Full wwPDB EM Validation Report (i)

Mar 17, 2026 – 09:40 PM UTC

PDB ID	:	8I9V / pdb_00008i9v
EMDB ID	:	EMD-35285
Title	:	Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit - State Dbp10-2
Authors	:	Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on	:	2023-02-07
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 (i) 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 (i)) were used in the production of this report:

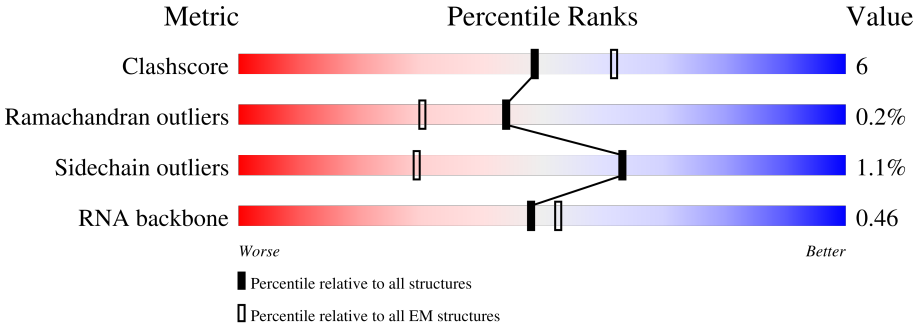
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

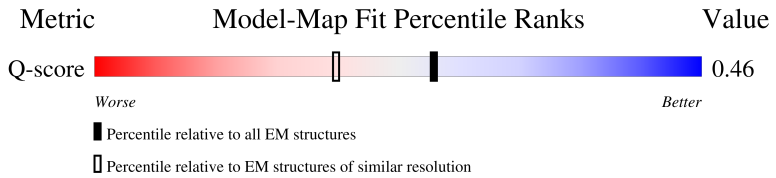
1 Overall quality at a glance (i)

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	C1	3341	• 39% 22% • 36%
2	C2	256	• 41% 18% • 38%
3	C3	161	5% 25% 29% 7% 39%

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Mol	Chain	Length	Quality of chain
4	CA	316	61% 21% 18%
5	CB	391	45% 20% 34%
6	CC	801	15% 30% 6% 64%
7	CE	598	65% 12% 23%
8	CF	270	75% 16% 9%
9	CG	184	71% 23%
10	CH	661	61% 11% 28%
11	CI	414	27% 8% 65%
12	CJ	679	28% 46% 10% 44%
13	CK	261	69% 20% 11%
14	CL	558	51% 66% 30%
15	CM	249	17% 60% 14% 25%
15	LF	249	84% 13%
16	CN	246	82% 18%
17	CO	120	47% 5% 48%
18	CP	751	33% 10% 57%
19	CQ	225	38% 12% 50%
20	CR	237	57% 13% 30%
21	CS	834	33% 35% 64%
22	CT	688	49% 65% 33%
23	CU	451	33% 6% 61%
24	CX	203	21% 38% 5% 57%
25	CY	788	22% 41% 59%
26	Cz	123	16% 50% 7% 43%
27	Cb	924	56% 14% 31%

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Mol	Chain	Length	Quality of chain
28	LB	392	67% 20% 13%
29	LC	365	85% 14%
30	LE	200	76% 9% 15%
31	LG	262	7% 60% 15% 25%
32	LH	192	88% 11%
33	LK	165	75% 13% 12%
34	LL	213	44% 11% 45%
35	LM	142	79% 18%
36	LN	203	77% 13% 10%
37	LO	204	94% 6%
38	LP	187	72% 10% 18%
39	LQ	213	51% 9% 39%
40	LS	174	83% 17%
41	LT	160	11% 71% 7% 21%
42	LV	139	72% 25%
43	LX	156	9% 14% 86%
44	LY	138	78% 18%
45	Ld	120	22% 69% 20% 9%
46	Le	131	88% 11%
47	Lf	109	83% 16%
48	Lh	935	11% 87%
49	Li	110	70% 10% 20%
50	Lj	95	67% 11% 22%
51	Lq	217	59% 83% 12% 5%
52	Cc	282	73% 10% 16%

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Mol	Chain	Length	Quality of chain
53	Cd	436	67% 12% 22%
54	Ce	336	49% 8% 42%
55	Cf	570	9% 90%

2 Entry composition (i)

There are 57 unique types of molecules in this entry. The entry contains 138001 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 (3341-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	C1	2152	46025	20547	8331	14995	2152	0	0

- Molecule 2 is a RNA chain called RNA (256-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	C2	158	3359	1502	593	1106	158	0	0

- Molecule 3 is a RNA chain called RNA (161-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C3	98	2097	933	381	685	98	0	0

- Molecule 4 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	CA	260	2144	1371	393	373	7	0	0

- Molecule 5 is a protein called Ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	CB	260	2063	1322	367	371	3	0	0

- Molecule 6 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	CC	289	2388	1520	399	462	7	0	0

- Molecule 7 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	CE	463	3673	2352	643	667	11	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	543	LYS	-	insertion	UNP G0RYU9
CE	544	SER	-	insertion	UNP G0RYU9
CE	545	PHE	-	insertion	UNP G0RYU9
CE	546	GLY	-	insertion	UNP G0RYU9
CE	547	PHE	-	insertion	UNP G0RYU9
CE	548	SER	-	insertion	UNP G0RYU9
CE	549	THR	-	insertion	UNP G0RYU9
CE	550	PRO	-	insertion	UNP G0RYU9
CE	551	PRO	-	insertion	UNP G0RYU9
CE	552	ARG	-	insertion	UNP G0RYU9
CE	553	VAL	-	insertion	UNP G0RYU9
CE	554	ASP	-	insertion	UNP G0RYU9
CE	555	ILE	-	insertion	UNP G0RYU9
CE	556	THR	-	insertion	UNP G0RYU9
CE	557	LEU	-	insertion	UNP G0RYU9
CE	558	SER	-	insertion	UNP G0RYU9
CE	559	ALA	-	insertion	UNP G0RYU9
CE	560	SER	-	insertion	UNP G0RYU9
CE	561	LEU	-	insertion	UNP G0RYU9
CE	562	SER	-	insertion	UNP G0RYU9
CE	563	ARG	-	insertion	UNP G0RYU9
CE	564	ASP	-	insertion	UNP G0RYU9
CE	565	LYS	-	insertion	UNP G0RYU9
CE	566	LYS	-	insertion	UNP G0RYU9
CE	567	PRO	-	insertion	UNP G0RYU9
CE	568	GLN	-	insertion	UNP G0RYU9
CE	569	GLY	-	insertion	UNP G0RYU9
CE	570	ARG	-	insertion	UNP G0RYU9
CE	571	ARG	-	insertion	UNP G0RYU9
CE	572	ALA	-	insertion	UNP G0RYU9
CE	573	TYR	-	insertion	UNP G0RYU9
CE	574	GLY	-	insertion	UNP G0RYU9
CE	575	SER	-	insertion	UNP G0RYU9
CE	576	GLN	-	insertion	UNP G0RYU9
CE	577	PRO	-	insertion	UNP G0RYU9
CE	578	ARG	-	insertion	UNP G0RYU9

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Chain	Residue	Modelled	Actual	Comment	Reference
CE	579	GLN	-	insertion	UNP G0RYU9
CE	580	GLY	-	insertion	UNP G0RYU9
CE	581	GLY	-	insertion	UNP G0RYU9
CE	582	ARG	-	insertion	UNP G0RYU9
CE	583	TYR	-	insertion	UNP G0RYU9
CE	584	LYS	-	insertion	UNP G0RYU9

- Molecule 8 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	CF	245	1945	1222	352	362	9	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CF	13	ILE	THR	conflict	UNP G0S616
CF	139	THR	PRO	conflict	UNP G0S616
CF	228	ASN	SER	conflict	UNP G0S616
CF	259	ILE	MET	conflict	UNP G0S616

- Molecule 9 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	CG	177	1396	884	247	253	12	0	0

- Molecule 10 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	CH	476	3851	2451	669	716	15	0	0

- Molecule 11 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	CI	146	1196	763	224	204	5	0	0

- Molecule 12 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	CJ	380	3109	2003	547	549	10	0	0

- Molecule 13 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	CK	232	1855	1165	363	323	4	0	0

- Molecule 14 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	CL	390	2173	1307	446	420	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CL	69	ARG	ILE	conflict	UNP G0SEW3

- Molecule 15 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	CM	187	1525	987	278	257	3	0	0
15	LF	240	1967	1264	368	332	3	0	0

- Molecule 16 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	CN	246	1856	1158	322	369	7	0	0

- Molecule 17 is a protein called DUF2423 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	CO	62	468	290	94	82	2	0	0

- Molecule 18 is a protein called RNA methyltransferase nop2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	CP	324	2535	1618	445	457	15	0	0

- Molecule 19 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	CQ	112	960	607	195	148	10	0	0

- Molecule 20 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	CR	167	1354	827	278	247	2	0	0

- Molecule 21 is a protein called AdoMet-dependent rRNA methyltransferase SPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	CS	298	1750	1072	330	347	1	0	0

- Molecule 22 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
22	CT	458	2269	1353	458	458	0	0

- Molecule 23 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	CU	178	1415	876	265	271	3	0	0

- Molecule 24 is a protein called 60S ribosomal subunit-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	CX	88	701	435	128	135	3	0	0

- Molecule 25 is a protein called Putative NOC2 family protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	CY	324	1608	960	324	324	0	0

- Molecule 26 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Cz	70	592	368	120	101	3	0	0

- Molecule 27 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Cb	642	5058	3216	918	911	13	0	0

- Molecule 28 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	LB	341	2708	1721	493	482	12	0	0

- Molecule 29 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	LC	362	2752	1738	526	479	9	0	0

- Molecule 30 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	LE	170	1338	861	241	233	3	0	0

- Molecule 31 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	LG	196	1583	1021	287	270	5	0	0

- Molecule 32 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	LH	190	1496	950	268	272	6	0	0

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	TYR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LEU	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

- Molecule 33 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	LK	146	1112	701	203	206	2	0	0

- Molecule 34 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	LL	117	964	608	206	148	2	0	0

- Molecule 35 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	LM	137	1101	699	211	190	1	0	0

- Molecule 36 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	LN	183	1563	974	332	253	4	0	0

- Molecule 37 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	LO	204	1618	1039	306	267	6	0	0

- Molecule 38 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	LP	154	1212	758	233	218	3	0	0

- Molecule 39 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	LQ	129	1021	646	200	173	2	0	0

- Molecule 40 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	LS	174	1433	922	267	239	5	0	0

- Molecule 41 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	LT	126	1014	643	196	173	2	0	0

- Molecule 42 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	LV	135	995	633	185	170	7	0	0

- Molecule 43 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
43	LX	22	148	91	31	26	0	0

- Molecule 44 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	LY	134	1065	664	215	184	2	0	0

- Molecule 45 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	Ld	109	890	563	171	155	1	0	0

- Molecule 46 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	Le	131	1055	663	213	172	7	0	0

- Molecule 47 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	Lf	108	862	546	171	144	1	0	0

- Molecule 48 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
48	Lh	121	995	633	196	166	0	0

- Molecule 49 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	Li	88	731	449	162	119	1	0	0

- Molecule 50 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	Lj	74	595	365	132	93	5	0	0

- Molecule 51 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	Lq	207	1600	1016	285	291	8	0	0

- Molecule 52 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	Cc	236	1898	1208	337	343	10	0	0

- Molecule 53 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	Cd	342	2763	1743	533	483	4	0	0

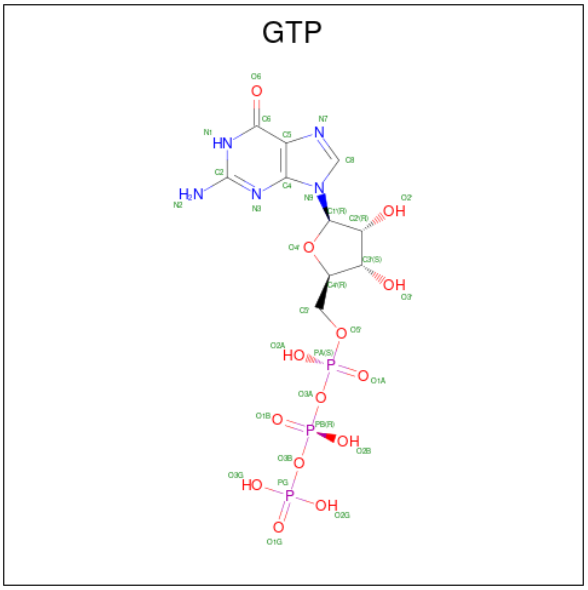
- Molecule 54 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	Ce	194	1609	1020	304	276	9	0	0

- Molecule 55 is a protein called 60S ribosome biogenesis protein Rrp14.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
55	Cf	59	513	310	111	92	0	0

- Molecule 56 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
56	CH	1	32	10	5	14	3	0

- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

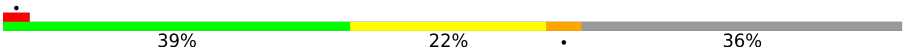
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
57	CQ	1	1	1	0
57	Lj	1	1	1	0
57	Ce	1	1	1	0

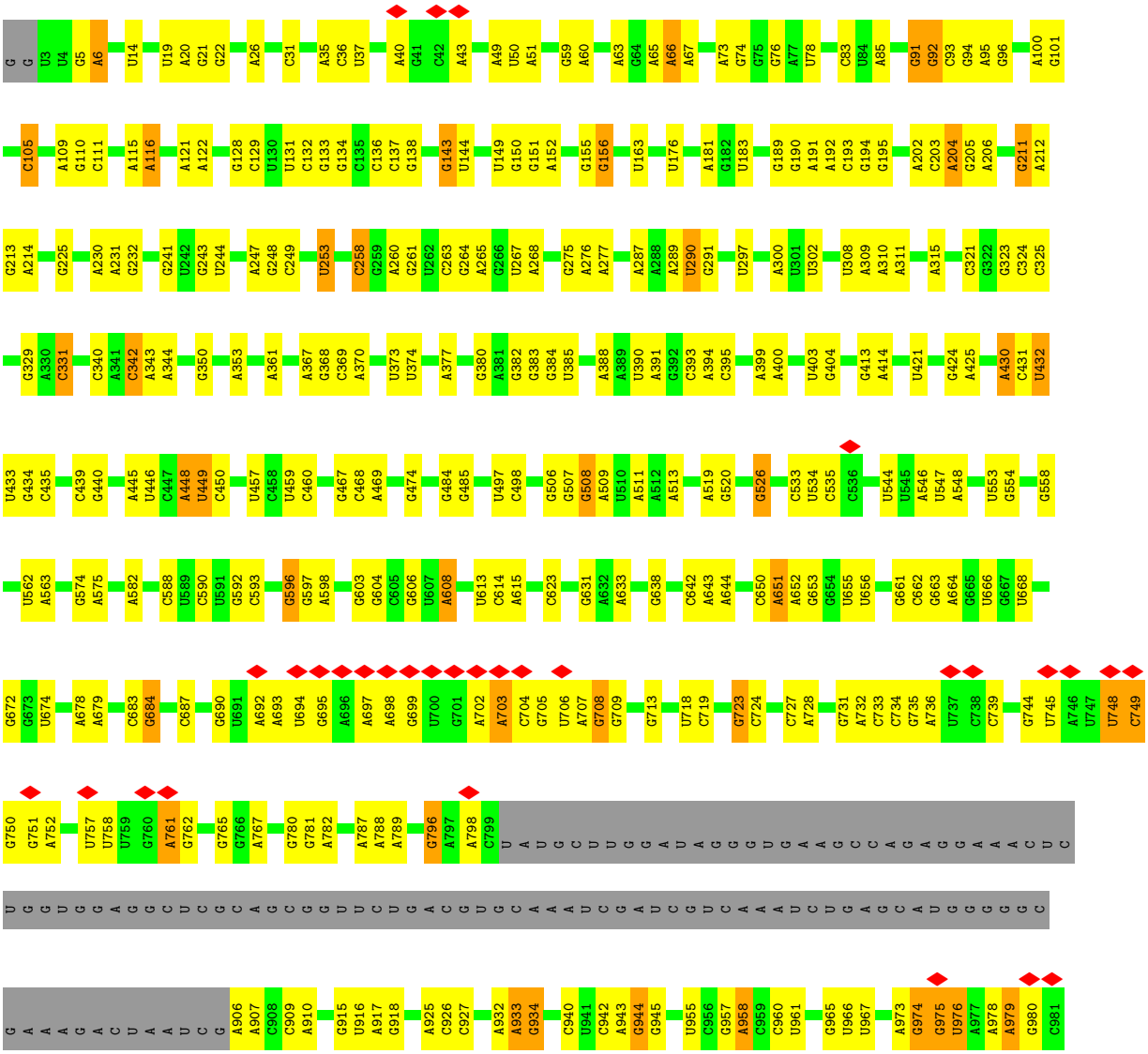
3 Residue-property plots (i)

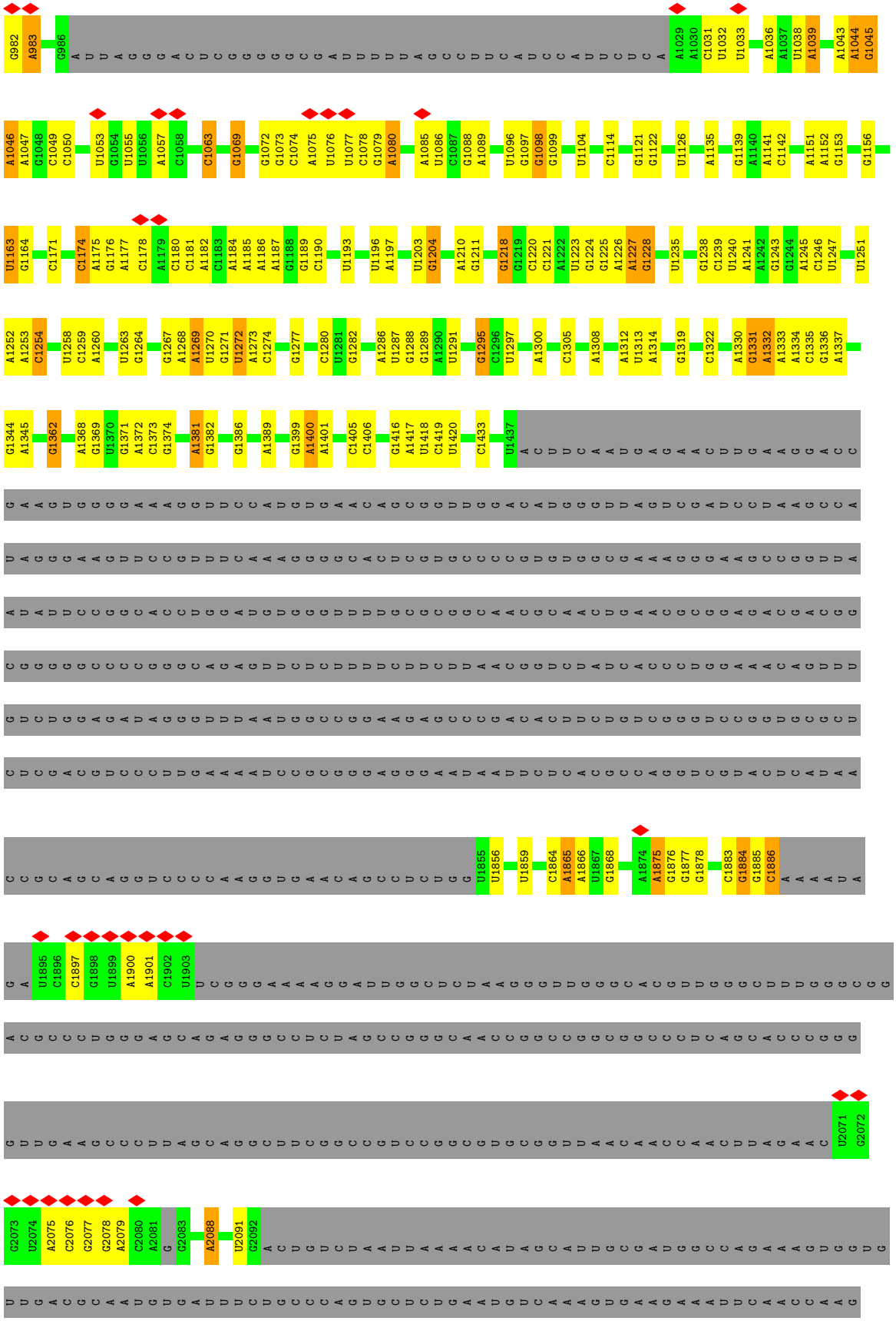
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

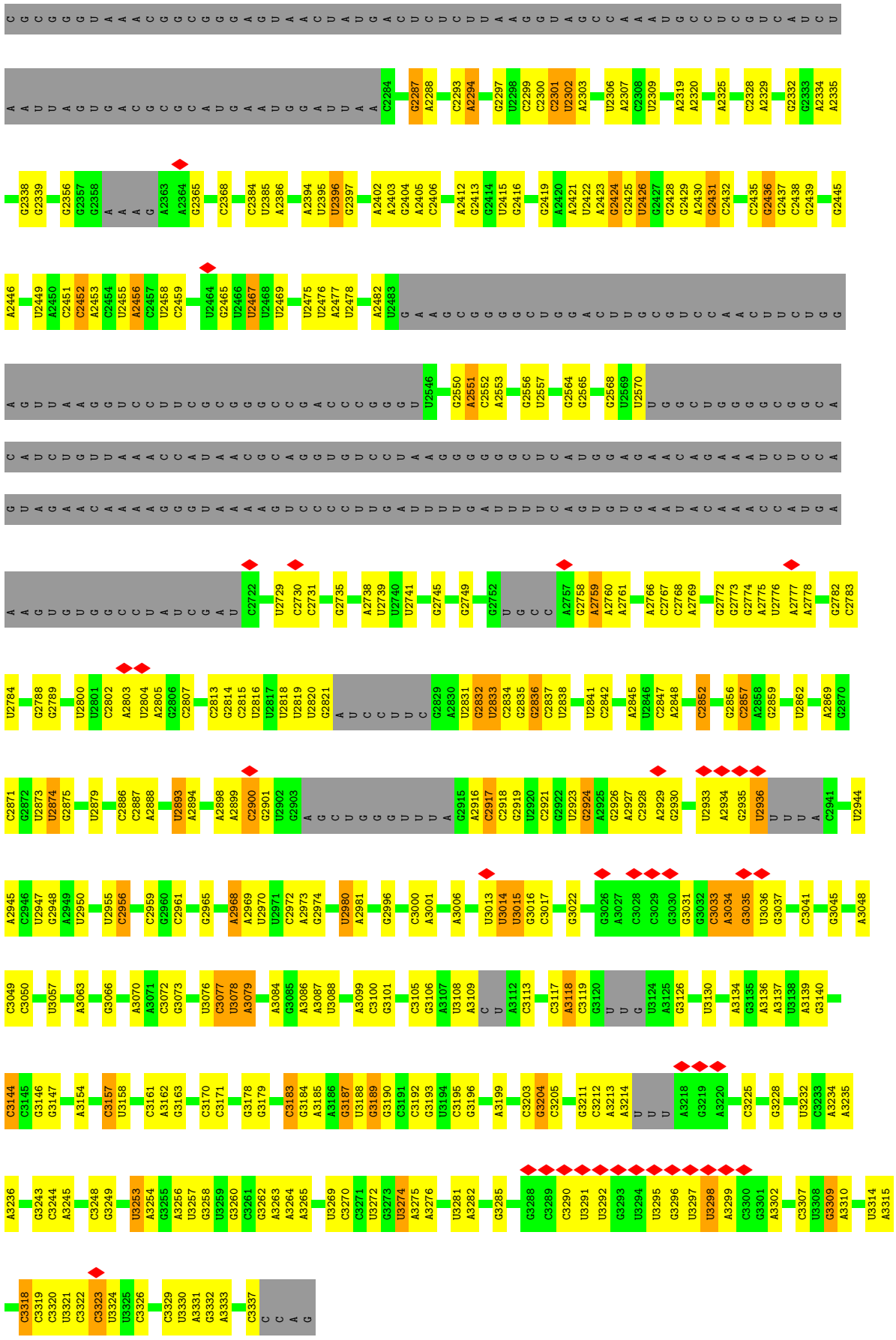
- Molecule 1: RNA (3341-MER)

Chain C1:



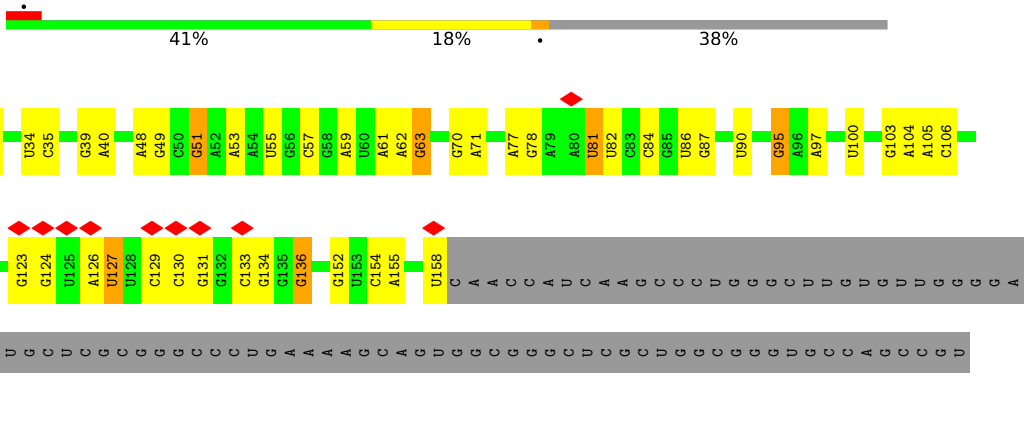



G982 A983 G986 A U U A G G G A C U C G G G G G C G A U U U U A G G C C U U C A U C C A U U C U C A A1029 A1030 C1031 U1032 U1033 A1036 A1037 U1038 A1039 A1043 A1044 G1045
A1046 A1047 G1048 C1049 C1050 U1053 G1054 U1055 U1056 A1057 C1058 C1063 G1069 G1072 G1073 C1074 A1075 U1076 U1077 C1078 G1079 A1080 A1085 U1086 C1087 G1088 A1089 U1096 G1097 G1098 G1099 U1104 C1114 G1121 G1122 U1126 A1135 G1139 A1140 A1141 C1142 A1151 A1152 G1153 G1156
U1163 G1164 C1171 C1174 A1175 G1176 A1177 C1178 A1179 C1180 C1181 A1182 C1183 A1184 A1185 A1186 A1187 G1188 G1189 C1190 U1193 U1196 A1197 U1203 G1204 A1210 G1211 G1218 G1219 C1220 C1221 A1222 U1223 G1224 G1225 A1226 A1227 G1228 U1235 C1238 C1239 U1240 A1241 A1242 G1243 G1244 A1245 C1246 U1247 U1251
A1252 A1253 C1254 U1258 C1259 A1260 U1263 G1264 G1267 A1268 A1269 U1270 G1271 U1272 A1273 C1274 G1277 C1280 U1281 G1282 A1286 U1287 G1288 G1289 A1290 U1291 G1295 C1296 U1297 A1300 C1305 A1308 A1312 U1313 A1314 G1319 C1322 A1330 G1331 A1332 A1333 A1334 C1335 C1246 U1336 A1337
G1344 A1345 G1362 A1368 G1369 U1370 G1371 A1372 C1373 G1374 A1381 G1382 G1386 A1389 G1399 A1400 A1401 C1405 C1406 G1416 A1417 U1418 C1419 U1420 C1433 U1437 A C U U C A A U U G A G A A C U U G G A A G G C C A U G G U U C A A C C G G G A A U C U A A G G C C A
G U A G A A G G G G U U C C A A U G U G G G G C C C C C G G G G U U U U U C C C C C G G G G A A C A A C A A C
U A G G U U A A G G U U C C G U U U C C A A A A U G G G G G C C C C C G U U U U U C C C C C G G G G A A C C
A U A U U U C C G G G C C A C C U U U U G C C G G C C A A C U G A A C C G G G G A A G C C G G G G A A C C G
C G G G G G C C C C C G G G C A G A A U U C C U U U U C C C G G C C A A C U U C A C C G G G G A A G C C G G
G U U C U G G G A G A U G G G U U U A A A A U G G G C C C C C G G G A A G G A G C C U U C A C C G G G G U U G
C U U C G A C G U C C U G G G A A A A U U C C C C C G G G G A A G G G C C C C C A A A A U U C C A C C G G G U U
C C G C A G C A A G G G C C C C U U U U G G G G G A A G G A G C C U U C G G G A A G G G G U U C A C C G G G G U U
G A U1895 C1896 C1897 G1898 U1899 A1900 A1901 C1902 U1903 U C G G G A A A A G G A U U G G G G U U G G G C U C U A A G G G G G U U G G G C A C G U U G G G C C A C C G G G
A C G C C C U G G G A G C A G A G G G G C C C A A C C G G G C C C G G G C C G G G C C G G G A C C C C U U C A G C A C C C G G G
G U U G A A G C C C C U U A G G C U U C C C G G G C G G G C A A C C C C A A C U U C A G G A A A C C G G G U U U
U U G A C G C A A G U G C C C U U G G G C C C A A A A G U G A A G G A A A U U C A A C C C A A G U U C U G C C C A A A A U G G G C A A G G G C A A A A U U C A A C C C A A G
G2073 U2074 A2075 C2076 G2077 G2078 A2079 C2080 A2081 G G2083 A2088 U2091 G2092 A C U G U C U A A A U A A A C A U A G C A U U G C C G A A U G G G C A A A A U U C A A C C C A A G U G G G U G
U2071 G2072



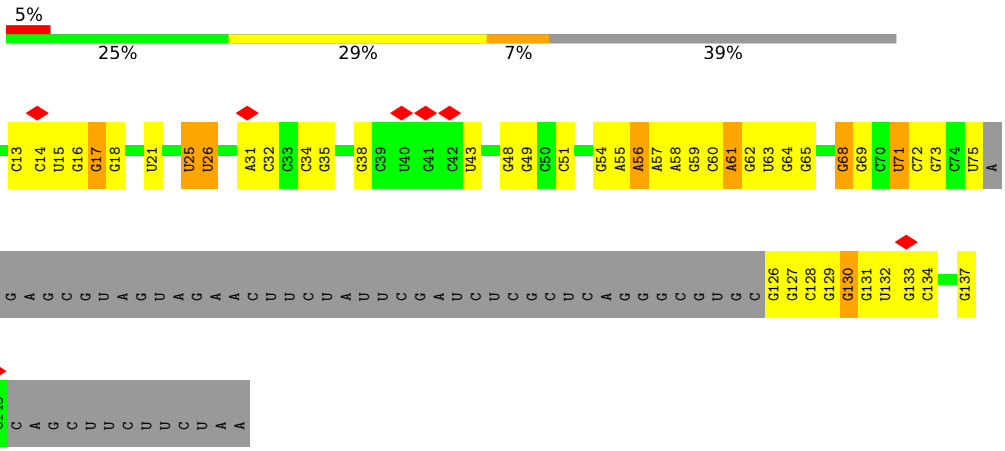
• Molecule 2: RNA (256-MER)

Chain C2:



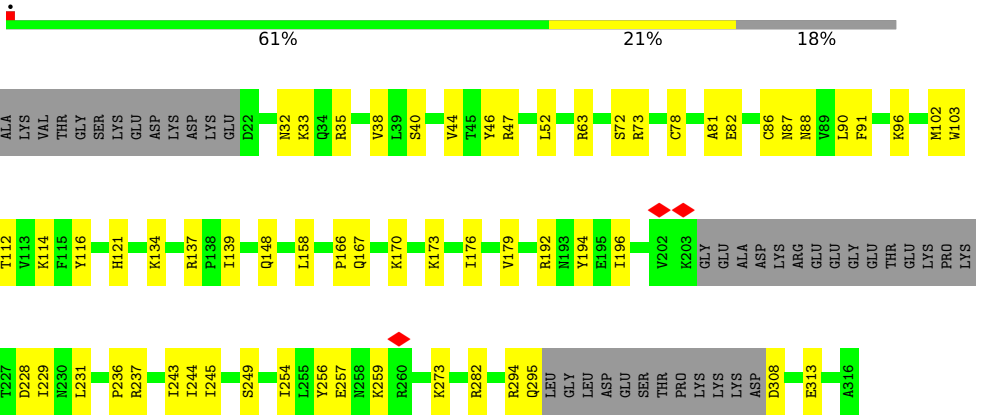
• Molecule 3: RNA (161-MER)

Chain C3:



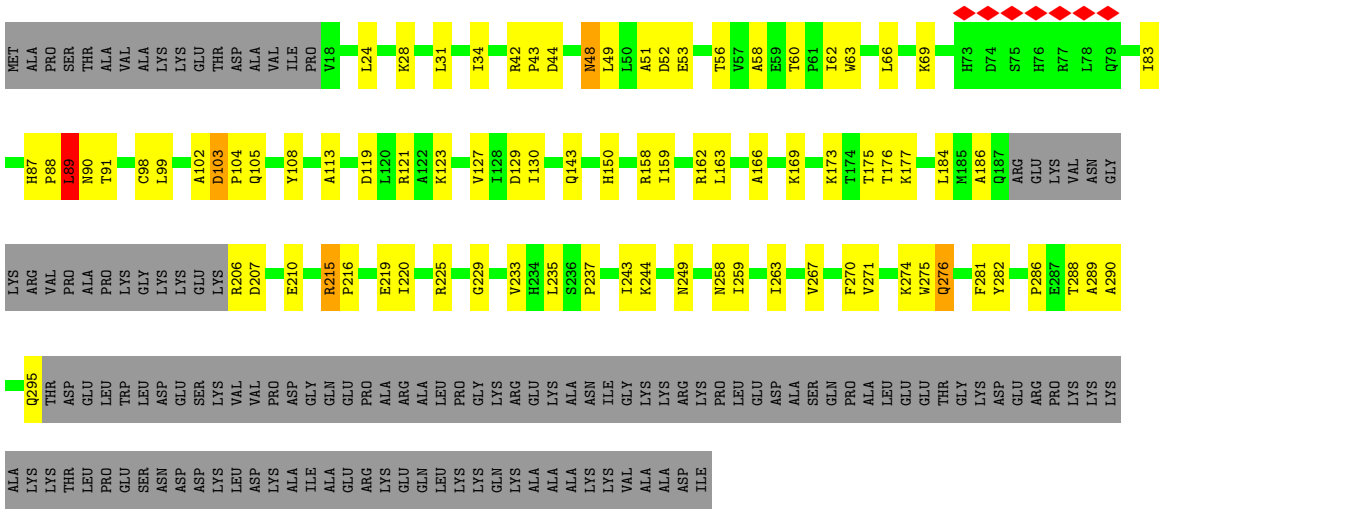
• Molecule 4: Brix domain-containing protein

Chain CA:



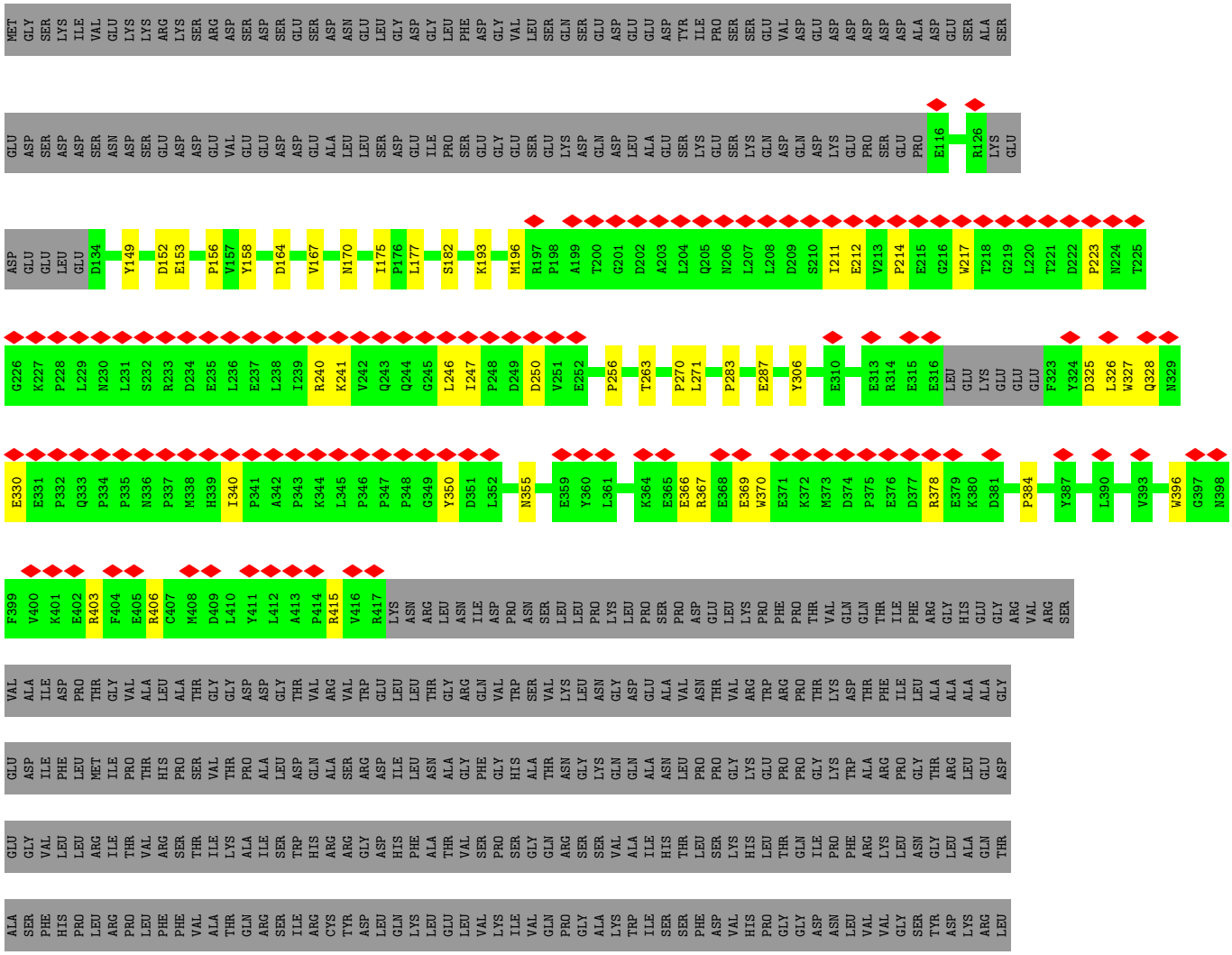
• Molecule 5: Ribosome biogenesis protein C8F11.04

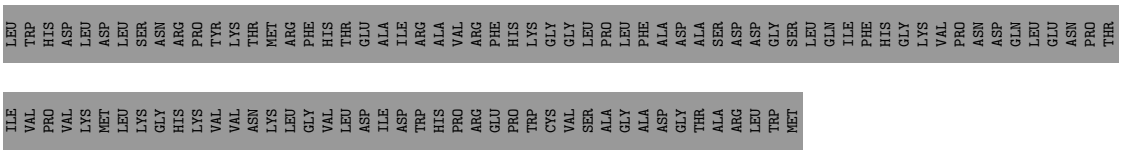
Chain CB:



- Molecule 6: Ribosome biogenesis protein ERB1

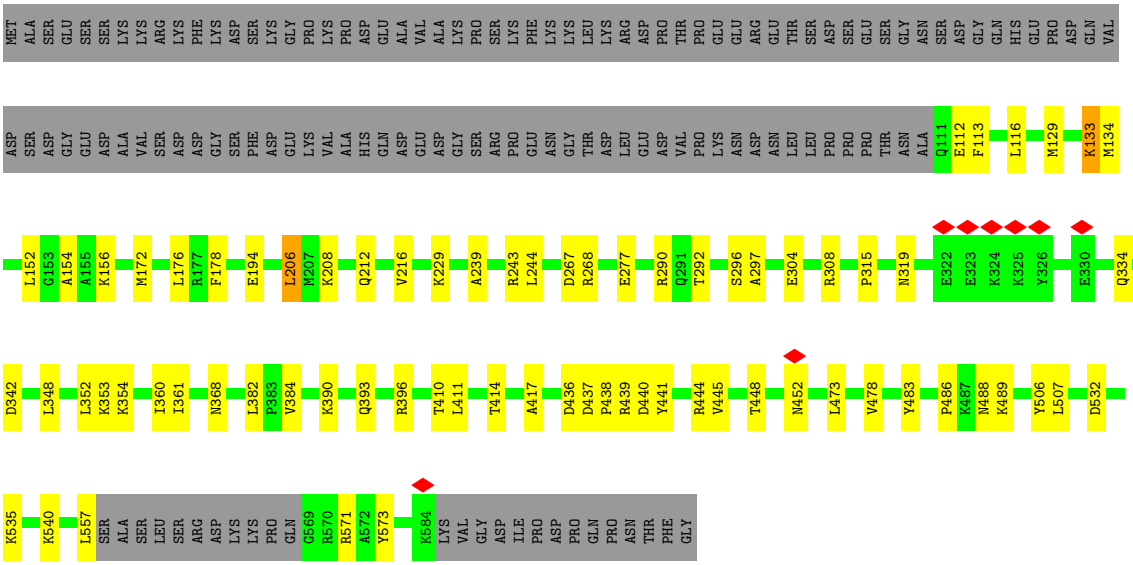
Chain CC:





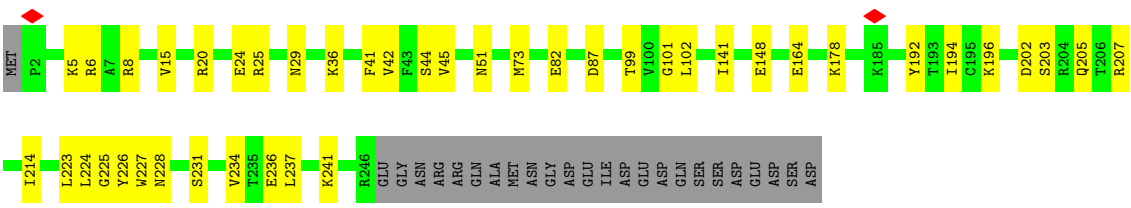
• Molecule 7: RNA helicase

Chain CE:



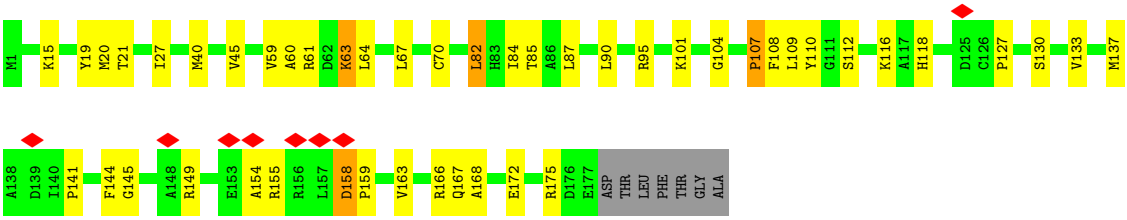
• Molecule 8: Ribosome assembly factor mrt4

Chain CF:



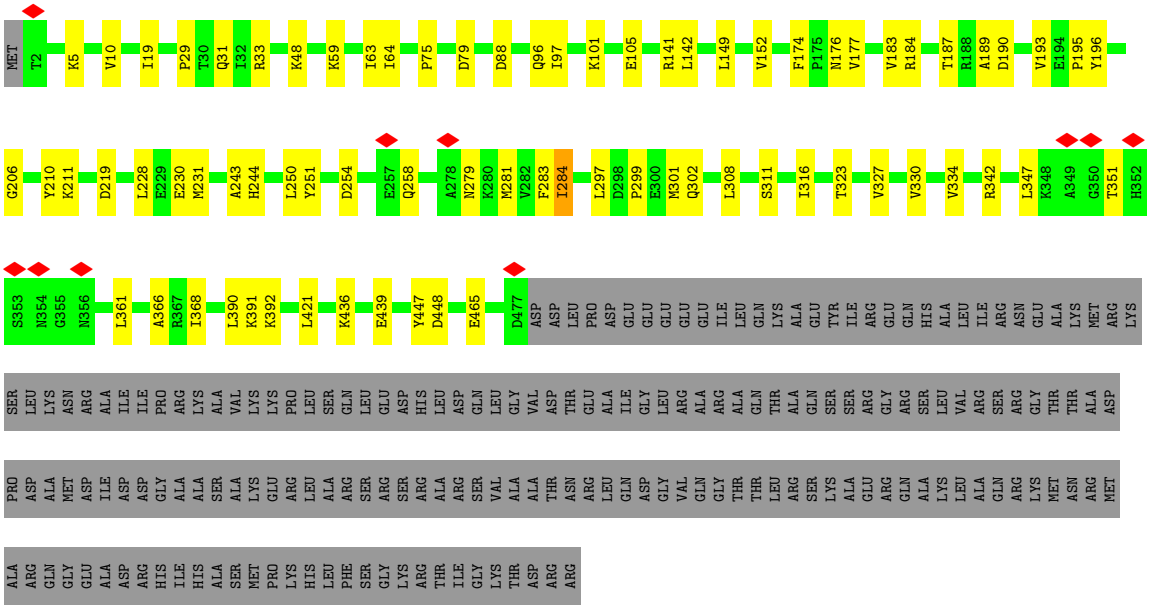
• Molecule 9: 60S ribosome subunit biogenesis protein NIP7

Chain CG:



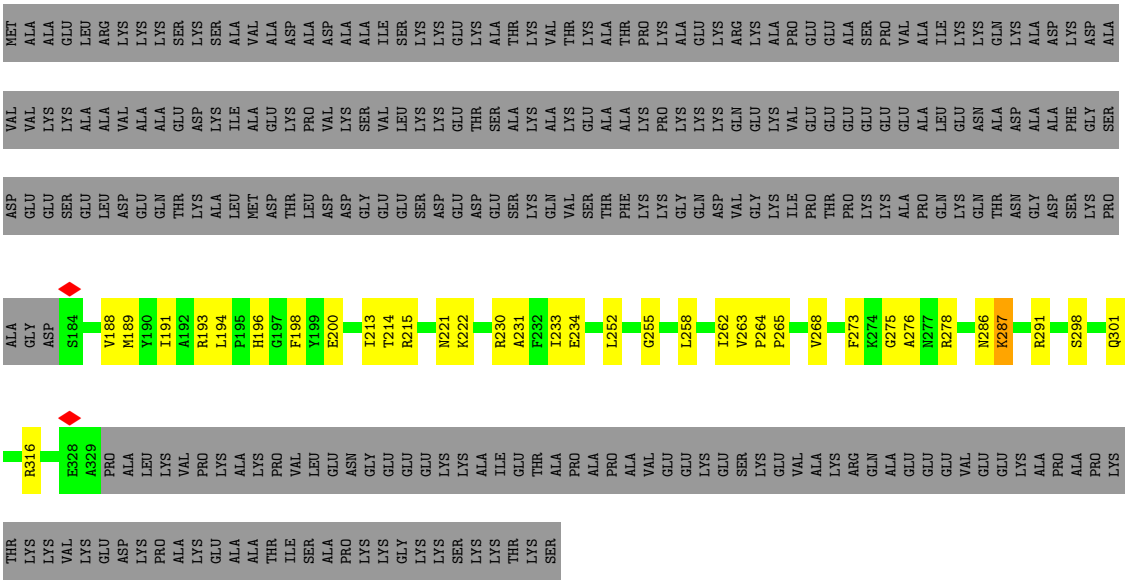
• Molecule 10: Nucleolar GTP-binding protein 1

Chain CH:



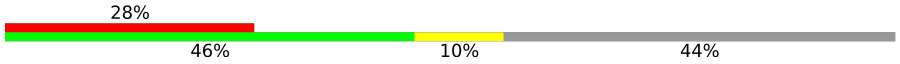
- Molecule 11: Putative RNA-binding protein

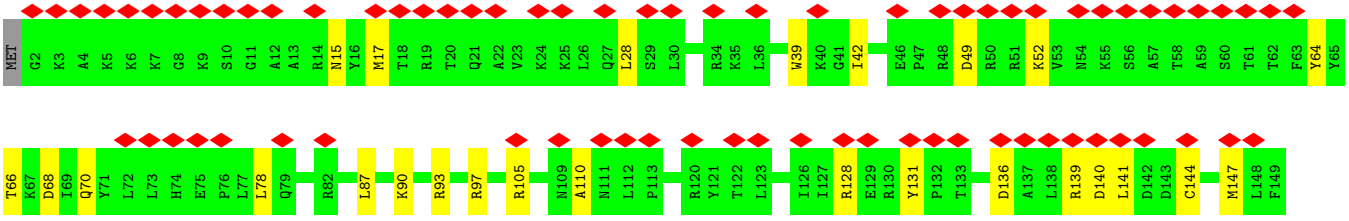
Chain CI:

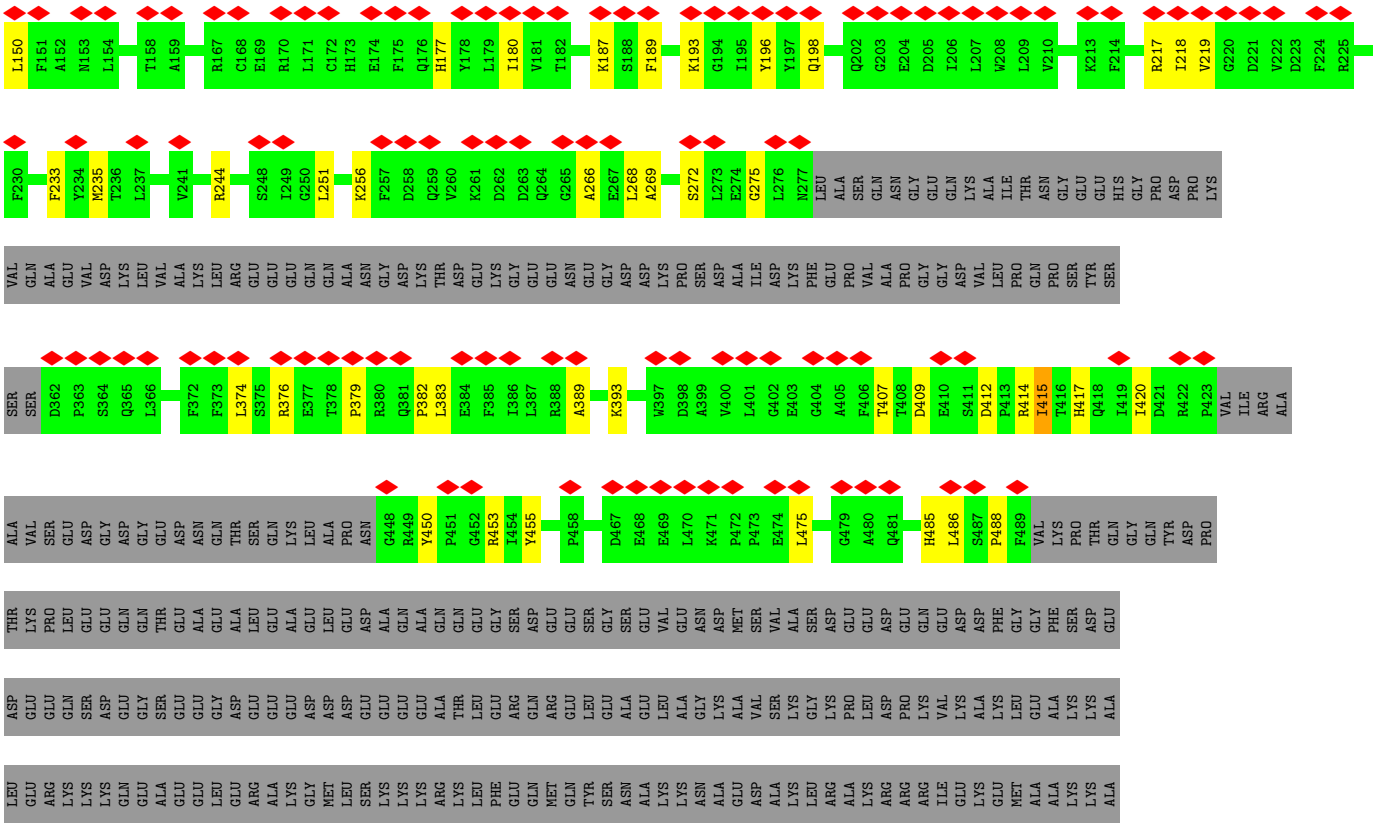


- Molecule 12: Pescadillo homolog

Chain CJ:

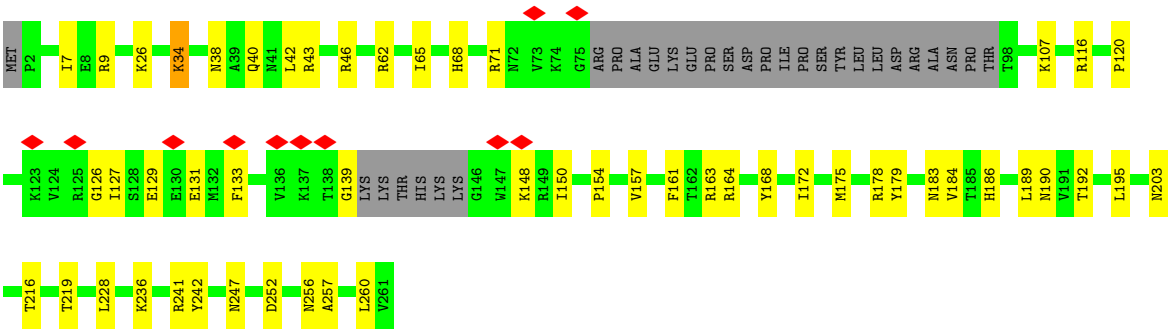






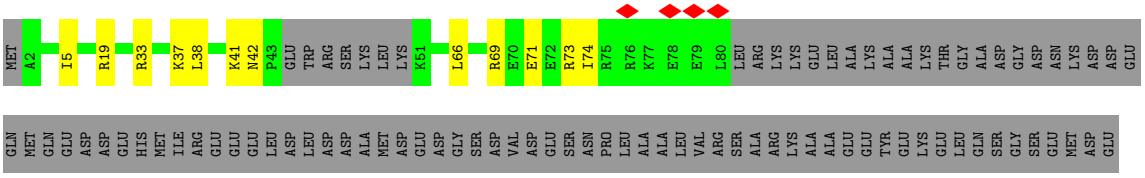
- Molecule 13: Ribosome biogenesis protein NSA2 homolog

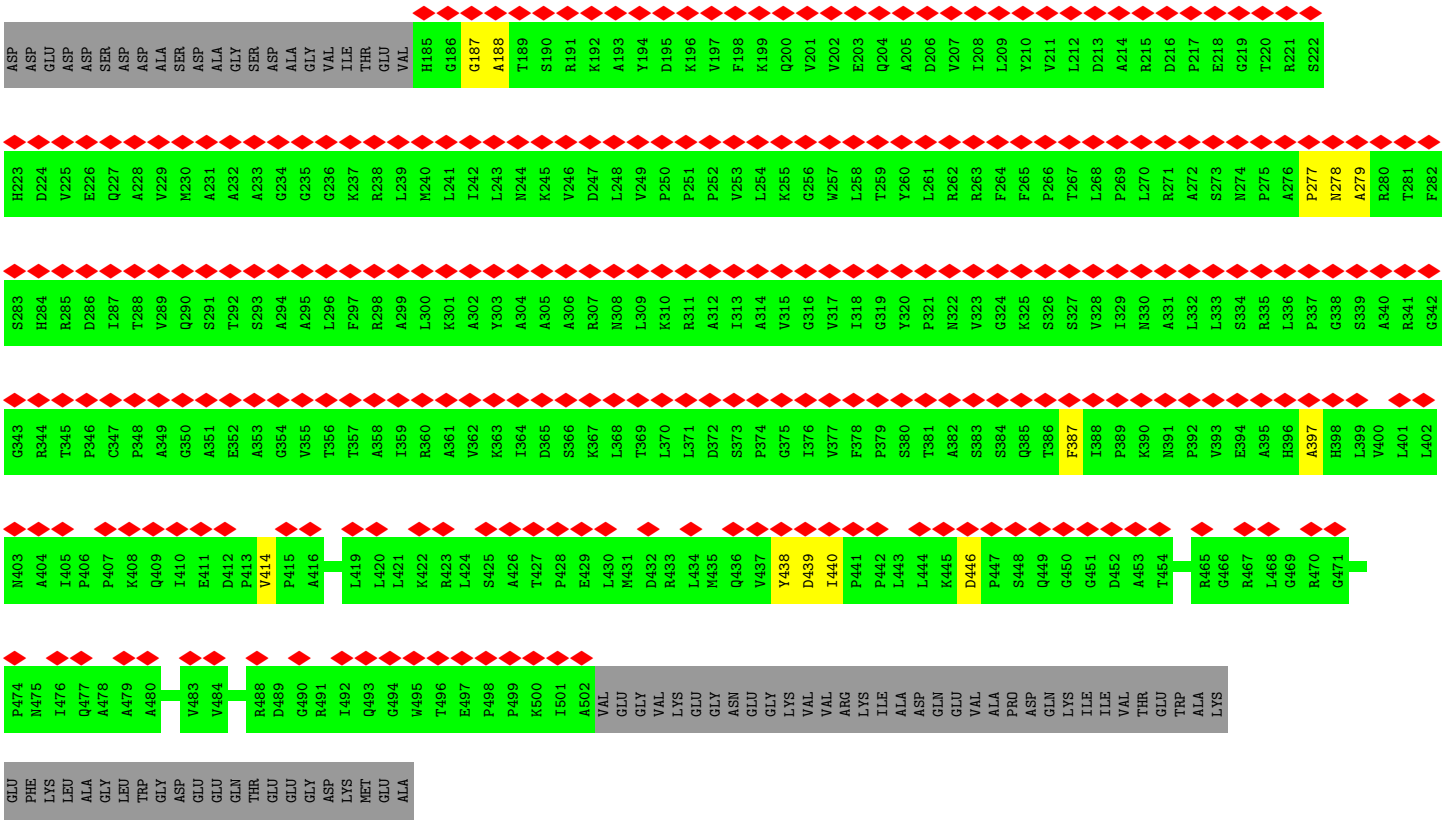
Chain CK:



- Molecule 14: Putative GTP binding protein

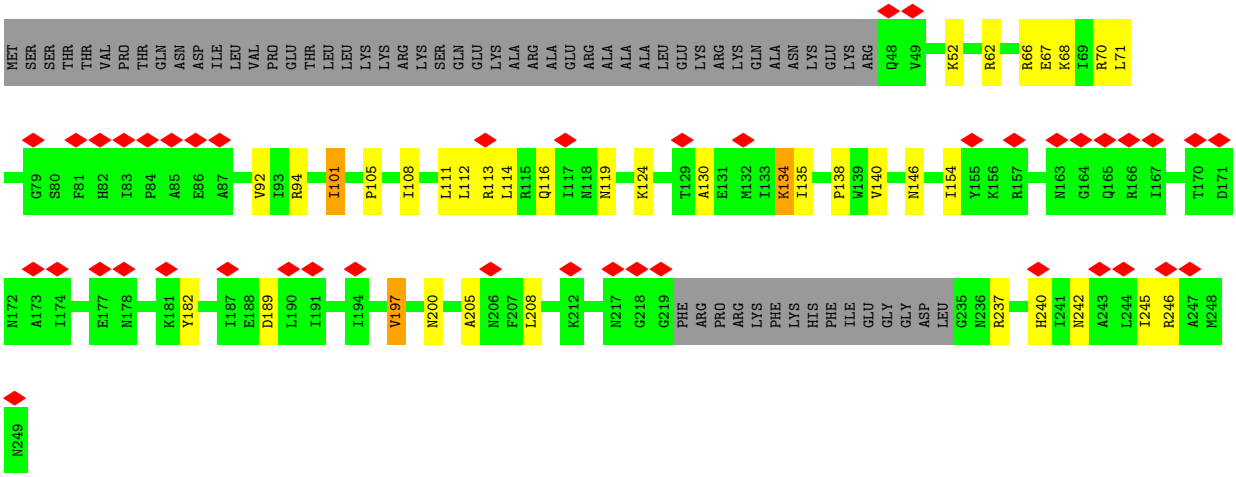
Chain CL:





- Molecule 15: 60S ribosomal protein l7-like protein

Chain CM:

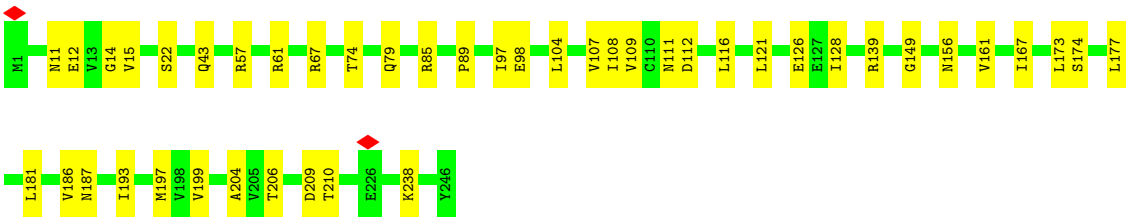


- Molecule 15: 60S ribosomal protein l7-like protein

Chain LF:

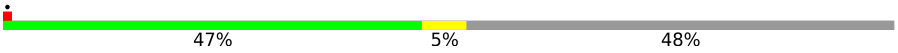
• Molecule 16: Eukaryotic translation initiation factor 6

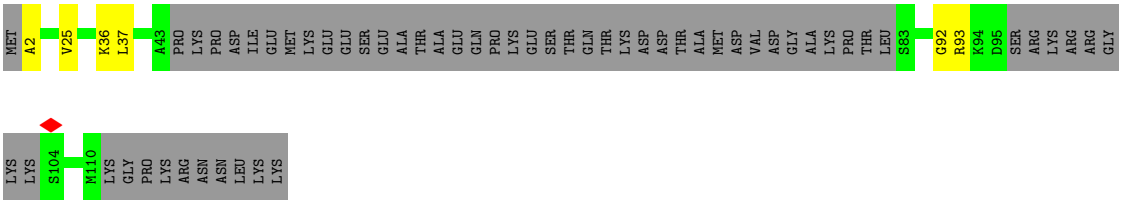
Chain CN:



• Molecule 17: DUF2423 domain-containing protein

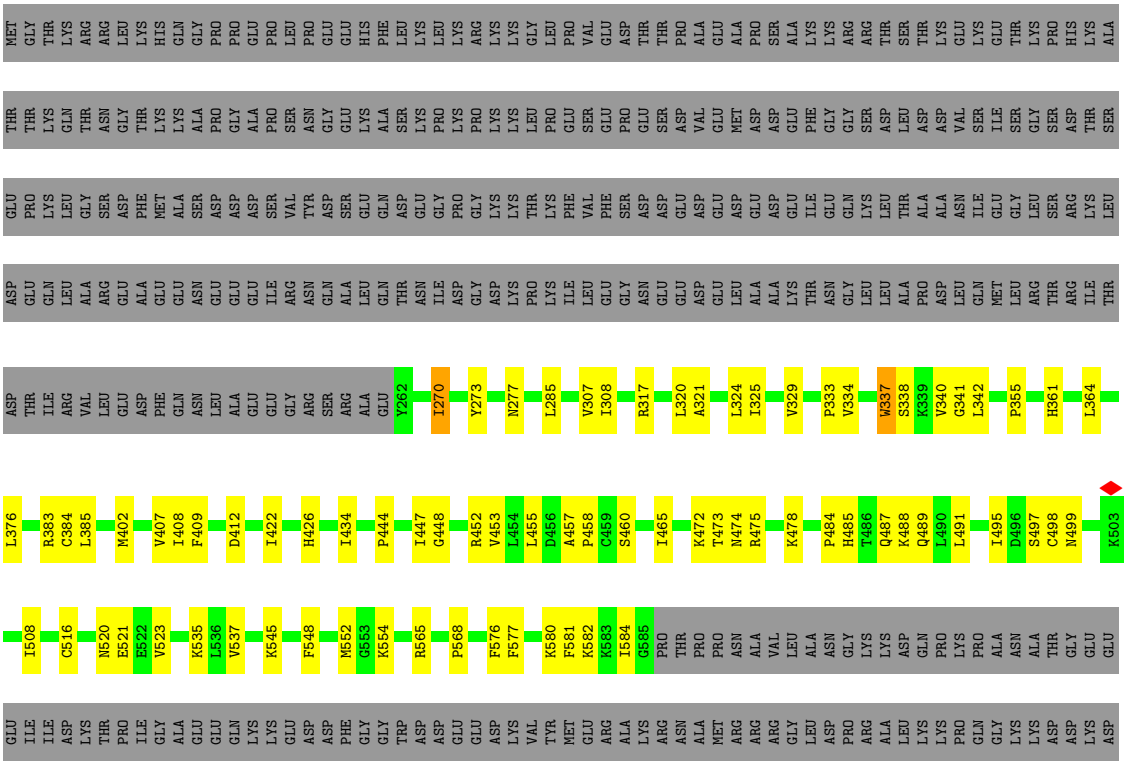
Chain CO:

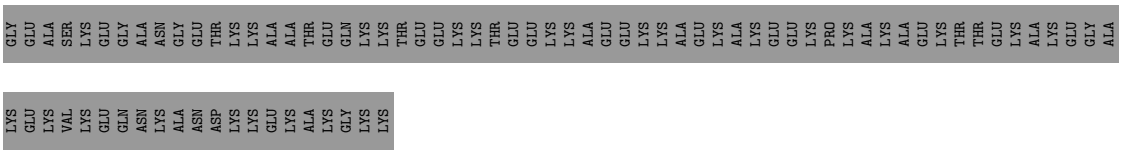




• Molecule 18: RNA methyltransferase nop2-like protein

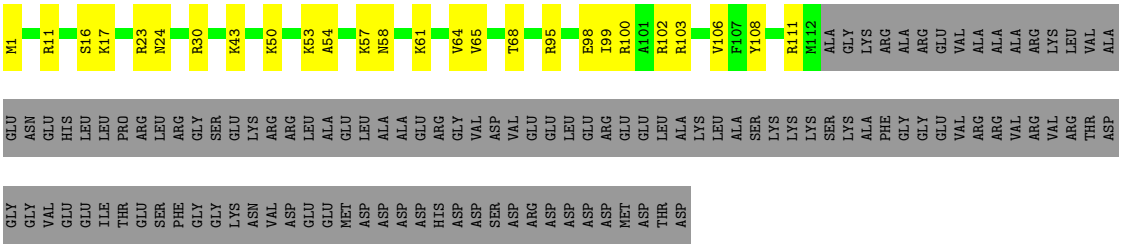
Chain CP:





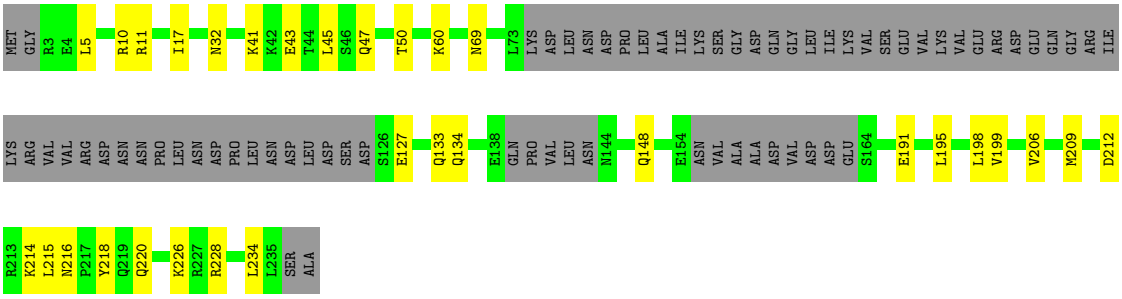
• Molecule 19: Ribosome biogenesis protein RLP24

Chain CQ:



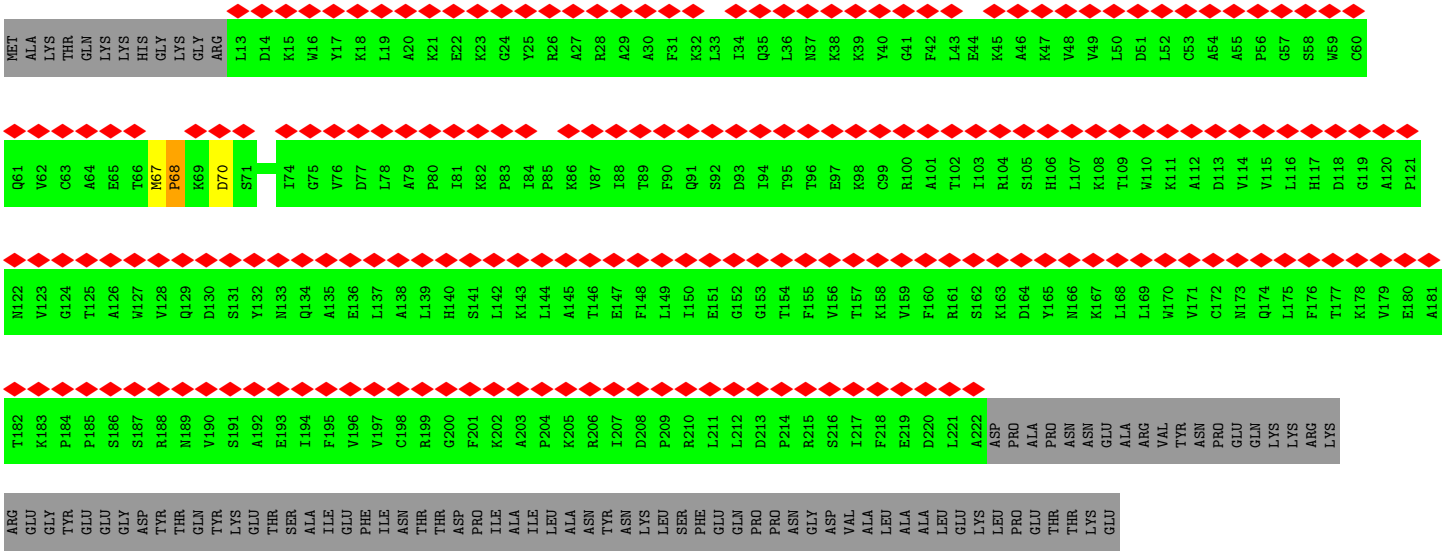
• Molecule 20: Nucleolar protein 16

Chain CR:



• Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1

Chain CS:



ILE ARG ALA CYS CYS ASP ASP LEU LYS VAL LEU GLY LYS LYS ASP PHE ARG LEU LEU LEU LYS TRP ARG LEU ARG VAL ARG GLU ILE PHE GLY LEU PRO SER LYS LYS THR ALA LYS GLN GLN PRO LEU VAL GLU GLU GLU ALA LYS VAL GLU PRO MET ASP GLU GLU LEU LYS ILE GLN

GLU GLU LEU GLU ARG ILE LYS GLU LYS GLU ARG ALA LYS LYS LYS ARG GLU ARG ARG LYS GLU ASN GLU ARG LYS HIS LYS GLU ILE VAL ARG MET GLN MET HIS MET THR THR PRO MET ASP ILE GLY MET GLU GLN GLU GLY PRO ARG GLY ASP GLY ALA PHE PHE ARG GLU GLU

ILE ASP GLN THR ASP ALA LEU ARG ARG ILE ALA LYS GLY LYS MET ALA MET LEU THR GLU ALA GLU GLN ALA ASP ARG ASP SER GLY ILE GLY LEU SER PRO ASP THR ASP ASP ASP SER ASP GLU ASP GLY ASP GLN LEU GLU ARG GLU LEU ASP ALA MET TYR GLU HIS TYR LYS GLU

ARG LYS ALA SER GLN ASP ALA LYS TYR ARG ALA LYS ARG ALA ARG GLN GLU VAL ASP ASP GLU GLU TRP GLU GLY LEU LEU SER ALA ASP GLU LYS GLY SER ASP VAL ASP MET ASP ASP ASP ASP SER GLU ARG LEU GLU GLU ASP SER SER ASP GLU ALA TRP SER ASP ASP ASP GLY GLU

LEU ASP THR SER LYS PRO LEU ILE LYS ASP LEU SER GLY ALA PRO GLN ASP GLY SER GLY LEU SER LYS ARG ALA ARG GLY PHE PHE SER GLN ASP VAL PHE GLN LYS ILE PRO GLY LEU LEU ASP THR VAL SER GLU SER GLU GLU GLU GLN ASP SER ASP ASN ASP GLY ILE PRO

SER ILE GLN GLU GLN LYS ARG MET GLN LYS GLU LYS LYS GLU LYS GLU ALA LYS LYS GLN ASP ASP ASP PHE GLU VAL VAL VAL LYS GLU HIS ASP SER ASP ASP W638 E639 E640 K641 E642 K643 K644 S645 K646 D647 G648 R649 P650 N651 I652 D653 I654 I655 T656 A657 E658 A659 M660 T661

L662 A663 H664 Q665 L666 A667 T668 G669 E670 K671 T672 K673 A674 D675 L676 I677 D678 E679 G680 Y681 N682 K683 K689 E690 G691 D694 W695 F696 L697 E698 D699 E700 A701 D704 K705 P706 T707 K708 P709 I710 T711 K712 E713 A714 A715 Q716 A717 I718 K719 E720 K721 L722 R723 A724 L725 ASN ALA

ARG PRO ILE LYS LYS VAL ALA GLU ALA ARG ALA ARG ARG LYS LEU ARG GLN ALA LYS LYS LEU GLU LYS LEU LYS LYS LYS ALA ASP LEU LEU VAL ASP GLU GLU GLY MET SER GLU LYS GLU LYS ALA THR THR ILE ALA LYS MET LEU SER ALA ALA ALA ARG LYS LYS ARG ARG PRO

GLN VAL LYS VAL VAL LYS ALA THR GLY ALA ASN ARG GLY ILE LYS GLY ARG PRO LYS GLY VAL LYS GLY ARG TYR LYS MET VAL ASP GLY ARG MET LYS LYS GLU MET ARG ALA LEU LYS ARG LEU ALA LYS LYS LYS ARG

- Molecule 22: Nucleolar complex-associated protein 3

Chain CT: 49% 65% • 33%

MET ALA THR ARG PRO LEU LYS ARG ARG LYS VAL THR PRO PRO ARG ASP ASP GLY GLN ASP ALA ALA GLU GLU ARG GLU ALA LYS ILE GLN LYS ALA PHE LEU LYS ASN ALA ALA SER TRP ASP LEU GLU GLU ALA TRP GLU SER ARG PRO ARG LYS GLY LYS LYS LYS ASP LYS LYS LYS ASP

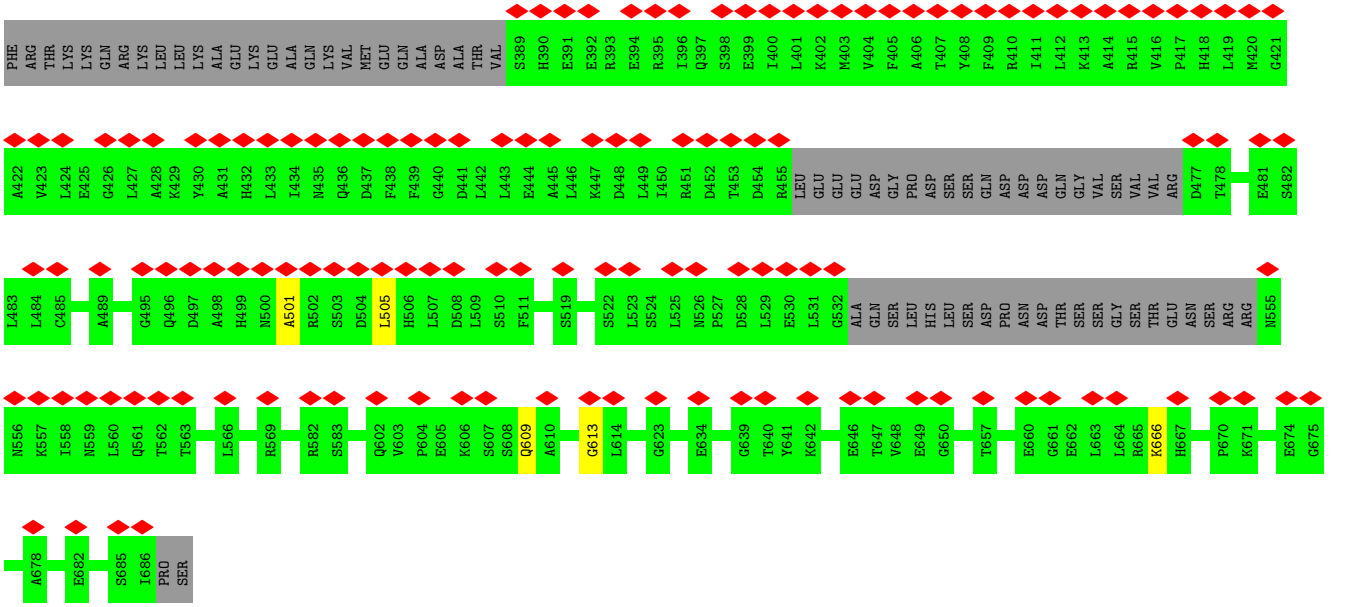
GLU GLU ARG PRO GLY ARG LEU PRO ILE ARG THR GLU GLN GLY THR TRP GLN VAL GLN ASP ASP VAL GLU SER ILE PRO SER ASP ALA GLU TRP LEU ASP SER ASP GLY GLU LEU ALA VAL GLU GLN GLN LEU GLU PRO VAL ALA PRO ALA PRO ALA PRO GLU PRO PRO LYS ILE SER GLU

LYS E122 Q123 I124 R125 Q126 A127 Q128 E129 E130 L131 A132 K133 I134 A135 T136 Q137 L138 N139 E140 N141 P142 E143 E144 Y145 P146 G147 H148 F149 K150 A151 L152 A153 R154 I155 G156 E157 T158 P159 I160 L161 A162 I163 Q164 K165 L166 C167 I168 V169 T170 Q171 M172 A173 V174 Y175 K176 D177 V178 I179 P180

G181 Y182 R183 I184 R185 P186 L187 G188 E189 ASP ALA VAL ASN GLU LYS VAL SER K198 E199 V200 K201 R202 L203 R204 T205 Y206 E207 Q208 A209 L210 V211 A212 C213 G216 Y217 L218 K219 T220 L221 A222 T223 Y224 A225 A226 S227 S228 I229 P230 E231 D232 R233 K234 G235 E236 P237 I238 S239 S240 I241

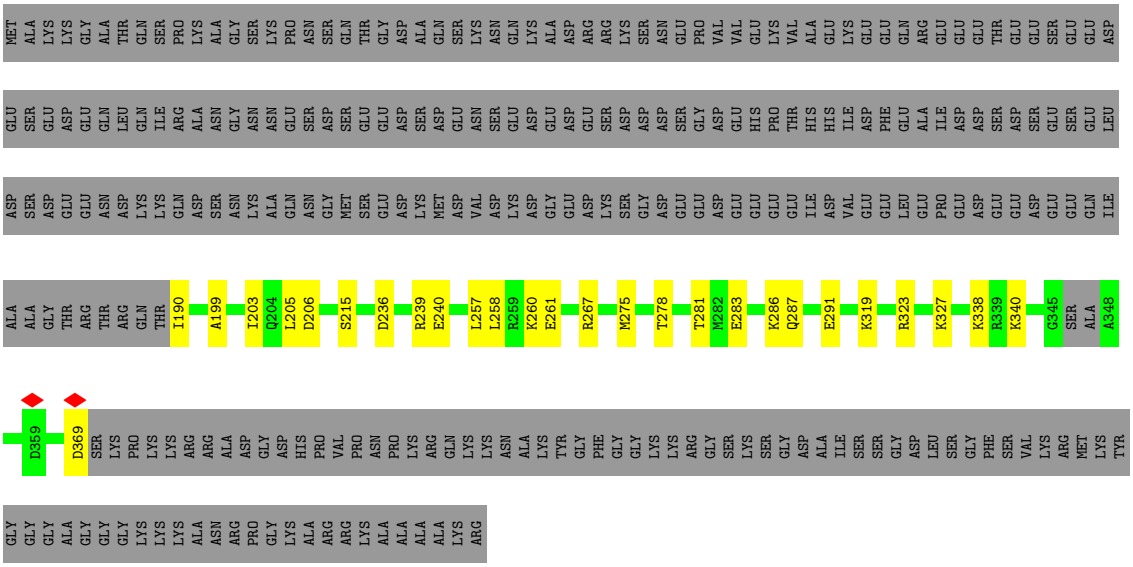
A242 F243 T244 C245 A246 C247 E248 L249 V250 N251 A252 V253 P254 H255 F256 N257 F258 R259 G260 D261 L262 L263 R264 I265 L266 V267 K268 K269 L270 S271 T272 R273 K274 I275 D276 R277 D278 F279 V280 K281 C282 R283 E284 A285 L286 E287 K288 L289 F290 Q291 D292 D293 E294 E295 G296 N297 A298 S299 Q300 E301

A302 V303 S304 L305 L306 S307 K308 M309 M310 K311 A312 R313 E314 Y315 R316 V317 D318 E319 S320 V321 L322 N323 L324 F325 L326 H327 L328 R329 L330 L331 S332 GLU PHE VAL GLY LYS GLY SER ARG ASP THR VAL ILE ARG PRO GLY ASP ASP ARG PRO ILE GLY LYS LYS PRO LYS LYS LYS TRP GLU



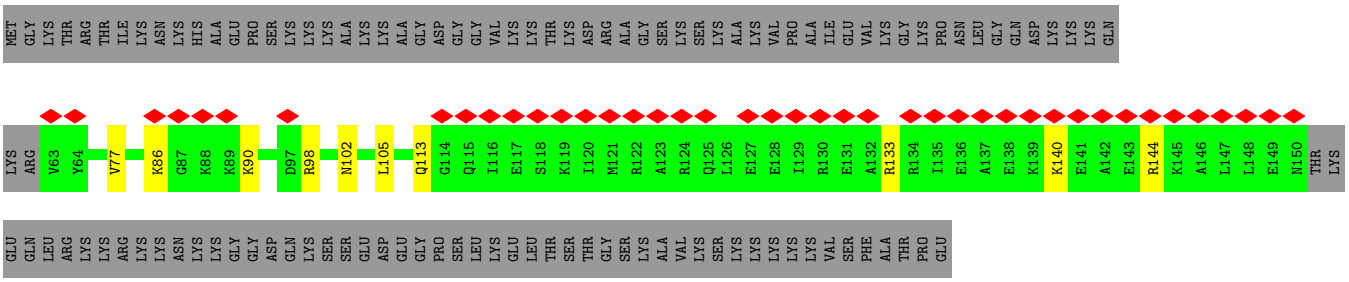
- Molecule 23: rRNA-processing protein EBP2

Chain CU:



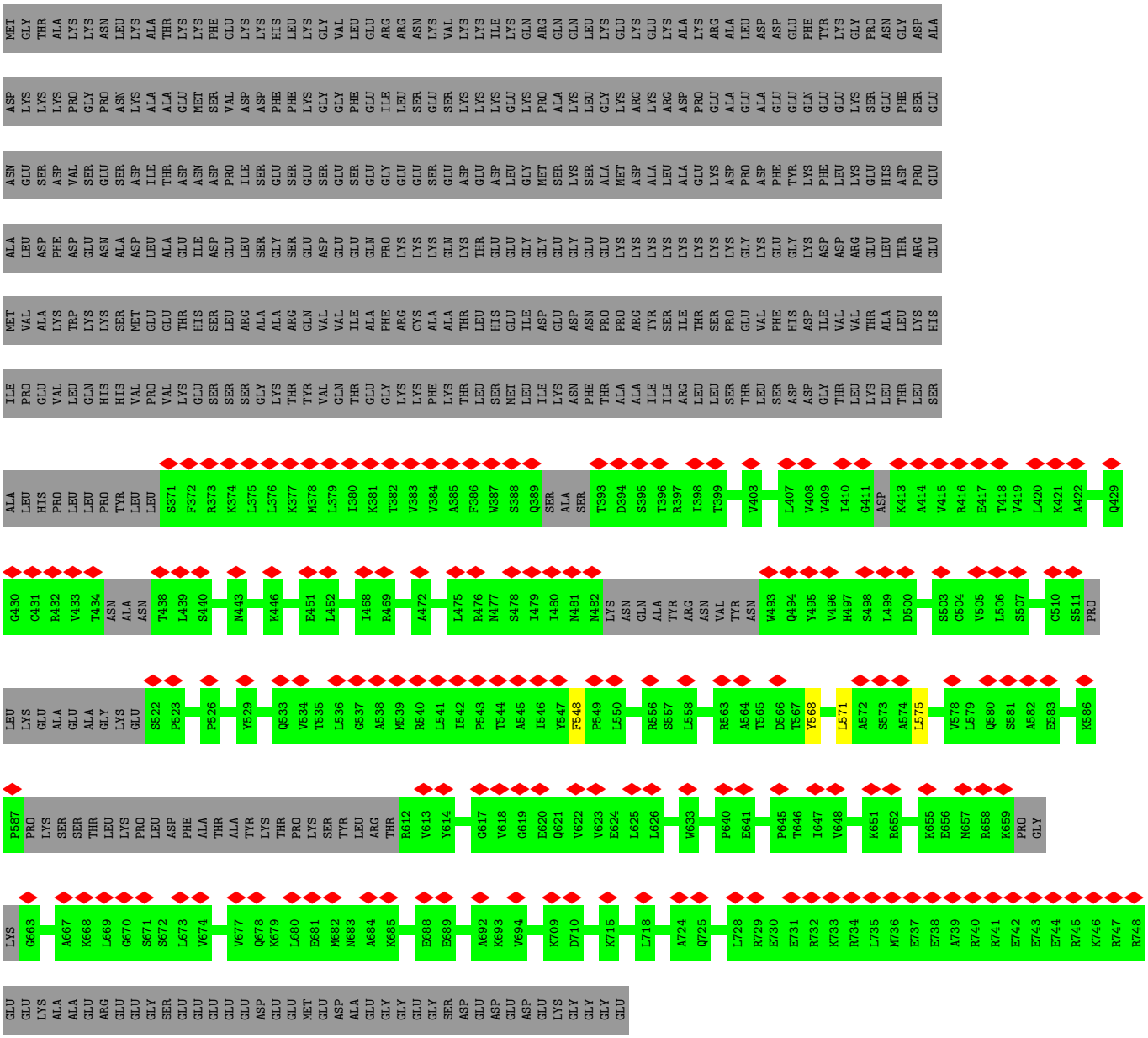
- Molecule 24: 60S ribosomal subunit-like protein

Chain CX:



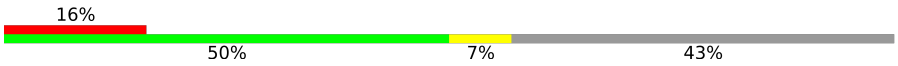
- Molecule 25: Putative NOC2 family protein

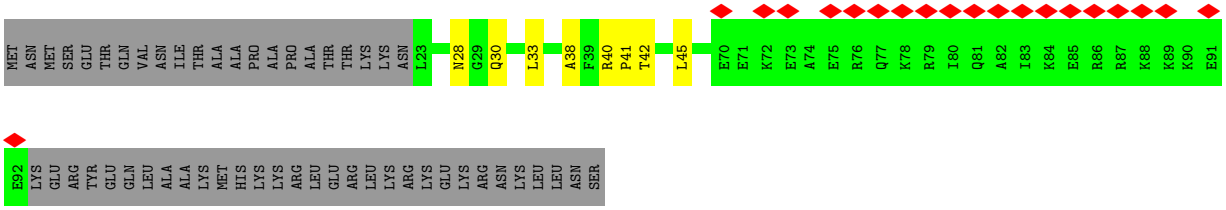
Chain CY:



- Molecule 26: rRNA-processing protein

Chain Cz:





• Molecule 27: ATP-dependent RNA helicase DBP10

Chain Cb: 56% 14% 31%

M1 P2 K3 R4 A9 P10 V15 D16 I17 A23 ASN GLU LEU ASP SER ASP SER ASP ALA PRO LYS ALA ASN PRO GLY THR ALA THR ASP LEU ASP PHE GLY ASP LEU LEU LEU ASN ALA THR HIS ASP GLY GLY SER ASP ASP SER GLY ASP GLU ALA PHE ILE ASP LEU HIS

GLN ARG SER SER ASN ARG LYS SER SER ASN LEU GLN G83 K84 T85 V86 K87 K88 G89 G90 M95 R107 Q117 I121 R127 R128 D129 V130 V131 G132 M133 A134 R135 T136 K140 M148 R151 L152 K153 R158 F159 G160 A161 R162 A163 L164 V165 P168 S169 R170

L174 L177 V180 K181 E182 K185 G186 T187 D188 L189 K190 T191 L200 E201 M207 A208 T209 N210 P211 D212 I213 I214 I215 R220 F221 L222 M228 S229 L230 I235 K236 Y237 A243 D244 R245 L246 L255 T256 E257 I258 L259 L262 Q267 T268 L269 L270 F271

L275 L279 L287 L295 D296 A297 K300 L305 L321 L322 H323 I324 I328 P332 P337 ARG SER GLU ASN ASP GLU GLU GLN PRO LYS SER LYS LYS ARG LYS ARG GLY SER ASP LYS PRO ASN PHE LYS GLU K363 H367 I371 K376 Y381

L388 V396 L400 D401 V422 T423 D424 A427 R428 I432 N440 Q446 P447 K448 I449 R453 R456 R459 V490 L491 G492 R493 K496 V505 L509 K510 R511 V512 E513 N516 E519 T538 E562 V563 I564 G568 Q571 R587 D588

L591 Q600 F604 E605 I606 GLY PRO LYS GLY LYS VAL SER GLN N615 K616 A617 A618 E619 A620 V621 R625 R631 K632 LEU PRO LYS GLN ASP GLU ASP THR GLU MET VAL ASP ALA GLU ALA LEU PRO ASP HIS VAL GLY ASN ALA GLU ARG LYS GLY GLN GLU GLU GLU GLU

SER VAL ASP GLU ASP GLY ALA THR GLN ASP SER VAL LEU TRP LYS HIS ASP SER ASN SER ASP SER ASN SER GLU SER GLU LEU GLU VAL THR VAL THR ASN SER ALA LYS ALA LYS LYS GLY GLN THR S708 M716 R721 THR THR SER LEU ALA GLU GLU HIS ALA TYR GLY VAL

HIS SER GLY GLY VAL ARG SER SER ASN PHE VAL GLU ALA ALA ARG ASP ALA THR MET ASP LEU THR ASN ASP GLU GLY ALA LYS GLY PHE GLY LEU PRO SER ARG PRO LYS TYR ARG TRP ASP LYS ARG HIS SER LYS TYR VAL SER THR ALA ASN ASP ASP ASP GLY SER LYS GLY V793

G798 I804 F813 H820 R824 L825 K833 A834 N835 L836 V837 R838 G845 R880 ILE GLY LYS PHE LYS ASP GLY GLU GLY ASN ARG ARG GLU LEU LYS THR GLU SER ASP ILE ARG LYS ALA LYS GLU LEU LYS GLU ARG ARG LYS GLU LYS ASN ALA ARG PRO SER

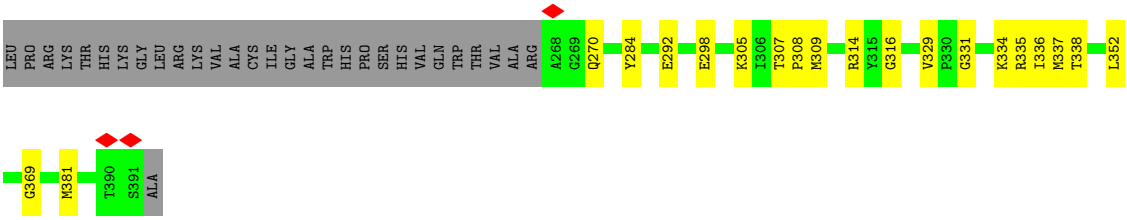
LYS LYS PRO LYS LYS LYS

• Molecule 28: 60S ribosomal protein L3-like protein

Chain LB: 67% 20% 13%

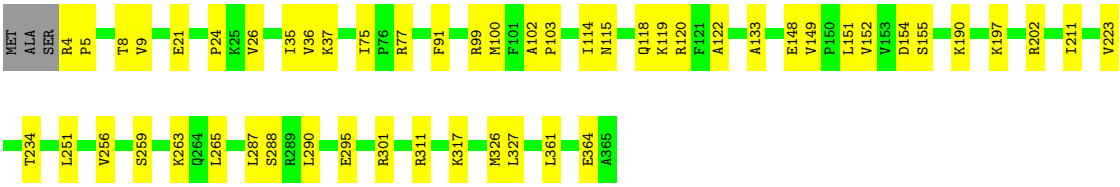
MET SER HIS ARG LYS TYR GLU ALA PRO ARG HIS G12 S13 R19 K20 R21 R26 V29 P33 K39 T44 M47 K50 M53 R58 R62 P63 K66 A67 H68 K69 V73 T77 M84 V85 I93 E94 T95 G98 L99 V105 W106

E113 V114 K115 R116 K126 K127 K128 A129 Y133 M141 E148 L149 E150 R151 C156 T157 V158 V159 T165 Q166 T170 P171 L172 K173 Q174 K175 K176 A177 M180 K192 V193 T208 E214 V218 I219 V228 GLY VAL THR ALA ARG TRP GLY THR LYS LYS



• Molecule 29: 60S ribosomal protein L4-like protein

Chain LC:

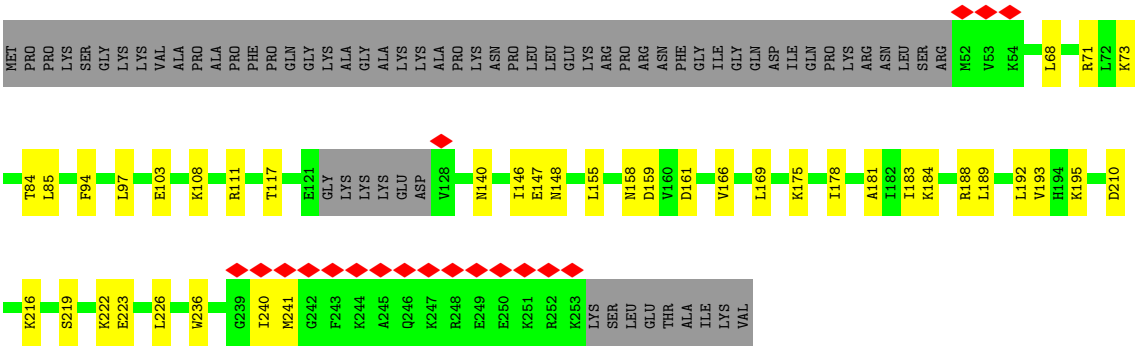


• Molecule 30: 60S ribosomal protein L6

Chain LE:

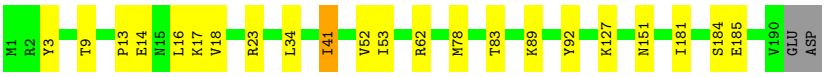
• Molecule 31: 60S ribosomal protein L8

Chain LG:



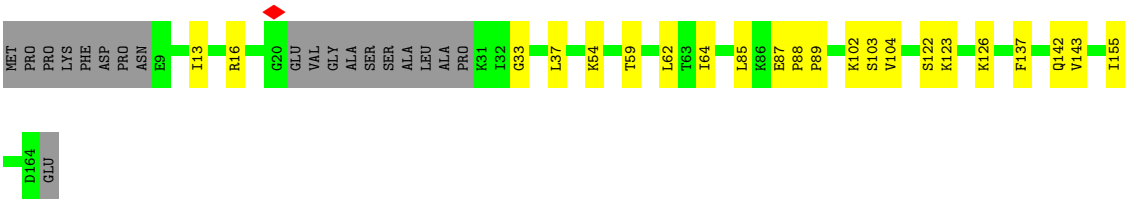
• Molecule 32: 60S ribosomal protein l9-like protein

Chain LH:



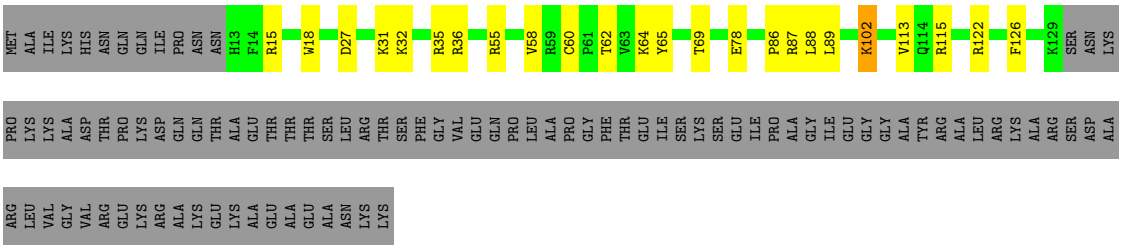
• Molecule 33: 60S ribosomal protein L12-like protein

Chain LK: 75% 13% 12%



- Molecule 34: 60S ribosomal protein L13

Chain LL: 44% 11% 45%

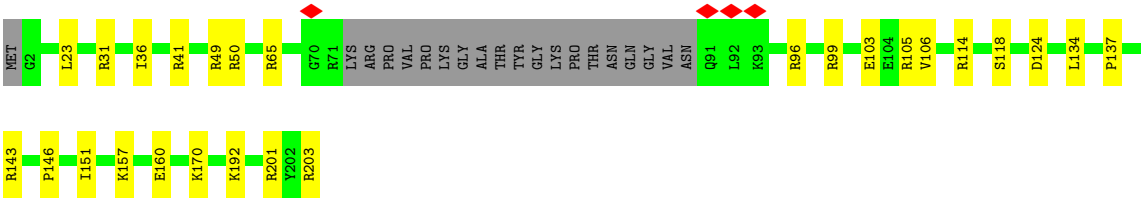


- Molecule 35: 60S ribosomal protein L14-like protein

Chain LM: 79% 18%

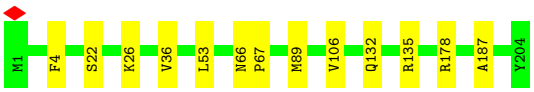
- Molecule 36: Ribosomal protein L15

Chain LN: 77% 13% 10%



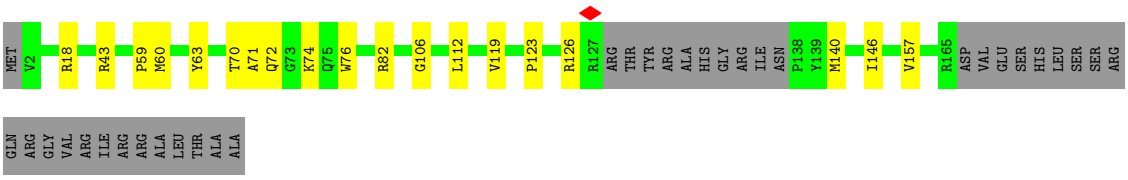
- Molecule 37: 60S ribosomal protein L16-like protein

Chain LO: 94% 6%



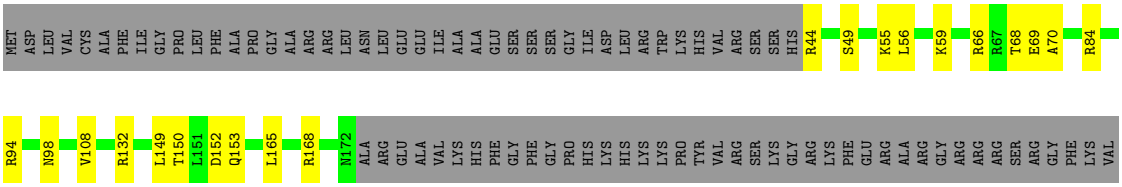
- Molecule 38: 60S ribosomal protein l17-like protein

Chain LP: 72% 10% 18%



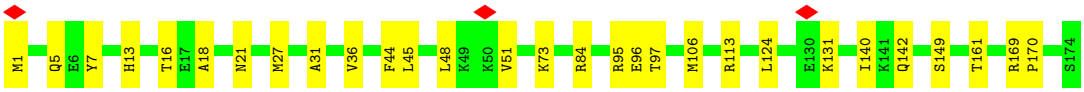
• Molecule 39: Ribosomal protein L18-like protein

Chain LQ:



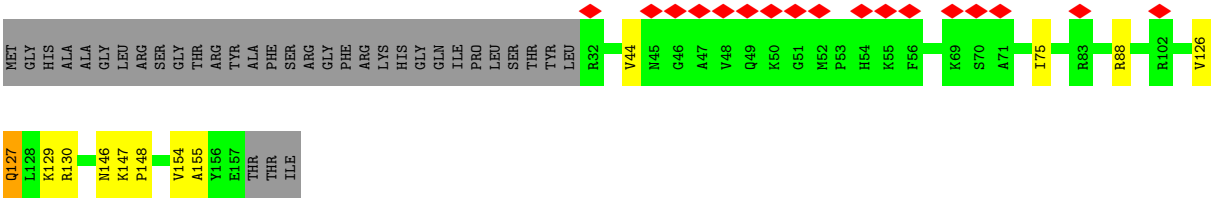
• Molecule 40: 60S ribosomal protein L20

Chain LS:



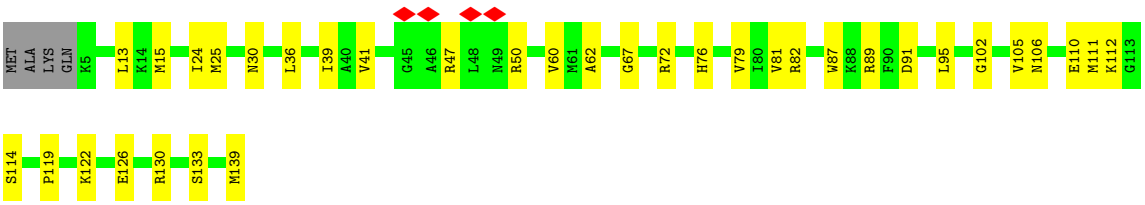
• Molecule 41: 60S ribosomal protein l21-like protein

Chain LT:



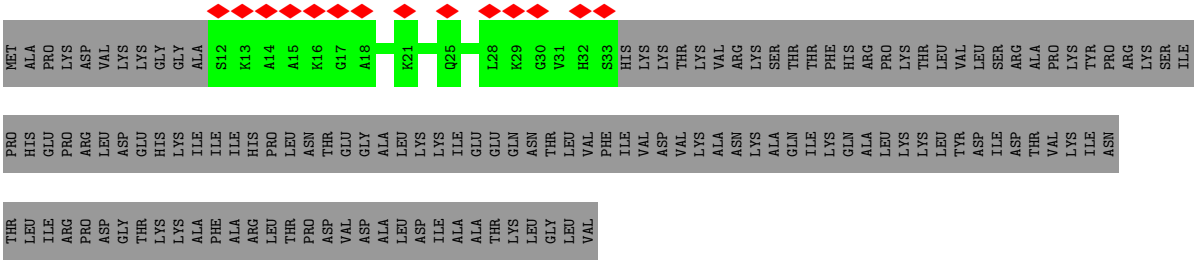
• Molecule 42: 60S ribosomal protein l23-like protein

Chain LV:



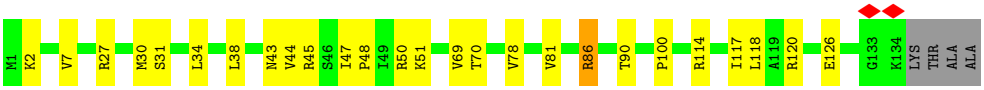
• Molecule 43: 60S ribosomal protein L25-like protein

Chain LX:



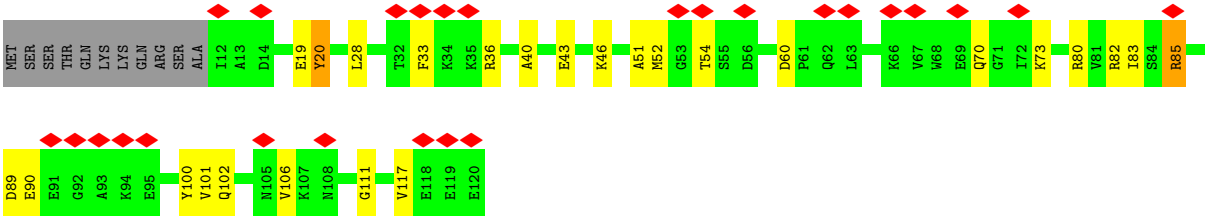
- Molecule 44: 60S ribosomal protein L26-like protein

Chain LY:



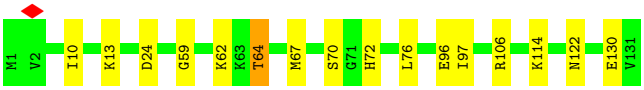
- Molecule 45: Putative 60S ribosomal protein

Chain Ld:



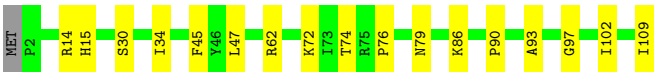
- Molecule 46: 60S ribosomal protein L32-like protein

Chain Le:



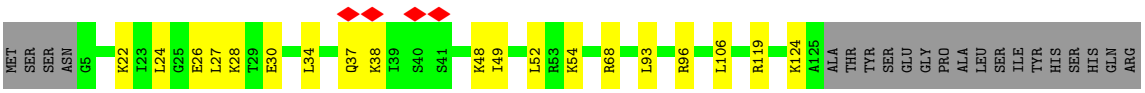
- Molecule 47: 60S ribosomal protein l33-like protein

Chain Lf:



- Molecule 48: dolichyl-diphosphooligosaccharide--protein glycotransferase

Chain Lh:



GLU ALA ARG CYS SER LEU VAL GLN CYS CYS THR PHE GLU PRO GLU LEU LEU ARG GLU SER LEU LEU LEU LEU PRO VAL ALA ALA SER LEU LYS GLY PRO ASN PHE THR ARG ARG GLU ARG GLN HIS ARG ASN PRO SER GLU ALA THR MET SER ALA ALA GLU PRO LEU LYS LEU LEU ALA SER

ALA GLY LYS GLY LYS SER THR ARG SER VAL LEU LEU ARG VAL ALA ILE LEU LEU VAL LEU ILE ALA GLY ALA ALA VAL ALA SER ARG LEU PHE SER VAL ILE ARG PHE GLU SER ILE ILE HIS GLU PHE ASP PRO TRP PHE ASN PHE ARG ALA THR LYS TYR LEU VAL ALA ASN GLY PHE TYR LYS

PHE TRP ASP TRP PHE ASP ASP ARG THR TRP HIS PRO LEU GLY ARG VAL THR GLY GLY THR LEU TYR PRO GLY LEU MET VAL THR SER GLY VAL ILE TYR HIS LEU LEU ARG PHE LEU THR VAL PRO VAL ASP ILE ARG ASN ILE CYS VAL LEU LEU ALA PRO GLY PHE SER GLY LEU THR

ALA ILE ALA ALA TYR LEU LEU THR ASN GLU MET THR THR SER PRO SER ALA GLY LEU LEU ALA ALA ALA PHE MET GLY ILE ALA PRO GLY TYR ILE SER ARG SER VAL ALA GLY SER TYR ASP ASN GLU ALA ILE ALA ILE PHE LEU LEU VAL PHE THR THR PHE PHE LEU TRP ILE LYS ALA

LEU LYS GLN GLY SER MET LEU TRP GLY ALA LEU CYS ALA LEU PHE TYR GLY TYR MET VAL ALA SER TRP GLY GLY TYR ALA PHE ILE THR CYS LEU LEU PRO LEU HIS SER PHE VAL LEU ILE CYS MET GLY ARG TYR SER THR ARG LEU TYR VAL ALA TYR THR TRP LEU ALA LEU

GLY THR LEU ALA SER MET GLN ILE PRO PHE VAL GLY PHE LEU PRO VAL LYS THR SER GLU HIS MET PRO ALA LEU GLY ILE PHE GLY PHE LEU GLN LEU LEU ALA PHE LEU ASP TYR VAL ARG SER THR ILE SER SER ARG GLN PHE GLN THR PHE LEU TRP LEU PHE ALA GLY GLY ILE

PHE GLY LEU GLY LEU LEU GLY LEU VAL ILE ALA THR SER ALA GLY LEU ILE ALA PRO TRP SER GLY ARG PHE TYR SER LEU TRP ASP THR GLY TYR ALA LYS ILE HIS ILE PRO ILE ILE ALA SER VAL SER GLU HIS GLN PRO THR ALA TRP PRO ALA ALA PHE PHE ASP LEU ASN MET

LEU VAL TRP LEU PHE PRO VAL GLY VAL TYR LEU CYS PHE GLN GLN LEU GLY ASP GLU HIS VAL PHE ILE ILE VAL TYR ALA LEU PHE GLY SER TYR PHE ALA GLY VAL MET VAL ARG LEU MET LEU THR LEU THR PRO VAL VAL CYS VAL ALA ALA ALA ILE ALA PHE SER SER LEU LEU

ASP THR TYR LEU ASN LEU LYS THR PRO ASN PRO GLY GLN ALA GLN ALA THR GLU ASP ALA GLY LYS LYS LYS SER GLY LEU LYS PRO ALA VAL GLY VAL TYR PHE ALA GLY VAL ILE LEU LYS ALA ALA ALA SER LYS PRO ALA VAL GLY LYS THR MET MET ILE SER GLY LEU THR ILE TYR LEU LEU LEU PHE VAL LEU HIS

CYS THR TRP VAL THR SER ASN ALA TYR SER SER PRO SER VAL VAL LEU ALA SER ARG LEU PRO ASP GLY SER GLN HIS ILE ILE ASP ASP TYR ARG GLU ALA TYR GLN TRP LEU ARG GLN ASN THR ARG GLU ASP ALA LYS ILE MET SER TRP TRP ASP TYR GLY TYR GLN ILE GLY GLY

MET ALA ASP ARG PRO THR LEU LEU VAL ASP ASN ASN THR TRP ASN ASN THR HIS ILE ALA THR VAL GLY LYS ALA MET ALA SER ARG GLU GLU VAL SER GLN HIS GLU VAL ASP TYR VAL LEU VAL VAL PHE GLY GLY LEU LEU GLY TYR SER GLY ASP ASP ILE ASN

LYS PHE LEU TRP MET VAL ARG ILE ALA GLU GLY ILE TRP PRO ASP GLU VAL SER GLU ARG ALA PHE PHE THR PRO ARG GLY GLU TYR ARG VAL ASP ALA GLU ALA THR ASP THR MET LYS ASN SER LEU MET TYR LYS MET CYS TYR TYR ASN TYR ASN ASN LEU PHE PRO PRO GLY GLN

ALA VAL ASP ARG MET ARG GLY VAL ARG LEU PRO GLU VAL GLY PRO THR LEU ASN THR LEU GLU GLU ALA PHE THR SER GLU ASN TRP ILE ILE ARG ILE TYR LYS VAL LYS ASP LEU ASP ASN LEU GLY ARG ASP HIS ALA SER ALA ALA ALA PHE GLU ARG GLY HIS LYS LYS LYS LYS

ALA THR LYS LYS ARG GLY PRO ARG VAL LEU ARG VAL GLU

- Molecule 49: 60S ribosomal protein L36

Chain Li:

MET SER GLU ASP ALA THR PRO LYS ALA PRO VAL GLU ARG THR GLY LEU ILE ARG GLY LEU ASN LYS G23 H24 K25 R29 K39 G40 A41 Q42 R45 T46 R50 E55 K76 R91 H110

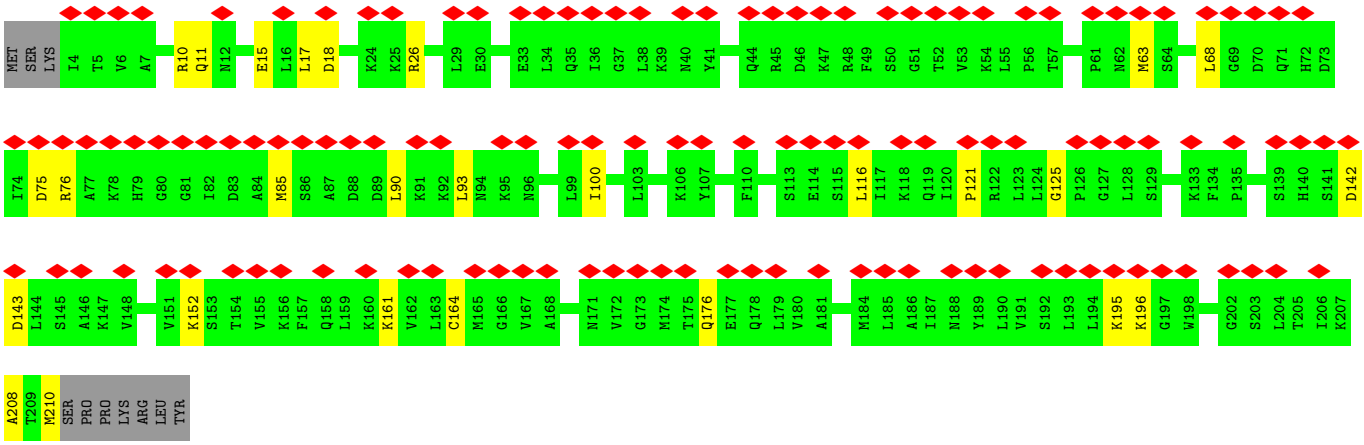
- Molecule 50: Ribosomal protein L37

Chain Lj:

MET THR LYS GLY THR SER SER PHE GLY LYS ARG HIS ASN K14 T15 H16 L27 C34 W49 V58 T59 G60 M64 S68 P71 R79 R87 GLY PRO ALA VAL SER THR SER SER

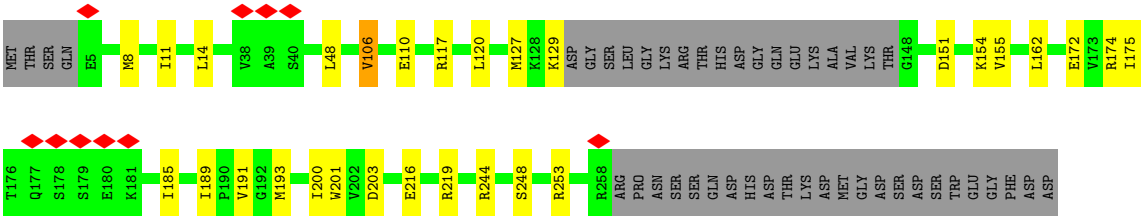
- Molecule 51: Ribosomal protein

Chain Lq:



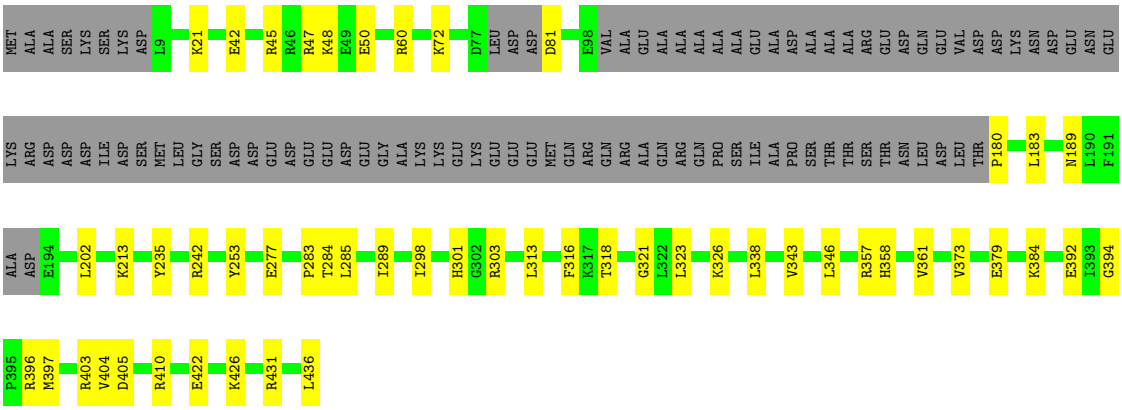
• Molecule 52: Ribosomal RNA-processing protein 1

Chain Cc:



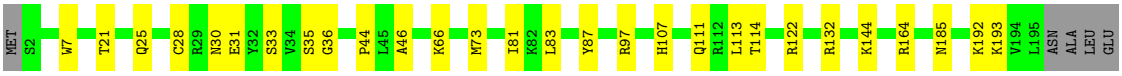
• Molecule 53: Brix domain-containing protein

Chain Cd:



• Molecule 54: Protein MAK16

Chain Ce:



ALA GLU GLY GLU GLY VAL ARG ASP LYS ASP HIS ASP LYS GLY ILE GLU ALA ASP GLU GLU GLY LEU GLU SER ALA GLU GLU SER GLU VAL GLU TYR GLU ARG GLU GLU GLU ASN GLU GLU ASP ASN VAL VAL GLU TYR VAL SER ASP PHE GLU GLU SER GLU ASP GLU LEU GLY ASP LEU

GLU ASP TRP LEU GLY SER ASP ASP GLU GLU PHE ASP ASP GLU ASP ASP ASP ASP GLU ASP ASP ASP GLU SER GLU GLU ASP ASP GLU GLU GLU LEU LYS LYS LYS LYS ALA GLY ASP LYS ARG LYS ARG GLY LYS ALA VAL LYS LYS PRO LYS ALA ARG LYS ARG LYS

GLU LEU GLU ILE GLU ARG GLU GLU ALA ASP ARG ALA LYS LEU LEU ALA PHE

- Molecule 55: 60S ribosome biogenesis protein Rrp14

Chain Cf: 9% 90%

MET SER ASP GLU ASP THR SER LEU GLN GLU ARG LEU ARG GLU HIS ALA ARG ALA PHE ASP GLY LEU LEU SER LEU ILE PRO ALA LYS VAL TYR TYR GLY ASP SER ASN ASN ASP ASN GLN TRP LYS LYS LYS LYS GLN THR LYS ASP GLU ALA LYS ALA ALA LYS ARG GLY LYS LEU ASP

PRO ASP SER GLU LEU ASN ARG SER ALA LYS ASP VAL MET ASP GLU ARG ALA ARG ASN LYS ARG LYS LEU GLN GLU LEU GLU ALA ASP GLU ALA SER ALA SER SER ASP GLN ASP ASP ASP SER SER ASP ILE SER ILE PRO GLY ILE ILE LYS GLU LYS PRO GLY GLU GLY LEU LYS LYS

LYS LYS PRO LYS LEU ALA GLU ASP ALA GLU GLU GLU GLU GLU GLU PRO GLU LYS PRO ALA ALA ASP ASN THR THR LYS GLU GLU GLU HIS GLU ALA PRO LYS GLN ASP PRO LEU SER LYS LYS GLN GLN ALA LYS GLU GLU LYS LYS LEU GLU LEU LYS LYS GLN ARG LYS GLU GLU ALA LYS LYS GLN LYS

GLU GLU GLU ALA LYS ALA THR THR PRO SER THR THR ASP LYS ALA GLU LYS PRO LYS GLN ASP THR VAL GLU LYS THR LEU LYS LYS GLU GLN LYS LYS LYS PRO PRO ARG PRO ALA GLU ASP GLU ALA GLU SER ASP SER GLU GLU GLY GLU GLU GLU PRO THR GLY LYS GLN PRO VAL LYS SER VAL

GLU ALA ALA GLU SER ASP SER GLU ASP ASP MET ALA PRO ILE ASP VAL SER GLY LEU ASP TYR LYS ASP GLU SER ALA ASP SER SER GLN GLU SER ALA THR ASN SER VAL PHE ASP GLY LYS ILE THR SER THR GLU PRO ALA SER THR THR THR SER MET SER SER ALA VAL PRO PRO

SER GLU LYS PRO LYS TYR LEU LYS ILE PRO ALA ASP THR SER ALA LYS ARG ALA ARG LEU GLU ALA LYS LEU ALA ALA LEU ARG ALA ARG LYS ALA ASP PRO GLU GLY LYS PRO ILE ARG THR ARG GLN GLU LEU ILE GLU ALA ARG ARG GLN LYS GLN ALA GLU ARG LYS ALA

ARG LYS LYS GLU LEU ARG ARG LEU ALA LYS GLU GLN GLU GLU ARG LYS ARG GLU GLU ALA LEU ALA SER ALA ALA ARG ASN SER PRO GLY LEU SER PRO LEU LEU GLY LYS GLU GLU ILE ASP PRO GLY GLU THR HIS PHE ALA PHE PHE GLY ARG VAL ASN PHE ASN ASP GLY THR GLN LEU SER

HIS ASP LEU THR TYR ALA LYS SER ALA ASP SER GLU LYS LYS LYS LYS GLY PRO SER ASP PRO LYS SER ALA LEU MET GLN LEU GLU ALA LYS LYS LYS ARG LEU GLU ALA LEU PRO GLU GLU LYS ARG LYS GLU ILE GLU GLU LYS LYS GLN TRP LEU ALA ALA ARG ARG ARG ALA GLU

GLY ILE LYS VAL HIS D486 D487 E488 S489 L490 L491 K492 K493 A494 L495 K503 E511 K514 K526 R527 E528 R532 G544 LYS GLY LYS LEU LYS GLY VAL GLN THR LYS LYS LYS ASN ARG PRO GLY PHE GLU GLY GLY PHE GLY GLY GLY LYS LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16465	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.458	Depositor
Minimum map value	-0.239	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	438.9, 438.9, 438.9	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	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, GTP

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	C1	0.22	0/51490	0.36	0/80245
2	C2	0.19	0/3754	0.32	0/5846
3	C3	0.19	0/2342	0.38	0/3649
4	CA	0.22	0/2190	0.57	2/2940 (0.1%)
5	CB	0.33	0/2109	0.72	1/2866 (0.0%)
6	CC	0.18	0/2459	0.44	0/3350
7	CE	0.21	0/3743	0.53	2/5045 (0.0%)
8	CF	0.19	0/1982	0.53	0/2671
9	CG	0.24	0/1422	0.63	3/1920 (0.2%)
10	CH	0.28	0/3927	0.61	1/5307 (0.0%)
11	CI	0.22	0/1225	0.61	1/1645 (0.1%)
12	CJ	0.16	0/3189	0.40	0/4309
13	CK	0.22	0/1885	0.54	1/2529 (0.0%)
14	CL	0.14	0/2178	0.39	0/2983
15	CM	0.23	0/1555	0.65	1/2091 (0.0%)
15	LF	0.20	0/2004	0.47	0/2686
16	CN	0.20	0/1881	0.53	0/2560
17	CO	0.18	0/470	0.42	0/619
18	CP	0.24	0/2594	0.62	2/3514 (0.1%)
19	CQ	0.22	0/981	0.62	1/1301 (0.1%)
20	CR	0.22	0/1369	0.47	0/1828
21	CS	0.21	0/1762	0.43	0/2417
22	CT	0.33	0/2264	0.61	0/3149
23	CU	0.24	0/1428	0.60	1/1910 (0.1%)
24	CX	0.17	0/705	0.51	0/938
25	CY	0.36	0/1600	0.62	0/2220
26	Cz	0.18	0/598	0.42	0/785
27	Cb	0.24	0/5150	0.59	2/6936 (0.0%)
28	LB	0.25	0/2760	0.54	1/3701 (0.0%)
29	LC	0.23	0/2809	0.45	0/3787
30	LE	0.19	0/1363	0.43	0/1833
31	LG	0.23	0/1606	0.53	0/2149

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	LH	0.20	0/1516	0.48	0/2038
33	LK	0.24	0/1124	0.65	0/1507
34	LL	0.39	0/983	0.59	0/1318
35	LM	0.19	0/1120	0.41	0/1507
36	LN	0.21	0/1595	0.42	0/2132
37	LO	0.21	0/1652	0.45	0/2215
38	LP	0.26	0/1231	0.46	0/1658
39	LQ	0.20	0/1033	0.45	0/1391
40	LS	0.22	0/1468	0.49	0/1975
41	LT	0.19	0/1033	0.53	0/1389
42	LV	0.25	0/1013	0.45	0/1361
43	LX	0.10	0/148	0.40	0/194
44	LY	0.21	0/1079	0.45	0/1443
45	Ld	0.19	0/904	0.48	0/1209
46	Le	0.20	0/1073	0.40	0/1431
47	Lf	0.23	0/883	0.47	0/1187
48	Lh	0.18	0/1006	0.44	0/1338
49	Li	0.19	0/738	0.39	0/971
50	Lj	0.28	0/606	0.46	0/803
51	Lq	0.16	0/1621	0.45	0/2180
52	Cc	0.21	0/1934	0.48	0/2614
53	Cd	0.26	0/2818	0.52	0/3786
54	Ce	0.22	0/1638	0.44	0/2196
55	Cf	0.15	0/514	0.38	0/669
All	All	0.23	0/145524	0.46	19/208241 (0.0%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	LB	171	PRO	CA-N-CD	-9.51	98.69	112.00
10	CH	195	PRO	CA-N-CD	-8.05	100.72	112.00
18	CP	568	PRO	CA-N-CD	-7.82	101.06	112.00
4	CA	148	GLN	CA-C-N	6.75	129.78	120.39
4	CA	148	GLN	C-N-CA	6.75	129.78	120.39
9	CG	107	PRO	CA-N-CD	-6.72	102.59	112.00
23	CU	275	MET	CB-CG-SD	5.93	130.50	112.70
7	CE	478	VAL	CB-CA-C	5.85	116.07	110.16
15	CM	101	ILE	CB-CA-C	5.78	115.00	109.33
19	CQ	64	VAL	N-CA-C	-5.76	107.88	113.53
9	CG	63	LYS	N-CA-C	-5.74	107.52	114.75
13	CK	120	PRO	CA-N-CD	-5.72	103.99	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
27	Cb	207	MET	CB-CG-SD	5.60	129.50	112.70
5	CB	215	ARG	CA-CB-CG	5.54	125.19	114.10
18	CP	340	VAL	N-CA-C	-5.53	108.46	113.71
11	CI	200	GLU	CA-CB-CG	5.24	124.58	114.10
7	CE	133	LYS	CA-CB-CG	5.22	124.54	114.10
27	Cb	201	GLU	N-CA-C	-5.18	107.61	114.04
9	CG	20	MET	CB-CG-SD	5.12	128.04	112.70

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	C1	46025	0	23207	422	0
2	C2	3359	0	1698	26	0
3	C3	2097	0	1065	36	0
4	CA	2144	0	2178	48	0
5	CB	2063	0	2131	56	0
6	CC	2388	0	2301	39	0
7	CE	3673	0	3778	46	0
8	CF	1945	0	1965	31	0
9	CG	1396	0	1420	32	0
10	CH	3851	0	3894	56	0
11	CI	1196	0	1202	25	0
12	CJ	3109	0	3122	47	0
13	CK	1855	0	1952	36	0
14	CL	2173	0	1423	11	0
15	CM	1525	0	1604	22	0
15	LF	1967	0	2080	23	0
16	CN	1856	0	1856	30	0
17	CO	468	0	503	7	0
18	CP	2535	0	2549	58	0
19	CQ	960	0	1000	19	0
20	CR	1354	0	1400	22	0
21	CS	1750	0	1195	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	CT	2269	0	1022	6	0
23	CU	1415	0	1457	21	0
24	CX	701	0	742	7	0
25	CY	1608	0	719	2	0
26	Cz	592	0	640	8	0
27	Cb	5058	0	5223	83	0
28	LB	2708	0	2811	55	0
29	LC	2752	0	2878	37	0
30	LE	1338	0	1423	13	0
31	LG	1583	0	1722	30	0
32	LH	1496	0	1575	16	0
33	LK	1112	0	1190	14	0
34	LL	964	0	1041	17	0
35	LM	1101	0	1170	16	0
36	LN	1563	0	1618	19	0
37	LO	1618	0	1714	13	0
38	LP	1212	0	1250	11	0
39	LQ	1021	0	1118	15	0
40	LS	1433	0	1496	20	0
41	LT	1014	0	1073	9	0
42	LV	995	0	1055	23	0
43	LX	148	0	163	0	0
44	LY	1065	0	1156	19	0
45	Ld	890	0	940	16	0
46	Le	1055	0	1133	11	0
47	Lf	862	0	891	12	0
48	Lh	995	0	1110	15	0
49	Li	731	0	797	12	0
50	Lj	595	0	625	7	0
51	Lq	1600	0	1703	18	0
52	Cc	1898	0	1931	19	0
53	Cd	2763	0	2859	38	0
54	Ce	1609	0	1681	17	0
55	Cf	513	0	556	5	0
56	CH	32	0	12	1	0
57	CQ	1	0	0	0	0
57	Ce	1	0	0	0	0
57	Lj	1	0	0	0	0
All	All	138001	0	112017	1433	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (1433) 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:C1:788:A:N6	1:C1:915:G:H1	1.47	1.11
1:C1:1055:U:C4	1:C1:1063:C:N4	2.22	1.06
1:C1:1055:U:O4	1:C1:1063:C:C4	2.10	1.04
3:C3:69:G:H1	3:C3:132:U:H3	0.99	0.94
3:C3:38:G:H1	3:C3:43:U:H3	0.96	0.93
1:C1:1204:G:HO2'	1:C1:1267:G:H1	1.01	0.93
1:C1:2848:A:N6	1:C1:2871:C:H42	1.66	0.93
21:CS:68:PRO:HA	27:Cb:820:HIS:HA	1.53	0.89
1:C1:2848:A:H61	1:C1:2871:C:N4	1.69	0.88
1:C1:2735:G:H1	1:C1:2741:U:H3	0.86	0.85
1:C1:2404:G:H1	1:C1:2467:U:H3	1.25	0.85
1:C1:2848:A:H61	1:C1:2871:C:H42	0.89	0.85
1:C1:91:G:H21	1:C1:95:A:H62	1.26	0.84
1:C1:788:A:H62	1:C1:915:G:H1	0.83	0.82
1:C1:526:G:N2	1:C1:544:U:C2	2.49	0.81
18:CP:535:LYS:HD3	18:CP:584:ILE:HD11	1.61	0.81
1:C1:1055:U:C4	1:C1:1063:C:C4	2.66	0.80
1:C1:3319:C:H4'	28:LB:316:GLY:HA2	1.66	0.77
46:Le:70:SER:HG	46:Le:72:HIS:HD1	1.35	0.75
3:C3:62:G:N7	11:CI:278:ARG:NH2	2.35	0.73
1:C1:974:G:H1	1:C1:1038:U:H3	0.81	0.73
1:C1:796:G:H1	1:C1:906:A:H61	1.39	0.71
27:Cb:17:ILE:HG23	27:Cb:448:LYS:HZ1	1.56	0.70
4:CA:243:ILE:HG22	4:CA:244:ILE:HG22	1.73	0.70
4:CA:91:PHE:HB3	4:CA:103:TRP:HB2	1.74	0.69
4:CA:137:ARG:HH12	4:CA:167:GLN:HG2	1.58	0.69
9:CG:19:TYR:HB3	9:CG:90:LEU:HD11	1.73	0.69
7:CE:129:MET:HE1	7:CE:206:LEU:HD22	1.75	0.69
15:CM:146:ASN:HD21	15:CM:246:ARG:HH12	1.40	0.69
12:CJ:376:ARG:HH21	15:CM:189:ASP:HA	1.58	0.68
1:C1:2927:A:O2'	9:CG:149:ARG:NH2	2.26	0.68
6:CC:325:ASP:HB3	6:CC:328:GLN:HG3	1.74	0.68
1:C1:1055:U:O4	1:C1:1063:C:N3	2.27	0.68
1:C1:1046:A:N1	1:C1:1074:C:N3	2.41	0.67
18:CP:537:VAL:H	18:CP:582:LYS:HZ1	1.42	0.67
1:C1:2848:A:N1	1:C1:2871:C:N3	2.42	0.67
12:CJ:87:LEU:HD21	12:CJ:110:ALA:HA	1.77	0.67
1:C1:3183:C:N3	17:CO:93:ARG:NH1	2.43	0.67
10:CH:258:GLN:HE22	33:LK:33:GLY:HA3	1.59	0.67
15:CM:70:ARG:HH12	15:CM:138:PRO:HD3	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1053:U:H3	1:C1:1069:G:H1	1.43	0.66
5:CB:215:ARG:HH21	5:CB:220:ILE:HG12	1.59	0.66
52:Cc:216:GLU:HA	52:Cc:219:ARG:HH12	1.59	0.66
18:CP:521:GLU:OE2	18:CP:565:ARG:NH1	2.27	0.66
8:CF:5:LYS:NZ	8:CF:6:ARG:O	2.29	0.66
35:LM:35:ASP:OD2	35:LM:38:ARG:NH1	2.28	0.66
10:CH:299:PRO:HA	10:CH:302:GLN:HG2	1.76	0.66
4:CA:78:CYS:SG	4:CA:249:SER:OG	2.53	0.66
18:CP:508:ILE:HB	18:CP:581:PHE:HB2	1.77	0.66
8:CF:194:ILE:O	8:CF:205:GLN:NE2	2.29	0.65
10:CH:439:GLU:OE2	19:CQ:1:MET:N	2.27	0.65
13:CK:175:MET:SD	13:CK:178:ARG:NH1	2.68	0.65
29:LC:155:SER:HG	29:LC:259:SER:HG	1.41	0.65
44:LY:30:MET:HB3	44:LY:100:PRO:HG2	1.76	0.65
1:C1:788:A:N6	1:C1:915:G:N1	2.32	0.65
39:LQ:68:THR:HG22	39:LQ:70:ALA:H	1.60	0.65
19:CQ:95:ARG:NH1	19:CQ:98:GLU:OE2	2.29	0.65
35:LM:106:GLN:HA	35:LM:109:ARG:HG2	1.78	0.65
3:C3:71:U:C2	3:C3:131:G:N1	2.65	0.65
32:LH:17:LYS:NZ	35:LM:3:GLU:OE1	2.30	0.65
7:CE:334:GLN:NE2	7:CE:441:TYR:OH	2.30	0.65
10:CH:183:VAL:HG21	10:CH:219:ASP:HB2	1.78	0.65
33:LK:85:LEU:HD21	33:LK:104:VAL:HG22	1.79	0.65
1:C1:2924:G:O6	9:CG:15:LYS:NZ	2.30	0.65
3:C3:71:U:O2	3:C3:131:G:C2	2.50	0.65
6:CC:325:ASP:OD1	12:CJ:244:ARG:NH1	2.30	0.64
1:C1:83:C:HO2'	1:C1:687:C:HO2'	1.42	0.64
1:C1:3188:U:OP2	17:CO:93:ARG:NH2	2.31	0.64
4:CA:121:HIS:HB2	4:CA:237:ARG:HB3	1.78	0.64
27:Cb:423:THR:OG1	27:Cb:424:ASP:N	2.30	0.64
27:Cb:491:LEU:HB3	27:Cb:568:GLY:HA3	1.80	0.64
41:LT:127:GLN:NE2	41:LT:129:LYS:O	2.29	0.64
5:CB:58:ALA:HA	5:CB:249:ASN:HB3	1.79	0.64
2:C2:39:G:C2	2:C2:105:A:C2	2.85	0.63
28:LB:331:GLY:HA3	28:LB:337:MET:HE1	1.80	0.63
9:CG:101:LYS:HA	9:CG:137:MET:HE1	1.79	0.63
1:C1:690:G:N7	4:CA:282:ARG:NH2	2.44	0.63
1:C1:1046:A:N6	1:C1:1074:C:O2	2.32	0.63
10:CH:29:PRO:O	10:CH:48:LYS:NZ	2.31	0.63
44:LY:51:LYS:NZ	44:LY:70:THR:O	2.32	0.63
47:Lf:15:HIS:NE2	47:Lf:30:SER:OG	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:CP:383:ARG:NH2	18:CP:448:GLY:O	2.32	0.62
6:CC:270:PRO:HB3	31:LG:148:ASN:HA	1.81	0.62
16:CN:126:GLU:OE1	16:CN:139:ARG:NH1	2.32	0.62
1:C1:2965:G:H4'	37:LO:67:PRO:HB2	1.82	0.62
5:CB:119:ASP:HB2	5:CB:225:ARG:HH12	1.64	0.62
1:C1:1080:A:OP2	41:LT:130:ARG:NH1	2.33	0.62
8:CF:25:ARG:O	8:CF:29:ASN:ND2	2.29	0.62
16:CN:12:GLU:OE2	42:LV:130:ARG:NH2	2.31	0.62
19:CQ:17:LYS:NZ	28:LB:369:GLY:O	2.33	0.62
53:Cd:42:GLU:OE1	53:Cd:45:ARG:NH2	2.32	0.62
24:CX:140:LYS:HB3	24:CX:144:ARG:HH21	1.64	0.62
1:C1:663:G:N7	39:LQ:132:ARG:NH2	2.48	0.62
13:CK:242:TYR:HB3	13:CK:260:LEU:HD12	1.81	0.62
29:LC:290:LEU:HD21	39:LQ:152:ASP:HB2	1.82	0.62
40:LS:31:ALA:HB1	40:LS:36:VAL:HG13	1.80	0.62
1:C1:2302:U:H2'	1:C1:2303:A:H8	1.64	0.62
7:CE:112:GLU:HG2	7:CE:133:LYS:HA	1.82	0.62
1:C1:974:G:O6	1:C1:1038:U:O4	2.18	0.61
5:CB:175:THR:HG22	5:CB:177:LYS:H	1.63	0.61
36:LN:114:ARG:NH1	36:LN:151:ILE:O	2.33	0.61
1:C1:1372:A:N6	1:C1:1400:A:O2'	2.33	0.61
15:CM:124:LYS:HD3	15:CM:197:VAL:HG21	1.82	0.61
1:C1:608:A:OP1	47:Lf:62:ARG:NH2	2.33	0.61
1:C1:1239:C:H42	1:C1:1243:G:N2	1.98	0.61
18:CP:460:SER:O	18:CP:475:ARG:NH1	2.33	0.61
45:Ld:89:ASP:OD1	45:Ld:90:GLU:N	2.31	0.61
4:CA:33:LYS:HE3	6:CC:156:PRO:HD2	1.82	0.61
10:CH:250:LEU:HD21	10:CH:334:VAL:HG21	1.83	0.61
18:CP:485:HIS:O	18:CP:489:GLN:NE2	2.33	0.61
1:C1:385:U:O2'	44:LY:86:ARG:NH2	2.34	0.61
1:C1:1153:G:OP2	15:LF:223:ARG:NH1	2.32	0.61
1:C1:2959:C:OP1	28:LB:26:ARG:NH1	2.33	0.61
18:CP:488:LYS:HG3	18:CP:523:VAL:HG13	1.82	0.61
42:LV:30:ASN:HD21	42:LV:114:SER:HB2	1.66	0.61
2:C2:55:U:OP1	20:CR:11:ARG:NH1	2.33	0.61
9:CG:104:GLY:HA3	9:CG:118:HIS:HB3	1.83	0.61
1:C1:2478:U:O4	1:C1:2550:G:N2	2.34	0.61
1:C1:596:G:OP2	29:LC:317:LYS:NZ	2.34	0.60
1:C1:796:G:H1	1:C1:906:A:N6	1.98	0.60
1:C1:2425:G:N1	1:C1:2455:U:N3	2.49	0.60
1:C1:3298:U:H2'	1:C1:3299:A:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1171:C:N3	1:C1:1297:U:O2	2.34	0.60
1:C1:1274:C:OP1	13:CK:62:ARG:NH2	2.32	0.60
6:CC:340:ILE:O	6:CC:415:ARG:NH1	2.34	0.60
13:CK:260:LEU:HD22	23:CU:338:LYS:HE3	1.84	0.60
4:CA:192:ARG:NH1	23:CU:240:GLU:OE1	2.35	0.60
29:LC:91:PHE:O	29:LC:99:ARG:NH2	2.35	0.60
54:Ce:33:SER:OG	54:Ce:35:SER:O	2.20	0.60
1:C1:1104:U:OP2	14:CL:33:ARG:NH1	2.34	0.60
47:Lf:34:ILE:HG23	47:Lf:102:ILE:HD13	1.84	0.60
9:CG:110:TYR:O	13:CK:163:ARG:NH1	2.33	0.60
27:Cb:148:MET:HE2	27:Cb:163:ALA:HB2	1.84	0.60
18:CP:491:LEU:HD11	18:CP:581:PHE:HE2	1.67	0.60
33:LK:37:LEU:HD21	33:LK:64:ILE:HG12	1.83	0.60
52:Cc:8:MET:HE3	52:Cc:11:ILE:HD11	1.83	0.60
9:CG:40:MET:HB2	9:CG:45:VAL:HG12	1.84	0.60
7:CE:440:ASP:OD1	7:CE:444:ARG:NE	2.28	0.59
27:Cb:161:ALA:HA	27:Cb:212:ASP:HA	1.83	0.59
36:LN:99:ARG:NH1	36:LN:118:SER:O	2.34	0.59
23:CU:236:ASP:OD1	23:CU:239:ARG:NH2	2.35	0.59
41:LT:75:ILE:HG12	41:LT:88:ARG:HG2	1.84	0.59
53:Cd:318:THR:H	53:Cd:436:LEU:HD22	1.67	0.59
20:CR:50:THR:OG1	20:CR:69:ASN:O	2.15	0.59
27:Cb:127:ARG:HG2	27:Cb:151:ARG:HH22	1.66	0.59
1:C1:2820:U:N3	10:CH:88:ASP:OD2	2.34	0.59
1:C1:264:G:H1'	49:Li:91:ARG:HH12	1.67	0.59
5:CB:103:ASP:HB3	5:CB:104:PRO:HD2	1.85	0.59
10:CH:97:ILE:HG13	10:CH:142:LEU:HD21	1.83	0.59
22:CT:609:GLN:O	22:CT:613:GLY:N	2.30	0.59
1:C1:2088:A:O3'	19:CQ:43:LYS:NZ	2.33	0.59
4:CA:105:SER:HB2	4:CA:112:THR:HG23	1.84	0.59
16:CN:107:VAL:HG23	16:CN:108:ILE:HG13	1.85	0.59
27:Cb:493:ARG:HE	27:Cb:571:GLN:HG2	1.68	0.59
27:Cb:588:ASP:HA	27:Cb:591:LEU:HB3	1.85	0.59
27:Cb:813:PHE:HZ	27:Cb:825:LEU:HD11	1.67	0.59
1:C1:2933:U:H2'	1:C1:2934:A:H8	1.68	0.58
10:CH:190:ASP:OD2	13:CK:9:ARG:NH2	2.36	0.58
33:LK:54:LYS:NZ	33:LK:87:GLU:OE2	2.35	0.58
1:C1:1139:G:OP2	15:LF:100:LYS:NZ	2.35	0.58
8:CF:227:TRP:HB2	8:CF:234:VAL:HG12	1.84	0.58
19:CQ:61:LYS:HG3	19:CQ:111:ARG:HH12	1.67	0.58
5:CB:60:THR:HB	5:CB:286:PRO:HG3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Cz:42:THR:HG23	26:Cz:45:LEU:HD12	1.84	0.58
11:CI:196:HIS:O	15:CM:62:ARG:NH2	2.33	0.58
12:CJ:376:ARG:NH2	15:CM:189:ASP:OD1	2.36	0.58
1:C1:2813:C:H2'	1:C1:2814:G:H8	1.67	0.58
1:C1:3184:G:H5'	1:C1:3187:G:H21	1.68	0.58
15:CM:113:ARG:NH2	15:CM:205:ALA:O	2.36	0.58
18:CP:277:ASN:HB2	18:CP:473:THR:HA	1.84	0.58
1:C1:121:A:O2'	31:LG:108:LYS:NZ	2.36	0.58
1:C1:143:G:N7	31:LG:140:ASN:ND2	2.52	0.58
1:C1:1239:C:H42	1:C1:1243:G:H22	1.50	0.58
8:CF:44:SER:HB3	8:CF:224:LEU:HD21	1.85	0.58
19:CQ:16:SER:HB3	28:LB:73:VAL:HG21	1.84	0.58
53:Cd:289:ILE:HG12	53:Cd:397:MET:HE2	1.86	0.58
53:Cd:410:ARG:NH2	53:Cd:422:GLU:OE2	2.36	0.58
1:C1:116:A:OP1	49:Li:45:ARG:NH1	2.29	0.58
5:CB:83:ILE:HD11	5:CB:270:PHE:HE2	1.69	0.58
30:LE:69:ARG:NH1	30:LE:185:SER:OG	2.36	0.58
32:LH:23:ARG:NH1	32:LH:41:ILE:O	2.37	0.58
34:LL:27:ASP:OD2	34:LL:31:LYS:NZ	2.37	0.58
1:C1:253:U:O4	7:CE:390:LYS:NZ	2.35	0.58
19:CQ:54:ALA:O	19:CQ:58:ASN:ND2	2.36	0.58
32:LH:34:LEU:HD13	32:LH:78:MET:HG2	1.85	0.58
1:C1:243:G:N2	20:CR:191:GLU:OE1	2.37	0.58
16:CN:112:ASP:H	16:CN:156:ASN:HD21	1.52	0.58
1:C1:342:C:OP1	20:CR:10:ARG:NH2	2.35	0.57
13:CK:42:LEU:HD22	13:CK:46:ARG:HE	1.69	0.57
18:CP:484:PRO:HA	18:CP:487:GLN:HG3	1.86	0.57
27:Cb:222:LEU:HD21	27:Cb:257:GLU:HB3	1.85	0.57
27:Cb:228:MET:HE2	27:Cb:230:LEU:HD13	1.85	0.57
29:LC:21:GLU:OE2	29:LC:263:LYS:NZ	2.37	0.57
29:LC:100:MET:HE2	29:LC:103:PRO:HA	1.86	0.57
1:C1:3001:A:H4'	28:LB:13:SER:HB2	1.86	0.57
6:CC:370:TRP:HE1	6:CC:378:ARG:HG2	1.69	0.57
16:CN:116:LEU:HD11	16:CN:177:LEU:HD21	1.86	0.57
28:LB:66:LYS:HZ1	42:LV:13:LEU:H	1.51	0.57
29:LC:288:SER:HB3	52:Cc:106:VAL:HG21	1.85	0.57
7:CE:438:PRO:HB2	7:CE:439:ARG:HH12	1.69	0.57
54:Ce:81:ILE:HG21	54:Ce:97:ARG:HE	1.68	0.57
1:C1:105:C:OP1	20:CR:60:LYS:NZ	2.36	0.57
1:C1:1046:A:N6	1:C1:1074:C:C2	2.64	0.57
1:C1:3045:G:OP1	28:LB:314:ARG:NH2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LH:14:GLU:HA	35:LM:2:ALA:HB2	1.85	0.57
4:CA:244:ILE:HD12	4:CA:257:GLU:HG3	1.87	0.57
12:CJ:90:LYS:HA	12:CJ:93:ARG:HG2	1.87	0.57
39:LQ:94:ARG:O	39:LQ:98:ASN:ND2	2.37	0.57
4:CA:245:ILE:HB	4:CA:256:TYR:HB3	1.86	0.57
10:CH:251:TYR:HB3	10:CH:284:ILE:HG22	1.86	0.57
12:CJ:180:ILE:HA	12:CJ:389:ALA:HA	1.86	0.57
27:Cb:244:ASP:OD2	27:Cb:428:ARG:NH2	2.37	0.57
34:LL:55:ARG:O	34:LL:115:ARG:NH1	2.37	0.57
39:LQ:49:SER:O	39:LQ:55:LYS:NZ	2.37	0.57
1:C1:694:U:O2'	1:C1:735:G:N3	2.38	0.57
5:CB:105:GLN:HB2	5:CB:129:ASP:HB2	1.85	0.57
1:C1:263:C:O2	49:Li:91:ARG:NH2	2.38	0.57
4:CA:88:ASN:OD1	4:CA:106:LYS:NZ	2.37	0.57
8:CF:164:GLU:OE2	8:CF:207:ARG:NH2	2.38	0.57
20:CR:195:LEU:HD11	20:CR:228:ARG:HG2	1.87	0.57
1:C1:705:G:OP2	1:C1:705:G:N2	2.38	0.57
1:C1:1865:A:N3	1:C1:3035:G:N2	2.52	0.57
7:CE:154:ALA:HB3	7:CE:319:ASN:HA	1.86	0.57
9:CG:104:GLY:HA2	9:CG:107:PRO:HG2	1.87	0.57
44:LY:34:LEU:HD23	44:LY:38:LEU:HB3	1.87	0.57
10:CH:243:ALA:O	27:Cb:587:ARG:NH2	2.38	0.56
11:CI:188:VAL:HG21	11:CI:268:VAL:HG21	1.86	0.56
3:C3:5:C:H2'	5:CB:162:ARG:HH12	1.68	0.56
12:CJ:414:ARG:O	12:CJ:414:ARG:NE	2.39	0.56
1:C1:1371:G:O6	29:LC:190:LYS:NZ	2.38	0.56
1:C1:2436:G:N2	1:C1:2437:G:O6	2.37	0.56
27:Cb:15:VAL:HG13	27:Cb:448:LYS:HE3	1.87	0.56
1:C1:695:G:H5'	1:C1:735:G:H21	1.70	0.56
1:C1:978:A:N6	1:C1:1032:U:O4	2.38	0.56
1:C1:1331:G:O6	52:Cc:244:ARG:NH2	2.38	0.56
6:CC:158:TYR:HE2	6:CC:164:ASP:HB2	1.70	0.56
1:C1:1228:G:O6	1:C1:1258:U:O4	2.24	0.56
42:LV:67:GLY:O	42:LV:72:ARG:NH2	2.39	0.56
1:C1:2424:G:O6	1:C1:2455:U:O2	2.23	0.56
5:CB:48:ASN:HD22	5:CB:51:ALA:HB3	1.69	0.56
27:Cb:212:ASP:OD2	27:Cb:212:ASP:N	2.36	0.56
27:Cb:401:ASP:OD2	42:LV:72:ARG:NH1	2.33	0.56
31:LG:71:ARG:NH1	31:LG:240:ILE:O	2.38	0.56
31:LG:84:THR:HG21	31:LG:158:ASN:HD22	1.70	0.56
51:Lq:63:MET:HG2	51:Lq:152:LYS:HD3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:780:G:H2'	1:C1:782:A:H62	1.71	0.56
15:LF:108:ILE:HG23	15:LF:132:MET:HE3	1.88	0.56
40:LS:21:ASN:ND2	41:LT:146:ASN:OD1	2.39	0.56
18:CP:337:TRP:CD1	18:CP:338:SER:HG	2.24	0.56
1:C1:1259:C:H2'	1:C1:1260:A:H8	1.71	0.56
1:C1:3314:U:H2'	1:C1:3318:C:H41	1.71	0.56
53:Cd:50:GLU:OE2	53:Cd:60:ARG:NH1	2.39	0.56
1:C1:3158:U:OP2	35:LM:128:ARG:NH2	2.39	0.56
7:CE:290:ARG:NH1	7:CE:292:THR:OG1	2.39	0.56
31:LG:210:ASP:OD1	31:LG:210:ASP:N	2.38	0.56
48:Lh:34:LEU:HD13	48:Lh:37:GLN:HE21	1.71	0.56
1:C1:289:A:O2'	49:Li:42:GLN:NE2	2.37	0.55
3:C3:17:G:H2'	3:C3:18:G:C8	2.41	0.55
34:LL:122:ARG:HG3	48:Lh:124:LYS:HB2	1.88	0.55
13:CK:203:ASN:ND2	13:CK:219:THR:OG1	2.39	0.55
29:LC:115:ASN:HB2	29:LC:118:GLN:HG3	1.87	0.55
5:CB:103:ASP:OD2	5:CB:206:ARG:NH1	2.39	0.55
9:CG:87:LEU:HD21	9:CG:141:PRO:HB2	1.88	0.55
35:LM:30:ILE:HD13	35:LM:39:VAL:HG21	1.88	0.55
52:Cc:172:GLU:OE2	52:Cc:174:ARG:NH2	2.40	0.55
1:C1:323:G:H5"	20:CR:5:LEU:HD22	1.88	0.55
1:C1:976:U:N3	1:C1:1036:A:C8	2.74	0.55
4:CA:170:LYS:HB3	6:CC:167:VAL:HG21	1.88	0.55
10:CH:368:ILE:HD13	16:CN:238:LYS:HG3	1.88	0.55
45:Ld:19:GLU:HB3	45:Ld:80:ARG:HD2	1.89	0.55
51:Lq:68:LEU:HB3	51:Lq:116:LEU:HD23	1.88	0.55
6:CC:170:ASN:ND2	6:CC:223:PRO:O	2.37	0.55
6:CC:355:ASN:H	12:CJ:485:HIS:HE1	1.54	0.55
6:CC:403:ARG:HH21	6:CC:406:ARG:HH22	1.54	0.55
9:CG:15:LYS:HZ3	9:CG:82:LEU:HD22	1.70	0.55
18:CP:521:GLU:OE1	18:CP:548:PHE:N	2.39	0.55
27:Cb:162:ARG:HA	27:Cb:235:ILE:HA	1.87	0.55
1:C1:2431:G:H21	1:C1:2432:C:H41	1.55	0.55
4:CA:196:ILE:HG23	4:CA:229:ILE:HD11	1.89	0.55
5:CB:158:ARG:HG2	5:CB:159:ILE:HD13	1.89	0.55
12:CJ:217:ARG:NH2	12:CJ:219:VAL:O	2.36	0.55
12:CJ:412:ASP:O	12:CJ:453:ARG:NH1	2.39	0.55
20:CR:43:GLU:HB3	20:CR:47:GLN:HG3	1.88	0.55
42:LV:25:MET:HE3	42:LV:102:GLY:HA3	1.89	0.55
45:Ld:82:ARG:HH11	45:Ld:117:VAL:HG21	1.72	0.55
1:C1:679:A:OP1	36:LN:201:ARG:NH2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:1218:G:N3	1:C1:1227:A:C5	2.74	0.55
1:C1:2729:U:C4	1:C1:2731:C:N4	2.75	0.55
1:C1:2874:U:C6	1:C1:2893:U:H2'	2.42	0.55
6:CC:263:THR:OG1	49:Li:55:GLU:OE1	2.23	0.55
16:CN:173:LEU:HD22	16:CN:181:LEU:HD11	1.89	0.55
18:CP:384:CYS:HB2	18:CP:408:ILE:HD12	1.88	0.55
18:CP:535:LYS:HG2	18:CP:582:LYS:HB2	1.87	0.55
25:CY:571:LEU:O	25:CY:575:LEU:N	2.36	0.55
46:Le:114:LYS:O	54:Ce:122:ARG:NH1	2.39	0.55
53:Cd:384:LYS:O	54:Ce:193:LYS:NZ	2.40	0.55
1:C1:374:U:OP2	53:Cd:47:ARG:NH2	2.40	0.55
18:CP:498:CYS:SG	18:CP:499:ASN:N	2.79	0.55
1:C1:507:G:OP1	15:LF:73:ARG:NH2	2.39	0.55
1:C1:2091:U:C2	1:C1:2287:G:N1	2.75	0.55
7:CE:304:GLU:HB3	7:CE:308:ARG:HH21	1.71	0.55
46:Le:97:ILE:HG21	46:Le:106:ARG:HG2	1.89	0.55
53:Cd:81:ASP:OD1	53:Cd:81:ASP:N	2.39	0.55
1:C1:695:G:N2	1:C1:698:A:OP2	2.39	0.54
3:C3:65:G:O2'	3:C3:142:A:OP1	2.22	0.54
4:CA:106:LYS:HB2	4:CA:110:GLY:HA3	1.89	0.54
12:CJ:256:LYS:HE3	12:CJ:272:SER:HB3	1.88	0.54
42:LV:106:ASN:OD1	42:LV:110:GLU:N	2.35	0.54
1:C1:2934:A:OP1	55:Cf:532:ARG:NH1	2.37	0.54
8:CF:82:GLU:N	8:CF:82:GLU:OE1	2.41	0.54
12:CJ:450:TYR:N	12:CJ:455:TYR:OH	2.41	0.54
27:Cb:159:PHE:HA	27:Cb:210:ASN:HD21	1.72	0.54
28:LB:94:GLU:HB2	28:LB:157:THR:HG21	1.89	0.54
29:LC:301:ARG:NH2	39:LQ:66:ARG:O	2.40	0.54
34:LL:86:PRO:HG2	34:LL:89:LEU:HB3	1.89	0.54
1:C1:588:C:H4'	29:LC:327:LEU:HD23	1.90	0.54
5:CB:263:ILE:HG23	5:CB:281:PHE:HE2	1.72	0.54
29:LC:295:GLU:HG2	52:Cc:191:VAL:HG13	1.88	0.54
33:LK:13:ILE:HB	33:LK:62:LEU:HB2	1.88	0.54
1:C1:674:U:OP2	34:LL:36:ARG:NH2	2.41	0.54
1:C1:3309:G:N2	28:LB:381:MET:O	2.41	0.54
3:C3:25:U:H3	5:CB:173:LYS:HG3	1.70	0.54
11:CI:213:ILE:HD13	11:CI:233:ILE:HD11	1.90	0.54
11:CI:214:THR:HG22	11:CI:215:ARG:HG2	1.89	0.54
55:Cf:511:GLU:HA	55:Cf:514:LYS:HE3	1.89	0.54
2:C2:48:A:O2'	2:C2:51:G:N2	2.41	0.54
2:C2:63:G:HO2'	48:Lh:54:LYS:HZ2	1.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CA:35:ARG:HB2	4:CA:86:CYS:HA	1.90	0.54
16:CN:97:ILE:HG22	16:CN:128:ILE:HD11	1.89	0.54
5:CB:31:LEU:HA	5:CB:34:ILE:HD12	1.90	0.54
5:CB:235:LEU:HD11	5:CB:270:PHE:HB3	1.90	0.54
32:LH:89:LYS:HB2	32:LH:185:GLU:HB3	1.88	0.54
44:LY:2:LYS:HD2	44:LY:7:VAL:HG13	1.89	0.54
53:Cd:180:PRO:HG2	53:Cd:183:LEU:HB3	1.90	0.54
1:C1:1046:A:N1	1:C1:1074:C:C4	2.76	0.54
1:C1:2996:G:OP1	28:LB:62:ARG:NH1	2.41	0.54
18:CP:334:VAL:HG13	18:CP:337:TRP:HE1	1.73	0.54
15:LF:94:ARG:HB2	15:LF:114:LEU:HD13	1.90	0.54
38:LP:126:ARG:HD3	38:LP:140:MET:HE1	1.89	0.54
1:C1:430:A:OP2	1:C1:606:G:N2	2.35	0.54
28:LB:58:ARG:NH1	28:LB:284:TYR:OH	2.41	0.54
1:C1:83:C:O2'	1:C1:687:C:O2'	2.19	0.54
2:C2:127:U:O2	12:CJ:15:ASN:ND2	2.41	0.54
51:Lq:76:ARG:HH12	51:Lq:143:ASP:HA	1.73	0.54
5:CB:282:TYR:HB3	5:CB:290:ALA:HB1	1.90	0.53
26:Cz:41:PRO:HG2	32:LH:62:ARG:HH12	1.73	0.53
1:C1:36:C:H4'	1:C1:789:A:H2	1.73	0.53
1:C1:37:U:O2	34:LL:15:ARG:NH2	2.39	0.53
1:C1:1331:G:H3'	15:LF:21:LYS:HE3	1.89	0.53
7:CE:239:ALA:HB3	7:CE:244:LEU:HD22	1.89	0.53
8:CF:45:VAL:O	8:CF:99:THR:OG1	2.26	0.53
29:LC:133:ALA:HA	29:LC:149:VAL:HG21	1.90	0.53
1:C1:3269:U:H5"	28:LB:309:MET:HE2	1.91	0.53
2:C2:40:A:OP2	2:C2:103:G:N1	2.36	0.53
6:CC:271:LEU:HD12	31:LG:147:GLU:HG2	1.90	0.53
28:LB:47:MET:H	28:LB:84:MET:HE3	1.73	0.53
42:LV:15:MET:HB2	42:LV:87:TRP:HB2	1.90	0.53
1:C1:2888:A:H5'	27:Cb:3:LYS:HB2	1.91	0.53
29:LC:8:THR:OG1	29:LC:148:GLU:OE1	2.27	0.53
15:LF:169:LEU:HA	15:LF:174:ILE:HD11	1.90	0.53
40:LS:27:MET:HE1	40:LS:44:PHE:HB2	1.91	0.53
1:C1:2395:U:H3'	1:C1:2396:U:H2'	1.90	0.53
1:C1:2424:G:O6	1:C1:2455:U:C2	2.62	0.53
1:C1:2973:A:H2'	1:C1:2974:G:H8	1.74	0.53
3:C3:58:A:H5"	11:CI:230:ARG:HH11	1.74	0.53
15:CM:113:ARG:NH2	15:CM:208:LEU:O	2.37	0.53
27:Cb:200:LEU:HD13	27:Cb:220:ARG:HE	1.74	0.53
1:C1:6:A:O5'	12:CJ:93:ARG:NH1	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:724:C:O2	39:LQ:168:ARG:NE	2.40	0.53
5:CB:99:LEU:HD22	5:CB:127:VAL:HG22	1.90	0.53
6:CC:211:ILE:HG22	6:CC:212:GLU:HG3	1.91	0.53
8:CF:42:VAL:HG13	8:CF:224:LEU:HB2	1.90	0.53
15:CM:105:PRO:HA	15:CM:108:ILE:HG22	1.89	0.53
1:C1:642:C:H2'	1:C1:643:A:H8	1.74	0.53
1:C1:983:A:N1	1:C1:1032:U:O2'	2.40	0.53
8:CF:228:ASN:HB3	8:CF:231:SER:HB3	1.89	0.53
10:CH:279:ASN:OD1	10:CH:279:ASN:N	2.41	0.53
12:CJ:189:PHE:HB3	12:CJ:196:TYR:HB2	1.90	0.53
13:CK:116:ARG:NH1	18:CP:273:TYR:OH	2.41	0.53
22:CT:666:LYS:O	25:CY:568:TYR:N	2.42	0.53
27:Cb:324:ILE:HA	27:Cb:328:ILE:HB	1.90	0.53
35:LM:33:ILE:HA	35:LM:39:VAL:HG23	1.88	0.53
38:LP:106:GLY:O	54:Ce:164:ARG:NH2	2.42	0.53
1:C1:92:G:H5'	1:C1:93:C:H5"	1.90	0.53
1:C1:297:U:OP2	4:CA:96:LYS:NZ	2.39	0.53
10:CH:342:ARG:NH2	27:Cb:519:GLU:OE2	2.41	0.53
18:CP:580:LYS:HG2	18:CP:582:LYS:HZ2	1.73	0.53
2:C2:133:C:H2'	2:C2:134:G:H8	1.74	0.53
5:CB:44:ASP:OD1	5:CB:44:ASP:N	2.41	0.53
10:CH:210:TYR:CZ	10:CH:211:LYS:HE2	2.44	0.53
13:CK:127:ILE:HD12	13:CK:131:GLU:HG3	1.91	0.53
1:C1:661:G:O6	39:LQ:84:ARG:NH2	2.36	0.53
1:C1:1055:U:O4	1:C1:1063:C:N4	2.24	0.53
1:C1:340:C:O2	1:C1:344:A:O2'	2.27	0.52
1:C1:734:C:H2'	1:C1:735:G:H8	1.73	0.52
1:C1:2886:C:O2'	27:Cb:4:ARG:NH2	2.41	0.52
1:C1:3033:C:OP2	45:Ld:73:LYS:NZ	2.43	0.52
2:C2:103:G:OP2	2:C2:105:A:O2'	2.25	0.52
9:CG:85:THR:HG23	18:CP:426:HIS:HB3	1.90	0.52
10:CH:390:LEU:HD11	16:CN:43:GLN:HB2	1.91	0.52
13:CK:154:PRO:HB3	13:CK:179:TYR:HE2	1.74	0.52
30:LE:25:GLN:NE2	30:LE:27:TRP:O	2.42	0.52
1:C1:2944:U:H2'	1:C1:2945:A:H8	1.75	0.52
1:C1:36:C:O2'	1:C1:915:G:N3	2.40	0.52
1:C1:1263:U:H2'	1:C1:1264:G:H8	1.75	0.52
1:C1:2475:U:O2	1:C1:2551:A:C6	2.63	0.52
5:CB:88:PRO:HB3	5:CB:229:GLY:HA3	1.90	0.52
7:CE:113:PHE:HD1	7:CE:134:MET:HE2	1.74	0.52
7:CE:342:ASP:OD2	7:CE:540:LYS:NZ	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Cb:297:ALA:HB1	27:Cb:300:LYS:HB2	1.91	0.52
30:LE:56:THR:OG1	30:LE:108:LYS:NZ	2.43	0.52
15:LF:216:PRO:HD3	15:LF:248:MET:HE3	1.91	0.52
5:CB:83:ILE:HD11	5:CB:270:PHE:CE2	2.44	0.52
1:C1:2426:U:O2'	51:Lq:164:CYS:SG	2.59	0.52
7:CE:152:LEU:HD23	7:CE:315:PRO:HB3	1.92	0.52
14:CL:5:ILE:HD13	37:LO:53:LEU:HD12	1.92	0.52
17:CO:37:LEU:HD22	28:LB:208:THR:HB	1.92	0.52
28:LB:50:LYS:HD3	28:LB:337:MET:HE3	1.92	0.52
1:C1:403:U:H2'	1:C1:404:G:H8	1.74	0.52
15:CM:182:TYR:O	15:CM:200:ASN:ND2	2.42	0.52
15:LF:104:LYS:HD3	15:LF:135:ILE:HD13	1.91	0.52
46:Le:24:ASP:OD1	46:Le:24:ASP:N	2.36	0.52
1:C1:3157:C:OP1	35:LM:132:ARG:NH2	2.33	0.52
5:CB:275:TRP:HZ3	5:CB:295:GLN:HB3	1.75	0.52
10:CH:176:ASN:ND2	10:CH:196:TYR:O	2.30	0.52
1:C1:230:A:H2'	1:C1:231:A:C8	2.44	0.52
4:CA:38:VAL:HG12	4:CA:90:LEU:HB3	1.92	0.52
5:CB:42:ARG:HD3	5:CB:43:PRO:HD2	1.90	0.52
7:CE:393:GLN:HG2	7:CE:396:ARG:HH21	1.74	0.52
7:CE:506:TYR:HD2	7:CE:507:LEU:HD12	1.75	0.52
1:C1:370:A:H4'	44:LY:90:THR:HG22	1.92	0.52
1:C1:597:G:N7	29:LC:311:ARG:NH2	2.57	0.52
9:CG:112:SER:HB2	13:CK:139:GLY:HA3	1.92	0.52
13:CK:236:LYS:HZ3	18:CP:474:ASN:HB3	1.74	0.52
31:LG:222:LYS:HG3	31:LG:226:LEU:HD12	1.92	0.52
42:LV:105:VAL:HA	42:LV:111:MET:HA	1.91	0.52
53:Cd:284:THR:HB	53:Cd:405:ASP:HB2	1.91	0.52
4:CA:244:ILE:HD11	4:CA:254:ILE:HD12	1.92	0.52
24:CX:98:ARG:NH1	24:CX:102:ASN:OD1	2.42	0.52
27:Cb:600:GLN:O	27:Cb:625:ARG:NH1	2.43	0.52
27:Cb:798:GLY:HA3	27:Cb:804:ILE:HD12	1.93	0.52
1:C1:1239:C:N4	1:C1:1243:G:H22	2.06	0.51
1:C1:2857:C:O2'	1:C1:2859:G:OP2	2.27	0.51
29:LC:364:GLU:OE2	41:LT:147:LYS:NZ	2.42	0.51
1:C1:3076:U:OP2	26:Cz:28:ASN:ND2	2.41	0.51
1:C1:2436:G:O3'	1:C1:2438:C:N4	2.43	0.51
1:C1:2947:U:OP1	37:LO:66:ASN:ND2	2.44	0.51
16:CN:22:SER:HB3	16:CN:67:ARG:HG3	1.91	0.51
16:CN:109:VAL:HB	16:CN:149:GLY:HA2	1.91	0.51
15:LF:155:TYR:OH	15:LF:188:GLU:OE2	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:350:G:N2	1:C1:353:A:OP2	2.37	0.51
1:C1:704:C:OP1	1:C1:732:A:O2'	2.26	0.51
1:C1:2936:U:H5"	55:Cf:526:LYS:HD3	1.92	0.51
6:CC:182:SER:HB2	24:CX:133:ARG:HH22	1.75	0.51
46:Le:10:ILE:HA	46:Le:64:THR:HG21	1.92	0.51
47:Lf:47:LEU:HD11	47:Lf:76:PRO:HD3	1.92	0.51
53:Cd:298:ILE:HD11	53:Cd:396:ARG:HG3	1.93	0.51
4:CA:109:ASN:ND2	6:CC:153:GLU:OE2	2.43	0.51
5:CB:42:ARG:HG3	5:CB:44:ASP:H	1.75	0.51
8:CF:236:GLU:O	8:CF:241:LYS:NZ	2.39	0.51
10:CH:79:ASP:OD2	10:CH:244:HIS:NE2	2.40	0.51
28:LB:26:ARG:HG3	28:LB:336:ILE:HD13	1.91	0.51
1:C1:1218:G:C2	1:C1:1227:A:C5	2.98	0.51
1:C1:1877:G:H2'	1:C1:1878:G:C8	2.45	0.51
1:C1:50:U:H2'	1:C1:51:A:H8	1.76	0.51
1:C1:653:G:OP1	36:LN:203:ARG:NH2	2.42	0.51
1:C1:2735:G:O6	1:C1:2741:U:O4	2.29	0.51
1:C1:2873:U:HO2'	1:C1:2893:U:HO2'	1.59	0.51
5:CB:216:PRO:HB2	5:CB:219:GLU:HG2	1.91	0.51
27:Cb:131:VAL:HG23	27:Cb:270:LEU:HD22	1.91	0.51
8:CF:141:ILE:HD11	8:CF:178:LYS:HD2	1.93	0.51
12:CJ:28:LEU:HD11	12:CJ:78:LEU:HD12	1.92	0.51
12:CJ:251:LEU:HG	12:CJ:275:GLY:HA2	1.92	0.51
18:CP:317:ARG:NH2	18:CP:341:GLY:O	2.44	0.51
15:LF:221:ARG:NH1	15:LF:232:GLY:O	2.42	0.51
5:CB:281:PHE:HB2	5:CB:295:GLN:HE22	1.76	0.51
7:CE:194:GLU:OE1	7:CE:194:GLU:N	2.42	0.51
31:LG:155:LEU:HD23	31:LG:183:ILE:HD13	1.93	0.51
38:LP:60:MET:HE3	38:LP:82:ARG:HB2	1.91	0.51
1:C1:213:G:C6	1:C1:1371:G:C2	2.99	0.51
3:C3:13:C:H2'	3:C3:14:C:H2'	1.91	0.51
27:Cb:130:VAL:HB	27:Cb:269:LEU:HD22	1.92	0.51
27:Cb:190:LYS:NZ	27:Cb:209:THR:O	2.43	0.51
1:C1:1218:G:C2	1:C1:1227:A:C6	2.99	0.50
18:CP:270:ILE:HD13	18:CP:285:LEU:HD21	1.93	0.50
28:LB:53:MET:HG2	28:LB:77:THR:HA	1.93	0.50
1:C1:432:U:OP2	53:Cd:235:TYR:OH	2.29	0.50
1:C1:1288:G:O6	1:C1:2328:C:O2'	2.29	0.50
1:C1:1875:A:H2'	1:C1:1876:G:C8	2.45	0.50
6:CC:177:LEU:HD11	6:CC:223:PRO:HA	1.93	0.50
13:CK:184:VAL:HG12	13:CK:257:ALA:HB3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Cb:95:MET:HE1	27:Cb:121:ILE:HD12	1.91	0.50
27:Cb:432:ILE:HG13	27:Cb:456:ARG:HD2	1.93	0.50
1:C1:137:C:OP1	12:CJ:105:ARG:NH2	2.40	0.50
1:C1:385:U:OP1	53:Cd:72:LYS:NZ	2.45	0.50
1:C1:2368:C:H5"	23:CU:323:ARG:HH12	1.76	0.50
6:CC:196:MET:SD	6:CC:196:MET:N	2.84	0.50
7:CE:384:VAL:HG23	7:CE:410:THR:HB	1.94	0.50
23:CU:206:ASP:OD1	23:CU:206:ASP:N	2.45	0.50
31:LG:159:ASP:N	31:LG:159:ASP:OD1	2.42	0.50
46:Le:130:GLU:OE2	53:Cd:403:ARG:NH2	2.44	0.50
1:C1:2973:A:H2'	1:C1:2974:G:C8	2.47	0.50
13:CK:68:HIS:HA	13:CK:71:ARG:HG2	1.93	0.50
13:CK:247:ASN:ND2	13:CK:252:ASP:OD2	2.44	0.50
23:CU:267:ARG:NH2	24:CX:77:VAL:O	2.44	0.50
27:Cb:180:VAL:HG11	27:Cb:191:THR:HG21	1.93	0.50
27:Cb:182:GLU:O	27:Cb:185:LYS:NZ	2.45	0.50
1:C1:66:A:N6	1:C1:76:G:H1'	2.26	0.50
1:C1:1269:A:O2'	26:Cz:40:ARG:NH1	2.42	0.50
1:C1:1332:A:H2'	1:C1:1333:A:C8	2.47	0.50
1:C1:3015:U:N3	1:C1:3036:U:O2	2.42	0.50
51:Lq:93:LEU:HB3	51:Lq:100:ILE:HD12	1.91	0.50
1:C1:3234:A:H5"	28:LB:128:LYS:HE3	1.92	0.50
10:CH:230:GLU:OE1	10:CH:230:GLU:N	2.45	0.50
23:CU:283:GLU:O	23:CU:286:LYS:N	2.45	0.50
15:LF:67:GLU:HA	15:LF:70:ARG:HG2	1.93	0.50
31:LG:85:LEU:HD11	31:LG:183:ILE:HG22	1.93	0.50
33:LK:54:LYS:HE3	33:LK:89:PRO:HB3	1.92	0.50
42:LV:79:VAL:HG23	42:LV:105:VAL:HG11	1.93	0.50
1:C1:2076:C:H2'	1:C1:2077:G:H8	1.75	0.50
3:C3:1:C:N4	11:CI:252:LEU:O	2.44	0.50
8:CF:73:MET:HE3	8:CF:102:LEU:HG	1.94	0.50
11:CI:255:GLY:O	31:LG:216:LYS:NZ	2.42	0.50
27:Cb:191:THR:HG22	27:Cb:213:ILE:HB	1.93	0.50
29:LC:24:PRO:HG2	29:LC:265:LEU:HD23	1.93	0.50
38:LP:70:THR:HG23	38:LP:72:GLN:H	1.77	0.50
51:Lq:76:ARG:NH1	51:Lq:142:ASP:O	2.45	0.50
1:C1:1171:C:H42	1:C1:1297:U:H1'	1.77	0.50
1:C1:1417:A:H5"	1:C1:1418:U:H5"	1.92	0.50
6:CC:214:PRO:HD2	6:CC:217:TRP:HB2	1.94	0.50
7:CE:216:VAL:O	7:CE:229:LYS:NZ	2.45	0.50
18:CP:307:VAL:HG22	27:Cb:716:MET:HE1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LB:170:THR:HG22	28:LB:172:LEU:HG	1.94	0.50
1:C1:2821:G:N2	10:CH:64:ILE:O	2.42	0.50
5:CB:143:GLN:NE2	5:CB:166:ALA:O	2.45	0.50
9:CG:109:LEU:HD11	18:CP:355:PRO:HB3	1.94	0.50
12:CJ:187:LYS:HD3	12:CJ:488:PRO:HB2	1.94	0.50
29:LC:9:VAL:HA	29:LC:152:VAL:HG23	1.93	0.50
1:C1:1277:G:OP1	40:LS:84:ARG:NE	2.45	0.49
1:C1:2832:G:N3	1:C1:2833:U:O2'	2.45	0.49
17:CO:36:LYS:HB3	28:LB:208:THR:HG22	1.92	0.49
27:Cb:165:VAL:HB	27:Cb:215:ILE:HG22	1.93	0.49
30:LE:140:GLU:O	30:LE:144:LYS:NZ	2.39	0.49
48:Lh:93:LEU:HD22	48:Lh:96:ARG:HH21	1.76	0.49
52:Cc:11:ILE:HA	52:Cc:14:LEU:HD12	1.94	0.49
53:Cd:45:ARG:HA	53:Cd:48:LYS:HZ2	1.77	0.49
1:C1:3307:C:OP1	19:CQ:111:ARG:NH2	2.41	0.49
5:CB:186:ALA:HA	5:CB:215:ARG:HB2	1.94	0.49
9:CG:60:ALA:HB3	9:CG:63:LYS:HB3	1.93	0.49
9:CG:155:ARG:O	9:CG:155:ARG:NH1	2.45	0.49
28:LB:149:LEU:HD12	28:LB:193:VAL:HG13	1.94	0.49
36:LN:146:PRO:HG2	48:Lh:106:LEU:HD13	1.93	0.49
3:C3:26:U:H5"	5:CB:169:LYS:HG3	1.94	0.49
13:CK:157:VAL:HG21	13:CK:178:ARG:HH21	1.77	0.49
51:Lq:121:PRO:HA	51:Lq:125:GLY:HA3	1.94	0.49
1:C1:2091:U:N3	1:C1:2287:G:N1	2.61	0.49
10:CH:96:GLN:HE21	10:CH:141:ARG:HH12	1.58	0.49
10:CH:187:THR:HG21	10:CH:206:GLY:HA3	1.95	0.49
29:LC:151:LEU:HD23	29:LC:256:VAL:HG12	1.93	0.49
32:LH:89:LYS:O	32:LH:184:SER:OG	2.29	0.49
1:C1:260:A:OP1	36:LN:50:ARG:NH1	2.46	0.49
1:C1:331:C:OP1	1:C1:1362:G:O2'	2.30	0.49
1:C1:2815:C:O2'	13:CK:183:ASN:OD1	2.25	0.49
1:C1:2898:A:OP2	1:C1:2900:C:O2'	2.26	0.49
6:CC:366:GLU:OE1	6:CC:366:GLU:N	2.37	0.49
10:CH:19:ILE:HG21	10:CH:59:LYS:HE2	1.94	0.49
13:CK:129:GLU:OE2	13:CK:164:ARG:NH1	2.45	0.49
22:CT:218:LEU:O	22:CT:222:ALA:N	2.43	0.49
23:CU:340:LYS:NZ	23:CU:369:ASP:OD1	2.44	0.49
53:Cd:373:VAL:HA	53:Cd:379:GLU:HA	1.94	0.49
4:CA:35:ARG:H	4:CA:87:ASN:HD21	1.59	0.49
23:CU:239:ARG:NH1	23:CU:240:GLU:OE2	2.45	0.49
29:LC:154:ASP:N	29:LC:154:ASP:OD1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:LH:9:THR:HG23	32:LH:52:VAL:HG13	1.95	0.49
34:LL:126:PHE:O	48:Lh:119:ARG:NH1	2.46	0.49
53:Cd:298:ILE:O	53:Cd:301:HIS:ND1	2.46	0.49
1:C1:258:C:O2	49:Li:39:LYS:NZ	2.38	0.49
1:C1:703:A:OP1	1:C1:733:C:O2'	2.31	0.49
1:C1:944:G:H2'	1:C1:945:G:C8	2.47	0.49
1:C1:2814:G:H21	13:CK:192:THR:HG21	1.77	0.49
1:C1:2918:C:H2'	1:C1:2919:G:H8	1.76	0.49
6:CC:283:PRO:HB2	20:CR:218:TYR:HE2	1.77	0.49
10:CH:31:GLN:OE1	10:CH:33:ARG:NH1	2.46	0.49
10:CH:439:GLU:OE2	16:CN:79:GLN:NE2	2.45	0.49
18:CP:520:ASN:HB3	18:CP:577:PHE:CD1	2.47	0.49
27:Cb:323:HIS:HD2	27:Cb:509:LEU:HD22	1.77	0.49
53:Cd:338:LEU:HD22	54:Ce:185:ASN:HD21	1.78	0.49
1:C1:781:G:H22	29:LC:102:ALA:HA	1.78	0.49
1:C1:1218:G:N1	1:C1:1227:A:N6	2.61	0.49
1:C1:3118:A:OP1	53:Cd:301:HIS:NE2	2.40	0.49
3:C3:49:G:OP1	5:CB:176:THR:N	2.45	0.49
8:CF:225:GLY:HA2	8:CF:237:LEU:HG	1.94	0.49
12:CJ:136:ASP:HA	12:CJ:139:ARG:HD2	1.95	0.49
12:CJ:407:THR:OG1	12:CJ:409:ASP:OD1	2.27	0.49
13:CK:126:GLY:HA3	13:CK:161:PHE:HB2	1.94	0.49
18:CP:383:ARG:HH12	18:CP:447:ILE:HG21	1.77	0.49
18:CP:516:CYS:O	18:CP:520:ASN:ND2	2.45	0.49
28:LB:63:PRO:HA	28:LB:68:HIS:HD1	1.77	0.49
31:LG:146:ILE:HB	31:LG:178:ILE:HD13	1.94	0.49
1:C1:19:U:H2'	1:C1:20:A:C8	2.47	0.49
1:C1:910:A:O2'	50:Lj:49:TRP:O	2.28	0.49
1:C1:2395:U:OP2	1:C1:2396:U:O2'	2.28	0.49
3:C3:25:U:H2'	5:CB:169:LYS:HG2	1.93	0.49
23:CU:319:LYS:O	23:CU:323:ARG:HG3	2.12	0.49
27:Cb:835:ASN:OD1	27:Cb:838:ARG:NH2	2.46	0.49
28:LB:335:ARG:HB3	28:LB:337:MET:HE2	1.94	0.49
35:LM:88:TYR:HD2	35:LM:90:VAL:HG12	1.77	0.49
37:LO:36:VAL:HB	37:LO:106:VAL:HG12	1.93	0.49
53:Cd:189:ASN:HD21	53:Cd:283:PRO:HD3	1.78	0.49
53:Cd:321:GLY:HA3	53:Cd:436:LEU:HD23	1.95	0.49
1:C1:1218:G:C2	1:C1:1227:A:N6	2.80	0.49
1:C1:1280:C:O2	13:CK:40:GLN:NE2	2.45	0.49
5:CB:52:ASP:O	5:CB:56:THR:OG1	2.23	0.49
6:CC:256:PRO:O	31:LG:236:TRP:NE1	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:CM:94:ARG:HG3	15:CM:114:LEU:HB3	1.95	0.49
20:CR:133:GLN:HE22	34:LL:113:VAL:HG11	1.76	0.49
27:Cb:134:ALA:HA	27:Cb:295:LEU:HD12	1.95	0.49
29:LC:326:MET:HE1	15:LF:155:TYR:CZ	2.48	0.49
46:Le:13:LYS:NZ	46:Le:59:GLY:O	2.45	0.49
48:Lh:24:LEU:O	48:Lh:28:LYS:NZ	2.46	0.49
4:CA:111:PRO:HG2	23:CU:203:ILE:HD11	1.93	0.48
6:CC:152:ASP:O	7:CE:573:TYR:OH	2.31	0.48
6:CC:287:GLU:OE1	31:LG:111:ARG:NH2	2.46	0.48
7:CE:441:TYR:O	7:CE:445:VAL:HG22	2.13	0.48
27:Cb:228:MET:HA	27:Cb:813:PHE:CD1	2.47	0.48
27:Cb:228:MET:HA	27:Cb:813:PHE:HD1	1.77	0.48
30:LE:108:LYS:HB2	30:LE:108:LYS:HZ3	1.77	0.48
1:C1:2091:U:N3	1:C1:2287:G:C6	2.81	0.48
1:C1:2852:C:H1'	1:C1:3063:A:H2	1.77	0.48
2:C2:71:A:OP1	44:LY:27:ARG:NH1	2.46	0.48
27:Cb:396:VAL:HA	27:Cb:400:LEU:HD22	1.93	0.48
28:LB:29:VAL:HA	28:LB:219:ILE:HD13	1.95	0.48
31:LG:103:GLU:OE2	31:LG:111:ARG:NH1	2.45	0.48
1:C1:3136:A:H2'	1:C1:3137:A:H8	1.78	0.48
14:CL:38:LEU:HD23	14:CL:41:LYS:HD2	1.94	0.48
42:LV:91:ASP:OD1	42:LV:91:ASP:N	2.41	0.48
1:C1:35:A:H2'	1:C1:36:C:H6	1.79	0.48
1:C1:553:U:H2'	1:C1:554:G:H8	1.78	0.48
1:C1:916:U:H2'	1:C1:917:A:C8	2.48	0.48
7:CE:438:PRO:HA	7:CE:441:TYR:HB3	1.94	0.48
12:CJ:374:LEU:HD22	12:CJ:383:LEU:HD13	1.96	0.48
22:CT:259:ARG:O	22:CT:263:LEU:N	2.45	0.48
27:Cb:174:LEU:HA	27:Cb:177:LEU:HB3	1.95	0.48
15:LF:184:ILE:HG23	15:LF:189:ASP:HB3	1.95	0.48
35:LM:130:GLU:HB3	37:LO:187:ALA:HB1	1.95	0.48
39:LQ:150:THR:OG1	39:LQ:152:ASP:OD1	2.28	0.48
44:LY:34:LEU:HD11	44:LY:47:ILE:HG12	1.95	0.48
45:Ld:33:PHE:HD1	45:Ld:73:LYS:HB2	1.79	0.48
1:C1:63:A:N3	1:C1:78:U:O2'	2.42	0.48
1:C1:324:C:H4'	50:Lj:71:PRO:HB3	1.96	0.48
3:C3:71:U:C2	3:C3:131:G:C2	3.01	0.48
4:CA:194:TYR:HB3	4:CA:231:LEU:HB3	1.95	0.48
7:CE:296:SER:OG	7:CE:297:ALA:N	2.47	0.48
16:CN:74:THR:HB	16:CN:98:GLU:HA	1.95	0.48
23:CU:278:THR:HG23	23:CU:281:THR:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:Ld:36:ARG:NH1	45:Ld:73:LYS:O	2.42	0.48
6:CC:367:ARG:NH1	6:CC:384:PRO:O	2.41	0.48
18:CP:402:MET:HE2	18:CP:402:MET:HB3	1.68	0.48
27:Cb:243:ALA:HA	27:Cb:246:LEU:HD12	1.94	0.48
34:LL:60:CYS:HB2	34:LL:65:TYR:O	2.13	0.48
51:Lq:75:ASP:OD1	51:Lq:75:ASP:N	2.46	0.48
1:C1:247:A:H2'	1:C1:248:G:H8	1.79	0.48
1:C1:3253:U:O5'	28:LB:174:GLN:NE2	2.47	0.48
5:CB:24:LEU:HD12	5:CB:28:LYS:HZ3	1.78	0.48
15:CM:130:ALA:O	15:CM:134:LYS:N	2.46	0.48
15:LF:15:PRO:HB3	52:Cc:110:GLU:HG2	1.95	0.48
44:LY:43:ASN:ND2	44:LY:126:GLU:OE2	2.43	0.48
1:C1:662:C:O2'	1:C1:666:U:OP1	2.29	0.48
1:C1:672:G:N7	34:LL:32:LYS:NZ	2.61	0.48
1:C1:672:G:OP2	34:LL:35:ARG:NH2	2.39	0.48
1:C1:1038:U:H2'	1:C1:1039:A:C8	2.49	0.48
1:C1:1264:G:H4'	8:CF:99:THR:HG22	1.95	0.48
1:C1:2319:A:H2'	1:C1:2320:A:H8	1.79	0.48
1:C1:2328:C:H2'	1:C1:2329:A:H8	1.79	0.48
4:CA:32:ASN:HB3	4:CA:166:PRO:HB3	1.96	0.48
11:CI:193:ARG:HB2	11:CI:258:LEU:HA	1.96	0.48
16:CN:85:ARG:NH2	16:CN:89:PRO:O	2.46	0.48
27:Cb:332:PRO:HD3	27:Cb:367:HIS:CE1	2.48	0.48
51:Lq:85:MET:HE2	51:Lq:90:LEU:HG	1.94	0.48
53:Cd:316:PHE:HA	53:Cd:436:LEU:HD21	1.95	0.48
1:C1:745:U:O2	1:C1:749:C:N3	2.46	0.48
3:C3:68:G:H2'	3:C3:69:G:H8	1.78	0.48
5:CB:69:LYS:NZ	5:CB:276:GLN:O	2.45	0.48
9:CG:145:GLY:HA2	9:CG:167:GLN:HB2	1.95	0.48
13:CK:186:HIS:CD2	13:CK:228:LEU:HD11	2.49	0.48
18:CP:320:LEU:HD13	18:CP:361:HIS:HB3	1.96	0.48
28:LB:115:LYS:NZ	28:LB:129:ALA:O	2.47	0.48
1:C1:2404:G:H2'	1:C1:2405:A:H8	1.79	0.48
1:C1:2729:U:O4	1:C1:2745:G:O6	2.31	0.48
8:CF:223:LEU:HB3	8:CF:237:LEU:HD12	1.95	0.48
9:CG:133:VAL:HG22	9:CG:144:PHE:HB3	1.96	0.48
12:CJ:379:PRO:HB2	12:CJ:382:PRO:HD2	1.95	0.48
51:Lq:17:LEU:HA	51:Lq:18:ASP:HA	1.59	0.48
11:CI:298:SER:HB2	11:CI:301:GLN:HG3	1.96	0.47
12:CJ:177:HIS:HA	12:CJ:180:ILE:HG12	1.95	0.47
53:Cd:285:LEU:HG	53:Cd:404:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CA:72:SER:OG	4:CA:73:ARG:N	2.47	0.47
4:CA:254:ILE:HG22	23:CU:190:ILE:HD11	1.96	0.47
5:CB:207:ASP:HB3	5:CB:210:GLU:HB3	1.95	0.47
20:CR:198:LEU:HD22	20:CR:209:MET:HB3	1.96	0.47
33:LK:16:ARG:HA	33:LK:59:THR:HA	1.95	0.47
54:Ce:44:PRO:O	54:Ce:66:LYS:NZ	2.32	0.47
1:C1:421:U:O2'	47:Lf:90:PRO:O	2.31	0.47
1:C1:2416:G:O6	1:C1:2446:A:N1	2.47	0.47
4:CA:46:TYR:OH	4:CA:47:ARG:NH2	2.46	0.47
30:LE:49:ARG:NH1	47:Lf:109:ILE:O	2.47	0.47
35:LM:5:ASN:OD1	35:LM:5:ASN:N	2.46	0.47
44:LY:69:VAL:HG22	44:LY:81:VAL:HG12	1.96	0.47
45:Ld:54:THR:HB	45:Ld:85:ARG:HH12	1.79	0.47
47:Lf:74:THR:HG21	47:Lf:86:LYS:HD3	1.97	0.47
53:Cd:242:ARG:NH2	54:Ce:132:ARG:O	2.47	0.47
1:C1:369:C:O2'	1:C1:383:G:N2	2.46	0.47
1:C1:934:G:H3'	1:C1:1098:G:N2	2.28	0.47
1:C1:1885:G:H5"	1:C1:1886:C:H5	1.78	0.47
1:C1:2385:U:H3	1:C1:2565:G:H1	1.61	0.47
5:CB:108:TYR:HE2	5:CB:184:LEU:HD13	1.79	0.47
12:CJ:39:TRP:HD1	12:CJ:233:PHE:HB2	1.79	0.47
20:CR:127:GLU:HB2	20:CR:134:GLN:HE22	1.80	0.47
1:C1:638:G:O2'	1:C1:1417:A:OP1	2.33	0.47
1:C1:1308:A:O2'	47:Lf:79:ASN:OD1	2.31	0.47
1:C1:2980:U:H2'	1:C1:2981:A:H8	1.79	0.47
1:C1:3315:A:O2'	1:C1:3318:C:OP2	2.27	0.47
4:CA:139:ILE:HG13	4:CA:176:ILE:HD11	1.96	0.47
10:CH:448:ASP:OD1	10:CH:448:ASP:N	2.48	0.47
15:CM:111:LEU:HD23	15:CM:112:LEU:HD23	1.96	0.47
21:CS:68:PRO:C	21:CS:70:ASP:H	2.22	0.47
1:C1:727:C:H2'	1:C1:728:A:H8	1.80	0.47
1:C1:1272:U:H2'	1:C1:1273:A:C8	2.49	0.47
1:C1:2788:G:H2'	1:C1:2789:G:C8	2.50	0.47
5:CB:49:LEU:HG	7:CE:483:TYR:HB3	1.95	0.47
11:CI:221:ASN:OD1	11:CI:222:LYS:N	2.48	0.47
19:CQ:68:THR:HG21	19:CQ:100:ARG:HB2	1.96	0.47
28:LB:172:LEU:HD22	28:LB:334:LYS:HG2	1.96	0.47
1:C1:155:G:H2'	1:C1:156:G:C8	2.50	0.47
1:C1:574:G:H2'	1:C1:575:A:H8	1.79	0.47
1:C1:2738:A:H5'	51:Lq:161:LYS:HE2	1.96	0.47
1:C1:2921:C:N4	1:C1:2927:A:N6	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:CG:67:LEU:HB2	18:CP:434:ILE:HG23	1.96	0.47
10:CH:10:VAL:HG21	10:CH:63:ILE:HD12	1.96	0.47
12:CJ:266:ALA:HB1	12:CJ:269:ALA:HB3	1.95	0.47
18:CP:334:VAL:HG21	27:Cb:716:MET:HE3	1.97	0.47
27:Cb:107:ARG:HH11	27:Cb:185:LYS:HE2	1.80	0.47
27:Cb:456:ARG:O	27:Cb:459:ARG:NH2	2.48	0.47
33:LK:104:VAL:HB	33:LK:143:VAL:HG22	1.96	0.47
51:Lq:195:LYS:HE2	51:Lq:196:LYS:HE2	1.95	0.47
14:CL:37:LYS:HG2	14:CL:41:LYS:HE3	1.97	0.47
22:CT:501:ALA:O	22:CT:505:LEU:N	2.46	0.47
23:CU:257:LEU:O	23:CU:260:LYS:NZ	2.48	0.47
27:Cb:604:PHE:HB2	27:Cb:621:VAL:HG21	1.95	0.47
1:C1:231:A:H2'	1:C1:232:G:C8	2.49	0.47
1:C1:1196:U:H2'	1:C1:1197:A:C8	2.50	0.47
6:CC:263:THR:HG23	31:LG:175:LYS:HB2	1.97	0.47
18:CP:321:ALA:O	18:CP:325:ILE:HG13	2.15	0.47
27:Cb:129:ASP:HB3	27:Cb:287:LEU:HD23	1.97	0.47
27:Cb:135:ARG:HH12	27:Cb:459:ARG:CZ	2.27	0.47
34:LL:78:GLU:OE1	49:Li:29:ARG:NH1	2.48	0.47
36:LN:114:ARG:HD3	36:LN:137:PRO:HG3	1.96	0.47
1:C1:2300:C:H2'	1:C1:2301:C:C6	2.50	0.47
4:CA:82:GLU:O	49:Li:76:LYS:NZ	2.48	0.47
5:CB:288:THR:OG1	5:CB:289:ALA:N	2.45	0.47
6:CC:366:GLU:HA	6:CC:369:GLU:HB2	1.97	0.47
8:CF:87:ASP:O	8:CF:227:TRP:NE1	2.48	0.47
40:LS:13:HIS:HD2	40:LS:51:VAL:HG12	1.79	0.47
42:LV:76:HIS:CE1	42:LV:112:LYS:NZ	2.83	0.47
1:C1:562:U:H2'	1:C1:563:A:H8	1.80	0.46
1:C1:3195:C:H2'	1:C1:3196:G:H8	1.80	0.46
12:CJ:17:MET:O	12:CJ:64:TYR:N	2.47	0.46
20:CR:206:VAL:HG21	20:CR:226:LYS:HE2	1.97	0.46
28:LB:21:ARG:HG3	28:LB:270:GLN:HG2	1.96	0.46
2:C2:63:G:H22	2:C2:97:A:H2	1.63	0.46
7:CE:348:LEU:HD23	7:CE:352:LEU:HD13	1.96	0.46
44:LY:31:SER:HA	44:LY:48:PRO:HA	1.97	0.46
45:Ld:60:ASP:OD2	45:Ld:100:TYR:OH	2.27	0.46
1:C1:2874:U:H2'	1:C1:2875:G:O4'	2.15	0.46
2:C2:154:C:H2'	2:C2:155:A:C8	2.51	0.46
10:CH:308:LEU:O	10:CH:311:SER:OG	2.30	0.46
18:CP:376:LEU:HD11	18:CP:452:ARG:HB3	1.97	0.46
18:CP:455:LEU:HD21	18:CP:457:ALA:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Cb:237:TYR:HD2	27:Cb:267:GLN:HB3	1.80	0.46
44:LY:44:VAL:HG21	44:LY:118:LEU:HG	1.97	0.46
48:Lh:22:LYS:O	48:Lh:26:GLU:HG3	2.16	0.46
52:Cc:120:LEU:HD11	52:Cc:162:LEU:HD21	1.96	0.46
52:Cc:151:ASP:OD1	52:Cc:154:LYS:N	2.45	0.46
53:Cd:358:HIS:CE1	53:Cd:392:GLU:HG3	2.50	0.46
1:C1:361:A:OP2	53:Cd:21:LYS:NZ	2.33	0.46
1:C1:631:G:H5"	1:C1:1098:G:C8	2.50	0.46
1:C1:3072:C:OP2	32:LH:62:ARG:NH2	2.49	0.46
1:C1:3243:G:O2'	1:C1:3245:A:N6	2.49	0.46
3:C3:126:G:H2'	3:C3:127:G:H8	1.80	0.46
10:CH:436:LYS:HA	10:CH:436:LYS:HD3	1.67	0.46
13:CK:184:VAL:HG21	13:CK:195:LEU:HD12	1.97	0.46
1:C1:975:G:N2	1:C1:976:U:O4	2.49	0.46
1:C1:2385:U:H2'	1:C1:2386:A:H8	1.81	0.46
24:CX:102:ASN:HA	24:CX:105:LEU:HG	1.98	0.46
29:LC:211:ILE:HB	29:LC:234:THR:HG23	1.96	0.46
1:C1:191:A:N3	1:C1:211:G:O2'	2.46	0.46
1:C1:1163:U:O4	37:LO:22:SER:OG	2.31	0.46
1:C1:2921:C:N3	1:C1:2927:A:N1	2.63	0.46
1:C1:2972:C:OP2	17:CO:2:ALA:N	2.49	0.46
9:CG:27:ILE:HD12	24:CX:105:LEU:HD21	1.96	0.46
20:CR:198:LEU:HB3	20:CR:209:MET:HE3	1.97	0.46
30:LE:71:VAL:HG11	30:LE:169:LEU:HD21	1.97	0.46
53:Cd:357:ARG:HB3	53:Cd:394:GLY:HA3	1.97	0.46
2:C2:154:C:H5"	31:LG:184:LYS:HB3	1.98	0.46
28:LB:116:ARG:HB3	28:LB:176:LYS:HG3	1.98	0.46
29:LC:287:LEU:HD21	39:LQ:59:LYS:HB3	1.98	0.46
15:LF:32:ARG:HD2	15:LF:32:ARG:HA	1.70	0.46
38:LP:59:PRO:HG3	38:LP:76:TRP:CG	2.50	0.46
1:C1:189:G:N1	1:C1:192:A:OP2	2.46	0.46
1:C1:1049:C:H2'	1:C1:1050:C:C6	2.51	0.46
1:C1:1176:G:H2'	1:C1:1177:A:C8	2.51	0.46
1:C1:2918:C:H2'	1:C1:2919:G:C8	2.51	0.46
1:C1:3073:G:C4	26:Cz:38:ALA:HB2	2.49	0.46
1:C1:3117:C:H3'	53:Cd:303:ARG:NH1	2.30	0.46
10:CH:250:LEU:HD23	10:CH:283:PHE:HB2	1.98	0.46
15:CM:68:LYS:HB3	15:CM:68:LYS:HZ2	1.81	0.46
17:CO:92:GLY:O	28:LB:151:ARG:NH2	2.39	0.46
18:CP:465:ILE:HG21	18:CP:472:LYS:HD3	1.98	0.46
15:LF:146:ASN:OD1	15:LF:242:ASN:ND2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:Li:41:ALA:HB3	49:Li:50:ARG:HH22	1.80	0.46
1:C1:267:U:H2'	1:C1:268:A:C8	2.51	0.46
3:C3:61:A:C8	11:CI:275:GLY:HA3	2.51	0.46
5:CB:63:TRP:HE3	5:CB:244:LYS:HG2	1.81	0.46
6:CC:350:TYR:HE1	12:CJ:486:LEU:HB3	1.81	0.46
8:CF:41:PHE:CE2	8:CF:226:TYR:HB3	2.51	0.46
12:CJ:141:LEU:HA	12:CJ:144:CYS:HB3	1.97	0.46
17:CO:25:VAL:HG21	28:LB:352:LEU:HD23	1.97	0.46
21:CS:696:PHE:CE1	31:LG:68:LEU:HD21	2.51	0.46
27:Cb:148:MET:HE1	27:Cb:237:TYR:HB3	1.98	0.46
29:LC:361:LEU:HD11	41:LT:148:PRO:HG2	1.98	0.46
1:C1:1225:G:N2	1:C1:1252:A:O2'	2.46	0.46
1:C1:2432:C:C2	1:C1:2451:C:H4'	2.50	0.46
3:C3:58:A:H2	11:CI:263:VAL:HG22	1.81	0.46
8:CF:36:LYS:HB2	8:CF:36:LYS:HE3	1.60	0.46
12:CJ:15:ASN:O	12:CJ:66:THR:OG1	2.31	0.46
1:C1:643:A:H2'	1:C1:644:A:C8	2.50	0.45
1:C1:2299:C:H2'	1:C1:2300:C:C6	2.51	0.45
3:C3:71:U:N3	3:C3:131:G:N1	2.64	0.45
48:Lh:30:GLU:HG2	48:Lh:52:LEU:HD11	1.97	0.45
1:C1:526:G:N2	1:C1:544:U:O2	2.48	0.45
1:C1:975:G:H4'	1:C1:976:U:H5'	1.98	0.45
1:C1:2452:C:H4'	51:Lq:210:MET:HE1	1.98	0.45
1:C1:3189:G:H2'	1:C1:3190:G:H8	1.81	0.45
16:CN:174:SER:HB2	16:CN:181:LEU:HB2	1.98	0.45
27:Cb:321:LEU:HD21	27:Cb:371:ILE:HD13	1.97	0.45
28:LB:33:PRO:HD2	28:LB:44:THR:HG21	1.98	0.45
36:LN:106:VAL:HG11	36:LN:134:LEU:HD21	1.97	0.45
40:LS:95:ARG:HB2	40:LS:140:ILE:HD12	1.98	0.45
53:Cd:285:LEU:HD21	53:Cd:323:LEU:HD23	1.97	0.45
1:C1:31:C:H4'	36:LN:96:ARG:HG2	1.98	0.45
10:CH:436:LYS:HG3	28:LB:298:GLU:HG2	1.98	0.45
19:CQ:98:GLU:O	19:CQ:102:ARG:HG2	2.16	0.45
19:CQ:103:ARG:HA	19:CQ:106:VAL:HG12	1.98	0.45
27:Cb:181:LYS:HE2	27:Cb:181:LYS:H	1.81	0.45
32:LH:16:LEU:HD21	32:LH:83:THR:HG23	1.98	0.45
39:LQ:108:VAL:HG22	39:LQ:165:LEU:HD23	1.96	0.45
45:Ld:52:MET:O	45:Ld:85:ARG:NH2	2.50	0.45
47:Lf:15:HIS:O	47:Lf:97:GLY:N	2.41	0.45
1:C1:3188:U:H2'	1:C1:3189:G:C8	2.52	0.45
3:C3:51:C:H5"	7:CE:488:ASN:ND2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CA:112:THR:OG1	4:CA:249:SER:O	2.32	0.45
16:CN:104:LEU:HA	16:CN:107:VAL:HG22	1.99	0.45
27:Cb:170:ARG:HH12	27:Cb:174:LEU:HD11	1.81	0.45
28:LB:106:TRP:HB2	28:LB:133:TYR:CE2	2.52	0.45
32:LH:18:VAL:HG11	32:LH:53:ILE:HD11	1.97	0.45
1:C1:6:A:O3'	12:CJ:97:ARG:NH2	2.44	0.45
1:C1:373:U:OP2	53:Cd:60:ARG:NH2	2.49	0.45
1:C1:631:G:H5'	1:C1:1099:G:H1'	1.97	0.45
1:C1:1295:G:O2'	1:C1:1300:A:N1	2.49	0.45
2:C2:14:C:H5"	38:LP:123:PRO:HD3	1.99	0.45
4:CA:90:LEU:HD11	4:CA:102:MET:HE2	1.99	0.45
18:CP:317:ARG:NH2	18:CP:338:SER:O	2.50	0.45
20:CR:148:GLN:OE1	34:LL:86:PRO:HB3	2.16	0.45
27:Cb:207:MET:HA	27:Cb:207:MET:HE3	1.98	0.45
28:LB:19:ARG:HA	28:LB:19:ARG:HD3	1.74	0.45
1:C1:1270:U:O5'	26:Cz:40:ARG:NH2	2.49	0.45
14:CL:187:GLY:HA2	14:CL:188:ALA:HA	1.68	0.45
27:Cb:140:LYS:HB3	27:Cb:271:PHE:HD2	1.81	0.45
40:LS:48:LEU:HD23	41:LT:155:ALA:HB2	1.99	0.45
1:C1:137:C:H2'	1:C1:138:G:O4'	2.17	0.45
1:C1:190:G:N7	54:Ce:144:LYS:NZ	2.65	0.45
1:C1:424:G:H2'	1:C1:425:A:H8	1.81	0.45
1:C1:966:U:H2'	1:C1:967:U:H6	1.81	0.45
1:C1:1121:G:H2'	1:C1:1122:G:H8	1.82	0.45
1:C1:2306:U:H2'	1:C1:2307:A:C8	2.51	0.45
1:C1:2841:U:H2'	1:C1:2842:C:H6	1.81	0.45
7:CE:488:ASN:N	7:CE:488:ASN:OD1	2.49	0.45
8:CF:51:ASN:OD1	8:CF:51:ASN:N	2.50	0.45
28:LB:218:VAL:HG11	28:LB:329:VAL:HG13	1.98	0.45
29:LC:301:ARG:HD3	39:LQ:69:GLU:HG3	1.99	0.45
45:Ld:43:GLU:HA	45:Ld:46:LYS:HB3	1.99	0.45
52:Cc:201:TRP:HE1	52:Cc:248:SER:HB3	1.81	0.45
1:C1:367:A:H1'	44:LY:86:ARG:HE	1.82	0.45
1:C1:614:C:H2'	1:C1:615:A:C8	2.51	0.45
1:C1:642:C:H2'	1:C1:643:A:C8	2.52	0.45
1:C1:708:G:H2'	1:C1:709:G:H8	1.82	0.45
1:C1:979:A:H2'	1:C1:980:G:C8	2.52	0.45
1:C1:2917:C:H2'	1:C1:2918:C:C6	2.52	0.45
18:CP:308:ILE:HD13	18:CP:308:ILE:HA	1.85	0.45
18:CP:385:LEU:HD22	18:CP:453:VAL:HB	1.99	0.45
29:LC:35:ILE:HG22	29:LC:122:ALA:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:574:G:H2'	1:C1:575:A:C8	2.52	0.45
4:CA:139:ILE:HB	4:CA:179:VAL:HG22	1.99	0.45
23:CU:287:GLN:O	23:CU:291:GLU:HG3	2.17	0.45
29:LC:24:PRO:HB2	29:LC:26:VAL:HG12	1.99	0.45
53:Cd:202:LEU:HB2	53:Cd:253:TYR:CD2	2.50	0.45
1:C1:603:G:H2'	1:C1:604:G:H8	1.82	0.45
1:C1:643:A:H2'	1:C1:644:A:H8	1.81	0.45
1:C1:933:A:N3	1:C1:1096:U:O2'	2.44	0.45
1:C1:3105:C:H2'	1:C1:3106:G:H8	1.82	0.45
3:C3:128:C:H2'	3:C3:129:G:H8	1.82	0.45
7:CE:361:ILE:HD13	7:CE:411:LEU:HB3	1.99	0.45
7:CE:445:VAL:HA	7:CE:448:THR:HG22	1.99	0.45
8:CF:73:MET:HE1	8:CF:101:GLY:HA2	1.98	0.45
10:CH:465:GLU:OE1	19:CQ:103:ARG:NH2	2.50	0.45
16:CN:15:VAL:HG13	16:CN:61:ARG:HG3	1.99	0.45
18:CP:321:ALA:HB2	18:CP:342:LEU:HD21	1.98	0.45
20:CR:41:LYS:HE2	20:CR:41:LYS:HB2	1.87	0.45
33:LK:126:LYS:NZ	33:LK:155:ILE:O	2.49	0.45
52:Cc:117:ARG:HH21	52:Cc:200:ILE:HG22	1.82	0.45
52:Cc:203:ASP:HB3	52:Cc:253:ARG:HH12	1.83	0.45
3:C3:69:G:O6	3:C3:132:U:O4	2.35	0.44
7:CE:360:ILE:HG22	7:CE:410:THR:HG23	1.98	0.44
20:CR:47:GLN:H	20:CR:47:GLN:HG2	1.66	0.44
40:LS:16:THR:HG22	40:LS:18:ALA:H	1.81	0.44
48:Lh:38:LYS:HD3	48:Lh:49:ILE:HG13	2.00	0.44
1:C1:553:U:H2'	1:C1:554:G:C8	2.52	0.44
1:C1:694:U:OP1	1:C1:761:A:O2'	2.34	0.44
3:C3:71:U:H3	3:C3:130:G:H1	1.64	0.44
11:CI:189:MET:HB2	11:CI:262:ILE:HD13	1.99	0.44
12:CJ:136:ASP:OD1	12:CJ:139:ARG:NH1	2.43	0.44
16:CN:187:ASN:H	16:CN:210:THR:HG22	1.81	0.44
16:CN:197:MET:HE3	16:CN:206:THR:HG22	1.99	0.44
27:Cb:163:ALA:HB3	27:Cb:213:ILE:HA	1.99	0.44
29:LC:197:LYS:HB2	29:LC:202:ARG:HH11	1.82	0.44
36:LN:96:ARG:HD2	36:LN:96:ARG:HA	1.83	0.44
55:Cf:503:LYS:HD2	55:Cf:503:LYS:HA	1.69	0.44
1:C1:3077:C:OP2	13:CK:26:LYS:NZ	2.38	0.44
5:CB:48:ASN:ND2	5:CB:51:ALA:O	2.50	0.44
8:CF:24:GLU:H	8:CF:24:GLU:HG2	1.60	0.44
8:CF:99:THR:OG1	8:CF:99:THR:O	2.35	0.44
10:CH:327:VAL:HA	10:CH:330:VAL:HG12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:LC:114:ILE:HB	29:LC:119:LYS:HD2	1.98	0.44
31:LG:193:VAL:HG12	31:LG:195:LYS:HG2	1.99	0.44
36:LN:31:ARG:O	36:LN:65:ARG:NH2	2.50	0.44
1:C1:20:A:H2'	1:C1:21:G:C8	2.52	0.44
1:C1:253:U:N3	7:CE:368:ASN:OD1	2.50	0.44
1:C1:788:A:H61	1:C1:915:G:H22	1.64	0.44
1:C1:3118:A:OP2	53:Cd:303:ARG:NH2	2.47	0.44
6:CC:403:ARG:HG3	12:CJ:150:LEU:HD22	1.98	0.44
16:CN:199:VAL:HG23	16:CN:204:ALA:HB2	1.98	0.44
49:Li:25:LYS:HE2	49:Li:25:LYS:HB2	1.66	0.44
1:C1:497:U:H2'	1:C1:498:C:C6	2.53	0.44
1:C1:978:A:H2'	1:C1:979:A:C8	2.53	0.44
1:C1:1420:U:OP1	29:LC:77:ARG:NH2	2.47	0.44
1:C1:3022:G:O6	1:C1:3034:A:N6	2.50	0.44
4:CA:35:ARG:H	4:CA:87:ASN:ND2	2.16	0.44
13:CK:236:LYS:NZ	18:CP:474:ASN:HB3	2.32	0.44
27:Cb:187:THR:OG1	27:Cb:188:ASP:N	2.50	0.44
32:LH:13:PRO:HD2	32:LH:16:LEU:HD12	1.99	0.44
34:LL:62:THR:HG23	34:LL:64:LYS:H	1.82	0.44
45:Ld:80:ARG:HG2	45:Ld:106:VAL:HG11	2.00	0.44
1:C1:1260:A:O2'	8:CF:15:VAL:O	2.35	0.44
1:C1:2735:G:N2	1:C1:2741:U:O2	2.31	0.44
5:CB:259:ILE:O	5:CB:263:ILE:HG13	2.18	0.44
7:CE:178:PHE:O	7:CE:212:GLN:NE2	2.46	0.44
7:CE:243:ARG:HH22	7:CE:557:LEU:HD22	1.83	0.44
7:CE:486:PRO:HB2	7:CE:489:LYS:HG2	1.99	0.44
12:CJ:187:LYS:HB2	12:CJ:198:GLN:HB3	1.99	0.44
12:CJ:235:MET:HE3	12:CJ:235:MET:HB3	1.83	0.44
13:CK:241:ARG:HD2	13:CK:241:ARG:HA	1.81	0.44
31:LG:166:VAL:HG12	31:LG:169:LEU:HD12	1.99	0.44
51:Lq:26:ARG:HH22	51:Lq:208:ALA:HB1	1.83	0.44
1:C1:14:U:H3	2:C2:136:G:H21	1.65	0.44
1:C1:944:G:H2'	1:C1:945:G:H8	1.81	0.44
1:C1:2078:G:H2'	1:C1:2079:A:H8	1.82	0.44
3:C3:17:G:H2'	3:C3:18:G:H8	1.81	0.44
3:C3:140:G:H3'	11:CI:291:ARG:HH12	1.83	0.44
4:CA:228:ASP:OD1	4:CA:228:ASP:N	2.46	0.44
5:CB:52:ASP:OD1	5:CB:53:GLU:N	2.51	0.44
5:CB:233:VAL:HG23	5:CB:243:ILE:HD12	2.00	0.44
18:CP:383:ARG:HG3	18:CP:407:VAL:HG13	2.00	0.44
22:CT:260:GLY:O	22:CT:264:ARG:N	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LB:47:MET:HE2	28:LB:180:MET:SD	2.58	0.44
51:Lq:18:ASP:OD1	51:Lq:18:ASP:N	2.49	0.44
1:C1:91:G:N2	1:C1:95:A:H62	2.05	0.44
1:C1:403:U:H2'	1:C1:404:G:C8	2.53	0.44
1:C1:1235:U:H5'	33:LK:137:PHE:HE2	1.83	0.44
1:C1:1875:A:H2'	1:C1:1876:G:H8	1.82	0.44
1:C1:2419:G:H2'	1:C1:2421:A:H62	1.83	0.44
1:C1:3187:G:O6	28:LB:151:ARG:NH1	2.42	0.44
1:C1:3275:A:H2'	1:C1:3276:A:C8	2.53	0.44
3:C3:71:U:N3	3:C3:131:G:C6	2.85	0.44
10:CH:149:LEU:HA	10:CH:152:VAL:HG22	2.00	0.44
14:CL:71:GLU:HA	14:CL:74:ILE:HD12	1.98	0.44
18:CP:333:PRO:HA	18:CP:342:LEU:HD12	1.99	0.44
18:CP:444:PRO:HB3	18:CP:497:SER:HB2	2.00	0.44
19:CQ:108:TYR:HD1	19:CQ:111:ARG:HD3	1.83	0.44
27:Cb:422:VAL:HG21	27:Cb:427:ALA:HB2	1.99	0.44
27:Cb:490:VAL:HG12	27:Cb:505:VAL:HA	1.99	0.44
1:C1:745:U:H3	1:C1:748:U:H3	1.65	0.44
1:C1:2887:C:O2'	27:Cb:3:LYS:O	2.29	0.44
4:CA:40:SER:HB3	4:CA:52:LEU:HD13	2.00	0.44
7:CE:414:THR:HG23	7:CE:417:ALA:H	1.83	0.44
12:CJ:131:TYR:OH	12:CJ:140:ASP:OD2	2.30	0.44
13:CK:133:PHE:HE2	13:CK:148:LYS:HG2	1.83	0.44
18:CP:308:ILE:HD11	18:CP:364:LEU:HD22	2.00	0.44
19:CQ:17:LYS:HA	19:CQ:17:LYS:HD2	1.78	0.44
20:CR:32:ASN:OD1	20:CR:32:ASN:N	2.51	0.44
33:LK:103:SER:OG	33:LK:142:GLN:O	2.32	0.44
35:LM:15:GLU:HB3	40:LS:149:SER:HB2	2.00	0.44
50:Lj:64:MET:HB3	50:Lj:68:SER:HB3	2.00	0.44
54:Ce:21:THR:OG1	54:Ce:25:GLN:O	2.34	0.44
1:C1:231:A:H2'	1:C1:232:G:H8	1.83	0.43
1:C1:264:G:H2'	1:C1:265:A:H8	1.82	0.43
1:C1:439:C:H2'	1:C1:440:G:C8	2.53	0.43
1:C1:749:C:H2'	1:C1:750:G:C8	2.52	0.43
3:C3:68:G:H2'	3:C3:69:G:C8	2.53	0.43
4:CA:158:LEU:HD23	4:CA:158:LEU:HA	1.87	0.43
10:CH:244:HIS:CE1	27:Cb:591:LEU:HD11	2.53	0.43
27:Cb:259:LEU:HA	27:Cb:262:LEU:HD12	2.00	0.43
40:LS:124:LEU:HD11	41:LT:154:VAL:HG12	2.00	0.43
45:Ld:28:LEU:HD11	45:Ld:40:ALA:HB2	2.00	0.43
1:C1:181:A:H3'	44:LY:45:ARG:HH22	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2076:C:H2'	1:C1:2077:G:C8	2.52	0.43
1:C1:2813:C:H2'	1:C1:2814:G:C8	2.48	0.43
4:CA:81:ALA:HB3	4:CA:107:VAL:HG11	2.00	0.43
4:CA:111:PRO:HG3	23:CU:199:ALA:HB1	1.99	0.43
5:CB:113:ALA:HA	5:CB:121:ARG:HH22	1.83	0.43
10:CH:184:ARG:NH1	10:CH:189:ALA:O	2.52	0.43
11:CI:191:ILE:HG23	11:CI:231:ALA:HB3	1.99	0.43
29:LC:36:VAL:HG21	29:LC:251:LEU:HD21	1.98	0.43
29:LC:75:ILE:HD12	29:LC:75:ILE:HA	1.90	0.43
31:LG:219:SER:O	31:LG:223:GLU:HG2	2.18	0.43
42:LV:89:ARG:CZ	42:LV:95:LEU:HD11	2.49	0.43
50:Lj:27:LEU:HA	50:Lj:34:CYS:HA	2.00	0.43
1:C1:247:A:H2'	1:C1:248:G:C8	2.52	0.43
4:CA:273:LYS:HB3	4:CA:273:LYS:HE2	1.75	0.43
5:CB:98:CYS:HB2	5:CB:150:HIS:CD2	2.53	0.43
10:CH:193:VAL:HG22	56:CH:701:GTP:H5'	2.00	0.43
13:CK:7:ILE:HD13	13:CK:7:ILE:HA	1.90	0.43
20:CR:199:VAL:HG11	20:CR:234:LEU:HD13	1.99	0.43
40:LS:131:LYS:HE3	40:LS:131:LYS:HB2	1.85	0.43
1:C1:2431:G:N1	1:C1:2438:C:N3	2.66	0.43
1:C1:3078:U:H1'	1:C1:3079:A:H5"	1.99	0.43
1:C1:3314:U:O2'	1:C1:3315:A:N7	2.52	0.43
9:CG:108:PHE:CE1	9:CG:166:ARG:HG2	2.54	0.43
12:CJ:475:LEU:HD23	12:CJ:475:LEU:HA	1.89	0.43
15:CM:67:GLU:OE2	15:CM:138:PRO:HG3	2.18	0.43
16:CN:57:ARG:NH2	42:LV:126:GLU:O	2.51	0.43
31:LG:85:LEU:HD23	31:LG:181:ALA:HB1	1.99	0.43
51:Lq:26:ARG:HG3	51:Lq:210:MET:HB3	2.01	0.43
1:C1:404:G:OP1	38:LP:63:TYR:OH	2.34	0.43
1:C1:916:U:H2'	1:C1:917:A:H8	1.83	0.43
1:C1:2458:U:H2'	1:C1:2459:C:C6	2.54	0.43
6:CC:246:LEU:HD12	6:CC:247:ILE:HG13	2.00	0.43
10:CH:281:MET:HE2	10:CH:281:MET:HB3	1.89	0.43
10:CH:447:TYR:HE2	16:CN:79:GLN:HE21	1.67	0.43
12:CJ:42:ILE:HD12	12:CJ:68:ASP:HB2	2.01	0.43
18:CP:545:LYS:HD2	18:CP:545:LYS:HA	1.71	0.43
33:LK:88:PRO:HA	33:LK:89:PRO:HD3	1.80	0.43
35:LM:19:VAL:HA	35:LM:29:ALA:HA	2.01	0.43
47:Lf:45:PHE:HZ	47:Lf:109:ILE:HD11	1.84	0.43
48:Lh:54:LYS:HA	48:Lh:54:LYS:HD3	1.78	0.43
1:C1:650:C:H2'	1:C1:651:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2570:U:N3	1:C1:2758:G:C6	2.87	0.43
5:CB:237:PRO:HB2	11:CI:286:ASN:HD21	1.84	0.43
18:CP:478:LYS:HE3	18:CP:478:LYS:HB3	1.74	0.43
19:CQ:17:LYS:O	19:CQ:30:ARG:NH2	2.44	0.43
27:Cb:136:THR:HA	27:Cb:140:LYS:NZ	2.33	0.43
27:Cb:164:LEU:HB2	27:Cb:235:ILE:HG21	2.00	0.43
30:LE:76:LEU:HB2	30:LE:80:VAL:HG23	2.00	0.43
37:LO:132:GLN:HB3	37:LO:135:ARG:HG3	1.99	0.43
45:Ld:83:ILE:HD12	45:Ld:101:VAL:HG22	2.00	0.43
51:Lq:10:ARG:HH22	51:Lq:176:GLN:HB3	1.83	0.43
51:Lq:11:GLN:NE2	51:Lq:15:GLU:OE1	2.42	0.43
54:Ce:83:LEU:HD13	54:Ce:113:LEU:HD13	2.00	0.43
1:C1:613:U:O2	1:C1:1381:A:O2'	2.31	0.43
1:C1:934:G:H3'	1:C1:1098:G:H21	1.84	0.43
1:C1:955:U:OP1	39:LQ:44:ARG:NH2	2.52	0.43
1:C1:1174:C:OP1	13:CK:43:ARG:NH1	2.48	0.43
1:C1:2836:G:H2'	1:C1:2837:C:C6	2.54	0.43
1:C1:2837:C:H2'	1:C1:2838:U:C6	2.54	0.43
11:CI:287:LYS:O	11:CI:291:ARG:HG2	2.19	0.43
14:CL:387:PHE:H	14:CL:397:ALA:HB2	1.84	0.43
16:CN:186:VAL:HG23	16:CN:193:ILE:HD12	2.01	0.43
27:Cb:230:LEU:HD12	27:Cb:230:LEU:HA	1.90	0.43
29:LC:4:ARG:HA	29:LC:5:PRO:HD3	1.90	0.43
30:LE:69:ARG:O	30:LE:90:ASN:ND2	2.52	0.43
36:LN:114:ARG:HH21	36:LN:157:LYS:HG2	1.84	0.43
52:Cc:175:ILE:HB	52:Cc:185:ILE:HB	2.00	0.43
1:C1:388:A:P	53:Cd:431:ARG:HH12	2.41	0.43
1:C1:2319:A:H2'	1:C1:2320:A:C8	2.54	0.43
1:C1:3105:C:H2'	1:C1:3106:G:C8	2.53	0.43
2:C2:9:A:H2'	2:C2:10:A:C8	2.54	0.43
2:C2:95:G:C2	50:Lj:79:ARG:HD2	2.54	0.43
3:C3:25:U:N3	5:CB:173:LYS:HG3	2.34	0.43
5:CB:52:ASP:O	5:CB:56:THR:N	2.50	0.43
5:CB:52:ASP:H	7:CE:354:LYS:NZ	2.17	0.43
10:CH:392:LYS:HB3	10:CH:392:LYS:HE3	1.72	0.43
11:CI:194:LEU:HD22	11:CI:198:PHE:HB3	2.00	0.43
23:CU:205:LEU:H	23:CU:205:LEU:HD23	1.84	0.43
27:Cb:168:PRO:HG3	27:Cb:246:LEU:HG	2.01	0.43
1:C1:2955:U:H2'	1:C1:2956:C:C6	2.53	0.43
2:C2:63:G:O2'	48:Lh:54:LYS:NZ	2.36	0.43
13:CK:203:ASN:ND2	13:CK:216:THR:OG1	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LB:95:THR:OG1	28:LB:98:GLY:O	2.26	0.43
53:Cd:183:LEU:HD11	53:Cd:323:LEU:HD12	2.01	0.43
1:C1:909:C:H2'	1:C1:910:A:C8	2.54	0.43
1:C1:976:U:C2	1:C1:1036:A:N7	2.87	0.43
1:C1:3319:C:H2'	1:C1:3320:C:C6	2.53	0.43
6:CC:263:THR:HG1	49:Li:55:GLU:CD	2.27	0.43
6:CC:396:TRP:HB2	12:CJ:193:LYS:HA	2.01	0.43
6:CC:406:ARG:NH2	12:CJ:147:MET:SD	2.92	0.43
9:CG:154:ALA:HB1	9:CG:163:VAL:HG23	2.01	0.43
16:CN:121:LEU:O	16:CN:139:ARG:NH2	2.52	0.43
31:LG:189:LEU:HD23	31:LG:189:LEU:HA	1.82	0.43
1:C1:1322:C:OP2	46:Le:62:LYS:NZ	2.46	0.42
1:C1:2841:U:H2'	1:C1:2842:C:C6	2.54	0.42
5:CB:102:ALA:HA	5:CB:130:ILE:HG22	2.01	0.42
10:CH:75:PRO:HB2	10:CH:244:HIS:ND1	2.34	0.42
16:CN:14:GLY:O	16:CN:61:ARG:NH1	2.52	0.42
19:CQ:95:ARG:O	19:CQ:99:ILE:HG13	2.19	0.42
37:LO:66:ASN:HA	37:LO:67:PRO:HD3	1.92	0.42
46:Le:96:GLU:HG3	46:Le:122:ASN:HD21	1.84	0.42
52:Cc:129:LYS:H	52:Cc:129:LYS:HG2	1.62	0.42
52:Cc:189:ILE:HG23	52:Cc:193:MET:HE3	2.00	0.42
1:C1:194:G:OP1	1:C1:213:G:O2'	2.34	0.42
1:C1:434:G:H2'	1:C1:435:C:C6	2.53	0.42
1:C1:727:C:H2'	1:C1:728:A:C8	2.54	0.42
1:C1:796:G:H5'	50:Lj:16:HIS:CE1	2.53	0.42
1:C1:1072:G:N2	1:C1:1073:G:N2	2.67	0.42
1:C1:1884:G:N3	1:C1:2294:A:C5	2.87	0.42
1:C1:2772:G:H2'	1:C1:2773:G:H8	1.83	0.42
1:C1:3323:C:N4	1:C1:3326:C:OP2	2.53	0.42
2:C2:130:C:H2'	2:C2:131:G:C8	2.54	0.42
5:CB:89:LEU:HD13	5:CB:89:LEU:HA	1.84	0.42
7:CE:172:MET:HG2	7:CE:176:LEU:HD13	2.01	0.42
8:CF:192:TYR:HD2	8:CF:194:ILE:HG22	1.84	0.42
9:CG:172:GLU:OE1	9:CG:175:ARG:NH2	2.52	0.42
13:CK:65:ILE:HD12	13:CK:65:ILE:HA	1.82	0.42
19:CQ:24:ASN:HA	42:LV:119:PRO:HD3	2.01	0.42
19:CQ:53:LYS:HG2	19:CQ:57:LYS:HE2	2.01	0.42
28:LB:219:ILE:HB	28:LB:338:THR:HB	2.01	0.42
33:LK:122:SER:OG	33:LK:123:LYS:N	2.52	0.42
54:Ce:107:HIS:NE2	54:Ce:111:GLN:OE1	2.52	0.42
1:C1:508:G:OP1	15:LF:73:ARG:NE	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:3158:U:C4	35:LM:121:MET:HG3	2.54	0.42
4:CA:116:TYR:HB2	4:CA:243:ILE:HD11	2.00	0.42
5:CB:267:VAL:HA	5:CB:271:VAL:HB	2.01	0.42
5:CB:274:LYS:HB3	5:CB:275:TRP:H	1.48	0.42
7:CE:268:ARG:NH2	7:CE:436:ASP:OD1	2.44	0.42
9:CG:116:LYS:HG2	9:CG:159:PRO:HA	2.01	0.42
10:CH:101:LYS:O	10:CH:105:GLU:HG3	2.19	0.42
28:LB:113:GLU:HB2	28:LB:177:ALA:HB2	2.00	0.42
30:LE:191:LYS:NZ	37:LO:4:PHE:O	2.52	0.42
36:LN:137:PRO:O	36:LN:143:ARG:NH1	2.52	0.42
53:Cd:313:LEU:HD23	53:Cd:346:LEU:HB2	2.01	0.42
1:C1:144:U:P	36:LN:49:ARG:HH22	2.42	0.42
1:C1:2816:U:OP1	13:CK:107:LYS:NZ	2.43	0.42
1:C1:2921:C:H42	1:C1:2927:A:N6	2.18	0.42
1:C1:3274:U:H5”	19:CQ:50:LYS:HZ2	1.84	0.42
6:CC:327:TRP:HB3	6:CC:330:GLU:HB2	2.01	0.42
12:CJ:39:TRP:CD1	12:CJ:233:PHE:HB2	2.54	0.42
13:CK:247:ASN:HB3	13:CK:256:ASN:HB2	2.02	0.42
30:LE:167:LYS:HE2	30:LE:167:LYS:HB2	1.93	0.42
52:Cc:127:MET:SD	52:Cc:155:VAL:HG23	2.59	0.42
1:C1:597:G:N1	1:C1:1319:G:OP1	2.41	0.42
1:C1:1044:A:N3	41:LT:130:ARG:NH2	2.68	0.42
1:C1:2078:G:H2’	1:C1:2079:A:C8	2.55	0.42
2:C2:57:C:H4’	2:C2:63:G:N7	2.35	0.42
13:CK:34:LYS:NZ	13:CK:38:ASN:OD1	2.39	0.42
20:CR:216:ASN:HD21	20:CR:220:GLN:HG3	1.85	0.42
27:Cb:117:GLN:O	27:Cb:121:ILE:HG12	2.19	0.42
32:LH:92:TYR:HB3	32:LH:181:ILE:HG23	2.01	0.42
40:LS:1:MET:HE3	40:LS:1:MET:HB2	1.81	0.42
40:LS:106:MET:HE3	40:LS:106:MET:HB3	1.85	0.42
40:LS:140:ILE:HD13	40:LS:140:ILE:HA	1.85	0.42
53:Cd:426:LYS:H	53:Cd:426:LYS:HG2	1.70	0.42
1:C1:1210:A:OP1	8:CF:203:SER:OG	2.32	0.42
1:C1:3203:C:H2’	1:C1:3204:G:C8	2.55	0.42
2:C2:71:A:H2’	44:LY:50:ARG:NH1	2.35	0.42
8:CF:41:PHE:CD2	8:CF:226:TYR:HB3	2.55	0.42
10:CH:421:LEU:HD13	28:LB:69:LYS:HD3	2.01	0.42
28:LB:292:GLU:HA	28:LB:305:LYS:HD3	2.02	0.42
31:LG:161:ASP:HB2	36:LN:41:ARG:HH12	1.84	0.42
42:LV:41:VAL:HA	42:LV:60:VAL:HG12	2.00	0.42
49:Li:41:ALA:HB1	49:Li:46:THR:HG21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:2556:G:H2'	1:C1:2557:U:C6	2.54	0.42
1:C1:3014:U:O2'	1:C1:3016:G:OP1	2.37	0.42
1:C1:3031:G:H5'	45:Ld:70:GLN:HE21	1.85	0.42
1:C1:3144:C:H4'	37:LO:178:ARG:HH22	1.84	0.42
10:CH:391:LYS:O	16:CN:43:GLN:NE2	2.51	0.42
15:CM:116:GLN:N	15:CM:119:ASN:HD21	2.18	0.42
18:CP:402:MET:H	18:CP:402:MET:HG2	1.68	0.42
18:CP:458:PRO:O	18:CP:487:GLN:NE2	2.48	0.42
28:LB:93:ILE:HG22	28:LB:156:CYS:HA	2.01	0.42
29:LC:148:GLU:O	29:LC:151:LEU:HB2	2.19	0.42
36:LN:31:ARG:NH1	36:LN:124:ASP:OD2	2.52	0.42
38:LP:119:VAL:HG22	38:LP:146:ILE:HG12	2.02	0.42
42:LV:47:ARG:HD2	42:LV:50:ARG:HB2	2.02	0.42
1:C1:1171:C:N3	1:C1:1297:U:C2	2.87	0.42
1:C1:3192:C:H2'	1:C1:3193:G:C8	2.55	0.42
2:C2:70:G:OP1	44:LY:120:ARG:NH2	2.53	0.42
3:C3:4:C:N3	15:CM:66:ARG:NH1	2.68	0.42
3:C3:141:U:OP2	11:CI:291:ARG:NH1	2.51	0.42
5:CB:87:HIS:ND1	5:CB:258:ASN:OD1	2.52	0.42
9:CG:59:VAL:HG11	9:CG:64:LEU:HD13	2.01	0.42
10:CH:5:LYS:HE2	10:CH:5:LYS:HB3	1.90	0.42
10:CH:63:ILE:HD11	10:CH:149:LEU:HD13	2.01	0.42
10:CH:361:LEU:HD12	10:CH:361:LEU:HA	1.92	0.42
16:CN:61:ARG:HD3	42:LV:133:SER:HA	2.01	0.42
15:LF:134:LYS:HE2	15:LF:134:LYS:HB2	1.82	0.42
32:LH:3:TYR:OH	32:LH:62:ARG:NH1	2.46	0.42
38:LP:43:ARG:HG2	38:LP:43:ARG:HH11	1.84	0.42
53:Cd:189:ASN:OD1	53:Cd:189:ASN:N	2.41	0.42
1:C1:100:A:H2'	1:C1:101:G:N3	2.34	0.42
1:C1:194:G:H2'	1:C1:195:G:H8	1.84	0.42
1:C1:399:A:C2	2:C2:17:A:H1'	2.55	0.42
1:C1:697:A:N6	1:C1:736:A:O3'	2.53	0.42
1:C1:2455:U:O2'	1:C1:2456:A:H5"	2.20	0.42
1:C1:3192:C:H2'	1:C1:3193:G:H8	1.84	0.42
1:C1:3265:A:H5'	45:Ld:111:GLY:H	1.84	0.42
9:CG:84:ILE:HG23	9:CG:168:ALA:HB1	2.00	0.42
10:CH:279:ASN:ND2	27:Cb:511:ARG:HH22	2.17	0.42
15:CM:242:ASN:HA	15:CM:245:ILE:HG22	2.02	0.42
36:LN:103:GLU:HB3	36:LN:160:GLU:HB2	2.02	0.42
44:LY:48:PRO:O	44:LY:114:ARG:NH2	2.52	0.42
1:C1:115:A:N6	1:C1:149:U:C2	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:506:G:O3'	15:LF:66:ARG:NH2	2.53	0.42
10:CH:228:LEU:HA	10:CH:231:MET:HE2	2.02	0.42
10:CH:301:MET:SD	10:CH:301:MET:N	2.92	0.42
18:CP:495:ILE:HD12	18:CP:495:ILE:H	1.85	0.42
23:CU:319:LYS:HB2	23:CU:319:LYS:HE2	1.92	0.42
54:Ce:30:ASN:ND2	54:Ce:44:PRO:HG2	2.35	0.42
1:C1:181:A:P	44:LY:45:ARG:HH21	2.43	0.41
1:C1:713:G:C5	1:C1:723:G:C2	3.08	0.41
2:C2:97:A:OP1	48:Lh:68:ARG:NH1	2.53	0.41
4:CA:114:LYS:HB3	4:CA:243:ILE:HB	2.01	0.41
8:CF:20:ARG:HD2	8:CF:20:ARG:HA	1.79	0.41
9:CG:64:LEU:HD11	18:CP:434:ILE:HG22	2.02	0.41
18:CP:409:PHE:CE2	18:CP:434:ILE:HD12	2.55	0.41
18:CP:422:ILE:HG23	18:CP:426:HIS:CE1	2.55	0.41
23:CU:215:SER:HB3	23:CU:261:GLU:OE1	2.20	0.41
23:CU:258:LEU:HD23	23:CU:258:LEU:HA	1.88	0.41
36:LN:36:ILE:HD11	36:LN:105:ARG:HB3	2.02	0.41
1:C1:380:G:H4'	38:LP:18:ARG:HB2	2.02	0.41
1:C1:575:A:H5"	47:Lf:72:LYS:HD3	2.00	0.41
1:C1:3118:A:H2'	1:C1:3119:C:C6	2.54	0.41
6:CC:326:LEU:O	12:CJ:128:ARG:NH1	2.53	0.41
9:CG:127:PRO:HD2	9:CG:130:SER:HB3	2.01	0.41
18:CP:453:VAL:HG23	18:CP:508:ILE:HG23	2.01	0.41
28:LB:105:VAL:HG22	28:LB:148:GLU:HB3	2.02	0.41
28:LB:159:VAL:HG22	28:LB:192:LYS:HD3	2.01	0.41
31:LG:223:GLU:HG2	31:LG:223:GLU:H	1.78	0.41
36:LN:192:LYS:HE2	36:LN:192:LYS:HB3	1.74	0.41
1:C1:2944:U:H2'	1:C1:2945:A:C8	2.55	0.41
5:CB:163:LEU:HD23	5:CB:163:LEU:HA	1.85	0.41
14:CL:438:TYR:O	14:CL:440:ILE:N	2.53	0.41
18:CP:552:MET:HB2	18:CP:554:LYS:HZ2	1.86	0.41
27:Cb:833:LYS:HB2	27:Cb:836:LEU:HB2	2.02	0.41
42:LV:24:ILE:HD13	42:LV:24:ILE:HA	1.90	0.41
42:LV:82:ARG:HD3	42:LV:119:PRO:HG2	2.02	0.41
52:Cc:48:LEU:HD23	52:Cc:48:LEU:HA	1.89	0.41
1:C1:655:U:H2'	1:C1:656:U:C6	2.55	0.41
1:C1:2774:G:H2'	1:C1:2775:A:H8	1.85	0.41
1:C1:2961:C:O2'	28:LB:99:LEU:O	2.33	0.41
6:CC:241:LYS:NZ	6:CC:250:ASP:OD1	2.53	0.41
11:CI:188:VAL:O	11:CI:263:VAL:N	2.49	0.41
27:Cb:133:MET:HE3	27:Cb:275:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Cb:381:TYR:HD2	27:Cb:538:THR:HG21	1.86	0.41
28:LB:126:LYS:HE3	28:LB:126:LYS:HB3	1.96	0.41
30:LE:114:VAL:HG21	30:LE:169:LEU:HD13	2.02	0.41
35:LM:17:GLY:HA2	35:LM:72:LEU:HD22	2.02	0.41
40:LS:5:GLN:HB2	40:LS:7:TYR:CE1	2.55	0.41
50:Lj:60:GLY:HA2	50:Lj:64:MET:HE2	2.01	0.41
1:C1:3235:A:H2'	1:C1:3236:A:C8	2.55	0.41
8:CF:202:ASP:OD1	8:CF:202:ASP:N	2.42	0.41
14:CL:277:PRO:O	14:CL:279:ALA:N	2.53	0.41
15:CM:71:LEU:HD21	15:CM:135:ILE:HG23	2.02	0.41
18:CP:385:LEU:HD13	18:CP:453:VAL:HG12	2.01	0.41
20:CR:214:LYS:HG2	20:CR:215:LEU:HG	2.02	0.41
26:Cz:30:GLN:H	26:Cz:30:GLN:HG2	1.64	0.41
27:Cb:446:GLN:HB2	27:Cb:449:ILE:HG12	2.02	0.41
55:Cf:528:GLU:O	55:Cf:532:ARG:HG3	2.20	0.41
1:C1:926:C:H2'	1:C1:927:C:C6	2.55	0.41
1:C1:1088:G:H2'	1:C1:1089:A:C8	2.56	0.41
1:C1:2077:G:H2'	1:C1:2078:G:H8	1.85	0.41
4:CA:40:SER:HB2	4:CA:44:VAL:HG11	2.03	0.41
4:CA:134:LYS:O	4:CA:173:LYS:NZ	2.53	0.41
7:CE:352:LEU:HD21	7:CE:410:THR:HG21	2.03	0.41
7:CE:353:LYS:HG3	7:CE:382:LEU:HD11	2.03	0.41
12:CJ:393:LYS:HA	12:CJ:393:LYS:HD3	1.87	0.41
18:CP:324:LEU:HB3	18:CP:329:VAL:HB	2.03	0.41
27:Cb:513:GLU:HA	27:Cb:516:ASN:ND2	2.35	0.41
28:LB:39:LYS:HB3	28:LB:39:LYS:HE2	1.88	0.41
31:LG:222:LYS:HA	31:LG:226:LEU:HB2	2.03	0.41
34:LL:87:ARG:NH2	34:LL:88:LEU:HD13	2.36	0.41
40:LS:45:LEU:HD12	40:LS:45:LEU:HA	1.89	0.41
1:C1:5:G:O3'	12:CJ:93:ARG:NH2	2.47	0.41
1:C1:957:G:H2'	1:C1:958:A:H8	1.86	0.41
1:C1:1344:G:H2'	1:C1:1345:A:C8	2.56	0.41
1:C1:2759:A:N1	9:CG:61:ARG:NH2	2.47	0.41
1:C1:2836:G:H2'	1:C1:2837:C:H6	1.86	0.41
3:C3:65:G:H21	3:C3:143:A:N6	2.18	0.41
4:CA:63:ARG:HE	4:CA:63:ARG:HB2	1.54	0.41
12:CJ:49:ASP:HB3	12:CJ:52:LYS:HB2	2.02	0.41
14:CL:66:LEU:HA	14:CL:69:ARG:HG2	2.02	0.41
15:CM:92:VAL:HG22	15:CM:140:VAL:HG22	2.02	0.41
15:CM:237:ARG:HB3	15:CM:240:HIS:HB2	2.01	0.41
27:Cb:564:ILE:HD13	27:Cb:564:ILE:HA	1.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:LB:47:MET:HB2	28:LB:165:THR:HG21	2.03	0.41
31:LG:94:PHE:CZ	31:LG:188:ARG:HG2	2.56	0.41
34:LL:102:LYS:HE3	34:LL:102:LYS:HB2	1.74	0.41
42:LV:89:ARG:NH1	42:LV:122:LYS:HE3	2.36	0.41
54:Ce:7:TRP:HB2	54:Ce:46:ALA:HB1	2.03	0.41
1:C1:448:A:H3'	1:C1:449:U:H4'	2.03	0.41
1:C1:683:C:O2'	1:C1:684:G:N7	2.48	0.41
1:C1:966:U:H2'	1:C1:967:U:C6	2.55	0.41
9:CG:70:CYS:HB3	9:CG:85:THR:HG21	2.03	0.41
12:CJ:415:ILE:HD11	12:CJ:417:HIS:O	2.21	0.41
28:LB:85:VAL:HG23	28:LB:166:GLN:HE21	1.86	0.41
15:LF:53:ARG:HE	15:LF:53:ARG:HB2	1.69	0.41
39:LQ:149:LEU:HD23	39:LQ:153:GLN:HB3	2.03	0.41
54:Ce:31:GLU:H	54:Ce:31:GLU:HG3	1.70	0.41
1:C1:713:G:C6	1:C1:723:G:C2	3.09	0.41
1:C1:1171:C:C4	1:C1:1297:U:O2	2.74	0.41
1:C1:1251:U:H1'	1:C1:1254:C:H5	1.85	0.41
1:C1:1272:U:OP1	8:CF:8:ARG:HD2	2.21	0.41
1:C1:1305:C:H4'	40:LS:1:MET:HA	2.03	0.41
1:C1:1405:C:H2'	1:C1:1406:C:C6	2.56	0.41
1:C1:3254:A:H5"	28:LB:175:LYS:HG3	2.03	0.41
6:CC:306:TYR:HB3	31:LG:117:THR:HG21	2.02	0.41
7:CE:116:LEU:HD23	7:CE:134:MET:HE1	2.03	0.41
7:CE:277:GLU:OE1	7:CE:277:GLU:N	2.54	0.41
9:CG:21:THR:HB	9:CG:95:ARG:HB3	2.01	0.41
9:CG:158:ASP:OD1	9:CG:159:PRO:HD2	2.20	0.41
23:CU:338:LYS:HA	23:CU:338:LYS:HE2	2.03	0.41
27:Cb:270:LEU:HD21	27:Cb:279:LEU:HD21	2.03	0.41
15:LF:237:ARG:HD2	15:LF:241:ILE:HD12	2.03	0.41
31:LG:97:LEU:HB3	31:LG:192:LEU:HD11	2.02	0.41
32:LH:151:ASN:OD1	32:LH:151:ASN:N	2.54	0.41
40:LS:169:ARG:HA	40:LS:170:PRO:HD3	1.93	0.41
42:LV:36:LEU:HB3	42:LV:62:ALA:HB1	2.02	0.41
46:Le:76:LEU:HD12	46:Le:76:LEU:HA	1.95	0.41
52:Cc:203:ASP:OD1	52:Cc:203:ASP:N	2.36	0.41
1:C1:1045:G:OP2	1:C1:1045:G:N2	2.45	0.41
1:C1:2412:A:H2'	1:C1:2413:G:C8	2.55	0.41
1:C1:2437:G:H3'	1:C1:2438:C:C6	2.56	0.41
1:C1:3041:C:O2'	1:C1:3272:U:OP1	2.27	0.41
3:C3:34:C:H2'	3:C3:35:G:H8	1.86	0.41
4:CA:137:ARG:NH1	4:CA:167:GLN:HG2	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CA:259:LYS:HE2	4:CA:259:LYS:HB2	1.90	0.41
20:CR:17:ILE:HD13	20:CR:17:ILE:HA	1.90	0.41
29:LC:287:LEU:HD22	39:LQ:56:LEU:HD12	2.03	0.41
40:LS:73:LYS:NZ	40:LS:97:THR:O	2.54	0.41
48:Lh:48:LYS:HB2	48:Lh:48:LYS:HE2	1.79	0.41
1:C1:603:G:H2'	1:C1:604:G:C8	2.56	0.40
1:C1:694:U:H1'	1:C1:735:G:H1'	2.04	0.40
1:C1:1185:A:H61	1:C1:1282:G:H1'	1.86	0.40
1:C1:1196:U:H2'	1:C1:1197:A:H8	1.87	0.40
1:C1:1386:G:N2	1:C1:1389:A:OP2	2.32	0.40
1:C1:2091:U:C2	1:C1:2287:G:C2	3.08	0.40
1:C1:2928:C:H5'	9:CG:149:ARG:NH2	2.36	0.40
1:C1:2947:U:H2'	1:C1:2948:G:C8	2.56	0.40
1:C1:2968:A:N1	1:C1:3000:C:O2'	2.45	0.40
1:C1:3016:G:H2'	1:C1:3017:C:C6	2.56	0.40
3:C3:56:A:H4'	11:CI:193:ARG:HE	1.86	0.40
4:CA:294:ARG:HA	4:CA:294:ARG:HD3	1.83	0.40
6:CC:149:TYR:OH	7:CE:571:ARG:NH2	2.54	0.40
7:CE:437:ASP:HB3	7:CE:440:ASP:HB3	2.03	0.40
10:CH:297:LEU:HD23	10:CH:297:LEU:H	1.86	0.40
13:CK:164:ARG:HD2	13:CK:168:TYR:O	2.20	0.40
16:CN:111:ASN:HB2	16:CN:156:ASN:ND2	2.37	0.40
27:Cb:10:PRO:HD3	27:Cb:376:LYS:HD2	2.02	0.40
32:LH:127:LYS:HB3	32:LH:127:LYS:HE3	1.90	0.40
33:LK:102:LYS:HB3	33:LK:102:LYS:HE2	1.90	0.40
35:LM:73:PRO:HG2	35:LM:76:ALA:HB2	2.03	0.40
46:Le:67:MET:HE3	46:Le:67:MET:HB2	1.88	0.40
54:Ce:28:CYS:N	54:Ce:36:GLY:O	2.40	0.40
1:C1:21:G:H3'	1:C1:22:G:H8	1.86	0.40
1:C1:202:A:O2'	1:C1:204:A:OP2	2.34	0.40
1:C1:290:U:H5"	1:C1:291:G:H5'	2.04	0.40
1:C1:1151:A:H2'	1:C1:1152:A:C8	2.56	0.40
1:C1:2403:A:H2'	1:C1:2404:G:C8	2.56	0.40
1:C1:2768:C:H2'	1:C1:2769:A:C8	2.55	0.40
2:C2:81:U:H2'	2:C2:82:U:C6	2.57	0.40
10:CH:366:ALA:HA	16:CN:167:ILE:HD11	2.03	0.40
11:CI:273:PHE:HB3	11:CI:276:ALA:HB2	2.02	0.40
24:CX:86:LYS:HA	24:CX:90:LYS:HD2	2.03	0.40
26:Cz:33:LEU:HD23	26:Cz:33:LEU:HA	1.91	0.40
42:LV:81:VAL:HG13	42:LV:82:ARG:HG3	2.03	0.40
45:Ld:20:TYR:HE2	45:Ld:51:ALA:HB1	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:Cd:326:LYS:HA	53:Cd:326:LYS:HD3	1.87	0.40
1:C1:683:C:OP2	29:LC:120:ARG:NH2	2.53	0.40
1:C1:780:G:O2'	34:LL:18:TRP:NE1	2.49	0.40
1:C1:1156:G:N2	37:LO:89:MET:SD	2.95	0.40
1:C1:2403:A:H2'	1:C1:2404:G:H8	1.86	0.40
1:C1:2570:U:C4	1:C1:2758:G:N1	2.89	0.40
2:C2:119:C:H5"	12:CJ:70:GLN:NE2	2.37	0.40
5:CB:48:ASN:OD1	5:CB:48:ASN:N	2.53	0.40
6:CC:240:ARG:HD3	21:CS:652:ILE:HG12	2.03	0.40
7:CE:267:ASP:OD1	7:CE:267:ASP:N	2.55	0.40
10:CH:316:ILE:HD13	10:CH:316:ILE:HA	1.97	0.40
18:CP:412:ASP:OD1	18:CP:412:ASP:N	2.54	0.40
30:LE:58:LEU:HD13	30:LE:102:VAL:HG11	2.02	0.40
37:LO:4:PHE:CZ	47:Lf:14:ARG:HG3	2.56	0.40
1:C1:1193:U:O2'	40:LS:113:ARG:NH1	2.55	0.40
1:C1:2837:C:H2'	1:C1:2838:U:H6	1.86	0.40
2:C2:70:G:H5"	44:LY:117:ILE:HD11	2.04	0.40
3:C3:38:G:O6	3:C3:43:U:O4	2.39	0.40
4:CA:308:ASP:N	4:CA:313:GLU:OE2	2.55	0.40
8:CF:148:GLU:HG3	8:CF:214:ILE:HG12	2.03	0.40
10:CH:177:VAL:HG13	10:CH:254:ASP:HB2	2.02	0.40
10:CH:297:LEU:HG	10:CH:302:GLN:OE1	2.22	0.40
15:CM:101:ILE:HD12	15:CM:101:ILE:HA	1.92	0.40
28:LB:307:THR:HA	28:LB:308:PRO:HD3	1.95	0.40
54:Ce:87:TYR:OH	54:Ce:114:THR:OG1	2.25	0.40
1:C1:1039:A:H5'	15:LF:104:LYS:NZ	2.37	0.40
7:CE:438:PRO:HB2	7:CE:439:ARG:NH1	2.34	0.40
7:CE:532:ASP:OD1	7:CE:535:LYS:HG3	2.22	0.40
10:CH:347:LEU:O	10:CH:351:THR:OG1	2.23	0.40
11:CI:188:VAL:HA	11:CI:234:GLU:OE1	2.21	0.40
11:CI:264:PRO:HA	11:CI:265:PRO:HD3	1.95	0.40
14:CL:73:ARG:NH1	14:CL:73:ARG:O	2.55	0.40
16:CN:11:ASN:HD22	16:CN:209:ASP:CG	2.29	0.40
27:Cb:151:ARG:NH2	27:Cb:267:GLN:OE1	2.54	0.40
27:Cb:388:LEU:HD23	27:Cb:388:LEU:HA	1.96	0.40
27:Cb:440:ASN:OD1	27:Cb:453:ARG:NH1	2.49	0.40
28:LB:113:GLU:H	28:LB:113:GLU:HG2	1.61	0.40
37:LO:26:LYS:HA	37:LO:26:LYS:HD2	1.78	0.40
38:LP:70:THR:OG1	38:LP:71:ALA:N	2.54	0.40
48:Lh:27:LEU:HD23	48:Lh:27:LEU:HA	1.95	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
4	CA	254/316 (80%)	234 (92%)	19 (8%)	1 (0%)	30 61
5	CB	256/391 (66%)	244 (95%)	10 (4%)	2 (1%)	16 47
6	CC	283/801 (35%)	272 (96%)	11 (4%)	0	100 100
7	CE	459/598 (77%)	445 (97%)	13 (3%)	1 (0%)	43 73
8	CF	243/270 (90%)	234 (96%)	9 (4%)	0	100 100
9	CG	175/184 (95%)	167 (95%)	8 (5%)	0	100 100
10	CH	474/661 (72%)	456 (96%)	18 (4%)	0	100 100
11	CI	144/414 (35%)	136 (94%)	8 (6%)	0	100 100
12	CJ	374/679 (55%)	365 (98%)	9 (2%)	0	100 100
13	CK	226/261 (87%)	216 (96%)	10 (4%)	0	100 100
14	CL	384/558 (69%)	357 (93%)	22 (6%)	5 (1%)	9 35
15	CM	183/249 (74%)	175 (96%)	8 (4%)	0	100 100
15	LF	238/249 (96%)	228 (96%)	9 (4%)	1 (0%)	30 61
16	CN	244/246 (99%)	236 (97%)	8 (3%)	0	100 100
17	CO	56/120 (47%)	56 (100%)	0	0	100 100
18	CP	322/751 (43%)	307 (95%)	15 (5%)	0	100 100
19	CQ	110/225 (49%)	106 (96%)	4 (4%)	0	100 100
20	CR	159/237 (67%)	155 (98%)	4 (2%)	0	100 100
21	CS	294/834 (35%)	286 (97%)	6 (2%)	2 (1%)	18 49
22	CT	448/688 (65%)	425 (95%)	21 (5%)	2 (0%)	30 61
23	CU	174/451 (39%)	166 (95%)	8 (5%)	0	100 100
24	CX	86/203 (42%)	82 (95%)	4 (5%)	0	100 100
25	CY	308/788 (39%)	292 (95%)	15 (5%)	1 (0%)	36 67
26	Cz	68/123 (55%)	67 (98%)	1 (2%)	0	100 100
27	Cb	630/924 (68%)	597 (95%)	33 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	LB	337/392 (86%)	320 (95%)	17 (5%)	0	100	100
29	LC	360/365 (99%)	348 (97%)	12 (3%)	0	100	100
30	LE	166/200 (83%)	160 (96%)	6 (4%)	0	100	100
31	LG	192/262 (73%)	188 (98%)	4 (2%)	0	100	100
32	LH	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
33	LK	142/165 (86%)	132 (93%)	10 (7%)	0	100	100
34	LL	115/213 (54%)	109 (95%)	6 (5%)	0	100	100
35	LM	135/142 (95%)	131 (97%)	4 (3%)	0	100	100
36	LN	179/203 (88%)	174 (97%)	5 (3%)	0	100	100
37	LO	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
38	LP	150/187 (80%)	149 (99%)	1 (1%)	0	100	100
39	LQ	127/213 (60%)	123 (97%)	4 (3%)	0	100	100
40	LS	172/174 (99%)	166 (96%)	6 (4%)	0	100	100
41	LT	124/160 (78%)	117 (94%)	6 (5%)	1 (1%)	16	47
42	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
43	LX	20/156 (13%)	20 (100%)	0	0	100	100
44	LY	132/138 (96%)	130 (98%)	2 (2%)	0	100	100
45	Ld	107/120 (89%)	102 (95%)	5 (5%)	0	100	100
46	Le	129/131 (98%)	126 (98%)	3 (2%)	0	100	100
47	Lf	106/109 (97%)	102 (96%)	3 (3%)	1 (1%)	14	44
48	Lh	119/935 (13%)	117 (98%)	2 (2%)	0	100	100
49	Li	86/110 (78%)	84 (98%)	2 (2%)	0	100	100
50	Lj	72/95 (76%)	70 (97%)	2 (3%)	0	100	100
51	Lq	205/217 (94%)	186 (91%)	19 (9%)	0	100	100
52	Cc	232/282 (82%)	226 (97%)	6 (3%)	0	100	100
53	Cd	334/436 (77%)	323 (97%)	11 (3%)	0	100	100
54	Ce	192/336 (57%)	185 (96%)	7 (4%)	0	100	100
55	Cf	57/570 (10%)	57 (100%)	0	0	100	100
All	All	11105/18067 (62%)	10656 (96%)	432 (4%)	17 (0%)	44	73

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CA	236	PRO
5	CB	103	ASP
14	CL	414	VAL
21	CS	67	MET
22	CT	254	PRO
25	CY	548	PHE
14	CL	446	ASP
15	LF	12	ILE
47	Lf	93	ALA
14	CL	42	ASN
14	CL	278	ASN
14	CL	439	ASP
5	CB	89	LEU
7	CE	452	ASN
41	LT	44	VAL
21	CS	68	PRO
22	CT	237	PRO

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	
4	CA	231/276 (84%)	230 (100%)	1 (0%)	84	86
5	CB	222/329 (68%)	214 (96%)	8 (4%)	31	62
6	CC	266/710 (38%)	264 (99%)	2 (1%)	73	81
7	CE	398/517 (77%)	394 (99%)	4 (1%)	68	79
8	CF	214/236 (91%)	213 (100%)	1 (0%)	81	85
9	CG	150/155 (97%)	148 (99%)	2 (1%)	61	77
10	CH	424/575 (74%)	421 (99%)	3 (1%)	76	82
11	CI	121/336 (36%)	119 (98%)	2 (2%)	53	74
12	CJ	332/579 (57%)	328 (99%)	4 (1%)	63	78
13	CK	198/225 (88%)	193 (98%)	5 (2%)	42	69
14	CL	65/458 (14%)	64 (98%)	1 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	CM	161/215 (75%)	157 (98%)	4 (2%)	42	69
15	LF	206/215 (96%)	206 (100%)	0	100	100
16	CN	206/206 (100%)	205 (100%)	1 (0%)	81	85
17	CO	48/99 (48%)	48 (100%)	0	100	100
18	CP	273/632 (43%)	270 (99%)	3 (1%)	65	78
19	CQ	100/192 (52%)	97 (97%)	3 (3%)	36	65
20	CR	144/206 (70%)	142 (99%)	2 (1%)	59	76
21	CS	73/716 (10%)	73 (100%)	0	100	100
23	CU	149/376 (40%)	148 (99%)	1 (1%)	76	82
24	CX	76/172 (44%)	75 (99%)	1 (1%)	61	77
26	Cz	60/107 (56%)	60 (100%)	0	100	100
27	Cb	540/779 (69%)	534 (99%)	6 (1%)	65	78
28	LB	290/331 (88%)	289 (100%)	1 (0%)	86	87
29	LC	283/285 (99%)	281 (99%)	2 (1%)	76	82
30	LE	143/166 (86%)	142 (99%)	1 (1%)	76	82
31	LG	168/222 (76%)	166 (99%)	2 (1%)	63	78
32	LH	167/169 (99%)	166 (99%)	1 (1%)	78	83
33	LK	121/136 (89%)	121 (100%)	0	100	100
34	LL	99/176 (56%)	96 (97%)	3 (3%)	36	65
35	LM	115/117 (98%)	113 (98%)	2 (2%)	53	74
36	LN	164/180 (91%)	162 (99%)	2 (1%)	63	78
37	LO	163/163 (100%)	163 (100%)	0	100	100
38	LP	125/152 (82%)	122 (98%)	3 (2%)	43	69
39	LQ	110/178 (62%)	110 (100%)	0	100	100
40	LS	154/154 (100%)	151 (98%)	3 (2%)	50	73
41	LT	109/135 (81%)	107 (98%)	2 (2%)	51	73
42	LV	99/102 (97%)	97 (98%)	2 (2%)	48	72
43	LX	12/129 (9%)	12 (100%)	0	100	100
44	LY	117/119 (98%)	115 (98%)	2 (2%)	53	74
45	Ld	95/105 (90%)	92 (97%)	3 (3%)	34	64
46	Le	114/114 (100%)	113 (99%)	1 (1%)	70	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	Lf	89/90 (99%)	89 (100%)	0	100	100
48	Lh	108/781 (14%)	108 (100%)	0	100	100
49	Li	75/93 (81%)	75 (100%)	0	100	100
50	Lj	61/78 (78%)	60 (98%)	1 (2%)	55	75
51	Lq	179/189 (95%)	179 (100%)	0	100	100
52	Cc	204/244 (84%)	203 (100%)	1 (0%)	81	85
53	Cd	291/367 (79%)	287 (99%)	4 (1%)	59	76
54	Ce	173/297 (58%)	171 (99%)	2 (1%)	63	78
55	Cf	53/482 (11%)	53 (100%)	0	100	100
All	All	8538/14065 (61%)	8446 (99%)	92 (1%)	63	78

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	CA	295	GLN
5	CB	48	ASN
5	CB	62	ILE
5	CB	66	LEU
5	CB	89	LEU
5	CB	90	ASN
5	CB	91	THR
5	CB	123	LYS
5	CB	276	GLN
6	CC	175	ILE
6	CC	193	LYS
7	CE	156	LYS
7	CE	206	LEU
7	CE	208	LYS
7	CE	473	LEU
8	CF	196	LYS
9	CG	82	LEU
9	CG	158	ASP
10	CH	174	PHE
10	CH	284	ILE
10	CH	323	THR
11	CI	287	LYS
11	CI	316	ARG
12	CJ	218	ILE
12	CJ	268	LEU

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Mol	Chain	Res	Type
12	CJ	415	ILE
12	CJ	420	ILE
13	CK	34	LYS
13	CK	150	ILE
13	CK	172	ILE
13	CK	189	LEU
13	CK	190	ASN
14	CL	19	ARG
15	CM	52	LYS
15	CM	134	LYS
15	CM	154	ILE
15	CM	197	VAL
16	CN	161	VAL
18	CP	270	ILE
18	CP	337	TRP
18	CP	576	PHE
19	CQ	11	ARG
19	CQ	23	ARG
19	CQ	65	VAL
20	CR	45	LEU
20	CR	212	ASP
23	CU	327	LYS
24	CX	113	GLN
27	Cb	121	ILE
27	Cb	212	ASP
27	Cb	214	ILE
27	Cb	255	LEU
27	Cb	305	LEU
27	Cb	562	GLU
28	LB	214	GLU
29	LC	37	LYS
29	LC	223	VAL
30	LE	191	LYS
31	LG	73	LYS
31	LG	241	MET
32	LH	41	ILE
34	LL	58	VAL
34	LL	69	THR
34	LL	102	LYS
35	LM	14	VAL
35	LM	20	LEU
36	LN	23	LEU

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Mol	Chain	Res	Type
36	LN	170	LYS
38	LP	74	LYS
38	LP	112	LEU
38	LP	157	VAL
40	LS	96	GLU
40	LS	142	GLN
40	LS	161	THR
41	LT	126	VAL
41	LT	127	GLN
42	LV	39	ILE
42	LV	139	MET
44	LY	78	VAL
44	LY	86	ARG
45	Ld	20	TYR
45	Ld	85	ARG
45	Ld	102	GLN
46	Le	64	THR
50	Lj	58	VAL
52	Cc	106	VAL
53	Cd	213	LYS
53	Cd	277	GLU
53	Cd	343	VAL
53	Cd	361	VAL
54	Ce	73	MET
54	Ce	192	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
4	CA	25	ASN
4	CA	119	ASN
4	CA	121	HIS
5	CB	47	GLN
5	CB	249	ASN
6	CC	286	ASN
7	CE	235	ASN
7	CE	280	GLN
7	CE	443	HIS
8	CF	14	GLN
9	CG	18	ASN
10	CH	226	HIS
10	CH	258	GLN

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Mol	Chain	Res	Type
10	CH	306	ASN
10	CH	389	ASN
12	CJ	485	HIS
13	CK	3	GLN
13	CK	105	GLN
13	CK	190	ASN
13	CK	203	ASN
15	CM	119	ASN
15	CM	192	HIS
16	CN	79	GLN
16	CN	156	ASN
18	CP	322	GLN
18	CP	411	ASN
18	CP	485	HIS
18	CP	489	GLN
18	CP	499	ASN
19	CQ	24	ASN
19	CQ	58	ASN
20	CR	148	GLN
20	CR	196	GLN
20	CR	216	ASN
20	CR	220	GLN
23	CU	364	ASN
26	Cz	58	GLN
27	Cb	367	HIS
27	Cb	377	HIS
27	Cb	446	GLN
28	LB	109	HIS
28	LB	183	GLN
29	LC	60	GLN
29	LC	203	HIS
29	LC	205	GLN
29	LC	250	HIS
29	LC	315	GLN
30	LE	145	GLN
15	LF	206	ASN
31	LG	62	GLN
31	LG	140	ASN
31	LG	158	ASN
31	LG	246	GLN
32	LH	44	ASN
32	LH	96	HIS

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Mol	Chain	Res	Type
32	LH	102	ASN
32	LH	142	GLN
33	LK	65	GLN
33	LK	100	HIS
34	LL	17	HIS
34	LL	25	HIS
35	LM	110	GLN
36	LN	138	ASN
37	LO	27	GLN
38	LP	49	GLN
38	LP	72	GLN
38	LP	75	GLN
38	LP	121	GLN
38	LP	142	ASN
39	LQ	86	ASN
40	LS	21	ASN
41	LT	146	ASN
42	LV	76	HIS
44	LY	56	GLN
45	Ld	29	HIS
46	Le	79	ASN
48	Lh	37	GLN
49	Li	42	GLN
52	Cc	187	GLN
52	Cc	257	ASN
53	Cd	291	ASN
53	Cd	347	HIS
53	Cd	349	GLN
54	Ce	86	ASN
54	Ce	185	ASN
55	Cf	518	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2134/3341 (63%)	480 (22%)	15 (0%)
2	C2	157/256 (61%)	30 (19%)	1 (0%)
3	C3	96/161 (59%)	34 (35%)	0
All	All	2387/3758 (63%)	544 (22%)	16 (0%)

All (544) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	6	A
1	C1	26	A
1	C1	40	A
1	C1	43	A
1	C1	49	A
1	C1	59	G
1	C1	60	A
1	C1	65	A
1	C1	66	A
1	C1	67	A
1	C1	73	A
1	C1	74	G
1	C1	85	A
1	C1	91	G
1	C1	92	G
1	C1	94	G
1	C1	96	G
1	C1	105	C
1	C1	109	A
1	C1	110	G
1	C1	111	C
1	C1	116	A
1	C1	122	A
1	C1	128	G
1	C1	129	C
1	C1	131	U
1	C1	132	C
1	C1	133	G
1	C1	134	G
1	C1	136	C
1	C1	143	G
1	C1	150	G
1	C1	151	G
1	C1	152	A
1	C1	156	G
1	C1	163	U
1	C1	176	U
1	C1	183	U
1	C1	193	C
1	C1	203	C
1	C1	204	A
1	C1	205	G
1	C1	206	A

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Mol	Chain	Res	Type
1	C1	211	G
1	C1	212	A
1	C1	214	A
1	C1	225	G
1	C1	241	G
1	C1	244	U
1	C1	249	C
1	C1	253	U
1	C1	258	C
1	C1	261	G
1	C1	275	G
1	C1	276	A
1	C1	277	A
1	C1	287	A
1	C1	290	U
1	C1	300	A
1	C1	302	U
1	C1	308	U
1	C1	309	A
1	C1	310	A
1	C1	311	A
1	C1	315	A
1	C1	321	C
1	C1	325	C
1	C1	329	G
1	C1	331	C
1	C1	342	C
1	C1	343	A
1	C1	368	G
1	C1	377	A
1	C1	382	G
1	C1	384	G
1	C1	390	U
1	C1	391	A
1	C1	393	C
1	C1	394	A
1	C1	395	C
1	C1	400	A
1	C1	413	G
1	C1	414	A
1	C1	430	A
1	C1	431	C

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Mol	Chain	Res	Type
1	C1	432	U
1	C1	433	U
1	C1	445	A
1	C1	446	U
1	C1	448	A
1	C1	449	U
1	C1	450	C
1	C1	457	U
1	C1	459	U
1	C1	460	C
1	C1	467	G
1	C1	468	C
1	C1	469	A
1	C1	474	G
1	C1	484	G
1	C1	485	G
1	C1	508	G
1	C1	509	A
1	C1	511	A
1	C1	513	A
1	C1	520	G
1	C1	526	G
1	C1	533	C
1	C1	534	U
1	C1	535	C
1	C1	546	A
1	C1	547	U
1	C1	548	A
1	C1	558	G
1	C1	582	A
1	C1	590	C
1	C1	592	G
1	C1	593	C
1	C1	596	G
1	C1	598	A
1	C1	608	A
1	C1	623	C
1	C1	633	A
1	C1	651	A
1	C1	652	A
1	C1	664	A
1	C1	668	U

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Mol	Chain	Res	Type
1	C1	678	A
1	C1	684	G
1	C1	692	A
1	C1	693	A
1	C1	699	G
1	C1	702	A
1	C1	703	A
1	C1	706	U
1	C1	707	A
1	C1	708	G
1	C1	718	U
1	C1	719	C
1	C1	723	G
1	C1	731	G
1	C1	739	C
1	C1	744	G
1	C1	748	U
1	C1	749	C
1	C1	751	G
1	C1	752	A
1	C1	757	U
1	C1	758	U
1	C1	761	A
1	C1	762	G
1	C1	765	G
1	C1	767	A
1	C1	787	A
1	C1	796	G
1	C1	798	A
1	C1	907	A
1	C1	918	G
1	C1	925	A
1	C1	932	A
1	C1	933	A
1	C1	934	G
1	C1	940	C
1	C1	942	C
1	C1	943	A
1	C1	944	G
1	C1	958	A
1	C1	960	C
1	C1	961	U

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Mol	Chain	Res	Type
1	C1	965	G
1	C1	973	A
1	C1	974	G
1	C1	975	G
1	C1	976	U
1	C1	979	A
1	C1	982	G
1	C1	983	A
1	C1	1031	C
1	C1	1033	U
1	C1	1039	A
1	C1	1043	A
1	C1	1045	G
1	C1	1046	A
1	C1	1047	A
1	C1	1057	A
1	C1	1063	C
1	C1	1069	G
1	C1	1075	A
1	C1	1076	U
1	C1	1077	U
1	C1	1078	C
1	C1	1079	G
1	C1	1080	A
1	C1	1085	A
1	C1	1086	U
1	C1	1097	G
1	C1	1098	G
1	C1	1114	C
1	C1	1126	U
1	C1	1135	A
1	C1	1141	A
1	C1	1142	C
1	C1	1163	U
1	C1	1164	G
1	C1	1174	C
1	C1	1175	A
1	C1	1178	C
1	C1	1180	C
1	C1	1181	C
1	C1	1182	A
1	C1	1184	A

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Mol	Chain	Res	Type
1	C1	1186	A
1	C1	1187	A
1	C1	1189	G
1	C1	1190	C
1	C1	1203	U
1	C1	1204	G
1	C1	1211	G
1	C1	1218	G
1	C1	1221	C
1	C1	1223	U
1	C1	1224	G
1	C1	1226	A
1	C1	1227	A
1	C1	1228	G
1	C1	1238	G
1	C1	1240	U
1	C1	1241	A
1	C1	1245	A
1	C1	1246	C
1	C1	1247	U
1	C1	1253	A
1	C1	1254	C
1	C1	1268	A
1	C1	1269	A
1	C1	1271	G
1	C1	1272	U
1	C1	1286	A
1	C1	1287	U
1	C1	1289	G
1	C1	1291	U
1	C1	1295	G
1	C1	1312	A
1	C1	1313	U
1	C1	1314	A
1	C1	1330	A
1	C1	1331	G
1	C1	1332	A
1	C1	1334	A
1	C1	1335	C
1	C1	1336	G
1	C1	1337	A
1	C1	1362	G

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Mol	Chain	Res	Type
1	C1	1368	A
1	C1	1369	G
1	C1	1373	C
1	C1	1374	G
1	C1	1381	A
1	C1	1382	G
1	C1	1399	G
1	C1	1400	A
1	C1	1401	A
1	C1	1416	G
1	C1	1419	C
1	C1	1433	C
1	C1	1856	U
1	C1	1859	U
1	C1	1864	C
1	C1	1865	A
1	C1	1866	A
1	C1	1868	G
1	C1	1875	A
1	C1	1883	C
1	C1	1884	G
1	C1	1886	C
1	C1	1897	C
1	C1	1900	A
1	C1	1901	A
1	C1	2075	A
1	C1	2088	A
1	C1	2287	G
1	C1	2288	A
1	C1	2293	C
1	C1	2294	A
1	C1	2297	G
1	C1	2302	U
1	C1	2309	U
1	C1	2325	A
1	C1	2332	G
1	C1	2334	A
1	C1	2335	A
1	C1	2338	G
1	C1	2339	G
1	C1	2356	G
1	C1	2365	G

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Mol	Chain	Res	Type
1	C1	2384	C
1	C1	2394	A
1	C1	2396	U
1	C1	2397	G
1	C1	2402	A
1	C1	2406	C
1	C1	2415	U
1	C1	2422	U
1	C1	2423	A
1	C1	2424	G
1	C1	2426	U
1	C1	2428	G
1	C1	2429	G
1	C1	2430	A
1	C1	2431	G
1	C1	2435	C
1	C1	2436	G
1	C1	2439	G
1	C1	2445	G
1	C1	2449	U
1	C1	2452	C
1	C1	2453	A
1	C1	2456	A
1	C1	2465	G
1	C1	2467	U
1	C1	2469	U
1	C1	2476	U
1	C1	2477	A
1	C1	2482	A
1	C1	2551	A
1	C1	2552	C
1	C1	2553	A
1	C1	2564	G
1	C1	2568	G
1	C1	2730	C
1	C1	2739	U
1	C1	2749	G
1	C1	2759	A
1	C1	2760	A
1	C1	2761	A
1	C1	2766	A
1	C1	2767	C

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Mol	Chain	Res	Type
1	C1	2776	U
1	C1	2777	A
1	C1	2778	A
1	C1	2782	G
1	C1	2783	C
1	C1	2784	U
1	C1	2800	U
1	C1	2802	C
1	C1	2803	A
1	C1	2804	U
1	C1	2805	A
1	C1	2807	C
1	C1	2818	U
1	C1	2819	U
1	C1	2831	U
1	C1	2832	G
1	C1	2833	U
1	C1	2834	C
1	C1	2835	G
1	C1	2836	G
1	C1	2845	A
1	C1	2847	C
1	C1	2852	C
1	C1	2856	G
1	C1	2857	C
1	C1	2862	U
1	C1	2869	A
1	C1	2874	U
1	C1	2879	U
1	C1	2893	U
1	C1	2894	A
1	C1	2899	A
1	C1	2900	C
1	C1	2901	G
1	C1	2916	A
1	C1	2917	C
1	C1	2923	U
1	C1	2924	G
1	C1	2926	G
1	C1	2929	A
1	C1	2930	G
1	C1	2935	G

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Mol	Chain	Res	Type
1	C1	2936	U
1	C1	2950	U
1	C1	2956	C
1	C1	2968	A
1	C1	2969	A
1	C1	2970	U
1	C1	2980	U
1	C1	3006	A
1	C1	3013	U
1	C1	3014	U
1	C1	3015	U
1	C1	3033	C
1	C1	3034	A
1	C1	3035	G
1	C1	3037	G
1	C1	3048	A
1	C1	3049	C
1	C1	3050	C
1	C1	3057	U
1	C1	3066	G
1	C1	3070	A
1	C1	3077	C
1	C1	3079	A
1	C1	3084	A
1	C1	3086	A
1	C1	3087	A
1	C1	3088	U
1	C1	3099	A
1	C1	3100	C
1	C1	3101	G
1	C1	3108	U
1	C1	3109	A
1	C1	3113	C
1	C1	3118	A
1	C1	3126	G
1	C1	3130	U
1	C1	3134	A
1	C1	3139	A
1	C1	3140	G
1	C1	3144	C
1	C1	3146	G
1	C1	3147	G

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Mol	Chain	Res	Type
1	C1	3154	A
1	C1	3157	C
1	C1	3161	C
1	C1	3162	A
1	C1	3163	G
1	C1	3170	C
1	C1	3171	C
1	C1	3178	G
1	C1	3179	G
1	C1	3183	C
1	C1	3185	A
1	C1	3187	G
1	C1	3189	G
1	C1	3199	A
1	C1	3205	C
1	C1	3211	G
1	C1	3212	C
1	C1	3213	A
1	C1	3214	A
1	C1	3225	C
1	C1	3228	G
1	C1	3232	U
1	C1	3244	C
1	C1	3248	C
1	C1	3249	G
1	C1	3253	U
1	C1	3256	A
1	C1	3257	U
1	C1	3258	G
1	C1	3260	G
1	C1	3262	G
1	C1	3263	A
1	C1	3264	A
1	C1	3270	C
1	C1	3274	U
1	C1	3281	U
1	C1	3282	A
1	C1	3285	G
1	C1	3290	C
1	C1	3291	U
1	C1	3292	U
1	C1	3295	U

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Mol	Chain	Res	Type
1	C1	3296	G
1	C1	3297	U
1	C1	3298	U
1	C1	3302	A
1	C1	3309	G
1	C1	3310	A
1	C1	3318	C
1	C1	3321	U
1	C1	3322	C
1	C1	3323	C
1	C1	3324	U
1	C1	3329	C
1	C1	3330	U
1	C1	3331	A
1	C1	3332	G
1	C1	3333	A
1	C1	3337	C
2	C2	34	U
2	C2	35	C
2	C2	49	G
2	C2	51	G
2	C2	53	A
2	C2	59	A
2	C2	61	A
2	C2	62	A
2	C2	63	G
2	C2	77	A
2	C2	78	G
2	C2	81	U
2	C2	84	C
2	C2	86	U
2	C2	87	G
2	C2	90	U
2	C2	95	G
2	C2	100	U
2	C2	104	A
2	C2	106	C
2	C2	109	A
2	C2	111	A
2	C2	113	U
2	C2	124	G
2	C2	126	A

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Mol	Chain	Res	Type
2	C2	127	U
2	C2	129	C
2	C2	136	G
2	C2	152	G
2	C2	158	U
3	C3	5	C
3	C3	6	A
3	C3	7	U
3	C3	8	C
3	C3	15	U
3	C3	16	G
3	C3	17	G
3	C3	21	U
3	C3	25	U
3	C3	26	U
3	C3	31	A
3	C3	32	C
3	C3	48	G
3	C3	54	G
3	C3	55	A
3	C3	56	A
3	C3	57	A
3	C3	59	G
3	C3	60	C
3	C3	61	A
3	C3	63	U
3	C3	64	G
3	C3	68	G
3	C3	71	U
3	C3	72	C
3	C3	73	G
3	C3	75	U
3	C3	130	G
3	C3	133	G
3	C3	134	C
3	C3	137	G
3	C3	141	U
3	C3	143	A
3	C3	144	A

All (16) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	150	G
1	C1	308	U
1	C1	519	A
1	C1	1044	A
1	C1	1046	A
1	C1	1220	C
1	C1	2301	C
1	C1	2929	A
1	C1	3078	U
1	C1	3162	A
1	C1	3204	G
1	C1	3257	U
1	C1	3263	A
1	C1	3296	G
1	C1	3297	U
2	C2	123	G

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
56	GTP	CH	701	-	33,34,34	0.89	1 (3%)	50,54,54	1.61	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	GTP	CH	701	-	-	6/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	CH	701	GTP	C2-N3	2.10	1.38	1.33

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
56	CH	701	GTP	C5-C4-N3	-5.11	120.26	128.39
56	CH	701	GTP	C2-N3-C4	4.62	120.27	112.30
56	CH	701	GTP	N9-C4-N3	3.35	132.65	125.95
56	CH	701	GTP	C2-N1-C6	-2.92	119.81	125.11
56	CH	701	GTP	N9-C8-N7	-2.55	108.67	113.40
56	CH	701	GTP	C5-C6-N1	2.46	119.51	113.25
56	CH	701	GTP	C8-N7-C5	2.41	108.55	104.26
56	CH	701	GTP	O6-C6-C5	-2.36	120.31	126.53
56	CH	701	GTP	C3'-C2'-C1'	2.11	105.46	101.46

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	CH	701	GTP	PB-O3B-PG-O2G
56	CH	701	GTP	PB-O3B-PG-O3G
56	CH	701	GTP	C5'-O5'-PA-O3A
56	CH	701	GTP	C4'-C5'-O5'-PA
56	CH	701	GTP	C5'-O5'-PA-O2A
56	CH	701	GTP	C3'-C4'-C5'-O5'

There are no ring outliers.

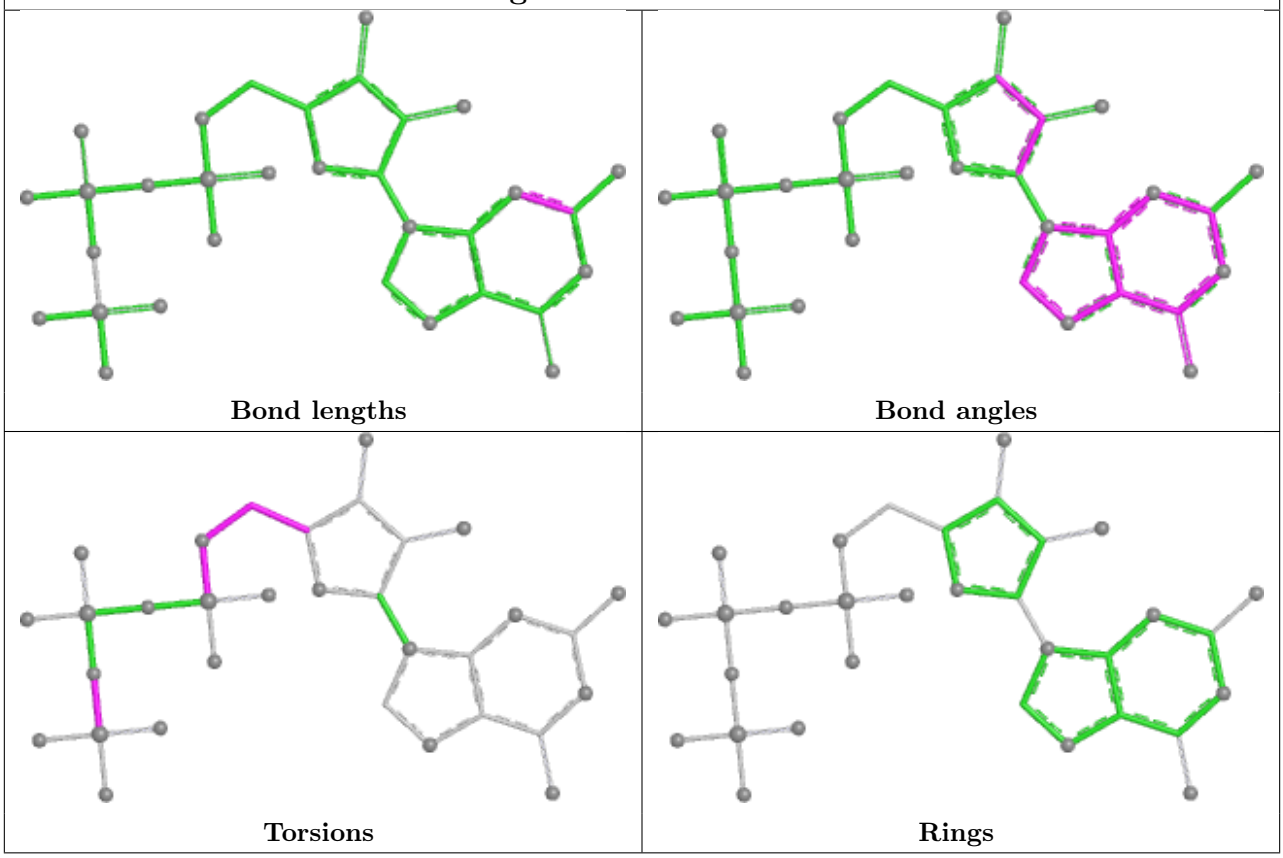
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	CH	701	GTP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GTP CH 701



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

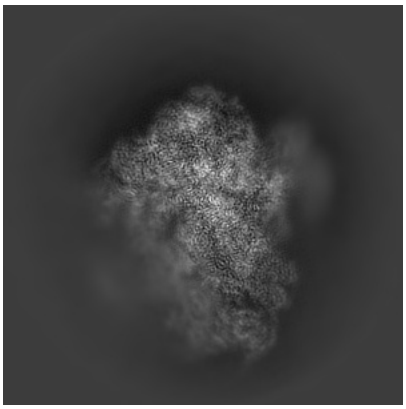
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-35285. These allow visual inspection of the internal detail of the map and identification of artifacts.

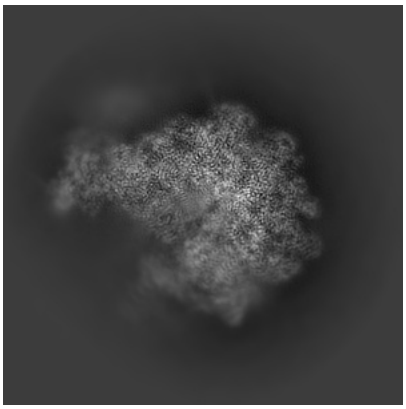
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

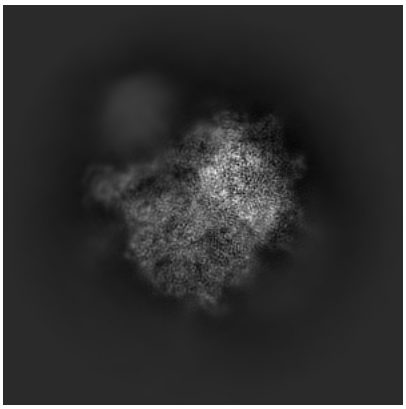
6.1.1 Primary map



X

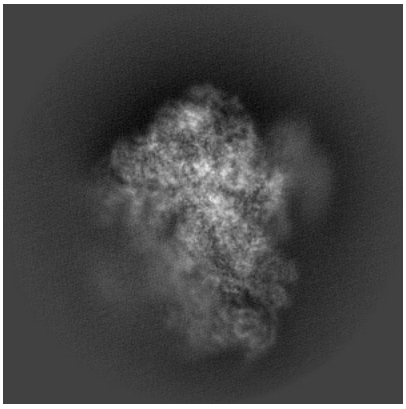


Y

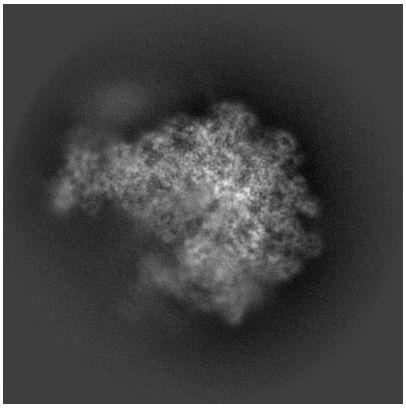


Z

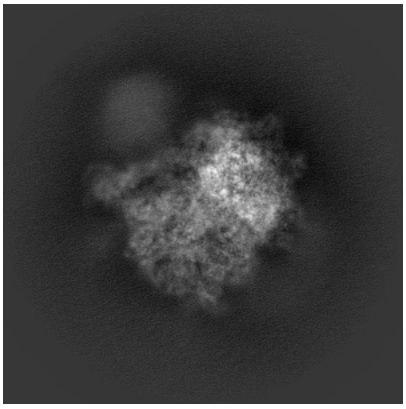
6.1.2 Raw map



X



Y

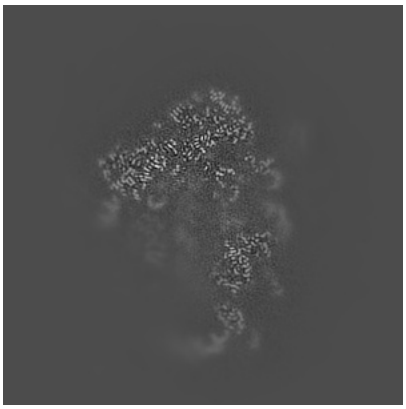


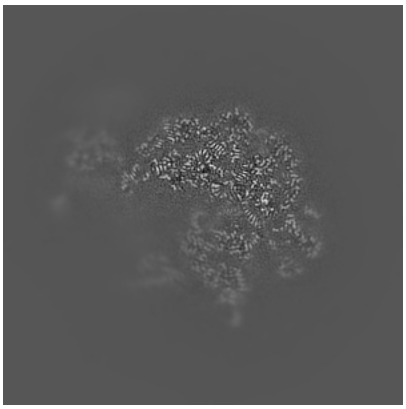
Z

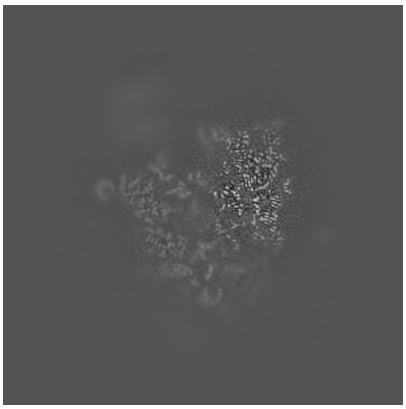
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

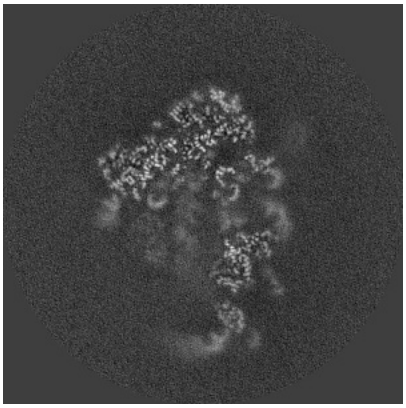
6.2.1 Primary map

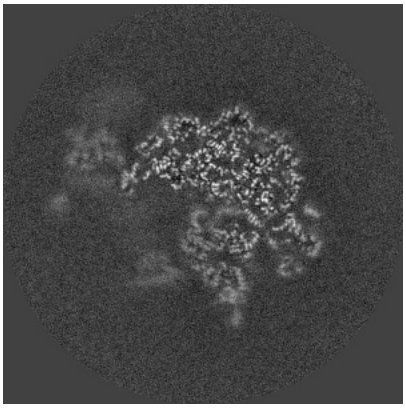

X Index: 210

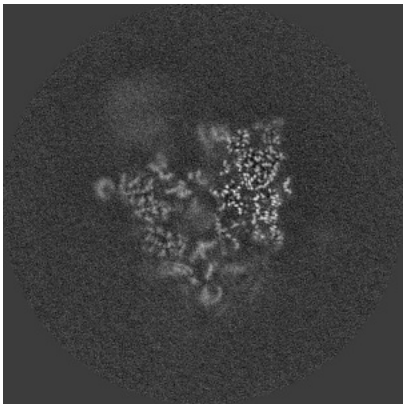

Y Index: 210


Z Index: 210

6.2.2 Raw map


X Index: 210


Y Index: 210

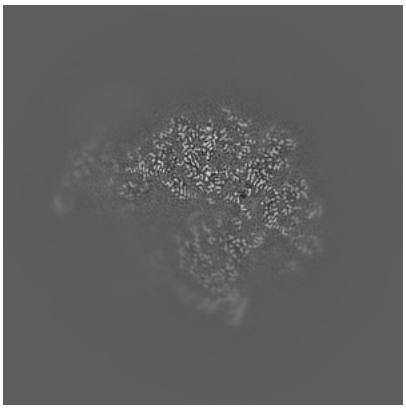

Z Index: 210

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

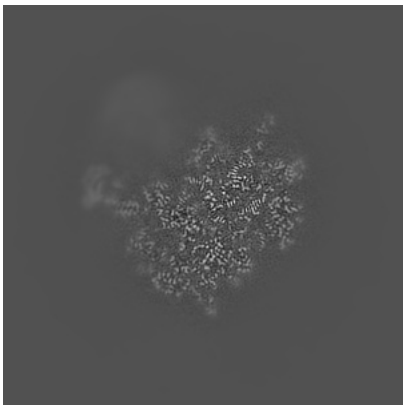
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 247

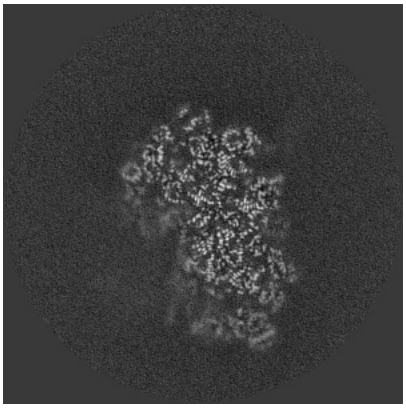


Y Index: 217

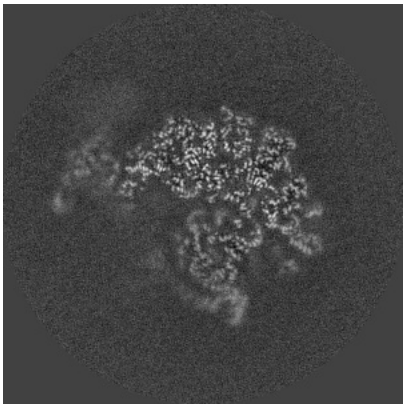


Z Index: 247

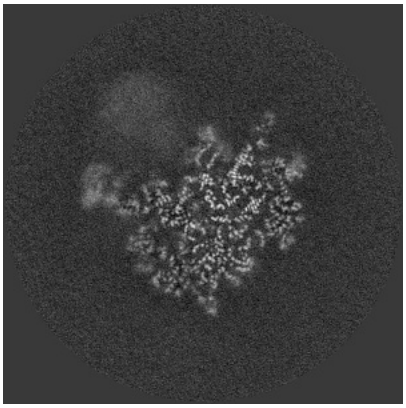
6.3.2 Raw map



X Index: 247



Y Index: 216

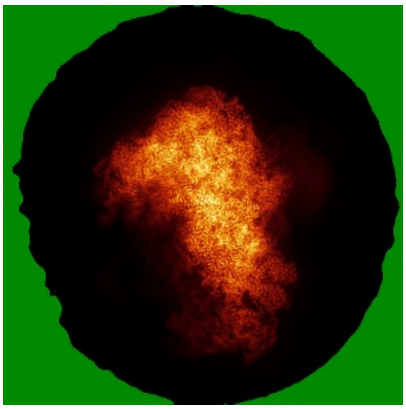


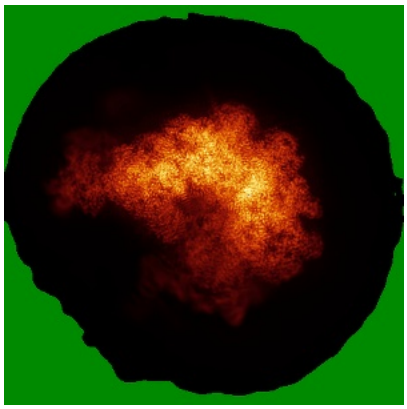
Z Index: 246

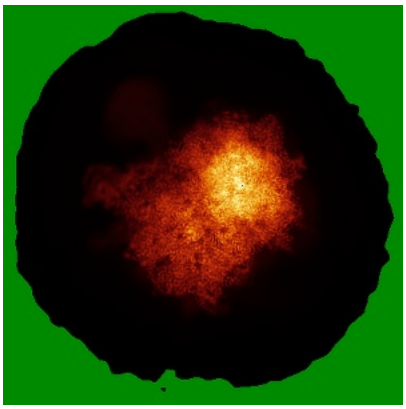
The images above show the largest variance slices of the map in three orthogonal directions.

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

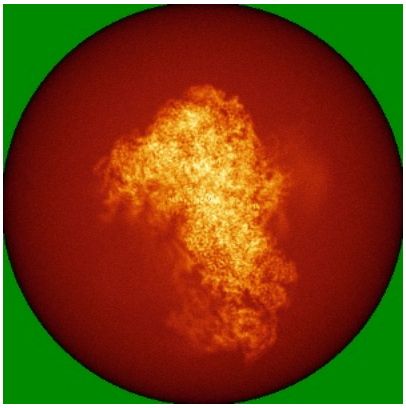
6.4.1 Primary map

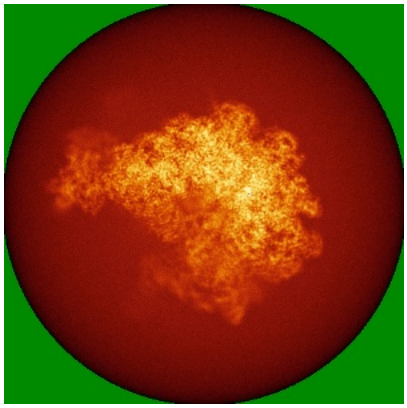

X

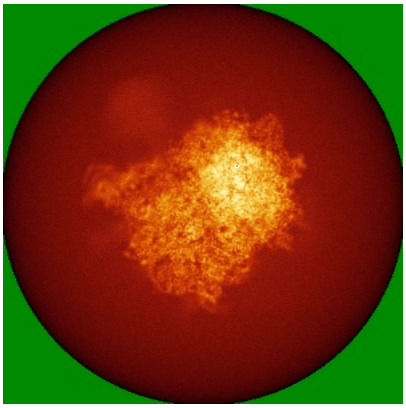

Y


Z

6.4.2 Raw map


X


Y


Z

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

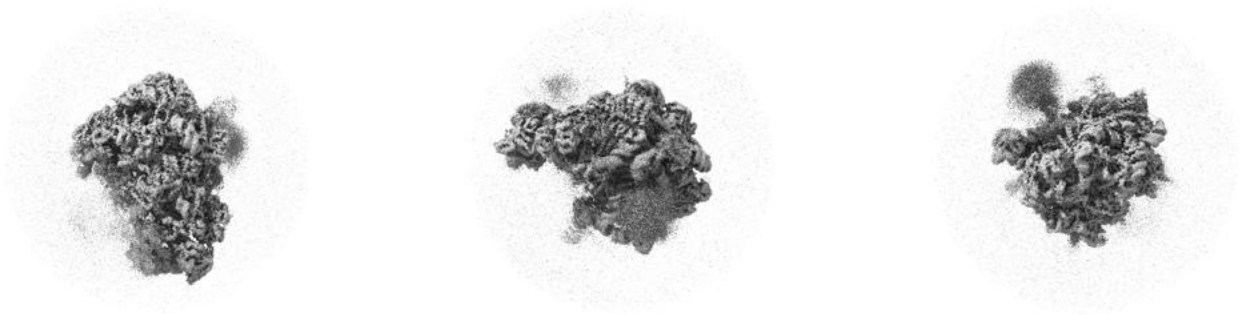
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

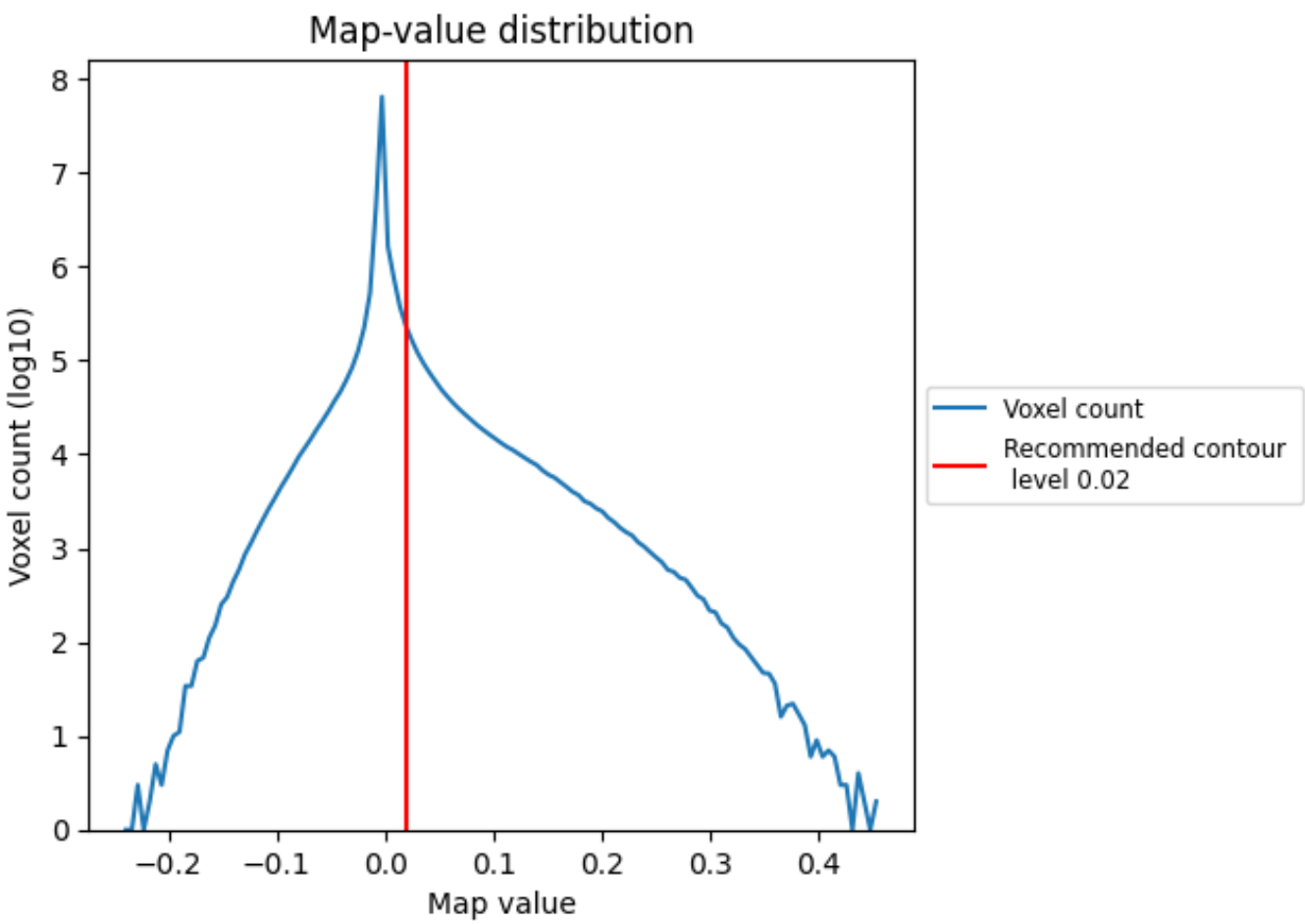
6.6 Mask visualisation (i)

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

7 Map analysis (i)

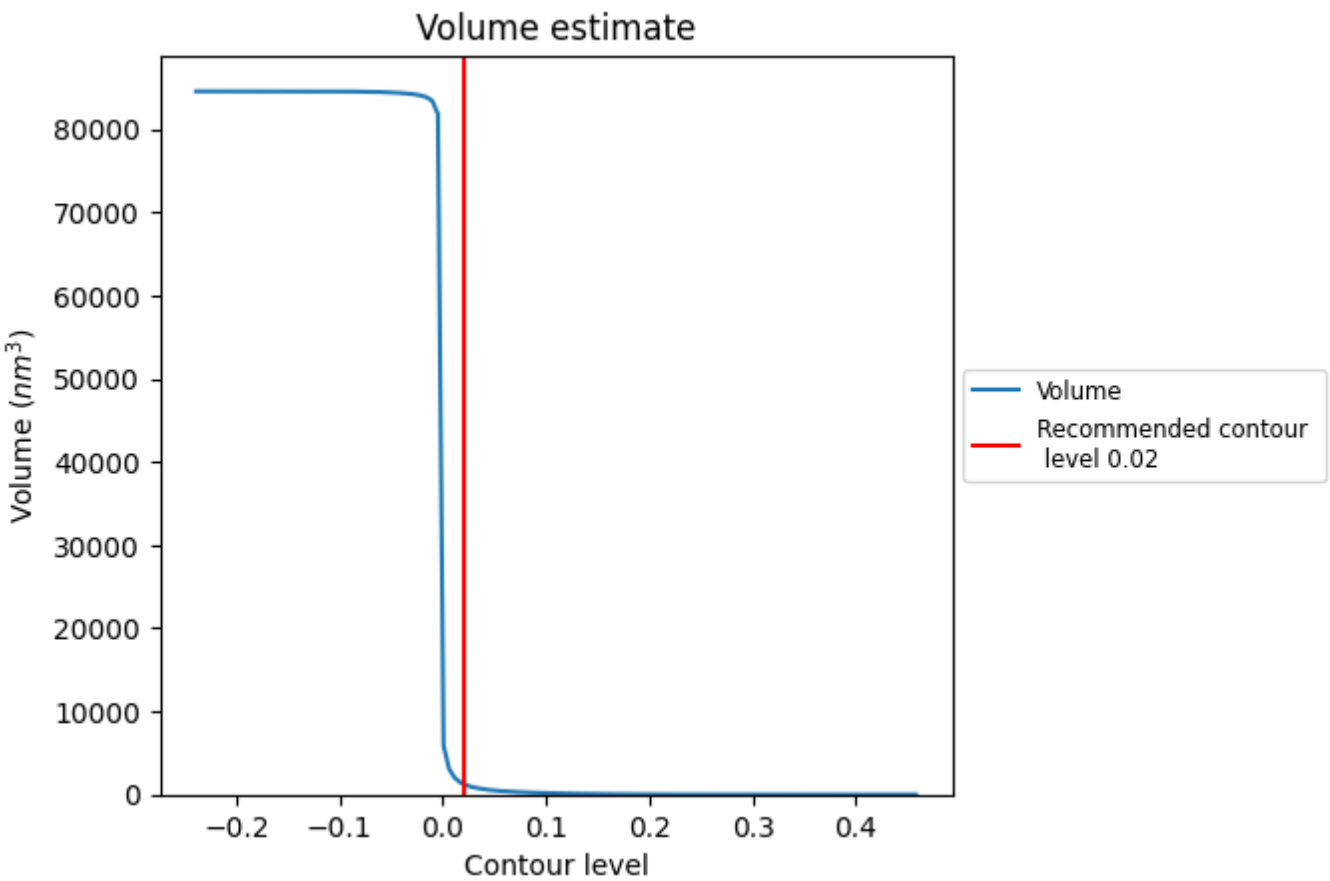
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

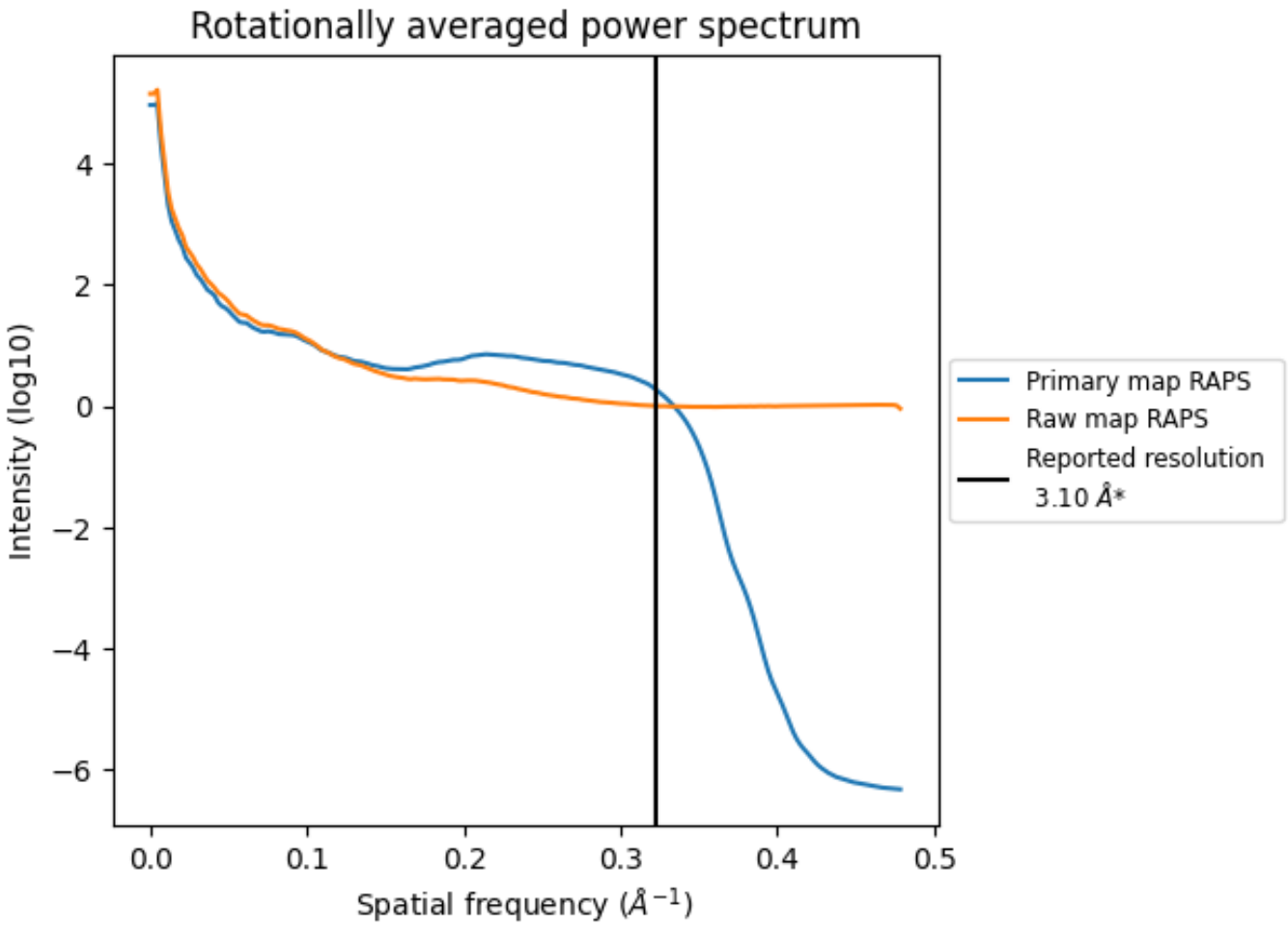
7.2 Volume estimate (i)



The volume at the recommended contour level is 1277 nm^3; this corresponds to an approximate mass of 1154 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)

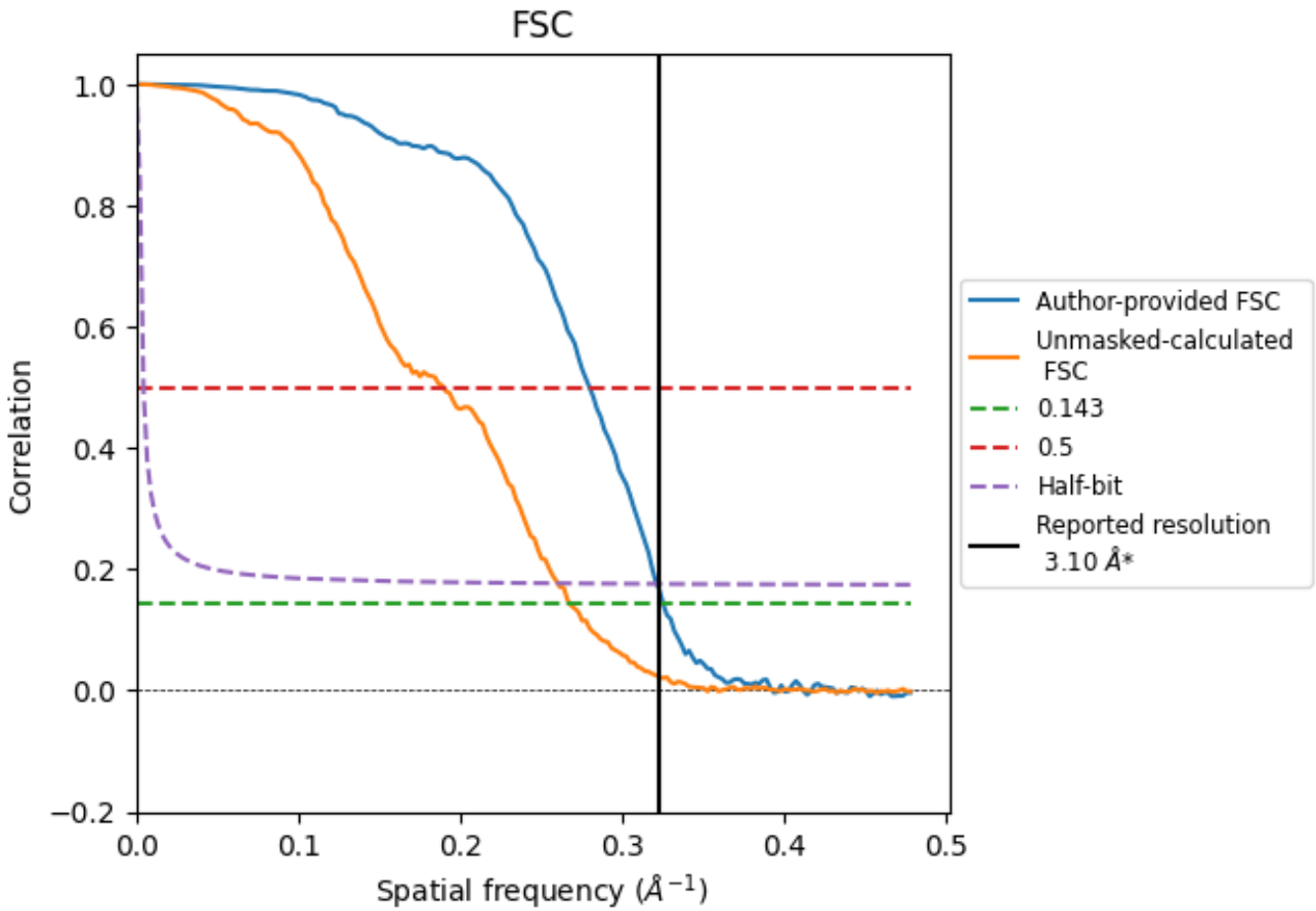


*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8.2 Resolution estimates (i)

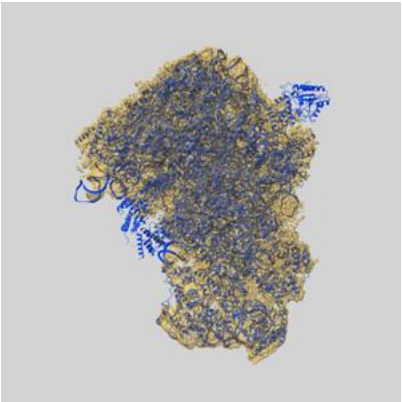
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.07	3.57	3.11
Unmasked-calculated*	3.73	5.27	3.84

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.73 differs from the reported value 3.1 by more than 10 %

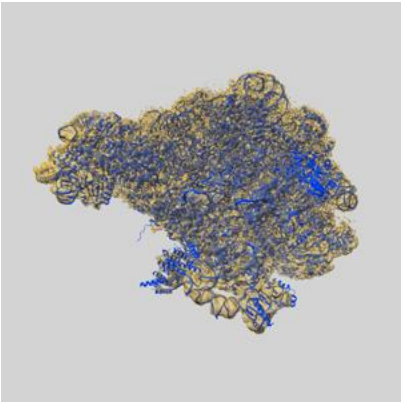
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-35285 and PDB model 8I9V. Per-residue inclusion information can be found in section 3 on page 17.

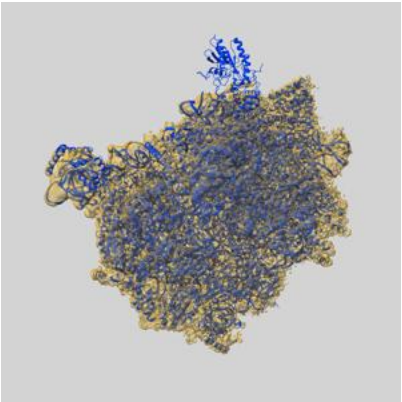
9.1 Map-model overlay (i)



X



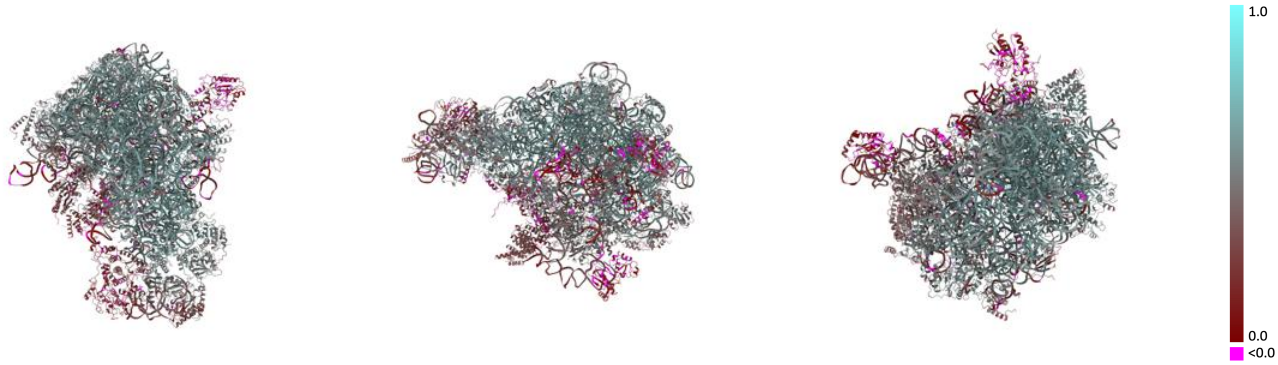
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

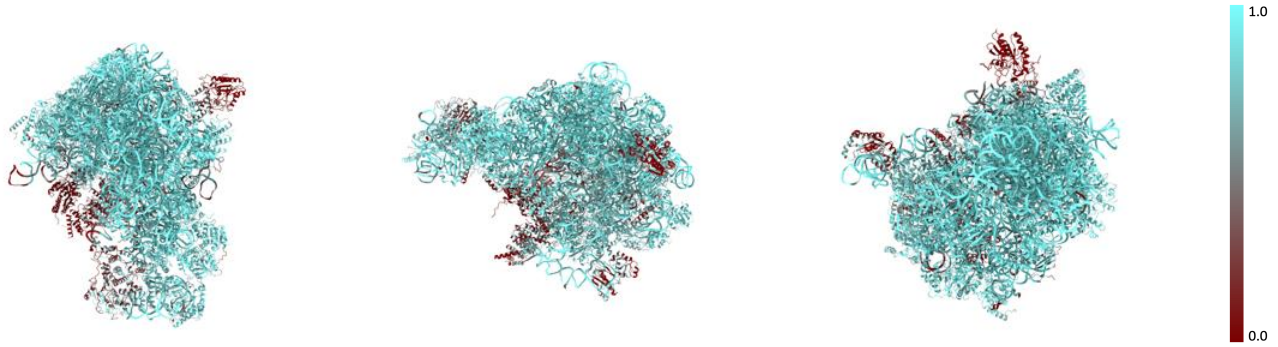
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

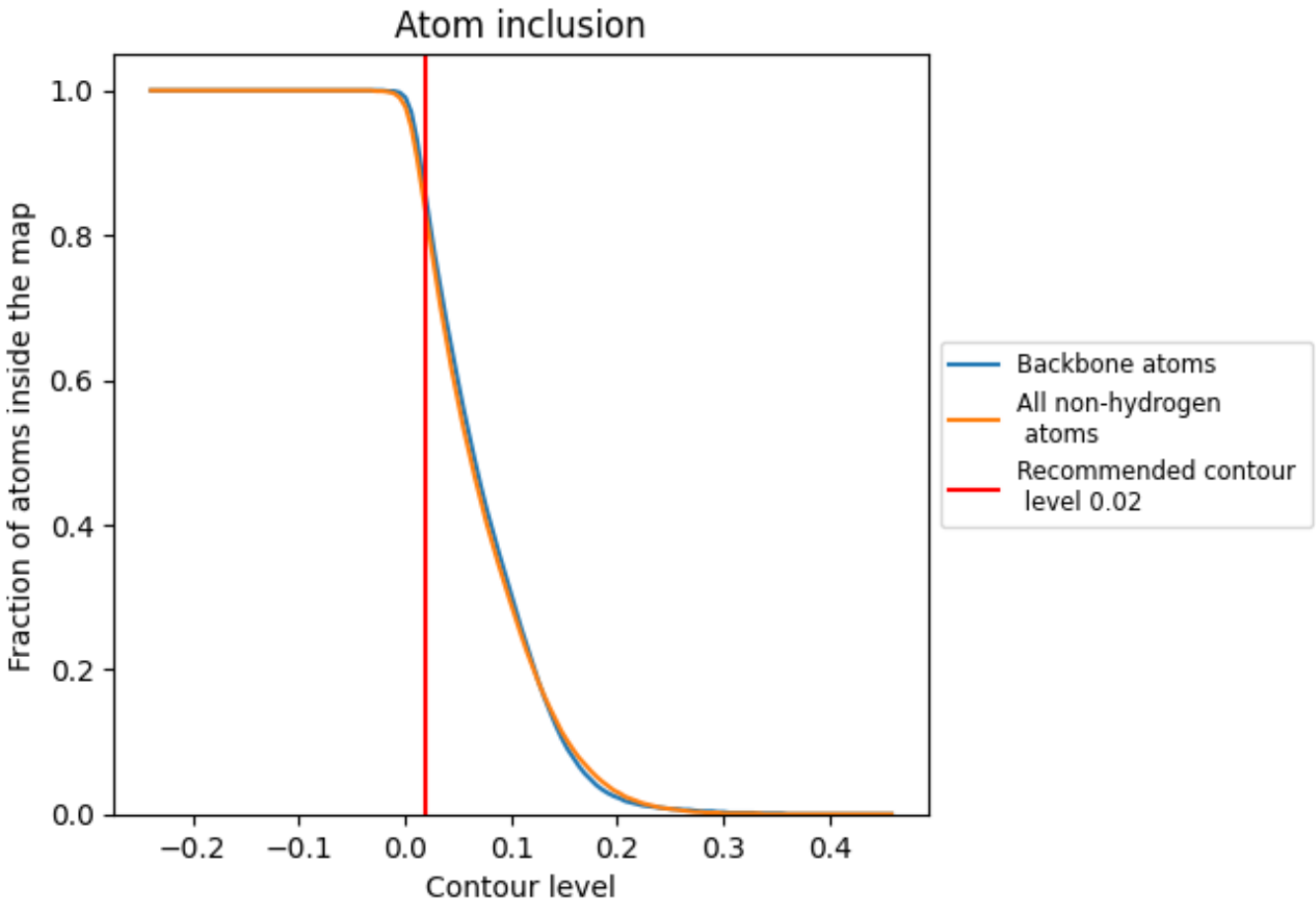
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 85% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8270	0.4600
C1	0.9160	0.4920
C2	0.8890	0.4890
C3	0.8700	0.3460
CA	0.9100	0.5190
CB	0.7890	0.3810
CC	0.5130	0.2890
CE	0.8820	0.4970
CF	0.8700	0.4630
CG	0.7850	0.4060
CH	0.8810	0.4950
CI	0.8400	0.4180
CJ	0.4520	0.1900
CK	0.8500	0.4840
CL	0.3040	0.1920
CM	0.6100	0.2570
CN	0.8960	0.5130
CO	0.9340	0.5560
CP	0.8240	0.4390
CQ	0.9170	0.5070
CR	0.9130	0.5330
CS	0.0980	0.2140
CT	0.2590	0.2500
CU	0.8290	0.4480
CX	0.3990	0.1990
CY	0.4070	0.2780
Cb	0.7750	0.4150
Cc	0.8570	0.5040
Cd	0.9220	0.5390
Ce	0.9420	0.5730
Cf	0.6860	0.3770
Cz	0.6190	0.3280
LB	0.9320	0.5570
LC	0.9480	0.5860
LE	0.9180	0.5360

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Chain	Atom inclusion	Q-score
LF	0.9230	0.5600
LG	0.8410	0.5040
LH	0.9300	0.5580
LK	0.8110	0.3740
LL	0.9530	0.5840
LM	0.9440	0.5590
LN	0.9430	0.5890
LO	0.9520	0.5830
LP	0.9240	0.5510
LQ	0.9390	0.5720
LS	0.9310	0.5570
LT	0.7100	0.3300
LV	0.8870	0.5150
LX	0.3240	0.2180
LY	0.9190	0.5550
Ld	0.6000	0.2850
Le	0.9510	0.5970
Lf	0.9530	0.5990
Lh	0.8630	0.4980
Li	0.8880	0.5080
Lj	0.9590	0.5960
Lq	0.3400	0.0810