



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:43 AM UTC

PDB ID : 7D63 / pdb_00007d63
EMDB ID : EMD-30588
Title : Cryo-EM structure of 90S preribosome with inactive Utp24 (state C)
Authors : Du, Y.; Zhang, J.; An, W.; Ye, K.
Deposited on : 2020-09-29
Resolution : 12.30 Å (reported)
Based on initial model : 6LQR

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

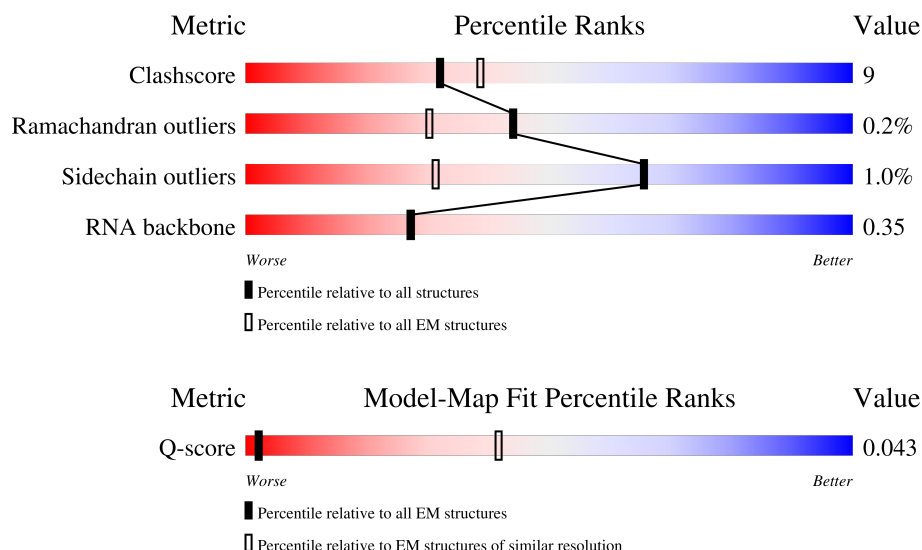
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 12.30 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	82 (11.80 - 12.80)

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	
2	5A	700	
3	SA	1812	

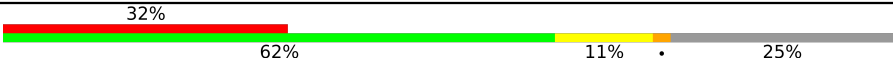
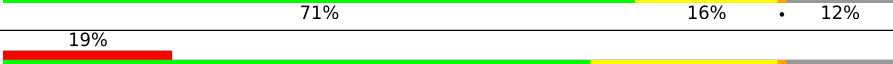
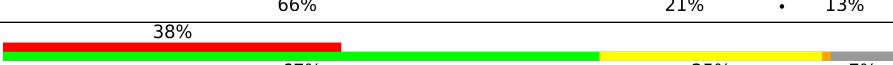
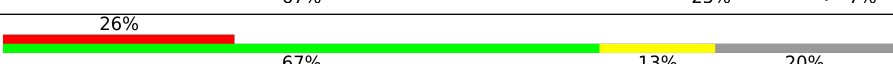
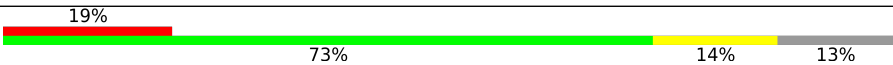
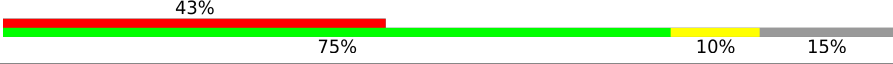
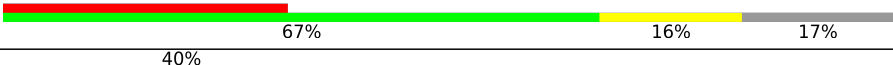
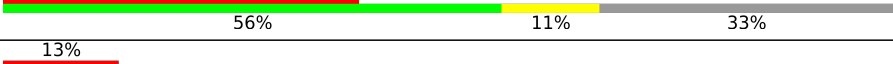
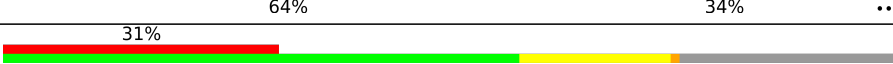
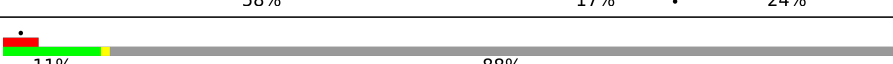
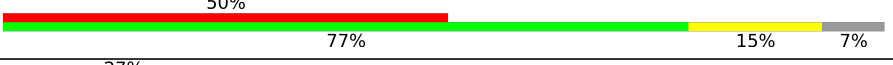
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	
9	SJ	200	
10	SK	197	
11	SM	155	
12	SO	151	
13	SP	137	
14	SR	143	
15	SX	130	
16	SY	145	
17	SZ	135	
18	Sc	82	
19	Sd	67	
20	3B	327	
20	3C	327	
21	3D	504	
22	3E	511	
23	3F	573	
24	3G	126	
24	3H	126	
25	A4	776	
26	A5	643	

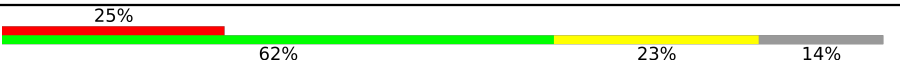
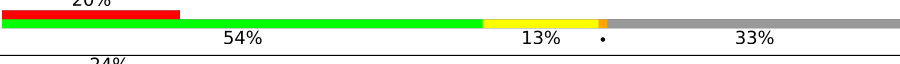
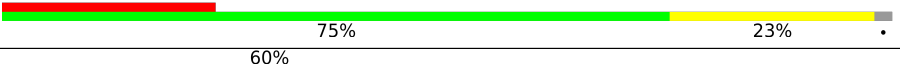
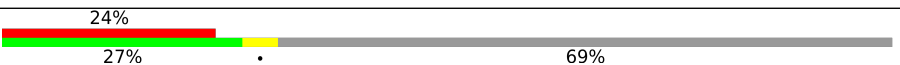
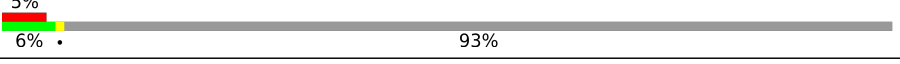
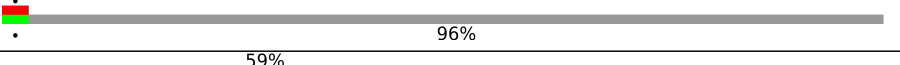
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	A8	713	
28	A9	575	
29	AE	1769	
30	AF	513	
31	AG	896	
32	B1	900	
33	B2	943	
34	B3	817	
35	B8	594	
36	BE	939	
37	B6	440	
38	5B	214	
39	5C	554	
40	5D	250	
41	5E	593	
42	5F	183	
43	5G	290	
44	5H	610	
45	5I	489	
46	5J	217	
47	5K	189	
48	RA	707	
49	RB	357	
50	RE	1237	
51	RF	297	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
52	RG	252	
52	RH	252	
53	RJ	1183	
54	RK	367	
55	RL	1056	
55	RM	1056	
56	RN	810	
57	RO	552	
58	RP	2493	
59	RQ	899	
60	RS	480	
61	RY	534	
62	X1	611	
63	RT	326	
64	ST	146	
65	SU	144	
66	RD	1729	
67	RZ	1267	

2 Entry composition

There are 71 unique types of molecules in this entry. The entry contains 225233 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 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	175	Total	C	N	O	P	0	0
			3711	1661	648	1227	175		

- Molecule 2 is a RNA chain called 5' ETS.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5A	192	Total	C	N	O	P	0	0
			4117	1838	746	1341	192		

- Molecule 3 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1331	Total	C	N	O	P	0	0
			28383	12684	5049	9319	1331		

- Molecule 4 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	230	Total	C	N	O	S	0	0
			1830	1156	335	335	4		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SF	229	Total	C	N	O	S	0	0
			1815	1161	331	320	3		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SG	213	Total	C	N	O	S	0	0
			1669	1045	307	314	3		

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SH	167	Total	C	N	O	S	0	0
			1327	834	256	235	2		

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SI	165	Total	C	N	O	S	0	0
			1321	853	226	242			

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SJ	166	Total	C	N	O	S	0	0
			1324	824	262	236	2		

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SK	171	Total	C	N	O	S	0	0
			1388	879	268	240	1		

- Molecule 11 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SM	123	Total	C	N	O	S	0	0
			997	641	189	164	3		

- Molecule 12 is a protein called 40S ribosomal protein S13.

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

- Molecule 13 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SP	118	Total	C	N	O	S	0	0
			868	536	164	165	3		

- Molecule 14 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S22-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SX	127	Total	C	N	O	S	0	0
			1003	640	183	177	3		

- Molecule 16 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SY	103	Total	C	N	O	S	0	0
			786	503	144	137	2		

- Molecule 17 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	SZ	102	Total	C	N	O	0	0
			809	517	148	144		

- Molecule 18 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Sc	80	Total	C	N	O	S	0	0
			603	377	109	112	5		

- Molecule 19 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 20 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
20	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 21 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	3D	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 22 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

- Molecule 23 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3F	454	Total	C	N	O	S	0	0
			3643	2315	638	680	10		

- Molecule 24 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
24	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 25 is a protein called U3 small nucleolar RNA-associated protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A4	662	Total	C	N	O	S	0	0
			5226	3309	910	986	21		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A5	514	Total	C	N	O	S	0	0
			3976	2520	688	755	13		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A8	532	Total	C	N	O	S	0	0
			3229	2008	592	626	3		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A9	128	Total	C	N	O	S	0	0
			939	594	173	170	2		

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AE	1534	Total	C	N	O	S	0	0
			9955	6242	1771	1923	19		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	493	Total	C	N	O	S	0	0
			3911	2462	702	735	12		

- Molecule 31 is a protein called NET1-associated nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AG	826	Total	C	N	O	S	0	0
			6570	4181	1111	1259	19		

- Molecule 32 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B1	793	Total	C	N	O	S	0	0
			6331	4046	1085	1182	18		

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B2	825	Total	C	N	O	S	0	0
			6502	4156	1096	1223	27		

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B3	757	Total	C	N	O	S	0	0
			5919	3769	993	1130	27		

- Molecule 35 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B8	477	Total	C	N	O	S	0	0
			3764	2387	662	705	10		

- Molecule 36 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BE	820	Total	C	N	O	S	0	0
			6450	4090	1114	1225	21		

- Molecule 37 is a protein called U3 small nucleolar RNA-associated protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B6	374	Total	C	N	O	S	0	0
			2800	1782	501	505	12		

- Molecule 38 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5B	60	Total	C	N	O		0	0
			495	310	101	84			

- Molecule 39 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5C	458	Total	C	N	O	S	0	0
			3612	2276	636	689	11		

- Molecule 40 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5D	167	Total	C	N	O	S	0	0
			1396	862	266	263	5		

- Molecule 41 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5E	193	Total	C	N	O	S	0	0
			1564	970	280	310	4		

- Molecule 42 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 43 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	5G	219	Total	C	N	O	S	0	0
			1756	1107	325	318	6		

- Molecule 44 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	5H	74	Total	C	N	O	S	0	0
			596	373	122	101			

- Molecule 45 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 46 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5J	134	Total	C	N	O	S	0	0
			1131	715	206	207	3		

- Molecule 47 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 48 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	RA	338	Total	C	N	O	S	0	0
			2709	1713	463	524	9		

- Molecule 49 is a protein called U3 small nucleolar ribonucleoprotein protein LCP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	RB	134	Total	C	N	O	S	0	0
			1108	664	227	214	3		

- Molecule 50 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	RE	1079	Total	C	N	O	S	0	0
			8716	5666	1437	1589	24		

- Molecule 51 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RF	241	Total	C	N	O	S	0	0
			1963	1253	335	367	8		

- Molecule 52 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	RG	216	Total	C	N	O	S	0	0
			1701	1079	296	315	11		
52	RH	230	Total	C	N	O	S	0	0
			1799	1142	313	333	11		

- Molecule 53 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RJ	796	Total	C	N	O	S	0	0
			6379	4086	1136	1128	29		

- Molecule 54 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	RK	360	Total	C	N	O	S	0	0
			2781	1781	473	516	11		

- Molecule 55 is a protein called RNA cytidine acetyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	RL	805	Total	C	N	O	S	0	0
			4539	2760	885	887	7		
55	RM	766	Total	C	N	O		0	0
			3779	2247	766	766			

- Molecule 56 is a protein called Nucleolar complex protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	RN	607	Total	C	N	O	S	0	0
			4529	2861	820	837	11		

- Molecule 57 is a protein called Nucleolar complex protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	RO	525	Total	C	N	O	S	0	0
			3766	2412	646	696	12		

- Molecule 58 is a protein called U3 small nucleolar RNA-associated protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	RP	2108	Total	C	N	O	S	0	0
			12171	7483	2291	2381	16		

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	RQ	275	Total	C	N	O	S	0	0
			1853	1139	356	356	2		

- Molecule 60 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RS	251	Total	C	N	O	S	0	0
			2051	1340	349	359	3		

- Molecule 61 is a protein called Protein BFR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	RY	37	Total	C	N	O	0	0
			299	191	48	60		

- Molecule 62 is a protein called Unassigned peptides 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	X1	22	Total	C	N	O	0	0
			110	66	22	22		

- Molecule 63 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	RT	212	Total	C	N	O	S	0	0
			1587	1010	290	283	4		

- Molecule 64 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	ST	110	Total	C	N	O	S	0	0
			896	565	170	159	2		

- Molecule 65 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SU	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 66 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RD	316	Total	C	N	O	S	0	0
			2412	1541	414	452	5		

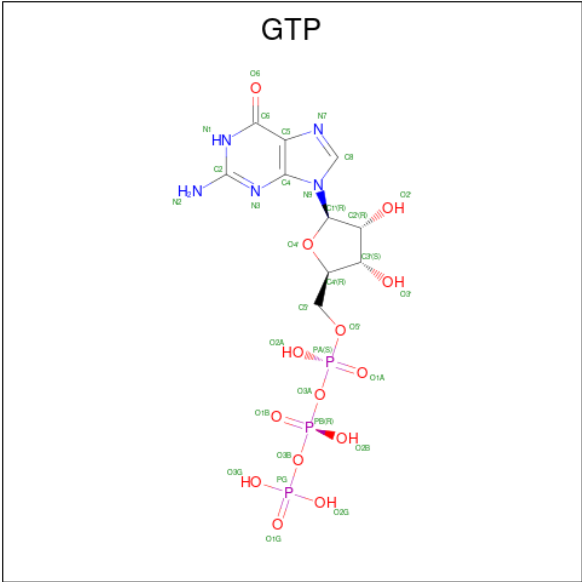
- Molecule 67 is a protein called Probable ATP-dependent RNA helicase DHR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	RZ	839	Total	C	N	O	S	1	0
			6604	4215	1146	1208	35		

- Molecule 68 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
68	Sc	1	Total	Zn	0
			1	1	
68	5K	1	Total	Zn	0
			1	1	

- Molecule 69 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

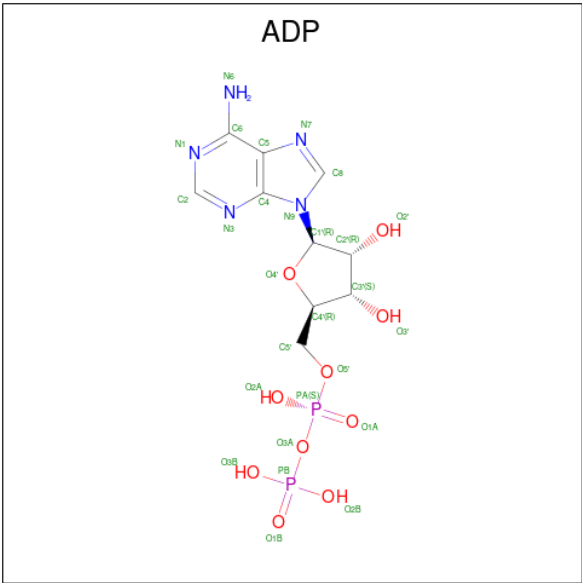


Mol	Chain	Residues	Atoms					AltConf
69	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

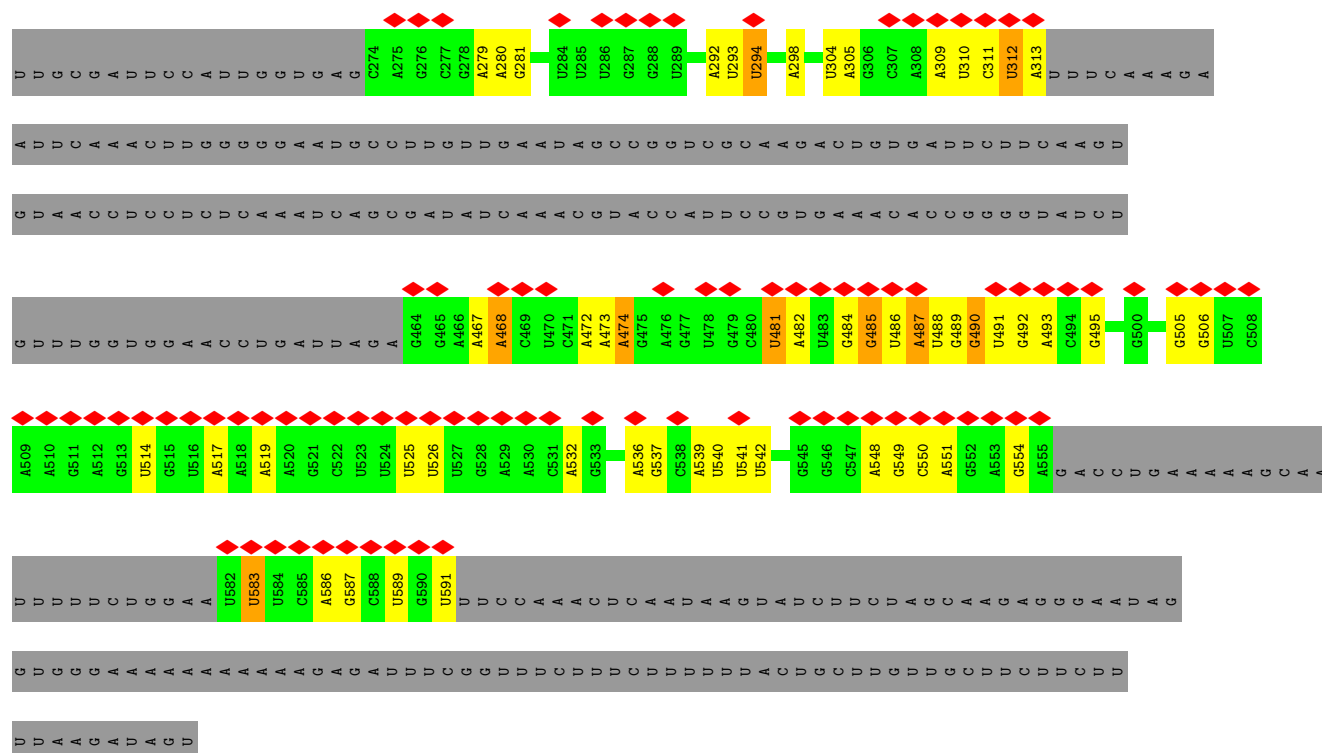
- Molecule 70 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
70	RJ	1	Total	Mg	0
			1	1	

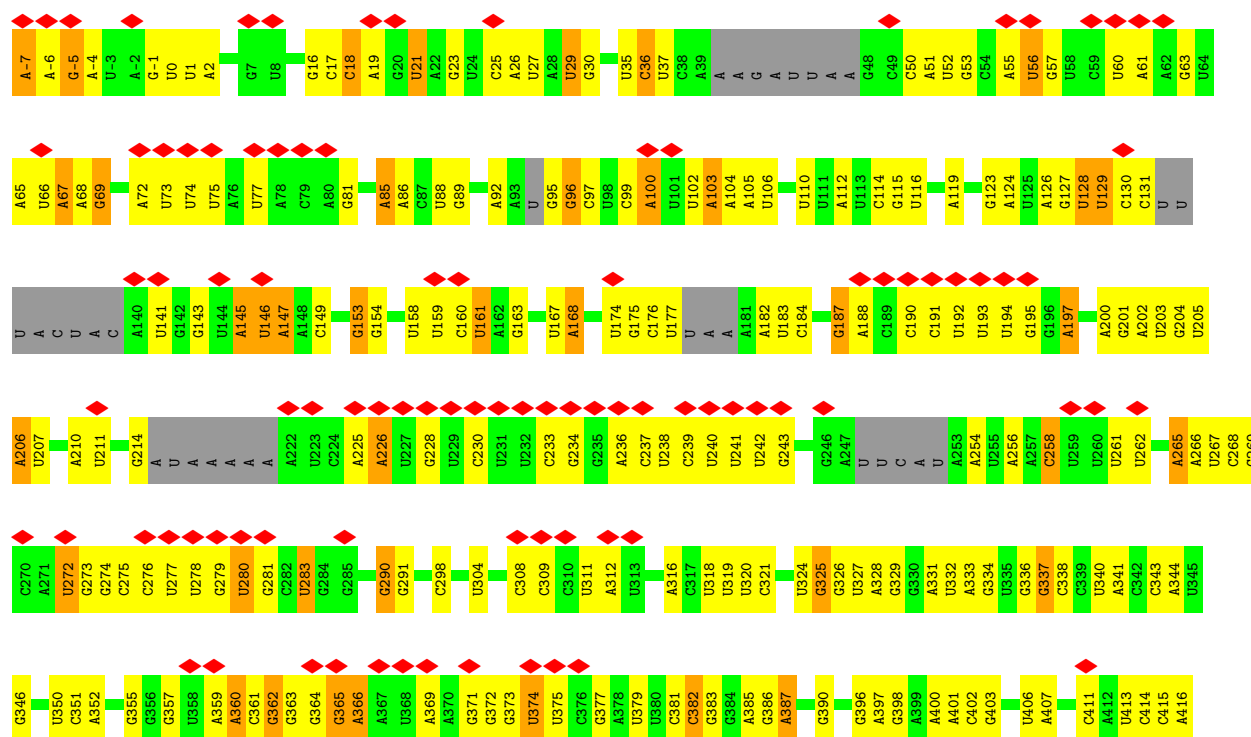
- Molecule 71 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



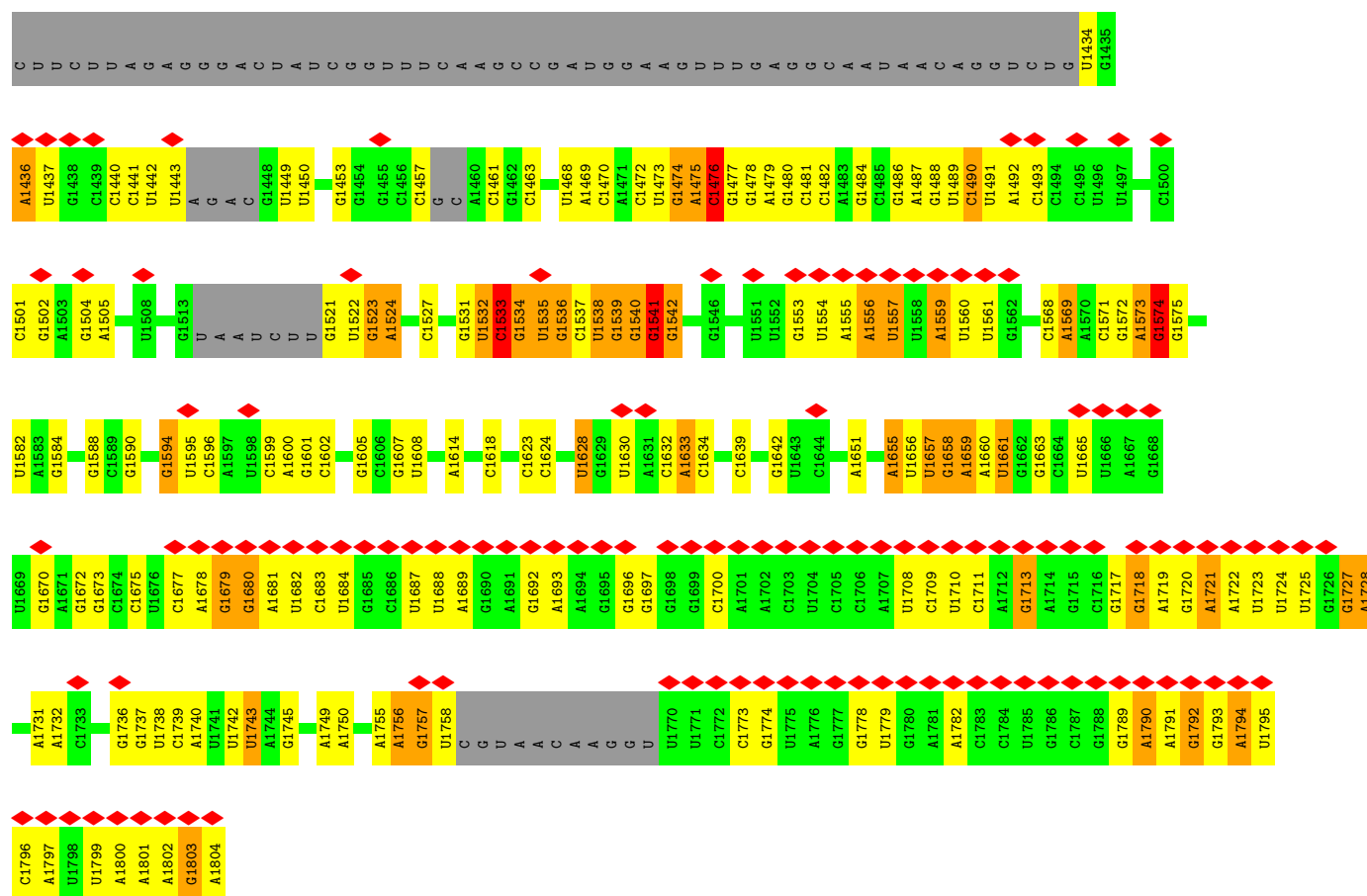
Mol	Chain	Residues	Atoms					AltConf
71	RZ	1	Total	C	N	O	P	0
			27	10	5	10	2	



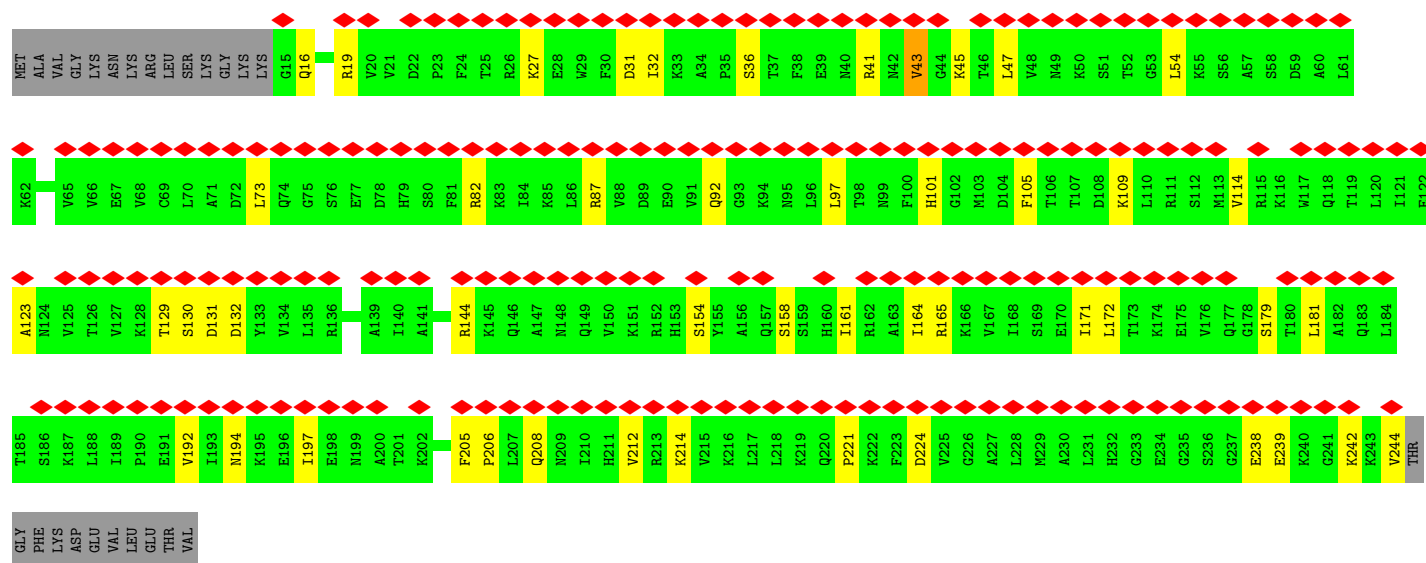
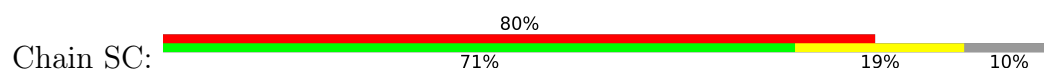
• Molecule 3: 18S rRNA



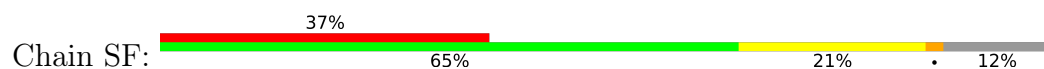


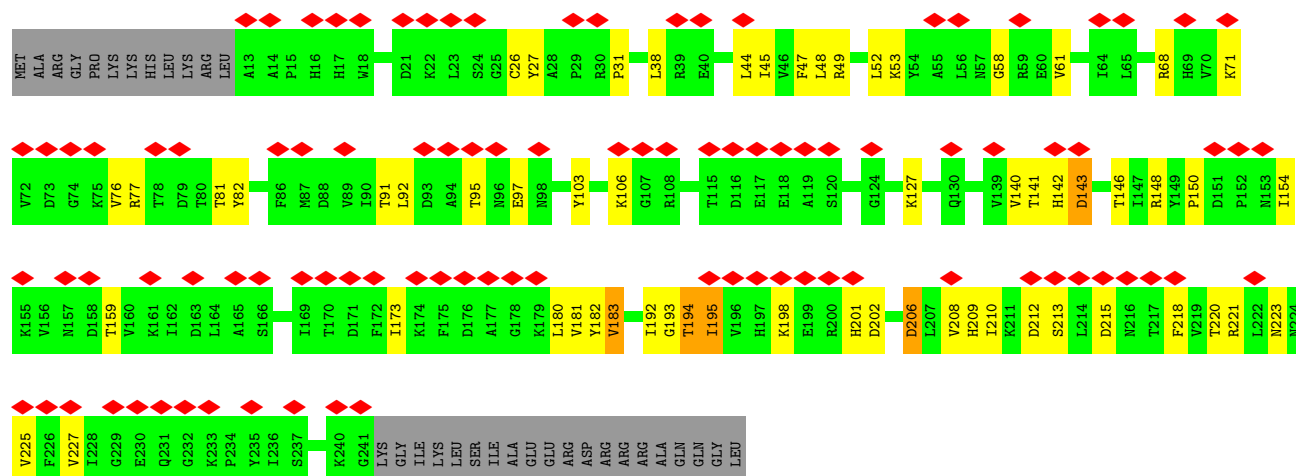


• Molecule 4: 40S ribosomal protein S1-A



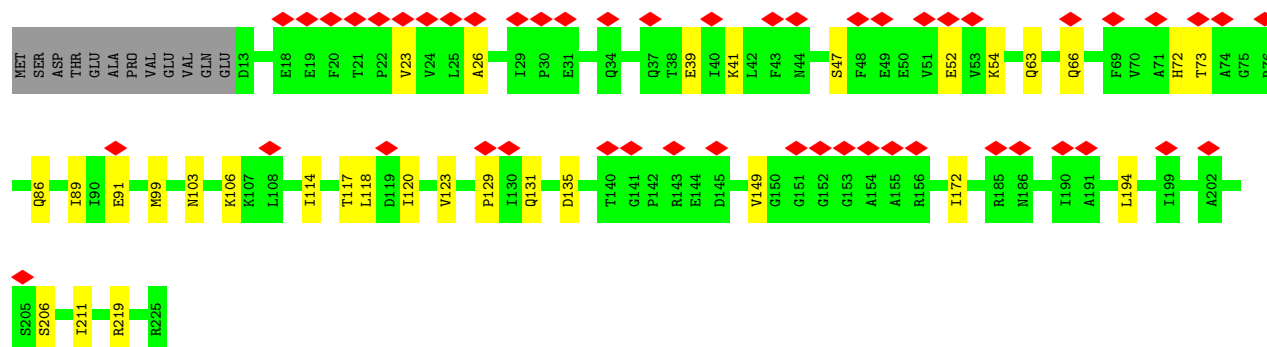
• Molecule 5: 40S ribosomal protein S4-A





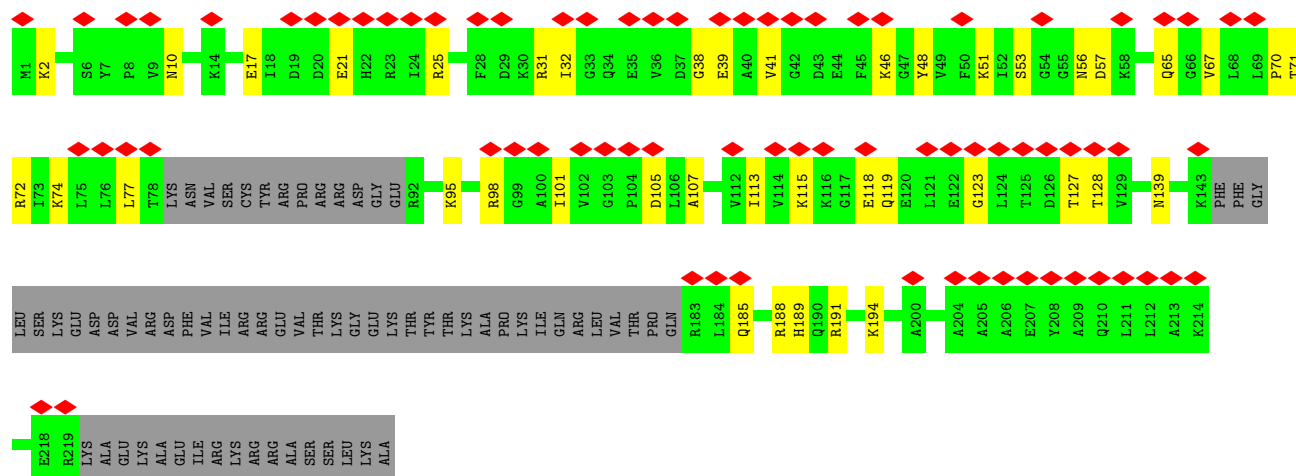
• Molecule 6: 40S ribosomal protein S5

Chain SG: 22% 81% 14% 5%

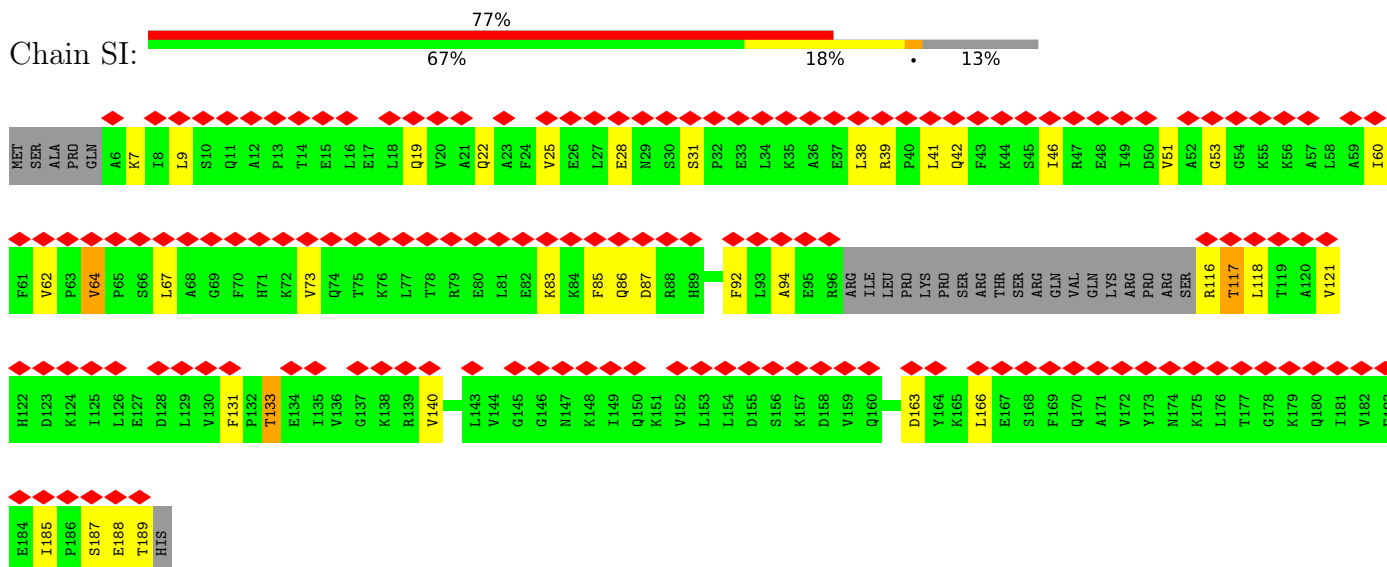


• Molecule 7: 40S ribosomal protein S6-A

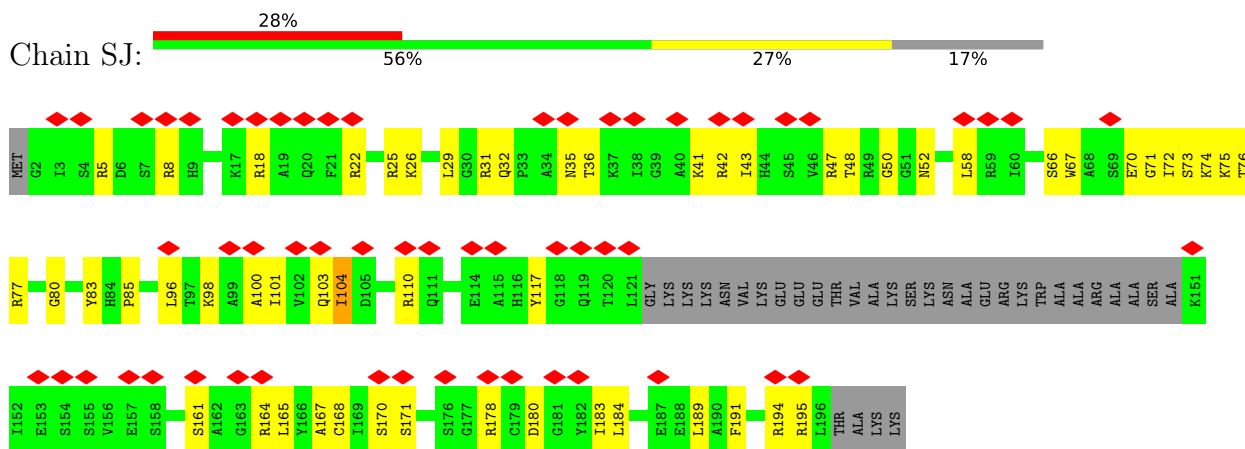
Chain SH: 32% 53% 17% 29%



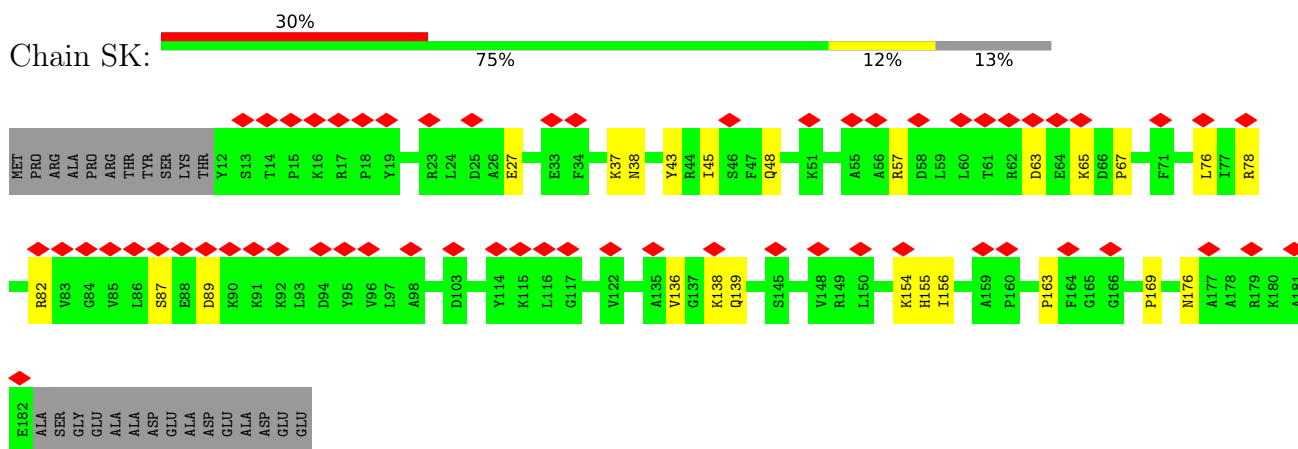
• Molecule 8: 40S ribosomal protein S7-A



- Molecule 9: 40S ribosomal protein S8-A

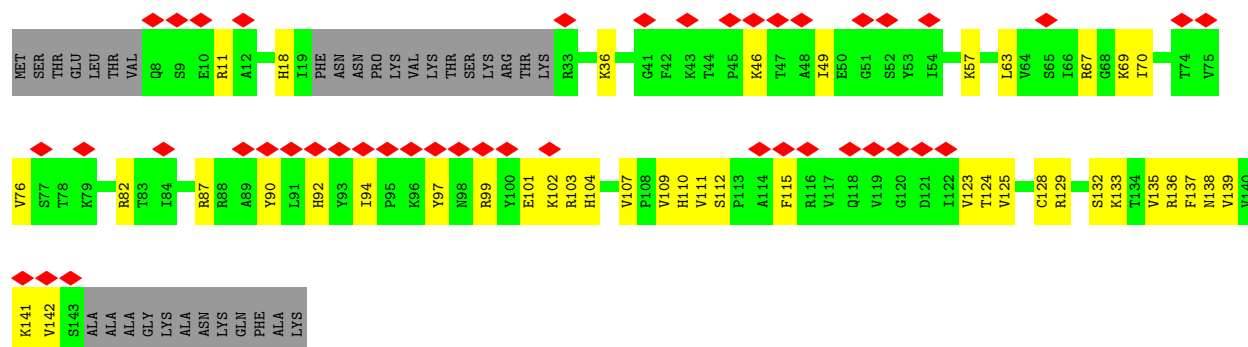


- Molecule 10: 40S ribosomal protein S9-A

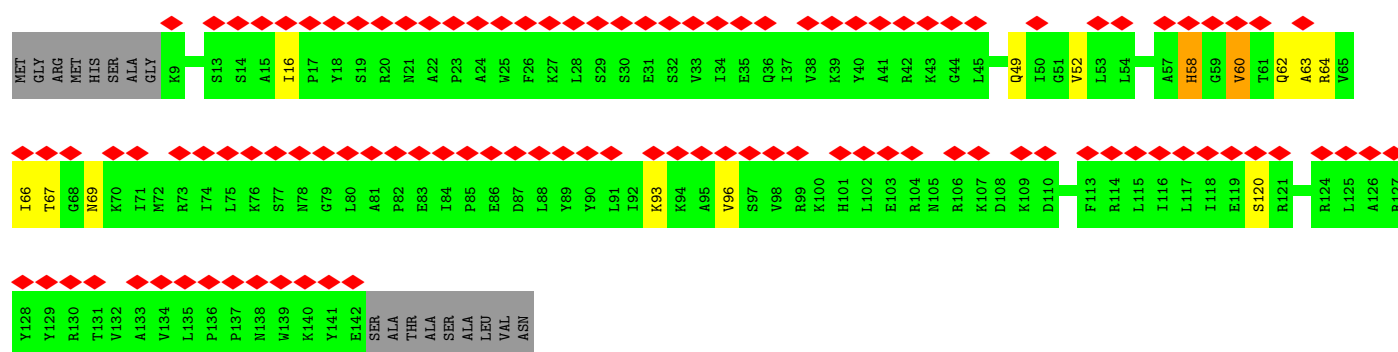
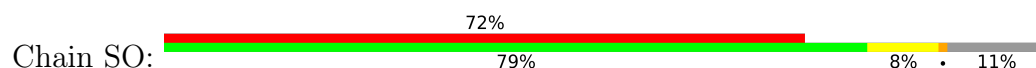


- Molecule 11: 40S ribosomal protein S11-A

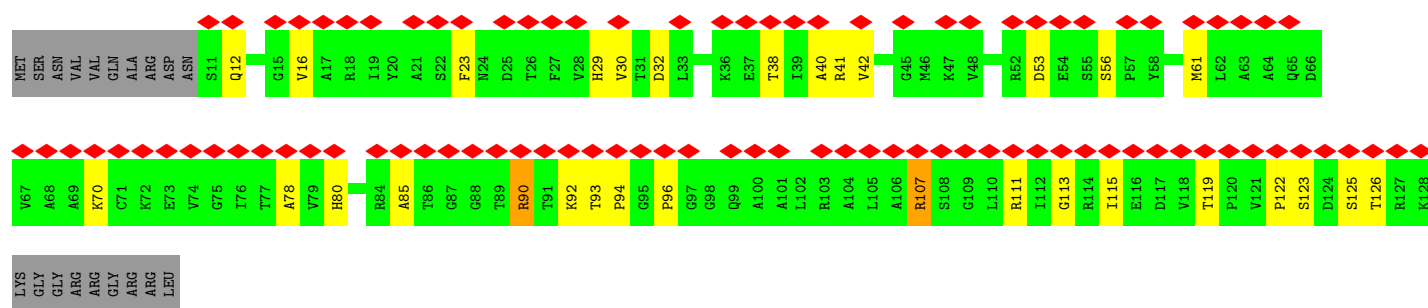




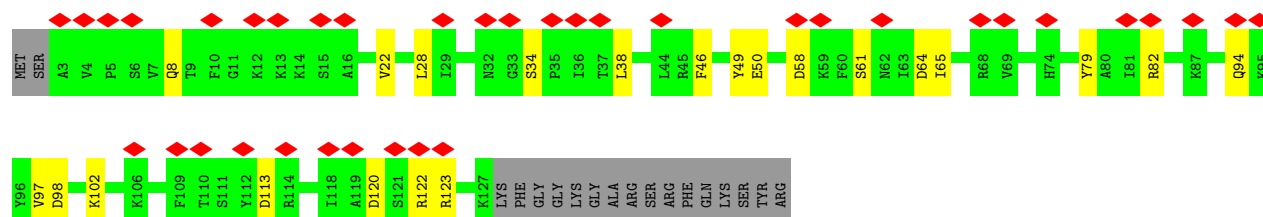
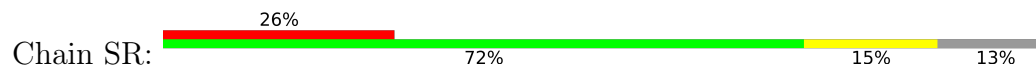
• Molecule 12: 40S ribosomal protein S13



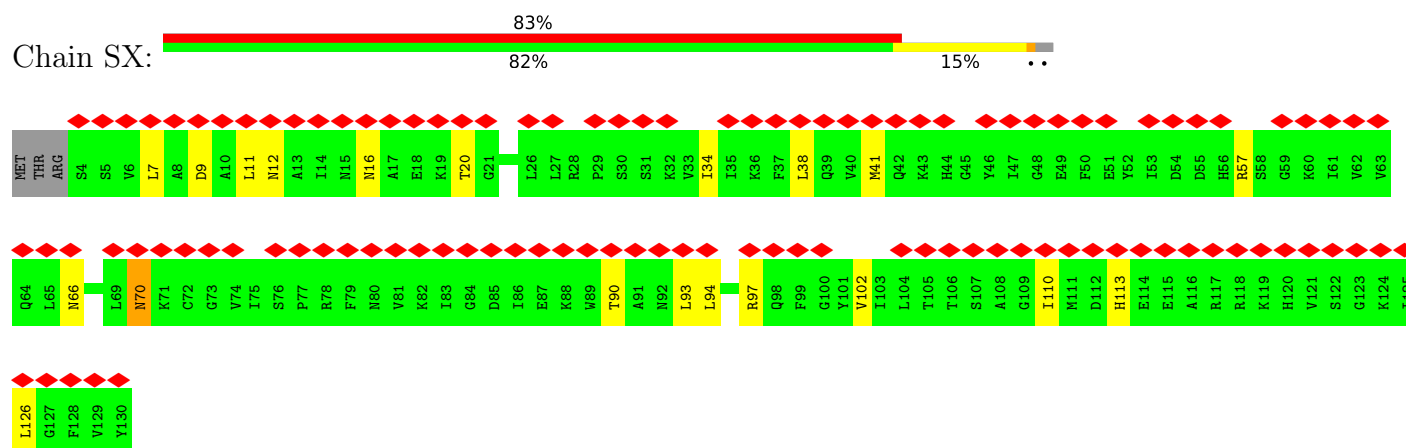
• Molecule 13: 40S ribosomal protein S14-A



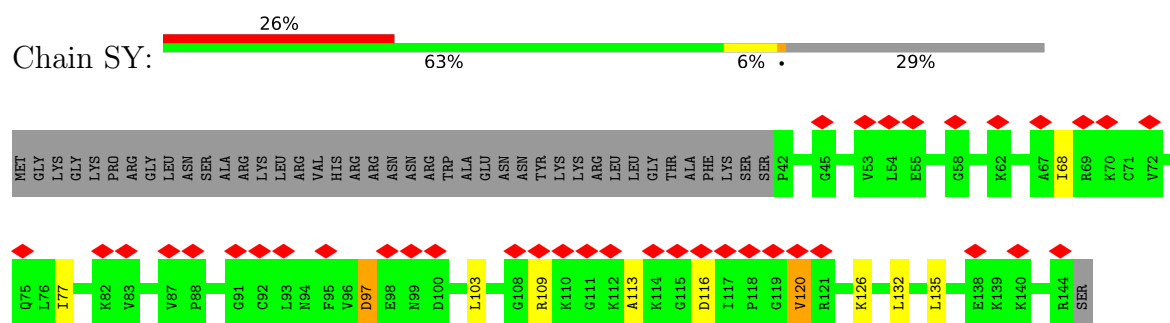
• Molecule 14: 40S ribosomal protein S16-A



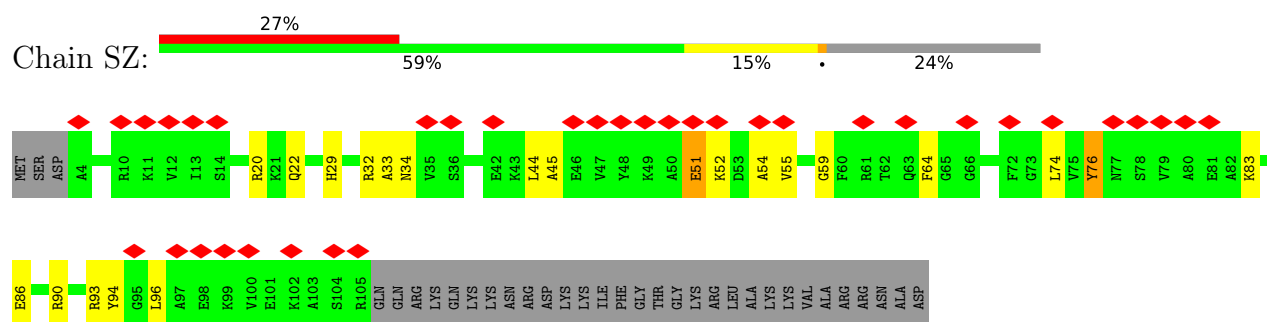
- Molecule 15: 40S ribosomal protein S22-B



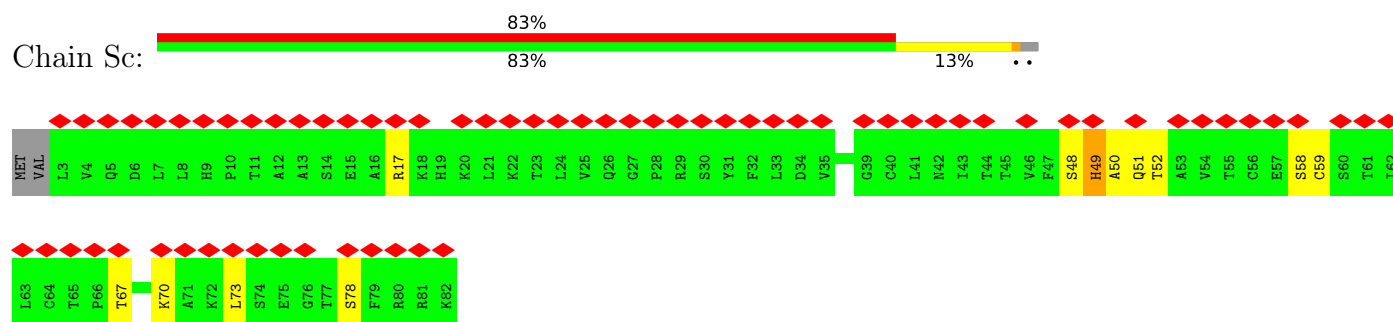
- Molecule 16: 40S ribosomal protein S23-A



- Molecule 17: 40S ribosomal protein S24-A

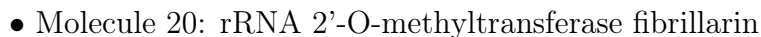


- Molecule 18: 40S ribosomal protein S27-A



- Molecule 19: 40S ribosomal protein S28-A

Chain Sd:



Chain 3B:

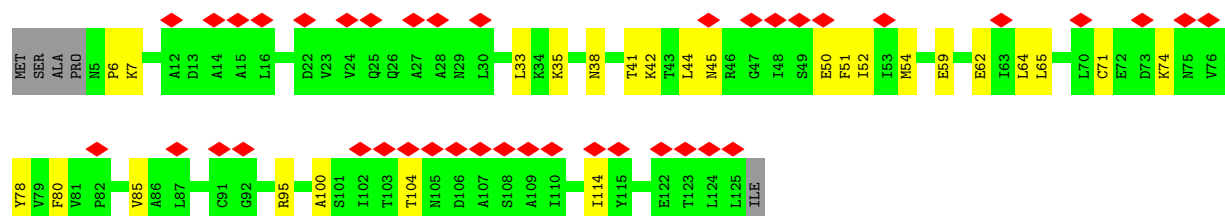
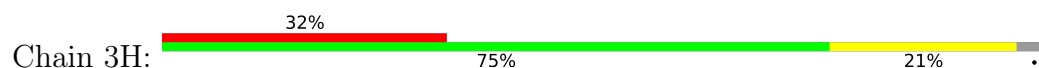
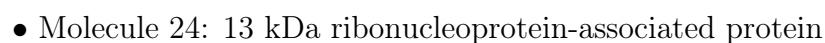
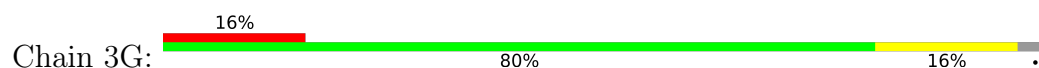
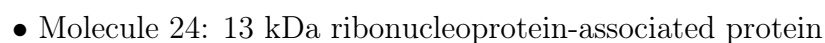
- Molecule 20: rRNA 2'-O-methyltransferase fibrillar

Chain 3C:

- Molecule 21: Nucleolar protein 56

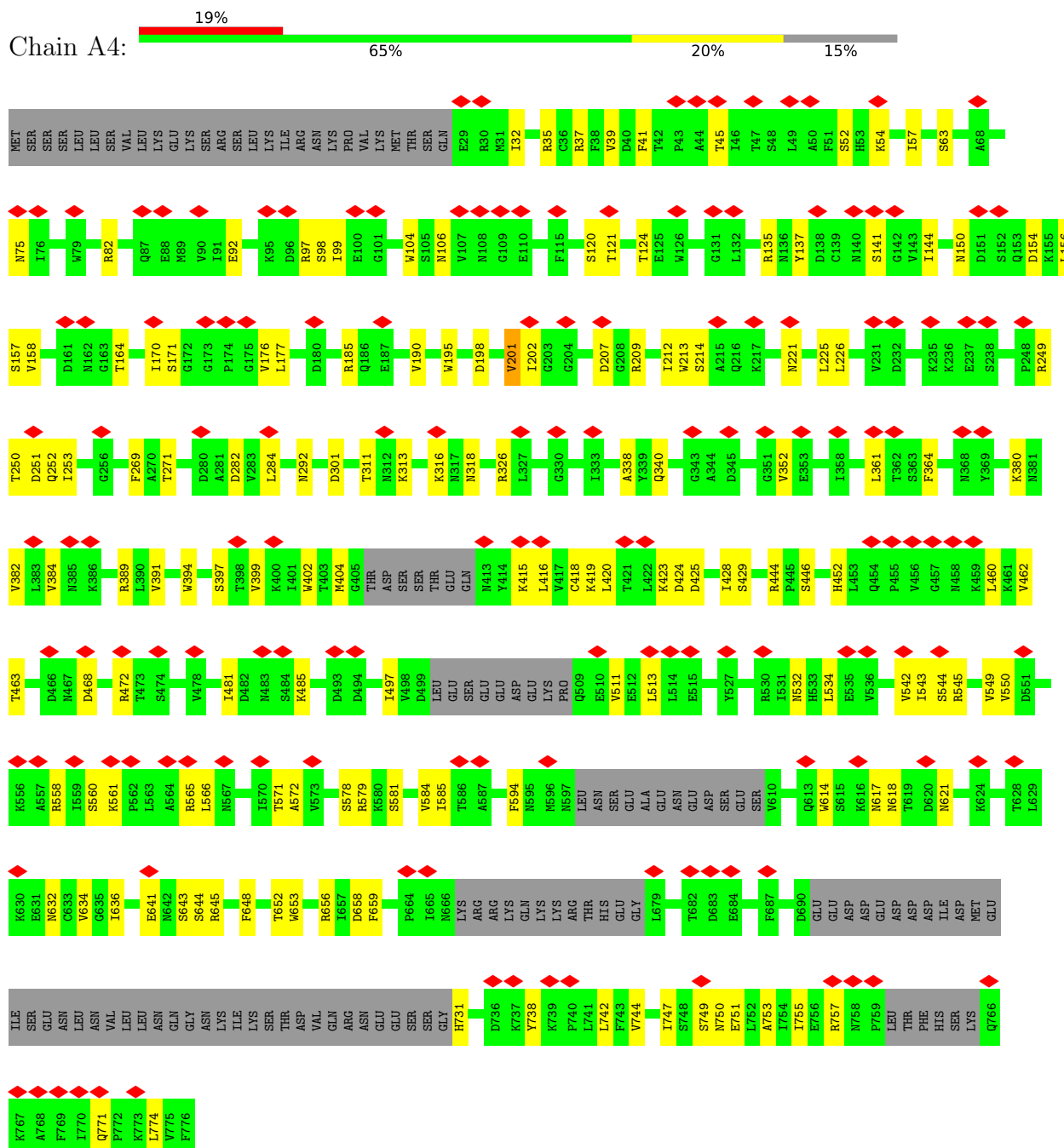


Chain 3F:



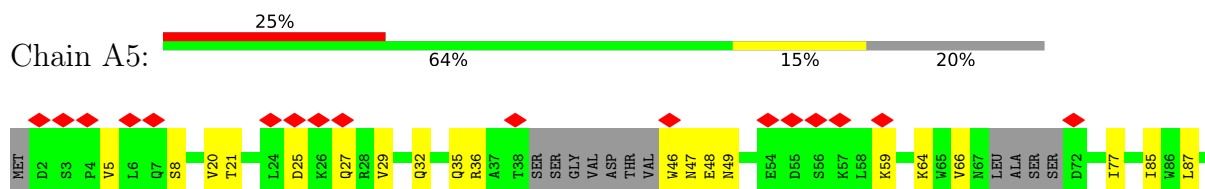
• Molecule 25: U3 small nucleolar RNA-associated protein 4

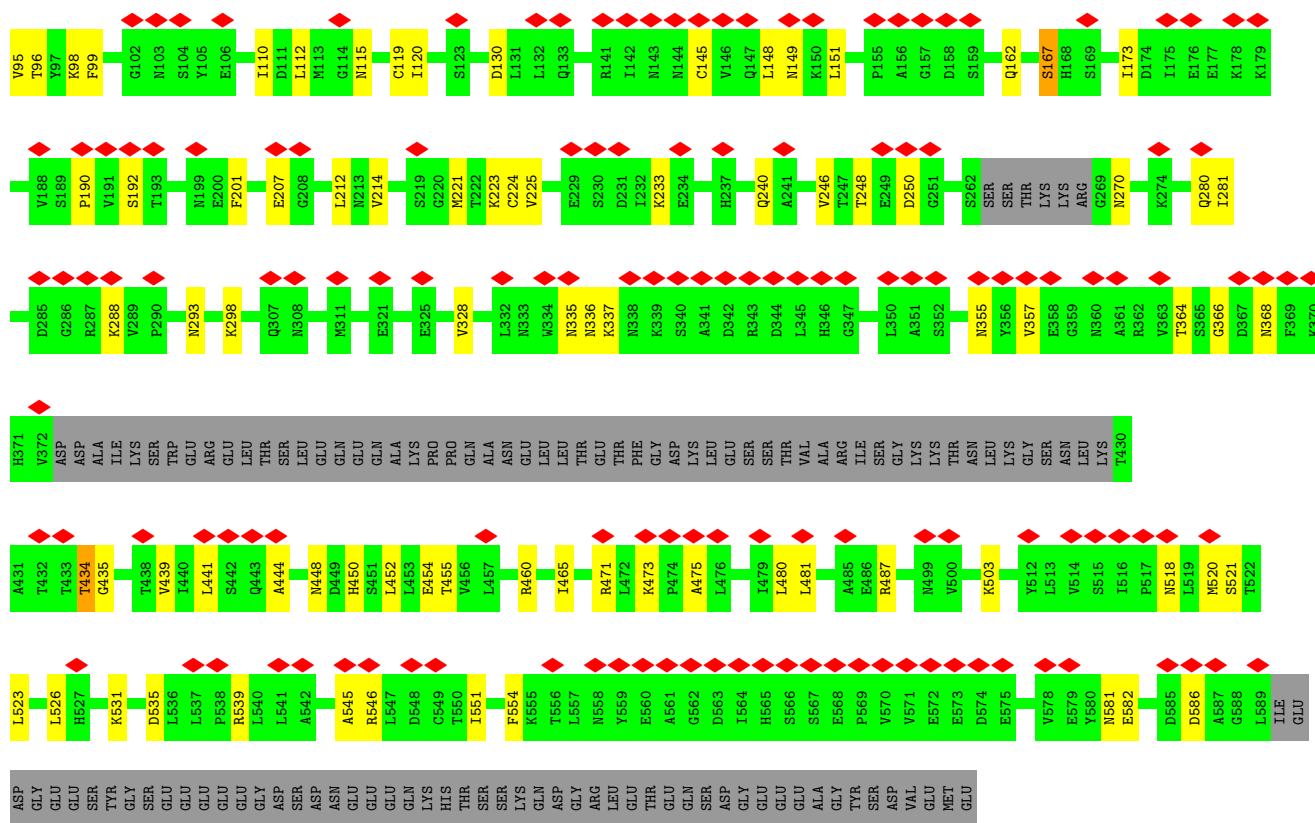
Chain A4:



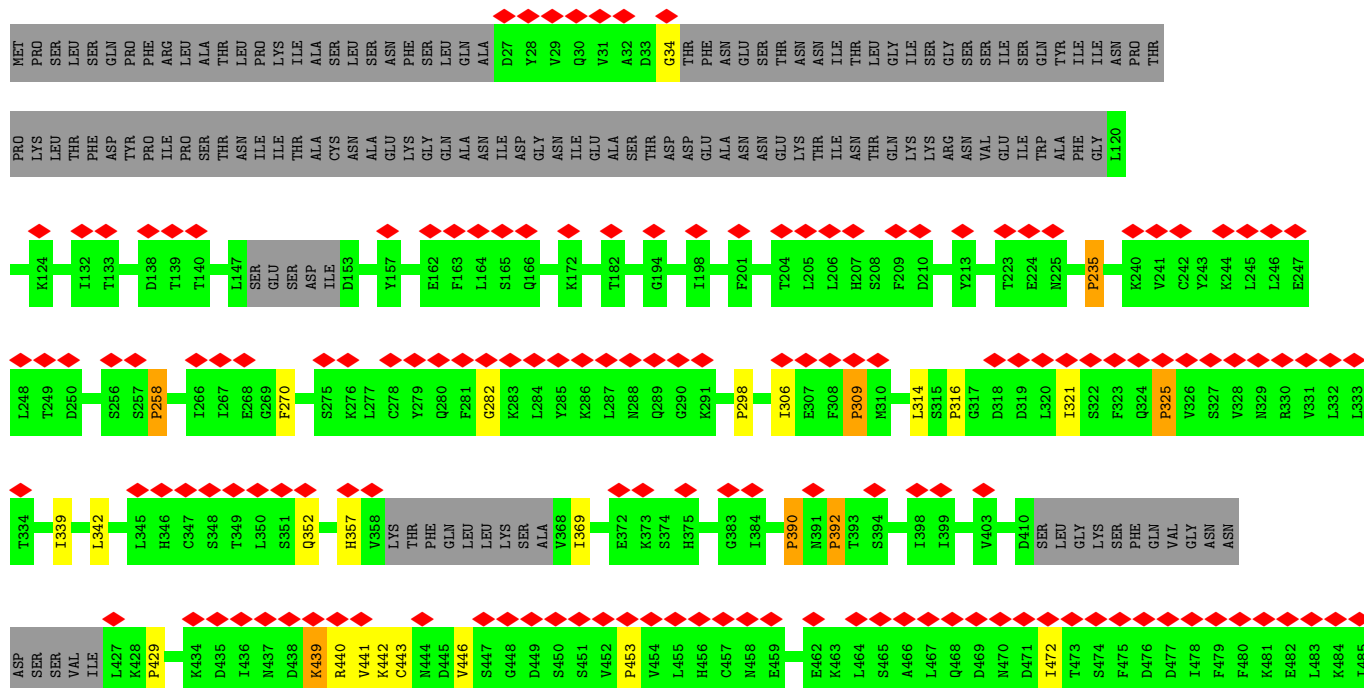
• Molecule 26: U3 small nucleolar RNA-associated protein 5

Chain A5:

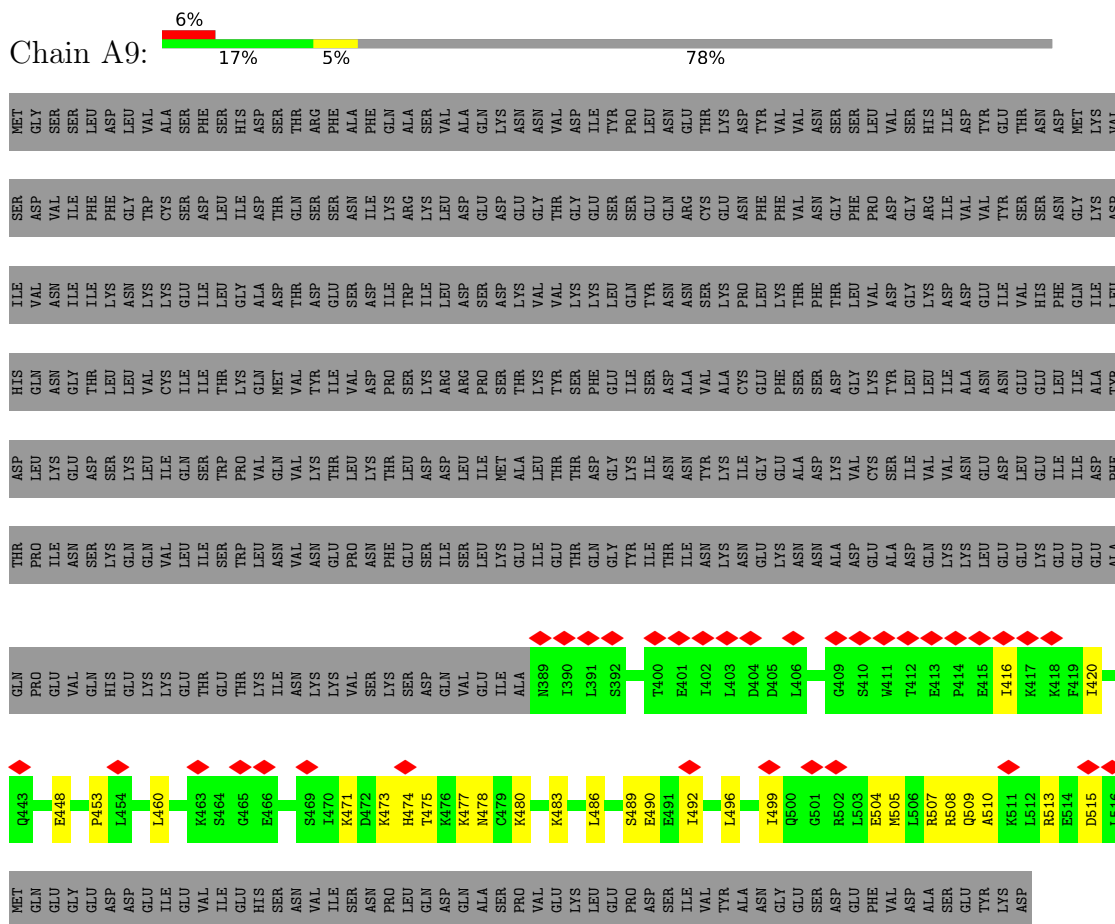




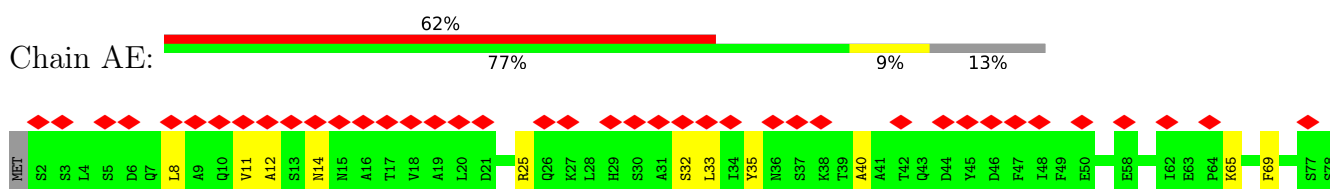
• Molecule 27: U3 small nucleolar RNA-associated protein 8



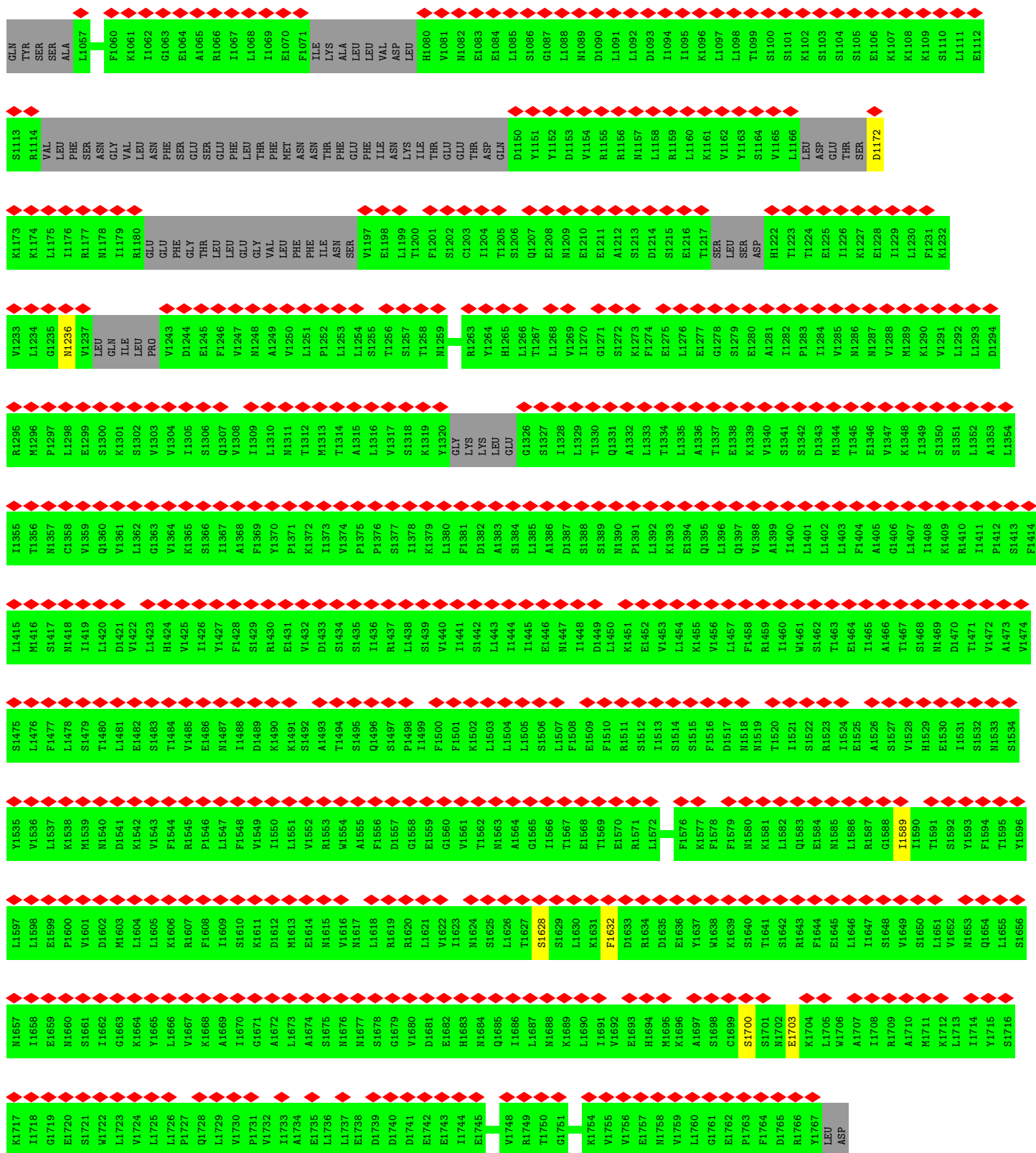
- Molecule 28: U3 small nucleolar RNA-associated protein 9



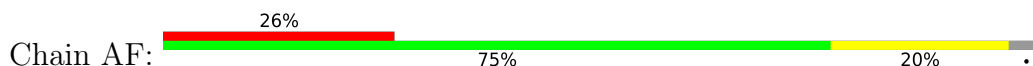
- Molecule 29: U3 small nucleolar RNA-associated protein 10

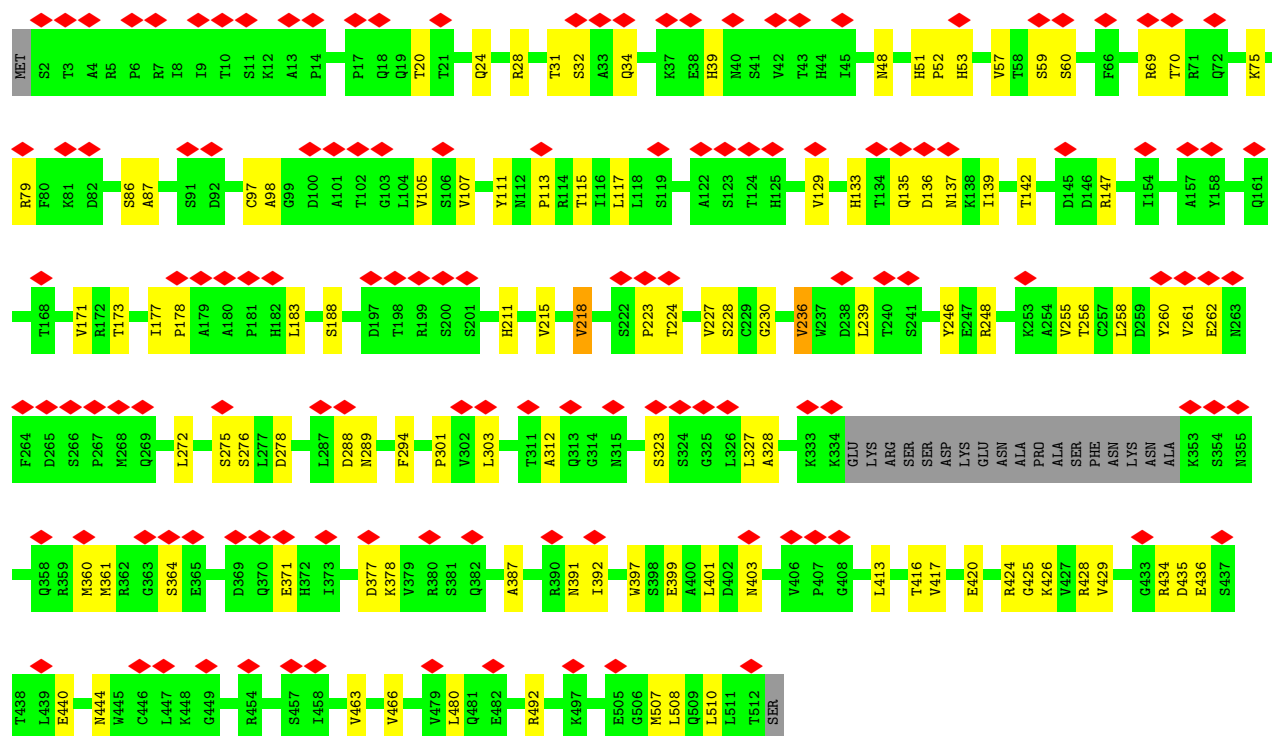




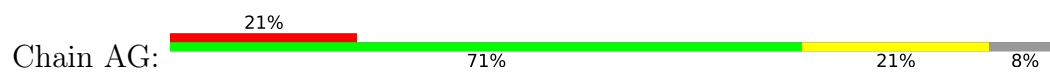


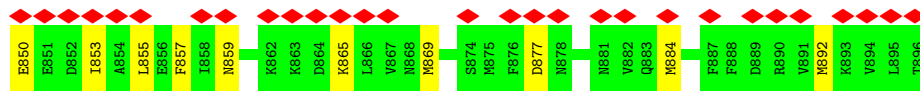
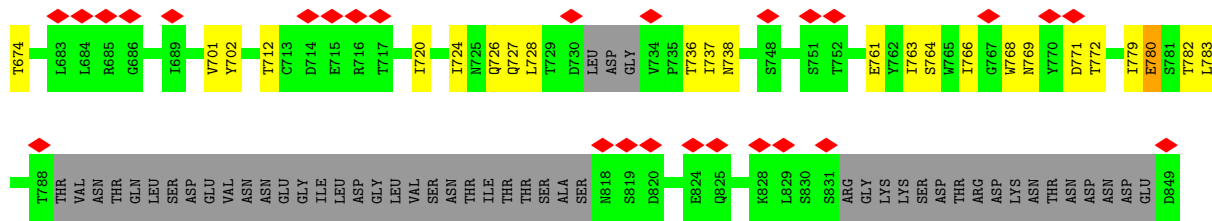
• Molecule 30: U3 small nucleolar RNA-associated protein 15



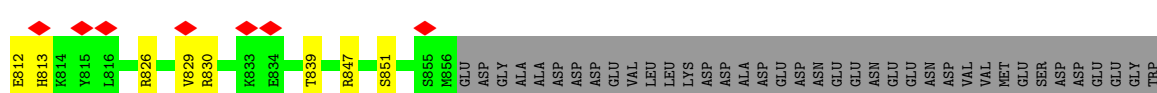
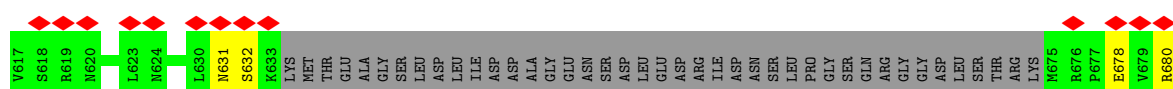
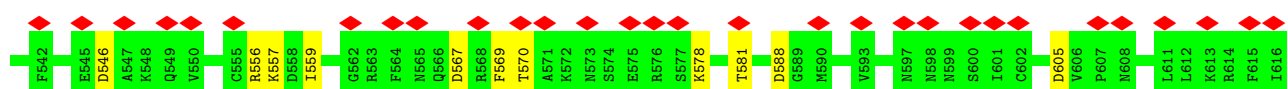
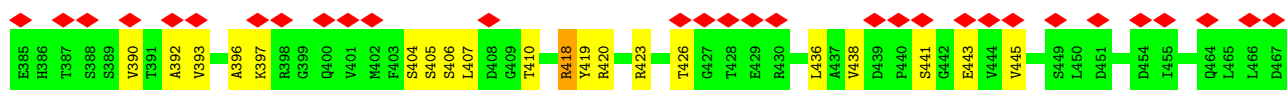
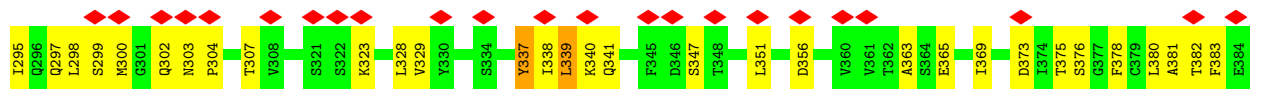
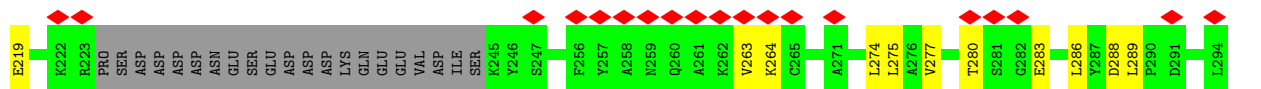
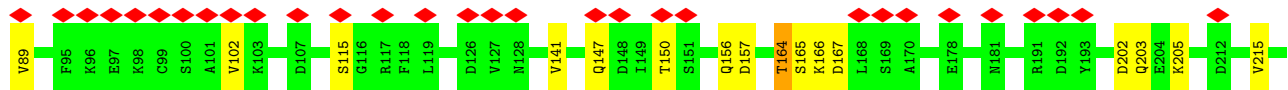
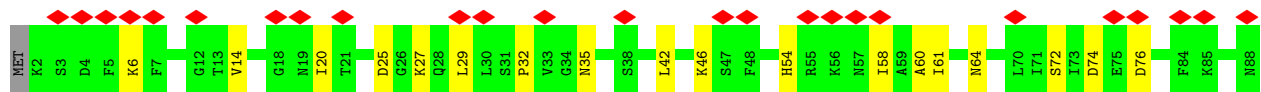
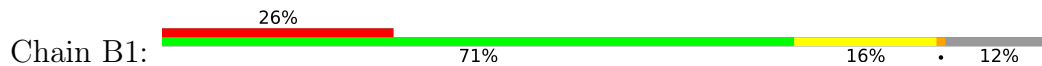


• Molecule 31: NET1-associated nuclear protein 1



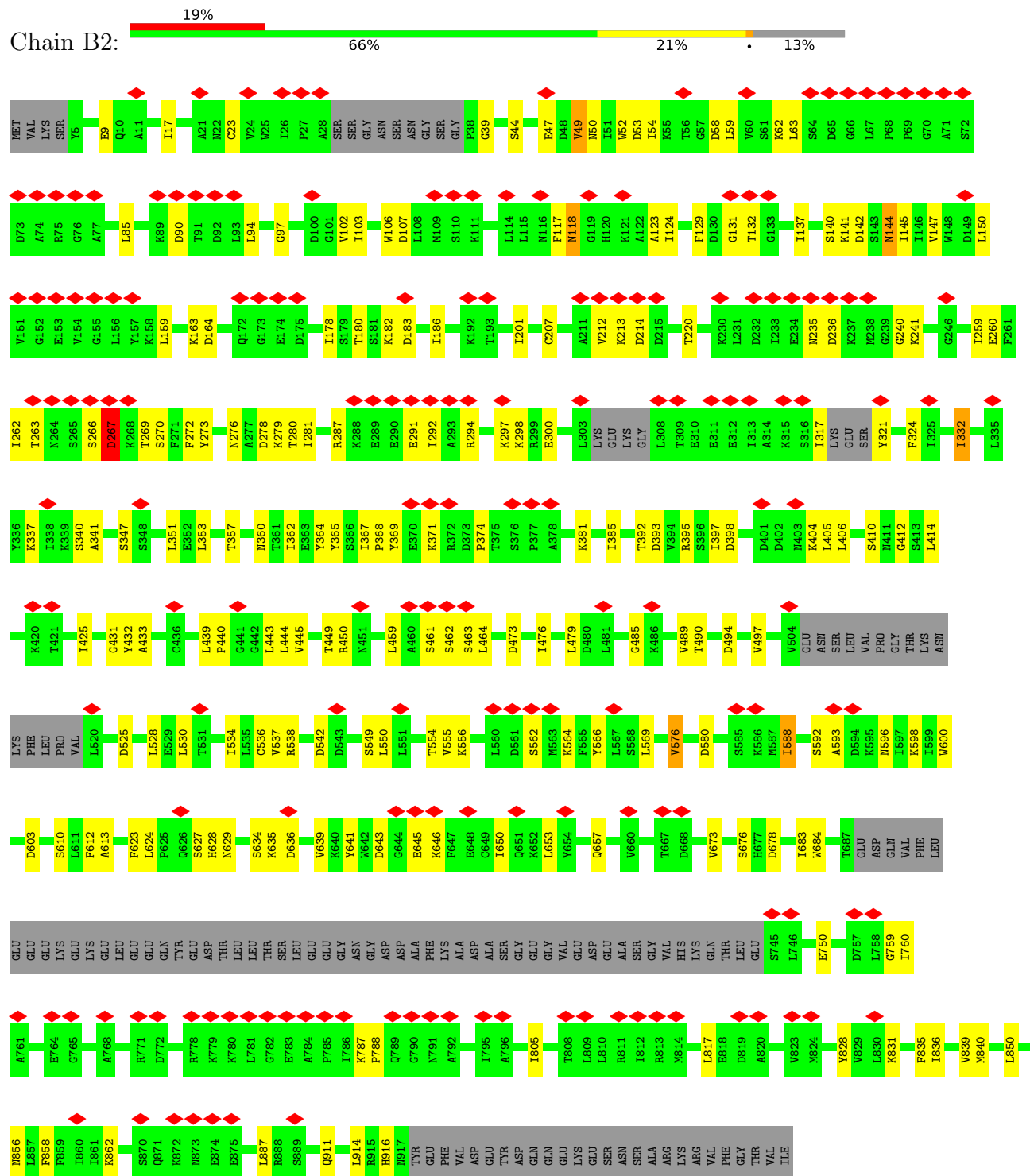


• Molecule 32: Periodic tryptophan protein 2



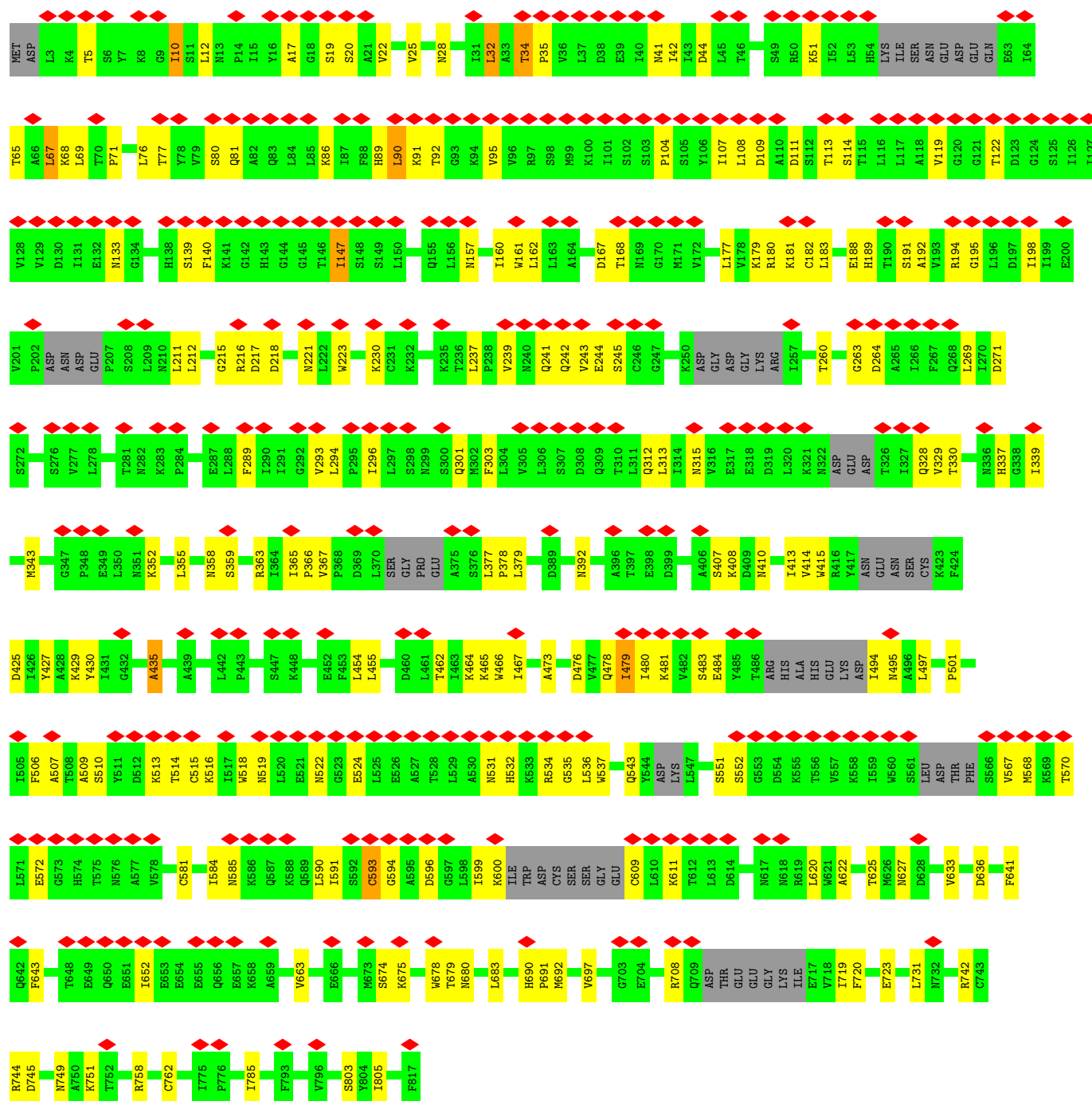
ILE
GLY
PHE
ASN
GLY
LYS

• Molecule 33: U3 small nucleolar RNA-associated protein 12

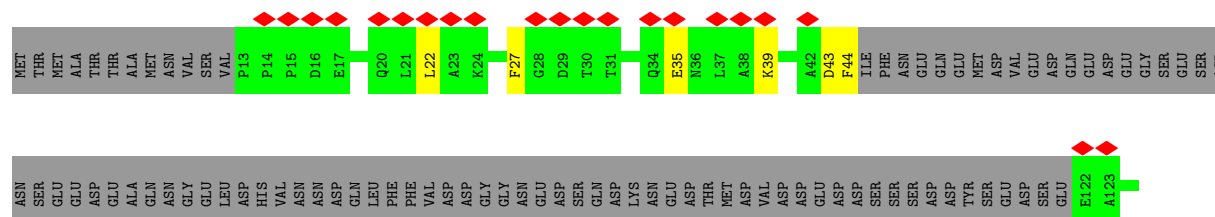


• Molecule 34: U3 small nucleolar RNA-associated protein 13



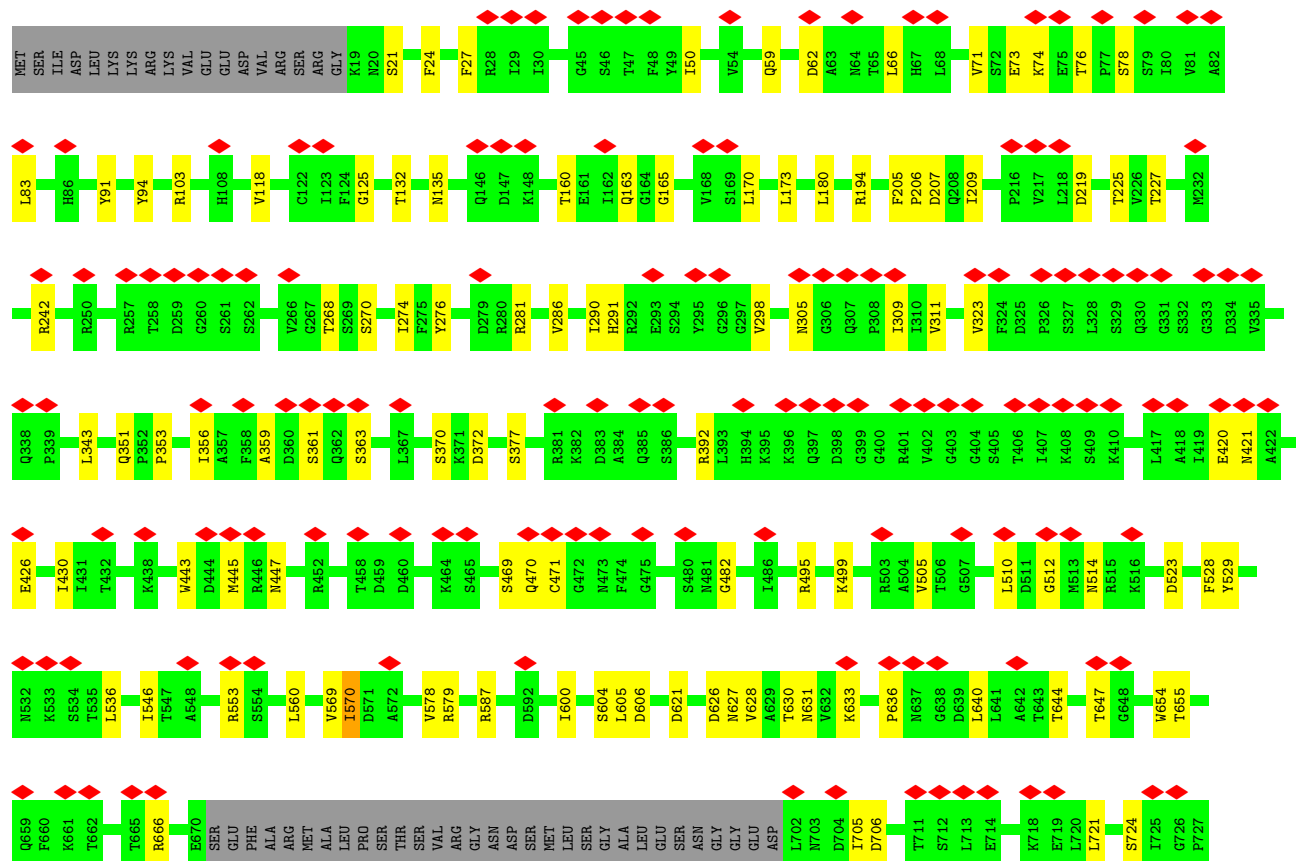
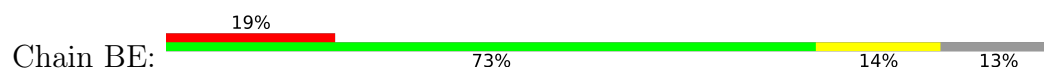


• Molecule 35: U3 small nucleolar RNA-associated protein 18



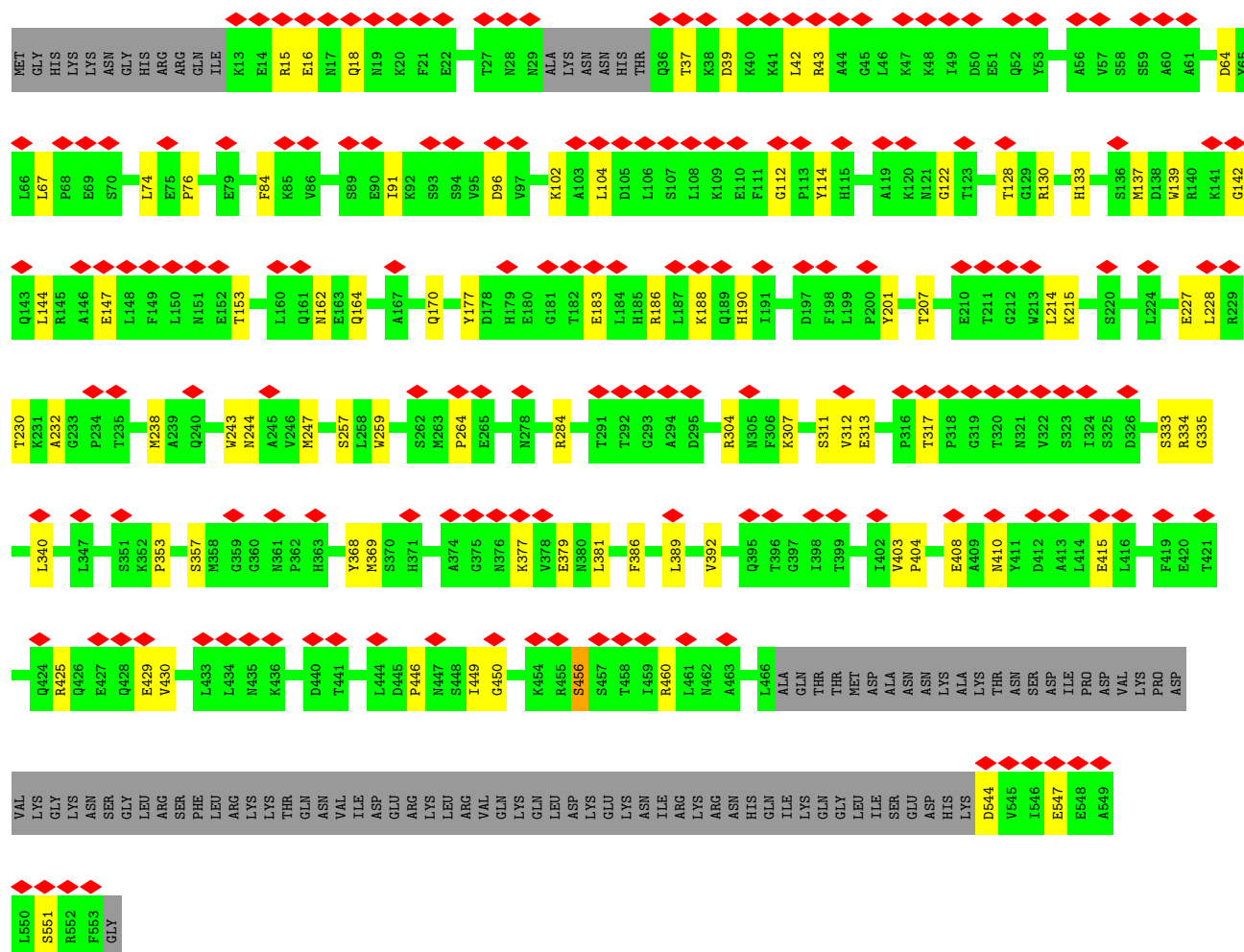


• Molecule 36: U3 small nucleolar RNA-associated protein 21

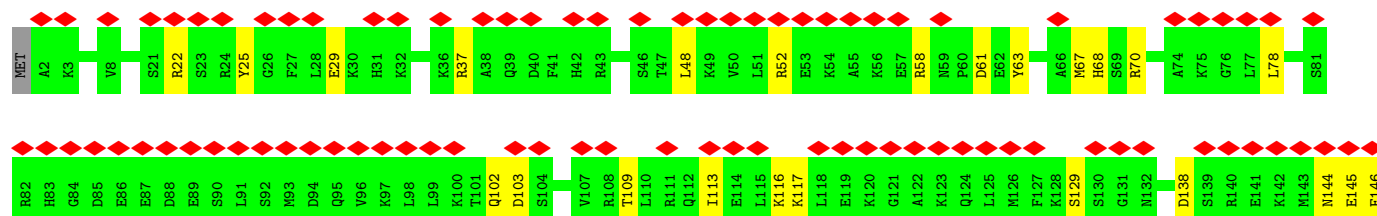
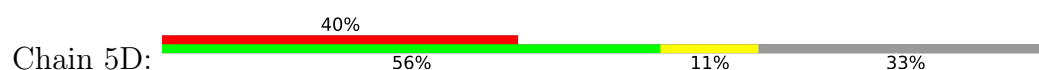


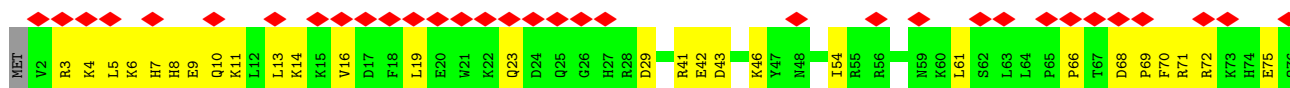


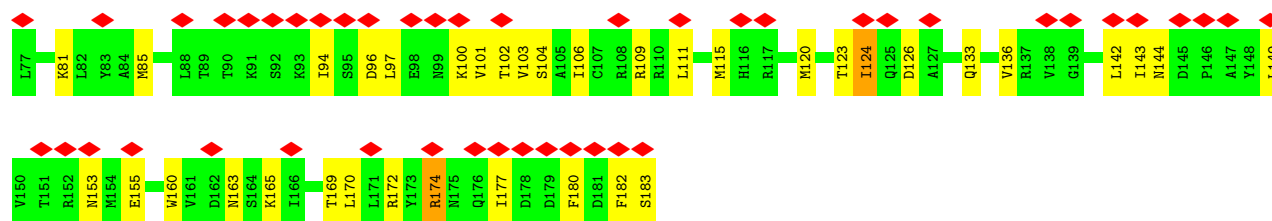
• Molecule 39: U3 small nucleolar RNA-associated protein 7



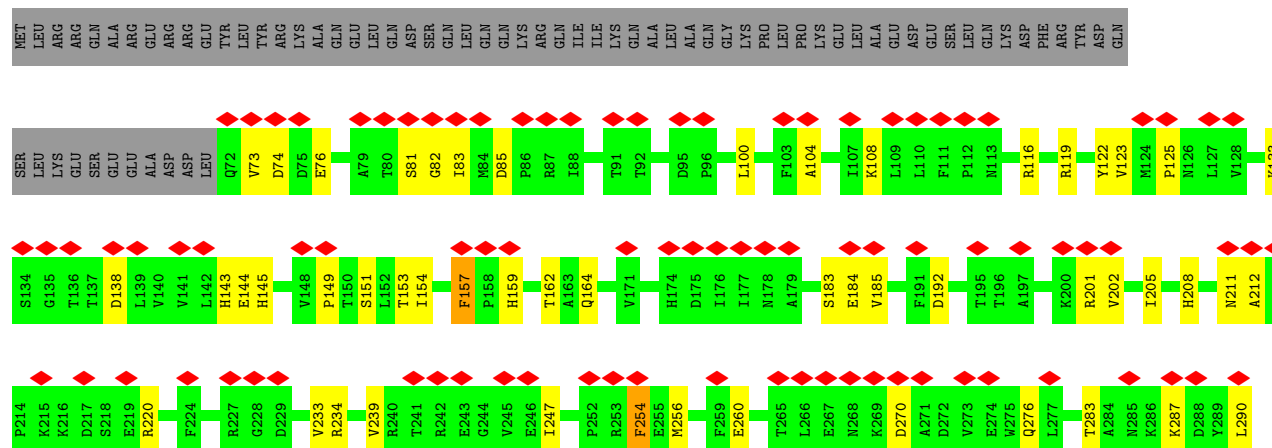
• Molecule 40: U3 small nucleolar RNA-associated protein 11



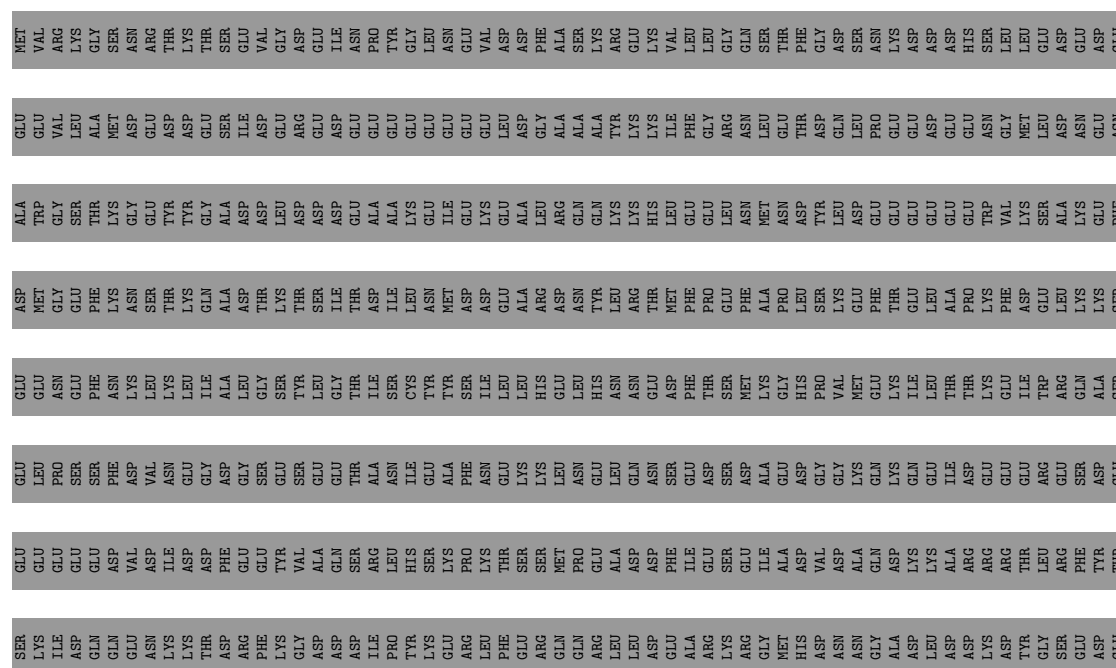




• Molecule 43: U3 small nucleolar ribonucleoprotein protein IMP4

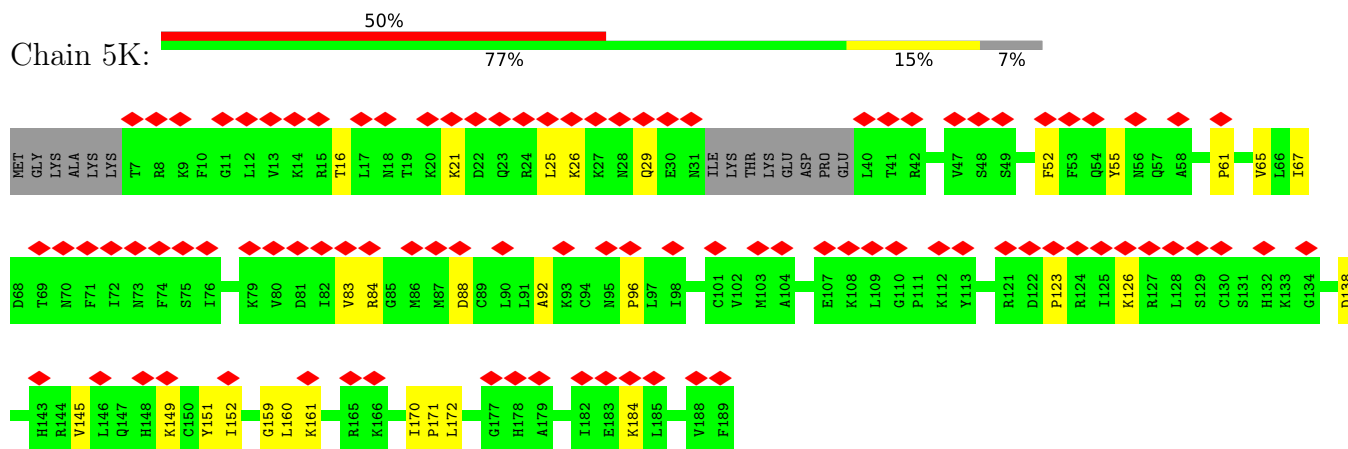


• Molecule 44: Something about silencing protein 10



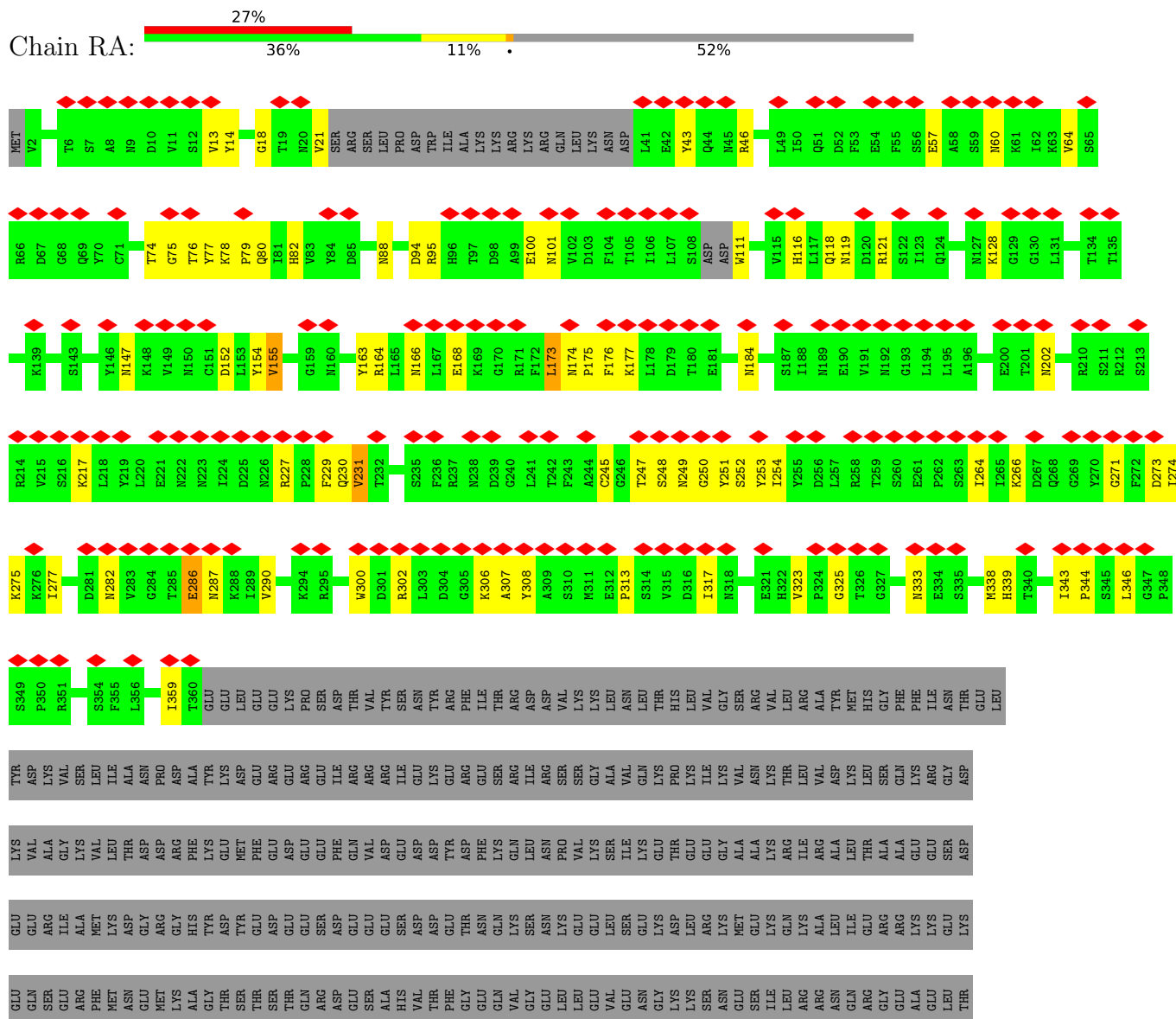
• Molecule 47: rRNA-processing protein FCF1

Chain 5K:



• Molecule 48: Ribosome biogenesis protein ENP2

Chain RA:

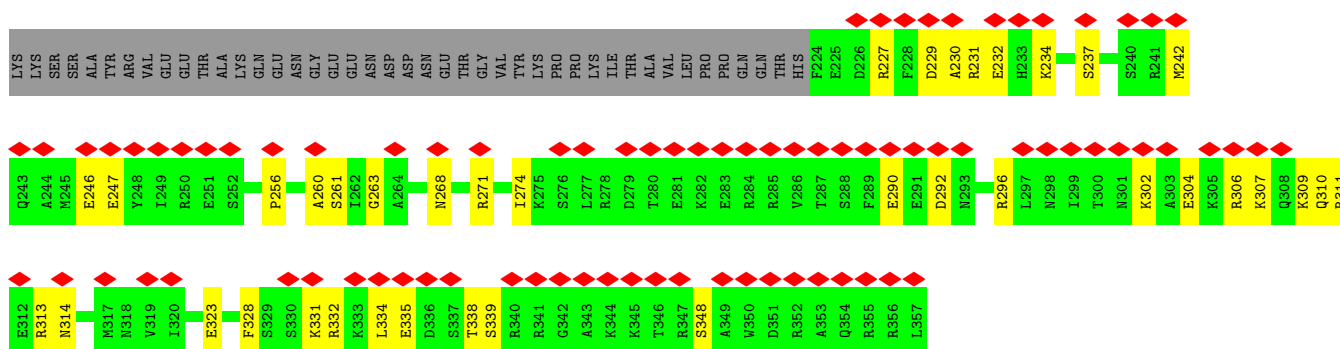


- Molecule 49: U3 small nucleolar ribonucleoprotein protein LCP5

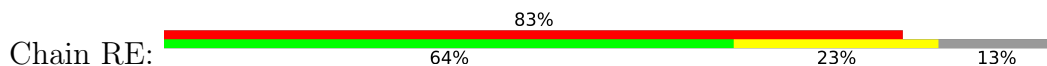


LEU SER LEU LEU LYS ASN GLY SER MET LEU LEU TYR TLE ASN SER SER LEU LEU LEU MET LEU TLE ASN SER SER ASP ASP GLU LYS CYS ASP PRO PRO SER SER ALA ALA ARG ARG GLU ARG SER SER TLE HIS VAL VAL LEU LEU GLU ARG GLY VAL LYS LYS LEU LEU ALA TTR

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



- Molecule 50: U3 small nucleolar RNA-associated protein 22

[illegible]

SER	PRO	GLU	SER	ASN	GLU	VAL	ALA	THR	ASN	THR	ALA	ALA	THR	GLU	SER	TYR	ASP	ILE	ILE	ALA	ARG	GLU	THR	ALA	GLU	LEU	PHE	LYS	S100	I101	I102	F103	K104	L105	Q106	T107	D108	E109	L110	L111	E112	G113	V114	K115	L116	K117	Q118	K119	H120
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

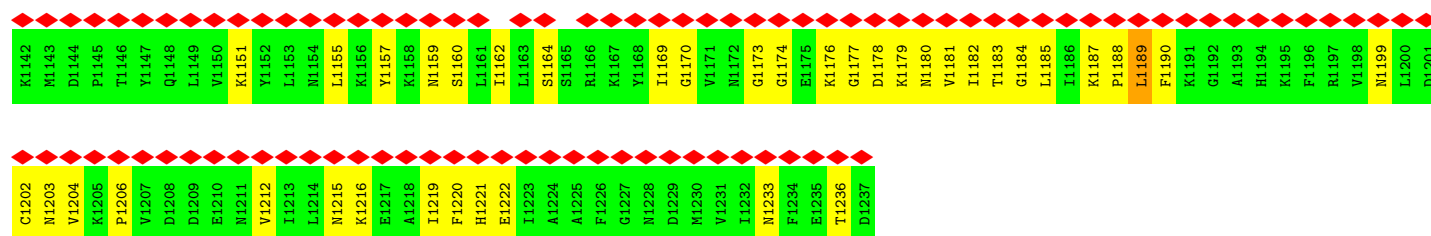
V121	L122	K123	E125	K126	F127	L128	H129	K130	L131	Y132	D133	I134	L135	Q136	I138	P139	D140	M141	E142	E143	K144	S145	L146	A147	E148	V149	D150	S151	F152	F153	K154	M155	K156	I157	V158	S159	V160	P161	F162	V163	D164	P165	K166	P167	I168	P169	Q170	M171	T172	T173	Y174	K175	F176	M177	V178	K179	M180
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

F181	F182	F183	F184	F185	F186	F187	F188	F189	F190	F191	F192	F193	F194	F195	F196	F197	F198	F199	F200	F201	F202	F203	F204	F205	F206	F207	F208	F209	F210	F211	F212	F213	F214	F215	F216	F217	F218	F219	F220	F221	F222	F223	F224	F225	F226	F227	F228	F229	F230	F231	F232	F233	F234	F235	F236	F237	F238	F239	F240
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

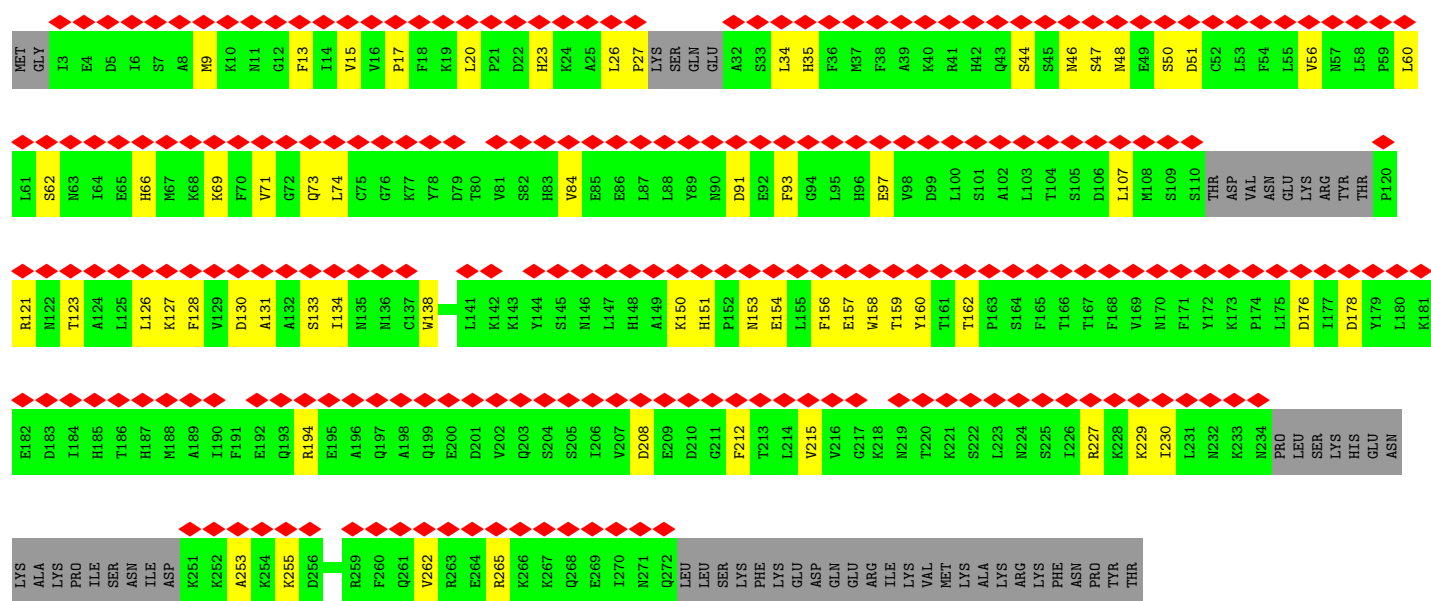
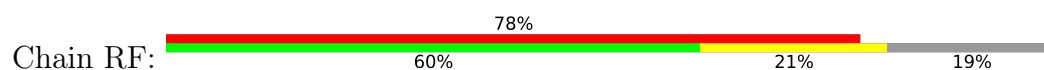
L241	L242	L243	L244	L245	L246	L247	L248	L249	S250	F251	L252	Q253	L254	E255	Y256	S257	F258	F259	D260	N261	D262	P263	L264	L265	P266	L267	L268	D269	L270	S271	C272	S273	K274	PRO	THR	GLY	ASP	SER	SER	LEU	SER	D282	Y283	N284	F285	Y286	K287	T288	R289	F290	S291	L292	N293	L294	L295	L296	G297	F298	P299	V300
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

K301	V302	F303	F304	P305	K306	K307	L308	L309	P310	N311	R312	N313	C314	I315	R316	I317	ALA	GLN	GLU	SER	LYS	GLU	GLN	SER	L326	P327	A328	T329	P330	L331	Y332	N333	F334	S335	V336	L337	S338	S339	S340	T341	H342	E343	N344	Y345	L346	K347	Y348	L349	Y350	K351	T352	K353	K354	Q355	T356	E357	S358	F359	V360
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

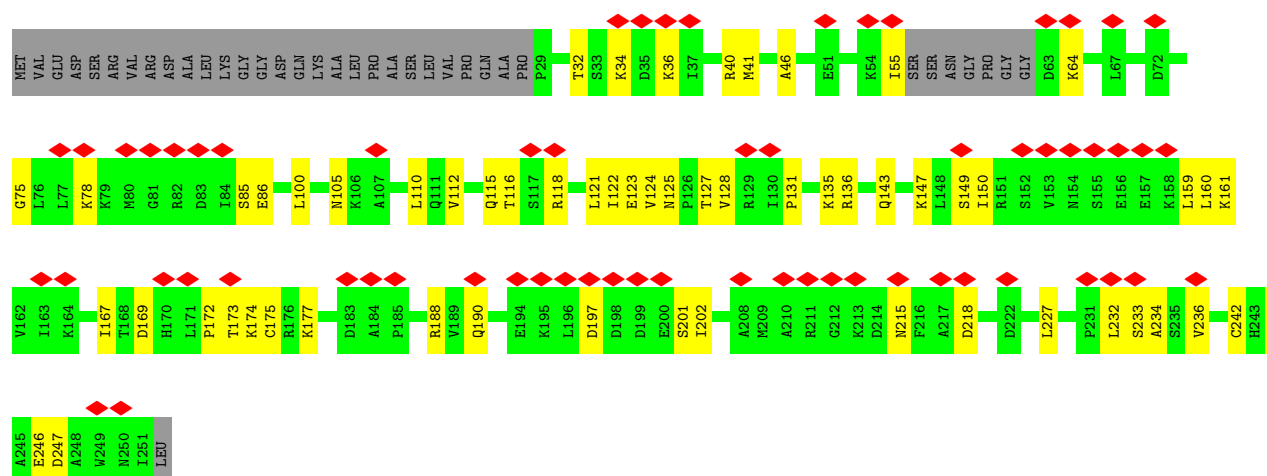
Q1082	M1022	L962	T902	L843	V782	L722	G661	S601	T541	T481	L421	E361
Q1083	M1023	K963	S903	L844	I783	N723	S662	N602	S542	V482	F422	A362
T1084	F1024	F964	H904	T844	L784	L724	T863	T603	L543	S483	K423	T363
M1085	T1025	I965	S905	P845	E785	S725	T664	G604	A544	S484	G424	V364
M1086	M1026	S966	S906	E846	F786	S726	H665	G605	A545	V485	V425	L365
L1087	L1027	Q967	Q907	Q847	E787	S727	G666	N606	T546	Q486	I426	G366
L1088	R1028	W968	F908	Y848	T788	F728	C667	H607	F547	I487	K427	L367
F1089	M1029	N969	S909	Q849	S789	N729	V668	F608	G548	L488	Y428	W369
T1090	S1030	W970	S910	F850	P790	L730	W669	N609	S549	L489	L429	L370
P1091	D1031	K971	S911	K851	K791	K731	S670	F610	M550	E490	A430	Q371
G1092	P1032	D972	V912	F852	W792	K732	T671	D611	E551	Y491	T431	Q372
L1093	M1033	D973	V913	R853	P793	S733	S672	F612	R552	A492	M432	R373
K1094	G1034	P974	R914	W854	D794	F734	S673	W613	G493	G493	D433	G374
D1095	T1035	L975	L915	L855	E795	D735	S674	R614	E494	E494	L434	F375
Y1096	H1036	T856	F916	T856	I796	D736	E875	W615	T495	L496	C435	S376
D1097	L1037	E857	Q917	E857	T797	L737	P676	K616	L497	R497	H436	S377
F1098	Q1038	R858	R918	R858	S798	K738	I677	L617	M498	G437	D437	N378
V1099	F1039	D859	W919	D859	L799	Y739	I678	I618	L499	G438	H439	M379
V1100	F1040	E860	S919	E860	E800	I740	S679	W619	N500	L440	L440	S380
D1101	V1041	T861	D921	T861	K801	I741	S680	N620	N501	Q441	Q441	H381
L1102	A1042	L862	T922	L862	A802	F742	I681	P621	F561	F442	F442	S382
R1103	S1043	Y863	H923	Y863	K803	Q743	V882	S622	V502	V503	V503	G383
T1104	K1044	L864	L924	L864	T804	W744	N883	E923	Q504	Q504	S444	S384
P1105	M1045	R865	L925	R865	A805	K745	F684	C624	Q505	Q505	N445	L385
T1106	D1046	A866	L926	A866	F806	L746	A885	D625	Q506	Q506	N445	G386
G1107	P1047	T867	Q927	T867	L807	L747	L686	K626	F507	F507	P40	C387
L1108	S1048	A868	H928	A868	L808	L748	Q887	L627	T567	T567	GLU	F388
K1109	G1049	N869	I929	N869	K809	S749	K688	W628	N568	N568	ASN	F389
S1110	I1050	A870	T930	A870	T810	V750	H889	T629	N509	N509	SER	G390
L1051	D1051	R871	D931	R871	Q811	K751	W690	K630	I510	I510	SER	T390
Y1052	G1052	N872	E932	N872	E812	S752	S691	G631	F511	F511	SER	F391
S1053	S1053	GLY	L933	GLY	E813	I753	K692	P632	L512	L512	A454	E392
A1054	S1054	ALA	A934	ALA	E814	L754	K693	A633	T513	T513	A454	F393
G1055	G1055	GLY	E935	GLY	L814	L754	K694	H634	N514	N514	A455	T394
L1056	I1056	S815	L936	S815	S815	F755	A694	H634	I515	I515	A456	I395
P1057	P1057	A816	L937	P876	A816	V756	Q695	S635	S516	S516	Y457	L396
L1058	L1058	E817	I937	E877	N817	S757	I696	E636	R517	R517	I458	M397
P1059	P1059	L878	I939	L878	S818	S758	S697	T637	F518	F518	D459	A398
I1060	I1060	S819	T939	E879	S819	A759	N698	M638	D519	D519	E460	A399
A1061	A1061	T820	I941	A890	T820	F760	E699	S639	N520	N520	G461	L400
L1062	T1062	Y821	P942	T881	Y821	R761	T700	T640	L521	L521	F462	L401
R1063	V943	R822	F942	R882	R822	V762	I701	E641	K522	K522	Q463	N402
L1064	D944	S823	V943	L883	S823	T763	K702	A642	I583	I583	T464	G403
A1065	P945	F824	D945	K884	F824	S764	H705	A643	Y523	Y523	P465	G404
T1066	A946	F825	A946	R885	F825	L765	W706	V644	D524	D524	P465	G405
L1067	P947	S826	P947	T886	S826	Q766	F707	F645	C526	C526	T466	I406
A1068	Y948	R827	Y948	A887	R827	Q767	L708	K646	Y527	Y527	L467	N407
K1069	F949	D828	F949	K888	D828	P768	W709	N647	D528	D528	F468	S408
F1070	I950	E829	I950	Y889	E829	V769	L710	F648	Q530	Q530	K470	N409
A1071	Q951	S830	P951	Y890	S830	P770	P711	W649	L531	L531	S471	K410
Y1072	G952	I831	G952	L890	I831	T771	W712	G650	F532	F532	T472	I411
K1073	S953	P832	S953	S892	P832	A772	W713	I651	L533	L533	K473	L412
L1074	I1075	N834	I1020	W893	N834	S774	L714	K652	V474	V474	H414	L413
Q1076	T1076	L835	E955	R894	L835	D775	S715	S653	N475	N475	I476	G415
T1077	Q1077	H895	N956	H895	S716	D776	S654	Y536	I476	I476	F416	F416
L1136	L1136	E836	G957	T896	E836	P776	S716	L655	N537	N537	L477	S417
N1137	D1138	R897	G957	R897	A717	D777	A717	R656	N538	N538	T478	S417
L1139	H1078	T898	L959	T898	K718	F778	K718	R657	L539	L539	K479	Y419
S1140	G1079	W838	L959	T898	K718	F778	K718	R657	M480	M480	M480	Q420
E1141	L1080	T839	V961	E900	T719	Q780	S720	F658				
	M1081	L840			S720	Q780	V721	K659				
		N841				D761		D660				



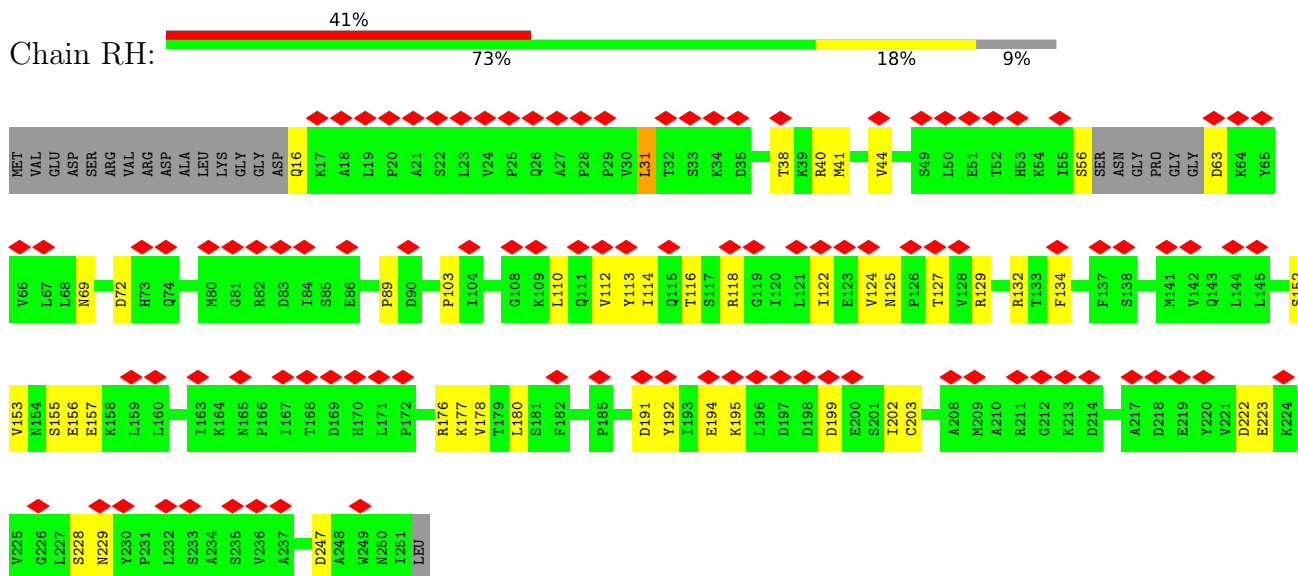
• Molecule 51: Ribosomal RNA-processing protein 7



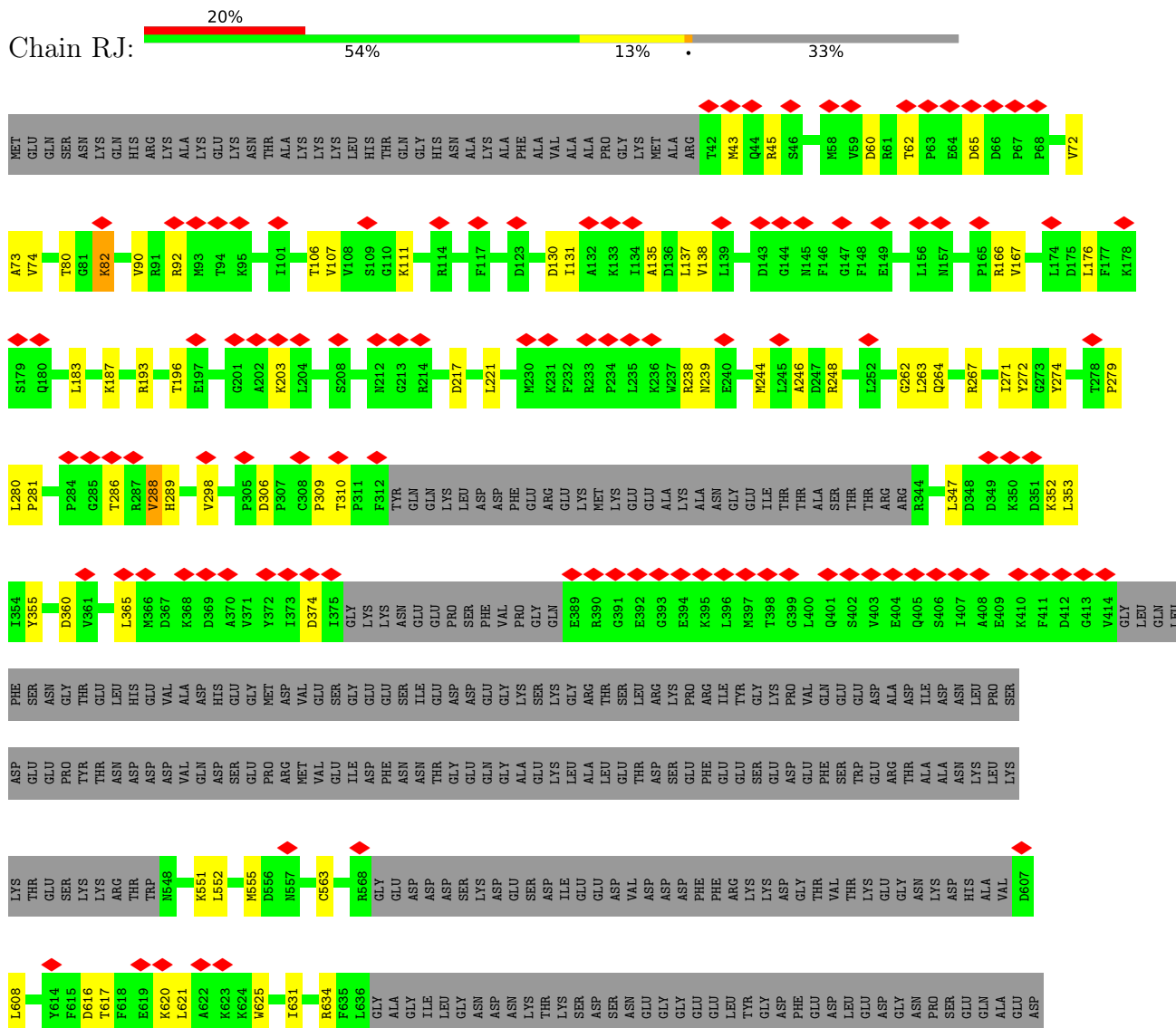
• Molecule 52: Ribosomal RNA small subunit methyltransferase NEP1

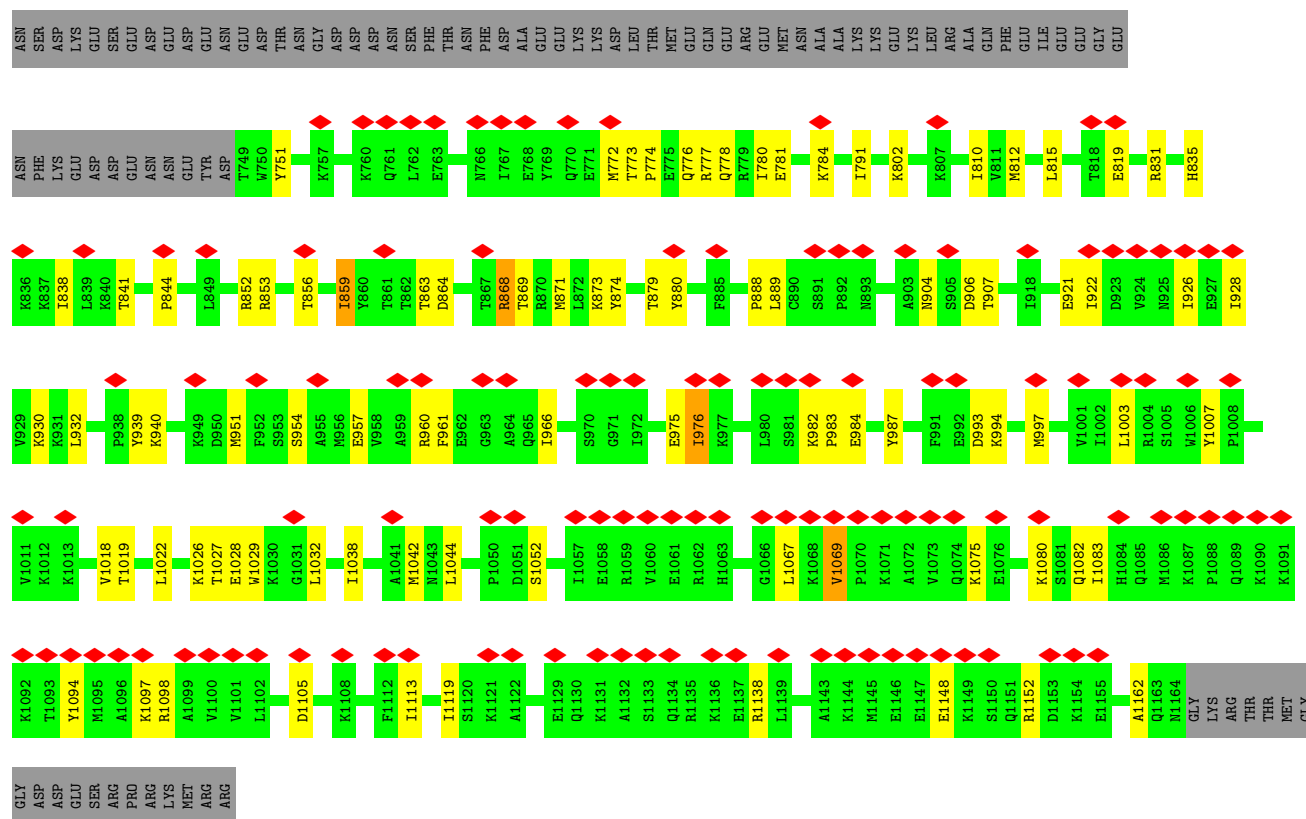


• Molecule 52: Ribosomal RNA small subunit methyltransferase NEP1

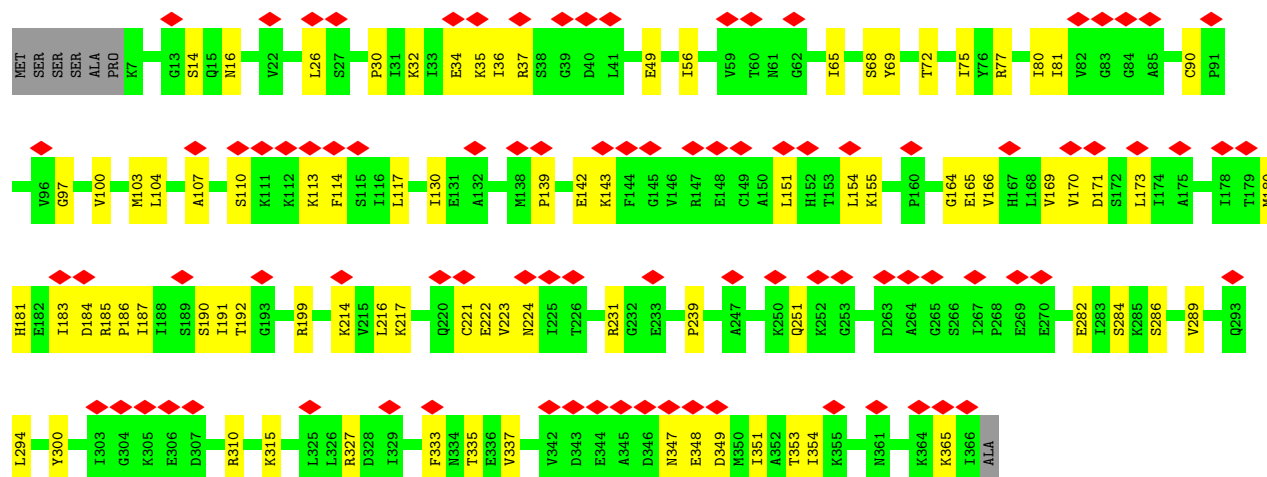
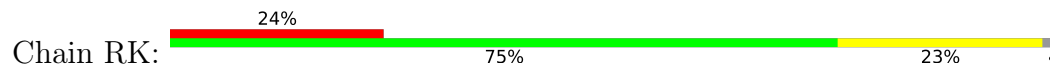


- Molecule 53: Ribosome biogenesis protein BMS1

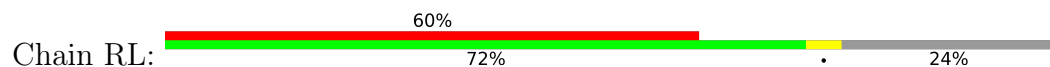




• Molecule 54: RNA 3'-terminal phosphate cyclase-like protein



• Molecule 55: RNA cytidine acetyltransferase



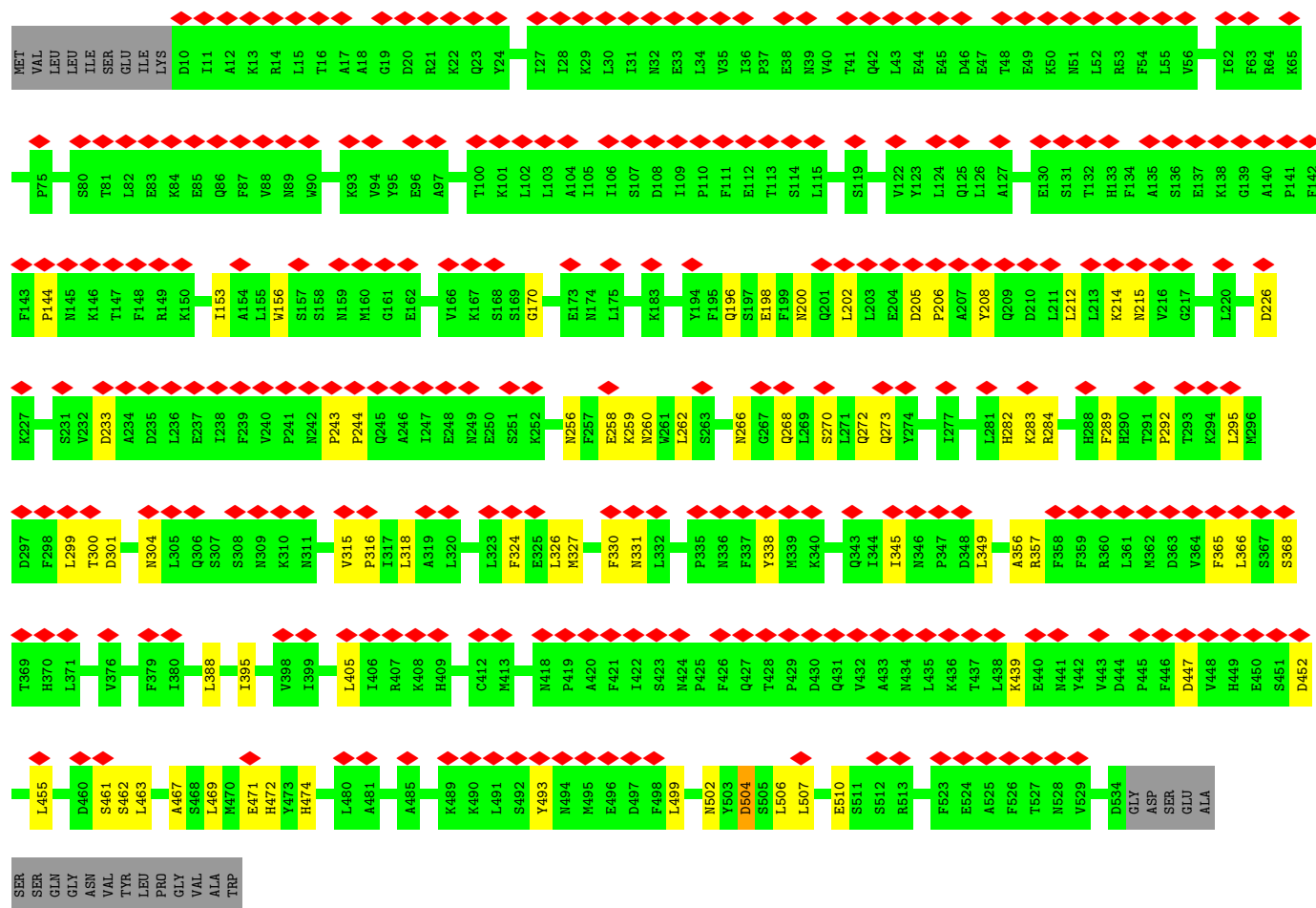


LEU	ASP	GLN	MET	GLU	GLU	ASP	ASP	GLU	GLU	GLU	GLU	THR	ALA	GLY	SER	SER	GLU	VAL	GLN	ALA	MET	ARG	GLU	LYS	GLN	LYS	GLU	LEU	ILE	ASN	SER	LEU	ASN	ASN	ASP	ASN	SER	SER	GLU	GLU	TRP	ALA	ALA	TYR	LYS	LYS	ASN	ASP	ILE	ALA	ALA	GLY
VAL	SER	LEU	LYS	THR	GLY	LYS	LYS	ARG	GLU	THR	THR	GLY	LYS	ALA	ASP	VAL	GLN	ILE	ASP	VAL	ALA	TYR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

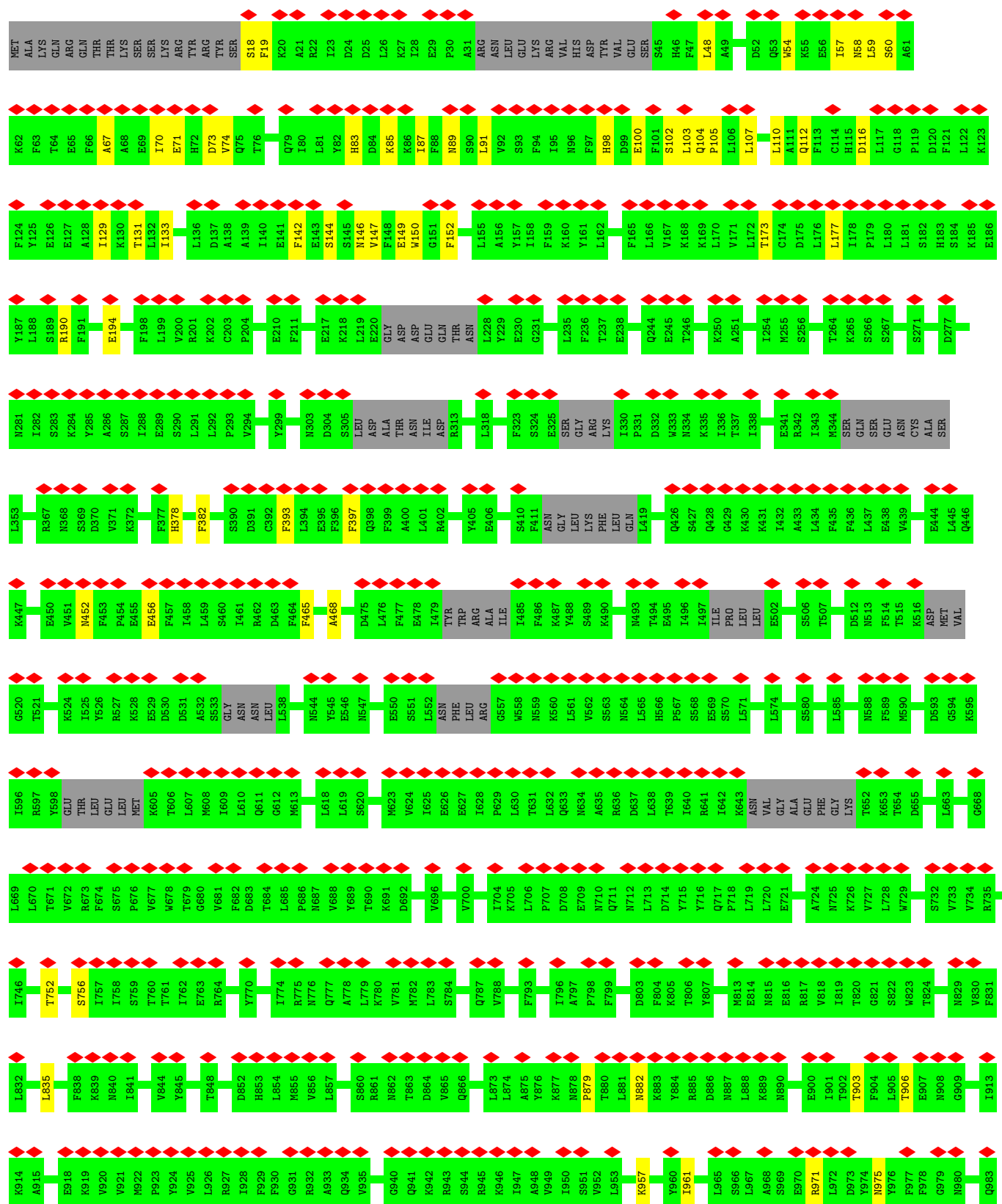
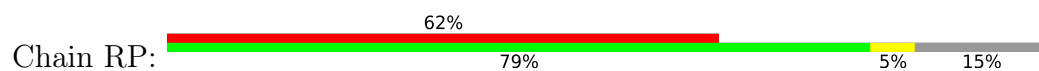
● Molecule 55: RNA cytidine acetyltransferase



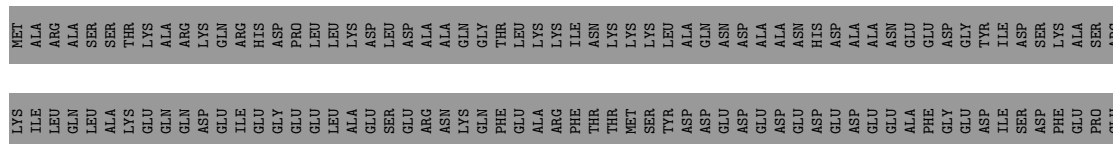
MET	ALA	K3	K4	A5	I6	D7	S8	R9	I10	P11	S12	L13	I14	R15	N16	G17	V18	Q19	T20	K21	Q22	R23	S24	I25	P26	V27	I28	V29	G30	D31	R32	A33	R34	N35	Q36	L37	P38	N39	H41	Y42	L43	M44	M45	S46	A47	D48	L49	M51	N52	K53	S54	V55	L56	W57	A58	Y59	K60							
K61	K62	L63	L64	G65	F66	THR	SER	HIS	ARG	LYS	LYS	ARG	GLU	ASN	ILE	LYS	GLU	ILE	LYS	ARG	THR	GLU	VAL	ASN	GLU	MET	D92	P93	F94	E95	S96	F97	I98	S99	N100	Q101	S102	I103	R104	Y105	V106	Y107	Y108	K109	E110	S111	E112	K113	I114	L115	G116	N117	T118	Y119	G120									
M121	C122	I123	L124	Q125	D126	F127	E128	A129	L130	T131	P132	N133	L134	L135	A136	R137	T138	I139	E140	T141	V142	E143	G144	G145	G146	I147	V148	V149	I150	L151	L152	K153	S154	M155	S156	S157	L158	K159	Q160	L161	Y162	T163	M164	T165	M166	D167	V168	H169	I170	R171	Y172	ARG	THR	GLU	ALA	HIS	GLY	ASP	V180					
V181	A182	R183	F184	N185	E186	R187	F188	I189	L190	S191	L192	G193	S194	N195	P196	N197	C198	L199	V200	V201	D202	D203	E204	L205	N206	V207	L208	P209	I270	S211	G212	K213	K214	N215	V216	K217	P218	LEU	PRO	PRO	LYS	GLU	D224	D225	E226	L227	P228	P229	K230	Q231	L232	E233	L234	Q235	E236	L237	K238	E239	SER					
LEU	GLU	D243	Q245	Q246	P247	G248	S249	L250	V251	S252	L253	S254	K255	T256	V257	N258	Q259	H261	A262	L263	L264	S265	F266	L267	D268	A269	I270	S271	E272	K273	T274	LEU	ASN	PHE	THR	V279	A280	L281	T282	A283	G284	R285	G286	R287	G288	K289	S290	A291	A292	L293	G294	I295	S296	I297	A298	A299	A300							
V301	S302	H303	G304	Y305	S306	N307	L308	F309	V310	T311	S312	P313	S314	P315	E316	N317	L318	K319	T320	L321	F322	E323	F324	I325	F326	K327	G328	F329	D330	A331	L332	K333	Y334	Q335	E336	H337	ILE	TYR	ASP	ILE	ILE	GLN	SER	THR	ASN	PRO	A403	Y404	L405	V406	F407	M408	A409	S410	T411	L412	N413	G414	T415	GLY	THR	GLY	ARG	K360
ARG	ASP	HIS	ARG	GLN	THR	ILE	Q368	Y369	L370	P372	Q373	D374	H375	Q376	V377	L378	G379	Q380	A381	L382	V384	V385	L386	D387	E388	A389	A390	A391	L392	PRO	LEU	PRO	L396	V397	K398	N399	L400	L401	G402	P403	Y404	L405	V406	F407	M408	A409	S410	T411	L412	N413	G414	T415	GLY	THR	GLY	ARG	K360							
SER	L422	S423	L424	K425	L426	L427	Q428	Q429	L430	R431	N432	Q433	ASN	ASN	THR	SER	GLY	ARG	GLU	THR	GLN	THR	ALA	VAL	VAL	ARG	ASP	ASN	LYS	GLU	LYS	ASP	SER	HIS	LEU	HIS	GLN	SER	ARG	GLN	LEU	ARG	E467	L468	S469	L470	D471	E472	P473	L474	R475	Y476	A477	P478	Q479	D480								
P481	L482	E483	K484	W485	L486	N487	K488	L489	L490	C491	L492	D493	V494	T495	L496	L497	K498	N499	P500	R501	F502	A503	T504	R505	G506	Y507	P508	H509	P510	S511	O512	C513	N514	L515	F516	V517	V518	N519	D520	D521	T522	L523	S524	S525	Y526	H527	P528	S530	V529	E531	N532	F533	E535	K536	W537	M538	A539	L540						
Y541	V542	S543	S544	H545	Y546	K547	N548	S549	P550	N551	D552	L553	Q554	L555	M556	S557	D558	A559	P560	A561	H562	K563	L564	F565	V566	L567	P568	P569	R570	S571	D572	P573	N574	D575	G576	G577	V578	L579	P580	P582	L583	C584	A653	S585	L586	Q587	L588	A589	LEU	GLU	D659	Y660	F661	GLY	GLY	LYS	PHE	THR	ASP					
N601	S602	L603	S604	H605	G606	Q607	R608	A609	G610	T614	P615	W616	L617	T618	S619	Q620	D621	F622	D623	E626	F627	L630	S631	O632	A633	R634	P635	V636	R637	L638	A639	T640	H641	F642	E643	Y644	A645	G650	S651	R652	A653	L654	E655	L656	L657	R658	D659	Y660	F661	GLY	GLY	LYS	PHE	THR	ASP									

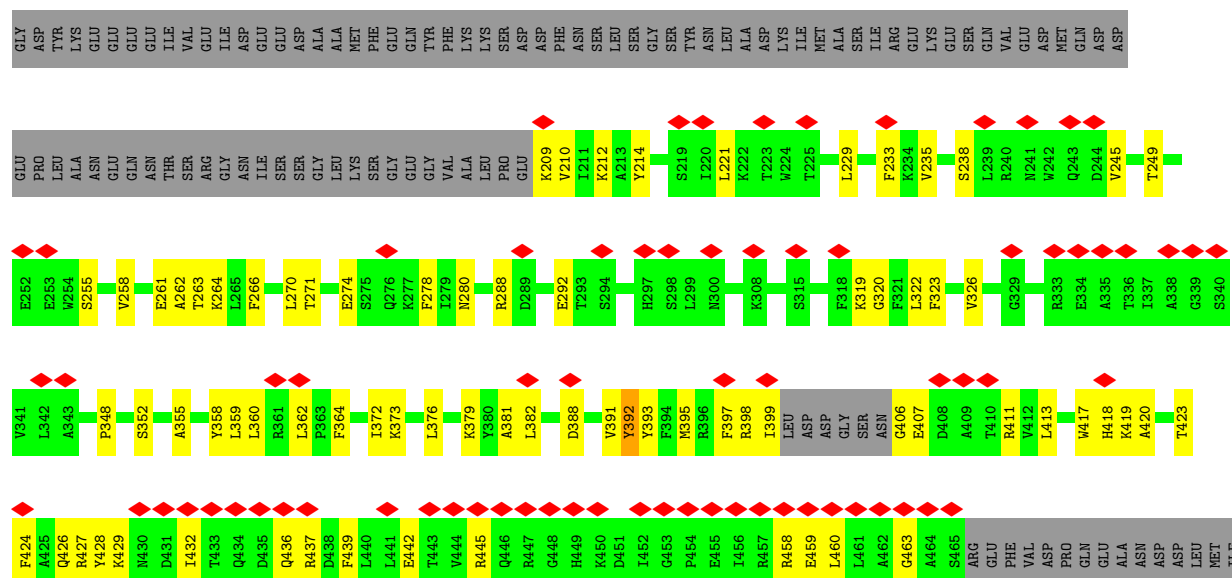


• Molecule 58: U3 small nucleolar RNA-associated protein 20

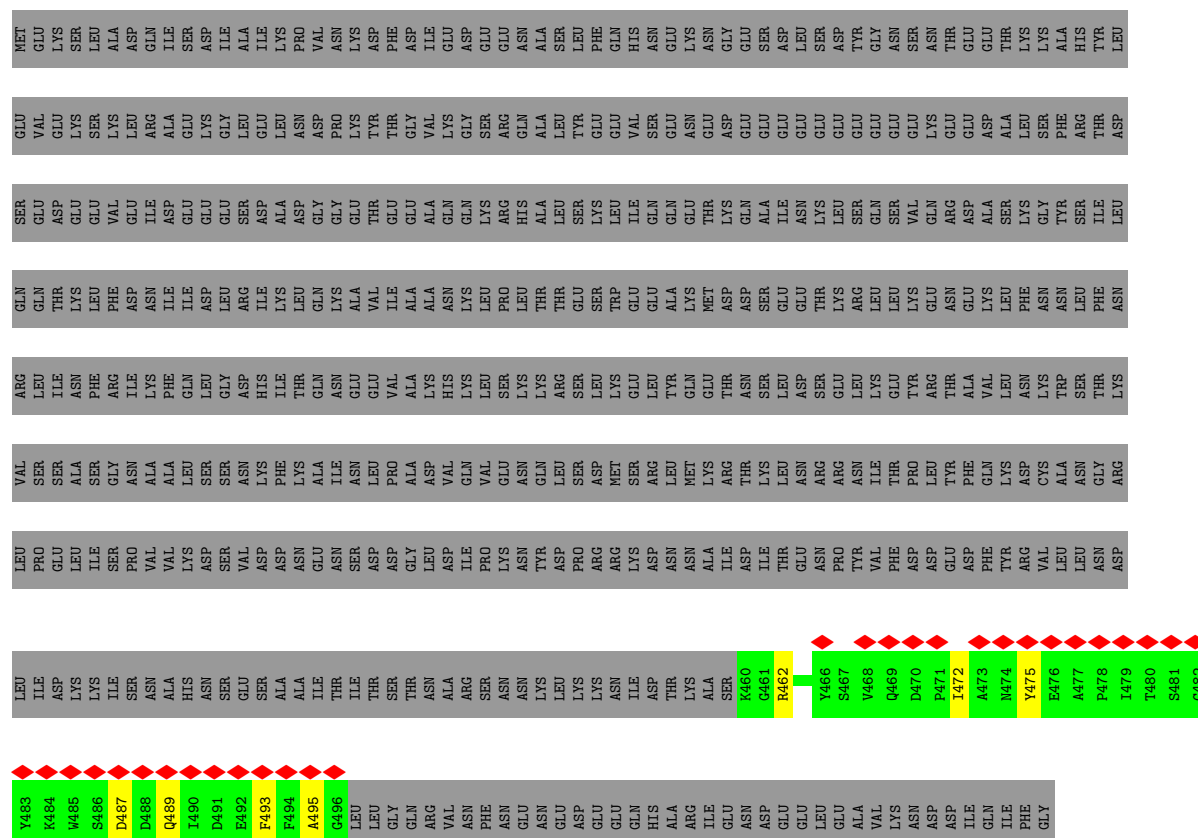


Tl768	L1769	L1770	S1771	P1772	V1773	K1774	A1775	L1776	L1777	M1778	V1779	R1780	I1781	M1782	L1783	R1784	N1785	Q1786	E1723	N1724	F1726	G1727	F1728	A1729	R1793	E1791	R1794	R1795	Y1796	L1797	L1800	H1801	H1802	N1803	S1804	L1805	S1806	E1807	S1808	E1809	S1810	I1811	L1812	K1813	F1814	C1815	H1816	Q1817	S1759	A1758	N1760	I1761	S1762	L1763	T1764	E1765	F1766	SER	ASN	SER	PRO
L1705	K1706	H1707	S1708	D1709	L1710	D1711	T1712	L1713	S1714	S1715	M1716	I1717	V1718	K1719	I1720	M1721	E1722	N1723	Y1724	I1725	F1726	G1727	F1728	A1729	R1733	D1734	S1735	E1736	H1739	T1740	K1741	V1742	K1743	E1744	L1745	K1746	S1747	N1748	Y1751	D1752	E1755	I1756	L1757	A1758	N1759	L1760	I1761	S1762	L1763	T1764	E1765	F1766	SER	ASN	SER	PRO					
L1643	R1644	S1645	K1646	S1647	E1648	E1649	L1650	R1651	D1652	A1653	V1654	R1655	V1656	T1657	L1658	G1659	K1660	S1662	I1663	I1664	L1665	G1666	A1667	E1668	Y1669	L1670	V1671	F1672	V1673	I1674	K1675	E1676	L1677	M1678	A1679	T1680	L1681	L1682	R1683	G1684	S1685	T1686	H1688	L1689	S1691	Y1692	T1693	V1694	H1695	Y1696	I1697	L1698	K1699	H1702							
GLU	PRO	ASN	PHE	ILE	LYS	GLN	GLU	LEU	TYR	PRO	THR	LEU	LYS	ILE	GLY	ARG	ASP	GLU	THR	ILE	E1608	R1609	M1610	I1611	I1612	A1613	E1614	A1615	L1616	V1617	M1618	I1619	V1620	L1621	G1622	L1623	T1624	M1625	L1626	D1627	I1628	T1629	M1630	F1631	L1632	P1633	S1634	I1635	L1636	T1637	M1638	I1639	C1640								
HIS	R1461	R1462	Q1463	R1464	A1465	I1466	R1467	D1468	L1469	G1470	E1471	H1472	A1473	H1474	L1475	L1476	K1477	D1478	N1479	S1480	T1481	S1482	H1483	Y1484	L1485	I1486	P1487	M1488	Y1430	F1431	D1432	F1433	F1434	A1435	D1436	M1437	A1438	L1439	L1440	L1441	Y1442	N1443	G1444	D1445	E1446	E1447	A1448	D1449	PHE	PHE	THR	ASN	ASN	VAL	HIS	ILE	GLN	LEU	ASP		
L1398	L1399	R1403	I1404	G1405	L1406	R1407	D1408	S1409	L1410	E1411	E1412	V1413	GLN	SER	GLU	TYR	VAL	SER	V1420	L1421	S1422	L1423	M1424	V1425	K1426	N1427	T1428	K1429	Y1430	F1431	D1432	D1433	F1434	A1435	D1436	M1437	A1438	L1439	L1440	L1441	Y1442	N1443	G1444	D1445	E1446	E1447	A1448	D1449	PHE	PHE	THR	ASN	ASN	VAL	HIS	ILE	GLN	LEU			
SER	TYR	SER	GLU	LEU	GLU	TRP	LEU	PRO	LEU	LEU	PHE	THR	PHE	THR	PHE	HIS	PHE	ILE	ASN	ASN	GLN	L1291	G1292	R1293	K1294	E1299	L1301	S1302	K1303	L1304	E1237	V1305	A1306	L1307	L1308	N1309	S1310	Y1311	S1312	S1313	S1314	R1315	M1316	H1317	E1318	Y1319	D1320	F1321	P1322	ARG	ILE	LEU	SER	THR	PHE	LYS	GLY	LEU	ASP	TYR	LYS
F1275	D1276	E1277	N1278	L1279	L1280	R1281	V1282	S1283	L1284	T1285	E1286	L1287	F1288	L1291	G1292	R1293	K1294	E1299	L1301	S1302	K1303	L1304	E1237	V1305	A1306	L1307	L1308	N1309	S1310	Y1311	S1312	S1313	S1314	R1315	M1316	H1317	E1318	Y1319	D1320	F1321	P1322	ARG	ILE	LEU	SER	THR	PHE	LYS	GLY	LEU	ASP	TYR	LYS								
F1210	I1211	Q1212	D1213	D1214	H1215	V1216	R1217	S1218	R1219	I1220	S1221	S1222	S1223	L1224	I1225	S1226	I1227	L1228	K1229	G1230	K1231	L1232	K1233	K1234	L1235	Q1236	E1237	N1238	D1239	T1240	Q1241	K1242	I1243	I1246	L1247	K1248	L1249	I1250	V1251	F1252	N1253	Y1254	C1256	S1257	E1262	E1263	L1264	Y1265	T1266	T1267	I1268	S1269	S1270	L1271	F1272	K1273					
P1149	I1150	I1151	E1152	A1153	A1154	D1155	L1156	I1157	I1158	P1161	V1162	M1163	D1164	D1165	H1166	Y1167	V1168	D1169	L1170	V1171	L1172	L1173	I1174	C1175	L1176	S1177	C1178	L1179	K1180	I1181	L1182	P1183	S1184	L1185	Y1186	V1187	K1188	L1189	S1190	D1191	S1192	M1193	S1194	I1195	S1196	T1197	F1198	L1199	N1199	Q1140	H1141	V1142	K1143	E1144	A1145	T1146	F1147	G1148			
I1082	Y1083	A1084	V1085	V1086	V1087	K1088	P1089	R1090	H1093	F1094	S1095	D1096	E1097	N1098	Y1028	S1029	I1030	A1031	M1032	A1033	V1036	L1037	D1038	T1039	E1040	S1041	T1042	E1043	E1044	V1045	L1046	L1047	R1048	K1049	M1050	A1051	S1052	N1053	L1054	G1058	L1059	K1060	C1061	V1069	G1070	N1071	T1072	S1076	T1077	S1078	M1079	E1080	D1081								



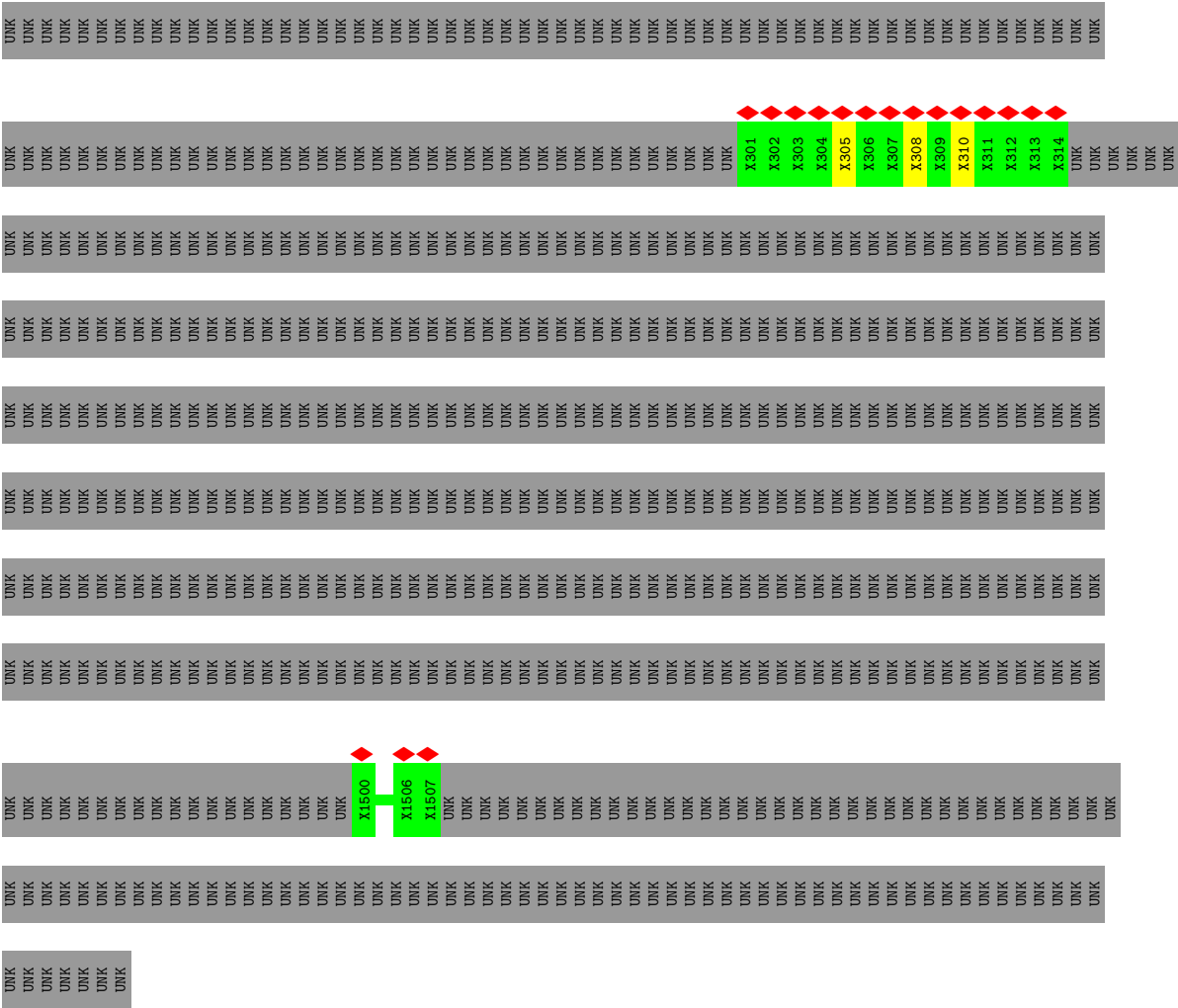


• Molecule 61: Protein BFR2

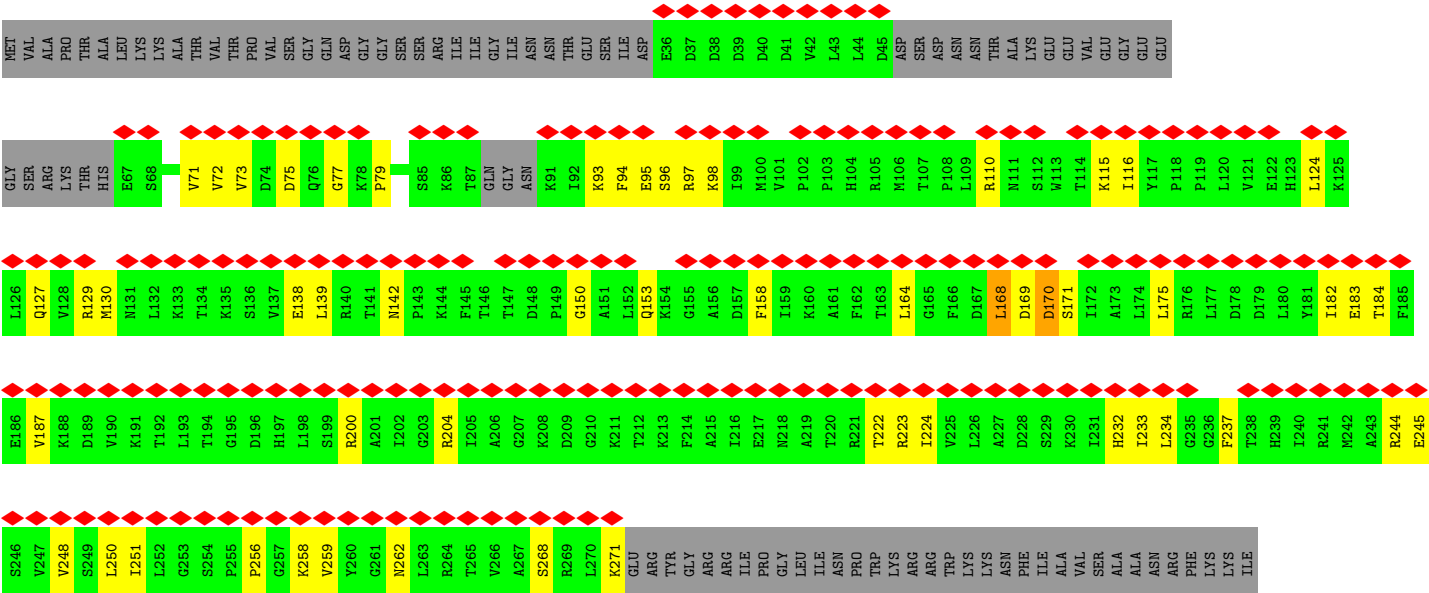


• Molecule 62: Unassigned peptides 1





● Molecule 63: Pno1



[illegible]





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3841	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.015	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	531.19995, 531.19995, 531.19995	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3279998, 1.3279998, 1.3279998	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.46	0/4141	0.62	3/6433 (0.0%)
2	5A	0.40	0/4605	0.46	1/7168 (0.0%)
3	SA	0.35	1/31727 (0.0%)	0.50	17/49393 (0.0%)
4	SC	0.44	0/1856	0.77	3/2490 (0.1%)
5	SF	0.29	0/1854	0.66	0/2504
6	SG	0.49	0/1690	0.67	2/2285 (0.1%)
7	SH	0.24	0/1341	0.61	1/1789 (0.1%)
8	SI	0.32	0/1341	0.69	2/1806 (0.1%)
9	SJ	0.26	0/1347	0.60	0/1801
10	SK	0.44	0/1410	0.63	0/1888
11	SM	0.27	0/1020	0.64	0/1374
12	SO	0.40	0/1109	0.63	0/1495
13	SP	0.48	0/879	0.83	0/1186
14	SR	0.52	0/990	0.77	3/1335 (0.2%)
15	SX	0.46	0/1020	0.63	0/1371
16	SY	0.48	0/798	0.65	0/1065
17	SZ	0.36	0/822	0.73	0/1103
18	Sc	0.40	0/613	0.63	0/828
19	Sd	0.50	0/499	0.72	2/670 (0.3%)
20	3B	0.51	0/1901	0.66	0/2567
20	3C	0.38	0/1796	0.69	2/2424 (0.1%)
21	3D	0.40	0/2891	0.62	0/3895
22	3E	0.38	0/3059	0.62	0/4153
23	3F	0.36	0/3715	0.64	0/5001
24	3G	0.51	0/928	0.72	1/1262 (0.1%)
24	3H	0.46	0/928	0.70	0/1262
25	A4	0.43	0/5321	0.66	0/7207
26	A5	0.44	0/4044	0.65	0/5493
27	A8	0.38	0/3249	0.86	12/4454 (0.3%)
28	A9	0.30	0/951	0.61	0/1287
29	AE	0.32	1/10049 (0.0%)	0.56	1/13737 (0.0%)
30	AF	0.48	0/3993	0.68	0/5413

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AG	0.42	0/6699	0.64	3/9077 (0.0%)
32	B1	0.59	0/6474	0.70	3/8763 (0.0%)
33	B2	0.39	0/6628	0.69	2/8954 (0.0%)
34	B3	0.35	0/6014	0.70	0/8137
35	B8	0.55	0/3848	0.63	0/5218
36	BE	0.54	0/6580	0.65	2/8901 (0.0%)
37	B6	0.37	0/2849	0.60	0/3853
38	5B	0.32	0/499	0.62	0/659
39	5C	0.58	0/3690	0.67	2/4991 (0.0%)
40	5D	0.47	0/1417	0.74	0/1885
41	5E	0.42	0/1580	0.87	1/2115 (0.0%)
42	5F	0.38	0/1559	0.81	2/2097 (0.1%)
43	5G	0.34	0/1792	0.76	3/2425 (0.1%)
44	5H	0.47	0/601	0.59	0/789
45	5I	0.56	0/3844	0.68	0/5174
46	5J	0.36	0/1151	0.56	0/1535
47	5K	0.52	0/1426	0.66	0/1917
48	RA	0.28	0/2769	0.66	2/3753 (0.1%)
49	RB	0.37	0/1121	0.79	0/1487
50	RE	0.33	0/8924	0.64	4/12070 (0.0%)
51	RF	0.28	0/2004	0.66	1/2697 (0.0%)
52	RG	0.32	0/1727	0.70	0/2329
52	RH	0.37	0/1828	0.59	0/2470
53	RJ	0.45	0/6514	0.62	0/8768
54	RK	0.39	0/2832	0.64	0/3825
55	RL	0.21	0/4549	0.51	1/6241 (0.0%)
55	RM	0.16	0/3765	0.44	1/5218 (0.0%)
56	RN	0.31	0/4591	0.63	1/6187 (0.0%)
57	RO	0.32	0/3849	0.63	0/5261
58	RP	0.21	0/12225	0.54	4/16812 (0.0%)
59	RQ	0.43	0/1879	0.73	3/2564 (0.1%)
60	RS	0.30	0/2104	0.70	1/2854 (0.0%)
61	RY	0.23	0/307	0.53	0/415
63	RT	0.43	0/1611	0.77	1/2174 (0.0%)
64	ST	0.35	0/908	0.74	2/1221 (0.2%)
65	SU	0.56	1/1130 (0.1%)	0.94	3/1517 (0.2%)
66	RD	0.26	0/2453	0.67	2/3308 (0.1%)
67	RZ	0.27	0/6737	0.60	3/9099 (0.0%)
All	All	0.39	3/232365 (0.0%)	0.63	97/322899 (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
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
12	SO	0	1
13	SP	0	1
17	SZ	0	1
18	Sc	0	1
21	3D	0	3
22	3E	0	1
23	3F	0	1
24	3G	0	2
24	3H	0	1
25	A4	0	1
26	A5	0	1
27	A8	0	2
31	AG	0	2
32	B1	0	2
33	B2	0	8
34	B3	0	11
36	BE	0	1
39	5C	0	1
40	5D	0	1
43	5G	0	2
45	5I	0	2
48	RA	0	2
49	RB	0	1
50	RE	0	1
51	RF	0	1
53	RJ	0	2
54	RK	0	1
55	RL	0	1
55	RM	0	1
56	RN	0	1
57	RO	0	1
58	RP	0	3
59	RQ	0	4
67	RZ	0	2
All	All	0	75

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	SU	46	PRO	C-N	12.73	1.50	1.33
29	AE	564	VAL	C-N	5.40	1.40	1.34
3	SA	1572	G	O3'-P	-5.25	1.53	1.61

All (97) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	SU	46	PRO	CA-C-N	17.60	137.85	119.89
65	SU	46	PRO	C-N-CA	17.60	137.85	119.89
3	SA	1541	G	P-O5'-C5'	-10.70	104.84	120.90
27	A8	316	PRO	N-CA-CB	10.50	109.84	102.81
3	SA	1541	G	O5'-C5'-C4'	9.05	125.08	111.50
1	3A	99	U	C4'-C3'-O3'	8.84	126.26	113.00
1	3A	317	A	C4'-C3'-O3'	8.44	125.66	113.00
27	A8	258	PRO	N-CA-CB	8.32	111.99	103.25
3	SA	1533	C	C2'-C3'-O3'	8.29	121.94	109.50
3	SA	1533	C	C3'-C2'-O2'	8.18	126.87	114.60
1	3A	321	C	N1-C1'-C2'	-8.05	99.92	112.00
66	RD	1223	PRO	N-CA-CB	8.04	111.70	103.25
27	A8	325	PRO	N-CA-CB	7.90	111.55	103.25
50	RE	1105	PRO	O-C-N	-7.87	112.02	122.64
66	RD	1205	PRO	N-CA-CB	7.67	110.59	103.15
27	A8	453	PRO	N-CA-CB	7.65	110.46	103.34
27	A8	392	PRO	N-CA-CB	7.58	111.21	103.25
27	A8	429	PRO	N-CA-CB	7.46	110.27	103.19
3	SA	1541	G	C2'-C3'-O3'	7.17	124.46	113.70
27	A8	309	PRO	N-CA-CB	7.11	110.72	103.25
33	B2	267	ASP	CA-C-N	6.86	134.64	121.54
33	B2	267	ASP	C-N-CA	6.86	134.64	121.54
2	5A	312	U	P-O3'-C3'	6.82	130.44	120.20
3	SA	1484	G	O3'-P-O5'	-6.82	93.77	104.00
67	RZ	658	PRO	N-CA-CB	6.76	110.35	103.25
27	A8	390	PRO	N-CA-CB	6.67	110.25	103.25
58	RP	2033	LYS	CA-C-N	6.63	134.21	121.54
58	RP	2033	LYS	C-N-CA	6.63	134.21	121.54
63	RT	79	PRO	N-CA-CB	6.62	110.33	103.38
27	A8	235	PRO	N-CA-CB	6.57	110.15	103.25
32	B1	339	LEU	CA-C-N	6.53	132.13	122.86
32	B1	339	LEU	C-N-CA	6.53	132.13	122.86
59	RQ	801	PRO	N-CA-CB	6.45	110.03	103.25
27	A8	298	PRO	N-CA-CB	6.36	110.26	103.52
32	B1	339	LEU	O-C-N	6.25	130.39	123.33
51	RF	157	GLU	N-CA-C	6.13	116.36	108.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	RL	744	PRO	N-CA-C	6.10	125.03	112.47
3	SA	1484	G	P-O3'-C3'	-6.03	111.16	120.20
55	RM	744	PRO	N-CA-C	6.00	124.82	112.47
31	AG	141	LEU	N-CA-C	5.91	117.82	110.91
24	3G	67	LEU	CA-CB-CG	5.87	136.85	116.30
8	SI	117	THR	CA-C-N	5.81	132.64	121.54
8	SI	117	THR	C-N-CA	5.81	132.64	121.54
58	RP	1745	ILE	CA-C-N	5.81	132.63	121.54
58	RP	1745	ILE	C-N-CA	5.81	132.63	121.54
20	3C	217	ILE	CA-C-N	-5.80	118.29	123.33
20	3C	217	ILE	C-N-CA	-5.80	118.29	123.33
43	5G	192	ASP	CA-C-N	5.77	132.56	121.54
43	5G	192	ASP	C-N-CA	5.77	132.56	121.54
64	ST	55	HIS	CA-C-N	-5.75	113.90	123.33
64	ST	55	HIS	C-N-CA	-5.75	113.90	123.33
3	SA	1052	U	O3'-P-O5'	5.68	112.52	104.00
59	RQ	789	PRO	N-CA-CB	5.68	109.21	103.25
36	BE	840	PHE	CA-C-N	5.66	130.09	121.03
36	BE	840	PHE	C-N-CA	5.66	130.09	121.03
65	SU	45	MET	N-CA-C	5.64	113.09	108.07
43	5G	157	PHE	N-CA-C	5.60	122.19	109.81
14	SR	123	ARG	CA-C-N	5.60	140.44	127.00
14	SR	123	ARG	C-N-CA	5.60	140.44	127.00
4	SC	54	LEU	CA-CB-CG	5.59	135.87	116.30
3	SA	1574	G	N9-C1'-C2'	-5.58	103.63	112.00
3	SA	1541	G	O4'-C4'-C3'	5.52	109.52	104.00
27	A8	640	LEU	CA-C-O	-5.49	115.04	120.70
50	RE	924	LEU	CA-CB-CG	5.49	135.51	116.30
27	A8	636	GLN	N-CA-C	-5.48	105.40	111.71
48	RA	286	GLU	CA-C-N	5.48	132.01	121.54
48	RA	286	GLU	C-N-CA	5.48	132.01	121.54
59	RQ	313	PHE	N-CA-C	5.44	121.84	109.81
3	SA	579	A	P-O3'-C3'	5.38	128.26	120.20
29	AE	1589	ILE	N-CA-C	-5.35	107.61	112.96
3	SA	1476	C	C4'-C3'-O3'	5.32	120.98	113.00
4	SC	54	LEU	CA-C-N	5.31	131.68	121.54
4	SC	54	LEU	C-N-CA	5.31	131.68	121.54
3	SA	272	U	P-O3'-C3'	5.30	128.15	120.20
3	SA	1541	G	C5'-C4'-O4'	5.29	117.74	109.80
3	SA	1803	G	P-O3'-C3'	5.24	128.05	120.20
7	SH	41	VAL	N-CA-C	-5.23	107.73	112.96
50	RE	1105	PRO	CA-C-N	5.23	130.70	122.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	RE	1105	PRO	C-N-CA	5.23	130.70	122.33
67	RZ	1141	LEU	CA-C-N	5.16	131.39	121.54
67	RZ	1141	LEU	C-N-CA	5.16	131.39	121.54
42	5F	174	ARG	CA-C-N	5.13	131.34	121.54
42	5F	174	ARG	C-N-CA	5.13	131.34	121.54
41	5E	448	LEU	CA-CB-CG	5.09	134.11	116.30
14	SR	123	ARG	C-N-CD	-5.06	109.47	120.60
3	SA	56	U	P-O3'-C3'	5.05	127.78	120.20
19	Sd	50	GLU	CA-C-N	5.03	131.15	121.54
19	Sd	50	GLU	C-N-CA	5.03	131.15	121.54
39	5C	456	SER	CA-C-N	5.03	128.80	121.31
39	5C	456	SER	C-N-CA	5.03	128.80	121.31
3	SA	1594	G	C4'-C3'-O3'	5.02	116.94	109.40
6	SG	99	MET	CA-C-N	5.02	131.12	121.54
6	SG	99	MET	C-N-CA	5.02	131.12	121.54
60	RS	392	TYR	CA-CB-CG	5.02	122.93	113.90
31	AG	138	ASP	CA-C-N	5.01	128.19	120.82
31	AG	138	ASP	C-N-CA	5.01	128.19	120.82
56	RN	592	ARG	CA-CB-CG	5.01	124.11	114.10

There are no chirality outliers.

All (75) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	3D	142	LEU	Peptide
21	3D	202	HIS	Peptide
21	3D	286	ARG	Peptide
22	3E	331	LYS	Peptide
23	3F	237	ASP	Peptide
24	3G	59	GLU	Peptide
24	3G	9	PHE	Peptide
24	3H	59	GLU	Peptide
39	5C	551	SER	Peptide
40	5D	138	ASP	Peptide
43	5G	254	PHE	Peptide
43	5G	74	ASP	Peptide
45	5I	230	ASN	Peptide
45	5I	283	ASP	Peptide
25	A4	54	LYS	Peptide
26	A5	167	SER	Peptide
27	A8	496	TYR	Peptide
27	A8	529	HIS	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
31	AG	178	PHE	Peptide
31	AG	780	GLU	Peptide
32	B1	288	ASP	Peptide
32	B1	690	ALA	Peptide
33	B2	131	GLY	Peptide
33	B2	213	LYS	Peptide
33	B2	266	SER	Peptide
33	B2	267	ASP	Peptide
33	B2	278	ASP	Peptide
33	B2	44	SER	Peptide
33	B2	613	ALA	Peptide
33	B2	916	HIS	Peptide
34	B3	34	THR	Peptide
34	B3	435	ALA	Peptide
34	B3	473	ALA	Peptide
34	B3	479	ILE	Peptide
34	B3	480	ILE	Peptide
34	B3	585	ASN	Peptide
34	B3	593	CYS	Peptide
34	B3	594	GLY	Peptide
34	B3	627	ASN	Peptide
34	B3	89	HIS	Peptide
34	B3	90	LEU	Peptide
36	BE	94	TYR	Peptide
48	RA	111	TRP	Peptide
48	RA	173	LEU	Peptide
49	RB	261	SER	Peptide
50	RE	767	GLN	Peptide
51	RF	253	ALA	Peptide
53	RJ	1026	LYS	Peptide
53	RJ	868	ARG	Peptide
54	RK	333	PHE	Peptide
55	RL	743	VAL	Peptide
55	RM	743	VAL	Peptide
56	RN	286	SER	Peptide
57	RO	144	PRO	Peptide
58	RP	1746	LYS	Peptide
58	RP	2051	ASP	Peptide
58	RP	835	LEU	Peptide
59	RQ	313	PHE	Peptide
59	RQ	786	THR	Peptide
59	RQ	787	THR	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
59	RQ	806	ARG	Peptide
67	RZ	1001	SER	Peptide
67	RZ	1069	SER	Peptide
4	SC	238	GLU	Peptide
5	SF	193	GLY	Peptide
5	SF	195	ILE	Peptide
8	SI	133	THR	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide
9	SJ	85	PRO	Peptide
11	SM	128	CYS	Peptide
12	SO	58	HIS	Peptide
13	SP	90	ARG	Peptide
17	SZ	76	TYR	Peptide
18	Sc	49	HIS	Peptide

5.2 Too-close contacts

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	3711	0	1882	58	0
2	5A	4117	0	2068	38	0
3	SA	28383	0	14310	307	0
4	SC	1830	0	1914	33	0
5	SF	1815	0	1870	43	0
6	SG	1669	0	1724	18	0
7	SH	1327	0	1403	31	0
8	SI	1321	0	1387	22	0
9	SJ	1324	0	1344	46	0
10	SK	1388	0	1467	32	0
11	SM	997	0	1048	34	0
12	SO	1087	0	1152	9	0
13	SP	868	0	894	63	0
14	SR	973	0	1029	18	0
15	SX	1003	0	1040	15	0
16	SY	786	0	843	7	0
17	SZ	809	0	842	15	0
18	Sc	603	0	623	9	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	Sd	497	0	535	3	0
20	3B	1865	0	1910	30	0
20	3C	1763	0	1805	46	0
21	3D	2848	0	2815	43	0
22	3E	3028	0	2813	58	0
23	3F	3643	0	3654	78	0
24	3G	916	0	964	11	0
24	3H	916	0	964	25	0
25	A4	5226	0	5199	96	0
26	A5	3976	0	3919	62	0
27	A8	3229	0	2281	131	0
28	A9	939	0	898	47	0
29	AE	9955	0	7968	102	0
30	AF	3911	0	3906	77	0
31	AG	6570	0	6473	142	0
32	B1	6331	0	6236	140	0
33	B2	6502	0	6493	126	0
34	B3	5919	0	6007	147	0
35	B8	3764	0	3757	54	0
36	BE	6450	0	6420	102	0
37	B6	2800	0	2517	32	0
38	5B	495	0	561	12	0
39	5C	3612	0	3578	62	0
40	5D	1396	0	1407	49	0
41	5E	1564	0	1592	180	0
42	5F	1530	0	1572	84	0
43	5G	1756	0	1765	56	0
44	5H	596	0	661	7	0
45	5I	3765	0	3714	79	0
46	5J	1131	0	1161	19	0
47	5K	1403	0	1484	20	0
48	RA	2709	0	2622	61	0
49	RB	1108	0	1087	27	0
50	RE	8716	0	8828	236	0
51	RF	1963	0	1942	48	0
52	RG	1701	0	1767	39	0
52	RH	1799	0	1872	28	0
53	RJ	6379	0	6506	152	0
54	RK	2781	0	2878	53	0
55	RL	4539	0	2874	26	0
55	RM	3779	0	1650	9	0
56	RN	4529	0	4262	87	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	RO	3766	0	3269	58	0
58	RP	12171	0	7749	78	0
59	RQ	1853	0	1474	30	0
60	RS	2051	0	2096	53	0
61	RY	299	0	275	6	0
62	X1	110	0	29	4	0
63	RT	1587	0	1583	73	0
64	ST	896	0	930	60	0
65	SU	1112	0	1124	65	0
66	RD	2412	0	2263	42	0
67	RZ	6604	0	6637	120	0
68	5K	1	0	0	0	0
68	Sc	1	0	0	0	0
69	RJ	32	0	12	2	0
70	RJ	1	0	0	0	0
71	RZ	27	0	12	1	0
All	All	225233	0	195610	3575	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 (3575) 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)
27:A8:596:LYS:HE3	27:A8:637:LEU:CD2	1.25	1.57
50:RE:1203:ASN:HD22	50:RE:1219:ILE:CG2	1.50	1.23
32:B1:382:THR:O	41:5E:481:PRO:HB3	1.40	1.21
3:SA:1478:G:OP1	65:SU:39:THR:HB	1.38	1.20
41:5E:366:GLU:OE2	43:5G:247:ILE:HG21	1.40	1.20
27:A8:596:LYS:HE3	27:A8:637:LEU:HD23	1.22	1.20
50:RE:1102:LEU:HD23	50:RE:1180:ASN:O	1.40	1.20
27:A8:443:CYS:HA	31:AG:728:LEU:HD13	1.25	1.19
27:A8:596:LYS:CE	27:A8:637:LEU:CD2	2.21	1.18
41:5E:520:LEU:HD11	41:5E:525:LYS:CG	1.74	1.17
27:A8:596:LYS:CE	27:A8:637:LEU:HD22	1.75	1.16
42:5F:8:HIS:HA	45:5I:53:MET:HE1	1.26	1.16
27:A8:563:LEU:HB2	27:A8:598:GLU:OE1	1.41	1.16
27:A8:633:GLN:O	27:A8:637:LEU:HG	1.44	1.14
39:5C:430:VAL:HG21	42:5F:3:ARG:HD3	1.25	1.14
27:A8:673:THR:HG22	28:A9:490:GLU:HB2	1.20	1.14
40:5D:78:LEU:HB2	53:RJ:1082:GLN:HE21	1.10	1.14

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:ST:41:ARG:HG3	65:SU:45:MET:HG2	1.18	1.12
27:A8:673:THR:HG22	28:A9:490:GLU:CB	1.80	1.12
13:SP:96:PRO:HG3	63:RT:237:PHE:CE1	1.84	1.12
41:5E:520:LEU:CD1	41:5E:525:LYS:HG3	1.80	1.11
41:5E:520:LEU:HD11	41:5E:525:LYS:HG3	1.29	1.10
36:BE:737:LEU:HA	36:BE:740:ILE:CG2	1.82	1.08
27:A8:631:SER:O	27:A8:634:LEU:HG	1.56	1.06
50:RE:1203:ASN:HD22	50:RE:1219:ILE:HG21	1.18	1.05
27:A8:443:CYS:N	31:AG:728:LEU:HD22	1.70	1.05
32:B1:298:LEU:HD12	41:5E:476:MET:SD	1.95	1.05
50:RE:518:PHE:CZ	50:RE:1075:LEU:HG	1.92	1.05
27:A8:443:CYS:CB	31:AG:728:LEU:HB3	1.86	1.04
65:SU:38:LYS:HE2	65:SU:43:ASN:O	1.56	1.04
50:RE:1204:VAL:HB	50:RE:1212:VAL:HG11	1.35	1.03
34:B3:690:HIS:CG	41:5E:519:GLU:HB2	1.94	1.03
32:B1:341:GLN:NE2	32:B1:378:PHE:HB3	1.73	1.03
32:B1:298:LEU:CD1	41:5E:476:MET:SD	2.47	1.02
42:5F:19:LEU:HG	47:5K:25:LEU:HB3	1.41	1.02
64:ST:54:LEU:HD12	65:SU:48:GLN:HE22	1.24	1.02
36:BE:740:ILE:HG13	41:5E:483:TYR:OH	1.58	1.02
33:B2:17:ILE:HG22	33:B2:52:TRP:CZ2	1.94	1.01
56:RN:527:GLN:O	56:RN:531:GLN:HB2	1.61	1.01
27:A8:592:ARG:HB2	27:A8:596:LYS:HZ1	0.88	1.01
32:B1:418:ARG:HD2	41:5E:489:SER:O	1.59	1.01
59:RQ:298:TRP:NE1	59:RQ:899:LYS:HG3	1.75	1.00
27:A8:631:SER:HA	27:A8:634:LEU:HD11	1.43	1.00
41:5E:343:GLU:OE2	53:RJ:1007:TYR:HE1	1.43	1.00
27:A8:592:ARG:HB2	27:A8:596:LYS:NZ	1.76	1.00
34:B3:157:ASN:HB2	63:RT:77:GLY:HA2	1.43	1.00
3:SA:36:C:H42	3:SA:472:U:H3	1.00	1.00
41:5E:384:ARG:HD2	43:5G:83:ILE:HD12	1.42	0.99
32:B1:337:TYR:OH	41:5E:474:ILE:HD13	1.61	0.98
39:5C:430:VAL:HG21	42:5F:3:ARG:CD	1.94	0.98
3:SA:1479:A:P	65:SU:57:ARG:HH21	1.88	0.97
27:A8:593:ASP:HA	27:A8:596:LYS:HD2	1.43	0.97
56:RN:86:ILE:HA	56:RN:89:GLN:HE21	1.26	0.97
50:RE:1203:ASN:ND2	50:RE:1219:ILE:CG2	2.28	0.96
50:RE:518:PHE:HZ	50:RE:1075:LEU:HG	1.28	0.96
10:SK:65:LYS:HZ2	23:3F:59:PRO:CD	1.78	0.95
32:B1:54:HIS:HE2	32:B1:72:SER:HG	1.13	0.95
10:SK:65:LYS:HZ2	23:3F:59:PRO:CG	1.78	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5E:341:LEU:HD12	64:ST:120:ARG:NH1	1.81	0.94
50:RE:918:ARG:HE	50:RE:1089:PHE:HE2	1.12	0.94
27:A8:443:CYS:CA	31:AG:728:LEU:HD22	1.96	0.94
1:3A:319:G:H5'	20:3C:121:LYS:NZ	1.82	0.94
50:RE:1204:VAL:HB	50:RE:1212:VAL:CG1	1.97	0.94
27:A8:596:LYS:HE2	27:A8:637:LEU:HA	1.48	0.93
64:ST:41:ARG:HG3	65:SU:45:MET:CG	1.99	0.93
41:5E:319:VAL:HG21	53:RJ:1038:ILE:CG2	1.97	0.93
10:SK:65:LYS:HZ2	23:3F:59:PRO:CB	1.82	0.93
50:RE:1203:ASN:ND2	50:RE:1219:ILE:HG21	1.83	0.92
36:BE:739:VAL:HG21	41:5E:487:ALA:HB2	1.51	0.92
13:SP:107:ARG:NH1	63:RT:150:GLY:CA	2.31	0.92
27:A8:596:LYS:CE	27:A8:637:LEU:HD23	1.91	0.92
36:BE:737:LEU:HA	36:BE:740:ILE:HG21	1.50	0.92
27:A8:443:CYS:HA	31:AG:728:LEU:CD1	2.00	0.91
2:5A:9:G:H5'	28:A9:483:LYS:NZ	1.85	0.91
13:SP:93:THR:HG21	63:RT:184:THR:HB	1.51	0.91
3:SA:1477:G:OP1	65:SU:43:ASN:HB3	1.71	0.91
32:B1:418:ARG:HH21	32:B1:418:ARG:HG3	1.33	0.91
50:RE:918:ARG:NE	50:RE:1089:PHE:HE2	1.68	0.91
50:RE:1098:PHE:HD2	50:RE:1184:GLY:H	1.12	0.90
3:SA:36:C:N4	3:SA:472:U:H3	1.70	0.90
56:RN:86:ILE:HA	56:RN:89:GLN:NE2	1.87	0.90
10:SK:65:LYS:NZ	23:3F:59:PRO:CG	2.35	0.89
34:B3:494:ILE:N	34:B3:510:SER:HG	1.71	0.89
41:5E:343:GLU:OE2	53:RJ:1007:TYR:CE1	2.25	0.89
50:RE:1157:TYR:HE1	50:RE:1203:ASN:HD21	1.17	0.89
27:A8:673:THR:HG22	28:A9:490:GLU:CA	2.02	0.88
66:RD:1473:ASN:HB3	66:RD:1509:GLU:OE2	1.72	0.88
53:RJ:871:MET:HE2	53:RJ:930:LYS:HZ2	1.37	0.88
27:A8:592:ARG:CB	27:A8:596:LYS:HZ1	1.82	0.88
45:5I:231:GLU:OE2	59:RQ:899:LYS:HD3	1.74	0.87
65:SU:38:LYS:CE	65:SU:43:ASN:O	2.22	0.87
41:5E:341:LEU:HD12	64:ST:120:ARG:HH12	1.37	0.87
50:RE:1203:ASN:HD22	50:RE:1219:ILE:HG22	1.37	0.87
1:3A:318:U:H3	20:3C:119:GLY:HA3	1.36	0.87
32:B1:418:ARG:CD	41:5E:489:SER:O	2.21	0.87
41:5E:493:GLN:NE2	41:5E:497:ASN:HB3	1.88	0.87
27:A8:673:THR:CG2	28:A9:490:GLU:CA	2.54	0.86
40:5D:78:LEU:HB2	53:RJ:1082:GLN:NE2	1.91	0.86
40:5D:78:LEU:HD22	53:RJ:1082:GLN:CG	2.05	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5E:319:VAL:HG21	53:RJ:1038:ILE:HG22	1.57	0.85
3:SA:1538:U:C5	3:SA:1540:G:O6	2.29	0.85
41:5E:384:ARG:HE	43:5G:82:GLY:H	1.22	0.85
10:SK:65:LYS:NZ	23:3F:59:PRO:CD	2.38	0.85
27:A8:596:LYS:HE3	27:A8:637:LEU:HD22	0.88	0.85
50:RE:1065:THR:O	50:RE:1069:LYS:HG3	1.75	0.85
55:RM:313:PRO:O	55:RM:372:PRO:HA	1.77	0.85
56:RN:86:ILE:CA	56:RN:89:GLN:HE21	1.89	0.85
41:5E:341:LEU:CD1	64:ST:120:ARG:HH12	1.88	0.85
60:RS:424:PHE:O	60:RS:428:TYR:HB2	1.78	0.84
39:5C:430:VAL:CG2	42:5F:3:ARG:HD3	2.07	0.84
50:RE:919:TRP:CZ2	50:RE:1067:LEU:HD22	2.12	0.84
1:3A:24:U:O2	42:5F:13:LEU:HB2	1.77	0.84
27:A8:643:ASP:HA	30:AF:510:LEU:CD1	2.06	0.84
27:A8:673:THR:CG2	28:A9:490:GLU:HA	2.07	0.84
5:SF:213:SER:HG	23:3F:102:ASP:N	1.74	0.84
50:RE:1216:LYS:HE3	50:RE:1236:THR:HG23	1.60	0.84
63:RT:75:ASP:CB	67:RZ:478:ARG:HH22	1.90	0.84
32:B1:382:THR:O	41:5E:481:PRO:CB	2.26	0.83
41:5E:341:LEU:CD1	64:ST:120:ARG:NH1	2.40	0.83
34:B3:691:PRO:HD2	41:5E:516:SER:HB3	1.60	0.83
1:3A:94:A:H61	1:3A:322:A:H61	1.27	0.83
53:RJ:960:ARG:HD3	64:ST:120:ARG:NH2	1.92	0.83
57:RO:502:ASN:O	57:RO:506:LEU:HB2	1.77	0.83
3:SA:1477:G:P	65:SU:43:ASN:HB3	2.19	0.83
67:RZ:600:PHE:CE1	67:RZ:684:ASP:O	2.32	0.82
41:5E:384:ARG:HD2	43:5G:83:ILE:CD1	2.10	0.82
36:BE:736:HIS:O	36:BE:740:ILE:HG22	1.78	0.82
13:SP:92:LYS:HE2	13:SP:122:PRO:HD3	1.62	0.82
41:5E:532:LEU:O	41:5E:536:ARG:HG2	1.78	0.82
1:3A:319:G:C5'	20:3C:121:LYS:NZ	2.42	0.82
40:5D:68:HIS:CE1	42:5F:169:THR:HG21	2.14	0.82
41:5E:384:ARG:HH21	43:5G:81:SER:HB3	1.45	0.82
41:5E:384:ARG:CD	43:5G:83:ILE:HD12	2.09	0.82
65:SU:39:THR:HG23	65:SU:57:ARG:NH1	1.95	0.82
66:RD:1509:GLU:HB3	66:RD:1512:GLU:HB2	1.60	0.82
57:RO:324:PHE:CZ	64:ST:4:VAL:HB	2.14	0.81
1:3A:318:U:OP1	1:3A:318:U:H3'	1.80	0.81
41:5E:520:LEU:HD11	41:5E:525:LYS:HG2	1.61	0.81
59:RQ:346:LEU:O	59:RQ:350:ASN:HA	1.80	0.81
24:3H:44:LEU:HD22	24:3H:52:ILE:CD1	2.10	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1477:G:OP1	65:SU:43:ASN:C	2.22	0.81
32:B1:298:LEU:HA	41:5E:472:PRO:HB2	1.62	0.81
29:AE:151:ILE:O	29:AE:155:ILE:HB	1.81	0.81
40:5D:58:ARG:HD2	42:5F:174:ARG:NH2	1.96	0.81
59:RQ:298:TRP:HE1	59:RQ:899:LYS:HG3	1.44	0.81
64:ST:44:ASN:ND2	65:SU:45:MET:SD	2.54	0.81
41:5E:345:LEU:O	41:5E:345:LEU:HD23	1.81	0.80
36:BE:737:LEU:HA	36:BE:740:ILE:HG22	1.63	0.80
3:SA:1478:G:OP1	65:SU:39:THR:CB	2.28	0.80
64:ST:54:LEU:HD12	65:SU:48:GLN:NE2	1.96	0.80
32:B1:14:VAL:HG21	32:B1:341:GLN:O	1.81	0.80
32:B1:678:GLU:OE2	41:5E:455:HIS:CE1	2.34	0.80
27:A8:596:LYS:HD3	27:A8:640:LEU:HD22	1.62	0.80
41:5E:533:LYS:HA	41:5E:536:ARG:NE	1.97	0.80
3:SA:1490:C:C4	40:5D:25:TYR:HE1	1.99	0.80
55:RM:746:TYR:O	55:RM:765:VAL:HA	1.82	0.79
34:B3:690:HIS:CD2	41:5E:519:GLU:HB2	2.18	0.79
50:RE:1174:GLY:HA3	50:RE:1179:LYS:HE2	1.62	0.79
64:ST:54:LEU:CD1	65:SU:48:GLN:HE22	1.95	0.79
41:5E:319:VAL:CG2	53:RJ:1038:ILE:CG2	2.61	0.79
27:A8:633:GLN:O	27:A8:637:LEU:CG	2.29	0.79
50:RE:1157:TYR:HE1	50:RE:1203:ASN:ND2	1.79	0.79
3:SA:1475:A:H5"	3:SA:1541:G:OP2	1.81	0.79
37:B6:319:TYR:O	37:B6:323:PHE:HB2	1.81	0.79
3:SA:1663:G:H1	3:SA:1738:U:H3	1.31	0.78
9:SJ:48:THR:O	9:SJ:52:ASN:HB2	1.83	0.78
56:RN:86:ILE:O	56:RN:89:GLN:HG3	1.84	0.78
1:3A:323:G:N3	1:3A:323:G:H2'	1.96	0.78
3:SA:1479:A:P	65:SU:57:ARG:NH2	2.56	0.78
27:A8:631:SER:CA	27:A8:634:LEU:HD21	2.14	0.78
56:RN:86:ILE:HA	56:RN:89:GLN:HG2	1.66	0.78
50:RE:1098:PHE:HD2	50:RE:1184:GLY:N	1.80	0.78
10:SK:65:LYS:NZ	23:3F:59:PRO:HD3	1.97	0.78
3:SA:825:U:H3	3:SA:845:G:H1	1.32	0.78
3:SA:868:G:H1	3:SA:960:U:H3	1.30	0.78
30:AF:224:THR:O	30:AF:239:LEU:HB2	1.83	0.77
50:RE:1189:LEU:HA	66:RD:1470:GLY:O	1.82	0.77
50:RE:1216:LYS:HG2	50:RE:1220:PHE:CE2	2.19	0.77
27:A8:673:THR:HG21	28:A9:490:GLU:HA	1.66	0.77
43:5G:239:VAL:HG21	56:RN:13:LEU:HD12	1.65	0.77
13:SP:107:ARG:NH1	63:RT:150:GLY:HA3	1.98	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A8:672:ASN:HB2	28:A9:489:SER:OG	1.83	0.77
13:SP:111:ARG:CZ	63:RT:93:LYS:HD2	2.15	0.77
27:A8:665:GLN:HB3	28:A9:496:LEU:HD21	1.64	0.77
50:RE:1169:ILE:HD12	50:RE:1177:GLY:O	1.84	0.77
2:5A:9:G:H5'	28:A9:483:LYS:HZ2	1.47	0.77
3:SA:153:G:H1	3:SA:161:U:H3	1.33	0.77
13:SP:107:ARG:NE	13:SP:107:ARG:HA	2.00	0.77
27:A8:631:SER:HA	27:A8:634:LEU:HD21	1.66	0.77
53:RJ:871:MET:HE2	53:RJ:930:LYS:NZ	2.00	0.77
27:A8:647:LEU:HB3	28:A9:509:GLN:HE22	1.50	0.77
41:5E:319:VAL:CG2	53:RJ:1038:ILE:HG21	2.14	0.76
40:5D:78:LEU:HD22	53:RJ:1082:GLN:HG3	1.67	0.76
3:SA:1538:U:C2	3:SA:1540:G:N7	2.54	0.76
41:5E:533:LYS:HA	41:5E:536:ARG:HE	1.47	0.76
3:SA:1688:U:H3	3:SA:1713:G:H1	1.34	0.76
42:5F:6:LYS:O	42:5F:9:GLU:HB2	1.84	0.76
13:SP:111:ARG:NH2	63:RT:93:LYS:HD2	2.00	0.76
50:RE:1203:ASN:ND2	50:RE:1219:ILE:HG22	1.98	0.75
10:SK:138:LYS:H	49:RB:263:GLY:HA3	1.51	0.75
32:B1:299:SER:O	41:5E:476:MET:HG2	1.87	0.75
64:ST:29:VAL:CG1	64:ST:54:LEU:HD22	2.15	0.75
40:5D:78:LEU:HD22	53:RJ:1082:GLN:HG2	1.68	0.75
42:5F:5:LEU:HB3	42:5F:9:GLU:HB3	1.67	0.75
41:5E:319:VAL:HG21	53:RJ:1038:ILE:HG21	1.69	0.75
41:5E:345:LEU:HD22	53:RJ:961:PHE:CZ	2.22	0.75
3:SA:1533:C:H5'	64:ST:27:LYS:HE2	1.67	0.75
14:SR:94:GLN:OE1	42:5F:182:PHE:CD1	2.39	0.75
41:5E:493:GLN:HE22	41:5E:497:ASN:ND2	1.84	0.75
41:5E:533:LYS:HA	41:5E:536:ARG:HG2	1.68	0.75
3:SA:415:C:H1'	3:SA:419:G:H22	1.50	0.74
32:B1:680:ARG:NH1	41:5E:455:HIS:CD2	2.55	0.74
41:5E:384:ARG:CD	43:5G:83:ILE:CD1	2.65	0.74
25:A4:614:TRP:O	25:A4:618:ASN:HB2	1.87	0.74
32:B1:419:TYR:HE2	41:5E:486:ASN:ND2	1.86	0.74
32:B1:298:LEU:HD11	41:5E:476:MET:HE1	1.69	0.74
39:5C:188:LYS:HE2	42:5F:23:GLN:OE1	1.87	0.74
53:RJ:871:MET:HE1	53:RJ:930:LYS:CE	2.17	0.74
46:5J:114:ARG:O	46:5J:118:GLN:HB3	1.88	0.74
50:RE:1102:LEU:CD2	50:RE:1180:ASN:O	2.30	0.74
27:A8:643:ASP:HA	30:AF:510:LEU:HD13	1.69	0.74
32:B1:420:ARG:HH22	41:5E:494:GLU:CD	1.96	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BE:737:LEU:CA	36:BE:740:ILE:CG2	2.64	0.73
1:3A:319:G:C5'	20:3C:121:LYS:HZ2	2.01	0.73
10:SK:65:LYS:HZ1	23:3F:59:PRO:HD3	1.53	0.73
63:RT:75:ASP:CB	67:RZ:478:ARG:NH2	2.50	0.73
34:B3:216:ARG:HH11	34:B3:241:GLN:HE22	1.36	0.73
3:SA:1051:G:H21	45:5I:447:THR:HG21	1.54	0.73
27:A8:669:ALA:HA	28:A9:489:SER:HB2	1.69	0.73
36:BE:855:PHE:CD1	36:BE:856:GLU:N	2.57	0.73
1:3A:319:G:H5'	20:3C:121:LYS:HZ2	1.50	0.73
14:SR:94:GLN:OE1	42:5F:182:PHE:HD1	1.69	0.73
65:SU:39:THR:HG22	65:SU:39:THR:O	1.89	0.73
3:SA:1477:G:O2'	65:SU:47:PRO:HA	1.89	0.72
2:5A:9:G:C5'	28:A9:483:LYS:NZ	2.51	0.72
41:5E:517:LYS:HD2	41:5E:517:LYS:C	2.14	0.72
41:5E:384:ARG:NE	43:5G:82:GLY:H	1.87	0.72
50:RE:919:TRP:CH2	50:RE:1067:LEU:HD22	2.24	0.72
3:SA:1534:G:C6	30:AF:79:ARG:NH2	2.58	0.72
3:SA:1756:A:H5'	41:5E:536:ARG:HB2	1.70	0.72
27:A8:596:LYS:CG	27:A8:637:LEU:HB3	2.20	0.72
32:B1:341:GLN:HE21	32:B1:378:PHE:HB3	1.55	0.72
53:RJ:871:MET:CE	53:RJ:930:LYS:NZ	2.53	0.72
1:3A:318:U:H3'	1:3A:318:U:P	2.30	0.72
3:SA:505:A:H61	3:SA:586:G:H8	1.38	0.72
41:5E:341:LEU:CB	64:ST:116:LEU:HD22	2.20	0.72
32:B1:298:LEU:HD11	41:5E:476:MET:SD	2.30	0.72
50:RE:1204:VAL:CB	50:RE:1212:VAL:HG11	2.19	0.71
22:3E:397:ARG:HH21	22:3E:400:GLN:HE21	1.38	0.71
27:A8:642:LEU:HD12	28:A9:499:ILE:HG23	1.70	0.71
10:SK:65:LYS:NZ	23:3F:59:PRO:CB	2.52	0.71
41:5E:493:GLN:HE21	41:5E:497:ASN:HB3	1.52	0.71
42:5F:8:HIS:HA	45:5I:53:MET:CE	2.14	0.71
3:SA:1470:C:N4	3:SA:1573:A:C2	2.59	0.71
55:RL:29:VAL:HG12	55:RL:152:LEU:HD12	1.72	0.71
31:AG:435:ASP:HB2	31:AG:702:TYR:CD1	2.26	0.71
56:RN:86:ILE:HA	56:RN:89:GLN:CG	2.21	0.71
27:A8:631:SER:HA	27:A8:634:LEU:CD1	2.18	0.71
51:RF:97:GLU:HG2	66:RD:1508:ARG:NH1	2.06	0.71
66:RD:1518:ILE:HG12	66:RD:1552:LYS:HG2	1.73	0.70
26:A5:545:ALA:CB	27:A8:674:GLU:HG3	2.20	0.70
3:SA:1533:C:H5'	64:ST:27:LYS:CE	2.20	0.70
3:SA:1756:A:N7	41:5E:532:LEU:HB2	2.07	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5E:345:LEU:HD23	41:5E:345:LEU:C	2.17	0.70
5:SF:92:LEU:HB2	5:SF:97:GLU:HB2	1.74	0.70
41:5E:493:GLN:HE22	41:5E:497:ASN:HD22	1.37	0.70
50:RE:1174:GLY:CA	50:RE:1179:LYS:HE2	2.22	0.70
50:RE:1189:LEU:HD23	50:RE:1189:LEU:C	2.16	0.70
41:5E:340:LEU:HB2	53:RJ:957:GLU:OE2	1.92	0.69
27:A8:596:LYS:CE	27:A8:637:LEU:HA	2.22	0.69
6:SG:206:SER:H	6:SG:211:ILE:HD11	1.55	0.69
13:SP:107:ARG:HB2	13:SP:107:ARG:NH2	2.07	0.69
32:B1:337:TYR:CD2	32:B1:340:LYS:HD3	2.27	0.69
1:3A:323:G:OP2	40:5D:116:LYS:HB3	1.92	0.69
50:RE:1108:LEU:O	50:RE:1112:CYS:HB2	1.91	0.69
41:5E:533:LYS:HA	41:5E:536:ARG:CG	2.22	0.69
13:SP:111:ARG:HH22	63:RT:93:LYS:CA	2.05	0.69
32:B1:58:ILE:HA	32:B1:74:ASP:HA	1.74	0.69
50:RE:1199:ASN:HD21	66:RD:1512:GLU:HG2	1.57	0.69
3:SA:1477:G:OP1	65:SU:43:ASN:CB	2.40	0.69
50:RE:441:GLN:O	50:RE:455:SER:HA	1.93	0.69
41:5E:517:LYS:NZ	41:5E:517:LYS:HB3	2.08	0.69
57:RO:324:PHE:HZ	64:ST:4:VAL:HB	1.57	0.69
41:5E:315:GLU:HB3	53:RJ:1032:LEU:HD11	1.74	0.68
56:RN:86:ILE:HG23	56:RN:89:GLN:NE2	2.07	0.68
17:SZ:29:HIS:HB2	17:SZ:32:ARG:HB2	1.76	0.68
13:SP:111:ARG:NH2	63:RT:93:LYS:CD	2.57	0.68
27:A8:664:LYS:O	27:A8:668:ILE:HG13	1.92	0.68
28:A9:480:LYS:O	28:A9:483:LYS:HG3	1.93	0.68
32:B1:678:GLU:CD	41:5E:455:HIS:ND1	2.52	0.68
54:RK:192:THR:HA	54:RK:224:ASN:O	1.92	0.68
59:RQ:297:LYS:HB2	59:RQ:899:LYS:HB3	1.76	0.68
10:SK:65:LYS:NZ	23:3F:59:PRO:HB3	2.08	0.68
50:RE:1096:TYR:CZ	50:RE:1183:THR:OG1	2.46	0.68
27:A8:443:CYS:CB	31:AG:728:LEU:HD22	2.23	0.68
27:A8:596:LYS:HG3	27:A8:637:LEU:HB3	1.74	0.68
41:5E:538:LYS:HD3	41:5E:538:LYS:C	2.19	0.68
30:AF:86:SER:O	30:AF:98:ALA:HA	1.93	0.68
13:SP:111:ARG:HH22	63:RT:93:LYS:HA	1.58	0.68
27:A8:643:ASP:HA	30:AF:510:LEU:HD12	1.75	0.68
30:AF:211:HIS:HD1	30:AF:228:SER:HG	1.42	0.68
58:RP:173:THR:O	58:RP:177:LEU:HB2	1.94	0.68
33:B2:17:ILE:HG22	33:B2:52:TRP:CH2	2.28	0.68
41:5E:384:ARG:NH2	43:5G:81:SER:HB3	2.08	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5I:345:THR:HG22	45:5I:347:ARG:H	1.58	0.68
3:SA:646:C:H2'	3:SA:647:G:H8	1.59	0.68
23:3F:443:LEU:HD21	23:3F:492:TRP:HE1	1.59	0.67
29:AE:692:ILE:HA	29:AE:695:TYR:HB3	1.76	0.67
41:5E:520:LEU:CG	41:5E:525:LYS:HG3	2.24	0.67
64:ST:41:ARG:CG	65:SU:45:MET:HG2	2.10	0.67
36:BE:209:ILE:HG22	36:BE:225:THR:HG22	1.76	0.67
3:SA:1679:G:H1'	3:SA:1722:A:H61	1.59	0.67
42:5F:11:LYS:HA	42:5F:14:LYS:HE3	1.75	0.67
56:RN:86:ILE:CB	56:RN:89:GLN:HE21	2.07	0.67
23:3F:185:LEU:H	23:3F:202:THR:HB	1.59	0.67
57:RO:324:PHE:HZ	64:ST:4:VAL:CG2	2.08	0.67
27:A8:648:PHE:CE1	28:A9:510:ALA:HA	2.29	0.67
43:5G:123:VAL:HG12	43:5G:125:PRO:HD2	1.77	0.67
10:SK:65:LYS:NZ	23:3F:59:PRO:HG3	2.08	0.67
33:B2:536:CYS:HB3	33:B2:549:SER:HB3	1.77	0.67
41:5E:384:ARG:HH21	43:5G:81:SER:CB	2.08	0.67
50:RE:1069:LYS:O	50:RE:1072:VAL:HG12	1.94	0.67
50:RE:1216:LYS:CE	50:RE:1236:THR:HG23	2.24	0.67
3:SA:187:G:N2	3:SA:197:A:N7	2.43	0.67
32:B1:20:ILE:H	32:B1:307:THR:HG21	1.58	0.67
35:B8:513:GLN:HG3	35:B8:551:VAL:HG21	1.76	0.67
56:RN:85:GLY:O	56:RN:89:GLN:HG2	1.95	0.67
25:A4:645:ARG:HD2	25:A4:656:ARG:HD3	1.77	0.66
27:A8:631:SER:C	27:A8:634:LEU:HG	2.19	0.66
41:5E:366:GLU:OE2	43:5G:247:ILE:CG2	2.33	0.66
41:5E:490:LEU:HD22	41:5E:494:GLU:OE1	1.95	0.66
57:RO:324:PHE:HZ	64:ST:4:VAL:CB	2.08	0.66
32:B1:337:TYR:CD2	36:BE:744:SER:O	2.48	0.66
50:RE:235:LEU:O	50:RE:239:LEU:HB2	1.95	0.66
20:3B:103:GLU:HG3	46:5J:134:ARG:HH12	1.60	0.66
27:A8:648:PHE:HE1	28:A9:510:ALA:HA	1.58	0.66
31:AG:435:ASP:HB3	31:AG:701:VAL:O	1.96	0.66
41:5E:517:LYS:HB3	41:5E:517:LYS:HZ2	1.60	0.66
30:AF:52:PRO:HG2	30:AF:312:ALA:HA	1.77	0.66
1:3A:323:G:H5'	40:5D:116:LYS:HG3	1.76	0.66
16:SY:103:LEU:HB3	16:SY:126:LYS:HB2	1.76	0.66
17:SZ:51:GLU:HB2	17:SZ:54:ALA:HB3	1.76	0.66
13:SP:107:ARG:NH1	63:RT:150:GLY:HA2	2.08	0.66
41:5E:342:THR:HG22	64:ST:119:ILE:HG13	1.78	0.66
13:SP:107:ARG:HG2	13:SP:107:ARG:HH21	1.60	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B3:462:THR:HA	34:B3:484:GLU:HG2	1.77	0.66
36:BE:209:ILE:HA	36:BE:225:THR:HA	1.76	0.66
42:5F:5:LEU:HB3	42:5F:9:GLU:CB	2.25	0.66
31:AG:16:SER:HB2	31:AG:783:LEU:HB2	1.77	0.66
11:SM:67:ARG:HH21	11:SM:129:ARG:H	1.44	0.65
53:RJ:248:ARG:HB3	53:RJ:272:TYR:HB2	1.78	0.65
27:A8:443:CYS:N	31:AG:728:LEU:CD2	2.56	0.65
50:RE:756:VAL:HA	50:RE:896:THR:HG21	1.78	0.65
25:A4:497:ILE:HD11	25:A4:511:VAL:HG23	1.78	0.65
65:SU:37:VAL:O	65:SU:46:PRO:HB3	1.95	0.65
3:SA:1538:U:N1	3:SA:1540:G:N7	2.45	0.65
27:A8:643:ASP:OD1	30:AF:510:LEU:HA	1.96	0.65
50:RE:518:PHE:HE2	50:RE:1075:LEU:HB3	1.62	0.65
67:RZ:785:ARG:HH22	67:RZ:794:GLN:HE21	1.45	0.65
27:A8:665:GLN:HB3	28:A9:496:LEU:CD2	2.26	0.65
3:SA:207:U:H3	3:SA:258:C:H42	1.45	0.65
3:SA:1490:C:C4	40:5D:25:TYR:CE1	2.84	0.65
55:RM:283:ALA:HA	55:RM:411:THR:O	1.96	0.65
55:RM:311:THR:O	55:RM:370:ILE:HA	1.97	0.65
66:RD:1525:ASN:HD22	66:RD:1556:ILE:HG22	1.62	0.65
1:3A:84:U:OP2	22:3E:361:ARG:NH2	2.30	0.65
11:SM:87:ARG:HE	11:SM:104:HIS:HB2	1.62	0.65
40:5D:61:ASP:O	42:5F:160:TRP:CH2	2.50	0.65
3:SA:1538:U:H2'	3:SA:1540:G:C8	2.32	0.64
10:SK:57:ARG:HE	47:5K:88:ASP:HB3	1.60	0.64
23:3F:125:VAL:O	23:3F:128:GLN:NE2	2.30	0.64
39:5C:170:GLN:NE2	39:5C:177:TYR:OH	2.30	0.64
67:RZ:396:GLU:HB2	67:RZ:583:VAL:CG2	2.27	0.64
32:B1:438:VAL:HG12	32:B1:445:VAL:HG23	1.79	0.64
4:SC:132:ASP:HB2	4:SC:221:PRO:HB3	1.79	0.64
33:B2:262:ILE:O	33:B2:270:SER:HA	1.97	0.64
34:B3:719:ILE:HD11	34:B3:762:CYS:HB3	1.78	0.64
50:RE:1101:ASP:HB3	50:RE:1233:ASN:HB2	1.78	0.64
53:RJ:263:LEU:HD23	53:RJ:267:ARG:HH22	1.63	0.64
57:RO:472:HIS:HD2	57:RO:474:HIS:H	1.46	0.64
57:RO:318:LEU:HA	57:RO:357:ARG:HH12	1.62	0.64
57:RO:324:PHE:CZ	64:ST:4:VAL:CB	2.81	0.64
13:SP:107:ARG:HH21	13:SP:107:ARG:CG	2.10	0.64
27:A8:576:ARG:HG2	27:A8:578:LEU:H	1.63	0.64
67:RZ:1097:ASP:HB3	67:RZ:1106:ILE:HG21	1.79	0.64
3:SA:1727:G:N2	3:SA:1728:A:N7	2.46	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BE:631:ASN:HB2	36:BE:644:THR:HB	1.80	0.64
56:RN:86:ILE:HG23	56:RN:89:GLN:HE21	1.63	0.64
2:5A:487:A:H62	59:RQ:876:GLN:HE22	1.45	0.64
9:SJ:5:ARG:NH2	9:SJ:29:LEU:O	2.31	0.64
10:SK:65:LYS:HZ2	23:3F:59:PRO:HB3	1.62	0.64
42:5F:8:HIS:CA	45:5I:53:MET:HE1	2.17	0.64
1:3A:319:G:C5'	20:3C:121:LYS:HZ1	2.08	0.64
9:SJ:42:ARG:HD3	48:RA:57:GLU:HB3	1.80	0.64
27:A8:664:LYS:HD2	28:A9:448:GLU:OE1	1.98	0.64
52:RG:122:ILE:HA	52:RG:161:LYS:O	1.97	0.64
3:SA:415:C:H1'	3:SA:419:G:N2	2.12	0.64
3:SA:1052:U:H5''	45:5I:449:LYS:HG2	1.79	0.64
33:B2:439:LEU:HB2	33:B2:444:LEU:HB3	1.79	0.64
3:SA:1475:A:H4'	3:SA:1540:G:H5''	1.80	0.63
16:SY:97:ASP:OD1	16:SY:97:ASP:N	2.31	0.63
48:RA:18:GLY:HA2	48:RA:339:HIS:HD2	1.62	0.63
26:A5:145:CYS:HB2	26:A5:148:LEU:HD21	1.80	0.63
23:3F:538:ARG:HA	23:3F:566:ALA:O	1.97	0.63
35:B8:521:LEU:HA	35:B8:531:CYS:O	1.98	0.63
3:SA:576:G:H4'	41:5E:327:LYS:HE2	1.80	0.63
3:SA:1475:A:H5'	3:SA:1540:G:H4'	1.79	0.63
34:B3:244:GLU:HG2	34:B3:293:VAL:H	1.64	0.63
52:RH:129:ARG:HH11	52:RH:132:ARG:HD3	1.63	0.63
57:RO:324:PHE:CE1	64:ST:4:VAL:HB	2.34	0.63
17:SZ:20:ARG:HD2	17:SZ:74:LEU:HD12	1.79	0.63
34:B3:531:ASN:HD21	34:B3:568:MET:HE2	1.63	0.63
52:RH:192:TYR:HA	52:RH:195:LYS:HD2	1.81	0.63
53:RJ:831:ARG:NH2	53:RJ:835:HIS:O	2.30	0.63
1:3A:319:G:O5'	20:3C:121:LYS:NZ	2.32	0.63
14:SR:94:GLN:HB2	14:SR:102:LYS:HG3	1.81	0.63
39:5C:386:PHE:O	45:5I:8:ARG:NH2	2.31	0.63
41:5E:370:ARG:NH1	56:RN:52:ARG:NH1	2.47	0.63
41:5E:381:LEU:HB2	43:5G:212:ALA:HA	1.80	0.63
3:SA:343:C:H2'	3:SA:344:A:H8	1.63	0.63
24:3H:44:LEU:HD22	24:3H:52:ILE:HD11	1.80	0.63
37:B6:285:TYR:HD2	37:B6:308:THR:HG22	1.63	0.63
41:5E:340:LEU:HD13	53:RJ:957:GLU:OE2	1.98	0.63
64:ST:45:LEU:HD21	64:ST:81:ILE:HD12	1.79	0.63
41:5E:533:LYS:CA	41:5E:536:ARG:HG2	2.29	0.63
3:SA:146:U:H3	3:SA:168:A:N6	1.97	0.63
30:AF:323:SER:OG	64:ST:5:VAL:HG12	1.99	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RJ:932:LEU:HD22	53:RJ:1007:TYR:HB2	1.80	0.63
8:SI:9:LEU:HD22	8:SI:42:GLN:HE22	1.63	0.62
48:RA:287:ASN:HB2	48:RA:302:ARG:HB2	1.80	0.62
22:3E:384:GLY:O	22:3E:388:LEU:HB2	1.99	0.62
32:B1:298:LEU:HD11	41:5E:476:MET:CE	2.28	0.62
48:RA:247:THR:HG23	48:RA:249:ASN:H	1.64	0.62
29:AE:638:SER:HA	29:AE:641:LEU:HD12	1.80	0.62
34:B3:691:PRO:CD	41:5E:516:SER:HB3	2.29	0.62
3:SA:1538:U:C6	3:SA:1540:G:N7	2.67	0.62
3:SA:1655:A:N6	3:SA:1743:U:O4	2.32	0.62
40:5D:29:GLU:OE2	40:5D:37:ARG:NH1	2.31	0.62
54:RK:221:CYS:SG	54:RK:222:GLU:N	2.71	0.62
3:SA:1220:C:H2'	3:SA:1221:A:H8	1.64	0.62
3:SA:1479:A:OP1	65:SU:57:ARG:NH2	2.33	0.62
13:SP:111:ARG:HH12	63:RT:94:PHE:H	1.47	0.62
27:A8:672:ASN:CB	28:A9:489:SER:OG	2.46	0.62
28:A9:432:LYS:HB3	28:A9:435:LEU:HB3	1.81	0.62
57:RO:300:THR:O	57:RO:304:ASN:ND2	2.32	0.62
13:SP:107:ARG:HH11	63:RT:150:GLY:CA	2.13	0.62
25:A4:399:VAL:HG22	25:A4:420:LEU:HB2	1.80	0.62
27:A8:592:ARG:HH11	31:AG:605:ASN:ND2	1.98	0.62
56:RN:95:ARG:HH12	56:RN:757:LYS:HG3	1.64	0.62
56:RN:482:GLN:HG2	57:RO:507:LEU:HD11	1.80	0.62
60:RS:379:LYS:HD2	60:RS:427:ARG:HE	1.64	0.62
42:5F:153:ASN:O	42:5F:153:ASN:ND2	2.32	0.62
53:RJ:871:MET:CE	53:RJ:930:LYS:HD2	2.30	0.62
60:RS:214:TYR:HB3	60:RS:249:THR:HG22	1.80	0.62
27:A8:631:SER:CA	27:A8:634:LEU:HD11	2.25	0.62
36:BE:733:THR:O	36:BE:737:LEU:HB3	2.00	0.62
24:3H:50:GLU:HG3	24:3H:104:THR:HG22	1.82	0.61
26:A5:120:ILE:HB	26:A5:151:LEU:HD23	1.82	0.61
32:B1:303:ASN:ND2	32:B1:323:LYS:HD3	2.15	0.61
34:B3:157:ASN:CB	63:RT:77:GLY:HA2	2.25	0.61
43:5G:239:VAL:HG21	56:RN:13:LEU:CD1	2.30	0.61
54:RK:155:LYS:HG2	54:RK:165:GLU:HG2	1.82	0.61
3:SA:521:A:N3	17:SZ:34:ASN:ND2	2.48	0.61
5:SF:95:THR:HG22	58:RP:59:LEU:HB3	1.82	0.61
27:A8:671:ARG:NH2	28:A9:453:PRO:HG2	2.15	0.61
27:A8:672:ASN:HB2	28:A9:489:SER:HG	1.66	0.61
30:AF:428:ARG:NH2	31:AG:518:ASP:O	2.34	0.61
36:BE:471:CYS:SG	36:BE:514:ASN:ND2	2.74	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:477:A:H5'	44:5H:560:ASN:HD22	1.64	0.61
30:AF:440:GLU:O	30:AF:444:ASN:HB2	2.00	0.61
60:RS:423:THR:HA	60:RS:426:GLN:HG2	1.81	0.61
65:SU:39:THR:HG23	65:SU:57:ARG:HH12	1.64	0.61
5:SF:212:ASP:H	5:SF:215:ASP:HA	1.65	0.61
13:SP:16:VAL:HG12	13:SP:80:HIS:HB2	1.82	0.61
27:A8:443:CYS:HA	31:AG:728:LEU:CG	2.30	0.61
35:B8:424:ILE:HG12	35:B8:434:GLU:HG2	1.83	0.61
41:5E:345:LEU:CD2	53:RJ:961:PHE:CZ	2.82	0.61
52:RG:36:LYS:HB3	52:RG:172:PRO:HA	1.83	0.61
13:SP:111:ARG:NH2	63:RT:93:LYS:HA	2.16	0.61
31:AG:335:PRO:HB2	31:AG:336:ARG:HD3	1.82	0.61
31:AG:769:ASN:ND2	31:AG:771:ASP:OD1	2.33	0.61
50:RE:1096:TYR:OH	50:RE:1183:THR:HG21	2.00	0.61
3:SA:362:G:H22	3:SA:382:C:H1'	1.66	0.61
25:A4:578:SER:HG	25:A4:643:SER:HG	1.48	0.61
26:A5:162:GLN:HA	26:A5:173:ILE:O	2.01	0.61
34:B3:160:ILE:HG22	34:B3:162:LEU:HD13	1.82	0.61
34:B3:591:ILE:HG12	34:B3:600:LYS:HZ1	1.65	0.61
50:RE:923:HIS:CD2	50:RE:1067:LEU:HD11	2.35	0.61
3:SA:1475:A:H4'	3:SA:1540:G:C5'	2.31	0.61
23:3F:356:ARG:NH1	49:RB:260:ALA:O	2.34	0.61
56:RN:511:SER:HA	56:RN:557:SER:HB2	1.82	0.61
20:3C:186:ASP:OD1	20:3C:214:ARG:NH1	2.33	0.61
58:RP:91:LEU:HD21	58:RP:110:LEU:HD12	1.83	0.61
13:SP:80:HIS:HA	13:SP:113:GLY:O	2.01	0.60
20:3B:142:ARG:NH1	20:3B:186:ASP:OD2	2.34	0.60
23:3F:328:ILE:HG13	23:3F:338:THR:HG22	1.82	0.60
37:B6:201:LYS:HZ1	46:5J:55:ILE:HG21	1.66	0.60
41:5E:371:ARG:NH1	41:5E:375:ASP:OD2	2.34	0.60
53:RJ:60:ASP:O	53:RJ:239:ASN:ND2	2.34	0.60
67:RZ:999:LYS:HD3	67:RZ:1000:PHE:H	1.66	0.60
13:SP:111:ARG:NH2	63:RT:93:LYS:HB3	2.16	0.60
26:A5:481:LEU:HD21	26:A5:526:LEU:HD22	1.82	0.60
50:RE:398:ALA:HA	50:RE:401:LEU:HD12	1.82	0.60
56:RN:548:ARG:NH1	56:RN:638:ASN:OD1	2.34	0.60
3:SA:435:C:H42	53:RJ:166:ARG:HH12	1.47	0.60
26:A5:545:ALA:HB2	27:A8:674:GLU:HG3	1.82	0.60
30:AF:51:HIS:O	30:AF:53:HIS:ND1	2.30	0.60
37:B6:286:ILE:HG22	37:B6:308:THR:HG21	1.83	0.60
50:RE:779:PHE:HB3	50:RE:851:LYS:HG3	1.82	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B1:14:VAL:HG11	32:B1:341:GLN:HB3	1.84	0.60
34:B3:581:CYS:HA	34:B3:590:LEU:O	2.01	0.60
40:5D:68:HIS:HE1	42:5F:169:THR:HG21	1.67	0.60
45:5I:260:GLN:NE2	45:5I:289:TYR:OH	2.35	0.60
56:RN:649:THR:HG23	56:RN:650:VAL:HG23	1.82	0.60
57:RO:452:ASP:HB3	57:RO:455:LEU:HB2	1.84	0.60
52:RG:147:LYS:HD3	52:RG:150:ILE:HG22	1.83	0.60
5:SF:194:THR:HG23	5:SF:195:ILE:HG12	1.83	0.60
33:B2:54:ILE:HD13	33:B2:364:TYR:HD2	1.66	0.60
52:RH:156:GLU:HG2	52:RH:157:GLU:HG2	1.81	0.60
57:RO:461:SER:OG	57:RO:462:SER:N	2.33	0.60
41:5E:493:GLN:NE2	41:5E:497:ASN:CB	2.61	0.60
42:5F:69:PRO:HA	42:5F:72:ARG:HG2	1.83	0.60
1:3A:319:G:H5'	20:3C:121:LYS:HZ1	1.59	0.60
3:SA:1478:G:OP2	65:SU:43:ASN:ND2	2.34	0.60
25:A4:429:SER:HB3	25:A4:444:ARG:HA	1.83	0.60
3:SA:374:U:H5''	49:RB:331:LYS:HE3	1.83	0.60
29:AE:699:ARG:NH1	29:AE:702:TRP:O	2.35	0.60
30:AF:301:PRO:HG2	30:AF:323:SER:HB3	1.84	0.60
50:RE:345:TYR:O	50:RE:349:LEU:HB3	2.02	0.60
27:A8:638:LEU:HD21	27:A8:658:LEU:HD11	1.82	0.59
40:5D:22:ARG:NH1	53:RJ:997:MET:O	2.35	0.59
48:RA:333:ASN:HD21	48:RA:338:MET:HA	1.67	0.59
50:RE:363:THR:HG22	50:RE:394:THR:HG21	1.83	0.59
3:SA:870:C:O2	18:Sc:51:GLN:NE2	2.35	0.59
8:SI:118:LEU:HA	8:SI:121:VAL:HB	1.82	0.59
9:SJ:32:GLN:HG2	48:RA:79:PRO:HD2	1.84	0.59
30:AF:248:ARG:NH1	30:AF:289:ASN:O	2.35	0.59
31:AG:90:LYS:HG2	31:AG:144:VAL:HG22	1.84	0.59
36:BE:737:LEU:CA	36:BE:740:ILE:HG22	2.28	0.59
43:5G:233:VAL:HG21	43:5G:256:MET:HE3	1.83	0.59
50:RE:344:ASN:HA	50:RE:347:LYS:HD2	1.84	0.59
50:RE:1100:VAL:O	50:RE:1181:VAL:HG12	2.01	0.59
58:RP:112:GLN:NE2	58:RP:116:ASP:OD2	2.36	0.59
13:SP:40:ALA:HB2	13:SP:70:LYS:HD2	1.84	0.59
21:3D:382:LYS:HD2	21:3D:404:LEU:HD22	1.83	0.59
34:B3:189:HIS:NE2	34:B3:217:ASP:OD1	2.35	0.59
54:RK:14:SER:HB2	54:RK:36:ILE:HG23	1.83	0.59
64:ST:29:VAL:HG13	64:ST:54:LEU:HD22	1.84	0.59
67:RZ:1060:VAL:HG23	67:RZ:1060:VAL:O	2.02	0.59
6:SG:131:GLN:NE2	6:SG:135:ASP:OD1	2.35	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A8:593:ASP:CA	27:A8:596:LYS:HD2	2.26	0.59
30:AF:133:HIS:HD2	30:AF:135:GLN:H	1.50	0.59
39:5C:96:ASP:OD1	39:5C:96:ASP:N	2.35	0.59
21:3D:29:SER:O	21:3D:35:GLN:NE2	2.35	0.59
42:5F:109:ARG:NH2	42:5F:155:GLU:OE2	2.36	0.59
50:RE:383:GLY:HA3	50:RE:585:MET:HG2	1.83	0.59
67:RZ:941:ILE:HB	67:RZ:1029:PHE:HB3	1.84	0.59
3:SA:85:A:H2'	3:SA:86:A:H8	1.65	0.59
10:SK:65:LYS:HZ2	23:3F:59:PRO:N	1.99	0.59
52:RG:125:ASN:ND2	52:RG:127:THR:OG1	2.36	0.59
5:SF:180:LEU:HA	5:SF:194:THR:HG21	1.85	0.59
7:SH:70:PRO:HB3	7:SH:101:ILE:HB	1.84	0.59
22:3E:210:LEU:HD23	22:3E:256:ASN:HD22	1.68	0.59
56:RN:614:ILE:HG22	56:RN:616:LEU:HB2	1.85	0.59
59:RQ:794:TRP:H	63:RT:129:ARG:HG3	1.67	0.59
15:SX:90:THR:O	15:SX:94:LEU:HB2	2.03	0.59
18:Sc:73:LEU:HB2	51:RF:215:VAL:HG21	1.85	0.59
34:B3:157:ASN:HB2	63:RT:77:GLY:CA	2.28	0.59
37:B6:15:MET:HA	37:B6:18:LEU:HB3	1.85	0.59
39:5C:257:SER:OG	39:5C:259:TRP:NE1	2.36	0.59
56:RN:86:ILE:CG2	56:RN:89:GLN:HE21	2.16	0.59
56:RN:535:ASN:OD1	56:RN:539:ARG:NH1	2.36	0.59
63:RT:115:LYS:HD2	63:RT:168:LEU:HD11	1.83	0.59
4:SC:92:GLN:HE21	4:SC:97:LEU:HD21	1.68	0.59
14:SR:122:ARG:NH2	43:5G:133:LYS:HD2	2.17	0.59
21:3D:286:ARG:HA	21:3D:289:TYR:HB3	1.85	0.59
31:AG:568:ASN:ND2	31:AG:586:SER:OG	2.35	0.59
32:B1:497:ILE:HG23	32:B1:512:ILE:HB	1.84	0.59
50:RE:381:HIS:NE2	50:RE:478:THR:O	2.36	0.59
50:RE:1111:SER:HA	50:RE:1129:PRO:HG3	1.85	0.59
31:AG:153:ILE:HG22	31:AG:174:TYR:HB2	1.85	0.59
41:5E:493:GLN:NE2	41:5E:497:ASN:HD22	2.01	0.59
43:5G:144:GLU:HA	43:5G:149:PRO:HA	1.84	0.59
58:RP:54:TRP:O	58:RP:58:ASN:ND2	2.35	0.59
13:SP:111:ARG:NH2	63:RT:93:LYS:CB	2.66	0.58
15:SX:97:ARG:HH11	47:5K:84:ARG:HH12	1.51	0.58
19:Sd:65:ARG:NH2	33:B2:750:GLU:OE2	2.36	0.58
50:RE:525:LEU:HB2	50:RE:617:LEU:HB2	1.84	0.58
50:RE:834:ASN:ND2	50:RE:863:TYR:OH	2.36	0.58
1:3A:30:A:N6	45:5I:341:GLU:OE2	2.36	0.58
20:3B:236:MET:HG3	21:3D:133:LEU:HA	1.84	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A5:546:ARG:NH1	27:A8:677:ASN:O	2.36	0.58
39:5C:190:HIS:HB3	39:5C:207:THR:HG21	1.84	0.58
40:5D:58:ARG:NH2	42:5F:174:ARG:NE	2.51	0.58
58:RP:1904:LEU:HD12	58:RP:1940:LYS:HE2	1.85	0.58
27:A8:647:LEU:C	28:A9:509:GLN:NE2	2.62	0.58
32:B1:300:MET:HE3	32:B1:328:LEU:HD13	1.85	0.58
58:RP:2030:ASN:O	58:RP:2036:ARG:NH2	2.35	0.58
20:3C:114:GLY:O	20:3C:122:ARG:NH1	2.35	0.58
39:5C:76:PRO:HA	45:5I:1:MET:HE2	1.86	0.58
50:RE:520:ASN:HD22	50:RE:959:LEU:HD12	1.68	0.58
50:RE:1096:TYR:OH	50:RE:1183:THR:CG2	2.51	0.58
52:RH:44:VAL:HA	52:RH:113:TYR:O	2.03	0.58
66:RD:1583:SER:HA	66:RD:1586:VAL:HG12	1.85	0.58
67:RZ:563:ARG:HD3	67:RZ:837:PHE:HE1	1.68	0.58
32:B1:501:SER:HB2	32:B1:508:GLN:HB2	1.84	0.58
41:5E:384:ARG:HE	43:5G:82:GLY:N	1.97	0.58
66:RD:1530:GLU:HA	66:RD:1533:LEU:HB2	1.85	0.58
1:3A:323:G:OP2	40:5D:116:LYS:CB	2.51	0.58
27:A8:632:THR:O	27:A8:636:GLN:HG3	2.04	0.58
29:AE:248:SER:OG	29:AE:253:CYS:SG	2.62	0.58
42:5F:54:ILE:HD11	42:5F:101:VAL:HG21	1.84	0.58
45:5I:411:LYS:O	45:5I:415:ARG:HB2	2.02	0.58
51:RF:91:ASP:O	51:RF:121:ARG:NH2	2.36	0.58
57:RO:202:LEU:HD22	57:RO:212:LEU:HD22	1.86	0.58
58:RP:144:SER:HB3	58:RP:147:VAL:HG12	1.86	0.58
3:SA:1468:U:O3'	65:SU:88:VAL:O	2.21	0.58
5:SF:44:LEU:HD13	5:SF:82:TYR:HB3	1.85	0.58
22:3E:11:GLY:HA2	22:3E:143:LEU:HD22	1.86	0.58
25:A4:565:ARG:HD3	29:AE:633:GLU:HB2	1.86	0.58
34:B3:494:ILE:N	34:B3:510:SER:OG	2.35	0.58
1:3A:58:A:OP1	42:5F:165:LYS:HE3	2.03	0.58
31:AG:118:VAL:HB	31:AG:130:LYS:HB2	1.85	0.58
34:B3:237:LEU:HD21	50:RE:663:ILE:HG21	1.86	0.58
36:BE:740:ILE:HG13	41:5E:483:TYR:HH	1.69	0.58
40:5D:37:ARG:NH2	53:RJ:994:LYS:O	2.36	0.58
56:RN:86:ILE:CA	56:RN:89:GLN:HG2	2.33	0.58
3:SA:126:A:N6	3:SA:291:G:O2'	2.37	0.58
31:AG:435:ASP:CB	31:AG:702:TYR:HA	2.34	0.58
35:B8:227:LEU:HB2	35:B8:528:GLN:HE22	1.67	0.58
39:5C:430:VAL:HG21	42:5F:3:ARG:NE	2.18	0.58
40:5D:113:ILE:HG23	40:5D:117:LYS:HE3	1.86	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:RA:75:GLY:HA3	48:RA:80:GLN:H	1.68	0.58
50:RE:412:LEU:HD21	50:RE:424:GLY:HA3	1.84	0.58
58:RP:2036:ARG:HH12	58:RP:2074:SER:HB2	1.69	0.58
34:B3:742:ARG:NH1	41:5E:506:GLU:OE1	2.36	0.58
36:BE:482:GLY:HA2	36:BE:505:VAL:HG23	1.86	0.58
42:5F:9:GLU:HA	42:5F:9:GLU:OE2	2.04	0.58
55:RL:29:VAL:HG22	55:RL:202:ASP:HA	1.86	0.58
63:RT:224:ILE:HG22	63:RT:233:ILE:HG23	1.85	0.58
23:3F:241:THR:HG21	23:3F:285:SER:HA	1.86	0.57
25:A4:269:PHE:O	35:B8:446:ARG:NH2	2.36	0.57
29:AE:671:LEU:O	29:AE:675:ASN:HB3	2.04	0.57
34:B3:744:ARG:HA	34:B3:785:ILE:HG21	1.86	0.57
50:RE:373:ARG:NH2	50:RE:510:ILE:O	2.37	0.57
50:RE:918:ARG:NE	50:RE:1089:PHE:CE2	2.59	0.57
3:SA:1196:A:N3	52:RG:136:ARG:NH2	2.52	0.57
17:SZ:83:LYS:HD2	17:SZ:96:LEU:HD21	1.86	0.57
26:A5:545:ALA:HB1	27:A8:674:GLU:HG3	1.86	0.57
29:AE:186:MET:HE1	29:AE:234:LEU:HD12	1.86	0.57
31:AG:86:GLU:OE1	31:AG:113:ASN:ND2	2.36	0.57
33:B2:97:GLY:HA3	33:B2:124:ILE:HD11	1.84	0.57
35:B8:221:THR:OG1	35:B8:222:LEU:N	2.38	0.57
41:5E:384:ARG:HE	43:5G:81:SER:HB3	1.69	0.57
43:5G:183:SER:HB3	43:5G:220:ARG:HD2	1.86	0.57
53:RJ:773:THR:HA	53:RJ:777:ARG:HH11	1.69	0.57
54:RK:114:PHE:HB2	54:RK:170:VAL:HG22	1.86	0.57
3:SA:205:U:H2'	3:SA:206:A:H8	1.68	0.57
3:SA:1684:U:H3	3:SA:1718:G:H1	1.52	0.57
5:SF:206:ASP:OD1	5:SF:206:ASP:N	2.38	0.57
9:SJ:167:ALA:HB2	9:SJ:183:ILE:HD12	1.87	0.57
27:A8:631:SER:HA	27:A8:634:LEU:CD2	2.34	0.57
34:B3:392:ASN:H	34:B3:407:SER:HA	1.69	0.57
38:5B:194:LYS:HD2	38:5B:199:ILE:HG13	1.86	0.57
39:5C:317:THR:HG23	39:5C:334:ARG:HB3	1.86	0.57
39:5C:450:GLY:O	59:RQ:857:TYR:OH	2.21	0.57
57:RO:270:SER:H	57:RO:273:GLN:HE21	1.50	0.57
58:RP:2073:GLU:OE2	58:RP:2076:ARG:NH1	2.36	0.57
3:SA:146:U:N3	3:SA:168:A:N6	2.51	0.57
13:SP:115:ILE:HD11	63:RT:97:ARG:CZ	2.34	0.57
22:3E:339:TYR:HB3	22:3E:343:TYR:HB2	1.85	0.57
24:3H:44:LEU:HD13	24:3H:52:ILE:HD11	1.86	0.57
31:AG:144:VAL:HG12	31:AG:153:ILE:HG13	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:157:PHE:HB2	31:AG:170:SER:HB3	1.86	0.57
45:5I:87:SER:OG	45:5I:89:ASP:OD1	2.22	0.57
48:RA:152:ASP:HA	48:RA:166:ASN:HA	1.86	0.57
1:3A:251:G:H2'	23:3F:155:ASN:HD21	1.67	0.57
3:SA:826:U:O2'	3:SA:827:C:O2	2.23	0.57
3:SA:1536:G:N7	3:SA:1539:G:O6	2.37	0.57
30:AF:24:GLN:O	30:AF:28:ARG:HB3	2.05	0.57
30:AF:303:LEU:HD13	30:AF:323:SER:HB2	1.86	0.57
33:B2:259:ILE:HA	33:B2:273:TYR:O	2.03	0.57
36:BE:359:ALA:O	36:BE:421:ASN:ND2	2.38	0.57
64:ST:29:VAL:HG11	64:ST:54:LEU:HD22	1.84	0.57
67:RZ:1095:ARG:NH1	67:RZ:1148:PRO:O	2.37	0.57
1:3A:57:A:H5''	42:5F:165:LYS:HG3	1.87	0.57
34:B3:584:ILE:HD11	34:B3:599:ILE:HD11	1.86	0.57
35:B8:146:LEU:O	35:B8:163:ARG:NH1	2.37	0.57
51:RF:134:ILE:O	51:RF:138:TRP:HB3	2.05	0.57
60:RS:209:LYS:HE3	60:RS:212:LYS:HG3	1.87	0.57
3:SA:559:C:OP1	53:RJ:868:ARG:NH2	2.37	0.57
20:3C:267:VAL:HG21	20:3C:298:ILE:HD12	1.87	0.57
21:3D:264:SER:OG	21:3D:265:GLU:N	2.37	0.57
26:A5:434:THR:HG23	57:RO:266:ASN:HD21	1.68	0.57
27:A8:655:LEU:HD23	28:A9:507:ARG:HB3	1.86	0.57
32:B1:264:LYS:HD3	32:B1:280:THR:HG22	1.87	0.57
36:BE:666:ARG:NH1	36:BE:706:ASP:OD2	2.38	0.57
48:RA:227:ARG:NH2	48:RA:248:SER:O	2.34	0.57
50:RE:440:LEU:HA	50:RE:456:LYS:O	2.05	0.57
2:5A:481:U:O2'	37:B6:102:LYS:NZ	2.37	0.57
16:SY:109:ARG:NH2	16:SY:120:VAL:O	2.37	0.57
23:3F:442:ILE:HA	23:3F:472:PRO:HA	1.86	0.57
32:B1:298:LEU:HA	41:5E:472:PRO:CB	2.33	0.57
33:B2:365:TYR:HA	33:B2:381:LYS:HA	1.85	0.57
35:B8:129:ASP:OD1	36:BE:194:ARG:NH2	2.36	0.57
40:5D:113:ILE:CG2	40:5D:117:LYS:HE3	2.34	0.57
41:5E:507:ILE:HD11	41:5E:528:LEU:HD23	1.85	0.57
53:RJ:1042:MET:HG3	53:RJ:1044:LEU:HD13	1.86	0.57
55:RL:32:ARG:HE	55:RL:35:ASN:HD21	1.53	0.57
67:RZ:776:VAL:HG22	67:RZ:813:ALA:HB2	1.86	0.57
3:SA:1197:C:OP1	52:RG:136:ARG:NH1	2.38	0.57
3:SA:1542:G:N2	3:SA:1569:A:OP2	2.36	0.57
13:SP:23:PHE:CE2	63:RT:244:ARG:NH2	2.69	0.57
26:A5:148:LEU:HD23	26:A5:167:SER:HB3	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B1:405:SER:HB3	32:B1:436:LEU:HD23	1.85	0.57
34:B3:690:HIS:ND1	41:5E:519:GLU:HB2	2.20	0.57
50:RE:443:HIS:HB3	50:RE:470:LYS:HB2	1.86	0.57
64:ST:62:THR:OG1	64:ST:63:GLN:N	2.38	0.57
67:RZ:600:PHE:CZ	67:RZ:684:ASP:O	2.57	0.57
3:SA:112:A:O2'	11:SM:67:ARG:NH1	2.37	0.57
8:SI:187:SER:OG	8:SI:188:GLU:N	2.38	0.57
20:3C:142:ARG:NH1	20:3C:186:ASP:OD2	2.36	0.57
23:3F:142:ILE:HA	23:3F:568:ILE:HD11	1.86	0.57
29:AE:559:ASN:HA	29:AE:592:ARG:HD3	1.85	0.57
40:5D:78:LEU:CB	53:RJ:1082:GLN:HE21	2.01	0.57
41:5E:350:THR:OG1	53:RJ:975:GLU:CD	2.48	0.57
50:RE:1160:SER:O	50:RE:1187:LYS:HG2	2.04	0.57
52:RH:31:LEU:HD13	52:RH:40:ARG:HE	1.69	0.57
58:RP:54:TRP:HA	58:RP:57:ILE:HG22	1.87	0.57
61:RY:487:ASP:N	61:RY:487:ASP:OD1	2.36	0.57
1:3A:94:A:H61	1:3A:322:A:N6	2.01	0.56
3:SA:1477:G:OP1	65:SU:43:ASN:CA	2.53	0.56
23:3F:545:LYS:HG2	23:3F:561:ASN:HD21	1.70	0.56
27:A8:596:LYS:HG2	27:A8:637:LEU:HB3	1.86	0.56
45:5I:81:ASN:ND2	45:5I:96:ASN:OD1	2.38	0.56
50:RE:1170:GLY:HA3	50:RE:1177:GLY:HA2	1.87	0.56
65:SU:39:THR:O	65:SU:39:THR:CG2	2.53	0.56
67:RZ:1055:LYS:HG3	67:RZ:1056:GLU:CD	2.29	0.56
27:A8:673:THR:CG2	28:A9:490:GLU:CB	2.68	0.56
32:B1:418:ARG:HH21	32:B1:418:ARG:CG	2.09	0.56
34:B3:180:ARG:O	34:B3:180:ARG:HG2	2.06	0.56
45:5I:15:PRO:HB3	45:5I:20:GLN:HE21	1.70	0.56
3:SA:505:A:H62	3:SA:585:A:HO2'	1.51	0.56
3:SA:1680:G:N2	3:SA:1720:G:O6	2.38	0.56
16:SY:132:LEU:HA	16:SY:135:LEU:HB2	1.88	0.56
22:3E:414:ARG:NH1	29:AE:187:ASP:OD2	2.36	0.56
23:3F:417:SER:OG	23:3F:418:ASP:N	2.37	0.56
26:A5:212:LEU:HD11	26:A5:246:VAL:HG11	1.87	0.56
28:A9:473:LYS:O	28:A9:477:LYS:NZ	2.39	0.56
30:AF:147:ARG:NH2	52:RH:16:GLN:O	2.39	0.56
31:AG:473:LEU:HB2	31:AG:495:ILE:HD11	1.87	0.56
32:B1:479:LEU:HD12	32:B1:488:LEU:HD11	1.87	0.56
47:5K:26:LYS:HD3	47:5K:29:GLN:HG3	1.87	0.56
55:RL:12:SER:O	55:RL:16:ASN:ND2	2.38	0.56
67:RZ:563:ARG:CD	67:RZ:837:PHE:HE1	2.18	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:318:U:H3	20:3C:119:GLY:CA	2.12	0.56
2:5A:484:G:OP2	37:B6:3:LYS:NZ	2.38	0.56
3:SA:143:G:OP2	7:SH:139:ASN:ND2	2.38	0.56
25:A4:32:ILE:O	25:A4:751:GLU:HA	2.06	0.56
43:5G:76:GLU:OE2	43:5G:201:ARG:NH2	2.36	0.56
45:5I:45:LEU:HD13	45:5I:410:ILE:HG22	1.86	0.56
49:RB:230:ALA:O	49:RB:234:LYS:HB2	2.05	0.56
50:RE:919:TRP:CZ2	50:RE:1067:LEU:CD2	2.87	0.56
57:RO:170:GLY:O	57:RO:272:GLN:NE2	2.32	0.56
63:RT:110:ARG:HH12	63:RT:130:MET:HG2	1.70	0.56
25:A4:37:ARG:NH1	27:A8:704:PRO:O	2.38	0.56
32:B1:373:ASP:HB2	32:B1:380:LEU:HD21	1.86	0.56
41:5E:474:ILE:HG23	41:5E:476:MET:H	1.71	0.56
50:RE:223:ARG:HA	50:RE:226:HIS:HB2	1.86	0.56
50:RE:606:ASN:ND2	50:RE:608:PHE:O	2.39	0.56
52:RG:41:MET:HG3	52:RG:202:ILE:HG23	1.87	0.56
2:5A:5:G:N2	2:5A:8:A:OP2	2.39	0.56
3:SA:337:G:N2	3:SA:340:U:OP2	2.38	0.56
26:A5:435:GLY:HA3	57:RO:262:LEU:HD11	1.88	0.56
30:AF:39:HIS:ND1	64:ST:60:GLU:OE2	2.38	0.56
34:B3:12:LEU:HG	34:B3:641:PHE:HB2	1.87	0.56
41:5E:310:GLN:HA	41:5E:313:GLN:HG2	1.86	0.56
50:RE:822:ARG:HE	50:RE:1136:LEU:HD21	1.71	0.56
51:RF:69:LYS:HZ3	51:RF:159:THR:H	1.52	0.56
55:RL:71:LYS:O	55:RL:75:ASN:ND2	2.38	0.56
56:RN:478:ILE:HD13	56:RN:520:PRO:HB2	1.87	0.56
32:B1:329:VAL:HG12	32:B1:339:LEU:HG	1.87	0.56
33:B2:463:SER:OG	33:B2:464:LEU:N	2.39	0.56
39:5C:284:ARG:NH1	39:5C:408:GLU:OE1	2.38	0.56
50:RE:241:ILE:HA	50:RE:244:LYS:HD2	1.88	0.56
63:RT:258:LYS:O	63:RT:262:ASN:ND2	2.39	0.56
67:RZ:840:PRO:HB2	67:RZ:842:ILE:HG22	1.87	0.56
3:SA:439:U:H4'	3:SA:465:G:H22	1.69	0.56
13:SP:96:PRO:CG	63:RT:237:PHE:CE1	2.76	0.56
21:3D:389:ILE:HA	24:3H:62:GLU:HB2	1.87	0.56
22:3E:136:LEU:HG	22:3E:139:MET:HE2	1.88	0.56
25:A4:301:ASP:O	25:A4:771:GLN:NE2	2.38	0.56
29:AE:272:LYS:NZ	29:AE:310:GLY:O	2.39	0.56
33:B2:598:LYS:NZ	33:B2:610:SER:OG	2.38	0.56
45:5I:340:ARG:NH2	45:5I:377:SER:O	2.39	0.56
47:5K:123:PRO:O	47:5K:126:LYS:NZ	2.39	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:RA:101:ASN:HA	48:RA:118:GLN:HA	1.88	0.56
50:RE:1199:ASN:HB2	66:RD:1509:GLU:HG2	1.87	0.56
4:SC:87:ARG:HH21	4:SC:101:HIS:HD2	1.52	0.56
7:SH:46:LYS:HB3	7:SH:118:GLU:HG2	1.88	0.56
20:3C:225:ARG:NH2	20:3C:246:GLN:OE1	2.38	0.56
26:A5:25:ASP:OD2	35:B8:590:LYS:NZ	2.37	0.56
32:B1:341:GLN:HG3	32:B1:378:PHE:CD1	2.41	0.56
51:RF:262:VAL:HA	51:RF:265:ARG:HG2	1.88	0.56
56:RN:512:ASP:OD1	56:RN:512:ASP:N	2.38	0.56
1:3A:94:A:N6	1:3A:322:A:H61	2.00	0.56
3:SA:128:U:H3	58:RP:906:THR:H	1.53	0.56
20:3C:189:GLY:O	20:3C:216:ASN:ND2	2.39	0.56
27:A8:596:LYS:HE2	27:A8:637:LEU:CA	2.29	0.56
32:B1:419:TYR:CE2	41:5E:486:ASN:ND2	2.73	0.56
33:B2:347:SER:O	33:B2:371:LYS:NZ	2.39	0.56
33:B2:461:SER:OG	33:B2:462:SER:N	2.38	0.56
50:RE:228:ARG:HE	50:RE:296:ILE:HG12	1.71	0.56
50:RE:560:ASN:OD1	50:RE:560:ASN:N	2.39	0.56
53:RJ:960:ARG:CD	64:ST:120:ARG:HH21	2.19	0.56
58:RP:1981:TYR:OH	58:RP:1985:ARG:NH1	2.39	0.56
64:ST:49:LYS:NZ	64:ST:79:TYR:O	2.39	0.56
3:SA:444:C:O2	3:SA:460:A:N6	2.39	0.55
3:SA:606:A:N3	3:SA:607:G:N1	2.50	0.55
13:SP:111:ARG:CZ	63:RT:93:LYS:HB3	2.36	0.55
26:A5:364:THR:OG1	26:A5:368:ASN:ND2	2.38	0.55
26:A5:471:ARG:NH2	57:RO:301:ASP:OD2	2.39	0.55
33:B2:858:PHE:O	33:B2:862:LYS:HB2	2.06	0.55
39:5C:162:ASN:HB3	39:5C:164:GLN:H	1.71	0.55
45:5I:73:ILE:HG12	45:5I:85:THR:HG22	1.88	0.55
54:RK:34:GLU:HG3	54:RK:35:LYS:HG2	1.88	0.55
3:SA:1479:A:OP1	65:SU:80:TYR:CE2	2.59	0.55
3:SA:1533:C:H5'	64:ST:27:LYS:CD	2.36	0.55
3:SA:1678:A:N6	3:SA:1723:U:O4	2.39	0.55
9:SJ:104:ILE:O	9:SJ:164:ARG:HA	2.06	0.55
17:SZ:54:ALA:HB1	17:SZ:76:TYR:HB2	1.88	0.55
20:3B:225:ARG:NH1	20:3B:248:ASP:OD2	2.38	0.55
29:AE:95:ASP:HB2	29:AE:131:ASN:HD21	1.71	0.55
31:AG:435:ASP:HB3	31:AG:702:TYR:HA	1.88	0.55
33:B2:145:ILE:HG23	33:B2:159:LEU:HB2	1.88	0.55
34:B3:179:LYS:O	34:B3:181:LYS:NZ	2.38	0.55
35:B8:181:GLU:HB3	36:BE:281:ARG:HH12	1.71	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5I:329:ILE:HG12	45:5I:343:TYR:HB2	1.89	0.55
58:RP:67:ALA:O	58:RP:71:GLU:HB2	2.07	0.55
58:RP:1760:ASN:ND2	58:RP:1805:ASP:OD2	2.39	0.55
9:SJ:195:ARG:NH2	11:SM:11:ARG:O	2.39	0.55
31:AG:510:TYR:HH	31:AG:527:HIS:HD1	1.52	0.55
33:B2:124:ILE:HA	33:B2:140:SER:HA	1.89	0.55
33:B2:787:LYS:NZ	33:B2:788:PRO:O	2.38	0.55
42:5F:4:LYS:O	42:5F:4:LYS:HG2	2.07	0.55
50:RE:412:LEU:HD13	50:RE:421:LEU:HD12	1.89	0.55
50:RE:578:ILE:HG22	50:RE:619:VAL:HG12	1.88	0.55
50:RE:707:PHE:O	50:RE:918:ARG:NH1	2.39	0.55
53:RJ:871:MET:HE1	53:RJ:930:LYS:HE2	1.87	0.55
54:RK:154:LEU:HB2	54:RK:165:GLU:HG3	1.88	0.55
3:SA:1232:U:O4	3:SA:1234:A:N6	2.39	0.55
9:SJ:98:LYS:NZ	9:SJ:170:SER:O	2.35	0.55
10:SK:139:GLN:NE2	17:SZ:64:PHE:O	2.39	0.55
20:3C:320:TYR:OH	20:3C:322:ARG:NH2	2.39	0.55
23:3F:337:VAL:HG23	23:3F:407:MET:HE2	1.88	0.55
23:3F:552:TRP:HB3	24:3H:85:VAL:HG13	1.88	0.55
24:3H:41:THR:O	24:3H:45:ASN:ND2	2.39	0.55
25:A4:57:ILE:HD13	25:A4:340:GLN:HG2	1.89	0.55
26:A5:5:VAL:HA	26:A5:21:THR:HG22	1.89	0.55
31:AG:262:MET:HA	31:AG:272:ALA:O	2.07	0.55
45:5I:26:ARG:NH1	59:RQ:867:GLN:O	2.40	0.55
46:5J:129:ALA:HB1	53:RJ:1119:ILE:HG22	1.89	0.55
53:RJ:279:PRO:HB3	53:RJ:784:LYS:HA	1.88	0.55
53:RJ:608:LEU:HB2	54:RK:16:ASN:HD22	1.72	0.55
54:RK:139:PRO:HA	54:RK:142:GLU:HB2	1.89	0.55
55:RL:7:ASP:HB2	55:RL:10:ILE:HG12	1.88	0.55
3:SA:1657:U:OP1	3:SA:1658:G:O2'	2.23	0.55
23:3F:293:ASP:N	23:3F:293:ASP:OD1	2.37	0.55
34:B3:366:PRO:HG2	34:B3:378:PRO:HB3	1.89	0.55
40:5D:58:ARG:NH2	42:5F:174:ARG:CZ	2.69	0.55
40:5D:61:ASP:HA	42:5F:160:TRP:HZ3	1.71	0.55
42:5F:13:LEU:CD1	42:5F:16:VAL:HG11	2.37	0.55
48:RA:175:PRO:O	48:RA:177:LYS:NZ	2.36	0.55
50:RE:1174:GLY:N	50:RE:1179:LYS:CE	2.70	0.55
53:RJ:130:ASP:OD2	53:RJ:853:ARG:NH2	2.40	0.55
53:RJ:921:GLU:HB2	54:RK:365:LYS:HG3	1.88	0.55
59:RQ:896:ALA:HB1	59:RQ:897:PRO:HD2	1.89	0.55
66:RD:1674:LEU:HD23	66:RD:1677:ARG:HD3	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:365:G:N7	49:RB:231:ARG:NH1	2.55	0.55
5:SF:45:ILE:HG13	5:SF:61:VAL:HG11	1.88	0.55
12:SO:60:VAL:HG23	12:SO:66:ILE:HD12	1.88	0.55
23:3F:289:ARG:NH2	23:3F:332:ALA:O	2.39	0.55
24:3G:57:ASP:O	24:3G:84:ARG:NH1	2.40	0.55
33:B2:163:LYS:HG2	41:5E:522:ARG:HH22	1.71	0.55
35:B8:561:PRO:O	35:B8:587:ARG:NH1	2.39	0.55
53:RJ:871:MET:SD	53:RJ:930:LYS:HD2	2.47	0.55
53:RJ:939:TYR:HA	53:RJ:997:MET:HE1	1.88	0.55
53:RJ:960:ARG:CD	64:ST:120:ARG:NH2	2.67	0.55
54:RK:155:LYS:HG3	54:RK:164:GLY:HA2	1.89	0.55
56:RN:86:ILE:O	56:RN:89:GLN:CG	2.54	0.55
56:RN:682:ARG:O	56:RN:686:ASN:ND2	2.40	0.55
3:SA:448:C:OP2	5:SF:49:ARG:NH2	2.38	0.55
3:SA:862:A:OP2	12:SO:64:ARG:NH2	2.40	0.55
4:SC:192:VAL:HG21	50:RE:751:LYS:HA	1.88	0.55
11:SM:125:VAL:HB	11:SM:137:PHE:HB3	1.89	0.55
29:AE:1172:ASP:N	29:AE:1236:ASN:O	2.40	0.55
31:AG:510:TYR:OH	31:AG:527:HIS:ND1	2.35	0.55
33:B2:142:ASP:OD2	33:B2:144:ASN:ND2	2.39	0.55
37:B6:278:MET:HA	37:B6:312:LEU:HD11	1.89	0.55
45:5I:173:ILE:HG13	45:5I:174:ARG:HG2	1.87	0.55
57:RO:368:SER:HG	64:ST:3:LEU:N	2.04	0.55
64:ST:41:ARG:CG	65:SU:45:MET:CG	2.78	0.55
3:SA:96:G:N2	3:SA:387:A:N1	2.55	0.55
3:SA:207:U:H3	3:SA:258:C:N4	2.04	0.55
13:SP:90:ARG:O	13:SP:92:LYS:HG3	2.06	0.55
14:SR:122:ARG:CZ	43:5G:133:LYS:HD2	2.37	0.55
20:3C:160:ASP:OD1	20:3C:160:ASP:N	2.37	0.55
30:AF:420:GLU:O	30:AF:424:ARG:HB3	2.07	0.55
31:AG:51:GLN:HE21	31:AG:53:LYS:HD3	1.72	0.55
31:AG:583:LYS:HE2	31:AG:599:ILE:HD13	1.88	0.55
39:5C:186:ARG:NH1	42:5F:42:GLU:OE2	2.40	0.55
50:RE:356:THR:HB	50:RE:414:HIS:HB2	1.89	0.55
1:3A:318:U:N3	20:3C:119:GLY:HA3	2.16	0.55
3:SA:396:G:O6	9:SJ:26:LYS:NZ	2.37	0.55
3:SA:453:U:O2'	3:SA:455:C:OP2	2.24	0.55
7:SH:10:ASN:O	7:SH:128:THR:OG1	2.25	0.55
26:A5:454:GLU:OE2	26:A5:487:ARG:NH1	2.39	0.55
26:A5:531:LYS:O	26:A5:535:ASP:HB2	2.07	0.55
29:AE:558:VAL:O	29:AE:592:ARG:NH1	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B8:526:ASP:OD1	35:B8:526:ASP:N	2.38	0.55
45:5I:324:SER:OG	45:5I:326:ASP:OD1	2.23	0.55
48:RA:166:ASN:ND2	48:RA:168:GLU:O	2.40	0.55
49:RB:304:GLU:OE1	49:RB:309:LYS:NZ	2.40	0.55
53:RJ:360:ASP:OD1	53:RJ:360:ASP:N	2.35	0.55
54:RK:37:ARG:NH2	54:RK:49:GLU:OE2	2.36	0.55
56:RN:290:LYS:O	60:RS:458:ARG:NH1	2.40	0.55
57:RO:156:TRP:O	57:RO:215:ASN:ND2	2.40	0.55
67:RZ:534:ARG:NH2	67:RZ:864:ASN:O	2.40	0.55
67:RZ:1113:ILE:HD12	67:RZ:1166:ARG:HH22	1.71	0.55
67:RZ:1124:ARG:NH1	67:RZ:1127:ASN:O	2.40	0.55
3:SA:1475:A:C5'	3:SA:1540:G:H4'	2.37	0.55
3:SA:1684:U:N3	3:SA:1718:G:N1	2.55	0.55
9:SJ:41:LYS:HE2	9:SJ:43:ILE:HD11	1.89	0.55
21:3D:63:LEU:O	21:3D:67:ASN:ND2	2.40	0.55
25:A4:534:LEU:HA	25:A4:542:VAL:O	2.07	0.55
27:A8:441:VAL:C	31:AG:728:LEU:CD2	2.80	0.55
27:A8:441:VAL:C	31:AG:728:LEU:HD21	2.32	0.55
29:AE:519:LEU:HD23	29:AE:523:ILE:HD13	1.88	0.55
29:AE:636:ASP:OD1	29:AE:639:ARG:NH1	2.40	0.55
35:B8:176:LYS:O	35:B8:180:ASP:CB	2.55	0.55
37:B6:187:LYS:HE3	46:5J:63:PRO:HB2	1.89	0.55
39:5C:369:MET:HE1	39:5C:404:PRO:HD2	1.88	0.55
45:5I:402:GLU:O	45:5I:405:ARG:NH2	2.40	0.55
50:RE:267:ILE:HD12	50:RE:293:ASN:HB3	1.89	0.55
50:RE:508:SER:HA	50:RE:512:LEU:HB2	1.89	0.55
53:RJ:551:LYS:O	53:RJ:555:MET:HB2	2.07	0.55
54:RK:347:ASN:ND2	54:RK:349:ASP:OD2	2.40	0.55
57:RO:345:ILE:HA	57:RO:349:LEU:HD13	1.89	0.55
60:RS:445:ARG:NH1	60:RS:445:ARG:O	2.40	0.55
3:SA:103:A:OP1	9:SJ:18:ARG:NH1	2.40	0.54
3:SA:1684:U:O2	3:SA:1718:G:N2	2.40	0.54
14:SR:22:VAL:HG22	14:SR:65:ILE:HG23	1.89	0.54
23:3F:398:CYS:O	23:3F:419:ASN:ND2	2.40	0.54
27:A8:563:LEU:HB2	27:A8:598:GLU:CD	2.27	0.54
29:AE:12:ALA:HB2	39:5C:142:GLY:HA3	1.89	0.54
29:AE:196:LEU:HD11	29:AE:213:THR:HG21	1.88	0.54
32:B1:356:ASP:HB2	32:B1:826:ARG:HG3	1.88	0.54
33:B2:267:ASP:OD1	33:B2:267:ASP:N	2.36	0.54
34:B3:107:ILE:HD11	34:B3:147:ILE:HG22	1.88	0.54
50:RE:190:ALA:O	50:RE:350:TYR:OH	2.25	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RE:536:TYR:OH	50:RE:552:ARG:NH1	2.40	0.54
53:RJ:289:HIS:HB2	53:RJ:815:LEU:HD21	1.89	0.54
67:RZ:444:MET:HE2	67:RZ:490:LYS:HE2	1.89	0.54
67:RZ:732:LEU:HD13	67:RZ:746:VAL:HA	1.89	0.54
3:SA:258:C:O2	9:SJ:178:ARG:NH2	2.40	0.54
3:SA:332:U:OP1	9:SJ:31:ARG:NH2	2.37	0.54
3:SA:545:A:O2'	3:SA:546:U:O4'	2.22	0.54
3:SA:1628:U:OP2	41:5E:534:ARG:NH1	2.40	0.54
10:SK:78:ARG:NH2	49:RB:247:GLU:OE1	2.33	0.54
13:SP:122:PRO:HB2	13:SP:125:SER:HB3	1.89	0.54
25:A4:641:GLU:OE2	25:A4:645:ARG:NH1	2.40	0.54
27:A8:638:LEU:HA	27:A8:641:VAL:HG12	1.89	0.54
32:B1:202:ASP:N	32:B1:202:ASP:OD1	2.40	0.54
33:B2:592:SER:OG	33:B2:593:ALA:N	2.40	0.54
34:B3:537:TRP:N	34:B3:551:SER:O	2.37	0.54
45:5I:133:GLN:NE2	45:5I:151:ASN:OD1	2.40	0.54
59:RQ:898:PHE:N	59:RQ:898:PHE:CD1	2.73	0.54
3:SA:562:G:H8	43:5G:283:THR:HB	1.72	0.54
21:3D:21:LYS:HE2	21:3D:49:GLU:HB2	1.88	0.54
30:AF:75:LYS:HD3	30:AF:113:PRO:HD3	1.89	0.54
34:B3:5:THR:O	34:B3:611:LYS:NZ	2.39	0.54
44:5H:565:LYS:HA	44:5H:568:LYS:HG2	1.89	0.54
52:RH:114:ILE:HG12	52:RH:122:ILE:HB	1.89	0.54
1:3A:58:A:P	42:5F:165:LYS:HE3	2.47	0.54
22:3E:280:MET:HG3	22:3E:288:THR:HG22	1.89	0.54
29:AE:652:MET:HE3	29:AE:683:SER:HB3	1.89	0.54
31:AG:850:GLU:HA	31:AG:853:ILE:HD12	1.89	0.54
32:B1:396:ALA:HB2	32:B1:438:VAL:HG21	1.90	0.54
40:5D:61:ASP:C	42:5F:160:TRP:CH2	2.86	0.54
48:RA:121:ARG:HH22	61:RY:462:ARG:HD2	1.72	0.54
48:RA:250:GLY:HA2	48:RA:274:ILE:HG23	1.88	0.54
67:RZ:1209:ARG:HG2	67:RZ:1211:CYS:HB3	1.90	0.54
3:SA:576:G:C5'	41:5E:327:LYS:HE2	2.37	0.54
6:SG:26:ALA:HB3	14:SR:28:LEU:HB3	1.90	0.54
25:A4:252:GLN:NE2	25:A4:318:ASN:OD1	2.40	0.54
29:AE:274:ILE:HD11	35:B8:215:THR:HG21	1.90	0.54
33:B2:287:ARG:NH1	33:B2:324:PHE:O	2.41	0.54
34:B3:328:GLN:NE2	34:B3:329:VAL:O	2.41	0.54
50:RE:1189:LEU:HD23	50:RE:1189:LEU:O	2.07	0.54
50:RE:1216:LYS:HG2	50:RE:1220:PHE:HE2	1.68	0.54
53:RJ:966:ILE:HD13	53:RJ:976:ILE:HG22	1.88	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RJ:1018:VAL:O	53:RJ:1029:TRP:NE1	2.41	0.54
65:SU:109:GLU:OE2	65:SU:122:ARG:NE	2.40	0.54
9:SJ:8:ARG:HD2	9:SJ:22:ARG:HH11	1.72	0.54
10:SK:76:LEU:HB2	49:RB:328:PHE:CE1	2.43	0.54
14:SR:34:SER:HB2	14:SR:38:LEU:HD12	1.90	0.54
20:3C:268:VAL:HG22	20:3C:317:VAL:HG12	1.89	0.54
21:3D:379:LEU:O	21:3D:383:CYS:HB2	2.07	0.54
23:3F:481:ILE:HD12	23:3F:486:VAL:HG13	1.90	0.54
24:3G:13:ASP:OD1	24:3G:13:ASP:N	2.39	0.54
26:A5:20:VAL:HG22	26:A5:29:VAL:HG22	1.89	0.54
27:A8:527:LEU:HD11	27:A8:549:ARG:HH22	1.71	0.54
29:AE:205:THR:HB	29:AE:210:LEU:HD21	1.89	0.54
30:AF:387:ALA:O	30:AF:391:ASN:ND2	2.41	0.54
41:5E:437:ILE:HD11	42:5F:70:PHE:HE2	1.73	0.54
49:RB:242:MET:HE2	49:RB:332:ARG:HE	1.73	0.54
49:RB:335:GLU:HA	49:RB:339:SER:HB2	1.89	0.54
50:RE:578:ILE:HG21	50:RE:617:LEU:HD12	1.90	0.54
60:RS:319:LYS:HA	60:RS:323:PHE:HB2	1.89	0.54
3:SA:511:A:OP2	10:SK:176:ASN:ND2	2.40	0.54
30:AF:360:MET:HE3	30:AF:361:MET:HE3	1.89	0.54
33:B2:317:ILE:O	33:B2:321:TYR:N	2.41	0.54
35:B8:486:SER:OG	35:B8:487:GLU:N	2.41	0.54
36:BE:626:ASP:N	36:BE:626:ASP:OD1	2.35	0.54
39:5C:449:ILE:HD11	45:5I:38:ALA:HA	1.89	0.54
45:5I:349:GLN:O	45:5I:367:SER:OG	2.24	0.54
48:RA:78:LYS:O	48:RA:80:GLN:NE2	2.41	0.54
50:RE:174:TYR:HE2	50:RE:227:LYS:HB3	1.73	0.54
54:RK:214:LYS:O	54:RK:217:LYS:NZ	2.40	0.54
58:RP:1939:ARG:HG3	58:RP:1974:LEU:HD11	1.88	0.54
67:RZ:445:VAL:HB	67:RZ:489:VAL:HA	1.90	0.54
1:3A:258:U:O4	21:3D:377:ARG:NH2	2.41	0.54
3:SA:1108:G:O2'	3:SA:1109:G:N7	2.37	0.54
3:SA:1541:G:H3'	3:SA:1542:G:C8	2.42	0.54
3:SA:1605:G:OP1	43:5G:119:ARG:NH2	2.40	0.54
23:3F:414:ILE:HD11	23:3F:480:ALA:HB2	1.90	0.54
30:AF:215:VAL:HA	30:AF:230:GLY:HA3	1.90	0.54
31:AG:727:GLN:OE1	31:AG:738:ASN:ND2	2.39	0.54
34:B3:745:ASP:O	41:5E:512:GLY:O	2.26	0.54
41:5E:315:GLU:HB3	53:RJ:1032:LEU:CD1	2.37	0.54
45:5I:75:LYS:NZ	45:5I:356:TYR:O	2.34	0.54
48:RA:64:VAL:HG21	48:RA:323:VAL:HG12	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RJ:73:ALA:HB1	53:RJ:131:ILE:HD12	1.90	0.54
53:RJ:960:ARG:HD3	64:ST:120:ARG:HH21	1.72	0.54
53:RJ:1027:THR:HG23	53:RJ:1028:GLU:HG2	1.89	0.54
3:SA:494:U:OP1	53:RJ:1138:ARG:NH2	2.32	0.54
5:SF:198:LYS:HG3	5:SF:208:VAL:HG23	1.89	0.54
18:Sc:67:THR:OG1	18:Sc:70:LYS:O	2.26	0.54
21:3D:392:TYR:HB3	24:3H:65:LEU:HD22	1.90	0.54
24:3H:38:ASN:HA	24:3H:41:THR:HG22	1.90	0.54
25:A4:271:THR:HG21	35:B8:443:VAL:HG21	1.90	0.54
31:AG:325:GLN:NE2	31:AG:328:THR:OG1	2.41	0.54
31:AG:368:ASP:OD1	31:AG:368:ASP:N	2.38	0.54
35:B8:176:LYS:O	35:B8:180:ASP:HB3	2.07	0.54
36:BE:73:GLU:OE2	36:BE:74:LYS:NZ	2.40	0.54
49:RB:310:GLN:O	49:RB:314:ASN:ND2	2.40	0.54
50:RE:931:ASP:OD1	50:RE:931:ASP:N	2.37	0.54
56:RN:86:ILE:HA	56:RN:89:GLN:CD	2.33	0.54
3:SA:146:U:O4	3:SA:168:A:N7	2.41	0.54
3:SA:1175:U:OP1	56:RN:748:ARG:NH1	2.41	0.54
20:3B:90:PRO:HD3	46:5J:106:LEU:HD12	1.90	0.54
33:B2:260:GLU:O	33:B2:272:PHE:HA	2.08	0.54
35:B8:352:GLN:HE21	35:B8:385:ASN:HD22	1.54	0.54
36:BE:160:THR:OG1	36:BE:163:GLN:NE2	2.41	0.54
50:RE:227:LYS:HA	50:RE:230:VAL:HG12	1.90	0.54
50:RE:691:SER:OG	50:RE:692:LYS:N	2.40	0.54
53:RJ:954:SER:HA	53:RJ:984:GLU:HG3	1.89	0.54
56:RN:515:HIS:HB3	56:RN:518:ILE:HG22	1.90	0.54
56:RN:780:LYS:HG2	56:RN:781:MET:HE2	1.90	0.54
20:3B:124:SER:HB3	46:5J:153:ILE:HD11	1.90	0.53
31:AG:724:ILE:HD11	31:AG:763:ILE:HG22	1.90	0.53
34:B3:157:ASN:HD22	63:RT:77:GLY:HA2	1.73	0.53
34:B3:510:SER:O	34:B3:514:THR:OG1	2.26	0.53
36:BE:604:SER:OG	36:BE:606:ASP:OD1	2.25	0.53
50:RE:375:PHE:HZ	50:RE:487:ILE:HG23	1.73	0.53
55:RL:37:LEU:HD13	55:RL:123:ILE:HD13	1.90	0.53
56:RN:605:ASP:OD1	56:RN:610:ARG:NH1	2.41	0.53
3:SA:325:G:H2'	3:SA:326:G:H8	1.73	0.53
22:3E:380:ARG:NH1	22:3E:382:ASP:OD1	2.40	0.53
23:3F:162:CYS:SG	23:3F:525:GLN:NE2	2.79	0.53
27:A8:443:CYS:CB	31:AG:728:LEU:CB	2.76	0.53
29:AE:651:LEU:HD21	29:AE:680:TYR:HB2	1.90	0.53
30:AF:173:THR:HG21	30:AF:218:VAL:H	1.74	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:157:PHE:O	31:AG:169:GLN:NE2	2.41	0.53
33:B2:412:GLY:HA2	33:B2:431:GLY:H	1.73	0.53
36:BE:430:ILE:HB	36:BE:443:TRP:HB2	1.89	0.53
36:BE:743:ARG:O	36:BE:743:ARG:HD3	2.08	0.53
47:5K:145:VAL:HG23	47:5K:151:TYR:HB2	1.89	0.53
50:RE:1183:THR:HG23	50:RE:1183:THR:O	2.07	0.53
52:RG:36:LYS:NZ	52:RG:169:ASP:O	2.40	0.53
52:RH:125:ASN:ND2	52:RH:127:THR:OG1	2.42	0.53
53:RJ:871:MET:CE	53:RJ:930:LYS:CE	2.86	0.53
66:RD:1633:ASP:OD2	66:RD:1636:ARG:NH1	2.42	0.53
3:SA:1633:A:O3'	32:B1:418:ARG:NH2	2.38	0.53
3:SA:1738:U:OP1	33:B2:279:LYS:NZ	2.40	0.53
6:SG:73:THR:OG1	6:SG:91:GLU:OE1	2.27	0.53
9:SJ:184:LEU:HD23	9:SJ:189:LEU:HA	1.90	0.53
23:3F:399:GLU:OE2	23:3F:417:SER:OG	2.26	0.53
24:3H:45:ASN:HA	24:3H:74:LYS:HE2	1.90	0.53
25:A4:311:THR:HG22	25:A4:313:LYS:H	1.74	0.53
50:RE:969:ASN:ND2	50:RE:972:ASP:OD1	2.41	0.53
53:RJ:374:ASP:OD1	53:RJ:374:ASP:N	2.40	0.53
11:SM:82:ARG:HA	11:SM:111:VAL:HG13	1.91	0.53
21:3D:157:ALA:O	37:B6:293:TYR:OH	2.26	0.53
25:A4:641:GLU:HB3	25:A4:749:SER:HB3	1.90	0.53
26:A5:46:TRP:HD1	26:A5:48:GLU:HG3	1.74	0.53
32:B1:283:GLU:OE2	32:B1:297:GLN:NE2	2.42	0.53
34:B3:596:ASP:OD1	34:B3:596:ASP:N	2.42	0.53
41:5E:338:ASP:OD2	64:ST:116:LEU:HD11	2.08	0.53
42:5F:136:VAL:HA	42:5F:160:TRP:HA	1.90	0.53
45:5I:192:SER:HB2	45:5I:206:VAL:HG22	1.89	0.53
50:RE:687:GLN:NE2	50:RE:694:ALA:O	2.41	0.53
54:RK:289:VAL:HG21	54:RK:294:LEU:HD13	1.90	0.53
67:RZ:779:SER:O	67:RZ:781:ARG:NH1	2.42	0.53
1:3A:25:U:H5'	42:5F:11:LYS:O	2.07	0.53
7:SH:48:TYR:OH	7:SH:119:GLN:O	2.27	0.53
21:3D:392:TYR:HB2	24:3H:62:GLU:HB3	1.90	0.53
29:AE:40:ALA:HB1	29:AE:123:ARG:HH12	1.73	0.53
31:AG:291:ARG:HD2	31:AG:329:ASN:HD21	1.73	0.53
48:RA:202:ASN:ND2	48:RA:229:PHE:O	2.41	0.53
56:RN:96:LYS:HD2	56:RN:761:PHE:HZ	1.73	0.53
2:5A:9:G:H5'	28:A9:483:LYS:HZ1	1.72	0.53
3:SA:396:G:N7	9:SJ:47:ARG:NH1	2.56	0.53
4:SC:32:ILE:HB	4:SC:43:VAL:HG22	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:404:SER:OG	31:AG:405:ALA:N	2.40	0.53
36:BE:737:LEU:O	36:BE:740:ILE:HG23	2.09	0.53
39:5C:312:VAL:HG21	39:5C:353:PRO:HG2	1.90	0.53
51:RF:107:LEU:HD12	51:RF:194:ARG:HG3	1.89	0.53
65:SU:65:ILE:HD13	65:SU:71:VAL:HG22	1.91	0.53
65:SU:66:TYR:HA	65:SU:124:ILE:HD11	1.91	0.53
3:SA:513:U:H2'	3:SA:514:G:C8	2.44	0.53
20:3B:230:TYR:OH	20:3B:256:ASN:OD1	2.25	0.53
31:AG:213:LYS:HA	31:AG:223:LYS:HA	1.91	0.53
42:5F:123:THR:HG23	42:5F:126:ASP:H	1.74	0.53
50:RE:1098:PHE:HE2	50:RE:1182:ILE:HG22	1.72	0.53
52:RG:169:ASP:N	52:RG:169:ASP:OD1	2.40	0.53
66:RD:1473:ASN:CB	66:RD:1509:GLU:OE2	2.51	0.53
1:3A:98:U:OP2	1:3A:98:U:H6	1.92	0.53
23:3F:357:LEU:HD22	49:RB:256:PRO:HB2	1.90	0.53
27:A8:647:LEU:O	28:A9:509:GLN:NE2	2.41	0.53
28:A9:513:ARG:HH21	28:A9:515:ASP:HA	1.72	0.53
32:B1:418:ARG:HG3	32:B1:418:ARG:NH2	2.12	0.53
32:B1:419:TYR:CD2	41:5E:482:LEU:HD12	2.44	0.53
33:B2:525:ASP:OD1	33:B2:525:ASP:N	2.41	0.53
41:5E:493:GLN:HE21	41:5E:497:ASN:CB	2.20	0.53
67:RZ:851:VAL:HG23	67:RZ:862:ILE:HG21	1.91	0.53
67:RZ:884:GLN:NE2	67:RZ:893:GLU:OE2	2.42	0.53
30:AF:87:ALA:HA	30:AF:97:CYS:O	2.08	0.53
50:RE:417:SER:OG	50:RE:418:SER:N	2.42	0.53
52:RG:121:LEU:HD21	52:RG:167:ILE:HG13	1.90	0.53
55:RL:131:THR:OG1	55:RL:133:ASN:ND2	2.42	0.53
58:RP:18:SER:OG	58:RP:19:PHE:N	2.42	0.53
59:RQ:298:TRP:HE1	59:RQ:899:LYS:CG	2.19	0.53
67:RZ:447:ILE:HG13	67:RZ:514:ILE:HD13	1.89	0.53
67:RZ:794:GLN:HE22	67:RZ:908:SER:HB3	1.74	0.53
67:RZ:1042:ARG:NH1	67:RZ:1067:LEU:O	2.42	0.53
3:SA:1209:C:N3	3:SA:1210:C:N4	2.56	0.53
5:SF:209:HIS:ND1	5:SF:218:PHE:O	2.41	0.53
21:3D:102:ASP:HB3	21:3D:105:LEU:HB3	1.91	0.53
29:AE:626:PHE:HB3	29:AE:629:GLU:HB2	1.90	0.53
31:AG:283:VAL:HG12	31:AG:290:ILE:HG22	1.91	0.53
32:B1:812:GLU:HG3	32:B1:813:HIS:HD2	1.74	0.53
41:5E:500:LYS:O	41:5E:508:ARG:NH2	2.42	0.53
50:RE:179:LYS:HB2	50:RE:210:PRO:HG2	1.90	0.53
63:RT:164:LEU:HD22	63:RT:182:ILE:HD11	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:153:G:H2'	3:SA:154:G:H8	1.74	0.52
3:SA:258:C:H4'	9:SJ:75:LYS:HD2	1.91	0.52
3:SA:331:A:N3	9:SJ:5:ARG:NH1	2.57	0.52
3:SA:1136:U:O2'	33:B2:596:ASN:ND2	2.43	0.52
11:SM:97:TYR:O	11:SM:99:ARG:NH1	2.42	0.52
13:SP:96:PRO:HB3	63:RT:237:PHE:CD1	2.44	0.52
25:A4:35:ARG:HH11	25:A4:738:TYR:HD1	1.57	0.52
33:B2:676:SER:OG	33:B2:678:ASP:OD1	2.22	0.52
41:5E:322:LYS:HD2	41:5E:327:LYS:HB2	1.90	0.52
50:RE:398:ALA:O	50:RE:402:ASN:ND2	2.43	0.52
50:RE:443:HIS:HB3	50:RE:470:LYS:HE2	1.91	0.52
50:RE:518:PHE:CE2	50:RE:1075:LEU:HG	2.43	0.52
52:RH:116:THR:HG22	52:RH:118:ARG:H	1.73	0.52
67:RZ:808:GLN:OE1	67:RZ:812:ARG:NH1	2.42	0.52
3:SA:153:G:N2	7:SH:56:ASN:OD1	2.42	0.52
32:B1:418:ARG:NH1	41:5E:492:PRO:HD3	2.24	0.52
36:BE:578:VAL:O	36:BE:579:ARG:NH1	2.42	0.52
41:5E:384:ARG:HD3	43:5G:83:ILE:CD1	2.38	0.52
48:RA:13:VAL:HG12	48:RA:343:ILE:HG12	1.89	0.52
50:RE:437:ASP:N	50:RE:437:ASP:OD1	2.42	0.52
52:RG:188:ARG:NH2	52:RH:247:ASP:OD2	2.41	0.52
54:RK:180:MET:HE3	54:RK:181:HIS:H	1.75	0.52
55:RL:117:ASN:O	55:RL:141:THR:OG1	2.26	0.52
56:RN:587:ASP:OD1	56:RN:587:ASP:N	2.42	0.52
60:RS:437:ARG:NH2	60:RS:459:GLU:O	2.42	0.52
3:SA:1535:U:O2	3:SA:1536:G:N1	2.41	0.52
9:SJ:191:PHE:O	9:SJ:195:ARG:NH1	2.41	0.52
20:3B:281:ASP:OD1	20:3B:281:ASP:N	2.41	0.52
22:3E:289:GLN:HE21	22:3E:388:LEU:HD13	1.74	0.52
24:3H:54:MET:HE1	24:3H:78:TYR:HB2	1.90	0.52
29:AE:502:ILE:HG23	29:AE:542:ILE:HG13	1.90	0.52
29:AE:556:LYS:O	29:AE:592:ARG:NH2	2.43	0.52
32:B1:678:GLU:OE2	41:5E:455:HIS:HE1	1.92	0.52
41:5E:341:LEU:HD13	64:ST:120:ARG:NH1	2.22	0.52
43:5G:185:VAL:O	43:5G:220:ARG:NH1	2.39	0.52
53:RJ:982:LYS:HG3	53:RJ:983:PRO:HD3	1.92	0.52
57:RO:233:ASP:N	57:RO:233:ASP:OD1	2.42	0.52
66:RD:1547:TYR:OH	66:RD:1583:SER:OG	2.27	0.52
67:RZ:594:PHE:HE1	67:RZ:823:ARG:HH11	1.57	0.52
3:SA:647:G:H22	3:SA:687:G:H22	1.57	0.52
20:3C:297:ARG:HD3	20:3C:322:ARG:HA	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:39:VAL:H	25:A4:755:ILE:HD11	1.75	0.52
25:A4:420:LEU:HD23	26:A5:581:ASN:HA	1.91	0.52
29:AE:571:LEU:HD11	29:AE:582:VAL:HG11	1.92	0.52
32:B1:680:ARG:HH11	41:5E:455:HIS:CD2	2.27	0.52
50:RE:270:ILE:HB	50:RE:292:ILE:HG23	1.91	0.52
53:RJ:135:ALA:O	53:RJ:238:ARG:NH2	2.42	0.52
54:RK:171:ASP:N	54:RK:171:ASP:OD1	2.39	0.52
58:RP:452:ASN:O	58:RP:456:GLU:N	2.43	0.52
1:3A:323:G:N3	1:3A:323:G:C2'	2.71	0.52
5:SF:53:LYS:O	23:3F:120:ARG:NH2	2.42	0.52
8:SI:163:ASP:HA	8:SI:166:LEU:HG	1.90	0.52
27:A8:443:CYS:CA	31:AG:728:LEU:CD2	2.79	0.52
50:RE:186:ILE:HD11	50:RE:206:LEU:HB2	1.92	0.52
50:RE:526:CYS:O	50:RE:698:ASN:ND2	2.43	0.52
50:RE:596:LYS:HZ2	50:RE:600:TYR:HD1	1.56	0.52
53:RJ:90:VAL:HG23	53:RJ:107:VAL:HG11	1.92	0.52
53:RJ:844:PRO:HA	53:RJ:856:THR:O	2.08	0.52
54:RK:97:GLY:HA2	54:RK:100:VAL:HG12	1.92	0.52
67:RZ:396:GLU:HB2	67:RZ:583:VAL:HG23	1.91	0.52
1:3A:97:C:O2	1:3A:320:G:C2	2.62	0.52
26:A5:481:LEU:HD22	26:A5:523:LEU:HD22	1.92	0.52
28:A9:504:GLU:OE2	28:A9:507:ARG:NH1	2.43	0.52
30:AF:364:SER:O	30:AF:364:SER:OG	2.26	0.52
33:B2:398:ASP:HB2	33:B2:406:LEU:HB3	1.92	0.52
33:B2:554:THR:OG1	33:B2:556:LYS:NZ	2.39	0.52
36:BE:268:THR:HG22	36:BE:270:SER:H	1.74	0.52
36:BE:470:GLN:NE2	36:BE:512:GLY:O	2.42	0.52
42:5F:66:PRO:O	42:5F:72:ARG:NH2	2.43	0.52
48:RA:147:ASN:ND2	48:RA:154:TYR:OH	2.43	0.52
50:RE:469:ASP:OD2	50:RE:472:THR:OG1	2.27	0.52
50:RE:1108:LEU:HB2	50:RE:1169:ILE:HD11	1.91	0.52
3:SA:594:A:OP1	10:SK:38:ASN:ND2	2.43	0.52
3:SA:1436:A:H1'	60:RS:419:LYS:HD2	1.91	0.52
7:SH:105:ASP:OD1	7:SH:105:ASP:N	2.43	0.52
20:3B:277:ASP:N	20:3B:277:ASP:OD1	2.43	0.52
22:3E:251:ASP:OD1	22:3E:251:ASP:N	2.43	0.52
25:A4:658:ASP:OD2	25:A4:731:HIS:N	2.42	0.52
30:AF:256:THR:N	30:AF:275:SER:O	2.39	0.52
33:B2:281:ILE:HB	33:B2:332:ILE:HG23	1.91	0.52
35:B8:216:TYR:OH	36:BE:276:TYR:OH	2.27	0.52
36:BE:819:LYS:NZ	36:BE:823:GLU:OE2	2.40	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RE:315:ILE:HG13	50:RE:329:THR:HG21	1.92	0.52
51:RF:227:ARG:HA	51:RF:230:ILE:HD12	1.91	0.52
58:RP:1880:ILE:HD11	58:RP:1892:LEU:HD21	1.91	0.52
67:RZ:507:LEU:O	67:RZ:539:ARG:NH2	2.43	0.52
1:3A:256:G:OP1	21:3D:382:LYS:NZ	2.37	0.52
3:SA:283:U:OP1	7:SH:191:ARG:NH1	2.40	0.52
3:SA:862:A:H4'	15:SX:57:ARG:HG3	1.90	0.52
6:SG:120:ILE:HA	6:SG:123:VAL:HG12	1.92	0.52
9:SJ:110:ARG:NH1	9:SJ:161:SER:O	2.43	0.52
9:SJ:171:SER:HB3	9:SJ:180:ASP:H	1.74	0.52
10:SK:67:PRO:HB2	49:RB:334:LEU:HD23	1.91	0.52
22:3E:426:ALA:HB2	36:BE:305:ASN:HD21	1.75	0.52
31:AG:64:LYS:NZ	31:AG:123:GLY:O	2.39	0.52
31:AG:319:LYS:HD2	31:AG:339:GLY:H	1.74	0.52
33:B2:53:ASP:OD2	33:B2:58:ASP:OD1	2.27	0.52
34:B3:680:ASN:N	34:B3:680:ASN:OD1	2.42	0.52
36:BE:605:LEU:HD23	36:BE:628:VAL:HG11	1.92	0.52
45:5I:319:GLU:OE2	45:5I:356:TYR:OH	2.27	0.52
46:5J:58:ASN:HA	46:5J:61:LYS:HG2	1.92	0.52
53:RJ:246:ALA:HB3	53:RJ:810:ILE:HB	1.91	0.52
54:RK:30:PRO:HB3	54:RK:77:ARG:HG3	1.90	0.52
58:RP:1892:LEU:HA	58:RP:1895:PHE:HB2	1.92	0.52
59:RQ:298:TRP:CD1	59:RQ:899:LYS:HG3	2.44	0.52
60:RS:397:PHE:HD1	60:RS:407:GLU:HG2	1.75	0.52
67:RZ:423:GLN:OE1	67:RZ:426:GLN:NE2	2.42	0.52
26:A5:503:LYS:HD3	28:A9:508:ARG:HH22	1.75	0.52
39:5C:130:ARG:NH2	39:5C:379:GLU:OE2	2.42	0.52
43:5G:108:LYS:HD2	43:5G:116:ARG:HB2	1.92	0.52
50:RE:596:LYS:HG3	50:RE:598:LYS:H	1.74	0.52
53:RJ:616:ASP:HB2	53:RJ:621:LEU:HG	1.90	0.52
67:RZ:936:VAL:HG11	67:RZ:1038:ILE:HB	1.92	0.52
2:5A:294:U:OP1	32:B1:631:ASN:ND2	2.43	0.52
8:SI:83:LYS:O	8:SI:86:GLN:NE2	2.43	0.52
21:3D:169:LYS:HA	21:3D:299:VAL:HG22	1.92	0.52
25:A4:63:SER:HA	25:A4:82:ARG:HH12	1.75	0.52
32:B1:506:SER:OG	32:B1:507:GLN:N	2.43	0.52
33:B2:54:ILE:CD1	33:B2:364:TYR:CD2	2.93	0.52
33:B2:634:SER:OG	33:B2:635:LYS:N	2.41	0.52
36:BE:59:GLN:HG2	36:BE:71:VAL:HG22	1.91	0.52
39:5C:410:ASN:O	45:5I:27:ASN:ND2	2.43	0.52
42:5F:6:LYS:HB2	42:5F:9:GLU:HG2	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RE:529:VAL:HB	50:RE:613:VAL:HB	1.91	0.52
5:SF:201:HIS:H	5:SF:206:ASP:HB3	1.75	0.51
11:SM:18:HIS:HB2	11:SM:63:LEU:HD21	1.92	0.51
22:3E:218:ALA:O	22:3E:236:LYS:NZ	2.41	0.51
29:AE:659:LEU:HD13	29:AE:690:GLU:HB3	1.92	0.51
31:AG:407:ASN:ND2	31:AG:416:SER:OG	2.44	0.51
32:B1:420:ARG:NH2	41:5E:494:GLU:CD	2.66	0.51
32:B1:722:THR:HG22	32:B1:724:HIS:H	1.75	0.51
36:BE:377:SER:HB2	36:BE:445:MET:HE1	1.92	0.51
49:RB:348:SER:HB2	58:RP:1728:PHE:HB3	1.93	0.51
50:RE:634:HIS:HB2	50:RE:655:LEU:HD11	1.91	0.51
51:RF:44:SER:H	51:RF:50:SER:HA	1.75	0.51
51:RF:128:PHE:HD2	51:RF:134:ILE:HG22	1.75	0.51
54:RK:315:LYS:HB2	54:RK:348:GLU:HB3	1.92	0.51
55:RL:589:ALA:HB3	55:RL:593:GLU:H	1.75	0.51
60:RS:229:LEU:HD11	60:RS:233:PHE:HD2	1.74	0.51
65:SU:37:VAL:O	65:SU:46:PRO:CB	2.58	0.51
67:RZ:1042:ARG:NH1	67:RZ:1068:LYS:O	2.43	0.51
1:3A:312:U:H5''	46:5J:167:LYS:HG2	1.91	0.51
3:SA:419:G:H5''	3:SA:419:G:H8	1.75	0.51
3:SA:1599:C:H4'	43:5G:145:HIS:CD2	2.45	0.51
21:3D:126:ASP:HA	21:3D:129:ARG:HG2	1.93	0.51
22:3E:359:ILE:HA	22:3E:362:VAL:HG12	1.92	0.51
25:A4:402:TRP:HB3	25:A4:416:LEU:HA	1.91	0.51
33:B2:362:ILE:HG12	33:B2:385:ILE:HB	1.91	0.51
34:B3:337:HIS:HD2	34:B3:363:ARG:HD3	1.74	0.51
34:B3:414:VAL:HG23	34:B3:427:TYR:HB3	1.92	0.51
35:B8:306:ASN:OD1	35:B8:306:ASN:N	2.43	0.51
53:RJ:193:ARG:NH2	53:RJ:196:THR:OG1	2.43	0.51
53:RJ:864:ASP:OD1	53:RJ:864:ASP:N	2.44	0.51
53:RJ:871:MET:HE1	53:RJ:930:LYS:HD2	1.91	0.51
57:RO:324:PHE:HZ	64:ST:4:VAL:HG21	1.75	0.51
60:RS:360:LEU:HD21	60:RS:393:TYR:HB2	1.92	0.51
5:SF:202:ASP:OD1	5:SF:202:ASP:N	2.41	0.51
9:SJ:100:ALA:O	9:SJ:168:CYS:HA	2.10	0.51
17:SZ:59:GLY:O	49:RB:296:ARG:NH2	2.44	0.51
22:3E:3:TYR:N	22:3E:21:LYS:O	2.43	0.51
31:AG:736:THR:HG23	31:AG:738:ASN:H	1.74	0.51
32:B1:588:ASP:OD1	32:B1:588:ASP:N	2.43	0.51
32:B1:678:GLU:OE2	41:5E:455:HIS:ND1	2.43	0.51
36:BE:854:SER:HB2	36:BE:895:VAL:HG21	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:RG:105:ASN:HD21	52:RG:110:LEU:HD22	1.75	0.51
57:RO:356:ALA:HA	57:RO:499:LEU:HD22	1.91	0.51
65:SU:130:ARG:HH21	65:SU:134:ARG:HB2	1.76	0.51
2:5A:473:A:H5''	39:5C:164:GLN:HE22	1.76	0.51
3:SA:29:U:H2'	3:SA:30:G:H8	1.74	0.51
3:SA:1790:A:O2'	3:SA:1792:G:N2	2.43	0.51
29:AE:558:VAL:HG13	29:AE:615:ASN:HA	1.93	0.51
34:B3:679:THR:HG21	34:B3:723:GLU:HB2	1.93	0.51
45:5I:327:LYS:HG2	45:5I:350:HIS:H	1.76	0.51
48:RA:282:ASN:HD21	48:RA:325:GLY:H	1.58	0.51
50:RE:261:ASN:HB3	50:RE:379:MET:HB2	1.91	0.51
50:RE:1215:ASN:HD21	51:RF:35:HIS:HA	1.75	0.51
51:RF:51:ASP:HB2	51:RF:134:ILE:HG21	1.91	0.51
52:RG:150:ILE:HD11	52:RG:160:LEU:HD23	1.92	0.51
53:RJ:72:VAL:HG22	53:RJ:137:LEU:HB3	1.91	0.51
57:RO:258:GLU:HG3	57:RO:289:PHE:HD1	1.74	0.51
59:RQ:298:TRP:NE1	59:RQ:899:LYS:CG	2.62	0.51
67:RZ:1107:THR:OG1	67:RZ:1109:ARG:NH2	2.44	0.51
3:SA:-5:G:N1	39:5C:39:ASP:OD1	2.36	0.51
3:SA:1720:G:N7	3:SA:1721:A:N6	2.58	0.51
4:SC:164:ILE:HD11	4:SC:205:PHE:HB2	1.92	0.51
13:SP:12:GLN:HE21	13:SP:78:ALA:HB2	1.76	0.51
20:3B:120:GLU:OE2	20:3B:142:ARG:NE	2.41	0.51
27:A8:587:LEU:HD23	27:A8:587:LEU:O	2.10	0.51
27:A8:596:LYS:CD	27:A8:637:LEU:HD22	2.38	0.51
29:AE:586:LEU:O	29:AE:590:ALA:CB	2.58	0.51
30:AF:399:GLU:O	30:AF:403:ASN:ND2	2.42	0.51
33:B2:759:GLY:HA3	33:B2:805:ILE:HD11	1.91	0.51
36:BE:370:SER:OG	36:BE:372:ASP:OD1	2.20	0.51
37:B6:296:SER:HB3	37:B6:300:MET:HB2	1.91	0.51
43:5G:143:HIS:HB2	43:5G:151:SER:HB2	1.91	0.51
45:5I:122:ARG:HB2	45:5I:192:SER:HB3	1.93	0.51
56:RN:661:ILE:HG22	56:RN:665:GLN:HG3	1.92	0.51
57:RO:200:ASN:ND2	57:RO:256:ASN:O	2.43	0.51
64:ST:40:ARG:O	65:SU:45:MET:SD	2.69	0.51
2:5A:293:U:H3	32:B1:632:SER:HB3	1.75	0.51
3:SA:340:U:H2'	3:SA:341:A:H8	1.75	0.51
3:SA:1538:U:C5	3:SA:1540:G:C6	2.98	0.51
7:SH:39:GLU:HG3	7:SH:46:LYS:HG3	1.91	0.51
20:3C:94:ALA:HB3	20:3C:166:PRO:HG3	1.92	0.51
23:3F:136:PHE:HE1	23:3F:484:SER:HB2	1.74	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:420:LEU:HD11	25:A4:462:VAL:HG21	1.92	0.51
26:A5:439:VAL:HG11	57:RO:300:THR:HG21	1.92	0.51
30:AF:258:LEU:HD22	30:AF:272:LEU:HD21	1.93	0.51
32:B1:329:VAL:HG13	32:B1:338:ILE:HB	1.92	0.51
34:B3:17:ALA:HB3	34:B3:35:PRO:HA	1.91	0.51
41:5E:341:LEU:HB2	64:ST:116:LEU:HD22	1.90	0.51
50:RE:1162:ILE:HG23	50:RE:1187:LYS:NZ	2.26	0.51
51:RF:178:ASP:OD1	51:RF:178:ASP:N	2.43	0.51
67:RZ:775:TYR:HD1	67:RZ:820:HIS:HB2	1.75	0.51
1:3A:93:U:OP2	22:3E:302:HIS:ND1	2.42	0.51
2:5A:90:G:O2'	2:5A:91:U:O4'	2.25	0.51
3:SA:1634:C:P	32:B1:418:ARG:HH22	2.33	0.51
23:3F:284:LEU:O	23:3F:548:ARG:NH2	2.38	0.51
31:AG:434:GLN:OE1	31:AG:434:GLN:N	2.43	0.51
31:AG:877:ASP:N	31:AG:877:ASP:OD1	2.43	0.51
34:B3:497:LEU:HA	34:B3:507:ALA:O	2.11	0.51
45:5I:54:PHE:O	45:5I:382:ARG:NH2	2.44	0.51
48:RA:101:ASN:HD21	48:RA:116:HIS:HB3	1.76	0.51
50:RE:111:LEU:HA	50:RE:114:VAL:HG12	1.93	0.51
60:RS:263:THR:HA	60:RS:266:PHE:HB2	1.93	0.51
3:SA:1541:G:H2'	3:SA:1542:G:C4	2.45	0.51
8:SI:67:LEU:HD13	8:SI:94:ALA:HB2	1.93	0.51
9:SJ:67:TRP:NE1	9:SJ:70:GLU:OE1	2.42	0.51
13:SP:107:ARG:NH2	13:SP:107:ARG:CB	2.73	0.51
17:SZ:86:GLU:OE2	17:SZ:90:ARG:NH1	2.43	0.51
21:3D:26:ASP:OD1	45:5I:98:SER:OG	2.29	0.51
25:A4:481:ILE:HB	25:A4:485:LYS:HB2	1.91	0.51
34:B3:501:PRO:HG3	34:B3:543:GLN:HG3	1.91	0.51
39:5C:74:LEU:HD23	39:5C:404:PRO:HG2	1.93	0.51
40:5D:61:ASP:HB3	42:5F:160:TRP:CZ3	2.46	0.51
41:5E:350:THR:HG21	53:RJ:975:GLU:HB2	1.92	0.51
50:RE:298:PHE:HB2	50:RE:340:SER:HA	1.93	0.51
50:RE:777:ASP:O	50:RE:780:GLN:NE2	2.43	0.51
51:RF:71:VAL:HA	51:RF:74:LEU:HD12	1.92	0.51
57:RO:214:LYS:O	57:RO:268:GLN:NE2	2.44	0.51
63:RT:97:ARG:NH1	63:RT:153:GLN:OE1	2.42	0.51
63:RT:187:VAL:HG13	63:RT:251:ILE:HD11	1.93	0.51
67:RZ:561:THR:OG1	67:RZ:563:ARG:NH2	2.43	0.51
1:3A:305:G:H2'	1:3A:306:G:H8	1.76	0.51
7:SH:70:PRO:HD3	7:SH:101:ILE:HD12	1.93	0.51
7:SH:74:LYS:HB2	48:RA:88:ASN:HD21	1.75	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SP:96:PRO:HG3	63:RT:237:PHE:HE1	1.61	0.51
20:3B:91:HIS:HD2	20:3B:93:HIS:H	1.57	0.51
22:3E:355:ASN:HB2	22:3E:401:LEU:HD13	1.93	0.51
33:B2:562:SER:HB2	33:B2:564:LYS:HB2	1.93	0.51
39:5C:91:ILE:HG23	45:5I:3:ILE:HD11	1.92	0.51
45:5I:329:ILE:HG22	45:5I:351:VAL:HG11	1.93	0.51
50:RE:1202:CYS:SG	50:RE:1203:ASN:N	2.83	0.51
52:RH:178:VAL:HG12	52:RH:223:GLU:HB2	1.93	0.51
2:5A:7:A:N7	31:AG:578:ASN:ND2	2.55	0.51
3:SA:1538:U:H2'	3:SA:1540:G:N7	2.26	0.51
20:3B:111:MET:HB2	20:3B:186:ASP:HB3	1.92	0.51
27:A8:441:VAL:CA	31:AG:728:LEU:HD21	2.41	0.51
27:A8:443:CYS:CA	31:AG:728:LEU:HD13	2.17	0.51
27:A8:587:LEU:HD23	27:A8:587:LEU:C	2.35	0.51
32:B1:392:ALA:O	32:B1:404:SER:HA	2.10	0.51
32:B1:732:GLU:HG2	32:B1:734:GLN:HE22	1.76	0.51
36:BE:135:ASN:ND2	36:BE:165:GLY:O	2.42	0.51
39:5C:238:MET:HE3	39:5C:247:MET:HE2	1.92	0.51
50:RE:1189:LEU:HD22	50:RE:1190:PHE:CD2	2.46	0.51
53:RJ:776:GLN:HA	53:RJ:780:ILE:HG22	1.93	0.51
53:RJ:776:GLN:NE2	53:RJ:781:GLU:OE2	2.40	0.51
58:RP:1896:ILE:HG13	58:RP:1897:PRO:HD3	1.92	0.51
65:SU:39:THR:HG21	65:SU:57:ARG:NH2	2.26	0.51
1:3A:316:A:H2'	1:3A:317:A:H8	1.76	0.50
20:3B:142:ARG:NH2	20:3B:182:SER:OG	2.44	0.50
20:3C:223:ASP:OD2	20:3C:225:ARG:NH1	2.44	0.50
24:3H:44:LEU:HD22	24:3H:52:ILE:HD12	1.90	0.50
29:AE:522:ARG:HH12	29:AE:561:PHE:HB2	1.76	0.50
30:AF:59:SER:OG	30:AF:60:SER:N	2.43	0.50
31:AG:855:LEU:HD23	35:B8:477:LYS:HE3	1.94	0.50
34:B3:413:ILE:HG22	34:B3:429:LYS:HA	1.92	0.50
50:RE:1107:GLY:HA3	50:RE:1176:LYS:HG2	1.93	0.50
53:RJ:772:MET:HE3	53:RJ:773:THR:H	1.76	0.50
55:RL:539:ALA:O	55:RL:543:SER:CB	2.59	0.50
58:RP:85:LYS:NZ	58:RP:89:ASN:OD1	2.40	0.50
58:RP:1873:LEU:HD22	58:RP:1917:ILE:HG13	1.93	0.50
65:SU:39:THR:CG2	65:SU:57:ARG:NH1	2.72	0.50
65:SU:131:ASP:OD1	65:SU:134:ARG:NH1	2.35	0.50
3:SA:1194:A:OP2	3:SA:1195:C:N4	2.40	0.50
3:SA:1477:G:H4'	65:SU:47:PRO:HA	1.93	0.50
3:SA:1794:A:OP2	63:RT:200:ARG:NH1	2.44	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:SG:118:LEU:HG	6:SG:129:PRO:HB2	1.92	0.50
31:AG:668:THR:OG1	31:AG:669:ASN:OD1	2.30	0.50
41:5E:336:PRO:HB2	41:5E:339:ALA:HB2	1.93	0.50
55:RL:80:GLU:OE2	55:RL:85:THR:OG1	2.29	0.50
67:RZ:546:ASN:ND2	67:RZ:549:GLU:OE2	2.44	0.50
3:SA:340:U:H2'	3:SA:341:A:C8	2.47	0.50
3:SA:647:G:H1	3:SA:687:G:H1	1.59	0.50
20:3C:171:LEU:HD23	20:3C:240:VAL:HG12	1.92	0.50
33:B2:627:SER:OG	33:B2:628:HIS:N	2.45	0.50
46:5J:120:ASP:HB2	46:5J:173:ILE:HD12	1.92	0.50
54:RK:65:ILE:HB	56:RN:112:VAL:HG12	1.93	0.50
54:RK:183:ILE:HG22	54:RK:351:ILE:HD13	1.93	0.50
60:RS:439:PHE:HA	60:RS:442:GLU:HG3	1.94	0.50
1:3A:59:G:H5'	32:B1:570:THR:HG23	1.92	0.50
3:SA:1192:C:H1'	52:RG:131:PRO:HA	1.92	0.50
3:SA:1796:C:H2'	3:SA:1797:A:H8	1.76	0.50
4:SC:36:SER:HA	4:SC:41:ARG:HD3	1.91	0.50
9:SJ:104:ILE:HD13	9:SJ:167:ALA:HB3	1.91	0.50
26:A5:192:SER:HB3	26:A5:207:GLU:HG3	1.93	0.50
27:A8:647:LEU:CB	28:A9:509:GLN:HE22	2.23	0.50
30:AF:323:SER:OG	64:ST:5:VAL:CG1	2.60	0.50
30:AF:401:LEU:HB3	30:AF:434:ARG:HH22	1.77	0.50
33:B2:201:ILE:HG13	34:B3:663:VAL:HG11	1.92	0.50
41:5E:319:VAL:HG23	53:RJ:1038:ILE:HG21	1.91	0.50
41:5E:345:LEU:HD21	53:RJ:961:PHE:CE2	2.46	0.50
50:RE:404:GLY:H	50:RE:455:SER:HB3	1.76	0.50
50:RE:1096:TYR:CD2	50:RE:1185:LEU:HD12	2.47	0.50
58:RP:1746:LYS:O	58:RP:1748:ASN:ND2	2.41	0.50
65:SU:50:ALA:HA	65:SU:53:TRP:HD1	1.76	0.50
2:5A:505:G:H2'	2:5A:506:G:C8	2.47	0.50
3:SA:290:G:H3'	3:SA:291:G:H8	1.76	0.50
3:SA:304:U:OP1	11:SM:136:ARG:NH2	2.45	0.50
3:SA:413:U:H2'	3:SA:414:C:H6	1.77	0.50
4:SC:27:LYS:HB3	4:SC:47:LEU:HD22	1.93	0.50
7:SH:21:GLU:OE2	7:SH:25:ARG:NH2	2.44	0.50
25:A4:382:VAL:HG11	25:A4:755:ILE:HG21	1.92	0.50
26:A5:8:SER:OG	26:A5:293:ASN:ND2	2.43	0.50
26:A5:115:ASN:ND2	26:A5:130:ASP:OD1	2.45	0.50
27:A8:34:GLY:HA2	27:A8:352:GLN:HA	1.92	0.50
27:A8:712:ASP:OD1	27:A8:712:ASP:N	2.39	0.50
30:AF:224:THR:O	30:AF:239:LEU:CB	2.57	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:207:LEU:HG	31:AG:264:ILE:HD12	1.93	0.50
31:AG:249:THR:HG22	31:AG:256:THR:HB	1.93	0.50
52:RG:150:ILE:HG12	52:RG:160:LEU:HB2	1.94	0.50
52:RH:41:MET:HG3	52:RH:202:ILE:HG23	1.92	0.50
53:RJ:634:ARG:HD2	54:RK:185:ARG:HH21	1.77	0.50
54:RK:114:PHE:O	54:RK:169:VAL:HA	2.12	0.50
65:SU:133:ASP:OD1	65:SU:133:ASP:N	2.43	0.50
3:SA:420:A:C8	3:SA:420:A:H3'	2.47	0.50
3:SA:1134:C:H1'	33:B2:610:SER:HB2	1.94	0.50
11:SM:109:VAL:HG11	11:SM:139:VAL:HG13	1.94	0.50
22:3E:385:ASP:OD1	22:3E:385:ASP:N	2.42	0.50
25:A4:156:LEU:HD22	25:A4:170:ILE:HD11	1.93	0.50
32:B1:328:LEU:HD21	41:5E:476:MET:HG3	1.93	0.50
32:B1:375:THR:OG1	32:B1:376:SER:N	2.41	0.50
50:RE:711:PRO:HG3	50:RE:767:GLN:HE21	1.76	0.50
66:RD:1674:LEU:HA	66:RD:1677:ARG:HG2	1.93	0.50
3:SA:420:A:H3'	3:SA:420:A:H8	1.76	0.50
3:SA:442:C:O2'	3:SA:525:A:N1	2.35	0.50
4:SC:144:ARG:HB3	4:SC:206:PRO:HB2	1.93	0.50
5:SF:26:CYS:SG	5:SF:27:TYR:N	2.84	0.50
31:AG:370:GLN:NE2	31:AG:384:SER:OG	2.44	0.50
36:BE:587:ARG:HB3	36:BE:605:LEU:HD12	1.92	0.50
38:5B:173:ARG:HE	40:5D:146:PHE:HA	1.76	0.50
39:5C:37:THR:O	39:5C:43:ARG:NH2	2.45	0.50
40:5D:149:GLU:HB3	40:5D:153:ASN:HA	1.94	0.50
58:RP:1769:LEU:HD21	58:RP:1797:LEU:HD22	1.94	0.50
3:SA:123:G:H21	5:SF:146:THR:HG21	1.76	0.50
8:SI:28:GLU:OE2	8:SI:39:ARG:NH2	2.45	0.50
13:SP:85:ALA:H	13:SP:119:THR:HB	1.76	0.50
13:SP:115:ILE:CD1	63:RT:97:ARG:NE	2.75	0.50
25:A4:415:LYS:NZ	25:A4:416:LEU:O	2.45	0.50
26:A5:355:ASN:OD1	31:AG:479:ASN:ND2	2.44	0.50
27:A8:539:ASN:ND2	27:A8:560:ASN:O	2.44	0.50
27:A8:631:SER:O	27:A8:634:LEU:CG	2.45	0.50
29:AE:306:LEU:HD22	29:AE:311:ASN:HA	1.94	0.50
30:AF:133:HIS:HB2	30:AF:139:ILE:HG13	1.94	0.50
32:B1:557:LYS:NZ	36:BE:426:GLU:OE1	2.44	0.50
34:B3:407:SER:OG	34:B3:408:LYS:N	2.45	0.50
37:B6:297:ASP:OD1	37:B6:297:ASP:N	2.44	0.50
45:5I:76:ASN:HA	45:5I:118:VAL:HG21	1.93	0.50
50:RE:261:ASN:OD1	50:RE:588:GLN:NE2	2.42	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RE:1062:THR:HG21	62:X1:310:UNK:HA	1.94	0.50
53:RJ:262:GLY:O	53:RJ:264:GLN:NE2	2.44	0.50
53:RJ:852:ARG:HD2	53:RJ:888:PRO:HG3	1.94	0.50
53:RJ:1069:VAL:HG11	53:RJ:1083:ILE:HD13	1.94	0.50
53:RJ:1094:TYR:HA	53:RJ:1097:LYS:HG2	1.94	0.50
65:SU:138:GLN:HA	65:SU:141:GLU:HB3	1.93	0.50
67:RZ:1055:LYS:HG3	67:RZ:1056:GLU:OE1	2.11	0.50
3:SA:268:C:H2'	3:SA:269:G:H8	1.76	0.50
3:SA:1588:G:H1	3:SA:1608:U:H3	1.60	0.50
4:SC:158:SER:HA	4:SC:161:ILE:HB	1.93	0.50
9:SJ:80:GLY:O	9:SJ:103:GLN:NE2	2.45	0.50
11:SM:109:VAL:HG13	11:SM:138:ASN:HA	1.94	0.50
18:Sc:78:SER:HB3	51:RF:212:PHE:HB3	1.94	0.50
22:3E:430:ASP:HA	36:BE:125:GLY:HA2	1.93	0.50
30:AF:260:TYR:OH	30:AF:262:GLU:OE1	2.30	0.50
31:AG:80:GLN:NE2	31:AG:83:GLU:OE1	2.44	0.50
33:B2:90:ASP:N	33:B2:90:ASP:OD1	2.39	0.50
34:B3:22:VAL:O	34:B3:68:LYS:NZ	2.45	0.50
34:B3:65:THR:HA	34:B3:80:SER:HA	1.94	0.50
34:B3:455:LEU:HA	34:B3:464:LYS:O	2.12	0.50
36:BE:225:THR:OG1	36:BE:227:THR:O	2.29	0.50
40:5D:113:ILE:O	40:5D:117:LYS:HG3	2.12	0.50
52:RH:41:MET:O	52:RH:110:LEU:HA	2.11	0.50
52:RH:228:SER:OG	52:RH:229:ASN:N	2.44	0.50
58:RP:73:ASP:OD2	58:RP:83:HIS:ND1	2.45	0.50
60:RS:322:LEU:HD21	60:RS:359:LEU:HD11	1.92	0.50
2:5A:20:C:H2'	2:5A:21:A:H8	1.77	0.49
2:5A:484:G:O6	59:RQ:872:ARG:NH1	2.45	0.49
3:SA:898:A:N1	3:SA:911:U:O2'	2.41	0.49
5:SF:181:VAL:HA	5:SF:227:VAL:HA	1.94	0.49
20:3C:170:VAL:HG23	20:3C:194:VAL:HG13	1.93	0.49
25:A4:566:LEU:HD11	25:A4:584:VAL:HG21	1.94	0.49
31:AG:139:GLU:HB3	31:AG:155:THR:HB	1.94	0.49
33:B2:102:VAL:HA	33:B2:118:ASN:HA	1.93	0.49
33:B2:828:TYR:HA	33:B2:831:LYS:HG2	1.93	0.49
34:B3:466:TRP:HZ3	34:B3:478:GLN:HA	1.77	0.49
35:B8:410:ASP:OD1	35:B8:479:ASN:ND2	2.45	0.49
40:5D:67:MET:SD	42:5F:170:LEU:HB3	2.52	0.49
42:5F:96:ASP:HB3	42:5F:100:LYS:HE2	1.94	0.49
50:RE:138:ILE:HD11	50:RE:238:HIS:HB3	1.94	0.49
50:RE:177:ASN:ND2	50:RE:213:LEU:O	2.44	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RE:345:TYR:O	50:RE:349:LEU:CB	2.59	0.49
57:RO:327:MET:O	57:RO:331:ASN:HA	2.11	0.49
61:RY:472:ILE:HA	61:RY:475:TYR:HB2	1.93	0.49
2:5A:293:U:H2'	32:B1:631:ASN:HA	1.93	0.49
3:SA:123:G:OP1	5:SF:77:ARG:NH2	2.40	0.49
9:SJ:70:GLU:OE2	9:SJ:117:TYR:OH	2.30	0.49
20:3B:228:GLN:O	20:3B:231:ARG:NH2	2.43	0.49
30:AF:48:ASN:ND2	30:AF:111:TYR:OH	2.45	0.49
30:AF:378:LYS:NZ	35:B8:292:GLY:O	2.44	0.49
31:AG:628:ASP:H	31:AG:658:GLU:HA	1.77	0.49
31:AG:736:THR:OG1	31:AG:737:ILE:N	2.45	0.49
32:B1:406:SER:OG	32:B1:407:LEU:N	2.46	0.49
32:B1:839:THR:HG22	36:BE:882:GLU:HG3	1.95	0.49
33:B2:476:ILE:HD11	33:B2:490:THR:HB	1.93	0.49
33:B2:817:LEU:HD11	33:B2:856:ASN:HD21	1.77	0.49
35:B8:520:ASN:HB2	35:B8:533:ALA:HB3	1.94	0.49
41:5E:533:LYS:HA	41:5E:536:ARG:CD	2.42	0.49
48:RA:252:SER:HB2	48:RA:266:LYS:HB3	1.94	0.49
50:RE:566:ILE:HD13	50:RE:690:VAL:HG21	1.94	0.49
50:RE:606:ASN:ND2	50:RE:610:PHE:O	2.45	0.49
52:RH:38:THR:O	52:RH:40:ARG:NH1	2.45	0.49
67:RZ:1086:ALA:HB2	67:RZ:1181:ILE:HD12	1.94	0.49
24:3H:54:MET:O	24:3H:80:PHE:HA	2.12	0.49
29:AE:387:LEU:HD21	29:AE:403:LEU:HD13	1.93	0.49
29:AE:558:VAL:HG22	29:AE:615:ASN:HD22	1.76	0.49
33:B2:180:THR:OG1	33:B2:207:CYS:SG	2.62	0.49
43:5G:202:VAL:HA	43:5G:205:ILE:HG22	1.94	0.49
52:RH:112:VAL:O	52:RH:124:VAL:HB	2.12	0.49
53:RJ:106:THR:HG23	53:RJ:355:TYR:HB3	1.94	0.49
56:RN:623:ASP:O	56:RN:627:HIS:HB3	2.13	0.49
58:RP:1473:ALA:O	58:RP:1477:LYS:CB	2.61	0.49
58:RP:1794:ARG:HH22	58:RP:1870:LYS:HD2	1.77	0.49
64:ST:27:LYS:O	64:ST:31:ALA:HB2	2.13	0.49
3:SA:562:G:C8	43:5G:283:THR:HB	2.46	0.49
23:3F:343:ASP:OD1	23:3F:343:ASP:N	2.46	0.49
24:3G:105:ASN:HB3	24:3G:108:SER:HB2	1.94	0.49
24:3H:7:LYS:HB3	24:3H:65:LEU:HD11	1.95	0.49
24:3H:52:ILE:HG22	24:3H:54:MET:SD	2.52	0.49
25:A4:418:CYS:SG	25:A4:419:LYS:N	2.85	0.49
25:A4:452:HIS:HB3	25:A4:463:THR:HG23	1.94	0.49
27:A8:673:THR:CG2	28:A9:490:GLU:N	2.74	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AE:637:ILE:HA	29:AE:640:ILE:HG22	1.94	0.49
31:AG:584:PHE:HB3	31:AG:598:LYS:HB2	1.94	0.49
39:5C:84:PHE:HA	39:5C:369:MET:HA	1.95	0.49
43:5G:287:LYS:HE2	43:5G:290:LEU:HA	1.94	0.49
53:RJ:138:VAL:HB	53:RJ:167:VAL:HG22	1.93	0.49
53:RJ:871:MET:HE1	53:RJ:930:LYS:CD	2.43	0.49
54:RK:180:MET:O	54:RK:181:HIS:ND1	2.45	0.49
66:RD:1519:ALA:HA	66:RD:1522:ASN:HD22	1.77	0.49
2:5A:485:G:H4'	2:5A:486:U:H5'	1.94	0.49
13:SP:111:ARG:NH1	63:RT:95:GLU:CG	2.75	0.49
15:SX:70:ASN:N	15:SX:70:ASN:OD1	2.43	0.49
20:3B:116:SER:OG	20:3B:120:GLU:OE1	2.28	0.49
23:3F:365:PRO:HB3	23:3F:397:PHE:HA	1.93	0.49
24:3H:54:MET:HB3	24:3H:64:LEU:HD13	1.93	0.49
31:AG:116:VAL:O	31:AG:131:HIS:HA	2.13	0.49
34:B3:182:CYS:SG	34:B3:183:LEU:N	2.84	0.49
34:B3:343:MET:HE2	34:B3:622:ALA:HB1	1.95	0.49
34:B3:513:LYS:HG3	34:B3:532:HIS:HB2	1.95	0.49
40:5D:67:MET:SD	42:5F:170:LEU:CB	3.01	0.49
48:RA:300:TRP:HB3	48:RA:307:ALA:HA	1.95	0.49
49:RB:268:ASN:HB3	49:RB:271:ARG:HB3	1.94	0.49
53:RJ:951:MET:SD	53:RJ:987:TYR:OH	2.63	0.49
54:RK:107:ALA:HB1	54:RK:170:VAL:HG21	1.94	0.49
55:RL:57:TRP:NE1	55:RL:125:GLN:OE1	2.39	0.49
67:RZ:750:PRO:HD3	67:RZ:756:LEU:HD12	1.94	0.49
1:3A:321:C:H2'	1:3A:322:A:C8	2.47	0.49
3:SA:1779:U:O2	3:SA:1782:A:N6	2.36	0.49
7:SH:57:ASP:HA	7:SH:107:ALA:H	1.78	0.49
13:SP:115:ILE:HD11	63:RT:97:ARG:NH1	2.27	0.49
25:A4:389:ARG:HE	25:A4:404:MET:HB2	1.78	0.49
32:B1:286:LEU:HD12	32:B1:295:ILE:HB	1.94	0.49
32:B1:567:ASP:HB3	42:5F:144:ASN:ND2	2.28	0.49
33:B2:397:ILE:HD11	33:B2:405:LEU:HD21	1.94	0.49
33:B2:862:LYS:HE2	34:B3:805:ILE:HD13	1.93	0.49
36:BE:118:VAL:HA	36:BE:132:THR:HA	1.94	0.49
36:BE:469:SER:HB3	36:BE:510:LEU:HD23	1.95	0.49
38:5B:186:ASP:HA	38:5B:189:THR:HG22	1.93	0.49
39:5C:183:GLU:HB3	47:5K:16:THR:HG22	1.94	0.49
52:RG:46:ALA:HA	52:RG:115:GLN:HG3	1.93	0.49
53:RJ:176:LEU:HD12	53:RJ:183:LEU:HA	1.94	0.49
53:RJ:309:PRO:HD2	53:RJ:353:LEU:HD22	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RP:752:THR:O	58:RP:756:SER:CB	2.59	0.49
60:RS:388:ASP:HA	60:RS:391:VAL:HG22	1.93	0.49
65:SU:116:ILE:HD13	65:SU:122:ARG:HB3	1.93	0.49
13:SP:111:ARG:NH1	63:RT:93:LYS:HB3	2.28	0.49
27:A8:631:SER:HA	27:A8:634:LEU:CG	2.43	0.49
30:AF:428:ARG:HH21	31:AG:518:ASP:HB3	1.76	0.49
32:B1:569:PHE:CZ	42:5F:142:LEU:HD21	2.48	0.49
33:B2:624:LEU:HD12	33:B2:629:ASN:HB2	1.93	0.49
34:B3:80:SER:OG	34:B3:81:GLN:N	2.46	0.49
35:B8:233:LEU:HD11	35:B8:543:LEU:HD12	1.95	0.49
36:BE:173:LEU:HD13	36:BE:219:ASP:HA	1.95	0.49
36:BE:737:LEU:C	36:BE:740:ILE:CG2	2.85	0.49
45:5I:315:PRO:HG2	45:5I:360:SER:HB3	1.93	0.49
45:5I:421:GLN:HG3	45:5I:425:LYS:HD2	1.94	0.49
49:RB:230:ALA:O	49:RB:234:LYS:CB	2.61	0.49
51:RF:56:VAL:HG22	51:RF:123:THR:HG22	1.93	0.49
53:RJ:777:ARG:O	53:RJ:778:GLN:NE2	2.46	0.49
56:RN:752:MET:HA	56:RN:755:ILE:HG12	1.93	0.49
59:RQ:797:ALA:O	63:RT:142:ASN:ND2	2.45	0.49
67:RZ:522:ASN:HB2	67:RZ:525:THR:HG23	1.94	0.49
3:SA:129:U:O2'	58:RP:903:THR:O	2.30	0.49
22:3E:24:LYS:O	22:3E:28:LEU:CB	2.60	0.49
29:AE:1628:SER:O	29:AE:1632:PHE:CB	2.60	0.49
31:AG:96:ILE:HG12	31:AG:108:THR:HG21	1.95	0.49
33:B2:291:GLU:HA	33:B2:294:ARG:HG2	1.94	0.49
33:B2:440:PRO:HG3	33:B2:485:GLY:HA3	1.94	0.49
34:B3:749:ASN:ND2	41:5E:511:ASN:OD1	2.45	0.49
36:BE:274:ILE:HG23	36:BE:286:VAL:HG22	1.94	0.49
36:BE:528:PHE:HZ	36:BE:570:ILE:HD11	1.78	0.49
39:5C:456:SER:O	39:5C:456:SER:OG	2.28	0.49
47:5K:65:VAL:HG22	47:5K:152:ILE:HB	1.94	0.49
50:RE:972:ASP:OD1	50:RE:972:ASP:N	2.45	0.49
53:RJ:274:TYR:OH	53:RJ:306:ASP:OD1	2.29	0.49
3:SA:153:G:N2	3:SA:161:U:O2	2.43	0.49
3:SA:622:A:HI'	3:SA:623:A:C8	2.48	0.49
20:3B:269:ILE:O	20:3B:315:ILE:HA	2.13	0.49
25:A4:150:ASN:ND2	25:A4:198:ASP:OD1	2.37	0.49
26:A5:149:ASN:HD21	26:A5:190:PRO:HB3	1.77	0.49
29:AE:482:SER:HB2	29:AE:484:LEU:HG	1.94	0.49
30:AF:75:LYS:HD2	30:AF:111:TYR:HA	1.95	0.49
31:AG:31:ASN:HD21	31:AG:201:ILE:HB	1.78	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B8:148:THR:OG1	35:B8:152:GLU:OE2	2.31	0.49
35:B8:462:GLY:HA2	35:B8:527:GLY:HA3	1.95	0.49
36:BE:902:ASN:HB3	36:BE:905:ILE:HG22	1.95	0.49
45:5I:140:SER:OG	45:5I:141:ASP:N	2.44	0.49
50:RE:858:ARG:HD2	50:RE:861:ILE:HD11	1.95	0.49
51:RF:23:HIS:HD2	51:RF:26:LEU:HG	1.78	0.49
59:RQ:853:ASN:OD1	59:RQ:853:ASN:N	2.45	0.49
67:RZ:414:GLY:HA3	67:RZ:420:LYS:HD3	1.95	0.49
67:RZ:468:ASP:N	67:RZ:468:ASP:OD1	2.44	0.49
1:3A:57:A:N3	42:5F:133:GLN:NE2	2.61	0.49
3:SA:895:G:H1	3:SA:917:U:H3	1.61	0.49
3:SA:1133:A:OP1	54:RK:231:ARG:NE	2.42	0.49
3:SA:1474:G:H2'	3:SA:1475:A:C8	2.48	0.49
24:3H:51:PHE:HE1	24:3H:114:ILE:HG23	1.78	0.49
27:A8:583:SER:HA	27:A8:586:ILE:HG22	1.94	0.49
27:A8:635:PHE:HD2	28:A9:492:ILE:CD1	2.26	0.49
33:B2:392:THR:HG21	33:B2:410:SER:HB3	1.93	0.49
33:B2:643:ASP:HB3	33:B2:650:ILE:HD11	1.95	0.49
34:B3:600:LYS:HA	34:B3:609:CYS:HA	1.95	0.49
39:5C:340:LEU:O	39:5C:368:TYR:N	2.43	0.49
47:5K:149:LYS:HD3	47:5K:170:ILE:HD11	1.95	0.49
52:RG:190:GLN:HE22	52:RG:247:ASP:HB2	1.78	0.49
52:RG:197:ASP:OD1	52:RG:197:ASP:N	2.45	0.49
53:RJ:634:ARG:NH2	54:RK:186:PRO:O	2.42	0.49
67:RZ:534:ARG:HH12	67:RZ:861:ASN:HB3	1.77	0.49
67:RZ:1043:LYS:NZ	67:RZ:1062:ILE:O	2.44	0.49
3:SA:886:U:H2'	3:SA:887:A:H8	1.78	0.48
3:SA:1476:C:H2'	3:SA:1477:G:H8	1.78	0.48
6:SG:219:ARG:NH2	52:RH:222:ASP:OD2	2.45	0.48
10:SK:82:ARG:NH1	49:RB:323:GLU:OE2	2.46	0.48
11:SM:109:VAL:HG21	11:SM:125:VAL:HG11	1.95	0.48
23:3F:305:ARG:HG2	23:3F:317:ILE:HD13	1.94	0.48
25:A4:338:ALA:HB1	25:A4:361:LEU:HD11	1.95	0.48
34:B3:454:LEU:O	34:B3:465:LYS:HA	2.12	0.48
35:B8:266:GLY:HA3	35:B8:295:ILE:HD11	1.95	0.48
37:B6:63:VAL:HG13	37:B6:88:ILE:HD11	1.94	0.48
50:RE:592:PHE:HB3	50:RE:599:VAL:HG22	1.95	0.48
50:RE:1189:LEU:C	50:RE:1189:LEU:CD2	2.84	0.48
53:RJ:951:MET:HE1	53:RJ:1003:LEU:HB2	1.94	0.48
56:RN:600:LEU:HD21	56:RN:636:LEU:HD13	1.94	0.48
56:RN:646:THR:HA	56:RN:649:THR:HG22	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:RN:786:ASN:HA	56:RN:789:ASN:HB2	1.95	0.48
58:RP:1802:HIS:HE1	58:RP:1882:ARG:HB2	1.77	0.48
67:RZ:1039:VAL:HG12	67:RZ:1042:ARG:HH21	1.77	0.48
21:3D:160:ARG:NH2	22:3E:243:MET:O	2.43	0.48
21:3D:297:HIS:NE2	21:3D:309:GLU:OE2	2.46	0.48
25:A4:207:ASP:OD2	25:A4:209:ARG:NH1	2.37	0.48
29:AE:8:LEU:HD12	39:5C:144:LEU:HD23	1.96	0.48
33:B2:263:THR:HA	33:B2:269:THR:O	2.14	0.48
33:B2:549:SER:OG	33:B2:576:VAL:O	2.28	0.48
35:B8:183:ASP:OD1	36:BE:281:ARG:NH2	2.45	0.48
35:B8:458:ILE:HG13	35:B8:484:VAL:HG22	1.95	0.48
58:RP:393:PHE:O	58:RP:397:PHE:CB	2.60	0.48
67:RZ:783:LYS:HB2	67:RZ:798:VAL:HG22	1.95	0.48
1:3A:64:A:OP2	36:BE:392:ARG:NH2	2.45	0.48
4:SC:129:THR:OG1	4:SC:179:SER:O	2.31	0.48
13:SP:111:ARG:NH1	63:RT:95:GLU:HG3	2.28	0.48
13:SP:115:ILE:HD12	63:RT:97:ARG:NE	2.28	0.48
18:Sc:58:SER:OG	18:Sc:59:CYS:N	2.46	0.48
22:3E:164:ILE:HG12	22:3E:301:ALA:HA	1.93	0.48
32:B1:680:ARG:HH11	41:5E:455:HIS:CG	2.31	0.48
34:B3:536:LEU:HA	34:B3:552:SER:HA	1.96	0.48
36:BE:630:THR:N	36:BE:644:THR:O	2.44	0.48
45:5I:145:VAL:HB	45:5I:176:PHE:HB2	1.94	0.48
45:5I:260:GLN:NE2	45:5I:460:GLN:OE1	2.47	0.48
50:RE:132:TYR:HA	50:RE:135:LEU:HG	1.95	0.48
51:RF:97:GLU:HB3	66:RD:1508:ARG:HH12	1.78	0.48
52:RH:69:ASN:HD22	52:RH:72:ASP:HB3	1.77	0.48
53:RJ:863:THR:O	53:RJ:863:THR:OG1	2.30	0.48
3:SA:364:G:N7	3:SA:366:A:N6	2.62	0.48
14:SR:58:ASP:OD1	14:SR:58:ASP:N	2.43	0.48
21:3D:225:ASP:OD1	21:3D:226:LYS:N	2.46	0.48
22:3E:214:ILE:HD11	22:3E:252:LEU:HD22	1.94	0.48
23:3F:421:ASN:HD22	23:3F:437:ARG:HA	1.78	0.48
27:A8:570:LEU:HD23	27:A8:582:ILE:HD11	1.95	0.48
27:A8:668:ILE:O	27:A8:671:ARG:HG3	2.14	0.48
29:AE:684:TYR:HB2	29:AE:687:LEU:HD23	1.95	0.48
30:AF:246:TYR:OH	30:AF:289:ASN:ND2	2.44	0.48
31:AG:771:ASP:OD1	31:AG:771:ASP:N	2.46	0.48
37:B6:16:ASP:OD2	39:5C:15:ARG:NH2	2.46	0.48
40:5D:78:LEU:HD13	53:RJ:1082:GLN:HG2	1.95	0.48
41:5E:384:ARG:NE	43:5G:81:SER:HB3	2.28	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:5G:85:ASP:OD1	43:5G:211:ASN:ND2	2.42	0.48
47:5K:67:ILE:HD11	47:5K:96:PRO:HB2	1.95	0.48
50:RE:803:LYS:NZ	50:RE:859:ASP:OD2	2.43	0.48
54:RK:103:MET:O	54:RK:107:ALA:HB2	2.13	0.48
63:RT:72:VAL:CB	67:RZ:1056:GLU:HB3	2.43	0.48
66:RD:1662:GLU:HG3	66:RD:1671:VAL:HG22	1.95	0.48
9:SJ:72:ILE:HG22	9:SJ:74:LYS:HG2	1.96	0.48
23:3F:523:LYS:O	23:3F:541:ALA:HA	2.13	0.48
26:A5:280:GLN:HB2	26:A5:288:LYS:HE2	1.95	0.48
29:AE:395:GLU:OE2	29:AE:397:LYS:NZ	2.44	0.48
34:B3:198:ILE:HG12	34:B3:211:LEU:HD13	1.95	0.48
36:BE:529:TYR:HA	36:BE:536:LEU:HA	1.95	0.48
37:B6:273:ILE:HA	37:B6:276:VAL:HG22	1.95	0.48
38:5B:155:ILE:HD12	38:5B:158:LYS:HE3	1.95	0.48
39:5C:112:GLY:HA3	39:5C:130:ARG:HB3	1.94	0.48
41:5E:475:SER:C	41:5E:477:GLU:H	2.22	0.48
41:5E:538:LYS:C	41:5E:538:LYS:CD	2.86	0.48
50:RE:146:LEU:HA	50:RE:149:VAL:HG12	1.94	0.48
51:RF:97:GLU:OE2	51:RF:121:ARG:NH1	2.45	0.48
56:RN:734:ARG:HA	56:RN:737:ILE:HG12	1.95	0.48
58:RP:190:ARG:NH1	58:RP:194:GLU:OE2	2.46	0.48
3:SA:153:G:O3'	7:SH:2:LYS:NZ	2.41	0.48
3:SA:158:U:H3	3:SA:420:A:HO2'	1.59	0.48
3:SA:895:G:H21	13:SP:38:THR:HG21	1.79	0.48
11:SM:132:SER:OG	11:SM:133:LYS:N	2.46	0.48
17:SZ:52:LYS:O	17:SZ:94:TYR:OH	2.23	0.48
23:3F:448:PHE:HA	23:3F:451:ILE:HG22	1.95	0.48
25:A4:579:ARG:NH2	25:A4:644:SER:OG	2.47	0.48
27:A8:596:LYS:CE	27:A8:640:LEU:HD13	2.43	0.48
30:AF:276:SER:OG	30:AF:278:ASP:OD1	2.30	0.48
33:B2:414:LEU:HD11	33:B2:445:VAL:HG11	1.94	0.48
42:5F:19:LEU:HG	47:5K:25:LEU:CB	2.29	0.48
50:RE:886:THR:HG23	50:RE:890:LEU:HD12	1.96	0.48
55:RM:507:THR:H	61:RY:495:ALA:HB3	1.77	0.48
55:RM:716:PRO:O	55:RM:720:LEU:CB	2.61	0.48
56:RN:560:TYR:OH	57:RO:388:LEU:O	2.30	0.48
59:RQ:322:ASN:OD1	59:RQ:322:ASN:N	2.46	0.48
67:RZ:600:PHE:CZ	67:RZ:684:ASP:C	2.91	0.48
3:SA:647:G:H22	3:SA:687:G:H1	1.60	0.48
3:SA:1478:G:P	65:SU:43:ASN:HD22	2.37	0.48
20:3C:170:VAL:HG12	20:3C:239:CYS:HB3	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AE:329:THR:HG21	29:AE:365:ILE:HG21	1.95	0.48
31:AG:855:LEU:O	31:AG:859:ASN:HB2	2.13	0.48
32:B1:717:LEU:HD12	36:BE:578:VAL:HB	1.95	0.48
34:B3:167:ASP:OD1	34:B3:168:THR:N	2.47	0.48
35:B8:43:ASP:N	35:B8:43:ASP:OD1	2.40	0.48
48:RA:273:ASP:O	48:RA:275:LYS:NZ	2.47	0.48
50:RE:209:MET:HB2	50:RE:299:PRO:HD3	1.96	0.48
50:RE:373:ARG:HA	50:RE:515:ILE:HG12	1.96	0.48
50:RE:1174:GLY:N	50:RE:1179:LYS:HE2	2.28	0.48
52:RG:173:THR:OG1	52:RG:174:LYS:N	2.46	0.48
53:RJ:298:VAL:HG23	53:RJ:791:ILE:HG23	1.94	0.48
58:RP:1778:MET:HG2	58:RP:1864:LEU:HD22	1.96	0.48
3:SA:464:A:H2'	3:SA:465:G:H8	1.78	0.48
3:SA:1041:G:H2'	3:SA:1042:G:C8	2.49	0.48
3:SA:1538:U:C2	3:SA:1540:G:C8	3.01	0.48
3:SA:1573:A:H5'	3:SA:1574:G:H5'	1.96	0.48
5:SF:223:ASN:OD1	5:SF:223:ASN:N	2.47	0.48
10:SK:136:VAL:HG12	10:SK:156:ILE:HG12	1.96	0.48
11:SM:90:TYR:H	11:SM:103:ARG:HB3	1.79	0.48
11:SM:112:SER:HB3	11:SM:139:VAL:HG23	1.95	0.48
31:AG:105:HIS:HB2	31:AG:122:LYS:HG3	1.95	0.48
33:B2:118:ASN:OD1	33:B2:118:ASN:N	2.46	0.48
34:B3:161:TRP:HB3	34:B3:177:LEU:HG	1.96	0.48
35:B8:183:ASP:HB2	36:BE:242:ARG:HA	1.96	0.48
53:RJ:1105:ASP:N	53:RJ:1105:ASP:OD1	2.47	0.48
55:RL:55:VAL:HG23	55:RL:121:MET:HB3	1.95	0.48
57:RO:447:ASP:OD1	57:RO:447:ASP:N	2.46	0.48
58:RP:1709:ASP:HA	58:RP:1758:ALA:HA	1.94	0.48
67:RZ:373:ALA:N	67:RZ:437:ASP:OD1	2.46	0.48
67:RZ:583:VAL:HG13	67:RZ:583:VAL:O	2.12	0.48
1:3A:332:G:H21	31:AG:869:MET:HE3	1.79	0.48
5:SF:103:TYR:O	5:SF:182:TYR:OH	2.32	0.48
26:A5:335:ASN:O	26:A5:337:LYS:NZ	2.47	0.48
32:B1:150:THR:N	32:B1:164:THR:O	2.45	0.48
34:B3:44:ASP:OD1	34:B3:44:ASP:N	2.46	0.48
34:B3:301:GLN:HG2	34:B3:315:ASN:HA	1.95	0.48
37:B6:426:ASP:O	37:B6:430:TYR:N	2.47	0.48
41:5E:477:GLU:HG2	41:5E:477:GLU:O	2.14	0.48
50:RE:1216:LYS:HE3	50:RE:1236:THR:CG2	2.39	0.48
52:RG:232:LEU:HD21	52:RH:103:PRO:HG3	1.96	0.48
54:RK:130:ILE:HG23	54:RK:151:LEU:HD23	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RP:48:LEU:HG	58:RP:74:VAL:HG22	1.95	0.48
67:RZ:600:PHE:HE1	67:RZ:684:ASP:O	1.92	0.48
3:SA:1082:C:H5''	15:SX:20:THR:HA	1.96	0.48
3:SA:1624:C:H5''	43:5G:185:VAL:HG22	1.96	0.48
17:SZ:20:ARG:NH1	17:SZ:22:GLN:OE1	2.47	0.48
22:3E:225:GLU:HG2	22:3E:226:ILE:HG13	1.96	0.48
23:3F:477:SER:OG	23:3F:521:VAL:O	2.27	0.48
26:A5:460:ARG:HA	26:A5:465:ILE:HD11	1.96	0.48
27:A8:593:ASP:OD1	27:A8:596:LYS:NZ	2.34	0.48
29:AE:336:LEU:HD22	29:AE:373:ILE:HG21	1.96	0.48
32:B1:205:LYS:HG2	32:B1:219:GLU:HG2	1.96	0.48
32:B1:441:SER:O	32:B1:443:GLU:N	2.43	0.48
33:B2:9:GLU:O	33:B2:684:TRP:HA	2.14	0.48
34:B3:271:ASP:OD1	34:B3:271:ASP:N	2.47	0.48
37:B6:14:GLU:OE2	37:B6:91:ARG:NH2	2.38	0.48
50:RE:400:LEU:HB3	50:RE:412:LEU:HD12	1.95	0.48
55:RL:388:GLU:HA	55:RL:410:SER:O	2.14	0.48
57:RO:153:ILE:HD13	57:RO:202:LEU:HD21	1.94	0.48
63:RT:256:PRO:HA	63:RT:259:VAL:HG12	1.96	0.48
67:RZ:1239:LYS:HB2	67:RZ:1248:ILE:HD11	1.95	0.48
1:3A:94:A:H2'	1:3A:95:A:H8	1.79	0.47
3:SA:280:U:H2'	7:SH:188:ARG:HH22	1.80	0.47
3:SA:1642:G:OP2	41:5E:530:ARG:NH2	2.47	0.47
13:SP:53:ASP:O	13:SP:56:SER:OG	2.28	0.47
25:A4:560:SER:OG	25:A4:561:LYS:N	2.46	0.47
25:A4:747:ILE:HD11	25:A4:753:ALA:HB2	1.96	0.47
29:AE:376:GLU:H	29:AE:379:GLU:HG3	1.79	0.47
29:AE:484:LEU:HD13	29:AE:663:SER:HB3	1.95	0.47
30:AF:420:GLU:O	30:AF:424:ARG:CB	2.61	0.47
31:AG:498:LEU:HA	31:AG:508:ILE:O	2.14	0.47
33:B2:235:ASN:ND2	33:B2:240:GLY:O	2.40	0.47
34:B3:77:THR:HG22	34:B3:86:LYS:HB3	1.96	0.47
39:5C:133:HIS:HE1	39:5C:147:GLU:HG3	1.79	0.47
41:5E:517:LYS:NZ	41:5E:518:GLU:HG3	2.29	0.47
50:RE:264:LEU:HD12	50:RE:265:LEU:HG	1.95	0.47
50:RE:1108:LEU:O	50:RE:1112:CYS:CB	2.60	0.47
51:RF:9:MET:HB2	51:RF:13:PHE:HB2	1.96	0.47
51:RF:176:ASP:OD1	51:RF:176:ASP:N	2.37	0.47
66:RD:1644:LEU:HD13	66:RD:1654:LEU:HD22	1.96	0.47
67:RZ:1102:ASP:N	67:RZ:1102:ASP:OD1	2.47	0.47
3:SA:1061:A:OP1	51:RF:229:LYS:NZ	2.46	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SP:107:ARG:NH2	13:SP:107:ARG:CG	2.72	0.47
13:SP:111:ARG:NE	63:RT:93:LYS:HD2	2.29	0.47
22:3E:207:ARG:HH11	22:3E:226:ILE:HG12	1.78	0.47
25:A4:157:SER:OG	25:A4:195:TRP:NE1	2.47	0.47
30:AF:135:GLN:HE22	30:AF:178:PRO:HA	1.79	0.47
31:AG:141:LEU:HD11	31:AG:153:ILE:HD11	1.96	0.47
31:AG:431:SER:OG	31:AG:432:ARG:N	2.42	0.47
33:B2:54:ILE:CD1	33:B2:364:TYR:HD2	2.27	0.47
33:B2:479:LEU:HA	33:B2:489:VAL:O	2.14	0.47
36:BE:363:SER:O	36:BE:363:SER:OG	2.31	0.47
48:RA:250:GLY:HA3	48:RA:271:GLY:HA2	1.96	0.47
49:RB:290:GLU:OE2	49:RB:296:ARG:NH1	2.47	0.47
50:RE:627:LEU:HD12	50:RE:628:VAL:HG23	1.96	0.47
50:RE:1157:TYR:HE1	50:RE:1203:ASN:CG	2.22	0.47
51:RF:46:ASN:OD1	51:RF:46:ASN:N	2.39	0.47
54:RK:282:GLU:O	54:RK:286:SER:HB3	2.14	0.47
57:RO:507:LEU:HA	57:RO:510:GLU:HB3	1.95	0.47
63:RT:158:PHE:O	63:RT:171:SER:OG	2.31	0.47
67:RZ:1135:ILE:HG23	67:RZ:1169:THR:HG21	1.95	0.47
2:5A:517:A:OP2	58:RP:1939:ARG:NH1	2.46	0.47
3:SA:336:G:H1	9:SJ:5:ARG:HB2	1.79	0.47
3:SA:954:G:H2'	3:SA:955:A:C8	2.49	0.47
7:SH:31:ARG:HE	48:RA:359:ILE:HD13	1.78	0.47
8:SI:64:VAL:HG23	8:SI:67:LEU:HB3	1.95	0.47
10:SK:87:SER:OG	10:SK:89:ASP:OD1	2.33	0.47
11:SM:124:THR:HG22	11:SM:141:LYS:HB3	1.96	0.47
26:A5:248:THR:OG1	26:A5:250:ASP:OD1	2.31	0.47
29:AE:141:ASN:ND2	29:AE:206:TYR:OH	2.46	0.47
31:AG:249:THR:O	31:AG:257:ARG:NH1	2.41	0.47
31:AG:440:VAL:HG11	31:AG:449:LEU:HD12	1.95	0.47
34:B3:10:ILE:HG23	34:B3:643:PHE:HB2	1.95	0.47
39:5C:137:MET:HA	39:5C:144:LEU:HA	1.96	0.47
50:RE:1063:ARG:HD2	62:X1:305:UNK:CB	2.44	0.47
52:RH:153:VAL:HA	56:RN:716:LYS:HB2	1.96	0.47
53:RJ:80:THR:O	69:RJ:1201:GTP:O2B	2.31	0.47
55:RL:200:VAL:HG12	55:RL:208:LEU:HD13	1.97	0.47
59:RQ:341:LYS:HA	59:RQ:344:GLN:HE21	1.79	0.47
65:SU:15:ILE:HG22	65:SU:56:LYS:HZ2	1.79	0.47
1:3A:315:A:H2'	1:3A:316:A:C8	2.49	0.47
3:SA:869:A:H61	3:SA:958:U:H3	1.62	0.47
3:SA:1556:A:H1'	3:SA:1557:U:H2'	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1757:G:H2'	41:5E:500:LYS:HD2	1.96	0.47
22:3E:355:ASN:HA	22:3E:358:LYS:HB2	1.97	0.47
25:A4:284:LEU:HD21	38:5B:206:LEU:HD21	1.95	0.47
25:A4:744:VAL:HA	25:A4:753:ALA:O	2.14	0.47
32:B1:537:GLY:HA3	32:B1:556:ARG:HB3	1.96	0.47
33:B2:530:LEU:HD13	33:B2:550:LEU:HD11	1.94	0.47
34:B3:593:CYS:HB2	34:B3:620:LEU:HB3	1.95	0.47
40:5D:58:ARG:HD2	42:5F:174:ARG:CZ	2.45	0.47
40:5D:58:ARG:HH21	42:5F:174:ARG:CZ	2.28	0.47
47:5K:152:ILE:HG12	47:5K:171:PRO:HG2	1.95	0.47
51:RF:66:HIS:HA	51:RF:69:LYS:HG3	1.94	0.47
57:RO:198:GLU:O	57:RO:202:LEU:HB2	2.13	0.47
67:RZ:477:ILE:HG13	67:RZ:478:ARG:HG3	1.95	0.47
67:RZ:1112:ILE:HG13	67:RZ:1145:GLY:HA3	1.96	0.47
3:SA:163:G:O2'	7:SH:53:SER:OG	2.30	0.47
3:SA:1556:A:N6	3:SA:1559:A:OP1	2.47	0.47
6:SG:52:GLU:OE2	6:SG:54:LYS:NZ	2.48	0.47
13:SP:16:VAL:O	13:SP:30:VAL:HA	2.14	0.47
13:SP:92:LYS:CE	13:SP:122:PRO:HD3	2.40	0.47
14:SR:120:ASP:OD1	14:SR:120:ASP:N	2.41	0.47
25:A4:534:LEU:HB3	25:A4:543:ILE:HG22	1.95	0.47
34:B3:245:SER:O	34:B3:245:SER:OG	2.32	0.47
34:B3:622:ALA:HB3	34:B3:636:ASP:H	1.78	0.47
50:RE:1025:THR:O	50:RE:1029:ASN:ND2	2.47	0.47
50:RE:1159:ASN:O	50:RE:1187:LYS:HG3	2.14	0.47
53:RJ:111:LYS:O	53:RJ:310:THR:OG1	2.32	0.47
53:RJ:631:ILE:HG13	53:RJ:634:ARG:HB2	1.97	0.47
67:RZ:417:GLY:O	67:RZ:815:ARG:NH2	2.44	0.47
67:RZ:815:ARG:O	67:RZ:815:ARG:NH1	2.42	0.47
1:3A:198:U:O4	23:3F:151:ARG:NE	2.38	0.47
3:SA:1470:C:OP1	3:SA:1541:G:H4'	2.14	0.47
20:3C:173:LEU:HA	20:3C:197:VAL:HG13	1.97	0.47
25:A4:511:VAL:HA	25:A4:558:ARG:HB3	1.96	0.47
26:A5:473:LYS:HE3	26:A5:475:ALA:HB3	1.96	0.47
31:AG:581:GLY:HA2	31:AG:602:PRO:HD2	1.97	0.47
32:B1:156:GLN:HB2	32:B1:203:GLN:HE21	1.79	0.47
34:B3:139:SER:OG	34:B3:140:PHE:N	2.48	0.47
36:BE:207:ASP:N	36:BE:207:ASP:OD1	2.47	0.47
45:5I:201:ILE:HD12	45:5I:225:LEU:HD21	1.97	0.47
48:RA:245:CYS:HB3	48:RA:253:TYR:HB2	1.96	0.47
48:RA:313:PRO:HG3	48:RA:317:ILE:HD11	1.94	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RE:1087:LEU:HA	50:RE:1090:THR:HG23	1.97	0.47
50:RE:1103:ARG:HA	50:RE:1178:ASP:HB2	1.96	0.47
50:RE:1174:GLY:CA	50:RE:1179:LYS:CE	2.91	0.47
51:RF:69:LYS:NZ	51:RF:159:THR:H	2.12	0.47
53:RJ:92:ARG:HH21	53:RJ:221:LEU:HG	1.79	0.47
53:RJ:879:THR:OG1	53:RJ:880:TYR:N	2.48	0.47
4:SC:16:GLN:HB2	34:B3:358:ASN:HD22	1.80	0.47
7:SH:32:ILE:HD12	7:SH:65:GLN:HA	1.96	0.47
22:3E:262:ILE:HA	22:3E:265:PHE:HB2	1.96	0.47
32:B1:515:TYR:CE2	42:5F:180:PHE:HZ	2.33	0.47
32:B1:680:ARG:HH12	41:5E:455:HIS:CD2	2.29	0.47
33:B2:137:ILE:HG22	33:B2:147:VAL:HG22	1.97	0.47
33:B2:588:ILE:HG12	33:B2:600:TRP:HB2	1.97	0.47
34:B3:113:THR:OG1	34:B3:114:SER:N	2.48	0.47
34:B3:339:ILE:HG13	34:B3:358:ASN:HD21	1.80	0.47
34:B3:481:LYS:HE2	34:B3:522:ASN:HA	1.97	0.47
35:B8:238:LEU:HD11	35:B8:590:LYS:HB2	1.97	0.47
35:B8:568:VAL:HG23	35:B8:579:VAL:HG22	1.96	0.47
36:BE:430:ILE:HD11	36:BE:445:MET:HB2	1.97	0.47
39:5C:333:SER:HB3	39:5C:381:LEU:HD11	1.95	0.47
48:RA:80:GLN:HB2	48:RA:82:HIS:HD2	1.78	0.47
48:RA:164:ARG:NH2	48:RA:174:ASN:OD1	2.46	0.47
50:RE:253:GLN:NE2	50:RE:254:LEU:O	2.48	0.47
50:RE:348:TYR:HA	50:RE:351:LYS:HD3	1.97	0.47
50:RE:578:ILE:HA	50:RE:619:VAL:HA	1.96	0.47
56:RN:451:THR:O	56:RN:455:LEU:HB2	2.15	0.47
58:RP:1278:ARG:O	58:RP:1282:VAL:HA	2.15	0.47
67:RZ:381:SER:H	67:RZ:384:ILE:HD11	1.78	0.47
67:RZ:563:ARG:CD	67:RZ:837:PHE:CE1	2.98	0.47
67:RZ:761:THR:HG22	67:RZ:762:ASN:H	1.78	0.47
67:RZ:852:LEU:HG	67:RZ:903:SER:HB2	1.97	0.47
3:SA:158:U:N3	3:SA:420:A:O2'	2.46	0.47
12:SO:16:ILE:HG23	12:SO:62:GLN:HE22	1.79	0.47
25:A4:97:ARG:NE	38:5B:191:PRO:O	2.39	0.47
27:A8:635:PHE:HD2	28:A9:492:ILE:HD12	1.79	0.47
29:AE:136:LEU:HD21	29:AE:155:ILE:HG12	1.97	0.47
30:AF:435:ASP:OD1	30:AF:435:ASP:N	2.45	0.47
33:B2:367:ILE:HD12	33:B2:368:PRO:HD2	1.97	0.47
34:B3:680:ASN:HA	34:B3:683:LEU:HG	1.96	0.47
50:RE:793:PRO:HG2	50:RE:799:LEU:HA	1.96	0.47
53:RJ:347:LEU:O	53:RJ:352:LYS:NZ	2.48	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:RL:729:LEU:HA	55:RL:764:ASN:HA	1.97	0.47
67:RZ:610:THR:HA	67:RZ:613:ILE:HD12	1.96	0.47
13:SP:23:PHE:HZ	63:RT:183:GLU:OE2	1.98	0.47
22:3E:176:GLU:HA	22:3E:179:THR:HG22	1.97	0.47
32:B1:418:ARG:HD3	41:5E:489:SER:O	2.10	0.47
33:B2:214:ASP:OD1	33:B2:214:ASP:N	2.45	0.47
34:B3:19:SER:OG	34:B3:20:SER:N	2.48	0.47
40:5D:52:ARG:NH2	43:5G:270:ASP:OD1	2.43	0.47
41:5E:493:GLN:NE2	41:5E:497:ASN:ND2	2.58	0.47
51:RF:17:PRO:HB2	51:RF:34:LEU:HD11	1.96	0.47
60:RS:258:VAL:HA	60:RS:261:GLU:HG2	1.97	0.47
60:RS:379:LYS:HA	60:RS:379:LYS:HD3	1.72	0.47
66:RD:1592:LEU:HB3	66:RD:1597:GLU:HB2	1.97	0.47
3:SA:576:G:OP2	53:RJ:873:LYS:NZ	2.36	0.47
5:SF:53:LYS:NZ	49:RB:292:ASP:OD2	2.38	0.47
7:SH:17:GLU:N	55:RL:604:SER:O	2.47	0.47
31:AG:22:LEU:HD12	31:AG:32:LYS:HB2	1.97	0.47
31:AG:530:LYS:HG2	31:AG:546:LYS:HB3	1.97	0.47
32:B1:29:LEU:HD22	32:B1:42:LEU:HD11	1.96	0.47
32:B1:32:PRO:HG3	32:B1:61:ILE:HG13	1.97	0.47
32:B1:165:SER:OG	32:B1:166:LYS:N	2.48	0.47
33:B2:23:CYS:HG	33:B2:340:SER:HG	1.61	0.47
33:B2:163:LYS:HG2	41:5E:522:ARG:NH2	2.30	0.47
33:B2:393:ASP:OD1	33:B2:393:ASP:N	2.46	0.47
34:B3:69:LEU:HD13	34:B3:109:ASP:HA	1.96	0.47
34:B3:189:HIS:HD2	34:B3:191:SER:H	1.62	0.47
34:B3:352:LYS:HA	34:B3:365:ILE:O	2.15	0.47
34:B3:534:ARG:HH11	34:B3:535:GLY:H	1.63	0.47
36:BE:170:LEU:HG	36:BE:180:LEU:HD21	1.97	0.47
57:RO:504:ASP:OD1	57:RO:504:ASP:N	2.48	0.47
64:ST:41:ARG:NH2	65:SU:36:ILE:O	2.34	0.47
2:5A:69:U:O4	2:5A:70:A:N6	2.48	0.46
3:SA:328:A:H2'	3:SA:329:G:C8	2.50	0.46
3:SA:406:U:H2'	3:SA:407:A:C8	2.50	0.46
3:SA:420:A:C8	3:SA:420:A:C3'	2.98	0.46
3:SA:545:A:OP2	44:5H:542:TYR:OH	2.33	0.46
4:SC:224:ASP:OD2	50:RE:981:LYS:NZ	2.43	0.46
13:SP:107:ARG:HH11	63:RT:150:GLY:HA2	1.77	0.46
14:SR:113:ASP:N	14:SR:113:ASP:OD1	2.48	0.46
26:A5:366:GLY:O	31:AG:583:LYS:NZ	2.48	0.46
28:A9:471:LYS:HZ3	28:A9:474:HIS:H	1.63	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:175:ALA:O	31:AG:187:VAL:HA	2.15	0.46
32:B1:115:SER:O	32:B1:115:SER:OG	2.33	0.46
34:B3:32:LEU:HD12	34:B3:68:LYS:HE2	1.97	0.46
34:B3:108:LEU:HG	34:B3:119:VAL:HG12	1.96	0.46
41:5E:448:LEU:HD12	42:5F:85:MET:SD	2.55	0.46
50:RE:718:LYS:NZ	66:RD:1183:ILE:CB	2.78	0.46
56:RN:510:THR:HB	56:RN:518:ILE:HD13	1.96	0.46
58:RP:1721:ILE:HD11	58:RP:1751:TYR:HB2	1.96	0.46
65:SU:105:LEU:HD12	65:SU:122:ARG:HD2	1.96	0.46
2:5A:485:G:H2'	21:3D:22:LEU:HD21	1.97	0.46
3:SA:677:G:O2'	58:RP:1884:ARG:NH2	2.48	0.46
4:SC:19:ARG:HH21	34:B3:359:SER:HA	1.80	0.46
10:SK:65:LYS:HZ2	23:3F:59:PRO:CA	2.27	0.46
14:SR:50:GLU:OE2	14:SR:82:ARG:NH2	2.47	0.46
15:SX:9:ASP:OD1	15:SX:9:ASP:N	2.45	0.46
29:AE:509:SER:HA	29:AE:512:LEU:HD12	1.98	0.46
31:AG:43:ASN:OD1	31:AG:43:ASN:N	2.48	0.46
31:AG:443:ASN:ND2	31:AG:446:ASN:OD1	2.48	0.46
33:B2:63:LEU:HD21	33:B2:106:TRP:CD2	2.50	0.46
34:B3:749:ASN:HB3	34:B3:751:LYS:H	1.81	0.46
36:BE:737:LEU:C	36:BE:740:ILE:HG22	2.41	0.46
38:5B:173:ARG:NH2	40:5D:144:ASN:O	2.48	0.46
45:5I:283:ASP:OD2	45:5I:287:TYR:OH	2.30	0.46
48:RA:300:TRP:HA	48:RA:308:TYR:H	1.80	0.46
50:RE:1063:ARG:CD	62:X1:305:UNK:CB	2.93	0.46
50:RE:1189:LEU:HD22	50:RE:1190:PHE:CE2	2.51	0.46
50:RE:1199:ASN:ND2	66:RD:1512:GLU:HG2	2.28	0.46
53:RJ:819:GLU:O	53:RJ:852:ARG:NH2	2.47	0.46
54:RK:282:GLU:O	54:RK:286:SER:CB	2.64	0.46
58:RP:1756:ILE:HD13	58:RP:1800:LEU:HB3	1.98	0.46
3:SA:1477:G:O2'	65:SU:47:PRO:CA	2.62	0.46
20:3C:308:PRO:HG3	40:5D:129:SER:HA	1.96	0.46
22:3E:191:HIS:HD2	22:3E:246:GLU:HA	1.80	0.46
29:AE:374:ARG:NH1	29:AE:375:LEU:O	2.49	0.46
31:AG:446:ASN:OD1	31:AG:446:ASN:N	2.46	0.46
34:B3:476:ASP:N	34:B3:476:ASP:OD1	2.48	0.46
45:5I:280:ALA:HB2	45:5I:311:VAL:HB	1.97	0.46
48:RA:251:TYR:HA	48:RA:266:LYS:O	2.16	0.46
50:RE:209:MET:HB3	50:RE:213:LEU:HD21	1.98	0.46
54:RK:337:VAL:HG23	54:RK:354:ILE:HG12	1.98	0.46
56:RN:56:ASN:HD21	56:RN:59:GLU:HG3	1.81	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RP:1725:ILE:HD11	58:RP:1793:LEU:HD22	1.98	0.46
65:SU:44:GLU:HG2	65:SU:44:GLU:O	2.16	0.46
2:5A:18:G:H2'	2:5A:19:A:C8	2.50	0.46
2:5A:86:C:N4	31:AG:482:GLY:O	2.45	0.46
10:SK:37:LYS:HB3	10:SK:37:LYS:HE2	1.76	0.46
17:SZ:45:ALA:HB2	17:SZ:55:VAL:HG11	1.97	0.46
20:3C:194:VAL:HB	20:3C:217:ILE:HD13	1.97	0.46
25:A4:326:ARG:NH2	25:A4:364:PHE:O	2.49	0.46
25:A4:418:CYS:HB2	25:A4:460:LEU:HB2	1.97	0.46
29:AE:262:VAL:HG21	31:AG:892:MET:HE1	1.96	0.46
32:B1:299:SER:O	41:5E:475:SER:HA	2.15	0.46
34:B3:67:LEU:HD23	34:B3:68:LYS:H	1.80	0.46
35:B8:278:ASP:N	35:B8:278:ASP:OD1	2.46	0.46
35:B8:472:GLN:NE2	35:B8:474:SER:OG	2.49	0.46
37:B6:185:TYR:HE2	59:RQ:338:LEU:HD21	1.81	0.46
41:5E:384:ARG:HD3	43:5G:83:ILE:HD11	1.97	0.46
41:5E:521:THR:HG23	41:5E:524:ASP:H	1.80	0.46
42:5F:61:LEU:O	42:5F:71:ARG:NE	2.47	0.46
42:5F:103:VAL:HA	42:5F:106:ILE:HG22	1.96	0.46
46:5J:110:ASP:OD1	46:5J:110:ASP:N	2.36	0.46
54:RK:104:LEU:O	54:RK:300:TYR:OH	2.33	0.46
57:RO:202:LEU:HD23	57:RO:208:TYR:HB3	1.98	0.46
63:RT:250:LEU:HD12	63:RT:259:VAL:HG11	1.96	0.46
67:RZ:1175:SER:OG	67:RZ:1232:ASN:ND2	2.49	0.46
2:5A:514:U:OP2	58:RP:1975:LYS:NZ	2.37	0.46
21:3D:175:ILE:HD12	21:3D:317:SER:HA	1.98	0.46
23:3F:417:SER:HB3	23:3F:421:ASN:HB2	1.96	0.46
24:3G:57:ASP:HB3	24:3G:84:ARG:HG2	1.97	0.46
25:A4:742:LEU:HD12	25:A4:757:ARG:HG3	1.96	0.46
30:AF:436:GLU:HG2	30:AF:480:LEU:HD23	1.98	0.46
31:AG:204:ASN:OD1	31:AG:204:ASN:N	2.47	0.46
31:AG:435:ASP:HB2	31:AG:702:TYR:HD1	1.75	0.46
34:B3:708:ARG:NH2	34:B3:720:PHE:O	2.49	0.46
48:RA:286:GLU:HG3	48:RA:287:ASN:H	1.80	0.46
49:RB:309:LYS:HB3	49:RB:313:ARG:HH11	1.80	0.46
55:RM:249:SER:O	55:RM:253:LEU:CB	2.63	0.46
58:RP:104:GLN:HG3	58:RP:105:PRO:HD3	1.97	0.46
60:RS:270:LEU:HB3	60:RS:278:PHE:HZ	1.80	0.46
60:RS:392:TYR:HA	60:RS:395:MET:HB2	1.96	0.46
63:RT:169:ASP:OD1	63:RT:169:ASP:N	2.46	0.46
2:5A:485:G:OP2	21:3D:46:LYS:NZ	2.39	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1160:A:H2'	3:SA:1161:C:H6	1.80	0.46
3:SA:1541:G:N2	3:SA:1571:C:N3	2.64	0.46
5:SF:143:ASP:OD1	5:SF:143:ASP:N	2.35	0.46
8:SI:7:LYS:O	8:SI:42:GLN:NE2	2.49	0.46
25:A4:214:SER:OG	25:A4:221:ASN:O	2.28	0.46
26:A5:85:ILE:HB	26:A5:99:PHE:HB2	1.98	0.46
33:B2:341:ALA:HB1	33:B2:353:LEU:HD11	1.96	0.46
33:B2:542:ASP:N	33:B2:542:ASP:OD1	2.45	0.46
34:B3:625:THR:HG22	34:B3:633:VAL:HG13	1.97	0.46
40:5D:61:ASP:CA	42:5F:160:TRP:CZ3	2.99	0.46
42:5F:163:ASN:N	42:5F:183:SER:OG	2.45	0.46
50:RE:501:ASN:OD1	50:RE:501:ASN:N	2.49	0.46
52:RG:55:ILE:O	52:RG:64:LYS:HB2	2.16	0.46
52:RH:152:SER:OG	52:RH:155:SER:N	2.49	0.46
58:RP:1691:SER:HA	58:RP:1724:ASN:HD21	1.81	0.46
58:RP:1948:SER:O	58:RP:1985:ARG:NH2	2.48	0.46
63:RT:268:SER:HA	63:RT:271:LYS:HD2	1.97	0.46
1:3A:56:A:O2'	40:5D:63:TYR:OH	2.34	0.46
3:SA:225:A:H2'	3:SA:226:A:H8	1.79	0.46
3:SA:381:C:H2'	3:SA:382:C:H4'	1.97	0.46
3:SA:1273:G:H1	3:SA:1437:U:H2'	1.80	0.46
3:SA:1276:U:H3	3:SA:1434:U:H3	1.64	0.46
8:SI:62:VAL:HG12	8:SI:64:VAL:H	1.80	0.46
26:A5:66:VAL:HG12	26:A5:112:LEU:HD21	1.97	0.46
27:A8:638:LEU:HD12	27:A8:641:VAL:CG1	2.46	0.46
28:A9:505:MET:HB2	30:AF:507:MET:HE3	1.98	0.46
29:AE:568:ILE:HD11	29:AE:673:ASN:HD21	1.80	0.46
29:AE:583:LYS:HE2	29:AE:627:LEU:HA	1.98	0.46
32:B1:280:THR:HA	32:B1:304:PRO:HB3	1.98	0.46
33:B2:183:ASP:OD1	33:B2:183:ASP:N	2.42	0.46
36:BE:323:VAL:HB	36:BE:343:LEU:HD22	1.98	0.46
36:BE:351:GLN:HG3	36:BE:372:ASP:HB3	1.97	0.46
42:5F:115:MET:HG3	42:5F:120:MET:HB3	1.98	0.46
50:RE:377:SER:HB3	50:RE:389:GLY:HA3	1.97	0.46
50:RE:928:HIS:HE1	50:RE:1164:SER:HB2	1.80	0.46
52:RG:227:LEU:HA	52:RG:227:LEU:HD23	1.79	0.46
53:RJ:360:ASP:HB3	53:RJ:365:LEU:HB2	1.98	0.46
54:RK:199:ARG:HB2	54:RK:239:PRO:HA	1.97	0.46
56:RN:547:VAL:HA	56:RN:550:VAL:HG12	1.97	0.46
56:RN:554:GLN:HE21	56:RN:559:ARG:H	1.63	0.46
57:RO:366:LEU:HD13	57:RO:405:LEU:HD11	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:RT:96:SER:HA	63:RT:139:LEU:O	2.16	0.46
67:RZ:502:MET:HG3	67:RZ:858:ALA:HB3	1.98	0.46
1:3A:36:C:O2'	45:5I:389:ARG:NH1	2.48	0.46
3:SA:1111:G:C8	53:RJ:1162:ALA:HA	2.51	0.46
21:3D:371:ASN:OD1	21:3D:374:ARG:NH1	2.48	0.46
22:3E:381:ASP:OD1	22:3E:381:ASP:N	2.49	0.46
25:A4:164:THR:HG22	25:A4:185:ARG:HG2	1.98	0.46
31:AG:212:CYS:HB2	31:AG:224:SER:HB3	1.98	0.46
32:B1:300:MET:HE2	32:B1:300:MET:HB3	1.78	0.46
34:B3:157:ASN:HD21	63:RT:73:VAL:CB	2.28	0.46
35:B8:512:ASP:OD1	35:B8:512:ASP:N	2.48	0.46
50:RE:1157:TYR:CE1	50:RE:1203:ASN:ND2	2.59	0.46
53:RJ:1082:GLN:OE1	53:RJ:1082:GLN:HA	2.15	0.46
57:RO:462:SER:OG	57:RO:463:LEU:N	2.48	0.46
60:RS:413:LEU:O	60:RS:418:HIS:NE2	2.49	0.46
64:ST:52:VAL:HG21	64:ST:61:LEU:HD11	1.97	0.46
2:5A:486:U:H4'	2:5A:487:A:H5''	1.98	0.46
3:SA:689:G:C6	3:SA:690:G:O6	2.69	0.46
9:SJ:83:TYR:HB3	9:SJ:101:ILE:HD11	1.98	0.46
27:A8:631:SER:C	27:A8:634:LEU:CG	2.86	0.46
29:AE:495:LEU:HA	29:AE:498:PHE:HB2	1.97	0.46
40:5D:48:LEU:HG	53:RJ:1067:LEU:HD11	1.98	0.46
41:5E:384:ARG:HD2	43:5G:83:ILE:N	2.30	0.46
45:5I:210:LYS:HA	45:5I:210:LYS:HD3	1.68	0.46
45:5I:281:ASN:ND2	45:5I:283:ASP:OD1	2.49	0.46
47:5K:83:VAL:HG12	47:5K:96:PRO:HG3	1.98	0.46
50:RE:333:ASN:HA	50:RE:336:VAL:HG22	1.96	0.46
50:RE:822:ARG:HB2	50:RE:843:LEU:HB2	1.97	0.46
52:RG:112:VAL:HB	52:RG:124:VAL:HG22	1.97	0.46
56:RN:423:GLY:O	56:RN:426:THR:OG1	2.31	0.46
58:RP:971:ARG:O	58:RP:975:ASN:HA	2.15	0.46
60:RS:359:LEU:HB2	60:RS:372:ILE:HD11	1.97	0.46
65:SU:9:VAL:HG21	65:SU:136:ALA:HB1	1.97	0.46
67:RZ:603:THR:HB	67:RZ:635:MET:HE3	1.98	0.46
3:SA:397:A:H5''	9:SJ:50:GLY:HA2	1.98	0.46
3:SA:1470:C:H5''	3:SA:1540:G:H21	1.80	0.46
9:SJ:48:THR:O	9:SJ:52:ASN:CB	2.58	0.46
11:SM:76:VAL:HG21	11:SM:87:ARG:HH11	1.81	0.46
16:SY:113:ALA:HB3	16:SY:116:ASP:HB2	1.96	0.46
21:3D:379:LEU:HD13	21:3D:408:VAL:HG21	1.98	0.46
25:A4:444:ARG:HG3	25:A4:446:SER:H	1.81	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A5:539:ARG:NH1	31:AG:524:ASP:OD2	2.49	0.46
30:AF:69:ARG:HG3	30:AF:70:THR:HG23	1.97	0.46
33:B2:360:ASN:OD1	33:B2:360:ASN:N	2.47	0.46
36:BE:420:GLU:HG2	36:BE:470:GLN:HA	1.97	0.46
36:BE:851:SER:O	36:BE:851:SER:OG	2.31	0.46
38:5B:211:LEU:HD13	38:5B:213:LYS:HE3	1.96	0.46
39:5C:335:GLY:HA2	39:5C:377:LYS:HG3	1.98	0.46
42:5F:5:LEU:HD23	42:5F:9:GLU:HB3	1.98	0.46
43:5G:119:ARG:HG3	43:5G:122:TYR:HB2	1.98	0.46
45:5I:255:THR:HG22	59:RQ:288:TYR:HD1	1.81	0.46
45:5I:306:SER:HB3	45:5I:326:ASP:H	1.81	0.46
48:RA:21:VAL:HG12	48:RA:46:ARG:HH12	1.81	0.46
50:RE:380:SER:HB2	50:RE:481:THR:HG22	1.98	0.46
52:RG:143:GLN:HE22	52:RG:149:SER:HA	1.81	0.46
56:RN:495:ASN:HD22	56:RN:617:HIS:HB2	1.80	0.46
57:RO:395:ILE:HG23	57:RO:469:LEU:HD21	1.98	0.46
60:RS:271:THR:OG1	60:RS:274:GLU:OE1	2.31	0.46
66:RD:1520:MET:HE3	66:RD:1536:VAL:HB	1.98	0.46
2:5A:485:G:N2	45:5I:386:LYS:O	2.41	0.45
3:SA:385:A:OP1	9:SJ:25:ARG:NH2	2.46	0.45
3:SA:895:G:H22	3:SA:917:U:H3	1.64	0.45
3:SA:1474:G:C8	3:SA:1474:G:OP2	2.69	0.45
3:SA:1502:G:O6	65:SU:102:ARG:NH2	2.48	0.45
3:SA:1573:A:C5'	3:SA:1574:G:H5'	2.47	0.45
5:SF:127:LYS:HB2	5:SF:140:VAL:HG23	1.99	0.45
26:A5:452:LEU:HA	26:A5:455:THR:HG22	1.98	0.45
31:AG:726:GLN:NE2	31:AG:736:THR:O	2.42	0.45
33:B2:220:THR:HG22	33:B2:259:ILE:HD11	1.97	0.45
33:B2:580:ASP:OD2	33:B2:623:PHE:N	2.40	0.45
33:B2:760:ILE:HD11	33:B2:835:PHE:HB2	1.98	0.45
37:B6:186:VAL:HG12	37:B6:273:ILE:HG13	1.98	0.45
38:5B:200:ARG:O	38:5B:204:ARG:HB3	2.15	0.45
41:5E:437:ILE:HD11	42:5F:70:PHE:CE2	2.51	0.45
60:RS:280:ASN:ND2	60:RS:320:GLY:O	2.46	0.45
67:RZ:873:ARG:HA	67:RZ:876:LEU:HG	1.98	0.45
67:RZ:1118:ILE:HG23	67:RZ:1131:CYS:HB3	1.98	0.45
3:SA:1463:C:H4'	56:RN:63:ALA:HB1	1.98	0.45
3:SA:1639:C:H41	34:B3:692:MET:HE1	1.82	0.45
4:SC:144:ARG:HG3	4:SC:208:GLN:HB3	1.98	0.45
13:SP:32:ASP:OD1	13:SP:32:ASP:N	2.47	0.45
21:3D:195:VAL:HG12	21:3D:216:PHE:HE2	1.81	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3F:70:TYR:OH	49:RB:246:GLU:OE2	2.29	0.45
25:A4:124:THR:HG21	38:5B:191:PRO:HG3	1.97	0.45
25:A4:545:ARG:HG3	25:A4:549:VAL:HB	1.98	0.45
34:B3:157:ASN:HD22	63:RT:77:GLY:CA	2.29	0.45
34:B3:509:ALA:HB1	34:B3:515:CYS:HA	1.98	0.45
36:BE:640:LEU:HD23	36:BE:655:THR:HG22	1.98	0.45
48:RA:60:ASN:ND2	48:RA:100:GLU:OE2	2.50	0.45
48:RA:164:ARG:HH12	48:RA:176:PHE:H	1.64	0.45
50:RE:308:LEU:HG	50:RE:337:LEU:HD21	1.99	0.45
51:RF:255:LYS:O	51:RF:265:ARG:NH1	2.45	0.45
53:RJ:853:ARG:HE	53:RJ:853:ARG:HB2	1.61	0.45
64:ST:25:ASN:O	64:ST:57:ARG:NH2	2.49	0.45
6:SG:39:GLU:OE2	6:SG:47:SER:OG	2.33	0.45
9:SJ:32:GLN:HE21	48:RA:78:LYS:HG2	1.81	0.45
20:3B:261:LEU:O	21:3D:129:ARG:NH1	2.49	0.45
22:3E:392:ALA:O	22:3E:396:ASN:ND2	2.49	0.45
26:A5:518:ASN:HB2	26:A5:521:SER:HB3	1.98	0.45
27:A8:440:ARG:O	31:AG:728:LEU:HD21	2.17	0.45
29:AE:583:LYS:HD3	29:AE:631:VAL:HG21	1.98	0.45
30:AF:171:VAL:HG22	30:AF:188:SER:HB3	1.99	0.45
33:B2:404:LYS:HZ1	33:B2:425:ILE:HD11	1.80	0.45
34:B3:195:GLY:O	34:B3:245:SER:OG	2.29	0.45
39:5C:15:ARG:HB2	39:5C:18:GLN:HG3	1.98	0.45
39:5C:39:ASP:HB3	39:5C:42:LEU:HB3	1.97	0.45
41:5E:330:VAL:HG21	53:RJ:932:LEU:HD12	1.97	0.45
45:5I:94:TYR:OH	45:5I:134:ASN:ND2	2.41	0.45
50:RE:521:LEU:HD22	50:RE:960:LYS:HG3	1.97	0.45
52:RH:191:ASP:HA	52:RH:194:GLU:HG2	1.98	0.45
56:RN:13:LEU:HD22	56:RN:16:ARG:HE	1.81	0.45
56:RN:804:LYS:HD3	56:RN:804:LYS:HA	1.75	0.45
66:RD:1675:PHE:HE1	66:RD:1691:PHE:HB3	1.82	0.45
2:5A:550:C:H2'	2:5A:551:A:C8	2.52	0.45
5:SF:58:GLY:HA2	5:SF:61:VAL:HG12	1.99	0.45
23:3F:164:GLN:HE21	23:3F:527:VAL:HG13	1.81	0.45
24:3G:58:CYS:HB3	24:3G:98:ILE:HD12	1.98	0.45
27:A8:631:SER:N	27:A8:634:LEU:HD21	2.31	0.45
50:RE:218:ASP:N	50:RE:218:ASP:OD1	2.46	0.45
53:RJ:772:MET:HG3	53:RJ:774:PRO:HD2	1.98	0.45
53:RJ:871:MET:CE	53:RJ:930:LYS:CD	2.95	0.45
55:RL:846:SER:O	55:RL:850:LEU:CB	2.65	0.45
56:RN:600:LEU:HD22	56:RN:633:VAL:HG22	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RP:2006:LEU:HG	58:RP:2011:ILE:HD12	1.97	0.45
60:RS:271:THR:H	60:RS:274:GLU:HB2	1.82	0.45
1:3A:316:A:H2'	1:3A:317:A:C8	2.51	0.45
3:SA:67:A:H2'	3:SA:69:G:C8	2.52	0.45
3:SA:145:A:O2'	3:SA:146:U:O5'	2.33	0.45
4:SC:129:THR:OG1	4:SC:130:SER:N	2.47	0.45
9:SJ:103:GLN:HB3	9:SJ:164:ARG:HG2	1.98	0.45
11:SM:57:LYS:O	11:SM:138:ASN:ND2	2.50	0.45
12:SO:63:ALA:O	12:SO:67:THR:OG1	2.24	0.45
23:3F:452:SER:HB3	23:3F:460:ARG:HG2	1.99	0.45
25:A4:137:TYR:HB2	25:A4:177:LEU:HD12	1.99	0.45
25:A4:380:LYS:NZ	25:A4:634:VAL:O	2.35	0.45
25:A4:424:ASP:N	25:A4:424:ASP:OD1	2.45	0.45
25:A4:652:THR:HG23	25:A4:653:TRP:HD1	1.81	0.45
29:AE:864:VAL:O	29:AE:868:LYS:CB	2.65	0.45
30:AF:227:VAL:HG22	30:AF:236:VAL:HG12	1.99	0.45
31:AG:143:ASN:N	31:AG:143:ASN:OD1	2.47	0.45
31:AG:253:SER:O	31:AG:256:THR:OG1	2.33	0.45
34:B3:42:ILE:HD11	34:B3:379:LEU:HD13	1.98	0.45
39:5C:243:TRP:NE1	39:5C:304:ARG:HH22	2.15	0.45
41:5E:520:LEU:HD11	41:5E:525:LYS:CA	2.46	0.45
42:5F:111:LEU:HD13	42:5F:143:ILE:HG21	1.97	0.45
45:5I:288:TYR:O	45:5I:298:LEU:N	2.42	0.45
48:RA:14:TYR:HE2	48:RA:344:PRO:HG3	1.81	0.45
51:RF:71:VAL:HG21	51:RF:84:VAL:HB	1.98	0.45
67:RZ:515:ILE:HD12	67:RZ:528:LEU:HD21	1.97	0.45
1:3A:12:U:H3	3:SA:1112:G:H1	1.65	0.45
3:SA:360:A:OP2	3:SA:362:G:O2'	2.34	0.45
11:SM:92:HIS:HD2	11:SM:94:ILE:HG13	1.82	0.45
29:AE:11:VAL:HA	29:AE:14:ASN:HD22	1.80	0.45
33:B2:54:ILE:HD13	33:B2:364:TYR:CD2	2.48	0.45
33:B2:566:TYR:OH	33:B2:603:ASP:O	2.33	0.45
33:B2:641:TYR:O	33:B2:650:ILE:N	2.49	0.45
35:B8:264:LEU:HD11	35:B8:272:LEU:HD12	1.97	0.45
36:BE:76:THR:OG1	36:BE:78:SER:O	2.29	0.45
39:5C:104:LEU:HD21	39:5C:139:TRP:HB2	1.99	0.45
42:5F:29:ASP:OD2	42:5F:41:ARG:NH1	2.49	0.45
43:5G:100:LEU:HD22	43:5G:144:GLU:HB3	1.97	0.45
50:RE:151:SER:HA	50:RE:154:LYS:HB2	1.98	0.45
66:RD:1708:ILE:HA	66:RD:1711:VAL:HG22	1.99	0.45
3:SA:608:U:O2'	3:SA:609:U:O4'	2.34	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1634:C:O2	32:B1:397:LYS:NZ	2.50	0.45
3:SA:1660:A:H2'	3:SA:1661:U:C6	2.52	0.45
5:SF:159:THR:HB	5:SF:173:ILE:HB	1.99	0.45
19:Sd:35:ASP:N	19:Sd:35:ASP:OD1	2.45	0.45
20:3B:210:MET:HE2	20:3B:210:MET:HB3	1.79	0.45
20:3C:253:ILE:HD11	20:3C:293:LEU:HD21	1.99	0.45
25:A4:636:ILE:HG23	25:A4:648:PHE:HD2	1.82	0.45
27:A8:635:PHE:CD2	28:A9:492:ILE:HD12	2.51	0.45
29:AE:255:ILE:HD11	31:AG:884:MET:HB3	1.98	0.45
29:AE:718:ARG:HA	29:AE:721:VAL:HG12	1.99	0.45
29:AE:1700:SER:O	29:AE:1703:GLU:N	2.49	0.45
33:B2:107:ASP:OD1	33:B2:107:ASP:N	2.46	0.45
36:BE:377:SER:O	36:BE:377:SER:OG	2.35	0.45
42:5F:13:LEU:HG	42:5F:13:LEU:O	2.16	0.45
49:RB:229:ASP:HB3	49:RB:232:GLU:HG2	1.97	0.45
50:RE:1155:LEU:HD23	51:RF:93:PHE:HB3	1.98	0.45
52:RH:56:SER:HA	52:RH:63:ASP:HB2	1.99	0.45
60:RS:399:ILE:O	60:RS:406:GLY:N	2.50	0.45
63:RT:245:GLU:HA	63:RT:248:VAL:HG12	1.97	0.45
66:RD:1670:LYS:HG2	66:RD:1674:LEU:HG	1.99	0.45
3:SA:1223:A:H2'	3:SA:1224:A:C8	2.52	0.45
5:SF:150:PRO:HB2	5:SF:154:ILE:HG13	1.98	0.45
29:AE:65:LYS:HB3	29:AE:104:LEU:HD11	1.99	0.45
30:AF:51:HIS:O	30:AF:53:HIS:N	2.49	0.45
31:AG:38:SER:OG	31:AG:43:ASN:O	2.35	0.45
31:AG:140:LYS:HA	31:AG:140:LYS:HD3	1.78	0.45
33:B2:103:ILE:HB	33:B2:117:PHE:HB2	1.99	0.45
34:B3:157:ASN:HD22	63:RT:77:GLY:C	2.25	0.45
41:5E:325:SER:OG	53:RJ:1007:TYR:CE1	2.69	0.45
48:RA:164:ARG:HH12	48:RA:176:PHE:N	2.15	0.45
50:RE:585:MET:HB3	50:RE:610:PHE:HB3	1.99	0.45
54:RK:187:ILE:HB	54:RK:251:GLN:HE22	1.82	0.45
57:RO:259:LYS:HB3	57:RO:259:LYS:HE2	1.72	0.45
58:RP:378:HIS:O	58:RP:382:PHE:CB	2.65	0.45
58:RP:465:PHE:HA	58:RP:468:ALA:HB3	1.98	0.45
60:RS:235:VAL:HG12	60:RS:238:SER:HB3	1.98	0.45
63:RT:222:THR:OG1	63:RT:223:ARG:N	2.50	0.45
65:SU:77:ASN:HA	65:SU:96:ALA:HB3	1.99	0.45
3:SA:326:G:H4'	11:SM:82:ARG:HD2	1.98	0.45
3:SA:420:A:C8	3:SA:420:A:O5'	2.70	0.45
3:SA:1532:U:H2'	3:SA:1533:C:C6	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:31:ASP:HB3	4:SC:45:LYS:HG2	1.99	0.45
4:SC:242:LYS:N	50:RE:655:LEU:O	2.48	0.45
11:SM:94:ILE:HD12	11:SM:101:GLU:H	1.81	0.45
12:SO:49:GLN:HA	12:SO:52:VAL:HG12	1.99	0.45
20:3C:261:LEU:O	22:3E:118:ARG:NH2	2.34	0.45
29:AE:659:LEU:HD21	29:AE:691:PHE:HA	1.98	0.45
31:AG:761:GLU:HG3	31:AG:779:ILE:HG22	1.99	0.45
32:B1:369:ILE:HD11	32:B1:390:VAL:HG11	1.99	0.45
34:B3:343:MET:HB3	34:B3:355:LEU:HD23	1.98	0.45
43:5G:104:ALA:HB3	43:5G:116:ARG:HE	1.82	0.45
43:5G:138:ASP:N	43:5G:138:ASP:OD1	2.48	0.45
45:5I:297:SER:OG	45:5I:299:ASN:O	2.33	0.45
58:RP:70:ILE:HG21	58:RP:87:ILE:HG22	1.98	0.45
60:RS:429:LYS:HD2	60:RS:437:ARG:HH22	1.82	0.45
2:5A:554:G:H1	2:5A:583:U:H3	1.64	0.45
3:SA:592:A:O2'	3:SA:596:C:OP1	2.35	0.45
3:SA:884:A:H2'	3:SA:885:G:C8	2.52	0.45
3:SA:1070:C:H5''	18:Sc:17:ARG:HH21	1.82	0.45
3:SA:1541:G:N2	3:SA:1571:C:N4	2.64	0.45
6:SG:117:THR:HG21	6:SG:194:LEU:HD23	1.99	0.45
15:SX:66:ASN:OD1	15:SX:66:ASN:N	2.50	0.45
18:Sc:48:SER:OG	18:Sc:49:HIS:ND1	2.50	0.45
20:3C:175:ALA:N	20:3C:198:GLU:OE2	2.48	0.45
24:3H:33:LEU:HD23	24:3H:35:LYS:HE3	1.98	0.45
25:A4:249:ARG:HB2	25:A4:292:ASN:HD22	1.81	0.45
27:A8:547:GLN:O	27:A8:551:PHE:HB2	2.16	0.45
29:AE:641:LEU:O	29:AE:644:LYS:NZ	2.42	0.45
32:B1:475:PRO:HD2	32:B1:493:TRP:HB2	1.99	0.45
35:B8:358:PHE:HA	35:B8:376:LEU:O	2.17	0.45
36:BE:207:ASP:OD2	36:BE:227:THR:OG1	2.27	0.45
36:BE:546:ILE:HG21	36:BE:560:LEU:HD22	1.99	0.45
36:BE:921:ARG:O	36:BE:925:LEU:HB2	2.17	0.45
45:5I:8:ARG:HD3	45:5I:8:ARG:HA	1.80	0.45
49:RB:302:LYS:HB3	49:RB:306:ARG:HH22	1.81	0.45
52:RH:199:ASP:OD1	52:RH:199:ASP:N	2.48	0.45
66:RD:1544:MET:HB2	66:RD:1544:MET:HE2	1.67	0.45
67:RZ:803:LYS:HB2	67:RZ:836:GLN:HA	1.98	0.45
3:SA:351:C:N3	11:SM:102:LYS:NZ	2.52	0.44
3:SA:930:A:H2'	4:SC:114:VAL:HG11	1.99	0.44
20:3B:88:ILE:HD11	20:3B:123:ILE:HG21	1.98	0.44
20:3B:218:ILE:HD11	21:3D:152:LEU:HD22	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:3D:120:SER:O	21:3D:120:SER:OG	2.33	0.44
30:AF:31:THR:OG1	30:AF:32:SER:N	2.46	0.44
33:B2:49:VAL:HG22	33:B2:63:LEU:HD22	1.98	0.44
33:B2:140:SER:OG	33:B2:142:ASP:OD1	2.31	0.44
41:5E:447:LYS:HA	41:5E:450:VAL:HG12	1.98	0.44
41:5E:520:LEU:HG	41:5E:525:LYS:HG3	1.96	0.44
42:5F:85:MET:HE3	42:5F:149:LEU:HD11	1.98	0.44
53:RJ:288:VAL:HG11	53:RJ:812:MET:HE2	1.98	0.44
53:RJ:889:LEU:HD22	53:RJ:922:ILE:HB	2.00	0.44
56:RN:443:LYS:HG3	56:RN:448:PHE:HE2	1.81	0.44
58:RP:60:SER:HB3	58:RP:102:SER:HB3	1.99	0.44
60:RS:373:LYS:HG3	60:RS:420:ALA:HA	1.99	0.44
3:SA:265:A:OP2	7:SH:194:LYS:NZ	2.37	0.44
3:SA:406:U:H2'	3:SA:407:A:H8	1.82	0.44
3:SA:1169:G:N1	3:SA:1575:G:OP2	2.44	0.44
4:SC:36:SER:OG	4:SC:41:ARG:NH1	2.50	0.44
4:SC:242:LYS:HD2	4:SC:244:VAL:H	1.82	0.44
8:SI:163:ASP:O	59:RQ:277:ARG:NH2	2.50	0.44
12:SO:69:ASN:OD1	12:SO:69:ASN:N	2.47	0.44
25:A4:579:ARG:HH12	25:A4:659:PHE:HD1	1.65	0.44
27:A8:633:GLN:O	27:A8:637:LEU:CD2	2.65	0.44
29:AE:109:TRP:HA	29:AE:114:THR:HG21	1.99	0.44
30:AF:117:LEU:HD12	30:AF:117:LEU:HA	1.80	0.44
30:AF:371:GLU:OE2	35:B8:273:ARG:NH2	2.50	0.44
33:B2:337:LYS:O	33:B2:357:THR:OG1	2.25	0.44
34:B3:111:ASP:OD1	34:B3:111:ASP:N	2.48	0.44
36:BE:853:ASN:ND2	36:BE:860:GLU:OE1	2.50	0.44
39:5C:122:GLY:O	39:5C:139:TRP:NE1	2.34	0.44
39:5C:214:LEU:HD23	39:5C:228:LEU:HD12	1.99	0.44
39:5C:460:ARG:HB3	59:RQ:847:VAL:HB	1.99	0.44
42:5F:5:LEU:CD2	42:5F:13:LEU:HD21	2.47	0.44
42:5F:43:ASP:HA	42:5F:46:LYS:HG2	1.99	0.44
48:RA:247:THR:HG21	48:RA:251:TYR:HB2	1.99	0.44
50:RE:165:PRO:HD2	50:RE:222:PHE:HZ	1.82	0.44
50:RE:822:ARG:NH1	50:RE:1133:PRO:O	2.50	0.44
56:RN:640:MET:HE2	56:RN:640:MET:HB3	1.81	0.44
66:RD:1628:GLU:HG3	66:RD:1640:LEU:HD22	1.99	0.44
67:RZ:527:ILE:HG12	67:RZ:854:MET:HE2	1.99	0.44
67:RZ:622:ILE:HA	67:RZ:775:TYR:O	2.16	0.44
67:RZ:728:PRO:O	67:RZ:754:SER:HA	2.16	0.44
4:SC:194:ASN:HD21	4:SC:212:VAL:HG23	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A5:520:MET:H	26:A5:520:MET:HG3	1.60	0.44
29:AE:763:LEU:HD12	29:AE:768:LYS:HD3	2.00	0.44
31:AG:600:SER:O	31:AG:600:SER:OG	2.33	0.44
33:B2:292:ILE:HG23	33:B2:324:PHE:HE2	1.83	0.44
34:B3:430:TYR:HD2	34:B3:454:LEU:HD23	1.82	0.44
39:5C:311:SER:OG	39:5C:313:GLU:OE2	2.33	0.44
42:5F:68:ASP:OD1	42:5F:68:ASP:N	2.50	0.44
44:5H:555:ASN:HB3	44:5H:558:ASN:HB2	1.98	0.44
52:RG:242:CYS:O	52:RG:246:GLU:HG3	2.18	0.44
57:RO:282:HIS:CD2	57:RO:283:LYS:HG2	2.52	0.44
58:RP:107:LEU:HD21	58:RP:150:TRP:HB3	1.98	0.44
58:RP:1741:LYS:HD3	58:RP:1741:LYS:HA	1.90	0.44
64:ST:48:LYS:HD3	65:SU:35:ASP:HB3	1.99	0.44
6:SG:63:GLN:HE22	6:SG:66:GLN:HB3	1.82	0.44
13:SP:107:ARG:CB	13:SP:107:ARG:CZ	2.93	0.44
20:3C:92:ARG:HH12	40:5D:151:PHE:HB2	1.81	0.44
21:3D:281:LEU:HD23	22:3E:261:GLN:HE21	1.82	0.44
29:AE:422:LEU:HD12	29:AE:422:LEU:HA	1.87	0.44
31:AG:559:LYS:HE2	31:AG:559:LYS:HB2	1.79	0.44
32:B1:25:ASP:O	32:B1:27:LYS:N	2.49	0.44
36:BE:356:ILE:HG22	36:BE:633:LYS:HG3	2.00	0.44
51:RF:15:VAL:HG12	51:RF:17:PRO:HD3	1.98	0.44
53:RJ:617:THR:HG23	53:RJ:620:LYS:HE2	1.99	0.44
53:RJ:841:THR:HB	53:RJ:859:ILE:HA	1.99	0.44
53:RJ:1148:GLU:OE2	53:RJ:1152:ARG:NH1	2.49	0.44
57:RO:196:GLN:OE1	57:RO:260:ASN:ND2	2.37	0.44
58:RP:1183:PRO:O	58:RP:1187:VAL:CB	2.65	0.44
66:RD:1483:ALA:HA	66:RD:1486:LEU:HB2	1.99	0.44
67:RZ:507:LEU:HD21	67:RZ:510:TYR:HB2	1.99	0.44
67:RZ:590:VAL:HG23	67:RZ:813:ALA:HB3	1.99	0.44
67:RZ:714:GLY:N	67:RZ:716:GLU:OE2	2.48	0.44
3:SA:532:U:O2'	17:SZ:33:ALA:O	2.27	0.44
3:SA:1541:G:H2'	3:SA:1542:G:C5	2.53	0.44
6:SG:86:GLN:HE22	32:B1:546:ASP:HB3	1.83	0.44
11:SM:36:LYS:HD2	11:SM:36:LYS:HA	1.74	0.44
22:3E:372:ARG:HG3	24:3G:63:ILE:HA	2.00	0.44
25:A4:75:ASN:HB3	25:A4:92:GLU:HA	2.00	0.44
25:A4:468:ASP:OD2	25:A4:472:ARG:NH1	2.44	0.44
26:A5:582:GLU:O	26:A5:586:ASP:N	2.50	0.44
32:B1:157:ASP:N	32:B1:157:ASP:OD1	2.50	0.44
32:B1:356:ASP:OD1	32:B1:356:ASP:N	2.50	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B2:443:LEU:HG	33:B2:459:LEU:HD13	2.00	0.44
34:B3:32:LEU:HD22	34:B3:76:LEU:HD12	2.00	0.44
41:5E:341:LEU:HG	64:ST:116:LEU:HD22	1.98	0.44
41:5E:384:ARG:CD	43:5G:82:GLY:H	2.30	0.44
43:5G:234:ARG:NH1	43:5G:254:PHE:O	2.51	0.44
48:RA:152:ASP:OD1	48:RA:152:ASP:N	2.51	0.44
48:RA:231:VAL:HA	48:RA:247:THR:HA	1.98	0.44
51:RF:131:ALA:HA	51:RF:134:ILE:HG12	1.99	0.44
55:RL:111:SER:HB3	55:RL:134:LEU:HD12	1.99	0.44
67:RZ:420:LYS:N	71:RZ:1301:ADP:O1B	2.51	0.44
3:SA:1146:G:H2'	3:SA:1147:A:H8	1.83	0.44
3:SA:1623:C:O2'	43:5G:184:GLU:HB2	2.18	0.44
12:SO:93:LYS:HA	12:SO:96:VAL:HG12	1.99	0.44
14:SR:8:GLN:OE1	42:5F:177:ILE:HG23	2.18	0.44
21:3D:31:LEU:HD21	45:5I:59:VAL:HG13	1.99	0.44
23:3F:209:LYS:HA	23:3F:209:LYS:HD2	1.82	0.44
25:A4:201:VAL:HG13	25:A4:213:TRP:HB2	1.99	0.44
26:A5:87:LEU:O	26:A5:96:THR:N	2.50	0.44
27:A8:573:ILE:HG22	27:A8:575:ASN:H	1.83	0.44
27:A8:642:LEU:HD12	28:A9:499:ILE:CG2	2.44	0.44
29:AE:100:ALA:HB1	35:B8:44:PHE:HZ	1.82	0.44
29:AE:488:GLY:HA2	29:AE:491:TYR:HB3	1.98	0.44
30:AF:20:THR:HA	30:AF:24:GLN:HE21	1.82	0.44
31:AG:510:TYR:HE1	31:AG:527:HIS:HB3	1.83	0.44
31:AG:768:TRP:HE1	31:AG:772:THR:HA	1.83	0.44
32:B1:418:ARG:CZ	41:5E:491:ALA:HA	2.47	0.44
34:B3:188:GLU:O	34:B3:221:ASN:ND2	2.50	0.44
34:B3:531:ASN:OD1	34:B3:531:ASN:N	2.49	0.44
34:B3:749:ASN:OD1	41:5E:511:ASN:OD1	2.36	0.44
48:RA:60:ASN:HB3	48:RA:74:THR:HB	2.00	0.44
50:RE:174:TYR:CE2	50:RE:227:LYS:HB3	2.53	0.44
50:RE:804:THR:HG21	50:RE:838:VAL:HB	1.99	0.44
50:RE:1160:SER:C	50:RE:1187:LYS:HG2	2.43	0.44
51:RF:84:VAL:HG13	51:RF:126:LEU:HD11	1.99	0.44
51:RF:150:LYS:HG3	51:RF:151:HIS:ND1	2.33	0.44
56:RN:737:ILE:HA	56:RN:740:MET:HG2	2.00	0.44
56:RN:755:ILE:HG22	64:ST:122:HIS:HE1	1.83	0.44
66:RD:1181:ASP:HA	66:RD:1191:GLY:HA2	1.98	0.44
2:5A:20:C:H2'	2:5A:21:A:C8	2.52	0.44
3:SA:362:G:H2'	3:SA:363:G:C8	2.52	0.44
3:SA:863:A:H4'	15:SX:57:ARG:HG2	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1080:U:H5'	45:5I:425:LYS:HE2	1.99	0.44
5:SF:52:LEU:O	23:3F:120:ARG:NH1	2.48	0.44
20:3B:125:VAL:HG12	46:5J:150:GLY:HA3	2.00	0.44
21:3D:206:LEU:HD11	21:3D:219:LEU:HD11	2.00	0.44
23:3F:405:VAL:HG12	23:3F:415:THR:HG22	2.00	0.44
24:3H:95:ARG:HA	24:3H:95:ARG:HD2	1.88	0.44
25:A4:45:THR:HB	25:A4:352:VAL:HA	1.99	0.44
25:A4:212:ILE:O	25:A4:226:LEU:N	2.50	0.44
27:A8:676:TRP:CE3	27:A8:676:TRP:O	2.70	0.44
29:AE:729:LYS:HA	29:AE:733:MET:HG3	2.00	0.44
31:AG:364:ASN:OD1	31:AG:364:ASN:N	2.42	0.44
31:AG:484:VAL:O	31:AG:487:GLU:N	2.51	0.44
31:AG:516:PRO:HG2	31:AG:519:LEU:HD21	2.00	0.44
31:AG:712:THR:HG23	31:AG:720:ILE:HD13	1.99	0.44
32:B1:476:VAL:HA	32:B1:492:SER:HB3	1.99	0.44
34:B3:104:PRO:O	34:B3:122:THR:OG1	2.35	0.44
35:B8:277:ILE:HA	35:B8:282:ASN:HD22	1.83	0.44
39:5C:162:ASN:ND2	39:5C:429:GLU:OE1	2.51	0.44
41:5E:319:VAL:CG1	53:RJ:1044:LEU:HD22	2.47	0.44
50:RE:976:ILE:HG22	50:RE:1042:ALA:HB3	2.00	0.44
59:RQ:284:ARG:HE	59:RQ:284:ARG:HB3	1.51	0.44
60:RS:348:PRO:O	60:RS:352:SER:OG	2.30	0.44
66:RD:1670:LYS:HA	66:RD:1673:ASP:HB2	1.98	0.44
1:3A:88:U:OP2	22:3E:338:LYS:NZ	2.41	0.44
3:SA:1540:G:H2'	3:SA:1540:G:N3	2.32	0.44
11:SM:57:LYS:HG3	11:SM:110:HIS:CE1	2.53	0.44
16:SY:77:ILE:HG22	53:RJ:751:TYR:HB2	1.99	0.44
25:A4:120:SER:OG	25:A4:121:THR:N	2.50	0.44
25:A4:571:THR:HG21	25:A4:632:ASN:HB3	2.00	0.44
27:A8:633:GLN:H	27:A8:633:GLN:HG3	1.41	0.44
31:AG:296:HIS:NE2	31:AG:314:SER:OG	2.37	0.44
31:AG:532:TRP:HB3	31:AG:541:TRP:HB3	1.99	0.44
53:RJ:187:LYS:HB2	53:RJ:187:LYS:HE3	1.75	0.44
54:RK:143:LYS:HE3	54:RK:143:LYS:HB2	1.75	0.44
57:RO:315:VAL:HG23	57:RO:316:PRO:HD3	1.98	0.44
58:RP:103:LEU:HD11	58:RP:147:VAL:HG23	1.99	0.44
61:RY:489:GLN:O	61:RY:493:PHE:CB	2.66	0.44
64:ST:41:ARG:HA	65:SU:45:MET:SD	2.58	0.44
3:SA:1146:G:H2'	3:SA:1147:A:C8	2.53	0.44
4:SC:123:ALA:HB2	4:SC:165:ARG:HG3	2.00	0.44
4:SC:129:THR:HG23	4:SC:131:ASP:H	1.83	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SF:140:VAL:HG12	5:SF:146:THR:HG22	2.00	0.44
11:SM:46:LYS:HD3	11:SM:49:ILE:HD12	1.98	0.44
20:3B:169:LYS:HA	20:3B:193:VAL:O	2.18	0.44
24:3H:52:ILE:HD12	24:3H:71:CYS:SG	2.58	0.44
27:A8:633:GLN:HE21	27:A8:633:GLN:HB2	1.55	0.44
29:AE:715:HIS:HA	29:AE:718:ARG:HG2	2.00	0.44
31:AG:437:THR:OG1	31:AG:764:SER:O	2.31	0.44
34:B3:467:ILE:H	34:B3:479:ILE:HD11	1.83	0.44
35:B8:27:PHE:HB3	37:B6:31:LEU:HD23	1.98	0.44
38:5B:164:LYS:HE3	38:5B:164:LYS:HB3	1.76	0.44
45:5I:444:GLU:OE2	45:5I:448:ARG:NH2	2.37	0.44
50:RE:159:SER:O	50:RE:256:TYR:OH	2.27	0.44
50:RE:1098:PHE:CD2	50:RE:1184:GLY:N	2.72	0.44
50:RE:1222:GLU:HG2	51:RF:60:LEU:HB2	2.00	0.44
51:RF:50:SER:O	51:RF:127:LYS:NZ	2.51	0.44
53:RJ:625:TRP:HZ2	54:RK:284:SER:HB3	1.83	0.44
55:RL:195:ASN:HB3	55:RL:198:CYS:HB3	1.99	0.44
56:RN:755:ILE:CG2	64:ST:122:HIS:HE1	2.31	0.44
65:SU:89:ARG:HA	65:SU:89:ARG:HD3	1.81	0.44
3:SA:1234:A:O2'	3:SA:1236:A:N6	2.50	0.43
7:SH:65:GLN:NE2	48:RA:43:TYR:O	2.51	0.43
8:SI:19:GLN:HB3	8:SI:85:PHE:HZ	1.83	0.43
8:SI:38:LEU:HD12	8:SI:41:LEU:HD12	2.00	0.43
9:SJ:67:TRP:HD1	9:SJ:70:GLU:H	1.66	0.43
22:3E:227:LEU:HG	22:3E:231:ILE:HB	2.00	0.43
25:A4:572:ALA:HB3	25:A4:585:ILE:HD11	2.00	0.43
26:A5:221:MET:HB3	26:A5:221:MET:HE3	1.75	0.43
29:AE:238:LEU:HA	29:AE:241:ILE:HG22	1.99	0.43
32:B1:743:PHE:HZ	32:B1:778:ILE:HD13	1.83	0.43
33:B2:129:PHE:HE1	33:B2:150:LEU:HD11	1.82	0.43
34:B3:157:ASN:ND2	63:RT:77:GLY:HA2	2.32	0.43
34:B3:223:TRP:CD1	34:B3:230:LYS:HZ1	2.36	0.43
50:RE:1189:LEU:HD12	66:RD:1472:PRO:HG2	2.00	0.43
58:RP:1756:ILE:HG21	58:RP:1800:LEU:HB3	2.00	0.43
58:RP:1941:VAL:HA	58:RP:1944:ILE:HD12	1.99	0.43
60:RS:221:LEU:HD22	60:RS:258:VAL:HG11	2.00	0.43
67:RZ:601:ASN:OD1	67:RZ:603:THR:OG1	2.34	0.43
67:RZ:1129:GLU:HA	67:RZ:1132:PHE:HB2	2.00	0.43
3:SA:415:C:O2'	3:SA:418:G:O6	2.36	0.43
8:SI:87:ASP:OD1	58:RP:2031:HIS:NE2	2.49	0.43
14:SR:64:ASP:OD1	14:SR:64:ASP:N	2.50	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:144:ILE:HD12	25:A4:158:VAL:HB	2.00	0.43
27:A8:635:PHE:CD2	28:A9:492:ILE:CD1	3.01	0.43
27:A8:675:LEU:CB	28:A9:486:LEU:HD13	2.47	0.43
29:AE:348:ILE:HG21	29:AE:373:ILE:HD11	2.00	0.43
29:AE:538:ALA:HA	29:AE:541:LEU:HB2	2.00	0.43
29:AE:586:LEU:O	29:AE:590:ALA:HB2	2.18	0.43
33:B2:59:LEU:HD21	33:B2:62:LYS:HE2	1.99	0.43
33:B2:432:TYR:O	33:B2:450:ARG:N	2.48	0.43
36:BE:852:LEU:HD22	36:BE:860:GLU:HG2	2.00	0.43
39:5C:228:LEU:HD22	39:5C:264:PRO:HA	1.99	0.43
42:5F:124:ILE:H	42:5F:124:ILE:HG13	1.48	0.43
45:5I:107:LYS:NZ	45:5I:109:HIS:O	2.45	0.43
45:5I:139:CYS:HB3	45:5I:145:VAL:HG22	1.99	0.43
45:5I:241:ASP:OD1	45:5I:241:ASP:N	2.39	0.43
47:5K:161:LYS:HG2	47:5K:172:LEU:HD21	1.99	0.43
48:RA:184:ASN:OD1	48:RA:230:GLN:NE2	2.51	0.43
49:RB:237:SER:O	49:RB:237:SER:OG	2.32	0.43
50:RE:1188:PRO:HG3	62:X1:308:UNK:CB	2.48	0.43
50:RE:1221:HIS:CE1	51:RF:20:LEU:HB3	2.52	0.43
53:RJ:904:ASN:HA	53:RJ:907:THR:HB	2.00	0.43
55:RM:281:LEU:HA	55:RM:409:ALA:HB3	1.99	0.43
56:RN:314:MET:HA	56:RN:512:ASP:HA	1.99	0.43
60:RS:359:LEU:HD23	60:RS:362:LEU:HD12	2.00	0.43
66:RD:1479:MET:HE2	66:RD:1519:ALA:HB2	1.99	0.43
67:RZ:613:ILE:HG23	67:RZ:617:LEU:HD12	1.99	0.43
67:RZ:930:ILE:HD11	67:RZ:1007:LEU:HB2	1.99	0.43
3:SA:1599:C:H2'	3:SA:1600:A:C8	2.53	0.43
9:SJ:66:SER:HA	9:SJ:73:SER:HA	1.99	0.43
13:SP:111:ARG:HG3	63:RT:95:GLU:OE2	2.19	0.43
20:3B:221:ILE:HD13	21:3D:163:VAL:HB	2.00	0.43
24:3G:62:GLU:HA	24:3G:65:LEU:HG	2.00	0.43
25:A4:750:ASN:N	25:A4:750:ASN:OD1	2.51	0.43
26:A5:240:GLN:HE22	26:A5:298:LYS:HB3	1.83	0.43
27:A8:634:LEU:HD23	27:A8:634:LEU:H	1.83	0.43
30:AF:288:ASP:OD1	30:AF:288:ASP:N	2.48	0.43
31:AG:50:ASN:HD21	31:AG:782:THR:HG22	1.84	0.43
33:B2:645:GLU:HG2	33:B2:646:LYS:HG3	1.99	0.43
34:B3:194:ARG:HD3	34:B3:243:VAL:HG13	1.99	0.43
41:5E:325:SER:OG	53:RJ:1007:TYR:CD1	2.71	0.43
42:5F:29:ASP:N	42:5F:29:ASP:OD1	2.50	0.43
43:5G:164:GLN:HE21	43:5G:260:GLU:HB3	1.84	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5I:358:MET:HB3	59:RQ:890:VAL:HG23	2.00	0.43
50:RE:518:PHE:HD1	50:RE:520:ASN:H	1.67	0.43
50:RE:527:TYR:HB2	50:RE:615:VAL:HG13	2.01	0.43
50:RE:1109:LYS:HZ1	50:RE:1170:GLY:H	1.66	0.43
52:RG:135:LYS:HD3	52:RG:135:LYS:HA	1.87	0.43
56:RN:590:ASN:OD1	56:RN:590:ASN:N	2.50	0.43
65:SU:48:GLN:HG3	65:SU:48:GLN:O	2.17	0.43
67:RZ:1099:LEU:HD21	67:RZ:1229:TRP:HB3	1.99	0.43
2:5A:467:A:N1	2:5A:468:A:N6	2.66	0.43
3:SA:327:U:OP2	11:SM:57:LYS:NZ	2.38	0.43
3:SA:328:A:H2'	3:SA:329:G:H8	1.83	0.43
3:SA:526:A:OP1	17:SZ:93:ARG:NE	2.48	0.43
3:SA:1132:A:O3'	54:RK:231:ARG:NH1	2.43	0.43
3:SA:1789:G:H2'	3:SA:1790:A:H8	1.83	0.43
5:SF:183:VAL:HB	5:SF:225:VAL:HG23	2.00	0.43
6:SG:39:GLU:OE1	6:SG:41:LYS:NZ	2.45	0.43
10:SK:38:ASN:HA	44:5H:565:LYS:HE2	1.99	0.43
13:SP:111:ARG:NH2	63:RT:93:LYS:CA	2.74	0.43
23:3F:415:THR:OG1	23:3F:425:TRP:NE1	2.39	0.43
25:A4:214:SER:HB3	25:A4:226:LEU:HD13	1.99	0.43
29:AE:655:ALA:O	29:AE:659:LEU:HB2	2.18	0.43
31:AG:228:VAL:HG23	31:AG:236:ASN:HB3	2.00	0.43
32:B1:829:VAL:HG23	32:B1:830:ARG:HG2	2.01	0.43
33:B2:596:ASN:HB3	33:B2:612:PHE:HA	1.99	0.43
35:B8:376:LEU:HG	35:B8:386:ILE:HG12	1.99	0.43
36:BE:569:VAL:HB	36:BE:579:ARG:HB2	2.01	0.43
41:5E:323:LYS:HG2	41:5E:325:SER:H	1.84	0.43
47:5K:52:PHE:HB3	47:5K:55:TYR:HB3	2.01	0.43
50:RE:870:ALA:O	50:RE:875:LYS:NZ	2.51	0.43
51:RF:208:ASP:N	51:RF:212:PHE:O	2.41	0.43
52:RH:89:PRO:HG2	52:RH:134:PHE:HZ	1.83	0.43
58:RP:1782:ASN:OD1	58:RP:1782:ASN:N	2.44	0.43
63:RT:200:ARG:O	63:RT:204:ARG:HB2	2.18	0.43
2:5A:489:G:O6	37:B6:120:ARG:NH1	2.51	0.43
3:SA:18:C:O2'	3:SA:21:U:O4'	2.37	0.43
3:SA:398:G:OP2	9:SJ:47:ARG:NH2	2.40	0.43
3:SA:1468:U:H4'	65:SU:88:VAL:O	2.19	0.43
4:SC:171:ILE:HD11	4:SC:197:ILE:HA	1.99	0.43
4:SC:239:GLU:HG2	50:RE:658:PHE:HA	2.00	0.43
8:SI:131:PHE:O	8:SI:133:THR:N	2.52	0.43
9:SJ:76:THR:OG1	9:SJ:77:ARG:N	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:SK:155:HIS:NE2	23:3F:321:HIS:O	2.50	0.43
16:SY:68:ILE:HD12	56:RN:785:VAL:HG23	2.00	0.43
26:A5:281:ILE:HG12	26:A5:328:VAL:HB	2.01	0.43
27:A8:643:ASP:OD1	30:AF:510:LEU:O	2.37	0.43
31:AG:780:GLU:O	31:AG:782:THR:N	2.49	0.43
32:B1:369:ILE:HB	32:B1:383:PHE:HB2	1.99	0.43
32:B1:847:ARG:O	32:B1:851:SER:OG	2.30	0.43
34:B3:41:ASN:OD1	34:B3:41:ASN:N	2.49	0.43
40:5D:58:ARG:HD2	42:5F:174:ARG:HH22	1.82	0.43
41:5E:384:ARG:CZ	43:5G:81:SER:HB3	2.49	0.43
45:5I:133:GLN:HA	45:5I:150:ILE:O	2.18	0.43
45:5I:306:SER:OG	45:5I:307:ALA:N	2.50	0.43
47:5K:171:PRO:HA	47:5K:184:LYS:HB2	2.01	0.43
50:RE:257:SER:O	50:RE:266:PRO:HA	2.18	0.43
50:RE:611:ASP:OD1	50:RE:611:ASP:N	2.51	0.43
53:RJ:280:LEU:HD12	53:RJ:281:PRO:HD2	2.01	0.43
54:RK:36:ILE:HB	54:RK:72:THR:HA	2.01	0.43
56:RN:616:LEU:HB3	56:RN:619:LEU:HD13	2.01	0.43
67:RZ:627:THR:OG1	67:RZ:628:GLY:N	2.51	0.43
67:RZ:781:ARG:HB2	67:RZ:798:VAL:HG12	2.01	0.43
6:SG:89:ILE:HD11	6:SG:172:ILE:HD11	2.00	0.43
8:SI:22:GLN:HA	8:SI:25:VAL:HG22	1.99	0.43
11:SM:123:VAL:HG12	11:SM:142:VAL:HA	1.99	0.43
15:SX:38:LEU:HA	15:SX:41:MET:HG2	2.01	0.43
22:3E:206:ALA:HB2	22:3E:262:ILE:HD11	2.00	0.43
23:3F:201:ILE:HG12	23:3F:538:ARG:HD3	2.00	0.43
26:A5:336:ASN:OD1	26:A5:336:ASN:N	2.49	0.43
27:A8:439:LYS:HA	27:A8:442:LYS:CB	2.48	0.43
30:AF:413:LEU:HA	30:AF:416:THR:HG22	2.00	0.43
32:B1:35:ASN:HA	32:B1:58:ILE:HG23	1.99	0.43
33:B2:123:ALA:HB3	33:B2:141:LYS:HD3	2.00	0.43
35:B8:35:GLU:O	35:B8:39:LYS:HB2	2.18	0.43
45:5I:272:MET:HE3	45:5I:272:MET:HB3	1.95	0.43
48:RA:155:VAL:HG13	48:RA:163:TYR:HB2	2.00	0.43
50:RE:1216:LYS:HA	50:RE:1219:ILE:HG12	2.00	0.43
53:RJ:80:THR:C	69:RJ:1201:GTP:O2B	2.61	0.43
54:RK:80:ILE:HD13	54:RK:80:ILE:HA	1.90	0.43
67:RZ:646:LYS:HA	67:RZ:646:LYS:HD2	1.79	0.43
67:RZ:847:VAL:HA	67:RZ:850:ILE:HB	2.00	0.43
67:RZ:1066:ASP:N	67:RZ:1066:ASP:OD1	2.49	0.43
3:SA:513:U:H2'	3:SA:514:G:H8	1.82	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1501:C:H2'	3:SA:1502:G:C8	2.54	0.43
6:SG:72:HIS:O	14:SR:79:TYR:OH	2.37	0.43
12:SO:58:HIS:O	12:SO:60:VAL:N	2.49	0.43
20:3C:185:SER:HB3	20:3C:217:ILE:HD11	2.01	0.43
22:3E:191:HIS:HB2	22:3E:247:ILE:HG23	1.99	0.43
22:3E:330:LEU:HD13	40:5D:109:THR:HG21	2.00	0.43
22:3E:372:ARG:O	22:3E:376:LEU:HB2	2.18	0.43
26:A5:270:ASN:OD1	26:A5:270:ASN:N	2.49	0.43
27:A8:270:PHE:HA	27:A8:282:GLY:HA2	2.00	0.43
29:AE:700:SER:O	29:AE:700:SER:OG	2.32	0.43
30:AF:24:GLN:HB2	30:AF:294:PHE:HD1	1.83	0.43
30:AF:377:ASP:OD1	30:AF:377:ASP:N	2.51	0.43
33:B2:657:GLN:HE21	33:B2:657:GLN:HB3	1.64	0.43
34:B3:34:THR:HG23	34:B3:68:LYS:HE3	2.00	0.43
34:B3:519:ASN:HD22	34:B3:524:GLU:H	1.67	0.43
36:BE:24:PHE:HB3	36:BE:654:TRP:HB3	2.01	0.43
39:5C:64:ASP:HA	39:5C:67:LEU:HG	1.99	0.43
41:5E:316:ASN:O	41:5E:320:ALA:CB	2.66	0.43
45:5I:6:ILE:HG21	45:5I:8:ARG:HH21	1.84	0.43
45:5I:344:HIS:NE2	45:5I:418:HIS:O	2.51	0.43
50:RE:224:CYS:O	50:RE:227:LYS:HG3	2.19	0.43
3:SA:360:A:O2'	3:SA:362:G:N2	2.44	0.43
3:SA:1478:G:H5'	65:SU:39:THR:HG21	2.01	0.43
6:SG:103:ASN:HA	6:SG:106:LYS:HD2	2.01	0.43
21:3D:52:SER:HB2	21:3D:85:ASN:HD21	1.84	0.43
23:3F:303:LYS:HB3	23:3F:317:ILE:HD11	2.01	0.43
23:3F:414:ILE:HG13	23:3F:478:LEU:HD21	2.00	0.43
25:A4:566:LEU:HA	25:A4:566:LEU:HD23	1.83	0.43
25:A4:617:ASN:O	25:A4:621:ASN:HB2	2.19	0.43
32:B1:25:ASP:OD1	32:B1:25:ASP:N	2.50	0.43
32:B1:341:GLN:OE1	32:B1:341:GLN:HA	2.19	0.43
32:B1:493:TRP:HA	32:B1:517:ASP:HB2	2.01	0.43
33:B2:473:ASP:N	33:B2:494:ASP:OD2	2.47	0.43
34:B3:678:TRP:HE3	34:B3:697:VAL:HG23	1.84	0.43
40:5D:102:GLN:HE21	53:RJ:1098:ARG:NH1	2.17	0.43
41:5E:493:GLN:C	41:5E:493:GLN:CD	2.86	0.43
44:5H:550:LEU:HD23	44:5H:550:LEU:HA	1.88	0.43
54:RK:68:SER:OG	54:RK:69:TYR:N	2.52	0.43
56:RN:475:ARG:HH22	56:RN:516:LEU:HB3	1.84	0.43
56:RN:669:SER:HA	56:RN:672:THR:HG22	2.01	0.43
57:RO:472:HIS:CD2	57:RO:474:HIS:H	2.31	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RP:1610:MET:O	58:RP:1614:GLU:CB	2.67	0.43
59:RQ:767:GLU:C	59:RQ:769:GLN:N	2.75	0.43
61:RY:489:GLN:O	61:RY:493:PHE:HB3	2.19	0.43
64:ST:42:TYR:HA	64:ST:84:TRP:HH2	1.84	0.43
65:SU:37:VAL:O	65:SU:46:PRO:HA	2.19	0.43
67:RZ:1033:LYS:HD3	67:RZ:1033:LYS:HA	1.86	0.43
1:3A:94:A:H2'	1:3A:95:A:C8	2.53	0.43
3:SA:578:U:OP2	53:RJ:874:TYR:OH	2.29	0.43
3:SA:1541:G:N2	3:SA:1571:C:C4	2.87	0.43
7:SH:115:LYS:HE3	7:SH:115:LYS:HB2	1.76	0.43
8:SI:46:ILE:HD12	8:SI:60:ILE:HG13	2.01	0.43
9:SJ:31:ARG:HH12	9:SJ:48:THR:HB	1.84	0.43
10:SK:154:LYS:HE2	10:SK:154:LYS:HB3	1.88	0.43
13:SP:107:ARG:NH1	63:RT:150:GLY:N	2.66	0.43
13:SP:111:ARG:HH22	63:RT:93:LYS:CB	2.27	0.43
22:3E:319:ILE:HD12	22:3E:326:LEU:HD22	2.01	0.43
25:A4:313:LYS:HA	25:A4:316:LYS:HG2	2.01	0.43
27:A8:443:CYS:CA	31:AG:728:LEU:HB3	2.47	0.43
31:AG:87:SER:O	31:AG:111:THR:OG1	2.32	0.43
31:AG:252:LEU:HD23	31:AG:256:THR:HG21	2.00	0.43
33:B2:178:ILE:HD11	33:B2:186:ILE:HD11	2.01	0.43
34:B3:188:GLU:HB2	34:B3:223:TRP:HZ2	1.83	0.43
34:B3:192:ALA:HB3	34:B3:216:ARG:HG3	2.00	0.43
36:BE:50:ILE:HD13	36:BE:311:VAL:HG11	2.01	0.43
36:BE:499:LYS:HE2	36:BE:499:LYS:HB3	1.85	0.43
37:B6:5:ARG:HD2	37:B6:5:ARG:HA	1.80	0.43
39:5C:369:MET:HB3	39:5C:369:MET:HE2	1.79	0.43
39:5C:544:ASP:HB3	39:5C:547:GLU:HB3	2.00	0.43
41:5E:533:LYS:CA	41:5E:536:ARG:HE	2.24	0.43
46:5J:134:ARG:HD2	46:5J:134:ARG:HA	1.83	0.43
50:RE:207:LEU:HB2	50:RE:296:ILE:HA	2.00	0.43
50:RE:911:PRO:HB2	50:RE:954:LEU:HD13	2.01	0.43
50:RE:1206:PRO:HB3	50:RE:1212:VAL:HG22	2.01	0.43
51:RF:130:ASP:HB2	51:RF:133:SER:HB2	2.01	0.43
52:RG:75:GLY:HA2	52:RG:78:LYS:HE3	2.01	0.43
57:RO:292:PRO:HG2	57:RO:330:PHE:HE2	1.82	0.43
58:RP:1975:LYS:HA	58:RP:1975:LYS:HD2	1.80	0.43
64:ST:41:ARG:HB2	65:SU:45:MET:HG3	2.01	0.43
65:SU:105:LEU:HD13	65:SU:105:LEU:HA	1.77	0.43
66:RD:1592:LEU:HB2	66:RD:1601:ALA:HB2	2.01	0.43
67:RZ:842:ILE:HG13	67:RZ:850:ILE:HD13	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:341:A:OP1	48:RA:121:ARG:NH2	2.48	0.43
3:SA:1533:C:H5'	64:ST:27:LYS:HD3	2.00	0.43
5:SF:182:TYR:CD2	5:SF:192:ILE:HD11	2.54	0.43
5:SF:194:THR:H	5:SF:210:ILE:HG23	1.82	0.43
10:SK:27:GLU:OE2	10:SK:43:TYR:OH	2.37	0.43
15:SX:12:ASN:O	15:SX:16:ASN:ND2	2.52	0.43
25:A4:532:ASN:N	25:A4:544:SER:O	2.50	0.43
26:A5:110:ILE:HG22	26:A5:119:CYS:HB2	2.00	0.43
26:A5:448:ASN:OD1	26:A5:450:HIS:NE2	2.52	0.43
27:A8:547:GLN:O	27:A8:551:PHE:CB	2.66	0.43
30:AF:463:VAL:HA	30:AF:466:VAL:HG12	2.01	0.43
32:B1:749:TYR:HE2	36:BE:705:ILE:HG13	1.84	0.43
35:B8:426:VAL:HG11	35:B8:455:ILE:HG21	2.01	0.43
36:BE:627:ASN:ND2	36:BE:647:THR:OG1	2.52	0.43
37:B6:72:LYS:HD2	37:B6:72:LYS:HA	1.78	0.43
39:5C:230:THR:HG22	39:5C:232:ALA:H	1.83	0.43
40:5D:145:GLU:OE1	40:5D:146:PHE:N	2.51	0.43
42:5F:169:THR:HA	42:5F:172:ARG:HG2	2.01	0.43
43:5G:164:GLN:NE2	43:5G:260:GLU:OE1	2.52	0.43
48:RA:277:ILE:HA	48:RA:290:VAL:O	2.19	0.43
50:RE:208:THR:OG1	50:RE:209:MET:N	2.52	0.43
53:RJ:940:LYS:HE2	53:RJ:940:LYS:HB2	1.73	0.43
54:RK:56:ILE:HD13	54:RK:56:ILE:HA	1.89	0.43
56:RN:86:ILE:HG13	56:RN:89:GLN:NE2	2.34	0.43
56:RN:484:ARG:HB3	56:RN:492:ALA:HB1	2.01	0.43
60:RS:437:ARG:HH21	60:RS:463:GLY:HA3	1.84	0.43
63:RT:170:ASP:OD1	63:RT:170:ASP:N	2.48	0.43
3:SA:1739:C:H2'	3:SA:1740:A:C8	2.53	0.42
8:SI:51:VAL:HG23	8:SI:53:GLY:H	1.84	0.42
13:SP:107:ARG:NE	13:SP:107:ARG:CA	2.73	0.42
20:3B:198:GLU:O	20:3B:221:ILE:HA	2.18	0.42
20:3C:185:SER:HA	20:3C:188:VAL:HG12	2.01	0.42
27:A8:595:ILE:O	27:A8:599:MET:HB2	2.19	0.42
31:AG:857:PHE:HE2	35:B8:226:LYS:HB3	1.84	0.42
32:B1:150:THR:OG1	32:B1:164:THR:OG1	2.31	0.42
33:B2:351:LEU:HB2	33:B2:367:ILE:HG23	2.00	0.42
37:B6:15:MET:HE2	37:B6:15:MET:HB3	1.67	0.42
37:B6:35:LYS:HE3	37:B6:35:LYS:HB3	1.88	0.42
47:5K:61:PRO:HB3	47:5K:92:ALA:HB1	2.01	0.42
48:RA:95:ARG:NH2	48:RA:128:LYS:O	2.51	0.42
48:RA:217:LYS:HE2	48:RA:217:LYS:HB3	1.87	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RJ:831:ARG:HD3	53:RJ:838:ILE:HD12	2.01	0.42
53:RJ:1019:THR:HB	53:RJ:1022:LEU:HD12	2.01	0.42
54:RK:286:SER:OG	54:RK:289:VAL:O	2.33	0.42
55:RL:203:ASP:OD1	55:RL:203:ASP:N	2.52	0.42
56:RN:481:MET:HE3	56:RN:481:MET:HB2	1.92	0.42
60:RS:266:PHE:O	60:RS:270:LEU:HB3	2.18	0.42
60:RS:382:LEU:HD11	60:RS:428:TYR:CG	2.54	0.42
60:RS:398:ARG:H	60:RS:406:GLY:HA3	1.83	0.42
2:5A:298:A:OP2	36:BE:103:ARG:NH2	2.45	0.42
3:SA:99:C:H2'	3:SA:100:A:C8	2.54	0.42
3:SA:1504:G:H2'	3:SA:1505:A:C4	2.54	0.42
7:SH:74:LYS:O	48:RA:88:ASN:ND2	2.52	0.42
8:SI:185:ILE:HG13	8:SI:187:SER:HB3	2.01	0.42
9:SJ:67:TRP:O	9:SJ:71:GLY:HA2	2.18	0.42
15:SX:93:LEU:HD11	15:SX:102:VAL:HG22	2.01	0.42
22:3E:218:ALA:HA	22:3E:221:THR:HG22	2.00	0.42
24:3G:64:LEU:O	24:3G:66:HIS:N	2.43	0.42
28:A9:475:THR:HA	28:A9:478:ASN:HB2	1.99	0.42
29:AE:549:LYS:HD3	29:AE:549:LYS:HA	1.91	0.42
31:AG:414:ILE:HA	31:AG:414:ILE:HD12	1.79	0.42
33:B2:39:GLY:O	33:B2:54:ILE:HG13	2.19	0.42
33:B2:673:VAL:HG23	33:B2:683:ILE:HD13	2.01	0.42
34:B3:260:THR:HG22	34:B3:269:LEU:HD13	2.01	0.42
34:B3:483:SER:O	34:B3:483:SER:OG	2.35	0.42
36:BE:27:PHE:HB2	36:BE:655:THR:HG23	2.00	0.42
42:5F:94:ILE:HG23	42:5F:97:LEU:HD12	2.02	0.42
43:5G:119:ARG:HA	43:5G:122:TYR:HD2	1.84	0.42
50:RE:713:LEU:HB2	50:RE:716:SER:HB2	2.01	0.42
52:RG:190:GLN:NE2	52:RG:244:GLY:HA2	2.34	0.42
57:RO:243:PRO:HA	57:RO:244:PRO:HD3	1.81	0.42
57:RO:324:PHE:CZ	64:ST:4:VAL:HG21	2.54	0.42
57:RO:338:TYR:OH	57:RO:365:PHE:O	2.33	0.42
60:RS:210:VAL:HG23	60:RS:212:LYS:HG2	2.00	0.42
3:SA:200:A:H2'	3:SA:201:G:H8	1.83	0.42
3:SA:555:A:N6	3:SA:571:G:O2'	2.50	0.42
3:SA:1068:C:H2'	3:SA:1069:A:C8	2.54	0.42
5:SF:71:LYS:N	5:SF:91:THR:O	2.52	0.42
10:SK:63:ASP:OD1	10:SK:63:ASP:N	2.46	0.42
20:3B:272:LYS:HD3	20:3B:275:CYS:HB3	2.01	0.42
21:3D:182:ASP:OD1	21:3D:314:ARG:NH2	2.39	0.42
25:A4:513:LEU:HD12	25:A4:513:LEU:HA	1.89	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A5:441:LEU:HD11	26:A5:480:LEU:HD13	2.01	0.42
29:AE:476:ILE:HG23	29:AE:515:PHE:HE2	1.84	0.42
31:AG:313:LEU:HD23	31:AG:323:LEU:HB3	2.01	0.42
31:AG:551:HIS:HA	31:AG:583:LYS:HE3	2.00	0.42
34:B3:652:ILE:HD12	34:B3:652:ILE:HA	1.92	0.42
36:BE:470:GLN:HB3	36:BE:553:ARG:NH1	2.34	0.42
50:RE:1151:LYS:HE3	50:RE:1151:LYS:HB2	1.92	0.42
50:RE:1189:LEU:HD12	66:RD:1472:PRO:CG	2.49	0.42
54:RK:81:ILE:HG22	54:RK:110:SER:HB3	2.01	0.42
56:RN:700:LEU:HD21	57:RO:467:ALA:HB2	2.00	0.42
60:RS:264:LYS:HB2	60:RS:264:LYS:HE3	1.81	0.42
3:SA:628:G:OP1	12:SO:120:SER:OG	2.37	0.42
3:SA:1233:G:H1	3:SA:1253:U:H2'	1.83	0.42
5:SF:45:ILE:O	5:SF:49:ARG:HB3	2.19	0.42
10:SK:45:ILE:HD12	10:SK:48:GLN:HE21	1.84	0.42
11:SM:92:HIS:NE2	11:SM:101:GLU:O	2.52	0.42
15:SX:66:ASN:O	45:5I:325:TYR:OH	2.27	0.42
20:3C:124:SER:HA	20:3C:139:VAL:O	2.19	0.42
20:3C:149:SER:OG	20:3C:150:LYS:N	2.52	0.42
21:3D:4:ILE:HG23	21:3D:20:VAL:HG21	2.01	0.42
22:3E:132:SER:OG	22:3E:134:ASN:OD1	2.34	0.42
22:3E:160:ASP:HB3	22:3E:283:ILE:HG21	2.01	0.42
23:3F:160:ILE:HG12	23:3F:542:SER:HB2	2.00	0.42
23:3F:502:SER:OG	23:3F:504:ASN:OD1	2.32	0.42
29:AE:539:LEU:HD12	29:AE:540:LYS:HG3	2.01	0.42
30:AF:177:ILE:HA	30:AF:178:PRO:HD3	1.84	0.42
31:AG:865:LYS:HE2	31:AG:865:LYS:HB3	1.81	0.42
32:B1:76:ASP:N	32:B1:76:ASP:OD1	2.51	0.42
32:B1:275:LEU:HD22	32:B1:289:LEU:HD13	2.02	0.42
33:B2:236:ASP:OD1	33:B2:236:ASP:N	2.46	0.42
33:B2:297:LYS:HA	33:B2:300:GLU:HB2	2.02	0.42
33:B2:369:TYR:HA	33:B2:374:PRO:HA	2.01	0.42
33:B2:534:ILE:HD11	33:B2:537:VAL:HG12	2.01	0.42
34:B3:28:ASN:OD1	34:B3:28:ASN:N	2.48	0.42
34:B3:572:GLU:HG3	34:B3:600:LYS:HD2	2.01	0.42
48:RA:164:ARG:NH2	48:RA:174:ASN:O	2.51	0.42
49:RB:307:LYS:O	49:RB:311:ARG:HB3	2.19	0.42
50:RE:379:MET:HE3	50:RE:381:HIS:HB2	2.02	0.42
50:RE:918:ARG:HD3	50:RE:1089:PHE:CZ	2.54	0.42
51:RF:153:ASN:HD22	51:RF:154:GLU:HG2	1.83	0.42
56:RN:501:PHE:HB3	56:RN:549:ILE:HG21	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:SU:124:ILE:H	65:SU:124:ILE:HG13	1.55	0.42
66:RD:1695:TRP:HE1	66:RD:1711:VAL:HG11	1.84	0.42
67:RZ:1079:LEU:O	67:RZ:1083:MET:HG2	2.19	0.42
1:3A:62:C:O2'	36:BE:447:ASN:O	2.35	0.42
1:3A:97:C:C2	1:3A:320:G:N2	2.86	0.42
3:SA:-7:A:N7	45:5I:292:ARG:NH1	2.68	0.42
3:SA:200:A:O2'	58:RP:1061:CYS:O	2.36	0.42
3:SA:1659:A:H2'	3:SA:1660:A:C8	2.53	0.42
9:SJ:67:TRP:O	9:SJ:71:GLY:CA	2.68	0.42
10:SK:163:PRO:HB3	10:SK:169:PRO:HA	2.01	0.42
20:3C:210:MET:HE2	20:3C:210:MET:HB2	1.97	0.42
20:3C:291:GLN:HA	20:3C:294:ARG:HG2	2.01	0.42
24:3G:44:LEU:HD23	24:3G:44:LEU:HA	1.87	0.42
29:AE:323:PHE:CZ	29:AE:332:ILE:HD11	2.54	0.42
29:AE:354:SER:O	29:AE:358:TYR:HB2	2.20	0.42
30:AF:492:ARG:HA	30:AF:492:ARG:HD3	1.80	0.42
32:B1:60:ALA:HB1	32:B1:102:VAL:HG12	2.02	0.42
32:B1:492:SER:OG	32:B1:494:ASP:OD1	2.28	0.42
32:B1:498:ARG:HH11	32:B1:498:ARG:HD3	1.72	0.42
33:B2:276:ASN:ND2	33:B2:280:THR:O	2.47	0.42
33:B2:636:ASP:N	33:B2:636:ASP:OD1	2.52	0.42
33:B2:840:MET:HE1	33:B2:887:LEU:HD13	2.02	0.42
34:B3:674:SER:OG	34:B3:675:LYS:N	2.52	0.42
36:BE:606:ASP:OD1	36:BE:606:ASP:N	2.41	0.42
43:5G:153:THR:HG23	43:5G:164:GLN:HB3	2.02	0.42
43:5G:154:ILE:O	43:5G:162:THR:HA	2.20	0.42
50:RE:360:VAL:O	50:RE:363:THR:OG1	2.30	0.42
50:RE:919:TRP:HE3	50:RE:920:LEU:HD12	1.85	0.42
50:RE:1044:LYS:HE3	50:RE:1044:LYS:HB3	1.94	0.42
52:RG:128:VAL:HG22	52:RG:159:LEU:HD22	2.01	0.42
52:RH:176:ARG:NH2	52:RH:192:TYR:OH	2.52	0.42
53:RJ:217:ASP:O	53:RJ:221:LEU:HB2	2.20	0.42
53:RJ:773:THR:HG23	53:RJ:777:ARG:HD3	2.02	0.42
53:RJ:1075:LYS:HE3	53:RJ:1075:LYS:HB2	1.84	0.42
54:RK:310:ARG:HB3	54:RK:353:THR:HG22	2.01	0.42
56:RN:65:ASN:OD1	56:RN:65:ASN:N	2.50	0.42
57:RO:395:ILE:HD12	57:RO:469:LEU:HD11	2.02	0.42
59:RQ:767:GLU:C	59:RQ:769:GLN:H	2.26	0.42
60:RS:382:LEU:HD21	60:RS:428:TYR:CZ	2.53	0.42
1:3A:113:G:O6	24:3H:42:LYS:NZ	2.44	0.42
3:SA:147:A:N7	3:SA:167:U:O2	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:646:C:H2'	3:SA:647:G:C8	2.47	0.42
4:SC:154:SER:O	4:SC:154:SER:OG	2.32	0.42
20:3B:150:LYS:NZ	20:3B:310:GLU:OE2	2.44	0.42
22:3E:117:TYR:HA	22:3E:120:ILE:HG12	2.01	0.42
25:A4:774:LEU:HD12	25:A4:774:LEU:HA	1.83	0.42
27:A8:314:LEU:HA	27:A8:321:ILE:HA	2.00	0.42
27:A8:556:VAL:O	27:A8:585:ARG:NH1	2.52	0.42
27:A8:638:LEU:HA	27:A8:641:VAL:CG1	2.48	0.42
29:AE:25:ARG:HH21	45:5I:16:VAL:HG22	1.83	0.42
30:AF:424:ARG:HA	31:AG:477:VAL:HG11	2.01	0.42
32:B1:157:ASP:OD1	32:B1:203:GLN:NE2	2.38	0.42
32:B1:515:TYR:HE2	42:5F:180:PHE:HZ	1.67	0.42
33:B2:497:VAL:HG12	33:B2:528:LEU:HB3	2.01	0.42
41:5E:341:LEU:HB3	64:ST:116:LEU:HD22	1.99	0.42
50:RE:976:ILE:HA	50:RE:1042:ALA:O	2.19	0.42
51:RF:73:GLN:HE21	51:RF:156:PHE:HD2	1.66	0.42
57:RO:208:TYR:O	57:RO:212:LEU:HB2	2.19	0.42
58:RP:1877:ARG:NH2	58:RP:1913:SER:O	2.51	0.42
60:RS:364:PHE:HE1	60:RS:417:TRP:HE1	1.67	0.42
60:RS:437:ARG:HD2	60:RS:460:LEU:HG	2.02	0.42
4:SC:109:LYS:HA	4:SC:109:LYS:HD2	1.87	0.42
5:SF:31:PRO:HA	5:SF:81:THR:HB	2.01	0.42
5:SF:47:PHE:HD2	5:SF:48:LEU:HD12	1.84	0.42
6:SG:23:VAL:HG23	14:SR:61:SER:HB3	2.00	0.42
6:SG:114:ILE:HA	6:SG:117:THR:HG22	2.02	0.42
13:SP:107:ARG:HH12	63:RT:150:GLY:HA3	1.79	0.42
13:SP:111:ARG:NH1	63:RT:95:GLU:HG2	2.35	0.42
26:A5:49:ASN:OD1	26:A5:49:ASN:N	2.49	0.42
27:A8:596:LYS:HG3	27:A8:637:LEU:HD22	2.00	0.42
29:AE:487:THR:HG22	29:AE:488:GLY:H	1.85	0.42
31:AG:478:ASN:OD1	31:AG:478:ASN:N	2.51	0.42
33:B2:836:ILE:HA	33:B2:839:VAL:HG12	2.00	0.42
34:B3:133:ASN:OD1	34:B3:133:ASN:N	2.51	0.42
34:B3:367:VAL:HG12	34:B3:643:PHE:HE2	1.85	0.42
36:BE:353:PRO:HA	36:BE:370:SER:HA	2.01	0.42
37:B6:106:ASP:OD1	37:B6:106:ASP:N	2.38	0.42
39:5C:215:LYS:HG2	39:5C:227:GLU:HG2	2.00	0.42
41:5E:508:ARG:HG2	41:5E:514:ALA:HB2	2.02	0.42
48:RA:306:LYS:HA	48:RA:306:LYS:HD2	1.83	0.42
50:RE:652:LYS:HA	50:RE:652:LYS:HD2	1.83	0.42
54:RK:190:SER:OG	54:RK:191:ILE:N	2.51	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:RS:373:LYS:HE2	60:RS:373:LYS:HB3	1.84	0.42
65:SU:103:LYS:HD3	65:SU:103:LYS:HA	1.81	0.42
67:RZ:1153:LEU:O	67:RZ:1169:THR:HA	2.19	0.42
1:3A:58:A:OP2	42:5F:165:LYS:CE	2.68	0.42
5:SF:68:ARG:HH21	5:SF:76:VAL:HG11	1.85	0.42
7:SH:77:LEU:HD12	7:SH:95:LYS:HD3	2.00	0.42
8:SI:116:ARG:HB3	8:SI:117:THR:H	1.55	0.42
11:SM:115:PHE:CG	11:SM:142:VAL:HG21	2.55	0.42
18:Sc:50:ALA:O	18:Sc:52:THR:N	2.53	0.42
23:3F:301:ASP:OD1	23:3F:301:ASP:N	2.51	0.42
31:AG:31:ASN:OD1	31:AG:31:ASN:N	2.52	0.42
42:5F:41:ARG:HA	42:5F:41:ARG:HD2	1.89	0.42
43:5G:157:PHE:O	43:5G:159:HIS:N	2.51	0.42
45:5I:456:GLU:HA	45:5I:459:LYS:HE2	2.01	0.42
45:5I:464:THR:HG21	45:5I:468:TYR:HE1	1.85	0.42
53:RJ:203:LYS:HD2	53:RJ:203:LYS:HA	1.78	0.42
55:RL:37:LEU:HD22	55:RL:149:VAL:HG11	2.01	0.42
58:RP:1935:LYS:HZ2	58:RP:1935:LYS:HG3	1.69	0.42
58:RP:1945:ILE:HA	58:RP:1948:SER:HB2	2.01	0.42
66:RD:1597:GLU:HB3	66:RD:1600:GLU:HB3	2.00	0.42
3:SA:1156:C:H2'	3:SA:1157:A:C8	2.54	0.42
4:SC:181:LEU:HA	4:SC:181:LEU:HD23	1.86	0.42
8:SI:188:GLU:HG3	45:5I:465:VAL:HG22	2.00	0.42
22:3E:172:ASP:O	22:3E:176:GLU:HG2	2.20	0.42
22:3E:333:LYS:HD3	40:5D:103:ASP:HB3	2.02	0.42
25:A4:106:ASN:OD1	25:A4:106:ASN:N	2.51	0.42
26:A5:27:GLN:HG3	26:A5:59:LYS:HA	2.02	0.42
26:A5:224:CYS:SG	26:A5:225:VAL:N	2.93	0.42
27:A8:673:THR:HG22	28:A9:490:GLU:N	2.35	0.42
41:5E:341:LEU:HG	64:ST:116:LEU:HD13	2.01	0.42
46:5J:106:LEU:O	46:5J:146:ARG:NH1	2.44	0.42
50:RE:217:LYS:HD3	50:RE:217:LYS:HA	1.83	0.42
50:RE:501:ASN:HD21	50:RE:506:GLN:HE22	1.66	0.42
50:RE:554:LYS:HA	50:RE:554:LYS:HD2	1.82	0.42
50:RE:745:LYS:HA	50:RE:745:LYS:HD2	1.83	0.42
50:RE:902:ILE:HD13	50:RE:902:ILE:HA	1.90	0.42
52:RG:175:CYS:SG	52:RG:201:SER:OG	2.67	0.42
54:RK:216:LEU:HB3	54:RK:223:VAL:HG21	2.01	0.42
60:RS:255:SER:HB3	60:RS:258:VAL:HG22	2.01	0.42
60:RS:355:ALA:HA	60:RS:358:TYR:CE2	2.55	0.42
60:RS:432:ILE:HG23	60:RS:436:GLN:HB2	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:RT:98:LYS:HG2	63:RT:138:GLU:HB3	2.02	0.42
67:RZ:791:ASN:OD1	67:RZ:791:ASN:N	2.52	0.42
67:RZ:800:TRP:HB3	67:RZ:834:PHE:HE1	1.84	0.42
1:3A:118:A:C5	23:3F:218:ALA:HB2	2.55	0.42
3:SA:274:G:N1	3:SA:283:U:O2'	2.50	0.42
3:SA:565:C:N4	53:RJ:993:ASP:HB3	2.35	0.42
3:SA:647:G:N2	3:SA:687:G:H22	2.17	0.42
3:SA:1656:U:H3	3:SA:1743:U:H3	1.67	0.42
11:SM:70:ILE:HA	11:SM:125:VAL:O	2.20	0.42
14:SR:97:VAL:HG12	14:SR:98:ASP:H	1.83	0.42
20:3C:242:ALA:HB3	20:3C:269:ILE:HA	2.01	0.42
23:3F:303:LYS:HE3	23:3F:319:TYR:HE2	1.85	0.42
23:3F:368:LEU:HB3	23:3F:396:PHE:HE2	1.83	0.42
25:A4:98:SER:OG	25:A4:99:ILE:N	2.53	0.42
25:A4:213:TRP:HA	25:A4:225:LEU:HA	2.02	0.42
26:A5:233:LYS:HD3	26:A5:233:LYS:HA	1.82	0.42
29:AE:91:ILE:HD13	29:AE:91:ILE:HA	1.90	0.42
31:AG:502:LYS:HD2	31:AG:564:PRO:HA	2.02	0.42
32:B1:147:GLN:HB2	32:B1:167:ASP:H	1.85	0.42
32:B1:410:THR:HG22	32:B1:426:THR:HG22	2.01	0.42
34:B3:303:PHE:HA	34:B3:312:GLN:O	2.20	0.42
34:B3:516:LYS:HE2	34:B3:516:LYS:HB2	1.89	0.42
41:5E:533:LYS:HG3	41:5E:536:ARG:HE	1.83	0.42
50:RE:486:GLN:HE22	50:RE:571:ARG:HH22	1.68	0.42
50:RE:1072:VAL:HA	50:RE:1075:LEU:HB2	2.02	0.42
51:RF:26:LEU:HA	51:RF:27:PRO:HD2	1.93	0.42
56:RN:616:LEU:HD13	56:RN:619:LEU:HD22	2.01	0.42
67:RZ:449:GLN:HG3	67:RZ:455:ALA:HA	2.01	0.42
67:RZ:492:MET:HE2	67:RZ:492:MET:HB3	1.75	0.42
67:RZ:729:LEU:HD23	67:RZ:731:VAL:HG22	2.01	0.42
1:3A:49:C:H42	2:5A:467:A:H61	1.67	0.41
3:SA:576:G:C4'	41:5E:327:LYS:HE2	2.48	0.41
3:SA:1049:U:H5''	18:Sc:70:LYS:HG3	2.01	0.41
5:SF:220:THR:OG1	5:SF:221:ARG:N	2.53	0.41
15:SX:7:LEU:HD13	15:SX:34:ILE:HG12	2.02	0.41
20:3C:212:LYS:HA	20:3C:212:LYS:HD3	1.89	0.41
23:3F:260:LEU:HD21	23:3F:283:VAL:HG11	2.02	0.41
25:A4:423:LYS:NZ	38:5B:167:ARG:HH11	2.18	0.41
26:A5:32:GLN:HE22	26:A5:47:ASN:HB3	1.85	0.41
27:A8:662:ILE:HA	27:A8:665:GLN:HB2	2.02	0.41
29:AE:755:ARG:O	29:AE:759:ILE:HG12	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:511:GLU:HG2	31:AG:528:ILE:HB	2.00	0.41
31:AG:659:ILE:HG22	31:AG:674:THR:HB	2.00	0.41
32:B1:274:LEU:HD11	32:B1:286:LEU:HD13	2.02	0.41
33:B2:241:LYS:HB2	33:B2:241:LYS:HE3	1.89	0.41
34:B3:495:ASN:N	34:B3:510:SER:OG	2.45	0.41
34:B3:803:SER:O	34:B3:803:SER:OG	2.31	0.41
36:BE:62:ASP:O	36:BE:66:LEU:N	2.48	0.41
36:BE:724:SER:O	36:BE:728:ARG:NH2	2.39	0.41
41:5E:352:LYS:HE2	56:RN:764:ARG:HE	1.85	0.41
50:RE:209:MET:HE3	50:RE:213:LEU:HD11	2.02	0.41
50:RE:1010:GLU:HG2	50:RE:1011:ARG:HG2	2.01	0.41
55:RL:26:PHE:O	55:RL:149:VAL:HA	2.20	0.41
55:RL:59:TYR:O	55:RL:108:TYR:N	2.53	0.41
56:RN:700:LEU:HD23	56:RN:702:LEU:HG	2.01	0.41
57:RO:153:ILE:HD12	57:RO:153:ILE:HA	1.92	0.41
65:SU:108:LEU:HA	65:SU:111:ILE:HB	2.01	0.41
67:RZ:997:LEU:H	67:RZ:1004:PHE:HE2	1.68	0.41
3:SA:886:U:OP1	4:SC:214:LYS:NZ	2.54	0.41
7:SH:51:LYS:HE2	7:SH:51:LYS:HB3	1.91	0.41
21:3D:206:LEU:HB3	21:3D:216:PHE:HE1	1.84	0.41
23:3F:308:SER:OG	23:3F:313:SER:OG	2.36	0.41
23:3F:476:THR:HG22	23:3F:491:SER:HA	2.02	0.41
25:A4:154:ASP:OD1	25:A4:154:ASP:N	2.49	0.41
29:AE:480:ASN:HA	29:AE:518:THR:HG21	2.02	0.41
29:AE:559:ASN:HB2	29:AE:614:LEU:HD12	2.02	0.41
29:AE:572:ARG:NH2	29:AE:632:THR:O	2.40	0.41
30:AF:105:VAL:HG21	30:AF:142:THR:HG21	2.02	0.41
32:B1:46:LYS:HE2	32:B1:46:LYS:HB3	1.87	0.41
32:B1:605:ASP:OD1	32:B1:605:ASP:N	2.40	0.41
32:B1:721:VAL:O	36:BE:579:ARG:NH2	2.53	0.41
33:B2:405:LEU:HD11	33:B2:673:VAL:HG21	2.02	0.41
34:B3:218:ASP:OD1	34:B3:218:ASP:N	2.52	0.41
34:B3:313:LEU:O	34:B3:330:THR:OG1	2.33	0.41
34:B3:690:HIS:CE1	41:5E:519:GLU:HB2	2.55	0.41
36:BE:21:SER:OG	36:BE:621:ASP:OD2	2.28	0.41
36:BE:361:SER:HA	36:BE:636:PRO:HB2	2.02	0.41
42:5F:7:HIS:C	42:5F:9:GLU:N	2.77	0.41
48:RA:254:ILE:HD12	48:RA:254:ILE:HA	1.84	0.41
50:RE:518:PHE:CE2	50:RE:1075:LEU:HB3	2.48	0.41
52:RG:177:LYS:HE2	52:RG:177:LYS:HB3	1.68	0.41
52:RH:180:LEU:HD23	52:RH:180:LEU:HA	1.87	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:RN:456:ILE:HA	56:RN:456:ILE:HD13	1.79	0.41
58:RP:1752:ASP:HA	58:RP:1755:GLU:HG2	2.02	0.41
67:RZ:621:ALA:HB3	67:RZ:773:VAL:HA	2.02	0.41
67:RZ:1027:LYS:O	67:RZ:1027:LYS:NZ	2.43	0.41
2:5A:490:G:H1'	2:5A:495:G:H5'	2.01	0.41
3:SA:318:U:O2	3:SA:346:G:O6	2.37	0.41
3:SA:575:C:O2	53:RJ:1052:SER:OG	2.28	0.41
7:SH:101:ILE:H	7:SH:101:ILE:HG13	1.72	0.41
9:SJ:36:THR:O	9:SJ:96:LEU:N	2.52	0.41
14:SR:46:PHE:HA	14:SR:49:TYR:HB2	2.02	0.41
23:3F:158:THR:HG23	23:3F:548:ARG:HB2	2.02	0.41
23:3F:321:HIS:CE1	23:3F:340:GLY:H	2.39	0.41
23:3F:421:ASN:ND2	23:3F:437:ARG:HA	2.34	0.41
23:3F:457:GLU:HG3	23:3F:461:LYS:HE2	2.02	0.41
27:A8:443:CYS:CB	31:AG:728:LEU:CD2	2.97	0.41
30:AF:392:ILE:HD11	30:AF:417:VAL:HG23	2.03	0.41
31:AG:625:GLY:HA3	31:AG:662:VAL:HG11	2.02	0.41
32:B1:363:ALA:HB2	32:B1:393:VAL:HG13	2.01	0.41
33:B2:433:ALA:HA	33:B2:449:THR:HA	2.03	0.41
33:B2:555:VAL:HG22	33:B2:569:LEU:HB2	2.02	0.41
39:5C:244:ASN:HB3	39:5C:446:PRO:HG3	2.02	0.41
40:5D:78:LEU:HD12	40:5D:78:LEU:HA	1.82	0.41
45:5I:1:MET:HE3	45:5I:1:MET:HB2	1.83	0.41
50:RE:974:PRO:HB2	50:RE:976:ILE:HG23	2.02	0.41
53:RJ:193:ARG:HA	53:RJ:193:ARG:HD2	1.88	0.41
53:RJ:802:LYS:HB2	53:RJ:802:LYS:HE3	1.92	0.41
53:RJ:906:ASP:OD1	53:RJ:906:ASP:N	2.45	0.41
59:RQ:313:PHE:HE2	59:RQ:883:ILE:HD12	1.84	0.41
60:RS:373:LYS:HA	60:RS:376:LEU:HG	2.02	0.41
67:RZ:1215:PRO:HG2	67:RZ:1231:LEU:HB2	2.02	0.41
2:5A:474:A:OP2	39:5C:425:ARG:NH2	2.37	0.41
2:5A:532:A:O2'	59:RQ:332:ASP:OD2	2.37	0.41
3:SA:88:U:H2'	3:SA:89:G:H8	1.85	0.41
3:SA:110:U:OP1	49:RB:227:ARG:NH1	2.53	0.41
3:SA:1475:A:H4'	3:SA:1540:G:O5'	2.21	0.41
3:SA:1538:U:H5	3:SA:1540:G:O6	1.95	0.41
7:SH:123:GLY:O	7:SH:127:THR:OG1	2.39	0.41
13:SP:85:ALA:HB2	13:SP:94:PRO:N	2.35	0.41
17:SZ:44:LEU:HD12	17:SZ:44:LEU:HA	1.89	0.41
19:Sd:43:ASN:OD1	19:Sd:43:ASN:N	2.53	0.41
20:3B:107:VAL:HG13	20:3B:141:TYR:HB3	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:258:TYR:CD1	31:AG:414:ILE:HD11	2.56	0.41
31:AG:386:ASN:HD21	31:AG:389:LEU:HD11	1.86	0.41
32:B1:275:LEU:HB2	32:B1:289:LEU:HD22	2.02	0.41
32:B1:381:ALA:HA	41:5E:481:PRO:HA	2.01	0.41
33:B2:50:ASN:HB3	33:B2:62:LYS:HG3	2.02	0.41
33:B2:538:ARG:HD3	33:B2:580:ASP:HA	2.02	0.41
34:B3:506:PHE:CE1	34:B3:518:TRP:HB2	2.55	0.41
34:B3:745:ASP:OD2	41:5E:508:ARG:HD2	2.20	0.41
35:B8:296:GLN:HB3	35:B8:316:GLY:HA2	2.03	0.41
41:5E:314:LEU:HA	41:5E:317:GLU:HB2	2.03	0.41
41:5E:350:THR:CG2	53:RJ:975:GLU:HB2	2.51	0.41
42:5F:6:LYS:N	42:5F:9:GLU:HB2	2.36	0.41
45:5I:58:PHE:HE1	45:5I:373:ARG:HB3	1.85	0.41
45:5I:336:HIS:CE1	45:5I:338:HIS:HB2	2.55	0.41
50:RE:1094:LYS:HB3	50:RE:1096:TYR:HD1	1.85	0.41
53:RJ:244:MET:HE2	53:RJ:271:ILE:HG22	2.02	0.41
58:RP:129:ILE:O	58:RP:133:ILE:HG12	2.20	0.41
63:RT:116:ILE:HG23	63:RT:158:PHE:HE2	1.84	0.41
67:RZ:1000:PHE:HA	67:RZ:1140:ILE:HD13	2.02	0.41
3:SA:200:A:H2'	3:SA:201:G:C8	2.56	0.41
5:SF:181:VAL:HG23	5:SF:227:VAL:HG22	2.02	0.41
20:3C:89:GLU:HG2	20:3C:98:ILE:HB	2.03	0.41
23:3F:304:ILE:HB	23:3F:318:LEU:HG	2.03	0.41
25:A4:389:ARG:HG2	25:A4:747:ILE:HG21	2.02	0.41
25:A4:428:ILE:HD12	25:A4:444:ARG:HH21	1.85	0.41
27:A8:553:GLN:O	27:A8:557:THR:OG1	2.31	0.41
28:A9:416:ILE:O	28:A9:420:ILE:CB	2.69	0.41
29:AE:148:PHE:HA	29:AE:151:ILE:HG12	2.01	0.41
29:AE:526:LEU:HA	29:AE:529:VAL:HG12	2.02	0.41
29:AE:664:PRO:HB2	29:AE:716:PHE:HE2	1.85	0.41
30:AF:34:GLN:O	30:AF:328:ALA:HA	2.21	0.41
30:AF:255:VAL:HA	30:AF:276:SER:HA	2.02	0.41
31:AG:97:THR:OG1	31:AG:98:VAL:N	2.54	0.41
32:B1:501:SER:O	32:B1:506:SER:OG	2.38	0.41
37:B6:268:ASP:N	37:B6:268:ASP:OD1	2.53	0.41
42:5F:7:HIS:C	42:5F:9:GLU:H	2.28	0.41
50:RE:978:ASP:HB3	50:RE:1012:LEU:HG	2.02	0.41
52:RG:116:THR:HG22	52:RG:118:ARG:H	1.86	0.41
52:RG:215:ASN:HB2	52:RG:218:ASP:HB2	2.01	0.41
52:RG:232:LEU:HB3	52:RG:236:VAL:HG13	2.02	0.41
53:RJ:1080:LYS:HA	53:RJ:1080:LYS:HD2	1.80	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:RT:127:GLN:NE2	63:RT:142:ASN:OD1	2.54	0.41
65:SU:107:ALA:HA	65:SU:110:LYS:HE3	2.02	0.41
66:RD:1695:TRP:HD1	66:RD:1696:LEU:HD22	1.86	0.41
67:RZ:865:PHE:HB3	67:RZ:867:PHE:CZ	2.55	0.41
67:RZ:928:VAL:HA	67:RZ:931:VAL:HG12	2.02	0.41
1:3A:312:U:O4	1:3A:313:A:N6	2.53	0.41
3:SA:418:G:O2'	7:SH:72:ARG:NH2	2.38	0.41
9:SJ:35:ASN:HD21	48:RA:119:ASN:HD22	1.69	0.41
11:SM:82:ARG:HD3	11:SM:110:HIS:CD2	2.55	0.41
13:SP:111:ARG:HH11	63:RT:95:GLU:HG2	1.86	0.41
20:3C:151:LEU:HD13	20:3C:241:PHE:HE1	1.86	0.41
21:3D:268:MET:HA	21:3D:271:VAL:HG12	2.02	0.41
22:3E:192:PHE:CD2	22:3E:195:LEU:HB2	2.56	0.41
25:A4:135:ARG:HD2	25:A4:135:ARG:HA	1.89	0.41
25:A4:313:LYS:HA	25:A4:316:LYS:HZ3	1.84	0.41
26:A5:64:LYS:HB3	26:A5:77:ILE:HG13	2.02	0.41
29:AE:32:SER:OG	29:AE:33:LEU:N	2.54	0.41
29:AE:35:TYR:O	29:AE:150:ARG:NH1	2.53	0.41
29:AE:109:TRP:HB2	29:AE:142:TYR:CZ	2.56	0.41
29:AE:214:THR:HG23	29:AE:260:ILE:HG13	2.03	0.41
29:AE:328:ASP:N	29:AE:328:ASP:OD1	2.49	0.41
29:AE:420:LYS:HB2	29:AE:420:LYS:HE2	1.92	0.41
32:B1:6:LYS:HD3	32:B1:6:LYS:HA	1.91	0.41
32:B1:298:LEU:HD12	41:5E:474:ILE:CG2	2.51	0.41
32:B1:300:MET:HG2	32:B1:328:LEU:HD22	2.01	0.41
32:B1:347:SER:HB2	32:B1:365:GLU:HB3	2.03	0.41
32:B1:423:ARG:HD3	32:B1:423:ARG:HA	1.88	0.41
32:B1:523:MET:HE2	32:B1:523:MET:HB2	1.76	0.41
32:B1:559:ILE:HG21	32:B1:578:LYS:HA	2.03	0.41
34:B3:195:GLY:HA3	34:B3:245:SER:H	1.85	0.41
34:B3:758:ARG:HA	34:B3:758:ARG:HD2	1.93	0.41
35:B8:278:ASP:H	35:B8:282:ASN:HD22	1.67	0.41
37:B6:311:TYR:O	37:B6:315:GLU:HG2	2.21	0.41
39:5C:357:SER:O	39:5C:357:SER:OG	2.39	0.41
43:5G:73:VAL:HG23	43:5G:208:HIS:HE1	1.85	0.41
48:RA:164:ARG:HB2	48:RA:173:LEU:HB2	2.03	0.41
53:RJ:926:ILE:HG12	53:RJ:928:ILE:HG23	2.01	0.41
56:RN:283:ALA:HA	60:RS:381:ALA:HB1	2.03	0.41
56:RN:766:ARG:NH2	56:RN:769:GLU:OE2	2.54	0.41
56:RN:784:ILE:HA	56:RN:787:THR:HG22	2.03	0.41
63:RT:164:LEU:HD21	63:RT:232:HIS:CG	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
66:RD:1652:ILE:H	66:RD:1652:ILE:HG13	1.77	0.41
67:RZ:536:VAL:HA	67:RZ:553:LEU:HD23	2.03	0.41
3:SA:27:U:H4'	53:RJ:45:ARG:HG3	2.02	0.41
3:SA:1655:A:O2'	33:B2:395:ARG:NH1	2.53	0.41
3:SA:1672:G:H2'	3:SA:1673:G:C8	2.55	0.41
4:SC:82:ARG:HD3	4:SC:105:PHE:HE1	1.86	0.41
20:3B:134:VAL:HA	20:3B:135:PRO:HD3	1.89	0.41
21:3D:157:ALA:HB2	37:B6:292:TYR:CZ	2.56	0.41
25:A4:425:ASP:OD2	25:A4:444:ARG:NH2	2.53	0.41
27:A8:555:ILE:O	27:A8:585:ARG:NE	2.53	0.41
28:A9:475:THR:HA	28:A9:478:ASN:HD22	1.86	0.41
34:B3:264:ASP:HA	34:B3:289:PHE:HB2	2.03	0.41
34:B3:377:LEU:HA	34:B3:378:PRO:HD3	1.85	0.41
34:B3:415:TRP:HA	34:B3:425:ASP:O	2.20	0.41
35:B8:159:HIS:O	35:B8:163:ARG:HG2	2.21	0.41
36:BE:739:VAL:CG2	41:5E:487:ALA:HB2	2.37	0.41
36:BE:870:GLN:HA	36:BE:873:LYS:HE3	2.03	0.41
42:5F:6:LYS:O	42:5F:10:GLN:N	2.52	0.41
43:5G:260:GLU:HG3	43:5G:276:GLN:HB3	2.03	0.41
46:5J:51:LYS:HE2	46:5J:51:LYS:HB2	1.95	0.41
46:5J:117:VAL:HG11	46:5J:149:ILE:HG13	2.02	0.41
52:RG:233:SER:OG	52:RG:234:ALA:N	2.54	0.41
57:RO:226:ASP:OD1	57:RO:284:ARG:NE	2.54	0.41
58:RP:1756:ILE:HG22	58:RP:1760:ASN:HD21	1.85	0.41
67:RZ:385:GLN:O	67:RZ:389:ILE:HG12	2.20	0.41
67:RZ:1234:ILE:HD12	67:RZ:1234:ILE:HA	1.91	0.41
3:SA:1523:G:H1'	3:SA:1524:A:H5'	2.02	0.41
7:SH:70:PRO:O	7:SH:98:ARG:NH2	2.54	0.41
8:SI:60:ILE:HB	8:SI:92:PHE:HD1	1.86	0.41
20:3C:202:ARG:HA	20:3C:202:ARG:HD2	1.96	0.41
23:3F:132:VAL:HG21	23:3F:505:LEU:HD21	2.01	0.41
25:A4:39:VAL:HG12	25:A4:41:PHE:H	1.85	0.41
25:A4:141:SER:O	25:A4:141:SER:OG	2.34	0.41
29:AE:33:LEU:HD11	29:AE:151:ILE:HG22	2.03	0.41
30:AF:115:THR:O	30:AF:115:THR:OG1	2.35	0.41
31:AG:455:SER:O	31:AG:455:SER:OG	2.34	0.41
33:B2:294:ARG:O	33:B2:298:LYS:NZ	2.44	0.41
34:B3:90:LEU:O	34:B3:92:THR:N	2.54	0.41
34:B3:242:GLN:HA	34:B3:263:GLY:HA3	2.02	0.41
34:B3:296:ILE:HD13	34:B3:296:ILE:HA	1.93	0.41
35:B8:231:LYS:HA	35:B8:231:LYS:HD2	1.91	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BE:495:ARG:HD3	36:BE:495:ARG:HA	1.83	0.41
40:5D:150:LYS:HE2	40:5D:150:LYS:HB2	1.92	0.41
41:5E:522:ARG:HA	41:5E:525:LYS:HE3	2.02	0.41
44:5H:542:TYR:CZ	44:5H:546:LYS:HG3	2.56	0.41
47:5K:138:ASP:OD1	47:5K:160:LEU:HD22	2.20	0.41
50:RE:841:ASN:ND2	50:RE:851:LYS:HG2	2.35	0.41
50:RE:975:LEU:HG	50:RE:1041:VAL:HG23	2.01	0.41
50:RE:1216:LYS:CE	50:RE:1236:THR:CG2	2.97	0.41
51:RF:153:ASN:ND2	51:RF:154:GLU:HG2	2.36	0.41
52:RG:34:LYS:HD3	52:RG:34:LYS:HA	1.84	0.41
52:RG:40:ARG:O	52:RG:201:SER:HA	2.20	0.41
54:RK:32:LYS:HG2	54:RK:75:ILE:HG13	2.02	0.41
56:RN:611:SER:OG	56:RN:612:THR:N	2.52	0.41
56:RN:644:ASP:OD1	56:RN:687:LYS:NZ	2.51	0.41
58:RP:879:PRO:O	58:RP:882:ASN:C	2.64	0.41
60:RS:288:ARG:O	60:RS:292:GLU:HG2	2.21	0.41
3:SA:413:U:H2'	3:SA:414:C:C6	2.56	0.41
9:SJ:58:LEU:HD21	48:RA:77:TYR:HB2	2.02	0.41
9:SJ:74:LYS:HD3	9:SJ:74:LYS:HA	1.68	0.41
11:SM:115:PHE:HB2	11:SM:142:VAL:HG11	2.02	0.41
15:SX:102:VAL:O	15:SX:113:HIS:N	2.54	0.41
15:SX:110:ILE:HD12	15:SX:126:LEU:HD22	2.02	0.41
22:3E:359:ILE:HD13	22:3E:398:LEU:HD13	2.03	0.41
23:3F:465:GLN:HG2	24:3H:6:PRO:HG3	2.02	0.41
25:A4:581:SER:HA	25:A4:594:PHE:O	2.21	0.41
26:A5:551:ILE:HA	26:A5:554:PHE:CE2	2.56	0.41
27:A8:342:LEU:HA	27:A8:357:HIS:HA	2.02	0.41
29:AE:227:ASN:OD1	29:AE:227:ASN:N	2.53	0.41
29:AE:597:HIS:HB3	29:AE:615:ASN:HB3	2.03	0.41
31:AG:591:GLU:O	31:AG:593:ASN:N	2.54	0.41
31:AG:712:THR:HG22	31:AG:766:ILE:HG23	2.01	0.41
33:B2:17:ILE:CG2	33:B2:52:TRP:CH2	3.01	0.41
33:B2:164:ASP:HB3	33:B2:182:LYS:HB3	2.02	0.41
33:B2:911:GLN:HA	33:B2:914:LEU:HG	2.03	0.41
34:B3:51:LYS:H	34:B3:51:LYS:HG2	1.66	0.41
34:B3:678:TRP:CE3	34:B3:697:VAL:HG23	2.56	0.41
35:B8:278:ASP:H	35:B8:282:ASN:ND2	2.18	0.41
36:BE:205:PHE:HA	36:BE:206:PRO:HD3	1.91	0.41
39:5C:307:LYS:HA	39:5C:307:LYS:HD3	1.89	0.41
40:5D:70:ARG:HD3	40:5D:78:LEU:HD11	2.02	0.41
41:5E:341:LEU:HD13	64:ST:120:ARG:HH12	1.75	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5E:341:LEU:CG	64:ST:116:LEU:HD22	2.51	0.41
41:5E:533:LYS:O	41:5E:537:SER:HB2	2.21	0.41
48:RA:94:ASP:OD1	48:RA:94:ASP:N	2.54	0.41
50:RE:110:LEU:HD21	50:RE:368:LEU:HD23	2.03	0.41
50:RE:144:LYS:HA	50:RE:144:LYS:HD3	1.87	0.41
50:RE:177:ASN:HB2	50:RE:213:LEU:HB2	2.03	0.41
50:RE:202:SER:OG	50:RE:203:ILE:N	2.54	0.41
51:RF:62:SER:HA	51:RF:66:HIS:NE2	2.36	0.41
51:RF:69:LYS:HZ1	51:RF:158:TRP:HA	1.86	0.41
53:RJ:60:ASP:OD2	53:RJ:62:THR:OG1	2.32	0.41
53:RJ:74:VAL:HG11	53:RJ:82:LYS:HA	2.03	0.41
54:RK:117:LEU:HA	54:RK:166:VAL:O	2.21	0.41
54:RK:184:ASP:OD1	54:RK:185:ARG:N	2.53	0.41
55:RM:743:VAL:O	55:RM:745:VAL:N	2.47	0.41
56:RN:668:LEU:HD23	56:RN:671:TYR:HD2	1.86	0.41
56:RN:710:ILE:HD13	56:RN:710:ILE:HA	1.91	0.41
57:RO:326:LEU:HD12	57:RO:326:LEU:HA	1.90	0.41
58:RP:957:LYS:O	58:RP:961:ILE:N	2.44	0.41
58:RP:2073:GLU:HA	58:RP:2076:ARG:HG2	2.03	0.41
60:RS:238:SER:O	60:RS:238:SER:OG	2.33	0.41
60:RS:407:GLU:HB2	60:RS:411:ARG:HD2	2.03	0.41
67:RZ:391:LEU:HA	67:RZ:392:PRO:HD3	1.89	0.41
67:RZ:986:LYS:HA	67:RZ:989:LYS:HD2	2.02	0.41
1:3A:253:G:OP2	24:3H:95:ARG:NH1	2.54	0.41
2:5A:18:G:H2'	2:5A:19:A:H8	1.85	0.41
3:SA:304:U:H5''	11:SM:136:ARG:HH21	1.86	0.41
7:SH:38:GLY:N	7:SH:48:TYR:O	2.54	0.41
13:SP:29:HIS:CD2	13:SP:41:ARG:HB2	2.56	0.41
13:SP:125:SER:HB2	13:SP:126:THR:H	1.73	0.41
20:3B:104:ASP:OD1	20:3B:104:ASP:N	2.38	0.41
20:3C:322:ARG:HA	20:3C:322:ARG:HD2	1.80	0.41
22:3E:201:ASP:HB3	22:3E:204:ALA:HB3	2.03	0.41
22:3E:283:ILE:HD13	22:3E:283:ILE:HA	1.88	0.41
22:3E:299:LEU:HD22	22:3E:320:LEU:HD23	2.03	0.41
23:3F:488:ILE:HG22	23:3F:524:ILE:HD13	2.02	0.41
24:3G:85:VAL:O	24:3G:89:ARG:HG2	2.21	0.41
25:A4:394:TRP:HB3	25:A4:399:VAL:HG12	2.03	0.41
30:AF:426:LYS:HB3	30:AF:429:VAL:HB	2.03	0.41
31:AG:334:LEU:HA	31:AG:335:PRO:HD3	1.85	0.41
31:AG:439:ASN:ND2	31:AG:496:THR:O	2.54	0.41
34:B3:25:VAL:HG22	34:B3:294:LEU:HD13	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B8:137:ILE:HD13	35:B8:137:ILE:HA	1.86	0.41
37:B6:26:LYS:HA	37:B6:29:VAL:HG12	2.02	0.41
39:5C:340:LEU:HD22	39:5C:403:VAL:HG11	2.03	0.41
50:RE:676:PRO:HB2	50:RE:678:ILE:HG22	2.03	0.41
50:RE:1204:VAL:O	50:RE:1204:VAL:HG23	2.21	0.41
51:RF:9:MET:HE1	51:RF:15:VAL:HG23	2.02	0.41
51:RF:47:SER:OG	51:RF:48:ASN:N	2.54	0.41
56:RN:424:LYS:O	56:RN:428:VAL:HG23	2.20	0.41
56:RN:504:ILE:HA	56:RN:507:LEU:HG	2.03	0.41
58:RP:1923:ARG:HD3	58:RP:1923:ARG:HA	1.71	0.41
3:SA:16:G:H4'	47:5K:159:GLY:HA2	2.03	0.40
3:SA:124:A:O2'	5:SF:148:ARG:NH2	2.33	0.40
5:SF:141:THR:OG1	5:SF:142:HIS:N	2.52	0.40
7:SH:185:GLN:O	7:SH:189:HIS:ND1	2.44	0.40
20:3C:259:MET:HE3	20:3C:259:MET:HB2	1.85	0.40
21:3D:7:LEU:HD12	21:3D:99:ALA:HB3	2.02	0.40
25:A4:52:SER:HA	25:A4:104:TRP:CG	2.56	0.40
28:A9:460:LEU:HD23	28:A9:460:LEU:HA	1.96	0.40
31:AG:409:LYS:HG2	31:AG:489:ASN:HA	2.03	0.40
31:AG:514:TYR:HA	31:AG:515:PRO:HD3	1.93	0.40
32:B1:519:LEU:HD13	32:B1:581:THR:HG22	2.03	0.40
36:BE:523:ASP:OD1	36:BE:523:ASP:N	2.38	0.40
37:B6:306:LYS:HE3	37:B6:306:LYS:HB2	1.77	0.40
40:5D:61:ASP:O	42:5F:160:TRP:HH2	2.03	0.40
41:5E:362:THR:HA	41:5E:365:LEU:HD23	2.03	0.40
42:5F:102:THR:HG22	42:5F:104:SER:H	1.87	0.40
50:RE:310:PRO:HA	50:RE:333:ASN:HD21	1.87	0.40
50:RE:566:ILE:HD11	50:RE:686:LEU:HD21	2.03	0.40
53:RJ:43:MET:N	53:RJ:43:MET:SD	2.94	0.40
53:RJ:552:LEU:HD23	53:RJ:552:LEU:HA	1.92	0.40
58:RP:149:GLU:HA	58:RP:152:PHE:CD2	2.56	0.40
66:RD:1622:ARG:NH1	66:RD:1626:GLN:HE21	2.19	0.40
67:RZ:494:ASP:O	67:RZ:498:LEU:HG	2.21	0.40
67:RZ:867:PHE:HD2	67:RZ:870:PRO:HA	1.86	0.40
67:RZ:993:GLN:HB3	67:RZ:994:PHE:H	1.74	0.40
3:SA:153:G:O6	3:SA:161:U:O4	2.39	0.40
3:SA:625:C:H2'	3:SA:626:U:C6	2.57	0.40
11:SM:69:LYS:HD2	11:SM:69:LYS:HA	1.89	0.40
22:3E:367:ALA:O	22:3E:371:LEU:HB3	2.22	0.40
24:3G:41:THR:HG21	24:3G:66:HIS:CE1	2.55	0.40
24:3H:33:LEU:HD11	24:3H:100:ALA:HB1	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AE:69:PHE:HE2	29:AE:104:LEU:HD13	1.85	0.40
30:AF:136:ASP:OD1	30:AF:137:ASN:N	2.54	0.40
30:AF:397:TRP:CZ3	30:AF:425:GLY:HA3	2.56	0.40
30:AF:420:GLU:OE1	30:AF:424:ARG:NH1	2.37	0.40
31:AG:29:THR:HB	31:AG:198:LEU:HD11	2.03	0.40
31:AG:560:ILE:HG22	31:AG:575:THR:HG22	2.03	0.40
33:B2:850:LEU:HD23	33:B2:850:LEU:HA	1.90	0.40
41:5E:384:ARG:HD2	43:5G:83:ILE:CG1	2.51	0.40
41:5E:445:VAL:HG13	42:5F:81:LYS:HE2	2.03	0.40
48:RA:18:GLY:H	48:RA:21:VAL:HB	1.86	0.40
50:RE:356:THR:HG23	50:RE:359:PHE:HB2	2.02	0.40
50:RE:1173:GLY:CA	50:RE:1179:LYS:HB2	2.52	0.40
52:RH:177:LYS:HG2	52:RH:203:CYS:HB3	2.03	0.40
53:RJ:563:CYS:SG	54:RK:327:ARG:NH2	2.95	0.40
58:RP:100:GLU:OE2	58:RP:146:ASN:ND2	2.54	0.40
60:RS:245:VAL:O	60:RS:249:THR:HG23	2.22	0.40
63:RT:124:LEU:HD22	63:RT:175:LEU:HD11	2.02	0.40
64:ST:68:ARG:O	64:ST:72:ILE:HG12	2.21	0.40
67:RZ:466:LEU:HB3	67:RZ:469:HIS:HB2	2.03	0.40
67:RZ:915:LEU:HD13	67:RZ:1049:ILE:HG21	2.03	0.40
3:SA:153:G:H2'	3:SA:154:G:C8	2.54	0.40
3:SA:844:A:H2'	3:SA:845:G:C8	2.57	0.40
3:SA:1773:C:H2'	3:SA:1774:G:C8	2.56	0.40
21:3D:69:ILE:HD13	21:3D:69:ILE:HA	1.95	0.40
22:3E:88:ILE:HA	22:3E:106:ASN:O	2.22	0.40
22:3E:169:LEU:HD23	22:3E:169:LEU:HA	1.92	0.40
23:3F:419:ASN:OD1	23:3F:419:ASN:N	2.43	0.40
25:A4:202:ILE:HD13	25:A4:253:ILE:HG12	2.03	0.40
25:A4:250:THR:OG1	25:A4:251:ASP:N	2.53	0.40
26:A5:201:PHE:CZ	26:A5:223:LYS:HD2	2.56	0.40
26:A5:444:ALA:HB2	26:A5:452:LEU:HD12	2.03	0.40
29:AE:107:SER:OG	29:AE:108:LYS:NZ	2.52	0.40
30:AF:57:VAL:HG21	30:AF:327:LEU:HD11	2.04	0.40
30:AF:178:PRO:HD2	30:AF:223:PRO:HA	2.02	0.40
32:B1:64:ASN:OD1	32:B1:64:ASN:N	2.49	0.40
32:B1:263:VAL:HG13	32:B1:277:VAL:HG13	2.03	0.40
32:B1:419:TYR:HB2	41:5E:482:LEU:CD1	2.50	0.40
33:B2:393:ASP:OD2	33:B2:395:ARG:NH1	2.41	0.40
34:B3:745:ASP:OD2	41:5E:508:ARG:CD	2.70	0.40
36:BE:290:ILE:HG23	36:BE:291:HIS:CD2	2.56	0.40
36:BE:927:LYS:HD3	36:BE:927:LYS:HA	1.92	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5C:114:TYR:HA	39:5C:128:THR:O	2.22	0.40
39:5C:201:TYR:OH	39:5C:415:GLU:OE1	2.29	0.40
41:5E:448:LEU:HD11	42:5F:81:LYS:HE3	2.03	0.40
45:5I:467:LYS:H	45:5I:467:LYS:HG2	1.69	0.40
46:5J:195:GLN:O	46:5J:199:THR:HG22	2.22	0.40
50:RE:970:TRP:HB2	50:RE:971:LYS:HD3	2.02	0.40
51:RF:71:VAL:HG11	51:RF:84:VAL:HG21	2.02	0.40
52:RG:123:GLU:HB2	52:RG:161:LYS:HB2	2.03	0.40
57:RO:439:LYS:HE2	57:RO:439:LYS:HB3	1.83	0.40
58:RP:98:HIS:HD1	58:RP:142:PHE:HE2	1.68	0.40
67:RZ:782:SER:HB3	67:RZ:809:ARG:HH22	1.85	0.40
3:SA:298:C:H5'	5:SF:38:LEU:HG	2.02	0.40
3:SA:1470:C:C4	3:SA:1573:A:C2	3.09	0.40
4:SC:31:ASP:HA	4:SC:45:LYS:HA	2.03	0.40
9:SJ:191:PHE:HA	9:SJ:194:ARG:HE	1.85	0.40
13:SP:61:MET:HE2	13:SP:61:MET:HB3	1.97	0.40
20:3C:165:ALA:HB3	20:3C:168:LYS:HD3	2.04	0.40
25:A4:171:SER:O	25:A4:171:SER:OG	2.32	0.40
29:AE:401:VAL:O	29:AE:405:GLU:HG2	2.22	0.40
32:B1:382:THR:H	41:5E:481:PRO:HB3	1.87	0.40
33:B2:85:LEU:HD12	33:B2:94:LEU:HD11	2.04	0.40
33:B2:639:VAL:HG22	33:B2:653:LEU:HB2	2.03	0.40
34:B3:189:HIS:NE2	34:B3:215:GLY:HA3	2.37	0.40
34:B3:410:ASN:OD1	34:B3:435:ALA:N	2.52	0.40
35:B8:431:GLU:H	35:B8:431:GLU:HG2	1.71	0.40
37:B6:110:TRP:CD2	37:B6:136:LEU:HD13	2.56	0.40
41:5E:432:LYS:HA	41:5E:432:LYS:HD2	1.88	0.40
45:5I:231:GLU:HG2	59:RQ:298:TRP:HE1	1.86	0.40
45:5I:450:ASP:OD1	45:5I:450:ASP:N	2.55	0.40
46:5J:119:ARG:HD3	53:RJ:1113:ILE:HG13	2.02	0.40
48:RA:343:ILE:HG22	48:RA:346:LEU:H	1.87	0.40
52:RG:85:SER:OG	52:RG:86:GLU:OE1	2.39	0.40
53:RJ:65:ASP:OD1	53:RJ:65:ASP:N	2.46	0.40
53:RJ:286:THR:H	53:RJ:298:VAL:HG12	1.86	0.40
55:RL:60:LYS:HB3	55:RL:108:TYR:CD2	2.56	0.40
58:RP:2009:LYS:HD3	58:RP:2009:LYS:HA	1.88	0.40
60:RS:258:VAL:O	60:RS:262:ALA:CB	2.69	0.40
67:RZ:1111:SER:OG	67:RZ:1114:ASN:OD1	2.39	0.40
67:RZ:1159:LEU:HA	67:RZ:1165:THR:HA	2.03	0.40
3:SA:268:C:H2'	3:SA:269:G:C8	2.56	0.40
3:SA:1071:U:H2'	3:SA:1072:C:C6	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1480:G:H2'	3:SA:1481:C:O4'	2.22	0.40
4:SC:73:LEU:HA	4:SC:73:LEU:HD23	1.83	0.40
5:SF:106:LYS:HB3	5:SF:106:LYS:HE3	1.89	0.40
13:SP:107:ARG:HB2	13:SP:107:ARG:CZ	2.51	0.40
20:3B:227:PRO:HG2	20:3B:255:LEU:HB3	2.02	0.40
21:3D:86:LEU:HD21	21:3D:98:LEU:HD13	2.03	0.40
22:3E:162:MET:HE2	22:3E:162:MET:HB3	1.86	0.40
22:3E:215:ARG:NH1	22:3E:244:GLY:O	2.54	0.40
23:3F:263:TRP:HA	23:3F:269:SER:O	2.22	0.40
25:A4:397:SER:O	25:A4:397:SER:OG	2.34	0.40
26:A5:35:GLN:OE1	26:A5:36:ARG:N	2.55	0.40
26:A5:98:LYS:HE3	26:A5:98:LYS:HB2	1.88	0.40
27:A8:441:VAL:HA	31:AG:728:LEU:HD21	2.03	0.40
29:AE:585:ILE:HD12	29:AE:585:ILE:HA	1.86	0.40
30:AF:183:LEU:HD12	30:AF:183:LEU:HA	1.85	0.40
32:B1:14:VAL:CG2	32:B1:341:GLN:O	2.62	0.40
32:B1:302:GLN:CD	32:B1:302:GLN:N	2.79	0.40
34:B3:567:VAL:HG22	34:B3:568:MET:HG2	2.02	0.40
34:B3:690:HIS:CE1	41:5E:519:GLU:HA	2.57	0.40
36:BE:83:LEU:HA	36:BE:91:TYR:O	2.21	0.40
36:BE:743:ARG:NH2	41:5E:481:PRO:O	2.46	0.40
39:5C:102:LYS:HB3	39:5C:389:LEU:HD11	2.04	0.40
46:5J:106:LEU:HD23	46:5J:106:LEU:HA	1.95	0.40
47:5K:21:LYS:HD3	47:5K:21:LYS:HA	1.87	0.40
51:RF:160:TYR:CZ	51:RF:162:THR:HG23	2.57	0.40
53:RJ:1042:MET:HE2	53:RJ:1042:MET:HB3	1.87	0.40
54:RK:113:LYS:HG2	54:RK:173:LEU:HD11	2.03	0.40
56:RN:14:LYS:HA	56:RN:14:LYS:HD2	1.84	0.40
57:RO:205:ASP:HA	57:RO:206:PRO:HD3	1.89	0.40
57:RO:295:LEU:O	57:RO:299:LEU:HG	2.22	0.40
66:RD:1457:ALA:HA	66:RD:1458:PRO:HD3	1.95	0.40
66:RD:1617:HIS:HA	66:RD:1620:VAL:HG22	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100	100
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	30	67
6	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
7	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
8	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
9	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/155 (77%)	103 (87%)	16 (13%)	0	100	100
12	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
13	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	14	51
14	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
15	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
16	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
17	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	12	49
18	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100
19	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
20	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
20	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
21	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
22	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
23	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	43	78
24	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	16	54
24	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
25	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
26	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
27	A8	516/713 (72%)	397 (77%)	107 (21%)	12 (2%)	5	28
28	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
29	AE	1496/1769 (85%)	1367 (91%)	129 (9%)	0	100	100
30	AF	489/513 (95%)	443 (91%)	46 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	AG	812/896 (91%)	732 (90%)	79 (10%)	1 (0%)	48	83
32	B1	787/900 (87%)	732 (93%)	55 (7%)	0	100	100
33	B2	813/943 (86%)	723 (89%)	88 (11%)	2 (0%)	43	78
34	B3	733/817 (90%)	605 (82%)	126 (17%)	2 (0%)	36	72
35	B8	469/594 (79%)	440 (94%)	29 (6%)	0	100	100
36	BE	814/939 (87%)	764 (94%)	50 (6%)	0	100	100
37	B6	368/440 (84%)	342 (93%)	26 (7%)	0	100	100
38	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
39	5C	452/554 (82%)	419 (93%)	32 (7%)	1 (0%)	43	78
40	5D	165/250 (66%)	146 (88%)	19 (12%)	0	100	100
41	5E	187/593 (32%)	175 (94%)	10 (5%)	2 (1%)	11	46
42	5F	180/183 (98%)	164 (91%)	16 (9%)	0	100	100
43	5G	217/290 (75%)	203 (94%)	14 (6%)	0	100	100
44	5H	72/610 (12%)	65 (90%)	7 (10%)	0	100	100
45	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
46	5J	130/217 (60%)	121 (93%)	9 (7%)	0	100	100
47	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
48	RA	332/707 (47%)	276 (83%)	56 (17%)	0	100	100
49	RB	132/357 (37%)	117 (89%)	14 (11%)	1 (1%)	16	54
50	RE	1067/1237 (86%)	998 (94%)	69 (6%)	0	100	100
51	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
52	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
52	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
53	RJ	784/1183 (66%)	722 (92%)	61 (8%)	1 (0%)	48	83
54	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
55	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	36	72
55	RM	738/1056 (70%)	626 (85%)	108 (15%)	4 (0%)	24	63
56	RN	593/810 (73%)	546 (92%)	46 (8%)	1 (0%)	43	78
57	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
58	RP	2042/2493 (82%)	1816 (89%)	226 (11%)	0	100	100
59	RQ	267/899 (30%)	227 (85%)	40 (15%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	RS	247/480 (52%)	225 (91%)	22 (9%)	0	100	100
61	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
63	RT	206/326 (63%)	178 (86%)	27 (13%)	1 (0%)	24	63
64	ST	106/146 (73%)	89 (84%)	17 (16%)	0	100	100
65	SU	141/144 (98%)	124 (88%)	16 (11%)	1 (1%)	18	56
66	RD	310/1729 (18%)	284 (92%)	23 (7%)	3 (1%)	12	49
67	RZ	834/1267 (66%)	739 (89%)	91 (11%)	4 (0%)	24	63
All	All	25032/35454 (71%)	22530 (90%)	2459 (10%)	43 (0%)	44	78

All (43) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	A8	258	PRO
27	A8	309	PRO
27	A8	325	PRO
27	A8	390	PRO
27	A8	392	PRO
27	A8	446	VAL
27	A8	472	ILE
55	RL	744	PRO
55	RM	744	PRO
55	RM	905	PRO
66	RD	1223	PRO
67	RZ	583	VAL
67	RZ	676	ILE
67	RZ	682	VAL
17	SZ	51	GLU
53	RJ	82	LYS
67	RZ	1058	ILE
27	A8	235	PRO
31	AG	434	GLN
33	B2	132	THR
34	B3	91	LYS
55	RM	904	LEU
56	RN	285	PRO
65	SU	44	GLU
23	3F	552	TRP
27	A8	369	ILE
41	5E	476	MET
33	B2	118	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
41	5E	481	PRO
49	RB	274	ILE
55	RL	743	VAL
55	RM	743	VAL
66	RD	1204	VAL
66	RD	1222	LYS
5	SF	194	THR
13	SP	123	SER
27	A8	439	LYS
34	B3	71	PRO
39	5C	16	GLU
63	RT	71	VAL
24	3G	10	PRO
27	A8	306	ILE
27	A8	339	ILE

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	
4	SC	203/224 (91%)	201 (99%)	2 (1%)	68	78
5	SF	196/222 (88%)	193 (98%)	3 (2%)	57	72
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	83
7	SH	139/201 (69%)	136 (98%)	3 (2%)	45	64
8	SI	146/170 (86%)	143 (98%)	3 (2%)	47	65
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	57	72
10	SK	147/166 (89%)	147 (100%)	0	100	100
11	SM	110/136 (81%)	108 (98%)	2 (2%)	51	68
12	SO	117/128 (91%)	116 (99%)	1 (1%)	70	79
13	SP	90/105 (86%)	88 (98%)	2 (2%)	45	64
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	106 (98%)	2 (2%)	50	67

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	SY	85/120 (71%)	83 (98%)	2 (2%)	43	64
17	SZ	85/113 (75%)	85 (100%)	0	100	100
18	Sc	69/71 (97%)	69 (100%)	0	100	100
19	Sd	56/60 (93%)	56 (100%)	0	100	100
20	3B	201/240 (84%)	201 (100%)	0	100	100
20	3C	190/240 (79%)	188 (99%)	2 (1%)	65	76
21	3D	296/435 (68%)	295 (100%)	1 (0%)	86	86
22	3E	262/433 (60%)	261 (100%)	1 (0%)	84	84
23	3F	396/503 (79%)	392 (99%)	4 (1%)	68	78
24	3G	100/104 (96%)	100 (100%)	0	100	100
24	3H	100/104 (96%)	100 (100%)	0	100	100
25	A4	591/713 (83%)	584 (99%)	7 (1%)	63	75
26	A5	433/574 (75%)	429 (99%)	4 (1%)	70	79
27	A8	174/657 (26%)	168 (97%)	6 (3%)	32	54
28	A9	89/533 (17%)	89 (100%)	0	100	100
29	AE	708/1633 (43%)	705 (100%)	3 (0%)	84	84
30	AF	437/454 (96%)	431 (99%)	6 (1%)	59	72
31	AG	750/826 (91%)	739 (98%)	11 (2%)	57	72
32	B1	696/789 (88%)	685 (98%)	11 (2%)	55	70
33	B2	712/832 (86%)	705 (99%)	7 (1%)	68	78
34	B3	665/719 (92%)	656 (99%)	9 (1%)	59	72
35	B8	421/529 (80%)	417 (99%)	4 (1%)	68	78
36	BE	718/819 (88%)	712 (99%)	6 (1%)	73	80
37	B6	251/414 (61%)	249 (99%)	2 (1%)	73	80
38	5B	57/196 (29%)	56 (98%)	1 (2%)	51	68
39	5C	394/480 (82%)	392 (100%)	2 (0%)	81	83
40	5D	156/234 (67%)	156 (100%)	0	100	100
41	5E	175/535 (33%)	162 (93%)	13 (7%)	13	33
42	5F	171/172 (99%)	169 (99%)	2 (1%)	63	75
43	5G	194/258 (75%)	194 (100%)	0	100	100
44	5H	63/538 (12%)	63 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	5I	416/443 (94%)	412 (99%)	4 (1%)	68	78
46	5J	125/200 (62%)	125 (100%)	0	100	100
47	5K	157/169 (93%)	157 (100%)	0	100	100
48	RA	303/636 (48%)	299 (99%)	4 (1%)	61	74
49	RB	117/315 (37%)	116 (99%)	1 (1%)	70	79
50	RE	984/1125 (88%)	976 (99%)	8 (1%)	73	80
51	RF	221/274 (81%)	221 (100%)	0	100	100
52	RG	195/222 (88%)	193 (99%)	2 (1%)	68	78
52	RH	206/222 (93%)	205 (100%)	1 (0%)	81	83
53	RJ	683/1039 (66%)	678 (99%)	5 (1%)	76	81
54	RK	307/312 (98%)	304 (99%)	3 (1%)	68	78
55	RL	164/934 (18%)	164 (100%)	0	100	100
56	RN	422/732 (58%)	421 (100%)	1 (0%)	87	87
57	RO	329/506 (65%)	326 (99%)	3 (1%)	70	79
58	RP	499/2307 (22%)	496 (99%)	3 (1%)	78	83
59	RQ	136/808 (17%)	133 (98%)	3 (2%)	45	64
60	RS	225/421 (53%)	224 (100%)	1 (0%)	84	84
61	RY	31/482 (6%)	31 (100%)	0	100	100
63	RT	158/282 (56%)	155 (98%)	3 (2%)	50	67
64	ST	98/129 (76%)	96 (98%)	2 (2%)	48	66
65	SU	115/116 (99%)	113 (98%)	2 (2%)	53	69
66	RD	226/1544 (15%)	224 (99%)	2 (1%)	70	79
67	RZ	718/1140 (63%)	715 (100%)	3 (0%)	84	84
All	All	18207/30620 (60%)	18031 (99%)	176 (1%)	65	78

All (176) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	SC	43	VAL
4	SC	172	LEU
5	SF	143	ASP
5	SF	183	VAL
5	SF	206	ASP
6	SG	149	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	SH	67	VAL
7	SH	71	THR
7	SH	113	ILE
8	SI	73	VAL
8	SI	140	VAL
8	SI	189	THR
9	SJ	104	ILE
9	SJ	165	LEU
11	SM	107	VAL
11	SM	135	VAL
12	SO	60	VAL
13	SP	42	VAL
13	SP	107	ARG
15	SX	11	LEU
15	SX	70	ASN
16	SY	97	ASP
16	SY	120	VAL
20	3C	197	VAL
20	3C	237	VAL
21	3D	219	LEU
22	3E	371	LEU
23	3F	262	VAL
23	3F	273	VAL
23	3F	301	ASP
23	3F	408	VAL
25	A4	176	VAL
25	A4	190	VAL
25	A4	201	VAL
25	A4	282	ASP
25	A4	384	VAL
25	A4	391	VAL
25	A4	550	VAL
26	A5	95	VAL
26	A5	214	VAL
26	A5	357	VAL
26	A5	434	THR
27	A8	526	LEU
27	A8	563	LEU
27	A8	633	GLN
27	A8	634	LEU
27	A8	636	GLN
27	A8	637	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
29	AE	210	LEU
29	AE	227	ASN
29	AE	734	ILE
30	AF	107	VAL
30	AF	129	VAL
30	AF	218	VAL
30	AF	236	VAL
30	AF	261	VAL
30	AF	508	LEU
31	AG	109	VAL
31	AG	141	LEU
31	AG	259	VAL
31	AG	368	ASP
31	AG	391	VAL
31	AG	434	GLN
31	AG	435	ASP
31	AG	436	PHE
31	AG	508	ILE
31	AG	547	VAL
31	AG	650	VAL
32	B1	89	VAL
32	B1	141	VAL
32	B1	164	THR
32	B1	215	VAL
32	B1	337	TYR
32	B1	351	LEU
32	B1	418	ARG
32	B1	497	ILE
32	B1	519	LEU
32	B1	530	VAL
32	B1	745	LEU
33	B2	47	GLU
33	B2	49	VAL
33	B2	144	ASN
33	B2	212	VAL
33	B2	332	ILE
33	B2	576	VAL
33	B2	588	ILE
34	B3	10	ILE
34	B3	32	LEU
34	B3	67	LEU
34	B3	95	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
34	B3	147	ILE
34	B3	212	LEU
34	B3	239	VAL
34	B3	570	THR
34	B3	731	LEU
35	B8	22	LEU
35	B8	146	LEU
35	B8	178	VAL
35	B8	544	VAL
36	BE	298	VAL
36	BE	309	ILE
36	BE	570	ILE
36	BE	600	ILE
36	BE	721	LEU
36	BE	740	ILE
37	B6	4	THR
37	B6	106	ASP
38	5B	211	LEU
39	5C	153	THR
39	5C	392	VAL
41	5E	345	LEU
41	5E	365	LEU
41	5E	428	GLU
41	5E	439	GLU
41	5E	448	LEU
41	5E	451	LEU
41	5E	494	GLU
41	5E	515	MET
41	5E	516	SER
41	5E	517	LYS
41	5E	520	LEU
41	5E	537	SER
41	5E	538	LYS
42	5F	75	GLU
42	5F	124	ILE
45	5I	14	VAL
45	5I	113	VAL
45	5I	201	ILE
45	5I	351	VAL
48	RA	76	THR
48	RA	155	VAL
48	RA	231	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	RA	264	ILE
49	RB	338	THR
50	RE	102	ILE
50	RE	292	ILE
50	RE	560	ASN
50	RE	742	PHE
50	RE	753	ILE
50	RE	929	ILE
50	RE	1075	LEU
50	RE	1189	LEU
52	RG	32	THR
52	RG	100	LEU
52	RH	31	LEU
53	RJ	288	VAL
53	RJ	859	ILE
53	RJ	869	THR
53	RJ	976	ILE
53	RJ	1069	VAL
54	RK	26	LEU
54	RK	90	CYS
54	RK	335	THR
56	RN	766	ARG
57	RO	471	GLU
57	RO	493	TYR
57	RO	504	ASP
58	RP	131	THR
58	RP	1770	LEU
58	RP	1896	ILE
59	RQ	330	THR
59	RQ	898	PHE
59	RQ	899	LYS
60	RS	326	VAL
63	RT	168	LEU
63	RT	170	ASP
63	RT	234	LEU
64	ST	52	VAL
64	ST	55	HIS
65	SU	108	LEU
65	SU	124	ILE
66	RD	1521	LEU
66	RD	1670	LYS
67	RZ	564	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
67	RZ	584	ASP
67	RZ	590	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (431) such sidechains are listed below:

Mol	Chain	Res	Type
4	SC	74	GLN
4	SC	92	GLN
4	SC	101	HIS
4	SC	194	ASN
6	SG	63	GLN
6	SG	66	GLN
6	SG	169	ASN
7	SH	119	GLN
7	SH	140	ASN
8	SI	29	ASN
8	SI	42	GLN
8	SI	74	GLN
8	SI	122	HIS
8	SI	170	GLN
8	SI	174	ASN
8	SI	180	GLN
9	SJ	32	GLN
9	SJ	103	GLN
9	SJ	159	GLN
10	SK	48	GLN
10	SK	142	ASN
11	SM	8	GLN
11	SM	81	HIS
11	SM	98	ASN
11	SM	106	ASN
12	SO	36	GLN
12	SO	58	HIS
13	SP	12	GLN
13	SP	24	ASN
14	SR	74	HIS
15	SX	12	ASN
15	SX	16	ASN
15	SX	120	HIS
16	SY	48	HIS
18	Sc	5	GLN
18	Sc	19	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
18	Sc	42	ASN
20	3B	91	HIS
20	3B	228	GLN
20	3C	264	GLN
21	3D	39	ASN
21	3D	85	ASN
21	3D	168	GLN
21	3D	172	ASN
21	3D	183	GLN
21	3D	213	ASN
21	3D	324	ASN
21	3D	398	ASN
22	3E	191	HIS
22	3E	256	ASN
22	3E	261	GLN
22	3E	286	ASN
22	3E	289	GLN
22	3E	396	ASN
22	3E	400	GLN
23	3F	129	GLN
23	3F	155	ASN
23	3F	156	ASN
23	3F	164	GLN
23	3F	195	GLN
23	3F	226	HIS
23	3F	525	GLN
23	3F	561	ASN
24	3G	29	ASN
24	3H	5	ASN
24	3H	18	GLN
24	3H	45	ASN
25	A4	140	ASN
25	A4	279	HIS
25	A4	292	ASN
25	A4	317	ASN
25	A4	331	ASN
25	A4	438	GLN
25	A4	467	ASN
25	A4	483	ASN
25	A4	529	ASN
25	A4	574	HIS
25	A4	589	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
25	A4	621	ASN
25	A4	731	HIS
26	A5	32	GLN
26	A5	67	ASN
26	A5	103	ASN
26	A5	133	GLN
26	A5	302	ASN
26	A5	308	ASN
26	A5	316	ASN
26	A5	318	GLN
26	A5	333	ASN
26	A5	527	HIS
27	A8	588	GLN
27	A8	677	ASN
28	A9	474	HIS
28	A9	478	ASN
28	A9	509	GLN
29	AE	14	ASN
29	AE	96	ASN
29	AE	141	ASN
29	AE	166	ASN
29	AE	219	ASN
29	AE	224	ASN
29	AE	258	HIS
29	AE	304	GLN
29	AE	477	ASN
29	AE	480	ASN
29	AE	545	ASN
29	AE	673	ASN
29	AE	698	ASN
29	AE	730	GLN
30	AF	18	GLN
30	AF	48	ASN
30	AF	125	HIS
30	AF	133	HIS
30	AF	135	GLN
30	AF	156	ASN
30	AF	217	ASN
30	AF	250	ASN
30	AF	269	GLN
30	AF	289	ASN
30	AF	419	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	AF	481	GLN
30	AF	496	HIS
31	AG	50	ASN
31	AG	105	HIS
31	AG	131	HIS
31	AG	166	ASN
31	AG	184	GLN
31	AG	190	GLN
31	AG	266	ASN
31	AG	269	GLN
31	AG	289	GLN
31	AG	325	GLN
31	AG	332	GLN
31	AG	370	GLN
31	AG	393	ASN
31	AG	407	ASN
31	AG	410	ASN
31	AG	418	ASN
31	AG	453	HIS
31	AG	467	GLN
31	AG	568	ASN
31	AG	579	ASN
31	AG	603	ASN
31	AG	605	ASN
31	AG	706	HIS
31	AG	719	ASN
31	AG	880	GLN
32	B1	57	ASN
32	B1	92	HIS
32	B1	142	HIS
32	B1	201	HIS
32	B1	254	HIS
32	B1	297	GLN
32	B1	303	ASN
32	B1	349	ASN
32	B1	386	HIS
32	B1	452	ASN
32	B1	456	HIS
32	B1	461	GLN
32	B1	483	GLN
32	B1	549	GLN
32	B1	552	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	B1	707	ASN
32	B1	734	GLN
32	B1	752	ASN
32	B1	813	HIS
32	B1	837	ASN
32	B1	842	ASN
33	B2	172	GLN
33	B2	327	HIS
33	B2	390	GLN
33	B2	455	GLN
33	B2	523	HIS
33	B2	524	HIS
33	B2	656	HIS
33	B2	657	GLN
33	B2	770	ASN
33	B2	798	ASN
33	B2	856	ASN
33	B2	871	GLN
33	B2	881	ASN
34	B3	81	GLN
34	B3	157	ASN
34	B3	187	GLN
34	B3	241	GLN
34	B3	309	GLN
34	B3	312	GLN
34	B3	322	ASN
34	B3	337	HIS
34	B3	358	ASN
34	B3	387	HIS
34	B3	392	ASN
34	B3	478	GLN
34	B3	495	ASN
34	B3	519	ASN
34	B3	522	ASN
34	B3	642	GLN
34	B3	667	GLN
34	B3	735	GLN
34	B3	749	ASN
34	B3	767	HIS
35	B8	151	ASN
35	B8	162	ASN
35	B8	167	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
35	B8	224	ASN
35	B8	276	HIS
35	B8	282	ASN
35	B8	308	ASN
35	B8	322	HIS
35	B8	352	GLN
35	B8	472	GLN
35	B8	492	ASN
35	B8	498	ASN
35	B8	528	GLN
35	B8	592	ASN
35	B8	593	HIS
36	BE	32	ASN
36	BE	64	ASN
36	BE	120	HIS
36	BE	163	GLN
36	BE	289	ASN
36	BE	305	ASN
36	BE	349	HIS
36	BE	362	GLN
36	BE	447	ASN
36	BE	481	ASN
36	BE	501	HIS
36	BE	514	ASN
36	BE	627	ASN
36	BE	708	ASN
36	BE	736	HIS
36	BE	877	ASN
36	BE	911	ASN
36	BE	916	HIS
37	B6	62	ASN
37	B6	64	ASN
37	B6	90	GLN
37	B6	115	ASN
37	B6	166	ASN
37	B6	169	GLN
37	B6	287	ASN
37	B6	289	HIS
38	5B	207	ASN
39	5C	101	ASN
39	5C	133	HIS
39	5C	143	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
39	5C	151	ASN
39	5C	155	HIS
39	5C	164	GLN
39	5C	170	GLN
39	5C	185	HIS
39	5C	308	GLN
39	5C	371	HIS
39	5C	394	HIS
40	5D	42	HIS
40	5D	68	HIS
40	5D	144	ASN
40	5D	153	ASN
41	5E	303	GLN
41	5E	434	HIS
41	5E	493	GLN
42	5F	7	HIS
42	5F	10	GLN
42	5F	27	HIS
42	5F	48	ASN
42	5F	144	ASN
42	5F	153	ASN
43	5G	118	ASN
43	5G	145	HIS
43	5G	164	GLN
43	5G	182	GLN
43	5G	188	HIS
43	5G	211	ASN
43	5G	235	GLN
44	5H	560	ASN
45	5I	20	GLN
45	5I	46	ASN
45	5I	81	ASN
45	5I	109	HIS
45	5I	242	ASN
45	5I	260	GLN
45	5I	276	ASN
45	5I	281	ASN
45	5I	336	HIS
45	5I	371	ASN
45	5I	406	HIS
45	5I	418	HIS
45	5I	421	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	5J	53	GLN
46	5J	135	HIS
46	5J	139	GLN
46	5J	184	ASN
46	5J	192	ASN
46	5J	195	GLN
47	5K	29	GLN
48	RA	60	ASN
48	RA	82	HIS
48	RA	96	HIS
48	RA	118	GLN
48	RA	119	ASN
48	RA	147	ASN
48	RA	230	GLN
48	RA	268	GLN
48	RA	282	ASN
49	RB	314	ASN
49	RB	318	ASN
50	RE	136	GLN
50	RE	170	GLN
50	RE	237	HIS
50	RE	293	ASN
50	RE	342	HIS
50	RE	344	ASN
50	RE	402	ASN
50	RE	409	ASN
50	RE	506	GLN
50	RE	520	ASN
50	RE	537	ASN
50	RE	568	ASN
50	RE	602	ASN
50	RE	683	ASN
50	RE	729	ASN
50	RE	767	GLN
50	RE	834	ASN
50	RE	841	ASN
50	RE	869	ASN
50	RE	872	ASN
50	RE	956	ASN
50	RE	969	ASN
50	RE	1029	ASN
50	RE	1073	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
50	RE	1078	HIS
50	RE	1086	ASN
50	RE	1194	HIS
50	RE	1199	ASN
50	RE	1203	ASN
50	RE	1215	ASN
50	RE	1228	ASN
51	RF	23	HIS
51	RF	73	GLN
51	RF	135	ASN
51	RF	136	ASN
51	RF	187	HIS
51	RF	197	GLN
51	RF	261	GLN
52	RG	105	ASN
52	RG	125	ASN
52	RH	69	ASN
52	RH	74	GLN
52	RH	105	ASN
52	RH	125	ASN
52	RH	250	ASN
53	RJ	126	ASN
53	RJ	157	ASN
53	RJ	254	HIS
53	RJ	289	HIS
53	RJ	761	GLN
53	RJ	778	GLN
53	RJ	944	ASN
53	RJ	1082	GLN
54	RK	16	ASN
54	RK	61	ASN
54	RK	317	GLN
54	RK	334	ASN
55	RL	16	ASN
55	RL	75	ASN
55	RL	117	ASN
55	RL	133	ASN
56	RN	8	ASN
56	RN	56	ASN
56	RN	89	GLN
56	RN	432	HIS
56	RN	495	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
56	RN	683	ASN
56	RN	686	ASN
56	RN	703	GLN
56	RN	705	HIS
56	RN	713	HIS
56	RN	771	ASN
56	RN	797	ASN
57	RO	192	GLN
57	RO	249	ASN
57	RO	266	ASN
57	RO	268	GLN
57	RO	273	GLN
57	RO	304	ASN
57	RO	306	GLN
57	RO	343	GLN
57	RO	434	ASN
57	RO	449	HIS
57	RO	472	HIS
57	RO	474	HIS
58	RP	58	ASN
58	RP	79	GLN
58	RP	153	ASN
58	RP	1686	GLN
58	RP	1702	HIS
58	RP	1707	HIS
58	RP	1785	ASN
58	RP	1787	ASN
58	RP	1802	HIS
58	RP	1803	ASN
58	RP	1816	HIS
58	RP	1943	ASN
58	RP	2045	GLN
59	RQ	344	GLN
59	RQ	867	GLN
60	RS	241	ASN
60	RS	276	GLN
60	RS	300	ASN
61	RY	469	GLN
63	RT	123	HIS
63	RT	127	GLN
63	RT	218	ASN
64	ST	78	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
64	ST	122	HIS
65	SU	25	GLN
65	SU	43	ASN
65	SU	48	GLN
65	SU	64	HIS
66	RD	1473	ASN
66	RD	1522	ASN
66	RD	1525	ASN
66	RD	1626	GLN
67	RZ	519	HIS
67	RZ	550	HIS
67	RZ	595	ASN
67	RZ	794	GLN
67	RZ	884	GLN
67	RZ	1057	ASN
67	RZ	1114	ASN
67	RZ	1232	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	55 (32%)	8 (4%)
2	5A	186/700 (26%)	54 (29%)	4 (2%)
3	SA	1311/1812 (72%)	501 (38%)	32 (2%)
All	All	1666/2845 (58%)	610 (36%)	44 (2%)

All (610) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	2	U
1	3A	14	A
1	3A	15	U
1	3A	24	U
1	3A	25	U
1	3A	27	U
1	3A	28	A
1	3A	30	A
1	3A	33	A
1	3A	35	U
1	3A	38	U
1	3A	56	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	3A	60	A
1	3A	61	G
1	3A	87	G
1	3A	88	U
1	3A	89	C
1	3A	90	C
1	3A	91	C
1	3A	97	C
1	3A	98	U
1	3A	99	U
1	3A	101	G
1	3A	103	A
1	3A	111	G
1	3A	115	G
1	3A	198	U
1	3A	199	G
1	3A	201	C
1	3A	204	U
1	3A	205	G
1	3A	206	C
1	3A	246	A
1	3A	248	G
1	3A	249	G
1	3A	252	C
1	3A	264	C
1	3A	267	A
1	3A	305	G
1	3A	310	G
1	3A	311	G
1	3A	313	A
1	3A	314	C
1	3A	317	A
1	3A	318	U
1	3A	319	G
1	3A	320	G
1	3A	321	C
1	3A	322	A
1	3A	323	G
1	3A	324	U
1	3A	325	C
1	3A	328	A
1	3A	329	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	3A	332	G
2	5A	5	G
2	5A	6	A
2	5A	7	A
2	5A	8	A
2	5A	11	A
2	5A	13	U
2	5A	14	U
2	5A	15	G
2	5A	63	G
2	5A	64	U
2	5A	70	A
2	5A	83	U
2	5A	86	C
2	5A	87	C
2	5A	90	G
2	5A	279	A
2	5A	280	A
2	5A	281	G
2	5A	292	A
2	5A	294	U
2	5A	304	U
2	5A	305	A
2	5A	309	A
2	5A	310	U
2	5A	311	C
2	5A	312	U
2	5A	313	A
2	5A	468	A
2	5A	472	A
2	5A	474	A
2	5A	481	U
2	5A	482	A
2	5A	485	G
2	5A	487	A
2	5A	488	U
2	5A	490	G
2	5A	491	U
2	5A	493	A
2	5A	519	A
2	5A	525	U
2	5A	526	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	5A	536	A
2	5A	537	G
2	5A	539	A
2	5A	540	U
2	5A	541	U
2	5A	542	U
2	5A	548	A
2	5A	549	G
2	5A	583	U
2	5A	586	A
2	5A	587	G
2	5A	589	U
2	5A	591	U
3	SA	-6	A
3	SA	-5	G
3	SA	-4	A
3	SA	-1	G
3	SA	0	U
3	SA	1	U
3	SA	2	A
3	SA	17	C
3	SA	18	C
3	SA	19	A
3	SA	21	U
3	SA	23	G
3	SA	25	C
3	SA	26	A
3	SA	29	U
3	SA	35	U
3	SA	36	C
3	SA	37	U
3	SA	50	C
3	SA	51	A
3	SA	52	U
3	SA	53	G
3	SA	55	A
3	SA	56	U
3	SA	57	G
3	SA	60	U
3	SA	61	A
3	SA	63	G
3	SA	65	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	66	U
3	SA	67	A
3	SA	68	A
3	SA	69	G
3	SA	72	A
3	SA	73	U
3	SA	74	U
3	SA	75	U
3	SA	77	U
3	SA	81	G
3	SA	85	A
3	SA	92	A
3	SA	95	G
3	SA	96	G
3	SA	97	C
3	SA	100	A
3	SA	102	U
3	SA	103	A
3	SA	104	A
3	SA	105	A
3	SA	106	U
3	SA	114	C
3	SA	115	G
3	SA	116	U
3	SA	119	A
3	SA	127	G
3	SA	128	U
3	SA	129	U
3	SA	130	C
3	SA	131	C
3	SA	141	U
3	SA	145	A
3	SA	146	U
3	SA	147	A
3	SA	149	C
3	SA	153	G
3	SA	159	U
3	SA	160	C
3	SA	161	U
3	SA	168	A
3	SA	174	U
3	SA	175	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	176	C
3	SA	177	U
3	SA	182	A
3	SA	183	U
3	SA	184	C
3	SA	187	G
3	SA	188	A
3	SA	190	C
3	SA	191	C
3	SA	192	U
3	SA	193	U
3	SA	194	U
3	SA	195	G
3	SA	197	A
3	SA	202	A
3	SA	203	U
3	SA	204	G
3	SA	206	A
3	SA	210	A
3	SA	211	U
3	SA	214	G
3	SA	226	A
3	SA	228	G
3	SA	230	C
3	SA	233	C
3	SA	234	G
3	SA	236	A
3	SA	237	C
3	SA	238	U
3	SA	239	C
3	SA	240	U
3	SA	241	U
3	SA	242	U
3	SA	243	G
3	SA	254	A
3	SA	256	A
3	SA	258	C
3	SA	261	U
3	SA	262	U
3	SA	265	A
3	SA	266	A
3	SA	267	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	272	U
3	SA	273	G
3	SA	275	C
3	SA	276	C
3	SA	277	U
3	SA	278	U
3	SA	279	G
3	SA	280	U
3	SA	281	G
3	SA	283	U
3	SA	290	G
3	SA	308	C
3	SA	309	C
3	SA	311	U
3	SA	312	A
3	SA	316	A
3	SA	319	U
3	SA	320	U
3	SA	321	C
3	SA	324	U
3	SA	325	G
3	SA	333	A
3	SA	334	G
3	SA	337	G
3	SA	338	C
3	SA	350	U
3	SA	352	A
3	SA	355	G
3	SA	357	G
3	SA	359	A
3	SA	360	A
3	SA	361	C
3	SA	362	G
3	SA	365	G
3	SA	366	A
3	SA	369	A
3	SA	371	G
3	SA	373	G
3	SA	374	U
3	SA	375	U
3	SA	377	G
3	SA	379	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	382	C
3	SA	383	G
3	SA	386	G
3	SA	387	A
3	SA	390	G
3	SA	400	A
3	SA	401	A
3	SA	402	C
3	SA	403	G
3	SA	411	C
3	SA	416	A
3	SA	417	A
3	SA	418	G
3	SA	419	G
3	SA	421	A
3	SA	422	G
3	SA	423	G
3	SA	424	C
3	SA	425	A
3	SA	426	G
3	SA	429	G
3	SA	436	A
3	SA	437	A
3	SA	439	U
3	SA	440	U
3	SA	441	A
3	SA	444	C
3	SA	445	A
3	SA	448	C
3	SA	454	U
3	SA	455	C
3	SA	456	A
3	SA	457	G
3	SA	468	A
3	SA	469	C
3	SA	470	A
3	SA	471	A
3	SA	473	A
3	SA	477	A
3	SA	480	G
3	SA	486	G
3	SA	487	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	496	G
3	SA	501	U
3	SA	502	U
3	SA	505	A
3	SA	506	A
3	SA	514	G
3	SA	520	A
3	SA	534	A
3	SA	538	A
3	SA	539	G
3	SA	541	A
3	SA	542	A
3	SA	543	C
3	SA	545	A
3	SA	557	G
3	SA	558	U
3	SA	563	U
3	SA	564	G
3	SA	565	C
3	SA	570	A
3	SA	572	C
3	SA	574	G
3	SA	575	C
3	SA	578	U
3	SA	579	A
3	SA	580	A
3	SA	583	C
3	SA	584	C
3	SA	585	A
3	SA	586	G
3	SA	587	C
3	SA	594	A
3	SA	595	G
3	SA	602	U
3	SA	603	U
3	SA	604	A
3	SA	606	A
3	SA	608	U
3	SA	609	U
3	SA	610	G
3	SA	611	U
3	SA	612	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	613	G
3	SA	614	C
3	SA	615	A
3	SA	616	G
3	SA	635	A
3	SA	636	A
3	SA	638	U
3	SA	644	C
3	SA	648	G
3	SA	652	G
3	SA	654	C
3	SA	656	G
3	SA	657	U
3	SA	658	C
3	SA	677	G
3	SA	678	A
3	SA	686	C
3	SA	687	G
3	SA	688	G
3	SA	689	G
3	SA	691	C
3	SA	692	C
3	SA	827	C
3	SA	828	U
3	SA	840	U
3	SA	841	U
3	SA	848	C
3	SA	859	A
3	SA	860	U
3	SA	863	A
3	SA	864	U
3	SA	865	A
3	SA	873	U
3	SA	877	G
3	SA	894	U
3	SA	901	G
3	SA	904	G
3	SA	906	A
3	SA	912	U
3	SA	913	G
3	SA	914	G
3	SA	926	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	930	A
3	SA	933	A
3	SA	934	C
3	SA	935	U
3	SA	945	U
3	SA	951	A
3	SA	953	G
3	SA	960	U
3	SA	966	A
3	SA	969	C
3	SA	970	A
3	SA	1037	C
3	SA	1039	A
3	SA	1040	G
3	SA	1052	U
3	SA	1053	G
3	SA	1056	U
3	SA	1057	U
3	SA	1059	U
3	SA	1060	U
3	SA	1062	A
3	SA	1063	U
3	SA	1076	A
3	SA	1079	U
3	SA	1081	A
3	SA	1082	C
3	SA	1084	A
3	SA	1085	G
3	SA	1086	A
3	SA	1106	U
3	SA	1107	G
3	SA	1108	G
3	SA	1109	G
3	SA	1110	G
3	SA	1111	G
3	SA	1114	G
3	SA	1118	G
3	SA	1119	G
3	SA	1122	G
3	SA	1125	A
3	SA	1126	G
3	SA	1127	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	1128	C
3	SA	1129	U
3	SA	1131	A
3	SA	1132	A
3	SA	1145	U
3	SA	1146	G
3	SA	1158	C
3	SA	1164	G
3	SA	1178	G
3	SA	1191	U
3	SA	1192	C
3	SA	1193	A
3	SA	1195	C
3	SA	1196	A
3	SA	1197	C
3	SA	1198	G
3	SA	1199	G
3	SA	1200	G
3	SA	1201	G
3	SA	1202	A
3	SA	1205	C
3	SA	1206	U
3	SA	1208	A
3	SA	1210	C
3	SA	1213	G
3	SA	1217	A
3	SA	1218	G
3	SA	1219	A
3	SA	1220	C
3	SA	1223	A
3	SA	1227	A
3	SA	1228	G
3	SA	1229	G
3	SA	1230	A
3	SA	1232	U
3	SA	1233	G
3	SA	1235	C
3	SA	1236	A
3	SA	1252	C
3	SA	1253	U
3	SA	1254	U
3	SA	1255	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	1258	U
3	SA	1263	G
3	SA	1266	U
3	SA	1268	G
3	SA	1271	G
3	SA	1272	U
3	SA	1273	G
3	SA	1275	A
3	SA	1276	U
3	SA	1436	A
3	SA	1440	C
3	SA	1441	C
3	SA	1442	U
3	SA	1443	U
3	SA	1449	U
3	SA	1450	U
3	SA	1453	G
3	SA	1457	C
3	SA	1461	C
3	SA	1469	A
3	SA	1472	C
3	SA	1473	U
3	SA	1474	G
3	SA	1475	A
3	SA	1476	C
3	SA	1482	C
3	SA	1486	G
3	SA	1487	A
3	SA	1488	G
3	SA	1489	U
3	SA	1490	C
3	SA	1491	U
3	SA	1492	A
3	SA	1493	C
3	SA	1522	U
3	SA	1523	G
3	SA	1524	A
3	SA	1527	C
3	SA	1531	G
3	SA	1532	U
3	SA	1533	C
3	SA	1534	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	1535	U
3	SA	1536	G
3	SA	1537	C
3	SA	1538	U
3	SA	1539	G
3	SA	1540	G
3	SA	1541	G
3	SA	1542	G
3	SA	1553	G
3	SA	1554	U
3	SA	1555	A
3	SA	1556	A
3	SA	1557	U
3	SA	1559	A
3	SA	1560	U
3	SA	1561	U
3	SA	1569	A
3	SA	1573	A
3	SA	1574	G
3	SA	1582	U
3	SA	1584	G
3	SA	1590	G
3	SA	1594	G
3	SA	1595	U
3	SA	1596	C
3	SA	1601	G
3	SA	1602	C
3	SA	1607	G
3	SA	1614	A
3	SA	1618	C
3	SA	1628	U
3	SA	1630	U
3	SA	1633	A
3	SA	1651	A
3	SA	1655	A
3	SA	1657	U
3	SA	1658	G
3	SA	1659	A
3	SA	1661	U
3	SA	1665	U
3	SA	1670	G
3	SA	1675	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	1677	C
3	SA	1679	G
3	SA	1680	G
3	SA	1681	A
3	SA	1682	U
3	SA	1683	C
3	SA	1687	U
3	SA	1689	A
3	SA	1692	G
3	SA	1693	A
3	SA	1696	G
3	SA	1697	G
3	SA	1700	C
3	SA	1708	U
3	SA	1709	C
3	SA	1710	U
3	SA	1711	C
3	SA	1713	G
3	SA	1717	G
3	SA	1718	G
3	SA	1719	A
3	SA	1721	A
3	SA	1724	U
3	SA	1725	U
3	SA	1727	G
3	SA	1728	A
3	SA	1731	A
3	SA	1732	A
3	SA	1736	G
3	SA	1737	G
3	SA	1742	U
3	SA	1743	U
3	SA	1745	G
3	SA	1749	A
3	SA	1750	A
3	SA	1755	A
3	SA	1756	A
3	SA	1757	G
3	SA	1758	U
3	SA	1778	G
3	SA	1790	A
3	SA	1791	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	1792	G
3	SA	1793	G
3	SA	1794	A
3	SA	1795	U
3	SA	1799	U
3	SA	1800	A
3	SA	1801	A
3	SA	1802	A
3	SA	1803	G
3	SA	1804	A

All (44) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3A	97	C
1	3A	98	U
1	3A	198	U
1	3A	248	G
1	3A	312	U
1	3A	318	U
1	3A	322	A
1	3A	323	G
2	5A	312	U
2	5A	487	A
2	5A	492	G
2	5A	536	A
3	SA	-7	A
3	SA	0	U
3	SA	56	U
3	SA	68	A
3	SA	272	U
3	SA	372	G
3	SA	401	A
3	SA	417	A
3	SA	538	A
3	SA	542	A
3	SA	579	A
3	SA	602	U
3	SA	1052	U
3	SA	1084	A
3	SA	1197	C
3	SA	1474	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	1475	A
3	SA	1486	G
3	SA	1487	A
3	SA	1490	C
3	SA	1521	G
3	SA	1531	G
3	SA	1532	U
3	SA	1533	C
3	SA	1539	G
3	SA	1540	G
3	SA	1541	G
3	SA	1568	C
3	SA	1573	A
3	SA	1594	G
3	SA	1632	C
3	SA	1803	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
69	GTP	RJ	1201	70	33,34,34	0.57	0	50,54,54	0.72	1 (2%)
71	ADP	RZ	1301	-	28,29,29	1.43	5 (17%)	43,45,45	1.84	10 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
69	GTP	RJ	1201	70	-	3/22/38/38	0/3/3/3
71	ADP	RZ	1301	-	-	4/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
71	RZ	1301	ADP	C5-C4	4.64	1.47	1.39
71	RZ	1301	ADP	C5-C6	2.81	1.48	1.41
71	RZ	1301	ADP	C8-N7	2.37	1.36	1.31
71	RZ	1301	ADP	C5-N7	-2.24	1.35	1.39
71	RZ	1301	ADP	PA-O3A	2.17	1.61	1.59

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
71	RZ	1301	ADP	C5-C4-N3	-5.89	118.61	126.72
71	RZ	1301	ADP	N3-C4-N9	4.59	134.98	127.17
71	RZ	1301	ADP	C2-N3-C4	3.87	121.27	111.83
71	RZ	1301	ADP	C4-C5-N7	-3.68	106.37	110.58
71	RZ	1301	ADP	N3-C2-N1	-3.47	123.33	128.58
71	RZ	1301	ADP	C5-N7-C8	2.74	107.75	103.45
71	RZ	1301	ADP	C4-N9-C8	2.69	108.56	105.74
71	RZ	1301	ADP	C6-C5-N7	2.26	136.44	132.09
71	RZ	1301	ADP	C3'-C2'-C1'	2.15	105.53	101.46
71	RZ	1301	ADP	N9-C8-N7	-2.15	110.89	113.94
69	RJ	1201	GTP	C4'-O4'-C1'	-2.14	104.73	109.47

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
71	RZ	1301	ADP	C5'-O5'-PA-O2A
71	RZ	1301	ADP	C5'-O5'-PA-O3A
69	RJ	1201	GTP	O4'-C4'-C5'-O5'
69	RJ	1201	GTP	C3'-C4'-C5'-O5'
69	RJ	1201	GTP	C4'-C5'-O5'-PA
71	RZ	1301	ADP	O4'-C4'-C5'-O5'

Continued on next page...

Continued from previous page...

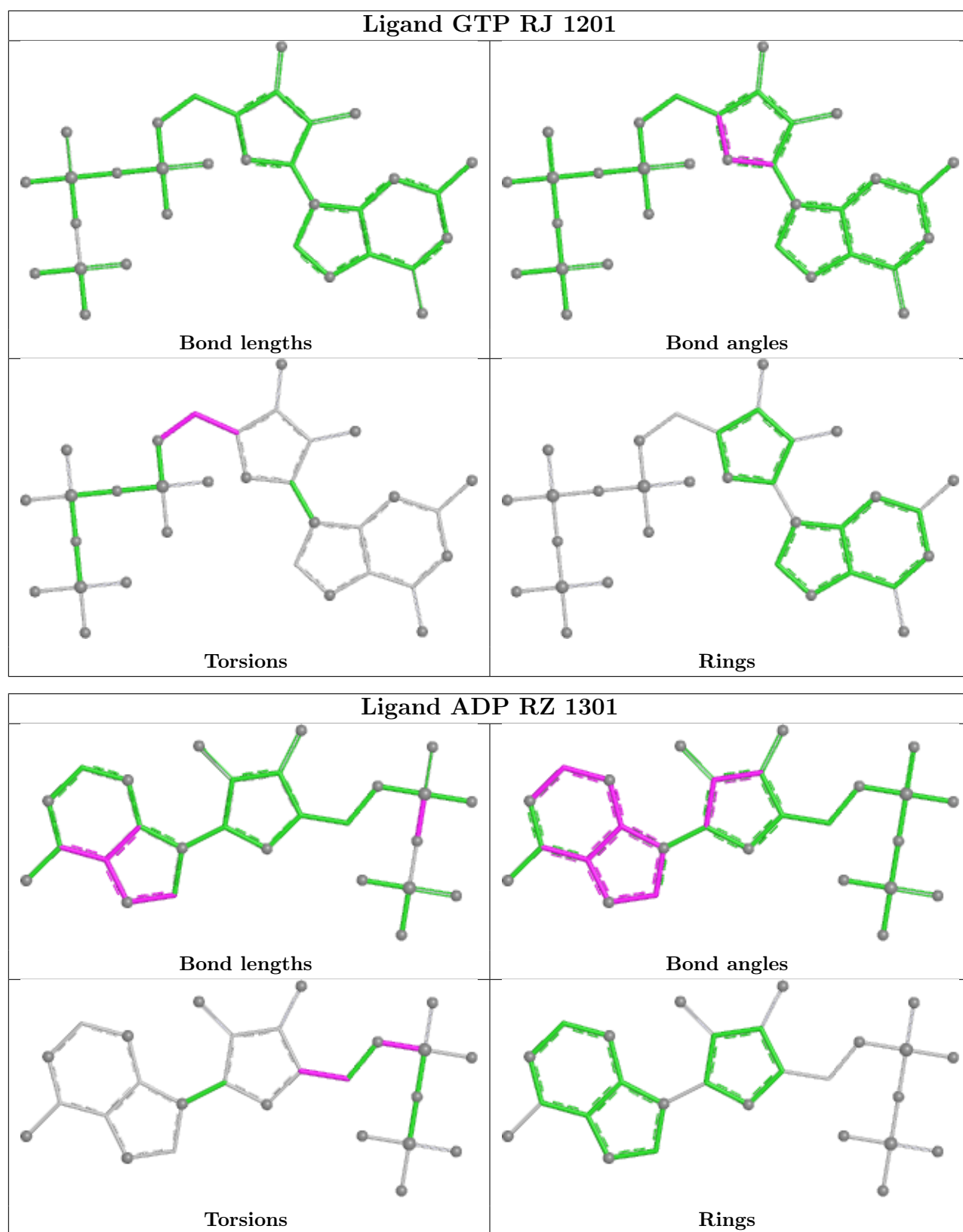
Mol	Chain	Res	Type	Atoms
71	RZ	1301	ADP	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
69	RJ	1201	GTP	2	0
71	RZ	1301	ADP	1	0

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

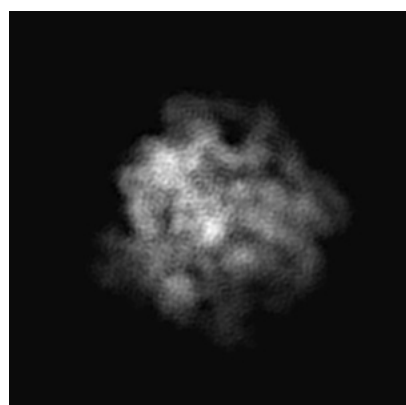
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30588. These allow visual inspection of the internal detail of the map and identification of artifacts.

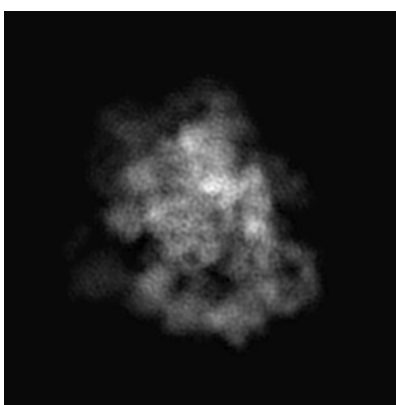
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

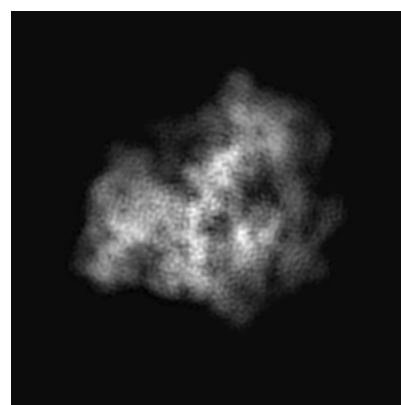
6.1.1 Primary map



X



Y

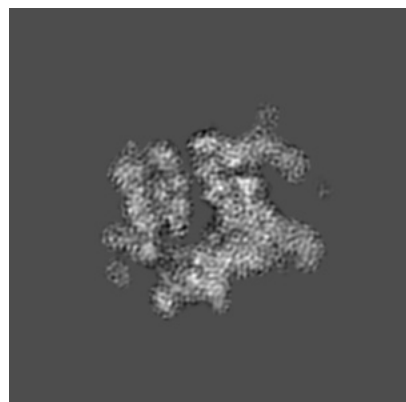


Z

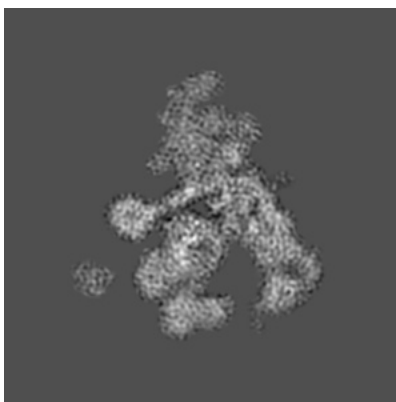
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

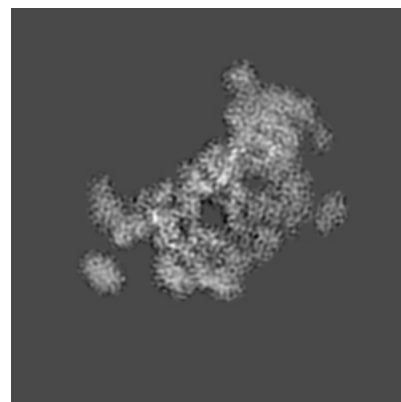
6.2.1 Primary map



X Index: 200



Y Index: 200

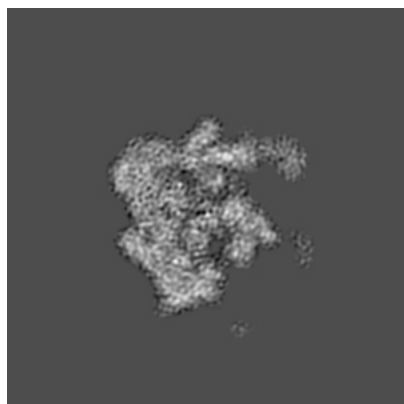


Z Index: 200

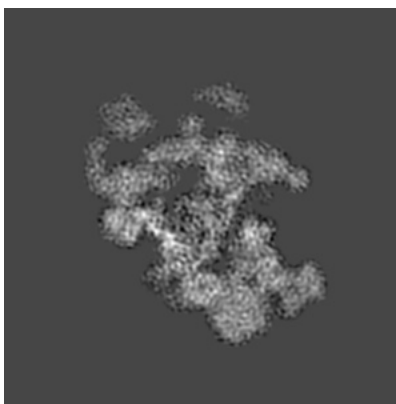
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

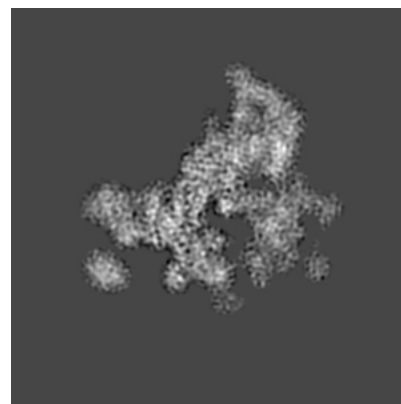
6.3.1 Primary map



X Index: 185



Y Index: 174

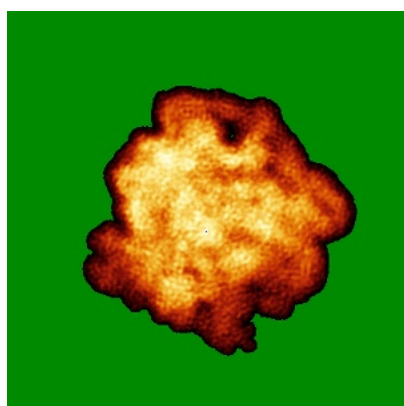


Z Index: 185

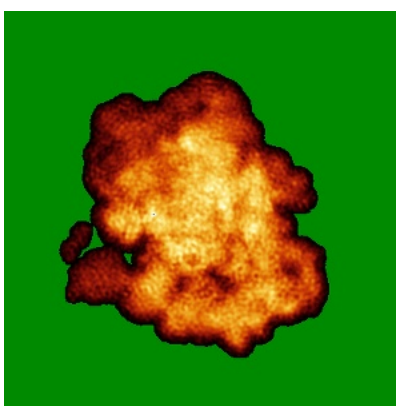
The images above show the largest variance slices of the map in three orthogonal directions.

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

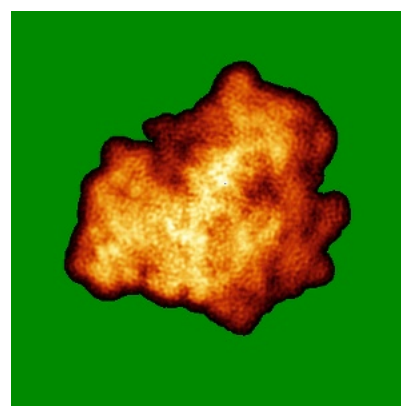
6.4.1 Primary map



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

This section was not generated.

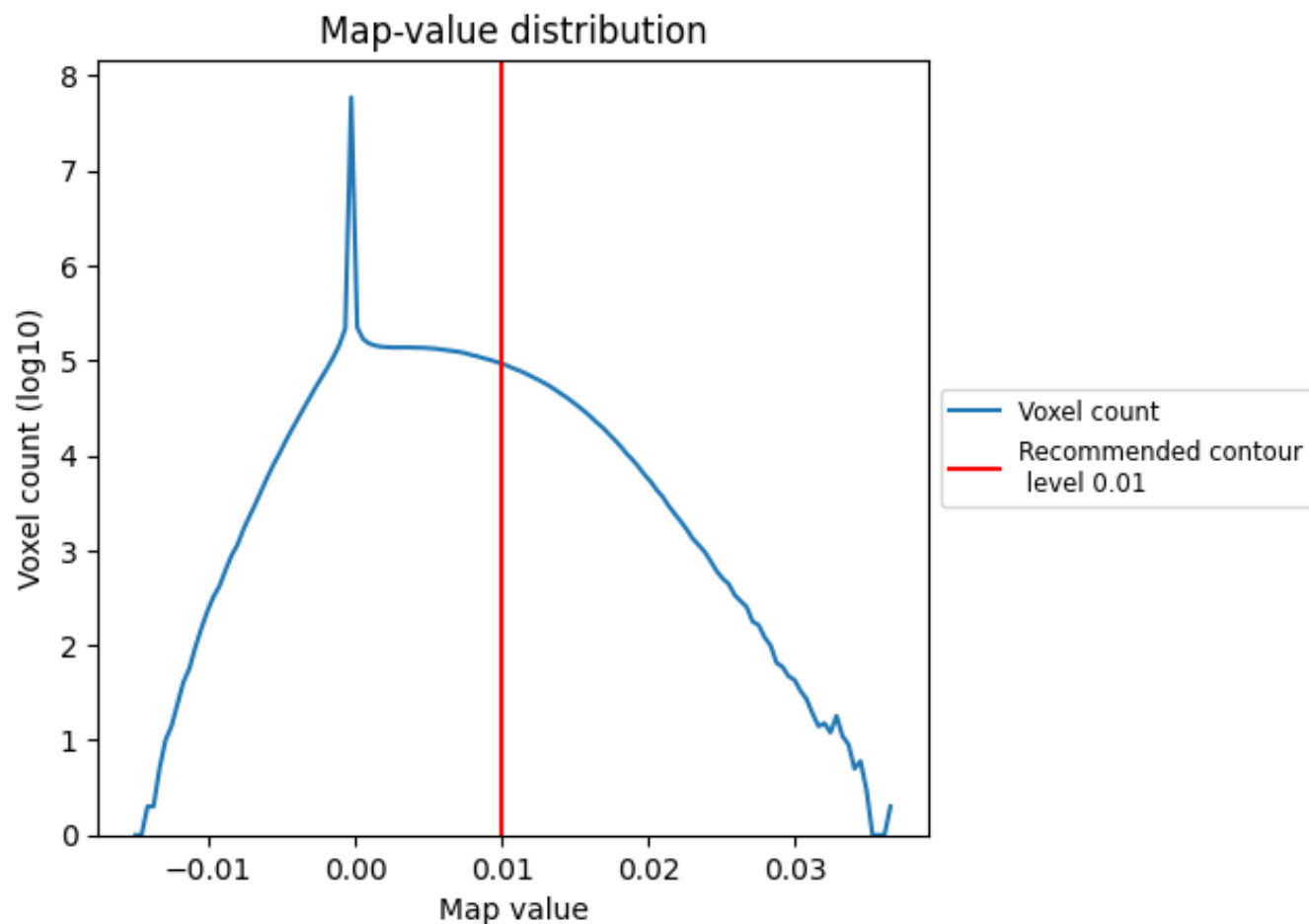
6.6 Mask visualisation

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

7 Map analysis [i](#)

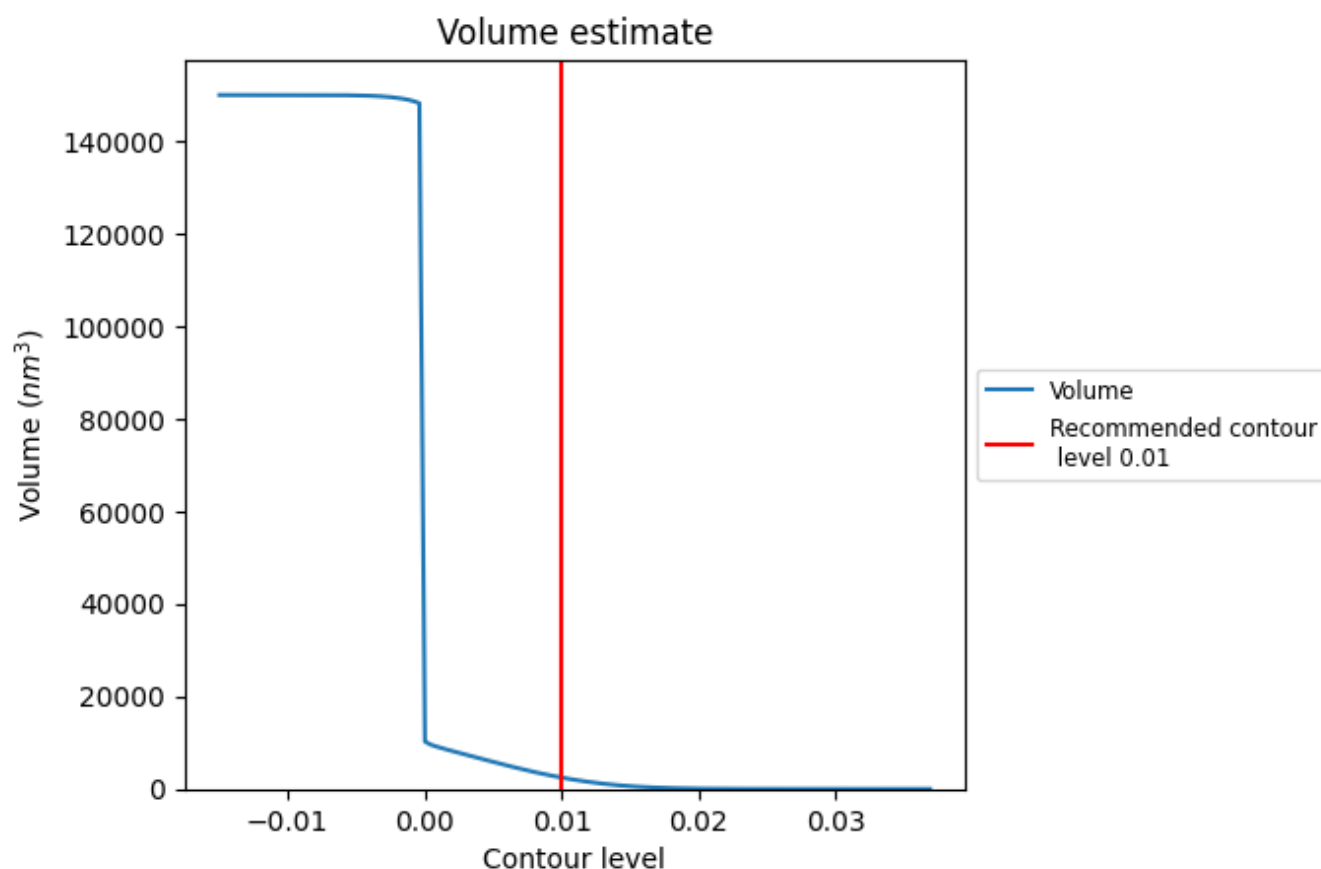
This section contains the results of statistical analysis of the map.

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.

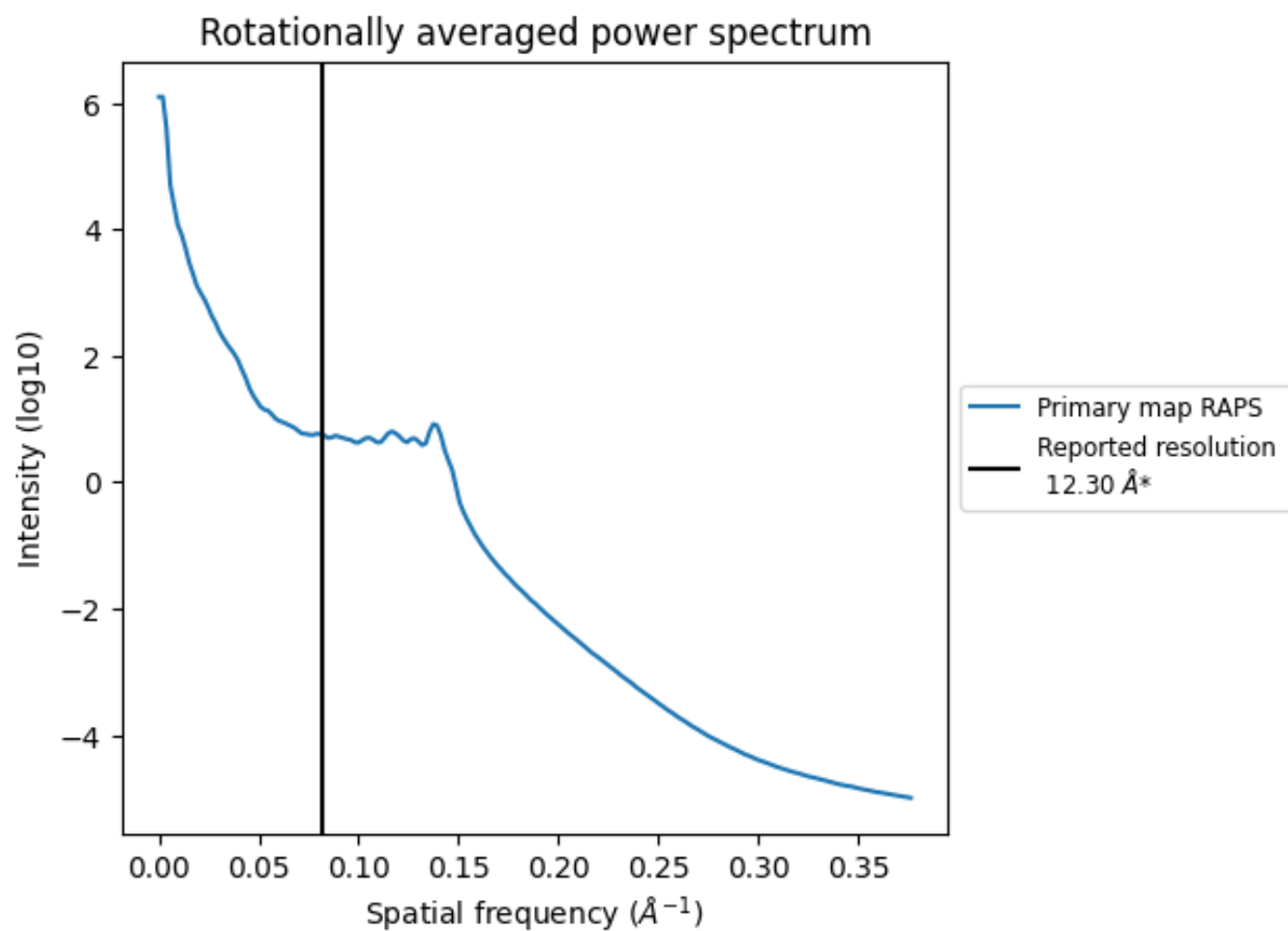
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2465 nm³; this corresponds to an approximate mass of 2227 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 0.081 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

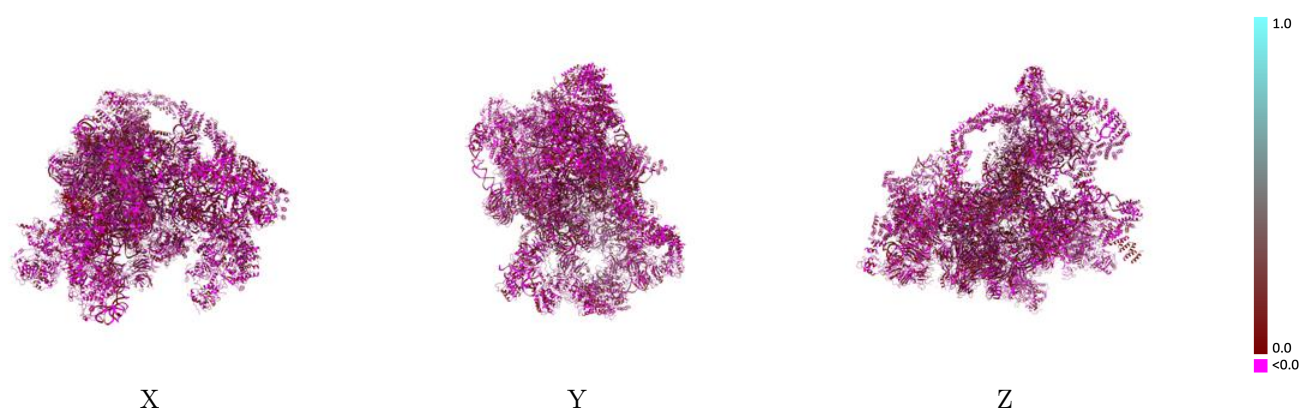
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30588 and PDB model 7D63. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)

This section was not generated.

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

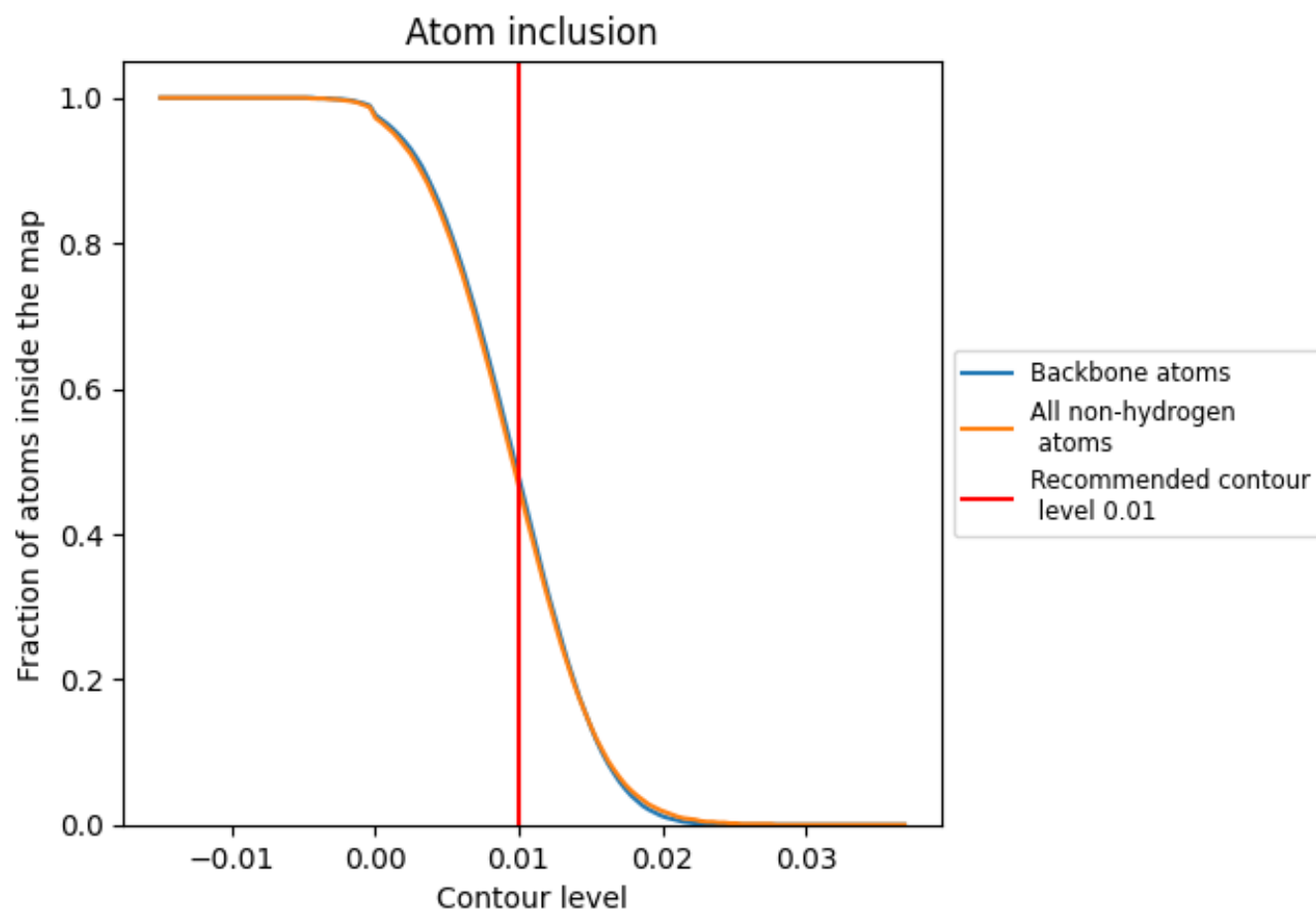


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 47% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4660	 0.0430
3A	 0.7300	 0.0750
3B	 0.4850	 0.0720
3C	 0.5050	 0.0300
3D	 0.6480	 0.0740
3E	 0.5400	 0.0530
3F	 0.6800	 0.0520
3G	 0.7000	 0.0700
3H	 0.5480	 0.0570
5A	 0.4620	 0.0410
5B	 0.1730	 0.0220
5C	 0.5190	 0.0420
5D	 0.3620	 0.0510
5E	 0.4860	 0.0690
5F	 0.4840	 0.0750
5G	 0.4940	 0.0710
5H	 0.5400	 0.0360
5I	 0.6100	 0.0490
5J	 0.3960	 0.0810
5K	 0.3810	 0.0530
A4	 0.6800	 0.0470
A5	 0.6300	 0.0460
A8	 0.5600	 0.0260
A9	 0.6910	 0.0700
AE	 0.3060	 0.0360
AF	 0.6460	 0.0650
AG	 0.7180	 0.0530
B1	 0.6050	 0.0590
B2	 0.7070	 0.0560
B3	 0.5320	 0.0300
B6	 0.4550	 0.0650
B8	 0.5910	 0.0510
BE	 0.6960	 0.0560
RA	 0.3730	 0.0180
RB	 0.3330	 0.0360



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
RD	 0.0000	 -0.0180
RE	 0.0600	 0.0080
RF	 0.0430	 0.0160
RG	 0.6280	 0.0530
RH	 0.4680	 0.0300
RJ	 0.5960	 0.0590
RK	 0.6340	 0.0620
RL	 0.2220	 0.0320
RM	 0.0710	 0.0130
RN	 0.4700	 0.0370
RO	 0.4470	 0.0330
RP	 0.2620	 0.0280
RQ	 0.2180	 0.0110
RS	 0.6410	 0.0240
RT	 0.0870	 -0.0040
RY	 0.1740	 -0.0020
RZ	 0.0700	 0.0220
SA	 0.5940	 0.0540
SC	 0.1120	 0.0220
SF	 0.5140	 0.0200
SG	 0.6420	 0.0910
SH	 0.4740	 0.0360
SI	 0.1110	 0.0190
SJ	 0.5740	 0.0260
SK	 0.5500	 0.0880
SM	 0.5310	 -0.0050
SO	 0.1890	 0.0210
SP	 0.1960	 0.0140
SR	 0.5560	 0.0800
ST	 0.1510	 0.0370
SU	 0.1310	 0.0350
SX	 0.1590	 0.0140
SY	 0.5430	 0.0730
SZ	 0.5910	 0.0530
Sc	 0.1360	 0.0130
Sd	 0.6440	 0.0760
X1	 0.2730	 0.0560