:2:115:G:H5"	1.96	0.48
7:A:137:MET:HG2	7:A:222:GLY:HA3	1.95	0.48
38:x:174:PHE:HB3	38:x:272:MET:HB3	1.94	0.48
1:1:1386:G:N2	1:1:1393:U:OP1	2.46	0.48
1:1:3275:A:C4	20:O:115:LYS:HA	2.47	0.48
1:1:3359:U:H5"	1:1:3361:U:C5	2.48	0.48
19:N:16:SER:HB2	30:i:46:ALA:O	2.14	0.48
1:1:662:C:O2'	1:1:663:C:O5'	2.30	0.48
2:2:126:C:H2'	2:2:127:U:C6	2.48	0.48
9:C:109:ARG:HG2	9:C:110:LYS:N	2.28	0.48
10:D:327:LEU:HD21	10:D:352:MET:HE1	1.96	0.48
17:L:46:ILE:HD12	17:L:49:ARG:HE	1.79	0.48
20:O:111:PRO:N	20:O:112:PRO:HD2	2.29	0.48
1:1:224:U:H4'	25:Y:99:ASP:OD2	2.13	0.48
1:1:444:A:C4	1:1:649:G:N2	2.82	0.48
1:1:499:G:H4'	1:1:499:G:OP1	2.13	0.48
4:4:37:GLU:HG2	4:4:40:ASP:H	1.79	0.48
6:6:92:G:N2	13:G:216:SER:OG	2.37	0.48
10:D:316:VAL:HG23	10:D:438:LEU:HD11	1.94	0.48
26:b:434:GLU:HA	26:b:442:ALA:HB2	1.94	0.48
27:e:103:VAL:O	27:e:107:GLU:HG2	2.12	0.48
38:x:70:PRO:HB2	38:x:75:GLN:HE22	1.79	0.48
1:1:1401:G:N2	1:1:1402:U:O4	2.45	0.48
4:4:34:LYS:HE3	4:4:36:PHE:CE1	2.48	0.48
9:C:208:LEU:HD11	9:C:230:VAL:HG12	1.94	0.48
19:N:96:ARG:HH21	19:N:104:GLU:HG3	1.77	0.48
20:O:92:LYS:HE3	20:O:92:LYS:HB3	1.75	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:O:148:TRP:CD1	20:O:148:TRP:C	2.92	0.48
38:x:8:ILE:O	38:x:12:GLN:HG2	2.14	0.48
1:1:393:A:H4'	38:x:26:LEU:HD13	1.96	0.48
1:1:500:U:O2'	1:1:501:G:OP1	2.26	0.48
1:1:601:C:O2'	1:1:603:C:OP1	2.30	0.48
1:1:1224:A:H3'	1:1:1225:G:H8	1.77	0.48
1:1:3156:C:O3'	1:1:3472:G:N2	2.47	0.48
5:5:222:CYS:HB3	5:5:224:HIS:CE1	2.48	0.48
5:5:323:ASP:O	5:5:325:LYS:NZ	2.37	0.48
7:A:68:MET:HE2	7:A:68:MET:HA	1.95	0.48
10:D:185:LEU:HD11	10:D:214:LEU:HD13	1.95	0.48
21:P:19:GLY:N	21:P:146:ILE:O	2.43	0.48
23:S:45:LYS:HZ2	23:S:51:LYS:HE3	1.79	0.48
1:1:120:G:P	13:G:128:LYS:HZ1	2.34	0.48
1:1:1454:C:OP2	9:C:195:LYS:NZ	2.45	0.48
1:1:1481:G:H22	1:1:2443:G:H3'	1.79	0.48
9:C:110:LYS:HE3	19:N:201:ARG:H	1.79	0.48
9:C:286:ASN:HD21	9:C:291:ARG:HD2	1.79	0.48
9:C:286:ASN:ND2	9:C:291:ARG:HD2	2.28	0.48
10:D:150:MET:HA	10:D:150:MET:HE2	1.94	0.48
13:G:201:THR:OG1	13:G:202:GLU:N	2.46	0.48
17:L:69:VAL:HG21	30:i:11:LYS:HB2	1.96	0.48
28:f:56:SER:OG	28:f:66:ARG:NH1	2.47	0.48
37:v:122:ASP:OD1	37:v:122:ASP:N	2.46	0.48
1:1:620:C:O2	9:C:329:ARG:HD3	2.13	0.48
1:1:1206:C:H1'	20:O:88:MET:HE3	1.96	0.48
1:1:3208:G:H21	1:1:3218:A:H62	1.62	0.48
1:1:3418:U:O2	1:1:3419:G:N2	2.47	0.48
2:2:19:C:H2'	2:2:20:A:C8	2.49	0.48
4:4:68:LEU:HA	4:4:71:LEU:HG	1.96	0.48
10:D:198:GLY:O	10:D:499:GLN:NE2	2.46	0.48
11:E:85:PRO:O	11:E:89:ASN:N	2.43	0.48
17:L:46:ILE:O	17:L:46:ILE:HG13	2.14	0.48
24:V:105:VAL:HA	24:V:111:MET:HA	1.95	0.48
27:e:102:ARG:NH1	27:e:121:ALA:HB3	2.29	0.48
1:1:1012:A:O2'	1:1:1013:U:O5'	2.32	0.47
1:1:3351:U:H2'	1:1:3352:A:H8	1.79	0.47
4:4:50:TYR:HA	4:4:53:TRP:HB2	1.96	0.47
5:5:71:GLN:HE21	5:5:75:ILE:HG22	1.79	0.47
5:5:205:GLU:HA	5:5:224:HIS:HB2	1.96	0.47
10:D:417:PRO:HB3	10:D:448:PHE:HE1	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:G:231:ARG:HG2	32:m:202:TYR:CD2	2.48	0.47
1:1:716:G:H1	25:Y:5:ARG:HD2	1.79	0.47
1:1:1381:G:N2	1:1:1389:A:H62	2.11	0.47
17:L:122:HIS:CD2	30:i:3:PRO:HD3	2.49	0.47
18:M:38:LEU:HA	18:M:50:VAL:HA	1.96	0.47
37:v:194:ASN:ND2	37:v:196:SER:OG	2.47	0.47
1:1:451:C:H5"	11:E:26:LYS:NZ	2.30	0.47
1:1:979:G:H5"	27:e:52:ILE:HB	1.96	0.47
1:1:1327:C:H2'	1:1:1328:C:C6	2.50	0.47
1:1:3128:A:H2'	1:1:3129:A:C8	2.50	0.47
4:4:27:GLN:OE1	4:4:74:ILE:HD12	2.15	0.47
5:5:122:ARG:NH2	5:5:170:LEU:O	2.46	0.47
11:E:152:GLU:H	11:E:152:GLU:CD	2.22	0.47
23:S:77:TRP:CD1	23:S:90:TYR:HB2	2.49	0.47
32:m:102:ILE:HG13	32:m:104:ALA:H	1.78	0.47
1:1:157:A:P	19:N:147:ARG:HH12	2.38	0.47
1:1:280:G:N2	30:i:75:LEU:O	2.42	0.47
3:3:162:GLU:OE2	38:x:261:THR:N	2.47	0.47
9:C:362:GLU:OE2	23:S:25:ARG:NH1	2.47	0.47
24:V:37:TYR:O	24:V:63:THR:N	2.47	0.47
30:i:56:MET:HE3	30:i:60:ARG:HH12	1.79	0.47
1:1:359:A:N3	1:1:359:A:H2'	2.29	0.47
1:1:1473:U:H2'	1:1:1474:G:C8	2.49	0.47
1:1:3303:C:H2'	1:1:3304:U:C6	2.50	0.47
20:O:4:PHE:HB2	20:O:32:GLN:NE2	2.29	0.47
1:1:778:G:H4'	1:1:778:G:OP1	2.14	0.47
1:1:832:G:N2	9:C:104:PRO:HD2	2.28	0.47
1:1:1357:A:O2'	28:f:78:ASN:ND2	2.45	0.47
1:1:3210:A:N6	1:1:3215:U:O2	2.47	0.47
1:1:3403:U:O2'	1:1:3405:C:N4	2.34	0.47
2:2:45:A:OP2	29:h:88:ARG:NH1	2.47	0.47
4:4:76:TRP:CD1	4:4:77:ILE:H	2.32	0.47
5:5:136:HIS:NE2	5:5:205:GLU:OE1	2.40	0.47
5:5:276:GLN:OE1	5:5:290:ARG:NH1	2.48	0.47
13:G:160:ILE:O	13:G:164:VAL:HG13	2.14	0.47
1:1:447:C:O3'	1:1:449:U:OP1	2.33	0.47
1:1:548:U:H1'	1:1:581:A:C8	2.50	0.47
1:1:1022:U:H3	1:1:1091:G:H1	1.63	0.47
1:1:1382:C:OP1	3:3:103:ARG:NE	2.45	0.47
1:1:3147:U:H3	1:1:3187:A:H61	1.63	0.47
5:5:14:PHE:HB3	5:5:34:GLN:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:6:2:C:C6	35:t:55:GLU:HG3	2.49	0.47
11:E:84:GLY:H	11:E:91:VAL:HB	1.79	0.47
13:G:118:ASN:OD1	13:G:119:GLY:N	2.48	0.47
13:G:225:LYS:HB2	13:G:225:LYS:NZ	2.30	0.47
19:N:143:ARG:O	19:N:149:ASN:ND2	2.26	0.47
20:O:4:PHE:HB2	20:O:32:GLN:HE22	1.79	0.47
20:O:12:ALA:HB1	20:O:42:LEU:HG	1.97	0.47
30:i:84:LYS:HG3	30:i:88:LEU:HD23	1.96	0.47
1:1:86:G:O2'	1:1:98:G:O6	2.32	0.47
1:1:652:U:H2'	1:1:653:U:C6	2.50	0.47
7:A:104:ARG:HG3	7:A:105:ARG:HD2	1.96	0.47
38:x:54:THR:HG23	38:x:57:SER:H	1.78	0.47
1:1:497:C:H2'	1:1:498:U:O4'	2.15	0.47
1:1:1388:G:OP2	3:3:41:GLN:HG3	2.15	0.47
9:C:46:LYS:HB3	9:C:49:ARG:HH11	1.78	0.47
24:V:26:ASN:O	24:V:102:GLY:N	2.47	0.47
25:Y:80:LEU:HD13	25:Y:80:LEU:HA	1.78	0.47
29:h:98:GLU:HA	29:h:101:ARG:HG2	1.97	0.47
1:1:547:G:H1'	1:1:548:U:H5	1.80	0.47
1:1:551:C:H1'	1:1:575:G:H1	1.79	0.47
1:1:731:A:H3'	1:1:732:A:H5"	1.97	0.47
1:1:3115:U:O2'	26:b:410:GLY:N	2.48	0.47
7:A:150:SER:OG	7:A:189:CYS:O	2.24	0.47
9:C:333:TYR:CE1	12:F:56:GLU:HG2	2.46	0.47
16:K:13:LEU:O	16:K:15:LYS:N	2.48	0.47
25:Y:30:MET:O	25:Y:49:VAL:HG22	2.15	0.47
27:e:100:ARG:O	27:e:103:VAL:HG22	2.15	0.47
1:1:232:C:OP1	25:Y:46:SER:HB3	2.14	0.46
1:1:416:A:N3	1:1:680:C:O2'	2.44	0.46
1:1:1419:U:H4'	3:3:29:ARG:NH1	2.30	0.46
10:D:165:ILE:HG13	10:D:237:LEU:HD11	1.97	0.46
12:F:148:HIS:HB2	12:F:196:TYR:CE1	2.50	0.46
24:V:33:ALA:HA	24:V:68:LYS:H	1.80	0.46
32:m:197:ASP:OD1	32:m:197:ASP:N	2.48	0.46
1:1:1161:A:H3'	1:1:1162:G:C8	2.45	0.46
4:4:141:TRP:HB3	4:4:146:PHE:HD2	1.79	0.46
7:A:194:ALA:HB3	7:A:199:TRP:HE1	1.79	0.46
10:D:173:LEU:O	10:D:177:ILE:HG12	2.14	0.46
38:x:237:ARG:HG3	38:x:304:PHE:CZ	2.50	0.46
1:1:165:A:H2'	1:1:166:A:O4'	2.15	0.46
1:1:454:G:H2'	1:1:455:G:H8	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:106:U:H5'	29:h:61:ASN:OD1	2.15	0.46
13:G:197:VAL:O	13:G:198:LEU:HD23	2.16	0.46
20:O:114:ASP:OD1	20:O:115:LYS:N	2.48	0.46
27:e:9:LYS:NZ	27:e:55:GLY:O	2.40	0.46
1:1:765:G:H2'	1:1:766:G:C8	2.50	0.46
1:1:3104:G:H2'	1:1:3105:G:H8	1.80	0.46
9:C:94:ASN:OD1	9:C:94:ASN:N	2.47	0.46
9:C:208:LEU:HD23	9:C:250:VAL:HG22	1.96	0.46
12:F:82:TYR:HE1	23:S:9:VAL:HG11	1.80	0.46
29:h:99:GLN:O	29:h:99:GLN:HG3	2.15	0.46
1:1:53:G:P	31:j:48:ASN:HD22	2.36	0.46
1:1:505:G:P	1:1:505:G:H8	2.38	0.46
1:1:3369:A:OP2	11:E:64:ARG:NH1	2.47	0.46
5:5:315:ARG:HH21	38:x:290:PHE:HZ	1.62	0.46
11:E:93:ILE:HB	11:E:124:PHE:HZ	1.81	0.46
11:E:114:VAL:HA	11:E:163:LYS:HD3	1.96	0.46
24:V:24:ILE:HA	24:V:37:TYR:HA	1.97	0.46
38:x:1:MET:HG3	38:x:2:GLY:H	1.80	0.46
4:4:194:HIS:CG	22:Q:79:ASN:HD21	2.33	0.46
7:A:46:LEU:HB3	7:A:98:ILE:HA	1.98	0.46
10:D:315:TYR:HA	10:D:439:MET:HB3	1.97	0.46
1:1:33:G:O6	1:1:49:A:H1'	2.16	0.46
4:4:159:PHE:HB3	4:4:205:ARG:HH21	1.81	0.46
5:5:95:MET:HA	5:5:103:MET:O	2.15	0.46
7:A:50:SER:OG	7:A:51:ARG:N	2.49	0.46
13:G:227[B]:ASP:O	13:G:231:ARG:NH1	2.48	0.46
17:L:48:PRO:HG3	37:v:33:ASN:HD22	1.80	0.46
20:O:23:VAL:HG21	20:O:121:VAL:HG11	1.97	0.46
24:V:116:ILE:H	24:V:134:ASN:C	2.24	0.46
33:o:132:LEU:N	33:o:152:GLU:O	2.48	0.46
1:1:118:U:H1'	32:m:230:HIS:NE2	2.31	0.46
1:1:584:C:H2'	1:1:585:C:C6	2.51	0.46
2:2:150:C:O2'	19:N:136:ASP:OD2	2.24	0.46
9:C:145:GLU:HB2	9:C:178:ARG:NH1	2.30	0.46
9:C:195:LYS:HD2	9:C:200:ARG:NH1	2.30	0.46
10:D:171:ARG:HD2	10:D:197:GLY:O	2.16	0.46
10:D:445:GLU:OE2	10:D:501:TYR:OH	2.27	0.46
1:1:74:A:H5"	17:L:104:ARG:HH11	1.80	0.46
1:1:997:A:H3'	1:1:998:U:H5"	1.96	0.46
1:1:3286:U:H3	1:1:3301:C:H42	1.64	0.46
5:5:103:MET:O	5:5:104:LEU:HD22	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:290:ARG:H	5:5:324:ARG:HE	1.63	0.46
6:6:82:A:O2'	6:6:83:A:H8	1.99	0.46
10:D:126:GLY:HA2	10:D:270:GLN:HE21	1.81	0.46
13:G:80:LYS:HE2	13:G:229:SER:HB3	1.97	0.46
17:L:121:ALA:HB2	37:v:128:ILE:HB	1.98	0.46
1:1:1150:C:H2'	1:1:1151:A:H8	1.81	0.46
5:5:17:ILE:HG13	5:5:21:THR:HB	1.98	0.46
9:C:35:ASP:OD1	9:C:36:LEU:N	2.49	0.46
11:E:139:PHE:HE1	38:x:127:ARG:HA	1.81	0.46
13:G:166:LEU:HD23	13:G:166:LEU:HA	1.80	0.46
17:L:48:PRO:CB	29:h:119:ALA:HB2	2.46	0.46
2:2:151:U:H2'	2:2:152:G:O4'	2.17	0.45
3:3:51:ALA:HB2	3:3:100:TRP:CZ3	2.51	0.45
5:5:321:ASP:OD1	5:5:325:LYS:N	2.40	0.45
7:A:68:MET:HE1	7:A:174:ILE:HG12	1.98	0.45
10:D:200:ASN:O	10:D:204:GLU:N	2.48	0.45
12:F:146:PRO:HA	12:F:243:ASN:OD1	2.16	0.45
13:G:85:ASN:C	13:G:85:ASN:OD1	2.59	0.45
13:G:130:TYR:HE1	13:G:202:GLU:HB3	1.81	0.45
1:1:14:U:H5"	1:1:15:C:OP2	2.16	0.45
1:1:762:U:H5'	1:1:764:U:O4	2.15	0.45
1:1:984:A:O2'	1:1:1145:U:O2	2.32	0.45
1:1:2440:A:OP1	21:P:83:TRP:N	2.42	0.45
1:1:3222:C:H2'	1:1:3223:A:C8	2.50	0.45
5:5:286:LYS:HB2	5:5:286:LYS:HE2	1.76	0.45
10:D:418:ARG:CD	10:D:418:ARG:H	2.29	0.45
13:G:90:VAL:HG22	13:G:214:ILE:HG21	1.99	0.45
17:L:59:LYS:HD3	17:L:66:ASN:O	2.16	0.45
23:S:136:ARG:HB2	23:S:139:VAL:HG12	1.98	0.45
29:h:72:TYR:CE2	29:h:79:PRO:HD3	2.51	0.45
37:v:187:LYS:HD2	37:v:187:LYS:N	2.30	0.45
38:x:142:LYS:NZ	38:x:143:ARG:HH21	2.13	0.45
1:1:265:C:H4'	17:L:81:LYS:HZ1	1.81	0.45
1:1:1157:G:H1	1:1:1163:C:N4	2.10	0.45
11:E:47:LYS:HA	11:E:47:LYS:HD3	1.64	0.45
27:e:94:ALA:HB3	27:e:97:VAL:HG23	1.98	0.45
1:1:201:U:H2'	1:1:202:U:H6	1.81	0.45
1:1:762:U:H5'	1:1:764:U:C4	2.52	0.45
1:1:1423:G:H5"	27:e:98:SER:HB3	1.97	0.45
1:1:3271:G:N7	11:E:185:SER:HB2	2.32	0.45
1:1:3327:A:C5	1:1:3328:U:H1'	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:E:49:ARG:H	11:E:52:LEU:HD12	1.81	0.45
12:F:223:GLU:HG2	12:F:224:ARG:H	1.81	0.45
17:L:62:THR:O	17:L:66:ASN:HB3	2.17	0.45
23:S:142:LEU:HA	23:S:147:LEU:HD11	1.98	0.45
24:V:27:CYS:HA	24:V:102:GLY:O	2.17	0.45
1:1:184:C:H4'	37:v:37:GLN:NE2	2.31	0.45
1:1:446:U:H2'	1:1:447:C:C4	2.51	0.45
1:1:710:G:N2	37:v:65:GLY:H	2.04	0.45
1:1:716:G:H1	25:Y:5:ARG:HE	1.65	0.45
1:1:3107:A:N3	1:1:3108:A:O2'	2.46	0.45
1:1:3367:A:N6	11:E:86:TYR:O	2.47	0.45
17:L:127:PRO:HD2	37:v:148:LYS:HE3	1.99	0.45
1:1:22:G:N2	2:2:48:A:N3	2.49	0.45
1:1:27:C:N4	1:1:57:A:H61	2.14	0.45
1:1:66:A:H3'	1:1:324:U:H5"	1.99	0.45
1:1:388:U:OP1	38:x:46:ARG:NH1	2.45	0.45
1:1:1162:G:N3	1:1:1162:G:H2'	2.32	0.45
4:4:46:LYS:HE2	4:4:46:LYS:HB2	1.51	0.45
4:4:118:PHE:HB2	4:4:172:VAL:HG21	1.98	0.45
9:C:295:SER:OG	9:C:297:GLU:OE1	2.29	0.45
10:D:195:VAL:HG21	10:D:225:HIS:HD2	1.81	0.45
10:D:241:VAL:HG13	10:D:272:LEU:HB2	1.98	0.45
13:G:233:TRP:NE1	32:m:200:PRO:O	2.48	0.45
19:N:119:TYR:OH	19:N:131:GLU:OE1	2.21	0.45
20:O:75:ARG:HG2	20:O:147:GLY:HA3	1.97	0.45
25:Y:68:LYS:H	25:Y:82:GLU:CD	2.24	0.45
25:Y:68:LYS:N	25:Y:82:GLU:OE2	2.47	0.45
27:e:102:ARG:CZ	27:e:121:ALA:HB3	2.47	0.45
1:1:481:A:OP1	3:3:61:TYR:OH	2.27	0.45
1:1:2462:C:O2	1:1:2463:G:N1	2.50	0.45
1:1:3135:G:H2'	1:1:3136:A:H8	1.81	0.45
7:A:43:GLN:HA	7:A:96:ASN:HD21	1.81	0.45
7:A:79:SER:HB3	7:A:82:ARG:HB2	1.98	0.45
10:D:336:LYS:HB3	10:D:336:LYS:HE2	1.80	0.45
10:D:415:ASP:OD1	10:D:415:ASP:N	2.46	0.45
11:E:150:PRO:HG2	11:E:153:ARG:HG3	1.99	0.45
12:F:217:PRO:HD3	12:F:249:MET:HE2	1.98	0.45
25:Y:73:TYR:HE1	25:Y:76:LYS:HD2	1.82	0.45
38:x:81:ASP:OD1	38:x:81:ASP:C	2.60	0.45
1:1:709:G:H5"	17:L:35:ARG:NH1	2.32	0.45
5:5:90:ALA:HB2	5:5:108:ASP:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:188:VAL:N	7:A:203:TYR:O	2.48	0.45
19:N:9:GLU:HA	19:N:12:LYS:HD2	1.99	0.45
29:h:3:LEU:HB2	29:h:52:ASP:OD1	2.17	0.45
29:h:107:ILE:HD13	29:h:107:ILE:HA	1.82	0.45
37:v:179:PHE:O	37:v:182:MET:HG2	2.17	0.45
1:1:220:A:H2	25:Y:8:THR:O	2.00	0.45
1:1:447:C:C5	38:x:103:ARG:HD3	2.51	0.45
1:1:1163:C:C2	1:1:1164:A:C8	3.05	0.45
9:C:13:LYS:HD3	9:C:157:ALA:HB1	1.98	0.45
20:O:28:LEU:HD13	20:O:28:LEU:HA	1.85	0.45
1:1:330:U:H5"	1:1:331:A:OP1	2.17	0.45
1:1:361:G:O2'	31:j:56:ARG:HG2	2.17	0.45
1:1:486:G:N2	1:1:488:A:H62	2.10	0.45
1:1:592:U:O2	9:C:345:SER:HA	2.17	0.45
1:1:646:A:HO2'	1:1:647:A:H8	1.65	0.45
1:1:1422:U:O4	9:C:188:LYS:HD2	2.17	0.45
1:1:1455:A:H2'	1:1:1456:G:C8	2.52	0.45
1:1:3135:G:H2'	1:1:3136:A:C8	2.51	0.45
2:2:141:A:H2'	2:2:142:A:C8	2.52	0.45
7:A:200:PHE:O	7:A:224:ARG:HA	2.17	0.45
12:F:79:GLU:OE1	12:F:81:ASN:ND2	2.49	0.45
19:N:47:LYS:HD2	19:N:50:ARG:HH11	1.82	0.45
22:Q:28:LEU:HD11	22:Q:125:LEU:HB2	1.99	0.45
27:e:64:MET:HE2	27:e:64:MET:HB3	1.78	0.45
38:x:83:PHE:HB2	38:x:213:ARG:NH1	2.32	0.45
1:1:389:U:H2'	1:1:390:U:C6	2.52	0.44
1:1:1205:G:H21	20:O:88:MET:CE	2.29	0.44
1:1:3332:U:H2'	1:1:3333:G:C8	2.52	0.44
5:5:208:ILE:HG12	5:5:282:HIS:HD2	1.82	0.44
9:C:333:TYR:OH	12:F:56:GLU:OE2	2.30	0.44
12:F:160:PHE:HD2	12:F:167:ARG:HG2	1.82	0.44
19:N:179:ARG:HD2	19:N:179:ARG:HA	1.72	0.44
21:P:11:GLU:HA	21:P:105:LYS:HZ3	1.83	0.44
1:1:428:G:H1'	1:1:2472:A:H2'	1.99	0.44
1:1:642:A:H2'	1:1:643:C:O4'	2.17	0.44
1:1:761:U:H1'	1:1:762:U:OP2	2.17	0.44
3:3:133:LEU:HD12	3:3:133:LEU:HA	1.87	0.44
5:5:271:ALA:HB2	5:5:277:ILE:HG23	1.98	0.44
11:E:61:LEU:HD11	11:E:102:ILE:HG12	1.99	0.44
12:F:210:TRP:CD1	12:F:211:PRO:HD2	2.52	0.44
13:G:80:LYS:HB3	13:G:226:TYR:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:L:105:SER:O	17:L:108:SER:OG	2.32	0.44
30:i:86:GLU:HA	30:i:89:THR:HG22	1.99	0.44
39:y:35:TYR:O	39:y:39:GLU:N	2.44	0.44
1:1:166:A:N6	1:1:167:G:O6	2.50	0.44
1:1:699:G:H2'	1:1:700:C:O4'	2.16	0.44
1:1:1158:G:C3'	1:1:1159:U:H5'	2.48	0.44
1:1:2463:G:H1'	1:1:2464:G:H3'	1.99	0.44
3:3:106:HIS:NE2	3:3:110:GLN:OE1	2.50	0.44
4:4:76:TRP:HD1	4:4:77:ILE:H	1.64	0.44
9:C:211:PHE:HB3	9:C:217:ILE:HD13	1.99	0.44
9:C:331:ASN:ND2	12:F:189:GLU:OE2	2.50	0.44
16:K:152:ARG:C	16:K:154:LEU:H	2.25	0.44
21:P:11:GLU:HA	21:P:105:LYS:NZ	2.32	0.44
21:P:50:ASN:HB3	21:P:55:LYS:HB2	1.99	0.44
22:Q:107:PHE:CE2	22:Q:122:VAL:HB	2.52	0.44
1:1:391:G:N2	1:1:394:A:OP2	2.31	0.44
1:1:3243:A:H4'	8:B:103:THR:HA	2.00	0.44
1:1:3343:A:C8	20:O:111:PRO:HG3	2.52	0.44
5:5:303:CYS:HA	5:5:308:VAL:HA	1.98	0.44
10:D:312:GLU:N	10:D:458:SER:HG	2.15	0.44
21:P:30:ARG:NH2	21:P:62:ARG:HD2	2.33	0.44
27:e:17:HIS:HB2	27:e:47:ILE:HD11	2.00	0.44
1:1:49:A:H4'	1:1:49:A:OP1	2.18	0.44
1:1:3242:G:H2'	1:1:3243:A:C8	2.52	0.44
5:5:103:MET:HG2	5:5:113:PHE:HE1	1.83	0.44
5:5:129:PRO:O	5:5:147:GLY:HA3	2.18	0.44
9:C:22:LEU:HD21	9:C:254:LYS:HZ2	1.82	0.44
9:C:297:GLU:CD	9:C:297:GLU:H	2.25	0.44
13:G:91:PHE:HE2	13:G:185:ARG:HB3	1.82	0.44
17:L:25:TRP:O	19:N:199:ARG:HD3	2.17	0.44
17:L:102:ARG:HH21	30:i:23:ARG:NH1	2.16	0.44
38:x:108:CYS:HB2	38:x:153:GLU:OE1	2.18	0.44
1:1:676:G:O2'	1:1:1469:A:OP1	2.32	0.44
5:5:172:ARG:HB2	5:5:175:ASN:HB2	2.00	0.44
10:D:245:ALA:HB2	10:D:273:LEU:HD11	2.00	0.44
11:E:86:TYR:HE1	11:E:92:PRO:HA	1.82	0.44
11:E:139:PHE:CE2	38:x:136:ILE:HD12	2.53	0.44
20:O:110:PRO:HB2	20:O:112:PRO:HD2	1.99	0.44
30:i:56:MET:HG2	30:i:88:LEU:HD12	1.99	0.44
1:1:307:G:H2'	1:1:308:G:C8	2.52	0.44
1:1:443:C:H2'	1:1:444:A:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:529:G:OP2	12:F:74:ARG:NH2	2.48	0.44
1:1:1324:U:H2'	1:1:1325:A:C8	2.53	0.44
3:3:172:GLY:HA2	3:3:174:TYR:CZ	2.52	0.44
3:3:180:ASN:OD1	3:3:181:VAL:N	2.50	0.44
23:S:131:LYS:HG3	23:S:143:LEU:HD11	2.00	0.44
29:h:78:ILE:HG13	29:h:83:ARG:HG3	1.99	0.44
38:x:82:GLU:HG2	38:x:169:GLY:HA2	2.00	0.44
1:1:726:C:H5'	7:A:266:TYR:HE1	1.82	0.44
1:1:1152:U:H2'	1:1:1153:U:O4'	2.18	0.44
1:1:2440:A:H5'	21:P:83:TRP:O	2.17	0.44
5:5:4:LEU:HD21	5:5:12:LEU:HD23	2.00	0.44
5:5:113:PHE:HE2	5:5:124:LEU:HD22	1.83	0.44
5:5:145:ALA:O	5:5:152:VAL:HA	2.18	0.44
22:Q:28:LEU:HA	22:Q:28:LEU:HD23	1.72	0.44
1:1:86:G:H22	1:1:98:G:H2'	1.81	0.44
1:1:200:C:OP1	5:5:292:GLN:NE2	2.51	0.44
1:1:282:G:OP2	7:A:76:LYS:NZ	2.51	0.44
1:1:419:U:H2'	1:1:420:G:C8	2.53	0.44
1:1:444:A:H4'	1:1:1435:G:H4'	2.00	0.44
1:1:776:U:O4	1:1:777:C:N4	2.51	0.44
1:1:1221:A:N3	1:1:1221:A:H2'	2.33	0.44
1:1:3406:A:H1'	1:1:3412:C:O2	2.18	0.44
1:1:3415:U:O2'	1:1:3422:G:H4'	2.16	0.44
7:A:258:ILE:O	7:A:262:ALA:N	2.45	0.44
9:C:31:PRO:HD2	9:C:280:PRO:HG2	2.00	0.44
9:C:232:VAL:HG13	9:C:233:ARG:HG3	2.00	0.44
27:e:6:ILE:HA	27:e:60:THR:CG2	2.48	0.44
39:y:159:ALA:N	39:y:180:PRO:O	2.41	0.44
1:1:119:U:H5"	32:m:224:ARG:HG2	2.00	0.43
1:1:235:U:H5"	25:Y:7:VAL:HG11	2.00	0.43
1:1:295:G:H2'	1:1:296:C:O4'	2.18	0.43
1:1:1157:G:H2'	1:1:1158:G:H1'	2.00	0.43
1:1:1460:C:H4'	9:C:42:THR:HG23	1.99	0.43
1:1:3132:G:N3	26:b:410:GLY:HA3	2.33	0.43
5:5:222:CYS:O	5:5:224:HIS:ND1	2.47	0.43
7:A:86:LEU:O	7:A:90:ALA:N	2.45	0.43
19:N:168:GLY:O	19:N:172:ARG:HG2	2.18	0.43
20:O:47:HIS:HE2	20:O:49:PHE:HB2	1.82	0.43
23:S:63:ILE:HD12	23:S:63:ILE:N	2.33	0.43
27:e:19:SER:OG	27:e:27:GLU:HG2	2.17	0.43
28:f:30:ILE:HD12	28:f:76:HIS:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:v:63:THR:O	37:v:63:THR:OG1	2.30	0.43
38:x:55:ILE:HD13	38:x:55:ILE:HA	1.83	0.43
1:1:604:U:H2'	1:1:605:G:H8	1.83	0.43
1:1:3147:U:H2'	1:1:3148:G:C8	2.53	0.43
2:2:141:A:H2'	2:2:142:A:H8	1.83	0.43
6:6:84:U:H4'	33:o:204:ALA:HA	1.99	0.43
11:E:55:GLY:N	11:E:72:VAL:O	2.38	0.43
11:E:118:LYS:HE2	11:E:118:LYS:HB2	1.75	0.43
17:L:77:LEU:HA	17:L:80:LEU:HD12	2.00	0.43
22:Q:50:ARG:HH12	22:Q:140:LEU:HG	1.81	0.43
29:h:31:ARG:HH21	29:h:46:ILE:HD11	1.83	0.43
38:x:195:ILE:HD12	38:x:224:GLN:HG3	1.99	0.43
1:1:119:U:H4'	1:1:120:G:H3'	2.01	0.43
1:1:184:C:H4'	37:v:37:GLN:HE22	1.84	0.43
1:1:461:A:OP1	5:5:186:LYS:HB2	2.17	0.43
1:1:835:C:H4'	9:C:94:ASN:HD21	1.83	0.43
1:1:3277:A:H2	1:1:3284:G:H5'	1.83	0.43
1:1:3343:A:N9	20:O:111:PRO:HG3	2.34	0.43
9:C:7:THR:HB	9:C:21:THR:OG1	2.18	0.43
10:D:141:LEU:HD11	10:D:184:LEU:HD11	2.00	0.43
19:N:17:ASP:OD1	19:N:18:VAL:N	2.51	0.43
19:N:104:GLU:HA	19:N:160:GLU:HG3	1.99	0.43
22:Q:25:LEU:HA	22:Q:25:LEU:HD12	1.76	0.43
29:h:22:GLU:OE2	29:h:22:GLU:N	2.51	0.43
38:x:155:ARG:HA	38:x:155:ARG:HD2	1.68	0.43
1:1:27:C:O2'	1:1:335:A:N3	2.47	0.43
1:1:504:A:H8	1:1:504:A:OP2	2.00	0.43
1:1:3343:A:H1'	1:1:3344:A:H2'	2.00	0.43
1:1:3368:A:C5	11:E:86:TYR:CE2	3.05	0.43
2:2:140:A:H2'	2:2:141:A:C8	2.54	0.43
5:5:97:TYR:OH	5:5:100:GLY:HA2	2.18	0.43
28:f:19:ARG:CB	28:f:24:ILE:HG12	2.49	0.43
37:v:183:ALA:HA	37:v:189:ASN:ND2	2.33	0.43
1:1:254:G:C2	1:1:255:C:C2	3.06	0.43
1:1:1473:U:H2'	1:1:1474:G:H8	1.83	0.43
1:1:2473:A:H1'	1:1:3239:A:C6	2.53	0.43
1:1:3316:G:H8	1:1:3316:G:OP2	2.01	0.43
3:3:174:TYR:CD2	3:3:178:PRO:HG3	2.54	0.43
7:A:178:ALA:O	7:A:181:SER:OG	2.29	0.43
9:C:235:LEU:HB3	9:C:240:LEU:HD11	2.00	0.43
11:E:149:LEU:HD12	11:E:149:LEU:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:36:ALA:C	12:F:40:LYS:HZ2	2.26	0.43
17:L:87:ARG:HE	17:L:87:ARG:HB2	1.57	0.43
19:N:122:ASN:OD1	19:N:123:GLN:N	2.49	0.43
24:V:37:TYR:N	24:V:63:THR:O	2.52	0.43
25:Y:31:SER:HA	25:Y:48:PRO:HA	2.00	0.43
36:u:62:GLU:HA	36:u:108:PHE:HA	2.00	0.43
1:1:452:C:H2'	1:1:453:U:C6	2.53	0.43
1:1:716:G:H1	25:Y:5:ARG:NE	2.16	0.43
1:1:3115:U:H3	1:1:3131:C:H42	1.65	0.43
3:3:156:LYS:HA	21:P:11:GLU:OE1	2.18	0.43
7:A:43:GLN:HB2	7:A:175:PRO:HG3	2.00	0.43
10:D:166:ILE:HG23	10:D:241:VAL:HB	2.00	0.43
28:f:18:GLN:OE1	28:f:83:ARG:NH1	2.51	0.43
37:v:202:TYR:O	37:v:205:MET:HG3	2.18	0.43
1:1:534:A:H3'	1:1:535:G:H8	1.83	0.43
1:1:574:U:H3'	1:1:575:G:H8	1.84	0.43
1:1:589:U:H2'	1:1:590:U:C5	2.54	0.43
1:1:847:G:H22	1:1:957:A:H2	1.66	0.43
1:1:2461:A:C5	1:1:2462:C:H1'	2.53	0.43
1:1:3407:U:O2'	1:1:3409:C:OP2	2.21	0.43
1:1:3420:U:H3'	1:1:3421:G:C5'	2.49	0.43
2:2:51:A:H5"	31:j:57:ARG:HH22	1.84	0.43
3:3:10:VAL:HG22	9:C:34:PRO:HG3	2.00	0.43
3:3:53:VAL:HG12	3:3:115:LEU:HD12	2.01	0.43
9:C:170:LEU:HD11	9:C:174:ILE:HD11	2.00	0.43
20:O:107:GLU:HG2	20:O:148:TRP:CH2	2.53	0.43
25:Y:30:MET:SD	25:Y:77:PHE:HA	2.59	0.43
1:1:697:A:C6	1:1:698:U:C4	3.06	0.43
1:1:983:A:H3'	1:1:984:A:H8	1.83	0.43
1:1:3422:G:H2'	1:1:3423:A:C8	2.54	0.43
3:3:115:LEU:HD23	3:3:115:LEU:HA	1.91	0.43
9:C:175:LYS:HE2	9:C:175:LYS:HB2	1.84	0.43
38:x:124:PHE:CD1	38:x:124:PHE:C	2.97	0.43
1:1:536:A:H2'	1:1:537:A:O4'	2.18	0.43
1:1:1183:G:H21	1:1:1183:G:P	2.40	0.43
1:1:3106:U:O2'	1:1:3107:A:H2'	2.19	0.43
1:1:3336:G:O6	1:1:3337:A:N6	2.52	0.43
1:1:3486:U:H2'	1:1:3487:C:C6	2.54	0.43
9:C:331:ASN:C	9:C:333:TYR:H	2.27	0.43
17:L:31:ARG:O	17:L:35:ARG:HG3	2.19	0.43
1:1:17:G:H2'	1:1:18:G:O4'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:121:A:C8	32:m:231:GLU:OE1	2.71	0.43
1:1:587:U:H3'	1:1:588:G:H8	1.83	0.43
1:1:1201:A:H2'	1:1:1202:G:O4'	2.19	0.43
1:1:3397:A:H2'	1:1:3398:U:C6	2.53	0.43
4:4:26:LEU:HD22	4:4:30:LEU:HD13	2.00	0.43
5:5:3:LEU:HA	5:5:342:ILE:H	1.84	0.43
5:5:229:THR:OG1	5:5:233:GLN:O	2.25	0.43
9:C:260:LEU:HD23	9:C:260:LEU:HA	1.77	0.43
9:C:350:LYS:HE2	9:C:350:LYS:HB2	1.87	0.43
11:E:83:THR:OG1	11:E:91:VAL:O	2.33	0.43
20:O:86:ARG:HG2	20:O:100:LEU:HD11	2.01	0.43
29:h:115:LEU:HA	29:h:115:LEU:HD12	1.70	0.43
37:v:72:ASP:HA	37:v:73:PRO:HD3	1.81	0.43
1:1:216:A:H4'	1:1:218:A:N7	2.34	0.42
3:3:56:ASP:HB3	3:3:61:TYR:CE1	2.54	0.42
14:H:90:MET:HA	14:H:180:SER:H	1.83	0.42
30:i:9:LEU:HD23	30:i:9:LEU:HA	1.83	0.42
1:1:26:A:H4'	1:1:337:U:H2'	2.01	0.42
1:1:362:U:H2'	1:1:363:A:C8	2.55	0.42
1:1:412:G:H1	2:2:27:C:H42	1.67	0.42
1:1:643:C:O2'	1:1:646:A:N3	2.47	0.42
2:2:14:U:H2'	2:2:15:U:C6	2.54	0.42
2:2:45:A:OP1	2:2:46:U:O2'	2.37	0.42
3:3:121:LYS:HE3	3:3:121:LYS:HB2	1.89	0.42
5:5:54:ASN:OD1	5:5:55:VAL:N	2.52	0.42
5:5:124:LEU:HD21	5:5:176:VAL:HG11	2.01	0.42
13:G:91:PHE:CE2	13:G:185:ARG:HB3	2.54	0.42
13:G:225:LYS:HG2	13:G:226:TYR:CD2	2.55	0.42
20:O:90:PRO:HB2	20:O:93:THR:HB	2.01	0.42
21:P:49:ASP:HA	21:P:52:LYS:HD2	2.01	0.42
22:Q:126:ASP:OD1	22:Q:127:GLN:N	2.52	0.42
29:h:4:LYS:HB2	29:h:7:GLU:OE1	2.20	0.42
1:1:138:U:H3	29:h:70:GLU:HG2	1.84	0.42
1:1:710:G:H21	37:v:65:GLY:N	2.03	0.42
1:1:985:G:H1	1:1:1173:G:H2'	1.83	0.42
2:2:57:G:H1'	29:h:43:LEU:HD13	2.00	0.42
5:5:300:SER:HB3	5:5:338:SER:HA	2.01	0.42
7:A:137:MET:HG2	7:A:222:GLY:CA	2.50	0.42
9:C:156:ASP:OD1	9:C:156:ASP:N	2.52	0.42
14:H:88:TYR:HA	14:H:182:ARG:HA	2.01	0.42
19:N:39:ALA:HB3	19:N:61:ILE:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:V:79:ILE:N	24:V:103:VAL:O	2.52	0.42
1:1:982:G:N1	1:1:1402:U:OP2	2.30	0.42
1:1:1158:G:H3'	1:1:1159:U:C6	2.53	0.42
1:1:1397:A:H2'	1:1:1398:C:O4'	2.20	0.42
1:1:1433:U:H5	2:2:17:A:H4'	1.84	0.42
1:1:3308:G:H4'	1:1:3309:U:O5'	2.19	0.42
4:4:190:ILE:HD13	4:4:203:PRO:HD3	2.02	0.42
5:5:183:LYS:HD3	5:5:244:ARG:HG3	2.02	0.42
25:Y:5:ARG:HD3	37:v:24:LYS:CG	2.50	0.42
39:y:64:CYS:O	39:y:70:LEU:HA	2.18	0.42
1:1:153:U:O4	13:G:183:LYS:HE2	2.19	0.42
1:1:646:A:O2'	1:1:647:A:H8	2.02	0.42
1:1:835:C:H4'	9:C:94:ASN:ND2	2.34	0.42
1:1:1419:U:H3'	1:1:1420:U:C5'	2.50	0.42
1:1:1481:G:O2'	1:1:2443:G:O6	2.36	0.42
2:2:29:C:O2'	2:2:30:U:O5'	2.35	0.42
3:3:147:ARG:HH12	38:x:301:ARG:HH21	1.68	0.42
5:5:170:LEU:HB3	5:5:171:TRP:CE3	2.55	0.42
7:A:126:VAL:HG12	7:A:129:LEU:HD21	2.00	0.42
9:C:110:LYS:HA	9:C:110:LYS:HD2	1.90	0.42
12:F:93:VAL:HA	12:F:143:TYR:HB3	2.01	0.42
22:Q:107:PHE:CZ	22:Q:122:VAL:HB	2.55	0.42
29:h:24:ARG:O	29:h:24:ARG:HD2	2.20	0.42
1:1:964:U:H1'	1:1:966:G:OP2	2.19	0.42
1:1:1223:C:O2'	1:1:1224:A:H5'	2.20	0.42
1:1:2462:C:H2'	1:1:2463:G:C4	2.54	0.42
1:1:3186:U:H2'	1:1:3187:A:C8	2.55	0.42
1:1:3338:A:H2'	1:1:3339:A:C8	2.54	0.42
1:1:3345:G:N2	1:1:3346:U:O4	2.51	0.42
5:5:47:PHE:HB2	5:5:95:MET:HE3	2.01	0.42
9:C:359:VAL:O	23:S:25:ARG:NH2	2.52	0.42
10:D:234:PHE:O	10:D:237:LEU:HD23	2.19	0.42
10:D:418:ARG:H	10:D:418:ARG:HD3	1.84	0.42
21:P:114:ILE:HD13	21:P:150:VAL:HG12	2.00	0.42
1:1:178:U:H2'	1:1:179:G:O4'	2.20	0.42
1:1:382:A:N3	1:1:384:G:H5"	2.35	0.42
1:1:3108:A:H2'	1:1:3109:U:C6	2.55	0.42
1:1:3109:U:H2'	1:1:3110:U:C6	2.54	0.42
1:1:3270:U:O2'	28:f:7:ARG:HB2	2.18	0.42
1:1:3367:A:H61	11:E:88:VAL:C	2.28	0.42
3:3:34:VAL:HG22	3:3:50:TYR:OH	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:63:LYS:HB2	4:4:63:LYS:HE3	1.76	0.42
9:C:208:LEU:HD12	9:C:228:GLU:O	2.20	0.42
10:D:223:LEU:HD13	10:D:260:ILE:HG13	2.01	0.42
13:G:107:GLN:O	13:G:110:VAL:HG12	2.20	0.42
22:Q:126:ASP:OD1	22:Q:126:ASP:C	2.63	0.42
23:S:130:LYS:HD2	23:S:130:LYS:HA	1.86	0.42
30:i:27:ARG:O	30:i:27:ARG:HG3	2.19	0.42
38:x:233:ILE:HD11	38:x:242:PHE:HD2	1.85	0.42
39:y:27:ALA:HB2	39:y:59:ILE:CB	2.50	0.42
1:1:431:A:H2'	1:1:432:G:O4'	2.19	0.42
1:1:505:G:H8	1:1:505:G:OP1	2.03	0.42
1:1:585:C:H2'	1:1:586:U:C6	2.54	0.42
1:1:701:G:N2	1:1:818:A:N3	2.67	0.42
1:1:998:U:H2'	1:1:999:A:O4'	2.19	0.42
1:1:3248:U:H2'	1:1:3497:G:C6	2.55	0.42
5:5:290:ARG:O	5:5:292:GLN:HG2	2.20	0.42
7:A:62:ASN:O	7:A:65:VAL:HG12	2.19	0.42
7:A:79:SER:CB	7:A:82:ARG:HB2	2.49	0.42
19:N:19:ASN:O	19:N:23:SER:N	2.45	0.42
20:O:51:ASN:HA	20:O:54:LYS:HD2	2.01	0.42
1:1:33:G:N3	1:1:52:A:N6	2.67	0.42
1:1:113:C:P	19:N:147:ARG:HH21	2.41	0.42
1:1:485:U:H2'	1:1:486:G:C8	2.54	0.42
1:1:772:A:H2'	1:1:773:C:O4'	2.20	0.42
1:1:3300:A:H3'	1:1:3301:C:H5"	2.02	0.42
1:1:3374:A:H3'	1:1:3375:U:C6	2.55	0.42
2:2:51:A:OP1	31:j:57:ARG:NH2	2.53	0.42
2:2:79:A:C2	2:2:88:A:H1'	2.54	0.42
9:C:231:ASN:HB3	9:C:234:ARG:HG2	2.01	0.42
10:D:321:ASP:OD1	10:D:322:LYS:N	2.52	0.42
10:D:408:ILE:HD12	10:D:423:ARG:HH22	1.84	0.42
13:G:70:LYS:HG3	13:G:233:TRP:HE3	1.85	0.42
19:N:113:LEU:HB3	19:N:134:LEU:HB3	2.01	0.42
25:Y:49:VAL:HG11	25:Y:79:LEU:HD21	2.02	0.42
27:e:16:ARG:HB3	27:e:19:SER:HB2	2.02	0.42
1:1:677:G:H2'	1:1:2449:A:H5'	2.00	0.42
1:1:712:U:O4	17:L:32:LYS:HE3	2.19	0.42
1:1:1142:U:O2'	1:1:1143:A:O5'	2.36	0.42
1:1:3351:U:H2'	1:1:3352:A:C8	2.55	0.42
5:5:314:ASP:O	5:5:316:ASN:ND2	2.50	0.42
7:A:250:SER:O	7:A:254:VAL:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:252:THR:O	7:A:255:ARG:HB3	2.20	0.42
9:C:147:ILE:HD13	9:C:147:ILE:HA	1.82	0.42
19:N:48:ALA:O	19:N:53:TYR:HB3	2.20	0.42
1:1:119:U:C2	13:G:138:HIS:CE1	3.08	0.41
1:1:329:C:OP1	19:N:159:ARG:NH1	2.53	0.41
1:1:488:A:C5	1:1:489:C:H5	2.38	0.41
1:1:3156:C:H4'	1:1:3473:A:N3	2.35	0.41
1:1:3222:C:H2'	1:1:3223:A:H8	1.85	0.41
2:2:71:G:O2'	29:h:51:LYS:NZ	2.53	0.41
4:4:100:ILE:HG23	9:C:291:ARG:HA	2.02	0.41
7:A:92:LEU:HD11	30:i:68:ARG:HB3	2.01	0.41
10:D:325:LEU:HD12	10:D:470:ALA:O	2.21	0.41
20:O:148:TRP:HE1	20:O:150:TYR:C	2.28	0.41
29:h:21:GLN:HA	29:h:21:GLN:OE1	2.20	0.41
39:y:162:HIS:HA	39:y:184:GLY:O	2.20	0.41
1:1:685:A:N1	1:1:973:G:O2'	2.46	0.41
1:1:3354:U:H2'	1:1:3355:G:C8	2.55	0.41
8:B:223:GLY:HA2	8:B:271:GLY:HA3	2.02	0.41
9:C:133:VAL:O	9:C:137:LEU:HD13	2.20	0.41
13:G:159:PRO:HG2	13:G:162:LEU:HD13	2.02	0.41
17:L:111:ARG:NH2	30:i:11:LYS:HB3	2.34	0.41
20:O:38:ARG:HD3	20:O:109:ILE:HD11	2.01	0.41
23:S:12:LYS:HG2	23:S:21:PRO:HB3	2.02	0.41
25:Y:35:SER:O	25:Y:39:ARG:N	2.43	0.41
25:Y:59:ARG:HB2	25:Y:102:LYS:HD2	2.03	0.41
31:j:60:GLY:HA3	37:v:5:ARG:HA	2.02	0.41
1:1:356:A:H4'	1:1:375:A:N6	2.36	0.41
1:1:1154:U:H3	1:1:1166:A:N6	2.18	0.41
5:5:317:VAL:HG23	5:5:332:ILE:HG13	2.02	0.41
9:C:183:VAL:HG22	9:C:204:ARG:HB2	2.02	0.41
10:D:145:ILE:HD13	10:D:145:ILE:HA	1.95	0.41
11:E:189:ARG:HG3	28:f:35:GLY:HA3	2.02	0.41
27:e:76:VAL:O	27:e:79:VAL:HG12	2.21	0.41
1:1:1169:U:H2'	1:1:1170:G:C8	2.55	0.41
1:1:1439:U:H1'	27:e:51:LYS:O	2.21	0.41
1:1:1446:G:H5"	27:e:121:ALA:HB2	2.03	0.41
1:1:3231:U:H2'	1:1:3232:G:H8	1.85	0.41
12:F:59:GLU:OE2	12:F:63:ARG:NH2	2.53	0.41
22:Q:77:SER:HA	22:Q:80:LYS:HE2	2.02	0.41
25:Y:47:LEU:HD12	25:Y:47:LEU:HA	1.88	0.41
29:h:94:LEU:HD22	29:h:98:GLU:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:x:86:TYR:HE2	38:x:216:GLN:HG3	1.85	0.41
1:1:19:U:H2'	1:1:20:A:C8	2.55	0.41
1:1:543:G:H2'	1:1:544:A:C8	2.55	0.41
1:1:1157:G:O3'	1:1:1158:G:H4'	2.19	0.41
5:5:59:ARG:HD2	5:5:63:THR:HB	2.01	0.41
9:C:50:GLN:HA	9:C:51:PRO:HD3	1.91	0.41
9:C:110:LYS:NZ	9:C:112:HIS:O	2.53	0.41
10:D:200:ASN:HB3	10:D:203:ALA:HB3	2.01	0.41
10:D:494:TYR:CE2	10:D:530:PRO:HD2	2.55	0.41
12:F:102:ILE:O	12:F:107:ARG:NH2	2.53	0.41
17:L:92:THR:HB	29:h:114:PRO:O	2.20	0.41
18:M:8:VAL:O	23:S:148:LYS:HA	2.21	0.41
22:Q:50:ARG:HA	22:Q:53:GLN:HG3	2.01	0.41
1:1:20:A:C6	1:1:21:G:C6	3.09	0.41
1:1:582:G:H2'	1:1:583:C:C6	2.55	0.41
1:1:684:G:H5"	1:1:685:A:OP1	2.20	0.41
1:1:3246:A:H2'	1:1:3247:U:O4'	2.21	0.41
1:1:3401:A:H2	1:1:3416:A:H1'	1.85	0.41
3:3:160:ASN:HA	3:3:163:LYS:NZ	2.35	0.41
6:6:58:A:H2'	6:6:59:A:C8	2.54	0.41
9:C:147:ILE:HD11	9:C:176:ALA:HA	2.03	0.41
10:D:314:GLY:O	10:D:439:MET:N	2.53	0.41
12:F:108:LYS:HA	12:F:108:LYS:HD2	1.86	0.41
21:P:47:PHE:HZ	21:P:58:VAL:HG12	1.86	0.41
37:v:134:LYS:HE2	37:v:134:LYS:HB2	1.84	0.41
39:y:69:GLY:HA2	39:y:93:LYS:N	2.36	0.41
1:1:1158:G:N3	1:1:1158:G:C2'	2.79	0.41
4:4:76:TRP:CD1	4:4:77:ILE:N	2.88	0.41
5:5:126:LEU:HD22	5:5:155:TYR:CE2	2.55	0.41
7:A:155:PHE:HA	7:A:161:LEU:HB3	2.02	0.41
9:C:42:THR:O	9:C:46:LYS:HE3	2.21	0.41
10:D:161:GLY:O	10:D:213:ASN:ND2	2.41	0.41
10:D:358:TYR:CD2	10:D:479:LEU:HD21	2.55	0.41
13:G:71:VAL:N	13:G:234:GLY:O	2.53	0.41
20:O:6:LYS:HB2	20:O:6:LYS:HE2	1.79	0.41
23:S:175:PHE:HD1	23:S:176:TYR:H	1.68	0.41
25:Y:50:ARG:NH1	25:Y:111:ASP:OD2	2.48	0.41
29:h:24:ARG:HH11	29:h:24:ARG:C	2.24	0.41
1:1:592:U:OP1	9:C:347:LYS:NZ	2.31	0.41
1:1:1341:G:H2'	1:1:1342:G:C8	2.53	0.41
2:2:26:U:O4	2:2:27:C:N4	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:267:LEU:HD12	5:5:267:LEU:HA	1.80	0.41
6:6:83:A:H2'	6:6:84:U:C6	2.56	0.41
9:C:100:ARG:HE	9:C:100:ARG:HB3	1.56	0.41
10:D:207:LYS:HE3	10:D:207:LYS:HB3	1.82	0.41
23:S:147:LEU:HD23	23:S:147:LEU:HA	1.85	0.41
1:1:28:G:H4'	1:1:61:A:N3	2.35	0.41
1:1:49:A:C5	1:1:287:U:H4'	2.55	0.41
1:1:184:C:H4'	37:v:37:GLN:OE1	2.21	0.41
1:1:193:U:H6	1:1:193:U:H2'	1.66	0.41
1:1:433:C:O2	1:1:660:G:N2	2.54	0.41
1:1:531:A:N1	9:C:349:PRO:HD2	2.35	0.41
1:1:533:A:H62	1:1:594:A:H2	1.68	0.41
1:1:544:A:N6	1:1:577:U:O2	2.53	0.41
1:1:763:G:H3'	1:1:764:U:H6	1.86	0.41
1:1:3116:U:H1'	1:1:3131:C:N3	2.36	0.41
1:1:3281:A:H2'	1:1:3281:A:N3	2.36	0.41
2:2:61:A:H2'	2:2:62:A:O4'	2.20	0.41
3:3:54:ARG:HA	3:3:115:LEU:HD11	2.01	0.41
4:4:58:PRO:HA	4:4:61:GLN:HG2	2.02	0.41
5:5:15:ILE:HG22	5:5:17:ILE:H	1.86	0.41
7:A:187:ARG:HD2	7:A:202:ASN:HD21	1.86	0.41
9:C:101:MET:H	9:C:101:MET:HG3	1.66	0.41
9:C:159:GLN:HA	9:C:217:ILE:HB	2.02	0.41
9:C:292:LEU:HD23	9:C:292:LEU:HA	1.87	0.41
10:D:356:LEU:HD23	10:D:359:ILE:HD11	2.03	0.41
10:D:363:VAL:HG13	10:D:389:ILE:HG13	2.03	0.41
12:F:116:LEU:HD12	12:F:116:LEU:H	1.86	0.41
13:G:185:ARG:O	13:G:188:THR:OG1	2.36	0.41
13:G:210:GLU:OE2	13:G:214:ILE:HD11	2.21	0.41
17:L:60:PRO:HB2	17:L:65:TYR:HB2	2.01	0.41
17:L:81:LYS:HD2	17:L:81:LYS:HA	1.84	0.41
21:P:7:SER:OG	21:P:8:PRO:HD3	2.21	0.41
27:e:29:TRP:CE2	27:e:50:PRO:HD2	2.56	0.41
32:m:238:LEU:HD23	32:m:238:LEU:HA	1.86	0.41
38:x:240:LEU:HD21	38:x:306:LEU:HD12	2.03	0.41
39:y:149:GLY:O	39:y:194:GLY:HA3	2.20	0.41
3:3:119:LEU:HD23	3:3:119:LEU:HA	1.86	0.41
5:5:143:ILE:HD11	5:5:171:TRP:CD1	2.56	0.41
5:5:255:PRO:HG2	5:5:273:LYS:HD3	2.02	0.41
7:A:38:PHE:CD2	32:m:108:SER:HB3	2.56	0.41
9:C:212:ASN:OD1	9:C:233:ARG:NH2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:171:ARG:HE	10:D:196:ILE:HD12	1.86	0.41
12:F:72:LEU:HD22	40:T:140:PHE:CE1	2.54	0.41
13:G:232:LYS:HD2	13:G:232:LYS:HA	1.82	0.41
19:N:20:LEU:HD12	19:N:20:LEU:HA	1.81	0.41
21:P:30:ARG:HD2	21:P:63:PHE:CE2	2.55	0.41
1:1:176:A:N1	29:h:101:ARG:NH1	2.70	0.40
1:1:430:A:H2'	1:1:431:A:O4'	2.20	0.40
1:1:460:G:O2'	1:1:461:A:O5'	2.39	0.40
1:1:1156:U:H2'	1:1:1157:G:O4'	2.19	0.40
1:1:3140:A:H2'	1:1:3141:G:C8	2.56	0.40
1:1:3195:C:N3	1:1:3232:G:H1'	2.36	0.40
2:2:148:G:C6	2:2:149:C:C4	3.09	0.40
3:3:45:LEU:HD13	9:C:139:ALA:HB2	2.03	0.40
10:D:223:LEU:HB2	10:D:260:ILE:HD11	2.02	0.40
13:G:227[A]:ASP:O	13:G:231:ARG:NH1	2.53	0.40
17:L:122:HIS:CE1	30:i:3:PRO:HD3	2.55	0.40
19:N:65:ARG:HD2	19:N:127:TYR:CE1	2.56	0.40
24:V:57:GLY:HA3	24:V:124:CYS:HA	2.03	0.40
30:i:88:LEU:HD13	30:i:88:LEU:HA	1.92	0.40
38:x:63:GLU:OE1	38:x:63:GLU:N	2.41	0.40
1:1:136:U:H6	1:1:136:U:H2'	1.70	0.40
1:1:233:C:H2'	1:1:234:G:O4'	2.21	0.40
1:1:299:C:H2'	1:1:300:U:C6	2.56	0.40
1:1:385:A:H1'	1:1:400:G:N2	2.36	0.40
1:1:501:G:H2'	1:1:502:G:C8	2.56	0.40
1:1:965:A:H4'	1:1:966:G:OP1	2.22	0.40
1:1:987:U:O4	1:1:999:A:H1'	2.20	0.40
1:1:3213:C:H2'	1:1:3214:C:O4'	2.21	0.40
2:2:85:A:H2'	2:2:86:G:O4'	2.21	0.40
7:A:74:ASP:OD1	7:A:75:SER:N	2.51	0.40
19:N:124:ASP:OD1	19:N:127:TYR:N	2.53	0.40
27:e:86:ASN:HA	27:e:114:VAL:HG23	2.01	0.40
30:i:48:PHE:CZ	30:i:91:VAL:HG11	2.56	0.40
32:m:240:TYR:O	32:m:244:LYS:HG2	2.21	0.40
38:x:66:ILE:HG21	38:x:209:MET:HE1	2.03	0.40
38:x:254:ASN:OD1	38:x:254:ASN:N	2.54	0.40
39:y:24:ALA:HB3	39:y:48:VAL:HA	2.01	0.40
1:1:148:C:H2'	1:1:149:G:O4'	2.21	0.40
1:1:759:C:H2'	1:1:760:C:C6	2.57	0.40
3:3:183:GLU:OE2	3:3:187:ASN:ND2	2.50	0.40
4:4:120:ASP:OD2	4:4:137:TYR:OH	2.33	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:F:79:GLU:OE2	12:F:81:ASN:HB2	2.21	0.40
13:G:82:LEU:HD12	13:G:82:LEU:HA	1.95	0.40
23:S:15:THR:HG23	23:S:17:HIS:N	2.36	0.40
33:o:105:GLY:N	33:o:153:PHE:O	2.46	0.40
37:v:53:LEU:HD22	37:v:137:VAL:HG11	2.01	0.40
1:1:716:G:H1	25:Y:5:ARG:CD	2.33	0.40
1:1:3100:C:O2'	8:B:99:LEU:O	2.35	0.40
2:2:26:U:C4	2:2:27:C:C4	3.09	0.40
10:D:340:ILE:HD12	10:D:390:LEU:O	2.21	0.40
12:F:82:TYR:CE1	23:S:9:VAL:HG11	2.57	0.40
12:F:193:HIS:CE1	12:F:197:THR:HG21	2.57	0.40
13:G:85:ASN:O	13:G:88:THR:OG1	2.33	0.40
17:L:76:THR:HG23	17:L:79:GLU:H	1.87	0.40
19:N:96:ARG:NH2	19:N:104:GLU:OE2	2.53	0.40
28:f:21:LYS:HG2	28:f:22:HIS:CE1	2.56	0.40
30:i:64:ASP:HB2	30:i:68:ARG:HH22	1.86	0.40
38:x:30:LYS:HB3	38:x:34:LYS:NZ	2.36	0.40
39:y:14:GLY:HA3	39:y:194:GLY:O	2.22	0.40
1:1:58:G:H1'	1:1:61:A:H5'	2.03	0.40
1:1:647:A:H2'	1:1:648:U:O4'	2.21	0.40
1:1:1152:U:C4	1:1:1153:U:C4	3.09	0.40
1:1:3396:A:H2'	1:1:3397:A:C8	2.56	0.40
3:3:190:LEU:HD23	3:3:193:ARG:HD3	2.03	0.40
4:4:201:THR:HG21	9:C:301:ILE:HD11	2.03	0.40
5:5:267:LEU:HD11	5:5:281:ASP:HA	2.03	0.40
10:D:333:ARG:NH2	16:K:47:GLN:HA	2.36	0.40
11:E:171:ILE:HD12	11:E:171:ILE:H	1.86	0.40
16:K:239:ILE:O	16:K:251:LEU:N	2.55	0.40
17:L:64:ARG:O	17:L:67:MET:HE1	2.22	0.40
29:h:66:LEU:HD23	29:h:66:LEU:HA	1.95	0.40
30:i:34:ARG:O	30:i:38:VAL:HG23	2.21	0.40
33:o:106:VAL:HA	33:o:152:GLU:HA	2.03	0.40
39:y:62:LEU:C	39:y:105:GLY:H	2.30	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	192/302 (64%)	185 (96%)	7 (4%)	0	100	100
4	4	205/217 (94%)	198 (97%)	7 (3%)	0	100	100
5	5	334/387 (86%)	297 (89%)	37 (11%)	0	100	100
7	A	249/295 (84%)	235 (94%)	12 (5%)	2 (1%)	16	48
8	B	311/388 (80%)	306 (98%)	5 (2%)	0	100	100
9	C	324/363 (89%)	295 (91%)	29 (9%)	0	100	100
10	D	390/578 (68%)	380 (97%)	10 (3%)	0	100	100
11	E	168/195 (86%)	152 (90%)	16 (10%)	0	100	100
12	F	237/250 (95%)	223 (94%)	12 (5%)	2 (1%)	16	48
13	G	161/259 (62%)	144 (89%)	15 (9%)	2 (1%)	11	38
14	H	171/190 (90%)	170 (99%)	1 (1%)	0	100	100
15	J	92/333 (28%)	86 (94%)	5 (5%)	1 (1%)	12	39
16	K	243/373 (65%)	236 (97%)	6 (2%)	1 (0%)	30	63
17	L	114/208 (55%)	107 (94%)	7 (6%)	0	100	100
18	M	121/134 (90%)	118 (98%)	3 (2%)	0	100	100
19	N	160/201 (80%)	153 (96%)	7 (4%)	0	100	100
20	O	177/197 (90%)	175 (99%)	2 (1%)	0	100	100
21	P	124/187 (66%)	112 (90%)	12 (10%)	0	100	100
22	Q	132/187 (71%)	123 (93%)	9 (7%)	0	100	100
23	S	164/176 (93%)	155 (94%)	9 (6%)	0	100	100
24	V	122/139 (88%)	112 (92%)	10 (8%)	0	100	100
25	Y	123/126 (98%)	116 (94%)	7 (6%)	0	100	100
26	b	143/642 (22%)	139 (97%)	3 (2%)	1 (1%)	19	51
27	e	122/127 (96%)	112 (92%)	10 (8%)	0	100	100
28	f	104/108 (96%)	97 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	h	118/122 (97%)	115 (98%)	3 (2%)	0	100	100
30	i	96/99 (97%)	88 (92%)	8 (8%)	0	100	100
31	j	69/91 (76%)	64 (93%)	5 (7%)	0	100	100
32	m	69/740 (9%)	66 (96%)	3 (4%)	0	100	100
33	o	134/276 (49%)	128 (96%)	6 (4%)	0	100	100
34	r	54/260 (21%)	53 (98%)	1 (2%)	0	100	100
35	t	21/249 (8%)	21 (100%)	0	0	100	100
36	u	98/192 (51%)	96 (98%)	2 (2%)	0	100	100
37	v	154/209 (74%)	144 (94%)	9 (6%)	1 (1%)	22	53
38	x	304/306 (99%)	288 (95%)	16 (5%)	0	100	100
39	y	220/244 (90%)	201 (91%)	19 (9%)	0	100	100
40	T	16/160 (10%)	16 (100%)	0	0	100	100
All	All	6036/9510 (64%)	5706 (94%)	320 (5%)	10 (0%)	50	74

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	A	249	VAL
15	J	126	PRO
37	v	130	ILE
7	A	248	PHE
16	K	153	ILE
13	G	227[A]	ASP
13	G	227[B]	ASP
26	b	94	ILE
12	F	13	ILE
12	F	15	ALA

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	171/271 (63%)	170 (99%)	1 (1%)	84 91
4	4	188/197 (95%)	187 (100%)	1 (0%)	86 92
5	5	299/345 (87%)	298 (100%)	1 (0%)	91 95
7	A	227/266 (85%)	227 (100%)	0	100 100
9	C	275/297 (93%)	275 (100%)	0	100 100
10	D	306/505 (61%)	305 (100%)	1 (0%)	91 95
11	E	139/155 (90%)	138 (99%)	1 (1%)	81 90
12	F	201/210 (96%)	200 (100%)	1 (0%)	86 92
13	G	136/212 (64%)	136 (100%)	0	100 100
17	L	97/167 (58%)	97 (100%)	0	100 100
19	N	146/176 (83%)	146 (100%)	0	100 100
20	O	149/162 (92%)	148 (99%)	1 (1%)	81 90
21	P	109/149 (73%)	109 (100%)	0	100 100
22	Q	115/159 (72%)	115 (100%)	0	100 100
23	S	150/154 (97%)	150 (100%)	0	100 100
25	Y	110/111 (99%)	110 (100%)	0	100 100
27	e	106/107 (99%)	104 (98%)	2 (2%)	52 75
28	f	89/91 (98%)	89 (100%)	0	100 100
29	h	106/107 (99%)	105 (99%)	1 (1%)	75 88
30	i	83/84 (99%)	83 (100%)	0	100 100
31	j	58/71 (82%)	58 (100%)	0	100 100
32	m	65/659 (10%)	65 (100%)	0	100 100
35	t	12/223 (5%)	12 (100%)	0	100 100
37	v	135/181 (75%)	134 (99%)	1 (1%)	81 90
38	x	273/273 (100%)	272 (100%)	1 (0%)	89 94
40	T	12/139 (9%)	11 (92%)	1 (8%)	9 33
All	All	3757/5471 (69%)	3744 (100%)	13 (0%)	90 95

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	3	163	LYS
4	4	46	LYS
5	5	95	MET

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Mol	Chain	Res	Type
10	D	188	HIS
11	E	169	LYS
12	F	116	LEU
20	O	150	TYR
27	e	125	SER
27	e	127	GLU
29	h	83	ARG
37	v	123	VAL
38	x	154	ASP
40	T	151	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
3	3	129	HIS
4	4	62	GLN
4	4	122	GLN
5	5	68	ASN
5	5	70	ASN
5	5	71	GLN
5	5	282	HIS
7	A	70	HIS
7	A	140	ASN
9	C	50	GLN
9	C	344	ASN
10	D	188	HIS
10	D	200	ASN
10	D	227	GLN
11	E	173	ASN
12	F	173	ASN
12	F	193	HIS
20	O	51	ASN
22	Q	78	GLN
27	e	18	GLN
27	e	66	ASN
27	e	96	ASN
28	f	43	GLN
29	h	13	GLN
29	h	25	GLN
30	i	19	GLN
30	i	63	GLN
32	m	232	GLN

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Mol	Chain	Res	Type
35	t	60	ASN
37	v	10	GLN
37	v	152	GLN
37	v	200	ASN
38	x	216	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1398/3497 (39%)	420 (30%)	19 (1%)
2	2	142/165 (86%)	31 (21%)	0
6	6	52/300 (17%)	16 (30%)	0
All	All	1592/3962 (40%)	467 (29%)	19 (1%)

All (467) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	9	U
1	1	11	A
1	1	16	A
1	1	18	G
1	1	21	G
1	1	22	G
1	1	34	A
1	1	35	A
1	1	49	A
1	1	50	U
1	1	51	A
1	1	53	G
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	67	A
1	1	68	A
1	1	69	U
1	1	71	A
1	1	72	C
1	1	74	A
1	1	87	U
1	1	101	G

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Mol	Chain	Res	Type
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	117	U
1	1	118	U
1	1	122	A
1	1	123	A
1	1	124	U
1	1	131	A
1	1	138	U
1	1	139	U
1	1	149	G
1	1	154	G
1	1	161	C
1	1	162	A
1	1	163	A
1	1	167	G
1	1	170	G
1	1	175	G
1	1	177	G
1	1	179	G
1	1	185	G
1	1	194	A
1	1	197	U
1	1	198	U
1	1	207	C
1	1	209	G
1	1	213	G
1	1	217	G
1	1	218	A
1	1	225	G
1	1	226	A
1	1	238	U
1	1	239	U
1	1	240	G
1	1	244	G
1	1	245	A
1	1	246	U
1	1	258	U
1	1	260	U
1	1	268	U

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Mol	Chain	Res	Type
1	1	269	U
1	1	276	A
1	1	277	G
1	1	301	C
1	1	303	A
1	1	306	U
1	1	331	A
1	1	336	U
1	1	337	U
1	1	338	G
1	1	346	A
1	1	347	C
1	1	354	C
1	1	358	C
1	1	359	A
1	1	360	A
1	1	361	G
1	1	362	U
1	1	383	A
1	1	384	G
1	1	393	A
1	1	403	A
1	1	405	A
1	1	406	U
1	1	407	A
1	1	410	A
1	1	411	C
1	1	428	G
1	1	429	G
1	1	430	A
1	1	437	G
1	1	443	C
1	1	445	G
1	1	446	U
1	1	447	C
1	1	448	U
1	1	449	U
1	1	458	G
1	1	459	A
1	1	461	A
1	1	462	U
1	1	465	G

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Mol	Chain	Res	Type
1	1	466	U
1	1	478	G
1	1	479	A
1	1	482	C
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	509	A
1	1	514	C
1	1	521	C
1	1	522	G
1	1	529	G
1	1	530	A
1	1	531	A
1	1	532	A
1	1	534	A
1	1	539	A
1	1	540	A
1	1	546	G
1	1	547	G
1	1	548	U
1	1	549	G
1	1	550	G
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	587	U
1	1	591	G
1	1	592	U
1	1	602	A
1	1	603	C

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Mol	Chain	Res	Type
1	1	616	A
1	1	618	U
1	1	624	U
1	1	629	G
1	1	632	A
1	1	634	G
1	1	635	G
1	1	636	A
1	1	641	G
1	1	644	A
1	1	645	U
1	1	646	A
1	1	647	A
1	1	649	G
1	1	661	C
1	1	662	C
1	1	663	C
1	1	671	A
1	1	673	C
1	1	675	C
1	1	685	A
1	1	686	G
1	1	702	A
1	1	706	U
1	1	708	U
1	1	714	A
1	1	716	G
1	1	717	A
1	1	724	A
1	1	732	A
1	1	753	G
1	1	759	C
1	1	761	U
1	1	762	U
1	1	763	G
1	1	765	G
1	1	768	G
1	1	770	G
1	1	776	U
1	1	777	C
1	1	778	G
1	1	779	A

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Mol	Chain	Res	Type
1	1	817	G
1	1	830	G
1	1	831	G
1	1	837	G
1	1	840	A
1	1	964	U
1	1	965	A
1	1	966	G
1	1	968	A
1	1	969	G
1	1	971	U
1	1	973	G
1	1	976	C
1	1	986	U
1	1	987	U
1	1	989	C
1	1	990	C
1	1	996	G
1	1	997	A
1	1	998	U
1	1	1003	G
1	1	1004	A
1	1	1009	C
1	1	1011	G
1	1	1012	A
1	1	1013	U
1	1	1014	C
1	1	1016	G
1	1	1017	U
1	1	1133	G
1	1	1135	G
1	1	1137	G
1	1	1141	C
1	1	1142	U
1	1	1143	A
1	1	1147	G
1	1	1154	U
1	1	1155	U
1	1	1156	U
1	1	1157	G
1	1	1158	G
1	1	1159	U

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Mol	Chain	Res	Type
1	1	1160	A
1	1	1161	A
1	1	1162	G
1	1	1163	C
1	1	1166	A
1	1	1167	A
1	1	1168	C
1	1	1173	G
1	1	1176	G
1	1	1184	A
1	1	1186	C
1	1	1188	G
1	1	1191	C
1	1	1205	G
1	1	1211	A
1	1	1212	U
1	1	1217	G
1	1	1221	A
1	1	1223	C
1	1	1224	A
1	1	1239	U
1	1	1243	A
1	1	1244	G
1	1	1249	U
1	1	1320	G
1	1	1324	U
1	1	1346	U
1	1	1347	U
1	1	1348	A
1	1	1352	G
1	1	1361	A
1	1	1363	A
1	1	1366	U
1	1	1380	A
1	1	1381	G
1	1	1382	C
1	1	1383	U
1	1	1387	A
1	1	1388	G
1	1	1389	A
1	1	1390	A
1	1	1420	U

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Mol	Chain	Res	Type
1	1	1421	G
1	1	1425	C
1	1	1426	G
1	1	1433	U
1	1	1436	G
1	1	1451	G
1	1	1452	A
1	1	1453	A
1	1	1459	U
1	1	1468	G
1	1	1471	C
1	1	1484	G
1	1	1935	U
1	1	1936	A
1	1	2440	A
1	1	2443	G
1	1	2454	C
1	1	2455	U
1	1	2456	G
1	1	2459	G
1	1	2460	A
1	1	2462	C
1	1	2463	G
1	1	2464	G
1	1	2465	G
1	1	2466	C
1	1	2467	C
1	1	2468	A
1	1	2469	G
1	1	2470	G
1	1	2473	A
1	1	3096	G
1	1	3104	G
1	1	3107	A
1	1	3108	A
1	1	3109	U
1	1	3113	A
1	1	3118	G
1	1	3119	U
1	1	3120	A
1	1	3125	A
1	1	3126	G

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Mol	Chain	Res	Type
1	1	3128	A
1	1	3130	C
1	1	3135	G
1	1	3137	U
1	1	3142	A
1	1	3146	U
1	1	3148	G
1	1	3149	G
1	1	3152	U
1	1	3154	U
1	1	3179	G
1	1	3180	C
1	1	3182	G
1	1	3188	U
1	1	3189	C
1	1	3190	A
1	1	3192	C
1	1	3193	U
1	1	3195	C
1	1	3197	G
1	1	3199	A
1	1	3200	U
1	1	3205	G
1	1	3212	G
1	1	3216	C
1	1	3219	A
1	1	3222	C
1	1	3225	A
1	1	3227	U
1	1	3237	A
1	1	3238	A
1	1	3239	A
1	1	3240	G
1	1	3248	U
1	1	3271	G
1	1	3272	U
1	1	3273	A
1	1	3275	A
1	1	3276	A
1	1	3281	A
1	1	3282	G
1	1	3286	U

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Mol	Chain	Res	Type
1	1	3301	C
1	1	3307	U
1	1	3309	U
1	1	3310	A
1	1	3315	A
1	1	3316	G
1	1	3317	A
1	1	3318	A
1	1	3319	G
1	1	3322	G
1	1	3324	G
1	1	3327	A
1	1	3328	U
1	1	3332	U
1	1	3335	U
1	1	3336	G
1	1	3337	A
1	1	3338	A
1	1	3342	G
1	1	3343	A
1	1	3344	A
1	1	3345	G
1	1	3346	U
1	1	3348	U
1	1	3349	U
1	1	3351	U
1	1	3352	A
1	1	3356	A
1	1	3359	U
1	1	3360	G
1	1	3362	C
1	1	3368	A
1	1	3369	A
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3375	U
1	1	3404	G
1	1	3405	C
1	1	3406	A
1	1	3408	A
1	1	3413	U

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Mol	Chain	Res	Type
1	1	3418	U
1	1	3419	G
1	1	3420	U
1	1	3421	G
1	1	3423	A
1	1	3425	C
1	1	3427	G
1	1	3431	A
1	1	3472	G
1	1	3475	U
1	1	3476	A
1	1	3477	A
1	1	3478	G
1	1	3479	C
1	1	3483	U
1	1	3490	A
1	1	3491	A
1	1	3492	G
2	2	9	A
2	2	30	U
2	2	42	U
2	2	43	C
2	2	57	G
2	2	58	C
2	2	59	G
2	2	60	A
2	2	67	A
2	2	69	A
2	2	71	G
2	2	72	U
2	2	76	G
2	2	79	A
2	2	84	C
2	2	87	A
2	2	98	U
2	2	99	C
2	2	103	G
2	2	104	A
2	2	112	A
2	2	114	C
2	2	115	G
2	2	124	G

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Mol	Chain	Res	Type
2	2	130	G
2	2	132	G
2	2	144	G
2	2	157	A
2	2	159	U
2	2	160	G
2	2	165	U
6	6	3	A
6	6	5	U
6	6	6	C
6	6	8	U
6	6	9	C
6	6	47	U
6	6	58	A
6	6	59	A
6	6	82	A
6	6	83	A
6	6	85	U
6	6	92	G
6	6	93	A
6	6	94	A
6	6	97	C
6	6	99	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	48	A
1	1	360	A
1	1	382	A
1	1	447	C
1	1	487	C
1	1	488	A
1	1	493	G
1	1	496	C
1	1	500	U
1	1	661	C
1	1	761	U
1	1	965	A
1	1	996	G
1	1	1159	U
1	1	1185	A

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Mol	Chain	Res	Type
1	1	1380	A
1	1	1389	A
1	1	3337	A
1	1	3407	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	505:G	O3'	506:G	P	6.68

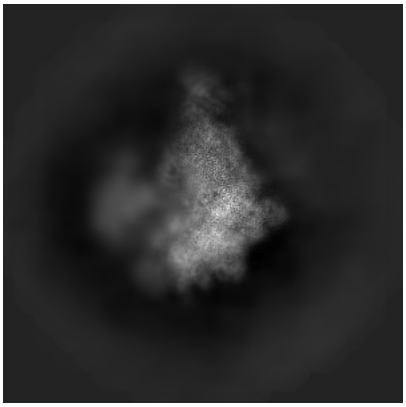
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24410. These allow visual inspection of the internal detail of the map and identification of artifacts.

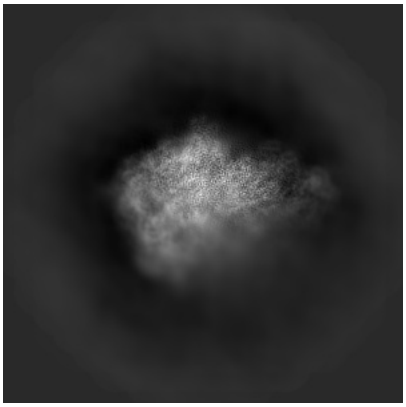
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

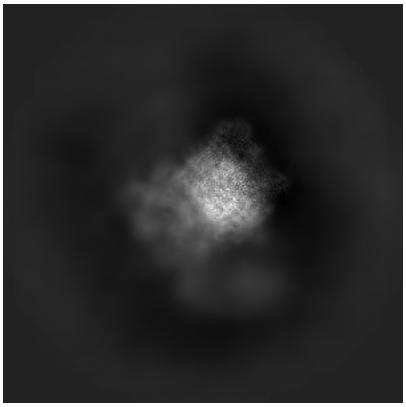
6.1.1 Primary map



X



Y

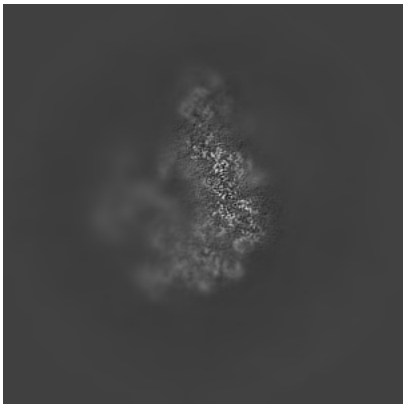


Z

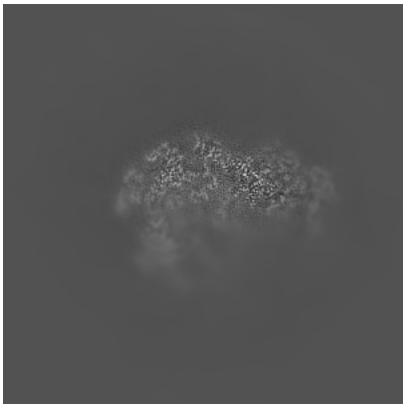
The images above show the map projected in three orthogonal directions.

6.2 Central slices

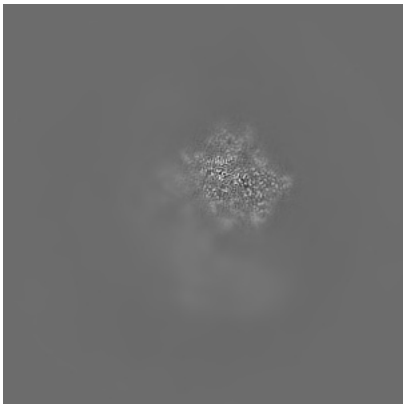
6.2.1 Primary map



X Index: 256



Y Index: 256

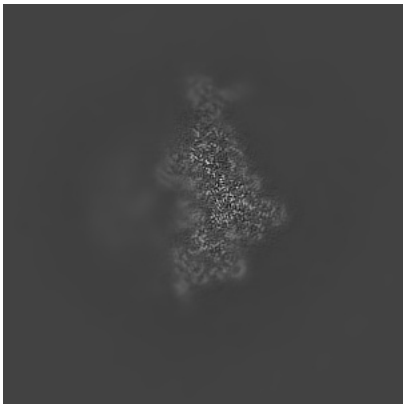


Z Index: 256

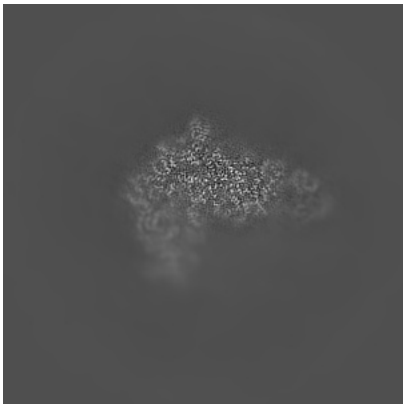
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

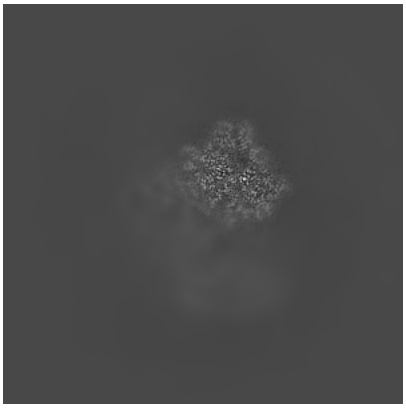
6.3.1 Primary map



X Index: 286



Y Index: 274

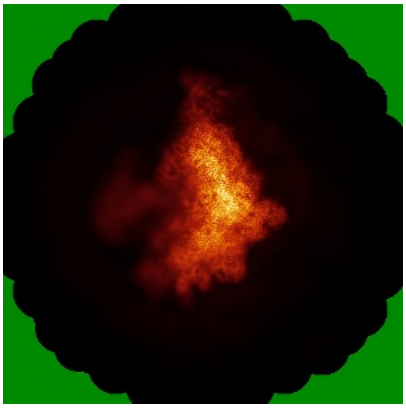


Z Index: 249

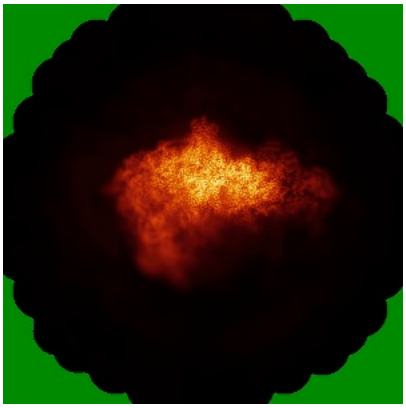
The images above show the largest variance slices of the map in three orthogonal directions.

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

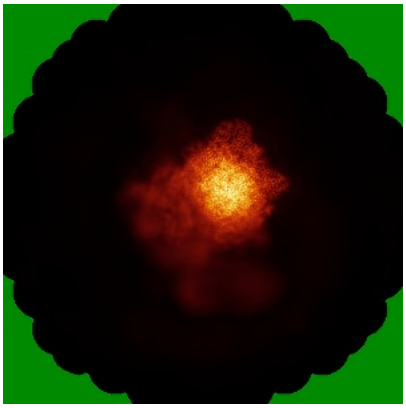
6.4.1 Primary map



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.

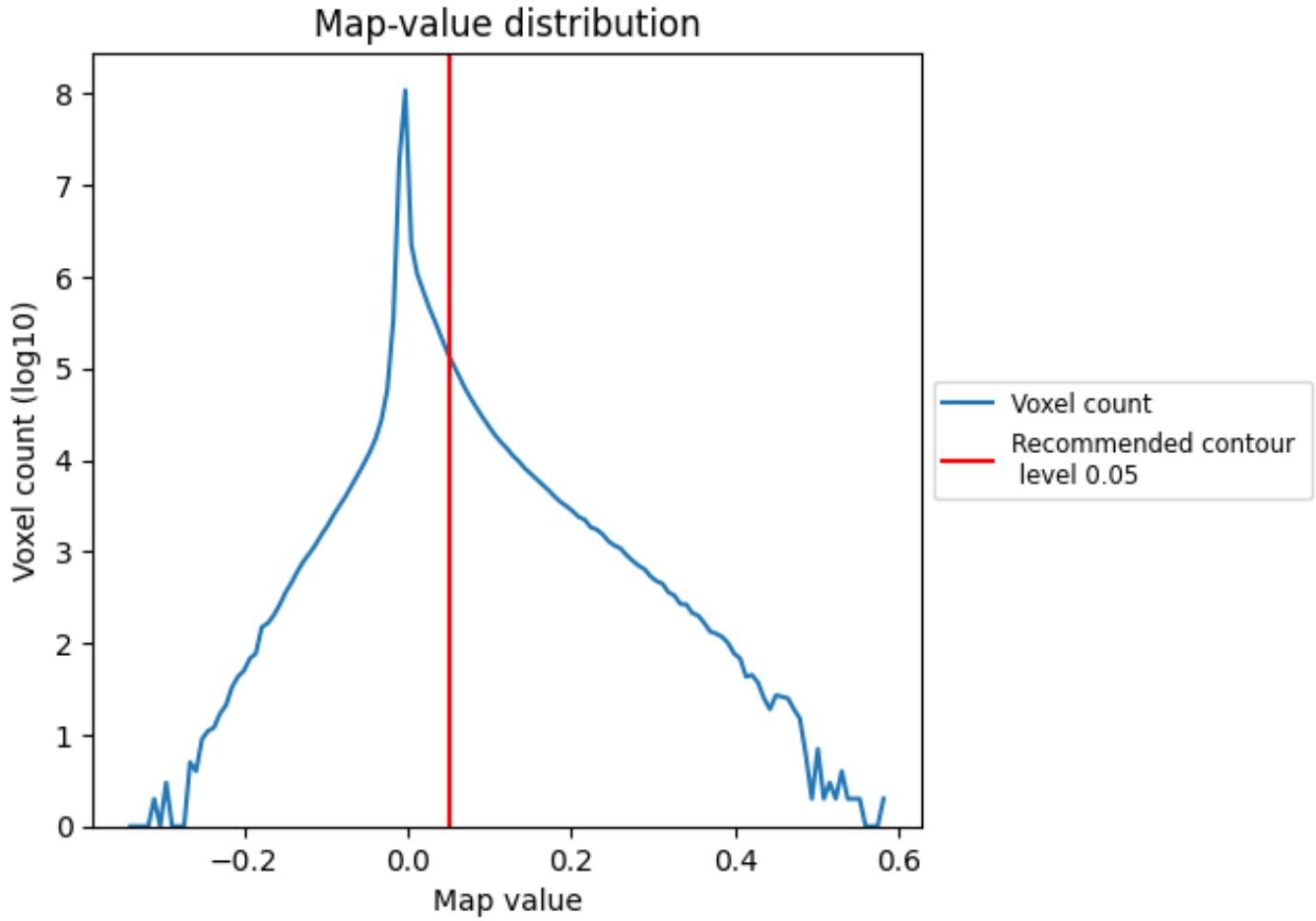
6.6 Mask visualisation (i)

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

7 Map analysis

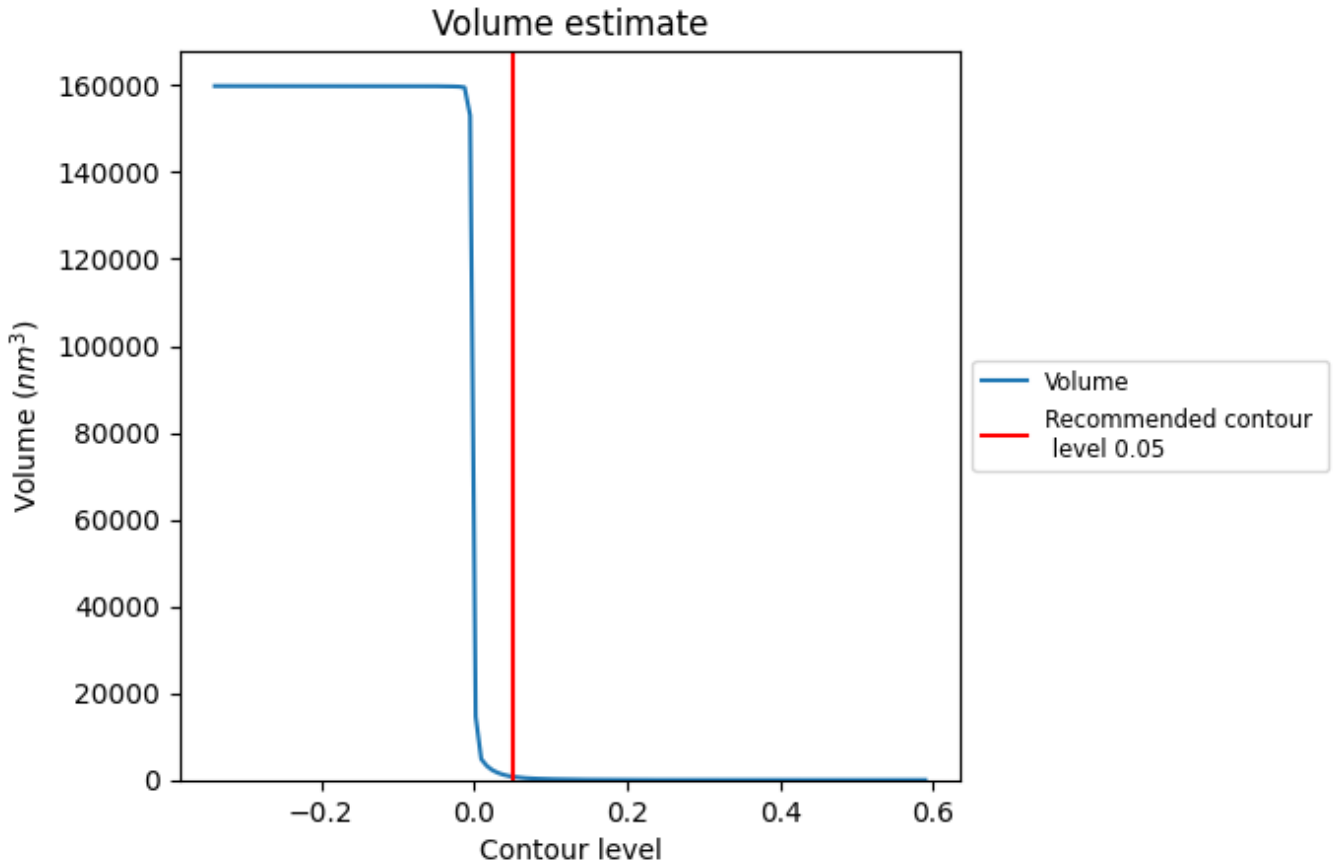
This section contains the results of statistical analysis of the map.

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.

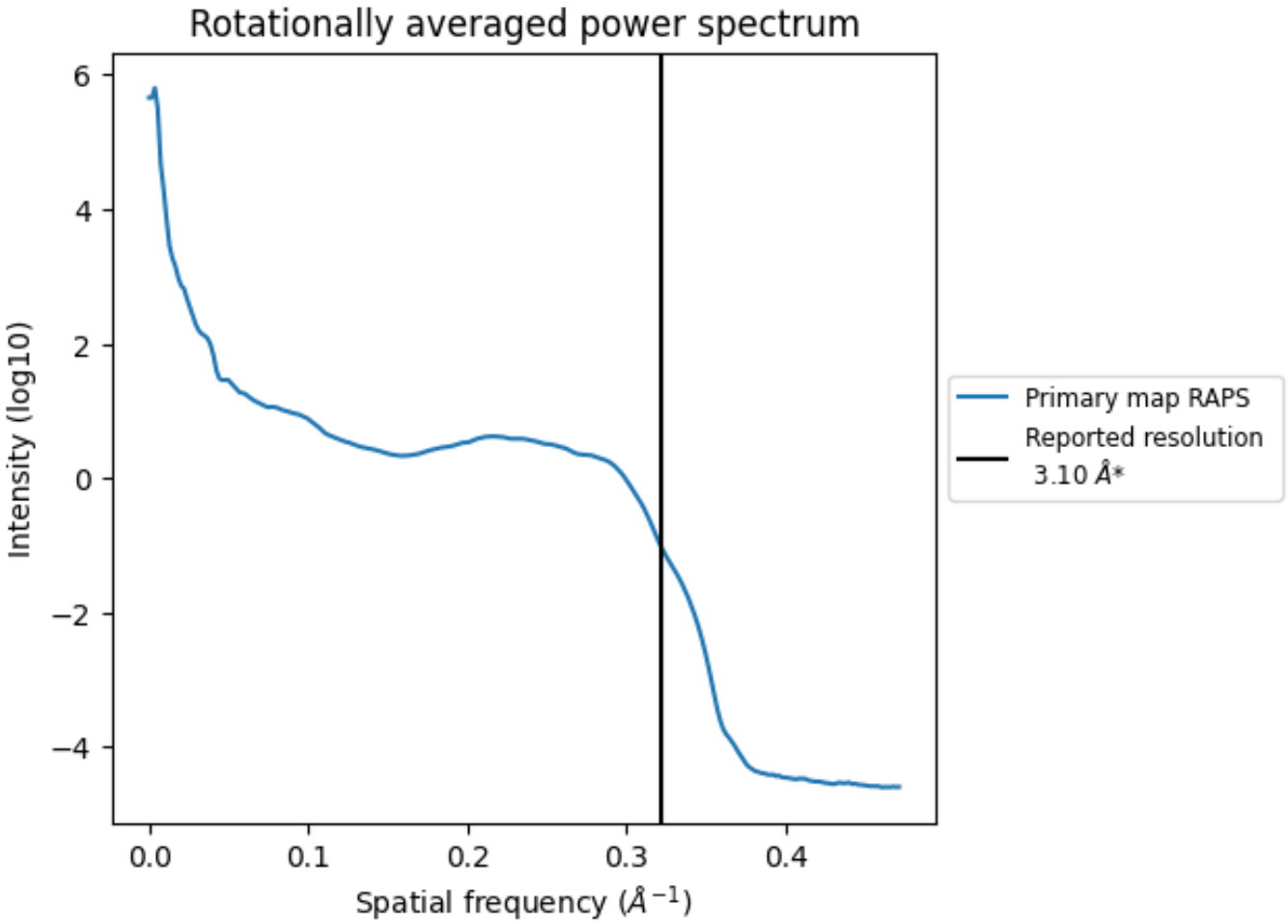
7.2 Volume estimate



The volume at the recommended contour level is 765 nm^3; this corresponds to an approximate mass of 691 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 0.323 $Å^{-1}$

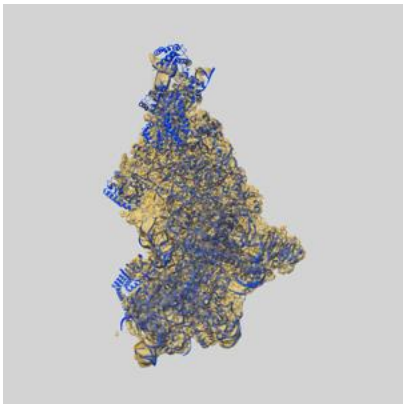
8 Fourier-Shell correlation (i)

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

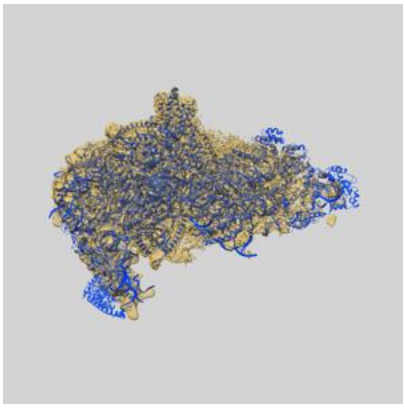
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-24410 and PDB model 8EUP. Per-residue inclusion information can be found in section 3 on page 11.

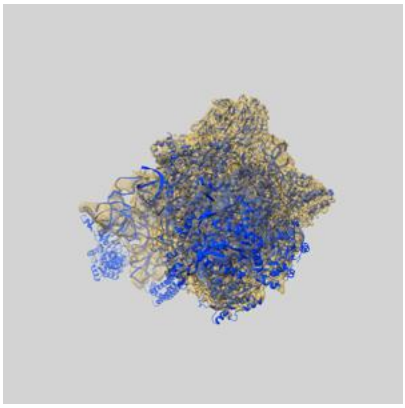
9.1 Map-model overlay



X



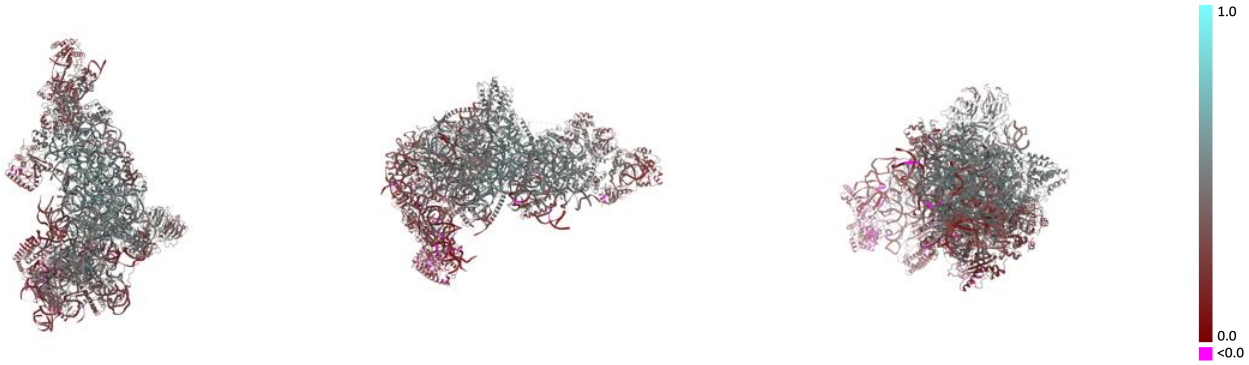
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

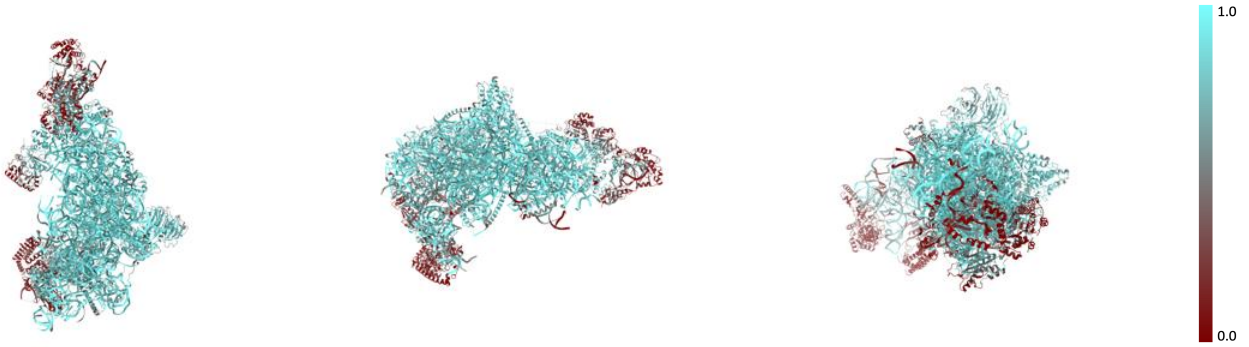
9.2 Q-score mapped to coordinate model



X Y Z

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

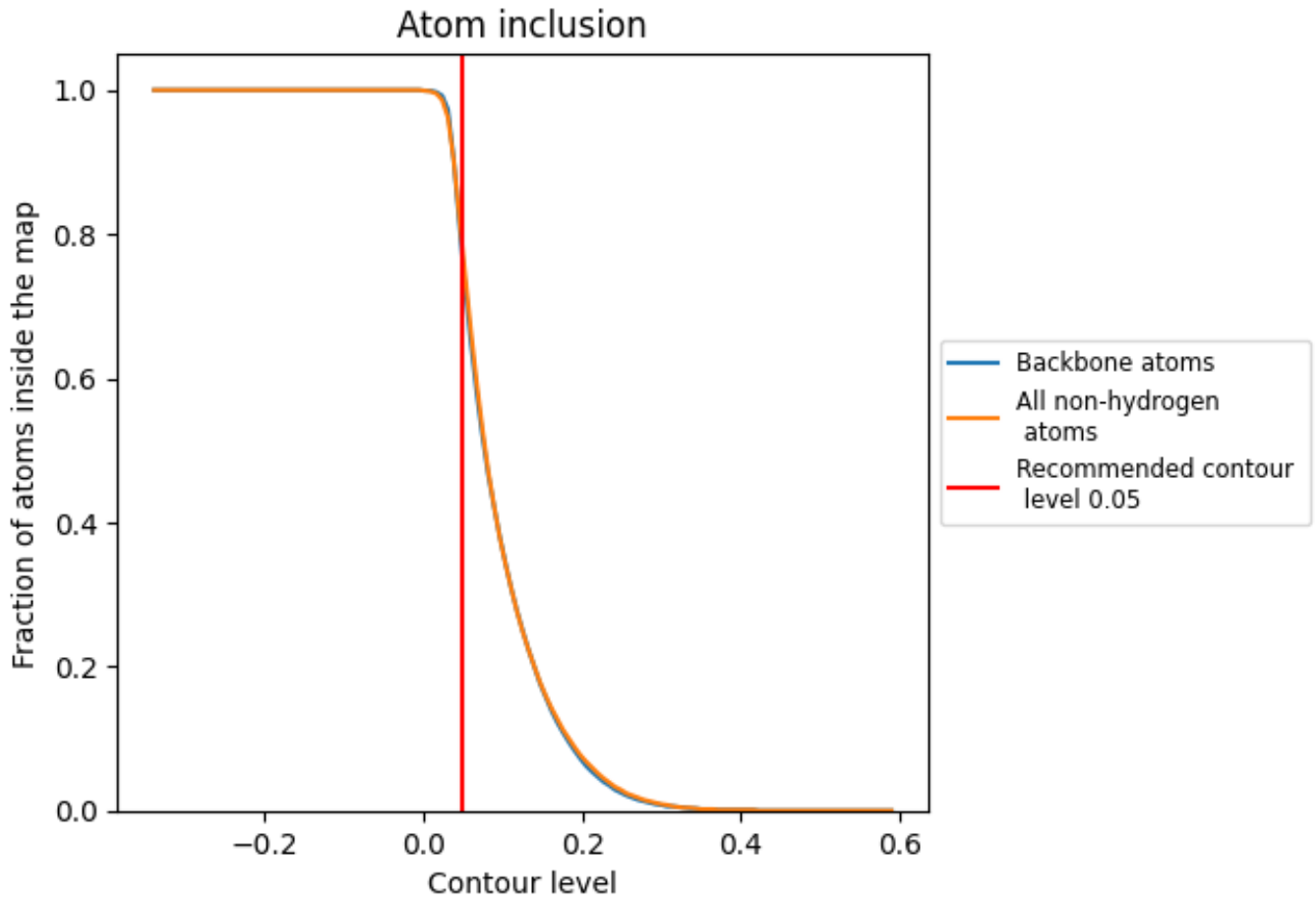
9.3 Atom inclusion mapped to coordinate model



X Y Z

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

9.4 Atom inclusion (i)



At the recommended contour level, 75% of all backbone atoms, 77% 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	0.7700	0.3950
1	0.8880	0.3820
2	0.8200	0.3820
3	0.8760	0.5110
4	0.8410	0.4880
5	0.7830	0.4390
6	0.3820	0.2380
A	0.6610	0.3020
B	0.6580	0.2340
C	0.9210	0.5340
D	0.4050	0.3710
E	0.8230	0.4210
F	0.8600	0.4750
G	0.8810	0.4930
H	0.1430	0.2360
J	0.2520	0.2300
K	0.2720	0.3170
L	0.9540	0.5490
M	0.9520	0.3990
N	0.9590	0.5460
O	0.7290	0.3420
P	0.8560	0.4510
Q	0.9000	0.5080
S	0.7220	0.3540
T	0.2400	0.3360
V	0.0290	0.1220
Y	0.9100	0.5150
b	0.0070	0.1780
e	0.9470	0.5390
f	0.9290	0.5070
h	0.7600	0.4280
i	0.8840	0.4760
j	0.8940	0.5020
m	0.7880	0.4440
o	0.2660	0.3230

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Chain	Atom inclusion	Q-score
r	0.0110	0.2110
t	0.1790	0.3170
u	0.1420	0.1310
v	0.8220	0.4710
x	0.8360	0.4730
y	0.0010	0.1050