



Full wwPDB EM Validation Report ⓘ

Mar 29, 2026 – 04:05 AM UTC

PDB ID : 5WYJ / pdb_00005wyj
EMDB ID : EMD-6695
Title : Cryo-EM structure of the 90S small subunit pre-ribosome (Dhr1-depleted, Enp1-TAP, state 1)
Authors : Ye, K.; Zhu, X.; Sun, Q.
Deposited on : 2017-01-13
Resolution : 8.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

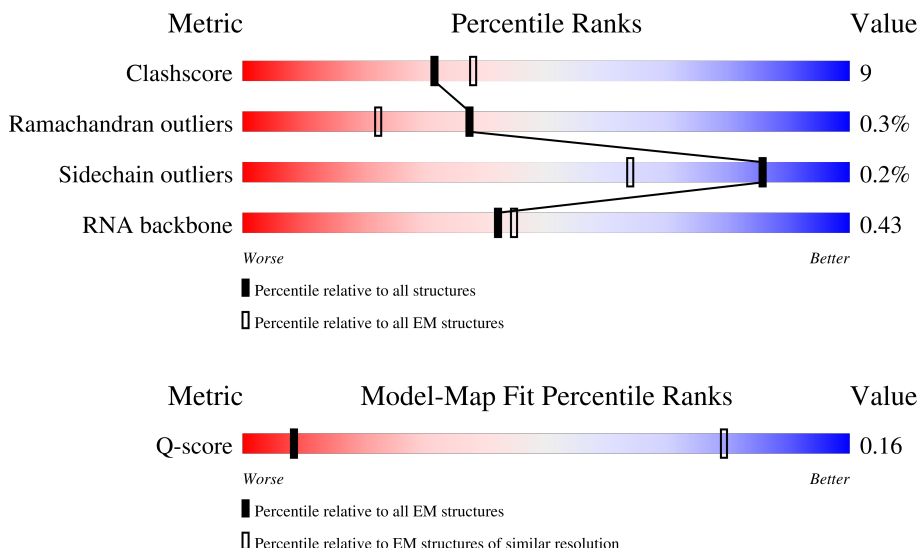
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.70 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	282 (8.20 - 9.20)

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

Mol	Chain	Length	Quality of chain
1	3A	333	5% 25% 20% 53%
2	3B	327	20% 57% 16% 27%
2	3C	327	38% 62% 11% 27%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	3D	504	
4	3E	511	
5	3F	573	
6	3G	126	
6	3H	126	
7	5A	700	
8	AA	776	
9	AB	643	
10	AC	713	
11	AD	575	
12	AE	1769	
13	AF	513	
14	AG	896	
15	B1	1183	
16	BA	923	
17	BB	943	
18	BC	817	
19	BD	594	
20	BE	939	
21	CA	297	
22	CB	1237	
23	E1	252	
23	E2	252	
24	E3	483	
25	E4	707	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
26	K1	316	
27	MA	183	
28	MB	290	
29	MC	593	
30	P1	274	
31	R1	367	
32	R2	1729	
33	S1	489	
34	SA	1812	
35	SC	255	
36	SF	261	
37	SG	225	
38	SH	236	
39	SI	190	
40	SJ	200	
41	SK	197	
42	SM	156	
43	SN	143	
44	SO	151	
45	SP	137	
46	SR	143	
47	SX	130	
48	SY	145	
49	SZ	135	
50	Sc	82	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
51	Sd	67	
52	Sf	63	
53	Sg	152	
54	U1	554	
55	U2	250	
56	U3	2493	
57	U4	189	
58	U5	274	
59	UA	1615	
60	UB	987	
61	UC	1033	

2 Entry composition [i](#)

There are 61 unique types of molecules in this entry. The entry contains 173863 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 U3 RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	157	Total	C	N	O	P	0	0
			3327	1488	575	1107	157		

- Molecule 2 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3B	239	Total	C	N	O	S	0	0
			1866	1183	332	341	10		
2	3C	239	Total	C	N	O	S	0	0
			1866	1183	332	341	10		

- Molecule 3 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3D	370	Total	C	N	O	S	0	0
			2915	1843	503	560	9		

- Molecule 4 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3E	382	Total	C	N	O	S	0	0
			2935	1859	498	570	8		

- Molecule 5 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3F	365	Total	C	N	O	S	0	0
			2916	1871	506	529	10		

- Molecule 6 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	3G	122	Total	C	N	O	S	0	0
			924	589	159	172	4		
6	3H	122	Total	C	N	O	S	0	0
			924	589	159	172	4		

- Molecule 7 is a RNA chain called 5ETS RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	5A	462	Total	C	N	O	P	0	0
			9867	4406	1749	3250	462		

- Molecule 8 is a protein called Utp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	AA	569	Total	C	N	O	0	0
			2845	1707	569	569		

- Molecule 9 is a protein called Utp5.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	AB	403	Total	C	N	O	0	0
			2015	1209	403	403		

- Molecule 10 is a protein called Utp8.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	AC	472	Total	C	N	O	0	0
			2360	1416	472	472		

- Molecule 11 is a protein called Utp9.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	AD	101	Total	C	N	O	0	0
			505	303	101	101		

- Molecule 12 is a protein called U3 small nucleolar RNA-associated protein 10,Utp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AE	1536	Total	C	N	O	S	0	0
			9970	6261	1772	1918	19		

- Molecule 13 is a protein called Utp15.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	AF	376	Total	C	N	O	0	0
			1880	1128	376	376		

- Molecule 14 is a protein called Utp17.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AG	612	Total	C	N	O	0	0
			3060	1836	612	612		

- Molecule 15 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	B1	536	Total	C	N	O	S	0	0
			4325	2801	758	746	20		

- Molecule 16 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BA	755	Total	C	N	O	S	0	0
			6026	3862	1025	1123	16		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BB	778	Total	C	N	O	S	0	0
			6138	3931	1019	1161	27		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BC	783	Total	C	N	O	S	0	0
			6117	3870	1033	1187	27		

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BD	325	Total	C	N	O	S	0	0
			2539	1606	458	466	9		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BE	753	Total	C	N	O	S	0	0
			5936	3769	1020	1126	21		

- Molecule 21 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CA	196	Total	C	N	O	S	0	0
			1582	1016	259	300	7		

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CB	1098	Total	C	N	O	S	0	0
			8870	5763	1462	1621	24		

- Molecule 23 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	E1	217	Total	C	N	O	S	0	0
			1689	1073	293	312	11		
23	E2	216	Total	C	N	O	S	0	0
			1695	1078	295	313	9		

- Molecule 24 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	E3	260	Total	C	N	O	S	0	0
			2114	1378	359	374	3		

- Molecule 25 is a protein called Enp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	E4	285	Total	C	N	O	0	0
			1425	855	285	285		

- Molecule 26 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	K1	175	Total	C	N	O	S	0	0
			1410	903	252	245	10		

- Molecule 27 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	MA	133	Total	C	N	O	S	0	0
			1097	692	204	194	7		

- Molecule 28 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	MB	184	Total	C	N	O	S	0	0
			1465	926	273	260	6		

- Molecule 29 is a protein called Mpp10,U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	MC	46	Total	C	N	O	0	0
			307	193	52	62		

- Molecule 30 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	P1	173	Total	C	N	O	S	0	0
			1368	876	245	243	4		

- Molecule 31 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	R1	355	Total	C	N	O	S	0	0
			2742	1756	466	509	11		

- Molecule 32 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R2	272	Total	C	N	O	S	0	0
			2228	1433	374	416	5		

- Molecule 33 is a protein called Sof1.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	S1	285	Total	C	N	O	0	0
			1425	855	285	285		

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	SA	1115	Total	C	N	O	P	0	0
			23759	10623	4225	7796	1115		

- Molecule 35 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	SC	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 36 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	SF	237	Total	C	N	O	S	0	0
			1881	1205	345	328	3		

- Molecule 37 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	SG	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 38 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SH	174	Total	C	N	O	S	0	0
			1369	856	262	248	3		

- Molecule 39 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	SI	165	Total	C	N	O		0	0
			1322	856	227	239			

- Molecule 40 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	SJ	170	Total	C	N	O	S	0	0
			1350	839	268	241	2		

- Molecule 41 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	SK	175	Total	C	N	O	S	0	0
			1412	892	272	247	1		

- Molecule 42 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	SM	141	Total	C	N	O	S	0	0
			1143	733	216	191	3		

- Molecule 43 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SN	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 44 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SO	134	Total	C	N	O	S	0	0
			1087	698	202	186	1		

- Molecule 45 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SP	109	Total	C	N	O	S	0	0
			750	462	147	140	1		

- Molecule 46 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	SR	125	Total	C	N	O	0	0
			973	625	174	174		

- Molecule 47 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SX	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 48 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SY	103	Total	C	N	O	S	0	0
			785	501	144	138	2		

- Molecule 49 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SZ	101	Total	C	N	O		0	0
			801	512	144	145			

- Molecule 50 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Sc	79	Total	C	N	O	S	0	0
			595	371	108	111	5		

- Molecule 51 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Sd	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 52 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	Sf	30	Total	C	N	O		0
			251	162	50	39		0

- Molecule 53 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Sg	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 54 is a protein called Utp7.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	U1	285	Total	C	N	O		0
			1425	855	285	285		0

- Molecule 55 is a protein called Utp11.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	U2	73	Total	C	N	O	0	0
			365	219	73	73		

- Molecule 56 is a protein called Utp20.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	U3	1407	Total	C	N	O	0	0
			7035	4221	1407	1407		

- Molecule 57 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	U4	126	Total	C	N	O	S	0	0
			990	633	179	168	10		

- Molecule 58 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	U5	248	Total	C	N	O	S	0	0
			2009	1285	357	359	8		

- Molecule 59 is a protein called Helical domain protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	UA	338	Total	C	N	O	0	0
			1690	1014	338	338		

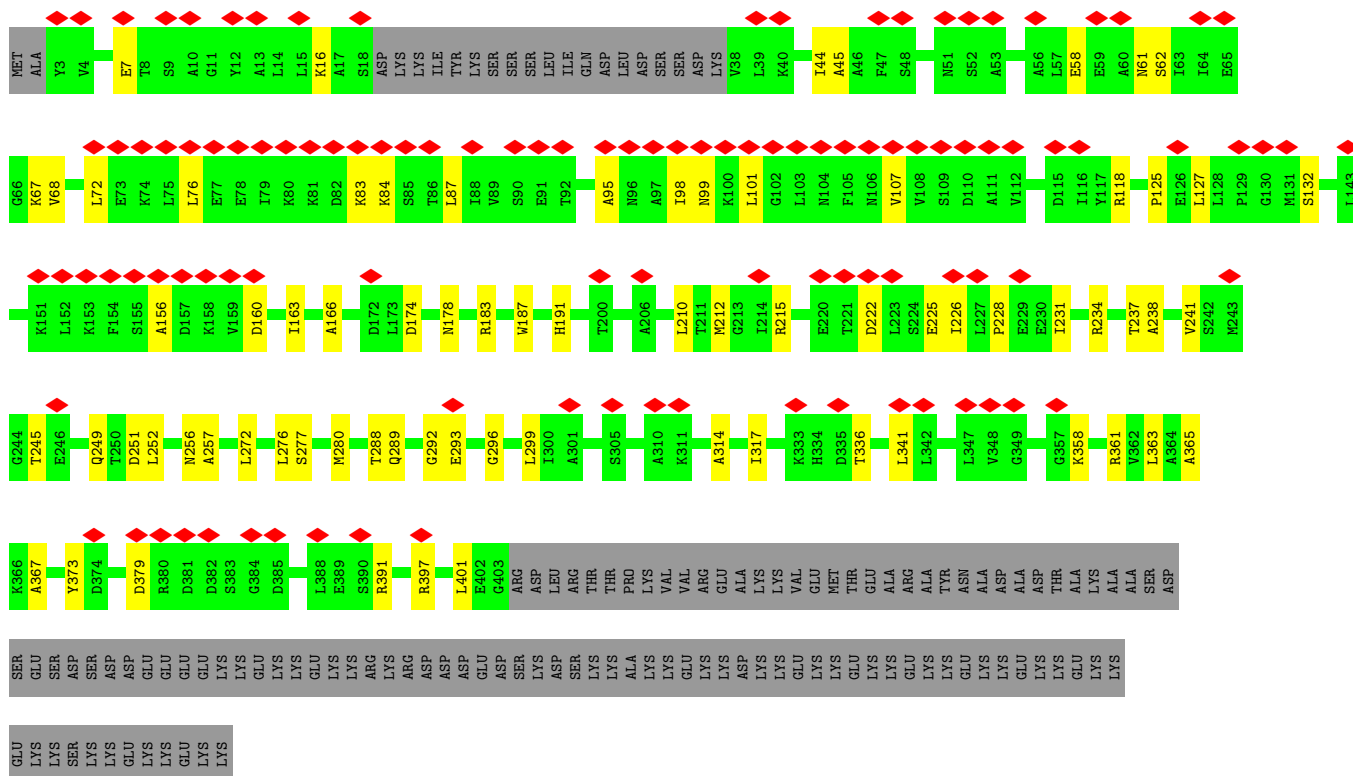
- Molecule 60 is a protein called Helical domain protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	UB	555	Total	C	N	O	0	0
			2775	1665	555	555		

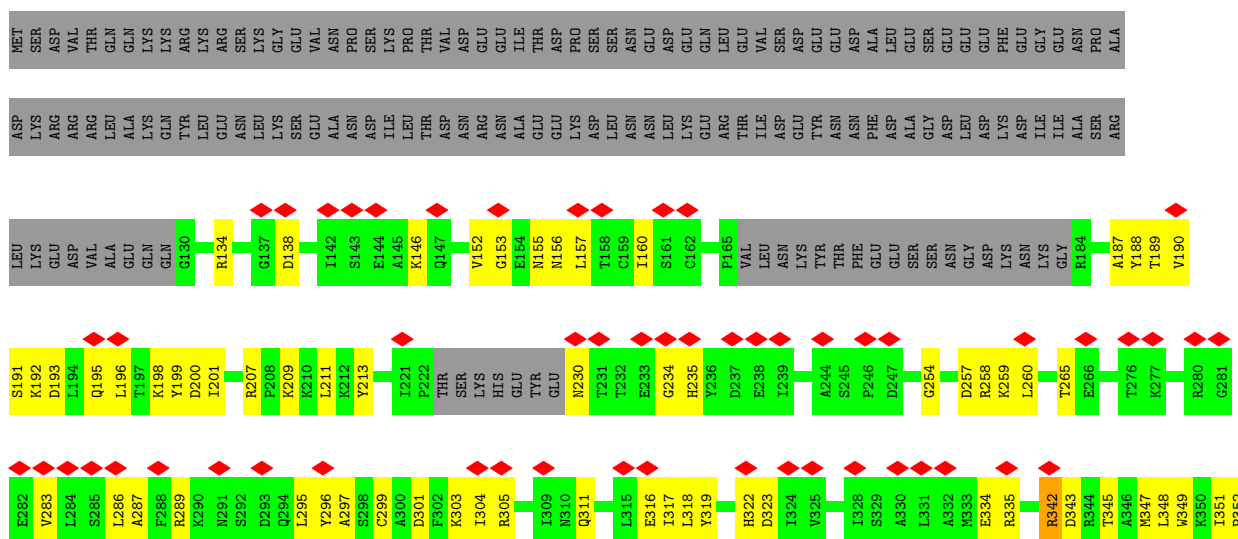
- Molecule 61 is a protein called Unassigned helices.

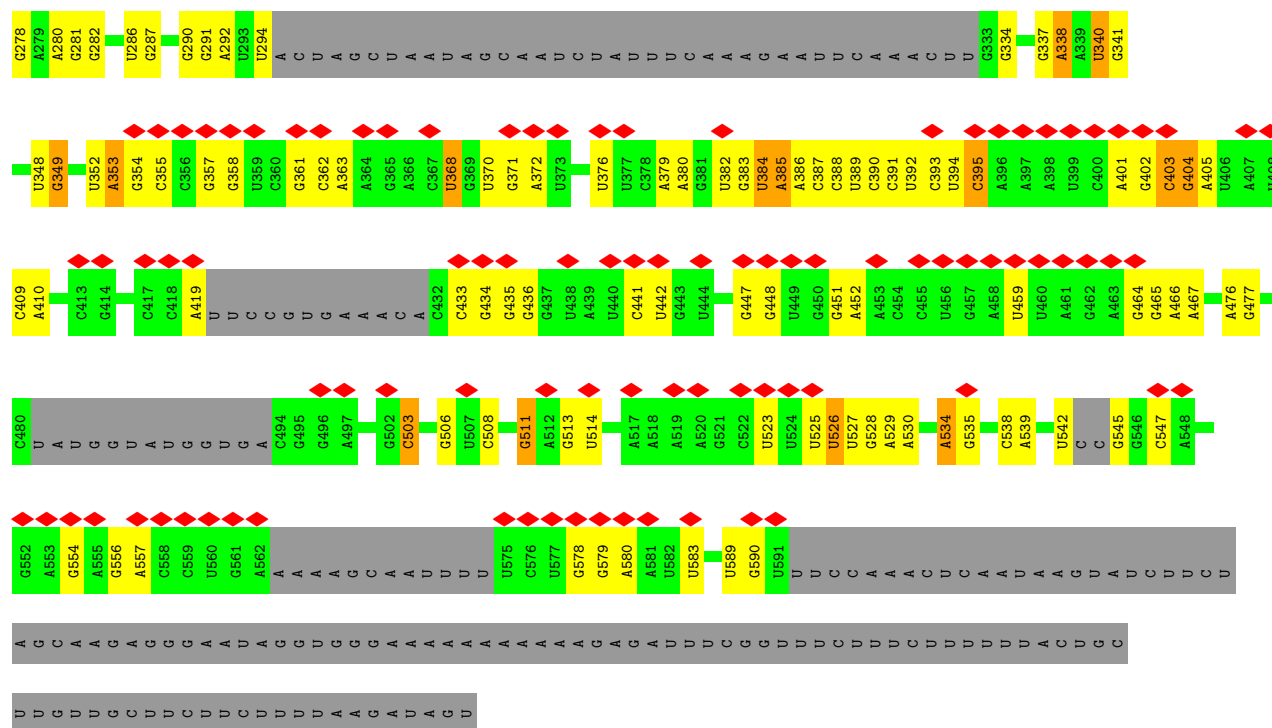
Mol	Chain	Residues	Atoms				AltConf	Trace
61	UC	660	Total	C	N	O	0	0
			3300	1980	660	660		

- Molecule 4: Nucleolar protein 58

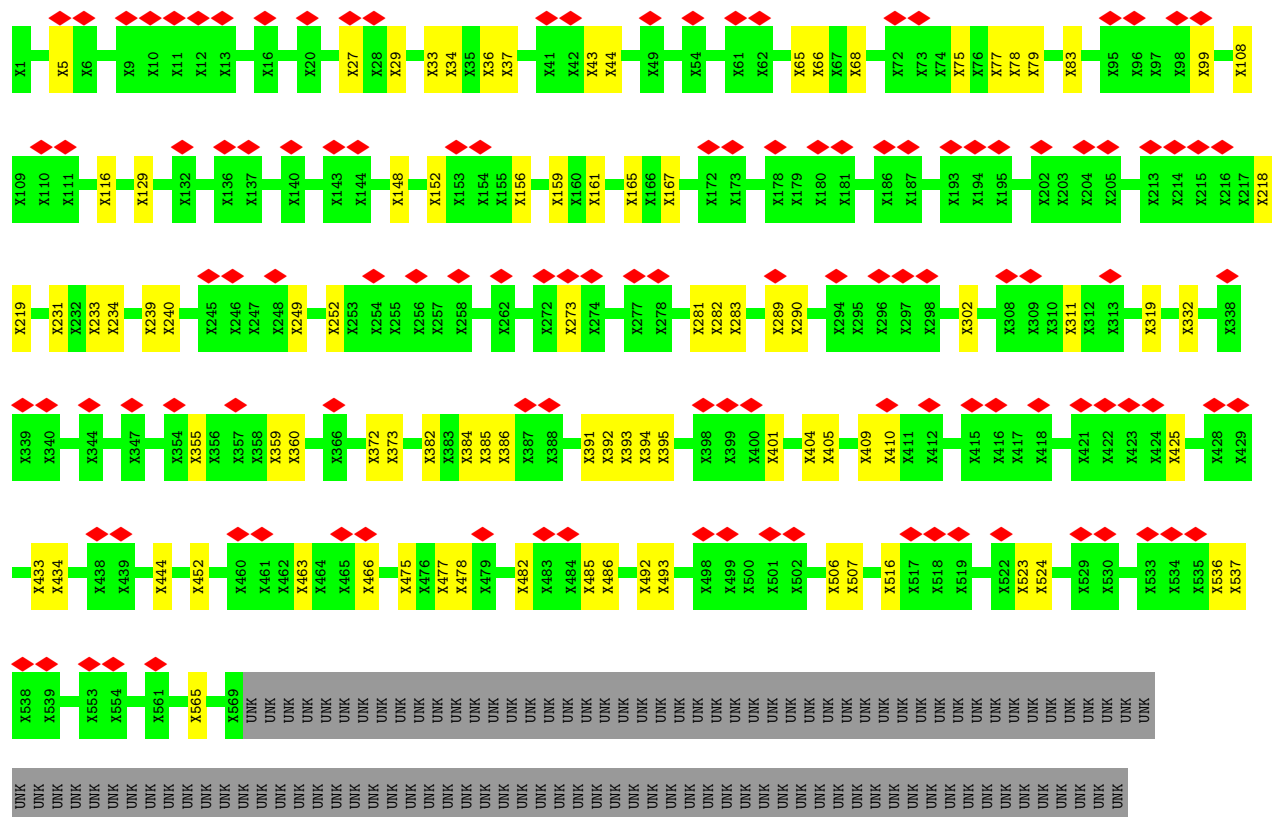


- Molecule 5: Ribosomal RNA-processing protein 9



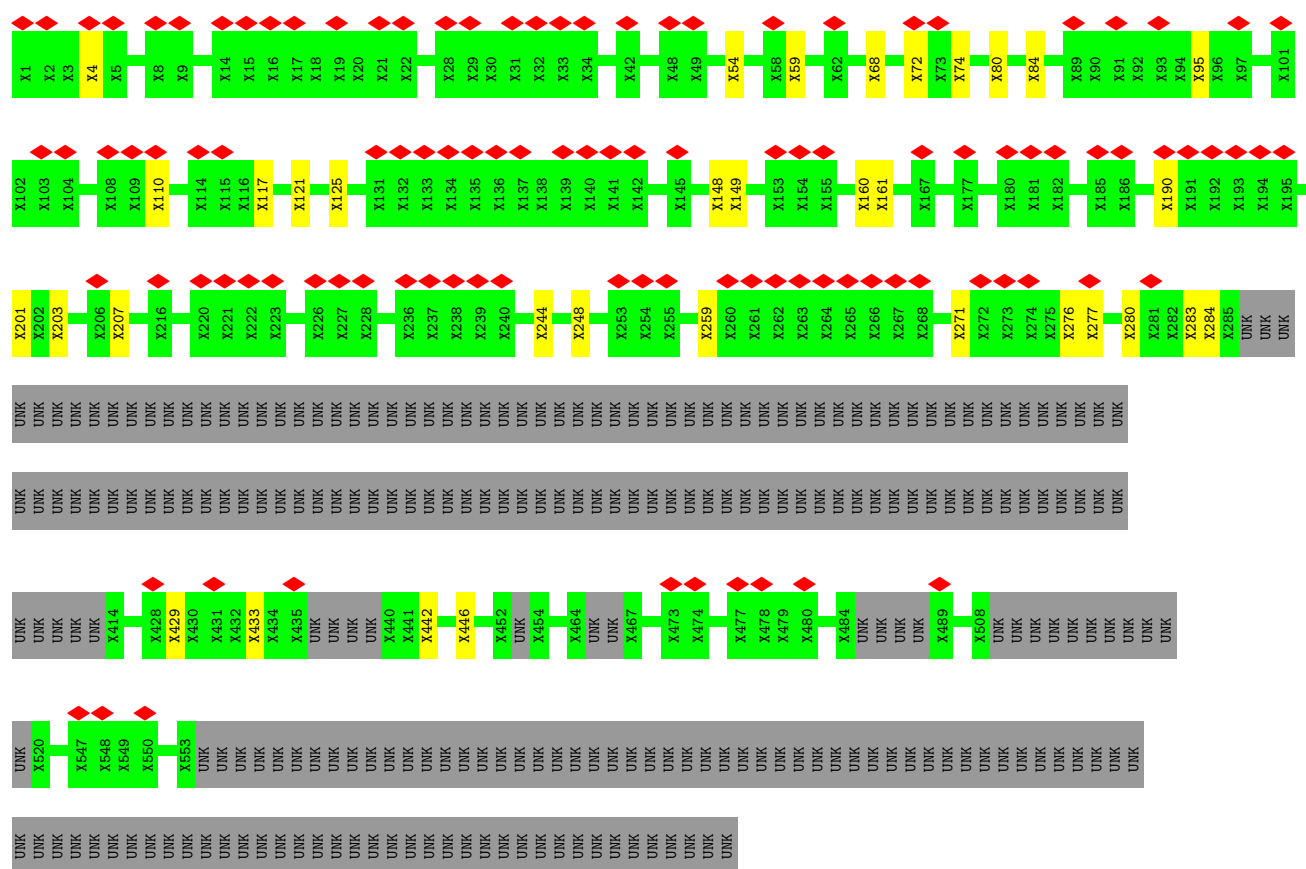


• Molecule 8: Utp4

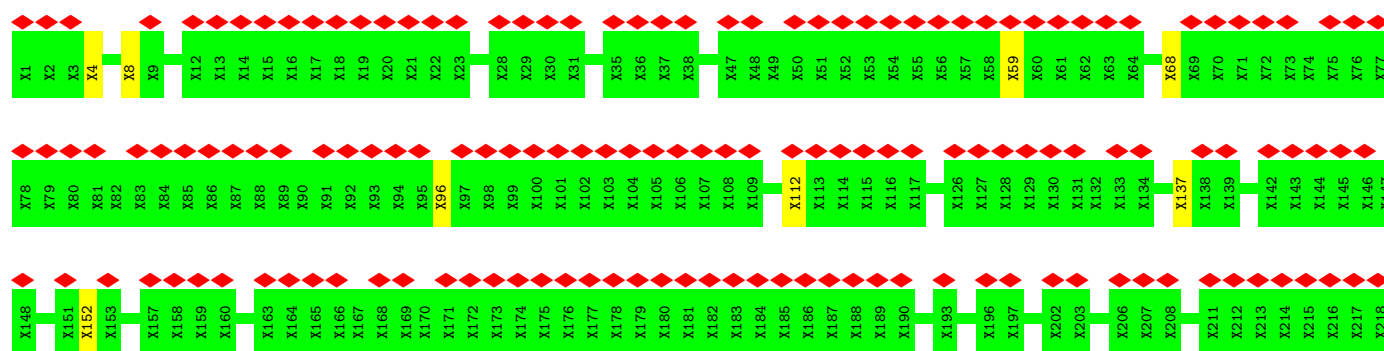


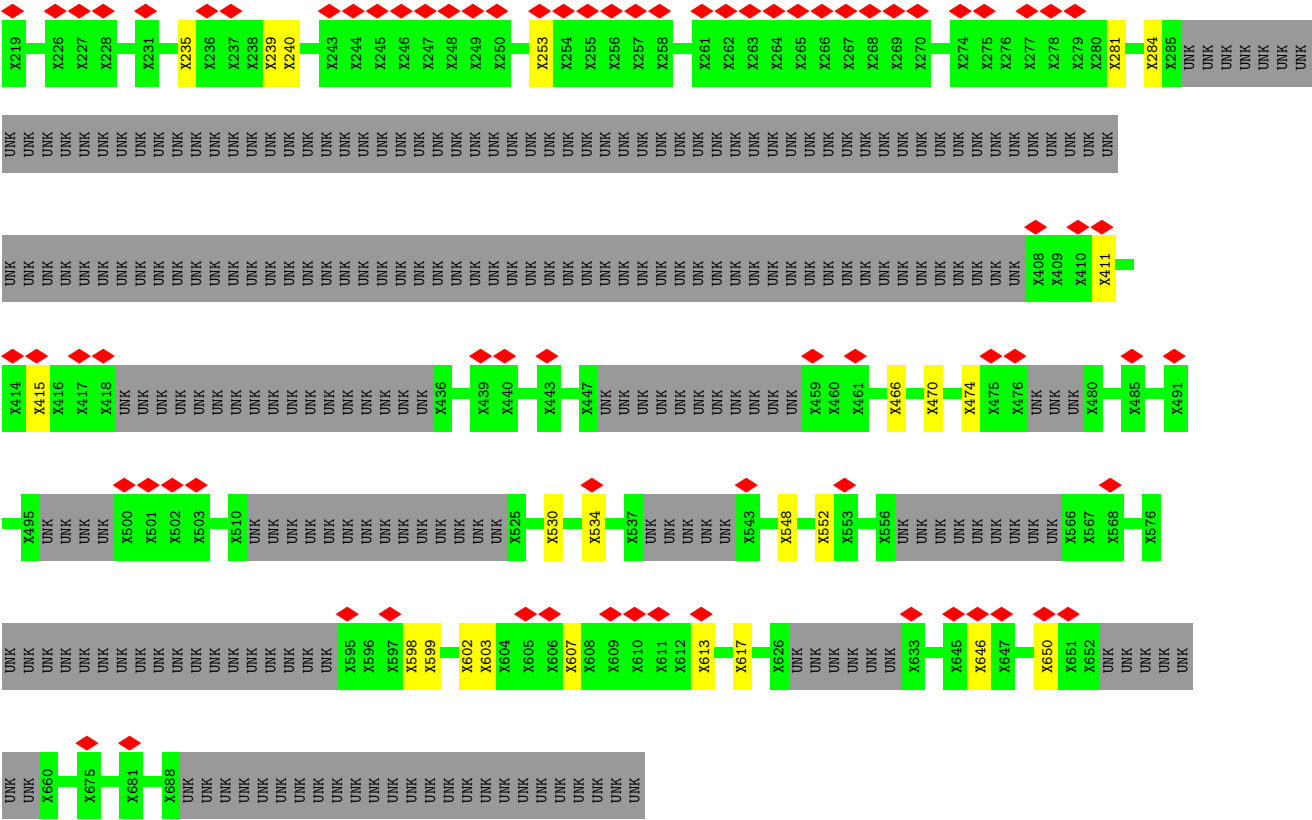
[illegible]

Chain AB:

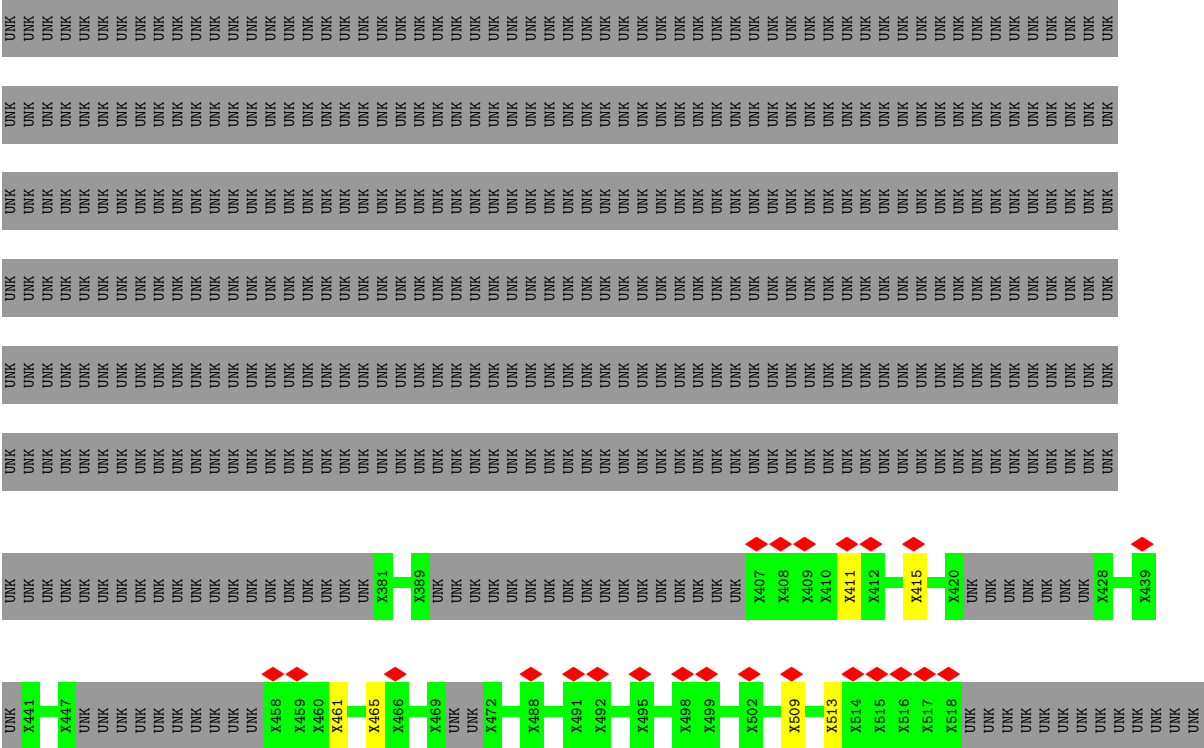


Chain AC:



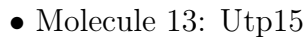


• Molecule 11: Utp9

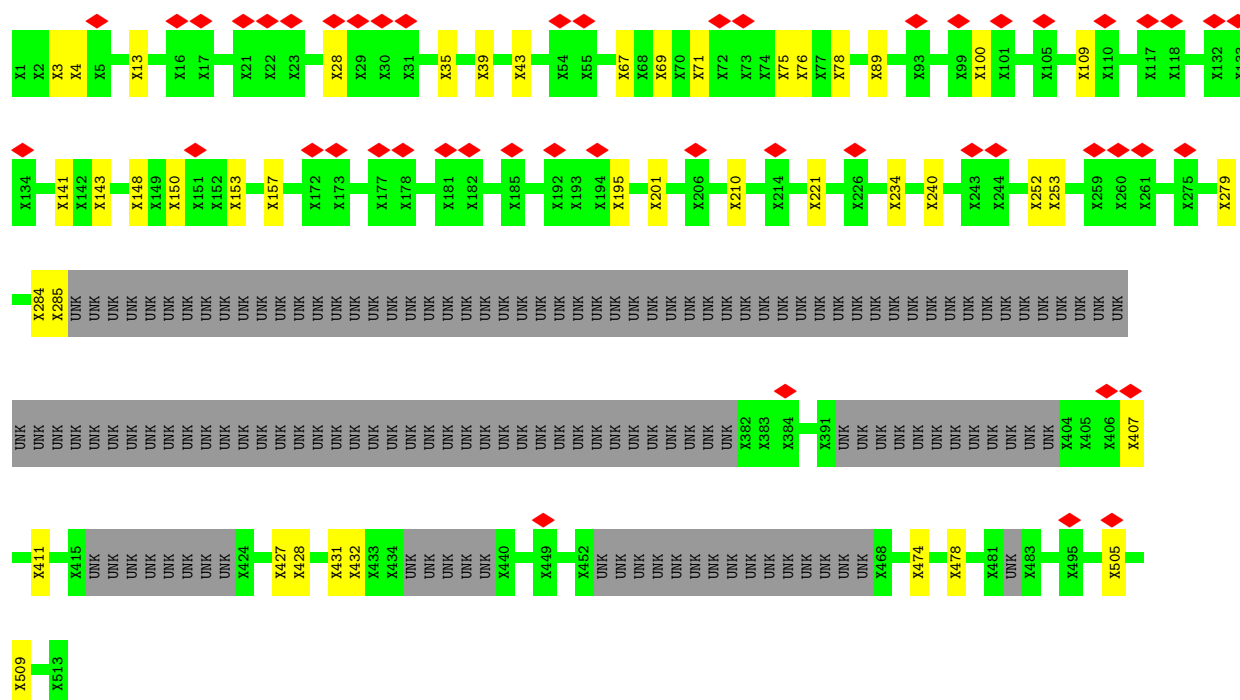


- Molecule 12: U3 small nucleolar RNA-associated protein 10,Utp10



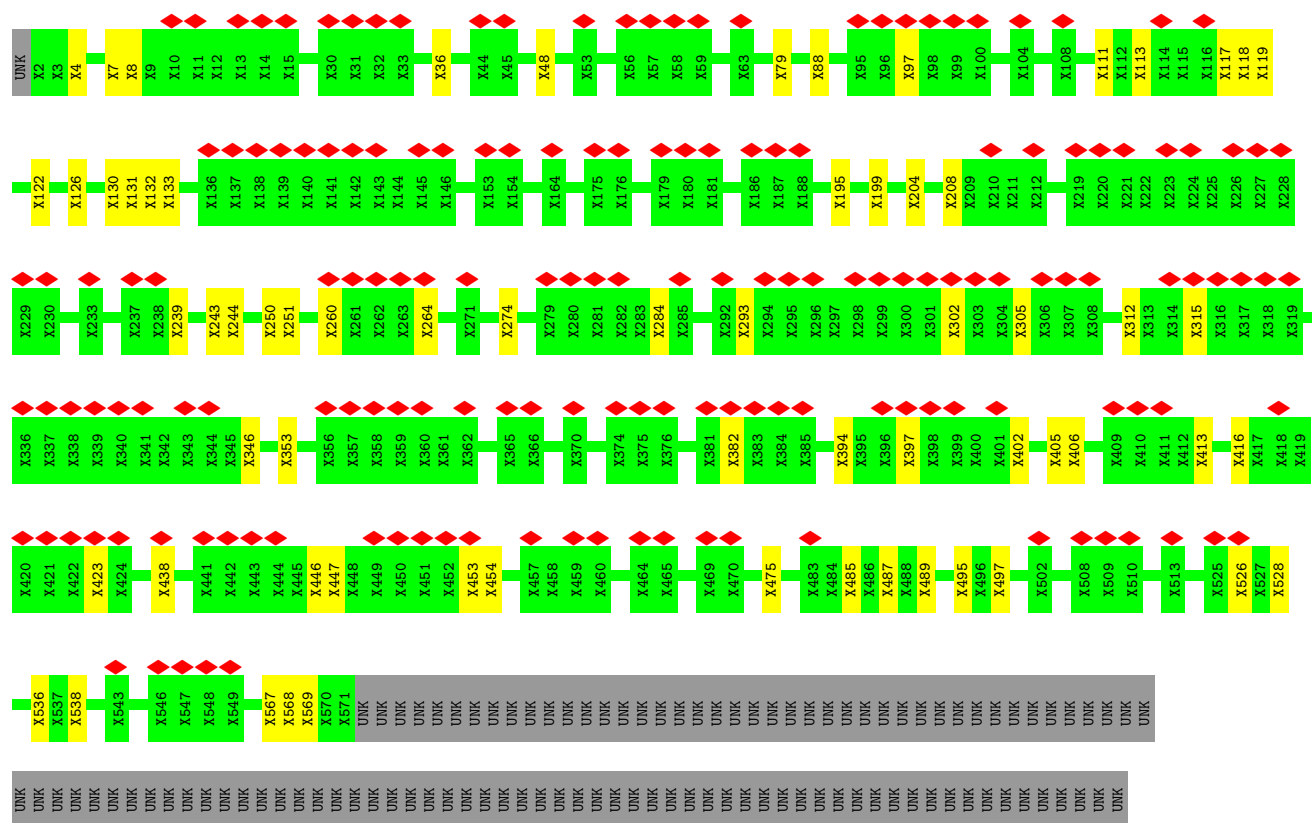


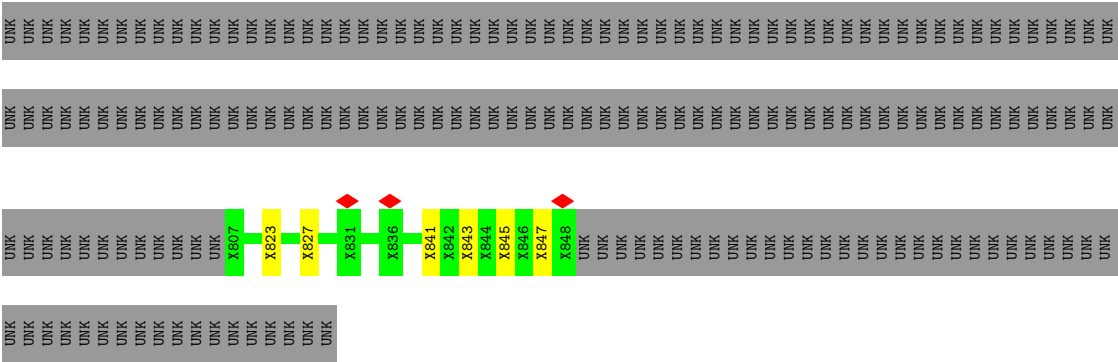
Chain AF: 



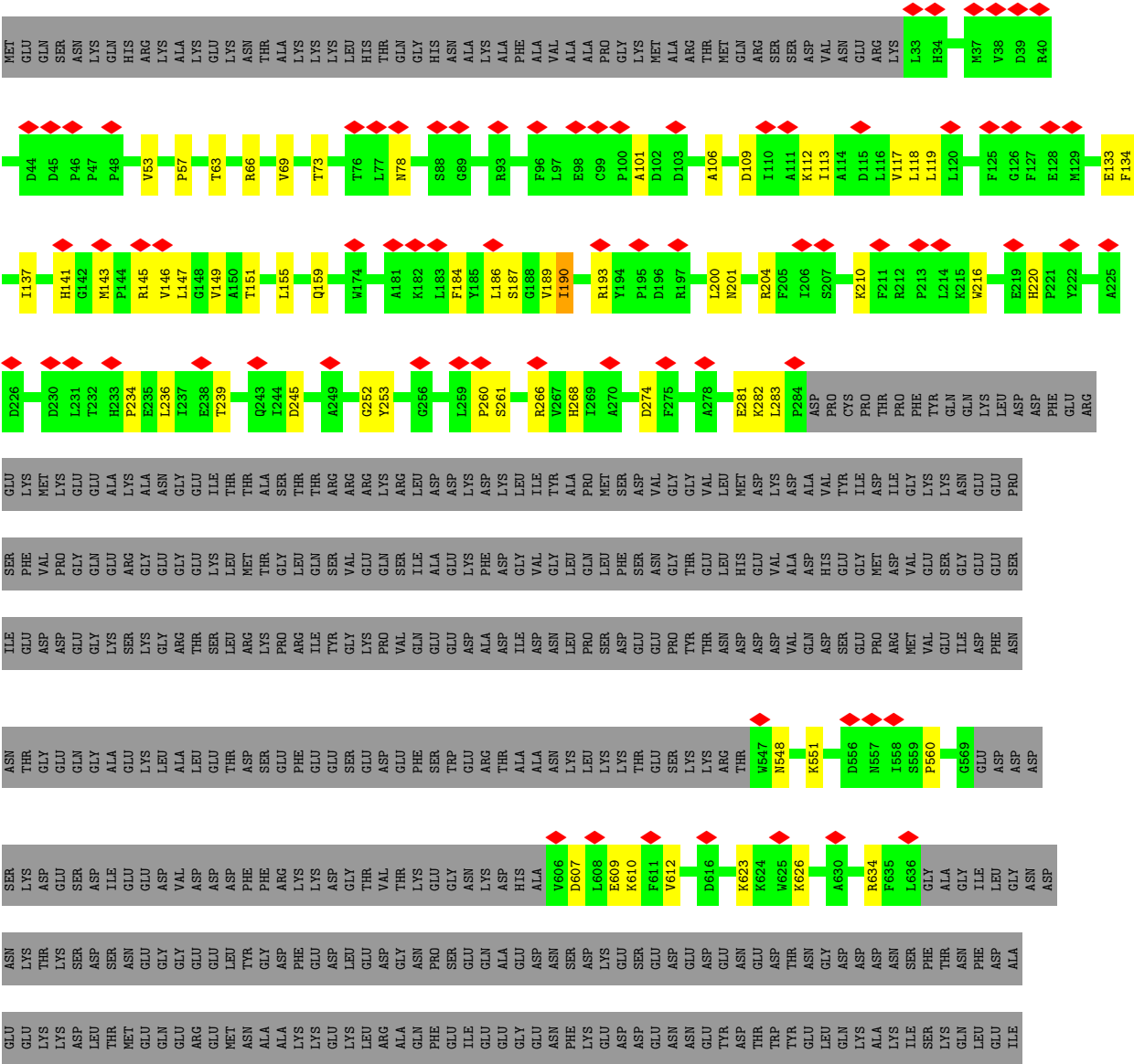
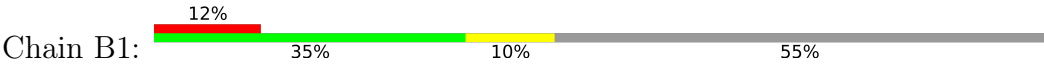
• Molecule 14: Utp17

Chain AG: 

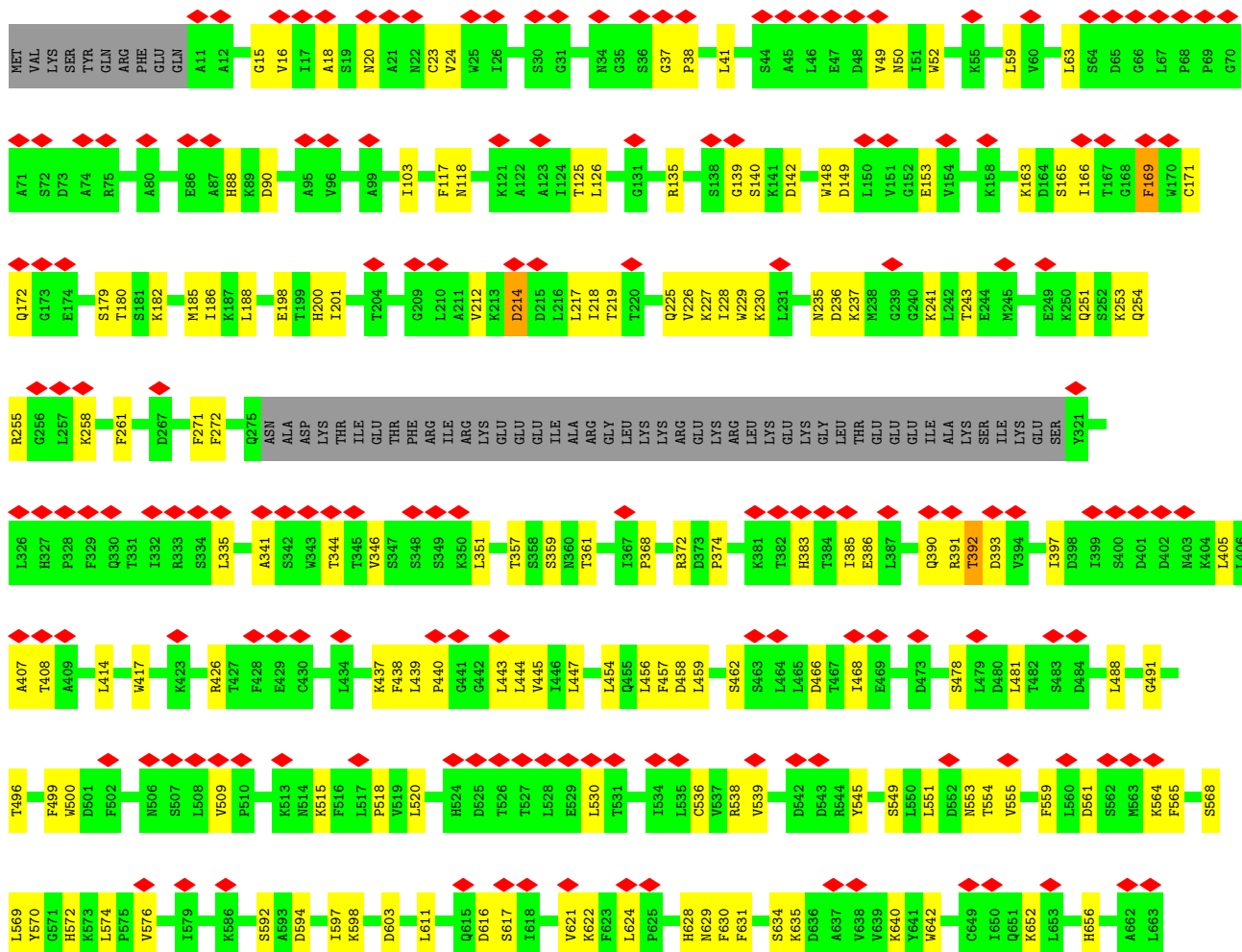


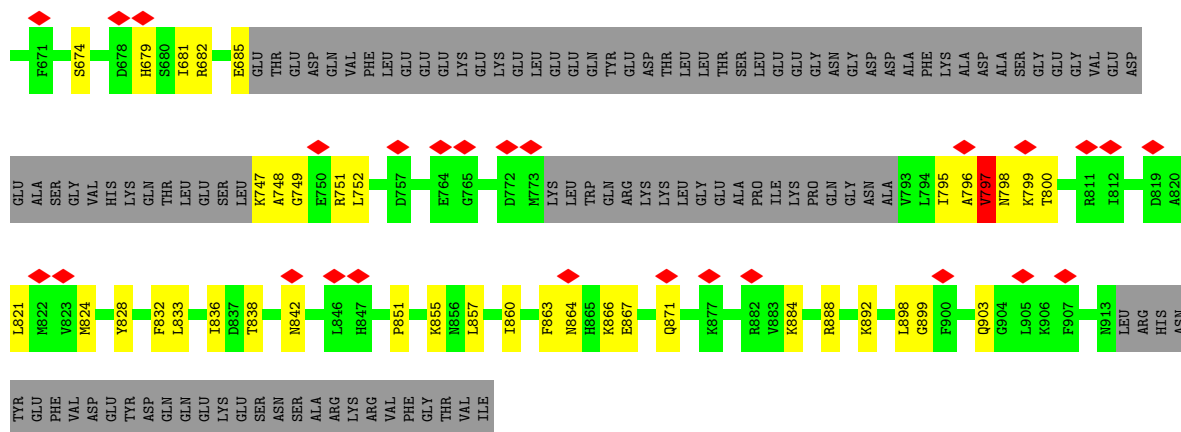


• Molecule 15: Ribosome biogenesis protein BMS1

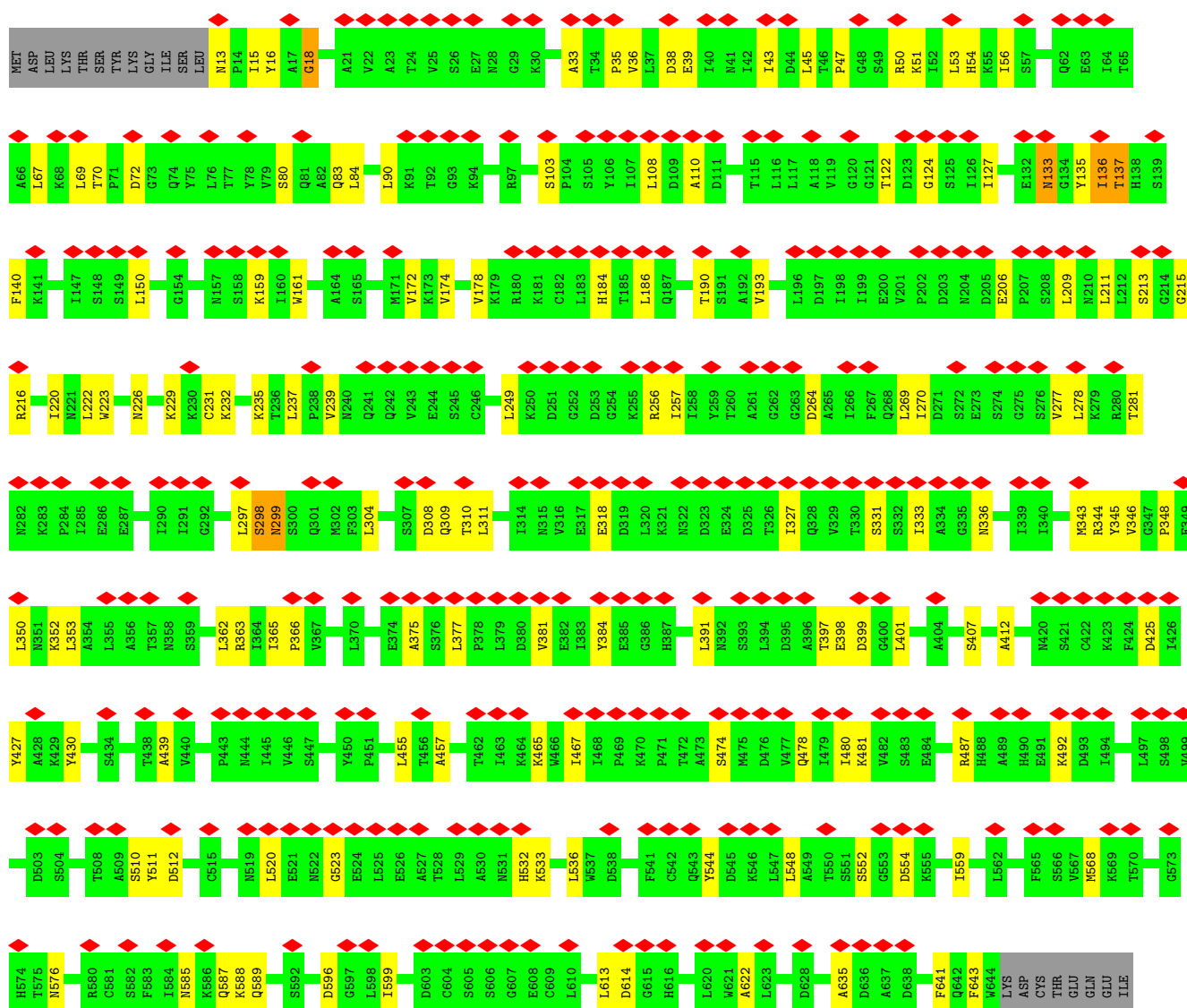
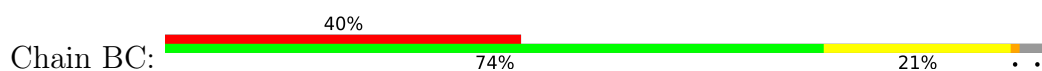


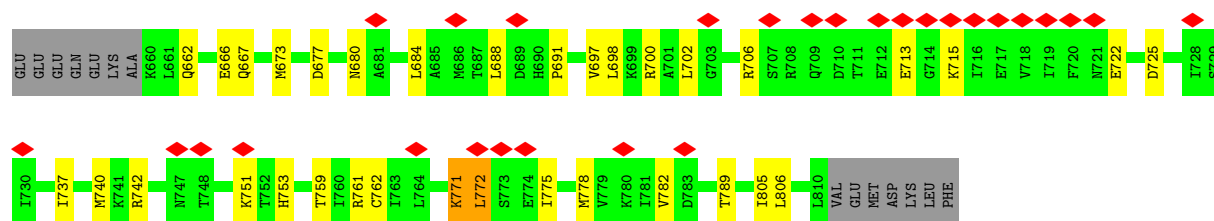
- Molecule 17: U3 small nucleolar RNA-associated protein 12



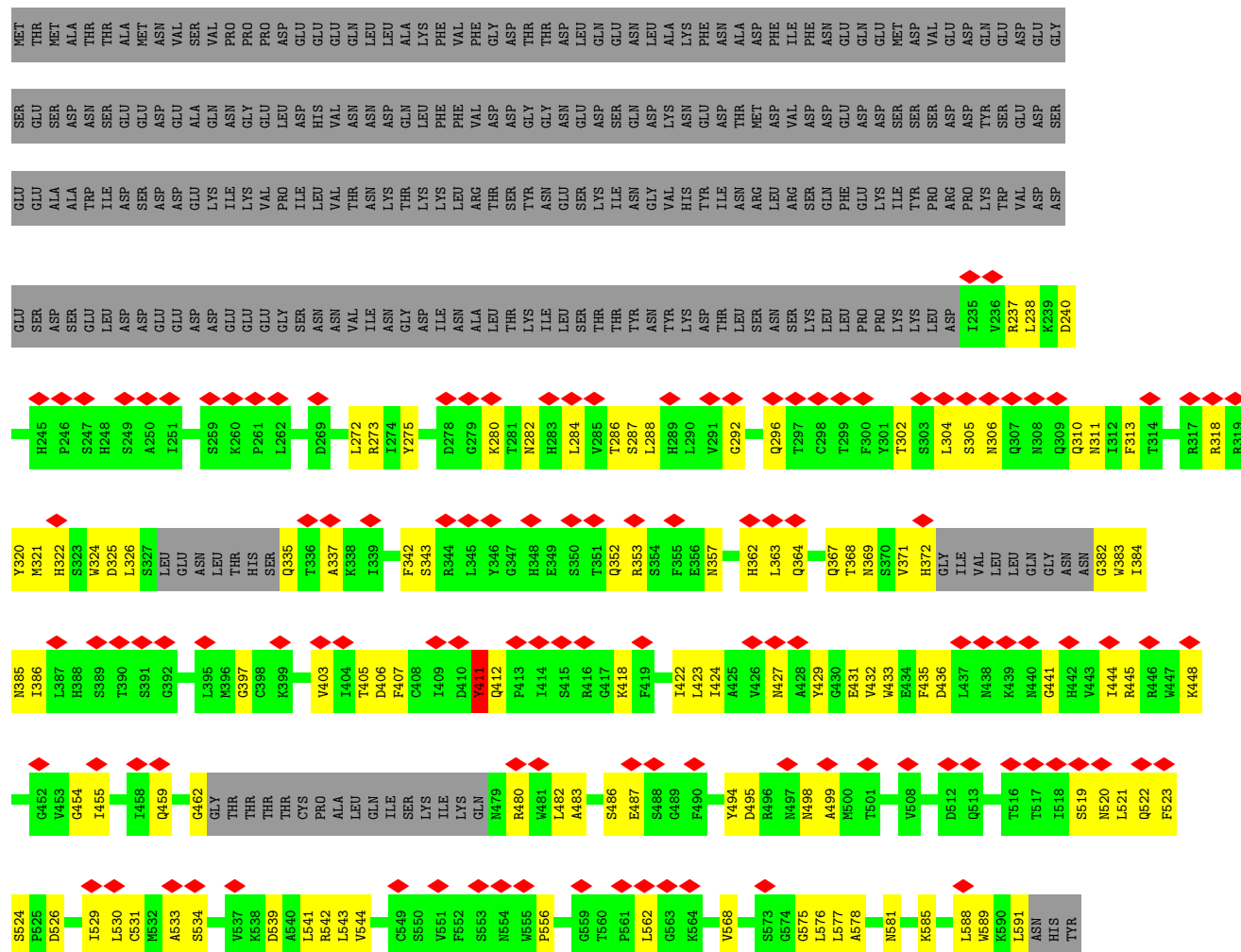


• Molecule 18: U3 small nucleolar RNA-associated protein 13



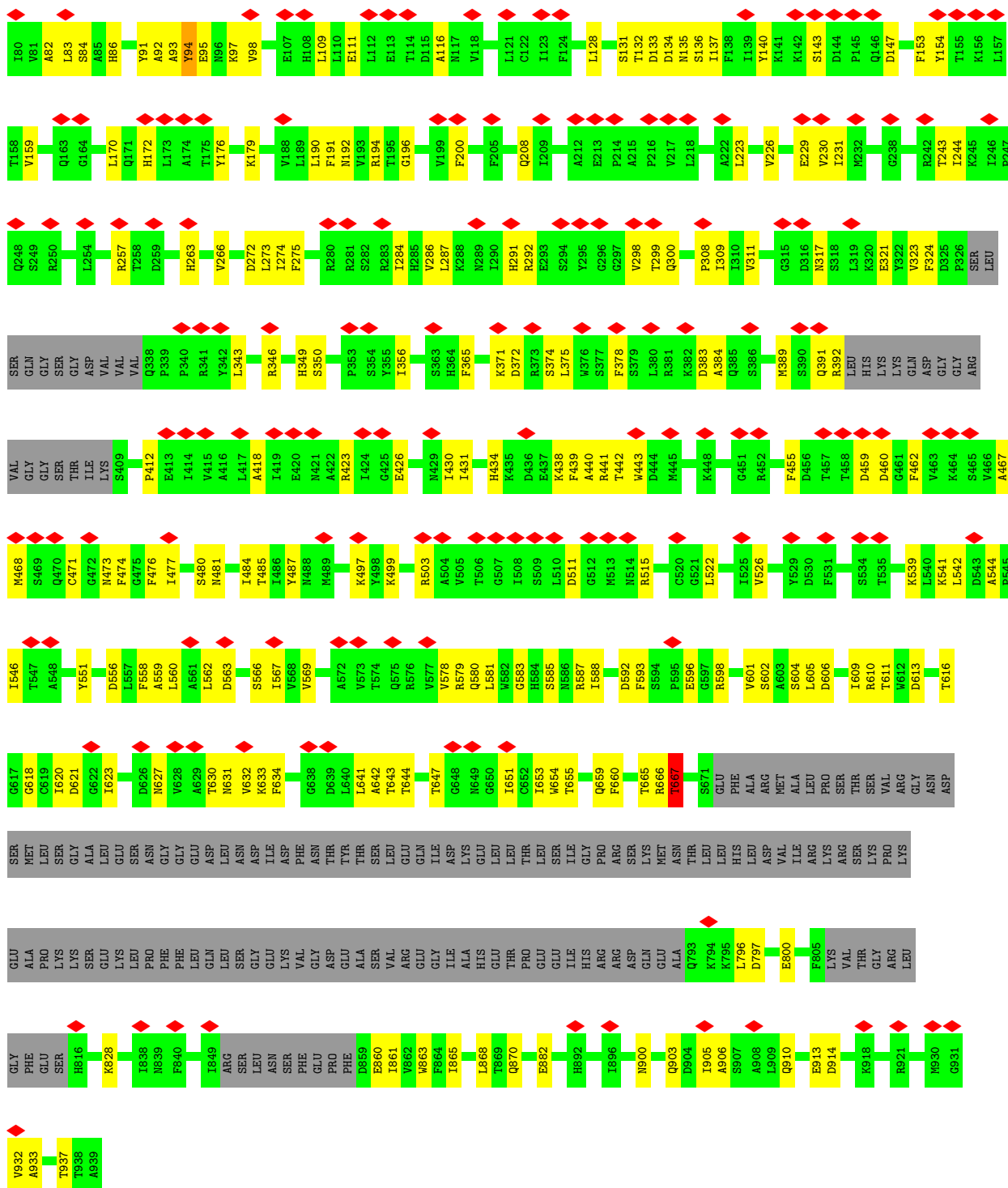


• Molecule 19: U3 small nucleolar RNA-associated protein 18

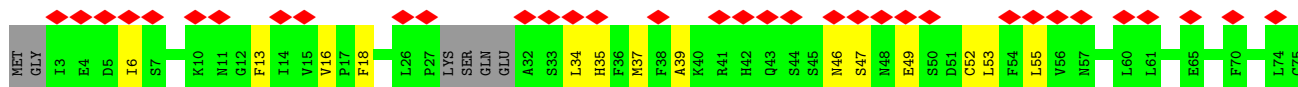


• Molecule 20: U3 small nucleolar RNA-associated protein 21

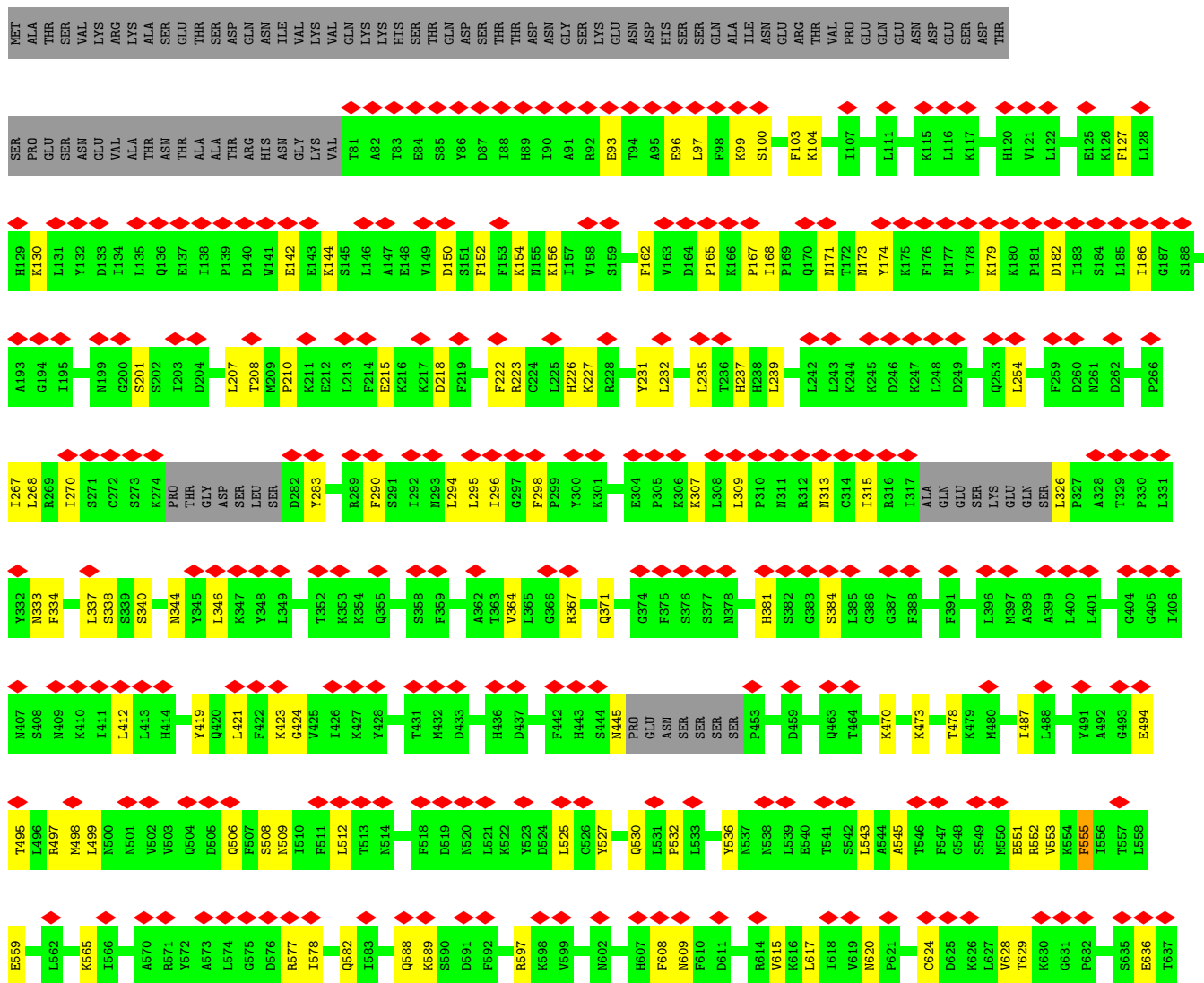


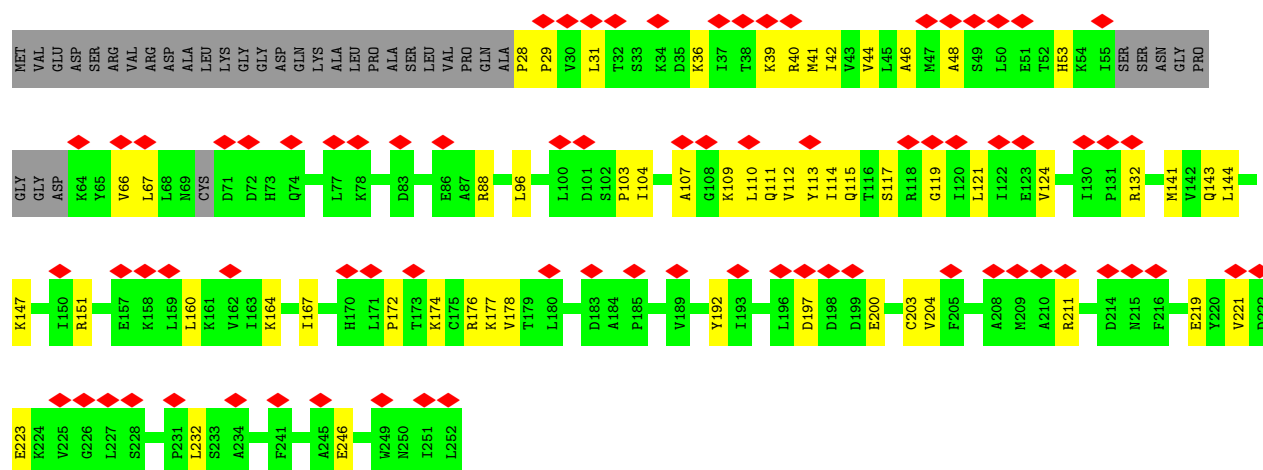


• Molecule 21: Ribosomal RNA-processing protein 7

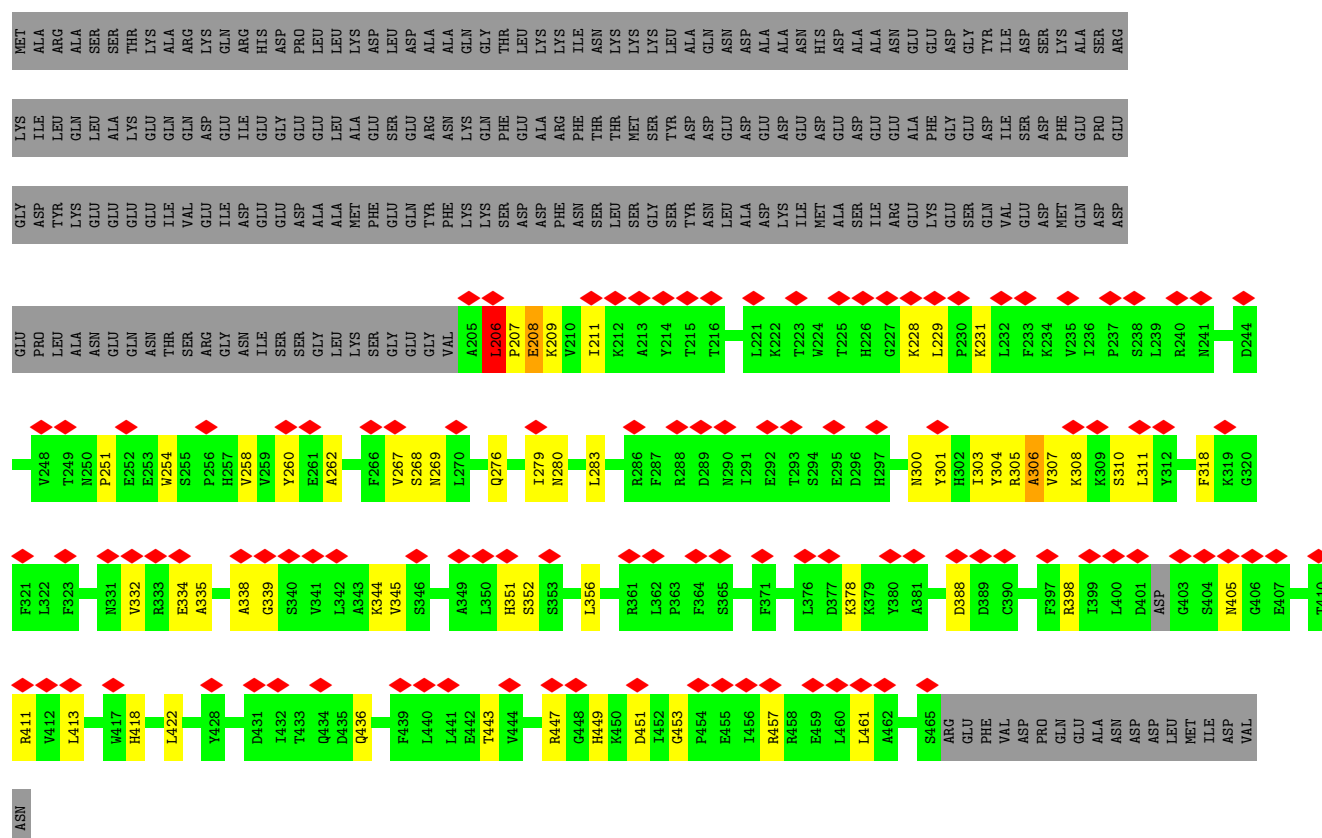
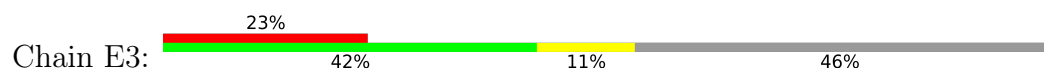


- Molecule 22: U3 small nucleolar RNA-associated protein 22

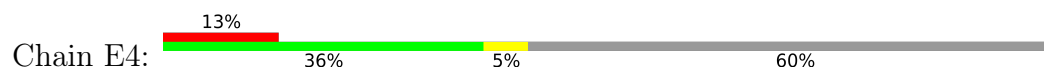


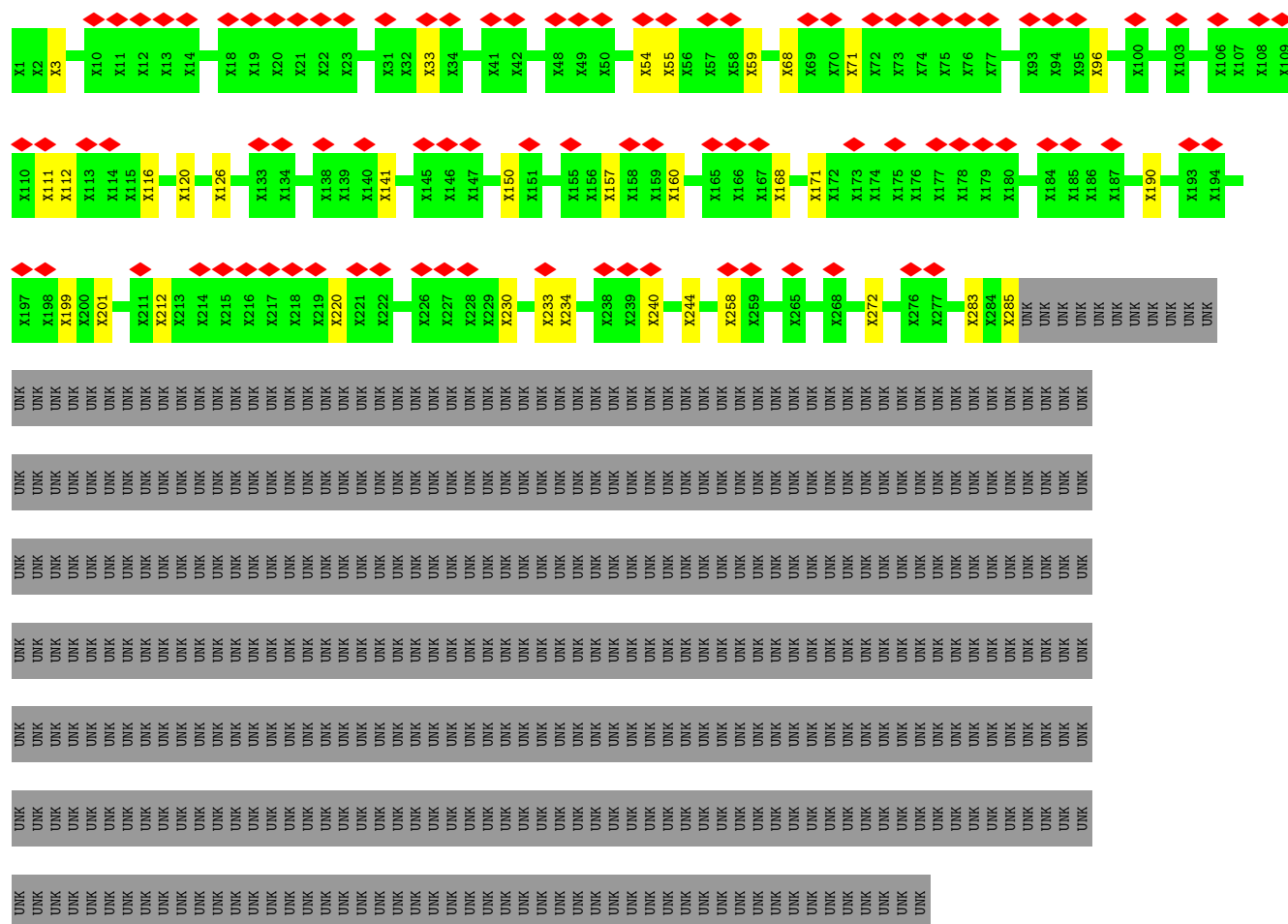


• Molecule 24: Essential nuclear protein 1

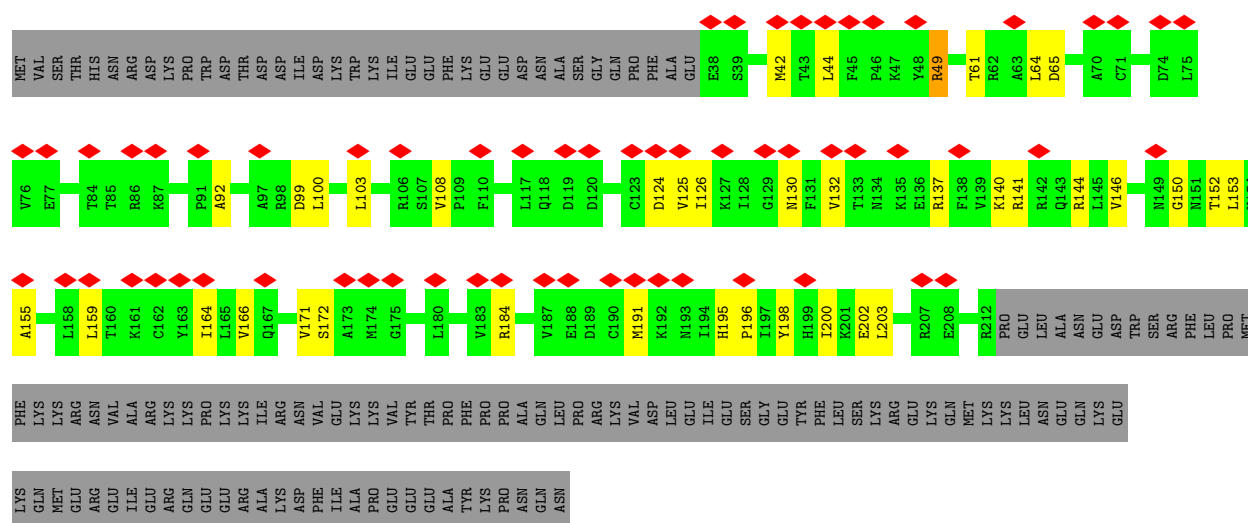
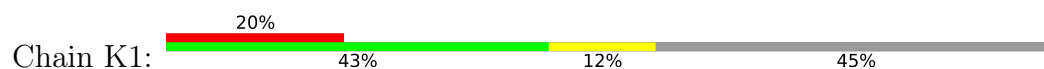


• Molecule 25: Enp2

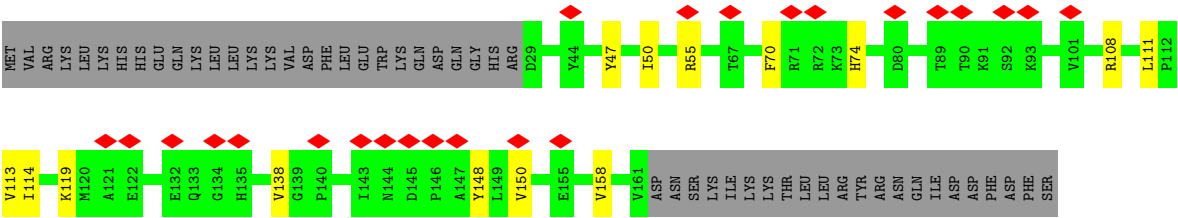




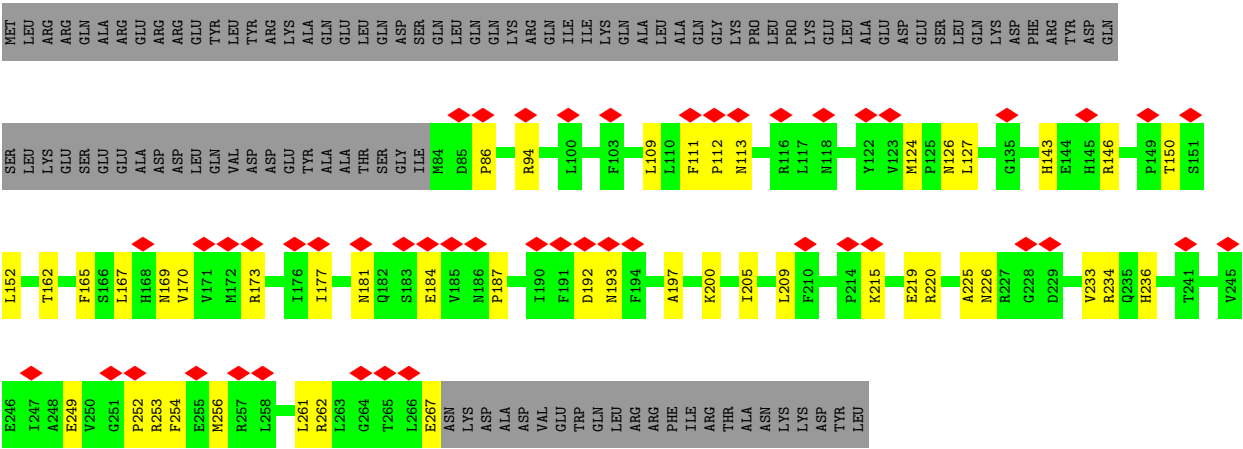
• Molecule 26: KRR1 small subunit processome component



• Molecule 27: U3 small nucleolar ribonucleoprotein protein IMP3



• Molecule 28: U3 small nucleolar ribonucleoprotein protein IMP4



• Molecule 29: Mpp10,U3 small nucleolar RNA-associated protein MPP10



[illegible]

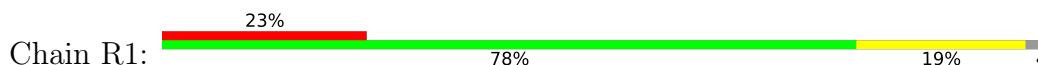
- Molecule 30: Pre-rRNA-processing protein PNO1



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

SER	GLY
ARG	SER
LEU	ARG
LYS	LYS
GLU	THR
ARG	HIS
TYR	GLU
	SER
	LYS
	THR
	VAL
	VAL
	ASP
	ASP
	GLN
	GLY
	LYS
	PRO
	ARG
	PHE
	THR
	SER
	SER
	ALA
	SER
	LYS
	THR
	GLN
	GLY
	ASN
	LYS
	ILE
	LYS
	F94
	P103
	H104
	R105
	M106
	L109
	W113
	H123
	L126
	T134
	K135
	S136
	K144
	F145
	T146
	T147
	D148
	P149
	L152
	F158
	A161
	F162
	T163
	L164
	G165
	F166
	D170
	L174
	L175
	R176
	L177
	D178
	D179
	F185
	E186
	V187
	K188
	K191
	T192
	L193
	T194
	G195
	D196
	H197
	L198
	A201
	I202
	G203
	R204
	I205
	A219
	T220
	R221
	T222
	H232
	F237
	I240
	V248
	I251
	S254
	P255
	P256
	V266

- Molecule 31: RNA 3'-terminal phosphate cyclase-like protein

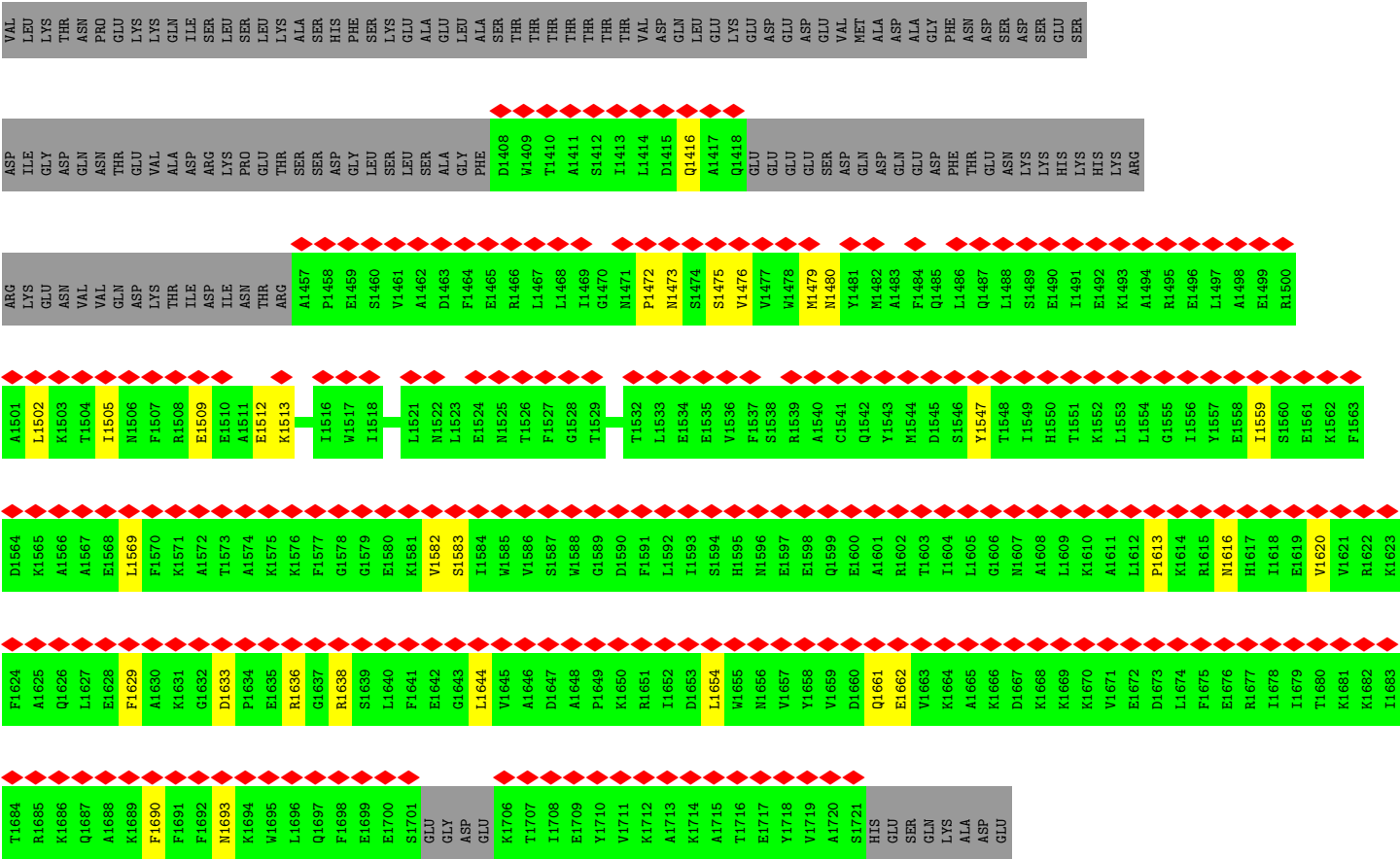


M301	G304	E306	D307	I308	G309	R310	L311	R312	I313	E316	E320	R321	I332	F333	N334	T335	D343	E344	A345	D346	N347	E348	D349	M350	I351	A352	T353	I354	R355	G358	F359	T360	N361	THR	SER	LYS	LYS	ILE	ALA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
	T192	T198	V200	S201	P202	S203	L204	V205	N206	R207	W208	L216	L219	E222	A227	D228	W229	W230	R231	W234	S235	G236	Q248	K252	Y256	F257	A258	E259	D260	G262	D263	A264	G265	L271	G278	E281	K285	A287	A288	G289	R291																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							

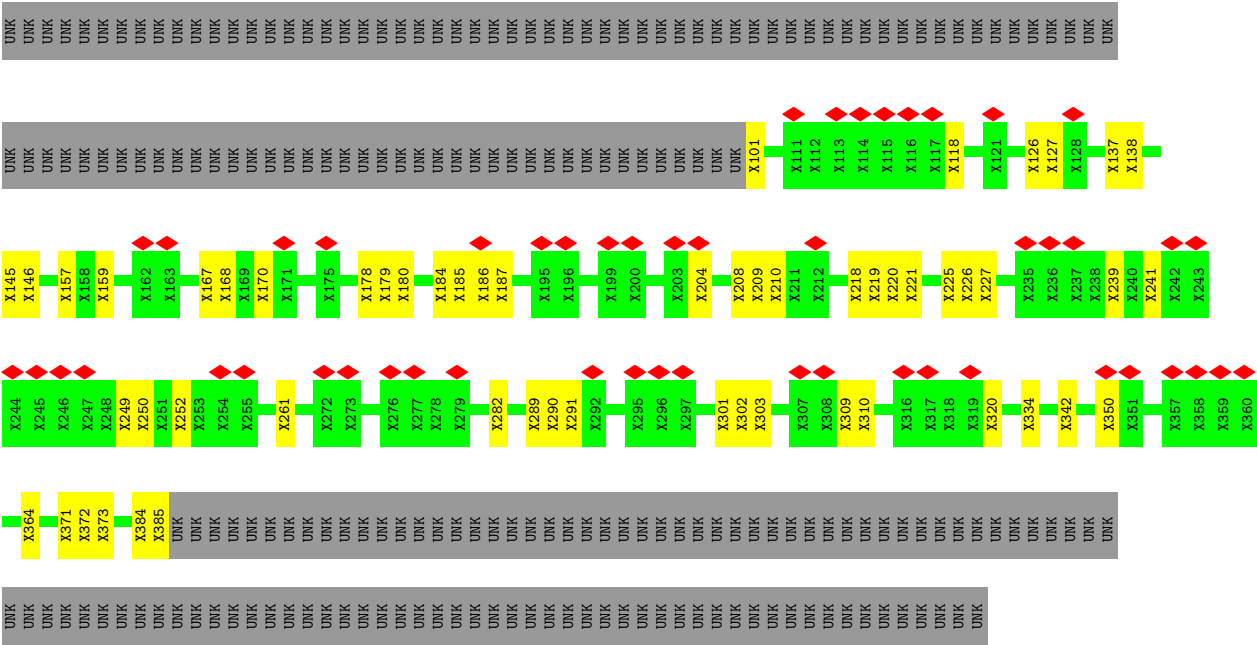
- Molecule 32: rRNA biogenesis protein RRP5

[illegible]

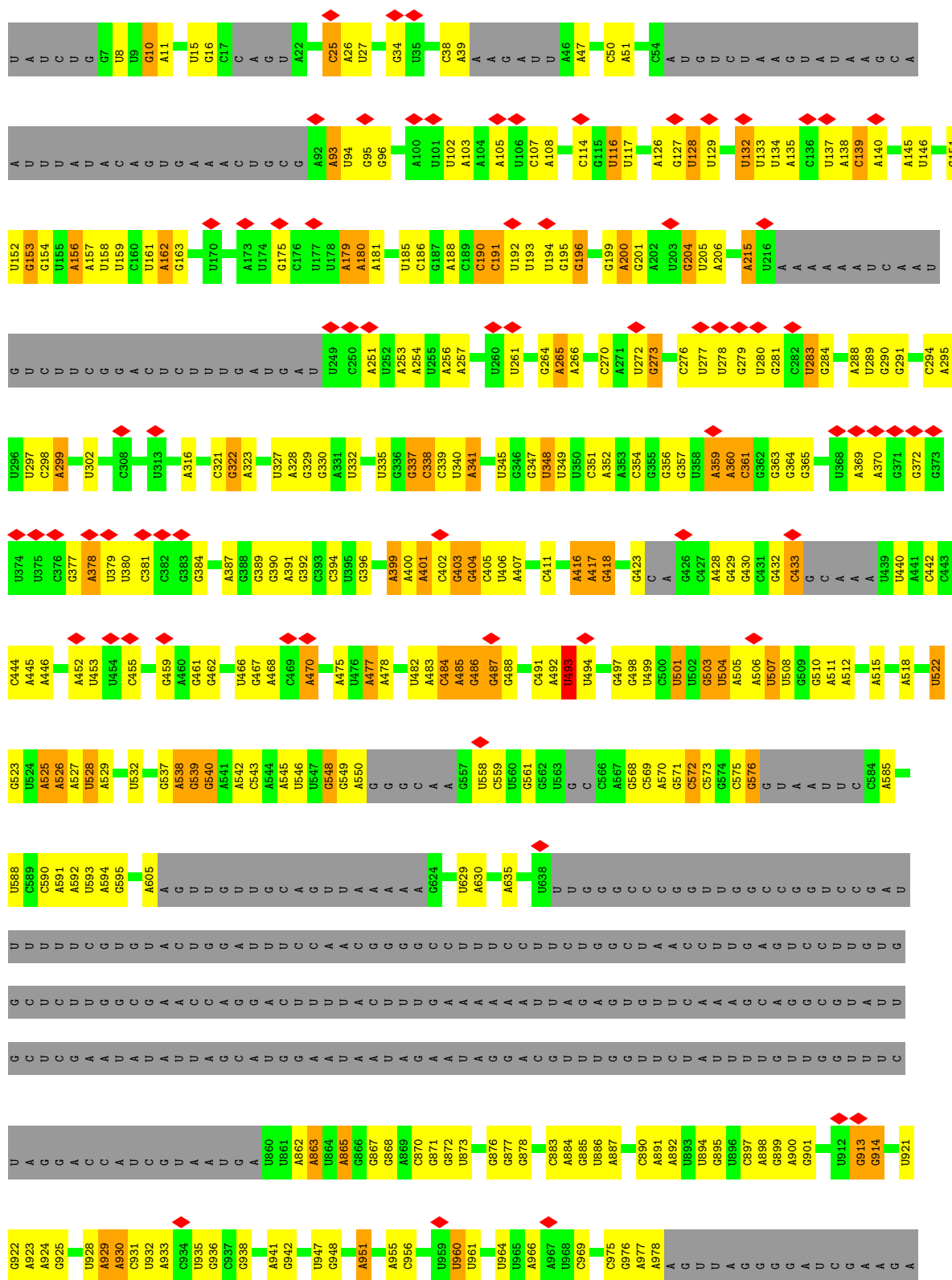
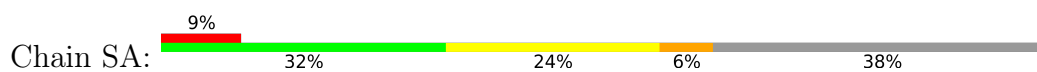


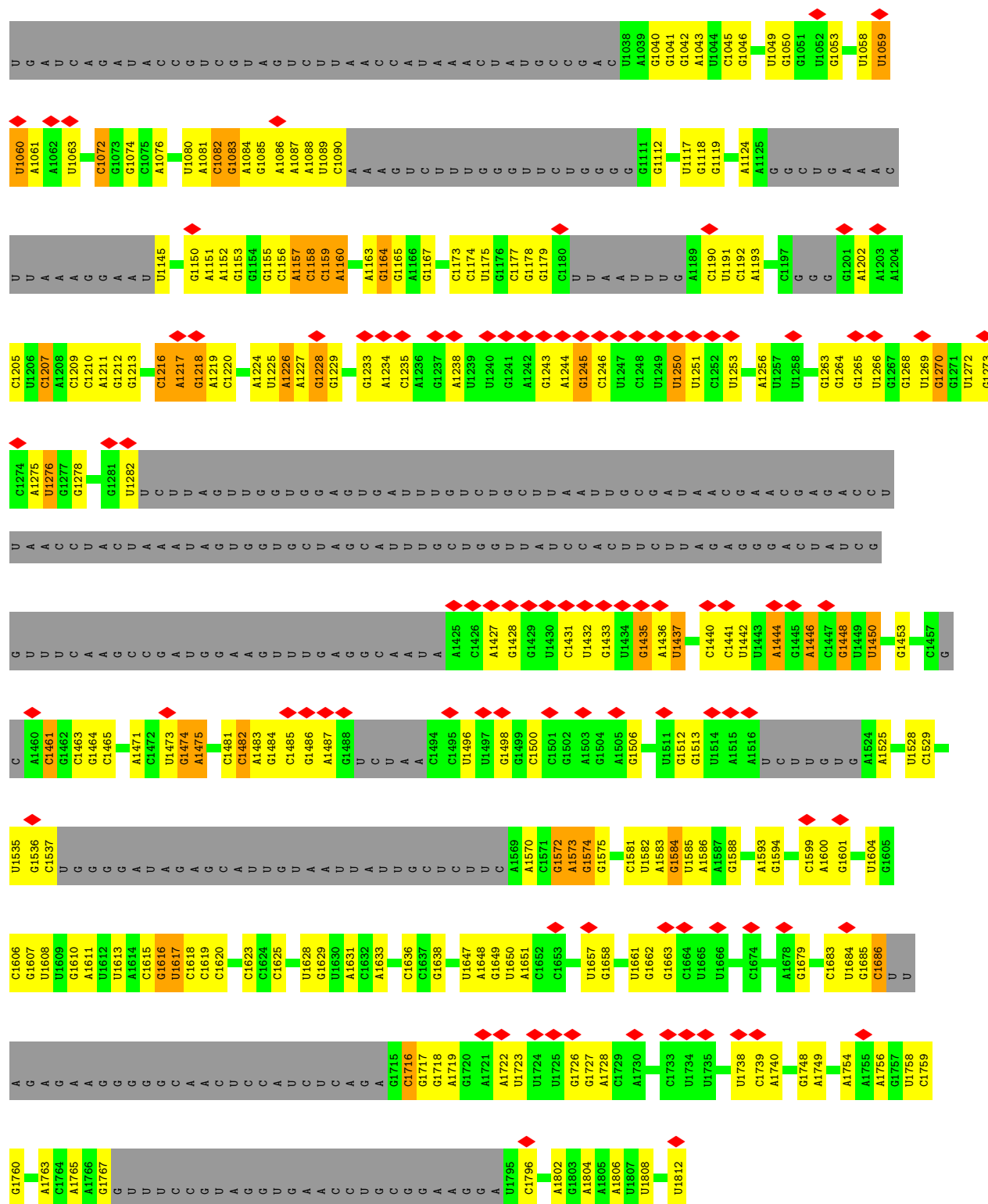


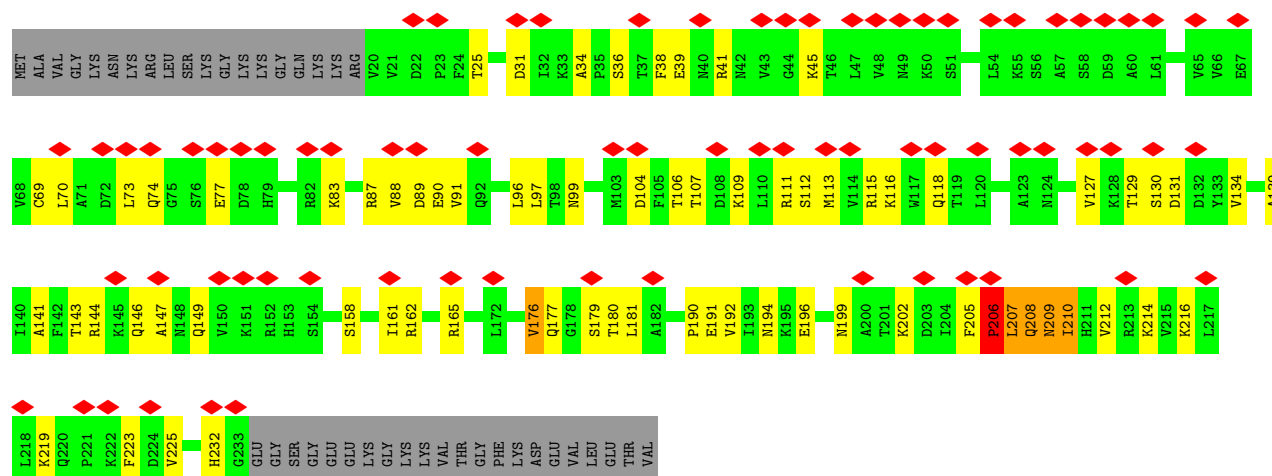
• Molecule 33: Sof1



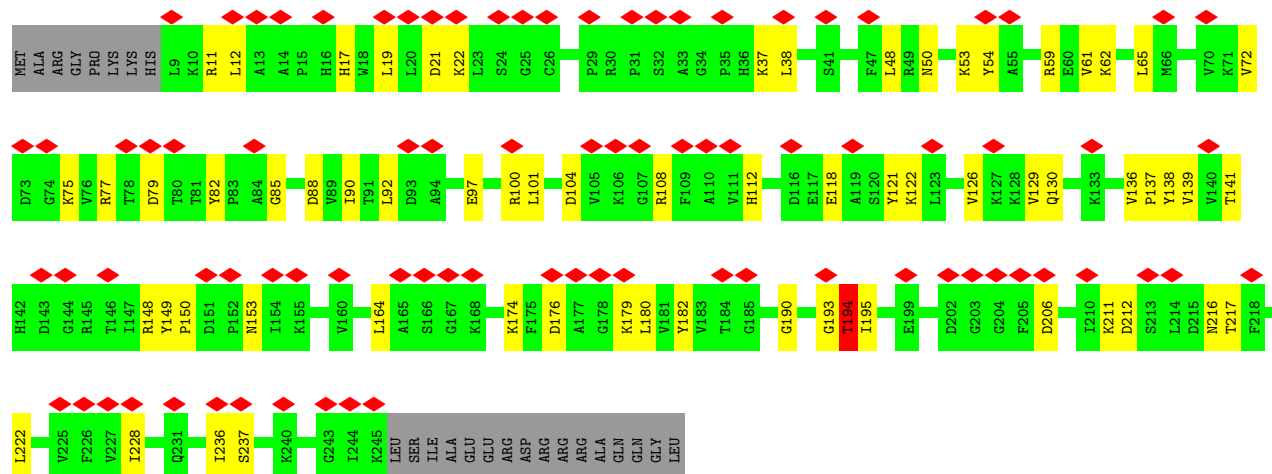
• Molecule 34: 18S ribosomal RNA



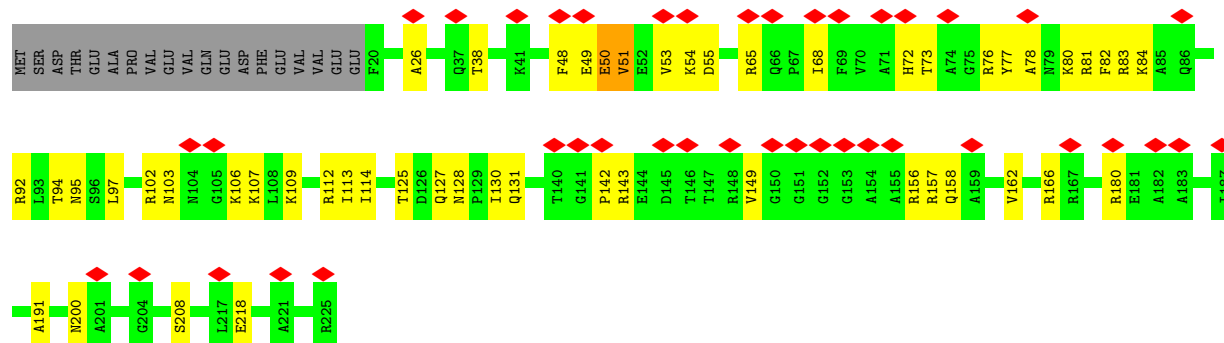




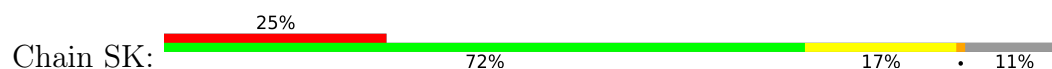
• Molecule 36: 40S ribosomal protein S4-A



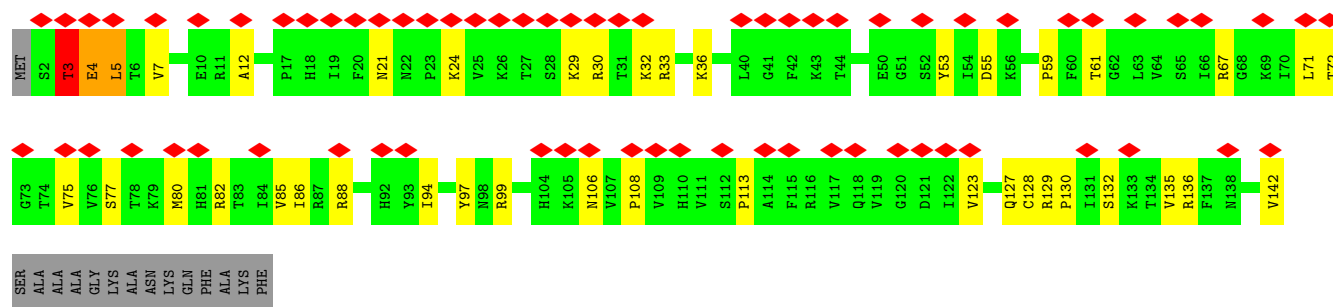
• Molecule 37: 40S ribosomal protein S5



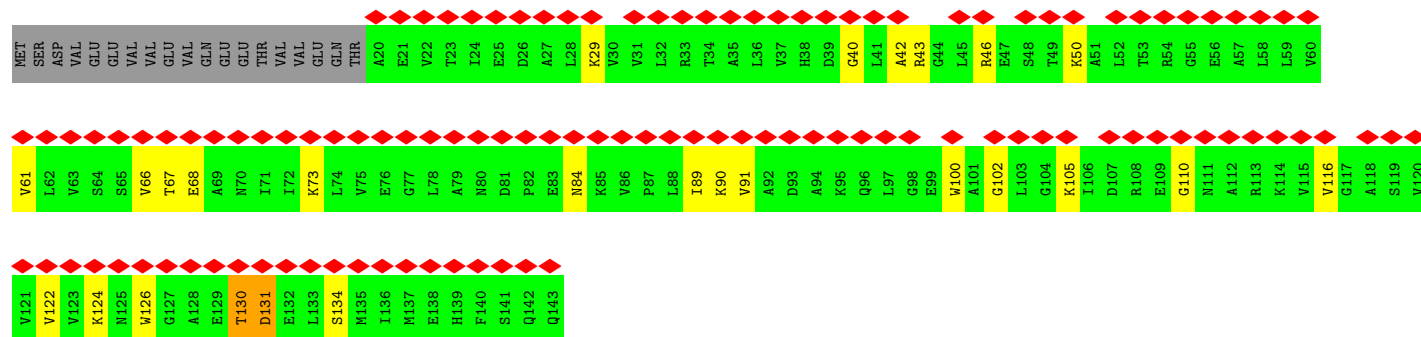
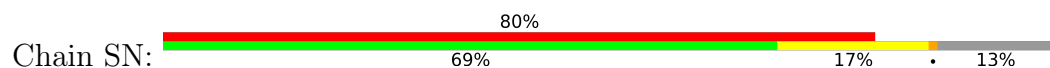
• Molecule 38: 40S ribosomal protein S6-A



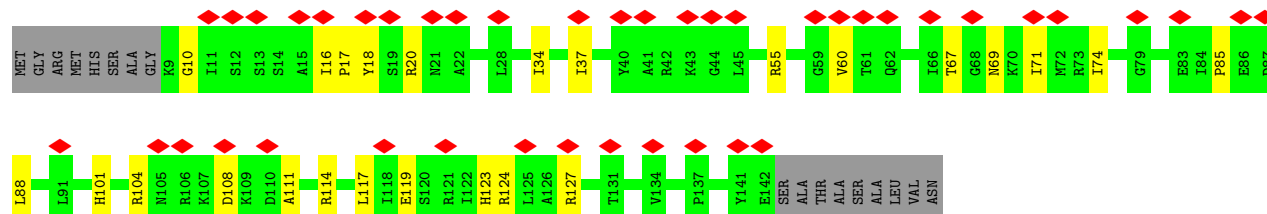
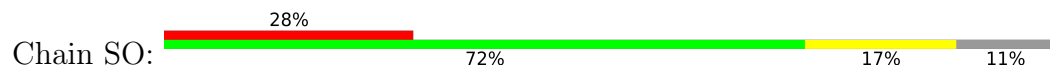
- Molecule 42: 40S ribosomal protein S11-A



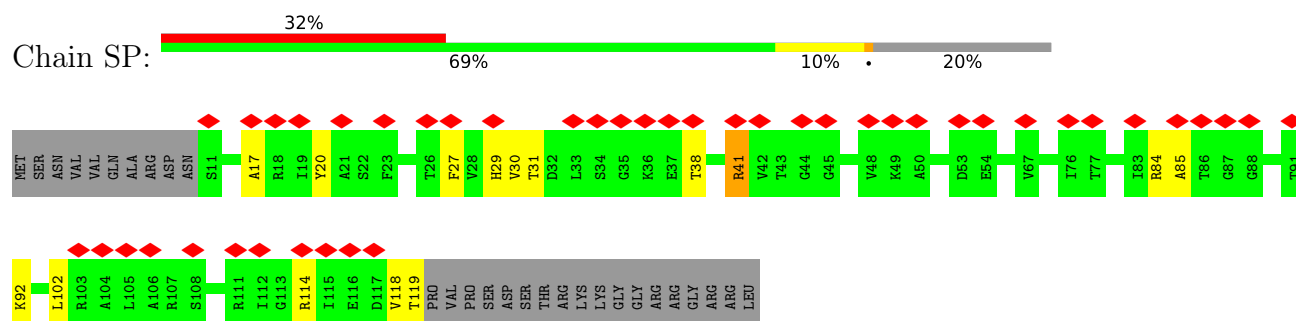
- Molecule 43: 40S ribosomal protein S12



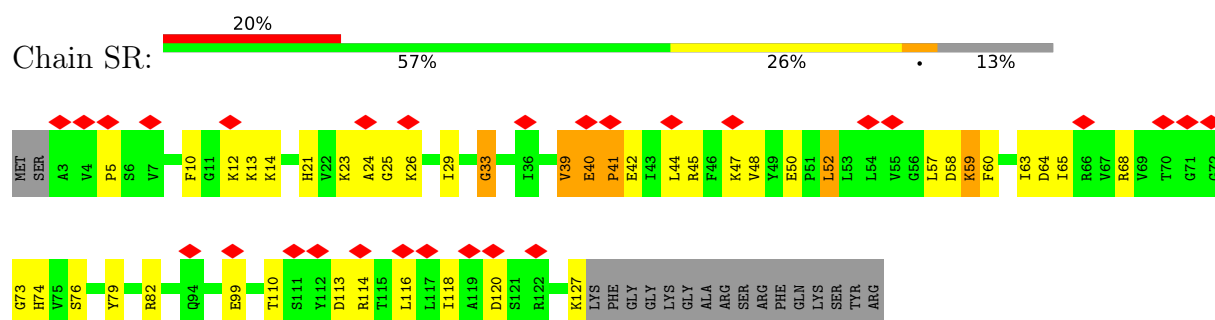
- Molecule 44: 40S ribosomal protein S13



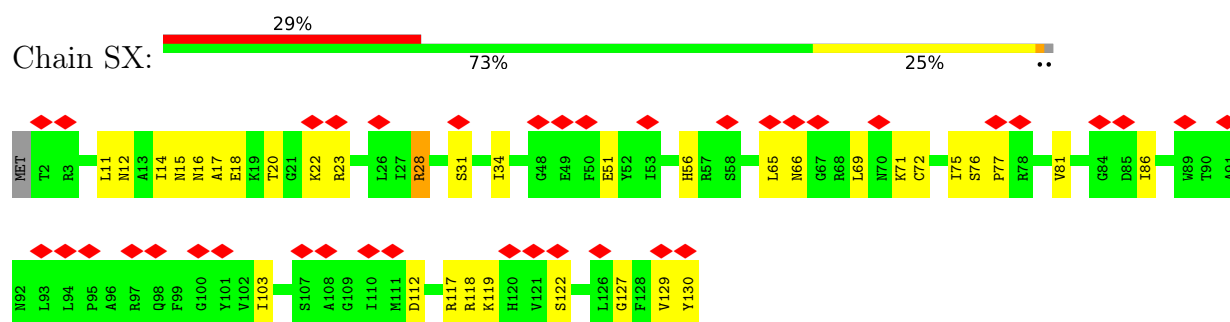
- Molecule 45: 40S ribosomal protein S14-A



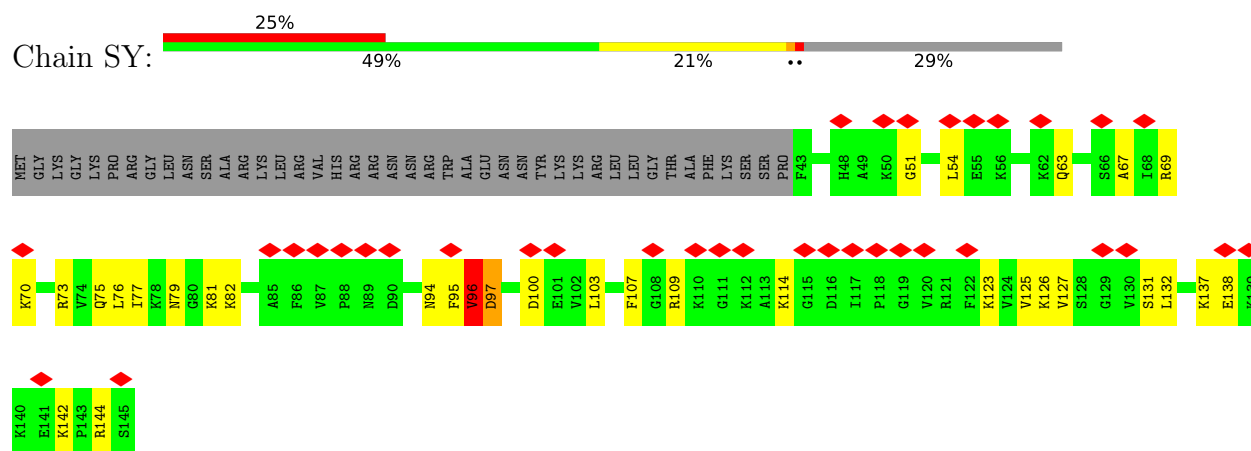
- Molecule 46: 40S ribosomal protein S16-A



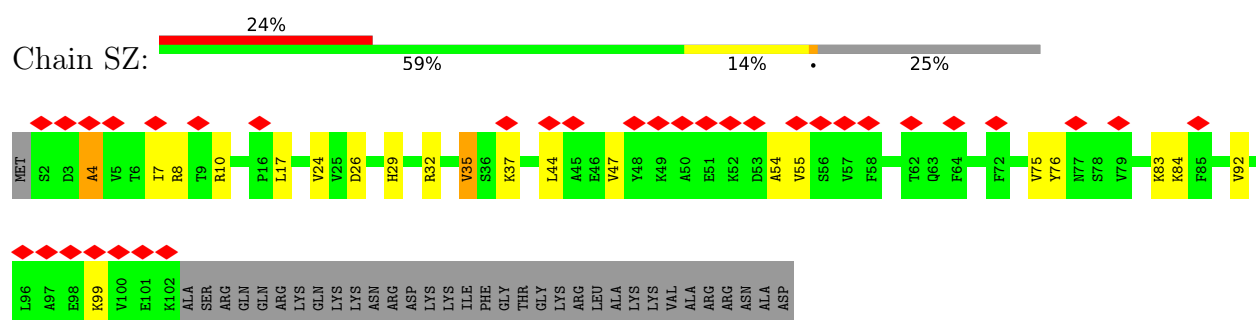
- Molecule 47: 40S ribosomal protein S22-A



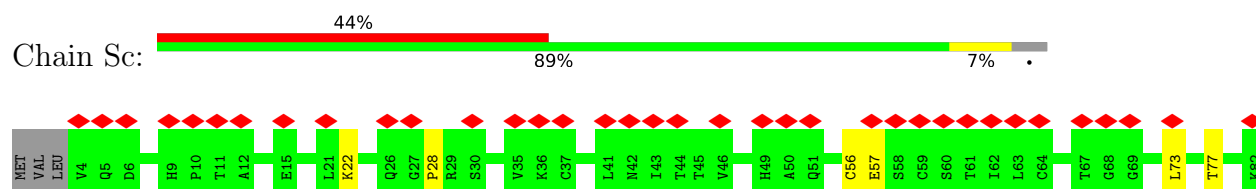
- Molecule 48: 40S ribosomal protein S23-A



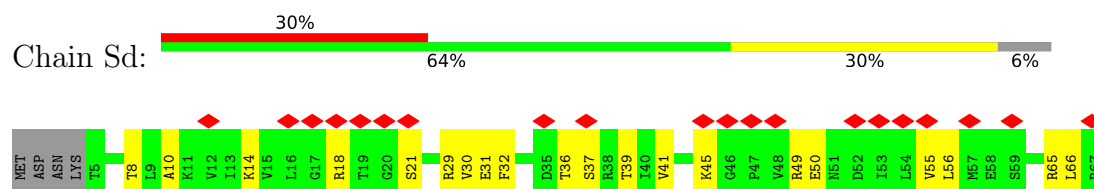
- Molecule 49: 40S ribosomal protein S24-A



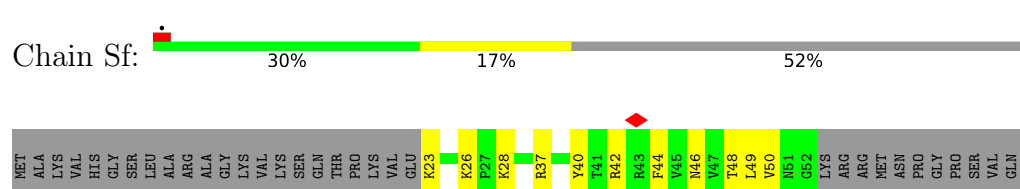
- Molecule 50: 40S ribosomal protein S27-A



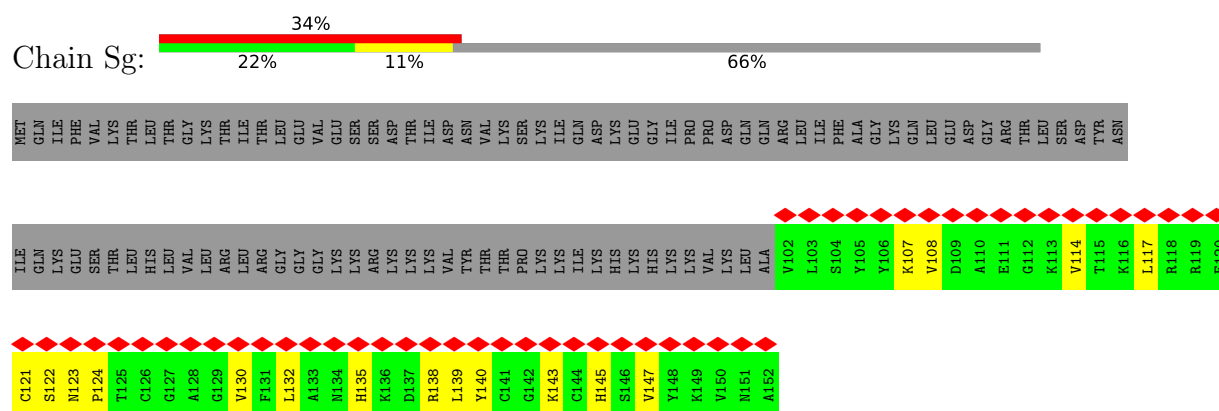
- Molecule 51: 40S ribosomal protein S28-A



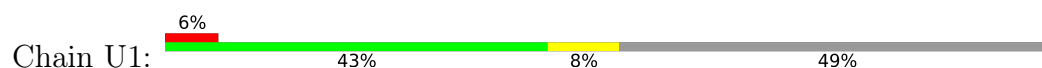
- Molecule 52: 40S ribosomal protein S30-A

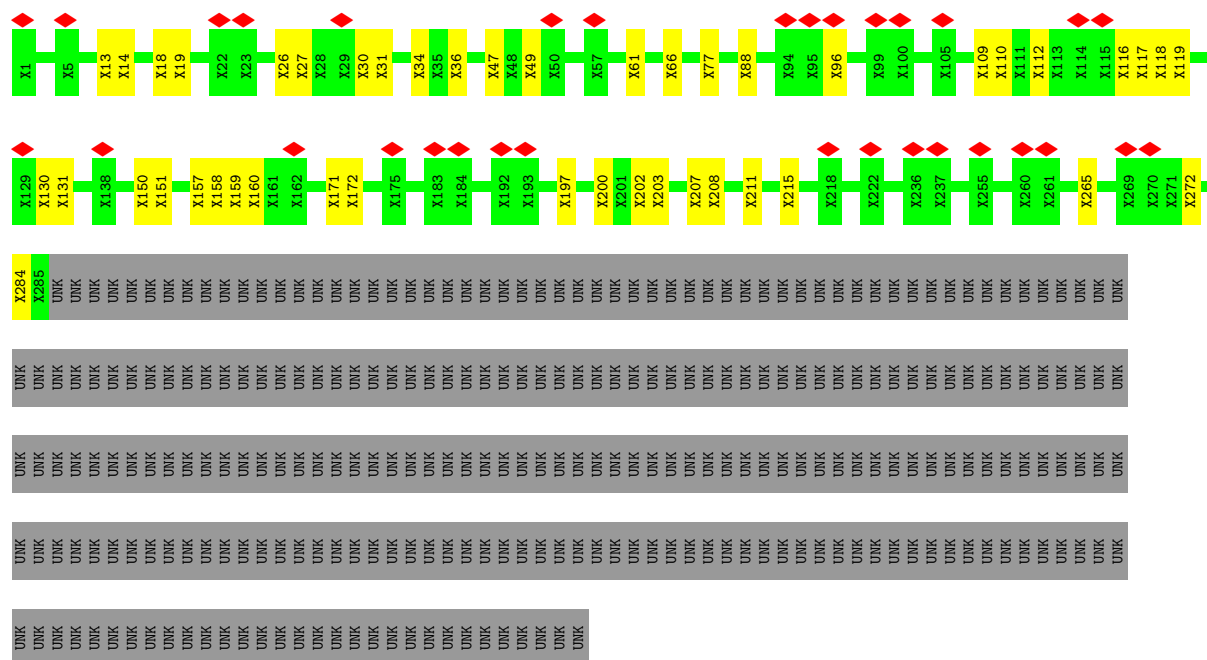


- Molecule 53: Ubiquitin-40S ribosomal protein S31

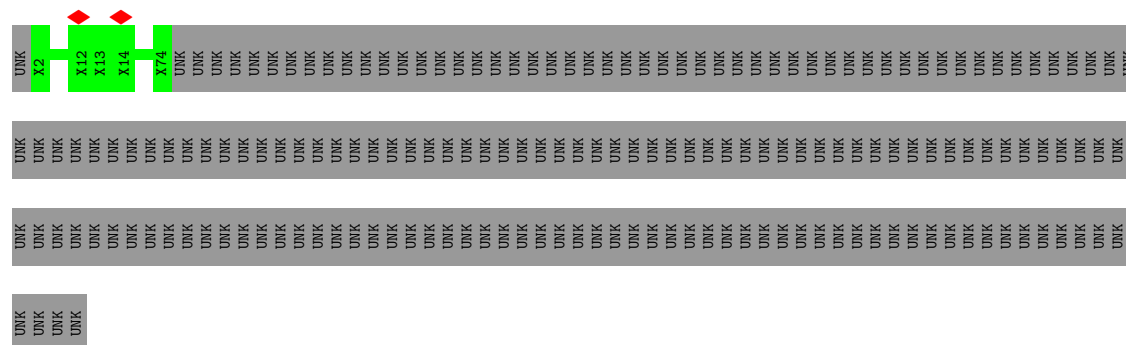


- Molecule 54: Utp7

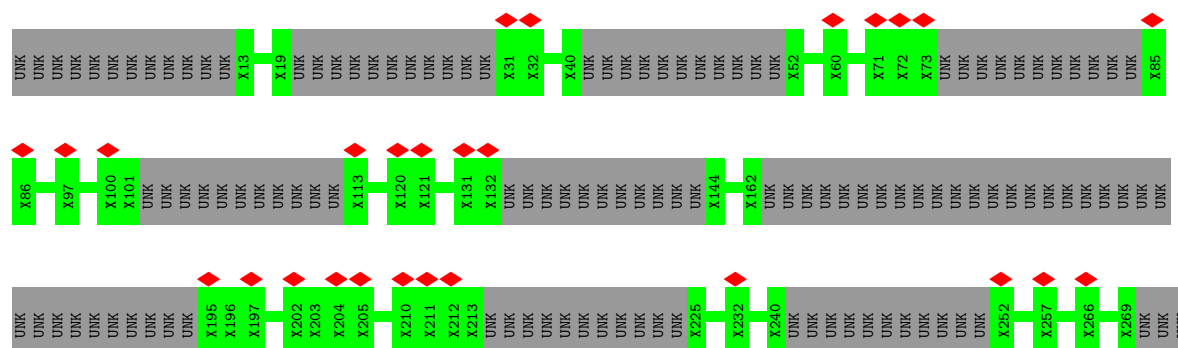




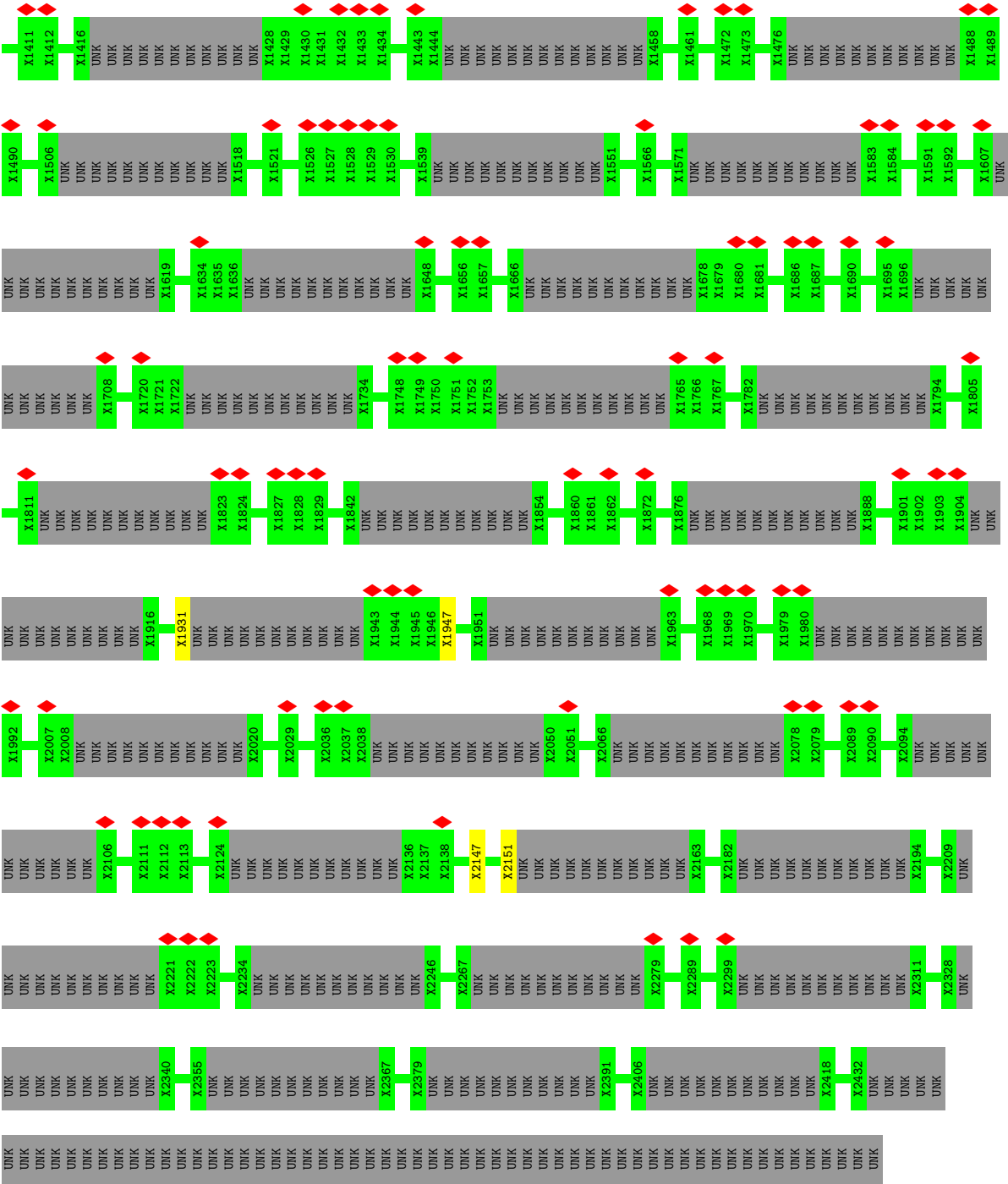
• Molecule 55: Utp11



• Molecule 56: Utp20





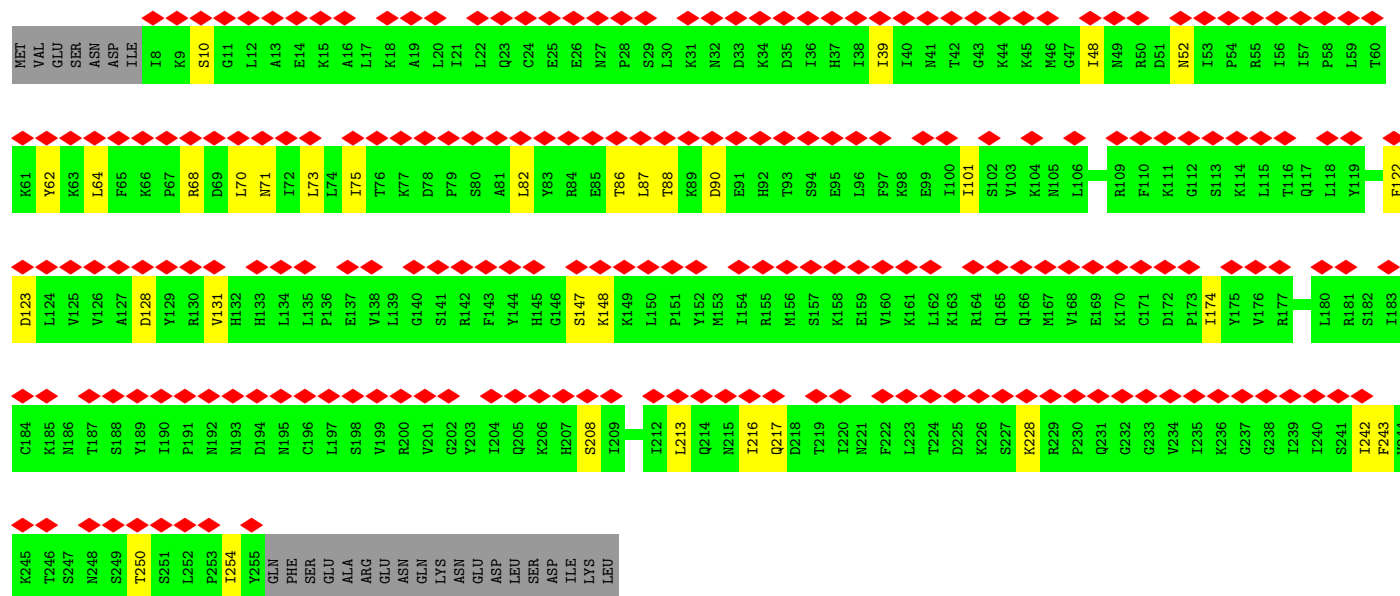
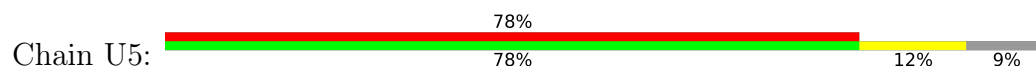


• Molecule 57: rRNA-processing protein FCF1

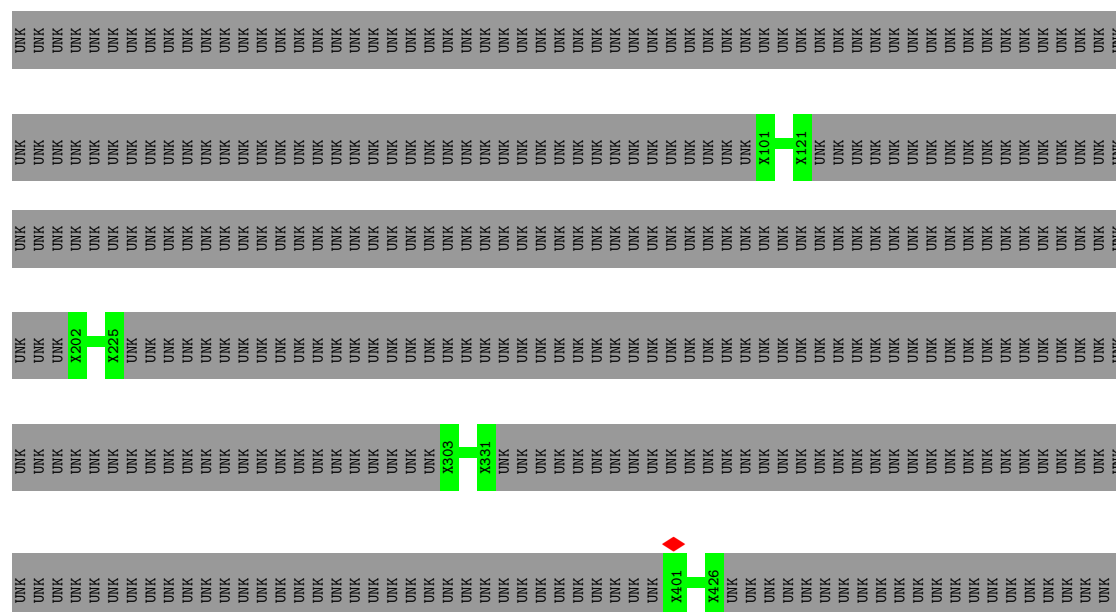


MET	GLY	LYS	ALA	LYS	LYS	THR	ARG	LYS	PHE	GLY	LEU	VAL	LYS	ARG	THR	LEU	ASN	THR	LYS	LYS	ASP	GLN	ARG	LEU	LYS	LYS	ASN	GLN	GLU	ASN	THR	LYS	THR	LYS	GLU	ASP	PRO	GLU	THR	ARG	ASN	THR	LEU	PRO	GLN	VAL	SER	ALA	LEU	PHE	PHE	GLN	TYR	ASN	Q57	A58	I59	R60
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

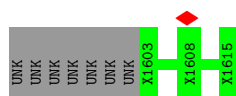
- Molecule 58: Ribosome biogenesis protein UTP30



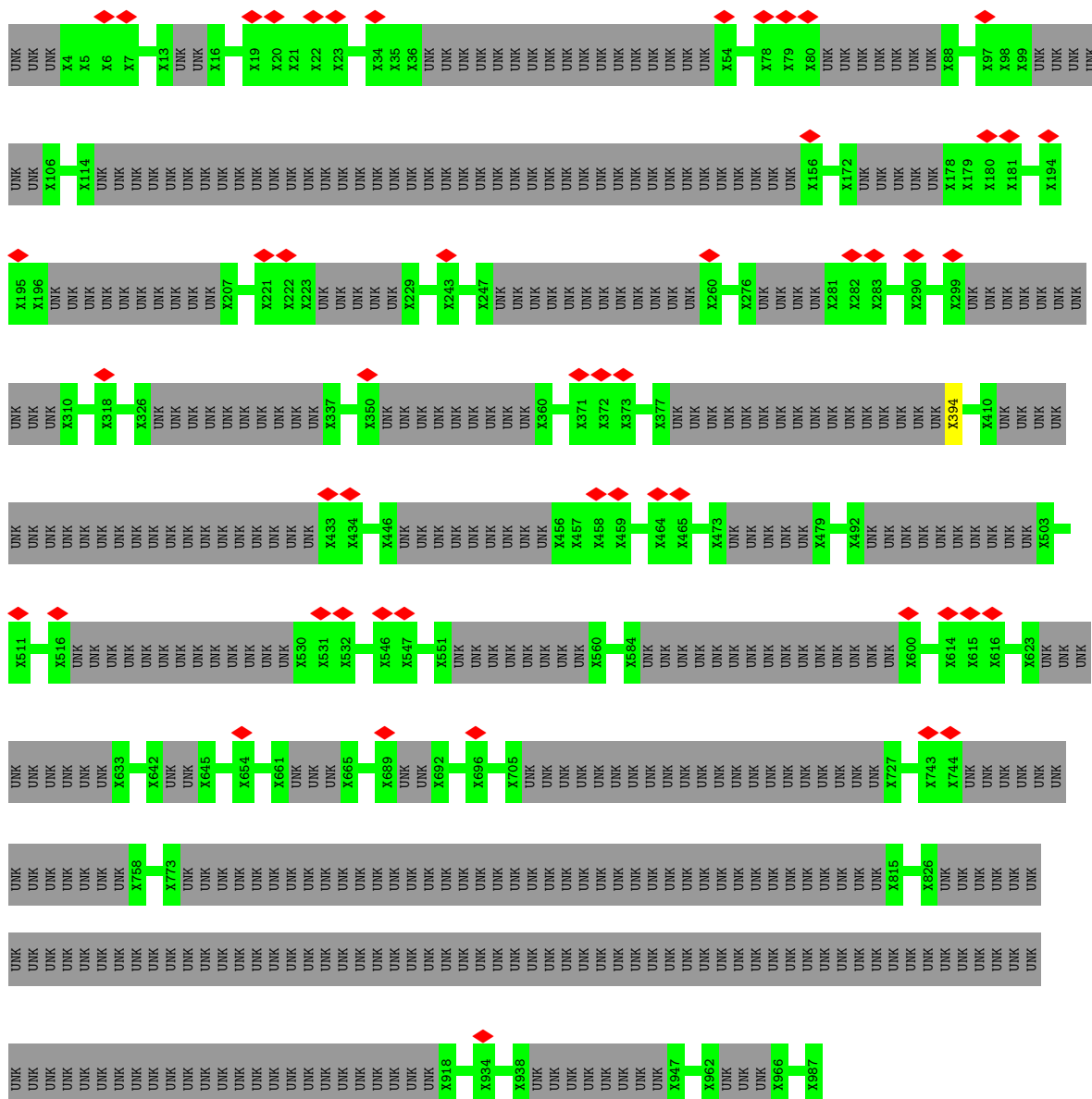
- Molecule 59: Helical domain protein



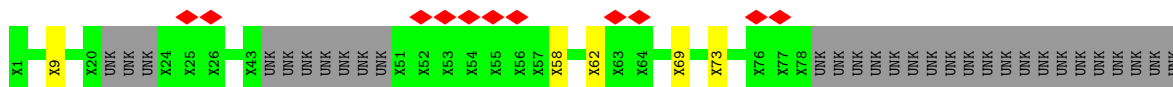




• Molecule 60: Helical domain protein



• Molecule 61: Unassigned helices





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30995	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	79545	Depositor
Image detector	OTHER	Depositor
Maximum map value	0.342	Depositor
Minimum map value	-0.265	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.09	Depositor
Map size ($\text{\AA}$)	704.0, 704.0, 704.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.76, 1.76, 1.76	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	3A	0.17	0/3710	0.35	0/5763
2	3B	0.25	0/1903	0.64	4/2572 (0.2%)
2	3C	0.23	0/1903	0.59	2/2572 (0.1%)
3	3D	0.24	0/2960	0.65	4/3987 (0.1%)
4	3E	0.19	0/2970	0.55	1/4004 (0.0%)
5	3F	0.23	0/2975	0.61	0/4008
6	3G	0.23	0/936	0.53	0/1273
6	3H	0.20	0/936	0.50	0/1273
7	5A	0.16	0/11029	0.34	0/17170
12	AE	0.94	2/6194 (0.0%)	0.72	11/8384 (0.1%)
15	B1	0.25	0/4431	0.68	3/5988 (0.1%)
16	BA	0.25	0/6164	0.68	6/8349 (0.1%)
17	BB	0.25	0/6264	0.72	7/8473 (0.1%)
18	BC	0.25	0/6226	0.71	10/8442 (0.1%)
19	BD	0.36	1/2597 (0.0%)	0.73	5/3520 (0.1%)
20	BE	0.23	0/6056	0.61	6/8189 (0.1%)
21	CA	0.18	0/1621	0.49	0/2196
22	CB	0.18	0/9081	0.48	0/12283
23	E1	0.17	0/1716	0.46	0/2319
23	E2	0.19	0/1721	0.47	0/2323
24	E3	0.25	0/2168	0.63	3/2942 (0.1%)
26	K1	0.24	0/1432	0.61	2/1926 (0.1%)
27	MA	0.21	0/1117	0.51	0/1509
28	MB	0.25	0/1496	0.63	1/2025 (0.0%)
29	MC	0.16	0/209	0.43	0/282
30	P1	0.22	0/1394	0.61	0/1881
31	R1	0.20	0/2793	0.49	2/3774 (0.1%)
32	R2	0.16	0/2271	0.48	0/3054
34	SA	0.31	7/26553 (0.0%)	0.39	3/41320 (0.0%)
35	SC	0.30	0/1735	0.94	7/2335 (0.3%)
36	SF	0.28	0/1920	0.75	1/2589 (0.0%)
37	SG	0.32	0/1629	0.81	0/2202
38	SH	0.23	0/1385	0.65	0/1851
39	SI	0.31	0/1343	0.76	0/1808

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
40	SJ	0.24	0/1373	0.76	2/1834 (0.1%)
41	SK	0.26	0/1434	0.74	0/1920
42	SM	0.29	0/1169	0.68	3/1576 (0.2%)
43	SN	0.32	0/898	1.09	2/1220 (0.2%)
44	SO	0.22	0/1109	0.66	0/1495
45	SP	0.24	0/758	0.74	0/1028
46	SR	0.28	0/990	1.01	4/1335 (0.3%)
47	SX	0.23	0/1038	0.62	1/1395 (0.1%)
48	SY	0.27	0/796	0.85	3/1062 (0.3%)
49	SZ	0.25	0/814	0.74	3/1093 (0.3%)
50	Sc	0.24	0/605	0.62	0/817
51	Sd	0.22	0/499	0.64	0/670
52	Sf	0.29	0/255	0.79	1/339 (0.3%)
53	Sg	0.26	0/404	0.76	0/542
57	U4	0.24	0/1007	0.63	0/1357
58	U5	0.22	0/2043	0.62	3/2747 (0.1%)
All	All	0.31	10/144030 (0.0%)	0.58	100/203016 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	3D	0	2
5	3F	0	2
12	AE	0	1
15	B1	0	3
16	BA	0	2
17	BB	0	7
18	BC	0	6
19	BD	0	3
20	BE	0	4
21	CA	0	1
22	CB	0	1
34	SA	0	1
35	SC	0	2
36	SF	0	2
37	SG	0	7
38	SH	0	1
39	SI	0	3
41	SK	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
42	SM	0	1
43	SN	0	4
45	SP	0	1
46	SR	0	3
48	SY	0	1
53	Sg	0	1
58	U5	0	1
61	UC	0	2
All	All	0	65

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	AE	571	LEU	CA-C	71.11	2.11	1.52
34	SA	283	U	C2-N3	18.61	1.75	1.37
34	SA	283	U	N3-C4	18.24	1.75	1.38
34	SA	283	U	N1-C2	17.93	1.74	1.38
34	SA	283	U	N1-C6	16.42	1.70	1.38
34	SA	283	U	C4-C5	14.59	1.72	1.43
34	SA	283	U	C5-C6	13.17	1.60	1.34
19	BD	411	TYR	CB-CG	-7.39	1.35	1.51
12	AE	112	ALA	C-N	5.29	1.40	1.34
34	SA	493	U	C2-N3	-5.09	1.27	1.37

All (100) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	AE	571	LEU	O-C-N	-23.75	98.51	121.79
12	AE	571	LEU	CB-CA-C	14.79	134.94	112.31
46	SR	40	GLU	CA-C-N	13.02	133.51	119.05
46	SR	40	GLU	C-N-CA	13.02	133.51	119.05
19	BD	455	ILE	N-CA-C	-10.49	102.20	112.17
12	AE	571	LEU	N-CA-CB	-9.54	91.37	111.21
12	AE	571	LEU	CA-C-N	8.00	132.48	120.31
12	AE	571	LEU	C-N-CA	8.00	132.48	120.31
34	SA	487	G	C5-C6-O6	7.67	151.60	128.60
18	BC	136	ILE	CA-C-N	7.63	136.12	121.54
18	BC	136	ILE	C-N-CA	7.63	136.12	121.54
18	BC	133	ASN	CA-C-N	7.49	135.18	121.70
18	BC	133	ASN	C-N-CA	7.49	135.18	121.70
19	BD	411	TYR	CA-CB-CG	-7.48	100.44	113.90
15	B1	808	PHE	CA-C-N	7.46	127.91	119.93

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	B1	808	PHE	C-N-CA	7.46	127.91	119.93
12	AE	571	LEU	N-CA-C	7.40	122.36	111.34
46	SR	41	PRO	N-CA-C	7.39	123.80	113.53
49	SZ	47	VAL	N-CA-C	-7.34	106.73	113.71
24	E3	211	ILE	CA-C-N	7.13	134.53	121.70
24	E3	211	ILE	C-N-CA	7.13	134.53	121.70
12	AE	34	ILE	N-CA-C	-7.03	105.93	112.96
43	SN	89	ILE	CA-C-N	6.94	134.80	121.54
43	SN	89	ILE	C-N-CA	6.94	134.80	121.54
18	BC	18	GLY	CA-C-N	6.90	134.13	121.70
18	BC	18	GLY	C-N-CA	6.90	134.13	121.70
18	BC	161	TRP	N-CA-C	-6.78	106.21	114.75
34	SA	487	G	N1-C6-O6	-6.72	99.72	119.90
42	SM	5	LEU	N-CA-C	6.53	119.18	111.02
12	AE	517	THR	CA-C-N	6.45	133.85	121.54
12	AE	517	THR	C-N-CA	6.45	133.85	121.54
12	AE	571	LEU	CA-C-O	6.36	126.40	119.40
4	3E	16	LYS	N-CA-C	-6.33	105.21	114.39
2	3B	144	TRP	CA-C-N	6.22	130.26	121.61
2	3B	144	TRP	C-N-CA	6.22	130.26	121.61
58	U5	48	ILE	N-CA-C	-6.17	106.79	112.96
35	SC	206	PRO	CA-C-N	6.09	133.17	121.54
35	SC	206	PRO	C-N-CA	6.09	133.17	121.54
17	BB	24	VAL	N-CA-C	-6.07	105.45	111.88
3	3D	393	SER	N-CA-C	5.97	117.90	110.91
17	BB	169	PHE	CA-C-N	5.89	132.78	121.54
17	BB	169	PHE	C-N-CA	5.89	132.78	121.54
2	3B	175	ALA	CA-C-N	5.87	129.62	120.82
2	3B	175	ALA	C-N-CA	5.87	129.62	120.82
42	SM	3	THR	CA-C-N	5.85	132.71	121.54
42	SM	3	THR	C-N-CA	5.85	132.71	121.54
2	3C	306	LEU	CA-C-N	5.80	135.96	121.80
2	3C	306	LEU	C-N-CA	5.80	135.96	121.80
20	BE	86	HIS	CA-C-N	5.77	129.47	120.82
20	BE	86	HIS	C-N-CA	5.77	129.47	120.82
47	SX	28	ARG	N-CA-C	-5.76	101.28	110.10
3	3D	44	PHE	CA-C-N	5.73	132.01	121.70
3	3D	44	PHE	C-N-CA	5.73	132.01	121.70
48	SY	96	VAL	CA-C-N	5.72	132.47	121.54
48	SY	96	VAL	C-N-CA	5.72	132.47	121.54
58	U5	208	SER	CA-C-N	5.68	123.82	120.24
58	U5	208	SER	C-N-CA	5.68	123.82	120.24

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	BB	392	THR	N-CA-C	5.67	115.51	108.19
20	BE	94	TYR	CA-C-N	5.59	130.09	121.19
20	BE	94	TYR	C-N-CA	5.59	130.09	121.19
16	BA	346	ASP	CA-C-N	5.58	129.03	120.82
16	BA	346	ASP	C-N-CA	5.58	129.03	120.82
16	BA	431	ILE	N-CA-C	-5.51	107.90	113.47
35	SC	176	VAL	CA-C-N	5.49	131.87	123.47
35	SC	176	VAL	C-N-CA	5.49	131.87	123.47
52	Sf	28	LYS	N-CA-C	-5.46	107.63	114.56
19	BD	427	ASN	CA-C-N	5.41	131.88	121.54
19	BD	427	ASN	C-N-CA	5.41	131.88	121.54
40	SJ	22	ARG	CA-CB-CG	5.39	124.88	114.10
18	BC	544	TYR	CA-C-N	5.38	130.05	122.46
18	BC	544	TYR	C-N-CA	5.38	130.05	122.46
31	R1	100	VAL	CA-C-N	5.34	127.63	120.58
31	R1	100	VAL	C-N-CA	5.34	127.63	120.58
35	SC	209	ASN	N-CA-C	5.31	122.12	110.80
46	SR	39	VAL	N-CA-C	5.31	115.45	110.30
24	E3	405	ASN	N-CA-C	5.29	119.30	109.56
40	SJ	199	LYS	N-CA-C	-5.29	108.09	114.75
20	BE	667	THR	CA-C-N	5.27	131.45	121.97
20	BE	667	THR	C-N-CA	5.27	131.45	121.97
17	BB	214	ASP	N-CA-C	-5.21	108.68	114.62
26	K1	49	ARG	CA-C-N	5.20	127.56	120.54
26	K1	49	ARG	C-N-CA	5.20	127.56	120.54
48	SY	125	VAL	N-CA-C	-5.19	107.69	111.90
16	BA	526	ASP	N-CA-C	-5.18	106.87	114.39
12	AE	182	LEU	N-CA-C	-5.15	108.02	114.56
28	MB	219	GLU	N-CA-C	-5.14	108.03	114.56
15	B1	261	SER	N-CA-C	-5.10	108.33	114.75
35	SC	147	ALA	CA-C-N	5.10	129.57	122.08
35	SC	147	ALA	C-N-CA	5.10	129.57	122.08
18	BC	425	ASP	N-CA-C	-5.08	106.65	114.16
17	BB	797	VAL	CA-C-N	5.07	131.22	121.54
17	BB	797	VAL	C-N-CA	5.07	131.22	121.54
3	3D	236	ASP	N-CA-C	-5.06	107.05	114.39
16	BA	545	GLU	CA-C-N	5.05	131.18	121.54
16	BA	545	GLU	C-N-CA	5.05	131.18	121.54
36	SF	194	THR	N-CA-C	5.02	121.50	110.80
49	SZ	4	ALA	CA-C-N	5.02	127.61	120.53
49	SZ	4	ALA	C-N-CA	5.02	127.61	120.53
34	SA	493	U	C5-C4-O4	5.02	140.96	125.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	BD	280	LYS	N-CA-C	-5.00	108.21	114.56

There are no chirality outliers.

All (65) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3D	392	TYR	Peptide
3	3D	91	SER	Peptide
5	3F	342	ARG	Peptide
5	3F	437	ARG	Peptide
12	AE	64	PRO	Peptide
15	B1	190	ILE	Peptide
15	B1	234	PRO	Peptide
15	B1	73	THR	Peptide
16	BA	515	TYR	Peptide
16	BA	702	LEU	Peptide
17	BB	169	PHE	Peptide
17	BB	235	ASN	Peptide
17	BB	335	LEU	Peptide
17	BB	795	ILE	Peptide
17	BB	796	ALA	Peptide
17	BB	797	VAL	Peptide
17	BB	864	ASN	Peptide
18	BC	133	ASN	Peptide
18	BC	136	ILE	Peptide
18	BC	299	ASN	Peptide
18	BC	365	ILE	Peptide
18	BC	771	LYS	Peptide
18	BC	772	LEU	Peptide
19	BD	304	LEU	Peptide
19	BD	411	TYR	Sidechain,Peptide
20	BE	660	PHE	Peptide
20	BE	665	THR	Peptide
20	BE	667	THR	Peptide
20	BE	94	TYR	Peptide
21	CA	199	GLN	Peptide
22	CB	555	PHE	Peptide
34	SA	493	U	Sidechain
35	SC	206	PRO	Peptide
35	SC	208	GLN	Peptide
36	SF	193	GLY	Peptide
36	SF	194	THR	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
37	SG	125	THR	Peptide
37	SG	127	GLN	Peptide
37	SG	128	ASN	Peptide
37	SG	48	PHE	Peptide
37	SG	49	GLU	Peptide
37	SG	50	GLU	Peptide
37	SG	65	ARG	Peptide
38	SH	68	LEU	Peptide
39	SI	131	PHE	Peptide
39	SI	156	SER	Peptide
39	SI	64	VAL	Peptide
41	SK	117	GLY	Peptide
41	SK	133	HIS	Peptide
41	SK	163	PRO	Peptide
42	SM	3	THR	Peptide
43	SN	105	LYS	Peptide
43	SN	110	GLY	Peptide
43	SN	130	THR	Peptide
43	SN	84	ASN	Peptide
45	SP	41	ARG	Peptide
46	SR	33	GLY	Peptide
46	SR	40	GLU	Peptide
46	SR	52	LEU	Peptide
48	SY	96	VAL	Peptide
53	Sg	147	VAL	Peptide
58	U5	62	TYR	Peptide
61	UC	233	UNK	Peptide,Mainchain

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	3A	3327	0	1687	58	0
2	3B	1866	0	1904	31	0
2	3C	1866	0	1904	21	0
3	3D	2915	0	2930	44	0
4	3E	2935	0	3033	50	0
5	3F	2916	0	2947	82	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	3G	924	0	975	21	0
6	3H	924	0	975	17	0
7	5A	9867	0	4954	84	0
8	AA	2845	0	658	47	0
9	AB	2015	0	454	19	0
10	AC	2360	0	534	17	0
11	AD	505	0	116	3	0
12	AE	9970	0	7056	161	0
13	AF	1880	0	425	23	0
14	AG	3060	0	707	36	0
15	B1	4325	0	4434	85	0
16	BA	6026	0	5940	129	0
17	BB	6138	0	6163	119	0
18	BC	6117	0	6141	104	0
19	BD	2539	0	2520	72	0
20	BE	5936	0	5882	139	0
21	CA	1582	0	1528	36	0
22	CB	8870	0	8975	148	0
23	E1	1689	0	1738	33	0
23	E2	1695	0	1757	39	0
24	E3	2114	0	2154	57	0
25	E4	1425	0	322	18	0
26	K1	1410	0	1503	27	0
27	MA	1097	0	1130	8	0
28	MB	1465	0	1486	32	0
29	MC	307	0	231	1	0
30	P1	1368	0	1436	9	0
31	R1	2742	0	2829	43	0
32	R2	2228	0	2228	17	0
33	S1	1425	0	334	35	0
34	SA	23759	0	11991	353	0
35	SC	1709	0	1784	49	0
36	SF	1881	0	1958	50	0
37	SG	1609	0	1675	43	0
38	SH	1369	0	1414	69	0
39	SI	1322	0	1394	29	0
40	SJ	1350	0	1374	41	0
41	SK	1412	0	1486	22	0
42	SM	1143	0	1210	28	0
43	SN	890	0	887	13	0
44	SO	1087	0	1152	17	0
45	SP	750	0	728	9	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	SR	973	0	1029	37	0
47	SX	1021	0	1060	26	0
48	SY	785	0	840	22	0
49	SZ	801	0	828	14	0
50	Sc	595	0	613	5	0
51	Sd	497	0	535	19	0
52	Sf	251	0	277	18	0
53	Sg	397	0	399	12	0
54	U1	1425	0	329	23	0
55	U2	365	0	75	0	0
56	U3	7035	0	1590	5	0
57	U4	990	0	1054	13	0
58	U5	2009	0	2130	16	0
59	UA	1690	0	370	0	0
60	UB	2775	0	620	1	0
61	UC	3300	0	727	12	0
All	All	173863	0	129519	2554	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 9.

All (2554) 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)
12:AE:630:TYR:CE1	12:AE:637:ILE:CD1	1.86	1.56
34:SA:283:U:N3	34:SA:283:U:C2	1.75	1.54
34:SA:283:U:N1	34:SA:283:U:C6	1.70	1.54
34:SA:283:U:N3	34:SA:283:U:C4	1.74	1.53
34:SA:283:U:C2	34:SA:283:U:N1	1.74	1.52
34:SA:283:U:N1	38:SH:188:ARG:CG	1.79	1.44
52:Sf:40:TYR:O	52:Sf:44:PHE:CD2	1.72	1.40
34:SA:283:U:N1	38:SH:188:ARG:HG3	1.04	1.37
12:AE:630:TYR:CZ	12:AE:637:ILE:HD13	1.63	1.33
12:AE:630:TYR:CE1	12:AE:637:ILE:HD12	1.52	1.32
12:AE:571:LEU:CA	12:AE:571:LEU:C	2.11	1.23
38:SH:188:ARG:NH1	38:SH:191:ARG:CD	2.05	1.20
38:SH:188:ARG:NH1	38:SH:191:ARG:HD2	1.57	1.19
24:E3:206:LEU:H	24:E3:207:PRO:CD	1.54	1.17
34:SA:283:U:H5''	38:SH:188:ARG:HD2	1.23	1.17
12:AE:630:TYR:OH	12:AE:637:ILE:HD13	1.43	1.17
12:AE:630:TYR:CE1	12:AE:637:ILE:HD13	1.66	1.16

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SA:283:U:OP2	38:SH:188:ARG:CZ	1.95	1.12
12:AE:571:LEU:HB3	12:AE:630:TYR:CD2	1.83	1.12
38:SH:188:ARG:NH2	38:SH:191:ARG:HH21	1.53	1.07
12:AE:630:TYR:HE1	12:AE:637:ILE:CB	1.68	1.07
12:AE:630:TYR:HE1	12:AE:637:ILE:CG1	1.67	1.06
24:E3:206:LEU:H	24:E3:207:PRO:HD3	1.08	1.05
52:Sf:40:TYR:O	52:Sf:44:PHE:HD2	1.14	1.04
16:BA:538:GLN:HA	16:BA:552:ASN:O	1.57	1.03
34:SA:283:U:C1'	38:SH:188:ARG:HG3	1.88	1.03
12:AE:630:TYR:HE1	12:AE:637:ILE:CD1	1.37	1.02
34:SA:126:A:H62	34:SA:291:G:N2	1.57	1.02
34:SA:126:A:N6	34:SA:291:G:H21	1.57	1.02
1:3A:254:A:OP2	6:3G:95:ARG:NH1	1.91	1.02
12:AE:630:TYR:CZ	12:AE:637:ILE:CD1	2.31	1.01
34:SA:588:U:OP2	52:Sf:26:LYS:NZ	1.95	0.99
38:SH:188:ARG:CZ	38:SH:191:ARG:HD2	1.94	0.98
34:SA:283:U:C5'	38:SH:188:ARG:HD2	1.93	0.98
34:SA:877:G:H1	34:SA:951:A:H61	1.03	0.98
15:B1:283:LEU:O	15:B1:788:TYR:HB3	1.64	0.97
12:AE:630:TYR:CE1	12:AE:637:ILE:CB	2.47	0.97
34:SA:1175:U:H3	34:SA:1464:G:H1	1.03	0.97
12:AE:630:TYR:CE1	12:AE:637:ILE:HG21	2.00	0.97
52:Sf:40:TYR:CG	52:Sf:44:PHE:CE2	2.22	0.96
34:SA:330:G:OP2	40:SJ:172:ARG:NH1	1.99	0.96
38:SH:188:ARG:HH12	38:SH:191:ARG:HD3	1.32	0.95
8:AA:66:UNK:O	8:AA:77:UNK:HA	1.67	0.95
15:B1:847:LEU:O	15:B1:853:ARG:HA	1.67	0.94
34:SA:1213:G:H1	34:SA:1450:U:H3	1.10	0.94
1:3A:7:G:H1	34:SA:1117:U:H3	1.08	0.94
5:3F:421:ASN:HA	5:3F:436:GLU:O	1.68	0.93
20:BE:27:PHE:HB3	20:BE:653:ILE:O	1.68	0.93
7:5A:506:G:H1	7:5A:530:A:H61	1.04	0.92
5:3F:539:ILE:O	5:3F:565:SER:HA	1.70	0.92
17:BB:597:ILE:O	17:BB:611:LEU:HB2	1.69	0.92
7:5A:506:G:H1	7:5A:530:A:N6	1.67	0.92
34:SA:1663:G:H1	34:SA:1738:U:H3	0.92	0.91
34:SA:283:U:H5''	38:SH:188:ARG:CD	2.00	0.91
28:MB:197:ALA:O	28:MB:200:LYS:NZ	2.04	0.91
34:SA:499:U:O2'	52:Sf:49:LEU:HD22	1.71	0.91
20:BE:631:ASN:O	20:BE:643:THR:HA	1.71	0.90
24:E3:206:LEU:N	24:E3:207:PRO:CD	2.27	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:5A:250:G:H1	7:5A:262:U:H3	0.95	0.90
34:SA:283:U:C4	38:SH:188:ARG:HB2	2.06	0.90
47:SX:23:ARG:HH12	47:SX:66:ASN:HA	1.35	0.89
12:AE:571:LEU:C	12:AE:630:TYR:CD2	2.49	0.89
19:BD:367:GLN:O	19:BD:386:ILE:HA	1.70	0.89
5:3F:497:LYS:NZ	5:3F:513:GLU:OE2	2.05	0.89
38:SH:188:ARG:NH1	38:SH:191:ARG:HD3	1.88	0.89
8:AA:359:UNK:HA	8:AA:373:UNK:O	1.72	0.89
6:3G:57:ASP:O	6:3G:84:ARG:NH1	2.06	0.89
34:SA:1219:A:H62	34:SA:1264:G:N2	1.71	0.88
12:AE:571:LEU:CB	12:AE:630:TYR:CD2	2.56	0.88
17:BB:555:VAL:O	17:BB:568:SER:HA	1.72	0.88
12:AE:630:TYR:CE1	12:AE:637:ILE:HB	2.08	0.88
15:B1:281:GLU:HB2	15:B1:790:ARG:O	1.73	0.87
12:AE:571:LEU:CA	12:AE:630:TYR:CD2	2.57	0.87
37:SG:84:LYS:HG2	37:SG:92:ARG:HH12	1.40	0.87
1:3A:326:U:OP1	6:3H:46:ARG:NH1	2.09	0.86
12:AE:630:TYR:CE1	12:AE:637:ILE:CG2	2.58	0.86
5:3F:235:HIS:ND1	5:3F:257:ASP:OD2	2.09	0.86
5:3F:347:MET:HA	5:3F:357:LEU:O	1.75	0.86
34:SA:877:G:H1	34:SA:951:A:N6	1.74	0.86
19:BD:482:LEU:HB2	19:BD:494:TYR:O	1.76	0.85
12:AE:571:LEU:C	12:AE:571:LEU:HA	1.98	0.85
52:Sf:46:ASN:O	52:Sf:50:VAL:HG23	1.75	0.85
36:SF:153:ASN:O	36:SF:174:LYS:NZ	2.10	0.84
52:Sf:44:PHE:O	52:Sf:48:THR:HG23	1.76	0.84
22:CB:150:ASP:O	22:CB:154:LYS:HB2	1.77	0.84
13:AF:75:UNK:HA	13:AF:89:UNK:O	1.77	0.84
34:SA:1529:C:OP1	37:SG:112:ARG:NH1	2.10	0.84
34:SA:523:G:N2	34:SA:529:A:OP2	2.10	0.84
39:SI:76:LYS:HG2	39:SI:79:ARG:HH12	1.42	0.84
5:3F:146:LYS:O	5:3F:566:ALA:HA	1.77	0.84
7:5A:513:G:H1	7:5A:523:U:H3	1.25	0.84
31:R1:29:LYS:NZ	31:R1:332:ILE:O	2.10	0.84
40:SJ:110:ARG:NH1	40:SJ:160:PHE:O	2.10	0.84
1:3A:84:U:OP2	4:3E:361:ARG:NH2	2.11	0.83
26:K1:124:ASP:OD1	26:K1:184:ARG:NH1	2.11	0.83
36:SF:75:LYS:NZ	36:SF:77:ARG:HH12	1.76	0.83
34:SA:1482:C:N4	34:SA:1525:A:OP2	2.10	0.83
22:CB:536:TYR:OH	22:CB:552:ARG:NH1	2.12	0.83
8:AA:360:UNK:O	8:AA:372:UNK:HA	1.77	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SA:283:U:N3	38:SH:188:ARG:HB2	1.92	0.82
34:SA:1072:C:OP1	50:Sc:22:LYS:NZ	2.11	0.82
42:SM:72:THR:O	42:SM:88:ARG:NH1	2.12	0.82
5:3F:551:ARG:NH1	6:3G:93:VAL:O	2.12	0.82
17:BB:554:THR:HA	17:BB:569:LEU:O	1.80	0.82
34:SA:1588:G:H1	34:SA:1608:U:H3	0.85	0.82
22:CB:152:PHE:O	22:CB:156:LYS:NZ	2.13	0.82
22:CB:307:LYS:NZ	34:SA:1683:C:OP1	2.13	0.81
20:BE:423:ARG:NH1	20:BE:426:GLU:OE1	2.13	0.81
34:SA:322:G:O2'	40:SJ:10:LYS:NZ	2.13	0.81
1:3A:5:A:H2	34:SA:1119:G:H1	1.22	0.81
34:SA:396:G:N1	34:SA:399:A:OP2	2.13	0.81
1:3A:5:A:C2	34:SA:1119:G:N1	2.48	0.81
5:3F:495:SER:HA	5:3F:514:LEU:O	1.80	0.81
22:CB:779:PHE:HA	22:CB:849:GLY:O	1.80	0.81
20:BE:24:PHE:HA	20:BE:655:THR:O	1.81	0.80
47:SX:20:THR:OG1	47:SX:22:LYS:NZ	2.13	0.80
20:BE:66:LEU:O	20:BE:346:ARG:NH1	2.12	0.80
22:CB:707:PHE:O	22:CB:918:ARG:NH1	2.14	0.80
12:AE:571:LEU:C	12:AE:630:TYR:HD2	1.89	0.80
34:SA:283:U:OP2	38:SH:188:ARG:NH2	2.14	0.80
34:SA:1216:C:O2'	34:SA:1217:A:O5'	1.97	0.80
14:AG:118:UNK:O	14:AG:130:UNK:HA	1.81	0.80
22:CB:367:ARG:O	22:CB:371:GLN:HB2	1.82	0.80
42:SM:132:SER:O	42:SM:136:ARG:NH1	2.14	0.80
15:B1:988:ARG:HH12	28:MB:146:ARG:HH11	1.29	0.80
34:SA:1636:C:H42	34:SA:1765:A:H61	1.28	0.79
12:AE:571:LEU:CB	12:AE:630:TYR:CE2	2.66	0.79
15:B1:845:LEU:O	15:B1:855:GLN:HA	1.81	0.79
20:BE:796:LEU:O	20:BE:800:GLU:HB2	1.83	0.79
23:E1:178:VAL:HA	23:E1:223:GLU:O	1.83	0.79
34:SA:163:G:N2	34:SA:163:G:OP2	2.14	0.79
3:3D:158:TYR:O	3:3D:162:LYS:HB2	1.82	0.79
51:Sd:49:ARG:NH1	51:Sd:50:GLU:O	2.16	0.79
24:E3:334:GLU:O	24:E3:338:ALA:HB3	1.83	0.78
34:SA:1085:G:N2	34:SA:1088:A:OP2	2.16	0.78
20:BE:356:ILE:O	20:BE:633:LYS:NZ	2.16	0.78
34:SA:1584:G:N2	34:SA:1611:A:OP2	2.17	0.78
36:SF:75:LYS:HZ2	36:SF:77:ARG:NH1	1.80	0.78
23:E2:44:VAL:HA	23:E2:113:TYR:O	1.83	0.78
34:SA:522:U:OP1	49:SZ:37:LYS:NZ	2.16	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AA:524:UNK:O	8:AA:536:UNK:HA	1.84	0.77
1:3A:80:U:OP2	6:3H:95:ARG:NH1	2.17	0.77
23:E2:88:ARG:NH1	34:SA:1191:U:OP1	2.17	0.77
26:K1:141:ARG:NH1	26:K1:191:MET:O	2.16	0.77
38:SH:188:ARG:NH2	38:SH:191:ARG:NH2	2.32	0.77
36:SF:50:ASN:O	36:SF:53:LYS:NZ	2.18	0.77
6:3H:57:ASP:O	6:3H:84:ARG:NH1	2.18	0.77
12:AE:571:LEU:HB3	12:AE:630:TYR:CE2	2.19	0.77
36:SF:11:ARG:NH1	36:SF:21:ASP:OD1	2.18	0.76
38:SH:188:ARG:HH22	38:SH:191:ARG:HH21	1.34	0.76
15:B1:943:LYS:NZ	34:SA:572:C:OP2	2.14	0.76
19:BD:382:GLY:N	19:BD:405:THR:HG1	1.84	0.76
34:SA:1253:U:OP1	43:SN:50:LYS:NZ	2.18	0.76
14:AG:382:UNK:HA	14:AG:397:UNK:O	1.86	0.76
23:E1:42:ILE:O	23:E1:203:CYS:HA	1.86	0.76
35:SC:158:SER:O	35:SC:162:ARG:NH1	2.19	0.76
1:3A:206:C:N4	1:3A:242:U:OP2	2.18	0.76
20:BE:439:PHE:HA	20:BE:455:PHE:O	1.86	0.76
22:CB:921:ASP:OD2	22:CB:1172:ASN:ND2	2.19	0.76
34:SA:590:C:OP1	52:Sf:42:ARG:NH1	2.18	0.75
34:SA:364:G:OP2	34:SA:377:G:N2	2.18	0.75
34:SA:1216:C:O2'	34:SA:1217:A:P	2.44	0.75
24:E3:206:LEU:N	24:E3:207:PRO:HD3	1.85	0.75
34:SA:335:U:O2'	42:SM:129:ARG:NH1	2.19	0.75
9:AB:190:UNK:O	9:AB:201:UNK:HA	1.87	0.75
6:3H:29:ASN:O	6:3H:31:ARG:NH1	2.20	0.74
24:E3:301:TYR:O	24:E3:304:TYR:N	2.20	0.74
16:BA:21:THR:O	16:BA:30:LEU:HB2	1.87	0.74
26:K1:164:ILE:HA	26:K1:172:SER:O	1.88	0.74
2:3B:170:VAL:HA	2:3B:239:CYS:O	1.88	0.74
9:AB:110:UNK:O	9:AB:117:UNK:HA	1.87	0.73
1:3A:67:G:H1	7:5A:286:U:H3	1.37	0.73
52:Sf:40:TYR:O	52:Sf:44:PHE:CE2	2.41	0.73
14:AG:4:UNK:HA	14:AG:569:UNK:O	1.87	0.73
15:B1:607:ASP:O	31:R1:321:ARG:NH1	2.19	0.73
12:AE:571:LEU:CA	12:AE:630:TYR:CE2	2.71	0.72
34:SA:432:G:OP2	34:SA:433:C:N4	2.22	0.72
15:B1:610:LYS:NZ	15:B1:612:VAL:O	2.21	0.72
26:K1:198:TYR:O	26:K1:202:GLU:HB2	1.90	0.72
20:BE:132:THR:OG1	20:BE:134:ASP:OD1	2.06	0.72
12:AE:756:LEU:O	12:AE:760:PHE:HB2	1.89	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CB:100:SER:O	22:CB:104:LYS:HB2	1.88	0.72
22:CB:899:LEU:O	22:CB:903:SER:HB3	1.89	0.72
22:CB:1097:ASP:OD2	22:CB:1186:ILE:N	2.16	0.72
23:E2:41:MET:O	23:E2:110:LEU:HA	1.89	0.72
1:3A:83:A:OP2	4:3E:361:ARG:NE	2.23	0.72
36:SF:75:LYS:HZ2	36:SF:77:ARG:HH12	1.33	0.72
24:E3:301:TYR:CE2	34:SA:1217:A:N6	2.57	0.72
38:SH:188:ARG:HH12	38:SH:191:ARG:CD	1.88	0.72
34:SA:283:U:C2	34:SA:283:U:C1'	2.73	0.72
34:SA:405:C:O4'	38:SH:88:ARG:NH1	2.22	0.71
46:SR:42:GLU:HG3	46:SR:45:ARG:HH12	1.55	0.71
36:SF:118:GLU:OE2	36:SF:237:SER:N	2.23	0.71
41:SK:163:PRO:HA	41:SK:166:GLY:H	1.55	0.71
12:AE:120:TRP:O	12:AE:124:ARG:HB3	1.91	0.71
9:AB:271:UNK:HA	9:AB:284:UNK:O	1.90	0.71
17:BB:186:ILE:HB	17:BB:200:HIS:O	1.90	0.71
7:5A:337:G:H21	7:5A:338:A:H62	1.39	0.71
28:MB:234:ARG:NH1	28:MB:254:PHE:O	2.22	0.71
34:SA:538:A:H1'	34:SA:540:G:H1	1.56	0.71
16:BA:60:ALA:O	16:BA:72:SER:HA	1.91	0.70
19:BD:577:LEU:O	19:BD:588:LEU:HA	1.91	0.70
24:E3:206:LEU:H	24:E3:207:PRO:HD2	1.52	0.70
34:SA:337:G:OP2	34:SA:338:C:N4	2.24	0.70
12:AE:746:GLU:O	12:AE:750:ASN:HB2	1.91	0.70
16:BA:198:PHE:O	16:BA:207:TYR:HB3	1.91	0.70
34:SA:1174:C:H42	34:SA:1465:C:H42	1.39	0.70
20:BE:273:LEU:O	20:BE:286:VAL:HA	1.91	0.70
37:SG:76:ARG:NH1	46:SR:120:ASP:OD1	2.23	0.70
2:3C:299:LYS:HD2	2:3C:322:ARG:HB3	1.73	0.70
17:BB:447:LEU:O	17:BB:454:LEU:HA	1.90	0.70
20:BE:84:SER:HB2	20:BE:91:TYR:HB2	1.72	0.69
5:3F:198:LYS:NZ	5:3F:265:THR:O	2.25	0.69
19:BD:313:PHE:HA	19:BD:322:HIS:O	1.92	0.69
1:3A:1:G:C6	34:SA:1124:A:N1	2.60	0.69
18:BC:662:GLN:O	18:BC:666:GLU:HB2	1.93	0.69
18:BC:722:GLU:O	18:BC:725:ASP:HB2	1.92	0.69
19:BD:369:ASN:O	19:BD:384:ILE:HA	1.91	0.69
18:BC:698:LEU:O	18:BC:702:LEU:HB2	1.92	0.69
52:Sf:40:TYR:C	52:Sf:44:PHE:CD2	2.70	0.69
15:B1:200:LEU:O	15:B1:204:ARG:HB2	1.92	0.69
5:3F:155:ASN:N	5:3F:193:ASP:OD2	2.22	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CA:134:ILE:O	21:CA:138:TRP:HB2	1.93	0.69
23:E2:39:LYS:O	23:E2:109:LYS:NZ	2.22	0.69
48:SY:67:ALA:HB3	48:SY:69:ARG:HH12	1.58	0.69
19:BD:311:ASN:HA	19:BD:324:TRP:O	1.92	0.69
34:SA:478:A:OP1	52:Sf:37:ARG:NH1	2.25	0.68
18:BC:190:THR:OG1	22:CB:657:ARG:NH1	2.25	0.68
34:SA:938:G:N2	34:SA:941:A:OP2	2.19	0.68
34:SA:1217:A:H2	34:SA:1448:G:H21	1.41	0.68
5:3F:299:CYS:HB2	5:3F:303:LYS:O	1.92	0.68
21:CA:18:PHE:O	21:CA:34:LEU:HA	1.94	0.68
34:SA:867:G:H1	34:SA:961:U:H3	1.38	0.68
19:BD:325:ASP:HB2	19:BD:337:ALA:H	1.57	0.68
12:AE:571:LEU:CA	12:AE:630:TYR:HD2	2.06	0.68
36:SF:59:ARG:HA	36:SF:62:LYS:HZ3	1.59	0.68
12:AE:630:TYR:CD1	12:AE:637:ILE:HB	2.28	0.68
34:SA:1219:A:N6	34:SA:1264:G:N2	2.40	0.68
52:Sf:44:PHE:O	52:Sf:48:THR:CG2	2.41	0.68
7:5A:511:G:H1	7:5A:525:U:H3	1.42	0.67
16:BA:103:LYS:O	16:BA:112:ALA:HB3	1.94	0.67
40:SJ:105:ASP:OD2	40:SJ:107:THR:OG1	2.11	0.67
19:BD:424:ILE:HB	19:BD:433:TRP:HB3	1.75	0.67
12:AE:367:LEU:O	12:AE:371:LYS:HB2	1.95	0.67
14:AG:423:UNK:HA	14:AG:438:UNK:O	1.94	0.67
36:SF:11:ARG:NH1	36:SF:21:ASP:O	2.26	0.67
42:SM:36:LYS:NZ	42:SM:59:PRO:O	2.24	0.67
17:BB:488:LEU:HB2	17:BB:500:TRP:HB2	1.77	0.67
17:BB:851:PRO:O	17:BB:855:LYS:HB2	1.94	0.67
14:AG:402:UNK:HA	14:AG:416:UNK:O	1.95	0.67
34:SA:283:U:C6	34:SA:283:U:C1'	2.71	0.67
17:BB:393:ASP:HA	17:BB:679:HIS:HB3	1.77	0.67
20:BE:309:ILE:HG12	20:BE:323:VAL:HG12	1.75	0.67
47:SX:118:ARG:NH1	47:SX:119:LYS:HZ2	1.93	0.67
12:AE:571:LEU:C	12:AE:630:TYR:CE2	2.73	0.66
12:AE:597:HIS:HB3	12:AE:615:ASN:HB3	1.77	0.66
5:3F:189:THR:O	5:3F:196:LEU:HA	1.94	0.66
34:SA:323:A:H61	34:SA:345:U:H3	1.43	0.66
34:SA:394:C:O2	34:SA:401:A:N6	2.29	0.66
2:3B:298:ILE:HA	2:3B:319:ARG:O	1.96	0.66
22:CB:182:ASP:HB2	22:CB:208:THR:HB	1.78	0.66
34:SA:283:U:C5	38:SH:188:ARG:NE	2.50	0.66
20:BE:477:ILE:O	20:BE:484:ILE:HA	1.96	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:SH:188:ARG:HH11	38:SH:191:ARG:HB2	1.61	0.66
7:5A:348:U:H3	7:5A:376:U:H3	1.42	0.66
16:BA:59:ALA:HA	16:BA:73:ILE:O	1.96	0.66
35:SC:144:ARG:HB3	35:SC:208:GLN:HB3	1.76	0.66
38:SH:187:LYS:HZ1	38:SH:191:ARG:HH12	1.41	0.66
19:BD:411:TYR:OH	19:BD:423:LEU:N	2.29	0.66
20:BE:567:ILE:O	20:BE:580:GLN:HA	1.96	0.66
23:E2:44:VAL:HG22	23:E2:113:TYR:HB2	1.76	0.66
26:K1:140:LYS:O	26:K1:144:ARG:HB2	1.96	0.66
38:SH:79:LYS:HG3	38:SH:86:PRO:HG2	1.77	0.66
7:5A:538:C:H2'	7:5A:539:A:H8	1.60	0.66
15:B1:827:ALA:HA	15:B1:920:GLU:H	1.61	0.66
34:SA:629:U:OP2	34:SA:969:C:N4	2.28	0.66
39:SI:143:LEU:HD23	39:SI:145:GLY:H	1.60	0.66
7:5A:557:A:H61	7:5A:580:A:H61	1.43	0.66
5:3F:322:HIS:HB2	5:3F:343:ASP:HB3	1.78	0.65
12:AE:559:ASN:HB2	12:AE:616:PRO:HD3	1.77	0.65
34:SA:283:U:N1	38:SH:188:ARG:CB	2.58	0.65
22:CB:412:LEU:HD21	22:CB:424:GLY:HA3	1.78	0.65
34:SA:1163:A:H4'	37:SG:166:ARG:HH12	1.60	0.65
5:3F:335:ARG:HA	5:3F:349:TRP:O	1.96	0.65
20:BE:481:ASN:O	20:BE:499:LYS:NZ	2.30	0.65
28:MB:152:LEU:HB3	28:MB:165:PHE:HB2	1.78	0.65
39:SI:51:VAL:HG13	39:SI:53:GLY:H	1.61	0.65
18:BC:697:VAL:HG12	18:BC:700:ARG:HH21	1.61	0.65
28:MB:94:ARG:NH1	34:SA:1588:G:N7	2.45	0.65
7:5A:334:G:H1'	27:MA:55:ARG:HE	1.62	0.65
20:BE:630:THR:N	20:BE:644:THR:O	2.30	0.65
7:5A:503:C:H1'	7:5A:535:G:H1	1.61	0.65
8:AA:68:UNK:O	8:AA:75:UNK:HA	1.96	0.65
3:3D:23:GLN:HG2	3:3D:50:LEU:HA	1.79	0.65
36:SF:180:LEU:HA	36:SF:194:THR:HG22	1.77	0.65
2:3B:194:VAL:HB	2:3B:217:ILE:HA	1.78	0.65
15:B1:988:ARG:HH12	28:MB:146:ARG:NH1	1.94	0.65
17:BB:838:THR:O	17:BB:842:ASN:HB2	1.97	0.65
34:SA:1219:A:N6	34:SA:1264:G:H21	1.95	0.65
12:AE:579:ARG:HD2	12:AE:631:VAL:HG22	1.80	0.64
34:SA:537:G:OP2	41:SK:175:ARG:NH2	2.27	0.64
5:3F:496:LEU:HB2	5:3F:514:LEU:HB2	1.79	0.64
20:BE:223:LEU:HB2	20:BE:231:ILE:HB	1.79	0.64
24:E3:305:ARG:O	24:E3:307:VAL:N	2.30	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AA:218:UNK:HA	8:AA:234:UNK:HA	1.79	0.64
20:BE:609:ILE:HB	20:BE:623:ILE:HB	1.78	0.64
19:BD:483:ALA:H	19:BD:523:PHE:HZ	1.44	0.64
12:AE:37:SER:O	12:AE:41:ALA:HB2	1.98	0.64
31:R1:18:ARG:NH1	31:R1:98:TYR:O	2.29	0.64
37:SG:53:VAL:HG22	37:SG:55:ASP:H	1.62	0.64
23:E2:164:LYS:HZ1	34:SA:1575:G:P	2.19	0.64
5:3F:551:ARG:HH11	6:3G:94:SER:HA	1.63	0.64
8:AA:486:UNK:HA	8:AA:492:UNK:HA	1.78	0.64
16:BA:712:PHE:H	16:BA:746:ASN:HD21	1.43	0.64
20:BE:467:ALA:HB3	20:BE:476:PHE:HB2	1.80	0.64
24:E3:301:TYR:HA	24:E3:304:TYR:HB2	1.80	0.64
14:AG:485:UNK:O	14:AG:497:UNK:HA	1.98	0.63
16:BA:715:PHE:HB2	16:BA:744:ARG:HG2	1.80	0.63
20:BE:179:LYS:HA	20:BE:191:PHE:O	1.98	0.63
20:BE:430:ILE:HB	20:BE:443:TRP:HB2	1.79	0.63
20:BE:350:SER:N	20:BE:372:ASP:OD2	2.30	0.63
22:CB:99:LYS:O	22:CB:103:PHE:HB3	1.98	0.63
24:E3:301:TYR:CE2	34:SA:1217:A:C6	2.86	0.63
37:SG:68:ILE:HG22	46:SR:114:ARG:HH12	1.64	0.63
12:AE:465:PHE:HB2	12:AE:507:LYS:HG2	1.81	0.63
34:SA:283:U:C2	38:SH:188:ARG:CB	2.82	0.63
51:Sd:31:GLU:OE2	51:Sd:36:THR:OG1	2.17	0.63
3:3D:122:GLU:HG2	3:3D:124:ALA:H	1.63	0.63
22:CB:840:LEU:HB3	22:CB:852:PHE:HB2	1.79	0.63
38:SH:31:ARG:HG2	38:SH:101:ILE:HG12	1.80	0.63
42:SM:71:LEU:HB3	42:SM:88:ARG:NH1	2.13	0.63
52:Sf:40:TYR:C	52:Sf:44:PHE:HD2	2.04	0.63
7:5A:174:U:H3	7:5A:222:G:H1	1.47	0.63
15:B1:143:MET:N	48:SY:144:ARG:HH11	1.97	0.63
21:CA:192:GLU:O	21:CA:196:ALA:HB2	1.98	0.63
12:AE:465:PHE:H	12:AE:507:LYS:HE2	1.63	0.63
1:3A:5:A:N1	34:SA:1119:G:O6	2.31	0.63
20:BE:551:TYR:HD1	20:BE:558:PHE:HB3	1.64	0.63
22:CB:861:ILE:O	22:CB:865:ARG:HB2	1.99	0.63
24:E3:418:HIS:O	24:E3:422:LEU:HB2	1.99	0.63
7:5A:506:G:N2	7:5A:530:A:N1	2.47	0.62
16:BA:842:ASN:ND2	20:BE:882:GLU:OE1	2.32	0.62
18:BC:771:LYS:HB3	18:BC:775:ILE:HD12	1.80	0.62
21:CA:55:LEU:O	21:CA:123:THR:HA	1.98	0.62
34:SA:929:A:H4'	34:SA:930:A:OP2	1.98	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3F:138:ASP:OD1	5:3F:500:LYS:NZ	2.31	0.62
15:B1:159:GLN:NE2	34:SA:518:A:OP2	2.32	0.62
16:BA:817:PHE:O	16:BA:821:MET:HB2	1.99	0.62
20:BE:266:VAL:HB	20:BE:274:ILE:HB	1.81	0.62
51:Sd:10:ALA:HA	51:Sd:32:PHE:HA	1.80	0.62
24:E3:301:TYR:CZ	34:SA:1217:A:C6	2.88	0.62
34:SA:1619:C:H1'	51:Sd:21:SER:HA	1.80	0.62
1:3A:5:A:H2	34:SA:1119:G:N1	1.92	0.62
1:3A:12:U:H3	34:SA:1112:G:H1	1.46	0.62
20:BE:596:GLU:HG3	20:BE:598:ARG:NH1	2.14	0.62
22:CB:525:LEU:HB2	22:CB:617:LEU:HB2	1.80	0.62
22:CB:530:GLN:HB2	22:CB:695:GLN:HB2	1.81	0.62
34:SA:51:A:H62	34:SA:429:G:H21	1.47	0.62
40:SJ:172:ARG:HE	40:SJ:175:GLN:HG3	1.65	0.62
8:AA:523:UNK:HA	8:AA:537:UNK:O	2.00	0.62
12:AE:365:ILE:O	12:AE:369:LEU:HB3	1.99	0.62
18:BC:318:GLU:HB3	18:BC:327:ILE:HG22	1.82	0.62
40:SJ:5:ARG:NH2	40:SJ:27:PHE:O	2.33	0.62
20:BE:861:ILE:HD11	20:BE:905:ILE:HD12	1.82	0.62
21:CA:16:VAL:HB	21:CA:37:MET:O	1.99	0.62
40:SJ:103:GLN:HB3	40:SJ:164:ARG:NH1	2.15	0.62
34:SA:411:C:H1'	34:SA:423:G:H22	1.65	0.61
46:SR:73:GLY:H	46:SR:76:SER:HB3	1.63	0.61
48:SY:107:PHE:HB3	48:SY:114:LYS:HD3	1.81	0.61
17:BB:426:ARG:HG2	17:BB:462:SER:HA	1.82	0.61
22:CB:1070:VAL:O	22:CB:1074:LEU:HB2	2.00	0.61
35:SC:199:ASN:HA	35:SC:202:LYS:HE3	1.81	0.61
36:SF:88:ASP:HB2	36:SF:101:LEU:HD12	1.82	0.61
42:SM:7:VAL:HG11	42:SM:53:TYR:HA	1.82	0.61
47:SX:118:ARG:NH1	47:SX:119:LYS:NZ	2.47	0.61
34:SA:1219:A:N6	34:SA:1264:G:C2	2.68	0.61
30:P1:188:LYS:HA	30:P1:191:LYS:HZ3	1.64	0.61
34:SA:273:G:N7	38:SH:185:GLN:NE2	2.49	0.61
35:SC:130:SER:HG	35:SC:180:THR:HG1	1.46	0.61
1:3A:53:U:H3	7:5A:465:G:H1	1.49	0.61
18:BC:108:LEU:HD13	18:BC:150:LEU:HD22	1.82	0.61
20:BE:900:ASN:OD1	20:BE:903:GLN:NE2	2.34	0.61
32:R2:1416:GLN:HE21	32:R2:1559:ILE:HD12	1.66	0.61
5:3F:234:GLY:O	5:3F:259:LYS:NZ	2.31	0.61
26:K1:92:ALA:HB2	45:SP:102:LEU:HD12	1.81	0.61
36:SF:17:HIS:HA	36:SF:108:ARG:HG2	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:SJ:70:GLU:OE1	42:SM:24:LYS:NZ	2.33	0.61
4:3E:76:LEU:HD23	4:3E:84:LYS:NZ	2.15	0.61
38:SH:79:LYS:HE2	38:SH:90:GLY:H	1.64	0.61
2:3C:162:LEU:HG	2:3C:164:ILE:H	1.65	0.61
15:B1:112:LYS:HG3	15:B1:113:ILE:HG23	1.82	0.61
17:BB:251:GLN:HE21	17:BB:344:THR:HG23	1.66	0.61
17:BB:888:ARG:O	17:BB:892:LYS:HB2	2.00	0.61
24:E3:301:TYR:O	24:E3:304:TYR:CB	2.49	0.61
1:3A:5:A:N1	34:SA:1119:G:C6	2.68	0.61
15:B1:988:ARG:HH22	28:MB:146:ARG:HE	1.49	0.61
17:BB:218:ILE:HA	17:BB:227:LYS:O	2.01	0.61
20:BE:229:GLU:HA	20:BE:244:ILE:O	2.00	0.61
22:CB:679:SER:O	22:CB:683:ASN:HB2	2.01	0.61
23:E1:46:ALA:HA	23:E1:115:GLN:HB3	1.82	0.61
34:SA:102:U:O2'	34:SA:105:A:N6	2.34	0.61
42:SM:21:ASN:ND2	42:SM:30:ARG:O	2.34	0.61
5:3F:311:GLN:HB3	49:SZ:4:ALA:HB1	1.83	0.60
16:BA:82:VAL:HG12	16:BA:88:ASN:H	1.65	0.60
19:BD:462:GLY:HA2	19:BD:480:ARG:H	1.64	0.60
20:BE:569:VAL:HB	20:BE:579:ARG:HB2	1.84	0.60
26:K1:49:ARG:NH2	26:K1:108:VAL:O	2.34	0.60
40:SJ:74:LYS:HD3	40:SJ:108:PRO:HB2	1.83	0.60
5:3F:424:LEU:HB3	5:3F:434:PHE:HB3	1.82	0.60
20:BE:308:PRO:HB2	20:BE:324:PHE:HB2	1.82	0.60
23:E1:94:GLN:OE1	23:E2:132:ARG:NH1	2.34	0.60
3:3D:34:VAL:HG23	3:3D:36:GLU:H	1.67	0.60
34:SA:51:A:H62	34:SA:429:G:N2	1.98	0.60
38:SH:70:PRO:HB3	38:SH:101:ILE:HB	1.83	0.60
5:3F:497:LYS:HG2	5:3F:513:GLU:HG2	1.84	0.60
13:AF:28:UNK:O	13:AF:35:UNK:HA	2.01	0.60
18:BC:45:LEU:HD12	18:BC:54:HIS:HB3	1.82	0.60
21:CA:204:SER:O	21:CA:208:ASP:HB2	2.00	0.60
34:SA:900:A:H3'	34:SA:901:G:H21	1.65	0.60
16:BA:541:ILE:HG22	16:BA:550:VAL:HG22	1.84	0.60
47:SX:31:SER:H	47:SX:34:ILE:HD12	1.67	0.60
16:BA:533:SER:HB3	16:BA:580:PHE:HB2	1.83	0.60
17:BB:799:LYS:HD2	17:BB:800:THR:HG23	1.83	0.60
18:BC:83:GLN:NE2	18:BC:103:SER:O	2.35	0.60
20:BE:230:VAL:O	20:BE:243:THR:HA	2.02	0.60
28:MB:162:THR:HB	28:MB:262:ARG:HB3	1.83	0.60
34:SA:364:G:H3'	34:SA:365:G:H8	1.67	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SA:1216:C:HO2'	34:SA:1217:A:P	2.23	0.60
17:BB:135:ARG:NH1	17:BB:149:ASP:OD1	2.35	0.60
20:BE:587:ARG:HB3	20:BE:605:LEU:HD13	1.83	0.60
38:SH:188:ARG:HH11	38:SH:191:ARG:CB	2.15	0.60
1:3A:64:A:H4'	20:BE:392:ARG:HH12	1.66	0.60
5:3F:304:ILE:HB	5:3F:318:LEU:HB2	1.83	0.60
8:AA:282:UNK:O	8:AA:290:UNK:N	2.35	0.60
13:AF:67:UNK:O	13:AF:78:UNK:HA	2.01	0.60
16:BA:169:SER:HB2	16:BA:186:THR:HB	1.84	0.60
17:BB:397:ILE:HG22	17:BB:408:THR:HG22	1.84	0.60
20:BE:97:LYS:HZ3	20:BE:111:GLU:CD	2.10	0.60
22:CB:812:GLU:O	22:CB:816:ALA:HB2	2.01	0.60
5:3F:187:ALA:HB3	5:3F:199:TYR:HB2	1.84	0.60
22:CB:268:LEU:HD23	22:CB:294:LEU:HD12	1.84	0.60
31:R1:143:LYS:HZ1	31:R1:252:LYS:HB3	1.67	0.60
34:SA:477:A:N6	34:SA:540:G:O6	2.34	0.60
15:B1:609:GLU:OE2	31:R1:17:PHE:N	2.35	0.59
17:BB:828:TYR:O	17:BB:832:PHE:HB2	2.02	0.59
20:BE:641:LEU:O	20:BE:653:ILE:HA	2.02	0.59
43:SN:43:ARG:HH12	43:SN:102:GLY:HA3	1.66	0.59
4:3E:87:LEU:HB3	4:3E:107:VAL:HG22	1.83	0.59
17:BB:747:LYS:HA	51:Sd:65:ARG:NH1	2.16	0.59
3:3D:297:HIS:NE2	3:3D:309:GLU:OE2	2.33	0.59
15:B1:830:ARG:NH2	48:SY:138:GLU:OE2	2.35	0.59
34:SA:446:A:N1	34:SA:461:G:O2'	2.35	0.59
20:BE:434:HIS:CD2	20:BE:441:ARG:HH11	2.21	0.59
23:E1:144:LEU:HD13	23:E1:150:ILE:HG12	1.85	0.59
34:SA:1160:A:H1'	34:SA:1620:C:H42	1.66	0.59
34:SA:1216:C:O2	34:SA:1446:A:N6	2.35	0.59
12:AE:469:LEU:O	12:AE:473:SER:HB3	2.03	0.59
15:B1:932:LEU:H	15:B1:1006:TRP:HD1	1.49	0.59
16:BA:431:ILE:HG23	16:BA:432:GLN:HG3	1.85	0.59
16:BA:719:VAL:HB	16:BA:744:ARG:HH22	1.68	0.59
23:E1:44:VAL:HG22	23:E1:113:TYR:HB2	1.84	0.59
7:5A:209:G:N2	7:5A:209:G:OP2	2.33	0.59
34:SA:593:U:H4'	34:SA:595:G:H4'	1.84	0.59
39:SI:150:GLN:HB3	39:SI:181:ILE:HG22	1.84	0.59
47:SX:17:ALA:HA	47:SX:22:LYS:NZ	2.18	0.59
17:BB:867:GLU:O	17:BB:871:GLN:NE2	2.35	0.59
6:3G:34:LYS:HB2	6:3G:101:SER:HB3	1.84	0.59
22:CB:254:LEU:HG	22:CB:270:ILE:HG12	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CB:313:ASN:HD22	22:CB:326:LEU:HB3	1.67	0.59
34:SA:484:C:H42	34:SA:504:U:H3	1.48	0.59
3:3D:176:GLN:HG3	4:3E:187:TRP:HB3	1.85	0.59
6:3G:25:GLN:OE1	6:3G:29:ASN:ND2	2.36	0.59
7:5A:163:G:H1	7:5A:232:U:H3	1.50	0.59
13:AF:240:UNK:O	13:AF:252:UNK:HA	2.02	0.59
16:BA:846:TYR:HB3	20:BE:913:GLU:HG2	1.85	0.59
17:BB:359:SER:O	17:BB:391:ARG:NH2	2.36	0.59
19:BD:272:LEU:HD22	19:BD:288:LEU:HD23	1.85	0.59
34:SA:204:G:O6	34:SA:264:G:N2	2.36	0.59
14:AG:526:UNK:O	14:AG:538:UNK:HA	2.02	0.58
16:BA:554:ASP:O	16:BA:556:ARG:NH1	2.36	0.58
24:E3:279:ILE:HG12	24:E3:283:LEU:HD12	1.84	0.58
36:SF:126:VAL:HA	36:SF:141:THR:HA	1.85	0.58
38:SH:188:ARG:NH1	38:SH:191:ARG:CB	2.65	0.58
2:3B:142:ARG:NH2	2:3B:186:ASP:OD2	2.36	0.58
3:3D:36:GLU:OE1	3:3D:37:GLN:NE2	2.36	0.58
17:BB:747:LYS:HA	51:Sd:65:ARG:HH12	1.68	0.58
23:E2:178:VAL:HA	23:E2:223:GLU:O	2.03	0.58
50:Sc:56:CYS:SG	50:Sc:57:GLU:N	2.75	0.58
20:BE:644:THR:HG22	20:BE:651:ILE:HG12	1.85	0.58
21:CA:52:CYS:HA	21:CA:126:LEU:O	2.04	0.58
25:E4:258:UNK:HA	40:SJ:42:ARG:NH1	2.18	0.58
31:R1:143:LYS:NZ	31:R1:252:LYS:HB3	2.17	0.58
16:BA:477:SER:HB2	16:BA:519:LEU:HD12	1.85	0.58
20:BE:78:SER:OG	20:BE:95:GLU:OE2	2.11	0.58
28:MB:124:MET:HG2	28:MB:126:ASN:H	1.67	0.58
28:MB:193:ASN:HB3	28:MB:226:ASN:HB2	1.84	0.58
39:SI:67:LEU:O	39:SI:71:HIS:ND1	2.37	0.58
16:BA:430:ARG:HH12	16:BA:451:ASP:HB2	1.67	0.58
16:BA:540:SER:HA	16:BA:550:VAL:O	2.03	0.58
34:SA:1163:A:N3	34:SA:1613:U:O2'	2.35	0.58
40:SJ:61:GLU:HG3	40:SJ:62:THR:HG23	1.85	0.58
52:Sf:40:TYR:CD1	52:Sf:44:PHE:CE2	2.81	0.58
5:3F:442:ILE:HA	5:3F:472:PRO:HA	1.85	0.58
12:AE:349:THR:O	12:AE:353:ARG:HB2	2.04	0.58
13:AF:69:UNK:O	13:AF:76:UNK:HA	2.03	0.58
15:B1:253:TYR:HA	15:B1:787:SER:O	2.02	0.58
16:BA:306:ASN:H	16:BA:321:SER:HA	1.69	0.58
17:BB:565:PHE:O	31:R1:207:ARG:NH2	2.37	0.58
19:BD:272:LEU:HB2	19:BD:288:LEU:HB3	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:SH:187:LYS:NZ	38:SH:191:ARG:NH1	2.52	0.58
12:AE:365:ILE:O	12:AE:369:LEU:CB	2.52	0.58
16:BA:247:SER:O	16:BA:249:ARG:NH1	2.37	0.58
18:BC:412:ALA:HB3	18:BC:430:TYR:HB2	1.85	0.58
23:E1:85:SER:OG	23:E1:211:ARG:NH2	2.37	0.58
26:K1:44:LEU:HD22	35:SC:115:ARG:HH11	1.69	0.58
26:K1:146:VAL:HA	26:K1:153:LEU:HB2	1.84	0.58
54:U1:96:UNK:HA	54:U1:112:UNK:HA	1.85	0.58
16:BA:542:PHE:HB3	16:BA:548:LYS:HA	1.86	0.58
19:BD:568:VAL:HA	19:BD:578:ALA:O	2.03	0.58
22:CB:487:ILE:HD12	22:CB:582:GLN:HE21	1.68	0.58
37:SG:51:VAL:HG21	37:SG:131:GLN:HB2	1.85	0.58
48:SY:76:LEU:HD13	48:SY:79:ASN:HD22	1.67	0.58
6:3G:27:ALA:HB1	6:3G:32:GLN:HB3	1.86	0.58
12:AE:333:LEU:O	12:AE:337:ASP:HB2	2.04	0.58
17:BB:454:LEU:O	17:BB:468:ILE:HB	2.03	0.58
31:R1:156:ARG:NH2	31:R1:228:ASP:OD2	2.37	0.58
54:U1:202:UNK:HA	54:U1:208:UNK:HA	1.86	0.58
8:AA:485:UNK:O	8:AA:493:UNK:N	2.37	0.58
12:AE:480:ASN:ND2	12:AE:520:GLU:O	2.36	0.58
15:B1:117:VAL:HB	15:B1:146:VAL:HG12	1.86	0.58
15:B1:119:LEU:HB3	15:B1:147:LEU:O	2.03	0.58
24:E3:231:LYS:NZ	34:SA:1235:C:OP1	2.37	0.58
34:SA:897:C:O2'	34:SA:914:G:N2	2.37	0.58
2:3B:261:LEU:O	3:3D:129:ARG:NH2	2.37	0.57
2:3C:261:LEU:O	4:3E:118:ARG:NH2	2.37	0.57
5:3F:286:LEU:HB3	5:3F:295:LEU:HD11	1.84	0.57
12:AE:371:LYS:O	12:AE:374:ARG:NH2	2.36	0.57
16:BA:507:GLN:HB2	46:SR:127:LYS:HD3	1.85	0.57
17:BB:341:ALA:HA	17:BB:357:THR:HA	1.86	0.57
17:BB:439:LEU:HD23	17:BB:443:LEU:HB2	1.86	0.57
18:BC:759:THR:O	18:BC:762:CYS:HB3	2.03	0.57
21:CA:183:ASP:O	21:CA:187:HIS:HB2	2.04	0.57
26:K1:42:MET:SD	35:SC:112:SER:OG	2.61	0.57
34:SA:1253:U:H3'	43:SN:46:ARG:HH22	1.69	0.57
4:3E:289:GLN:O	4:3E:391:ARG:NH2	2.37	0.57
5:3F:537:PHE:O	5:3F:567:VAL:HA	2.04	0.57
6:3G:21:LEU:O	6:3G:25:GLN:HB2	2.03	0.57
8:AA:444:UNK:O	8:AA:452:UNK:N	2.37	0.57
17:BB:866:LYS:NZ	18:BC:806:LEU:O	2.36	0.57
18:BC:666:GLU:HG2	18:BC:688:LEU:HD11	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BE:546:ILE:HD13	20:BE:560:LEU:HD13	1.85	0.57
22:CB:532:PRO:HG2	22:CB:693:LYS:HE2	1.85	0.57
23:E2:46:ALA:HA	23:E2:115:GLN:HB3	1.86	0.57
28:MB:181:ASN:HA	34:SA:1623:C:H4'	1.86	0.57
34:SA:1118:G:H2'	34:SA:1119:G:H8	1.69	0.57
51:Sd:14:LYS:NZ	51:Sd:29:ARG:HD2	2.19	0.57
57:U4:69:THR:HG22	57:U4:73:ASN:HD21	1.70	0.57
7:5A:466:A:H2'	7:5A:467:A:H8	1.69	0.57
8:AA:433:UNK:O	8:AA:444:UNK:HA	2.05	0.57
20:BE:616:THR:HG23	20:BE:618:GLY:H	1.69	0.57
54:U1:36:UNK:HA	54:U1:47:UNK:HA	1.85	0.57
19:BD:320:TYR:HB3	19:BD:343:SER:HB2	1.87	0.57
3:3D:157:ALA:O	3:3D:161:ALA:HB3	2.04	0.57
12:AE:630:TYR:CZ	12:AE:637:ILE:HG21	2.38	0.57
15:B1:283:LEU:HB3	15:B1:788:TYR:HD2	1.68	0.57
16:BA:126:ASP:OD1	16:BA:128:ASN:ND2	2.38	0.57
16:BA:505:ARG:HD3	34:SA:1616:G:H5'	1.86	0.57
37:SG:84:LYS:O	37:SG:92:ARG:NH1	2.38	0.57
4:3E:228:PRO:HD2	4:3E:231:ILE:HD12	1.86	0.57
16:BA:153:THR:HG21	16:BA:198:PHE:HA	1.85	0.57
17:BB:554:THR:HG22	17:BB:570:TYR:HB2	1.87	0.57
23:E1:114:ILE:HB	23:E1:122:ILE:HB	1.87	0.57
37:SG:73:THR:OG1	46:SR:114:ARG:NH2	2.37	0.57
39:SI:154:LEU:HD21	39:SI:185:ILE:HG13	1.86	0.57
34:SA:297:U:H5''	36:SF:37:LYS:HG2	1.85	0.57
34:SA:1213:G:N2	34:SA:1450:U:O2	2.35	0.57
5:3F:496:LEU:O	5:3F:513:GLU:HA	2.05	0.57
6:3H:25:GLN:OE1	6:3H:29:ASN:ND2	2.37	0.57
14:AG:7:UNK:HA	14:AG:568:UNK:HA	1.87	0.57
17:BB:230:LYS:HD3	17:BB:237:LYS:HB3	1.87	0.57
19:BD:429:TYR:OH	20:BE:563:ASP:OD1	2.22	0.57
23:E2:42:ILE:O	23:E2:203:CYS:HA	2.05	0.57
25:E4:233:UNK:O	25:E4:240:UNK:HA	2.04	0.57
42:SM:128:CYS:SG	42:SM:129:ARG:N	2.76	0.57
1:3A:3:C:H2'	1:3A:4:G:H8	1.69	0.57
20:BE:172:HIS:NE2	20:BE:176:TYR:O	2.36	0.57
21:CA:88:LEU:HB2	21:CA:125:LEU:HB2	1.87	0.57
22:CB:527:TYR:HB2	22:CB:615:VAL:HB	1.87	0.57
34:SA:1486:G:OP2	34:SA:1486:G:N2	2.34	0.57
37:SG:68:ILE:HG22	46:SR:114:ARG:NH1	2.18	0.57
5:3F:305:ARG:HG2	5:3F:317:ILE:HG12	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:BA:585:TYR:HA	16:BA:592:ILE:HG22	1.87	0.56
18:BC:713:GLU:HB3	18:BC:762:CYS:HB2	1.86	0.56
21:CA:185:HIS:O	21:CA:189:ALA:HB2	2.05	0.56
24:E3:344:LYS:NZ	34:SA:1266:U:O2	2.37	0.56
17:BB:499:PHE:HB2	17:BB:518:PRO:HG2	1.87	0.56
51:Sd:29:ARG:HA	51:Sd:41:VAL:HA	1.87	0.56
3:3D:218:LYS:NZ	3:3D:240:LEU:HD22	2.19	0.56
5:3F:201:ILE:O	5:3F:538:ARG:NH1	2.38	0.56
5:3F:551:ARG:NH1	6:3G:94:SER:HA	2.21	0.56
12:AE:370:LEU:HD23	12:AE:400:LEU:HD13	1.88	0.56
15:B1:634:ARG:NH1	31:R1:185:ARG:HG2	2.20	0.56
16:BA:430:ARG:HE	16:BA:432:GLN:H	1.53	0.56
16:BA:553:ILE:HD13	46:SR:99:GLU:HG2	1.86	0.56
18:BC:737:ILE:HD12	18:BC:778:MET:HE2	1.87	0.56
19:BD:541:LEU:O	19:BD:542:ARG:NH1	2.36	0.56
20:BE:92:ALA:O	20:BE:98:VAL:HA	2.04	0.56
22:CB:344:ASN:HD21	22:CB:445:ASN:HD21	1.51	0.56
23:E2:96:LEU:HD21	23:E2:114:ILE:HD11	1.86	0.56
34:SA:1080:U:O4	34:SA:1081:A:N6	2.38	0.56
34:SA:1583:A:H61	34:SA:1611:A:H5''	1.70	0.56
37:SG:76:ARG:HH11	46:SR:120:ASP:CG	2.13	0.56
34:SA:1585:U:H3	34:SA:1611:A:H2	1.53	0.56
12:AE:25:ARG:O	12:AE:29:HIS:HB2	2.05	0.56
17:BB:171:CYS:SG	17:BB:172:GLN:N	2.79	0.56
18:BC:548:LEU:O	18:BC:559:ILE:HA	2.04	0.56
20:BE:311:VAL:HG22	20:BE:321:GLU:HG2	1.86	0.56
23:E1:104:ILE:N	23:E1:246:GLU:OE2	2.39	0.56
34:SA:349:U:OP2	42:SM:106:ASN:ND2	2.39	0.56
38:SH:4:ASN:HB3	38:SH:110:ALA:HA	1.88	0.56
40:SJ:9:HIS:O	40:SJ:18:ARG:NH2	2.39	0.56
42:SM:67:ARG:NH1	42:SM:127:GLN:OE1	2.38	0.56
47:SX:75:ILE:HG12	47:SX:127:GLY:HA2	1.86	0.56
5:3F:304:ILE:O	5:3F:317:ILE:HA	2.05	0.56
12:AE:653:PHE:O	12:AE:657:GLN:HB2	2.06	0.56
16:BA:847:ARG:HH22	18:BC:761:ARG:HH11	1.54	0.56
19:BD:321:MET:HE1	19:BD:367:GLN:HE22	1.70	0.56
20:BE:601:VAL:HA	20:BE:610:ARG:O	2.06	0.56
28:MB:261:LEU:H	34:SA:571:G:H21	1.54	0.56
34:SA:1072:C:P	50:Sc:22:LYS:HZ2	2.27	0.56
7:5A:556:G:H2'	7:5A:557:A:H8	1.70	0.56
16:BA:799:ILE:O	16:BA:803:LEU:HB3	2.05	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:BA:799:ILE:O	16:BA:803:LEU:CB	2.54	0.56
20:BE:190:LEU:HB3	20:BE:200:PHE:HB3	1.87	0.56
4:3E:76:LEU:HD23	4:3E:84:LYS:HZ1	1.71	0.56
12:AE:33:LEU:HD22	12:AE:150:ARG:HB3	1.86	0.56
24:E3:311:LEU:HD22	24:E3:345:VAL:HB	1.87	0.56
5:3F:289:ARG:NH1	5:3F:334:GLU:HB2	2.21	0.56
16:BA:541:ILE:HG23	16:BA:549:GLN:HB2	1.88	0.56
18:BC:465:LYS:H	18:BC:481:LYS:HD2	1.70	0.56
34:SA:1235:C:O2	53:Sg:138:ARG:NH1	2.39	0.56
2:3B:227:PRO:HB2	2:3B:259:MET:HG2	1.87	0.56
19:BD:292:GLY:O	19:BD:318:ARG:NH1	2.39	0.56
23:E2:176:ARG:NH2	23:E2:192:TYR:OH	2.39	0.56
34:SA:337:G:H1'	34:SA:339:C:OP2	2.05	0.56
15:B1:268:HIS:ND1	15:B1:274:ASP:OD1	2.37	0.55
17:BB:616:ASP:HB3	17:BB:635:LYS:HB3	1.88	0.55
20:BE:128:LEU:HB3	20:BE:140:TYR:HB2	1.87	0.55
35:SC:69:CYS:HA	35:SC:83:LYS:HA	1.88	0.55
58:U5:39:ILE:HB	58:U5:243:PHE:HB2	1.88	0.55
1:3A:82:G:N2	1:3A:327:G:O2'	2.35	0.55
4:3E:95:ALA:O	4:3E:99:ASN:HB2	2.06	0.55
4:3E:191:HIS:ND1	4:3E:245:THR:O	2.38	0.55
12:AE:671:LEU:O	12:AE:675:ASN:ND2	2.39	0.55
22:CB:970:TRP:O	22:CB:1028:ARG:NH2	2.39	0.55
34:SA:132:U:O4	56:U3:1015:UNK:N	2.39	0.55
34:SA:283:U:C2	38:SH:188:ARG:CG	2.89	0.55
17:BB:899:GLY:O	17:BB:903:GLN:NE2	2.40	0.55
19:BD:576:LEU:HA	19:BD:589:TRP:O	2.06	0.55
21:CA:53:LEU:HB2	21:CA:126:LEU:HB3	1.89	0.55
26:K1:146:VAL:HG22	26:K1:150:GLY:HA2	1.87	0.55
34:SA:1085:G:N1	34:SA:1089:U:O4	2.40	0.55
46:SR:48:VAL:HG23	46:SR:82:ARG:HB3	1.88	0.55
46:SR:52:LEU:O	46:SR:59:LYS:NZ	2.38	0.55
12:AE:333:LEU:O	12:AE:337:ASP:CB	2.54	0.55
18:BC:216:ARG:NH1	35:SC:25:THR:O	2.39	0.55
19:BD:520:ASN:HD22	19:BD:533:ALA:HB3	1.72	0.55
23:E1:89:PRO:HG2	23:E1:134:PHE:HZ	1.71	0.55
31:R1:311:LEU:HB3	31:R1:352:ALA:HB3	1.87	0.55
36:SF:59:ARG:HG3	36:SF:62:LYS:NZ	2.22	0.55
51:Sd:14:LYS:HD3	51:Sd:29:ARG:HB3	1.89	0.55
51:Sd:14:LYS:HZ3	51:Sd:29:ARG:HD2	1.70	0.55
6:3H:34:LYS:O	6:3H:100:ALA:HA	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AE:141:ASN:ND2	12:AE:209:GLN:OE1	2.40	0.55
16:BA:17:GLN:NE2	16:BA:306:ASN:OD1	2.40	0.55
17:BB:509:VAL:HG13	17:BB:515:LYS:HE2	1.88	0.55
34:SA:1250:U:O2	53:Sg:135:HIS:NE2	2.39	0.55
5:3F:440:HIS:HD1	5:3F:493:SER:HG	1.55	0.55
17:BB:16:VAL:HG13	17:BB:18:ALA:H	1.71	0.55
22:CB:494:GLU:OE1	22:CB:497:ARG:NH2	2.38	0.55
25:E4:55:UNK:HA	25:E4:71:UNK:HA	1.88	0.55
36:SF:59:ARG:HA	36:SF:62:LYS:NZ	2.21	0.55
16:BA:603:LEU:HB3	16:BA:611:LEU:HB2	1.88	0.55
34:SA:1498:G:H4'	58:U5:250:THR:HA	1.89	0.55
16:BA:117:ARG:NH2	16:BA:145:HIS:O	2.40	0.55
17:BB:640:LYS:HG2	17:BB:652:LYS:HG3	1.89	0.55
18:BC:270:ILE:HG22	18:BC:277:VAL:HG12	1.86	0.55
19:BD:524:SER:HB3	19:BD:529:ILE:HB	1.89	0.55
34:SA:483:A:N6	34:SA:504:U:O4	2.40	0.55
48:SY:97:ASP:HB2	48:SY:100:ASP:OD2	2.06	0.55
49:SZ:32:ARG:NH1	49:SZ:35:VAL:HG23	2.22	0.55
57:U4:115:ILE:HA	57:U4:118:LYS:HE2	1.87	0.55
3:3D:323:THR:HG22	3:3D:327:LYS:NZ	2.22	0.55
8:AA:79:UNK:N	8:AA:83:UNK:O	2.40	0.55
12:AE:661:ILE:HG12	12:AE:663:SER:H	1.71	0.55
22:CB:1100:VAL:HB	22:CB:1182:ILE:HB	1.88	0.55
26:K1:198:TYR:O	26:K1:202:GLU:CB	2.54	0.55
31:R1:66:GLU:HB2	31:R1:75:ILE:HB	1.89	0.55
39:SI:137:GLY:H	39:SI:153:LEU:HB2	1.71	0.55
46:SR:25:GLY:HA3	46:SR:64:ASP:OD2	2.07	0.55
3:3D:323:THR:HG22	3:3D:327:LYS:HZ2	1.71	0.54
16:BA:10:LEU:HA	16:BA:702:LEU:H	1.70	0.54
17:BB:391:ARG:HG3	17:BB:392:THR:HG23	1.89	0.54
34:SA:151:G:N3	38:SH:13:GLN:NE2	2.55	0.54
36:SF:176:ASP:HB3	36:SF:179:LYS:NZ	2.23	0.54
23:E2:31:LEU:HD13	23:E2:40:ARG:HE	1.72	0.54
24:E3:305:ARG:CG	24:E3:306:ALA:N	2.66	0.54
46:SR:10:PHE:HB2	46:SR:12:LYS:NZ	2.23	0.54
47:SX:118:ARG:HH12	47:SX:119:LYS:NZ	2.05	0.54
1:3A:86:A:N3	4:3E:336:THR:OG1	2.38	0.54
2:3C:198:GLU:HG3	2:3C:200:SER:H	1.73	0.54
24:E3:378:LYS:HD2	34:SA:1220:C:H4'	1.89	0.54
34:SA:442:C:O2'	34:SA:526:A:N6	2.41	0.54
15:B1:149:VAL:HG22	15:B1:184:PHE:HB2	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BE:272:ASP:HA	20:BE:287:LEU:O	2.06	0.54
21:CA:18:PHE:HB2	21:CA:35:HIS:HB3	1.90	0.54
23:E1:31:LEU:HD22	23:E1:40:ARG:HE	1.72	0.54
31:R1:11:PHE:HB3	31:R1:20:ARG:NH1	2.22	0.54
34:SA:1610:G:H5"	37:SG:107:LYS:HE3	1.88	0.54
44:SO:20:ARG:HH21	47:SX:56:HIS:HB3	1.71	0.54
2:3C:319:ARG:HD2	2:3C:322:ARG:HD3	1.90	0.54
12:AE:802:PHE:O	12:AE:806:LEU:HB2	2.08	0.54
15:B1:857:LEU:HD13	15:B1:1012:LYS:HD3	1.88	0.54
18:BC:310:THR:HB	18:BC:363:ARG:HH12	1.70	0.54
33:S1:209:UNK:HA	33:S1:219:UNK:HA	1.88	0.54
34:SA:955:A:H5"	44:SO:10:GLY:HA3	1.88	0.54
54:U1:109:UNK:HA	54:U1:119:UNK:HA	1.89	0.54
12:AE:367:LEU:HA	12:AE:400:LEU:HD11	1.88	0.54
18:BC:467:ILE:H	18:BC:480:ILE:HG21	1.71	0.54
28:MB:192:ASP:HB2	28:MB:225:ALA:HA	1.89	0.54
34:SA:1685:G:N2	34:SA:1716:C:N3	2.56	0.54
36:SF:104:ASP:N	36:SF:108:ARG:O	2.40	0.54
19:BD:237:ARG:NH1	19:BD:238:LEU:O	2.40	0.54
19:BD:576:LEU:HB3	19:BD:588:LEU:HD12	1.90	0.54
20:BE:131:SER:HB3	20:BE:170:LEU:HD11	1.89	0.54
23:E1:150:ILE:O	23:E1:158:LYS:HA	2.08	0.54
27:MA:138:VAL:HG22	27:MA:158:VAL:HG22	1.88	0.54
40:SJ:72:ILE:HD12	40:SJ:74:LYS:NZ	2.22	0.54
13:AF:195:UNK:O	60:UB:394:UNK:N	2.41	0.54
14:AG:346:UNK:HA	14:AG:353:UNK:HA	1.89	0.54
23:E1:179:THR:HB	23:E1:224:LYS:HG2	1.88	0.54
34:SA:1218:G:OP1	34:SA:1444:A:N6	2.40	0.54
35:SC:87:ARG:HH11	35:SC:99:ASN:HD22	1.53	0.54
38:SH:188:ARG:CZ	38:SH:191:ARG:CD	2.70	0.54
58:U5:128:ASP:HB3	58:U5:131:VAL:HG22	1.88	0.54
15:B1:931:LYS:HD3	15:B1:1004:ARG:HB3	1.90	0.54
16:BA:792:ILE:O	16:BA:796:LEU:HB2	2.08	0.54
19:BD:237:ARG:NH2	19:BD:240:ASP:OD1	2.41	0.54
24:E3:413:LEU:HG	24:E3:447:ARG:HH21	1.73	0.54
34:SA:273:G:O6	34:SA:283:U:O2	2.24	0.54
38:SH:187:LYS:NZ	38:SH:191:ARG:HH12	2.05	0.54
58:U5:71:ASN:HB2	58:U5:122:PHE:HA	1.90	0.54
14:AG:487:UNK:O	14:AG:495:UNK:N	2.41	0.54
17:BB:538:ARG:NH1	17:BB:539:VAL:O	2.40	0.54
23:E1:111:GLN:NE2	23:E1:113:TYR:OH	2.41	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:E4:160:UNK:O	25:E4:168:UNK:N	2.41	0.54
25:E4:272:UNK:O	25:E4:283:UNK:HA	2.08	0.54
33:S1:221:UNK:N	33:S1:225:UNK:O	2.40	0.54
54:U1:150:UNK:HA	54:U1:160:UNK:HA	1.89	0.54
2:3C:252:ILE:O	2:3C:256:ASN:ND2	2.40	0.53
14:AG:97:UNK:HA	14:AG:113:UNK:HA	1.90	0.53
17:BB:530:LEU:HB3	17:BB:551:LEU:HB3	1.90	0.53
20:BE:62:ASP:OD2	20:BE:65:THR:OG1	2.25	0.53
34:SA:1163:A:H4'	37:SG:166:ARG:NH1	2.23	0.53
42:SM:3:THR:OG1	42:SM:4:GLU:N	2.41	0.53
1:3A:83:A:H61	1:3A:327:G:H1'	1.73	0.53
8:AA:394:UNK:O	8:AA:401:UNK:HA	2.08	0.53
17:BB:536:CYS:H	17:BB:549:SER:HB2	1.73	0.53
20:BE:60:ILE:HB	20:BE:70:PHE:HB2	1.89	0.53
22:CB:162:PHE:HB2	22:CB:597:ARG:HD2	1.89	0.53
24:E3:301:TYR:OH	34:SA:1217:A:C2	2.55	0.53
27:MA:70:PHE:O	27:MA:74:HIS:ND1	2.40	0.53
28:MB:167:LEU:HA	28:MB:256:MET:HG2	1.90	0.53
34:SA:485:A:H1'	34:SA:503:G:H22	1.73	0.53
34:SA:1175:U:O4	34:SA:1464:G:O6	2.25	0.53
40:SJ:101:ILE:HD12	40:SJ:184:LEU:HD21	1.89	0.53
44:SO:119:GLU:O	44:SO:123:HIS:ND1	2.38	0.53
53:Sg:132:LEU:HD13	53:Sg:139:LEU:HB3	1.91	0.53
4:3E:68:VAL:HG13	4:3E:72:LEU:HD22	1.90	0.53
5:3F:190:VAL:HA	5:3F:195:GLN:O	2.08	0.53
6:3G:53:ILE:HB	6:3G:100:ALA:HB3	1.89	0.53
9:AB:259:UNK:O	9:AB:277:UNK:N	2.41	0.53
12:AE:630:TYR:OH	12:AE:637:ILE:CD1	2.35	0.53
19:BD:530:LEU:HB3	19:BD:544:VAL:HB	1.90	0.53
21:CA:103:LEU:O	22:CB:869:ASN:ND2	2.38	0.53
23:E2:104:ILE:N	23:E2:246:GLU:OE2	2.41	0.53
49:SZ:29:HIS:ND1	49:SZ:32:ARG:O	2.37	0.53
53:Sg:108:VAL:HG22	53:Sg:114:VAL:HG22	1.91	0.53
54:U1:197:UNK:O	54:U1:215:UNK:N	2.41	0.53
2:3B:171:LEU:HB3	2:3B:240:VAL:HG23	1.91	0.53
7:5A:403:C:OP2	7:5A:404:G:O2'	2.17	0.53
15:B1:822:PHE:HA	15:B1:888:PRO:HA	1.91	0.53
18:BC:510:SER:OG	18:BC:512:ASP:OD1	2.25	0.53
33:S1:208:UNK:N	33:S1:220:UNK:O	2.42	0.53
33:S1:290:UNK:N	33:S1:302:UNK:O	2.41	0.53
44:SO:111:ALA:HA	44:SO:114:ARG:HB2	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:SR:50:GLU:OE1	46:SR:82:ARG:NH2	2.41	0.53
1:3A:7:G:O6	34:SA:1117:U:O4	2.27	0.53
3:3D:223:ILE:HG22	3:3D:225:ASP:H	1.74	0.53
16:BA:328:LEU:HG	16:BA:343:GLY:HA2	1.90	0.53
18:BC:533:LYS:HB2	18:BC:554:ASP:HB3	1.90	0.53
18:BC:576:ASN:HD22	18:BC:596:ASP:HA	1.74	0.53
20:BE:418:ALA:HB3	20:BE:431:ILE:HB	1.89	0.53
22:CB:751:LYS:N	22:CB:785:GLU:O	2.41	0.53
12:AE:478:THR:HA	12:AE:490:ARG:HD2	1.90	0.53
12:AE:566:CYS:O	12:AE:570:ALA:HB2	2.09	0.53
15:B1:943:LYS:HD2	34:SA:573:C:OP2	2.09	0.53
16:BA:131:ARG:HG3	20:BE:27:PHE:HA	1.91	0.53
22:CB:797:THR:HG23	22:CB:836:GLU:HG3	1.90	0.53
23:E1:103:PRO:HG3	23:E2:232:LEU:HD21	1.90	0.53
24:E3:378:LYS:O	34:SA:1220:C:O2'	2.25	0.53
34:SA:38:C:O2'	34:SA:470:A:N6	2.42	0.53
35:SC:144:ARG:NH2	35:SC:207:LEU:O	2.39	0.53
40:SJ:79:ALA:HB3	40:SJ:164:ARG:HH11	1.73	0.53
12:AE:78:SER:HB2	12:AE:125:PHE:HZ	1.73	0.53
12:AE:354:SER:O	12:AE:357:ARG:NH2	2.42	0.53
17:BB:38:PRO:HD2	17:BB:41:LEU:HB2	1.91	0.53
20:BE:526:VAL:O	20:BE:539:LYS:HA	2.09	0.53
33:S1:220:UNK:HA	33:S1:226:UNK:HA	1.90	0.53
35:SC:223:PHE:HD2	35:SC:225:VAL:HG23	1.74	0.53
36:SF:54:TYR:HB3	49:SZ:17:LEU:HD11	1.91	0.53
1:3A:18:G:H2'	1:3A:19:A:C8	2.44	0.53
5:3F:287:ALA:HB3	5:3F:296:TYR:HB2	1.91	0.53
7:5A:174:U:O4	7:5A:222:G:O6	2.26	0.53
7:5A:534:A:H8	7:5A:534:A:OP2	1.92	0.53
17:BB:165:SER:HB2	17:BB:182:LYS:HD2	1.91	0.53
17:BB:478:SER:O	17:BB:491:GLY:N	2.41	0.53
17:BB:553:ASN:HB3	17:BB:572:HIS:HB2	1.91	0.53
17:BB:559:PHE:HE1	17:BB:564:LYS:HB2	1.74	0.53
18:BC:16:TYR:HB3	18:BC:641:PHE:H	1.74	0.53
20:BE:459:ASP:O	20:BE:481:ASN:ND2	2.42	0.53
22:CB:578:ILE:HA	22:CB:620:ASN:H	1.74	0.53
31:R1:202:PRO:HG3	31:R1:229:VAL:HG11	1.91	0.53
33:S1:342:UNK:O	33:S1:350:UNK:N	2.42	0.53
34:SA:298:C:H5''	36:SF:38:LEU:HB2	1.90	0.53
34:SA:478:A:O2'	41:SK:124:HIS:ND1	2.42	0.53
34:SA:1663:G:O6	34:SA:1738:U:O4	2.27	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:SJ:8:ARG:NE	40:SJ:19:ALA:O	2.40	0.53
47:SX:18:GLU:HG3	47:SX:69:LEU:HD12	1.91	0.53
54:U1:61:UNK:N	54:U1:66:UNK:O	2.41	0.53
18:BC:174:VAL:HB	18:BC:184:HIS:HB2	1.90	0.53
34:SA:299:A:OP2	36:SF:38:LEU:HG	2.09	0.53
34:SA:1042:G:H22	34:SA:1076:A:H2	1.57	0.53
34:SA:1647:U:H2'	34:SA:1648:A:H8	1.74	0.53
1:3A:66:U:H2'	1:3A:67:G:H8	1.73	0.53
5:3F:297:ALA:HB3	5:3F:305:ARG:O	2.09	0.53
7:5A:545:G:OP1	7:5A:547:C:N4	2.42	0.53
16:BA:36:ARG:HG2	16:BA:52:TYR:HB2	1.91	0.53
17:BB:898:LEU:HD11	18:BC:789:THR:HB	1.91	0.53
20:BE:275:PHE:O	20:BE:284:ILE:N	2.42	0.53
21:CA:46:ASN:HB3	21:CA:49:GLU:HB2	1.91	0.53
22:CB:174:TYR:HB3	22:CB:223:ARG:NH1	2.24	0.53
25:E4:190:UNK:O	25:E4:201:UNK:HA	2.09	0.53
34:SA:1216:C:H4'	34:SA:1217:A:OP1	2.09	0.53
36:SF:112:HIS:NE2	36:SF:237:SER:OG	2.38	0.53
34:SA:865:A:OP1	47:SX:28:ARG:NH1	2.43	0.52
34:SA:1611:A:O2'	37:SG:95:ASN:O	2.26	0.52
49:SZ:92:VAL:HG13	49:SZ:99:LYS:HD2	1.90	0.52
24:E3:418:HIS:O	24:E3:422:LEU:CB	2.57	0.52
34:SA:1217:A:H2'	34:SA:1217:A:N3	2.24	0.52
54:U1:19:UNK:HA	54:U1:26:UNK:HA	1.90	0.52
2:3B:271:ILE:HB	2:3B:314:CYS:O	2.08	0.52
12:AE:105:ALA:O	12:AE:109:TRP:NE1	2.42	0.52
17:BB:185:MET:HA	17:BB:201:ILE:HG22	1.90	0.52
17:BB:426:ARG:HD2	17:BB:457:PHE:HB3	1.91	0.52
18:BC:257:ILE:HG12	18:BC:299:ASN:HD22	1.74	0.52
20:BE:583:GLY:C	20:BE:610:ARG:HH12	2.16	0.52
24:E3:208:GLU:O	24:E3:209:LYS:HE2	2.09	0.52
33:S1:180:UNK:N	33:S1:184:UNK:O	2.43	0.52
34:SA:354:C:H5'	40:SJ:14:THR:HG21	1.92	0.52
41:SK:53:ARG:NH2	41:SK:97:LEU:O	2.41	0.52
2:3B:88:ILE:HD13	2:3B:107:VAL:HG21	1.90	0.52
23:E1:112:VAL:O	23:E1:124:VAL:HB	2.08	0.52
1:3A:66:U:H3	7:5A:287:G:H1	1.57	0.52
8:AA:382:UNK:N	8:AA:395:UNK:O	2.42	0.52
9:AB:4:UNK:HA	9:AB:283:UNK:O	2.09	0.52
18:BC:346:VAL:HB	18:BC:352:LYS:HB3	1.92	0.52
23:E2:178:VAL:HG12	23:E2:223:GLU:HB3	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:MB:143:HIS:HB2	34:SA:1604:U:H5''	1.91	0.52
31:R1:176:GLN:HG3	31:R1:305:LYS:HB3	1.92	0.52
34:SA:404:G:O2'	38:SH:88:ARG:NH1	2.42	0.52
38:SH:2:LYS:HB3	38:SH:108:VAL:HG22	1.92	0.52
39:SI:62:VAL:HG12	39:SI:64:VAL:H	1.74	0.52
42:SM:97:TYR:HB3	42:SM:99:ARG:HH11	1.74	0.52
48:SY:107:PHE:HE1	48:SY:123:LYS:HB3	1.74	0.52
7:5A:242:C:H2'	7:5A:243:A:H8	1.74	0.52
12:AE:316:PRO:HA	12:AE:319:ILE:HG22	1.91	0.52
15:B1:932:LEU:H	15:B1:1006:TRP:CD1	2.25	0.52
16:BA:60:ALA:HB3	16:BA:73:ILE:HB	1.91	0.52
16:BA:206:ILE:O	16:BA:217:VAL:HA	2.09	0.52
18:BC:691:PRO:HG3	18:BC:742:ARG:HE	1.74	0.52
34:SA:25:C:N4	34:SA:470:A:OP1	2.43	0.52
42:SM:33:ARG:HH11	42:SM:61:THR:HG21	1.75	0.52
2:3B:122:ARG:HG2	2:3B:142:ARG:HG2	1.91	0.52
7:5A:178:G:O6	7:5A:219:U:O2	2.26	0.52
16:BA:92:HIS:HD2	16:BA:135:PRO:HD2	1.74	0.52
19:BD:575:GLY:O	19:BD:591:LEU:N	2.43	0.52
23:E2:211:ARG:HH12	34:SA:1190:C:H3'	1.75	0.52
34:SA:283:U:C4	38:SH:188:ARG:CB	2.73	0.52
34:SA:361:C:H3'	34:SA:378:A:OP2	2.09	0.52
34:SA:1234:A:O2'	53:Sg:140:TYR:OH	2.24	0.52
39:SI:161:GLN:HG2	39:SI:162:ILE:HG13	1.92	0.52
40:SJ:48:THR:OG1	40:SJ:52:ASN:O	2.28	0.52
57:U4:66:LEU:N	57:U4:152:ILE:O	2.42	0.52
22:CB:904:HIS:O	22:CB:907:GLN:NE2	2.42	0.52
37:SG:80:LYS:HB2	37:SG:83:ARG:NH1	2.24	0.52
4:3E:125:PRO:HB3	4:3E:132:SER:HA	1.91	0.52
4:3E:249:GLN:HA	4:3E:252:LEU:HD12	1.92	0.52
17:BB:456:LEU:HB3	17:BB:466:ASP:O	2.10	0.52
20:BE:471:CYS:SG	20:BE:473:ASN:ND2	2.83	0.52
20:BE:641:LEU:HB3	20:BE:654:TRP:HB2	1.91	0.52
23:E1:188:ARG:HD3	23:E1:191:ASP:OD2	2.10	0.52
26:K1:61:THR:HA	26:K1:64:LEU:HB3	1.92	0.52
32:R2:1509:GLU:HB3	32:R2:1512:GLU:HB3	1.91	0.52
34:SA:297:U:OP1	36:SF:37:LYS:NZ	2.42	0.52
38:SH:4:ASN:HA	38:SH:15:THR:HG22	1.92	0.52
12:AE:478:THR:HG22	12:AE:490:ARG:HB3	1.91	0.52
18:BC:211:LEU:O	18:BC:223:TRP:HB2	2.10	0.52
19:BD:302:THR:HG21	19:BD:364:GLN:HB3	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CA:169:VAL:HG23	21:CA:173:LYS:NZ	2.25	0.52
22:CB:748:LEU:HD21	22:CB:791:LYS:HD2	1.92	0.52
26:K1:61:THR:O	26:K1:65:ASP:HB3	2.10	0.52
26:K1:159:LEU:HD13	26:K1:203:LEU:HB2	1.92	0.52
35:SC:141:ALA:HA	35:SC:210:ILE:HG12	1.91	0.52
43:SN:42:ALA:HB3	43:SN:122:VAL:HB	1.92	0.52
6:3G:24:VAL:HG22	6:3G:102:ILE:HD11	1.93	0.51
18:BC:122:THR:HG23	18:BC:124:GLY:H	1.75	0.51
19:BD:406:ASP:OD1	20:BE:371:LYS:NZ	2.43	0.51
33:S1:118:UNK:O	33:S1:127:UNK:N	2.43	0.51
35:SC:107:THR:HB	35:SC:111:ARG:NH1	2.24	0.51
42:SM:127:GLN:NE2	42:SM:128:CYS:O	2.42	0.51
2:3B:188:VAL:HG22	2:3B:192:GLY:HA3	1.91	0.51
5:3F:254:GLY:HA3	5:3F:260:LEU:HD23	1.93	0.51
9:AB:59:UNK:N	9:AB:68:UNK:O	2.43	0.51
17:BB:624:LEU:HB2	17:BB:629:ASN:H	1.75	0.51
20:BE:412:PRO:HD2	20:BE:441:ARG:HH12	1.75	0.51
22:CB:127:PHE:HD1	22:CB:283:TYR:HB3	1.75	0.51
22:CB:165:PRO:HD2	22:CB:222:PHE:HE2	1.75	0.51
35:SC:83:LYS:HZ1	35:SC:106:THR:HA	1.75	0.51
36:SF:59:ARG:HG3	36:SF:62:LYS:HZ3	1.74	0.51
39:SI:67:LEU:HG	39:SI:71:HIS:HE1	1.75	0.51
14:AG:36:UNK:O	14:AG:48:UNK:HA	2.10	0.51
16:BA:161:ILE:HB	16:BA:173:TRP:O	2.10	0.51
21:CA:134:ILE:O	21:CA:138:TRP:CB	2.57	0.51
26:K1:130:ASN:ND2	34:SA:930:A:OP1	2.42	0.51
28:MB:233:VAL:HB	28:MB:254:PHE:HB2	1.93	0.51
34:SA:1157:A:N6	34:SA:1618:C:O2	2.42	0.51
37:SG:38:THR:HG21	46:SR:57:LEU:HB3	1.91	0.51
40:SJ:11:ARG:HH12	40:SJ:17:LYS:HB2	1.75	0.51
44:SO:18:TYR:O	47:SX:56:HIS:NE2	2.43	0.51
5:3F:365:PRO:O	5:3F:368:LEU:HB2	2.10	0.51
7:5A:21:A:H2'	7:5A:22:A:H8	1.74	0.51
13:AF:4:UNK:HA	13:AF:284:UNK:HA	1.93	0.51
20:BE:611:THR:HB	20:BE:621:ASP:HB3	1.93	0.51
22:CB:99:LYS:O	22:CB:103:PHE:CB	2.57	0.51
34:SA:485:A:H3'	34:SA:486:G:H21	1.76	0.51
34:SA:1175:U:O2	34:SA:1464:G:N2	2.42	0.51
39:SI:46:ILE:HD11	39:SI:58:LEU:HB3	1.91	0.51
5:3F:358:THR:O	5:3F:430:LYS:NZ	2.34	0.51
12:AE:628:ASN:O	12:AE:632:THR:OG1	2.26	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:BA:142:HIS:NE2	16:BA:174:SER:O	2.40	0.51
17:BB:188:LEU:HD12	17:BB:198:GLU:HB3	1.93	0.51
31:R1:199:ARG:NH2	31:R1:236:GLY:O	2.38	0.51
33:S1:320:UNK:N	33:S1:334:UNK:O	2.44	0.51
34:SA:265:A:OP2	38:SH:194:LYS:NZ	2.29	0.51
34:SA:931:C:H5'	35:SC:116:LYS:HG2	1.93	0.51
35:SC:87:ARG:HH11	35:SC:99:ASN:ND2	2.08	0.51
3:3D:62:ALA:O	3:3D:66:ALA:HB2	2.10	0.51
18:BC:599:ILE:O	18:BC:613:LEU:HB2	2.10	0.51
19:BD:581:ASN:OD1	19:BD:585:LYS:N	2.43	0.51
20:BE:33:VAL:N	20:BE:317:ASN:OD1	2.41	0.51
22:CB:1222:GLU:O	22:CB:1226:PHE:HB2	2.11	0.51
28:MB:215:LYS:HZ2	34:SA:1625:C:H5'	1.75	0.51
33:S1:178:UNK:O	33:S1:186:UNK:N	2.43	0.51
34:SA:128:U:OP1	34:SA:264:G:O2'	2.28	0.51
7:5A:357:G:O6	7:5A:368:U:O2	2.28	0.51
14:AG:528:UNK:O	14:AG:536:UNK:N	2.44	0.51
16:BA:163:THR:O	16:BA:170:ALA:HA	2.11	0.51
16:BA:165:SER:OG	16:BA:166:LYS:N	2.43	0.51
17:BB:225:GLN:HG2	17:BB:243:THR:HA	1.93	0.51
22:CB:186:ILE:HG22	22:CB:346:LEU:HD22	1.93	0.51
22:CB:842:ILE:O	22:CB:849:GLY:HA2	2.10	0.51
23:E2:174:LYS:HE2	23:E2:200:GLU:HB2	1.92	0.51
31:R1:96:VAL:HG22	31:R1:122:THR:HA	1.92	0.51
31:R1:201:SER:HB3	31:R1:204:LEU:HD13	1.93	0.51
34:SA:512:A:OP2	41:SK:172:VAL:HG13	2.10	0.51
34:SA:1217:A:N3	34:SA:1217:A:C2'	2.73	0.51
35:SC:134:VAL:HB	35:SC:219:LYS:HB3	1.92	0.51
45:SP:85:ALA:H	45:SP:119:THR:HG22	1.75	0.51
46:SR:39:VAL:HG22	46:SR:41:PRO:HD2	1.92	0.51
3:3D:180:LEU:HD13	4:3E:183:ARG:HG2	1.93	0.51
10:AC:603:UNK:O	10:AC:607:UNK:CB	2.59	0.51
12:AE:43:GLN:HE21	12:AE:47:PHE:HB2	1.75	0.51
12:AE:288:ALA:HB3	12:AE:326:LYS:HB3	1.93	0.51
14:AG:117:UNK:HA	14:AG:131:UNK:O	2.11	0.51
16:BA:39:VAL:HB	16:BA:48:PHE:HB2	1.92	0.51
16:BA:78:ARG:HB2	16:BA:93:PHE:HA	1.91	0.51
18:BC:47:PRO:HD2	18:BC:51:LYS:H	1.76	0.51
19:BD:383:TRP:HZ3	19:BD:397:GLY:HA3	1.75	0.51
36:SF:85:GLY:N	36:SF:88:ASP:OD2	2.40	0.51
37:SG:156:ARG:HH12	37:SG:158:GLN:HB2	1.76	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:SK:83:VAL:O	41:SK:107:ARG:NE	2.39	0.51
3:3D:107:PRO:O	3:3D:111:GLU:HB2	2.11	0.51
5:3F:345:THR:HA	5:3F:359:PHE:O	2.10	0.51
6:3G:33:LEU:HA	6:3G:101:SER:O	2.11	0.51
8:AA:5:UNK:N	8:AA:565:UNK:O	2.44	0.51
8:AA:161:UNK:N	8:AA:165:UNK:O	2.44	0.51
12:AE:303:PHE:HB3	12:AE:346:LYS:HB3	1.92	0.51
12:AE:695:TYR:OH	12:AE:699:ARG:NH2	2.44	0.51
16:BA:752:ASN:O	16:BA:756:GLU:HB2	2.10	0.51
22:CB:215:GLU:N	22:CB:218:ASP:OD2	2.43	0.51
22:CB:738:TYR:O	22:CB:742:PHE:CB	2.59	0.51
23:E2:112:VAL:O	23:E2:124:VAL:HB	2.10	0.51
31:R1:138:MET:HA	31:R1:141:MET:HE3	1.93	0.51
33:S1:301:UNK:O	33:S1:309:UNK:N	2.44	0.51
37:SG:149:VAL:HG21	51:Sd:66:LEU:HD22	1.92	0.51
57:U4:64:GLN:HA	57:U4:95:ASN:HB3	1.92	0.51
5:3F:200:ASP:HB3	5:3F:209:LYS:HB2	1.93	0.51
16:BA:37:VAL:HB	16:BA:51:GLU:HB2	1.92	0.51
17:BB:629:ASN:ND2	17:BB:642:TRP:O	2.44	0.51
17:BB:674:SER:H	17:BB:681:ILE:HG23	1.76	0.51
34:SA:913:G:H5''	34:SA:914:G:H5'	1.92	0.51
36:SF:212:ASP:OD1	36:SF:216:ASN:N	2.43	0.51
45:SP:17:ALA:HA	45:SP:30:VAL:HA	1.92	0.51
6:3H:34:LYS:HB2	6:3H:101:SER:HB3	1.92	0.50
12:AE:572:ARG:N	12:AE:630:TYR:CE2	2.79	0.50
13:AF:221:UNK:O	13:AF:234:UNK:N	2.44	0.50
14:AG:111:UNK:CB	14:AG:119:UNK:O	2.59	0.50
19:BD:352:GLN:HG3	19:BD:371:VAL:HG13	1.92	0.50
22:CB:649:TRP:HB2	22:CB:653:SER:HB2	1.93	0.50
34:SA:548:G:H2'	34:SA:549:G:H8	1.76	0.50
34:SA:863:A:N7	34:SA:964:U:O4	2.44	0.50
54:U1:117:UNK:N	54:U1:130:UNK:O	2.44	0.50
12:AE:750:ASN:O	12:AE:754:GLU:CB	2.59	0.50
17:BB:180:THR:HG22	17:BB:186:ILE:HG23	1.92	0.50
22:CB:235:LEU:O	22:CB:239:LEU:CB	2.60	0.50
35:SC:190:PRO:HG2	35:SC:192:VAL:HG23	1.93	0.50
48:SY:54:LEU:HD12	48:SY:82:LYS:HD3	1.93	0.50
51:Sd:8:THR:HB	51:Sd:56:LEU:HB2	1.92	0.50
8:AA:506:UNK:HA	8:AA:516:UNK:O	2.11	0.50
12:AE:333:LEU:HD11	12:AE:369:LEU:HD12	1.92	0.50
12:AE:630:TYR:CD1	12:AE:637:ILE:HD12	2.31	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:BA:28:GLN:HA	16:BA:41:ASP:HA	1.92	0.50
16:BA:87:ARG:HH11	16:BA:89:VAL:HG22	1.75	0.50
20:BE:135:ASN:HB3	20:BE:159:VAL:HB	1.93	0.50
22:CB:334:PHE:O	22:CB:338:SER:CB	2.59	0.50
36:SF:48:LEU:HD11	36:SF:61:VAL:HG22	1.94	0.50
47:SX:103:ILE:HA	47:SX:112:ASP:HA	1.93	0.50
48:SY:76:LEU:HD12	48:SY:81:LYS:HB2	1.93	0.50
53:Sg:130:VAL:HG11	53:Sg:143:LYS:HB2	1.92	0.50
8:AA:425:UNK:O	8:AA:434:UNK:N	2.44	0.50
9:AB:203:UNK:N	9:AB:207:UNK:O	2.45	0.50
15:B1:840:LYS:HG2	15:B1:874:TYR:HB3	1.94	0.50
15:B1:978:ARG:HB3	15:B1:988:ARG:HE	1.77	0.50
15:B1:988:ARG:NH1	28:MB:146:ARG:HH11	2.06	0.50
19:BD:448:LYS:HE2	20:BE:563:ASP:HB3	1.93	0.50
19:BD:522:GLN:HB2	19:BD:531:CYS:HB3	1.92	0.50
22:CB:861:ILE:O	22:CB:865:ARG:CB	2.59	0.50
24:E3:352:SER:O	24:E3:356:LEU:HB2	2.12	0.50
34:SA:1083:G:H1	34:SA:1090:C:H42	1.58	0.50
40:SJ:43:ILE:HA	40:SJ:57:ALA:HA	1.93	0.50
2:3B:173:LEU:HB2	2:3B:242:ALA:HA	1.94	0.50
12:AE:384:ILE:HG23	12:AE:401:VAL:HG22	1.93	0.50
16:BA:168:LEU:O	16:BA:188:ASN:ND2	2.44	0.50
17:BB:125:THR:HG21	17:BB:165:SER:HB3	1.92	0.50
20:BE:438:LYS:NZ	20:BE:460:ASP:OD1	2.45	0.50
20:BE:485:THR:HG22	20:BE:497:LYS:HG3	1.92	0.50
30:P1:186:GLU:HG2	30:P1:188:LYS:H	1.76	0.50
46:SR:58:ASP:OD1	46:SR:58:ASP:N	2.41	0.50
53:Sg:107:LYS:NZ	53:Sg:117:LEU:HD11	2.27	0.50
12:AE:769:LEU:O	12:AE:773:GLN:NE2	2.45	0.50
15:B1:931:LYS:HB3	15:B1:1004:ARG:HE	1.76	0.50
21:CA:192:GLU:O	21:CA:196:ALA:CB	2.59	0.50
22:CB:93:GLU:O	22:CB:97:LEU:HB2	2.12	0.50
22:CB:309:LEU:O	22:CB:333:ASN:ND2	2.44	0.50
22:CB:333:ASN:O	22:CB:337:LEU:HB3	2.12	0.50
22:CB:367:ARG:O	22:CB:371:GLN:CB	2.58	0.50
24:E3:267:VAL:HG11	24:E3:310:SER:HB2	1.93	0.50
28:MB:86:PRO:O	28:MB:113:ASN:ND2	2.42	0.50
31:R1:11:PHE:HB2	31:R1:33:ILE:HG12	1.93	0.50
34:SA:327:U:OP1	42:SM:82:ARG:NH1	2.44	0.50
34:SA:1648:A:H2'	34:SA:1649:G:H8	1.76	0.50
38:SH:114:VAL:HG12	38:SH:115:LYS:HD3	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:SM:94:ILE:HG22	42:SM:97:TYR:H	1.76	0.50
58:U5:10:SER:OG	58:U5:217:GLN:NE2	2.41	0.50
12:AE:218:ILE:HG23	12:AE:263:VAL:HG11	1.92	0.50
16:BA:149:ILE:HD13	16:BA:165:SER:HB2	1.93	0.50
16:BA:751:ILE:O	16:BA:755:TYR:HB3	2.11	0.50
18:BC:80:SER:HB3	18:BC:84:LEU:HB2	1.94	0.50
19:BD:418:LYS:HB2	19:BD:422:ILE:HD11	1.93	0.50
26:K1:44:LEU:HD22	35:SC:115:ARG:NH1	2.25	0.50
34:SA:284:G:OP1	38:SH:196:ARG:NH1	2.19	0.50
34:SA:1661:U:H3	34:SA:1740:A:H61	1.59	0.50
35:SC:191:GLU:HB2	35:SC:194:ASN:HD22	1.77	0.50
47:SX:81:VAL:O	47:SX:122:SER:OG	2.30	0.50
54:U1:18:UNK:O	54:U1:27:UNK:N	2.44	0.50
56:U3:1931:UNK:HA	56:U3:1947:UNK:HA	1.93	0.50
9:AB:74:UNK:HA	9:AB:95:UNK:HA	1.94	0.50
19:BD:286:THR:HG21	19:BD:335:GLN:HE22	1.76	0.50
19:BD:357:ASN:O	19:BD:369:ASN:ND2	2.45	0.50
34:SA:1739:C:H2'	34:SA:1740:A:H8	1.77	0.50
35:SC:143:THR:HB	35:SC:205:PHE:HE2	1.77	0.50
7:5A:554:G:H1	7:5A:583:U:H3	1.59	0.50
12:AE:141:ASN:ND2	12:AE:206:TYR:OH	2.44	0.50
13:AF:201:UNK:CB	13:AF:210:UNK:O	2.60	0.50
15:B1:941:ILE:HG21	15:B1:995:ILE:H	1.76	0.50
17:BB:624:LEU:HB3	17:BB:628:HIS:H	1.77	0.50
18:BC:805:ILE:HD12	20:BE:932:VAL:HG23	1.94	0.50
25:E4:96:UNK:HA	25:E4:111:UNK:O	2.11	0.50
26:K1:152:THR:O	26:K1:155:ALA:HB3	2.11	0.50
31:R1:30:PRO:HB3	31:R1:77:ARG:HG2	1.94	0.50
34:SA:1216:C:O2'	34:SA:1217:A:H2'	2.12	0.50
34:SA:1615:C:N4	37:SG:78:ALA:O	2.44	0.50
41:SK:20:GLU:HB3	41:SK:23:ARG:HE	1.77	0.50
48:SY:109:ARG:NH1	48:SY:114:LYS:O	2.44	0.50
5:3F:515:SER:O	5:3F:518:LYS:NZ	2.29	0.49
8:AA:463:UNK:CB	8:AA:477:UNK:O	2.60	0.49
14:AG:405:UNK:O	14:AG:413:UNK:N	2.44	0.49
14:AG:843:UNK:O	14:AG:847:UNK:N	2.45	0.49
17:BB:622:LYS:O	17:BB:630:PHE:HA	2.12	0.49
20:BE:40:ALA:HB3	20:BE:51:VAL:HB	1.94	0.49
28:MB:124:MET:HE2	28:MB:127:LEU:HD23	1.94	0.49
33:S1:239:UNK:O	33:S1:252:UNK:N	2.45	0.49
38:SH:33:GLY:HA2	38:SH:51:LYS:NZ	2.27	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:SM:77:SER:HB3	42:SM:85:VAL:HB	1.93	0.49
4:3E:358:LYS:HG2	4:3E:361:ARG:HH12	1.77	0.49
12:AE:469:LEU:O	12:AE:473:SER:CB	2.60	0.49
16:BA:171:LYS:HG2	16:BA:186:THR:HG22	1.93	0.49
16:BA:356:ASP:OD2	16:BA:830:ARG:NH2	2.45	0.49
16:BA:825:GLN:HE22	20:BE:937:THR:HG1	1.56	0.49
17:BB:229:TRP:HZ3	17:BB:236:ASP:HB2	1.77	0.49
18:BC:226:ASN:HB3	18:BC:229:LYS:HB2	1.95	0.49
18:BC:344:ARG:NH1	18:BC:345:TYR:O	2.45	0.49
22:CB:777:ASP:O	22:CB:780:GLN:NE2	2.45	0.49
27:MA:108:ARG:HA	27:MA:113:VAL:HG11	1.94	0.49
36:SF:62:LYS:HA	36:SF:65:LEU:HB2	1.94	0.49
41:SK:121:SER:HB3	41:SK:124:HIS:HB3	1.95	0.49
1:3A:63:C:H2'	1:3A:64:A:H8	1.76	0.49
2:3B:124:SER:HA	2:3B:139:VAL:O	2.11	0.49
2:3B:299:LYS:O	2:3B:318:GLY:HA2	2.12	0.49
3:3D:21:LYS:NZ	3:3D:138:LEU:O	2.45	0.49
8:AA:37:UNK:HA	8:AA:43:UNK:HA	1.95	0.49
15:B1:634:ARG:NH1	31:R1:186:PRO:O	2.46	0.49
20:BE:35:ASN:ND2	20:BE:53:CYS:SG	2.80	0.49
22:CB:334:PHE:O	22:CB:338:SER:OG	2.26	0.49
34:SA:190:C:N4	34:SA:196:G:O6	2.45	0.49
34:SA:886:U:H2'	34:SA:887:A:H8	1.76	0.49
47:SX:15:ASN:HD21	47:SX:72:CYS:H	1.60	0.49
12:AE:8:LEU:O	12:AE:12:ALA:HB3	2.12	0.49
19:BD:411:TYR:CZ	19:BD:423:LEU:O	2.66	0.49
22:CB:841:ASN:HA	22:CB:850:PHE:O	2.13	0.49
34:SA:283:U:C2	38:SH:188:ARG:HB2	2.47	0.49
37:SG:72:HIS:ND1	46:SR:79:TYR:OH	2.43	0.49
2:3C:204:GLY:HA2	2:3C:207:LEU:HD12	1.94	0.49
7:5A:447:G:H2'	7:5A:448:G:C8	2.47	0.49
12:AE:1689:UNK:O	12:AE:1693:UNK:CB	2.60	0.49
16:BA:603:LEU:HB2	16:BA:612:LEU:H	1.76	0.49
16:BA:817:PHE:O	16:BA:821:MET:CB	2.59	0.49
23:E1:178:VAL:HG12	23:E1:223:GLU:HB3	1.93	0.49
28:MB:187:PRO:HB3	28:MB:220:ARG:HG3	1.95	0.49
34:SA:445:A:H61	34:SA:462:G:HI'	1.77	0.49
2:3B:88:ILE:HG12	2:3B:99:ALA:HA	1.93	0.49
2:3B:205:ARG:NH2	3:3D:163:VAL:O	2.45	0.49
5:3F:260:LEU:HD21	5:3F:283:VAL:HG11	1.94	0.49
5:3F:342:ARG:HH22	6:3G:90:ALA:HA	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3F:348:LEU:O	5:3F:356:ARG:HA	2.12	0.49
12:AE:980:UNK:O	12:AE:984:UNK:CB	2.61	0.49
31:R1:119:LYS:HG2	31:R1:165:GLU:HG2	1.94	0.49
33:S1:371:UNK:HA	33:S1:385:UNK:HA	1.93	0.49
36:SF:182:TYR:HB2	36:SF:228:ILE:HD11	1.95	0.49
38:SH:12:SER:OG	38:SH:127:THR:O	2.31	0.49
3:3D:146:ASP:HB2	4:3E:241:VAL:HG11	1.93	0.49
7:5A:62:C:H2'	7:5A:63:G:H8	1.77	0.49
9:AB:80:UNK:N	9:AB:84:UNK:O	2.45	0.49
10:AC:599:UNK:O	10:AC:603:UNK:CB	2.61	0.49
17:BB:574:LEU:HD23	17:BB:594:ASP:HB3	1.95	0.49
22:CB:577:ARG:NH1	22:CB:624:CYS:O	2.45	0.49
22:CB:1189:LEU:HD13	32:R2:1472:PRO:HD2	1.93	0.49
28:MB:267:GLU:HG2	61:UC:9:UNK:HA	1.95	0.49
30:P1:105:ARG:HH21	30:P1:163:THR:HA	1.77	0.49
31:R1:150:ALA:HB3	31:R1:169:VAL:HB	1.95	0.49
33:S1:301:UNK:N	33:S1:310:UNK:O	2.45	0.49
35:SC:129:THR:HA	35:SC:177:GLN:HA	1.94	0.49
42:SM:108:PRO:HB2	42:SM:135:VAL:HG22	1.93	0.49
54:U1:203:UNK:N	54:U1:207:UNK:O	2.46	0.49
3:3D:198:TRP:NE1	3:3D:268:MET:SD	2.78	0.49
3:3D:231:ASP:HA	3:3D:237:LEU:HB2	1.95	0.49
4:3E:76:LEU:HD11	4:3E:98:ILE:HG12	1.94	0.49
5:3F:200:ASP:HB2	5:3F:211:LEU:HD11	1.94	0.49
5:3F:303:LYS:HG3	5:3F:319:TYR:HE1	1.78	0.49
7:5A:184:U:H2'	7:5A:185:A:H8	1.76	0.49
10:AC:96:UNK:HA	10:AC:112:UNK:HA	1.95	0.49
12:AE:917:UNK:O	12:AE:921:UNK:CB	2.61	0.49
12:AE:1490:UNK:O	12:AE:1494:UNK:CB	2.61	0.49
16:BA:825:GLN:HE21	20:BE:933:ALA:HB1	1.77	0.49
18:BC:740:MET:HE1	18:BC:782:VAL:HG12	1.95	0.49
22:CB:628:VAL:HA	22:CB:667:CYS:O	2.12	0.49
22:CB:814:LEU:HD12	22:CB:818:SER:HB2	1.94	0.49
23:E2:48:ALA:O	23:E2:117:SER:N	2.45	0.49
24:E3:258:VAL:O	24:E3:262:ALA:CB	2.60	0.49
33:S1:208:UNK:O	33:S1:220:UNK:N	2.45	0.49
37:SG:149:VAL:HG13	37:SG:156:ARG:HG3	1.95	0.49
5:3F:526:VAL:HG22	5:3F:539:ILE:HG12	1.94	0.49
12:AE:102:LEU:O	12:AE:106:SER:OG	2.25	0.49
12:AE:750:ASN:O	12:AE:754:GLU:HB2	2.12	0.49
14:AG:204:UNK:N	14:AG:208:UNK:O	2.45	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:B1:831:ARG:HE	15:B1:835:HIS:HB3	1.77	0.49
16:BA:8:SER:HB2	16:BA:703:ILE:HD11	1.94	0.49
22:CB:100:SER:O	22:CB:104:LYS:CB	2.61	0.49
23:E1:91:ILE:HG12	23:E2:132:ARG:NH1	2.28	0.49
26:K1:125:VAL:O	45:SP:92:LYS:NZ	2.44	0.49
34:SA:1213:G:O6	34:SA:1450:U:O4	2.30	0.49
35:SC:89:ASP:OD2	35:SC:99:ASN:HB2	2.13	0.49
35:SC:109:LYS:NZ	35:SC:113:MET:HE3	2.28	0.49
4:3E:280:MET:HG2	4:3E:293:GLU:HA	1.94	0.49
15:B1:143:MET:O	48:SY:144:ARG:NH1	2.46	0.49
17:BB:49:VAL:HB	17:BB:63:LEU:HB2	1.94	0.49
18:BC:331:SER:HB2	18:BC:381:VAL:HG23	1.95	0.49
20:BE:613:ASP:HB2	20:BE:620:ILE:HD13	1.95	0.49
21:CA:91:ASP:OD1	21:CA:95:LEU:N	2.45	0.49
33:S1:372:UNK:N	33:S1:384:UNK:O	2.45	0.49
36:SF:100:ARG:NH2	36:SF:121:TYR:O	2.45	0.49
37:SG:54:LYS:HZ2	37:SG:131:GLN:HE22	1.61	0.49
40:SJ:36:THR:HG23	40:SJ:96:LEU:HB2	1.95	0.49
6:3G:33:LEU:HD11	6:3G:100:ALA:HB1	1.94	0.48
12:AE:487:THR:HG21	12:AE:490:ARG:HE	1.78	0.48
19:BD:486:SER:OG	19:BD:487:GLU:N	2.45	0.48
23:E2:144:LEU:HD22	23:E2:160:LEU:HD13	1.94	0.48
24:E3:229:LEU:HD21	24:E3:258:VAL:HG22	1.94	0.48
34:SA:340:U:H2'	34:SA:341:A:C8	2.48	0.48
35:SC:109:LYS:HZ3	35:SC:113:MET:HE3	1.78	0.48
53:Sg:140:TYR:OH	53:Sg:145:HIS:O	2.30	0.48
9:AB:429:UNK:O	9:AB:433:UNK:CB	2.61	0.48
12:AE:1511:UNK:O	12:AE:1515:UNK:CB	2.61	0.48
15:B1:236:LEU:O	15:B1:239:THR:OG1	2.32	0.48
15:B1:252:GLY:O	15:B1:788:TYR:HA	2.13	0.48
20:BE:116:ALA:HB1	20:BE:133:ASP:OD1	2.13	0.48
23:E2:178:VAL:HG23	23:E2:204:VAL:HG23	1.95	0.48
34:SA:126:A:H62	34:SA:291:G:H21	0.74	0.48
47:SX:23:ARG:NH1	47:SX:66:ASN:HA	2.17	0.48
2:3C:107:VAL:HG12	2:3C:143:VAL:HA	1.94	0.48
2:3C:238:ASP:OD1	2:3C:262:LYS:NZ	2.40	0.48
4:3E:76:LEU:HD13	4:3E:101:LEU:HD22	1.95	0.48
6:3H:56:ALA:N	6:3H:81:VAL:O	2.39	0.48
15:B1:266:ARG:HB3	15:B1:815:LEU:HD12	1.95	0.48
16:BA:548:LYS:HB2	46:SR:110:THR:HG21	1.93	0.48
16:BA:584:HIS:CG	16:BA:685:GLN:HA	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:BC:231:CYS:SG	18:BC:232:LYS:N	2.87	0.48
18:BC:559:ILE:HG22	18:BC:568:MET:HB3	1.95	0.48
20:BE:588:ILE:HG12	20:BE:604:SER:HB2	1.95	0.48
20:BE:632:VAL:HG12	20:BE:643:THR:HG22	1.95	0.48
37:SG:97:LEU:O	37:SG:180:ARG:NH2	2.47	0.48
42:SM:123:VAL:HG23	42:SM:142:VAL:HA	1.95	0.48
47:SX:11:LEU:HD23	47:SX:14:ILE:HD12	1.95	0.48
58:U5:73:LEU:HD13	58:U5:101:ILE:HD12	1.95	0.48
2:3C:220:ILE:HG21	2:3C:233:LEU:HD13	1.94	0.48
4:3E:212:MET:HE2	4:3E:222:ASP:HB2	1.94	0.48
7:5A:12:G:N2	7:5A:70:A:OP2	2.42	0.48
12:AE:37:SER:O	12:AE:41:ALA:CB	2.61	0.48
12:AE:748:LEU:O	12:AE:752:ALA:HB2	2.13	0.48
12:AE:1688:UNK:O	12:AE:1692:UNK:CB	2.61	0.48
16:BA:751:ILE:O	16:BA:755:TYR:CB	2.61	0.48
17:BB:851:PRO:O	17:BB:855:LYS:CB	2.61	0.48
18:BC:298:SER:OG	18:BC:299:ASN:N	2.45	0.48
21:CA:181:LYS:HZ3	22:CB:808:LEU:HB3	1.78	0.48
31:R1:107:ALA:HB1	31:R1:170:VAL:HG11	1.94	0.48
34:SA:883:C:H2'	34:SA:884:A:C8	2.49	0.48
49:SZ:10:ARG:O	49:SZ:24:VAL:N	2.44	0.48
54:U1:110:UNK:N	54:U1:118:UNK:O	2.46	0.48
3:3D:92:LYS:HA	3:3D:115:TYR:HB3	1.95	0.48
15:B1:66:ARG:HA	15:B1:69:VAL:HG22	1.96	0.48
15:B1:948:ILE:HG21	15:B1:951:MET:HB2	1.95	0.48
16:BA:538:GLN:HE21	16:BA:551:GLY:HA3	1.78	0.48
17:BB:218:ILE:HG22	17:BB:228:ILE:HG22	1.94	0.48
18:BC:127:ILE:HG23	18:BC:140:PHE:HB2	1.94	0.48
19:BD:310:GLN:HA	19:BD:326:LEU:HB2	1.95	0.48
20:BE:585:SER:OG	20:BE:606:ASP:OD2	2.29	0.48
34:SA:283:U:OP2	38:SH:188:ARG:NH1	2.42	0.48
34:SA:956:C:OP1	34:SA:1072:C:O2'	2.31	0.48
35:SC:214:LYS:NZ	35:SC:216:LYS:HB3	2.29	0.48
37:SG:54:LYS:NZ	37:SG:131:GLN:HE22	2.12	0.48
40:SJ:26:LYS:NZ	40:SJ:29:LEU:HD13	2.28	0.48
41:SK:78:ARG:HH12	41:SK:91:LYS:HD3	1.78	0.48
43:SN:29:LYS:HE2	43:SN:100:TRP:HE1	1.78	0.48
56:U3:649:UNK:HA	56:U3:666:UNK:HA	1.96	0.48
5:3F:366:GLN:O	5:3F:369:LEU:HB2	2.13	0.48
7:5A:334:G:O6	7:5A:390:C:N4	2.43	0.48
8:AA:239:UNK:CB	8:AA:252:UNK:O	2.61	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:B1:610:LYS:O	31:R1:321:ARG:NH2	2.40	0.48
16:BA:499:ILE:HG22	16:BA:510:GLU:HA	1.95	0.48
22:CB:855:LEU:HD22	22:CB:889:TYR:HB3	1.95	0.48
22:CB:1099:VAL:HB	22:CB:1235:GLU:HB2	1.96	0.48
32:R2:1475:SER:N	32:R2:1512:GLU:OE2	2.45	0.48
34:SA:1512:G:H2'	34:SA:1513:G:C8	2.49	0.48
4:3E:76:LEU:HA	4:3E:84:LYS:NZ	2.29	0.48
16:BA:784:ASP:OD1	16:BA:826:ARG:NH2	2.46	0.48
22:CB:807:LEU:HD23	22:CB:810:ILE:HD12	1.95	0.48
26:K1:140:LYS:O	26:K1:144:ARG:CB	2.61	0.48
27:MA:47:TYR:HD1	27:MA:50:ILE:HD12	1.79	0.48
31:R1:23:LEU:HB3	31:R1:332:ILE:HG13	1.95	0.48
36:SF:122:LYS:HG2	36:SF:164:LEU:HD21	1.96	0.48
57:U4:117:LEU:HG	57:U4:121:ARG:HE	1.79	0.48
61:UC:923:UNK:O	61:UC:927:UNK:N	2.46	0.48
1:3A:1:G:N1	34:SA:1124:A:C2	2.82	0.48
8:AA:385:UNK:HA	8:AA:392:UNK:HA	1.96	0.48
8:AA:466:UNK:O	8:AA:475:UNK:N	2.47	0.48
12:AE:81:LEU:HD11	12:AE:85:VAL:HG22	1.95	0.48
12:AE:1065:UNK:O	12:AE:1069:UNK:CB	2.62	0.48
14:AG:447:UNK:HA	14:AG:453:UNK:HA	1.95	0.48
18:BC:680:ASN:O	18:BC:684:LEU:CB	2.61	0.48
19:BD:539:ASP:HA	19:BD:562:LEU:HB2	1.95	0.48
20:BE:349:HIS:HD1	20:BE:374:SER:HG	1.44	0.48
34:SA:359:A:OP2	34:SA:360:A:N6	2.47	0.48
38:SH:77:LEU:HD13	38:SH:84:TYR:HB2	1.95	0.48
46:SR:5:PRO:HG2	46:SR:24:ALA:HB2	1.96	0.48
2:3C:208:ILE:HD12	4:3E:156:ALA:HA	1.95	0.48
4:3E:397:ARG:HE	4:3E:401:LEU:HG	1.79	0.48
5:3F:402:ILE:HA	5:3F:417:SER:HA	1.96	0.48
16:BA:81:LEU:HB2	16:BA:90:LEU:HB2	1.96	0.48
16:BA:825:GLN:NE2	20:BE:937:THR:OG1	2.37	0.48
20:BE:97:LYS:HD3	20:BE:109:LEU:HD21	1.96	0.48
20:BE:132:THR:OG1	20:BE:136:SER:O	2.32	0.48
20:BE:567:ILE:HB	20:BE:581:LEU:HB2	1.95	0.48
22:CB:551:GLU:O	22:CB:555:PHE:HB2	2.13	0.48
4:3E:363:LEU:O	4:3E:367:ALA:HB2	2.13	0.48
12:AE:817:UNK:O	12:AE:821:UNK:CB	2.62	0.48
15:B1:145:ARG:NE	15:B1:210:LYS:O	2.39	0.48
16:BA:446:CYS:HA	16:BA:456:HIS:O	2.14	0.48
17:BB:603:ASP:HA	31:R1:200:VAL:HG12	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:BC:38:ASP:OD2	18:BC:309:GLN:NE2	2.47	0.48
21:CA:183:ASP:O	21:CA:187:HIS:CB	2.62	0.48
22:CB:656:ARG:HH11	22:CB:658:PHE:HD1	1.62	0.48
22:CB:761:ARG:HB3	22:CB:896:THR:HG23	1.95	0.48
22:CB:1100:VAL:O	22:CB:1181:VAL:HA	2.13	0.48
46:SR:110:THR:HA	46:SR:113:ASP:HB2	1.95	0.48
49:SZ:83:LYS:HD2	49:SZ:84:LYS:HZ2	1.79	0.48
5:3F:134:ARG:HB2	5:3F:484:SER:HA	1.94	0.47
5:3F:152:VAL:HG22	5:3F:562:GLY:HA2	1.96	0.47
5:3F:541:ALA:O	5:3F:563:ILE:HA	2.14	0.47
6:3H:106:ASP:O	6:3H:111:LYS:NZ	2.33	0.47
7:5A:98:G:O6	7:5A:146:G:O6	2.31	0.47
12:AE:608:ASN:HD21	12:AE:662:PRO:HG3	1.79	0.47
15:B1:548:ASN:HD22	15:B1:551:LYS:HE3	1.78	0.47
16:BA:355:PRO:O	16:BA:822:ARG:NH1	2.47	0.47
19:BD:296:GLN:HG3	19:BD:353:ARG:HH12	1.78	0.47
21:CA:94:GLY:HA3	21:CA:121:ARG:HH12	1.79	0.47
34:SA:539:G:OP2	34:SA:539:G:H8	1.97	0.47
35:SC:139:ALA:HA	35:SC:212:VAL:HA	1.97	0.47
1:3A:260:U:O4	3:3D:377:ARG:NH2	2.46	0.47
7:5A:184:U:H2'	7:5A:185:A:C8	2.49	0.47
12:AE:347:PHE:O	12:AE:351:TYR:CB	2.62	0.47
12:AE:600:LEU:HD22	12:AE:611:ILE:HG22	1.96	0.47
14:AG:244:UNK:HA	14:AG:250:UNK:HA	1.96	0.47
15:B1:977:LYS:H	15:B1:989:ALA:HA	1.80	0.47
16:BA:57:ASN:OD1	16:BA:619:ARG:NH2	2.47	0.47
22:CB:545:ALA:HB2	22:CB:565:LYS:HE2	1.96	0.47
22:CB:589:LYS:O	22:CB:609:ASN:ND2	2.47	0.47
23:E2:115:GLN:HE21	23:E2:119:GLY:HA2	1.79	0.47
33:S1:167:UNK:N	33:S1:179:UNK:O	2.47	0.47
34:SA:283:U:C6	34:SA:283:U:O4'	2.67	0.47
34:SA:871:G:H2'	34:SA:872:G:C8	2.49	0.47
34:SA:1217:A:H2	34:SA:1448:G:N2	2.10	0.47
34:SA:1474:G:H2'	34:SA:1475:A:H8	1.78	0.47
35:SC:146:GLN:HB2	35:SC:149:GLN:HE21	1.78	0.47
37:SG:76:ARG:O	37:SG:83:ARG:NE	2.40	0.47
39:SI:14:THR:OG1	39:SI:15:GLU:N	2.46	0.47
44:SO:67:THR:HG23	44:SO:69:ASN:H	1.79	0.47
1:3A:80:U:OP2	6:3H:95:ARG:HD2	2.14	0.47
2:3B:233:LEU:O	3:3D:151:GLN:NE2	2.47	0.47
12:AE:261:LEU:O	12:AE:265:ALA:CB	2.62	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AE:288:ALA:HB1	12:AE:292:LYS:HG2	1.96	0.47
12:AE:728:GLU:HG3	12:AE:730:GLN:H	1.79	0.47
13:AF:39:UNK:N	13:AF:43:UNK:O	2.47	0.47
17:BB:20:ASN:HD21	17:BB:23:CYS:H	1.61	0.47
18:BC:487:ARG:HH11	18:BC:523:GLY:HA2	1.79	0.47
23:E2:174:LYS:NZ	23:E2:197:ASP:OD2	2.40	0.47
24:E3:411:ARG:O	24:E3:447:ARG:NH2	2.48	0.47
32:R2:1547:TYR:HH	32:R2:1583:SER:HG	1.62	0.47
36:SF:19:LEU:HD21	36:SF:108:ARG:HH21	1.79	0.47
38:SH:63:MET:SD	38:SH:98:ARG:NH2	2.87	0.47
40:SJ:64:ASN:HA	40:SJ:75:LYS:HA	1.96	0.47
5:3F:189:THR:HG21	5:3F:563:ILE:HD11	1.97	0.47
6:3G:77:PRO:HG2	6:3G:118:LYS:HE3	1.96	0.47
12:AE:134:MET:HA	12:AE:137:LEU:HD12	1.97	0.47
12:AE:196:LEU:HD11	12:AE:213:THR:HG21	1.95	0.47
17:BB:261:PHE:O	17:BB:272:PHE:HA	2.15	0.47
20:BE:865:ILE:HA	20:BE:868:LEU:HD12	1.95	0.47
22:CB:173:ASN:ND2	34:SA:1686:C:OP1	2.46	0.47
22:CB:508:SER:HA	22:CB:512:LEU:HB2	1.96	0.47
24:E3:301:TYR:O	24:E3:304:TYR:HB3	2.13	0.47
32:R2:1629:PHE:HB2	32:R2:1661:GLN:HE21	1.79	0.47
34:SA:549:G:H2'	34:SA:550:A:H8	1.78	0.47
34:SA:629:U:H2'	34:SA:630:A:H8	1.80	0.47
34:SA:899:G:H2'	34:SA:900:A:H8	1.79	0.47
40:SJ:44:HIS:O	40:SJ:56:ARG:N	2.47	0.47
41:SK:17:ARG:O	41:SK:23:ARG:NH2	2.47	0.47
48:SY:127:VAL:HG13	48:SY:132:LEU:HD21	1.96	0.47
58:U5:87:LEU:HA	58:U5:88:THR:HA	1.66	0.47
1:3A:246:A:OP2	5:3F:207:ARG:NH2	2.48	0.47
3:3D:176:GLN:O	3:3D:180:LEU:CB	2.62	0.47
3:3D:221:LEU:HD13	3:3D:275:ALA:HB3	1.95	0.47
8:AA:152:UNK:CB	8:AA:156:UNK:O	2.62	0.47
8:AA:273:UNK:CB	8:AA:281:UNK:O	2.62	0.47
8:AA:302:UNK:O	8:AA:311:UNK:N	2.47	0.47
8:AA:384:UNK:O	8:AA:393:UNK:N	2.47	0.47
12:AE:261:LEU:O	12:AE:265:ALA:HB2	2.14	0.47
12:AE:1148:UNK:O	12:AE:1152:UNK:CB	2.62	0.47
17:BB:592:SER:HB3	17:BB:598:LYS:HZ1	1.80	0.47
18:BC:304:LEU:HD22	18:BC:311:LEU:HD11	1.97	0.47
18:BC:465:LYS:HE3	18:BC:520:LEU:HD11	1.95	0.47
22:CB:235:LEU:O	22:CB:239:LEU:HB3	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CB:1159:ASN:HD22	22:CB:1201:ASP:HB3	1.79	0.47
25:E4:141:UNK:O	25:E4:150:UNK:N	2.46	0.47
34:SA:418:G:O2'	38:SH:72:ARG:NH1	2.48	0.47
41:SK:57:ARG:NH1	57:U4:88:ASP:O	2.47	0.47
2:3C:240:VAL:HG23	2:3C:261:LEU:HD13	1.95	0.47
5:3F:553:ILE:HD13	5:3F:556:VAL:HG12	1.95	0.47
7:5A:145:A:H2'	7:5A:146:G:C8	2.50	0.47
14:AG:823:UNK:O	14:AG:827:UNK:CB	2.63	0.47
18:BC:15:ILE:N	18:BC:641:PHE:O	2.47	0.47
18:BC:585:ASN:O	18:BC:587:GLN:NE2	2.47	0.47
23:E1:48:ALA:HB3	23:E1:116:THR:HA	1.97	0.47
24:E3:268:SER:HB2	34:SA:1233:G:H5'	1.97	0.47
30:P1:158:PHE:HE1	30:P1:174:LEU:HB2	1.80	0.47
37:SG:113:ILE:HG23	37:SG:191:ALA:HB2	1.97	0.47
42:SM:33:ARG:NH1	42:SM:61:THR:HG21	2.29	0.47
46:SR:21:HIS:CE1	46:SR:68:ARG:HH12	2.32	0.47
1:3A:1:G:C6	34:SA:1124:A:C2	3.02	0.47
1:3A:47:G:H2'	1:3A:48:A:H8	1.79	0.47
5:3F:316:GLU:OE2	5:3F:351:ILE:HG23	2.15	0.47
6:3G:56:ALA:HB3	6:3G:82:PRO:HA	1.96	0.47
8:AA:507:UNK:O	8:AA:516:UNK:CB	2.62	0.47
9:AB:59:UNK:O	9:AB:68:UNK:N	2.48	0.47
11:AD:461:UNK:O	11:AD:465:UNK:CB	2.62	0.47
12:AE:506:TYR:O	12:AE:510:SER:HB2	2.14	0.47
18:BC:362:LEU:HB2	18:BC:384:TYR:HB2	1.97	0.47
18:BC:673:MET:HE3	18:BC:677:ASP:H	1.80	0.47
19:BD:454:GLY:N	19:BD:487:GLU:OE1	2.40	0.47
21:CA:13:PHE:HA	21:CA:39:ALA:O	2.15	0.47
22:CB:207:LEU:HD11	22:CB:294:LEU:HD22	1.97	0.47
22:CB:826:SER:O	22:CB:838:VAL:HA	2.14	0.47
22:CB:924:LEU:HD21	22:CB:1181:VAL:HG13	1.95	0.47
25:E4:157:UNK:HA	25:E4:171:UNK:O	2.14	0.47
32:R2:1502:LEU:HA	32:R2:1513:LYS:HE3	1.96	0.47
32:R2:1505:ILE:HB	32:R2:1513:LYS:HD3	1.96	0.47
34:SA:179:A:H4'	34:SA:180:A:C4	2.49	0.47
34:SA:417:A:OP1	38:SH:59:GLN:NE2	2.48	0.47
34:SA:1226:A:H3'	43:SN:116:VAL:HG11	1.96	0.47
34:SA:1584:G:N2	34:SA:1585:U:O4	2.37	0.47
34:SA:1718:G:H5'	34:SA:1719:A:OP2	2.15	0.47
36:SF:139:VAL:HG13	36:SF:150:PRO:HG3	1.97	0.47
39:SI:137:GLY:HA3	39:SI:153:LEU:HD12	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:SI:139:ARG:HB3	47:SX:51:GLU:OE2	2.14	0.47
41:SK:171:ARG:HH21	41:SK:175:ARG:HH22	1.63	0.47
46:SR:52:LEU:C	46:SR:59:LYS:HZ1	2.20	0.47
49:SZ:83:LYS:HD2	49:SZ:84:LYS:NZ	2.29	0.47
2:3C:96:VAL:HG11	2:3C:155:ILE:HG21	1.97	0.47
2:3C:231:ARG:NH1	4:3E:7:GLU:O	2.41	0.47
3:3D:199:TYR:HE2	3:3D:206:LEU:HB3	1.80	0.47
4:3E:191:HIS:O	4:3E:215:ARG:NH2	2.48	0.47
5:3F:195:GLN:HE21	5:3F:213:TYR:HB2	1.79	0.47
8:AA:319:UNK:CB	8:AA:332:UNK:O	2.63	0.47
16:BA:155:SER:HB2	16:BA:160:PHE:HB3	1.97	0.47
18:BC:345:TYR:HD2	18:BC:350:LEU:HD12	1.80	0.47
20:BE:275:PHE:HE2	20:BE:287:LEU:HG	1.80	0.47
20:BE:551:TYR:OH	20:BE:556:ASP:OD1	2.30	0.47
22:CB:207:LEU:HB2	22:CB:295:LEU:O	2.14	0.47
34:SA:870:C:H2'	34:SA:871:G:H8	1.79	0.47
1:3A:329:C:H2'	1:3A:330:A:C8	2.50	0.47
2:3B:169:LYS:O	2:3B:238:ASP:N	2.47	0.47
7:5A:226:U:O2'	7:5A:228:A:N7	2.48	0.47
12:AE:8:LEU:O	12:AE:12:ALA:CB	2.63	0.47
16:BA:50:PHE:H	16:BA:86:ALA:HB2	1.80	0.47
16:BA:605:ASP:HB3	16:BA:611:LEU:HD21	1.96	0.47
17:BB:621:VAL:HA	17:BB:631:PHE:O	2.14	0.47
17:BB:824:MET:O	51:Sd:29:ARG:NH2	2.48	0.47
33:S1:118:UNK:N	33:S1:127:UNK:O	2.48	0.47
61:UC:702:UNK:O	61:UC:706:UNK:N	2.48	0.47
12:AE:1439:UNK:O	12:AE:1443:UNK:CB	2.63	0.47
17:BB:125:THR:H	17:BB:140:SER:HA	1.80	0.47
17:BB:545:TYR:HA	17:BB:559:PHE:HA	1.97	0.47
18:BC:455:LEU:HD13	18:BC:465:LYS:HD3	1.96	0.47
20:BE:511:ASP:OD2	20:BE:515:ARG:HB2	2.15	0.47
21:CA:169:VAL:HB	22:CB:1140:SER:HB2	1.95	0.47
24:E3:332:VAL:H	34:SA:1435:G:H5'	1.80	0.47
34:SA:1463:C:H2'	34:SA:1464:G:C8	2.50	0.47
37:SG:103:ASN:HA	37:SG:106:LYS:HD2	1.97	0.47
38:SH:188:ARG:HD3	38:SH:188:ARG:HA	1.40	0.47
41:SK:53:ARG:HH12	57:U4:92:ALA:HB2	1.80	0.47
47:SX:72:CYS:HB3	47:SX:129:VAL:HG23	1.96	0.47
54:U1:272:UNK:N	54:U1:284:UNK:O	2.48	0.47
2:3B:110:ASN:HB3	2:3B:140:GLU:HB2	1.98	0.46
6:3H:111:LYS:HA	6:3H:114:ILE:HD12	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:5A:340:U:H2'	7:5A:341:G:H8	1.81	0.46
7:5A:578:G:H2'	7:5A:579:G:H8	1.80	0.46
8:AA:405:UNK:N	8:AA:409:UNK:O	2.47	0.46
12:AE:109:TRP:HH2	12:AE:118:THR:HG21	1.80	0.46
12:AE:738:LEU:HD22	12:AE:774:ASN:HB3	1.96	0.46
12:AE:1742:UNK:O	12:AE:1746:UNK:CB	2.63	0.46
16:BA:193:TYR:HB3	16:BA:211:LYS:HD3	1.97	0.46
20:BE:53:CYS:HB2	20:BE:83:LEU:HD11	1.96	0.46
20:BE:633:LYS:HB2	20:BE:642:ALA:HB3	1.95	0.46
24:E3:335:ALA:O	24:E3:339:GLY:HA3	2.15	0.46
34:SA:884:A:H2'	34:SA:885:G:C8	2.50	0.46
34:SA:1588:G:N2	34:SA:1608:U:O2	2.31	0.46
35:SC:34:ALA:HB3	35:SC:41:ARG:HA	1.96	0.46
39:SI:76:LYS:HA	39:SI:79:ARG:NH1	2.30	0.46
43:SN:131:ASP:HA	43:SN:134:SER:HB2	1.98	0.46
48:SY:75:GLN:HA	48:SY:82:LYS:HA	1.97	0.46
10:AC:411:UNK:O	10:AC:415:UNK:CB	2.63	0.46
10:AC:613:UNK:O	10:AC:617:UNK:CB	2.63	0.46
12:AE:120:TRP:O	12:AE:124:ARG:CB	2.63	0.46
20:BE:76:THR:OG1	20:BE:78:SER:O	2.30	0.46
20:BE:257:ARG:HD3	20:BE:263:HIS:HD2	1.79	0.46
22:CB:536:TYR:HH	22:CB:552:ARG:NH1	2.12	0.46
23:E2:164:LYS:NZ	34:SA:1575:G:OP1	2.48	0.46
34:SA:356:G:H2'	34:SA:357:G:H8	1.80	0.46
35:SC:70:LEU:HA	35:SC:73:LEU:HB2	1.96	0.46
36:SF:79:ASP:HB3	36:SF:82:TYR:HB2	1.97	0.46
58:U5:242:ILE:HB	58:U5:254:ILE:HB	1.97	0.46
3:3D:373:GLY:O	3:3D:377:ARG:HB2	2.15	0.46
12:AE:1382:UNK:O	12:AE:1386:UNK:CB	2.64	0.46
17:BB:149:ASP:HB3	17:BB:153:GLU:H	1.80	0.46
17:BB:437:LYS:HG2	17:BB:481:LEU:HD13	1.97	0.46
19:BD:275:TYR:HE2	19:BD:282:ASN:HD22	1.62	0.46
22:CB:419:TYR:O	22:CB:423:LYS:HB2	2.14	0.46
24:E3:206:LEU:N	24:E3:207:PRO:HD2	2.17	0.46
29:MC:54:UNK:O	29:MC:58:UNK:N	2.49	0.46
30:P1:103:PRO:HB3	30:P1:135:LYS:HE2	1.96	0.46
33:S1:210:UNK:N	33:S1:218:UNK:O	2.48	0.46
39:SI:48:GLU:OE2	39:SI:88:ARG:NE	2.48	0.46
45:SP:29:HIS:HB3	45:SP:41:ARG:HG3	1.96	0.46
54:U1:158:UNK:N	54:U1:171:UNK:O	2.49	0.46
3:3D:291:TYR:OH	4:3E:251:ASP:OD1	2.12	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:5A:349:G:OP2	7:5A:349:G:H8	1.98	0.46
8:AA:219:UNK:N	8:AA:233:UNK:O	2.48	0.46
12:AE:227:ASN:HD22	12:AE:230:LYS:HD2	1.81	0.46
16:BA:307:THR:O	16:BA:320:GLY:N	2.47	0.46
17:BB:351:LEU:HA	17:BB:372:ARG:HG2	1.97	0.46
23:E1:91:ILE:HG12	23:E2:132:ARG:HH12	1.81	0.46
23:E1:103:PRO:O	23:E1:107:ALA:N	2.44	0.46
12:AE:736:PHE:O	12:AE:740:ALA:HB2	2.16	0.46
12:AE:1743:UNK:O	12:AE:1747:UNK:CB	2.63	0.46
15:B1:895:PRO:HA	15:B1:918:ILE:HG13	1.98	0.46
17:BB:88:HIS:CD2	17:BB:90:ASP:H	2.33	0.46
23:E1:149:SER:HB2	23:E1:158:LYS:HG2	1.98	0.46
26:K1:100:LEU:O	26:K1:103:LEU:HB2	2.16	0.46
34:SA:384:G:H5'	40:SJ:22:ARG:HB3	1.97	0.46
35:SC:39:GLU:N	35:SC:74:GLN:OE1	2.48	0.46
37:SG:200:ASN:HB2	37:SG:208:SER:HB3	1.97	0.46
43:SN:40:GLY:O	43:SN:124:LYS:N	2.40	0.46
1:3A:254:A:H5'	1:3A:255:U:H3'	1.97	0.46
2:3B:291:GLN:OE1	2:3B:294:ARG:NH2	2.45	0.46
7:5A:447:G:H2'	7:5A:448:G:H8	1.79	0.46
12:AE:502:ILE:HA	12:AE:508:ALA:HB2	1.96	0.46
15:B1:824:ILE:HA	15:B1:886:TYR:HA	1.96	0.46
17:BB:20:ASN:ND2	17:BB:23:CYS:H	2.14	0.46
17:BB:368:PRO:HA	17:BB:374:PRO:HA	1.97	0.46
19:BD:305:SER:OG	19:BD:306:ASN:N	2.49	0.46
22:CB:1059:PRO:O	22:CB:1063:ARG:CB	2.63	0.46
23:E2:31:LEU:HB3	23:E2:111:GLN:HE21	1.79	0.46
24:E3:269:ASN:ND2	34:SA:1233:G:O2'	2.33	0.46
34:SA:294:C:H2'	34:SA:295:A:C8	2.50	0.46
34:SA:1483:A:H2'	34:SA:1484:G:C8	2.50	0.46
38:SH:88:ARG:HB3	38:SH:91:GLU:HB2	1.98	0.46
41:SK:70:LEU:O	41:SK:74:ASN:ND2	2.49	0.46
48:SY:103:LEU:N	48:SY:126:LYS:O	2.47	0.46
58:U5:75:ILE:HG12	58:U5:101:ILE:HB	1.97	0.46
3:3D:19:LYS:HE3	3:3D:142:LEU:HD13	1.97	0.46
5:3F:405:VAL:HG23	5:3F:415:THR:HG22	1.98	0.46
9:AB:442:UNK:O	9:AB:446:UNK:CB	2.64	0.46
12:AE:10:GLN:O	12:AE:13:SER:OG	2.30	0.46
16:BA:8:SER:H	16:BA:703:ILE:HD11	1.79	0.46
16:BA:597:ASN:ND2	16:BA:681:VAL:O	2.48	0.46
17:BB:103:ILE:HB	17:BB:117:PHE:HB2	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BE:82:ALA:H	20:BE:93:ALA:HB3	1.81	0.46
20:BE:578:VAL:HB	20:BE:579:ARG:HH11	1.81	0.46
22:CB:805:ALA:HA	22:CB:808:LEU:HD12	1.97	0.46
34:SA:153:G:H1	34:SA:161:U:H3	1.63	0.46
35:SC:129:THR:OG1	35:SC:131:ASP:O	2.29	0.46
40:SJ:11:ARG:NH1	40:SJ:17:LYS:HB2	2.31	0.46
40:SJ:105:ASP:OD2	40:SJ:108:PRO:HD3	2.15	0.46
46:SR:29:ILE:HA	46:SR:65:ILE:HB	1.98	0.46
49:SZ:8:ARG:HB2	49:SZ:26:ASP:HB3	1.96	0.46
2:3B:268:VAL:HG22	2:3B:317:VAL:HG22	1.98	0.46
5:3F:192:LYS:NZ	5:3F:550:GLY:HA2	2.31	0.46
9:AB:276:UNK:CB	9:AB:280:UNK:O	2.64	0.46
12:AE:1069:UNK:O	12:AE:1073:UNK:CB	2.64	0.46
16:BA:495:LYS:N	16:BA:517:ASP:OD1	2.48	0.46
19:BD:436:ASP:HB2	19:BD:444:ILE:HD11	1.98	0.46
19:BD:521:LEU:HA	19:BD:531:CYS:O	2.15	0.46
20:BE:97:LYS:NZ	20:BE:111:GLU:HB2	2.30	0.46
33:S1:241:UNK:O	33:S1:250:UNK:N	2.49	0.46
34:SA:1648:A:H2'	34:SA:1649:G:C8	2.51	0.46
41:SK:67:PRO:HA	41:SK:70:LEU:HB2	1.98	0.46
41:SK:84:GLY:HA2	41:SK:150:LEU:HD22	1.98	0.46
42:SM:29:LYS:HZ1	42:SM:32:LYS:HB2	1.80	0.46
7:5A:250:G:O6	7:5A:262:U:O4	2.34	0.46
7:5A:291:G:H2'	7:5A:292:A:C8	2.51	0.46
7:5A:334:G:H1	7:5A:389:U:H3	1.62	0.46
12:AE:347:PHE:O	12:AE:351:TYR:HB2	2.16	0.46
14:AG:302:UNK:O	14:AG:315:UNK:CB	2.64	0.46
16:BA:75:GLU:HA	16:BA:98:LYS:HB3	1.98	0.46
18:BC:269:LEU:O	18:BC:278:LEU:N	2.41	0.46
20:BE:143:SER:OG	20:BE:147:ASP:OD2	2.30	0.46
22:CB:96:GLU:O	22:CB:100:SER:HB2	2.16	0.46
26:K1:126:ILE:HB	26:K1:171:VAL:HB	1.98	0.46
33:S1:249:UNK:N	33:S1:261:UNK:O	2.49	0.46
34:SA:478:A:H62	34:SA:539:G:H22	1.64	0.46
34:SA:1268:G:H2'	34:SA:1270:G:H8	1.80	0.46
34:SA:1474:G:H2'	34:SA:1475:A:C8	2.51	0.46
40:SJ:36:THR:OG1	40:SJ:59:ARG:N	2.44	0.46
1:3A:46:U:H2'	1:3A:47:G:H8	1.80	0.46
1:3A:113:G:H1'	1:3A:257:A:H61	1.80	0.46
3:3D:323:THR:C	3:3D:327:LYS:HZ3	2.24	0.46
5:3F:160:ILE:HB	5:3F:542:SER:HB3	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:5A:271:G:H2'	7:5A:272:A:H8	1.81	0.46
7:5A:511:G:O6	7:5A:525:U:O4	2.33	0.46
8:AA:355:UNK:CB	8:AA:359:UNK:O	2.64	0.46
16:BA:300:MET:N	16:BA:300:MET:SD	2.89	0.46
19:BD:372:HIS:HA	19:BD:407:PHE:H	1.81	0.46
21:CA:175:LEU:HD21	22:CB:827:ARG:HG2	1.97	0.46
22:CB:179:LYS:HB2	22:CB:210:PRO:HG2	1.97	0.46
24:E3:305:ARG:C	24:E3:307:VAL:N	2.74	0.46
34:SA:870:C:H2'	34:SA:871:G:C8	2.51	0.46
34:SA:1617:U:H4'	51:Sd:18:ARG:HG3	1.97	0.46
53:Sg:121:CYS:SG	53:Sg:122:SER:N	2.88	0.46
10:AC:646:UNK:O	10:AC:650:UNK:CB	2.65	0.45
13:AF:71:UNK:CB	13:AF:75:UNK:O	2.64	0.45
16:BA:150:THR:H	16:BA:165:SER:HA	1.80	0.45
16:BA:368:LYS:HG2	16:BA:384:GLU:HG2	1.97	0.45
22:CB:142:GLU:HB2	22:CB:144:LYS:HE2	1.97	0.45
22:CB:218:ASP:OD2	22:CB:227:LYS:NZ	2.50	0.45
22:CB:671:THR:OG1	22:CB:718:LYS:O	2.34	0.45
22:CB:738:TYR:O	22:CB:742:PHE:HB2	2.17	0.45
33:S1:137:UNK:N	33:S1:146:UNK:O	2.48	0.45
34:SA:429:G:H2'	34:SA:430:G:H8	1.81	0.45
34:SA:1588:G:O6	34:SA:1608:U:O4	2.34	0.45
47:SX:12:ASN:O	47:SX:16:ASN:ND2	2.49	0.45
49:SZ:7:ILE:HG21	49:SZ:44:LEU:HD21	1.98	0.45
53:Sg:123:ASN:HD22	53:Sg:124:PRO:HD2	1.80	0.45
5:3F:188:TYR:HB3	5:3F:196:LEU:HD11	1.97	0.45
15:B1:623:LYS:HA	15:B1:626:LYS:HE2	1.97	0.45
17:BB:749:GLY:HA2	17:BB:752:LEU:HD12	1.98	0.45
20:BE:630:THR:OG1	20:BE:644:THR:OG1	2.33	0.45
22:CB:975:LEU:HD23	22:CB:1041:VAL:HG22	1.97	0.45
36:SF:75:LYS:HZ1	36:SF:77:ARG:HH12	1.57	0.45
1:3A:46:U:H2'	1:3A:47:G:C8	2.51	0.45
12:AE:163:CYS:HA	12:AE:164:LEU:HA	1.70	0.45
12:AE:1057:UNK:HA	12:AE:1065:UNK:HA	1.99	0.45
13:AF:474:UNK:O	13:AF:478:UNK:CB	2.65	0.45
15:B1:965:GLN:HA	15:B1:975:GLU:HG2	1.98	0.45
18:BC:220:ILE:HB	18:BC:237:LEU:HB3	1.99	0.45
20:BE:430:ILE:O	20:BE:442:THR:HA	2.16	0.45
22:CB:897:ARG:HE	35:SC:179:SER:HB2	1.81	0.45
31:R1:155:LYS:HG2	31:R1:234:ASN:HA	1.97	0.45
34:SA:215:A:H3'	34:SA:215:A:OP2	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SA:1082:C:OP2	34:SA:1083:G:OP2	2.35	0.45
39:SI:143:LEU:HD22	39:SI:147:ASN:HD22	1.81	0.45
44:SO:101:HIS:HA	44:SO:104:ARG:HE	1.82	0.45
52:Sf:42:ARG:HG2	52:Sf:46:ASN:ND2	2.31	0.45
54:U1:151:UNK:N	54:U1:159:UNK:O	2.50	0.45
2:3B:107:VAL:HG12	2:3B:143:VAL:HA	1.99	0.45
2:3B:299:LYS:HB2	2:3B:319:ARG:HB2	1.97	0.45
4:3E:373:TYR:HB3	4:3E:379:ASP:OD2	2.16	0.45
16:BA:514:VAL:HA	46:SR:118:ILE:HD13	1.98	0.45
17:BB:59:LEU:H	17:BB:383:HIS:HB3	1.79	0.45
20:BE:383:ASP:OD1	20:BE:384:ALA:N	2.49	0.45
20:BE:474:PHE:HA	20:BE:487:TYR:O	2.17	0.45
23:E2:28:PRO:HA	23:E2:29:PRO:HD3	1.88	0.45
24:E3:449:HIS:CD2	24:E3:451:ASP:H	2.34	0.45
25:E4:112:UNK:CB	25:E4:116:UNK:O	2.65	0.45
34:SA:93:A:H61	34:SA:396:G:H1'	1.80	0.45
34:SA:332:U:H5'	40:SJ:30:GLY:HA2	1.98	0.45
34:SA:501:U:OP1	52:Sf:49:LEU:HD21	2.17	0.45
34:SA:1118:G:H2'	34:SA:1119:G:C8	2.51	0.45
34:SA:1647:U:H2'	34:SA:1648:A:C8	2.52	0.45
37:SG:143:ARG:HD2	51:Sd:55:VAL:HG11	1.97	0.45
38:SH:57:ASP:HB3	38:SH:106:LEU:HD23	1.98	0.45
40:SJ:81:VAL:HA	40:SJ:102:VAL:HG12	1.97	0.45
4:3E:45:ALA:HB1	4:3E:83:LYS:HZ3	1.82	0.45
4:3E:296:GLY:HA2	4:3E:299:LEU:HD12	1.99	0.45
7:5A:529:A:H2'	7:5A:530:A:C8	2.52	0.45
8:AA:283:UNK:HA	8:AA:289:UNK:HA	1.98	0.45
12:AE:29:HIS:CD2	12:AE:123:ARG:HH21	2.35	0.45
14:AG:394:UNK:O	14:AG:406:UNK:CB	2.64	0.45
16:BA:263:VAL:HG22	16:BA:279:PHE:HE1	1.82	0.45
17:BB:226:VAL:O	17:BB:241:LYS:HA	2.17	0.45
17:BB:253:LYS:NZ	17:BB:254:GLN:O	2.48	0.45
17:BB:386:GLU:HB3	17:BB:390:GLN:HE22	1.80	0.45
17:BB:617:SER:O	17:BB:634:SER:OG	2.29	0.45
18:BC:377:LEU:HD12	18:BC:381:VAL:HG12	1.99	0.45
22:CB:949:PHE:O	22:CB:960:LYS:NZ	2.49	0.45
22:CB:1059:PRO:O	22:CB:1063:ARG:HB2	2.16	0.45
28:MB:169:ASN:ND2	28:MB:253:ARG:O	2.49	0.45
31:R1:281:GLU:OE2	31:R1:285:LYS:HE2	2.17	0.45
34:SA:391:A:H2'	34:SA:392:G:C8	2.51	0.45
34:SA:913:G:H4'	34:SA:914:G:OP2	2.15	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:SH:70:PRO:HD3	38:SH:101:ILE:HD12	1.98	0.45
1:3A:67:G:H2'	1:3A:68:A:H8	1.81	0.45
1:3A:330:A:H2'	1:3A:331:A:H8	1.81	0.45
7:5A:589:U:H2'	7:5A:590:G:H8	1.82	0.45
11:AD:509:UNK:O	11:AD:513:UNK:CB	2.64	0.45
17:BB:748:ALA:HA	17:BB:751:ARG:HE	1.82	0.45
18:BC:751:LYS:H	18:BC:753:HIS:CE1	2.35	0.45
20:BE:541:LYS:NZ	20:BE:542:LEU:O	2.48	0.45
28:MB:205:ILE:O	28:MB:209:LEU:N	2.49	0.45
32:R2:1475:SER:HB2	32:R2:1479:MET:HE3	1.99	0.45
33:S1:219:UNK:O	33:S1:227:UNK:N	2.50	0.45
34:SA:15:U:H2'	34:SA:16:G:C8	2.52	0.45
34:SA:406:U:H2'	34:SA:407:A:C8	2.52	0.45
34:SA:1584:G:H1'	34:SA:1585:U:H5	1.82	0.45
58:U5:52:ASN:HD21	58:U5:228:LYS:HE3	1.82	0.45
1:3A:3:C:H2'	1:3A:4:G:C8	2.51	0.45
4:3E:225:GLU:HG3	4:3E:226:ILE:HG13	1.99	0.45
8:AA:116:UNK:O	8:AA:129:UNK:CB	2.65	0.45
12:AE:121:LEU:HA	12:AE:125:PHE:HD2	1.82	0.45
15:B1:201:ASN:OD1	15:B1:204:ARG:NH2	2.49	0.45
16:BA:16:ARG:HB2	16:BA:34:GLY:H	1.82	0.45
16:BA:60:ALA:H	16:BA:73:ILE:H	1.64	0.45
19:BD:273:ARG:HA	19:BD:287:SER:HA	1.99	0.45
21:CA:53:LEU:HD12	21:CA:126:LEU:HD23	1.99	0.45
22:CB:167:PRO:HD3	22:CB:226:HIS:CE1	2.51	0.45
22:CB:419:TYR:HE1	22:CB:499:LEU:HD22	1.82	0.45
34:SA:445:A:C4	34:SA:525:A:H4'	2.52	0.45
57:U4:81:ASP:OD2	57:U4:84:ARG:NE	2.36	0.45
3:3D:74:VAL:HB	3:3D:78:LEU:HD22	1.99	0.45
6:3G:111:LYS:HA	6:3G:114:ILE:HD12	1.98	0.45
7:5A:71:U:H2'	7:5A:72:G:C8	2.52	0.45
7:5A:357:G:H2'	7:5A:358:G:H8	1.82	0.45
12:AE:25:ARG:O	12:AE:29:HIS:CB	2.64	0.45
12:AE:1520:UNK:O	12:AE:1524:UNK:CB	2.65	0.45
15:B1:190:ILE:H	15:B1:190:ILE:HG13	1.60	0.45
17:BB:212:VAL:HB	17:BB:217:LEU:HD23	1.98	0.45
17:BB:530:LEU:HD23	17:BB:551:LEU:HG	1.99	0.45
18:BC:43:ILE:HB	18:BC:56:ILE:O	2.17	0.45
18:BC:680:ASN:O	18:BC:684:LEU:HB3	2.17	0.45
22:CB:232:LEU:HD13	22:CB:296:ILE:HD11	1.98	0.45
22:CB:268:LEU:HB3	22:CB:294:LEU:HB2	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:E3:388:ASP:OD1	24:E3:436:GLN:NE2	2.48	0.45
35:SC:118:GLN:OE1	35:SC:208:GLN:NE2	2.49	0.45
37:SG:80:LYS:HB3	37:SG:83:ARG:HB2	1.98	0.45
38:SH:102:VAL:HG13	38:SH:106:LEU:HD12	1.98	0.45
47:SX:12:ASN:OD1	47:SX:16:ASN:ND2	2.49	0.45
54:U1:265:UNK:HA	54:U1:272:UNK:HA	1.99	0.45
58:U5:70:LEU:HB3	58:U5:123:ASP:HB2	1.98	0.45
10:AC:4:UNK:HA	10:AC:284:UNK:HA	1.99	0.45
10:AC:530:UNK:O	10:AC:534:UNK:CB	2.65	0.45
12:AE:1095:UNK:O	12:AE:1099:UNK:CB	2.65	0.45
13:AF:3:UNK:O	13:AF:285:UNK:N	2.50	0.45
17:BB:426:ARG:NH1	17:BB:458:ASP:O	2.49	0.45
17:BB:555:VAL:HG22	17:BB:569:LEU:HB2	1.97	0.45
22:CB:879:GLU:O	22:CB:883:LEU:HB2	2.16	0.45
22:CB:1147:TYR:O	22:CB:1151:LYS:HB2	2.17	0.45
25:E4:230:UNK:HA	25:E4:244:UNK:HA	1.98	0.45
34:SA:499:U:O2'	52:Sf:49:LEU:CD2	2.54	0.45
35:SC:88:VAL:HG13	35:SC:96:LEU:HD11	1.99	0.45
37:SG:80:LYS:HZ3	37:SG:83:ARG:HH11	1.65	0.45
39:SI:21:ALA:HA	39:SI:24:PHE:HD2	1.82	0.45
46:SR:24:ALA:HA	46:SR:63:ILE:HA	1.99	0.45
46:SR:42:GLU:CG	46:SR:45:ARG:HH12	2.26	0.45
8:AA:478:UNK:CB	8:AA:482:UNK:O	2.65	0.45
12:AE:814:UNK:O	12:AE:818:UNK:CB	2.65	0.45
14:AG:122:UNK:N	14:AG:126:UNK:O	2.50	0.45
15:B1:143:MET:H	48:SY:144:ARG:HH11	1.64	0.45
15:B1:893:ASN:HD22	15:B1:919:VAL:HG12	1.81	0.45
16:BA:385:GLU:OE1	16:BA:421:ASN:ND2	2.49	0.45
20:BE:36:GLY:HA2	20:BE:299:THR:HG21	1.99	0.45
20:BE:418:ALA:HB1	20:BE:468:MET:HG3	1.98	0.45
32:R2:1613:PRO:HD2	32:R2:1616:ASN:HD22	1.82	0.45
34:SA:1473:U:C2	37:SG:102:ARG:NH1	2.85	0.45
34:SA:1638:G:H22	34:SA:1763:A:H2	1.64	0.45
44:SO:114:ARG:HG3	44:SO:117:LEU:HD12	1.99	0.45
1:3A:199:G:C2	5:3F:153:GLY:HA2	2.52	0.44
6:3H:84:ARG:HG3	6:3H:96:PRO:HB3	1.98	0.44
13:AF:505:UNK:O	13:AF:509:UNK:CB	2.65	0.44
15:B1:112:LYS:HB3	15:B1:141:HIS:HD1	1.81	0.44
15:B1:977:LYS:HB3	15:B1:988:ARG:HG3	1.99	0.44
16:BA:710:ILE:HA	20:BE:596:GLU:HB2	1.98	0.44
17:BB:478:SER:H	17:BB:491:GLY:HA3	1.81	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:BC:36:VAL:HB	18:BC:39:GLU:H	1.83	0.44
18:BC:308:ASP:OD1	18:BC:308:ASP:N	2.51	0.44
20:BE:666:ARG:HB3	20:BE:667:THR:H	1.64	0.44
20:BE:860:GLU:HA	20:BE:863:TRP:HE3	1.82	0.44
22:CB:315:ILE:HB	22:CB:553:VAL:HG13	1.99	0.44
22:CB:970:TRP:HZ3	22:CB:1034:GLY:HA3	1.83	0.44
23:E2:121:LEU:HD11	23:E2:167:ILE:HD13	1.99	0.44
25:E4:59:UNK:O	25:E4:68:UNK:N	2.51	0.44
34:SA:156:A:H2'	34:SA:157:A:C8	2.52	0.44
34:SA:568:G:N2	34:SA:569:C:N3	2.65	0.44
43:SN:67:THR:HG22	43:SN:68:GLU:HG3	1.99	0.44
61:UC:731:UNK:HA	61:UC:732:UNK:HA	1.74	0.44
6:3H:85:VAL:HG22	6:3H:96:PRO:HG3	1.99	0.44
7:5A:163:G:H2'	7:5A:164:G:C8	2.52	0.44
8:AA:36:UNK:O	8:AA:44:UNK:N	2.50	0.44
11:AD:411:UNK:O	11:AD:415:UNK:CB	2.65	0.44
12:AE:1070:UNK:O	12:AE:1074:UNK:CB	2.65	0.44
18:BC:213:SER:OG	18:BC:223:TRP:NE1	2.45	0.44
20:BE:349:HIS:ND1	20:BE:374:SER:OG	2.38	0.44
22:CB:643:ALA:O	22:CB:647:ASN:HB2	2.17	0.44
23:E1:98:THR:OG1	23:E1:235:SER:OG	2.30	0.44
23:E2:103:PRO:O	23:E2:107:ALA:N	2.42	0.44
23:E2:151:ARG:NH2	34:SA:1572:G:OP2	2.50	0.44
34:SA:1145:U:H3	34:SA:1633:A:H2'	1.82	0.44
42:SM:75:VAL:HG22	42:SM:86:ILE:HG22	1.99	0.44
47:SX:17:ALA:HA	47:SX:22:LYS:HZ1	1.81	0.44
54:U1:157:UNK:HA	54:U1:172:UNK:HA	1.99	0.44
57:U4:72:ILE:HG23	57:U4:82:ILE:HD11	1.99	0.44
2:3B:116:SER:HB3	2:3B:122:ARG:HH12	1.82	0.44
2:3B:117:VAL:HG11	2:3B:179:THR:HA	1.98	0.44
7:5A:281:G:H2'	7:5A:282:G:H8	1.82	0.44
10:AC:8:UNK:N	10:AC:281:UNK:O	2.50	0.44
12:AE:659:LEU:HD23	12:AE:692:ILE:HA	1.99	0.44
12:AE:769:LEU:HB3	12:AE:801:ILE:HG12	2.00	0.44
13:AF:427:UNK:O	13:AF:431:UNK:CB	2.65	0.44
16:BA:85:LYS:HE2	20:BE:659:GLN:HA	1.98	0.44
19:BD:423:LEU:HG	19:BD:432:VAL:HG13	1.99	0.44
19:BD:424:ILE:HD13	19:BD:433:TRP:HD1	1.81	0.44
20:BE:292:ARG:NH2	20:BE:350:SER:OG	2.46	0.44
20:BE:602:SER:O	20:BE:609:ILE:HA	2.17	0.44
21:CA:211:GLY:HA2	21:CA:214:LEU:HD12	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CB:864:LEU:HD23	22:CB:867:ILE:HD12	1.98	0.44
24:E3:251:PRO:HA	24:E3:254:TRP:CE2	2.52	0.44
30:P1:161:ALA:HA	30:P1:232:HIS:HE1	1.83	0.44
34:SA:10:G:H2'	34:SA:11:A:C8	2.52	0.44
36:SF:100:ARG:HH12	36:SF:236:ILE:HG21	1.81	0.44
46:SR:23:LYS:O	46:SR:64:ASP:N	2.43	0.44
61:UC:58:UNK:O	61:UC:62:UNK:N	2.50	0.44
10:AC:59:UNK:O	10:AC:68:UNK:N	2.51	0.44
10:AC:466:UNK:O	10:AC:470:UNK:CB	2.66	0.44
15:B1:106:ALA:HA	15:B1:109:ASP:HB2	1.99	0.44
17:BB:357:THR:OG1	17:BB:361:THR:O	2.34	0.44
18:BC:172:VAL:HB	18:BC:186:LEU:HB2	2.00	0.44
24:E3:276:GLN:O	24:E3:280:ASN:HB2	2.18	0.44
25:E4:199:UNK:O	25:E4:212:UNK:CB	2.66	0.44
26:K1:132:VAL:HG11	26:K1:137:ARG:HB3	1.98	0.44
26:K1:140:LYS:HB3	26:K1:144:ARG:HH22	1.82	0.44
34:SA:924:A:H2'	34:SA:925:G:C4	2.52	0.44
35:SC:83:LYS:NZ	35:SC:106:THR:HA	2.33	0.44
39:SI:30:SER:HB2	39:SI:34:LEU:HB2	1.99	0.44
41:SK:78:ARG:HH11	41:SK:81:VAL:HG21	1.83	0.44
57:U4:71:PHE:HB2	57:U4:155:THR:HA	1.99	0.44
5:3F:440:HIS:HA	5:3F:497:LYS:HE3	2.00	0.44
7:5A:101:G:N2	7:5A:102:A:N1	2.61	0.44
14:AG:132:UNK:HA	14:AG:133:UNK:HA	1.73	0.44
16:BA:445:VAL:HG13	16:BA:458:TRP:HB2	2.00	0.44
28:MB:249:GLU:HB3	28:MB:253:ARG:HE	1.82	0.44
33:S1:137:UNK:O	33:S1:145:UNK:N	2.50	0.44
33:S1:179:UNK:HA	33:S1:185:UNK:HA	1.99	0.44
46:SR:58:ASP:O	46:SR:60:PHE:N	2.51	0.44
46:SR:113:ASP:OD1	46:SR:116:LEU:N	2.46	0.44
6:3H:56:ALA:HB3	6:3H:82:PRO:HA	2.00	0.44
7:5A:290:G:H2'	7:5A:291:G:H8	1.83	0.44
8:AA:148:UNK:O	8:AA:159:UNK:HA	2.18	0.44
12:AE:1651:UNK:HA	12:AE:1659:UNK:HA	1.99	0.44
14:AG:284:UNK:CB	14:AG:293:UNK:O	2.66	0.44
34:SA:1216:C:O2'	34:SA:1217:A:OP1	2.35	0.44
34:SA:1650:U:H2'	34:SA:1651:A:H8	1.83	0.44
35:SC:97:LEU:HD22	35:SC:232:HIS:CE1	2.52	0.44
37:SG:92:ARG:HA	37:SG:95:ASN:HD22	1.82	0.44
42:SM:130:PRO:HA	42:SM:136:ARG:HG3	1.99	0.44
58:U5:147:SER:HA	58:U5:148:LYS:HA	1.67	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AC:598:UNK:O	10:AC:602:UNK:CB	2.66	0.44
12:AE:528:ARG:HA	12:AE:531:ILE:HG22	1.99	0.44
12:AE:564:VAL:HB	12:AE:614:LEU:HD11	2.00	0.44
12:AE:912:UNK:HA	12:AE:913:UNK:HA	1.78	0.44
16:BA:423:ARG:NH2	16:BA:461:GLN:O	2.50	0.44
18:BC:35:PRO:HG3	18:BC:67:LEU:HG	1.99	0.44
19:BD:445:ARG:NH1	19:BD:499:ALA:O	2.50	0.44
21:CA:185:HIS:O	21:CA:189:ALA:CB	2.66	0.44
25:E4:3:UNK:O	25:E4:285:UNK:N	2.51	0.44
34:SA:361:C:N4	34:SA:384:G:O6	2.51	0.44
57:U4:63:TYR:O	57:U4:95:ASN:N	2.50	0.44
2:3B:264:GLN:HE22	2:3B:322:ARG:HA	1.81	0.44
5:3F:442:ILE:HD12	5:3F:470:LEU:HD12	1.99	0.44
7:5A:168:G:H1	7:5A:228:A:N6	2.16	0.44
15:B1:957:GLU:HG2	15:B1:960:ARG:HH11	1.82	0.44
16:BA:45:ASN:HB2	16:BA:377:GLY:HA3	1.99	0.44
18:BC:348:PRO:HB3	18:BC:399:ASP:HA	1.99	0.44
22:CB:1138:ASP:O	22:CB:1141:GLU:HB2	2.18	0.44
23:E2:67:LEU:HD11	23:E2:141:MET:HB2	1.98	0.44
30:P1:248:VAL:HA	30:P1:251:ILE:HD12	2.00	0.44
31:R1:110:SER:OG	31:R1:112:LYS:O	2.35	0.44
44:SO:17:PRO:HG3	50:Sc:28:PRO:HG3	1.99	0.44
1:3A:18:G:H2'	1:3A:19:A:H8	1.82	0.44
5:3F:342:ARG:NH1	6:3G:89:ARG:O	2.51	0.44
8:AA:231:UNK:HA	8:AA:240:UNK:O	2.17	0.44
10:AC:548:UNK:O	10:AC:552:UNK:CB	2.66	0.44
12:AE:854:UNK:O	12:AE:858:UNK:CB	2.66	0.44
13:AF:428:UNK:O	13:AF:432:UNK:CB	2.66	0.44
19:BD:429:TYR:HD2	19:BD:431:GLU:HG2	1.81	0.44
20:BE:154:TYR:OH	20:BE:194:ARG:O	2.25	0.44
20:BE:230:VAL:HB	20:BE:244:ILE:HB	2.00	0.44
21:CA:146:ASN:HB3	21:CA:150:LYS:NZ	2.32	0.44
24:E3:260:TYR:HA	24:E3:306:ALA:HB2	1.99	0.44
24:E3:305:ARG:HA	34:SA:1217:A:C8	2.52	0.44
28:MB:236:HIS:HE1	28:MB:249:GLU:HG2	1.83	0.44
36:SF:136:VAL:HG21	36:SF:148:ARG:NH1	2.33	0.44
40:SJ:67:TRP:NE1	40:SJ:69:SER:OG	2.51	0.44
43:SN:73:LYS:NZ	53:Sg:108:VAL:HB	2.32	0.44
58:U5:213:LEU:HA	58:U5:216:ILE:HD12	1.98	0.44
1:3A:310:G:H2'	1:3A:311:G:H8	1.83	0.43
2:3B:253:ILE:O	2:3B:257:SER:OG	2.30	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:3E:277:SER:HA	4:3E:293:GLU:OE2	2.18	0.43
5:3F:367:LYS:HA	5:3F:370:ARG:HD3	2.00	0.43
15:B1:868:ARG:HH21	15:B1:928:ILE:HA	1.83	0.43
20:BE:38:PRO:HB3	20:BE:300:GLN:HE21	1.82	0.43
20:BE:291:HIS:HD2	20:BE:298:VAL:HG22	1.83	0.43
20:BE:412:PRO:O	20:BE:434:HIS:ND1	2.42	0.43
23:E2:219:GLU:HA	37:SG:157:ARG:HH22	1.83	0.43
24:E3:457:ARG:HE	24:E3:461:LEU:HD11	1.83	0.43
31:R1:301:MET:HG2	31:R1:354:ILE:HD13	2.01	0.43
34:SA:51:A:N6	34:SA:429:G:H21	2.14	0.43
34:SA:1585:U:H2'	34:SA:1586:A:H8	1.83	0.43
61:UC:69:UNK:O	61:UC:73:UNK:N	2.51	0.43
9:AB:244:UNK:N	9:AB:248:UNK:O	2.51	0.43
14:AG:79:UNK:CB	14:AG:88:UNK:O	2.66	0.43
15:B1:828:ARG:HD3	48:SY:94:ASN:HA	2.00	0.43
16:BA:603:LEU:HB2	16:BA:612:LEU:O	2.18	0.43
17:BB:219:THR:HG22	17:BB:227:LYS:HB2	2.00	0.43
17:BB:444:LEU:HD13	17:BB:456:LEU:HD11	1.99	0.43
18:BC:270:ILE:HA	18:BC:277:VAL:HA	2.01	0.43
18:BC:311:LEU:HD12	18:BC:333:ILE:HD11	2.01	0.43
27:MA:114:ILE:HG13	27:MA:150:VAL:HB	2.00	0.43
34:SA:894:U:H2'	34:SA:895:G:C8	2.54	0.43
34:SA:1628:U:H2'	34:SA:1629:G:H8	1.82	0.43
39:SI:159:VAL:HG23	39:SI:163:ASP:OD2	2.17	0.43
61:UC:771:UNK:O	61:UC:775:UNK:N	2.51	0.43
9:AB:148:UNK:HA	9:AB:161:UNK:O	2.17	0.43
10:AC:235:UNK:CB	10:AC:239:UNK:O	2.66	0.43
10:AC:240:UNK:O	10:AC:253:UNK:CB	2.66	0.43
12:AE:121:LEU:HB3	12:AE:127:ILE:HD13	2.00	0.43
12:AE:595:THR:HG22	12:AE:619:SER:HA	2.00	0.43
13:AF:100:UNK:O	13:AF:109:UNK:N	2.51	0.43
13:AF:153:UNK:CB	13:AF:157:UNK:O	2.66	0.43
14:AG:264:UNK:HA	14:AG:274:UNK:O	2.17	0.43
14:AG:841:UNK:O	14:AG:845:UNK:CB	2.66	0.43
16:BA:99:CYS:SG	16:BA:115:SER:OG	2.76	0.43
16:BA:347:SER:HB2	16:BA:698:THR:HA	2.01	0.43
16:BA:522:SER:HB2	16:BA:583:ILE:HG23	1.99	0.43
17:BB:634:SER:OG	17:BB:635:LYS:N	2.49	0.43
17:BB:857:LEU:HD21	17:BB:884:LYS:HE2	2.01	0.43
22:CB:364:VAL:HA	22:CB:367:ARG:HG2	1.99	0.43
22:CB:412:LEU:HD22	22:CB:421:LEU:HA	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CB:506:GLN:OE1	22:CB:509:ASN:ND2	2.48	0.43
30:P1:188:LYS:HD2	30:P1:191:LYS:NZ	2.34	0.43
33:S1:282:UNK:O	33:S1:291:UNK:N	2.51	0.43
34:SA:283:U:H5''	38:SH:188:ARG:NE	2.31	0.43
34:SA:328:A:H2'	34:SA:329:G:C8	2.53	0.43
34:SA:363:G:H2'	34:SA:364:G:H8	1.83	0.43
34:SA:975:C:N4	34:SA:976:G:O6	2.52	0.43
36:SF:100:ARG:NH1	36:SF:236:ILE:HG21	2.34	0.43
44:SO:85:PRO:HD2	44:SO:88:LEU:HD13	2.00	0.43
58:U5:86:THR:HA	58:U5:90:ASP:HB2	2.00	0.43
2:3B:271:ILE:O	2:3B:313:HIS:HA	2.19	0.43
15:B1:819:GLU:O	15:B1:852:ARG:NH1	2.52	0.43
16:BA:308:VAL:HA	16:BA:319:PHE:HA	2.01	0.43
16:BA:475:PRO:HD2	16:BA:493:TRP:HB3	2.01	0.43
16:BA:498:ARG:HB3	16:BA:500:TRP:HE1	1.84	0.43
17:BB:166:ILE:HD11	17:BB:179:SER:HB2	1.99	0.43
17:BB:622:LYS:HB2	17:BB:631:PHE:CZ	2.54	0.43
18:BC:492:LYS:HD3	18:BC:511:TYR:HD2	1.83	0.43
20:BE:627:ASN:ND2	20:BE:647:THR:O	2.41	0.43
23:E2:53:HIS:N	23:E2:66:VAL:O	2.51	0.43
24:E3:305:ARG:O	24:E3:306:ALA:C	2.60	0.43
31:R1:138:MET:HE1	31:R1:151:LEU:HB2	2.00	0.43
33:S1:289:UNK:HA	33:S1:303:UNK:HA	2.01	0.43
34:SA:491:C:H2'	34:SA:492:A:C8	2.53	0.43
34:SA:1679:G:N2	34:SA:1723:U:O4	2.51	0.43
34:SA:1802:A:N6	34:SA:1808:U:O4	2.50	0.43
35:SC:127:VAL:HG11	35:SC:176:VAL:HG11	2.01	0.43
37:SG:81:ARG:NH1	37:SG:82:PHE:HE2	2.16	0.43
38:SH:57:ASP:HA	38:SH:106:LEU:HA	2.01	0.43
5:3F:491:SER:OG	5:3F:492:TRP:N	2.51	0.43
7:5A:244:U:H3	7:5A:269:G:H1	1.66	0.43
7:5A:409:C:H2'	7:5A:410:A:C8	2.53	0.43
15:B1:236:LEU:HB3	15:B1:239:THR:HG23	1.99	0.43
17:BB:163:LYS:HD3	34:SA:1765:A:H4'	2.01	0.43
17:BB:385:ILE:HG23	17:BB:417:TRP:HH2	1.83	0.43
24:E3:301:TYR:O	24:E3:304:TYR:CA	2.66	0.43
28:MB:215:LYS:NZ	34:SA:1625:C:H5'	2.33	0.43
34:SA:886:U:H2'	34:SA:887:A:C8	2.53	0.43
34:SA:1210:C:H2'	34:SA:1211:A:H8	1.83	0.43
36:SF:149:TYR:HB3	38:SH:208:TYR:CZ	2.52	0.43
40:SJ:4:SER:OG	40:SJ:6:ASP:OD1	2.34	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:U1:200:UNK:HA	54:U1:211:UNK:HA	2.01	0.43
4:3E:45:ALA:HB1	4:3E:83:LYS:NZ	2.33	0.43
12:AE:272:LYS:HA	12:AE:275:ILE:HD12	2.00	0.43
12:AE:367:LEU:O	12:AE:371:LYS:CB	2.63	0.43
12:AE:894:UNK:O	12:AE:898:UNK:CB	2.66	0.43
18:BC:622:ALA:H	18:BC:635:ALA:HB3	1.84	0.43
19:BD:368:THR:HA	19:BD:385:ASN:O	2.18	0.43
20:BE:208:GLN:O	20:BE:226:VAL:N	2.49	0.43
34:SA:273:G:C6	34:SA:283:U:O2	2.72	0.43
34:SA:363:G:H2'	34:SA:364:G:C8	2.54	0.43
36:SF:92:LEU:HB2	36:SF:97:GLU:HB2	2.01	0.43
39:SI:67:LEU:HG	39:SI:71:HIS:CE1	2.54	0.43
45:SP:20:TYR:HB3	45:SP:27:PHE:HB2	2.00	0.43
46:SR:79:TYR:HD1	46:SR:82:ARG:HD3	1.84	0.43
54:U1:77:UNK:HA	54:U1:88:UNK:HA	2.00	0.43
61:UC:243:UNK:O	61:UC:247:UNK:N	2.52	0.43
61:UC:437:UNK:O	61:UC:441:UNK:N	2.52	0.43
1:3A:47:G:H2'	1:3A:48:A:C8	2.53	0.43
1:3A:84:U:H2'	1:3A:85:G:H8	1.84	0.43
3:3D:150:ALA:O	3:3D:154:LEU:HB2	2.18	0.43
8:AA:65:UNK:HA	8:AA:78:UNK:O	2.18	0.43
15:B1:836:LYS:H	15:B1:912:ARG:HH12	1.67	0.43
16:BA:412:ARG:HA	16:BA:423:ARG:O	2.19	0.43
20:BE:97:LYS:HZ2	20:BE:111:GLU:HB2	1.83	0.43
22:CB:812:GLU:O	22:CB:816:ALA:CB	2.67	0.43
30:P1:255:PRO:HA	30:P1:256:PRO:HD3	1.88	0.43
31:R1:67:ILE:HG23	31:R1:74:VAL:HG22	2.01	0.43
34:SA:389:G:H3'	34:SA:390:G:H21	1.83	0.43
34:SA:1263:G:C2	34:SA:1264:G:H1'	2.53	0.43
34:SA:1661:U:H2'	34:SA:1662:G:C8	2.54	0.43
35:SC:83:LYS:HB2	35:SC:104:ASP:HB3	2.01	0.43
36:SF:137:PRO:HG2	36:SF:149:TYR:HA	2.00	0.43
51:Sd:30:VAL:O	51:Sd:39:THR:OG1	2.27	0.43
7:5A:274:C:H2'	7:5A:275:A:C8	2.54	0.43
7:5A:379:A:H2'	7:5A:380:A:C8	2.54	0.43
8:AA:386:UNK:N	8:AA:391:UNK:O	2.51	0.43
15:B1:189:VAL:HG13	15:B1:193:ARG:HA	2.01	0.43
16:BA:66:GLN:HG3	16:BA:68:THR:HG22	2.00	0.43
18:BC:353:LEU:HD12	18:BC:366:PRO:HG2	2.00	0.43
21:CA:6:ILE:HD13	22:CB:1206:PRO:HB2	2.00	0.43
22:CB:896:THR:O	22:CB:900:GLU:HB2	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:E3:228:LYS:NZ	34:SA:1245:G:OP2	2.51	0.43
34:SA:523:G:H22	34:SA:528:U:H5''	1.83	0.43
34:SA:1679:G:H1'	34:SA:1722:A:H61	1.84	0.43
35:SC:91:VAL:HG23	35:SC:96:LEU:HB2	2.01	0.43
36:SF:12:LEU:HD21	36:SF:22:LYS:HG2	2.01	0.43
40:SJ:8:ARG:HH11	40:SJ:19:ALA:HB3	1.84	0.43
48:SY:137:LYS:NZ	52:Sf:23:LYS:HE2	2.34	0.43
2:3C:169:LYS:O	2:3C:238:ASP:N	2.42	0.43
15:B1:66:ARG:HH21	15:B1:78:ASN:HB3	1.83	0.43
18:BC:614:ASP:OD1	18:BC:614:ASP:N	2.50	0.43
22:CB:298:PHE:HB2	22:CB:340:SER:HA	2.00	0.43
22:CB:644:VAL:O	22:CB:648:PHE:HB2	2.19	0.43
22:CB:823:SER:HA	22:CB:841:ASN:O	2.19	0.43
28:MB:173:ARG:HD3	28:MB:252:PRO:HB3	2.00	0.43
32:R2:1690:PHE:HA	32:R2:1693:ASN:HD22	1.83	0.43
34:SA:205:U:H2'	34:SA:206:A:H8	1.84	0.43
34:SA:1528:U:P	37:SG:109:LYS:HZ1	2.41	0.43
37:SG:94:THR:HG22	37:SG:114:ILE:HG13	2.01	0.43
39:SI:26:GLU:OE2	39:SI:27:LEU:HG	2.19	0.43
40:SJ:85:PRO:HG3	42:SM:12:ALA:HB2	2.01	0.43
44:SO:101:HIS:HA	44:SO:104:ARG:HH11	1.83	0.43
2:3B:227:PRO:HA	2:3B:230:TYR:CE1	2.54	0.43
3:3D:62:ALA:O	3:3D:66:ALA:CB	2.67	0.43
3:3D:284:TYR:HE1	4:3E:257:ALA:HB1	1.84	0.43
4:3E:160:ASP:OD1	4:3E:163:ILE:HD12	2.18	0.43
7:5A:242:C:H2'	7:5A:243:A:C8	2.53	0.43
16:BA:114:ALA:HB1	16:BA:149:ILE:HB	2.01	0.43
16:BA:505:ARG:HH22	34:SA:1618:C:H41	1.66	0.43
16:BA:556:ARG:HB3	16:BA:557:LYS:H	1.70	0.43
17:BB:438:PHE:HA	17:BB:445:VAL:HG23	2.00	0.43
17:BB:576:VAL:HA	17:BB:592:SER:HA	2.01	0.43
18:BC:18:GLY:O	18:BC:336:ASN:N	2.52	0.43
18:BC:439:ALA:HB3	18:BC:457:ALA:HB3	2.01	0.43
20:BE:375:LEU:HB3	20:BE:389:MET:HB2	2.00	0.43
20:BE:391:GLN:HG2	20:BE:443:TRP:HH2	1.84	0.43
20:BE:588:ILE:HA	20:BE:604:SER:HA	2.01	0.43
22:CB:758:SER:O	22:CB:762:TYR:N	2.52	0.43
22:CB:1157:TYR:HB3	22:CB:1161:LEU:HB2	2.01	0.43
25:E4:33:UNK:HA	25:E4:54:UNK:HA	2.01	0.43
26:K1:99:ASP:O	26:K1:103:LEU:N	2.44	0.43
34:SA:1041:G:H2'	34:SA:1042:G:C8	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:SI:71:HIS:HD2	39:SI:131:PHE:CZ	2.36	0.43
1:3A:79:G:C5	6:3H:95:ARG:HD3	2.54	0.42
3:3D:18:PHE:CZ	3:3D:151:GLN:HB2	2.54	0.42
3:3D:158:TYR:O	3:3D:162:LYS:CB	2.62	0.42
4:3E:58:GLU:HA	4:3E:61:ASN:HD22	1.84	0.42
7:5A:133:U:H2'	7:5A:134:A:C8	2.54	0.42
7:5A:271:G:H2'	7:5A:272:A:C8	2.54	0.42
12:AE:576:ILE:HA	12:AE:579:ARG:HE	1.83	0.42
13:AF:143:UNK:N	13:AF:148:UNK:O	2.52	0.42
20:BE:559:ALA:HA	20:BE:569:VAL:HA	2.01	0.42
20:BE:592:ASP:OD1	20:BE:593:PHE:N	2.51	0.42
23:E1:105:ASN:HB2	23:E1:110:LEU:HD23	2.00	0.42
31:R1:177:PRO:HD2	31:R1:304:GLY:HA2	2.00	0.42
34:SA:878:G:O2'	44:SO:108:ASP:OD1	2.36	0.42
34:SA:891:A:H2'	34:SA:892:A:H8	1.83	0.42
34:SA:1606:C:H2'	34:SA:1607:G:C8	2.54	0.42
35:SC:36:SER:O	35:SC:38:PHE:N	2.51	0.42
37:SG:142:PRO:HA	37:SG:218:GLU:OE2	2.18	0.42
41:SK:66:ASP:O	41:SK:70:LEU:N	2.49	0.42
51:Sd:36:THR:OG1	51:Sd:37:SER:N	2.49	0.42
61:UC:769:UNK:O	61:UC:773:UNK:N	2.52	0.42
2:3C:100:ARG:HA	2:3C:101:GLY:HA2	1.77	0.42
5:3F:323:ASP:OD2	5:3F:342:ARG:HD3	2.20	0.42
5:3F:345:THR:HG22	5:3F:360:ARG:HG3	2.01	0.42
12:AE:506:TYR:O	12:AE:510:SER:CB	2.67	0.42
12:AE:816:UNK:O	12:AE:820:UNK:CB	2.67	0.42
15:B1:245:ASP:HB3	15:B1:797:PRO:HA	2.00	0.42
15:B1:846:VAL:HB	15:B1:899:VAL:HG23	2.00	0.42
17:BB:15:GLY:H	17:BB:685:GLU:HB3	1.84	0.42
17:BB:656:HIS:CE1	17:BB:682:ARG:HD2	2.55	0.42
25:E4:258:UNK:HA	40:SJ:42:ARG:HH11	1.81	0.42
31:R1:153:THR:HA	31:R1:166:VAL:HG12	2.00	0.42
33:S1:101:UNK:N	33:S1:385:UNK:O	2.48	0.42
34:SA:497:G:H2'	34:SA:498:G:C8	2.54	0.42
36:SF:211:LYS:HB3	36:SF:217:THR:HG22	2.01	0.42
44:SO:55:ARG:HA	44:SO:60:VAL:HB	2.01	0.42
47:SX:65:LEU:HD22	47:SX:66:ASN:H	1.85	0.42
1:3A:330:A:H2'	1:3A:331:A:C8	2.54	0.42
2:3C:180:SER:HA	2:3C:183:HIS:HD2	1.83	0.42
8:AA:27:UNK:O	8:AA:34:UNK:HA	2.19	0.42
8:AA:404:UNK:HA	8:AA:410:UNK:HA	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AE:1762:UNK:O	12:AE:1766:UNK:CB	2.67	0.42
14:AG:8:UNK:N	14:AG:567:UNK:O	2.51	0.42
18:BC:391:LEU:HD23	18:BC:407:SER:HB2	2.00	0.42
18:BC:397:THR:OG1	18:BC:398:GLU:N	2.53	0.42
20:BE:323:VAL:HG13	20:BE:343:LEU:HB2	2.00	0.42
22:CB:543:LEU:HG	22:CB:545:ALA:H	1.85	0.42
27:MA:111:LEU:HB2	27:MA:148:TYR:HB3	2.02	0.42
34:SA:283:U:O4'	38:SH:188:ARG:HG3	2.19	0.42
34:SA:1049:U:H2'	34:SA:1050:G:C8	2.54	0.42
34:SA:1179:G:O6	34:SA:1461:C:N4	2.53	0.42
35:SC:97:LEU:HD22	35:SC:232:HIS:HE1	1.84	0.42
36:SF:129:VAL:HB	36:SF:139:VAL:HG12	2.01	0.42
36:SF:137:PRO:HB2	36:SF:150:PRO:HD2	2.01	0.42
41:SK:58:ASP:O	41:SK:61:THR:OG1	2.32	0.42
58:U5:64:LEU:HB3	58:U5:68:ARG:HE	1.84	0.42
7:5A:251:C:H2'	7:5A:252:A:C8	2.54	0.42
12:AE:687:LEU:HB2	12:AE:691:PHE:HD2	1.83	0.42
15:B1:962:GLU:HA	15:B1:976:ILE:HB	2.01	0.42
16:BA:536:LYS:HG3	16:BA:538:GLN:H	1.85	0.42
19:BD:362:HIS:H	19:BD:418:LYS:HD3	1.85	0.42
21:CA:138:TRP:CD1	21:CA:142:LYS:HE3	2.54	0.42
23:E1:122:ILE:HA	23:E1:161:LYS:O	2.19	0.42
24:E3:308:LYS:HB3	24:E3:345:VAL:HG21	2.01	0.42
28:MB:177:ILE:HG21	34:SA:1159:C:H5'	2.02	0.42
32:R2:1582:VAL:HG13	32:R2:1620:VAL:HG12	2.00	0.42
34:SA:139:C:H42	34:SA:175:G:H21	1.67	0.42
34:SA:162:A:OP2	34:SA:162:A:H8	2.00	0.42
34:SA:200:A:H2'	34:SA:201:G:H8	1.83	0.42
34:SA:868:G:H1	34:SA:960:U:H3	1.67	0.42
34:SA:890:C:H2'	34:SA:891:A:H8	1.84	0.42
34:SA:1482:C:O4'	46:SR:74:HIS:NE2	2.52	0.42
48:SY:126:LYS:HG2	48:SY:131:SER:HA	2.01	0.42
7:5A:182:G:H2'	7:5A:183:A:H8	1.85	0.42
9:AB:54:UNK:O	9:AB:72:UNK:N	2.53	0.42
9:AB:121:UNK:N	9:AB:125:UNK:O	2.52	0.42
12:AE:132:THR:HG23	12:AE:155:ILE:HD11	2.01	0.42
16:BA:36:ARG:NH1	16:BA:699:GLU:OE2	2.53	0.42
16:BA:716:ASP:O	16:BA:744:ARG:NH2	2.46	0.42
17:BB:857:LEU:HD12	17:BB:860:ILE:HD11	2.02	0.42
18:BC:47:PRO:HD3	18:BC:53:LEU:HG	2.01	0.42
18:BC:343:MET:HB2	18:BC:353:LEU:HD21	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:BC:345:TYR:CD2	18:BC:350:LEU:HD12	2.54	0.42
18:BC:532:HIS:CG	18:BC:536:LEU:HD11	2.55	0.42
20:BE:914:ASP:OD1	20:BE:914:ASP:N	2.52	0.42
21:CA:146:ASN:HB3	21:CA:150:LYS:HZ2	1.84	0.42
22:CB:712:ASN:HA	22:CB:1115:LEU:HG	2.00	0.42
22:CB:752:SER:HB3	22:CB:754:LEU:HG	2.01	0.42
26:K1:195:HIS:HA	26:K1:196:PRO:HD3	1.88	0.42
34:SA:340:U:H2'	34:SA:341:A:H8	1.84	0.42
34:SA:1253:U:O5'	43:SN:46:ARG:NH2	2.51	0.42
34:SA:1573:A:H4'	34:SA:1574:G:H5'	2.01	0.42
35:SC:77:GLU:OE2	45:SP:114:ARG:NH2	2.53	0.42
50:Sc:73:LEU:HD23	50:Sc:77:THR:HG21	2.00	0.42
7:5A:26:C:N4	7:5A:54:A:OP2	2.52	0.42
7:5A:125:G:H2'	7:5A:126:A:C8	2.54	0.42
8:AA:99:UNK:O	8:AA:108:UNK:N	2.51	0.42
12:AE:33:LEU:HD12	12:AE:115:LEU:HD11	2.01	0.42
12:AE:405:GLU:HA	12:AE:414:LEU:HD13	2.02	0.42
12:AE:1506:UNK:HA	12:AE:1507:UNK:HA	1.80	0.42
18:BC:13:ASN:N	18:BC:643:PHE:O	2.53	0.42
20:BE:140:TYR:HE1	20:BE:153:PHE:HD1	1.66	0.42
22:CB:559:GLU:OE2	22:CB:608:PHE:HB3	2.20	0.42
23:E1:28:PRO:HA	23:E1:29:PRO:HD3	1.88	0.42
34:SA:153:G:H2'	34:SA:154:G:C8	2.54	0.42
34:SA:283:U:N3	38:SH:188:ARG:CB	2.75	0.42
34:SA:891:A:H2'	34:SA:892:A:C8	2.54	0.42
34:SA:1158:C:N3	34:SA:1581:C:H3'	2.35	0.42
35:SC:207:LEU:HD22	35:SC:210:ILE:HD11	2.01	0.42
46:SR:44:LEU:HD12	46:SR:47:LYS:HG3	2.01	0.42
54:U1:13:UNK:O	54:U1:31:UNK:N	2.52	0.42
57:U4:66:LEU:HD13	57:U4:141:LEU:HD22	2.01	0.42
61:UC:445:UNK:O	61:UC:449:UNK:N	2.53	0.42
1:3A:63:C:H2'	1:3A:64:A:C8	2.54	0.42
1:3A:102:U:H2'	1:3A:103:A:C8	2.54	0.42
2:3C:251:ARG:HH12	8:AA:249:UNK:HA	1.85	0.42
5:3F:481:ILE:HA	5:3F:482:PRO:HD3	1.88	0.42
6:3H:93:VAL:HG12	6:3H:95:ARG:H	1.84	0.42
7:5A:352:U:H5''	7:5A:353:A:OP2	2.20	0.42
7:5A:556:G:H2'	7:5A:557:A:C8	2.51	0.42
8:AA:159:UNK:O	8:AA:167:UNK:N	2.53	0.42
12:AE:106:SER:HA	12:AE:109:TRP:HE1	1.84	0.42
12:AE:666:ALA:HA	12:AE:669:VAL:HG12	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:B1:134:PHE:HA	15:B1:137:ILE:HD12	2.00	0.42
16:BA:119:LEU:HD23	16:BA:142:HIS:HB2	2.01	0.42
17:BB:126:LEU:N	17:BB:139:GLY:O	2.52	0.42
17:BB:135:ARG:HA	17:BB:148:TRP:O	2.19	0.42
18:BC:33:ALA:H	18:BC:69:LEU:HD21	1.85	0.42
18:BC:667:GLN:HE22	18:BC:688:LEU:HB3	1.85	0.42
19:BD:519:SER:HB2	19:BD:534:SER:HA	2.02	0.42
22:CB:156:LYS:HD2	22:CB:237:HIS:CE1	2.55	0.42
22:CB:419:TYR:O	22:CB:423:LYS:CB	2.67	0.42
22:CB:883:LEU:HD11	22:CB:1051:LEU:HA	2.02	0.42
22:CB:1103:ARG:HD3	22:CB:1179:LYS:HE2	2.02	0.42
24:E3:449:HIS:HB3	24:E3:453:GLY:H	1.85	0.42
25:E4:220:UNK:CB	25:E4:234:UNK:O	2.68	0.42
33:S1:126:UNK:N	33:S1:138:UNK:O	2.53	0.42
34:SA:156:A:H1'	34:SA:416:A:C5	2.54	0.42
34:SA:863:A:N6	34:SA:964:U:C2	2.88	0.42
34:SA:883:C:H2'	34:SA:884:A:H8	1.83	0.42
36:SF:206:ASP:HB2	36:SF:222:LEU:HB2	2.00	0.42
40:SJ:8:ARG:NH1	40:SJ:19:ALA:H	2.17	0.42
47:SX:76:SER:HA	47:SX:77:PRO:HA	1.92	0.42
1:3A:204:U:H2'	1:3A:205:G:C8	2.55	0.42
4:3E:210:LEU:HA	4:3E:256:ASN:HD22	1.84	0.42
5:3F:160:ILE:HG23	5:3F:525:GLN:HG2	2.01	0.42
5:3F:443:LEU:N	5:3F:471:GLN:O	2.46	0.42
12:AE:374:ARG:HE	12:AE:404:PHE:HE1	1.66	0.42
15:B1:133:GLU:OE1	15:B1:832:HIS:NE2	2.52	0.42
15:B1:634:ARG:HH12	31:R1:185:ARG:HG2	1.85	0.42
16:BA:516:SER:HA	16:BA:535:LEU:HB2	2.02	0.42
17:BB:630:PHE:O	17:BB:642:TRP:HB2	2.19	0.42
18:BC:222:LEU:HD12	18:BC:235:LYS:HB2	2.02	0.42
22:CB:334:PHE:O	22:CB:338:SER:HB3	2.20	0.42
24:E3:260:TYR:HD1	24:E3:306:ALA:HB2	1.84	0.42
32:R2:1473:ASN:HA	32:R2:1505:ILE:HG23	2.00	0.42
32:R2:1476:VAL:O	32:R2:1480:ASN:ND2	2.52	0.42
32:R2:1644:LEU:HB3	32:R2:1654:LEU:HD13	2.02	0.42
34:SA:568:G:N2	34:SA:575:C:N3	2.65	0.42
34:SA:1042:G:H2'	34:SA:1043:A:C8	2.55	0.42
34:SA:1726:G:H2'	34:SA:1727:G:H8	1.84	0.42
35:SC:90:GLU:HB2	35:SC:97:LEU:HD21	2.01	0.42
37:SG:77:TYR:HA	37:SG:83:ARG:HE	1.84	0.42
37:SG:162:VAL:HA	51:Sd:45:LYS:HB3	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:SH:98:ARG:HH12	38:SH:103:GLY:N	2.17	0.42
40:SJ:78:ILE:HA	40:SJ:104:ILE:HG22	2.02	0.42
44:SO:71:ILE:HA	44:SO:74:ILE:HD12	2.01	0.42
1:3A:84:U:H2'	1:3A:85:G:C8	2.55	0.42
6:3G:56:ALA:N	6:3G:81:VAL:O	2.47	0.42
8:AA:29:UNK:CB	8:AA:33:UNK:O	2.68	0.42
15:B1:938:PRO:HB2	15:B1:941:ILE:HD11	2.02	0.42
16:BA:619:ARG:HD3	16:BA:619:ARG:H	1.85	0.42
20:BE:365:PHE:HA	20:BE:378:PHE:O	2.20	0.42
22:CB:781:ASP:OD1	22:CB:781:ASP:N	2.52	0.42
23:E1:196:LEU:HD11	23:E1:202:ILE:HD12	2.02	0.42
32:R2:1633:ASP:HB3	32:R2:1636:ARG:HD3	2.00	0.42
34:SA:1177:C:H2'	34:SA:1178:G:C8	2.54	0.42
3:3D:54:ALA:HB2	3:3D:81:ILE:HD12	2.02	0.42
10:AC:137:UNK:HA	10:AC:152:UNK:O	2.20	0.42
15:B1:112:LYS:HB3	15:B1:141:HIS:ND1	2.35	0.42
15:B1:155:LEU:HD11	15:B1:190:ILE:HD11	2.02	0.42
15:B1:260:PRO:HG3	15:B1:282:LYS:HD3	2.00	0.42
17:BB:407:ALA:HB1	17:BB:414:LEU:HD11	2.02	0.42
17:BB:439:LEU:HD12	17:BB:440:PRO:HD2	2.01	0.42
18:BC:193:VAL:HG23	18:BC:215:GLY:H	1.85	0.42
23:E1:180:LEU:HD13	23:E1:237:ALA:HB1	2.01	0.42
31:R1:9:THR:HB	31:R1:31:ILE:HG22	2.02	0.42
31:R1:228:ASP:OD2	31:R1:230:TRP:NE1	2.52	0.42
34:SA:1202:A:H4'	34:SA:1205:C:H42	1.85	0.42
34:SA:1593:A:H2'	34:SA:1594:G:C8	2.55	0.42
7:5A:476:A:H2'	7:5A:477:G:C8	2.55	0.41
7:5A:578:G:H2'	7:5A:579:G:C8	2.55	0.41
15:B1:151:THR:HG22	15:B1:186:LEU:HB2	2.02	0.41
17:BB:255:ARG:HA	17:BB:346:VAL:HG11	2.01	0.41
18:BC:110:ALA:HB3	18:BC:150:LEU:HD11	2.01	0.41
19:BD:363:LEU:H	19:BD:418:LYS:NZ	2.18	0.41
19:BD:495:ASP:H	19:BD:498:ASN:HD22	1.68	0.41
19:BD:524:SER:OG	19:BD:526:ASP:OD1	2.38	0.41
21:CA:46:ASN:HD22	21:CA:47:SER:H	1.68	0.41
22:CB:470:LYS:O	22:CB:473:LYS:NZ	2.36	0.41
34:SA:256:A:H2'	34:SA:257:A:C8	2.54	0.41
34:SA:322:G:O3'	40:SJ:10:LYS:NZ	2.53	0.41
34:SA:347:G:H5'	42:SM:80:MET:HE3	2.02	0.41
34:SA:1059:U:H4'	34:SA:1060:U:H5'	2.02	0.41
35:SC:196:GLU:HA	35:SC:199:ASN:HD22	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:SH:57:ASP:HA	38:SH:107:ALA:H	1.84	0.41
58:U5:82:LEU:HG	58:U5:174:ILE:HG21	2.02	0.41
1:3A:82:G:OP2	4:3E:365:ALA:HB1	2.20	0.41
2:3B:165:ALA:HB3	2:3B:168:LYS:HE2	2.02	0.41
3:3D:30:ARG:NH2	33:S1:204:UNK:O	2.53	0.41
4:3E:44:ILE:HG23	4:3E:127:LEU:HD22	2.02	0.41
5:3F:352:PRO:HB3	49:SZ:10:ARG:NH1	2.34	0.41
7:5A:250:G:N2	7:5A:262:U:O2	2.33	0.41
7:5A:384:U:H2'	7:5A:385:A:C8	2.55	0.41
12:AE:95:ASP:HA	12:AE:98:ILE:HD12	2.02	0.41
14:AG:475:UNK:HA	14:AG:489:UNK:HA	2.01	0.41
15:B1:63:THR:HG22	15:B1:193:ARG:HE	1.84	0.41
16:BA:111:PHE:HB3	16:BA:122:TRP:O	2.20	0.41
16:BA:743:PHE:CZ	16:BA:777:ARG:HB3	2.55	0.41
18:BC:206:GLU:HA	18:BC:209:LEU:HB2	2.03	0.41
18:BC:552:SER:OG	18:BC:554:ASP:OD1	2.34	0.41
18:BC:706:ARG:HH21	18:BC:715:LYS:HA	1.84	0.41
22:CB:130:LYS:HD2	22:CB:283:TYR:CZ	2.56	0.41
25:E4:120:UNK:HA	25:E4:126:UNK:HA	2.02	0.41
34:SA:482:U:H2'	34:SA:483:A:C8	2.54	0.41
34:SA:947:U:H2'	34:SA:948:G:C8	2.55	0.41
34:SA:1748:G:H2'	34:SA:1749:A:C8	2.54	0.41
38:SH:187:LYS:HZ3	38:SH:191:ARG:CZ	2.32	0.41
39:SI:13:PRO:HA	39:SI:14:THR:HA	1.91	0.41
39:SI:122:HIS:HA	39:SI:125:ILE:HD12	2.02	0.41
44:SO:34:ILE:HA	44:SO:37:ILE:HD12	2.01	0.41
54:U1:116:UNK:HA	54:U1:131:UNK:HA	2.01	0.41
6:3H:79:VAL:HG23	6:3H:121:ILE:HG23	2.02	0.41
7:5A:529:A:H2'	7:5A:530:A:H8	1.85	0.41
9:AB:149:UNK:O	9:AB:160:UNK:HA	2.19	0.41
15:B1:969:VAL:HG22	15:B1:1000:ILE:H	1.84	0.41
16:BA:161:ILE:O	16:BA:172:ILE:HA	2.20	0.41
16:BA:600:SER:OG	16:BA:601:ILE:N	2.51	0.41
18:BC:401:LEU:O	18:BC:427:TYR:OH	2.33	0.41
20:BE:828:LYS:HA	20:BE:870:GLN:HE22	1.85	0.41
20:BE:906:ALA:O	20:BE:910:GLN:HB2	2.21	0.41
22:CB:201:SER:O	22:CB:290:PHE:HA	2.20	0.41
28:MB:109:LEU:HD12	28:MB:111:PHE:HE1	1.85	0.41
34:SA:576:G:H8	34:SA:576:G:OP2	2.03	0.41
39:SI:14:THR:OG1	39:SI:15:GLU:OE1	2.38	0.41
41:SK:38:ASN:HB2	41:SK:41:GLU:HG3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:SK:114:TYR:HD1	41:SK:119:ALA:HB3	1.86	0.41
47:SX:71:LYS:HB3	47:SX:130:TYR:CZ	2.55	0.41
56:U3:2147:UNK:O	56:U3:2151:UNK:N	2.53	0.41
2:3C:253:ILE:O	2:3C:257:SER:N	2.46	0.41
4:3E:166:ALA:HB1	4:3E:272:LEU:HD11	2.02	0.41
5:3F:485:ASN:O	5:3F:501:ILE:N	2.48	0.41
7:5A:133:U:H2'	7:5A:134:A:H8	1.84	0.41
13:AF:13:UNK:HA	13:AF:279:UNK:HA	2.03	0.41
14:AG:195:UNK:CB	14:AG:199:UNK:O	2.69	0.41
15:B1:187:SER:O	15:B1:193:ARG:NH2	2.51	0.41
16:BA:557:LYS:HE2	16:BA:598:ASN:HB2	2.02	0.41
17:BB:559:PHE:HE2	17:BB:561:ASP:HB2	1.85	0.41
20:BE:131:SER:HA	20:BE:137:ILE:HG12	2.02	0.41
23:E1:50:LEU:HD12	23:E1:116:THR:HG22	2.03	0.41
31:R1:52:PHE:HE1	31:R1:102:PRO:HG3	1.86	0.41
34:SA:283:U:OP2	38:SH:188:ARG:NE	2.49	0.41
35:SC:31:ASP:HB3	35:SC:45:LYS:NZ	2.35	0.41
38:SH:98:ARG:HH12	38:SH:103:GLY:H	1.67	0.41
44:SO:16:ILE:HA	44:SO:17:PRO:HD3	1.91	0.41
1:3A:60:A:H5''	1:3A:61:G:C8	2.55	0.41
2:3C:117:VAL:HG22	2:3C:210:MET:HE1	2.02	0.41
3:3D:146:ASP:OD2	4:3E:237:THR:HB	2.21	0.41
5:3F:301:ASP:OD1	5:3F:301:ASP:N	2.53	0.41
7:5A:286:U:H2'	7:5A:287:G:C8	2.56	0.41
17:BB:50:ASN:ND2	17:BB:52:TRP:HE1	2.17	0.41
22:CB:381:HIS:NE2	22:CB:478:THR:O	2.44	0.41
22:CB:939:ILE:HG12	22:CB:943:VAL:HG13	2.02	0.41
34:SA:328:A:H2'	34:SA:329:G:H8	1.85	0.41
34:SA:1276:U:N3	34:SA:1437:U:O2	2.54	0.41
36:SF:130:GLN:HB2	36:SF:138:TYR:CZ	2.55	0.41
46:SR:59:LYS:HE2	46:SR:60:PHE:CZ	2.56	0.41
61:UC:297:UNK:O	61:UC:301:UNK:N	2.53	0.41
1:3A:85:G:H2'	1:3A:86:A:H8	1.85	0.41
7:5A:281:G:H2'	7:5A:282:G:C8	2.56	0.41
12:AE:345:ASP:HB3	12:AE:375:LEU:HB3	2.02	0.41
12:AE:748:LEU:O	12:AE:752:ALA:CB	2.69	0.41
12:AE:1128:UNK:O	12:AE:1133:UNK:N	2.54	0.41
13:AF:240:UNK:CB	13:AF:253:UNK:O	2.68	0.41
15:B1:560:PRO:HB2	31:R1:320:GLU:HG2	2.02	0.41
17:BB:142:ASP:OD1	17:BB:142:ASP:N	2.54	0.41
19:BD:435:PHE:HZ	19:BD:441:GLY:H	1.68	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:BE:544:ALA:HB3	20:BE:562:LEU:HD23	2.03	0.41
21:CA:94:GLY:CA	21:CA:121:ARG:HH12	2.34	0.41
22:CB:629:THR:HB	22:CB:667:CYS:HB2	2.01	0.41
23:E1:113:TYR:HE1	23:E1:123:GLU:HG3	1.86	0.41
23:E2:177:LYS:HB3	23:E2:221:VAL:HG12	2.02	0.41
31:R1:192:THR:N	31:R1:248:GLN:HE22	2.18	0.41
33:S1:178:UNK:N	33:S1:187:UNK:O	2.53	0.41
33:S1:282:UNK:N	33:S1:291:UNK:O	2.53	0.41
36:SF:72:VAL:HG12	36:SF:90:ILE:HG12	2.02	0.41
39:SI:9:LEU:HD22	39:SI:17:GLU:HB3	2.02	0.41
39:SI:129:LEU:HD11	39:SI:173:TYR:HB2	2.02	0.41
45:SP:84:ARG:HB2	45:SP:118:VAL:HG23	2.03	0.41
47:SX:86:ILE:HD11	47:SX:117:ARG:NH1	2.36	0.41
54:U1:34:UNK:HA	54:U1:49:UNK:HA	2.02	0.41
3:3D:176:GLN:O	3:3D:180:LEU:HB3	2.20	0.41
4:3E:163:ILE:HG23	4:3E:276:LEU:HD22	2.03	0.41
5:3F:156:ASN:HA	5:3F:544:ALA:HB1	2.03	0.41
7:5A:191:U:H2'	7:5A:192:G:C8	2.56	0.41
12:AE:1167:UNK:O	12:AE:1171:UNK:CB	2.69	0.41
16:BA:329:VAL:HB	16:BA:342:GLN:HE21	1.85	0.41
16:BA:825:GLN:HA	16:BA:828:ILE:HD12	2.02	0.41
20:BE:503:ARG:NH1	20:BE:522:LEU:O	2.54	0.41
20:BE:592:ASP:HB3	20:BE:634:PHE:HD1	1.86	0.41
22:CB:855:LEU:HD13	22:CB:889:TYR:HD2	1.86	0.41
22:CB:1233:ASN:HD22	22:CB:1234:PHE:H	1.69	0.41
23:E1:36:LYS:HB3	23:E1:172:PRO:HA	2.02	0.41
31:R1:305:LYS:HA	31:R1:358:GLY:HA2	2.02	0.41
33:S1:364:UNK:O	33:S1:373:UNK:N	2.54	0.41
34:SA:1202:A:H1'	34:SA:1207:C:H42	1.85	0.41
36:SF:112:HIS:NE2	36:SF:237:SER:O	2.54	0.41
40:SJ:103:GLN:HG3	40:SJ:164:ARG:HB3	2.02	0.41
43:SN:29:LYS:HG3	43:SN:100:TRP:CD1	2.55	0.41
2:3C:296:GLU:HG3	2:3C:298:ILE:HG12	2.03	0.41
5:3F:334:GLU:HG2	5:3F:351:ILE:HB	2.03	0.41
6:3G:37:ALA:O	6:3G:41:THR:OG1	2.26	0.41
7:5A:589:U:H2'	7:5A:590:G:C8	2.56	0.41
13:AF:141:UNK:O	13:AF:150:UNK:N	2.54	0.41
18:BC:281:THR:HG23	18:BC:327:ILE:HD13	2.02	0.41
18:BC:588:LYS:HG2	18:BC:589:GLN:HE21	1.85	0.41
20:BE:566:SER:HA	20:BE:581:LEU:O	2.21	0.41
21:CA:191:PHE:O	21:CA:195:GLU:HB2	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:E3:207:PRO:C	24:E3:208:GLU:CG	2.93	0.41
31:R1:312:ARG:HH21	31:R1:347:ASN:HD21	1.69	0.41
34:SA:348:U:H5''	42:SM:106:ASN:HB2	2.02	0.41
34:SA:505:A:H2'	34:SA:507:U:H5'	2.02	0.41
34:SA:1173:C:O2'	34:SA:1601:G:N2	2.51	0.41
34:SA:1759:C:H2'	34:SA:1760:G:C8	2.56	0.41
38:SH:188:ARG:NH1	38:SH:191:ARG:CG	2.80	0.41
40:SJ:90:LEU:HD22	40:SJ:95:THR:HG21	2.02	0.41
46:SR:13:LYS:HG3	46:SR:14:LYS:H	1.85	0.41
48:SY:51:GLY:HA2	48:SY:77:ILE:HG13	2.03	0.41
48:SY:73:ARG:CZ	48:SY:82:LYS:HZ2	2.33	0.41
1:3A:9:A:H2'	1:3A:10:C:C6	2.56	0.41
1:3A:113:G:H1'	1:3A:257:A:N6	2.35	0.41
3:3D:218:LYS:HZ1	3:3D:240:LEU:HD22	1.85	0.41
4:3E:174:ASP:O	4:3E:178:ASN:HB2	2.21	0.41
4:3E:314:ALA:HA	4:3E:317:ILE:HD12	2.02	0.41
5:3F:364:GLU:HG2	5:3F:366:GLN:H	1.85	0.41
12:AE:767:GLN:HA	12:AE:770:LYS:HB3	2.03	0.41
12:AE:1477:UNK:O	12:AE:1481:UNK:CB	2.69	0.41
12:AE:1663:UNK:O	12:AE:1667:UNK:CB	2.69	0.41
13:AF:407:UNK:O	13:AF:411:UNK:CB	2.69	0.41
14:AG:243:UNK:O	14:AG:251:UNK:N	2.53	0.41
14:AG:305:UNK:HA	14:AG:312:UNK:HA	2.02	0.41
15:B1:57:PRO:HD3	15:B1:101:ALA:HB3	2.02	0.41
15:B1:978:ARG:HG2	15:B1:980:LEU:H	1.85	0.41
16:BA:139:HIS:NE2	16:BA:176:ASP:OD1	2.50	0.41
16:BA:162:LEU:HD23	16:BA:199:PHE:HB2	2.02	0.41
16:BA:795:ASN:HA	16:BA:798:TRP:HD1	1.85	0.41
17:BB:37:GLY:HA3	17:BB:38:PRO:HD3	1.90	0.41
17:BB:214:ASP:HB2	17:BB:258:LYS:HD3	2.01	0.41
17:BB:833:LEU:HD13	17:BB:836:ILE:HD13	2.03	0.41
18:BC:70:THR:OG1	18:BC:72:ASP:OD1	2.35	0.41
18:BC:256:ARG:NH1	18:BC:299:ASN:OD1	2.50	0.41
19:BD:273:ARG:HB2	19:BD:284:LEU:HD11	2.03	0.41
19:BD:543:LEU:HD23	19:BD:556:PRO:HG3	2.03	0.41
20:BE:462:PHE:O	20:BE:480:SER:N	2.54	0.41
21:CA:133:SER:O	21:CA:137:CYS:HB3	2.21	0.41
22:CB:168:ILE:HD12	22:CB:171:ASN:H	1.86	0.41
22:CB:384:SER:HB3	22:CB:588:GLN:HE22	1.85	0.41
22:CB:748:LEU:HA	22:CB:787:GLU:OE2	2.21	0.41
23:E2:104:ILE:HG23	23:E2:110:LEU:HD22	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SA:107:C:H2'	34:SA:108:A:H8	1.85	0.41
34:SA:253:A:H2'	34:SA:254:A:C8	2.56	0.41
34:SA:453:U:OP2	34:SA:455:C:N4	2.54	0.41
34:SA:576:G:O3'	48:SY:63:GLN:NE2	2.54	0.41
34:SA:877:G:H2'	34:SA:878:G:H8	1.86	0.41
34:SA:1049:U:H2'	34:SA:1050:G:H8	1.86	0.41
34:SA:1152:A:H2'	34:SA:1153:G:C8	2.56	0.41
35:SC:161:ILE:HG22	35:SC:165:ARG:NH1	2.35	0.41
37:SG:26:ALA:HB2	46:SR:26:LYS:NZ	2.36	0.41
37:SG:130:ILE:H	37:SG:130:ILE:HG13	1.71	0.41
42:SM:55:ASP:OD2	42:SM:113:PRO:HD2	2.20	0.41
44:SO:124:ARG:HG2	44:SO:127:ARG:HH21	1.86	0.41
45:SP:31:THR:HG22	45:SP:38:THR:HA	2.03	0.41
49:SZ:55:VAL:HG22	49:SZ:75:VAL:HG23	2.02	0.41
57:U4:70:ASN:HA	57:U4:73:ASN:HD22	1.84	0.41
1:3A:252:C:H2'	1:3A:253:G:C4	2.56	0.41
4:3E:62:SER:HA	4:3E:67:LYS:HB3	2.03	0.41
4:3E:288:THR:O	4:3E:292:GLY:HA2	2.21	0.41
7:5A:542:U:OP1	7:5A:545:G:O2'	2.33	0.41
12:AE:769:LEU:HB2	12:AE:773:GLN:HE22	1.85	0.41
16:BA:722:THR:O	16:BA:726:THR:OG1	2.29	0.41
17:BB:640:LYS:HE2	17:BB:652:LYS:HD2	2.02	0.41
18:BC:135:TYR:CD2	18:BC:137:THR:HG22	2.55	0.41
20:BE:797:ASP:OD1	20:BE:797:ASP:N	2.53	0.41
28:MB:150:THR:HG21	28:MB:170:VAL:HG21	2.03	0.41
33:S1:159:UNK:O	33:S1:168:UNK:N	2.54	0.41
34:SA:1042:G:H2'	34:SA:1043:A:H8	1.86	0.41
34:SA:1045:C:H2'	34:SA:1046:G:H8	1.86	0.41
35:SC:91:VAL:HB	35:SC:96:LEU:HD13	2.03	0.41
40:SJ:39:GLY:O	40:SJ:59:ARG:HB3	2.21	0.41
46:SR:21:HIS:CE1	46:SR:68:ARG:NH1	2.89	0.41
56:U3:395:UNK:HA	56:U3:440:UNK:HA	2.03	0.41
1:3A:66:U:H2'	1:3A:67:G:C8	2.55	0.40
3:3D:44:PHE:CE2	3:3D:46:LYS:HB3	2.56	0.40
7:5A:244:U:H2'	7:5A:245:C:C6	2.56	0.40
10:AC:470:UNK:O	10:AC:474:UNK:CB	2.68	0.40
12:AE:756:LEU:O	12:AE:760:PHE:CB	2.65	0.40
15:B1:216:TRP:O	15:B1:220:HIS:ND1	2.44	0.40
18:BC:150:LEU:HD12	18:BC:159:LYS:HG2	2.02	0.40
18:BC:264:ASP:OD1	18:BC:264:ASP:N	2.47	0.40
19:BD:403:VAL:HG12	20:BE:605:LEU:HG	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:424:ILE:O	19:BD:432:VAL:HA	2.21	0.40
22:CB:333:ASN:O	22:CB:337:LEU:CB	2.70	0.40
23:E1:129:ARG:HB3	34:SA:1192:C:H5''	2.02	0.40
23:E2:36:LYS:HD2	23:E2:172:PRO:HA	2.02	0.40
23:E2:143:GLN:O	23:E2:147:LYS:HB2	2.20	0.40
24:E3:300:ASN:HB3	24:E3:303:ILE:HG12	2.02	0.40
24:E3:334:GLU:O	24:E3:338:ALA:CB	2.60	0.40
28:MB:112:PRO:HD3	28:MB:184:GLU:HG2	2.03	0.40
32:R2:1638:ARG:NH2	32:R2:1662:GLU:OE1	2.52	0.40
34:SA:289:U:H2'	34:SA:290:G:H8	1.86	0.40
34:SA:1164:G:OP1	37:SG:166:ARG:NH2	2.55	0.40
34:SA:1224:A:H2'	34:SA:1225:U:H6	1.86	0.40
34:SA:1727:G:H2'	34:SA:1728:A:C8	2.55	0.40
49:SZ:54:ALA:O	49:SZ:76:TYR:N	2.43	0.40
2:3B:255:LEU:O	2:3B:259:MET:HB2	2.21	0.40
4:3E:234:ARG:O	4:3E:238:ALA:CB	2.69	0.40
4:3E:299:LEU:HD23	4:3E:341:LEU:HD12	2.03	0.40
5:3F:157:LEU:HA	5:3F:191:SER:HA	2.03	0.40
5:3F:230:ASN:HD21	5:3F:258:ARG:HG3	1.86	0.40
5:3F:323:ASP:OD2	5:3F:342:ARG:HB2	2.21	0.40
7:5A:395:C:OP1	27:MA:119:LYS:NZ	2.44	0.40
9:AB:4:UNK:HA	9:AB:284:UNK:HA	2.04	0.40
12:AE:566:CYS:O	12:AE:570:ALA:CB	2.68	0.40
14:AG:446:UNK:O	14:AG:454:UNK:N	2.55	0.40
16:BA:159:ARG:HA	16:BA:175:VAL:HB	2.03	0.40
17:BB:821:LEU:HB3	17:BB:863:PHE:HE2	1.87	0.40
18:BC:50:ARG:HB2	18:BC:375:ALA:HB2	2.03	0.40
18:BC:239:VAL:HB	22:CB:636:GLU:HG3	2.03	0.40
19:BD:411:TYR:CE1	19:BD:423:LEU:O	2.74	0.40
22:CB:495:THR:HA	22:CB:498:MET:HE3	2.03	0.40
22:CB:738:TYR:O	22:CB:742:PHE:HB3	2.22	0.40
33:S1:157:UNK:N	33:S1:170:UNK:O	2.54	0.40
34:SA:1228:G:H21	43:SN:66:VAL:HG22	1.86	0.40
54:U1:14:UNK:HA	54:U1:30:UNK:HA	2.02	0.40
17:BB:405:LEU:HD22	17:BB:459:LEU:HD21	2.03	0.40
18:BC:474:SER:H	18:BC:478:GLN:NE2	2.20	0.40
19:BD:288:LEU:HD22	19:BD:324:TRP:CD1	2.56	0.40
19:BD:424:ILE:HD13	19:BD:433:TRP:CD1	2.56	0.40
20:BE:192:ASN:O	20:BE:196:GLY:N	2.54	0.40
20:BE:440:ALA:HB3	20:BE:455:PHE:HB2	2.03	0.40
22:CB:267:ILE:HG21	22:CB:295:LEU:HG	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:SA:116:U:H2'	34:SA:117:U:C6	2.57	0.40
34:SA:190:C:H1'	34:SA:191:C:H5'	2.03	0.40
34:SA:200:A:H2'	34:SA:201:G:C8	2.56	0.40
34:SA:976:G:H2'	34:SA:977:A:C8	2.56	0.40
39:SI:50:ASP:HA	39:SI:56:LYS:HA	2.02	0.40
41:SK:171:ARG:HH21	41:SK:175:ARG:NH2	2.19	0.40
53:Sg:107:LYS:HZ3	53:Sg:117:LEU:HD11	1.86	0.40
7:5A:525:U:H2'	7:5A:526:U:C6	2.57	0.40
14:AG:239:UNK:HA	14:AG:260:UNK:HA	2.04	0.40
17:BB:496:THR:OG1	17:BB:520:LEU:O	2.31	0.40
18:BC:222:LEU:HB2	18:BC:235:LYS:H	1.86	0.40
19:BD:363:LEU:H	19:BD:418:LYS:HZ1	1.70	0.40
19:BD:412:GLN:NE2	19:BD:459:GLN:OE1	2.46	0.40
22:CB:227:LYS:O	22:CB:231:TYR:HB2	2.20	0.40
22:CB:853:ARG:HH21	22:CB:889:TYR:HE1	1.69	0.40
24:E3:258:VAL:O	24:E3:262:ALA:HB3	2.21	0.40
24:E3:300:ASN:HD22	24:E3:301:TYR:H	1.70	0.40
24:E3:318:PHE:HE2	24:E3:351:HIS:HB3	1.86	0.40
24:E3:398:ARG:HB3	24:E3:443:THR:HA	2.03	0.40
26:K1:166:VAL:HA	26:K1:171:VAL:HA	2.04	0.40
34:SA:96:G:N1	34:SA:403:G:OP1	2.55	0.40
34:SA:356:G:H2'	34:SA:357:G:C8	2.55	0.40
34:SA:922:G:H2'	34:SA:923:A:C8	2.56	0.40
34:SA:936:G:OP1	34:SA:1074:G:N2	2.45	0.40
48:SY:95:PHE:O	48:SY:142:LYS:NZ	2.48	0.40
51:Sd:29:ARG:HB2	51:Sd:41:VAL:HG22	2.03	0.40
3:3D:233:SER:HA	3:3D:234:LEU:HA	1.92	0.40
6:3G:84:ARG:HG3	6:3G:96:PRO:HB3	2.03	0.40
7:5A:291:G:H2'	7:5A:292:A:H8	1.86	0.40
12:AE:180:ILE:HD12	12:AE:223:PHE:HZ	1.86	0.40
15:B1:53:VAL:HG13	15:B1:118:LEU:HD22	2.02	0.40
19:BD:321:MET:HG3	19:BD:342:PHE:HD2	1.86	0.40
19:BD:411:TYR:CG	19:BD:412:GLN:N	2.90	0.40
21:CA:169:VAL:HG23	21:CA:173:LYS:HZ1	1.86	0.40
34:SA:921:U:H2'	34:SA:922:G:C8	2.57	0.40
36:SF:182:TYR:CZ	36:SF:190:GLY:HA2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	3B	237/327 (72%)	227 (96%)	10 (4%)	0	100	100
2	3C	237/327 (72%)	216 (91%)	21 (9%)	0	100	100
3	3D	366/504 (73%)	343 (94%)	23 (6%)	0	100	100
4	3E	378/511 (74%)	358 (95%)	20 (5%)	0	100	100
5	3F	353/573 (62%)	334 (95%)	19 (5%)	0	100	100
6	3G	120/126 (95%)	114 (95%)	6 (5%)	0	100	100
6	3H	120/126 (95%)	118 (98%)	2 (2%)	0	100	100
12	AE	751/1769 (42%)	703 (94%)	48 (6%)	0	100	100
15	B1	528/1183 (45%)	481 (91%)	47 (9%)	0	100	100
16	BA	747/923 (81%)	669 (90%)	76 (10%)	2 (0%)	36	72
17	BB	770/943 (82%)	682 (89%)	86 (11%)	2 (0%)	36	72
18	BC	779/817 (95%)	678 (87%)	96 (12%)	5 (1%)	21	59
19	BD	317/594 (53%)	278 (88%)	39 (12%)	0	100	100
20	BE	741/939 (79%)	699 (94%)	42 (6%)	0	100	100
21	CA	190/297 (64%)	180 (95%)	10 (5%)	0	100	100
22	CB	1086/1237 (88%)	1059 (98%)	27 (2%)	0	100	100
23	E1	213/252 (84%)	209 (98%)	4 (2%)	0	100	100
23	E2	210/252 (83%)	204 (97%)	6 (3%)	0	100	100
24	E3	256/483 (53%)	242 (94%)	12 (5%)	2 (1%)	16	54
26	K1	173/316 (55%)	167 (96%)	6 (4%)	0	100	100
27	MA	131/183 (72%)	128 (98%)	3 (2%)	0	100	100
28	MB	182/290 (63%)	168 (92%)	14 (8%)	0	100	100
29	MC	24/593 (4%)	24 (100%)	0	0	100	100
30	P1	171/274 (62%)	161 (94%)	10 (6%)	0	100	100
31	R1	353/367 (96%)	348 (99%)	5 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	R2	266/1729 (15%)	262 (98%)	4 (2%)	0	100	100
35	SC	212/255 (83%)	170 (80%)	37 (18%)	5 (2%)	4	27
36	SF	235/261 (90%)	210 (89%)	24 (10%)	1 (0%)	30	67
37	SG	204/225 (91%)	181 (89%)	21 (10%)	2 (1%)	12	49
38	SH	170/236 (72%)	159 (94%)	11 (6%)	0	100	100
39	SI	161/190 (85%)	142 (88%)	18 (11%)	1 (1%)	21	59
40	SJ	166/200 (83%)	146 (88%)	19 (11%)	1 (1%)	21	59
41	SK	173/197 (88%)	157 (91%)	15 (9%)	1 (1%)	21	59
42	SM	139/156 (89%)	124 (89%)	13 (9%)	2 (1%)	9	40
43	SN	122/143 (85%)	83 (68%)	35 (29%)	4 (3%)	3	21
44	SO	132/151 (87%)	129 (98%)	3 (2%)	0	100	100
45	SP	107/137 (78%)	95 (89%)	12 (11%)	0	100	100
46	SR	123/143 (86%)	113 (92%)	8 (6%)	2 (2%)	7	38
47	SX	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
48	SY	101/145 (70%)	82 (81%)	16 (16%)	3 (3%)	3	23
49	SZ	99/135 (73%)	88 (89%)	11 (11%)	0	100	100
50	Sc	77/82 (94%)	67 (87%)	10 (13%)	0	100	100
51	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
52	Sf	28/63 (44%)	28 (100%)	0	0	100	100
53	Sg	49/152 (32%)	37 (76%)	12 (24%)	0	100	100
57	U4	124/189 (66%)	115 (93%)	8 (6%)	1 (1%)	16	54
58	U5	246/274 (90%)	229 (93%)	17 (7%)	0	100	100
All	All	12555/19466 (64%)	11579 (92%)	942 (8%)	34 (0%)	37	72

All (34) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	BC	298	SER
24	E3	306	ALA
35	SC	207	LEU
35	SC	209	ASN
37	SG	50	GLU
37	SG	51	VAL
43	SN	130	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	SR	59	LYS
17	BB	798	ASN
18	BC	137	THR
24	E3	206	LEU
35	SC	181	LEU
35	SC	206	PRO
36	SF	195	ILE
42	SM	4	GLU
43	SN	131	ASP
48	SY	97	ASP
16	BA	130	ASP
18	BC	297	LEU
42	SM	3	THR
43	SN	90	LYS
16	BA	556	ARG
17	BB	797	VAL
18	BC	90	LEU
18	BC	772	LEU
40	SJ	23	LYS
43	SN	126	TRP
48	SY	70	LYS
35	SC	210	ILE
39	SI	131	PHE
41	SK	134	ILE
46	SR	33	GLY
48	SY	96	VAL
57	U4	175	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	3B	202/240 (84%)	202 (100%)	0	100	100
2	3C	202/240 (84%)	202 (100%)	0	100	100
3	3D	317/435 (73%)	317 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3E	314/433 (72%)	314 (100%)	0	100	100
5	3F	317/503 (63%)	317 (100%)	0	100	100
6	3G	101/104 (97%)	101 (100%)	0	100	100
6	3H	101/104 (97%)	101 (100%)	0	100	100
12	AE	698/744 (94%)	695 (100%)	3 (0%)	84	84
15	B1	471/1039 (45%)	471 (100%)	0	100	100
16	BA	663/812 (82%)	661 (100%)	2 (0%)	86	86
17	BB	687/832 (83%)	685 (100%)	2 (0%)	86	86
18	BC	687/719 (96%)	685 (100%)	2 (0%)	86	86
19	BD	281/529 (53%)	281 (100%)	0	100	100
20	BE	657/819 (80%)	657 (100%)	0	100	100
21	CA	178/274 (65%)	178 (100%)	0	100	100
22	CB	1000/1125 (89%)	1000 (100%)	0	100	100
23	E1	191/222 (86%)	191 (100%)	0	100	100
23	E2	193/222 (87%)	193 (100%)	0	100	100
24	E3	232/424 (55%)	230 (99%)	2 (1%)	70	79
26	K1	158/289 (55%)	157 (99%)	1 (1%)	78	83
27	MA	123/172 (72%)	123 (100%)	0	100	100
28	MB	164/258 (64%)	164 (100%)	0	100	100
29	MC	24/148 (16%)	24 (100%)	0	100	100
30	P1	151/238 (63%)	151 (100%)	0	100	100
31	R1	302/312 (97%)	302 (100%)	0	100	100
32	R2	235/1544 (15%)	234 (100%)	1 (0%)	84	84
35	SC	191/224 (85%)	191 (100%)	0	100	100
36	SF	203/222 (91%)	203 (100%)	0	100	100
37	SG	173/191 (91%)	173 (100%)	0	100	100
38	SH	141/201 (70%)	139 (99%)	2 (1%)	59	72
39	SI	146/170 (86%)	146 (100%)	0	100	100
40	SJ	138/161 (86%)	138 (100%)	0	100	100
41	SK	149/166 (90%)	148 (99%)	1 (1%)	76	81
42	SM	128/137 (93%)	127 (99%)	1 (1%)	73	80

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	SN	88/119 (74%)	86 (98%)	2 (2%)	44	64
44	SO	117/128 (91%)	117 (100%)	0	100	100
45	SP	66/105 (63%)	66 (100%)	0	100	100
46	SR	105/119 (88%)	105 (100%)	0	100	100
47	SX	110/111 (99%)	110 (100%)	0	100	100
48	SY	85/120 (71%)	85 (100%)	0	100	100
49	SZ	85/113 (75%)	84 (99%)	1 (1%)	63	75
50	Sc	68/71 (96%)	68 (100%)	0	100	100
51	Sd	56/60 (93%)	56 (100%)	0	100	100
52	Sf	27/54 (50%)	27 (100%)	0	100	100
53	Sg	43/135 (32%)	43 (100%)	0	100	100
57	U4	110/169 (65%)	110 (100%)	0	100	100
58	U5	231/256 (90%)	231 (100%)	0	100	100
All	All	11109/15813 (70%)	11089 (100%)	20 (0%)	85	87

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	AE	487	THR
12	AE	559	ASN
12	AE	630	TYR
16	BA	127	VAL
16	BA	530	VAL
17	BB	118	ASN
17	BB	271	PHE
18	BC	178	VAL
18	BC	249	LEU
24	E3	206	LEU
24	E3	208	GLU
26	K1	200	ILE
32	R2	1569	LEU
38	SH	68	LEU
38	SH	188	ARG
41	SK	99	LEU
42	SM	5	LEU
43	SN	61	VAL
43	SN	91	VAL
49	SZ	35	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (218) such sidechains are listed below:

Mol	Chain	Res	Type
2	3B	91	HIS
2	3B	145	ASN
2	3B	226	HIS
2	3C	216	ASN
3	3D	37	GLN
3	3D	67	ASN
3	3D	85	ASN
3	3D	125	GLN
3	3D	134	HIS
3	3D	318	HIS
3	3D	371	ASN
3	3D	391	ASN
4	3E	145	HIS
4	3E	178	ASN
4	3E	256	ASN
4	3E	289	GLN
4	3E	355	ASN
5	3F	155	ASN
5	3F	195	GLN
5	3F	294	GLN
5	3F	555	ASN
5	3F	570	GLN
6	3G	18	GLN
6	3G	105	ASN
6	3H	45	ASN
6	3H	105	ASN
12	AE	7	GLN
12	AE	14	ASN
12	AE	15	ASN
12	AE	29	HIS
12	AE	43	GLN
12	AE	219	ASN
12	AE	227	ASN
12	AE	232	ASN
12	AE	258	HIS
12	AE	615	ASN
12	AE	774	ASN
12	AE	781	ASN
15	B1	91	HIS
15	B1	136	ASN
15	B1	233	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	B1	548	ASN
15	B1	835	HIS
15	B1	893	ASN
15	B1	900	GLN
15	B1	925	ASN
16	BA	17	GLN
16	BA	45	ASN
16	BA	88	ASN
16	BA	92	HIS
16	BA	181	ASN
16	BA	201	HIS
16	BA	296	GLN
16	BA	306	ASN
16	BA	483	GLN
16	BA	538	GLN
16	BA	608	ASN
16	BA	791	HIS
16	BA	837	ASN
17	BB	20	ASN
17	BB	22	ASN
17	BB	118	ASN
17	BB	162	HIS
17	BB	360	ASN
17	BB	390	GLN
17	BB	411	ASN
17	BB	472	HIS
17	BB	608	HIS
17	BB	620	ASN
17	BB	628	HIS
17	BB	629	ASN
17	BB	656	HIS
17	BB	677	HIS
17	BB	770	ASN
17	BB	798	ASN
17	BB	803	GLN
17	BB	847	HIS
17	BB	879	GLN
18	BC	28	ASN
18	BC	54	HIS
18	BC	58	ASN
18	BC	83	GLN
18	BC	184	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
18	BC	322	ASN
18	BC	410	ASN
18	BC	433	HIS
18	BC	478	GLN
18	BC	490	HIS
18	BC	543	GLN
18	BC	576	ASN
18	BC	585	ASN
18	BC	587	GLN
18	BC	589	GLN
18	BC	667	GLN
18	BC	790	GLN
19	BD	282	ASN
19	BD	335	GLN
19	BD	357	ASN
19	BD	367	GLN
19	BD	369	ASN
19	BD	372	HIS
19	BD	440	ASN
20	BE	86	HIS
20	BE	135	ASN
20	BE	171	GLN
20	BE	291	HIS
20	BE	300	GLN
20	BE	470	GLN
20	BE	473	ASN
20	BE	631	ASN
20	BE	649	ASN
20	BE	870	GLN
20	BE	900	ASN
20	BE	903	GLN
20	BE	910	GLN
21	CA	35	HIS
21	CA	46	ASN
22	CB	120	HIS
22	CB	155	ASN
22	CB	253	GLN
22	CB	261	ASN
22	CB	409	ASN
22	CB	441	GLN
22	CB	443	HIS
22	CB	445	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
22	CB	514	ASN
22	CB	560	ASN
22	CB	568	ASN
22	CB	582	GLN
22	CB	588	GLN
22	CB	683	ASN
22	CB	705	HIS
22	CB	904	HIS
22	CB	1029	ASN
22	CB	1073	ASN
22	CB	1078	HIS
22	CB	1082	GLN
22	CB	1154	ASN
22	CB	1159	ASN
22	CB	1233	ASN
23	E1	111	GLN
23	E2	73	HIS
23	E2	115	GLN
24	E3	226	HIS
24	E3	257	HIS
24	E3	269	ASN
24	E3	276	GLN
24	E3	300	ASN
24	E3	302	HIS
24	E3	351	HIS
24	E3	449	HIS
26	K1	167	GLN
27	MA	48	ASN
27	MA	135	HIS
28	MB	145	HIS
28	MB	174	HIS
28	MB	226	ASN
28	MB	236	HIS
30	P1	127	GLN
30	P1	131	ASN
30	P1	142	ASN
30	P1	232	HIS
31	R1	181	HIS
31	R1	248	GLN
31	R1	317	GLN
32	R2	1416	GLN
32	R2	1515	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R2	1522	ASN
32	R2	1616	ASN
32	R2	1661	GLN
32	R2	1693	ASN
35	SC	49	ASN
35	SC	118	GLN
35	SC	149	GLN
35	SC	194	ASN
35	SC	199	ASN
35	SC	208	GLN
37	SG	37	GLN
37	SG	95	ASN
37	SG	100	ASN
37	SG	103	ASN
37	SG	116	HIS
37	SG	131	GLN
37	SG	158	GLN
37	SG	224	ASN
38	SH	13	GLN
38	SH	22	HIS
38	SH	119	GLN
38	SH	185	GLN
39	SI	147	ASN
40	SJ	64	ASN
41	SK	155	HIS
42	SM	18	HIS
43	SN	125	ASN
44	SO	36	GLN
44	SO	49	GLN
44	SO	58	HIS
44	SO	62	GLN
45	SP	80	HIS
46	SR	21	HIS
46	SR	32	ASN
47	SX	15	ASN
47	SX	16	ASN
47	SX	42	GLN
47	SX	92	ASN
48	SY	63	GLN
48	SY	79	ASN
57	U4	57	GLN
57	U4	73	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
58	U5	23	GLN
58	U5	32	ASN
58	U5	41	ASN
58	U5	105	ASN
58	U5	145	HIS
58	U5	205	GLN
58	U5	207	HIS
58	U5	217	GLN
58	U5	248	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	151/333 (45%)	31 (20%)	1 (0%)
34	SA	1091/1812 (60%)	268 (24%)	22 (2%)
7	5A	452/700 (64%)	102 (22%)	4 (0%)
All	All	1694/2845 (59%)	401 (23%)	27 (1%)

All (401) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	9	A
1	3A	14	A
1	3A	15	U
1	3A	22	A
1	3A	24	U
1	3A	55	A
1	3A	58	A
1	3A	61	G
1	3A	64	A
1	3A	65	C
1	3A	79	G
1	3A	106	C
1	3A	109	G
1	3A	111	G
1	3A	114	A
1	3A	207	A
1	3A	254	A
1	3A	255	U
1	3A	256	G
1	3A	261	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	3A	262	G
1	3A	267	A
1	3A	317	A
1	3A	318	U
1	3A	319	G
1	3A	322	A
1	3A	323	G
1	3A	324	U
1	3A	325	C
1	3A	328	A
1	3A	329	C
7	5A	12	G
7	5A	13	U
7	5A	14	U
7	5A	27	G
7	5A	58	U
7	5A	59	U
7	5A	60	G
7	5A	63	G
7	5A	67	G
7	5A	68	U
7	5A	69	U
7	5A	70	A
7	5A	76	U
7	5A	91	U
7	5A	101	G
7	5A	103	G
7	5A	106	A
7	5A	109	C
7	5A	121	G
7	5A	123	C
7	5A	124	A
7	5A	125	G
7	5A	129	U
7	5A	130	G
7	5A	142	U
7	5A	143	A
7	5A	145	A
7	5A	152	U
7	5A	153	U
7	5A	158	G
7	5A	169	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	5A	170	U
7	5A	171	G
7	5A	176	U
7	5A	178	G
7	5A	181	A
7	5A	200	A
7	5A	211	G
7	5A	225	U
7	5A	226	U
7	5A	227	U
7	5A	234	A
7	5A	236	C
7	5A	237	A
7	5A	238	G
7	5A	239	U
7	5A	240	C
7	5A	246	G
7	5A	253	U
7	5A	261	U
7	5A	266	U
7	5A	267	U
7	5A	278	G
7	5A	280	A
7	5A	294	U
7	5A	338	A
7	5A	340	U
7	5A	349	G
7	5A	353	A
7	5A	354	G
7	5A	355	C
7	5A	361	G
7	5A	362	C
7	5A	363	A
7	5A	368	U
7	5A	370	U
7	5A	371	G
7	5A	372	A
7	5A	382	U
7	5A	383	G
7	5A	384	U
7	5A	386	A
7	5A	387	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	5A	388	C
7	5A	391	C
7	5A	392	U
7	5A	393	C
7	5A	394	U
7	5A	395	C
7	5A	401	A
7	5A	402	G
7	5A	403	C
7	5A	404	G
7	5A	405	A
7	5A	419	A
7	5A	433	C
7	5A	434	G
7	5A	435	G
7	5A	436	G
7	5A	441	C
7	5A	442	U
7	5A	451	G
7	5A	452	A
7	5A	459	U
7	5A	464	G
7	5A	503	C
7	5A	508	C
7	5A	511	G
7	5A	514	U
7	5A	527	U
7	5A	528	G
7	5A	534	A
34	SA	8	U
34	SA	10	G
34	SA	25	C
34	SA	26	A
34	SA	27	U
34	SA	34	G
34	SA	39	A
34	SA	47	A
34	SA	50	C
34	SA	93	A
34	SA	94	U
34	SA	95	G
34	SA	103	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	SA	114	C
34	SA	116	U
34	SA	127	G
34	SA	128	U
34	SA	129	U
34	SA	132	U
34	SA	133	U
34	SA	134	U
34	SA	135	A
34	SA	137	U
34	SA	138	A
34	SA	139	C
34	SA	140	A
34	SA	145	A
34	SA	146	U
34	SA	152	U
34	SA	153	G
34	SA	156	A
34	SA	159	U
34	SA	162	A
34	SA	179	A
34	SA	180	A
34	SA	181	A
34	SA	185	U
34	SA	186	C
34	SA	188	A
34	SA	190	C
34	SA	191	C
34	SA	192	U
34	SA	193	U
34	SA	194	U
34	SA	195	G
34	SA	196	G
34	SA	199	G
34	SA	200	A
34	SA	204	G
34	SA	215	A
34	SA	251	A
34	SA	261	U
34	SA	265	A
34	SA	266	A
34	SA	270	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	SA	272	U
34	SA	273	G
34	SA	276	C
34	SA	277	U
34	SA	278	U
34	SA	279	G
34	SA	280	U
34	SA	281	G
34	SA	288	A
34	SA	299	A
34	SA	302	U
34	SA	316	A
34	SA	321	C
34	SA	322	G
34	SA	337	G
34	SA	338	C
34	SA	341	A
34	SA	348	U
34	SA	351	C
34	SA	352	A
34	SA	359	A
34	SA	360	A
34	SA	361	C
34	SA	369	A
34	SA	370	A
34	SA	372	G
34	SA	378	A
34	SA	379	U
34	SA	380	U
34	SA	381	C
34	SA	387	A
34	SA	399	A
34	SA	400	A
34	SA	401	A
34	SA	402	C
34	SA	403	G
34	SA	404	G
34	SA	416	A
34	SA	417	A
34	SA	418	G
34	SA	428	A
34	SA	433	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	SA	440	U
34	SA	444	C
34	SA	452	A
34	SA	459	G
34	SA	466	U
34	SA	467	G
34	SA	468	A
34	SA	470	A
34	SA	475	A
34	SA	477	A
34	SA	484	C
34	SA	485	A
34	SA	486	G
34	SA	487	G
34	SA	488	G
34	SA	493	U
34	SA	494	U
34	SA	501	U
34	SA	503	G
34	SA	504	U
34	SA	506	A
34	SA	507	U
34	SA	508	U
34	SA	510	G
34	SA	511	A
34	SA	515	A
34	SA	522	U
34	SA	525	A
34	SA	526	A
34	SA	527	A
34	SA	528	U
34	SA	532	U
34	SA	538	A
34	SA	539	G
34	SA	540	G
34	SA	542	A
34	SA	543	C
34	SA	545	A
34	SA	546	U
34	SA	548	G
34	SA	558	U
34	SA	559	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	SA	561	G
34	SA	570	A
34	SA	572	C
34	SA	576	G
34	SA	585	A
34	SA	592	A
34	SA	594	A
34	SA	605	A
34	SA	635	A
34	SA	862	A
34	SA	863	A
34	SA	865	A
34	SA	873	U
34	SA	876	G
34	SA	898	A
34	SA	914	G
34	SA	928	U
34	SA	929	A
34	SA	930	A
34	SA	932	U
34	SA	933	A
34	SA	935	U
34	SA	942	G
34	SA	951	A
34	SA	960	U
34	SA	966	A
34	SA	978	A
34	SA	1040	G
34	SA	1053	G
34	SA	1058	U
34	SA	1059	U
34	SA	1060	U
34	SA	1061	A
34	SA	1063	U
34	SA	1072	C
34	SA	1082	C
34	SA	1083	G
34	SA	1084	A
34	SA	1086	A
34	SA	1087	A
34	SA	1150	G
34	SA	1151	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	SA	1155	G
34	SA	1156	C
34	SA	1157	A
34	SA	1158	C
34	SA	1159	C
34	SA	1160	A
34	SA	1164	G
34	SA	1165	G
34	SA	1167	G
34	SA	1193	A
34	SA	1207	C
34	SA	1209	C
34	SA	1212	G
34	SA	1217	A
34	SA	1218	G
34	SA	1227	A
34	SA	1228	G
34	SA	1229	G
34	SA	1238	A
34	SA	1243	G
34	SA	1244	A
34	SA	1245	G
34	SA	1246	C
34	SA	1251	U
34	SA	1256	A
34	SA	1265	G
34	SA	1269	U
34	SA	1270	G
34	SA	1272	U
34	SA	1273	G
34	SA	1275	A
34	SA	1276	U
34	SA	1278	G
34	SA	1282	U
34	SA	1427	A
34	SA	1428	G
34	SA	1431	C
34	SA	1432	U
34	SA	1433	G
34	SA	1435	G
34	SA	1436	A
34	SA	1437	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	SA	1440	C
34	SA	1441	C
34	SA	1442	U
34	SA	1444	A
34	SA	1446	A
34	SA	1448	G
34	SA	1450	U
34	SA	1453	G
34	SA	1461	C
34	SA	1471	A
34	SA	1474	G
34	SA	1475	A
34	SA	1482	C
34	SA	1485	C
34	SA	1487	A
34	SA	1496	U
34	SA	1500	C
34	SA	1506	G
34	SA	1535	U
34	SA	1536	G
34	SA	1537	C
34	SA	1570	A
34	SA	1572	G
34	SA	1574	G
34	SA	1582	U
34	SA	1584	G
34	SA	1599	C
34	SA	1600	A
34	SA	1616	G
34	SA	1617	U
34	SA	1631	A
34	SA	1657	U
34	SA	1658	G
34	SA	1684	U
34	SA	1686	C
34	SA	1716	C
34	SA	1717	G
34	SA	1754	A
34	SA	1756	A
34	SA	1758	U
34	SA	1767	G
34	SA	1796	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	SA	1804	A
34	SA	1806	A
34	SA	1812	U

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3A	78	G
7	5A	382	U
7	5A	385	A
7	5A	526	U
7	5A	527	U
34	SA	25	C
34	SA	139	C
34	SA	158	U
34	SA	192	U
34	SA	278	U
34	SA	351	C
34	SA	417	A
34	SA	467	G
34	SA	487	G
34	SA	503	G
34	SA	591	A
34	SA	913	G
34	SA	929	A
34	SA	1083	G
34	SA	1157	A
34	SA	1216	C
34	SA	1226	A
34	SA	1244	A
34	SA	1250	U
34	SA	1441	C
34	SA	1481	C
34	SA	1573	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

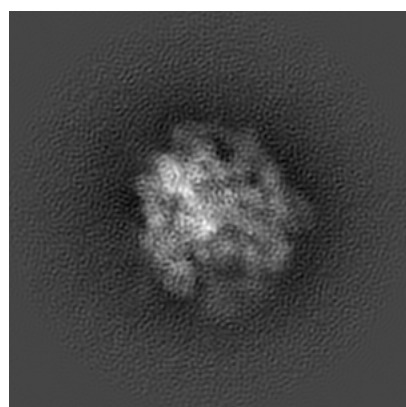
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6695. These allow visual inspection of the internal detail of the map and identification of artifacts.

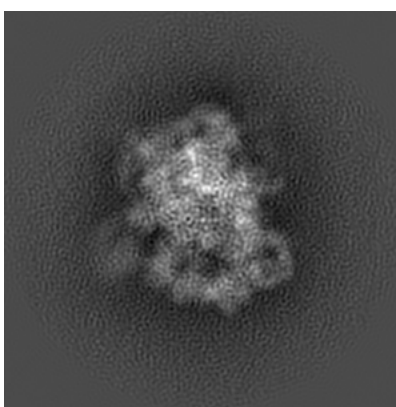
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

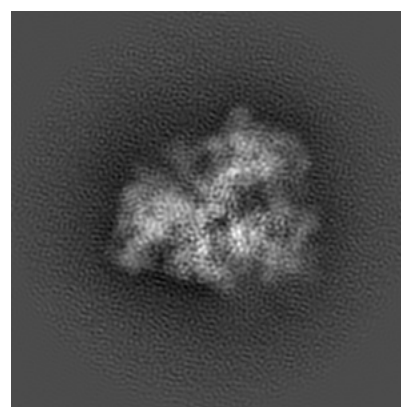
6.1.1 Primary map



X



Y

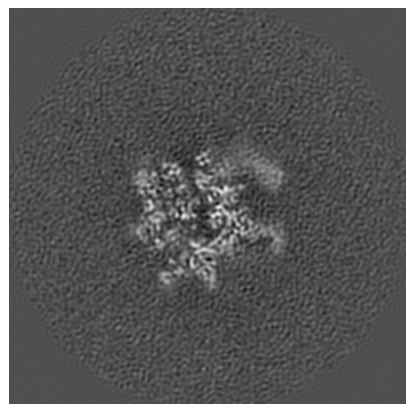


Z

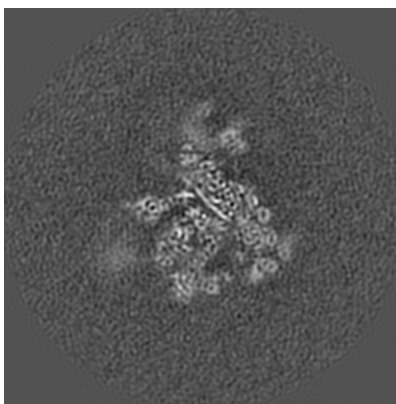
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

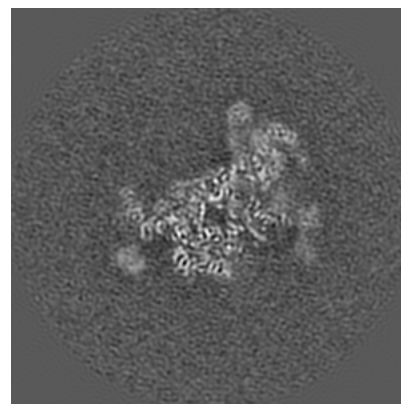
6.2.1 Primary map



X Index: 200



Y Index: 200

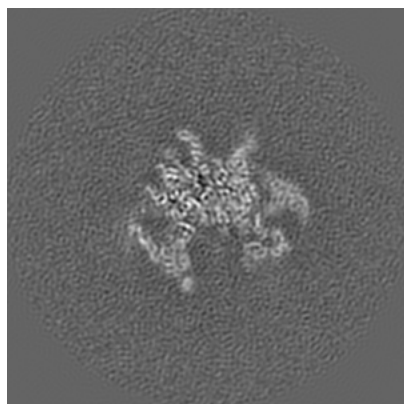


Z Index: 200

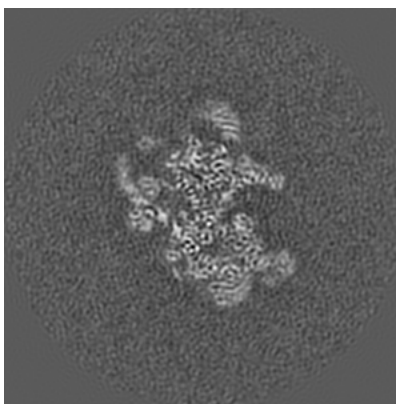
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

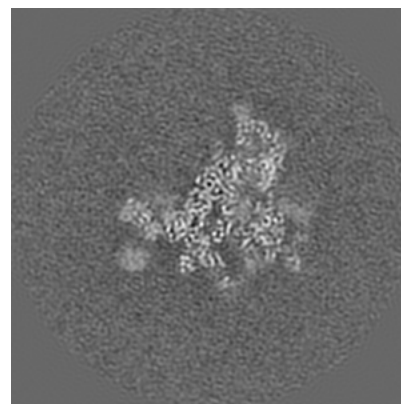
6.3.1 Primary map



X Index: 221



Y Index: 178

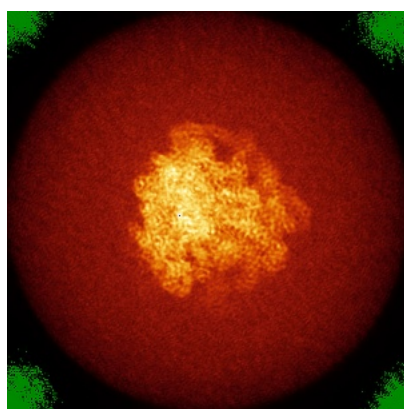


Z Index: 187

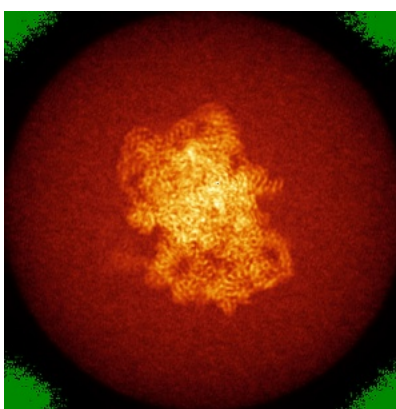
The images above show the largest variance slices of the map in three orthogonal directions.

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

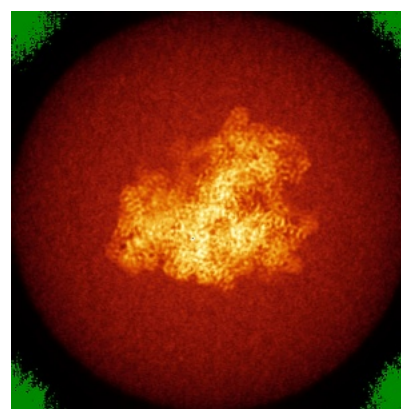
6.4.1 Primary map



X



Y

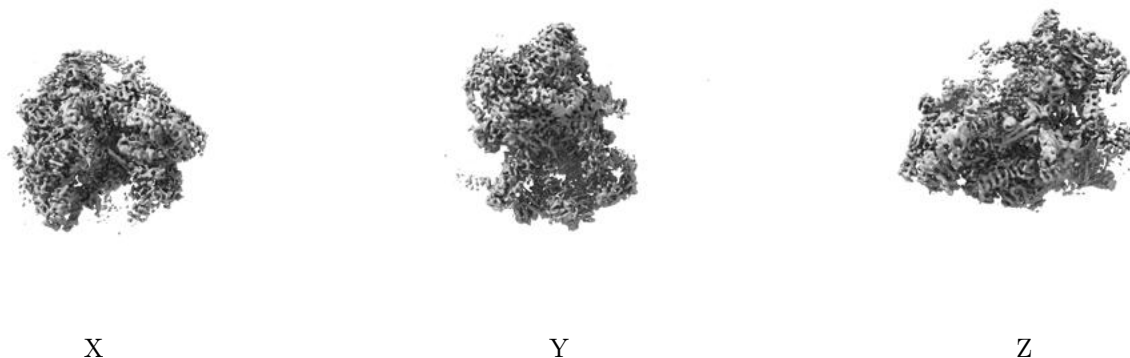


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

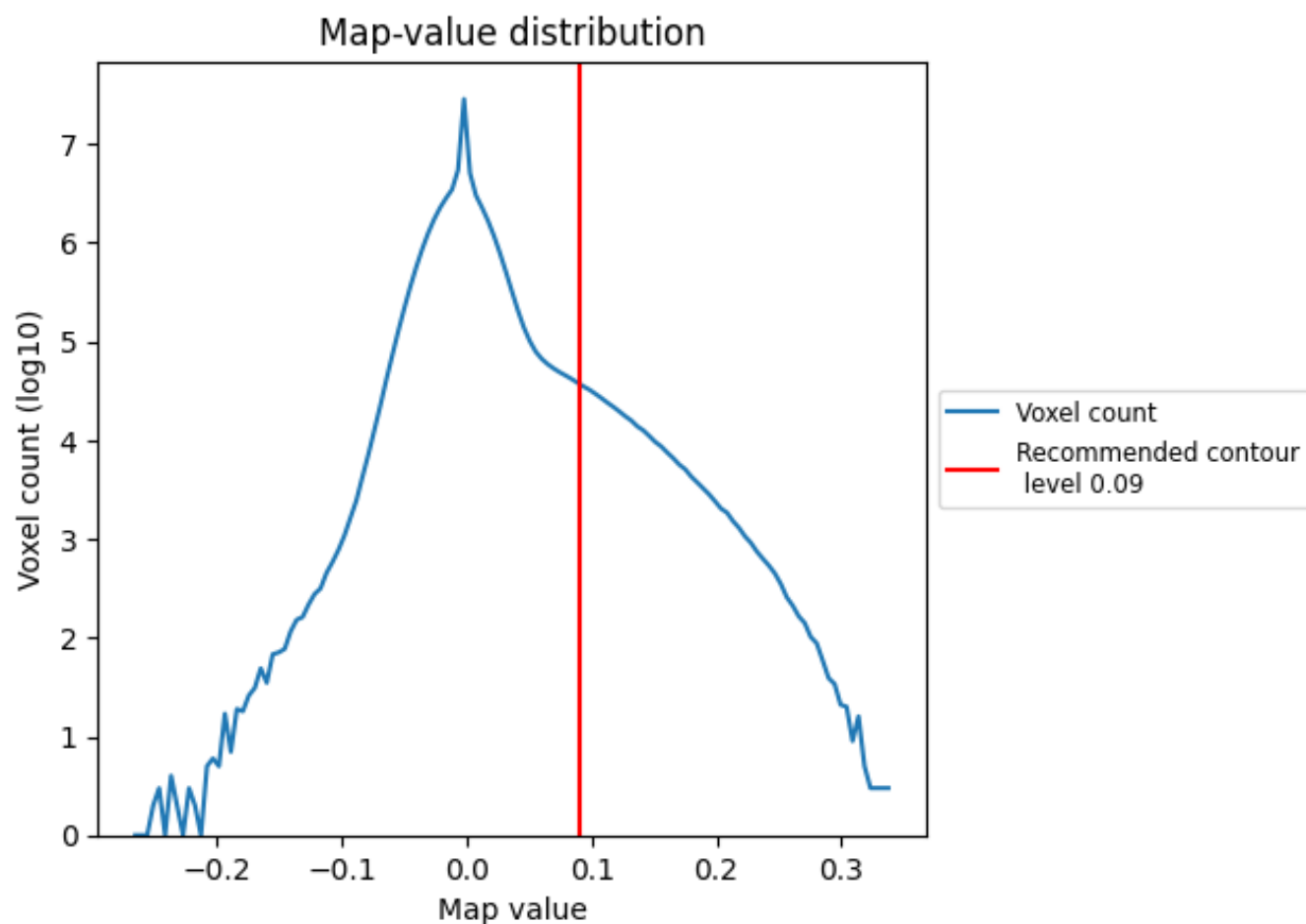
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

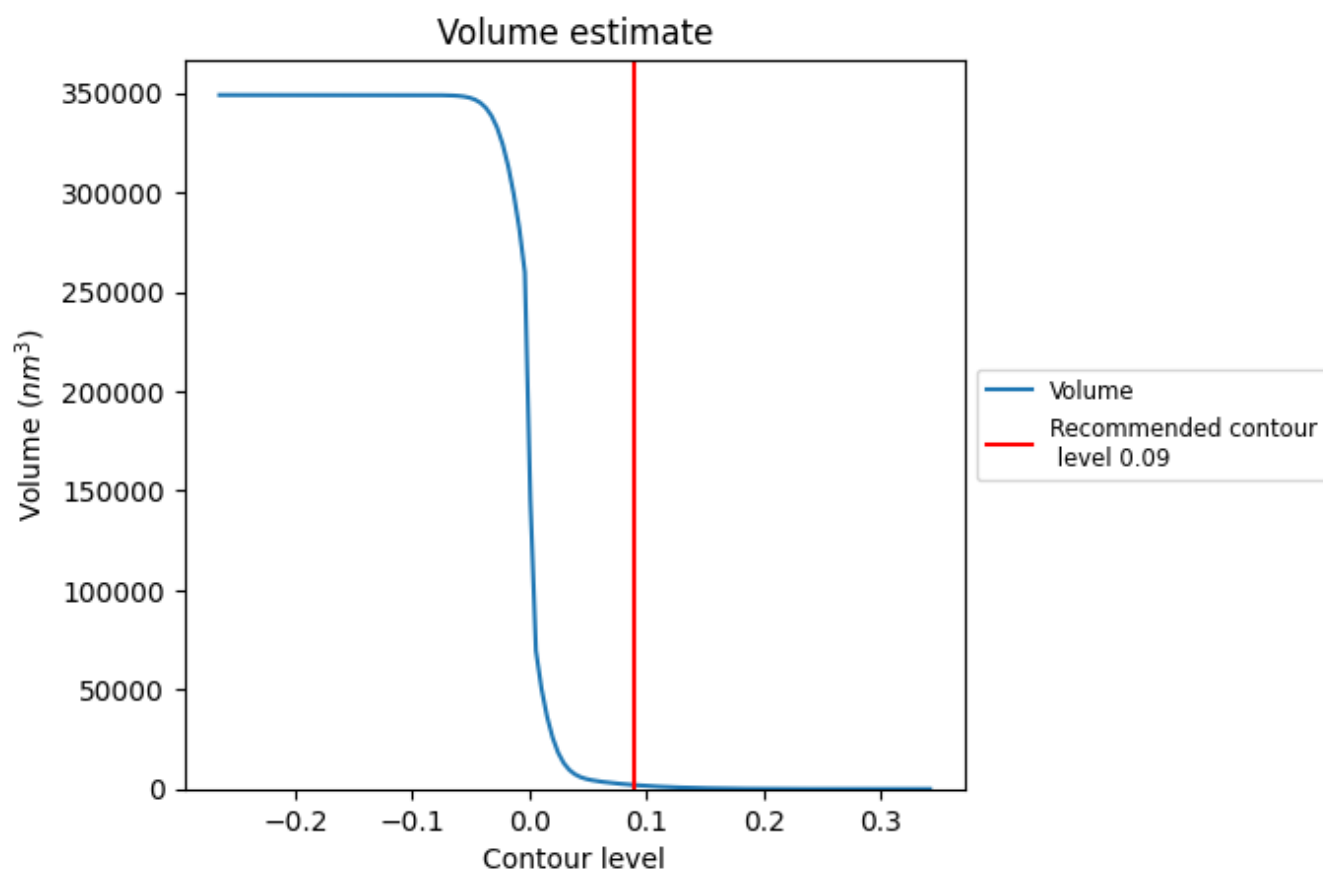
This section contains the results of statistical analysis of the map.

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.

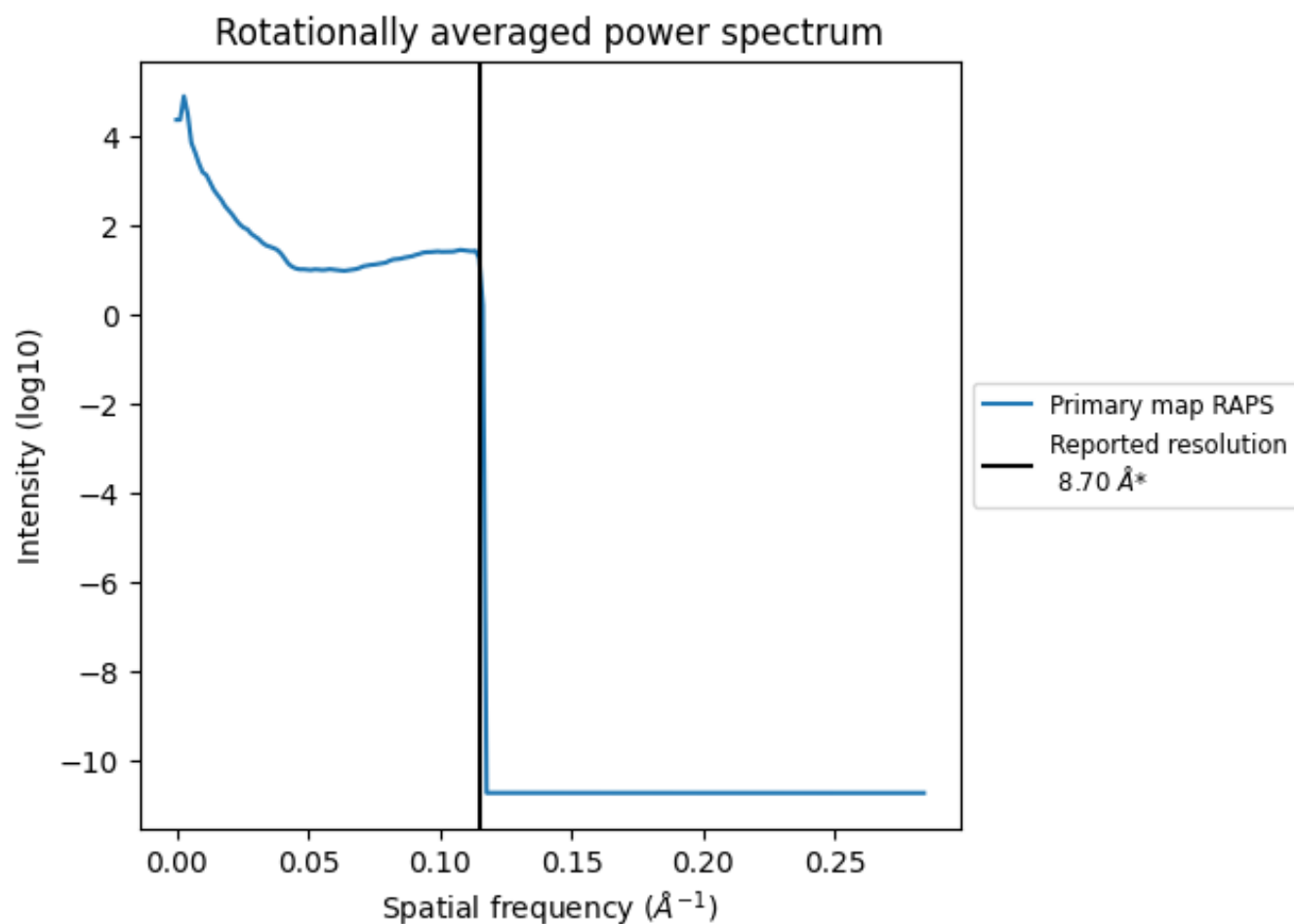
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1973 nm^3 ; this corresponds to an approximate mass of 1782 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

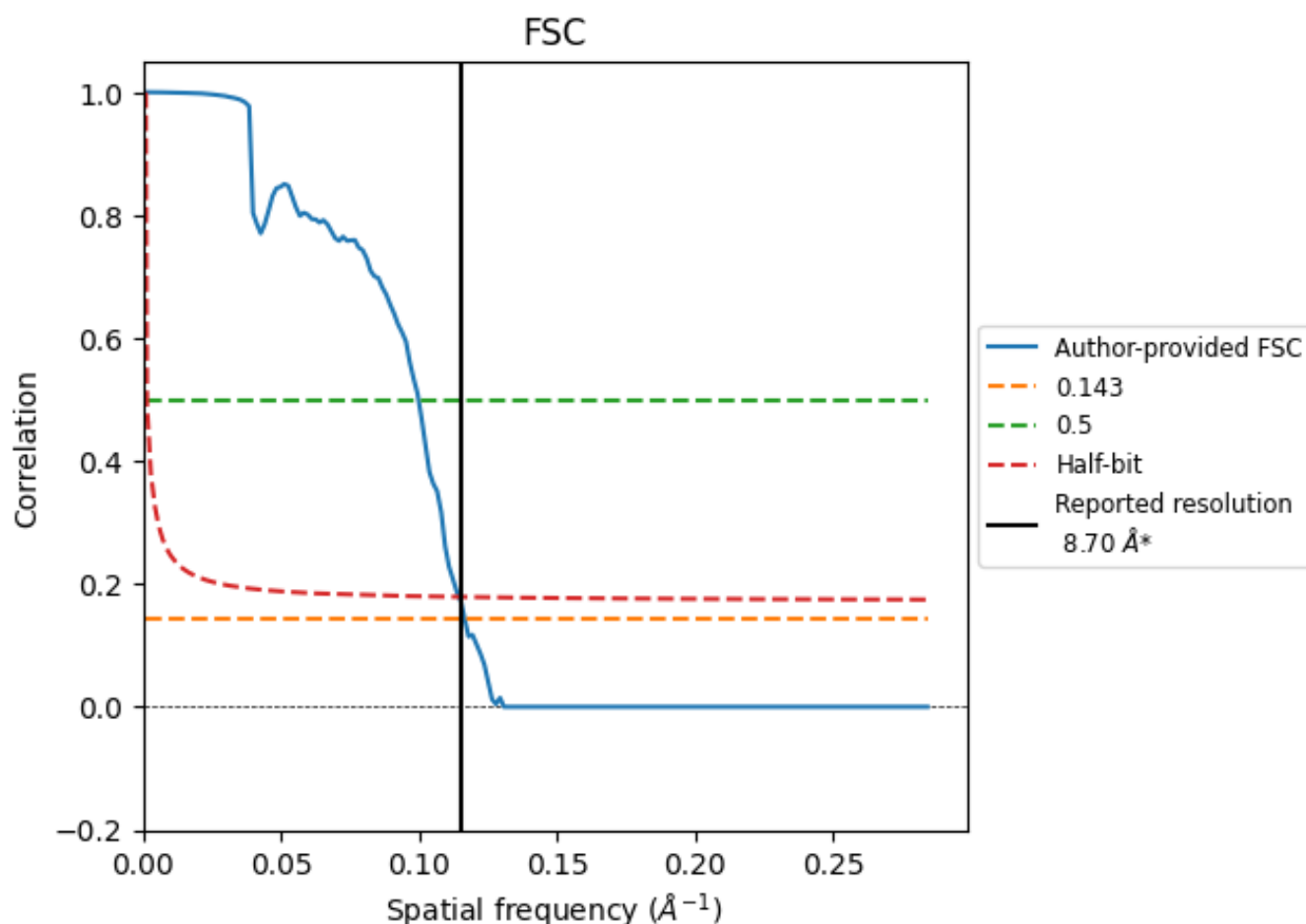


*Reported resolution corresponds to spatial frequency of 0.115 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.115 Å⁻¹

8.2 Resolution estimates [i](#)

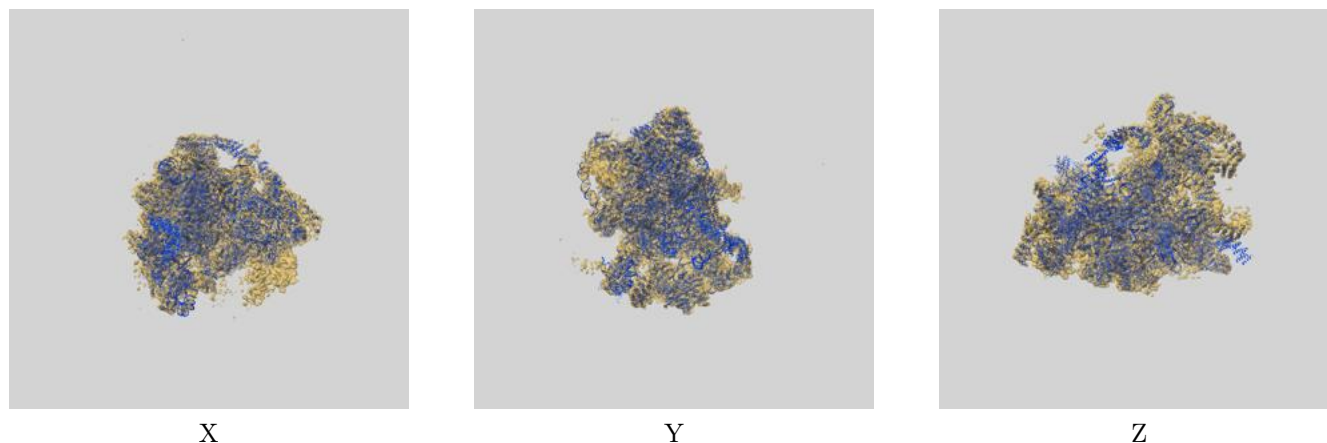
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.70	-	-
Author-provided FSC curve	8.58	10.02	8.74
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

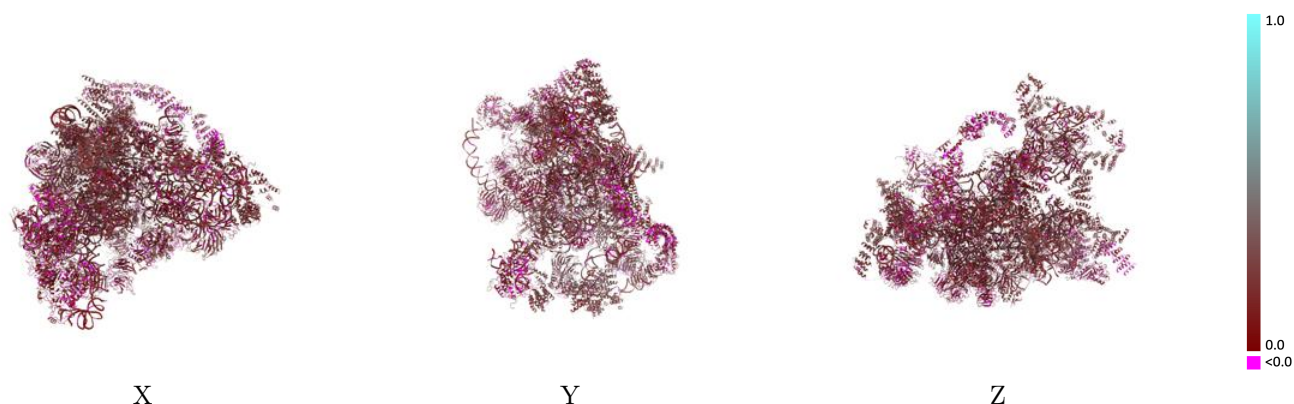
This section contains information regarding the fit between EMDB map EMD-6695 and PDB model 5WYJ. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



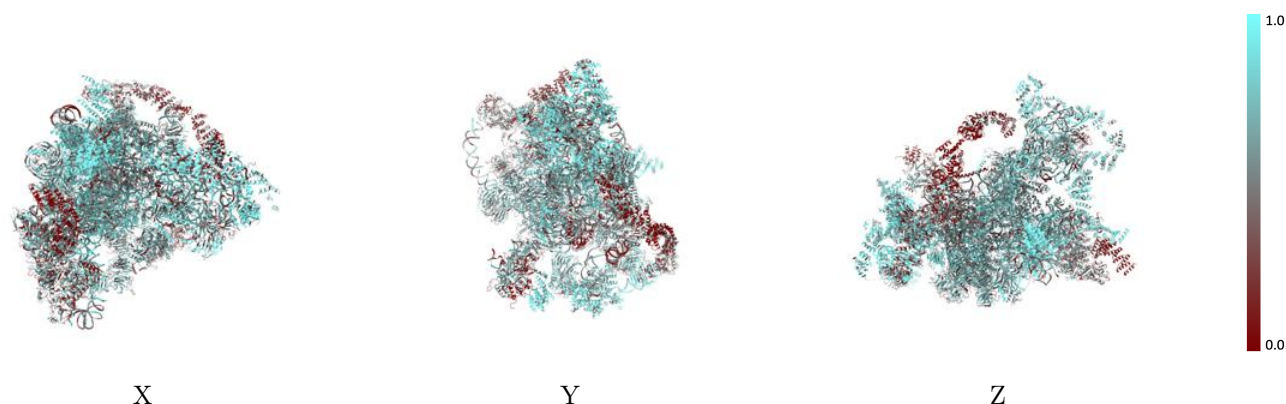
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



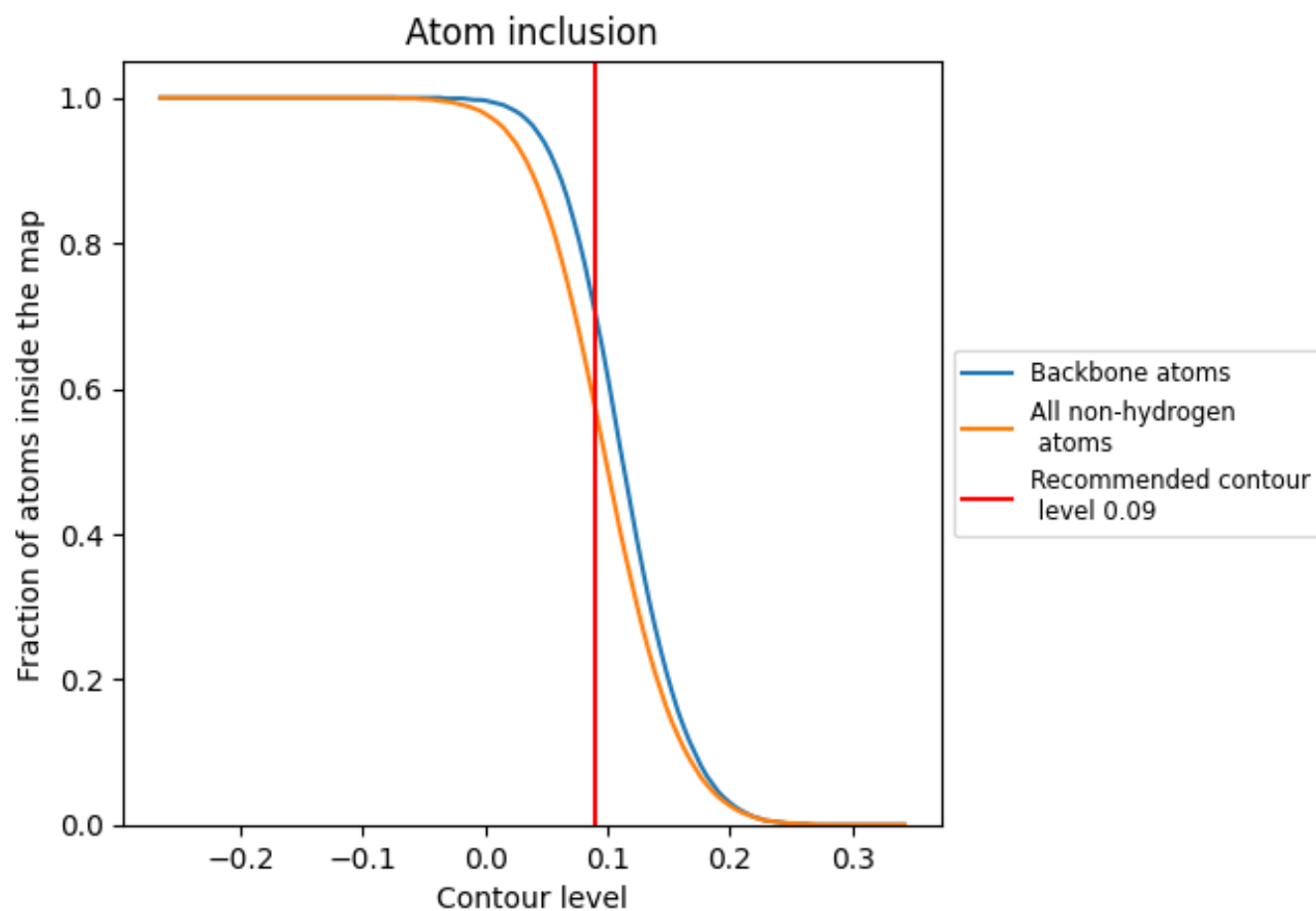
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 57% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5720	 0.1600
3A	 0.7480	 0.1830
3B	 0.5460	 0.1630
3C	 0.3770	 0.1290
3D	 0.5850	 0.1550
3E	 0.5060	 0.1500
3F	 0.5810	 0.1410
3G	 0.5820	 0.1580
3H	 0.5550	 0.1590
5A	 0.4970	 0.1750
AA	 0.7520	 0.2230
AB	 0.6860	 0.1990
AC	 0.5120	 0.1480
AD	 0.7390	 0.2190
AE	 0.3770	 0.1220
AF	 0.8140	 0.2410
AG	 0.6980	 0.2000
B1	 0.5600	 0.1420
BA	 0.5860	 0.1550
BB	 0.5860	 0.1320
BC	 0.4750	 0.1160
BD	 0.5210	 0.1110
BE	 0.5980	 0.1430
CA	 0.3850	 0.1130
CB	 0.4160	 0.1210
E1	 0.4620	 0.1290
E2	 0.4840	 0.1330
E3	 0.4820	 0.1220
E4	 0.6480	 0.2180
K1	 0.4880	 0.1450
MA	 0.6010	 0.1550
MB	 0.5300	 0.1350
MC	 0.7120	 0.2100
P1	 0.5510	 0.1530
R1	 0.5600	 0.1470



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
R2	 0.0520	 0.1040
S1	 0.7820	 0.2440
SA	 0.7160	 0.1710
SC	 0.4730	 0.1580
SF	 0.5000	 0.1300
SG	 0.5640	 0.1610
SH	 0.3790	 0.1150
SI	 0.4750	 0.1500
SJ	 0.4860	 0.1320
SK	 0.5270	 0.1470
SM	 0.4040	 0.1150
SN	 0.0690	 0.0710
SO	 0.5170	 0.1480
SP	 0.5060	 0.1440
SR	 0.5840	 0.1490
SX	 0.5150	 0.1580
SY	 0.5010	 0.1190
SZ	 0.5130	 0.1450
Sc	 0.4320	 0.1560
Sd	 0.5180	 0.1400
Sf	 0.6430	 0.1490
Sg	 0.0180	 0.0120
U1	 0.8200	 0.2560
U2	 0.9070	 0.2620
U3	 0.7750	 0.2360
U4	 0.5400	 0.1660
U5	 0.1590	 0.1000
UA	 0.9190	 0.2650
UB	 0.8290	 0.2540
UC	 0.8200	 0.2700