



Full wwPDB EM Validation Report ⓘ

Mar 17, 2026 – 06:52 PM UTC

PDB ID : 7D5S / pdb_00007d5s
EMDB ID : EMD-30584
Title : Cryo-EM structure of 90S preribosome with inactive Utp24 (state A2)
Authors : Du, Y.; Zhang, J.; An, W.; Ye, K.
Deposited on : 2020-09-28
Resolution : 4.60 Å(reported)
Based on initial model : 6LQU

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

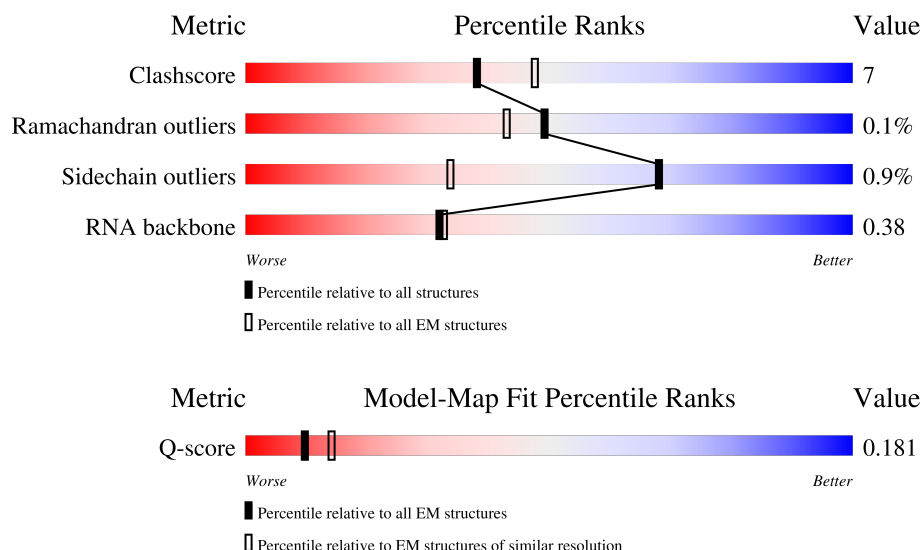
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 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	2407 (4.10 - 5.10)

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	1808	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	SG	225	
5	SK	197	
6	SN	143	
7	SO	151	
8	SP	137	
9	SR	143	
10	ST	146	
11	SY	145	
12	Sd	67	
13	3B	327	
13	3C	327	
14	3D	504	
15	3E	511	
16	3F	573	
17	3G	126	
17	3H	126	
18	A4	776	
19	A5	643	
20	A8	713	
21	A9	575	
22	AE	1769	
23	AF	513	
24	AG	896	
25	B1	923	
26	B2	943	

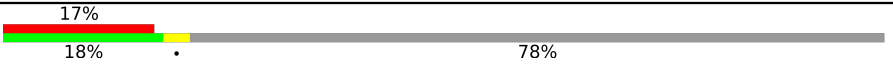
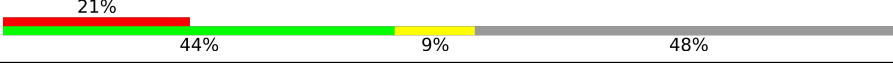
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	B3	817	
28	B8	594	
29	BE	939	
30	B6	440	
31	5B	214	
32	5C	554	
33	5D	250	
34	5E	593	
35	5F	183	
36	5G	290	
37	5H	610	
38	5I	489	
39	5J	217	
40	5K	189	
41	RC	316	
42	RD	1729	
43	RE	1237	
44	RF	297	
45	RG	252	
45	RH	252	
46	RI	274	
47	RJ	1183	
48	RK	367	
49	RN	810	
50	RO	552	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
51	RQ	899	
52	RS	483	
53	RT	326	
54	RW	206	
55	X1	347	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 179154 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	523	Total	C	N	O	P	0	0
			11163	4988	1984	3668	523		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	859	Total	C	N	O	P	0	0
			18356	8201	3302	5994	859		

- Molecule 4 is a protein called 40S ribosomal protein S5.

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

- Molecule 5 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 6 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SN	119	Total	C	N	O	S	0	0
			865	545	151	167	2		

- Molecule 7 is a protein called 40S ribosomal protein S13.

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

- Molecule 8 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 10 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	ST	117	Total	C	N	O	S	0	0
			964	610	184	168	2		

- Molecule 11 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 13 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	3B	240	Total	C	N	O	S	0	0
			1865	1184	333	338	10		
13	3C	225	Total	C	N	O	S	0	0
			1763	1120	316	317	10		

- Molecule 14 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	3D	369	Total	C	N	O	S	0	0
			2848	1811	489	540	8		

- Molecule 15 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	3E	431	Total	C	N	O	S	0	0
			3028	1888	543	588	9		

- Molecule 16 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	3F	406	Total	C	N	O	S	0	0
			3248	2075	566	597	10		

- Molecule 17 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	3G	121	Total	C	N	O	S	0	0
			916	583	158	171	4		
17	3H	121	Total	C	N	O	S	0	0
			916	583	158	171	4		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 4.

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

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 5.

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

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	A8	548	Total	C	N	O	S	0	0
			3307	2054	608	642	3		

- Molecule 21 is a protein called U3 small nucleolar RNA-associated protein 9.

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

- Molecule 22 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AE	649	Total	C	N	O	S	0	0
			5181	3355	849	960	17		

- Molecule 23 is a protein called U3 small nucleolar RNA-associated protein 15.

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

- Molecule 24 is a protein called NET1-associated nuclear protein 1.

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

- Molecule 25 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B1	834	Total	C	N	O	S	0	0
			6635	4223	1140	1253	19		

- Molecule 26 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B2	851	Total	C	N	O	S	0	0
			6723	4294	1133	1269	27		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B3	752	Total	C	N	O	S	0	0
			5882	3746	987	1122	27		

- Molecule 28 is a protein called U3 small nucleolar RNA-associated protein 18.

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

- Molecule 29 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BE	865	Total	C	N	O	S	0	0
			6810	4322	1175	1292	21		

- Molecule 30 is a protein called U3 small nucleolar RNA-associated protein 6.

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

- Molecule 31 is a protein called Bud site selection protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	5B	60	Total	C	N	O	0	0
			495	310	101	84		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5C	516	Total	C	N	O	S	0	0
			4084	2561	736	775	12		

- Molecule 33 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	5D	235	Total	C	N	O	S	0	0
			1972	1226	380	359	7		

- Molecule 34 is a protein called U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	5E	204	Total	C	N	O	S	0	0
			1647	1021	294	328	4		

- Molecule 35 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	5F	182	Total	C	N	O	S	0	0
			1530	967	287	269	7		

- Molecule 36 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5G	282	Total	C	N	O	S	0	0
			2296	1441	430	418	7		

- Molecule 37 is a protein called Something about silencing protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	5H	136	Total	C	N	O	S	0	0
			1065	658	211	196			

- Molecule 38 is a protein called Protein SOF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5I	461	Total	C	N	O	S	0	0
			3765	2354	686	709	16		

- Molecule 39 is a protein called rRNA-processing protein FCF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

- Molecule 40 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5K	175	Total	C	N	O	S	0	0
			1403	896	256	241	10		

- Molecule 41 is a protein called KRR1 small subunit processome component.

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

- Molecule 42 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	RD	265	Total	C	N	O	0	0
			1314	784	265	265		

- Molecule 43 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 44 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	RF	174	Total	C	N	O	S	0	0
			1404	905	230	261	8		

- Molecule 45 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 46 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	RI	252	Total	C	N	O	S	0	0
			2045	1309	362	366	8		

- Molecule 47 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	RJ	732	Total	C	N	O	S	0	0
			5953	3829	1057	1041	26		

- Molecule 48 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 49 is a protein called Nucleolar complex protein 14.

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

- Molecule 50 is a protein called Nucleolar complex protein 4.

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

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	RQ	194	Total	C	N	O	S	0	0
			1436	892	270	272	2		

- Molecule 52 is a protein called Essential nuclear protein 1.

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

- Molecule 53 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	RT	171	Total	C	N	O	S	0	0
			1357	864	249	240	4		

- Molecule 54 is a protein called Regulator of rDNA transcription protein 14.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	RW	63	Total	C	N	O	0	0
			381	234	69	78		

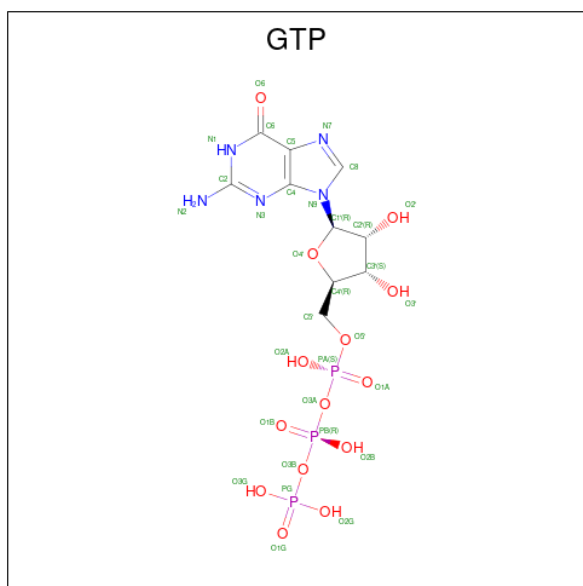
- Molecule 55 is a protein called Unassigned peptides 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	X1	61	Total	C	N	O	0	0
			305	183	61	61		

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	5K	1	Total	Zn	0
			1	1	

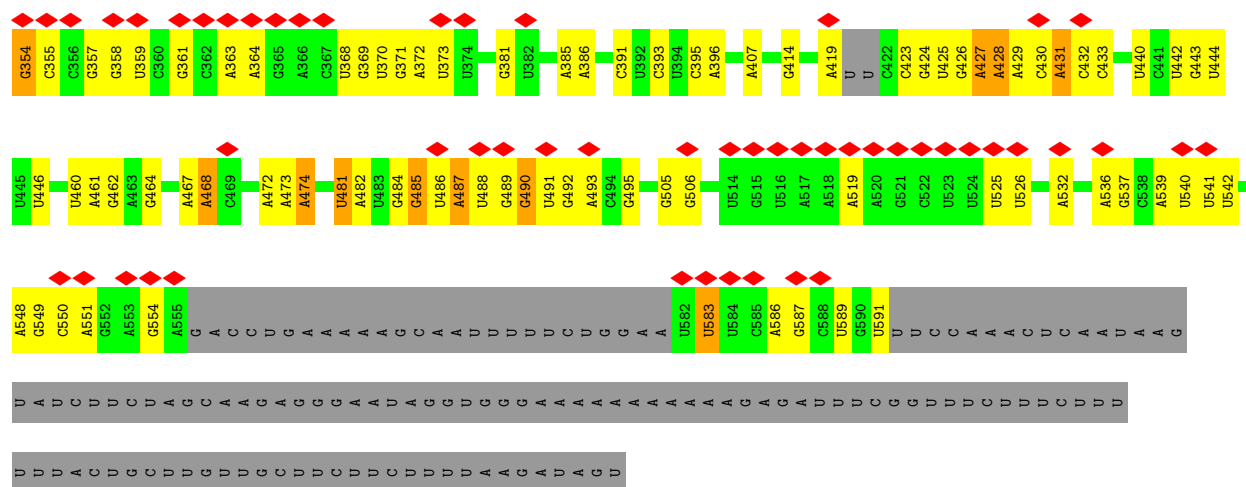
- Molecule 57 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



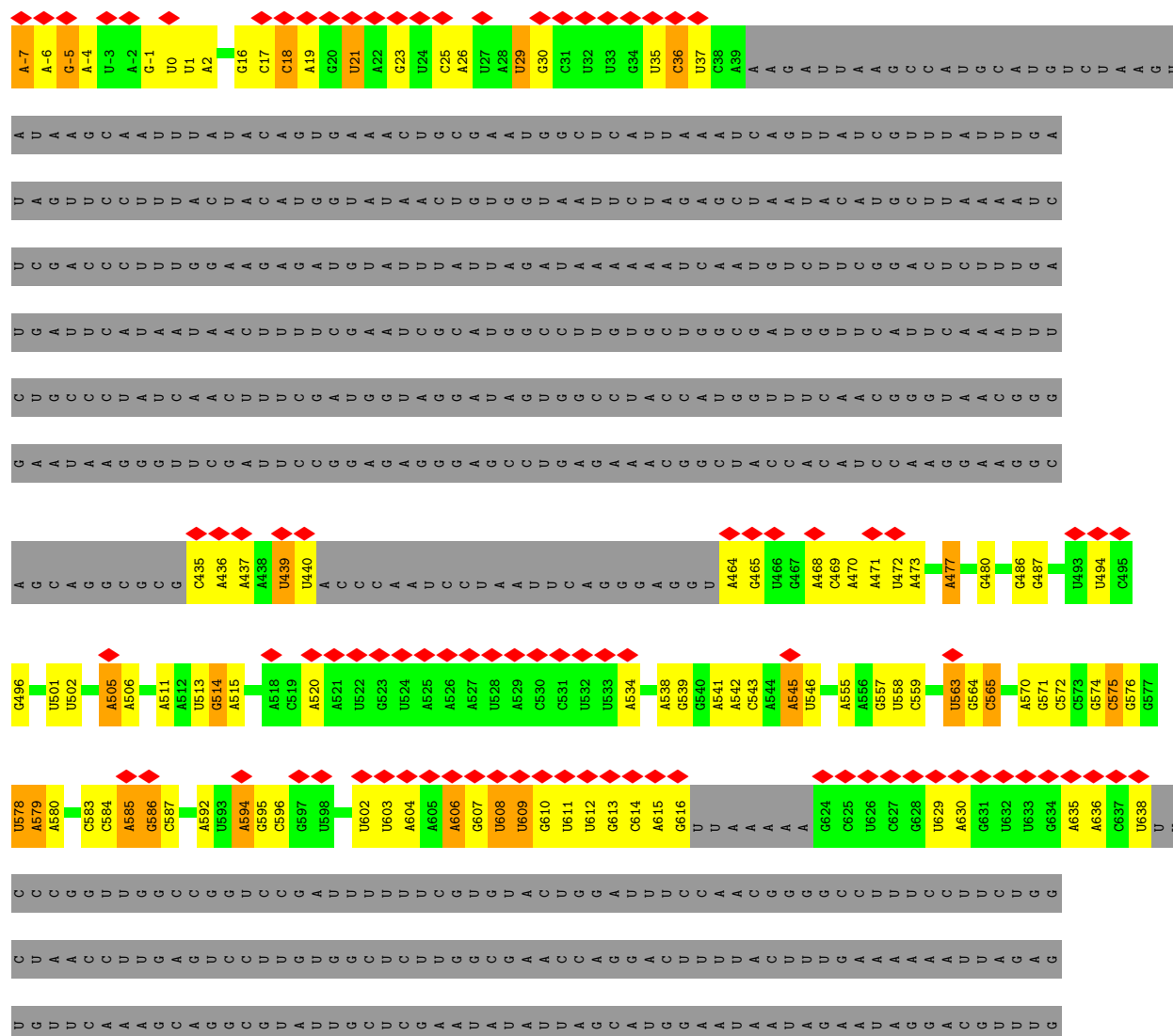
Mol	Chain	Residues	Atoms					AltConf
57	RJ	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

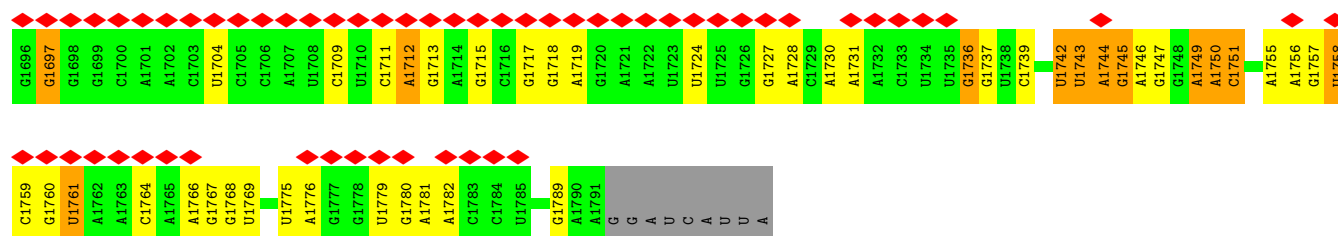
Mol	Chain	Residues	Atoms		AltConf
58	RJ	1	Total	Mg	0
			1	1	



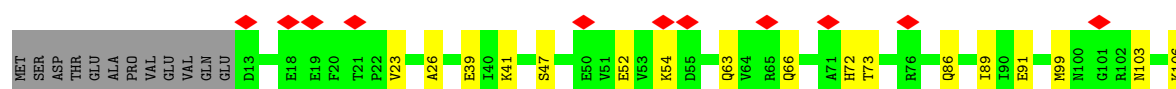
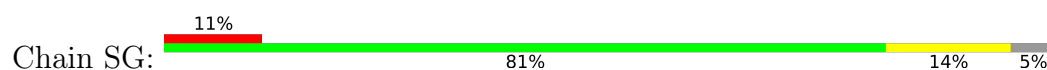
• Molecule 3: 18S rRNA



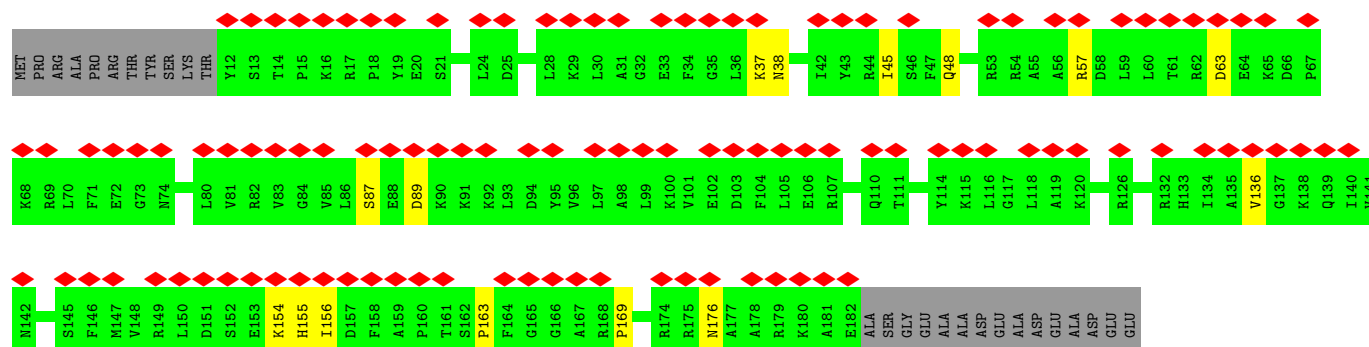
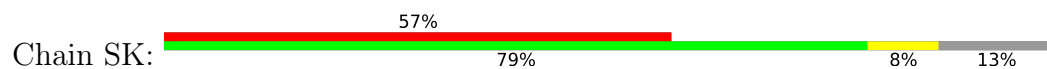




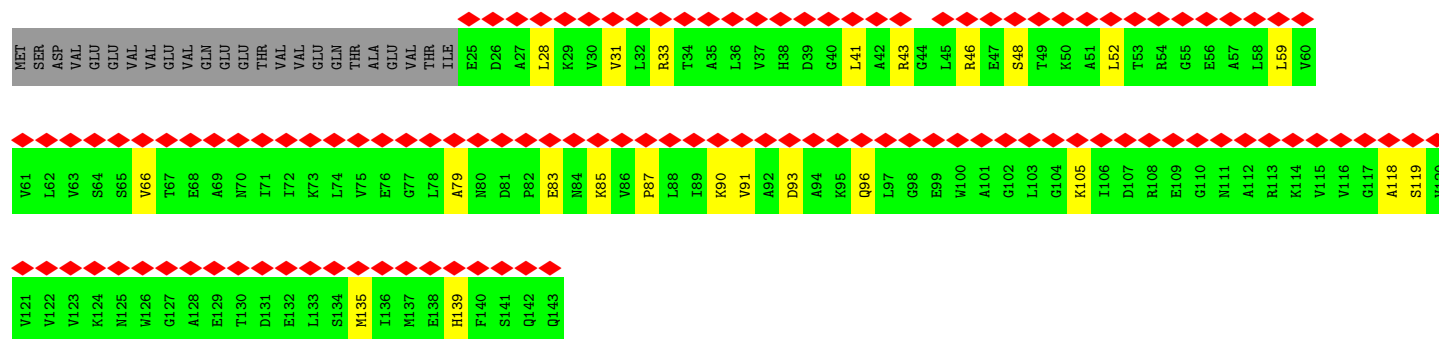
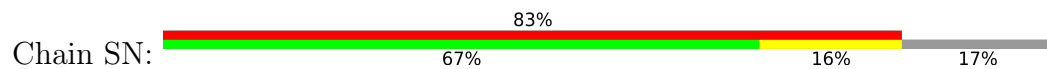
• Molecule 4: 40S ribosomal protein S5



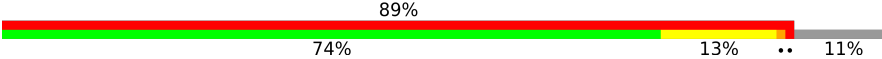
• Molecule 5: 40S ribosomal protein S9-A

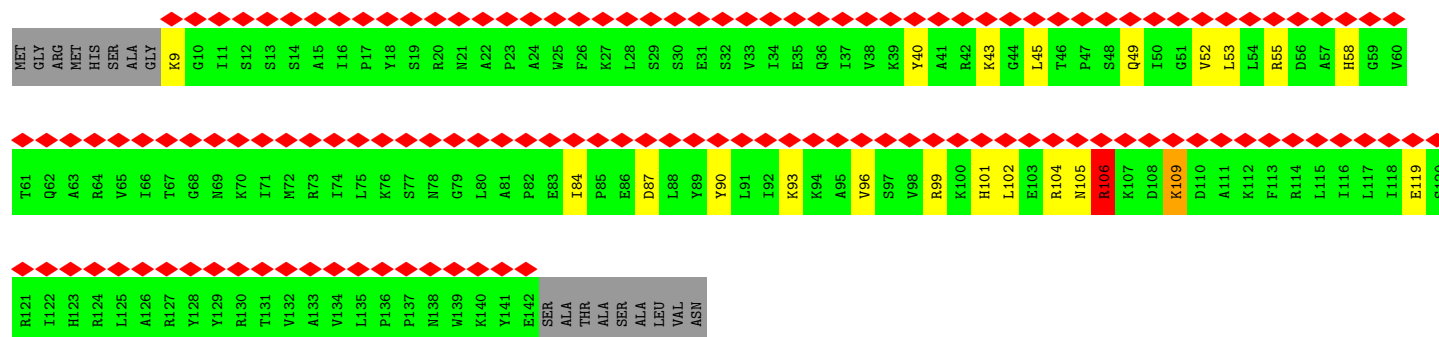


• Molecule 6: 40S ribosomal protein S12



• Molecule 7: 40S ribosomal protein S13

Chain SO: 



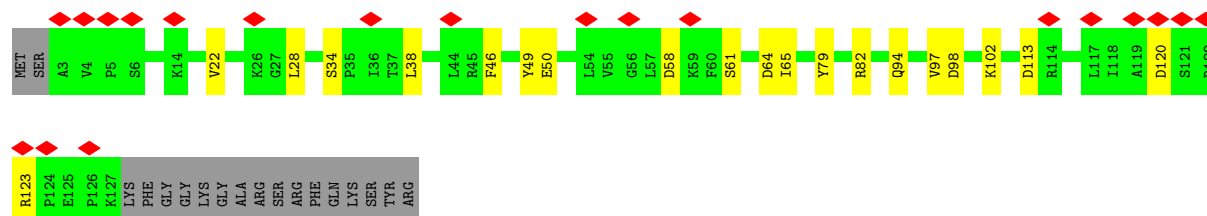
• Molecule 8: 40S ribosomal protein S14-A

Chain SP: 



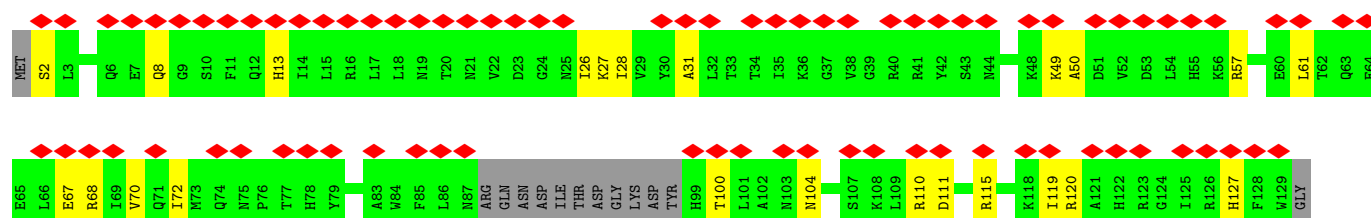
• Molecule 9: 40S ribosomal protein S16-A

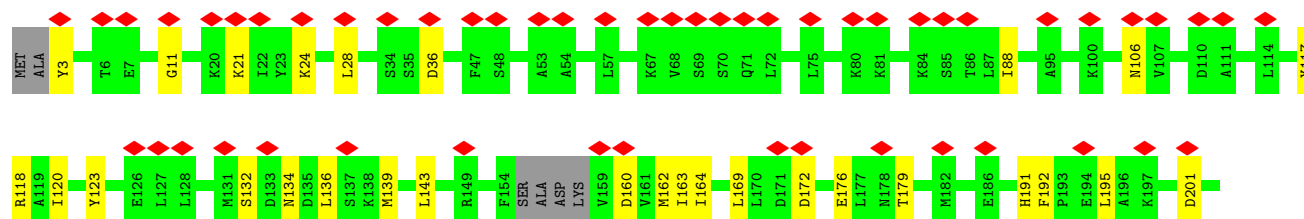
Chain SR: 

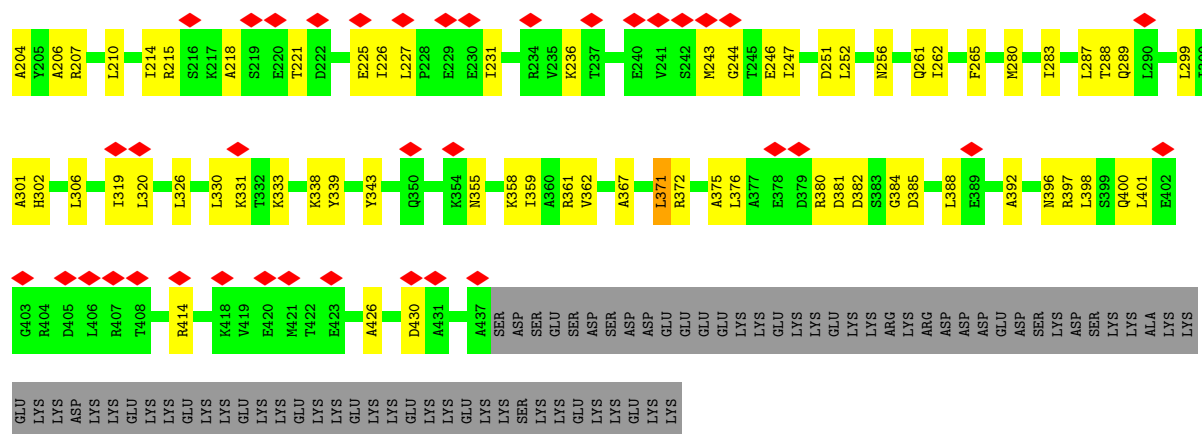


• Molecule 10: 40S ribosomal protein S18-A

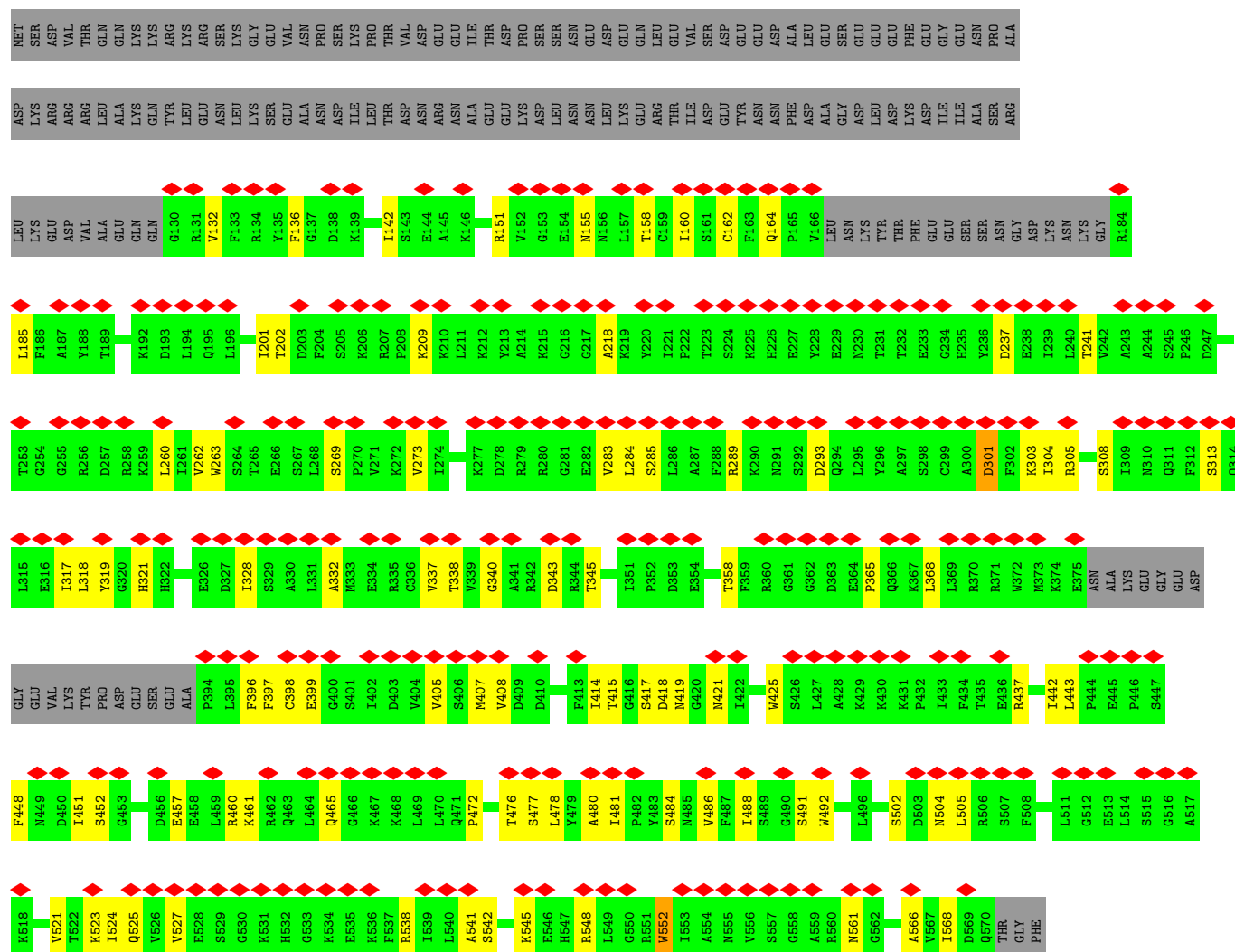
Chain ST: 



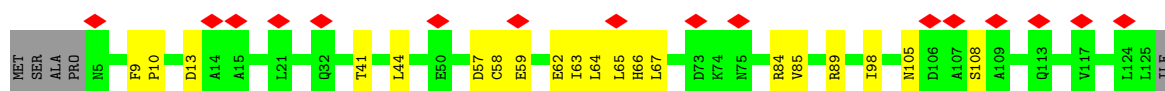
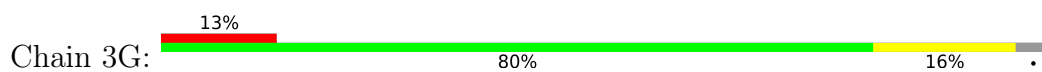




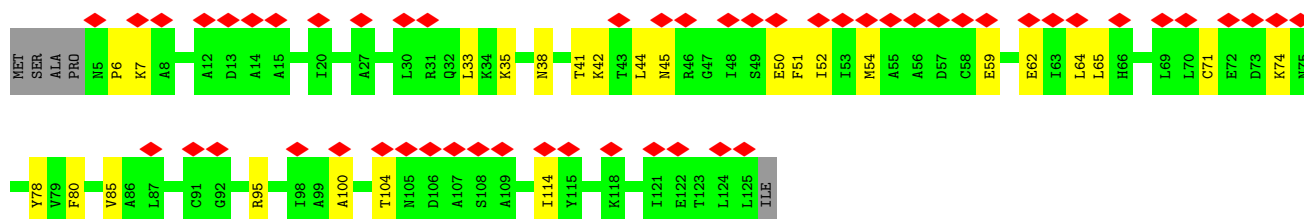
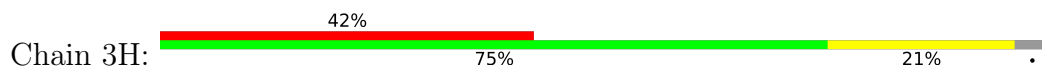
• Molecule 16: Ribosomal RNA-processing protein 9



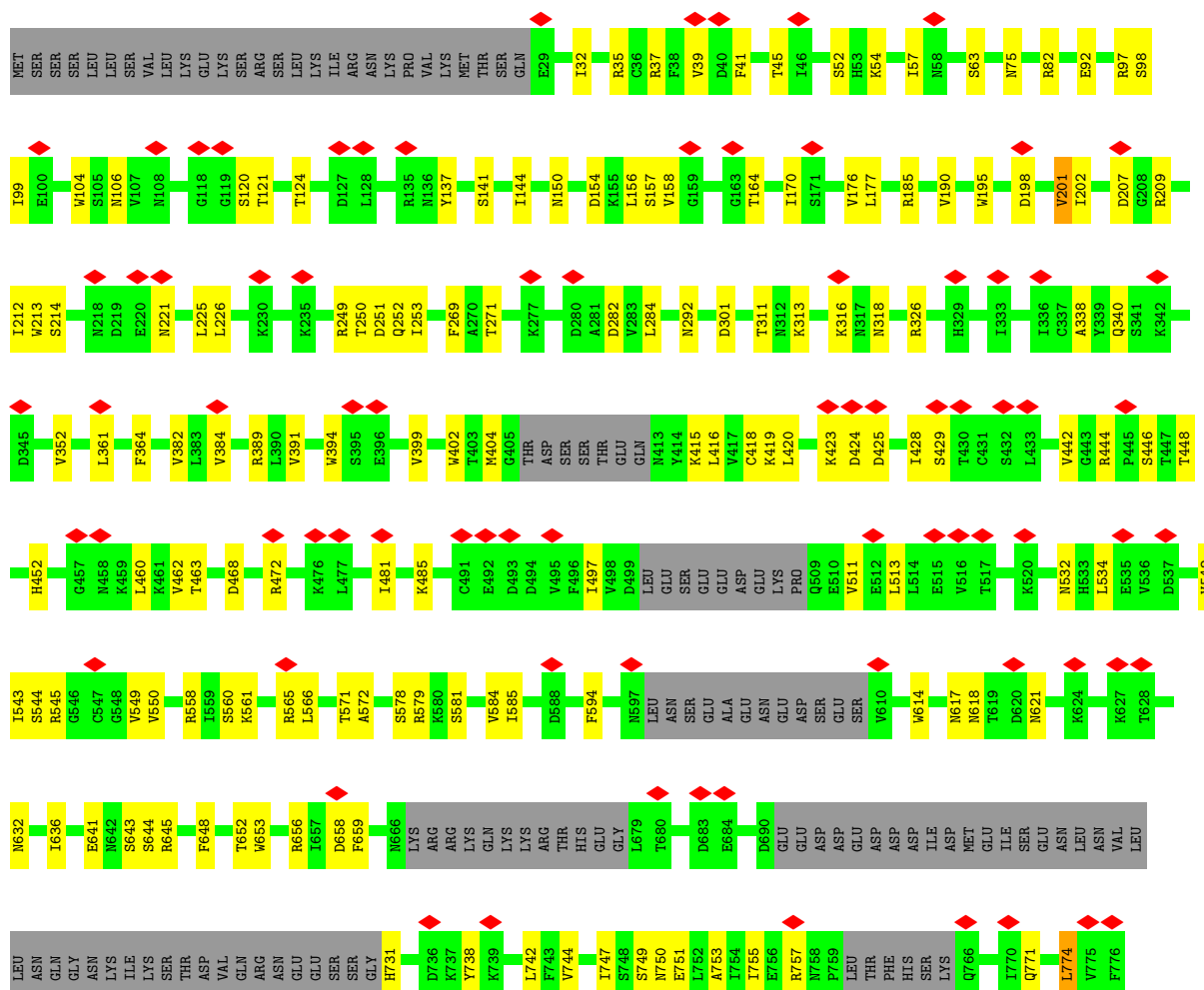
• Molecule 17: 13 kDa ribonucleoprotein-associated protein



- Molecule 17: 13 kDa ribonucleoprotein-associated protein



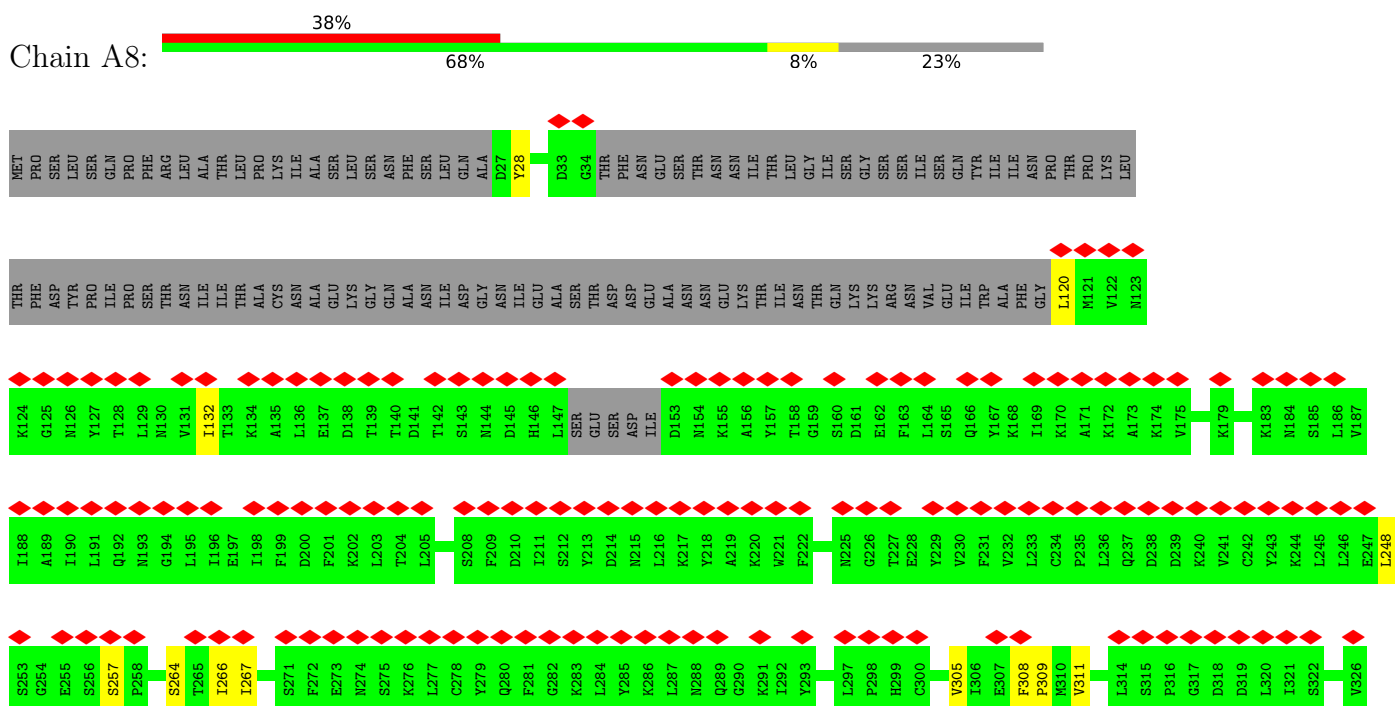
- Molecule 18: U3 small nucleolar RNA-associated protein 4



Chain A5:

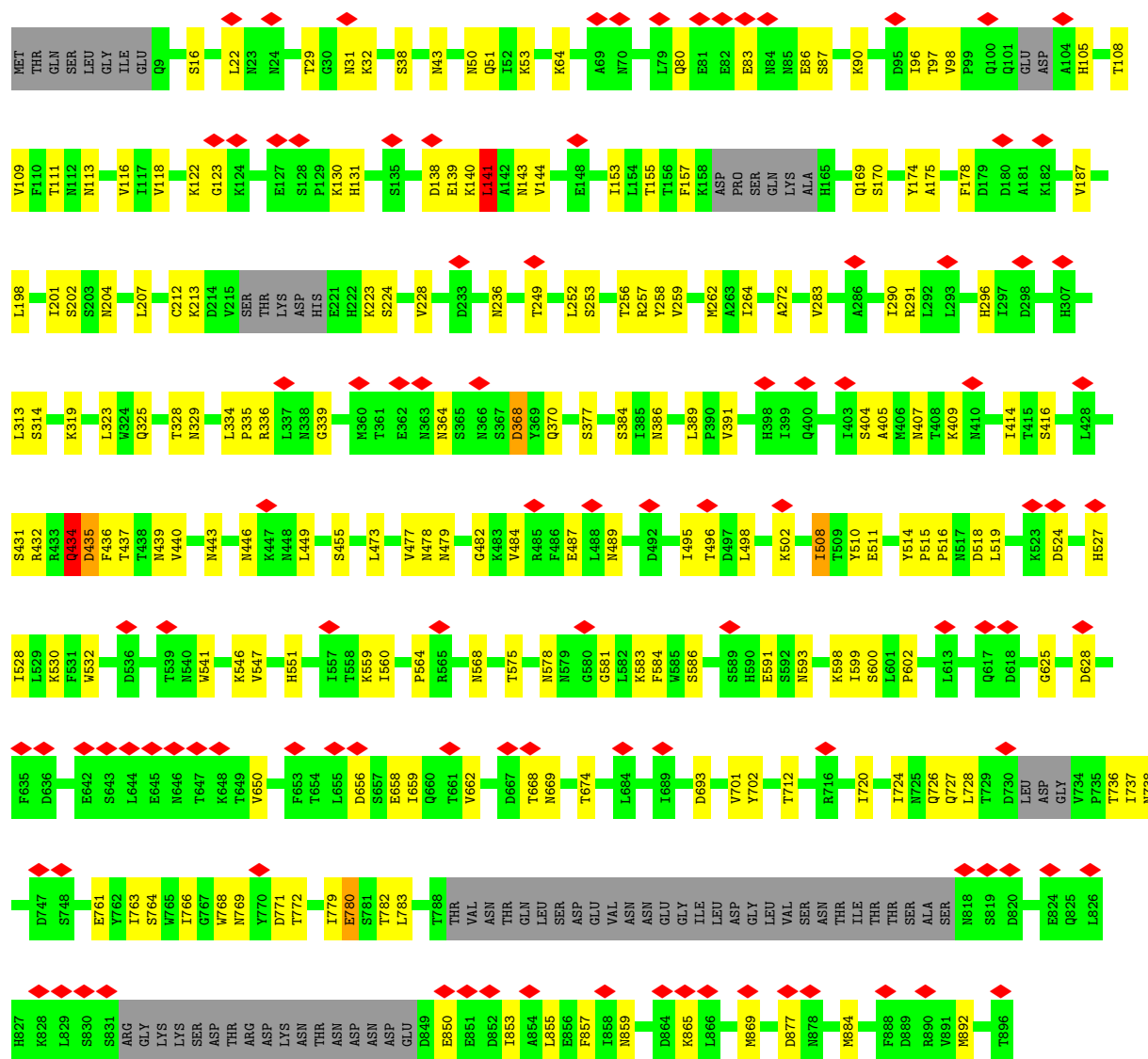


Chain A8:

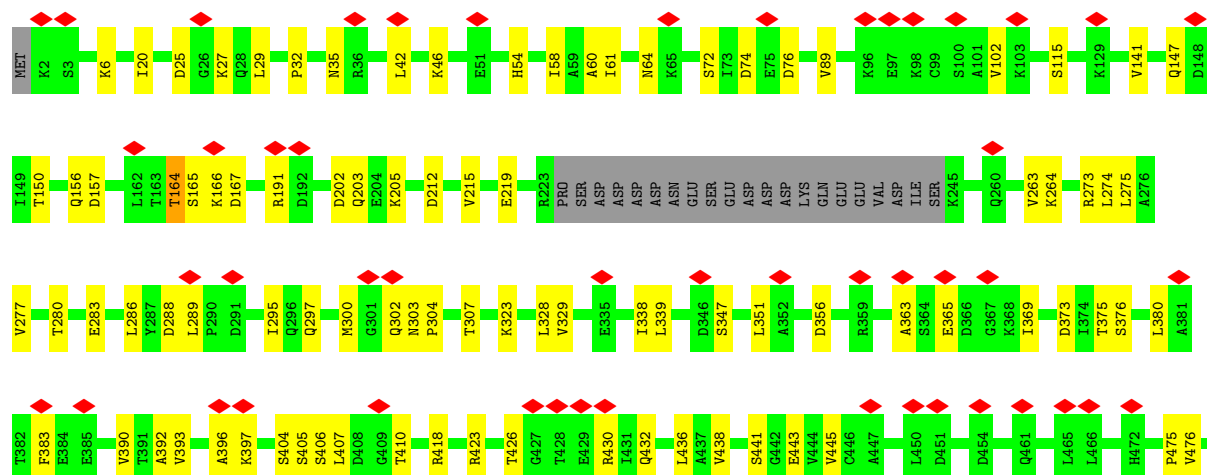
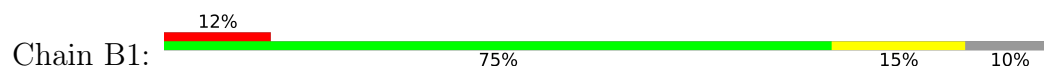


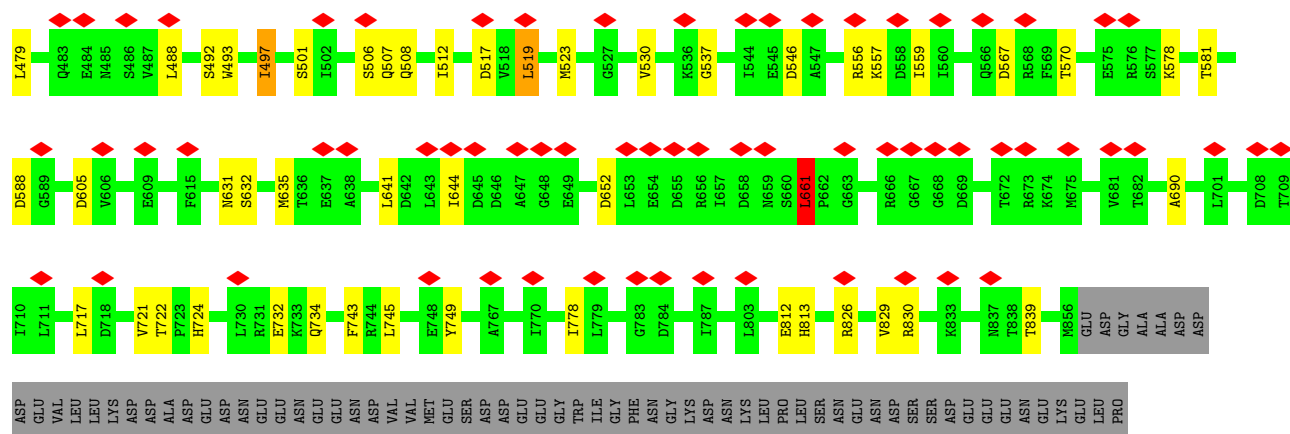




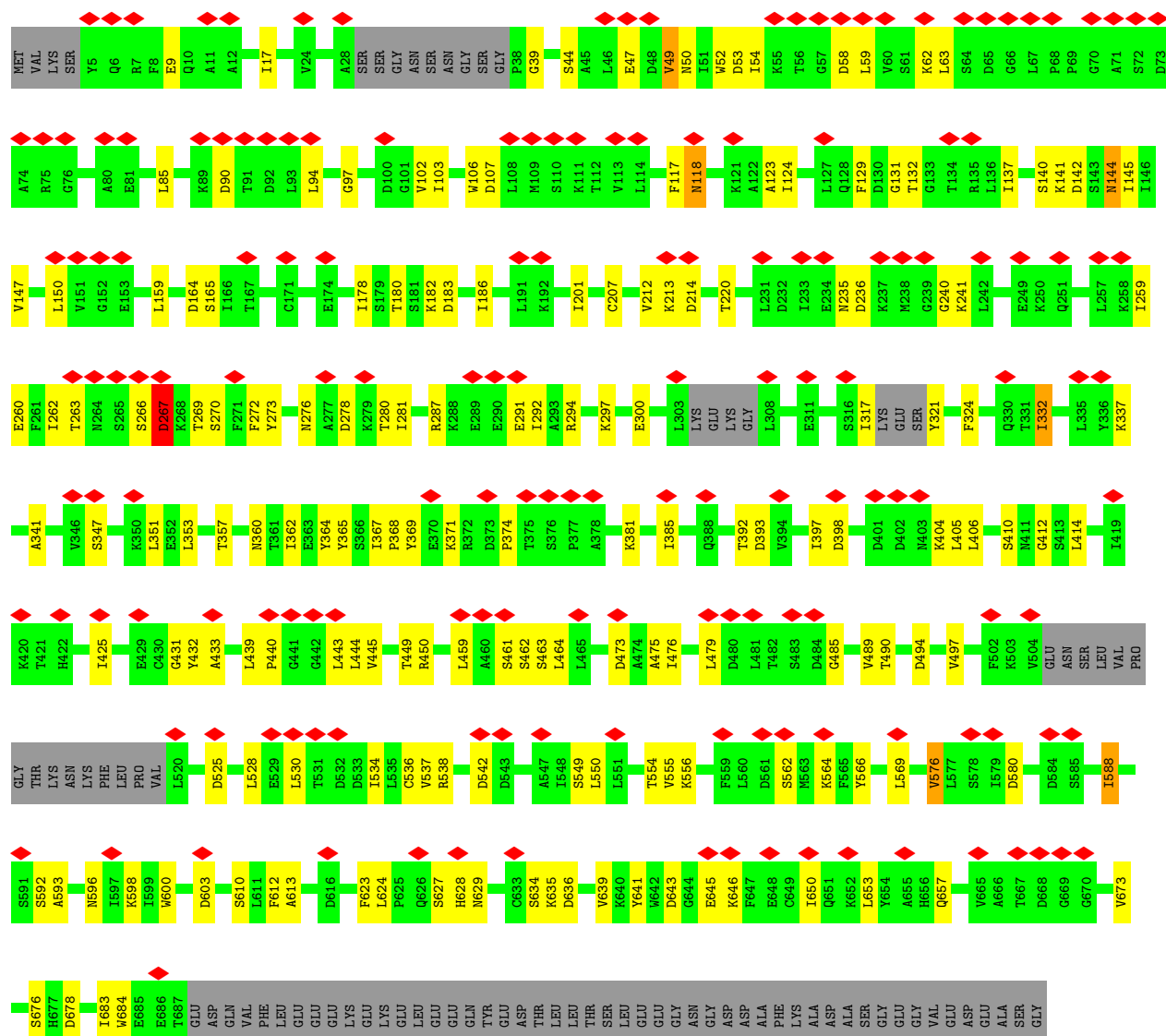


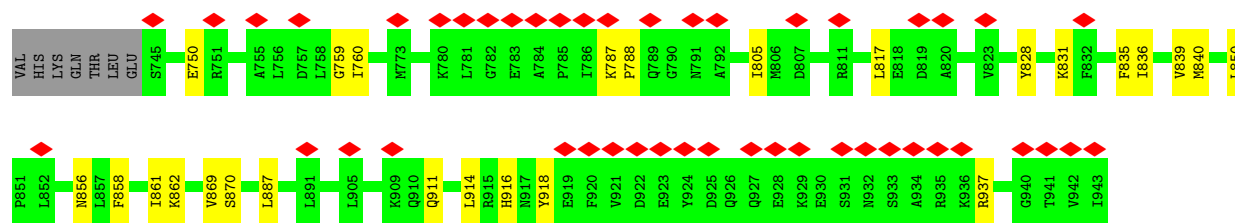
• Molecule 25: Periodic tryptophan protein 2



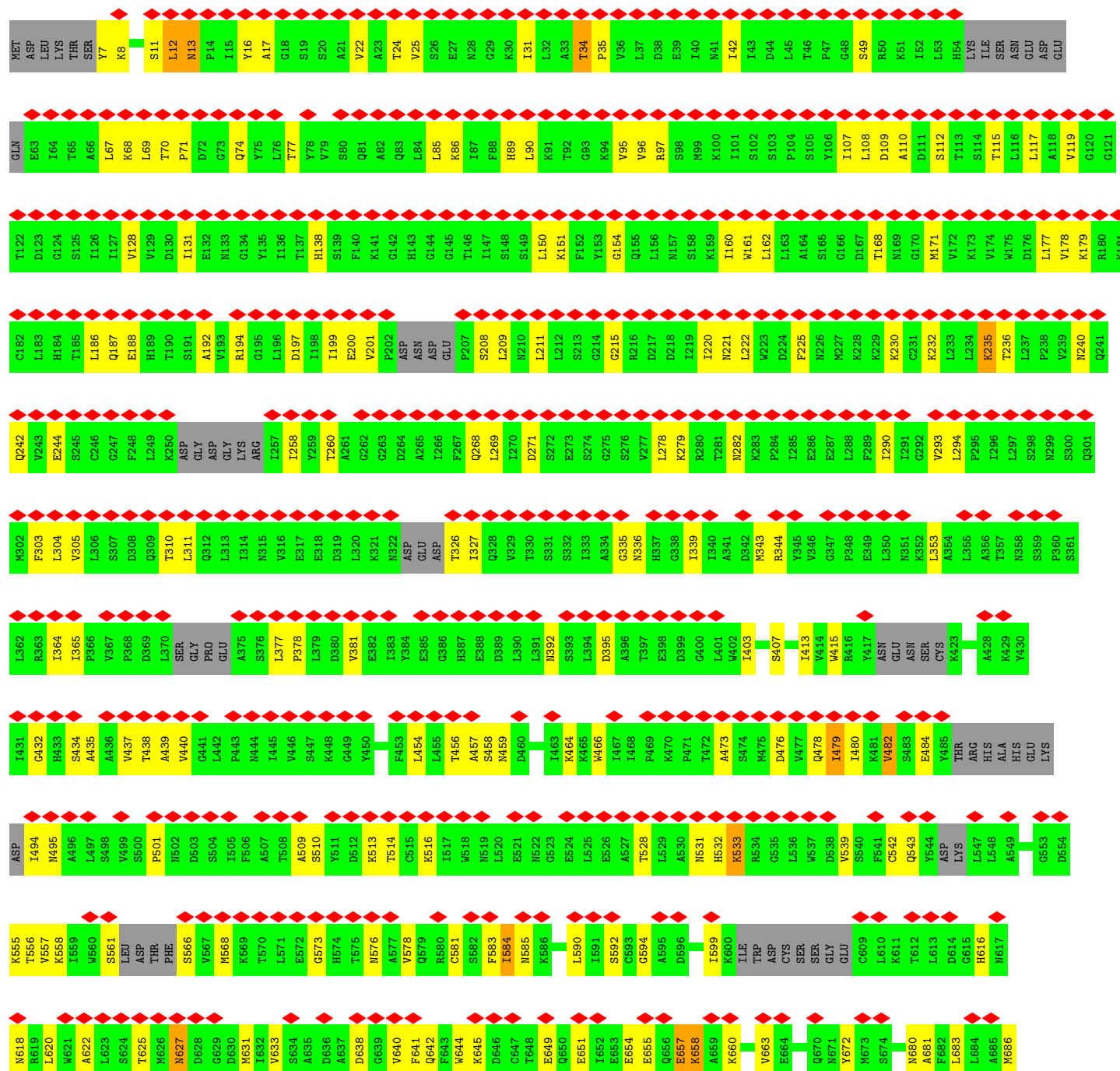


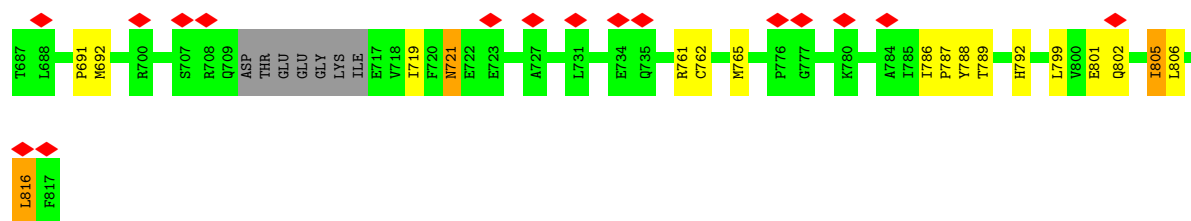
• Molecule 26: U3 small nucleolar RNA-associated protein 12



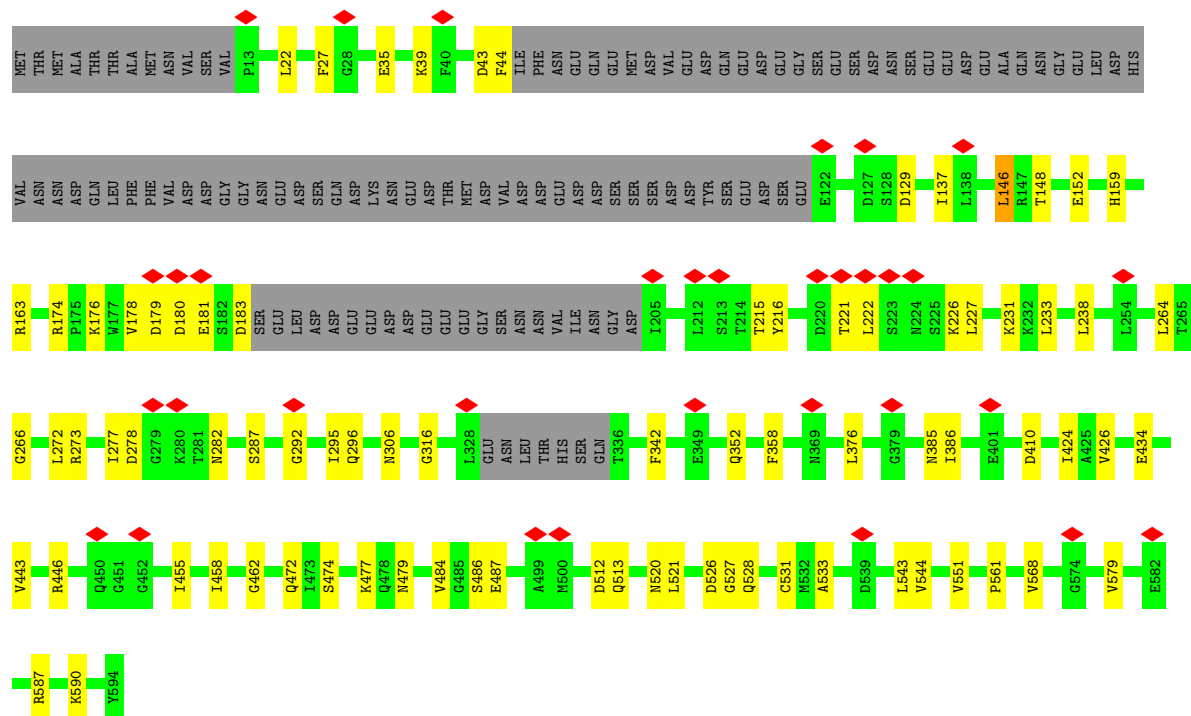


• Molecule 27: U3 small nucleolar RNA-associated protein 13

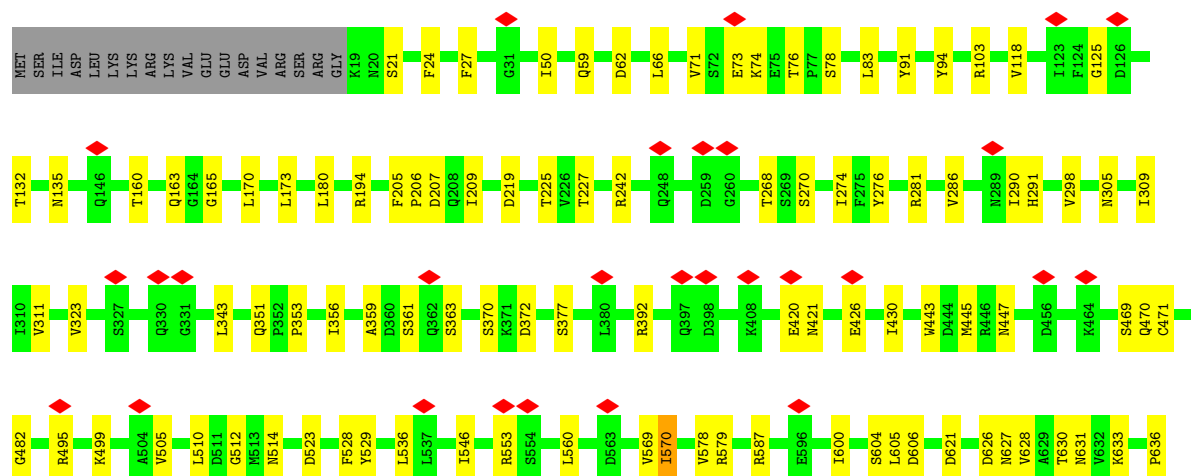
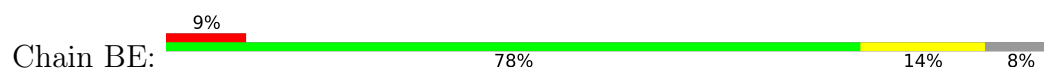


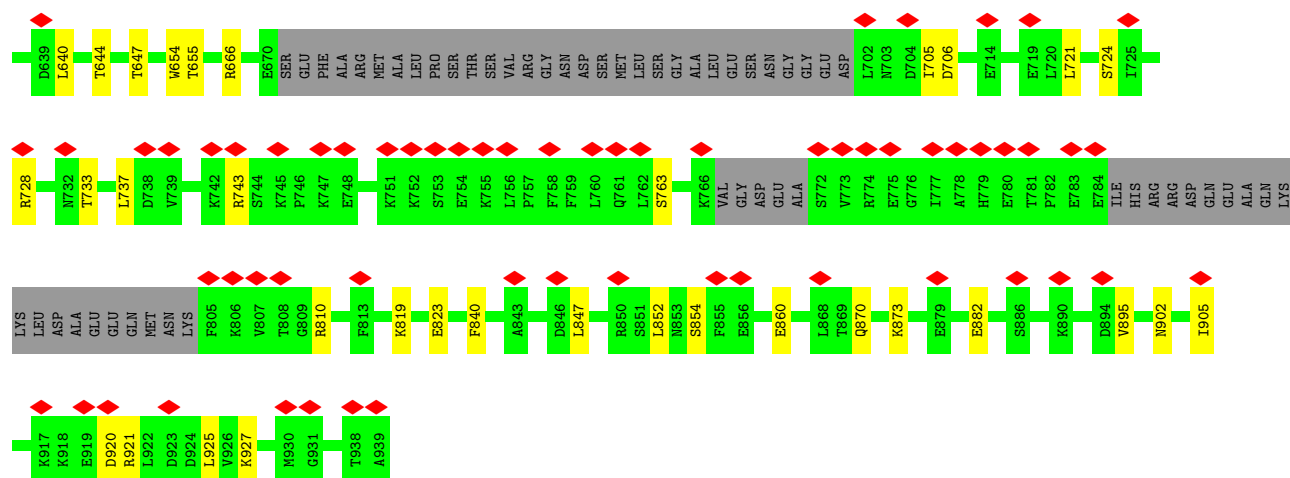


• Molecule 28: U3 small nucleolar RNA-associated protein 18

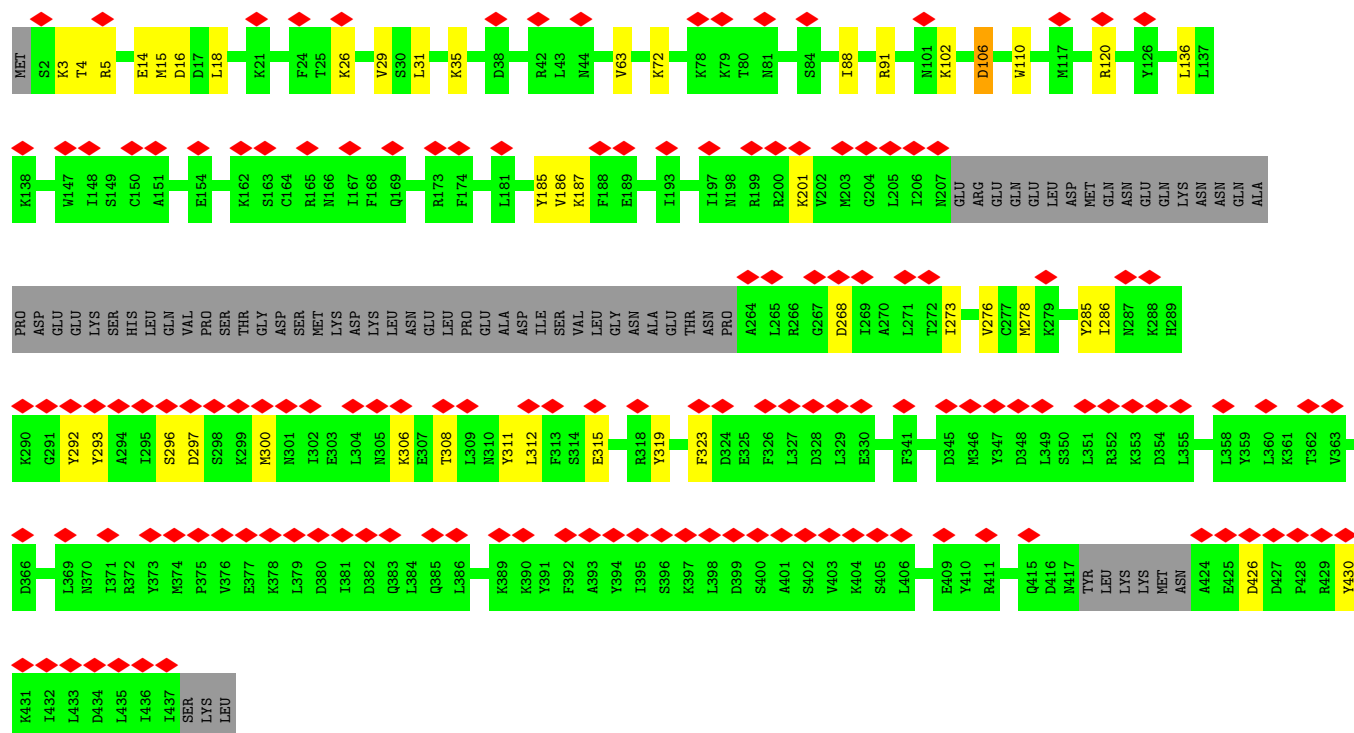
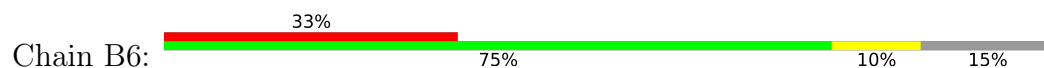


• Molecule 29: U3 small nucleolar RNA-associated protein 21

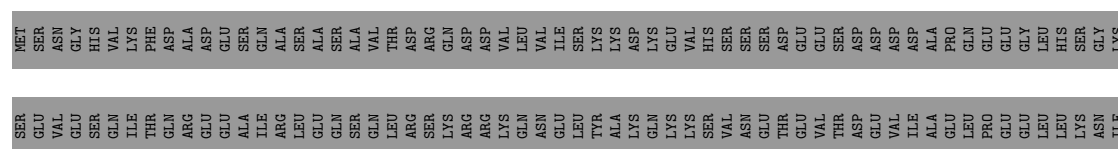


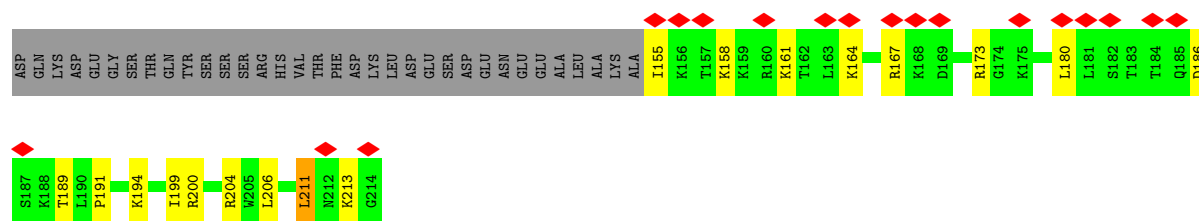


• Molecule 30: U3 small nucleolar RNA-associated protein 6

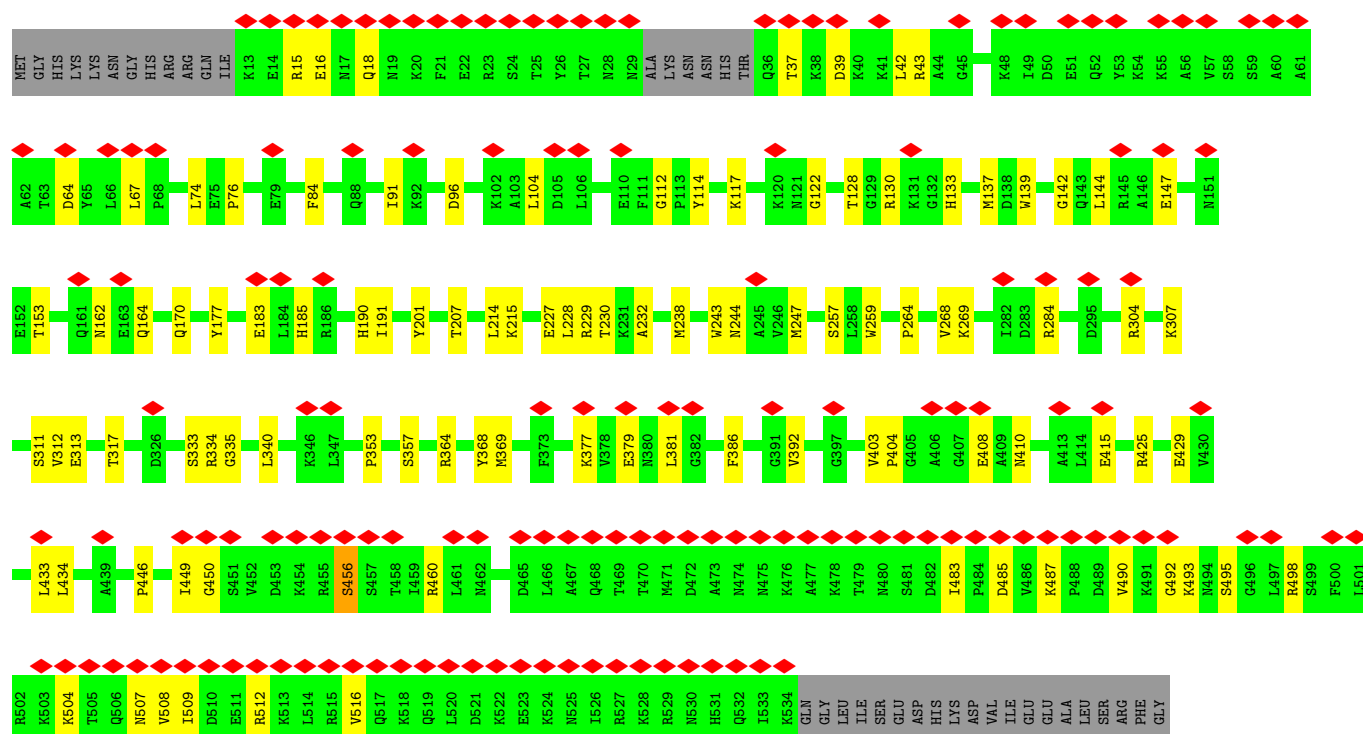
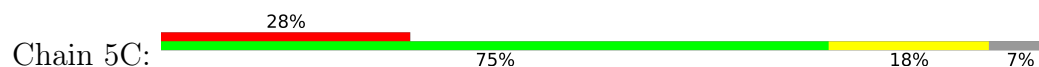


• Molecule 31: Bud site selection protein 21

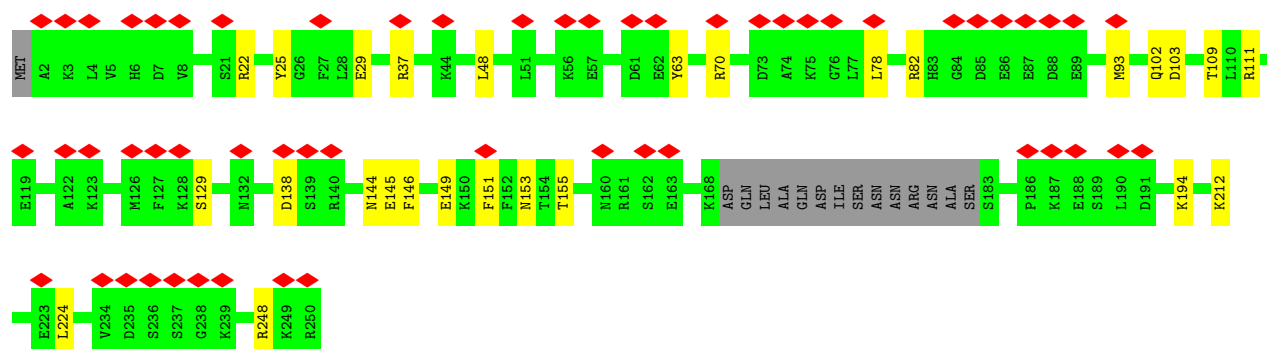
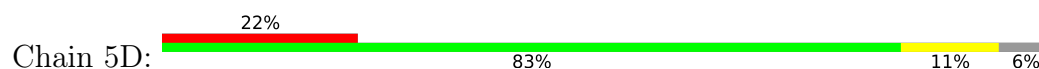




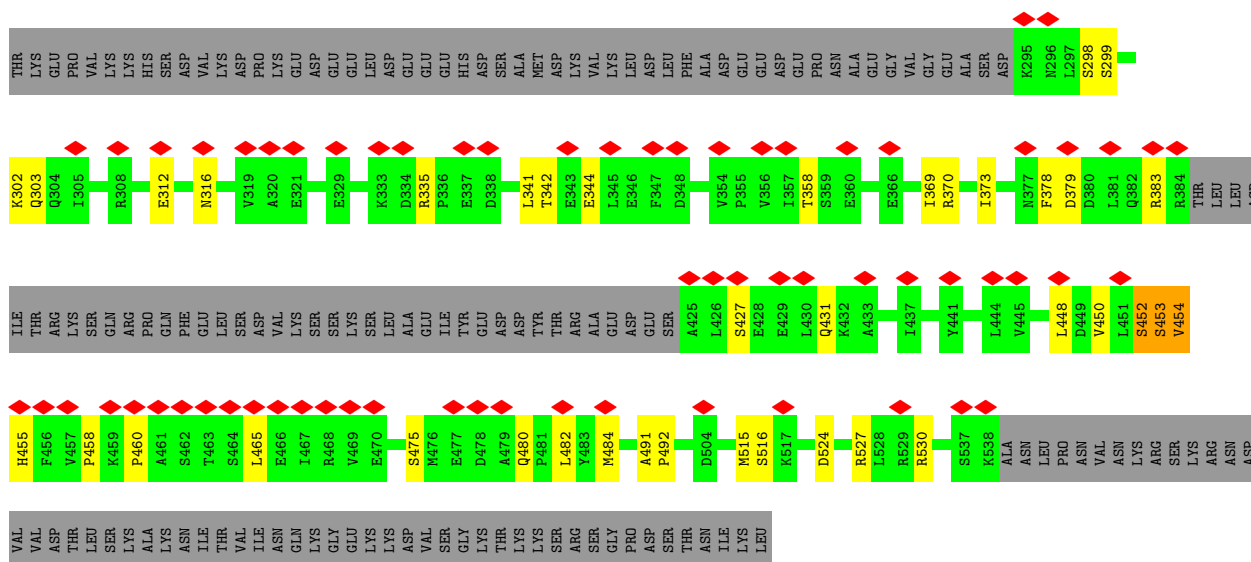
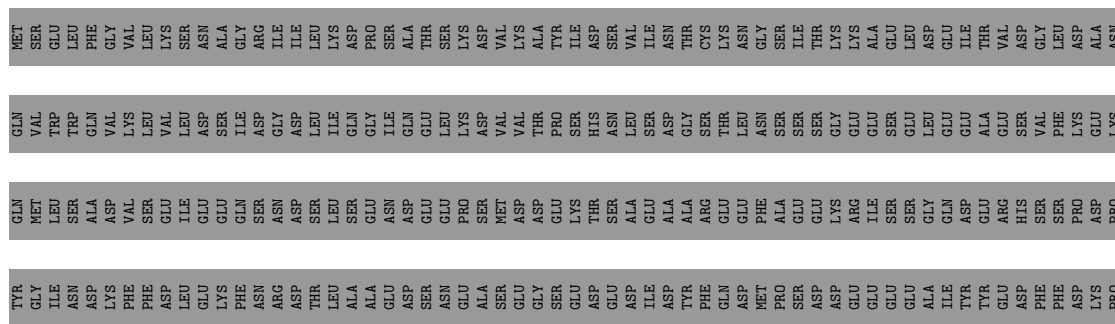
- Molecule 32: U3 small nucleolar RNA-associated protein 7



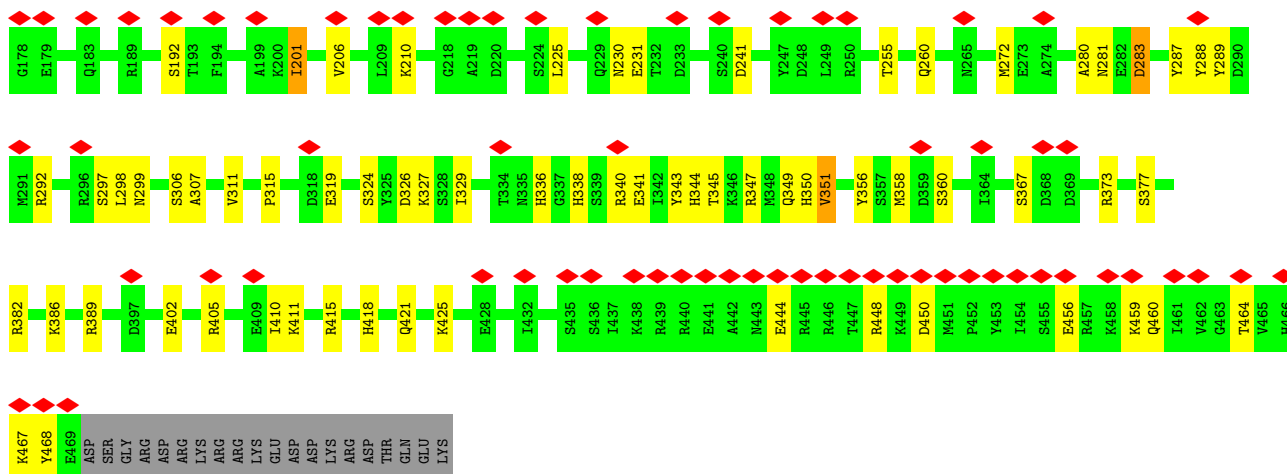
- Molecule 33: U3 small nucleolar RNA-associated protein 11



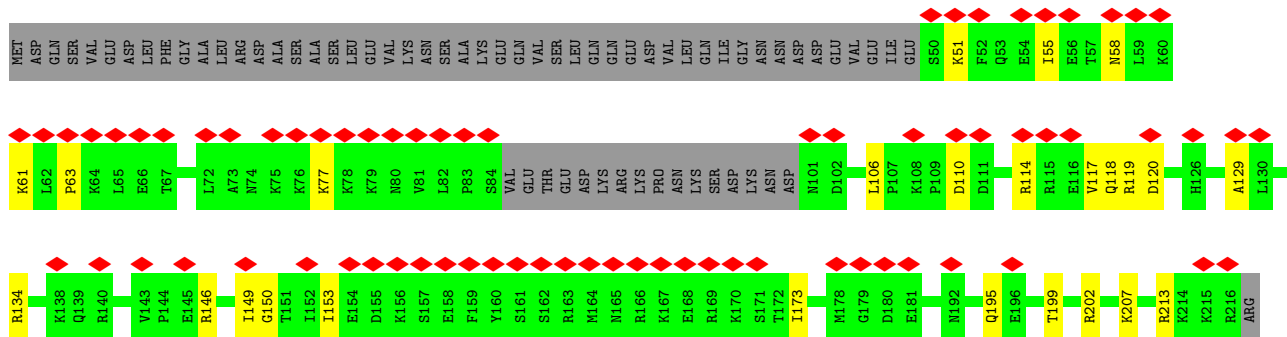
- Molecule 34: U3 small nucleolar RNA-associated protein MPP10

[illegible]

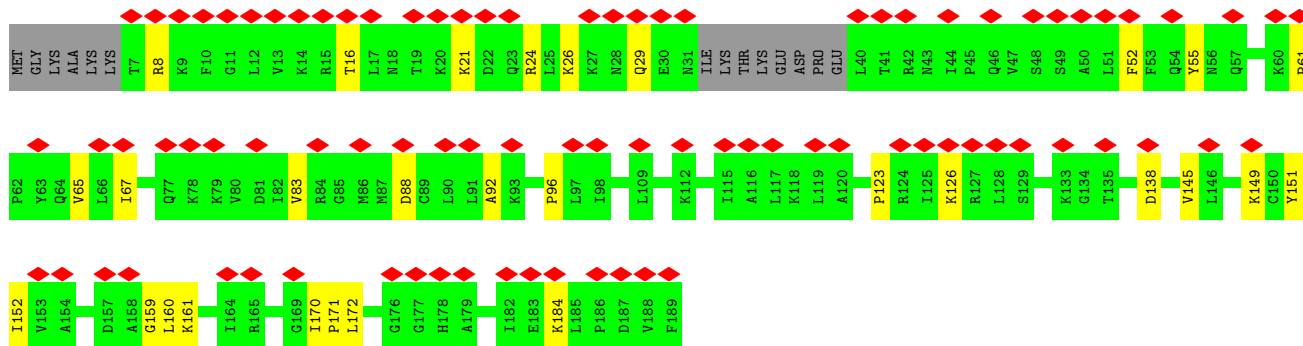
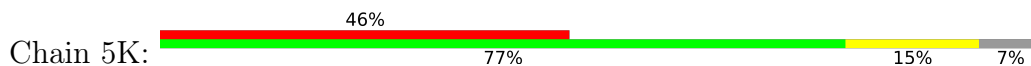
Layer	Input	Output
Encoder	GLU	M1
	GLU	L2
	ALA	R3
	ASP	R4
	ASP	Q5
	LEU	A6
	Q72	R9
	V73	R10
	D74	E11
	E75	Y12
Decoder	E76	L13
	Y77	K16
	A78	A17
	S81	Q18
	M84	L20
	R87	Q21
	I88	D22
	S93	S23
	S97	Q24
	L100	Q27
Bottleneck	K108	K28
	F111	R29
	R116	Q30
	L117	T31
	M118	K33
	R119	Q34
	G120	A35
	M121	L36
	Y122	A37
	V123	Q38
Decoder	M124	C39
	P125	K40
	N126	P41
	K133	L42
	D138	P43
	L139	K44
	L142	E45
	H143	A47
	E144	E48
	H145	D49
Decoder	R146	E50
	G147	S51
	V148	L52
	P149	D55
	T153	F56
	I154	D59
		Q60
		S61
		L62
		K63
GLU		



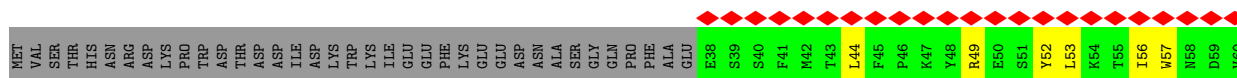
• Molecule 39: rRNA-processing protein FCF2

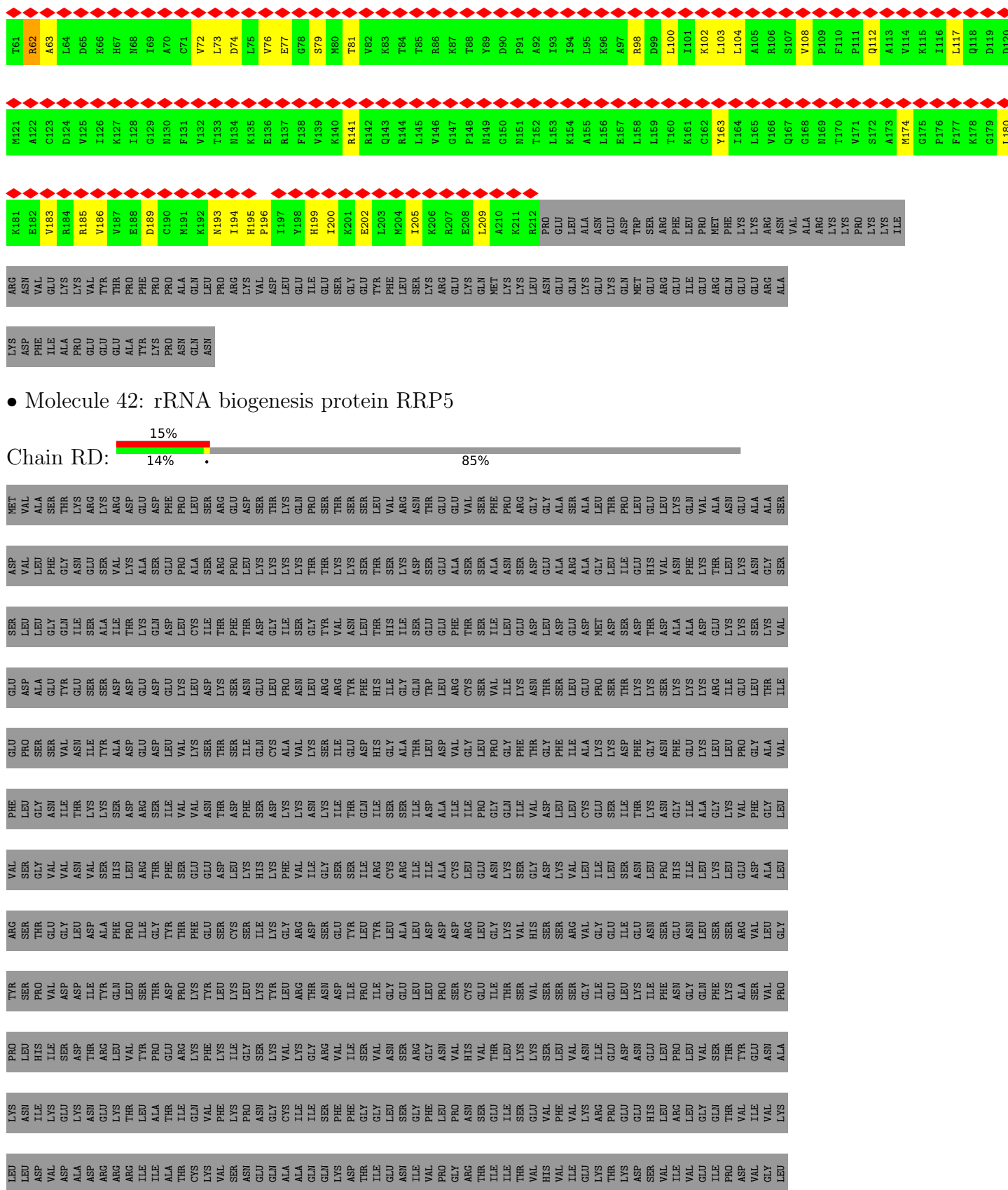


• Molecule 40: rRNA-processing protein FCF1

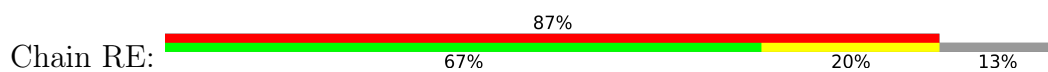


• Molecule 41: KRR1 small subunit processome component

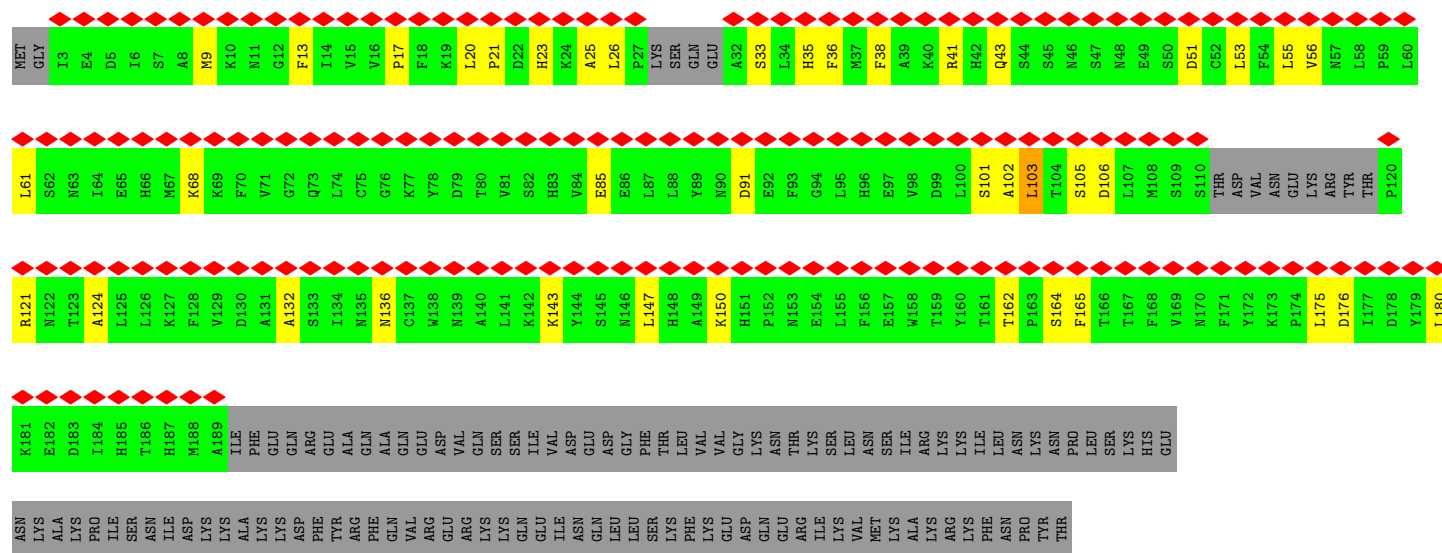




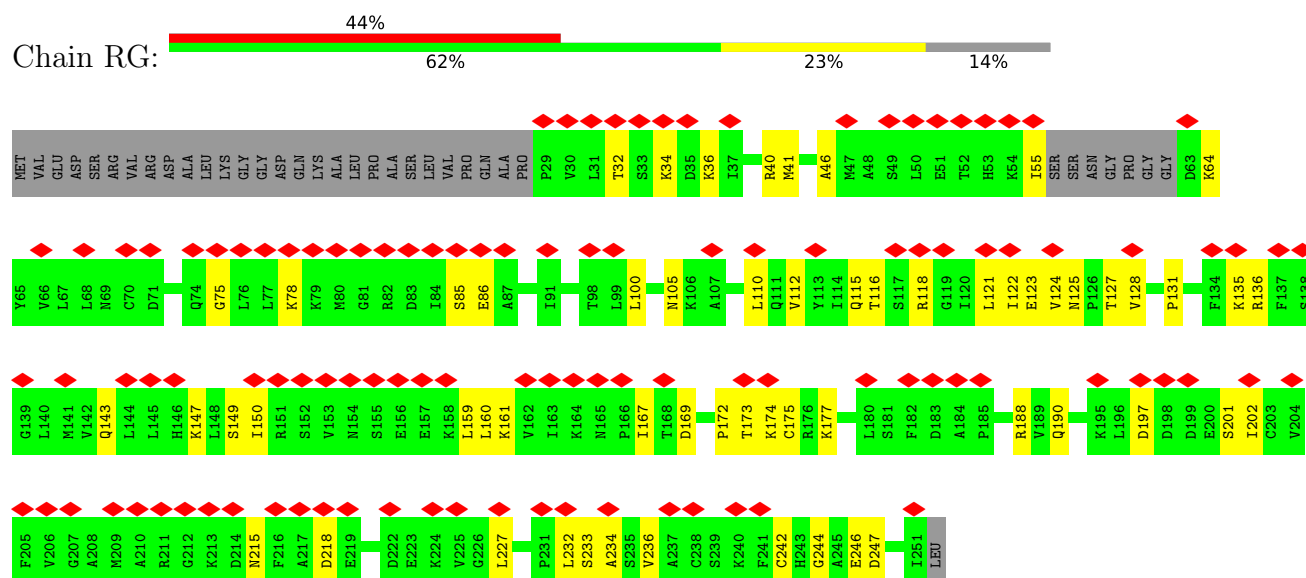
- Molecule 43: U3 small nucleolar RNA-associated protein 22



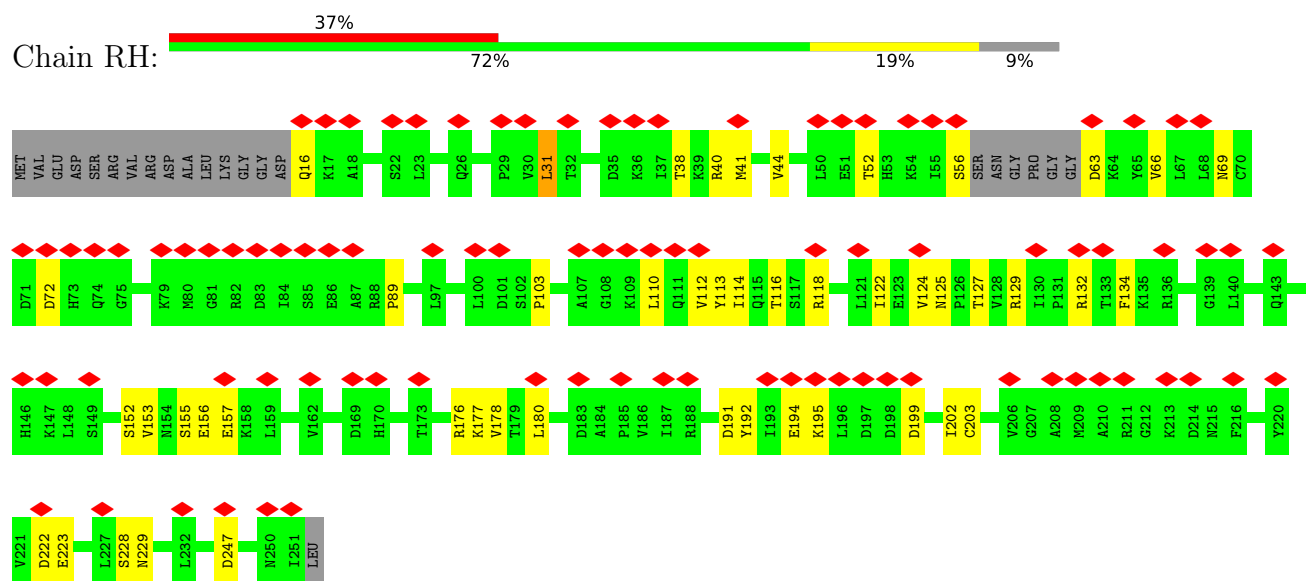
MET	ALA	THR	SER	VAL	GLY	ARG	LYS	ALA	SER	GLU	THR	ALA	SER	THR	ASP	GLN	ASN	ILE	VAL	LYS	VAL	GLN	LYS	LYS	HIS	SER	THR	GLN	ASP	ASN	GLY	SER	GLU	ASN	LEU	PHE	LYS	S100	N101	I102	F103	ILE	ASN	GLU	ARG	THR	VAL	PRO	GLU	GLU	ASP	GLU	SER	THR						
SER	PRO	GLU	SER	ASN	GLY	VAL	ALA	THR	ASN	THR	ALA	ALA	THR	THR	THR	ARG	HIS	ASN	GLY	LYS	VAL	THR	ALA	LYS	THR	GLU	SER	THR	TTR	ASP	ILE	HIS	ILE	ALA	ARG	THR	LYS	S100	N101	I102	F103	ILE	ASN	GLU	ARG	THR	VAL	PRO	GLU	GLU	ASP	GLU	SER	THR						
V121	L122	K123	V124	L125	K126	F127	L128	H129	L130	L131	Y132	I133	L135	Q136	I137	P138	P139	D140	W141	E142	E143	K144	S145	L146	A147	E148	V149	D150	S151	F152	F153	K154	N155	K156	L157	V158	I159	V160	P161	F162	V163	D164	P165	K166	P167	I168	S169	Q170	N171	T172	Y173	Y174	K175	F176	N177	Y178	K179	K180		
P181	D182	I183	S184	L185	I186	G187	S188	F189	A190	L191	K192	A193	G194	I195	Y196	Q197	P198	N199	G200	S201	S202	I203	D204	T205	L206	L207	T208	M209	P210	K211	E212	L213	F214	E215	K216	K217	D218	F219	L220	N221	F222	R223	C224	L225	H226	K227	R228	R229	V230	Y231	L232	A233	Y234	L235	T236	H237	N238	L239	L240	
I241	L242	L243	K244	K245	D246	K247	L248	D249	S250	F251	L252	Q253	L254	E255	Y256	S257	Y258	F259	D260	N261	D262	P263	L264	L265	P266	I267	L268	R269	I270	S271	C272	S273	K274	PRO	THR	GLY	ASP	SER	LEU	SER	D282	Y283	F285	Y286	K287	T288	R289	F290	S291	I292	N293	L294	L295	L296	G297	F298	P299	Y300		
K301	V302	F303	E304	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	F332	N333	F334	S335	V336	L337	S338	S339	S340	T341	H342	E343	N344	Y345	L346	K347	Y348	L349	Y350	K351	T352	K353	K354	Q355	T356	G357	S358	F359	V360	
E361	A362	T363	V364	L365	G366	R367	L368	N369	L370	Q371	Q372	R373	G374	F375	S376	S377	N378	K379	S380	H381	S382	G383	S384	L385	G386	G387	F388	G389	T390	F391	E392	F393	T394	I395	L396	K397	A398	A399	L400	L401	N402	G403	G404	G405	L406	T407	S408	N409	K410	I411	L412	L413	H414	G415	F416	S417	S418	Y419	Q420	
L421	F422	K423	G424	V425	L426	K427	Y428	L429	A430	T431	M432	D433	L434	C435	H436	D437	G438	H439	L440	Q441	F442	H443	S444	N445	PRO	GLU	ASN	SER	SER	SER	P453	A454	S455	K456	Y457	L458	D459	E460	G461	F462	Q463	T464	P465	T466	L467	F468	D469	K470	S471	T472	K473	V474	N475	L476	L477	T478	K479	N480		
T481	V482	S483	S484	Y485	Q486	L487	L488	K489	E490	Y491	A492	G493	K494	T495	L496	R497	M498	L499	N500	N501	V502	V503	Q504	D505	O506	F507	S508	N509	I510	F511	L512	T513	N514	I515	S516	R517	D518	N519	N520	L521	K522	Y523	D524	L525	C526	Y527	D528	V529	L531	P532	L533	Q534	K535	Y536	N537	N538	L539	E540		
T541	S542	L543	A544	A545	T546	F547	G548	S549	M550	E551	R552	V553	K554	F555	I556	T557	L558	E559	N560	F561	L562	A563	H564	K565	I566	T567	N568	V569	A570	R571	Y572	A573	L574	G575	D576	R577	L578	K579	Y580	I581	O582	L583	E584	M585	V586	G587	O588	K589	S590	D591	F592	P593	T594	T595	K596	R597	K598	V599	Y600	
S601	N602	T603	G604	G605	N606	H607	F608	N609	F610	D611	F612	V613	B614	V615	K616	L617	L618	V619	N620	P621	S622	K623	C624	D625	K626	L627	V628	T629	K630	G631	P632	A633	H634	S635	E636	T637	H638	S639	T640	S641	A642	A643	A644	V644	F645	K646	M647	F648	M649	G650	I651	K652	S653	S654	L655	R656	R657	F658	K659	D660
G661	S662	I663	T664	H665	C666	C667	V668	W669	S670	T671	S672	S673	S674	E675	P676	L677	L678	S679	S680	F681	V682	N683	F684	A685	L686	Q687	K688	H689	V690	S691	K692	K693	A694	Q695	L696	S697	N698	E699	T700	I701	K702	K703	F704	H705	M706	F707	L708	P709	L710	P711	N712	L713	P714	S715	S716	A717	K718	T719	S720	
V721	L722	M723	L724	S725	S726	F727	F728	M729	L730	K731	K732	S733	F734	S735	D736	L737	Y738	K739	I740	I741	F742	Q743	M744	K745	L746	P747	L748	S749	V750	K751	S752	I753	L754	F755	V756	G757	S758	A759	F760	R761	Y762	T763	S764	L765	C766	Q767	F768	V769	P770	F771	A772	Y773	S774	D775	P776	D777	F778	F779	Q780	



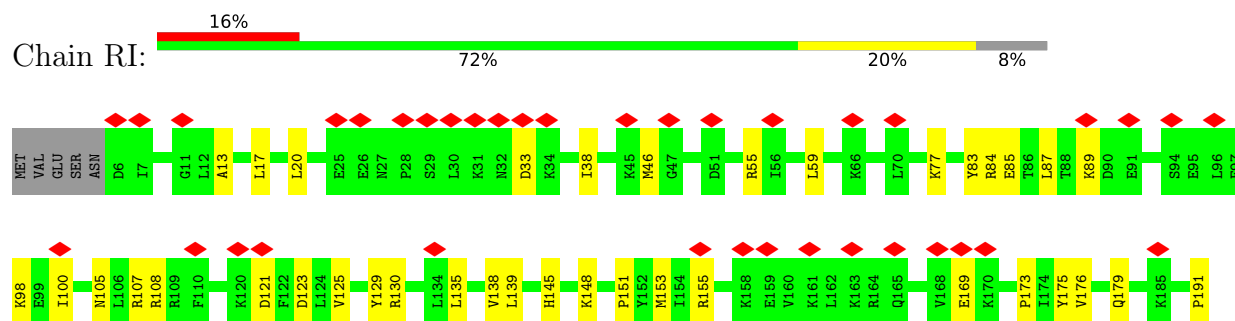
- Molecule 45: Ribosomal RNA small subunit methyltransferase NEP1

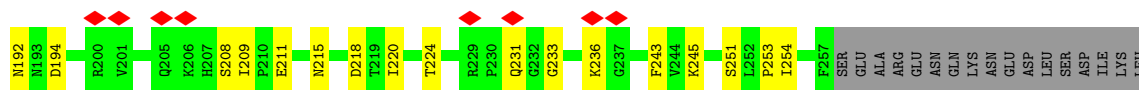


- Molecule 45: Ribosomal RNA small subunit methyltransferase NEP1

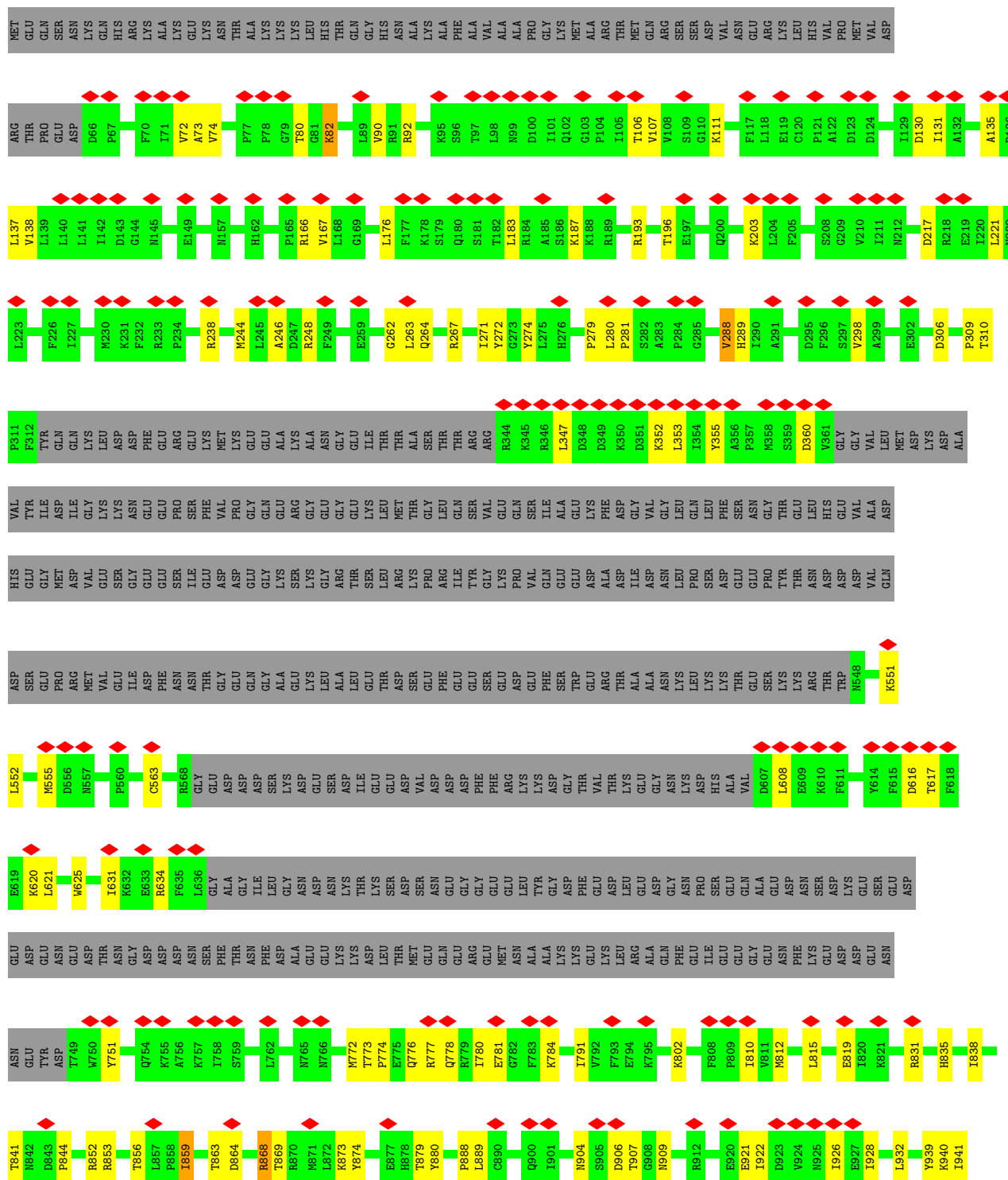


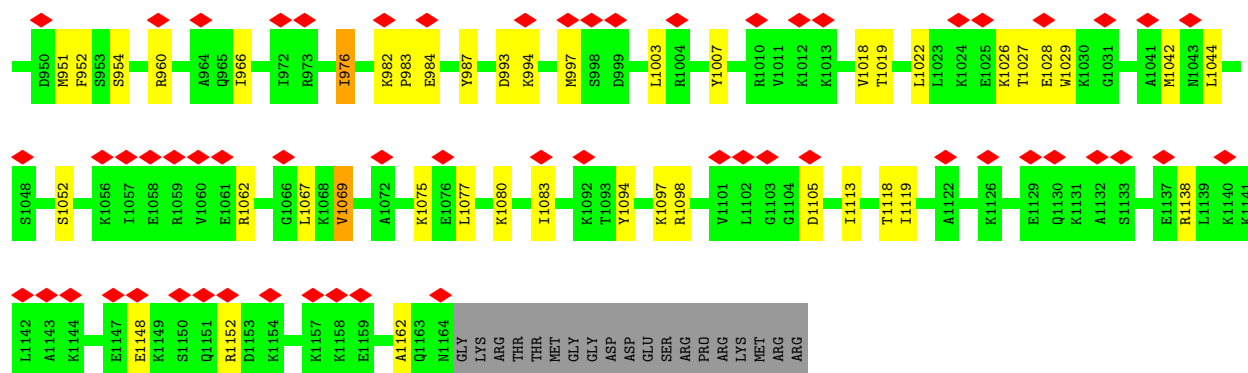
- Molecule 46: Ribosome biogenesis protein UTP30



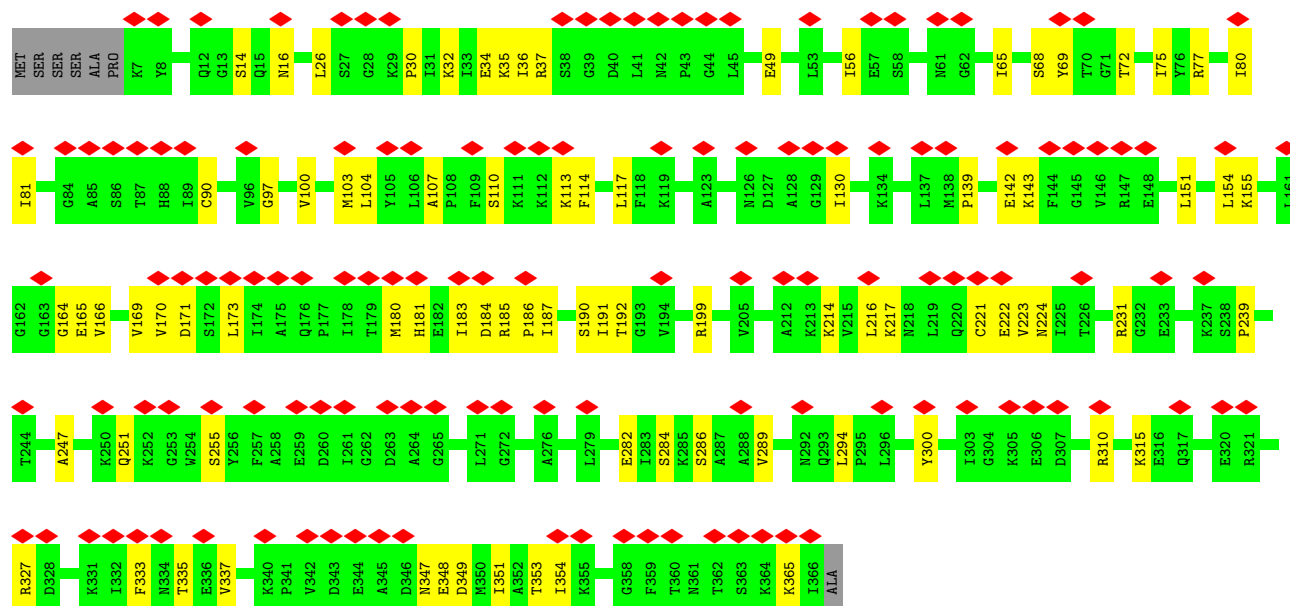
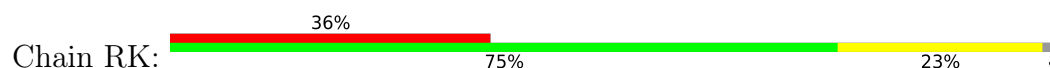


• Molecule 47: Ribosome biogenesis protein BMS1

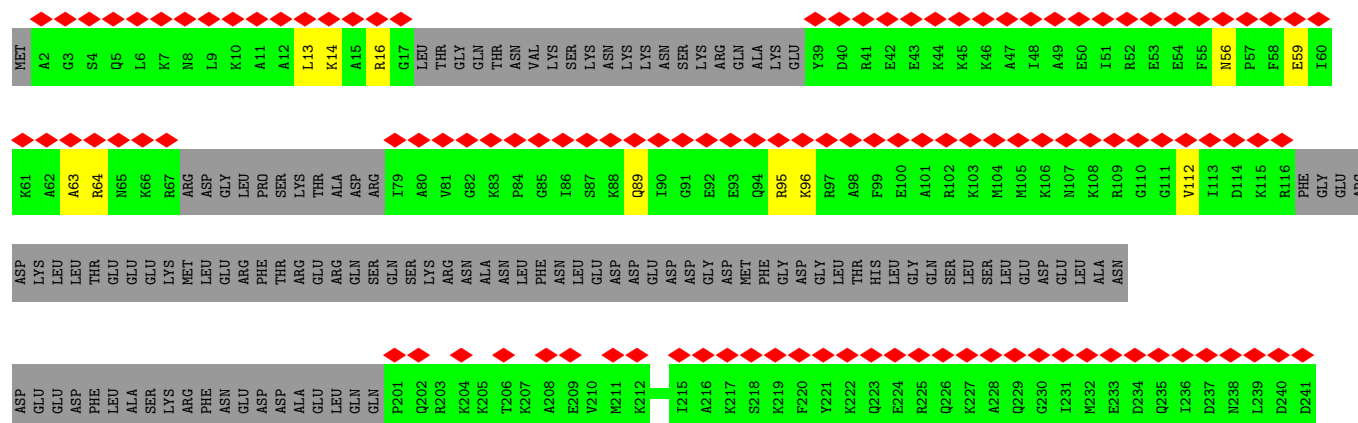
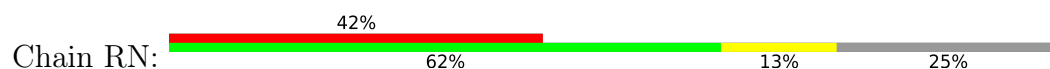


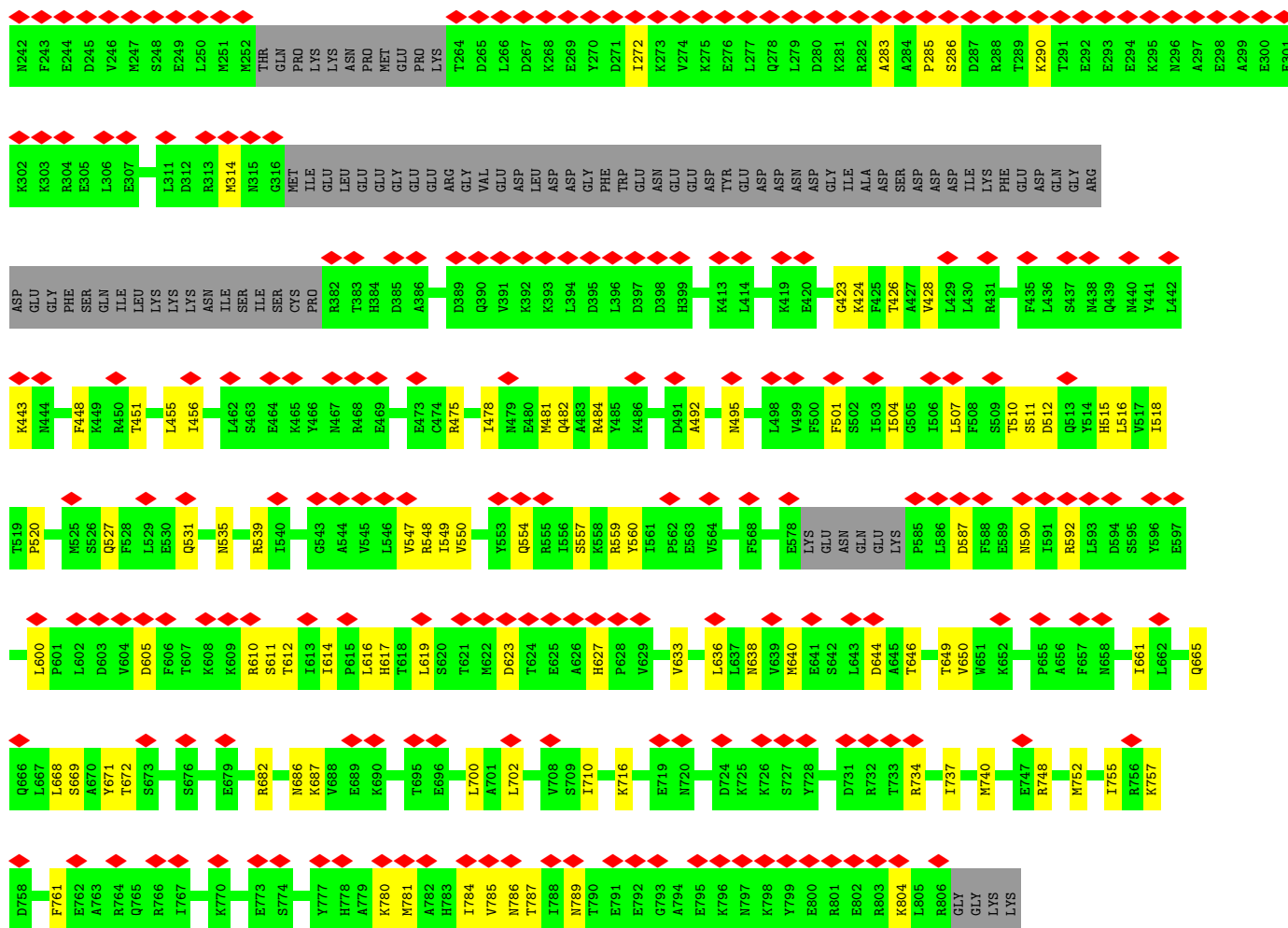


• Molecule 48: RNA 3'-terminal phosphate cyclase-like protein

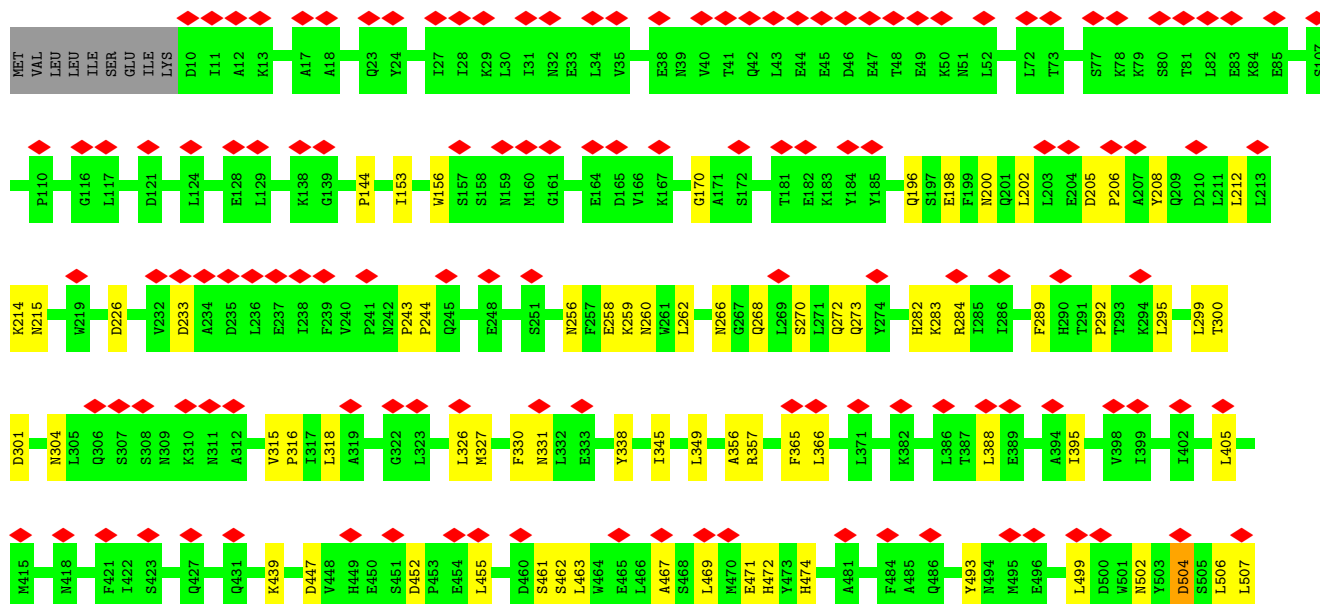
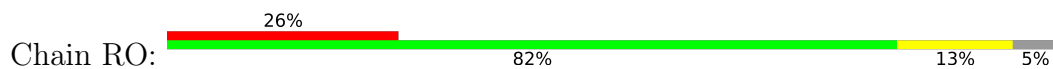


• Molecule 49: Nucleolar complex protein 14

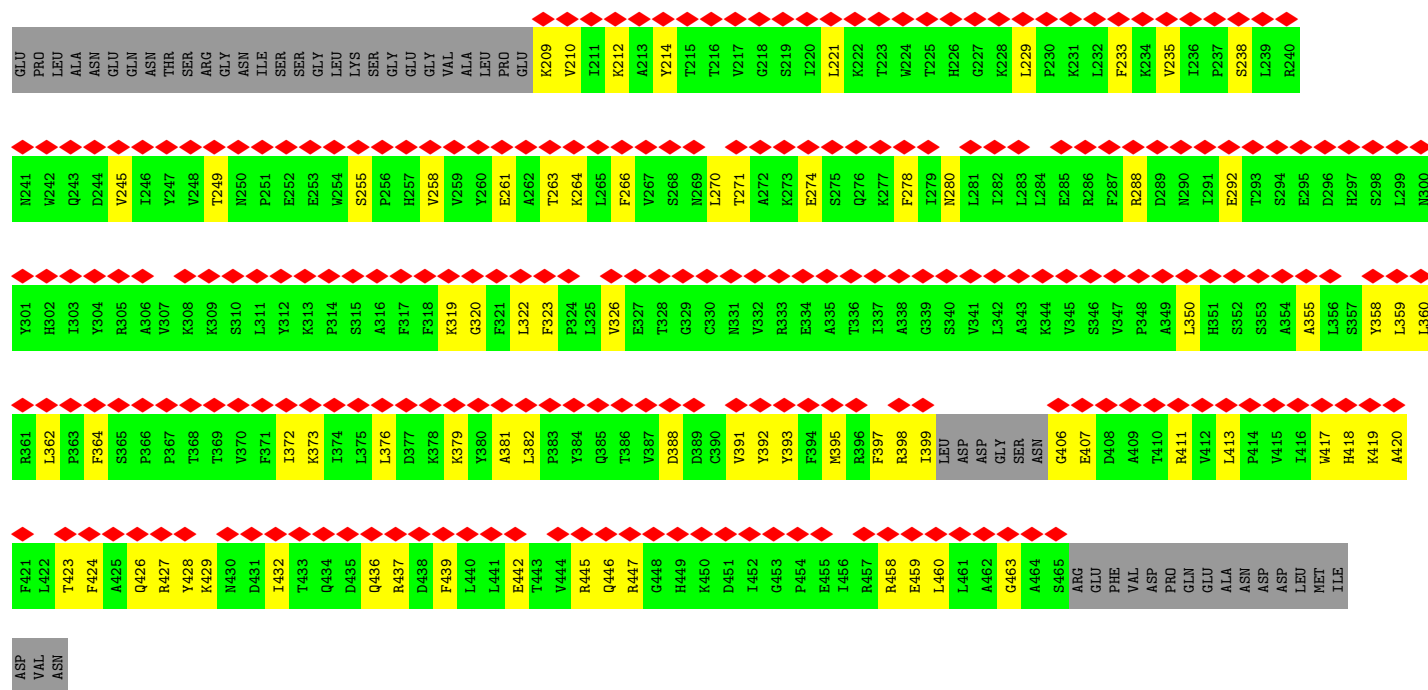
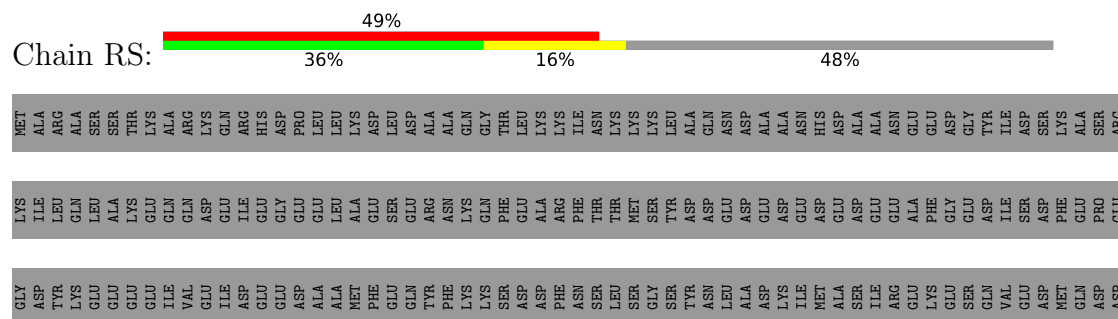




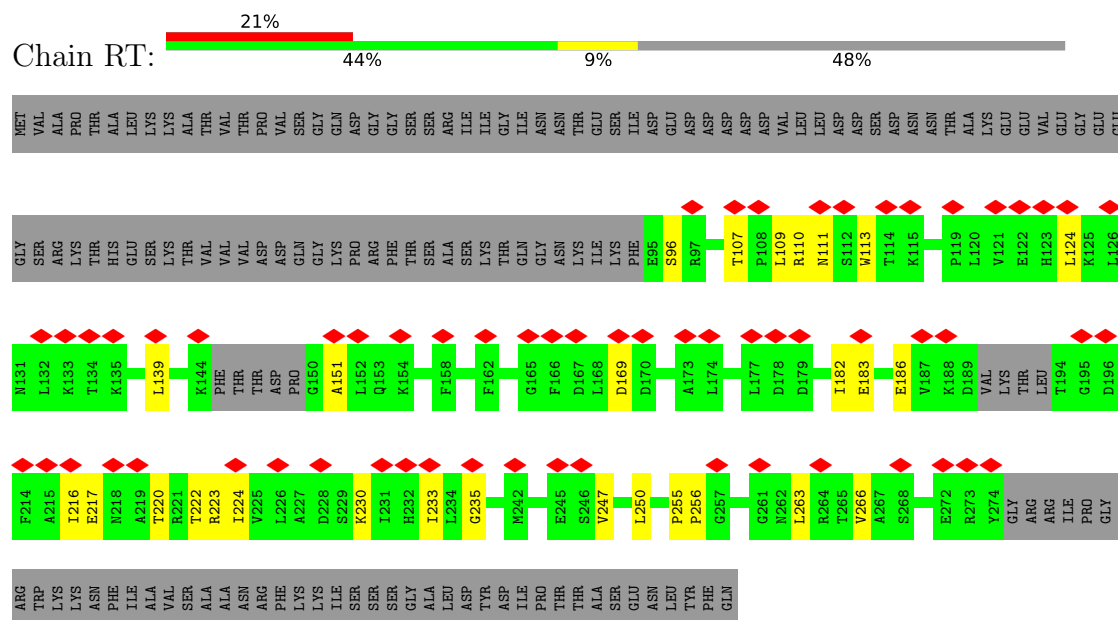
• Molecule 50: Nucleolar complex protein 4



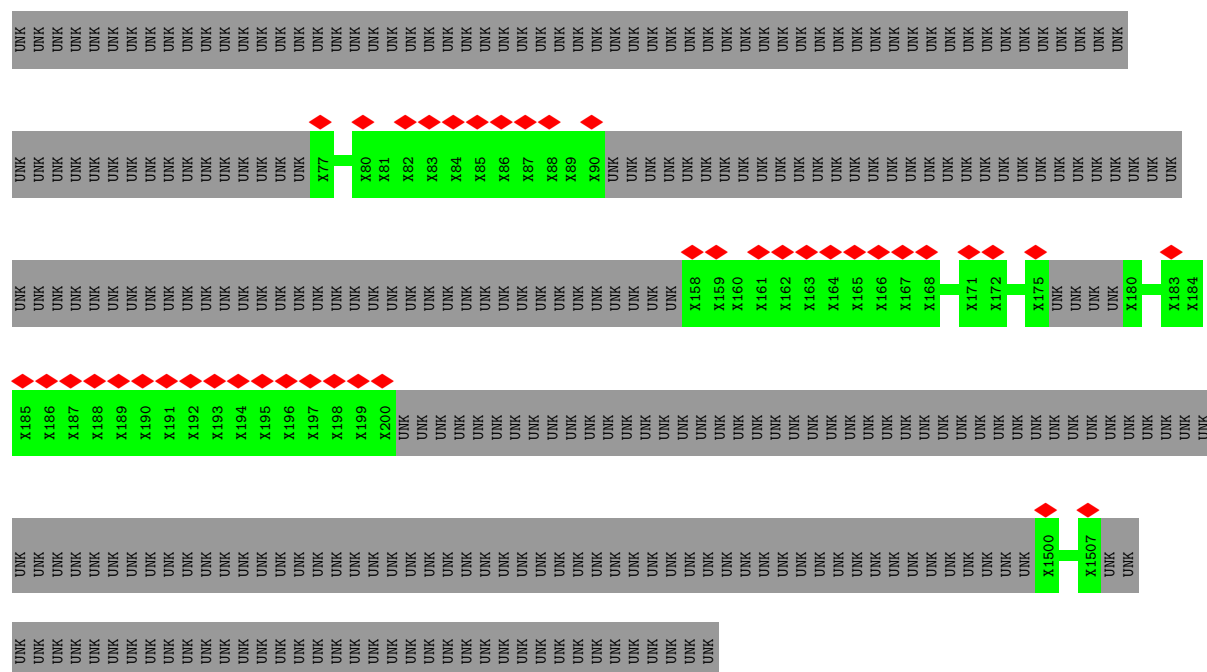
Chain RS:



Chain RT:



Chain RW:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40111	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	0.055	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.016	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: MG, ZN, GTP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	3A	0.45	0/4141	0.48	0/6433
2	5A	0.41	0/12485	0.47	2/19449 (0.0%)
3	SA	0.36	0/20532	0.53	18/31980 (0.1%)
4	SG	0.49	0/1690	0.67	2/2285 (0.1%)
5	SK	0.44	0/1410	0.63	0/1888
6	SN	0.29	0/873	0.79	0/1185
7	SO	0.35	0/1109	0.74	2/1495 (0.1%)
8	SP	0.38	0/879	0.85	3/1186 (0.3%)
9	SR	0.52	0/990	0.77	3/1335 (0.2%)
10	ST	0.31	0/980	0.65	0/1319
11	SY	0.48	0/798	0.65	0/1065
12	Sd	0.50	0/499	0.72	2/670 (0.3%)
13	3B	0.51	0/1901	0.66	1/2567 (0.0%)
13	3C	0.37	0/1796	0.66	0/2424
14	3D	0.40	0/2891	0.62	0/3895
15	3E	0.38	0/3059	0.62	0/4153
16	3F	0.37	0/3317	0.65	0/4469
17	3G	0.51	0/928	0.72	1/1262 (0.1%)
17	3H	0.46	0/928	0.70	0/1262
18	A4	0.43	0/5321	0.66	0/7207
19	A5	0.44	0/4044	0.65	0/5493
20	A8	0.24	0/3328	0.62	0/4565
21	A9	0.28	0/951	0.60	0/1287
22	AE	0.41	1/5274 (0.0%)	0.64	0/7142
23	AF	0.48	0/3993	0.68	0/5413
24	AG	0.42	0/6699	0.64	3/9077 (0.0%)
25	B1	0.58	0/6780	0.69	0/9175
26	B2	0.39	0/6853	0.69	2/9256 (0.0%)
27	B3	0.33	0/5977	0.78	4/8087 (0.0%)
28	B8	0.55	0/3848	0.63	0/5218
29	BE	0.53	0/6948	0.64	2/9391 (0.0%)
30	B6	0.37	0/2849	0.60	0/3853

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	5B	0.32	0/499	0.62	0/659
32	5C	0.56	0/4166	0.66	2/5624 (0.0%)
33	5D	0.46	0/1998	0.70	0/2644
34	5E	0.44	0/1665	0.66	2/2233 (0.1%)
35	5F	0.64	0/1559	0.72	1/2097 (0.0%)
36	5G	0.52	0/2337	0.67	2/3148 (0.1%)
37	5H	0.40	0/1074	0.57	0/1422
38	5I	0.56	0/3844	0.68	0/5174
39	5J	0.36	0/1302	0.58	0/1728
40	5K	0.52	0/1426	0.66	0/1917
41	RC	0.34	0/1432	0.66	0/1926
42	RD	0.26	0/1313	0.60	1/1830 (0.1%)
43	RE	0.25	0/8924	0.67	2/12070 (0.0%)
44	RF	0.26	0/1441	0.69	0/1951
45	RG	0.32	0/1727	0.70	0/2329
45	RH	0.37	0/1828	0.59	0/2470
46	RI	0.41	0/2080	0.65	0/2797
47	RJ	0.45	0/6085	0.62	0/8186
48	RK	0.39	0/2832	0.64	0/3825
49	RN	0.31	0/4591	0.63	1/6187 (0.0%)
50	RO	0.32	0/3849	0.63	0/5261
51	RQ	0.43	0/1459	0.62	1/1981 (0.1%)
52	RS	0.30	0/2104	0.70	0/2854
53	RT	0.38	0/1379	0.68	0/1853
54	RW	0.26	0/385	0.49	0/529
All	All	0.42	1/185370 (0.0%)	0.63	57/258181 (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
7	SO	0	1
10	ST	0	1
14	3D	0	3
15	3E	0	1
16	3F	0	1
17	3G	0	2
17	3H	0	1
18	A4	0	2
19	A5	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
20	A8	0	4
24	AG	0	2
25	B1	0	3
26	B2	0	9
27	B3	0	7
29	BE	0	1
33	5D	0	1
34	5E	0	1
35	5F	0	1
36	5G	0	1
38	5I	0	2
43	RE	0	2
47	RJ	0	2
48	RK	0	1
49	RN	0	1
50	RO	0	1
51	RQ	0	1
All	All	0	53

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	AE	564	VAL	C-N	5.35	1.40	1.34

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	SA	1746	A	C4'-C3'-O3'	8.88	126.33	113.00
3	SA	1147	A	C1'-C2'-O2'	-8.62	95.48	108.40
3	SA	915	A	C4'-C3'-O3'	8.19	125.29	113.00
3	SA	1746	A	C1'-C2'-O2'	-7.76	96.76	108.40
3	SA	1147	A	C4'-C3'-O3'	7.24	123.85	113.00
42	RD	1538	SER	N-CA-C	-6.97	103.76	111.36
26	B2	267	ASP	CA-C-N	6.86	134.65	121.54
26	B2	267	ASP	C-N-CA	6.86	134.65	121.54
2	5A	312	U	P-O3'-C3'	6.83	130.44	120.20
3	SA	1645	G	C4'-C3'-O3'	6.57	122.85	113.00
3	SA	1745	G	C1'-C2'-O2'	-6.53	98.61	108.40
35	5F	13	LEU	CA-CB-CG	6.48	138.97	116.30
3	SA	1656	U	C4'-C3'-O3'	6.45	122.67	113.00
27	B3	235	LYS	CA-C-N	6.34	133.65	121.54
27	B3	235	LYS	C-N-CA	6.34	133.65	121.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	SA	1751	C	C4'-C3'-O3'	6.08	122.12	113.00
3	SA	1651	A	C1'-C2'-O2'	-6.05	99.33	108.40
36	5G	157	PHE	N-CA-C	6.01	123.10	109.81
8	SP	45	GLY	O-C-N	-5.98	114.92	122.70
3	SA	1651	A	C4'-C3'-O3'	5.97	121.96	113.00
24	AG	141	LEU	N-CA-C	5.92	117.83	110.91
17	3G	67	LEU	CA-CB-CG	5.86	136.81	116.30
3	SA	1655	A	C4'-C3'-O3'	5.85	121.78	113.00
3	SA	975	C	C2'-C3'-O3'	-5.71	105.13	113.70
7	SO	84	ILE	N-CA-C	-5.71	104.51	109.19
43	RE	303	PHE	N-CA-C	5.69	116.89	108.86
29	BE	840	PHE	CA-C-N	5.66	130.08	121.03
29	BE	840	PHE	C-N-CA	5.66	130.08	121.03
9	SR	123	ARG	CA-C-N	5.58	140.39	127.00
9	SR	123	ARG	C-N-CA	5.58	140.39	127.00
34	5E	452	SER	CA-C-O	-5.47	110.15	118.91
51	RQ	313	PHE	N-CA-C	5.44	121.84	109.81
3	SA	579	A	P-O3'-C3'	5.41	128.32	120.20
27	B3	584	ILE	CA-C-N	5.40	131.86	121.54
27	B3	584	ILE	C-N-CA	5.40	131.86	121.54
3	SA	911	U	C4'-C3'-O3'	5.37	121.05	113.00
3	SA	971	A	C4'-C3'-O3'	5.37	121.05	113.00
8	SP	50	ALA	CA-C-N	5.34	131.75	121.54
8	SP	50	ALA	C-N-CA	5.34	131.75	121.54
7	SO	84	ILE	CB-CA-C	5.31	114.54	109.33
2	5A	173	G	P-O3'-C3'	5.30	128.15	120.20
3	SA	1751	C	C1'-C2'-O2'	-5.22	100.58	108.40
34	5E	454	VAL	N-CA-C	5.18	120.11	109.34
43	RE	305	PRO	N-CA-C	5.11	122.99	112.47
12	Sd	50	GLU	CA-C-N	5.06	131.21	121.54
12	Sd	50	GLU	C-N-CA	5.06	131.21	121.54
36	5G	120	GLY	N-CA-C	-5.05	101.20	113.18
32	5C	456	SER	CA-C-N	5.05	128.83	121.31
32	5C	456	SER	C-N-CA	5.05	128.83	121.31
9	SR	123	ARG	C-N-CD	-5.04	109.51	120.60
24	AG	138	ASP	CA-C-N	5.04	128.22	120.82
24	AG	138	ASP	C-N-CA	5.04	128.22	120.82
4	SG	99	MET	CA-C-N	5.02	131.14	121.54
4	SG	99	MET	C-N-CA	5.02	131.14	121.54
3	SA	1594	G	C4'-C3'-O3'	5.02	116.93	109.40
49	RN	592	ARG	CA-CB-CG	5.01	124.12	114.10
13	3B	306	LEU	CA-CB-CG	5.01	133.82	116.30

There are no chirality outliers.

All (53) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	3D	142	LEU	Peptide
14	3D	202	HIS	Peptide
14	3D	286	ARG	Peptide
15	3E	331	LYS	Peptide
16	3F	237	ASP	Peptide
17	3G	59	GLU	Peptide
17	3G	9	PHE	Peptide
17	3H	59	GLU	Peptide
33	5D	138	ASP	Peptide
34	5E	453	SER	Peptide
35	5F	101	VAL	Peptide
36	5G	74	ASP	Peptide
38	5I	230	ASN	Peptide
38	5I	283	ASP	Peptide
18	A4	54	LYS	Peptide
18	A4	774	LEU	Peptide
19	A5	167	SER	Peptide
20	A8	257	SER	Peptide
20	A8	266	ILE	Peptide
20	A8	496	TYR	Peptide
20	A8	529	HIS	Peptide
24	AG	178	PHE	Peptide
24	AG	780	GLU	Peptide
25	B1	288	ASP	Peptide
25	B1	661	LEU	Peptide
25	B1	690	ALA	Peptide
26	B2	131	GLY	Peptide
26	B2	213	LYS	Peptide
26	B2	266	SER	Peptide
26	B2	267	ASP	Peptide
26	B2	278	ASP	Peptide
26	B2	44	SER	Peptide
26	B2	613	ALA	Peptide
26	B2	916	HIS	Peptide
26	B2	918	TYR	Peptide
27	B3	235	LYS	Peptide
27	B3	34	THR	Peptide
27	B3	473	ALA	Peptide
27	B3	585	ASN	Peptide
27	B3	594	GLY	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
27	B3	627	ASN	Peptide
27	B3	90	LEU	Peptide
29	BE	94	TYR	Peptide
43	RE	116	LEU	Peptide
43	RE	173	ASN	Peptide
47	RJ	1026	LYS	Peptide
47	RJ	868	ARG	Peptide
48	RK	333	PHE	Peptide
49	RN	286	SER	Peptide
50	RO	144	PRO	Peptide
51	RQ	313	PHE	Peptide
7	SO	58	HIS	Peptide
10	ST	13	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	21	0
2	5A	11163	0	5611	81	0
3	SA	18356	0	9246	205	0
4	SG	1669	0	1724	18	0
5	SK	1388	0	1467	12	0
6	SN	865	0	874	15	0
7	SO	1087	0	1152	24	0
8	SP	868	0	894	26	0
9	SR	973	0	1029	13	0
10	ST	964	0	991	17	0
11	SY	786	0	843	7	0
12	Sd	497	0	535	3	0
13	3B	1865	0	1910	30	0
13	3C	1763	0	1805	36	0
14	3D	2848	0	2815	42	0
15	3E	3028	0	2813	63	0
16	3F	3248	0	3274	58	0
17	3G	916	0	964	11	0
17	3H	916	0	964	25	0
18	A4	5226	0	5199	93	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	A5	3976	0	3919	58	0
20	A8	3307	0	2316	40	0
21	A9	939	0	898	18	0
22	AE	5181	0	5373	87	0
23	AF	3911	0	3906	73	0
24	AG	6570	0	6473	129	0
25	B1	6635	0	6525	99	0
26	B2	6723	0	6698	132	0
27	B3	5882	0	5964	148	0
28	B8	3764	0	3757	57	0
29	BE	6810	0	6787	89	0
30	B6	2800	0	2517	32	0
31	5B	495	0	561	14	0
32	5C	4084	0	4092	77	0
33	5D	1972	0	2054	26	0
34	5E	1647	0	1678	33	0
35	5F	1530	0	1572	27	0
36	5G	2296	0	2325	39	0
37	5H	1065	0	1097	16	0
38	5I	3765	0	3714	72	0
39	5J	1280	0	1331	21	0
40	5K	1403	0	1484	20	0
41	RC	1410	0	1503	43	0
42	RD	1314	0	610	22	0
43	RE	8716	0	8828	160	0
44	RF	1404	0	1364	25	0
45	RG	1701	0	1767	39	0
45	RH	1799	0	1872	33	0
46	RI	2045	0	2162	37	0
47	RJ	5953	0	6152	105	0
48	RK	2781	0	2878	54	0
49	RN	4529	0	4262	68	0
50	RO	3766	0	3269	49	0
51	RQ	1436	0	1280	28	0
52	RS	2051	0	2096	53	0
53	RT	1357	0	1426	17	0
54	RW	381	0	255	4	0
55	X1	305	0	73	0	0
56	5K	1	0	0	0	0
57	RJ	32	0	12	2	0
58	RJ	1	0	0	0	0
All	All	179154	0	160842	2493	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 7.

All (2493) 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)
42:RD:1487:GLN:O	43:RE:411:ILE:HG23	1.40	1.18
27:B3:12:LEU:HD23	27:B3:377:LEU:HB2	1.23	1.17
8:SP:42:VAL:HG12	8:SP:67:VAL:HG23	1.31	1.12
8:SP:42:VAL:CG1	8:SP:67:VAL:HG23	1.82	1.09
27:B3:12:LEU:CB	27:B3:377:LEU:HD12	1.84	1.07
41:RC:112:GLN:NE2	41:RC:163:TYR:CD2	2.25	1.04
41:RC:112:GLN:NE2	41:RC:163:TYR:HD2	1.54	1.04
49:RN:527:GLN:O	49:RN:531:GLN:HB2	1.60	1.01
26:B2:17:ILE:HG22	26:B2:52:TRP:CZ2	1.94	1.01
20:A8:264:SER:O	20:A8:267:ILE:HA	1.61	1.01
51:RQ:298:TRP:NE1	51:RQ:899:LYS:HG3	1.76	1.00
3:SA:1697:G:O5'	43:RE:326:LEU:HD11	1.62	1.00
3:SA:36:C:H42	3:SA:472:U:H3	1.00	1.00
25:B1:54:HIS:HE2	25:B1:72:SER:HG	1.13	0.95
27:B3:494:ILE:N	27:B3:510:SER:HG	1.63	0.95
3:SA:925:G:C5'	42:RD:1611:ALA:HB1	1.96	0.95
3:SA:1697:G:OP1	43:RE:326:LEU:HD12	1.66	0.95
41:RC:112:GLN:HG2	41:RC:163:TYR:CE2	2.00	0.95
27:B3:12:LEU:HD21	27:B3:378:PRO:HD2	1.45	0.94
41:RC:112:GLN:CD	41:RC:163:TYR:CD2	2.46	0.94
27:B3:12:LEU:HB2	27:B3:377:LEU:HD12	1.46	0.94
8:SP:42:VAL:HG12	8:SP:67:VAL:CG2	1.98	0.93
3:SA:1665:U:H3	3:SA:1736:G:H1	1.17	0.93
7:SO:104:ARG:HG3	42:RD:1542:GLN:HA	1.50	0.93
3:SA:1658:G:N2	3:SA:1743:U:H1'	1.86	0.91
3:SA:36:C:N4	3:SA:472:U:H3	1.70	0.90
7:SO:106:ARG:HG2	7:SO:106:ARG:HH21	1.34	0.88
27:B3:12:LEU:HB3	27:B3:377:LEU:HD12	1.55	0.88
38:5I:231:GLU:OE2	51:RQ:899:LYS:HD3	1.74	0.87
27:B3:12:LEU:HB3	27:B3:377:LEU:CD1	2.05	0.87
3:SA:925:G:H5'	42:RD:1611:ALA:CB	2.07	0.85
52:RS:424:PHE:O	52:RS:428:TYR:HB2	1.78	0.84
42:RD:1489:SER:CB	43:RE:427:LYS:HD3	2.07	0.84
42:RD:1459:GLU:CB	43:RE:413:LEU:HD22	2.08	0.84
50:RO:502:ASN:O	50:RO:506:LEU:HB2	1.77	0.83
43:RE:656:ARG:O	43:RE:663:ILE:HA	1.79	0.83
27:B3:816:LEU:HD12	27:B3:816:LEU:O	1.78	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:12:LEU:HD23	27:B3:377:LEU:CB	2.07	0.82
27:B3:12:LEU:H	27:B3:12:LEU:HD12	1.43	0.82
17:3H:44:LEU:HD22	17:3H:52:ILE:CD1	2.10	0.81
43:RE:1224:ALA:O	43:RE:1228:ASN:HB3	1.81	0.81
51:RQ:346:LEU:O	51:RQ:350:ASN:HA	1.80	0.81
22:AE:151:ILE:O	22:AE:155:ILE:HB	1.81	0.81
51:RQ:298:TRP:HE1	51:RQ:899:LYS:HG3	1.44	0.81
3:SA:1697:G:P	43:RE:326:LEU:CD1	2.69	0.80
3:SA:925:G:H5'	42:RD:1611:ALA:HB1	1.62	0.79
30:B6:319:TYR:O	30:B6:323:PHE:HB2	1.81	0.79
3:SA:1697:G:P	43:RE:326:LEU:HD11	2.24	0.77
23:AF:224:THR:O	23:AF:239:LEU:HB2	1.83	0.77
41:RC:49:ARG:HH21	41:RC:52:TYR:HD2	1.32	0.77
42:RD:1488:LEU:HA	43:RE:411:ILE:O	1.84	0.76
3:SA:1658:G:C2	3:SA:1743:U:C2	2.75	0.75
41:RC:112:GLN:HG2	41:RC:163:TYR:CD2	2.21	0.75
3:SA:1697:G:H1	3:SA:1704:U:H3	1.34	0.75
18:A4:614:TRP:O	18:A4:618:ASN:HB2	1.87	0.74
39:5J:114:ARG:O	39:5J:118:GLN:HB3	1.88	0.74
42:RD:1487:GLN:O	43:RE:411:ILE:CG2	2.28	0.74
27:B3:12:LEU:CD2	27:B3:378:PRO:HD2	2.17	0.73
27:B3:533:LYS:HE2	27:B3:533:LYS:C	2.13	0.73
8:SP:42:VAL:HG11	8:SP:67:VAL:HG23	1.68	0.73
27:B3:12:LEU:CB	27:B3:377:LEU:CD1	2.63	0.72
27:B3:11:SER:HB3	27:B3:642:GLN:HG3	1.72	0.72
3:SA:505:A:H61	3:SA:586:G:H8	1.38	0.72
15:3E:397:ARG:HH21	15:3E:400:GLN:HE21	1.38	0.71
43:RE:1098:PHE:HB2	43:RE:1184:GLY:H	1.53	0.71
24:AG:435:ASP:HB2	24:AG:702:TYR:CD1	2.26	0.71
3:SA:1673:G:H1	3:SA:1728:A:N6	1.88	0.70
3:SA:1658:G:C5	3:SA:1743:U:C4	2.79	0.70
41:RC:112:GLN:CG	41:RC:163:TYR:CD2	2.75	0.70
46:RI:77:LYS:HD2	46:RI:130:ARG:HH11	1.57	0.69
3:SA:925:G:H5''	42:RD:1611:ALA:HB1	1.74	0.69
4:SG:206:SER:H	4:SG:211:ILE:HD11	1.55	0.69
3:SA:942:G:O5'	3:SA:977:A:H5'	1.91	0.69
2:5A:135:G:H4'	19:A5:494:ARG:HD3	1.74	0.69
3:SA:1697:G:P	43:RE:326:LEU:HD12	2.33	0.69
25:B1:58:ILE:HA	25:B1:74:ASP:HA	1.74	0.69
2:5A:316:U:H5'	32:5C:364:ARG:HH22	1.57	0.69
48:RK:192:THR:HA	48:RK:224:ASN:O	1.92	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:RQ:297:LYS:HB2	51:RQ:899:LYS:HB3	1.76	0.68
23:AF:86:SER:O	23:AF:98:ALA:HA	1.93	0.68
3:SA:1658:G:C6	3:SA:1743:U:C4	2.82	0.68
3:SA:1673:G:H1	3:SA:1728:A:H61	1.40	0.68
27:B3:533:LYS:HE2	27:B3:533:LYS:O	1.94	0.68
23:AF:211:HIS:HD1	23:AF:228:SER:HG	1.42	0.68
16:3F:443:LEU:HD21	16:3F:492:TRP:HE1	1.59	0.68
38:5I:345:THR:HG22	38:5I:347:ARG:H	1.58	0.68
26:B2:17:ILE:HG22	26:B2:52:TRP:CH2	2.28	0.67
27:B3:513:LYS:HD3	27:B3:513:LYS:N	2.09	0.67
29:BE:209:ILE:HG22	29:BE:225:THR:HG22	1.76	0.67
43:RE:377:SER:HB2	43:RE:389:GLY:HA3	1.76	0.67
43:RE:345:TYR:O	43:RE:349:LEU:HB2	1.95	0.67
16:3F:185:LEU:H	16:3F:202:THR:HB	1.59	0.67
26:B2:536:CYS:HB3	26:B2:549:SER:HB3	1.77	0.67
27:B3:531:ASN:ND2	27:B3:568:MET:SD	2.67	0.67
27:B3:719:ILE:HD11	27:B3:762:CYS:HB3	1.76	0.67
3:SA:868:G:H1	3:SA:960:U:H3	1.41	0.67
3:SA:1658:G:O6	3:SA:1742:U:C4	2.48	0.67
25:B1:20:ILE:H	25:B1:307:THR:HG21	1.58	0.66
28:B8:513:GLN:HG3	28:B8:551:VAL:HG21	1.76	0.66
13:3B:103:GLU:HG3	39:5J:134:ARG:HH12	1.60	0.66
18:A4:645:ARG:HD2	18:A4:656:ARG:HD3	1.77	0.66
3:SA:885:G:N2	8:SP:124:ASP:OD1	2.28	0.66
36:5G:123:VAL:HG12	36:5G:125:PRO:HD2	1.78	0.66
23:AF:52:PRO:HG2	23:AF:312:ALA:HA	1.77	0.66
24:AG:435:ASP:HB3	24:AG:701:VAL:O	1.96	0.66
11:SY:103:LEU:HB3	11:SY:126:LYS:HB2	1.76	0.66
24:AG:16:SER:HB2	24:AG:783:LEU:HB2	1.77	0.66
3:SA:1751:C:H5"	26:B2:142:ASP:HA	1.76	0.66
29:BE:209:ILE:HA	29:BE:225:THR:HA	1.77	0.65
47:RJ:248:ARG:HB3	47:RJ:272:TYR:HB2	1.78	0.65
43:RE:529:VAL:HB	43:RE:613:VAL:HB	1.79	0.65
18:A4:497:ILE:HD11	18:A4:511:VAL:HG23	1.78	0.65
8:SP:14:PHE:HA	8:SP:78:ALA:O	1.96	0.65
29:BE:847:LEU:HD11	53:RT:266:VAL:HG23	1.78	0.65
43:RE:822:ARG:HB2	43:RE:843:LEU:HB2	1.76	0.65
53:RT:222:THR:HG22	53:RT:235:GLY:HA3	1.79	0.65
1:3A:84:U:OP2	15:3E:361:ARG:NH2	2.30	0.65
20:A8:576:ARG:HG2	20:A8:578:LEU:H	1.61	0.65
5:SK:57:ARG:HE	40:5K:88:ASP:HB3	1.60	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B2:262:ILE:O	26:B2:270:SER:HA	1.97	0.64
3:SA:976:G:C2	3:SA:978:A:C5	2.84	0.64
25:B1:438:VAL:HG12	25:B1:445:VAL:HG23	1.79	0.64
32:5C:170:GLN:NE2	32:5C:177:TYR:OH	2.30	0.64
43:RE:1108:LEU:O	43:RE:1112:CYS:HB2	1.97	0.64
47:RJ:263:LEU:HD23	47:RJ:267:ARG:HH22	1.63	0.64
34:5E:299:SER:HA	34:5E:302:LYS:HE2	1.80	0.64
50:RO:472:HIS:HD2	50:RO:474:HIS:H	1.46	0.64
41:RC:49:ARG:NH1	41:RC:104:LEU:O	2.30	0.64
50:RO:318:LEU:HA	50:RO:357:ARG:HH12	1.62	0.64
29:BE:631:ASN:HB2	29:BE:644:THR:HB	1.80	0.64
2:5A:487:A:H62	51:RQ:876:GLN:HE22	1.45	0.64
26:B2:439:LEU:HB2	26:B2:444:LEU:HB3	1.79	0.64
27:B3:788:TYR:O	27:B3:792:HIS:ND1	2.31	0.64
45:RG:122:ILE:HA	45:RG:161:LYS:O	1.97	0.64
19:A5:145:CYS:HB2	19:A5:148:LEU:HD21	1.80	0.64
27:B3:278:LEU:HD12	27:B3:279:LYS:HG2	1.78	0.64
3:SA:879:G:O2'	7:SO:105:ASN:HB2	1.98	0.64
3:SA:1658:G:C5	3:SA:1743:U:N3	2.65	0.64
8:SP:122:PRO:HB2	8:SP:125:SER:HB3	1.80	0.63
11:SY:97:ASP:OD1	11:SY:97:ASP:N	2.31	0.63
26:B2:201:ILE:HG13	27:B3:663:VAL:HG11	1.80	0.63
35:5F:33:MET:HB2	35:5F:38:ILE:HB	1.79	0.63
3:SA:895:G:H1	3:SA:917:U:H3	1.46	0.63
3:SA:993:A:H62	3:SA:1011:G:H21	1.46	0.63
27:B3:11:SER:HB2	27:B3:641:PHE:O	1.98	0.63
28:B8:521:LEU:HA	28:B8:531:CYS:O	1.98	0.63
2:5A:173:G:N7	2:5A:175:A:N6	2.46	0.63
36:5G:32:ILE:HG22	36:5G:42:LEU:HD11	1.80	0.63
44:RF:68:LYS:HD2	44:RF:85:GLU:HA	1.81	0.63
47:RJ:831:ARG:NH2	47:RJ:835:HIS:O	2.30	0.63
16:3F:538:ARG:HA	16:3F:566:ALA:O	1.97	0.63
9:SR:94:GLN:HB2	9:SR:102:LYS:HG3	1.80	0.63
32:5C:386:PHE:O	38:5I:8:ARG:NH2	2.31	0.63
44:RF:38:PHE:HB2	44:RF:56:VAL:HB	1.80	0.63
45:RH:129:ARG:HH11	45:RH:132:ARG:HD3	1.63	0.63
2:5A:357:G:N7	32:5C:493:LYS:NZ	2.45	0.63
17:3H:44:LEU:HD22	17:3H:52:ILE:HD11	1.80	0.63
45:RH:192:TYR:HA	45:RH:195:LYS:HD2	1.81	0.63
27:B3:7:TYR:HB3	27:B3:644:TRP:HB3	1.80	0.63
43:RE:779:PHE:HB3	43:RE:851:LYS:HG3	1.80	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:108:LEU:HG	27:B3:119:VAL:HG12	1.81	0.63
47:RJ:932:LEU:HD22	47:RJ:1007:TYR:HB2	1.80	0.63
3:SA:1658:G:C6	3:SA:1743:U:C5	2.87	0.63
27:B3:651:GLU:HA	27:B3:651:GLU:OE1	1.99	0.63
30:B6:285:TYR:HD2	30:B6:308:THR:HG22	1.63	0.63
15:3E:384:GLY:O	15:3E:388:LEU:HB2	1.99	0.62
8:SP:16:VAL:HA	8:SP:80:HIS:O	1.99	0.62
20:A8:553:GLN:NE2	20:A8:557:THR:OG1	2.32	0.62
48:RK:221:CYS:SG	48:RK:222:GLU:N	2.71	0.62
33:5D:29:GLU:OE2	33:5D:37:ARG:NH1	2.31	0.62
20:A8:530:PRO:HG2	20:A8:553:GLN:HE22	1.64	0.62
3:SA:1220:C:H2'	3:SA:1221:A:H8	1.64	0.62
22:AE:638:SER:HA	22:AE:641:LEU:HD12	1.80	0.62
27:B3:8:LYS:HG2	27:B3:645:LYS:HB2	1.81	0.62
41:RC:189:ASP:HB3	41:RC:194:ILE:HD11	1.81	0.62
21:A9:432:LYS:HB3	21:A9:435:LEU:HB3	1.81	0.62
50:RO:300:THR:O	50:RO:304:ASN:ND2	2.32	0.62
52:RS:379:LYS:HD2	52:RS:427:ARG:HE	1.64	0.62
49:RN:482:GLN:HG2	50:RO:507:LEU:HD11	1.80	0.62
18:A4:399:VAL:HG22	18:A4:420:LEU:HB2	1.80	0.62
43:RE:268:LEU:HB2	43:RE:294:LEU:HB2	1.82	0.62
49:RN:95:ARG:HH12	49:RN:757:LYS:HG3	1.64	0.62
29:BE:733:THR:O	29:BE:737:LEU:HB3	2.00	0.62
3:SA:1538:U:H2'	3:SA:1569:A:H61	1.65	0.62
19:A5:120:ILE:HB	19:A5:151:LEU:HD23	1.82	0.62
52:RS:214:TYR:HB3	52:RS:249:THR:HG22	1.80	0.62
3:SA:925:G:H5'	42:RD:1611:ALA:HB2	1.80	0.61
17:3H:50:GLU:HG3	17:3H:104:THR:HG22	1.82	0.61
27:B3:494:ILE:N	27:B3:510:SER:OG	2.33	0.61
25:B1:303:ASN:ND2	25:B1:323:LYS:HD3	2.15	0.61
27:B3:655:GLU:OE1	27:B3:655:GLU:HA	2.00	0.61
3:SA:1498:G:HO2'	46:RI:251:SER:HG	1.48	0.61
23:AF:428:ARG:NH2	24:AG:518:ASP:O	2.34	0.61
27:B3:633:VAL:HB	27:B3:644:TRP:HB2	1.81	0.61
29:BE:471:CYS:SG	29:BE:514:ASN:ND2	2.74	0.61
48:RK:155:LYS:HG2	48:RK:165:GLU:HG2	1.82	0.61
3:SA:477:A:H5'	37:5H:560:ASN:HD22	1.64	0.61
27:B3:692:MET:SD	34:5E:515:MET:HG2	2.40	0.61
28:B8:424:ILE:HG12	28:B8:434:GLU:HG2	1.83	0.61
41:RC:103:LEU:HB3	41:RC:108:VAL:CG2	2.30	0.61
52:RS:423:THR:HA	52:RS:426:GLN:HG2	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1512:G:H5''	46:RI:148:LYS:HD2	1.83	0.61
7:SO:109:LYS:H	7:SO:109:LYS:HD2	1.65	0.61
23:AF:440:GLU:O	23:AF:444:ASN:HB2	2.00	0.61
45:RG:36:LYS:HB3	45:RG:172:PRO:HA	1.82	0.61
19:A5:162:GLN:HA	19:A5:173:ILE:O	2.01	0.61
24:AG:335:PRO:HB2	24:AG:336:ARG:HD3	1.82	0.61
44:RF:101:SER:O	44:RF:105:SER:HB2	2.00	0.61
53:RT:224:ILE:HG12	53:RT:233:ILE:HG12	1.83	0.61
23:AF:51:HIS:O	23:AF:53:HIS:ND1	2.30	0.61
24:AG:769:ASN:ND2	24:AG:771:ASP:OD1	2.33	0.61
27:B3:221:ASN:OD1	27:B3:232:LYS:NZ	2.33	0.61
26:B2:861:ILE:HD13	27:B3:806:LEU:HD23	1.81	0.61
27:B3:294:LEU:HB2	27:B3:303:PHE:HB2	1.82	0.61
30:B6:201:LYS:HZ1	39:5J:55:ILE:HG21	1.66	0.61
49:RN:511:SER:HA	49:RN:557:SER:HB2	1.82	0.61
3:SA:435:C:H42	47:RJ:166:ARG:HH12	1.47	0.60
3:SA:1658:G:N3	3:SA:1743:U:C2	2.69	0.60
49:RN:548:ARG:NH1	49:RN:638:ASN:OD1	2.33	0.60
13:3B:142:ARG:NH1	13:3B:186:ASP:OD2	2.34	0.60
13:3C:186:ASP:OD1	13:3C:214:ARG:NH1	2.33	0.60
16:3F:328:ILE:HG13	16:3F:338:THR:HG22	1.82	0.60
30:B6:286:ILE:HG22	30:B6:308:THR:HG21	1.83	0.60
43:RE:1111:SER:HA	43:RE:1129:PRO:HG3	1.83	0.60
19:A5:481:LEU:HD21	19:A5:526:LEU:HD22	1.83	0.60
45:RH:156:GLU:HG2	45:RH:157:GLU:HG2	1.81	0.60
38:5I:260:GLN:NE2	38:5I:289:TYR:OH	2.35	0.60
49:RN:649:THR:HG23	49:RN:650:VAL:HG23	1.82	0.60
50:RO:452:ASP:HB3	50:RO:455:LEU:HB2	1.84	0.60
27:B3:244:GLU:HG2	27:B3:293:VAL:H	1.66	0.60
34:5E:480:GLN:HG2	34:5E:482:LEU:H	1.66	0.60
45:RG:147:LYS:HD3	45:RG:150:ILE:HG22	1.83	0.60
50:RO:461:SER:OG	50:RO:462:SER:N	2.33	0.60
3:SA:1658:G:C4	3:SA:1743:U:C2	2.89	0.60
3:SA:1658:G:C4	3:SA:1743:U:N3	2.70	0.60
3:SA:606:A:N3	3:SA:607:G:N1	2.50	0.60
7:SO:106:ARG:HG2	7:SO:106:ARG:NH2	2.14	0.60
18:A4:578:SER:HG	18:A4:643:SER:HG	1.49	0.60
26:B2:54:ILE:HD13	26:B2:364:TYR:HD2	1.66	0.60
3:SA:941:A:N3	3:SA:976:G:O3'	2.35	0.60
27:B3:658:LYS:HB2	27:B3:658:LYS:NZ	2.15	0.60
18:A4:429:SER:HB3	18:A4:444:ARG:HA	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AF:301:PRO:HG2	23:AF:323:SER:HB3	1.84	0.60
33:5D:22:ARG:NH1	47:RJ:997:MET:O	2.35	0.60
37:5H:434:PHE:HA	45:RH:129:ARG:HH12	1.67	0.60
14:3D:382:LYS:HD2	14:3D:404:LEU:HD22	1.83	0.59
24:AG:90:LYS:HG2	24:AG:144:VAL:HG22	1.84	0.59
43:RE:711:PRO:HG3	43:RE:767:GLN:HE21	1.67	0.59
14:3D:29:SER:O	14:3D:35:GLN:NE2	2.34	0.59
23:AF:248:ARG:NH1	23:AF:289:ASN:O	2.35	0.59
32:5C:96:ASP:OD1	32:5C:96:ASP:N	2.35	0.59
48:RK:14:SER:HB2	48:RK:36:ILE:HG23	1.83	0.59
4:SG:131:GLN:NE2	4:SG:135:ASP:OD1	2.35	0.59
23:AF:133:HIS:HD2	23:AF:135:GLN:H	1.50	0.59
43:RE:128:LEU:HD21	43:RE:185:LEU:HD21	1.85	0.59
3:SA:1643:U:OP2	34:5E:530:ARG:NH1	2.36	0.59
15:3E:210:LEU:HD23	15:3E:256:ASN:HD22	1.68	0.59
25:B1:497:ILE:HG23	25:B1:512:ILE:HB	1.84	0.59
27:B3:392:ASN:ND2	27:B3:435:ALA:O	2.34	0.59
45:RG:125:ASN:ND2	45:RG:127:THR:OG1	2.36	0.59
43:RE:495:THR:HA	43:RE:498:MET:HG2	1.84	0.59
49:RN:614:ILE:HG22	49:RN:616:LEU:HB2	1.85	0.59
32:5C:257:SER:OG	32:5C:259:TRP:NE1	2.36	0.59
43:RE:1100:VAL:HB	43:RE:1182:ILE:HB	1.83	0.59
49:RN:535:ASN:OD1	49:RN:539:ARG:NH1	2.36	0.59
3:SA:991:G:N1	3:SA:1012:U:OP2	2.36	0.59
14:3D:286:ARG:HA	14:3D:289:TYR:HB3	1.85	0.59
20:A8:533:PRO:HA	20:A8:559:PRO:HG2	1.85	0.59
24:AG:568:ASN:ND2	24:AG:586:SER:OG	2.35	0.59
8:SP:17:ALA:HA	8:SP:30:VAL:HG22	1.85	0.59
12:Sd:65:ARG:NH2	26:B2:750:GLU:OE2	2.36	0.59
24:AG:153:ILE:HG22	24:AG:174:TYR:HB2	1.85	0.59
25:B1:300:MET:HE3	25:B1:328:LEU:HD13	1.85	0.59
30:B6:15:MET:HA	30:B6:18:LEU:HB3	1.85	0.58
43:RE:949:PHE:O	43:RE:960:LYS:NZ	2.36	0.58
53:RT:110:ARG:NH2	53:RT:130:MET:SD	2.76	0.58
3:SA:915:A:H2'	3:SA:916:U:H6	1.68	0.58
3:SA:1692:G:OP2	3:SA:1694:A:N6	2.37	0.58
2:5A:425:U:H3	2:5A:431:A:H61	1.51	0.58
13:3C:114:GLY:O	13:3C:122:ARG:NH1	2.35	0.58
1:3A:30:A:N6	38:5I:341:GLU:OE2	2.36	0.58
3:SA:563:U:H4'	36:5G:278:ARG:HG3	1.85	0.58
13:3B:236:MET:HG3	14:3D:133:LEU:HA	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:25:VAL:HG23	27:B3:31:ILE:HG22	1.85	0.58
27:B3:211:LEU:O	27:B3:222:LEU:HA	2.02	0.58
27:B3:556:THR:HA	27:B3:573:GLY:HA2	1.85	0.58
32:5C:190:HIS:HB3	32:5C:207:THR:HG21	1.84	0.58
7:SO:106:ARG:HH21	7:SO:106:ARG:CG	2.09	0.58
25:B1:501:SER:HB2	25:B1:508:GLN:HB2	1.84	0.58
32:5C:76:PRO:HA	38:5I:1:MET:HE2	1.86	0.58
38:5I:411:LYS:O	38:5I:415:ARG:HB2	2.02	0.58
45:RH:44:VAL:HA	45:RH:113:TYR:O	2.03	0.58
50:RO:202:LEU:HD22	50:RO:212:LEU:HD22	1.86	0.58
2:5A:177:U:O2'	2:5A:178:G:N7	2.35	0.58
15:3E:11:GLY:HA2	15:3E:143:LEU:HD22	1.86	0.58
43:RE:219:PHE:CZ	43:RE:303:PHE:CD2	2.91	0.58
18:A4:565:ARG:HD3	22:AE:633:GLU:HB2	1.86	0.58
22:AE:248:SER:OG	22:AE:253:CYS:SG	2.62	0.58
33:5D:37:ARG:NH2	47:RJ:994:LYS:O	2.36	0.58
27:B3:616:HIS:NE2	27:B3:642:GLN:OE1	2.37	0.58
24:AG:435:ASP:CB	24:AG:702:TYR:HA	2.34	0.58
27:B3:510:SER:O	27:B3:514:THR:OG1	2.22	0.58
29:BE:482:GLY:HA2	29:BE:505:VAL:HG23	1.86	0.58
22:AE:671:LEU:O	22:AE:675:ASN:HB3	2.04	0.58
24:AG:118:VAL:HB	24:AG:130:LYS:HB2	1.85	0.58
43:RE:443:HIS:HB3	43:RE:470:LYS:HE2	1.86	0.58
18:A4:269:PHE:O	28:B8:446:ARG:NH2	2.36	0.57
25:B1:432:GLN:HE22	34:5E:455:HIS:HA	1.69	0.57
26:B2:97:GLY:HA3	26:B2:124:ILE:HD11	1.84	0.57
28:B8:227:LEU:HB2	28:B8:528:GLN:HE22	1.67	0.57
50:RO:270:SER:H	50:RO:273:GLN:HE21	1.50	0.57
24:AG:86:GLU:OE1	24:AG:113:ASN:ND2	2.36	0.57
27:B3:509:ALA:HB3	27:B3:539:VAL:HG21	1.86	0.57
34:5E:369:ILE:HG12	36:5G:223:THR:HG21	1.86	0.57
37:5H:532:VAL:HA	47:RJ:909:ASN:HD21	1.69	0.57
38:5I:87:SER:OG	38:5I:89:ASP:OD1	2.22	0.57
48:RK:114:PHE:HB2	48:RK:170:VAL:HG22	1.86	0.57
1:3A:251:G:H2'	16:3F:155:ASN:HD21	1.67	0.57
16:3F:241:THR:HG21	16:3F:285:SER:HA	1.86	0.57
22:AE:186:MET:HE1	22:AE:234:LEU:HD12	1.86	0.57
24:AG:157:PHE:HB2	24:AG:170:SER:HB3	1.86	0.57
26:B2:861:ILE:CD1	27:B3:806:LEU:HD23	2.34	0.57
27:B3:12:LEU:CD2	27:B3:377:LEU:HB2	2.14	0.57
28:B8:221:THR:OG1	28:B8:222:LEU:N	2.38	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:5B:194:LYS:HD2	31:5B:199:ILE:HG13	1.86	0.57
32:5C:185:HIS:NE2	35:5F:19:LEU:O	2.36	0.57
32:5C:450:GLY:O	51:RQ:857:TYR:OH	2.21	0.57
47:RJ:773:THR:HA	47:RJ:777:ARG:HH11	1.69	0.57
3:SA:1196:A:N3	45:RG:136:ARG:NH2	2.52	0.57
26:B2:259:ILE:HA	26:B2:273:TYR:O	2.03	0.57
27:B3:16:TYR:O	27:B3:336:ASN:ND2	2.36	0.57
15:3E:339:TYR:HB3	15:3E:343:TYR:HB2	1.85	0.57
17:3H:44:LEU:HD13	17:3H:52:ILE:HD11	1.86	0.57
23:AF:303:LEU:HD13	23:AF:323:SER:HB2	1.86	0.57
29:BE:359:ALA:O	29:BE:421:ASN:ND2	2.38	0.57
32:5C:317:THR:HG23	32:5C:334:ARG:HB3	1.86	0.57
33:5D:111:ARG:HH11	33:5D:212:LYS:HD2	1.69	0.57
3:SA:942:G:H4'	3:SA:977:A:OP1	2.03	0.57
13:3C:267:VAL:HG21	13:3C:298:ILE:HD12	1.87	0.57
19:A5:434:THR:HG23	50:RO:266:ASN:HD21	1.69	0.57
23:AF:24:GLN:O	23:AF:28:ARG:HB3	2.05	0.57
24:AG:144:VAL:HG12	24:AG:153:ILE:HG13	1.86	0.57
28:B8:146:LEU:O	28:B8:163:ARG:NH1	2.37	0.57
34:5E:312:GLU:O	34:5E:316:ASN:ND2	2.38	0.57
43:RE:827:ARG:HB2	44:RF:175:LEU:HD11	1.87	0.57
3:SA:915:A:H2'	3:SA:916:U:C6	2.39	0.57
3:SA:1697:G:O5'	43:RE:326:LEU:CD1	2.45	0.57
11:SY:109:ARG:NH2	11:SY:120:VAL:O	2.37	0.57
25:B1:264:LYS:HD3	25:B1:280:THR:HG22	1.87	0.57
28:B8:129:ASP:OD1	29:BE:194:ARG:NH2	2.36	0.57
29:BE:666:ARG:NH1	29:BE:706:ASP:OD2	2.38	0.57
43:RE:242:LEU:HG	43:RE:245:LYS:HE3	1.87	0.57
43:RE:652:LYS:HG2	43:RE:667:CYS:HB2	1.87	0.57
52:RS:209:LYS:HE3	52:RS:212:LYS:HG3	1.87	0.57
13:3C:142:ARG:NH1	13:3C:186:ASP:OD2	2.36	0.57
14:3D:264:SER:OG	14:3D:265:GLU:N	2.37	0.57
26:B2:365:TYR:HA	26:B2:381:LYS:HA	1.85	0.57
26:B2:450:ARG:O	26:B2:475:ALA:HA	2.04	0.57
41:RC:141:ARG:NH2	41:RC:193:ASN:OD1	2.38	0.57
47:RJ:1042:MET:HG3	47:RJ:1044:LEU:HD13	1.86	0.57
2:5A:338:A:O2'	2:5A:340:U:O4	2.20	0.57
3:SA:559:C:OP1	47:RJ:868:ARG:NH2	2.37	0.57
7:SO:102:LEU:C	7:SO:104:ARG:H	2.13	0.57
20:A8:536:ARG:NH1	20:A8:537:THR:OG1	2.38	0.57
25:B1:405:SER:HB3	25:B1:436:LEU:HD23	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:581:CYS:HA	27:B3:590:LEU:O	2.04	0.57
45:RH:31:LEU:HD13	45:RH:40:ARG:HE	1.68	0.57
53:RT:217:GLU:HG2	53:RT:223:ARG:HA	1.86	0.57
3:SA:940:A:N1	3:SA:975:C:O2'	2.36	0.57
3:SA:1197:C:OP1	45:RG:136:ARG:NH1	2.38	0.57
3:SA:1657:U:H5''	26:B2:450:ARG:HH21	1.69	0.57
16:3F:442:ILE:HA	16:3F:472:PRO:HA	1.86	0.57
19:A5:148:LEU:HD23	19:A5:167:SER:HB3	1.86	0.57
22:AE:559:ASN:HA	22:AE:592:ARG:HD3	1.85	0.57
26:B2:432:TYR:HB3	26:B2:450:ARG:HB3	1.87	0.57
2:5A:481:U:O2'	30:B6:102:LYS:NZ	2.37	0.56
16:3F:545:LYS:HG2	16:3F:561:ASN:HD21	1.70	0.56
20:A8:614:ILE:HD12	20:A8:634:LEU:HD13	1.86	0.56
25:B1:479:LEU:HD12	25:B1:488:LEU:HD11	1.87	0.56
37:5H:438:ASP:OD1	37:5H:438:ASP:N	2.38	0.56
37:5H:498:VAL:HG21	46:RI:253:PRO:HD3	1.86	0.56
50:RO:170:GLY:O	50:RO:272:GLN:NE2	2.32	0.56
3:SA:1654:G:H2'	3:SA:1655:A:H8	1.71	0.56
24:AG:473:LEU:HB2	24:AG:495:ILE:HD11	1.87	0.56
24:AG:510:TYR:HH	24:AG:527:HIS:HD1	1.51	0.56
32:5C:493:LYS:O	32:5C:498:ARG:NH1	2.38	0.56
38:5I:15:PRO:HB3	38:5I:20:GLN:HE21	1.70	0.56
38:5I:81:ASN:ND2	38:5I:96:ASN:OD1	2.38	0.56
40:5K:26:LYS:HD3	40:5K:29:GLN:HG3	1.87	0.56
2:5A:323:A:N6	25:B1:212:ASP:OD2	2.37	0.56
11:SY:132:LEU:HA	11:SY:135:LEU:HB2	1.87	0.56
16:3F:142:ILE:HA	16:3F:568:ILE:HD11	1.87	0.56
16:3F:417:SER:OG	16:3F:418:ASP:N	2.37	0.56
18:A4:37:ARG:NH1	20:A8:704:PRO:O	2.38	0.56
19:A5:25:ASP:OD2	28:B8:590:LYS:NZ	2.37	0.56
19:A5:212:LEU:HD11	19:A5:246:VAL:HG11	1.87	0.56
20:A8:539:ASN:ND2	20:A8:560:ASN:O	2.38	0.56
21:A9:473:LYS:O	21:A9:477:LYS:NZ	2.38	0.56
23:AF:147:ARG:NH2	45:RH:16:GLN:O	2.39	0.56
25:B1:373:ASP:HB2	25:B1:380:LEU:HD21	1.86	0.56
38:5I:45:LEU:HD13	38:5I:410:ILE:HG22	1.86	0.56
43:RE:466:THR:HG22	43:RE:475:ASN:HD21	1.70	0.56
3:SA:1749:A:H8	3:SA:1749:A:OP2	1.88	0.56
18:A4:32:ILE:O	18:A4:751:GLU:HA	2.06	0.56
43:RE:486:GLN:HE22	43:RE:571:ARG:HH22	1.52	0.56
43:RE:828:ASP:OD2	43:RE:888:LYS:NZ	2.36	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:RG:41:MET:HG3	45:RG:202:ILE:HG23	1.87	0.56
2:5A:484:G:OP2	30:B6:3:LYS:NZ	2.39	0.56
10:ST:27:LYS:HA	10:ST:57:ARG:HA	1.88	0.56
15:3E:414:ARG:NH1	22:AE:187:ASP:OD2	2.36	0.56
25:B1:329:VAL:HG12	25:B1:339:LEU:HG	1.87	0.56
2:5A:173:G:N2	2:5A:224:G:O2'	2.38	0.56
18:A4:301:ASP:O	18:A4:771:GLN:NE2	2.38	0.56
2:5A:5:G:N2	2:5A:8:A:OP2	2.39	0.56
14:3D:389:ILE:HA	17:3H:62:GLU:HB2	1.87	0.56
26:B2:463:SER:OG	26:B2:464:LEU:N	2.39	0.56
26:B2:598:LYS:NZ	26:B2:610:SER:OG	2.38	0.56
46:RI:33:ASP:OD1	46:RI:33:ASP:N	2.37	0.56
49:RN:478:ILE:HD13	49:RN:520:PRO:HB2	1.88	0.56
49:RN:512:ASP:OD1	49:RN:512:ASP:N	2.38	0.56
3:SA:925:G:H4'	42:RD:1611:ALA:HA	1.87	0.56
19:A5:435:GLY:HA3	50:RO:262:LEU:HD11	1.88	0.56
32:5C:284:ARG:NH1	32:5C:408:GLU:OE1	2.39	0.56
40:5K:123:PRO:O	40:5K:126:LYS:NZ	2.39	0.56
43:RE:1232:ILE:HD12	43:RE:1233:ASN:HB2	1.87	0.56
2:5A:329:A:OP1	32:5C:229:ARG:NH2	2.36	0.56
3:SA:439:U:H4'	3:SA:465:G:H22	1.69	0.56
13:3C:225:ARG:NH2	13:3C:246:GLN:OE1	2.38	0.56
22:AE:272:LYS:NZ	22:AE:310:GLY:O	2.39	0.56
24:AG:435:ASP:HB3	24:AG:702:TYR:HA	1.88	0.56
26:B2:347:SER:O	26:B2:371:LYS:NZ	2.39	0.56
38:5I:340:ARG:NH2	38:5I:377:SER:O	2.39	0.56
43:RE:708:LEU:HG	43:RE:915:LEU:HD23	1.88	0.56
3:SA:958:U:O2'	7:SO:55:ARG:NH1	2.39	0.56
13:3C:189:GLY:O	13:3C:216:ASN:ND2	2.39	0.56
15:3E:136:LEU:HG	15:3E:139:MET:HE2	1.88	0.56
19:A5:364:THR:OG1	19:A5:368:ASN:ND2	2.38	0.56
19:A5:471:ARG:NH2	50:RO:301:ASP:OD2	2.39	0.56
26:B2:145:ILE:HG23	26:B2:159:LEU:HB2	1.88	0.56
27:B3:128:VAL:HB	27:B3:138:HIS:HB2	1.87	0.56
32:5C:433:LEU:HG	35:5F:13:LEU:HD11	1.88	0.56
36:5G:108:LYS:HD2	36:5G:116:ARG:HB2	1.87	0.56
36:5G:144:GLU:HA	36:5G:149:PRO:HA	1.88	0.56
22:AE:95:ASP:HB2	22:AE:131:ASN:HD21	1.71	0.55
26:B2:461:SER:OG	26:B2:462:SER:N	2.38	0.55
26:B2:858:PHE:O	26:B2:862:LYS:HB2	2.06	0.55
27:B3:12:LEU:HB3	27:B3:377:LEU:HD13	1.85	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:501:PRO:HG3	27:B3:543:GLN:HG3	1.86	0.55
35:5F:29:ASP:N	35:5F:29:ASP:OD1	2.38	0.55
38:5I:73:ILE:HG12	38:5I:85:THR:HG22	1.88	0.55
43:RE:777:ASP:O	43:RE:780:GLN:NE2	2.39	0.55
48:RK:154:LEU:HB2	48:RK:165:GLU:HG3	1.88	0.55
53:RT:109:LEU:O	53:RT:113:TRP:HB2	2.06	0.55
16:3F:337:VAL:HG23	16:3F:407:MET:HE2	1.88	0.55
26:B2:124:ILE:HA	26:B2:140:SER:HA	1.89	0.55
28:B8:181:GLU:HB3	29:BE:281:ARG:HH12	1.71	0.55
32:5C:162:ASN:HB3	32:5C:164:GLN:H	1.71	0.55
47:RJ:279:PRO:HB3	47:RJ:784:LYS:HA	1.88	0.55
3:SA:1655:A:H2'	3:SA:1656:U:C6	2.41	0.55
10:ST:8:GLN:NE2	23:AF:324:SER:O	2.39	0.55
26:B2:787:LYS:NZ	26:B2:788:PRO:O	2.38	0.55
38:5I:329:ILE:HG12	38:5I:343:TYR:HB2	1.89	0.55
39:5J:129:ALA:HB1	47:RJ:1119:ILE:HG22	1.89	0.55
48:RK:34:GLU:HG3	48:RK:35:LYS:HG2	1.88	0.55
48:RK:139:PRO:HA	48:RK:142:GLU:HB2	1.89	0.55
3:SA:1232:U:O4	3:SA:1234:A:N6	2.39	0.55
13:3B:225:ARG:NH1	13:3B:248:ASP:OD2	2.38	0.55
13:3C:320:TYR:OH	13:3C:322:ARG:NH2	2.39	0.55
17:3H:41:THR:O	17:3H:45:ASN:ND2	2.39	0.55
18:A4:57:ILE:HD13	18:A4:340:GLN:HG2	1.89	0.55
19:A5:5:VAL:HA	19:A5:21:THR:HG22	1.89	0.55
24:AG:262:MET:HA	24:AG:272:ALA:O	2.07	0.55
38:5I:26:ARG:NH1	51:RQ:867:GLN:O	2.40	0.55
41:RC:52:TYR:HE1	41:RC:56:ILE:HG21	1.70	0.55
47:RJ:608:LEU:HB2	48:RK:16:ASN:HD22	1.72	0.55
3:SA:1490:C:OP1	47:RJ:1062:ARG:NH2	2.38	0.55
3:SA:1542:G:O6	3:SA:1568:C:N4	2.36	0.55
8:SP:86:THR:OG1	8:SP:90:ARG:NH2	2.36	0.55
16:3F:289:ARG:NH2	16:3F:332:ALA:O	2.39	0.55
16:3F:552:TRP:HB3	17:3H:85:VAL:HG13	1.88	0.55
27:B3:513:LYS:HG3	27:B3:532:HIS:HB2	1.87	0.55
30:B6:278:MET:HA	30:B6:312:LEU:HD11	1.89	0.55
37:5H:432:ASP:O	45:RH:129:ARG:NH2	2.39	0.55
43:RE:526:CYS:O	43:RE:698:ASN:ND2	2.40	0.55
47:RJ:939:TYR:HA	47:RJ:997:MET:HE1	1.88	0.55
49:RN:682:ARG:O	49:RN:686:ASN:ND2	2.40	0.55
51:RQ:896:ALA:HB1	51:RQ:897:PRO:HD2	1.89	0.55
17:3G:57:ASP:O	17:3G:84:ARG:NH1	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AG:583:LYS:HE2	24:AG:599:ILE:HD13	1.88	0.55
27:B3:516:LYS:HA	27:B3:528:THR:HG22	1.89	0.55
28:B8:561:PRO:O	28:B8:587:ARG:NH1	2.39	0.55
38:5I:173:ILE:HG13	38:5I:174:ARG:HG2	1.87	0.55
47:RJ:130:ASP:OD2	47:RJ:853:ARG:NH2	2.40	0.55
48:RK:155:LYS:HG3	48:RK:164:GLY:HA2	1.89	0.55
13:3C:160:ASP:OD1	13:3C:160:ASP:N	2.37	0.55
16:3F:293:ASP:N	16:3F:293:ASP:OD1	2.37	0.55
19:A5:454:GLU:OE2	19:A5:487:ARG:NH1	2.39	0.55
23:AF:420:GLU:O	23:AF:424:ARG:HB3	2.07	0.55
24:AG:51:GLN:HE21	24:AG:53:LYS:HD3	1.72	0.55
26:B2:142:ASP:OD2	26:B2:144:ASN:ND2	2.39	0.55
43:RE:209:MET:SD	43:RE:227:LYS:NZ	2.70	0.55
43:RE:980:VAL:HG21	43:RE:1011:ARG:HG2	1.88	0.55
47:RJ:360:ASP:OD1	47:RJ:360:ASP:N	2.35	0.55
47:RJ:921:GLU:HB2	48:RK:365:LYS:HG3	1.88	0.55
48:RK:37:ARG:NH2	48:RK:49:GLU:OE2	2.36	0.55
19:A5:531:LYS:O	19:A5:535:ASP:HB2	2.07	0.55
20:A8:443:CYS:HA	24:AG:728:LEU:HD22	1.87	0.55
25:B1:418:ARG:HH22	34:5E:491:ALA:HA	1.72	0.55
26:B2:267:ASP:OD1	26:B2:267:ASP:N	2.36	0.55
28:B8:526:ASP:OD1	28:B8:526:ASP:N	2.38	0.55
34:5E:299:SER:O	34:5E:303:GLN:NE2	2.40	0.55
3:SA:545:A:O2'	3:SA:546:U:O4'	2.22	0.55
3:SA:1750:A:H2'	3:SA:1751:C:C6	2.42	0.55
3:SA:1758:U:O4	26:B2:937:ARG:NH2	2.40	0.55
22:AE:558:VAL:O	22:AE:592:ARG:NH1	2.40	0.55
27:B3:258:ILE:HD12	27:B3:271:ASP:HA	1.88	0.55
28:B8:176:LYS:O	28:B8:180:ASP:CB	2.55	0.55
32:5C:369:MET:HE1	32:5C:404:PRO:HD2	1.88	0.55
34:5E:344:GLU:HA	47:RJ:960:ARG:HH21	1.71	0.55
34:5E:448:LEU:HD22	35:5F:85:MET:HE1	1.89	0.55
6:SN:90:LYS:HE3	6:SN:91:VAL:HG12	1.88	0.55
18:A4:534:LEU:HA	18:A4:542:VAL:O	2.07	0.55
22:AE:196:LEU:HD11	22:AE:213:THR:HG21	1.88	0.55
24:AG:510:TYR:OH	24:AG:527:HIS:ND1	2.35	0.55
25:B1:430:ARG:HD2	34:5E:460:PRO:HA	1.89	0.55
35:5F:162:ASP:OD1	35:5F:162:ASP:N	2.40	0.55
47:RJ:289:HIS:HB2	47:RJ:815:LEU:HD21	1.89	0.55
47:RJ:551:LYS:O	47:RJ:555:MET:HB2	2.07	0.55
49:RN:290:LYS:O	52:RS:458:ARG:NH1	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RO:156:TRP:O	50:RO:215:ASN:ND2	2.40	0.55
52:RS:445:ARG:NH1	52:RS:445:ARG:O	2.40	0.55
2:5A:354:G:N1	32:5C:485:ASP:O	2.38	0.54
9:SR:22:VAL:HG22	9:SR:65:ILE:HG23	1.89	0.54
14:3D:21:LYS:HE2	14:3D:49:GLU:HB2	1.88	0.54
14:3D:63:LEU:O	14:3D:67:ASN:ND2	2.40	0.54
22:AE:12:ALA:HB2	32:5C:142:GLY:HA3	1.89	0.54
22:AE:636:ASP:OD1	22:AE:639:ARG:NH1	2.40	0.54
26:B2:592:SER:OG	26:B2:593:ALA:N	2.40	0.54
27:B3:721:ASN:OD1	27:B3:721:ASN:N	2.39	0.54
30:B6:187:LYS:HE3	39:5J:63:PRO:HB2	1.90	0.54
38:5I:402:GLU:O	38:5I:405:ARG:NH2	2.40	0.54
41:RC:103:LEU:HB3	41:RC:108:VAL:HG21	1.89	0.54
48:RK:347:ASN:ND2	48:RK:349:ASP:OD2	2.40	0.54
50:RO:345:ILE:HA	50:RO:349:LEU:HD13	1.89	0.54
2:5A:243:A:H4'	33:5D:224:LEU:HD21	1.89	0.54
16:3F:398:CYS:O	16:3F:419:ASN:ND2	2.40	0.54
22:AE:519:LEU:HD23	22:AE:523:ILE:HD13	1.88	0.54
25:B1:356:ASP:HB2	25:B1:826:ARG:HG3	1.88	0.54
25:B1:375:THR:OG1	25:B1:376:SER:N	2.41	0.54
27:B3:353:LEU:HD23	27:B3:365:ILE:HD11	1.88	0.54
35:5F:115:MET:HG3	35:5F:120:MET:HB3	1.89	0.54
38:5I:324:SER:OG	38:5I:326:ASP:OD1	2.23	0.54
45:RH:114:ILE:HG12	45:RH:122:ILE:HB	1.89	0.54
4:SG:26:ALA:HB3	9:SR:28:LEU:HB3	1.89	0.54
15:3E:280:MET:HG3	15:3E:288:THR:HG22	1.89	0.54
24:AG:850:GLU:HA	24:AG:853:ILE:HD12	1.89	0.54
25:B1:202:ASP:N	25:B1:202:ASP:OD1	2.40	0.54
25:B1:396:ALA:HB2	25:B1:438:VAL:HG21	1.90	0.54
25:B1:641:LEU:HD23	25:B1:644:ILE:HD12	1.89	0.54
27:B3:592:SER:HB3	27:B3:620:LEU:HD22	1.88	0.54
37:5H:565:LYS:HA	37:5H:568:LYS:HG2	1.89	0.54
43:RE:1014:LEU:HG	43:RE:1018:LYS:HE3	1.90	0.54
51:RQ:898:PHE:N	51:RQ:898:PHE:CD1	2.73	0.54
17:3G:13:ASP:OD1	17:3G:13:ASP:N	2.39	0.54
18:A4:641:GLU:OE2	18:A4:645:ARG:NH1	2.40	0.54
23:AF:360:MET:HE3	23:AF:361:MET:HE3	1.89	0.54
27:B3:343:MET:HE1	27:B3:622:ALA:HB1	1.89	0.54
38:5I:75:LYS:NZ	38:5I:356:TYR:O	2.34	0.54
38:5I:133:GLN:NE2	38:5I:151:ASN:OD1	2.40	0.54
43:RE:218:ASP:HA	43:RE:223:ARG:HH22	1.72	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RE:929:ILE:HG13	43:RE:933:LEU:HD23	1.90	0.54
14:3D:379:LEU:O	14:3D:383:CYS:HB2	2.07	0.54
18:A4:252:GLN:NE2	18:A4:318:ASN:OD1	2.40	0.54
24:AG:64:LYS:NZ	24:AG:123:GLY:O	2.39	0.54
26:B2:287:ARG:NH1	26:B2:324:PHE:O	2.41	0.54
27:B3:12:LEU:HD12	27:B3:12:LEU:N	2.17	0.54
27:B3:434:SER:H	27:B3:458:SER:HB2	1.73	0.54
29:BE:626:ASP:N	29:BE:626:ASP:OD1	2.35	0.54
38:5I:349:GLN:O	38:5I:367:SER:OG	2.24	0.54
43:RE:687:GLN:NE2	43:RE:694:ALA:O	2.41	0.54
47:RJ:1018:VAL:O	47:RJ:1029:TRP:NE1	2.41	0.54
3:SA:511:A:OP2	5:SK:176:ASN:ND2	2.40	0.54
16:3F:414:ILE:HD11	16:3F:480:ALA:HB2	1.90	0.54
19:A5:20:VAL:HG22	19:A5:29:VAL:HG22	1.89	0.54
22:AE:274:ILE:HD11	28:B8:215:THR:HG21	1.90	0.54
23:AF:387:ALA:O	23:AF:391:ASN:ND2	2.40	0.54
27:B3:17:ALA:HB3	27:B3:35:PRO:HA	1.90	0.54
42:RD:1488:LEU:CA	43:RE:411:ILE:O	2.55	0.54
47:RJ:966:ILE:HD13	47:RJ:976:ILE:HG22	1.88	0.54
9:SR:34:SER:HB2	9:SR:38:LEU:HD12	1.90	0.54
16:3F:481:ILE:HD12	16:3F:486:VAL:HG13	1.90	0.54
20:A8:666:VAL:HG22	21:A9:496:LEU:HB3	1.90	0.54
22:AE:205:THR:HB	22:AE:210:LEU:HD21	1.89	0.54
23:AF:75:LYS:HD3	23:AF:113:PRO:HD3	1.89	0.54
24:AG:727:GLN:OE1	24:AG:738:ASN:ND2	2.40	0.54
26:B2:317:ILE:O	26:B2:321:TYR:N	2.41	0.54
27:B3:279:LYS:NZ	27:B3:326:THR:OG1	2.39	0.54
28:B8:486:SER:OG	28:B8:487:GLU:N	2.41	0.54
32:5C:449:ILE:HD11	38:5I:38:ALA:HA	1.89	0.54
53:RT:169:ASP:OD1	53:RT:169:ASP:N	2.39	0.54
1:3A:258:U:O4	14:3D:377:ARG:NH2	2.41	0.54
3:SA:918:U:O3'	8:SP:18:ARG:NH1	2.41	0.54
13:3C:268:VAL:HG22	13:3C:317:VAL:HG12	1.89	0.54
14:3D:392:TYR:HB3	17:3H:65:LEU:HD22	1.90	0.54
23:AF:215:VAL:HA	23:AF:230:GLY:HA3	1.90	0.54
24:AG:368:ASP:OD1	24:AG:368:ASP:N	2.38	0.54
47:RJ:73:ALA:HB1	47:RJ:131:ILE:HD12	1.90	0.54
47:RJ:1027:THR:HG23	47:RJ:1028:GLU:HG2	1.89	0.54
49:RN:780:LYS:HG2	49:RN:781:MET:HE2	1.90	0.54
2:5A:354:G:N2	32:5C:495:SER:O	2.41	0.54
3:SA:494:U:OP1	47:RJ:1138:ARG:NH2	2.32	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1108:G:O2'	3:SA:1109:G:N7	2.37	0.54
28:B8:176:LYS:O	28:B8:180:ASP:HB3	2.07	0.54
37:5H:511:GLU:O	37:5H:515:ASN:ND2	2.40	0.54
48:RK:214:LYS:O	48:RK:217:LYS:NZ	2.40	0.54
49:RN:515:HIS:HB3	49:RN:518:ILE:HG22	1.90	0.54
52:RS:319:LYS:HA	52:RS:323:PHE:HB2	1.89	0.54
13:3B:124:SER:HB3	39:5J:153:ILE:HD11	1.90	0.54
15:3E:380:ARG:NH1	15:3E:382:ASP:OD1	2.40	0.54
24:AG:157:PHE:O	24:AG:169:GLN:NE2	2.40	0.54
26:B2:260:GLU:O	26:B2:272:PHE:HA	2.08	0.54
29:BE:73:GLU:OE2	29:BE:74:LYS:NZ	2.40	0.54
29:BE:160:THR:OG1	29:BE:163:GLN:NE2	2.41	0.54
3:SA:1159:C:N4	36:5G:184:GLU:OE2	2.38	0.53
3:SA:1175:U:OP1	49:RN:748:ARG:NH1	2.41	0.53
3:SA:1697:G:C5'	43:RE:326:LEU:HD11	2.38	0.53
13:3B:90:PRO:HD3	39:5J:106:LEU:HD12	1.90	0.53
16:3F:162:CYS:SG	16:3F:525:GLN:NE2	2.79	0.53
17:3H:38:ASN:HA	17:3H:41:THR:HG22	1.91	0.53
18:A4:271:THR:HG21	28:B8:443:VAL:HG21	1.91	0.53
20:A8:573:ILE:HG22	20:A8:575:ASN:H	1.72	0.53
22:AE:651:LEU:HD21	22:AE:680:TYR:HB2	1.90	0.53
24:AG:724:ILE:HD11	24:AG:763:ILE:HG22	1.90	0.53
43:RE:524:ASP:OD1	43:RE:956:ASN:ND2	2.39	0.53
43:RE:1202:CYS:SG	43:RE:1203:ASN:N	2.81	0.53
45:RG:36:LYS:NZ	45:RG:169:ASP:O	2.40	0.53
47:RJ:954:SER:HA	47:RJ:984:GLU:HG3	1.89	0.53
49:RN:605:ASP:OD1	49:RN:610:ARG:NH1	2.41	0.53
3:SA:1539:G:N1	3:SA:1569:A:OP2	2.41	0.53
6:SN:105:LYS:HA	52:RS:350:LEU:HD22	1.91	0.53
16:3F:399:GLU:OE2	16:3F:417:SER:OG	2.26	0.53
25:B1:661:LEU:HD11	34:5E:450:VAL:HG12	1.90	0.53
26:B2:412:GLY:HA2	26:B2:431:GLY:H	1.73	0.53
28:B8:352:GLN:HE21	28:B8:385:ASN:HD22	1.54	0.53
29:BE:604:SER:OG	29:BE:606:ASP:OD1	2.25	0.53
40:5K:145:VAL:HG23	40:5K:151:TYR:HB2	1.89	0.53
43:RE:207:LEU:O	43:RE:297:GLY:N	2.39	0.53
45:RH:125:ASN:ND2	45:RH:127:THR:OG1	2.42	0.53
4:SG:73:THR:OG1	4:SG:91:GLU:OE1	2.27	0.53
17:3H:45:ASN:HA	17:3H:74:LYS:HE2	1.90	0.53
18:A4:311:THR:HG22	18:A4:313:LYS:H	1.74	0.53
23:AF:173:THR:HG21	23: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)
25:B1:635:MET:HE1	40:5K:8:ARG:HH11	1.73	0.53
29:BE:430:ILE:HB	29:BE:443:TRP:HB2	1.89	0.53
36:5G:93:SER:O	36:5G:119:ARG:NH2	2.41	0.53
2:5A:175:A:N6	2:5A:177:U:O2	2.40	0.53
3:SA:867:G:H1	3:SA:961:U:H3	1.56	0.53
3:SA:976:G:C6	3:SA:978:A:H2'	2.44	0.53
7:SO:99:ARG:NH2	7:SO:119:GLU:OE2	2.40	0.53
18:A4:641:GLU:HB3	18:A4:749:SER:HB3	1.90	0.53
24:AG:291:ARG:HD2	24:AG:329:ASN:HD21	1.73	0.53
27:B3:151:LYS:NZ	27:B3:197:ASP:OD1	2.38	0.53
48:RK:289:VAL:HG21	48:RK:294:LEU:HD13	1.90	0.53
14:3D:157:ALA:O	30:B6:293:TYR:OH	2.26	0.53
14:3D:392:TYR:HB2	17:3H:62:GLU:HB3	1.90	0.53
19:A5:46:TRP:HD1	19:A5:48:GLU:HG3	1.74	0.53
25:B1:283:GLU:OE2	25:B1:297:GLN:NE2	2.42	0.53
26:B2:525:ASP:OD1	26:B2:525:ASP:N	2.40	0.53
27:B3:168:THR:HA	27:B3:192:ALA:HA	1.91	0.53
27:B3:625:THR:HG22	27:B3:633:VAL:HG13	1.90	0.53
45:RG:169:ASP:N	45:RG:169:ASP:OD1	2.40	0.53
46:RI:83:TYR:OH	46:RI:169:GLU:OE1	2.27	0.53
49:RN:96:LYS:HD2	49:RN:761:PHE:HZ	1.73	0.53
3:SA:513:U:H2'	3:SA:514:G:C8	2.44	0.53
22:AE:40:ALA:HB1	22:AE:123:ARG:HH12	1.73	0.53
24:AG:213:LYS:HA	24:AG:223:LYS:HA	1.91	0.53
38:5I:192:SER:HB2	38:5I:206:VAL:HG22	1.89	0.53
46:RI:83:TYR:O	46:RI:87:LEU:HB2	2.08	0.53
3:SA:629:U:H2'	3:SA:630:A:H8	1.74	0.53
26:B2:869:VAL:O	27:B3:816:LEU:HD22	2.09	0.53
35:5F:108:ARG:O	35:5F:117:ARG:NH1	2.42	0.53
3:SA:1658:G:O6	3:SA:1742:U:O4	2.26	0.53
24:AG:404:SER:OG	24:AG:405:ALA:N	2.40	0.53
32:5C:312:VAL:HG21	32:5C:353:PRO:HG2	1.90	0.53
36:5G:153:THR:HG23	36:5G:164:GLN:HG2	1.91	0.53
43:RE:162:PHE:HZ	43:RE:597:ARG:HH11	1.57	0.53
46:RI:231:GLN:NE2	54:RW:188:THR:O	2.42	0.53
14:3D:102:ASP:HB3	14:3D:105:LEU:HB3	1.91	0.53
21:A9:513:ARG:HH21	21:A9:515:ASP:HA	1.72	0.53
23:AF:87:ALA:HA	23:AF:97:CYS:O	2.08	0.53
27:B3:96:VAL:HG12	27:B3:97:ARG:HG3	1.90	0.53
32:5C:483:ILE:HG23	32:5C:516:VAL:HG22	1.90	0.53
43:RE:1101:ASP:OD2	43:RE:1103:ARG:NH1	2.42	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:RG:121:LEU:HD21	45:RG:167:ILE:HG13	1.90	0.53
3:SA:1671:A:N6	3:SA:1730:A:O2'	2.42	0.53
13:3B:230:TYR:OH	13:3B:256:ASN:OD1	2.25	0.53
24:AG:283:VAL:HG12	24:AG:290:ILE:HG22	1.91	0.53
25:B1:567:ASP:HB3	35:5F:144:ASN:HD21	1.74	0.53
27:B3:403:ILE:HB	27:B3:415:TRP:HB2	1.91	0.53
43:RE:257:SER:O	43:RE:266:PRO:HA	2.09	0.53
45:RG:188:ARG:NH2	45:RH:247:ASP:OD2	2.41	0.53
51:RQ:298:TRP:HE1	51:RQ:899:LYS:CG	2.19	0.53
1:3A:198:U:O4	16:3F:151:ARG:NE	2.38	0.52
2:5A:254:C:H2'	54:RW:183:ARG:HH21	1.74	0.52
3:SA:1136:U:O2'	26:B2:596:ASN:ND2	2.43	0.52
3:SA:1209:C:N3	3:SA:1210:C:N4	2.56	0.52
13:3B:281:ASP:OD1	13:3B:281:ASP:N	2.41	0.52
18:A4:35:ARG:HH11	18:A4:738:TYR:HD1	1.57	0.52
20:A8:558:CYS:O	20:A8:585:ARG:NH2	2.42	0.52
22:AE:626:PHE:HB3	22:AE:629:GLU:HB2	1.90	0.52
25:B1:812:GLU:HG3	25:B1:813:HIS:HD2	1.74	0.52
27:B3:616:HIS:HD2	27:B3:640:VAL:HG23	1.74	0.52
43:RE:254:LEU:HD11	43:RE:268:LEU:HD12	1.91	0.52
45:RH:116:THR:HG22	45:RH:118:ARG:H	1.73	0.52
50:RO:233:ASP:N	50:RO:233:ASP:OD1	2.42	0.52
15:3E:289:GLN:HE21	15:3E:388:LEU:HD13	1.74	0.52
26:B2:676:SER:OG	26:B2:678:ASP:OD1	2.22	0.52
27:B3:16:TYR:HD1	27:B3:34:THR:H	1.58	0.52
43:RE:128:LEU:HD11	43:RE:185:LEU:HD11	1.91	0.52
43:RE:1206:PRO:HB3	43:RE:1212:VAL:HG12	1.90	0.52
52:RS:437:ARG:NH2	52:RS:459:GLU:O	2.42	0.52
2:5A:135:G:O3'	19:A5:494:ARG:NH1	2.42	0.52
8:SP:42:VAL:HG11	8:SP:63:ALA:O	2.09	0.52
17:3H:54:MET:HE1	17:3H:78:TYR:HB2	1.90	0.52
18:A4:39:VAL:H	18:A4:755:ILE:HD11	1.75	0.52
22:AE:556:LYS:O	22:AE:592:ARG:NH2	2.43	0.52
22:AE:571:LEU:HD11	22:AE:582:VAL:HG11	1.91	0.52
29:BE:578:VAL:O	29:BE:579:ARG:NH1	2.42	0.52
36:5G:43:PRO:HG2	36:5G:46:LEU:HB2	1.91	0.52
47:RJ:90:VAL:HG23	47:RJ:107:VAL:HG11	1.92	0.52
47:RJ:135:ALA:O	47:RJ:238:ARG:NH2	2.42	0.52
48:RK:180:MET:HE3	48:RK:181:HIS:H	1.75	0.52
49:RN:587:ASP:OD1	49:RN:587:ASP:N	2.42	0.52
22:AE:502:ILE:HG23	22:AE:542:ILE:HG13	1.90	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:5F:123:THR:HG23	35:5F:126:ASP:H	1.73	0.52
46:RI:135:LEU:HD22	46:RI:139:LEU:HD13	1.91	0.52
47:RJ:982:LYS:HG3	47:RJ:983:PRO:HD3	1.92	0.52
2:5A:176:U:O2'	2:5A:178:G:OP2	2.23	0.52
13:3B:228:GLN:O	13:3B:231:ARG:NH2	2.43	0.52
18:A4:420:LEU:HD23	19:A5:581:ASN:HA	1.91	0.52
28:B8:216:TYR:OH	29:BE:276:TYR:OH	2.27	0.52
29:BE:470:GLN:NE2	29:BE:512:GLY:O	2.42	0.52
43:RE:1221:HIS:NE2	44:RF:21:PRO:O	2.42	0.52
47:RJ:844:PRO:HA	47:RJ:856:THR:O	2.08	0.52
48:RK:97:GLY:HA2	48:RK:100:VAL:HG12	1.92	0.52
48:RK:171:ASP:N	48:RK:171:ASP:OD1	2.39	0.52
3:SA:1533:C:OP1	10:ST:27:LYS:NZ	2.41	0.52
13:3C:297:ARG:HD3	13:3C:322:ARG:HA	1.92	0.52
15:3E:251:ASP:OD1	15:3E:251:ASP:N	2.43	0.52
18:A4:658:ASP:OD2	18:A4:731:HIS:N	2.42	0.52
19:A5:481:LEU:HD22	19:A5:523:LEU:HD22	1.92	0.52
20:A8:566:LEU:HG	20:A8:582:ILE:HD11	1.92	0.52
23:AF:364:SER:O	23:AF:364:SER:OG	2.26	0.52
26:B2:398:ASP:HB2	26:B2:406:LEU:HB3	1.92	0.52
27:B3:282:ASN:HD21	27:B3:327:ILE:HD11	1.75	0.52
42:RD:1489:SER:CB	43:RE:427:LYS:CD	2.83	0.52
43:RE:197:GLN:HB2	43:RE:200:GLY:H	1.73	0.52
43:RE:713:LEU:HB2	43:RE:716:SER:HB3	1.90	0.52
43:RE:834:ASN:ND2	43:RE:863:TYR:OH	2.42	0.52
43:RE:1109:LYS:HD3	43:RE:1114:ILE:HB	1.92	0.52
44:RF:101:SER:O	44:RF:105:SER:CB	2.58	0.52
44:RF:176:ASP:N	44:RF:176:ASP:OD1	2.41	0.52
3:SA:594:A:OP1	5:SK:38:ASN:ND2	2.43	0.52
21:A9:504:GLU:OE2	21:A9:507:ARG:NH1	2.43	0.52
24:AG:319:LYS:HD2	24:AG:339:GLY:H	1.74	0.52
26:B2:53:ASP:OD2	26:B2:58:ASP:OD1	2.27	0.52
26:B2:281:ILE:HB	26:B2:332:ILE:HG23	1.91	0.52
26:B2:554:THR:OG1	26:B2:556:LYS:NZ	2.39	0.52
29:BE:268:THR:HG22	29:BE:270:SER:H	1.75	0.52
29:BE:605:LEU:HD23	29:BE:628:VAL:HG11	1.92	0.52
29:BE:819:LYS:NZ	29:BE:823:GLU:OE2	2.40	0.52
38:5I:319:GLU:OE2	38:5I:356:TYR:OH	2.27	0.52
43:RE:270:ILE:HB	43:RE:292:ILE:HG13	1.92	0.52
46:RI:155:ARG:O	46:RI:179:GLN:NE2	2.42	0.52
1:3A:256:G:OP1	14:3D:382:LYS:NZ	2.37	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1004:U:OP2	3:SA:1006:C:N4	2.43	0.52
13:3B:277:ASP:N	13:3B:277:ASP:OD1	2.43	0.52
14:3D:169:LYS:HA	14:3D:299:VAL:HG22	1.91	0.52
39:5J:58:ASN:HA	39:5J:61:LYS:HG2	1.92	0.52
47:RJ:246:ALA:HB3	47:RJ:810:ILE:HB	1.91	0.52
47:RJ:616:ASP:HB2	47:RJ:621:LEU:HG	1.90	0.52
52:RS:397:PHE:HD1	52:RS:407:GLU:HG2	1.75	0.52
3:SA:1436:A:H1'	52:RS:419:LYS:HD2	1.90	0.52
4:SG:120:ILE:HA	4:SG:123:VAL:HG12	1.92	0.52
15:3E:426:ALA:HB2	29:BE:305:ASN:HD21	1.75	0.52
19:A5:503:LYS:HD3	21:A9:508:ARG:HH22	1.75	0.52
23:AF:256:THR:N	23:AF:275:SER:O	2.39	0.52
25:B1:506:SER:OG	25:B1:507:GLN:N	2.43	0.52
26:B2:54:ILE:CD1	26:B2:364:TYR:CD2	2.93	0.52
26:B2:861:ILE:HD13	27:B3:806:LEU:CD2	2.40	0.52
29:BE:59:GLN:HG2	29:BE:71:VAL:HG22	1.91	0.52
41:RC:103:LEU:O	41:RC:108:VAL:HG22	2.10	0.52
43:RE:307:LYS:HE3	43:RE:312:ARG:HD3	1.92	0.52
48:RK:30:PRO:HB3	48:RK:77:ARG:HG3	1.90	0.52
2:5A:294:U:OP1	25:B1:631:ASN:ND2	2.43	0.52
10:ST:28:ILE:HD13	10:ST:61:LEU:HD11	1.92	0.52
15:3E:359:ILE:HA	15:3E:362:VAL:HG12	1.92	0.52
32:5C:495:SER:O	32:5C:495:SER:OG	2.29	0.52
51:RQ:298:TRP:NE1	51:RQ:899:LYS:CG	2.62	0.52
51:RQ:298:TRP:CD1	51:RQ:899:LYS:HG3	2.44	0.52
52:RS:360:LEU:HD21	52:RS:393:TYR:HB2	1.92	0.52
3:SA:1533:C:OP2	23:AF:114:ARG:NH2	2.43	0.51
13:3B:120:GLU:OE2	13:3B:142:ARG:NE	2.41	0.51
18:A4:63:SER:HA	18:A4:82:ARG:HH12	1.75	0.51
18:A4:402:TRP:HB3	18:A4:416:LEU:HA	1.91	0.51
20:A8:28:TYR:HA	20:A8:356:THR:HA	1.92	0.51
24:AG:407:ASN:ND2	24:AG:416:SER:OG	2.44	0.51
25:B1:722:THR:HG22	25:B1:724:HIS:H	1.75	0.51
32:5C:130:ARG:NH2	32:5C:379:GLU:OE2	2.42	0.51
43:RE:756:VAL:HA	43:RE:896:THR:HG21	1.91	0.51
47:RJ:193:ARG:NH2	47:RJ:196:THR:OG1	2.43	0.51
47:RJ:864:ASP:OD1	47:RJ:864:ASP:N	2.43	0.51
8:SP:20:TYR:HB3	8:SP:27:PHE:HB2	1.93	0.51
14:3D:126:ASP:HA	14:3D:129:ARG:HG2	1.93	0.51
20:A8:563:LEU:HA	20:A8:566:LEU:HB2	1.92	0.51
20:A8:672:ASN:HB2	21:A9:486:LEU:HD22	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B2:634:SER:OG	26:B2:635:LYS:N	2.41	0.51
27:B3:787:PRO:HB2	34:5E:492:PRO:HG3	1.92	0.51
32:5C:410:ASN:O	38:5I:27:ASN:ND2	2.43	0.51
36:5G:139:LEU:HD23	36:5G:266:LEU:HD12	1.92	0.51
44:RF:9:MET:HB2	44:RF:13:PHE:HB2	1.92	0.51
45:RG:105:ASN:HD21	45:RG:110:LEU:HD22	1.75	0.51
48:RK:315:LYS:HB2	48:RK:348:GLU:HB3	1.92	0.51
50:RO:258:GLU:HG3	50:RO:289:PHE:HD1	1.74	0.51
3:SA:1670:G:N2	3:SA:1731:A:OP2	2.42	0.51
18:A4:420:LEU:HD11	18:A4:462:VAL:HG21	1.92	0.51
29:BE:377:SER:HB2	29:BE:445:MET:HE1	1.92	0.51
29:BE:854:SER:HB2	29:BE:895:VAL:HG21	1.92	0.51
34:5E:373:ILE:HG13	34:5E:378:PHE:HZ	1.76	0.51
42:RD:1537:PHE:HA	42:RD:1540:ALA:HB3	1.92	0.51
50:RO:356:ALA:HA	50:RO:499:LEU:HD22	1.91	0.51
52:RS:229:LEU:HD11	52:RS:233:PHE:HD2	1.74	0.51
2:5A:426:G:C2	2:5A:428:A:H5''	2.46	0.51
2:5A:460:U:OP1	40:5K:21:LYS:NZ	2.42	0.51
8:SP:42:VAL:O	8:SP:42:VAL:HG13	2.10	0.51
10:ST:67:GLU:HA	10:ST:70:VAL:HG12	1.91	0.51
15:3E:3:TYR:N	15:3E:21:LYS:O	2.43	0.51
24:AG:736:THR:HG23	24:AG:738:ASN:H	1.74	0.51
25:B1:588:ASP:OD1	25:B1:588:ASP:N	2.43	0.51
29:BE:370:SER:OG	29:BE:372:ASP:OD1	2.20	0.51
47:RJ:72:VAL:HG22	47:RJ:137:LEU:HB3	1.91	0.51
50:RO:200:ASN:ND2	50:RO:256:ASN:O	2.43	0.51
1:3A:93:U:OP2	15:3E:302:HIS:ND1	2.42	0.51
6:SN:48:SER:O	6:SN:52:LEU:HB2	2.10	0.51
10:ST:120:ARG:NH2	34:5E:341:LEU:O	2.44	0.51
13:3C:94:ALA:HB3	13:3C:166:PRO:HG3	1.92	0.51
19:A5:439:VAL:HG11	50:RO:300:THR:HG21	1.92	0.51
26:B2:362:ILE:HG12	26:B2:385:ILE:HB	1.91	0.51
27:B3:658:LYS:NZ	27:B3:658:LYS:CB	2.74	0.51
38:5I:122:ARG:HB2	38:5I:192:SER:HB3	1.93	0.51
38:5I:327:LYS:HG2	38:5I:350:HIS:H	1.76	0.51
41:RC:52:TYR:CE1	41:RC:56:ILE:HG12	2.45	0.51
43:RE:379:MET:O	43:RE:384:SER:OG	2.29	0.51
43:RE:584:GLU:HG3	43:RE:614:ARG:HB2	1.93	0.51
45:RG:150:ILE:HD11	45:RG:160:LEU:HD23	1.92	0.51
49:RN:661:ILE:HG22	49:RN:665:GLN:HG3	1.92	0.51
50:RO:214:LYS:O	50:RO:268:GLN:NE2	2.43	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:7:A:N7	24:AG:578:ASN:ND2	2.55	0.51
2:5A:293:U:H3	25:B1:632:SER:HB3	1.75	0.51
2:5A:473:A:H5''	32:5C:164:GLN:HE22	1.76	0.51
3:SA:-5:G:N1	32:5C:39:ASP:OD1	2.36	0.51
3:SA:29:U:H2'	3:SA:30:G:H8	1.74	0.51
16:3F:136:PHE:HE1	16:3F:484:SER:HB2	1.74	0.51
22:AE:558:VAL:HG13	22:AE:615:ASN:HA	1.93	0.51
22:AE:586:LEU:O	22:AE:590:ALA:CB	2.58	0.51
23:AF:258:LEU:HD22	23:AF:272:LEU:HD21	1.93	0.51
24:AG:877:ASP:N	24:AG:877:ASP:OD1	2.43	0.51
25:B1:273:ARG:NH1	29:BE:763:SER:O	2.43	0.51
26:B2:759:GLY:HA3	26:B2:805:ILE:HD11	1.91	0.51
30:B6:296:SER:HB3	30:B6:300:MET:HB2	1.91	0.51
1:3A:319:G:OP1	13:3C:122:ARG:NH2	2.44	0.51
14:3D:26:ASP:OD1	38:5I:98:SER:OG	2.29	0.51
18:A4:481:ILE:HB	18:A4:485:LYS:HB2	1.91	0.51
21:A9:471:LYS:HZ3	21:A9:474:HIS:H	1.59	0.51
23:AF:399:GLU:O	23:AF:403:ASN:ND2	2.42	0.51
24:AG:434:GLN:OE1	24:AG:434:GLN:N	2.44	0.51
25:B1:329:VAL:HG13	25:B1:338:ILE:HB	1.92	0.51
26:B2:562:SER:HB2	26:B2:564:LYS:HB2	1.93	0.51
28:B8:512:ASP:O	33:5D:248:ARG:NH1	2.42	0.51
38:5I:54:PHE:O	38:5I:382:ARG:NH2	2.44	0.51
43:RE:858:ARG:HD2	43:RE:861:ILE:HD11	1.93	0.51
46:RI:107:ARG:HB3	46:RI:138:VAL:HG13	1.93	0.51
47:RJ:776:GLN:NE2	47:RJ:781:GLU:OE2	2.40	0.51
52:RS:263:THR:HA	52:RS:266:PHE:HB2	1.93	0.51
13:3B:111:MET:HB2	13:3B:186:ASP:HB3	1.92	0.51
15:3E:355:ASN:HB2	15:3E:401:LEU:HD13	1.93	0.51
16:3F:284:LEU:O	16:3F:548:ARG:NH2	2.38	0.51
17:3H:44:LEU:HD22	17:3H:52:ILE:HD12	1.90	0.51
24:AG:325:GLN:NE2	24:AG:328:THR:OG1	2.41	0.51
27:B3:110:ALA:HB2	27:B3:117:LEU:HD12	1.92	0.51
27:B3:188:GLU:OE2	27:B3:232:LYS:NZ	2.44	0.51
38:5I:329:ILE:HG22	38:5I:351:VAL:HG11	1.93	0.51
1:3A:59:G:H5'	25:B1:570:THR:HG23	1.92	0.51
2:5A:427:A:H2'	2:5A:428:A:H4'	1.93	0.51
3:SA:630:A:C5	3:SA:970:A:N7	2.79	0.51
3:SA:976:G:N2	3:SA:978:A:C6	2.79	0.51
32:5C:74:LEU:HD23	32:5C:404:PRO:HG2	1.93	0.51
32:5C:434:LEU:HD11	35:5F:12:LEU:HD23	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RE:111:LEU:HA	43:RE:114:VAL:HG12	1.93	0.51
43:RE:498:MET:HE3	43:RE:510:ILE:HG22	1.93	0.51
46:RI:173:PRO:HA	46:RI:176:VAL:HG12	1.93	0.51
2:5A:90:G:O2'	2:5A:91:U:O4'	2.25	0.51
3:SA:910:C:H2'	3:SA:911:U:H6	1.76	0.51
3:SA:978:A:H5''	3:SA:979:A:H5'	1.92	0.51
3:SA:1194:A:OP2	3:SA:1195:C:N4	2.40	0.51
13:3B:91:HIS:HD2	13:3B:93:HIS:H	1.57	0.51
13:3B:142:ARG:NH2	13:3B:182:SER:OG	2.44	0.51
24:AG:855:LEU:HD23	28:B8:477:LYS:HE3	1.93	0.51
25:B1:392:ALA:O	25:B1:404:SER:HA	2.10	0.51
27:B3:654:GLU:OE1	27:B3:654:GLU:HA	2.10	0.51
32:5C:91:ILE:HG23	38:5I:3:ILE:HD11	1.92	0.51
39:5J:120:ASP:HB2	39:5J:173:ILE:HD12	1.92	0.51
47:RJ:776:GLN:HA	47:RJ:780:ILE:HG22	1.93	0.51
3:SA:886:U:H2'	3:SA:887:A:H8	1.75	0.50
13:3C:223:ASP:OD2	13:3C:225:ARG:NH1	2.44	0.50
20:A8:570:LEU:HD21	20:A8:637:LEU:HD21	1.91	0.50
24:AG:668:THR:OG1	24:AG:669:ASN:OD1	2.29	0.50
25:B1:732:GLU:HG2	25:B1:734:GLN:HE22	1.76	0.50
27:B3:658:LYS:HB2	27:B3:658:LYS:HZ3	1.75	0.50
32:5C:238:MET:HE3	32:5C:247:MET:HE2	1.92	0.50
45:RH:178:VAL:HG12	45:RH:223:GLU:HB2	1.93	0.50
46:RI:84:ARG:NH1	46:RI:100:ILE:O	2.42	0.50
47:RJ:772:MET:HE3	47:RJ:773:THR:H	1.76	0.50
3:SA:1499:G:N2	46:RI:194:ASP:OD2	2.44	0.50
4:SG:118:LEU:HG	4:SG:129:PRO:HB2	1.92	0.50
6:SN:93:ASP:HB3	6:SN:96:GLN:HG3	1.93	0.50
13:3C:171:LEU:HD23	13:3C:240:VAL:HG12	1.92	0.50
26:B2:627:SER:OG	26:B2:628:HIS:N	2.45	0.50
29:BE:135:ASN:ND2	29:BE:165:GLY:O	2.42	0.50
35:5F:86:GLY:HA3	35:5F:109:ARG:HD2	1.93	0.50
43:RE:765:LEU:HD21	43:RE:917:LYS:HB2	1.92	0.50
48:RK:183:ILE:HG22	48:RK:351:ILE:HD13	1.93	0.50
53:RT:107:THR:O	53:RT:111:ASN:ND2	2.44	0.50
3:SA:1192:C:H1'	45:RG:131:PRO:HA	1.92	0.50
18:A4:382:VAL:HG11	18:A4:755:ILE:HG21	1.92	0.50
20:A8:248:LEU:HA	20:A8:264:SER:HA	1.92	0.50
20:A8:712:ASP:OD1	20:A8:712:ASP:N	2.39	0.50
22:AE:522:ARG:HH12	22:AE:561:PHE:HB2	1.76	0.50
23:AF:59:SER:OG	23:AF:60:SER:N	2.43	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:186:LEU:HD11	27:B3:230:LYS:HD3	1.93	0.50
34:5E:298:SER:OG	34:5E:299:SER:N	2.43	0.50
43:RE:401:LEU:HD11	43:RE:414:HIS:HB3	1.93	0.50
44:RF:105:SER:OG	44:RF:106:ASP:N	2.44	0.50
8:SP:12:GLN:HE21	8:SP:78:ALA:HB2	1.76	0.50
23:AF:401:LEU:HB3	23:AF:434:ARG:HH22	1.77	0.50
24:AG:249:THR:HG22	24:AG:256:THR:HB	1.93	0.50
29:BE:810:ARG:NH2	53:RT:183:GLU:OE2	2.45	0.50
43:RE:219:PHE:CE2	43:RE:303:PHE:CD2	2.99	0.50
45:RG:150:ILE:HG12	45:RG:160:LEU:HB2	1.94	0.50
48:RK:65:ILE:HB	49:RN:112:VAL:HG12	1.93	0.50
52:RS:439:PHE:HA	52:RS:442:GLU:HG3	1.94	0.50
10:ST:49:LYS:HG3	10:ST:72:ILE:HD13	1.94	0.50
20:A8:671:ARG:NH1	21:A9:447:ASN:O	2.45	0.50
27:B3:618:ASN:ND2	27:B3:638:ASP:OD2	2.41	0.50
37:5H:496:GLN:HA	37:5H:499:GLN:HE21	1.75	0.50
41:RC:72:VAL:HG22	41:RC:81:THR:HG22	1.94	0.50
43:RE:186:ILE:HD11	43:RE:206:LEU:HB2	1.93	0.50
43:RE:214:PHE:HE2	43:RE:218:ASP:HB3	1.75	0.50
43:RE:426:ILE:HA	43:RE:429:LEU:HG	1.93	0.50
46:RI:211:GLU:O	46:RI:215:ASN:ND2	2.44	0.50
47:RJ:634:ARG:HD2	48:RK:185:ARG:HH21	1.77	0.50
2:5A:505:G:H2'	2:5A:506:G:C8	2.47	0.50
3:SA:1134:C:H1'	26:B2:610:SER:HB2	1.94	0.50
19:A5:115:ASN:ND2	19:A5:130:ASP:OD1	2.45	0.50
19:A5:192:SER:HB3	19:A5:207:GLU:HG3	1.93	0.50
24:AG:207:LEU:HG	24:AG:264:ILE:HD12	1.93	0.50
26:B2:90:ASP:N	26:B2:90:ASP:OD1	2.39	0.50
27:B3:115:THR:HA	27:B3:131:ILE:HG22	1.92	0.50
29:BE:587:ARG:HB3	29:BE:605:LEU:HD12	1.92	0.50
32:5C:37:THR:O	32:5C:43:ARG:NH2	2.45	0.50
38:5I:76:ASN:HA	38:5I:118:VAL:HG21	1.93	0.50
43:RE:253:GLN:NE2	43:RE:254:LEU:O	2.44	0.50
48:RK:114:PHE:O	48:RK:169:VAL:HA	2.12	0.50
3:SA:505:A:H62	3:SA:585:A:HO2'	1.57	0.50
15:3E:385:ASP:OD1	15:3E:385:ASP:N	2.42	0.50
19:A5:8:SER:OG	19:A5:293:ASN:ND2	2.43	0.50
23:AF:224:THR:O	23:AF:239:LEU:CB	2.57	0.50
24:AG:370:GLN:NE2	24:AG:384:SER:OG	2.44	0.50
26:B2:337:LYS:O	26:B2:357:THR:OG1	2.25	0.50
26:B2:828:TYR:HA	26:B2:831:LYS:HG2	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:42:ILE:HG22	27:B3:49:SER:HA	1.94	0.50
30:B6:297:ASP:OD1	30:B6:297:ASP:N	2.44	0.50
36:5G:153:THR:HG21	36:5G:266:LEU:HD21	1.93	0.50
41:RC:52:TYR:HE1	41:RC:56:ILE:CG2	2.25	0.50
41:RC:205:ILE:O	41:RC:209:LEU:HB2	2.12	0.50
45:RH:41:MET:HG3	45:RH:202:ILE:HG23	1.92	0.50
47:RJ:1069:VAL:HG11	47:RJ:1083:ILE:HD13	1.93	0.50
53:RT:216:ILE:O	53:RT:220:THR:OG1	2.28	0.50
15:3E:430:ASP:HA	29:BE:125:GLY:HA2	1.93	0.50
18:A4:415:LYS:NZ	18:A4:416:LEU:O	2.45	0.50
23:AF:378:LYS:NZ	28:B8:292:GLY:O	2.44	0.50
29:BE:225:THR:OG1	29:BE:227:THR:O	2.29	0.50
35:5F:174:ARG:NH2	47:RJ:1077:LEU:O	2.44	0.50
41:RC:195:HIS:HD2	41:RC:196:PRO:HD2	1.77	0.50
43:RE:887:ALA:O	43:RE:892:SER:OG	2.28	0.50
45:RH:41:MET:O	45:RH:110:LEU:HA	2.11	0.50
52:RS:322:LEU:HD21	52:RS:359:LEU:HD11	1.92	0.50
2:5A:20:C:H2'	2:5A:21:A:H8	1.77	0.50
3:SA:1588:G:H1	3:SA:1608:U:H3	1.60	0.50
18:A4:566:LEU:HD11	18:A4:584:VAL:HG21	1.94	0.50
19:A5:355:ASN:OD1	24:AG:479:ASN:ND2	2.44	0.50
20:A8:541:LEU:HA	20:A8:544:LEU:HD13	1.93	0.50
24:AG:80:GLN:NE2	24:AG:83:GLU:OE1	2.44	0.50
24:AG:139:GLU:HB3	24:AG:155:THR:HB	1.94	0.50
27:B3:160:ILE:HD13	27:B3:209:LEU:HD21	1.93	0.50
27:B3:484:GLU:O	42:RD:1642:GLU:CB	2.59	0.50
31:5B:173:ARG:HE	33:5D:146:PHE:HA	1.76	0.50
43:RE:753:ILE:HD13	43:RE:784:LEU:HB3	1.94	0.50
45:RH:228:SER:OG	45:RH:229:ASN:N	2.44	0.50
46:RI:233:GLY:O	46:RI:236:LYS:NZ	2.41	0.50
47:RJ:262:GLY:O	47:RJ:264:GLN:NE2	2.44	0.50
2:5A:484:G:O6	51:RQ:872:ARG:NH1	2.45	0.49
18:A4:156:LEU:HD22	18:A4:170:ILE:HD11	1.93	0.49
22:AE:306:LEU:HD22	22:AE:311:ASN:HA	1.94	0.49
23:AF:133:HIS:HB2	23:AF:139:ILE:HG13	1.94	0.49
23:AF:260:TYR:OH	23:AF:262:GLU:OE1	2.30	0.49
24:AG:628:ASP:H	24:AG:658:GLU:HA	1.77	0.49
24:AG:736:THR:OG1	24:AG:737:ILE:N	2.45	0.49
25:B1:839:THR:HG22	29:BE:882:GLU:HG3	1.94	0.49
26:B2:817:LEU:HD11	26:B2:856:ASN:HD21	1.77	0.49
28:B8:410:ASP:OD1	28:B8:479:ASN:ND2	2.45	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:5D:149:GLU:HB3	33:5D:153:ASN:HA	1.94	0.49
41:RC:199:HIS:HA	41:RC:202:GLU:HG2	1.93	0.49
43:RE:162:PHE:HE2	43:RE:597:ARG:HB2	1.77	0.49
45:RG:175:CYS:SG	45:RG:201:SER:OG	2.67	0.49
47:RJ:852:ARG:HD2	47:RJ:888:PRO:HG3	1.94	0.49
47:RJ:1094:TYR:HA	47:RJ:1097:LYS:HG2	1.94	0.49
3:SA:976:G:N2	3:SA:978:A:C5	2.81	0.49
22:AE:637:ILE:HA	22:AE:640:ILE:HG22	1.94	0.49
27:B3:437:VAL:N	27:B3:457:ALA:O	2.44	0.49
28:B8:520:ASN:HB2	28:B8:533:ALA:HB3	1.94	0.49
13:3C:170:VAL:HG23	13:3C:194:VAL:HG13	1.93	0.49
16:3F:343:ASP:OD1	16:3F:343:ASP:N	2.46	0.49
18:A4:418:CYS:SG	18:A4:419:LYS:N	2.85	0.49
20:A8:533:PRO:HG2	24:AG:656:ASP:HA	1.94	0.49
22:AE:558:VAL:HG22	22:AE:615:ASN:HD22	1.76	0.49
23:AF:48:ASN:ND2	23:AF:111:TYR:OH	2.45	0.49
24:AG:584:PHE:HB3	24:AG:598:LYS:HB2	1.94	0.49
25:B1:406:SER:OG	25:B1:407:LEU:N	2.46	0.49
26:B2:102:VAL:HA	26:B2:118:ASN:HA	1.94	0.49
27:B3:672:TYR:HB3	27:B3:681:ALA:HB2	1.95	0.49
32:5C:183:GLU:HB3	40:5K:16:THR:HG22	1.94	0.49
36:5G:192:ASP:OD2	36:5G:227:ARG:NH2	2.37	0.49
43:RE:1081:ASN:H	43:RE:1084:THR:HB	1.77	0.49
45:RG:46:ALA:HA	45:RG:115:GLN:HG3	1.93	0.49
45:RH:38:THR:O	45:RH:40:ARG:NH1	2.45	0.49
47:RJ:138:VAL:HB	47:RJ:167:VAL:HG22	1.93	0.49
49:RN:623:ASP:O	49:RN:627:HIS:HB3	2.13	0.49
50:RO:327:MET:O	50:RO:331:ASN:HA	2.11	0.49
53:RT:182:ILE:HA	53:RT:233:ILE:O	2.12	0.49
2:5A:293:U:H2'	25:B1:631:ASN:HA	1.93	0.49
6:SN:28:LEU:HA	6:SN:31:VAL:HG12	1.94	0.49
17:3H:7:LYS:HB3	17:3H:65:LEU:HD11	1.95	0.49
17:3H:54:MET:O	17:3H:80:PHE:HA	2.12	0.49
18:A4:442:VAL:O	18:A4:448:THR:OG1	2.26	0.49
18:A4:452:HIS:HB3	18:A4:463:THR:HG23	1.94	0.49
22:AE:387:LEU:HD21	22:AE:403:LEU:HD13	1.93	0.49
32:5C:84:PHE:HA	32:5C:369:MET:HA	1.95	0.49
44:RF:143:LYS:HD2	44:RF:147:LEU:HD23	1.94	0.49
46:RI:38:ILE:HA	46:RI:243:PHE:O	2.12	0.49
48:RK:180:MET:O	48:RK:181:HIS:ND1	2.45	0.49
53:RT:96:SER:HA	53:RT:139:LEU:O	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:323:A:OP1	25:B1:191:ARG:NH2	2.46	0.49
3:SA:1665:U:O4	3:SA:1736:G:O6	2.29	0.49
6:SN:33:ARG:HH12	49:RN:272:ILE:HA	1.76	0.49
10:ST:111:ASP:OD1	10:ST:115:ARG:NH1	2.46	0.49
17:3H:52:ILE:HG22	17:3H:54:MET:SD	2.52	0.49
17:3H:54:MET:HB3	17:3H:64:LEU:HD13	1.93	0.49
18:A4:150:ASN:ND2	18:A4:198:ASP:OD1	2.37	0.49
26:B2:180:THR:OG1	26:B2:207:CYS:SG	2.62	0.49
26:B2:476:ILE:HD11	26:B2:490:THR:HB	1.93	0.49
27:B3:13:ASN:N	27:B3:13:ASN:ND2	2.60	0.49
29:BE:118:VAL:HA	29:BE:132:THR:HA	1.94	0.49
32:5C:456:SER:O	32:5C:456:SER:OG	2.28	0.49
45:RH:112:VAL:O	45:RH:124:VAL:HB	2.12	0.49
47:RJ:106:THR:HG23	47:RJ:355:TYR:HB3	1.94	0.49
48:RK:107:ALA:HB1	48:RK:170:VAL:HG21	1.94	0.49
1:3A:88:U:OP2	15:3E:338:LYS:NZ	2.41	0.49
13:3B:116:SER:OG	13:3B:120:GLU:OE1	2.28	0.49
15:3E:24:LYS:O	15:3E:28:LEU:CB	2.60	0.49
18:A4:389:ARG:HE	18:A4:404:MET:HB2	1.78	0.49
24:AG:116:VAL:O	24:AG:131:HIS:HA	2.13	0.49
25:B1:286:LEU:HD12	25:B1:295:ILE:HB	1.94	0.49
26:B2:291:GLU:HA	26:B2:294:ARG:HG2	1.94	0.49
26:B2:624:LEU:HD12	26:B2:629:ASN:HB2	1.93	0.49
31:5B:186:ASP:HA	31:5B:189:THR:HG22	1.94	0.49
43:RE:1080:LEU:HD22	43:RE:1085:ILE:HD11	1.93	0.49
47:RJ:777:ARG:O	47:RJ:778:GLN:NE2	2.46	0.49
2:5A:485:G:H4'	2:5A:486:U:H5'	1.94	0.49
3:SA:1718:G:H2'	3:SA:1719:A:H8	1.77	0.49
17:3G:105:ASN:HB3	17:3G:108:SER:HB2	1.94	0.49
18:A4:207:ASP:OD2	18:A4:209:ARG:NH1	2.37	0.49
26:B2:392:THR:HG21	26:B2:410:SER:HB3	1.93	0.49
26:B2:397:ILE:HD11	26:B2:405:LEU:HD21	1.94	0.49
29:BE:274:ILE:HG23	29:BE:286:VAL:HG22	1.94	0.49
29:BE:469:SER:HB3	29:BE:510:LEU:HD23	1.95	0.49
33:5D:111:ARG:HE	33:5D:212:LYS:HB2	1.77	0.49
38:5I:421:GLN:HG3	38:5I:425:LYS:HD2	1.95	0.49
41:RC:52:TYR:CD1	41:RC:52:TYR:C	2.87	0.49
46:RI:85:GLU:OE2	46:RI:89:LYS:NZ	2.43	0.49
47:RJ:309:PRO:HD2	47:RJ:353:LEU:HD22	1.95	0.49
49:RN:752:MET:HA	49:RN:755:ILE:HG12	1.93	0.49
51:RQ:853:ASN:OD1	51:RQ:853:ASN:N	2.45	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:RS:388:ASP:HA	52:RS:391:VAL:HG22	1.93	0.49
13:3B:269:ILE:O	13:3B:315:ILE:HA	2.13	0.49
16:3F:365:PRO:HB3	16:3F:397:PHE:HA	1.93	0.49
20:A8:305:VAL:HA	20:A8:311:VAL:HA	1.95	0.49
22:AE:482:SER:HB2	22:AE:484:LEU:HG	1.94	0.49
24:AG:31:ASN:HD21	24:AG:201:ILE:HB	1.78	0.49
24:AG:96:ILE:HG12	24:AG:108:THR:HG21	1.95	0.49
28:B8:233:LEU:HD11	28:B8:543:LEU:HD12	1.95	0.49
29:BE:173:LEU:HD13	29:BE:219:ASP:HA	1.95	0.49
29:BE:528:PHE:HZ	29:BE:570:ILE:HD11	1.78	0.49
38:5I:315:PRO:HG2	38:5I:360:SER:HB3	1.93	0.49
41:RC:112:GLN:CG	41:RC:163:TYR:CE2	2.83	0.49
43:RE:146:LEU:HA	43:RE:149:VAL:HG22	1.93	0.49
46:RI:125:VAL:O	46:RI:151:PRO:HA	2.12	0.49
46:RI:155:ARG:NH1	46:RI:175:TYR:OH	2.46	0.49
47:RJ:176:LEU:HD12	47:RJ:183:LEU:HA	1.94	0.49
47:RJ:274:TYR:OH	47:RJ:306:ASP:OD1	2.29	0.49
3:SA:992:A:OP2	3:SA:1011:G:N1	2.38	0.49
3:SA:1133:A:OP1	48:RK:231:ARG:NE	2.42	0.49
20:A8:561:LEU:HD13	20:A8:566:LEU:HD11	1.95	0.49
23:AF:428:ARG:HH21	24:AG:518:ASP:HB3	1.76	0.49
26:B2:440:PRO:HG3	26:B2:485:GLY:HA3	1.94	0.49
28:B8:462:GLY:HA2	28:B8:527:GLY:HA3	1.95	0.49
29:BE:902:ASN:HB3	29:BE:905:ILE:HG22	1.95	0.49
32:5C:340:LEU:O	32:5C:368:TYR:N	2.43	0.49
32:5C:508:VAL:HG12	41:RC:72:VAL:HB	1.95	0.49
38:5I:140:SER:OG	38:5I:141:ASP:N	2.44	0.49
40:5K:65:VAL:HG22	40:5K:152:ILE:HB	1.94	0.49
43:RE:132:TYR:HB2	43:RE:183:ILE:HG21	1.94	0.49
43:RE:936:LEU:HA	43:RE:939:ILE:HG22	1.94	0.49
45:RG:197:ASP:OD1	45:RG:197:ASP:N	2.45	0.49
46:RI:13:ALA:HA	46:RI:254:ILE:HG12	1.95	0.49
49:RN:600:LEU:HD21	49:RN:636:LEU:HD13	1.94	0.49
19:A5:149:ASN:HD21	19:A5:190:PRO:HB3	1.77	0.49
26:B2:549:SER:OG	26:B2:576:VAL:O	2.29	0.49
27:B3:194:ARG:HG3	27:B3:244:GLU:H	1.78	0.49
30:B6:63:VAL:HG13	30:B6:88:ILE:HD11	1.94	0.49
32:5C:492:GLY:HA2	32:5C:495:SER:HB2	1.94	0.49
40:5K:149:LYS:HD3	40:5K:170:ILE:HD11	1.95	0.49
43:RE:749:SER:OG	43:RE:787:GLU:OE2	2.22	0.49
43:RE:1102:LEU:HD12	43:RE:1230:MET:HB3	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:RJ:634:ARG:NH2	48:RK:186:PRO:O	2.42	0.49
49:RN:646:THR:HA	49:RN:649:THR:HG22	1.95	0.49
3:SA:919:A:H5'	8:SP:18:ARG:HH12	1.77	0.48
4:SG:219:ARG:NH2	45:RH:222:ASP:OD2	2.45	0.48
14:3D:297:HIS:NE2	14:3D:309:GLU:OE2	2.46	0.48
15:3E:164:ILE:HG12	15:3E:301:ALA:HA	1.93	0.48
16:3F:305:ARG:HG2	16:3F:317:ILE:HD13	1.94	0.48
23:AF:75:LYS:HD2	23:AF:111:TYR:HA	1.95	0.48
26:B2:643:ASP:HB3	26:B2:650:ILE:HD11	1.95	0.48
27:B3:454:LEU:HB3	27:B3:466:TRP:HB2	1.95	0.48
28:B8:148:THR:OG1	28:B8:152:GLU:OE2	2.31	0.48
43:RE:151:SER:HA	43:RE:154:LYS:HB2	1.94	0.48
45:RG:190:GLN:HE22	45:RG:247:ASP:HB2	1.78	0.48
47:RJ:951:MET:SD	47:RJ:987:TYR:OH	2.63	0.48
49:RN:786:ASN:HA	49:RN:789:ASN:HB2	1.95	0.48
3:SA:1645:G:H2'	3:SA:1646:C:H6	1.78	0.48
17:3H:51:PHE:HE1	17:3H:114:ILE:HG23	1.78	0.48
18:A4:338:ALA:HB1	18:A4:361:LEU:HD11	1.95	0.48
26:B2:263:THR:HA	26:B2:269:THR:O	2.14	0.48
27:B3:305:VAL:HG12	27:B3:311:LEU:HG	1.95	0.48
28:B8:43:ASP:N	28:B8:43:ASP:OD1	2.40	0.48
28:B8:266:GLY:HA3	28:B8:295:ILE:HD11	1.95	0.48
29:BE:630:THR:N	29:BE:644:THR:O	2.44	0.48
38:5I:145:VAL:HB	38:5I:176:PHE:HB2	1.94	0.48
38:5I:260:GLN:NE2	38:5I:460:GLN:OE1	2.47	0.48
40:5K:67:ILE:HD11	40:5K:96:PRO:HB2	1.95	0.48
41:RC:52:TYR:CE1	41:RC:56:ILE:HG21	2.47	0.48
43:RE:125:GLU:OE2	43:RE:129:HIS:NE2	2.45	0.48
47:RJ:863:THR:O	47:RJ:863:THR:OG1	2.30	0.48
47:RJ:951:MET:HE1	47:RJ:1003:LEU:HB2	1.94	0.48
1:3A:64:A:OP2	29:BE:392:ARG:NH2	2.45	0.48
7:SO:49:GLN:HA	7:SO:52:VAL:HG12	1.94	0.48
19:A5:280:GLN:HB2	19:A5:288:LYS:HE2	1.95	0.48
23:AF:246:TYR:OH	23:AF:289:ASN:ND2	2.44	0.48
28:B8:458:ILE:HG13	28:B8:484:VAL:HG22	1.95	0.48
41:RC:183:VAL:HA	41:RC:186:VAL:HG12	1.93	0.48
43:RE:1027:LEU:HD11	43:RE:1037:LEU:HB3	1.95	0.48
45:RH:69:ASN:HD22	45:RH:72:ASP:HB3	1.77	0.48
3:SA:1465:C:N3	36:5G:146:ARG:NH1	2.58	0.48
14:3D:225:ASP:OD1	14:3D:226:LYS:N	2.46	0.48
16:3F:421:ASN:HD22	16:3F:437:ARG:HA	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AE:8:LEU:HD12	32:5C:144:LEU:HD23	1.96	0.48
25:B1:717:LEU:HD12	29:BE:578:VAL:HB	1.94	0.48
27:B3:290:ILE:HG12	27:B3:304:LEU:HD22	1.95	0.48
28:B8:183:ASP:OD1	29:BE:281:ARG:NH2	2.45	0.48
43:RE:704:PHE:CE2	43:RE:955:GLU:HB2	2.49	0.48
48:RK:103:MET:O	48:RK:107:ALA:HB2	2.13	0.48
49:RN:560:TYR:OH	50:RO:388:LEU:O	2.30	0.48
3:SA:884:A:H2'	3:SA:885:G:C8	2.48	0.48
3:SA:925:G:C5'	42:RD:1611:ALA:CB	2.70	0.48
9:SR:58:ASP:OD1	9:SR:58:ASP:N	2.43	0.48
14:3D:160:ARG:NH2	15:3E:243:MET:O	2.43	0.48
16:3F:523:LYS:O	16:3F:541:ALA:HA	2.13	0.48
18:A4:579:ARG:NH2	18:A4:644:SER:OG	2.47	0.48
24:AG:771:ASP:OD1	24:AG:771:ASP:N	2.46	0.48
30:B6:16:ASP:OD2	32:5C:15:ARG:NH2	2.46	0.48
31:5B:155:ILE:HD12	31:5B:158:LYS:HE3	1.95	0.48
32:5C:112:GLY:HA3	32:5C:130:ARG:HB3	1.94	0.48
43:RE:395:ILE:HD11	43:RE:476:ILE:HG21	1.95	0.48
43:RE:975:LEU:HD12	43:RE:1041:VAL:HG23	1.95	0.48
47:RJ:298:VAL:HG23	47:RJ:791:ILE:HG23	1.94	0.48
49:RN:734:ARG:HA	49:RN:737:ILE:HG12	1.95	0.48
3:SA:954:G:H2'	3:SA:955:A:C8	2.49	0.48
3:SA:976:G:N3	3:SA:978:A:C5	2.82	0.48
3:SA:1658:G:C2	3:SA:1743:U:N1	2.81	0.48
7:SO:101:HIS:HA	7:SO:104:ARG:HH21	1.78	0.48
13:3C:170:VAL:HG12	13:3C:239:CYS:HB3	1.96	0.48
15:3E:214:ILE:HD11	15:3E:252:LEU:HD22	1.94	0.48
16:3F:448:PHE:HA	16:3F:451:ILE:HG22	1.95	0.48
22:AE:395:GLU:OE2	22:AE:397:LYS:NZ	2.44	0.48
23:AF:276:SER:OG	23:AF:278:ASP:OD1	2.30	0.48
26:B2:183:ASP:OD1	26:B2:183:ASP:N	2.42	0.48
29:BE:529:TYR:HA	29:BE:536:LEU:HA	1.95	0.48
46:RI:98:LYS:NZ	46:RI:121:ASP:OD1	2.38	0.48
51:RQ:322:ASN:OD1	51:RQ:322:ASN:N	2.46	0.48
3:SA:464:A:H2'	3:SA:465:G:H8	1.79	0.48
5:SK:136:VAL:HG12	5:SK:156:ILE:HG12	1.96	0.48
22:AE:329:THR:HG21	22:AE:365:ILE:HG21	1.95	0.48
24:AG:105:HIS:HB2	24:AG:122:LYS:HG3	1.95	0.48
24:AG:855:LEU:O	24:AG:859:ASN:HB2	2.13	0.48
25:B1:441:SER:O	25:B1:443:GLU:N	2.43	0.48
27:B3:557:VAL:HG22	27:B3:578:VAL:HG11	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:B8:183:ASP:HB2	29:BE:242:ARG:HA	1.96	0.48
43:RE:412:LEU:HD21	43:RE:424:GLY:HA3	1.96	0.48
45:RG:173:THR:OG1	45:RG:174:LYS:N	2.47	0.48
50:RO:153:ILE:HD13	50:RO:202:LEU:HD21	1.94	0.48
22:AE:336:LEU:HD22	22:AE:373:ILE:HG21	1.96	0.48
26:B2:118:ASN:OD1	26:B2:118:ASN:N	2.46	0.48
26:B2:414:LEU:HD11	26:B2:445:VAL:HG11	1.94	0.48
30:B6:273:ILE:HA	30:B6:276:VAL:HG22	1.95	0.48
30:B6:426:ASP:O	30:B6:430:TYR:N	2.47	0.48
43:RE:507:PHE:HA	43:RE:510:ILE:HG12	1.95	0.48
47:RJ:1105:ASP:N	47:RJ:1105:ASP:OD1	2.47	0.48
50:RO:447:ASP:OD1	50:RO:447:ASP:N	2.46	0.48
3:SA:1659:A:O2'	3:SA:1660:A:O4'	2.31	0.48
16:3F:477:SER:OG	16:3F:521:VAL:O	2.27	0.48
19:A5:335:ASN:O	19:A5:337:LYS:NZ	2.47	0.48
24:AG:249:THR:O	24:AG:257:ARG:NH1	2.41	0.48
43:RE:308:LEU:HG	43:RE:337:LEU:HD21	1.96	0.48
45:RG:232:LEU:HD21	45:RH:103:PRO:HG3	1.96	0.48
48:RK:130:ILE:HG23	48:RK:151:LEU:HD23	1.95	0.48
1:3A:332:G:H21	24:AG:869:MET:HE3	1.79	0.48
9:SR:120:ASP:OD1	9:SR:120:ASP:N	2.40	0.48
15:3E:207:ARG:HH11	15:3E:226:ILE:HG12	1.78	0.48
18:A4:560:SER:OG	18:A4:561:LYS:N	2.47	0.48
18:A4:747:ILE:HD11	18:A4:753:ALA:HB2	1.96	0.48
20:A8:496:TYR:OH	24:AG:693:ASP:OD1	2.28	0.48
22:AE:376:GLU:H	22:AE:379:GLU:HG3	1.79	0.48
24:AG:141:LEU:HD11	24:AG:153:ILE:HD11	1.96	0.48
24:AG:431:SER:OG	24:AG:432:ARG:N	2.43	0.48
24:AG:498:LEU:HA	24:AG:508:ILE:O	2.14	0.48
25:B1:205:LYS:HG2	25:B1:219:GLU:HG2	1.96	0.48
32:5C:133:HIS:HE1	32:5C:147:GLU:HG3	1.79	0.48
43:RE:316:ARG:HH22	43:RE:552:ARG:HD3	1.78	0.48
43:RE:417:SER:OG	43:RE:420:GLN:OE1	2.32	0.48
3:SA:1645:G:H2'	3:SA:1646:C:C6	2.49	0.47
15:3E:225:GLU:HG2	15:3E:226:ILE:HG13	1.96	0.47
19:A5:460:ARG:HA	19:A5:465:ILE:HD11	1.96	0.47
24:AG:440:VAL:HG11	24:AG:449:LEU:HD12	1.95	0.47
26:B2:9:GLU:O	26:B2:684:TRP:HA	2.14	0.47
26:B2:54:ILE:CD1	26:B2:364:TYR:HD2	2.27	0.47
27:B3:22:VAL:HG22	27:B3:67:LEU:HD11	1.96	0.47
32:5C:137:MET:HA	32:5C:144:LEU:HA	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:5F:152:ARG:NH1	36:5G:11:GLU:OE2	2.46	0.47
23:AF:135:GLN:HE22	23:AF:178:PRO:HA	1.79	0.47
25:B1:150:THR:N	25:B1:164:THR:O	2.45	0.47
26:B2:479:LEU:HA	26:B2:489:VAL:O	2.14	0.47
43:RE:219:PHE:CZ	43:RE:303:PHE:CE2	3.02	0.47
3:SA:1658:G:N1	3:SA:1742:U:N3	2.62	0.47
4:SG:52:GLU:OE2	4:SG:54:LYS:NZ	2.48	0.47
5:SK:87:SER:OG	5:SK:89:ASP:OD1	2.32	0.47
18:A4:157:SER:OG	18:A4:195:TRP:NE1	2.47	0.47
22:AE:484:LEU:HD13	22:AE:663:SER:HB3	1.95	0.47
23:AF:420:GLU:O	23:AF:424:ARG:CB	2.61	0.47
29:BE:363:SER:O	29:BE:363:SER:OG	2.32	0.47
45:RH:153:VAL:HA	49:RN:716:LYS:HB2	1.96	0.47
46:RI:105:ASN:HA	46:RI:108:ARG:HB3	1.96	0.47
47:RJ:80:THR:O	57:RJ:1201:GTP:O2B	2.31	0.47
48:RK:282:GLU:O	48:RK:286:SER:HB3	2.14	0.47
2:5A:201:U:H2'	2:5A:202:U:H6	1.78	0.47
3:SA:1179:G:H3'	10:ST:127:HIS:HB2	1.96	0.47
3:SA:1511:U:H2'	3:SA:1512:G:C8	2.49	0.47
3:SA:1760:G:H5'	3:SA:1761:U:H5'	1.96	0.47
15:3E:355:ASN:HA	15:3E:358:LYS:HB2	1.97	0.47
18:A4:534:LEU:HB3	18:A4:543:ILE:HG22	1.95	0.47
18:A4:744:VAL:HA	18:A4:753:ALA:O	2.14	0.47
24:AG:581:GLY:HA2	24:AG:602:PRO:HD2	1.97	0.47
25:B1:537:GLY:HA3	25:B1:556:ARG:HB3	1.96	0.47
27:B3:432:GLY:O	27:B3:464:LYS:NZ	2.41	0.47
40:5K:152:ILE:HG12	40:5K:171:PRO:HG2	1.95	0.47
41:RC:195:HIS:CD2	41:RC:196:PRO:HD2	2.50	0.47
43:RE:940:LYS:HG3	43:RE:975:LEU:HD21	1.96	0.47
47:RJ:631:ILE:HG13	47:RJ:634:ARG:HB2	1.97	0.47
50:RO:507:LEU:HA	50:RO:510:GLU:HB3	1.95	0.47
51:RQ:341:LYS:HA	51:RQ:344:GLN:HE21	1.79	0.47
51:RQ:835:VAL:HG13	51:RQ:837:LYS:HG3	1.96	0.47
2:5A:116:U:H3	2:5A:130:G:H1	1.61	0.47
3:SA:576:G:OP2	47:RJ:873:LYS:NZ	2.36	0.47
3:SA:941:A:C2	3:SA:976:G:O3'	2.67	0.47
18:A4:284:LEU:HD21	31:5B:206:LEU:HD21	1.95	0.47
18:A4:511:VAL:HA	18:A4:558:ARG:HB3	1.96	0.47
22:AE:141:ASN:ND2	22:AE:206:TYR:OH	2.46	0.47
26:B2:530:LEU:HD13	26:B2:550:LEU:HD11	1.94	0.47
30:B6:14:GLU:OE2	30:B6:91:ARG:NH2	2.38	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:5E:452:SER:O	34:5E:452:SER:OG	2.29	0.47
43:RE:168:ILE:O	43:RE:172:THR:OG1	2.28	0.47
43:RE:177:ASN:HB2	43:RE:213:LEU:HB2	1.96	0.47
47:RJ:92:ARG:HH21	47:RJ:221:LEU:HG	1.79	0.47
50:RO:198:GLU:O	50:RO:202:LEU:HB2	2.13	0.47
13:3C:173:LEU:HA	13:3C:197:VAL:HG13	1.97	0.47
26:B2:235:ASN:ND2	26:B2:240:GLY:O	2.40	0.47
27:B3:786:ILE:O	27:B3:789:THR:OG1	2.31	0.47
44:RF:55:LEU:HB3	44:RF:124:ALA:HB3	1.96	0.47
47:RJ:111:LYS:O	47:RJ:310:THR:OG1	2.32	0.47
47:RJ:879:THR:OG1	47:RJ:880:TYR:N	2.48	0.47
3:SA:1512:G:O6	46:RI:145:HIS:NE2	2.42	0.47
3:SA:1677:C:H2'	3:SA:1678:A:C8	2.50	0.47
3:SA:1677:C:H2'	3:SA:1678:A:H8	1.80	0.47
15:3E:262:ILE:HA	15:3E:265:PHE:HB2	1.96	0.47
18:A4:97:ARG:NE	31:5B:191:PRO:O	2.39	0.47
19:A5:473:LYS:HE3	19:A5:475:ALA:HB3	1.96	0.47
23:AF:435:ASP:OD1	23:AF:435:ASP:N	2.45	0.47
26:B2:137:ILE:HG22	26:B2:147:VAL:HG22	1.97	0.47
28:B8:238:LEU:HD11	28:B8:590:LYS:HB2	1.97	0.47
28:B8:568:VAL:HG23	28:B8:579:VAL:HG22	1.96	0.47
29:BE:207:ASP:N	29:BE:207:ASP:OD1	2.47	0.47
32:5C:333:SER:HB3	32:5C:381:LEU:HD11	1.95	0.47
33:5D:25:TYR:HD1	39:5J:213:ARG:HE	1.62	0.47
37:5H:434:PHE:H	45:RH:129:ARG:HH22	1.63	0.47
38:5I:201:ILE:HD12	38:5I:225:LEU:HD21	1.97	0.47
43:RE:123:LYS:HE2	43:RE:123:LYS:HB3	1.77	0.47
52:RS:379:LYS:HA	52:RS:379:LYS:HD3	1.73	0.47
2:5A:207:G:H2'	2:5A:208:A:H8	1.79	0.47
8:SP:16:VAL:O	8:SP:30:VAL:HA	2.14	0.47
10:ST:2:SER:O	10:ST:2:SER:OG	2.32	0.47
22:AE:136:LEU:HD21	22:AE:155:ILE:HG12	1.97	0.47
24:AG:22:LEU:HD12	24:AG:32:LYS:HB2	1.97	0.47
24:AG:175:ALA:O	24:AG:187:VAL:HA	2.15	0.47
25:B1:156:GLN:HB2	25:B1:203:GLN:HE21	1.79	0.47
26:B2:201:ILE:HD12	27:B3:660:LYS:HA	1.97	0.47
29:BE:430:ILE:HD11	29:BE:445:MET:HB2	1.97	0.47
49:RN:451:THR:O	49:RN:455:LEU:HB2	2.15	0.47
52:RS:258:VAL:HA	52:RS:261:GLU:HG2	1.97	0.47
15:3E:176:GLU:HA	15:3E:179:THR:HG22	1.97	0.47
26:B2:214:ASP:OD1	26:B2:214:ASP:N	2.45	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B2:367:ILE:HD12	26:B2:368:PRO:HD2	1.97	0.47
26:B2:393:ASP:OD1	26:B2:393:ASP:N	2.46	0.47
26:B2:588:ILE:HG12	26:B2:600:TRP:HB2	1.97	0.47
34:5E:383:ARG:NH2	36:5G:212:ALA:O	2.48	0.47
47:RJ:347:LEU:O	47:RJ:352:LYS:NZ	2.48	0.47
50:RO:504:ASP:OD1	50:RO:504:ASP:N	2.48	0.47
2:5A:69:U:O4	2:5A:70:A:N6	2.48	0.47
3:SA:545:A:OP2	37:5H:542:TYR:OH	2.33	0.47
3:SA:1228:G:H22	6:SN:119:SER:HB2	1.79	0.47
9:SR:50:GLU:OE2	9:SR:82:ARG:NH2	2.47	0.47
25:B1:29:LEU:HD22	25:B1:42:LEU:HD11	1.96	0.47
25:B1:32:PRO:HG3	25:B1:61:ILE:HG13	1.97	0.47
25:B1:115:SER:O	25:B1:115:SER:OG	2.33	0.47
29:BE:170:LEU:HG	29:BE:180:LEU:HD21	1.97	0.47
35:5F:153:ASN:HB3	36:5G:4:ARG:HH22	1.80	0.47
36:5G:173:ARG:HH21	36:5G:250:VAL:HG23	1.80	0.47
47:RJ:819:GLU:O	47:RJ:852:ARG:NH2	2.47	0.47
2:5A:414:G:N1	2:5A:442:U:O2	2.48	0.46
2:5A:485:G:H2'	14:3D:22:LEU:HD21	1.97	0.46
9:SR:113:ASP:N	9:SR:113:ASP:OD1	2.48	0.46
19:A5:366:GLY:O	24:AG:583:LYS:NZ	2.48	0.46
24:AG:446:ASN:OD1	24:AG:446:ASN:N	2.46	0.46
24:AG:530:LYS:HG2	24:AG:546:LYS:HB3	1.97	0.46
26:B2:123:ALA:HB3	26:B2:141:LYS:CD	2.45	0.46
38:5I:283:ASP:OD2	38:5I:287:TYR:OH	2.30	0.46
43:RE:242:LEU:HA	43:RE:245:LYS:HG3	1.97	0.46
49:RN:510:THR:HB	49:RN:518:ILE:HD13	1.96	0.46
2:5A:446:U:H5'	47:RJ:1118:THR:HB	1.96	0.46
2:5A:485:G:OP2	14:3D:46:LYS:NZ	2.39	0.46
8:SP:91:THR:HG22	8:SP:93:THR:HG22	1.98	0.46
15:3E:191:HIS:HD2	15:3E:246:GLU:HA	1.80	0.46
22:AE:262:VAL:HG21	24:AG:892:MET:HE1	1.96	0.46
22:AE:509:SER:HA	22:AE:512:LEU:HD12	1.98	0.46
24:AG:43:ASN:OD1	24:AG:43:ASN:N	2.48	0.46
24:AG:443:ASN:ND2	24:AG:446:ASN:OD1	2.48	0.46
25:B1:165:SER:OG	25:B1:166:LYS:N	2.48	0.46
26:B2:63:LEU:HD21	26:B2:106:TRP:CD2	2.50	0.46
31:5B:173:ARG:NH2	33:5D:144:ASN:O	2.48	0.46
43:RE:203:ILE:HG22	43:RE:292:ILE:HA	1.97	0.46
44:RF:43:GLN:HG2	44:RF:51:ASP:HA	1.97	0.46
2:5A:116:U:O2	2:5A:130:G:N2	2.43	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:396:A:H62	36:5G:11:GLU:HG2	1.81	0.46
5:SK:37:LYS:HB3	5:SK:37:LYS:HE2	1.76	0.46
7:SO:93:LYS:HA	7:SO:96:VAL:HG12	1.97	0.46
18:A4:214:SER:OG	18:A4:221:ASN:O	2.28	0.46
18:A4:418:CYS:HB2	18:A4:460:LEU:HB2	1.97	0.46
22:AE:374:ARG:NH1	22:AE:375:LEU:O	2.48	0.46
24:AG:204:ASN:OD1	24:AG:204:ASN:N	2.47	0.46
24:AG:435:ASP:HB2	24:AG:702:TYR:HD1	1.75	0.46
39:5J:110:ASP:OD1	39:5J:110:ASP:N	2.36	0.46
43:RE:269:ARG:HA	43:RE:292:ILE:O	2.15	0.46
48:RK:282:GLU:O	48:RK:286:SER:CB	2.64	0.46
49:RN:56:ASN:HD21	49:RN:59:GLU:HG3	1.81	0.46
2:5A:18:G:H2'	2:5A:19:A:C8	2.50	0.46
2:5A:128:C:H5''	2:5A:129:U:H4'	1.98	0.46
2:5A:188:A:H61	2:5A:209:G:H1	1.63	0.46
3:SA:1673:G:N1	3:SA:1728:A:N6	2.50	0.46
18:A4:326:ARG:NH2	18:A4:364:PHE:O	2.49	0.46
18:A4:742:LEU:HD12	18:A4:757:ARG:HG3	1.96	0.46
23:AF:436:GLU:HG2	23:AF:480:LEU:HD23	1.98	0.46
30:B6:185:TYR:HE2	51:RQ:338:LEU:HD21	1.81	0.46
38:5I:280:ALA:HB2	38:5I:311:VAL:HB	1.97	0.46
45:RH:152:SER:OG	45:RH:155:SER:N	2.49	0.46
48:RK:104:LEU:O	48:RK:300:TYR:OH	2.33	0.46
50:RO:202:LEU:HD23	50:RO:208:TYR:HB3	1.98	0.46
2:5A:86:C:N4	24:AG:482:GLY:O	2.45	0.46
3:SA:925:G:H4'	42:RD:1611:ALA:CA	2.46	0.46
13:3C:194:VAL:HB	13:3C:217:ILE:HD13	1.97	0.46
13:3C:308:PRO:HG3	33:5D:129:SER:HA	1.96	0.46
16:3F:417:SER:HB3	16:3F:421:ASN:HB2	1.97	0.46
17:3G:57:ASP:HB3	17:3G:84:ARG:HG2	1.97	0.46
21:A9:505:MET:HB2	23:AF:507:MET:HE3	1.98	0.46
22:AE:568:ILE:HD11	22:AE:673:ASN:HD21	1.80	0.46
28:B8:472:GLN:NE2	28:B8:474:SER:OG	2.49	0.46
43:RE:1108:LEU:O	43:RE:1112:CYS:CB	2.61	0.46
46:RI:20:LEU:HD11	46:RI:245:LYS:HA	1.97	0.46
46:RI:55:ARG:HD2	46:RI:191:PRO:HD3	1.98	0.46
47:RJ:853:ARG:HE	47:RJ:853:ARG:HB2	1.61	0.46
48:RK:199:ARG:HB2	48:RK:239:PRO:HA	1.97	0.46
48:RK:337:VAL:HG23	48:RK:354:ILE:HG12	1.98	0.46
52:RS:270:LEU:HB3	52:RS:278:PHE:HZ	1.80	0.46
1:3A:306:G:H2'	1:3A:307:G:H8	1.80	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:1276:U:H3	3:SA:1434:U:H3	1.64	0.46
14:3D:175:ILE:HD12	14:3D:317:SER:HA	1.98	0.46
19:A5:66:VAL:HG12	19:A5:112:LEU:HD21	1.97	0.46
19:A5:85:ILE:HB	19:A5:99:PHE:HB2	1.98	0.46
24:AG:212:CYS:HB2	24:AG:224:SER:HB3	1.98	0.46
26:B2:341:ALA:HB1	26:B2:353:LEU:HD11	1.96	0.46
28:B8:278:ASP:N	28:B8:278:ASP:OD1	2.46	0.46
43:RE:223:ARG:HA	43:RE:226:HIS:HB2	1.97	0.46
43:RE:1224:ALA:O	43:RE:1228:ASN:CB	2.60	0.46
45:RG:55:ILE:O	45:RG:64:LYS:HB2	2.16	0.46
50:RO:462:SER:OG	50:RO:463:LEU:N	2.48	0.46
52:RS:392:TYR:HA	52:RS:395:MET:HB2	1.96	0.46
1:3A:56:A:O2'	33:5D:63:TYR:OH	2.34	0.46
20:A8:647:LEU:HG	21:A9:509:GLN:HE22	1.79	0.46
26:B2:542:ASP:N	26:B2:542:ASP:OD1	2.45	0.46
28:B8:512:ASP:OD1	28:B8:512:ASP:N	2.48	0.46
29:BE:323:VAL:HB	29:BE:343:LEU:HD22	1.98	0.46
29:BE:351:GLN:HG3	29:BE:372:ASP:HB3	1.97	0.46
43:RE:228:ARG:HG3	43:RE:296:ILE:HG12	1.98	0.46
44:RF:17:PRO:HA	44:RF:35:HIS:O	2.15	0.46
46:RI:59:LEU:HD22	46:RI:215:ASN:HB2	1.97	0.46
49:RN:547:VAL:HA	49:RN:550:VAL:HG12	1.97	0.46
50:RO:366:LEU:HD13	50:RO:405:LEU:HD11	1.96	0.46
52:RS:413:LEU:O	52:RS:418:HIS:NE2	2.49	0.46
1:3A:36:C:O2'	38:5I:389:ARG:NH1	2.48	0.46
3:SA:1111:G:C8	47:RJ:1162:ALA:HA	2.51	0.46
3:SA:1273:G:H1	3:SA:1437:U:H2'	1.80	0.46
18:A4:164:THR:HG22	18:A4:185:ARG:HG2	1.98	0.46
22:AE:583:LYS:HE2	22:AE:627:LEU:HA	1.98	0.46
25:B1:557:LYS:NZ	29:BE:426:GLU:OE1	2.44	0.46
27:B3:440:VAL:HG12	27:B3:456:THR:HA	1.97	0.46
29:BE:420:GLU:HG2	29:BE:470:GLN:HA	1.97	0.46
31:5B:211:LEU:HD13	31:5B:213:LYS:HE3	1.96	0.46
41:RC:44:LEU:HA	41:RC:79:SER:HA	1.97	0.46
49:RN:554:GLN:HE21	49:RN:559:ARG:H	1.63	0.46
52:RS:271:THR:OG1	52:RS:274:GLU:OE1	2.31	0.46
52:RS:359:LEU:HB2	52:RS:372:ILE:HD11	1.97	0.46
2:5A:426:G:H21	2:5A:428:A:H8	1.64	0.46
2:5A:486:U:H4'	2:5A:487:A:H5''	1.98	0.46
14:3D:371:ASN:OD1	14:3D:374:ARG:NH1	2.48	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:3E:381:ASP:OD1	15:3E:381:ASP:N	2.49	0.46
25:B1:280:THR:HA	25:B1:304:PRO:HB3	1.98	0.46
25:B1:300:MET:HE2	25:B1:300:MET:HB3	1.78	0.46
28:B8:306:ASN:OD1	28:B8:306:ASN:N	2.43	0.46
32:5C:335:GLY:HA2	32:5C:377:LYS:HG3	1.98	0.46
38:5I:255:THR:HG22	51:RQ:288:TYR:HD1	1.81	0.46
43:RE:243:LEU:HD13	43:RE:248:LEU:HG	1.96	0.46
45:RG:112:VAL:HB	45:RG:124:VAL:HG22	1.97	0.46
3:SA:1542:G:H2'	3:SA:1543:A:C4	2.51	0.46
19:A5:452:LEU:HA	19:A5:455:THR:HG22	1.98	0.46
20:A8:374:SER:HA	20:A8:408:LEU:HA	1.97	0.46
23:AF:69:ARG:HG3	23:AF:70:THR:HG23	1.97	0.46
26:B2:220:THR:HG22	26:B2:259:ILE:HD11	1.96	0.46
26:B2:360:ASN:OD1	26:B2:360:ASN:N	2.47	0.46
27:B3:85:LEU:HD23	27:B3:95:VAL:HG11	1.98	0.46
27:B3:584:ILE:HD11	27:B3:599:ILE:HD11	1.97	0.46
36:5G:76:GLU:HG2	36:5G:160:GLY:HA2	1.98	0.46
38:5I:288:TYR:O	38:5I:298:LEU:N	2.42	0.46
40:5K:83:VAL:HG12	40:5K:96:PRO:HG3	1.98	0.46
41:RC:112:GLN:NE2	41:RC:163:TYR:CE2	2.80	0.46
43:RE:188:SER:HB2	43:RE:367:ARG:HH12	1.81	0.46
50:RO:395:ILE:HG23	50:RO:469:LEU:HD21	1.98	0.46
52:RS:280:ASN:ND2	52:RS:320:GLY:O	2.46	0.46
8:SP:44:GLY:O	8:SP:46:MET:N	2.50	0.45
8:SP:85:ALA:H	8:SP:119:THR:HB	1.81	0.45
11:SY:113:ALA:HB3	11:SY:116:ASP:HB2	1.96	0.45
14:3D:195:VAL:HG12	14:3D:216:PHE:HE2	1.81	0.45
14:3D:379:LEU:HD13	14:3D:408:VAL:HG21	1.98	0.45
18:A4:545:ARG:HG3	18:A4:549:VAL:HB	1.98	0.45
22:AE:495:LEU:HA	22:AE:498:PHE:HB2	1.97	0.45
24:AG:726:GLN:NE2	24:AG:736:THR:O	2.42	0.45
29:BE:640:LEU:HD23	29:BE:655:THR:HG22	1.98	0.45
35:5F:95:SER:OG	36:5G:59:ASP:OD2	2.32	0.45
38:5I:94:TYR:OH	38:5I:134:ASN:ND2	2.41	0.45
38:5I:281:ASN:ND2	38:5I:283:ASP:OD1	2.49	0.45
43:RE:205:THR:HG22	43:RE:295:LEU:HD23	1.97	0.45
45:RG:143:GLN:HE22	45:RG:149:SER:HA	1.81	0.45
2:5A:192:G:H21	33:5D:155:THR:HG21	1.81	0.45
3:SA:891:A:H2'	3:SA:892:A:H8	1.82	0.45
3:SA:910:C:H2'	3:SA:911:U:C6	2.50	0.45
3:SA:976:G:C2	3:SA:978:A:C4	3.03	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:993:A:H62	3:SA:1011:G:N2	2.14	0.45
3:SA:1228:G:N2	6:SN:118:ALA:O	2.49	0.45
4:SG:39:GLU:OE2	4:SG:47:SER:OG	2.33	0.45
15:3E:392:ALA:O	15:3E:396:ASN:ND2	2.49	0.45
18:A4:444:ARG:HG3	18:A4:446:SER:H	1.81	0.45
19:A5:539:ARG:NH1	24:AG:524:ASP:OD2	2.49	0.45
26:B2:760:ILE:HD11	26:B2:835:PHE:HB2	1.98	0.45
27:B3:561:SER:O	27:B3:566:SER:N	2.49	0.45
30:B6:186:VAL:HG12	30:B6:273:ILE:HG13	1.98	0.45
31:5B:200:ARG:O	31:5B:204:ARG:HB3	2.15	0.45
33:5D:48:LEU:HG	47:RJ:1067:LEU:HD11	1.99	0.45
36:5G:97:SER:OG	36:5G:144:GLU:OE1	2.28	0.45
38:5I:306:SER:HB3	38:5I:326:ASP:H	1.82	0.45
43:RE:557:THR:HG23	43:RE:560:ASN:H	1.81	0.45
45:RG:227:LEU:HA	45:RG:227:LEU:HD23	1.79	0.45
49:RN:495:ASN:HD22	49:RN:617:HIS:HB2	1.80	0.45
2:5A:102:A:H61	23:AF:415:LEU:HD22	1.81	0.45
3:SA:1463:C:H4'	49:RN:63:ALA:HB1	1.98	0.45
13:3B:210:MET:HE2	13:3B:210:MET:HB3	1.79	0.45
13:3B:261:LEU:O	14:3D:129:ARG:NH1	2.49	0.45
23:AF:171:VAL:HG22	23:AF:188:SER:HB3	1.99	0.45
24:AG:253:SER:O	24:AG:256:THR:OG1	2.33	0.45
32:5C:243:TRP:NE1	32:5C:304:ARG:HH22	2.15	0.45
43:RE:298:PHE:HB2	43:RE:340:SER:HA	1.98	0.45
44:RF:132:ALA:O	44:RF:136:ASN:HB2	2.16	0.45
49:RN:423:GLY:O	49:RN:426:THR:OG1	2.31	0.45
50:RO:259:LYS:HB3	50:RO:259:LYS:HE2	1.72	0.45
2:5A:550:C:H2'	2:5A:551:A:C8	2.52	0.45
17:3G:58:CYS:HB3	17:3G:98:ILE:HD12	1.99	0.45
18:A4:124:THR:HG21	31:5B:191:PRO:HG3	1.97	0.45
18:A4:652:THR:HG23	18:A4:653:TRP:HD1	1.81	0.45
19:A5:518:ASN:HB2	19:A5:521:SER:HB3	1.98	0.45
22:AE:11:VAL:HA	22:AE:14:ASN:HD22	1.80	0.45
22:AE:583:LYS:HD3	22:AE:631:VAL:HG21	1.99	0.45
24:AG:143:ASN:N	24:AG:143:ASN:OD1	2.47	0.45
26:B2:54:ILE:HD13	26:B2:364:TYR:CD2	2.48	0.45
26:B2:580:ASP:OD2	26:B2:623:PHE:N	2.40	0.45
32:5C:39:ASP:HB3	32:5C:42:LEU:HB3	1.97	0.45
36:5G:19:GLU:O	36:5G:23:SER:HB2	2.17	0.45
43:RE:427:LYS:HA	43:RE:496:LEU:HD21	1.98	0.45
47:RJ:772:MET:HG3	47:RJ:774:PRO:HD2	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:RN:13:LEU:HD22	49:RN:16:ARG:HE	1.82	0.45
1:3A:12:U:H3	3:SA:1112:G:H1	1.65	0.45
18:A4:424:ASP:N	18:A4:424:ASP:OD1	2.45	0.45
26:B2:566:TYR:OH	26:B2:603:ASP:O	2.33	0.45
26:B2:641:TYR:O	26:B2:650:ILE:N	2.49	0.45
27:B3:24:THR:HG21	27:B3:70:THR:H	1.82	0.45
32:5C:15:ARG:HB2	32:5C:18:GLN:HG3	1.98	0.45
32:5C:104:LEU:HD21	32:5C:139:TRP:HB2	1.99	0.45
38:5I:210:LYS:HA	38:5I:210:LYS:HD3	1.69	0.45
43:RE:217:LYS:O	43:RE:223:ARG:NH1	2.50	0.45
43:RE:348:TYR:HA	43:RE:351:LYS:HD3	1.98	0.45
49:RN:600:LEU:HD22	49:RN:633:VAL:HG22	1.98	0.45
52:RS:271:THR:H	52:RS:274:GLU:HB2	1.82	0.45
7:SO:106:ARG:CD	42:RD:1544:MET:HA	2.47	0.45
16:3F:164:GLN:HE21	16:3F:527:VAL:HG13	1.82	0.45
16:3F:452:SER:HB3	16:3F:460:ARG:HG2	1.99	0.45
18:A4:137:TYR:HB2	18:A4:177:LEU:HD12	1.99	0.45
22:AE:255:ILE:HD11	24:AG:884:MET:HB3	1.98	0.45
23:AF:227:VAL:HG22	23:AF:236:VAL:HG12	1.99	0.45
27:B3:542:CYS:HB3	27:B3:583:PHE:HB2	1.99	0.45
29:BE:76:THR:OG1	29:BE:78:SER:O	2.29	0.45
43:RE:352:THR:HG21	43:RE:398:ALA:HB1	1.98	0.45
45:RH:191:ASP:HA	45:RH:194:GLU:HG2	1.98	0.45
2:5A:110:G:N2	2:5A:136:U:O2	2.49	0.45
3:SA:608:U:O2'	3:SA:609:U:O4'	2.34	0.45
3:SA:977:A:H2'	3:SA:978:A:C8	2.52	0.45
3:SA:1509:C:O2'	46:RI:192:ASN:ND2	2.50	0.45
12:Sd:35:ASP:N	12:Sd:35:ASP:OD1	2.45	0.45
18:A4:636:ILE:HG23	18:A4:648:PHE:HD2	1.82	0.45
20:A8:662:ILE:HA	20:A8:665:GLN:HB2	1.98	0.45
22:AE:348:ILE:HD13	22:AE:348:ILE:HA	1.87	0.45
24:AG:761:GLU:HG3	24:AG:779:ILE:HG22	1.99	0.45
26:B2:103:ILE:HB	26:B2:117:PHE:HB2	1.99	0.45
26:B2:870:SER:HA	27:B3:816:LEU:CD2	2.46	0.45
27:B3:162:LEU:HD21	27:B3:225:PHE:HE2	1.82	0.45
27:B3:801:GLU:HB3	29:BE:927:LYS:CD	2.47	0.45
32:5C:509:ILE:HG22	41:RC:76:VAL:HG21	1.99	0.45
43:RE:209:MET:HG2	43:RE:213:LEU:HD21	1.98	0.45
45:RH:56:SER:HA	45:RH:63:ASP:HB2	1.99	0.45
49:RN:804:LYS:HD3	49:RN:804:LYS:HA	1.75	0.45
52:RS:399:ILE:O	52:RS:406:GLY:N	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:866:G:OP1	7:SO:9:LYS:NZ	2.50	0.45
3:SA:1223:A:H2'	3:SA:1224:A:C8	2.52	0.45
3:SA:1537:C:N4	45:RH:155:SER:O	2.37	0.45
8:SP:84:ARG:HG3	8:SP:119:THR:HA	1.99	0.45
22:AE:641:LEU:O	22:AE:644:LYS:NZ	2.42	0.45
24:AG:38:SER:OG	24:AG:43:ASN:O	2.35	0.45
26:B2:140:SER:OG	26:B2:142:ASP:OD1	2.31	0.45
27:B3:112:SER:OG	27:B3:154:GLY:O	2.30	0.45
27:B3:799:LEU:HD12	27:B3:802:GLN:HE21	1.81	0.45
28:B8:264:LEU:HD11	28:B8:272:LEU:HD12	1.97	0.45
29:BE:377:SER:O	29:BE:377:SER:OG	2.35	0.45
41:RC:62:ARG:HH21	41:RC:63:ALA:HB2	1.82	0.45
2:5A:554:G:H1	2:5A:583:U:H3	1.64	0.45
3:SA:1634:C:O2	25:B1:397:LYS:NZ	2.50	0.45
3:SA:1775:U:H2'	3:SA:1776:A:C8	2.51	0.45
7:SO:109:LYS:HD2	7:SO:109:LYS:N	2.30	0.45
18:A4:249:ARG:HB2	18:A4:292:ASN:HD22	1.81	0.45
19:A5:520:MET:H	19:A5:520:MET:HG3	1.60	0.45
26:B2:107:ASP:OD1	26:B2:107:ASP:N	2.46	0.45
29:BE:546:ILE:HG21	29:BE:560:LEU:HD22	1.99	0.45
34:5E:358:THR:HB	49:RN:89:GLN:HB3	1.98	0.45
41:RC:98:ARG:HD2	41:RC:102:LYS:HE3	1.98	0.45
43:RE:1101:ASP:HB3	43:RE:1233:ASN:HB3	1.99	0.45
48:RK:187:ILE:HB	48:RK:251:GLN:HE22	1.82	0.45
49:RN:640:MET:HE2	49:RN:640:MET:HB3	1.81	0.45
52:RS:235:VAL:HG12	52:RS:238:SER:HB3	1.98	0.45
52:RS:429:LYS:HD2	52:RS:437:ARG:HH22	1.82	0.45
3:SA:592:A:O2'	3:SA:596:C:OP1	2.35	0.45
4:SG:117:THR:HG21	4:SG:194:LEU:HD23	1.98	0.45
13:3B:218:ILE:HD11	14:3D:152:LEU:HD22	1.98	0.45
13:3C:253:ILE:HD11	13:3C:293:LEU:HD21	1.99	0.45
14:3D:120:SER:O	14:3D:120:SER:OG	2.33	0.45
16:3F:209:LYS:HA	16:3F:209:LYS:HD2	1.82	0.45
17:3H:33:LEU:HD23	17:3H:35:LYS:HE3	1.98	0.45
20:A8:583:SER:HB2	20:A8:637:LEU:HD22	1.97	0.45
22:AE:65:LYS:HB3	22:AE:104:LEU:HD11	1.99	0.45
23:AF:117:LEU:HD12	23:AF:117:LEU:HA	1.79	0.45
24:AG:600:SER:O	24:AG:600:SER:OG	2.33	0.45
26:B2:49:VAL:HG22	26:B2:63:LEU:HD22	1.98	0.45
28:B8:358:PHE:HA	28:B8:376:LEU:O	2.17	0.45
29:BE:921:ARG:O	29:BE:925:LEU:HB2	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5C:460:ARG:HB3	51:RQ:847:VAL:HB	1.99	0.45
38:5I:8:ARG:HD3	38:5I:8:ARG:HA	1.80	0.45
38:5I:297:SER:OG	38:5I:299:ASN:O	2.33	0.45
41:RC:174:MET:HE2	41:RC:174:MET:HB3	1.86	0.45
47:RJ:288:VAL:HG11	47:RJ:812:MET:HE2	1.98	0.45
20:A8:574:ARG:H	20:A8:576:ARG:NH1	2.16	0.44
23:AF:31:THR:OG1	23:AF:32:SER:N	2.46	0.44
23:AF:51:HIS:O	23:AF:53:HIS:N	2.49	0.44
23:AF:371:GLU:OE2	28:B8:273:ARG:NH2	2.50	0.44
25:B1:369:ILE:HD11	25:B1:390:VAL:HG11	1.99	0.44
25:B1:475:PRO:HD2	25:B1:493:TRP:HB2	1.99	0.44
29:BE:920:ASP:OD1	29:BE:920:ASP:N	2.48	0.44
32:5C:433:LEU:HD21	35:5F:16:VAL:HG11	1.99	0.44
45:RH:199:ASP:OD1	45:RH:199:ASP:N	2.49	0.44
47:RJ:889:LEU:HD22	47:RJ:922:ILE:HB	2.00	0.44
47:RJ:1148:GLU:OE2	47:RJ:1152:ARG:NH1	2.49	0.44
52:RS:373:LYS:HG3	52:RS:420:ALA:HA	1.99	0.44
2:5A:228:A:H2'	2:5A:229:A:C8	2.52	0.44
4:SG:63:GLN:HE22	4:SG:66:GLN:HB3	1.82	0.44
8:SP:29:HIS:HD2	8:SP:41:ARG:HB2	1.82	0.44
13:3B:88:ILE:HD11	13:3B:123:ILE:HG21	1.98	0.44
14:3D:281:LEU:HD23	15:3E:261:GLN:HE21	1.82	0.44
20:A8:648:PHE:HD1	21:A9:509:GLN:HE21	1.64	0.44
24:AG:364:ASN:OD1	24:AG:364:ASN:N	2.42	0.44
26:B2:292:ILE:HG23	26:B2:324:PHE:HE2	1.83	0.44
27:B3:627:ASN:HB2	27:B3:631:MET:HB2	1.99	0.44
32:5C:214:LEU:HD23	32:5C:228:LEU:HD12	1.99	0.44
35:5F:169:THR:HA	35:5F:172:ARG:HG2	1.99	0.44
44:RF:23:HIS:CD2	44:RF:25:ALA:H	2.35	0.44
50:RO:196:GLN:OE1	50:RO:260:ASN:ND2	2.37	0.44
6:SN:41:LEU:HB3	6:SN:43:ARG:HG3	1.99	0.44
13:3C:175:ALA:N	13:3C:198:GLU:OE2	2.48	0.44
22:AE:109:TRP:HA	22:AE:114:THR:HG21	2.00	0.44
26:B2:443:LEU:HG	26:B2:459:LEU:HD13	1.99	0.44
27:B3:74:GLN:HA	27:B3:89:HIS:HB3	2.00	0.44
27:B3:392:ASN:H	27:B3:407:SER:HA	1.82	0.44
27:B3:691:PRO:HD2	34:5E:516:SER:HB2	1.97	0.44
32:5C:122:GLY:O	32:5C:139:TRP:NE1	2.34	0.44
37:5H:555:ASN:HB3	37:5H:558:ASN:HB2	1.98	0.44
43:RE:1098:PHE:HE1	43:RE:1216:LYS:HE2	1.82	0.44
46:RI:129:TYR:HB2	46:RI:153:MET:HE2	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RO:282:HIS:CD2	50:RO:283:LYS:HG2	2.52	0.44
10:ST:50:ALA:O	10:ST:68:ARG:NH1	2.50	0.44
13:3C:92:ARG:HH12	33:5D:151:PHE:HB2	1.81	0.44
13:3C:261:LEU:O	15:3E:118:ARG:NH2	2.35	0.44
15:3E:372:ARG:HG3	17:3G:63:ILE:HA	2.00	0.44
18:A4:579:ARG:HH12	18:A4:659:PHE:HD1	1.65	0.44
19:A5:582:GLU:O	19:A5:586:ASP:N	2.50	0.44
24:AG:559:LYS:HE2	24:AG:559:LYS:HB2	1.79	0.44
24:AG:768:TRP:HE1	24:AG:772:THR:HA	1.83	0.44
26:B2:404:LYS:HZ1	26:B2:425:ILE:HD11	1.82	0.44
32:5C:269:LYS:HB2	51:RQ:830:ILE:HG23	1.98	0.44
32:5C:311:SER:OG	32:5C:313:GLU:OE2	2.33	0.44
34:5E:524:ASP:OD2	34:5E:527:ARG:NH2	2.42	0.44
36:5G:166:SER:O	36:5G:256:MET:HA	2.17	0.44
43:RE:775:ASP:HB3	43:RE:778:PHE:HB2	1.98	0.44
44:RF:162:THR:HG22	44:RF:165:PHE:H	1.82	0.44
45:RG:242:CYS:O	45:RG:246:GLU:HG3	2.18	0.44
47:RJ:617:THR:HG23	47:RJ:620:LYS:HE2	1.99	0.44
49:RN:737:ILE:HA	49:RN:740:MET:HG2	2.00	0.44
2:5A:247:U:OP1	33:5D:82:ARG:NH1	2.50	0.44
4:SG:86:GLN:HE22	25:B1:546:ASP:HB3	1.83	0.44
8:SP:13:VAL:HG13	8:SP:76:ILE:HA	1.98	0.44
14:3D:31:LEU:HD21	38:5I:59:VAL:HG13	1.99	0.44
18:A4:75:ASN:HB3	18:A4:92:GLU:HA	2.00	0.44
18:A4:201:VAL:HG13	18:A4:213:TRP:HB2	1.99	0.44
19:A5:87:LEU:O	19:A5:96:THR:N	2.50	0.44
22:AE:488:GLY:HA2	22:AE:491:TYR:HB3	1.98	0.44
24:AG:712:THR:HG23	24:AG:720:ILE:HD13	1.99	0.44
25:B1:25:ASP:O	25:B1:27:LYS:N	2.49	0.44
25:B1:157:ASP:N	25:B1:157:ASP:OD1	2.50	0.44
25:B1:356:ASP:OD1	25:B1:356:ASP:N	2.50	0.44
29:BE:356:ILE:HG22	29:BE:633:LYS:HG3	2.00	0.44
32:5C:162:ASN:ND2	32:5C:429:GLU:OE1	2.51	0.44
41:RC:52:TYR:CD1	41:RC:52:TYR:O	2.70	0.44
43:RE:159:SER:HB2	43:RE:256:TYR:HE2	1.82	0.44
47:RJ:187:LYS:HB2	47:RJ:187:LYS:HE3	1.75	0.44
47:RJ:841:THR:HB	47:RJ:859:ILE:HA	2.00	0.44
49:RN:443:LYS:HG3	49:RN:448:PHE:HE2	1.81	0.44
2:5A:207:G:H2'	2:5A:208:A:C8	2.52	0.44
3:SA:1169:G:N1	3:SA:1575:G:OP2	2.44	0.44
15:3E:218:ALA:O	15:3E:236:LYS:NZ	2.41	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:3F:405:VAL:HG12	16:3F:415:THR:HG22	2.00	0.44
18:A4:120:SER:OG	18:A4:121:THR:N	2.50	0.44
22:AE:100:ALA:HB1	28:B8:44:PHE:HZ	1.82	0.44
24:AG:202:SER:OG	24:AG:204:ASN:OD1	2.30	0.44
24:AG:510:TYR:HE1	24:AG:527:HIS:HB3	1.83	0.44
25:B1:476:VAL:HA	25:B1:492:SER:HB3	1.98	0.44
35:5F:34:ARG:NH2	40:5K:16:THR:OG1	2.50	0.44
11:SY:77:ILE:HG22	47:RJ:751:TYR:HB2	1.99	0.44
18:A4:212:ILE:O	18:A4:226:LEU:N	2.50	0.44
18:A4:468:ASP:OD2	18:A4:472:ARG:NH1	2.44	0.44
18:A4:571:THR:HG21	18:A4:632:ASN:HB3	2.00	0.44
24:AG:140:LYS:HA	24:AG:140:LYS:HD3	1.78	0.44
24:AG:484:VAL:O	24:AG:487:GLU:N	2.51	0.44
24:AG:516:PRO:HG2	24:AG:519:LEU:HD21	2.00	0.44
24:AG:532:TRP:HB3	24:AG:541:TRP:HB3	1.99	0.44
26:B2:129:PHE:HE1	26:B2:150:LEU:HD11	1.82	0.44
27:B3:269:LEU:HB2	27:B3:279:LYS:HB2	1.99	0.44
28:B8:277:ILE:HA	28:B8:282:ASN:HD22	1.83	0.44
31:5B:164:LYS:HE3	31:5B:164:LYS:HB3	1.76	0.44
33:5D:194:LYS:HA	33:5D:194:LYS:HD3	1.83	0.44
36:5G:139:LEU:HB2	36:5G:157:PHE:CE2	2.53	0.44
45:RG:135:LYS:HD3	45:RG:135:LYS:HA	1.87	0.44
2:5A:20:C:H2'	2:5A:21:A:C8	2.52	0.44
13:3B:169:LYS:HA	13:3B:193:VAL:O	2.18	0.44
14:3D:206:LEU:HD11	14:3D:219:LEU:HD11	2.00	0.44
15:3E:36:ASP:O	15:3E:123:TYR:OH	2.34	0.44
18:A4:45:THR:HB	18:A4:352:VAL:HA	1.99	0.44
23:AF:20:THR:HA	23:AF:24:GLN:HE21	1.83	0.44
27:B3:304:LEU:O	27:B3:311:LEU:HA	2.18	0.44
34:5E:379:ASP:HB2	36:5G:191:PHE:HD2	1.83	0.44
38:5I:241:ASP:OD1	38:5I:241:ASP:N	2.39	0.44
42:RD:1524:GLU:HA	42:RD:1528:GLY:HA3	2.00	0.44
48:RK:143:LYS:HE3	48:RK:143:LYS:HB2	1.75	0.44
3:SA:1234:A:O2'	3:SA:1236:A:N6	2.50	0.44
7:SO:109:LYS:H	7:SO:109:LYS:CD	2.29	0.44
13:3B:125:VAL:HG12	39:5J:150:GLY:HA3	2.00	0.44
15:3E:227:LEU:HG	15:3E:231:ILE:HB	2.00	0.44
18:A4:144:ILE:HD12	18:A4:158:VAL:HB	2.00	0.44
19:A5:221:MET:HB3	19:A5:221:MET:HE3	1.75	0.44
22:AE:422:LEU:HD12	22:AE:422:LEU:HA	1.87	0.44
25:B1:743:PHE:HZ	25:B1:778:ILE:HD13	1.83	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:5I:139:CYS:HB3	38:5I:145:VAL:HG22	1.99	0.44
3:SA:1697:G:OP1	43:RE:326:LEU:CD1	2.48	0.43
9:SR:64:ASP:OD1	9:SR:64:ASP:N	2.50	0.43
17:3H:52:ILE:HD12	17:3H:71:CYS:SG	2.58	0.43
17:3H:95:ARG:HA	17:3H:95:ARG:HD2	1.88	0.43
18:A4:572:ALA:HB3	18:A4:585:ILE:HD11	2.00	0.43
22:AE:538:ALA:HA	22:AE:541:LEU:HB2	2.00	0.43
27:B3:476:ASP:N	27:B3:476:ASP:OD1	2.50	0.43
28:B8:27:PHE:HB3	30:B6:31:LEU:HD23	1.98	0.43
32:5C:228:LEU:HD22	32:5C:264:PRO:HA	1.99	0.43
40:5K:161:LYS:HG2	40:5K:172:LEU:HD21	1.99	0.43
46:RI:123:ASP:OD1	46:RI:123:ASP:N	2.49	0.43
50:RO:315:VAL:HG23	50:RO:316:PRO:HD3	1.98	0.43
52:RS:359:LEU:HD23	52:RS:362:LEU:HD12	2.00	0.43
3:SA:1132:A:O3'	48:RK:231:ARG:NH1	2.43	0.43
4:SG:39:GLU:OE1	4:SG:41:LYS:NZ	2.45	0.43
18:A4:750:ASN:N	18:A4:750:ASN:OD1	2.50	0.43
22:AE:238:LEU:HA	22:AE:241:ILE:HG22	1.99	0.43
24:AG:437:THR:OG1	24:AG:764:SER:O	2.31	0.43
26:B2:645:GLU:HG2	26:B2:646:LYS:HG3	1.99	0.43
27:B3:161:TRP:HB3	27:B3:177:LEU:HG	1.99	0.43
27:B3:464:LYS:HA	27:B3:482:VAL:HG21	2.00	0.43
29:BE:852:LEU:HD22	29:BE:860:GLU:HG2	2.00	0.43
38:5I:444:GLU:OE2	38:5I:448:ARG:NH2	2.37	0.43
45:RH:89:PRO:HG2	45:RH:134:PHE:HZ	1.83	0.43
47:RJ:904:ASN:HA	47:RJ:907:THR:HB	2.00	0.43
49:RN:590:ASN:OD1	49:RN:590:ASN:N	2.50	0.43
52:RS:221:LEU:HD22	52:RS:258:VAL:HG11	2.00	0.43
2:5A:467:A:N1	2:5A:468:A:N6	2.66	0.43
3:SA:886:U:H1'	8:SP:123:SER:HB3	2.00	0.43
3:SA:1599:C:H2'	3:SA:1600:A:C8	2.53	0.43
3:SA:1643:U:H2'	3:SA:1644:C:C6	2.52	0.43
3:SA:1658:G:C2	3:SA:1743:U:H1'	2.50	0.43
5:SK:38:ASN:HA	37:5H:565:LYS:HE2	1.99	0.43
13:3C:121:LYS:HA	13:3C:121:LYS:HD3	1.78	0.43
20:A8:638:LEU:HD21	20:A8:662:ILE:HD11	1.99	0.43
22:AE:348:ILE:HG21	22:AE:373:ILE:HD11	2.00	0.43
24:AG:296:HIS:NE2	24:AG:314:SER:OG	2.37	0.43
25:B1:35:ASN:HA	25:B1:58:ILE:HG23	1.99	0.43
26:B2:59:LEU:HD21	26:B2:62:LYS:HE2	1.99	0.43
27:B3:199:ILE:O	27:B3:209:LEU:HA	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5C:64:ASP:HA	32:5C:67:LEU:HG	1.99	0.43
35:5F:138:VAL:HG12	35:5F:158:VAL:HG22	2.00	0.43
38:5I:358:MET:HB3	51:RQ:890:VAL:HG23	2.00	0.43
40:5K:52:PHE:HB3	40:5K:55:TYR:HB3	2.01	0.43
40:5K:171:PRO:HA	40:5K:184:LYS:HB2	2.01	0.43
43:RE:380:SER:OG	43:RE:386:GLY:O	2.36	0.43
43:RE:970:TRP:HB2	43:RE:971:LYS:HD2	2.00	0.43
47:RJ:625:TRP:HZ2	48:RK:284:SER:HB3	1.83	0.43
49:RN:314:MET:HA	49:RN:512:ASP:HA	1.99	0.43
3:SA:18:C:O2'	3:SA:21:U:O4'	2.37	0.43
10:ST:110:ARG:NH1	49:RN:740:MET:HB2	2.33	0.43
11:SY:68:ILE:HD12	49:RN:785:VAL:HG23	2.00	0.43
13:3B:221:ILE:HD13	14:3D:163:VAL:HB	2.00	0.43
15:3E:191:HIS:HB2	15:3E:247:ILE:HG23	1.99	0.43
15:3E:330:LEU:HD13	33:5D:109:THR:HG21	2.00	0.43
17:3G:62:GLU:HA	17:3G:65:LEU:HG	2.00	0.43
18:A4:214:SER:HB3	18:A4:226:LEU:HD13	1.99	0.43
19:A5:240:GLN:HE22	19:A5:298:LYS:HB3	1.83	0.43
22:AE:655:ALA:O	22:AE:659:LEU:HB2	2.18	0.43
23:AF:413:LEU:HA	23:AF:416:THR:HG22	2.00	0.43
24:AG:228:VAL:HG23	24:AG:236:ASN:HB3	2.00	0.43
25:B1:369:ILE:HB	25:B1:383:PHE:HB2	1.99	0.43
26:B2:596:ASN:HB3	26:B2:612:PHE:HA	1.99	0.43
27:B3:532:HIS:CE1	27:B3:558:LYS:HD2	2.53	0.43
29:BE:569:VAL:HB	29:BE:579:ARG:HB2	2.01	0.43
30:B6:72:LYS:HD2	30:B6:72:LYS:HA	1.78	0.43
32:5C:508:VAL:HG12	41:RC:72:VAL:CB	2.48	0.43
36:5G:119:ARG:NH1	36:5G:122:TYR:O	2.52	0.43
51:RQ:284:ARG:HE	51:RQ:284:ARG:HB3	1.51	0.43
3:SA:871:G:H2'	3:SA:872:G:C8	2.53	0.43
3:SA:904:G:OP2	41:RC:185:ARG:NH2	2.52	0.43
4:SG:89:ILE:HD11	4:SG:172:ILE:HD11	2.00	0.43
13:3C:185:SER:HB3	13:3C:217:ILE:HD11	2.00	0.43
16:3F:415:THR:OG1	16:3F:425:TRP:NE1	2.39	0.43
19:A5:336:ASN:OD1	19:A5:336:ASN:N	2.49	0.43
22:AE:586:LEU:O	22:AE:590:ALA:HB2	2.18	0.43
23:AF:288:ASP:OD1	23:AF:288:ASP:N	2.48	0.43
23:AF:377:ASP:OD1	23:AF:377:ASP:N	2.51	0.43
24:AG:50:ASN:HD21	24:AG:782:THR:HG22	1.84	0.43
24:AG:780:GLU:O	24:AG:782:THR:N	2.49	0.43
25:B1:829:VAL:HG23	25:B1:830:ARG:HG2	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:B3:200:GLU:HB3	27:B3:209:LEU:HD23	2.01	0.43
27:B3:260:THR:HA	27:B3:268:GLN:O	2.18	0.43
27:B3:440:VAL:HB	27:B3:454:LEU:HD11	2.01	0.43
28:B8:376:LEU:HG	28:B8:386:ILE:HG12	1.99	0.43
32:5C:369:MET:HB3	32:5C:369:MET:HE2	1.79	0.43
36:5G:283:THR:HG22	36:5G:286:LYS:HB2	2.00	0.43
38:5I:133:GLN:HA	38:5I:150:ILE:O	2.18	0.43
46:RI:208:SER:OG	46:RI:209:ILE:N	2.52	0.43
47:RJ:280:LEU:HD12	47:RJ:281:PRO:HD2	2.01	0.43
48:RK:36:ILE:HB	48:RK:72:THR:HA	2.01	0.43
49:RN:616:LEU:HB3	49:RN:619:LEU:HD13	2.01	0.43
2:5A:192:G:H2'	2:5A:193:G:C8	2.53	0.43
2:5A:489:G:O6	30:B6:120:ARG:NH1	2.51	0.43
3:SA:513:U:H2'	3:SA:514:G:H8	1.82	0.43
3:SA:1655:A:H2'	3:SA:1656:U:H6	1.83	0.43
5:SK:155:HIS:NE2	16:3F:321:HIS:O	2.50	0.43
10:ST:119:ILE:HD13	34:5E:342:THR:HG22	2.00	0.43
16:3F:414:ILE:HG13	16:3F:478:LEU:HD21	2.00	0.43
18:A4:106:ASN:OD1	18:A4:106:ASN:N	2.51	0.43
23:AF:24:GLN:HB2	23:AF:294:PHE:HD1	1.83	0.43
28:B8:35:GLU:O	28:B8:39:LYS:HB2	2.18	0.43
32:5C:512:ARG:O	32:5C:516:VAL:HG23	2.18	0.43
35:5F:115:MET:HB2	35:5F:115:MET:HE3	1.58	0.43
36:5G:100:LEU:HD13	36:5G:144:GLU:HB3	2.01	0.43
38:5I:107:LYS:NZ	38:5I:109:HIS:O	2.45	0.43
38:5I:272:MET:HE3	38:5I:272:MET:HB3	1.95	0.43
43:RE:313:ASN:HD22	43:RE:326:LEU:HA	1.84	0.43
53:RT:186:GLU:HG3	53:RT:230:LYS:HG2	2.00	0.43
4:SG:72:HIS:O	9:SR:79:TYR:OH	2.37	0.43
4:SG:103:ASN:HA	4:SG:106:LYS:HD2	2.01	0.43
5:SK:154:LYS:HE2	5:SK:154:LYS:HB3	1.88	0.43
15:3E:372:ARG:O	15:3E:376:LEU:HB2	2.18	0.43
16:3F:201:ILE:HG12	16:3F:538:ARG:HD3	2.00	0.43
19:A5:281:ILE:HG12	19:A5:328:VAL:HB	2.01	0.43
22:AE:210:LEU:HD13	22:AE:210:LEU:HA	1.90	0.43
24:AG:414:ILE:HA	24:AG:414:ILE:HD12	1.80	0.43
26:B2:657:GLN:HE21	26:B2:657:GLN:HB3	1.64	0.43
27:B3:11:SER:CB	27:B3:641:PHE:O	2.64	0.43
27:B3:438:THR:OG1	27:B3:439:ALA:N	2.50	0.43
27:B3:657:GLU:CD	27:B3:657:GLU:C	2.85	0.43
38:5I:306:SER:OG	38:5I:307:ALA:N	2.50	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:RE:895:HIS:NE2	43:RE:935:GLU:OE1	2.39	0.43
47:RJ:80:THR:C	57:RJ:1201:GTP:O2B	2.61	0.43
48:RK:68:SER:OG	48:RK:69:TYR:N	2.52	0.43
50:RO:472:HIS:CD2	50:RO:474:HIS:H	2.31	0.43
14:3D:52:SER:HB2	14:3D:85:ASN:HD21	1.84	0.43
15:3E:206:ALA:HB2	15:3E:262:ILE:HD11	2.00	0.43
16:3F:303:LYS:HB3	16:3F:317:ILE:HD11	2.01	0.43
19:A5:270:ASN:OD1	19:A5:270:ASN:N	2.49	0.43
20:A8:583:SER:HA	20:A8:586:ILE:HG22	2.00	0.43
25:B1:493:TRP:HA	25:B1:517:ASP:HB2	2.01	0.43
26:B2:473:ASP:N	26:B2:494:ASP:OD2	2.47	0.43
43:RE:649:TRP:HB2	43:RE:653:SER:HB2	2.01	0.43
45:RG:75:GLY:HA2	45:RG:78:LYS:HE3	2.01	0.43
50:RO:292:PRO:HG2	50:RO:330:PHE:HE2	1.82	0.43
3:SA:1012:U:H2'	3:SA:1013:A:C8	2.53	0.43
6:SN:79:ALA:HA	6:SN:85:LYS:HD2	2.01	0.43
18:A4:532:ASN:N	18:A4:544:SER:O	2.50	0.43
26:B2:178:ILE:HD11	26:B2:186:ILE:HD11	2.01	0.43
29:BE:24:PHE:HB3	29:BE:654:TRP:HB3	2.01	0.43
29:BE:50:ILE:HD13	29:BE:311:VAL:HG11	2.01	0.43
29:BE:499:LYS:HE2	29:BE:499:LYS:HB3	1.85	0.43
32:5C:268:VAL:HG13	51:RQ:831:ILE:HG12	2.00	0.43
33:5D:102:GLN:HE21	47:RJ:1098:ARG:NH1	2.17	0.43
36:5G:28:LYS:HB2	36:5G:46:LEU:HD11	2.00	0.43
36:5G:29:ARG:HD2	36:5G:59:ASP:HB3	2.01	0.43
38:5I:6:ILE:HG21	38:5I:8:ARG:HH21	1.84	0.43
38:5I:344:HIS:NE2	38:5I:418:HIS:O	2.51	0.43
49:RN:475:ARG:HH22	49:RN:516:LEU:HB3	1.84	0.43
52:RS:437:ARG:HH21	52:RS:463:GLY:HA3	1.84	0.43
3:SA:909:U:H2'	3:SA:910:C:C6	2.54	0.43
3:SA:985:G:H2'	3:SA:986:G:C8	2.54	0.43
7:SO:40:TYR:HA	7:SO:43:LYS:HG2	2.00	0.43
13:3B:198:GLU:O	13:3B:221:ILE:HA	2.18	0.43
16:3F:160:ILE:HG12	16:3F:542:SER:HB2	2.00	0.43
18:A4:566:LEU:HA	18:A4:566:LEU:HD23	1.83	0.43
18:A4:617:ASN:O	18:A4:621:ASN:HB2	2.19	0.43
19:A5:110:ILE:HG22	19:A5:119:CYS:HB2	2.00	0.43
19:A5:448:ASN:OD1	19:A5:450:HIS:NE2	2.52	0.43
23:AF:463:VAL:HA	23:AF:466:VAL:HG12	2.01	0.43
24:AG:87:SER:O	24:AG:111:THR:OG1	2.32	0.43
24:AG:857:PHE:HE2	28:B8:226:LYS:HB3	1.84	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B1:25:ASP:OD1	25:B1:25:ASP:N	2.50	0.43
26:B2:861:ILE:HD11	27:B3:805:ILE:CD1	2.48	0.43
27:B3:160:ILE:HG22	27:B3:162:LEU:HB2	1.99	0.43
27:B3:225:PHE:HD1	27:B3:230:LYS:HD2	1.84	0.43
28:B8:426:VAL:HG11	28:B8:455:ILE:HG21	2.01	0.43
29:BE:627:ASN:ND2	29:BE:647:THR:OG1	2.52	0.43
33:5D:145:GLU:OE1	33:5D:146:PHE:N	2.52	0.43
40:5K:61:PRO:HB3	40:5K:92:ALA:HB1	2.01	0.43
44:RF:61:LEU:HD11	44:RF:164:SER:HA	2.00	0.43
49:RN:484:ARG:HB3	49:RN:492:ALA:HB1	2.01	0.43
49:RN:669:SER:HA	49:RN:672:THR:HG22	2.01	0.43
52:RS:266:PHE:O	52:RS:270:LEU:HB3	2.18	0.43
52:RS:398:ARG:H	52:RS:406:GLY:HA3	1.83	0.43
3:SA:899:G:H2'	3:SA:900:A:C8	2.54	0.42
3:SA:941:A:H2	3:SA:976:G:H4'	1.84	0.42
3:SA:960:U:H5'	7:SO:55:ARG:HD3	2.01	0.42
13:3C:185:SER:HA	13:3C:188:VAL:HG12	2.01	0.42
15:3E:319:ILE:HD12	15:3E:326:LEU:HD22	2.01	0.42
17:3G:64:LEU:O	17:3G:66:HIS:N	2.43	0.42
18:A4:313:LYS:HA	18:A4:316:LYS:HG2	2.01	0.42
23:AF:177:ILE:HA	23:AF:178:PRO:HD3	1.84	0.42
24:AG:252:LEU:HD23	24:AG:256:THR:HG21	2.00	0.42
25:B1:150:THR:OG1	25:B1:164:THR:OG1	2.31	0.42
25:B1:661:LEU:H	25:B1:661:LEU:HG	1.62	0.42
25:B1:749:TYR:HE2	29:BE:705:ILE:HG13	1.84	0.42
26:B2:276:ASN:ND2	26:B2:280:THR:O	2.47	0.42
32:5C:230:THR:HG22	32:5C:232:ALA:H	1.83	0.42
37:5H:496:GLN:HA	37:5H:499:GLN:HG2	2.00	0.42
37:5H:550:LEU:HD23	37:5H:550:LEU:HA	1.88	0.42
45:RG:190:GLN:NE2	45:RG:244:GLY:HA2	2.34	0.42
47:RJ:831:ARG:HD3	47:RJ:838:ILE:HD12	2.01	0.42
47:RJ:1019:THR:HB	47:RJ:1022:LEU:HD12	2.01	0.42
48:RK:56:ILE:HD13	48:RK:56:ILE:HA	1.89	0.42
48:RK:80:ILE:HD13	48:RK:80:ILE:HA	1.90	0.42
49:RN:481:MET:HE3	49:RN:481:MET:HB2	1.92	0.42
50:RO:338:TYR:OH	50:RO:365:PHE:O	2.33	0.42
52:RS:264:LYS:HB2	52:RS:264:LYS:HE3	1.81	0.42
52:RS:382:LEU:HD11	52:RS:428:TYR:CG	2.55	0.42
3:SA:1656:U:H1'	3:SA:1744:A:H61	1.84	0.42
21:A9:475:THR:HA	21:A9:478:ASN:HB2	1.99	0.42
25:B1:76:ASP:N	25:B1:76:ASP:OD1	2.51	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B2:351:LEU:HB2	26:B2:367:ILE:HG23	2.01	0.42
26:B2:432:TYR:CD1	26:B2:450:ARG:HB2	2.53	0.42
27:B3:77:THR:HG22	27:B3:86:LYS:HB3	2.01	0.42
27:B3:466:TRP:HZ3	27:B3:478:GLN:HA	1.82	0.42
29:BE:27:PHE:HB2	29:BE:655:THR:HG23	2.00	0.42
32:5C:487:LYS:HD3	32:5C:490:VAL:HG11	2.00	0.42
34:5E:335:ARG:HH22	47:RJ:952:PHE:HA	1.84	0.42
39:5J:134:ARG:HD2	39:5J:134:ARG:HA	1.83	0.42
47:RJ:1075:LYS:HE3	47:RJ:1075:LYS:HB2	1.84	0.42
48:RK:286:SER:OG	48:RK:289:VAL:O	2.33	0.42
52:RS:210:VAL:HG23	52:RS:212:LYS:HG2	2.00	0.42
3:SA:555:A:N6	3:SA:571:G:O2'	2.50	0.42
3:SA:578:U:OP2	47:RJ:874:TYR:OH	2.29	0.42
3:SA:1233:G:H1	3:SA:1253:U:H2'	1.83	0.42
5:SK:45:ILE:HD12	5:SK:48:GLN:HE21	1.84	0.42
10:ST:120:ARG:NH1	34:5E:344:GLU:OE2	2.50	0.42
14:3D:4:ILE:HG23	14:3D:20:VAL:HG21	2.01	0.42
15:3E:132:SER:OG	15:3E:134:ASN:OD1	2.34	0.42
22:AE:354:SER:O	22:AE:358:TYR:HB2	2.20	0.42
24:AG:313:LEU:HD23	24:AG:323:LEU:HB3	2.01	0.42
26:B2:39:GLY:O	26:B2:54:ILE:HG13	2.20	0.42
26:B2:673:VAL:HG23	26:B2:683:ILE:HD13	2.01	0.42
26:B2:840:MET:HE1	26:B2:887:LEU:HD13	2.02	0.42
29:BE:470:GLN:HB3	29:BE:553:ARG:NH1	2.34	0.42
30:B6:5:ARG:HD2	30:B6:5:ARG:HA	1.80	0.42
30:B6:35:LYS:HE3	30:B6:35:LYS:HB3	1.88	0.42
34:5E:370:ARG:HA	34:5E:373:ILE:HG22	2.01	0.42
41:RC:100:LEU:HD22	41:RC:117:LEU:HD21	2.02	0.42
42:RD:1535:GLU:O	42:RD:1539:ARG:N	2.45	0.42
47:RJ:940:LYS:HE2	47:RJ:940:LYS:HB2	1.73	0.42
48:RK:81:ILE:HG22	48:RK:110:SER:HB3	2.01	0.42
52:RS:373:LYS:HE2	52:RS:373:LYS:HB3	1.84	0.42
13:3B:272:LYS:HD3	13:3B:275:CYS:HB3	2.01	0.42
15:3E:218:ALA:HA	15:3E:221:THR:HG22	2.00	0.42
18:A4:774:LEU:HD12	18:A4:774:LEU:HA	1.83	0.42
20:A8:120:LEU:HA	20:A8:132:ILE:HA	2.01	0.42
22:AE:476:ILE:HG23	22:AE:515:PHE:HE2	1.84	0.42
24:AG:551:HIS:HA	24:AG:583:LYS:HE3	2.00	0.42
24:AG:865:LYS:HE2	24:AG:865:LYS:HB3	1.81	0.42
25:B1:60:ALA:HB1	25:B1:102:VAL:HG12	2.02	0.42
25:B1:275:LEU:HD22	25:B1:289:LEU:HD13	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B1:380:LEU:HD12	34:5E:484:MET:HE2	2.01	0.42
26:B2:297:LYS:HA	26:B2:300:GLU:HB2	2.02	0.42
26:B2:369:TYR:HA	26:B2:374:PRO:HA	2.01	0.42
26:B2:636:ASP:N	26:B2:636:ASP:OD1	2.52	0.42
26:B2:836:ILE:HA	26:B2:839:VAL:HG12	2.00	0.42
27:B3:479:ILE:HB	27:B3:480:ILE:HG23	2.02	0.42
29:BE:606:ASP:OD1	29:BE:606:ASP:N	2.41	0.42
36:5G:133:LYS:HE3	36:5G:133:LYS:HB3	1.85	0.42
47:RJ:203:LYS:HD2	47:RJ:203:LYS:HA	1.78	0.42
47:RJ:217:ASP:O	47:RJ:221:LEU:HB2	2.20	0.42
49:RN:501:PHE:HB3	49:RN:549:ILE:HG21	2.02	0.42
49:RN:700:LEU:HD21	50:RO:467:ALA:HB2	2.00	0.42
1:3A:113:G:O6	17:3H:42:LYS:NZ	2.44	0.42
2:5A:298:A:OP2	29:BE:103:ARG:NH2	2.45	0.42
3:SA:-7:A:N7	38:5I:292:ARG:NH1	2.68	0.42
3:SA:954:G:H2'	3:SA:955:A:H8	1.84	0.42
3:SA:1000:C:H41	3:SA:1003:A:H2'	1.83	0.42
3:SA:1229:G:O6	6:SN:46:ARG:NH1	2.52	0.42
10:ST:100:THR:O	10:ST:104:ASN:ND2	2.53	0.42
13:3C:124:SER:HA	13:3C:139:VAL:O	2.19	0.42
14:3D:182:ASP:OD1	14:3D:314:ARG:NH2	2.39	0.42
19:A5:441:LEU:HD11	19:A5:480:LEU:HD13	2.02	0.42
22:AE:323:PHE:CZ	22:AE:332:ILE:HD11	2.54	0.42
22:AE:487:THR:HG22	22:AE:488:GLY:H	1.85	0.42
25:B1:157:ASP:OD1	25:B1:203:GLN:NE2	2.38	0.42
26:B2:497:VAL:HG12	26:B2:528:LEU:HB3	2.01	0.42
27:B3:215:GLY:N	27:B3:242:GLN:OE1	2.52	0.42
27:B3:555:LYS:HG2	27:B3:576:ASN:HA	2.00	0.42
34:5E:453:SER:O	34:5E:455:HIS:ND1	2.52	0.42
36:5G:28:LYS:HB2	36:5G:46:LEU:HD21	2.01	0.42
45:RH:176:ARG:NH2	45:RH:192:TYR:OH	2.52	0.42
52:RS:382:LEU:HD21	52:RS:428:TYR:CZ	2.53	0.42
1:3A:62:C:O2'	29:BE:447:ASN:O	2.35	0.42
2:5A:192:G:H2'	2:5A:193:G:H8	1.85	0.42
3:SA:630:A:C6	3:SA:970:A:N7	2.87	0.42
5:SK:63:ASP:OD1	5:SK:63:ASP:N	2.46	0.42
5:SK:163:PRO:HB3	5:SK:169:PRO:HA	2.01	0.42
10:ST:27:LYS:O	10:ST:31:ALA:HB2	2.19	0.42
13:3C:291:GLN:HA	13:3C:294:ARG:HG2	2.01	0.42
15:3E:117:TYR:HA	15:3E:120:ILE:HG12	2.01	0.42
15:3E:160:ASP:HB3	15:3E:283:ILE:HG21	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:3F:502:SER:OG	16:3F:504:ASN:OD1	2.32	0.42
17:3G:44:LEU:HD23	17:3G:44:LEU:HA	1.87	0.42
18:A4:513:LEU:HD12	18:A4:513:LEU:HA	1.89	0.42
22:AE:539:LEU:HD12	22:AE:540:LYS:HG3	2.01	0.42
23:AF:424:ARG:HA	24:AG:477:VAL:HG11	2.01	0.42
26:B2:534:ILE:HD11	26:B2:537:VAL:HG12	2.01	0.42
27:B3:680:ASN:HA	27:B3:683:LEU:HG	2.02	0.42
29:BE:724:SER:O	29:BE:728:ARG:NH2	2.39	0.42
32:5C:215:LYS:HG2	32:5C:227:GLU:HG2	2.00	0.42
36:5G:154:ILE:O	36:5G:162:THR:HA	2.20	0.42
43:RE:135:LEU:HD21	43:RE:207:LEU:HD21	2.01	0.42
43:RE:566:ILE:HA	43:RE:569:VAL:HG22	2.00	0.42
43:RE:627:LEU:HD12	43:RE:628:VAL:HG23	2.01	0.42
45:RG:128:VAL:HG22	45:RG:159:LEU:HD22	2.01	0.42
47:RJ:773:THR:HG23	47:RJ:777:ARG:HD3	2.02	0.42
48:RK:190:SER:OG	48:RK:191:ILE:N	2.51	0.42
48:RK:310:ARG:HB3	48:RK:353:THR:HG22	2.02	0.42
50:RO:208:TYR:O	50:RO:212:LEU:HB2	2.19	0.42
50:RO:243:PRO:HA	50:RO:244:PRO:HD3	1.81	0.42
50:RO:395:ILE:HD12	50:RO:469:LEU:HD11	2.02	0.42
52:RS:364:PHE:HE1	52:RS:417:TRP:HE1	1.67	0.42
52:RS:437:ARG:HD2	52:RS:460:LEU:HG	2.02	0.42
53:RT:124:LEU:HG	53:RT:151:ALA:HB1	2.02	0.42
3:SA:976:G:N3	3:SA:978:A:N7	2.67	0.42
13:3C:210:MET:HE2	13:3C:210:MET:HB2	1.97	0.42
19:A5:27:GLN:HG3	19:A5:59:LYS:HA	2.02	0.42
19:A5:233:LYS:HD3	19:A5:233:LYS:HA	1.82	0.42
22:AE:25:ARG:HH21	38:5I:16:VAL:HG22	1.83	0.42
22:AE:549:LYS:HD3	22:AE:549:LYS:HA	1.91	0.42
24:AG:31:ASN:OD1	24:AG:31:ASN:N	2.52	0.42
24:AG:478:ASN:OD1	24:AG:478:ASN:N	2.51	0.42
26:B2:861:ILE:HD11	27:B3:805:ILE:HD13	2.01	0.42
29:BE:353:PRO:HA	29:BE:370:SER:HA	2.01	0.42
32:5C:117:LYS:HD2	32:5C:117:LYS:HA	1.85	0.42
33:5D:78:LEU:HD12	33:5D:78:LEU:HA	1.82	0.42
43:RE:433:ASP:OD1	43:RE:489:LYS:NZ	2.41	0.42
50:RO:153:ILE:HD12	50:RO:153:ILE:HA	1.91	0.42
3:SA:1492:A:N6	47:RJ:941:ILE:O	2.46	0.42
4:SG:23:VAL:HG23	9:SR:61:SER:HB3	2.00	0.42
4:SG:114:ILE:HA	4:SG:117:THR:HG22	2.02	0.42
6:SN:59:LEU:HB2	6:SN:87:PRO:HG2	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:3E:172:ASP:O	15:3E:176:GLU:HG2	2.20	0.42
16:3F:368:LEU:HB3	16:3F:396:PHE:HE2	1.83	0.42
19:A5:49:ASN:OD1	19:A5:49:ASN:N	2.49	0.42
19:A5:224:CYS:SG	19:A5:225:VAL:N	2.93	0.42
26:B2:236:ASP:OD1	26:B2:236:ASP:N	2.46	0.42
27:B3:201:VAL:O	27:B3:208:SER:HB3	2.20	0.42
27:B3:686:MET:HE3	27:B3:686:MET:HB3	1.93	0.42
36:5G:43:PRO:O	36:5G:47:ALA:HB2	2.20	0.42
36:5G:175:ASP:O	49:RN:64:ARG:NH2	2.53	0.42
38:5I:456:GLU:HA	38:5I:459:LYS:HE2	2.01	0.42
38:5I:464:THR:HG21	38:5I:468:TYR:HE1	1.85	0.42
43:RE:1206:PRO:HD2	44:RF:36:PHE:HD2	1.85	0.42
44:RF:20:LEU:HB2	44:RF:33:SER:HB2	2.01	0.42
44:RF:147:LEU:HA	44:RF:150:LYS:HD3	2.01	0.42
1:3A:49:C:H42	2:5A:467:A:H61	1.67	0.42
1:3A:118:A:C5	16:3F:218:ALA:HB2	2.55	0.42
9:SR:97:VAL:HG12	9:SR:98:ASP:H	1.83	0.42
16:3F:303:LYS:HE3	16:3F:319:TYR:HE2	1.85	0.42
18:A4:213:TRP:HA	18:A4:225:LEU:HA	2.02	0.42
22:AE:420:LYS:HB2	22:AE:420:LYS:HE2	1.91	0.42
52:RS:255:SER:HB3	52:RS:258:VAL:HG22	2.01	0.42
53:RT:263:LEU:HA	53:RT:266:VAL:HG12	2.02	0.42
3:SA:941:A:C2	3:SA:976:G:H4'	2.54	0.42
15:3E:333:LYS:HD3	33:5D:103:ASP:HB3	2.02	0.42
16:3F:301:ASP:OD1	16:3F:301:ASP:N	2.51	0.42
24:AG:502:LYS:HD2	24:AG:564:PRO:HA	2.02	0.42
24:AG:659:ILE:HG22	24:AG:674:THR:HB	2.01	0.42
25:B1:147:GLN:HB2	25:B1:167:ASP:H	1.85	0.42
26:B2:141:LYS:O	26:B2:165:SER:HA	2.20	0.42
27:B3:178:VAL:HG13	27:B3:179:LYS:HG2	2.02	0.42
39:5J:207:LYS:HE2	39:5J:207:LYS:HB3	1.88	0.42
43:RE:1100:VAL:HG22	43:RE:1234:PHE:HD1	1.85	0.42
45:RH:180:LEU:HD23	45:RH:180:LEU:HA	1.88	0.42
52:RS:355:ALA:HA	52:RS:358:TYR:CE2	2.55	0.42
52:RS:432:ILE:HG23	52:RS:436:GLN:HB2	2.00	0.42
3:SA:565:C:N4	47:RJ:993:ASP:HB3	2.35	0.41
6:SN:90:LYS:HD2	6:SN:90:LYS:HA	1.80	0.41
13:3B:150:LYS:NZ	13:3B:310:GLU:OE2	2.44	0.41
13:3C:242:ALA:HB3	13:3C:269:ILE:HA	2.01	0.41
16:3F:260:LEU:HD21	16:3F:283:VAL:HG11	2.02	0.41
16:3F:421:ASN:ND2	16:3F:437:ARG:HA	2.34	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:A4:98:SER:OG	18:A4:99:ILE:N	2.53	0.41
18:A4:154:ASP:OD1	18:A4:154:ASP:N	2.49	0.41
23:AF:492:ARG:HA	23:AF:492:ARG:HD3	1.80	0.41
25:B1:410:THR:HG22	25:B1:426:THR:HG22	2.01	0.41
25:B1:605:ASP:OD1	25:B1:605:ASP:N	2.40	0.41
25:B1:721:VAL:O	29:BE:579:ARG:NH2	2.53	0.41
30:B6:15:MET:HE2	30:B6:15:MET:HB3	1.67	0.41
38:5I:1:MET:HE3	38:5I:1:MET:HB2	1.83	0.41
48:RK:216:LEU:HB3	48:RK:223:VAL:HG21	2.01	0.41
49:RN:700:LEU:HD23	49:RN:702:LEU:HG	2.01	0.41
52:RS:373:LYS:HA	52:RS:376:LEU:HG	2.02	0.41
2:5A:150:G:C6	23:AF:380:ARG:HG3	2.54	0.41
2:5A:532:A:O2'	51:RQ:332:ASP:OD2	2.37	0.41
3:SA:1156:C:H2'	3:SA:1157:A:C8	2.54	0.41
9:SR:46:PHE:HA	9:SR:49:TYR:HB2	2.02	0.41
13:3C:149:SER:OG	13:3C:150:LYS:N	2.53	0.41
13:3C:212:LYS:HA	13:3C:212:LYS:HD3	1.89	0.41
14:3D:206:LEU:HB3	14:3D:216:PHE:HE1	1.84	0.41
18:A4:423:LYS:NZ	31:5B:167:ARG:HH11	2.19	0.41
19:A5:32:GLN:HE22	19:A5:47:ASN:HB3	1.85	0.41
22:AE:559:ASN:HB2	22:AE:614:LEU:HD12	2.02	0.41
24:AG:258:TYR:CD1	24:AG:414:ILE:HD11	2.55	0.41
25:B1:274:LEU:HD11	25:B1:286:LEU:HD13	2.02	0.41
26:B2:405:LEU:HD11	26:B2:673:VAL:HG21	2.02	0.41
26:B2:555:VAL:HG22	26:B2:569:LEU:HB2	2.02	0.41
27:B3:531:ASN:O	27:B3:558:LYS:NZ	2.53	0.41
41:RC:53:LEU:O	41:RC:57:TRP:HB2	2.20	0.41
43:RE:296:ILE:HD11	43:RE:339:SER:HB2	2.02	0.41
44:RF:102:ALA:HA	44:RF:105:SER:HB3	2.03	0.41
45:RG:177:LYS:HE2	45:RG:177:LYS:HB3	1.68	0.41
49:RN:616:LEU:HD13	49:RN:619:LEU:HD22	2.01	0.41
2:5A:223:C:O2	2:5A:224:G:O2'	2.38	0.41
13:3B:107:VAL:HG13	13:3B:141:TYR:HB3	2.01	0.41
16:3F:158:THR:HG23	16:3F:548:ARG:HB2	2.02	0.41
16:3F:476:THR:HG22	16:3F:491:SER:HA	2.02	0.41
22:AE:148:PHE:HA	22:AE:151:ILE:HG12	2.01	0.41
23:AF:105:VAL:HG21	23:AF:142:THR:HG21	2.01	0.41
23:AF:255:VAL:HA	23:AF:276:SER:HA	2.02	0.41
24:AG:386:ASN:HD21	24:AG:389:LEU:HD11	1.86	0.41
24:AG:455:SER:O	24:AG:455:SER:OG	2.34	0.41
25:B1:6:LYS:HD3	25:B1:6:LYS:HA	1.91	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:B1:46:LYS:HE2	25:B1:46:LYS:HB3	1.87	0.41
29:BE:361:SER:HA	29:BE:636:PRO:HB2	2.02	0.41
29:BE:495:ARG:HD3	29:BE:495:ARG:HA	1.84	0.41
32:5C:244:ASN:HB3	32:5C:446:PRO:HG3	2.02	0.41
34:5E:427:SER:O	34:5E:431:GLN:HB2	2.19	0.41
39:5J:106:LEU:O	39:5J:146:ARG:NH1	2.44	0.41
41:RC:180:LEU:HA	41:RC:183:VAL:HG12	2.01	0.41
45:RG:215:ASN:HB2	45:RG:218:ASP:HB2	2.01	0.41
46:RI:215:ASN:HA	46:RI:218:ASP:HB2	2.03	0.41
2:5A:490:G:H1'	2:5A:495:G:H5'	2.01	0.41
3:SA:867:G:H21	7:SO:87:ASP:CG	2.29	0.41
3:SA:939:A:H2'	3:SA:940:A:C8	2.56	0.41
3:SA:1658:G:N1	3:SA:1743:U:C6	2.88	0.41
12:Sd:43:ASN:OD1	12:Sd:43:ASN:N	2.53	0.41
16:3F:321:HIS:CE1	16:3F:340:GLY:H	2.39	0.41
23:AF:115:THR:O	23:AF:115:THR:OG1	2.35	0.41
24:AG:511:GLU:HG2	24:AG:528:ILE:HB	2.00	0.41
24:AG:625:GLY:HA3	24:AG:662:VAL:HG11	2.02	0.41
25:B1:275:LEU:HB2	25:B1:289:LEU:HD22	2.02	0.41
25:B1:300:MET:HG2	25:B1:328:LEU:HD22	2.01	0.41
25:B1:363:ALA:HB2	25:B1:393:VAL:HG13	2.02	0.41
25:B1:501:SER:O	25:B1:506:SER:OG	2.37	0.41
26:B2:433:ALA:HA	26:B2:449:THR:HA	2.03	0.41
26:B2:538:ARG:HD3	26:B2:580:ASP:HA	2.02	0.41
28:B8:296:GLN:HB3	28:B8:316:GLY:HA2	2.03	0.41
29:BE:21:SER:OG	29:BE:621:ASP:OD2	2.29	0.41
30:B6:106:ASP:OD1	30:B6:106:ASP:N	2.38	0.41
32:5C:357:SER:O	32:5C:357:SER:OG	2.38	0.41
35:5F:135:HIS:HB3	35:5F:160:TRP:CD1	2.55	0.41
36:5G:42:LEU:HD12	36:5G:43:PRO:HD2	2.02	0.41
38:5I:58:PHE:HE1	38:5I:373:ARG:HB3	1.85	0.41
38:5I:336:HIS:CE1	38:5I:338:HIS:HB2	2.55	0.41
41:RC:52:TYR:CE1	41:RC:56:ILE:CG2	3.01	0.41
46:RI:192:ASN:N	46:RI:192:ASN:OD1	2.53	0.41
47:RJ:802:LYS:HB2	47:RJ:802:LYS:HE3	1.92	0.41
47:RJ:1080:LYS:HA	47:RJ:1080:LYS:HD2	1.80	0.41
54:RW:180:LYS:HB2	54:RW:180:LYS:HE2	1.82	0.41
3:SA:1489:U:N3	39:5J:202:ARG:O	2.53	0.41
13:3C:89:GLU:HG2	13:3C:98:ILE:HB	2.03	0.41
13:3C:151:LEU:HD13	13:3C:241:PHE:HE1	1.86	0.41
14:3D:268:MET:HA	14:3D:271:VAL:HG12	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:3F:457:GLU:HG3	16:3F:461:LYS:HE2	2.02	0.41
18:A4:313:LYS:HA	18:A4:316:LYS:HZ3	1.84	0.41
18:A4:389:ARG:HG2	18:A4:747:ILE:HG21	2.02	0.41
18:A4:428:ILE:HD12	18:A4:444:ARG:HH21	1.85	0.41
20:A8:632:THR:HG22	21:A9:492:ILE:HD13	2.01	0.41
21:A9:416:ILE:O	21:A9:420:ILE:CB	2.69	0.41
22:AE:35:TYR:O	22:AE:150:ARG:NH1	2.53	0.41
22:AE:91:ILE:HD13	22:AE:91:ILE:HA	1.90	0.41
22:AE:480:ASN:HA	22:AE:518:THR:HG21	2.02	0.41
22:AE:526:LEU:HA	22:AE:529:VAL:HG12	2.02	0.41
23:AF:34:GLN:O	23:AF:328:ALA:HA	2.21	0.41
23:AF:392:ILE:HD11	23:AF:417:VAL:HG23	2.03	0.41
24:AG:97:THR:OG1	24:AG:98:VAL:N	2.54	0.41
26:B2:50:ASN:HB3	26:B2:62:LYS:HG3	2.02	0.41
26:B2:241:LYS:HB2	26:B2:241:LYS:HE3	1.89	0.41
27:B3:68:LYS:HE3	27:B3:68:LYS:HB3	1.81	0.41
29:BE:62:ASP:O	29:BE:66:LEU:N	2.48	0.41
30:B6:268:ASP:N	30:B6:268:ASP:OD1	2.53	0.41
30:B6:311:TYR:O	30:B6:315:GLU:HG2	2.21	0.41
36:5G:33:LYS:HB2	36:5G:33:LYS:HE3	1.79	0.41
38:5I:141:ASP:N	38:5I:141:ASP:OD1	2.49	0.41
39:5J:117:VAL:HG11	39:5J:149:ILE:HG13	2.02	0.41
41:RC:62:ARG:NH2	41:RC:63:ALA:HB2	2.35	0.41
43:RE:254:LEU:HD21	43:RE:268:LEU:HB3	2.02	0.41
43:RE:924:LEU:HD11	43:RE:1183:THR:HG22	2.01	0.41
43:RE:928:HIS:HB2	43:RE:1060:ILE:HG21	2.03	0.41
44:RF:91:ASP:O	44:RF:121:ARG:NH2	2.54	0.41
47:RJ:244:MET:HE2	47:RJ:271:ILE:HG22	2.01	0.41
49:RN:456:ILE:HA	49:RN:456:ILE:HD13	1.79	0.41
49:RN:611:SER:OG	49:RN:612:THR:N	2.52	0.41
49:RN:644:ASP:OD1	49:RN:687:LYS:NZ	2.51	0.41
49:RN:710:ILE:HD13	49:RN:710:ILE:HA	1.91	0.41
51:RQ:313:PHE:HE2	51:RQ:883:ILE:HD12	1.84	0.41
2:5A:474:A:OP2	32:5C:425:ARG:NH2	2.37	0.41
3:SA:1523:G:H1'	3:SA:1524:A:H5'	2.02	0.41
7:SO:106:ARG:NH2	7:SO:106:ARG:CG	2.72	0.41
16:3F:304:ILE:HB	16:3F:318:LEU:HG	2.03	0.41
18:A4:141:SER:O	18:A4:141:SER:OG	2.34	0.41
19:A5:64:LYS:HB3	19:A5:77:ILE:HG13	2.02	0.41
22:AE:32:SER:OG	22:AE:33:LEU:N	2.54	0.41
22:AE:33:LEU:HD11	22:AE:151:ILE:HG22	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AE:109:TRP:HB2	22:AE:142:TYR:CZ	2.56	0.41
25:B1:347:SER:HB2	25:B1:365:GLU:HB3	2.03	0.41
25:B1:559:ILE:HG21	25:B1:578:LYS:HA	2.03	0.41
27:B3:310:THR:HA	27:B3:335:GLY:HA2	2.02	0.41
27:B3:459:ASN:HA	27:B3:494:ILE:HD11	2.03	0.41
27:B3:495:ASN:N	27:B3:510:SER:OG	2.49	0.41
27:B3:801:GLU:HB3	29:BE:927:LYS:HD2	2.01	0.41
28:B8:159:HIS:O	28:B8:163:ARG:HG2	2.21	0.41
30:B6:306:LYS:HE3	30:B6:306:LYS:HB2	1.77	0.41
40:5K:138:ASP:OD1	40:5K:160:LEU:HD22	2.20	0.41
43:RE:508:SER:HA	43:RE:512:LEU:HB2	2.03	0.41
44:RF:23:HIS:HD2	44:RF:26:LEU:HG	1.85	0.41
49:RN:784:ILE:HA	49:RN:787:THR:HG22	2.03	0.41
2:5A:244:U:H1'	33:5D:93:MET:HE1	2.02	0.41
2:5A:248:G:OP1	33:5D:82:ARG:NH2	2.53	0.41
2:5A:485:G:N2	38:5I:386:LYS:O	2.41	0.41
3:SA:575:C:O2	47:RJ:1052:SER:OG	2.28	0.41
3:SA:899:G:H2'	3:SA:900:A:H8	1.85	0.41
10:ST:26:ILE:HG13	10:ST:31:ALA:HB2	2.03	0.41
15:3E:192:PHE:CD2	15:3E:195:LEU:HB2	2.56	0.41
15:3E:283:ILE:HD13	15:3E:283:ILE:HA	1.88	0.41
16:3F:308:SER:OG	16:3F:313:SER:OG	2.36	0.41
21:A9:475:THR:HA	21:A9:478:ASN:HD22	1.86	0.41
22:AE:214:THR:HG23	22:AE:260:ILE:HG13	2.03	0.41
22:AE:241:ILE:HD12	22:AE:241:ILE:HA	1.93	0.41
22:AE:572:ARG:NH2	22:AE:632:THR:O	2.40	0.41
25:B1:423:ARG:HD3	25:B1:423:ARG:HA	1.88	0.41
28:B8:137:ILE:HD13	28:B8:137:ILE:HA	1.86	0.41
36:5G:9:ARG:HD3	36:5G:159:HIS:CD2	2.56	0.41
37:5H:542:TYR:CZ	37:5H:546:LYS:HG3	2.56	0.41
39:5J:51:LYS:HE2	39:5J:51:LYS:HB2	1.95	0.41
43:RE:109:GLU:OE2	43:RE:113:GLN:NE2	2.47	0.41
43:RE:219:PHE:HZ	43:RE:303:PHE:CD2	2.35	0.41
43:RE:219:PHE:HZ	43:RE:303:PHE:CE2	2.37	0.41
43:RE:498:MET:O	43:RE:506:GLN:NE2	2.42	0.41
45:RG:34:LYS:HD3	45:RG:34:LYS:HA	1.84	0.41
45:RG:116:THR:HG22	45:RG:118:ARG:H	1.86	0.41
45:RG:232:LEU:HB3	45:RG:236:VAL:HG13	2.03	0.41
47:RJ:926:ILE:HG12	47:RJ:928:ILE:HG23	2.01	0.41
48:RK:32:LYS:HG2	48:RK:75:ILE:HG13	2.02	0.41
49:RN:283:ALA:HA	52:RS:381:ALA:HB1	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RO:226:ASP:OD1	50:RO:284:ARG:NE	2.54	0.41
2:5A:333:G:H5'	35:5F:49:ARG:HE	1.86	0.41
3:SA:976:G:N2	3:SA:978:A:C4	2.89	0.41
3:SA:1538:U:H1'	3:SA:1570:A:H61	1.84	0.41
8:SP:46:MET:O	8:SP:46:MET:SD	2.79	0.41
8:SP:70:LYS:HA	8:SP:73:GLU:HG2	2.02	0.41
13:3B:104:ASP:OD1	13:3B:104:ASP:N	2.38	0.41
14:3D:157:ALA:HB2	30:B6:292:TYR:CZ	2.56	0.41
16:3F:465:GLN:HG2	17:3H:6:PRO:HG3	2.02	0.41
18:A4:39:VAL:HG12	18:A4:41:PHE:H	1.85	0.41
18:A4:425:ASP:OD2	18:A4:444:ARG:NH2	2.53	0.41
19:A5:551:ILE:HA	19:A5:554:PHE:CE2	2.56	0.41
24:AG:514:TYR:HA	24:AG:515:PRO:HD3	1.94	0.41
27:B3:339:ILE:HG22	27:B3:638:ASP:HB2	2.03	0.41
28:B8:278:ASP:H	28:B8:282:ASN:HD22	1.67	0.41
43:RE:312:ARG:HH21	43:RE:333:ASN:HB3	1.86	0.41
45:RG:233:SER:OG	45:RG:234:ALA:N	2.54	0.41
47:RJ:193:ARG:HA	47:RJ:193:ARG:HD2	1.88	0.41
47:RJ:906:ASP:OD1	47:RJ:906:ASP:N	2.45	0.41
2:5A:211:G:OP1	31:5B:161:LYS:NZ	2.54	0.41
2:5A:329:A:O2'	2:5A:331:U:OP2	2.39	0.41
3:SA:976:G:N1	3:SA:978:A:H2'	2.36	0.41
3:SA:1689:A:H2	3:SA:1712:A:H62	1.67	0.41
6:SN:83:GLU:HG3	6:SN:85:LYS:HB2	2.03	0.41
6:SN:135:MET:HG3	6:SN:139:HIS:CE1	2.56	0.41
14:3D:7:LEU:HD12	14:3D:99:ALA:HB3	2.02	0.41
15:3E:201:ASP:HB3	15:3E:204:ALA:HB3	2.03	0.41
15:3E:359:ILE:HD13	15:3E:398:LEU:HD13	2.03	0.41
16:3F:132:VAL:HG21	16:3F:505:LEU:HD21	2.02	0.41
16:3F:345:THR:HG1	16:3F:358:THR:HG1	1.68	0.41
16:3F:488:ILE:HG22	16:3F:524:ILE:HD13	2.02	0.41
17:3G:85:VAL:O	17:3G:89:ARG:HG2	2.21	0.41
18:A4:394:TRP:HB3	18:A4:399:VAL:HG12	2.03	0.41
18:A4:581:SER:HA	18:A4:594:PHE:O	2.21	0.41
21:A9:460:LEU:HD23	21:A9:460:LEU:HA	1.96	0.41
22:AE:227:ASN:OD1	22:AE:227:ASN:N	2.53	0.41
22:AE:328:ASP:N	22:AE:328:ASP:OD1	2.49	0.41
24:AG:591:GLU:O	24:AG:593:ASN:N	2.54	0.41
24:AG:712:THR:HG22	24:AG:766:ILE:HG23	2.01	0.41
25:B1:652:ASP:N	25:B1:652:ASP:OD1	2.52	0.41
26:B2:17:ILE:CG2	26:B2:52:TRP:CH2	3.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:B2:911:GLN:HA	26:B2:914:LEU:HG	2.03	0.41
29:BE:870:GLN:HA	29:BE:873:LYS:HE3	2.03	0.41
32:5C:307:LYS:HA	32:5C:307:LYS:HD3	1.89	0.41
33:5D:70:ARG:HD3	33:5D:78:LEU:HD11	2.02	0.41
34:5E:465:LEU:HD12	34:5E:465:LEU:HA	1.96	0.41
43:RE:205:THR:HG21	43:RE:294:LEU:HA	2.03	0.41
43:RE:528:ASP:OD1	43:RE:697:SER:N	2.47	0.41
43:RE:794:ASP:OD1	43:RE:865:ARG:NH2	2.45	0.41
43:RE:870:ALA:HA	44:RF:103:LEU:HD21	2.03	0.41
43:RE:1146:THR:HG21	43:RE:1180:ASN:HD22	1.86	0.41
45:RG:40:ARG:O	45:RG:201:SER:HA	2.20	0.41
47:RJ:74:VAL:HG11	47:RJ:82:LYS:HA	2.03	0.41
48:RK:117:LEU:HA	48:RK:166:VAL:O	2.21	0.41
49:RN:504:ILE:HA	49:RN:507:LEU:HG	2.03	0.41
49:RN:668:LEU:HD23	49:RN:671:TYR:HD2	1.86	0.41
52:RS:238:SER:O	52:RS:238:SER:OG	2.33	0.41
52:RS:288:ARG:O	52:RS:292:GLU:HG2	2.21	0.41
52:RS:407:GLU:HB2	52:RS:411:ARG:HD2	2.03	0.41
1:3A:253:G:OP2	17:3H:95:ARG:NH1	2.54	0.41
2:5A:18:G:H2'	2:5A:19:A:H8	1.85	0.41
2:5A:210:U:H2'	2:5A:211:G:C8	2.55	0.41
2:5A:254:C:OP2	54:RW:184:TYR:OH	2.31	0.41
3:SA:909:U:H2'	3:SA:910:C:H6	1.86	0.41
3:SA:1648:A:H2'	3:SA:1649:G:C8	2.55	0.41
7:SO:45:LEU:HD21	7:SO:53:LEU:HD12	2.03	0.41
7:SO:104:ARG:HA	42:RD:1542:GLN:C	2.46	0.41
13:3C:202:ARG:HA	13:3C:202:ARG:HD2	1.96	0.41
15:3E:299:LEU:HD22	15:3E:320:LEU:HD23	2.03	0.41
15:3E:367:ALA:O	15:3E:371:LEU:HB3	2.21	0.41
17:3G:41:THR:HG21	17:3G:66:HIS:CE1	2.55	0.41
20:A8:539:ASN:OD1	20:A8:539:ASN:N	2.46	0.41
20:A8:670:GLU:OE2	23:AF:499:LYS:NZ	2.45	0.41
22:AE:597:HIS:HB3	22:AE:615:ASN:HB3	2.03	0.41
23:AF:397:TRP:CZ3	23:AF:425:GLY:HA3	2.56	0.41
23:AF:426:LYS:HB3	23:AF:429:VAL:HB	2.03	0.41
24:AG:334:LEU:HA	24:AG:335:PRO:HD3	1.85	0.41
24:AG:439:ASN:ND2	24:AG:496:THR:O	2.54	0.41
26:B2:164:ASP:HB3	26:B2:182:LYS:HB3	2.02	0.41
28:B8:278:ASP:H	28:B8:282:ASN:ND2	2.18	0.41
29:BE:743:ARG:HB2	34:5E:475:SER:HA	2.02	0.41
29:BE:927:LYS:HD3	29:BE:927:LYS:HA	1.92	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:5F:181:ASP:OD1	35:5F:181:ASP:N	2.42	0.41
43:RE:236:THR:HA	43:RE:239:LEU:HB2	2.03	0.41
43:RE:807:LEU:HB3	43:RE:840:LEU:HD23	2.02	0.41
44:RF:41:ARG:HA	44:RF:53:LEU:HA	2.02	0.41
45:RH:177:LYS:HG2	45:RH:203:CYS:HB3	2.02	0.41
2:5A:423:C:H2'	2:5A:424:G:H8	1.86	0.40
7:SO:90:TYR:HA	7:SO:93:LYS:HG2	2.02	0.40
18:A4:52:SER:HA	18:A4:104:TRP:CG	2.56	0.40
22:AE:69:PHE:HE2	22:AE:104:LEU:HD13	1.85	0.40
23:AF:136:ASP:OD1	23:AF:137:ASN:N	2.54	0.40
24:AG:29:THR:HB	24:AG:198:LEU:HD11	2.03	0.40
24:AG:409:LYS:HG2	24:AG:489:ASN:HA	2.03	0.40
25:B1:519:LEU:HD13	25:B1:581:THR:HG22	2.04	0.40
29:BE:205:PHE:HA	29:BE:206:PRO:HD3	1.91	0.40
39:5J:77:LYS:HA	39:5J:77:LYS:HD2	1.84	0.40
41:RC:62:ARG:C	41:RC:62:ARG:HD2	2.46	0.40
43:RE:168:ILE:HD12	43:RE:170:GLN:HE21	1.86	0.40
43:RE:248:LEU:HD12	43:RE:252:LEU:HD12	2.02	0.40
43:RE:708:LEU:HA	43:RE:709:PRO:HD3	1.94	0.40
46:RI:46:MET:H	46:RI:46:MET:HG2	1.65	0.40
46:RI:105:ASN:N	46:RI:105:ASN:OD1	2.48	0.40
48:RK:184:ASP:OD1	48:RK:185:ARG:N	2.53	0.40
49:RN:424:LYS:O	49:RN:428:VAL:HG23	2.20	0.40
53:RT:255:PRO:HA	53:RT:256:PRO:HD3	1.99	0.40
3:SA:16:G:H4'	40:5K:159:GLY:HA2	2.03	0.40
3:SA:973:A:H2'	3:SA:974:A:C8	2.56	0.40
13:3B:134:VAL:HA	13:3B:135:PRO:HD3	1.89	0.40
15:3E:88:ILE:HA	15:3E:106:ASN:O	2.22	0.40
15:3E:163:ILE:HD13	15:3E:163:ILE:HA	1.86	0.40
24:AG:560:ILE:HG22	24:AG:575:THR:HG22	2.03	0.40
25:B1:263:VAL:HG13	25:B1:277:VAL:HG13	2.03	0.40
25:B1:430:ARG:HH21	34:5E:458:PRO:HB2	1.85	0.40
27:B3:344:ARG:HE	27:B3:395:ASP:HA	1.86	0.40
28:B8:231:LYS:HA	28:B8:231:LYS:HD2	1.91	0.40
29:BE:290:ILE:HG23	29:BE:291:HIS:CD2	2.56	0.40
30:B6:26:LYS:HA	30:B6:29:VAL:HG12	2.03	0.40
31:5B:180:LEU:HD13	31:5B:180:LEU:HA	1.94	0.40
32:5C:340:LEU:HD22	32:5C:403:VAL:HG11	2.03	0.40
35:5F:73:LYS:HE2	35:5F:73:LYS:HB3	1.88	0.40
39:5J:195:GLN:O	39:5J:199:THR:HG22	2.22	0.40
43:RE:261:ASN:OD1	43:RE:588:GLN:NE2	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:RG:123:GLU:HB2	45:RG:161:LYS:HB2	2.03	0.40
47:RJ:563:CYS:SG	48:RK:327:ARG:NH2	2.95	0.40
50:RO:326:LEU:HD12	50:RO:326:LEU:HA	1.90	0.40
52:RS:245:VAL:O	52:RS:249:THR:HG23	2.22	0.40
3:SA:997:G:H2'	3:SA:998:A:C8	2.56	0.40
15:3E:162:MET:HB3	15:3E:162:MET:HE2	1.86	0.40
15:3E:287:LEU:HD12	15:3E:287:LEU:HA	1.90	0.40
18:A4:202:ILE:HD13	18:A4:253:ILE:HG12	2.03	0.40
18:A4:250:THR:OG1	18:A4:251:ASP:N	2.53	0.40
22:AE:677:SER:HA	22:AE:678:PRO:HD3	1.98	0.40
23:AF:371:GLU:HG3	28:B8:287:SER:OG	2.21	0.40
28:B8:174:ARG:NE	28:B8:179:ASP:OD2	2.44	0.40
29:BE:83:LEU:HA	29:BE:91:TYR:O	2.21	0.40
32:5C:504:LYS:HD3	32:5C:504:LYS:HA	1.82	0.40
39:5J:119:ARG:HD3	47:RJ:1113:ILE:HG13	2.02	0.40
41:RC:57:TRP:CD2	41:RC:73:LEU:HD22	2.56	0.40
41:RC:74:ASP:CG	41:RC:77:GLU:HG2	2.47	0.40
43:RE:225:LEU:HA	43:RE:228:ARG:HB3	2.03	0.40
45:RG:85:SER:OG	45:RG:86:GLU:OE1	2.39	0.40
46:RI:220:ILE:O	46:RI:224:THR:HG22	2.21	0.40
52:RS:446:GLN:HG2	52:RS:447:ARG:HE	1.86	0.40
3:SA:1480:G:H2'	3:SA:1481:C:O4'	2.22	0.40
7:SO:101:HIS:HA	7:SO:104:ARG:NH2	2.37	0.40
15:3E:169:LEU:HD23	15:3E:169:LEU:HA	1.92	0.40
15:3E:215:ARG:NH1	15:3E:244:GLY:O	2.54	0.40
15:3E:388:LEU:HD12	15:3E:388:LEU:HA	1.89	0.40
19:A5:444:ALA:HB2	19:A5:452:LEU:HD12	2.03	0.40
20:A8:532:PHE:HD1	20:A8:534:LEU:H	1.69	0.40
20:A8:642:LEU:HD12	21:A9:499:ILE:HG23	2.04	0.40
22:AE:401:VAL:O	22:AE:405:GLU:HG2	2.22	0.40
23:AF:57:VAL:HG21	23:AF:327:LEU:HD11	2.04	0.40
23:AF:178:PRO:HD2	23:AF:223:PRO:HA	2.02	0.40
23:AF:420:GLU:OE1	23:AF:424:ARG:NH1	2.37	0.40
25:B1:64:ASN:OD1	25:B1:64:ASN:N	2.49	0.40
25:B1:523:MET:HE2	25:B1:523:MET:HB2	1.76	0.40
26:B2:85:LEU:HD12	26:B2:94:LEU:HD11	2.04	0.40
26:B2:639:VAL:HG22	26:B2:653:LEU:HB2	2.03	0.40
27:B3:364:ILE:O	27:B3:381:VAL:HA	2.21	0.40
27:B3:761:ARG:HG2	27:B3:765:MET:HE3	2.03	0.40
27:B3:816:LEU:HD12	27:B3:816:LEU:C	2.39	0.40
29:BE:523:ASP:OD1	29:BE:523:ASP:N	2.38	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5C:114:TYR:HA	32:5C:128:THR:O	2.22	0.40
38:5I:467:LYS:H	38:5I:467:LYS:HG2	1.69	0.40
43:RE:492:ALA:HA	43:RE:495:THR:HG22	2.03	0.40
46:RI:85:GLU:O	46:RI:89:LYS:HG2	2.22	0.40
48:RK:113:LYS:HG2	48:RK:173:LEU:HD11	2.03	0.40
50:RO:439:LYS:HE2	50:RO:439:LYS:HB3	1.83	0.40
53:RT:247:VAL:HA	53:RT:250:LEU:HD23	2.04	0.40
3:SA:514:G:H2'	3:SA:515:A:H8	1.87	0.40
3:SA:1463:C:H2'	3:SA:1464:G:O4'	2.22	0.40
13:3B:227:PRO:HG2	13:3B:255:LEU:HB3	2.02	0.40
13:3C:165:ALA:HB3	13:3C:168:LYS:HD3	2.04	0.40
14:3D:86:LEU:HD21	14:3D:98:LEU:HD13	2.03	0.40
15:3E:306:LEU:HG	15:3E:375:ALA:HB2	2.04	0.40
16:3F:263:TRP:HA	16:3F:269:SER:O	2.22	0.40
17:3H:33:LEU:HD11	17:3H:100:ALA:HB1	2.03	0.40
19:A5:35:GLN:OE1	19:A5:36:ARG:N	2.55	0.40
19:A5:201:PHE:CZ	19:A5:223:LYS:HD2	2.56	0.40
24:AG:377:SER:HB2	28:B8:342:PHE:HE1	1.85	0.40
24:AG:869:MET:N	24:AG:869:MET:SD	2.95	0.40
25:B1:302:GLN:CD	25:B1:302:GLN:N	2.79	0.40
25:B1:567:ASP:HB3	35:5F:144:ASN:ND2	2.36	0.40
26:B2:850:LEU:HD23	26:B2:850:LEU:HA	1.90	0.40
27:B3:69:LEU:HD13	27:B3:109:ASP:HA	2.02	0.40
27:B3:171:MET:HB3	27:B3:187:GLN:NE2	2.37	0.40
30:B6:110:TRP:CD2	30:B6:136:LEU:HD13	2.56	0.40
32:5C:191:ILE:HD13	32:5C:191:ILE:HA	1.87	0.40
32:5C:201:TYR:OH	32:5C:415:GLU:OE1	2.29	0.40
35:5F:19:LEU:HD11	40:5K:24:ARG:HB3	2.04	0.40
38:5I:231:GLU:HG2	51:RQ:298:TRP:HE1	1.86	0.40
38:5I:450:ASP:OD1	38:5I:450:ASP:N	2.55	0.40
43:RE:691:SER:OG	43:RE:692:LYS:N	2.54	0.40
45:RH:52:THR:HA	45:RH:66:VAL:O	2.22	0.40
47:RJ:552:LEU:HD23	47:RJ:552:LEU:HA	1.92	0.40
48:RK:247:ALA:O	48:RK:255:SER:HA	2.22	0.40
49:RN:14:LYS:HA	49:RN:14:LYS:HD2	1.84	0.40
50:RO:205:ASP:HA	50:RO:206:PRO:HD3	1.90	0.40
50:RO:295:LEU:O	50:RO:299:LEU:HG	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
5	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
6	SN	117/143 (82%)	89 (76%)	28 (24%)	0	100	100
7	SO	132/151 (87%)	121 (92%)	10 (8%)	1 (1%)	16	53
8	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	14	49
9	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
10	ST	113/146 (77%)	103 (91%)	10 (9%)	0	100	100
11	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
12	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
13	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
13	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
14	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
15	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
16	3F	400/573 (70%)	362 (90%)	37 (9%)	1 (0%)	36	71
17	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	16	53
17	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
18	A4	648/776 (84%)	591 (91%)	57 (9%)	0	100	100
19	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
20	A8	534/713 (75%)	398 (74%)	134 (25%)	2 (0%)	30	67
21	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
22	AE	645/1769 (36%)	595 (92%)	50 (8%)	0	100	100
23	AF	489/513 (95%)	442 (90%)	47 (10%)	0	100	100
24	AG	812/896 (91%)	732 (90%)	79 (10%)	1 (0%)	48	83
25	B1	830/923 (90%)	767 (92%)	63 (8%)	0	100	100
26	B2	839/943 (89%)	748 (89%)	89 (11%)	2 (0%)	43	77

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	B3	728/817 (89%)	595 (82%)	131 (18%)	2 (0%)	36	71
28	B8	469/594 (79%)	438 (93%)	31 (7%)	0	100	100
29	BE	857/939 (91%)	803 (94%)	54 (6%)	0	100	100
30	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100	100
31	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
32	5C	512/554 (92%)	474 (93%)	37 (7%)	1 (0%)	43	77
33	5D	231/250 (92%)	205 (89%)	26 (11%)	0	100	100
34	5E	200/593 (34%)	183 (92%)	16 (8%)	1 (0%)	24	63
35	5F	180/183 (98%)	172 (96%)	8 (4%)	0	100	100
36	5G	278/290 (96%)	256 (92%)	22 (8%)	0	100	100
37	5H	132/610 (22%)	123 (93%)	9 (7%)	0	100	100
38	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
39	5J	147/217 (68%)	136 (92%)	11 (8%)	0	100	100
40	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
41	RC	173/316 (55%)	169 (98%)	4 (2%)	0	100	100
42	RD	263/1729 (15%)	254 (97%)	9 (3%)	0	100	100
43	RE	1067/1237 (86%)	998 (94%)	69 (6%)	0	100	100
44	RF	168/297 (57%)	145 (86%)	23 (14%)	0	100	100
45	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
45	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
46	RI	250/274 (91%)	233 (93%)	17 (7%)	0	100	100
47	RJ	722/1183 (61%)	670 (93%)	51 (7%)	1 (0%)	48	83
48	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
49	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	43	77
50	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
51	RQ	188/899 (21%)	177 (94%)	11 (6%)	0	100	100
52	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
53	RT	165/326 (51%)	150 (91%)	15 (9%)	0	100	100
54	RW	59/206 (29%)	54 (92%)	5 (8%)	0	100	100
All	All	18453/27161 (68%)	16810 (91%)	1628 (9%)	15 (0%)	49	83

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	5E	454	VAL
7	SO	106	ARG
8	SP	45	GLY
47	RJ	82	LYS
20	A8	309	PRO
24	AG	434	GLN
26	B2	132	THR
27	B3	236	THR
49	RN	285	PRO
16	3F	552	TRP
20	A8	308	PHE
26	B2	118	ASN
27	B3	71	PRO
32	5C	16	GLU
17	3G	10	PRO

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	SG	180/191 (94%)	179 (99%)	1 (1%)	78	80
5	SK	147/166 (89%)	147 (100%)	0	100	100
6	SN	88/119 (74%)	87 (99%)	1 (1%)	65	74
7	SO	117/128 (91%)	115 (98%)	2 (2%)	53	67
8	SP	90/105 (86%)	89 (99%)	1 (1%)	65	74
9	SR	105/119 (88%)	105 (100%)	0	100	100
10	ST	105/129 (81%)	105 (100%)	0	100	100
11	SY	85/120 (71%)	83 (98%)	2 (2%)	43	63
12	Sd	56/60 (93%)	56 (100%)	0	100	100
13	3B	201/240 (84%)	201 (100%)	0	100	100
13	3C	190/240 (79%)	188 (99%)	2 (1%)	65	74
14	3D	296/435 (68%)	295 (100%)	1 (0%)	86	84
15	3E	262/433 (60%)	261 (100%)	1 (0%)	84	82

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	3F	354/503 (70%)	350 (99%)	4 (1%)	65	74
17	3G	100/104 (96%)	100 (100%)	0	100	100
17	3H	100/104 (96%)	100 (100%)	0	100	100
18	A4	591/713 (83%)	584 (99%)	7 (1%)	63	73
19	A5	433/574 (75%)	429 (99%)	4 (1%)	70	76
20	A8	174/657 (26%)	173 (99%)	1 (1%)	78	80
21	A9	89/533 (17%)	89 (100%)	0	100	100
22	AE	589/1633 (36%)	587 (100%)	2 (0%)	86	84
23	AF	437/454 (96%)	431 (99%)	6 (1%)	59	71
24	AG	750/826 (91%)	739 (98%)	11 (2%)	57	70
25	B1	730/812 (90%)	720 (99%)	10 (1%)	59	71
26	B2	736/832 (88%)	729 (99%)	7 (1%)	68	76
27	B3	660/719 (92%)	644 (98%)	16 (2%)	43	63
28	B8	421/529 (80%)	417 (99%)	4 (1%)	68	76
29	BE	757/819 (92%)	752 (99%)	5 (1%)	76	79
30	B6	251/414 (61%)	249 (99%)	2 (1%)	73	77
31	5B	57/196 (29%)	56 (98%)	1 (2%)	51	67
32	5C	448/480 (93%)	445 (99%)	3 (1%)	76	79
33	5D	221/234 (94%)	221 (100%)	0	100	100
34	5E	185/535 (35%)	185 (100%)	0	100	100
35	5F	171/172 (99%)	168 (98%)	3 (2%)	51	67
36	5G	251/258 (97%)	246 (98%)	5 (2%)	48	65
37	5H	107/538 (20%)	107 (100%)	0	100	100
38	5I	416/443 (94%)	412 (99%)	4 (1%)	68	76
39	5J	140/200 (70%)	140 (100%)	0	100	100
40	5K	157/169 (93%)	157 (100%)	0	100	100
41	RC	158/289 (55%)	156 (99%)	2 (1%)	61	72
43	RE	984/1125 (88%)	972 (99%)	12 (1%)	63	73
44	RF	159/274 (58%)	157 (99%)	2 (1%)	61	72
45	RG	195/222 (88%)	193 (99%)	2 (1%)	68	76
45	RH	206/222 (93%)	205 (100%)	1 (0%)	81	81

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	RI	235/256 (92%)	234 (100%)	1 (0%)	84	82
47	RJ	648/1039 (62%)	643 (99%)	5 (1%)	73	77
48	RK	307/312 (98%)	304 (99%)	3 (1%)	68	76
49	RN	422/732 (58%)	422 (100%)	0	100	100
50	RO	329/506 (65%)	326 (99%)	3 (1%)	70	76
51	RQ	132/808 (16%)	129 (98%)	3 (2%)	44	63
52	RS	225/424 (53%)	224 (100%)	1 (0%)	84	82
53	RT	148/282 (52%)	148 (100%)	0	100	100
54	RW	22/192 (12%)	21 (96%)	1 (4%)	24	46
All	All	15417/22619 (68%)	15275 (99%)	142 (1%)	68	76

All (142) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	SG	149	VAL
6	SN	66	VAL
7	SO	106	ARG
7	SO	109	LYS
8	SP	46	MET
11	SY	97	ASP
11	SY	120	VAL
13	3C	197	VAL
13	3C	237	VAL
14	3D	219	LEU
15	3E	371	LEU
16	3F	262	VAL
16	3F	273	VAL
16	3F	301	ASP
16	3F	408	VAL
18	A4	176	VAL
18	A4	190	VAL
18	A4	201	VAL
18	A4	282	ASP
18	A4	384	VAL
18	A4	391	VAL
18	A4	550	VAL
19	A5	95	VAL
19	A5	214	VAL
19	A5	357	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
19	A5	434	THR
20	A8	563	LEU
22	AE	210	LEU
22	AE	227	ASN
23	AF	107	VAL
23	AF	129	VAL
23	AF	218	VAL
23	AF	236	VAL
23	AF	261	VAL
23	AF	508	LEU
24	AG	109	VAL
24	AG	141	LEU
24	AG	259	VAL
24	AG	368	ASP
24	AG	391	VAL
24	AG	434	GLN
24	AG	435	ASP
24	AG	436	PHE
24	AG	508	ILE
24	AG	547	VAL
24	AG	650	VAL
25	B1	89	VAL
25	B1	141	VAL
25	B1	164	THR
25	B1	215	VAL
25	B1	351	LEU
25	B1	497	ILE
25	B1	519	LEU
25	B1	530	VAL
25	B1	661	LEU
25	B1	745	LEU
26	B2	47	GLU
26	B2	49	VAL
26	B2	144	ASN
26	B2	212	VAL
26	B2	332	ILE
26	B2	576	VAL
26	B2	588	ILE
27	B3	12	LEU
27	B3	13	ASN
27	B3	107	ILE
27	B3	150	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	B3	220	ILE
27	B3	240	ASN
27	B3	413	ILE
27	B3	479	ILE
27	B3	482	VAL
27	B3	533	LYS
27	B3	649	GLU
27	B3	657	GLU
27	B3	658	LYS
27	B3	721	ASN
27	B3	805	ILE
27	B3	816	LEU
28	B8	22	LEU
28	B8	146	LEU
28	B8	178	VAL
28	B8	544	VAL
29	BE	298	VAL
29	BE	309	ILE
29	BE	570	ILE
29	BE	600	ILE
29	BE	721	LEU
30	B6	4	THR
30	B6	106	ASP
31	5B	211	LEU
32	5C	153	THR
32	5C	392	VAL
32	5C	507	ASN
35	5F	32	VAL
35	5F	102	THR
35	5F	159	THR
36	5G	176	ILE
36	5G	209	LEU
36	5G	222	ILE
36	5G	239	VAL
36	5G	245	VAL
38	5I	14	VAL
38	5I	113	VAL
38	5I	201	ILE
38	5I	351	VAL
41	RC	62	ARG
41	RC	200	ILE
43	RE	216	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
43	RE	243	LEU
43	RE	303	PHE
43	RE	308	LEU
43	RE	309	LEU
43	RE	365	LEU
43	RE	368	LEU
43	RE	400	LEU
43	RE	503	VAL
43	RE	562	LEU
43	RE	730	LEU
43	RE	1087	LEU
44	RF	103	LEU
44	RF	180	LEU
45	RG	32	THR
45	RG	100	LEU
45	RH	31	LEU
46	RI	17	LEU
47	RJ	288	VAL
47	RJ	859	ILE
47	RJ	869	THR
47	RJ	976	ILE
47	RJ	1069	VAL
48	RK	26	LEU
48	RK	90	CYS
48	RK	335	THR
50	RO	471	GLU
50	RO	493	TYR
50	RO	504	ASP
51	RQ	330	THR
51	RQ	898	PHE
51	RQ	899	LYS
52	RS	326	VAL
54	RW	179	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (364) such sidechains are listed below:

Mol	Chain	Res	Type
4	SG	63	GLN
4	SG	66	GLN
4	SG	169	ASN
5	SK	74	ASN
7	SO	36	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	SO	105	ASN
8	SP	12	GLN
9	SR	74	HIS
10	ST	13	HIS
10	ST	103	ASN
10	ST	104	ASN
13	3B	91	HIS
13	3B	228	GLN
13	3C	264	GLN
14	3D	39	ASN
14	3D	85	ASN
14	3D	168	GLN
14	3D	172	ASN
14	3D	183	GLN
14	3D	213	ASN
14	3D	324	ASN
14	3D	398	ASN
15	3E	191	HIS
15	3E	256	ASN
15	3E	261	GLN
15	3E	286	ASN
15	3E	289	GLN
15	3E	396	ASN
15	3E	400	GLN
16	3F	155	ASN
16	3F	156	ASN
16	3F	164	GLN
16	3F	195	GLN
16	3F	226	HIS
16	3F	525	GLN
16	3F	561	ASN
17	3G	29	ASN
17	3H	5	ASN
17	3H	18	GLN
17	3H	45	ASN
17	3H	113	GLN
18	A4	140	ASN
18	A4	279	HIS
18	A4	292	ASN
18	A4	317	ASN
18	A4	331	ASN
18	A4	438	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
18	A4	467	ASN
18	A4	483	ASN
18	A4	529	ASN
18	A4	574	HIS
18	A4	589	ASN
18	A4	621	ASN
18	A4	731	HIS
19	A5	32	GLN
19	A5	67	ASN
19	A5	103	ASN
19	A5	133	GLN
19	A5	139	HIS
19	A5	302	ASN
19	A5	308	ASN
19	A5	316	ASN
19	A5	318	GLN
19	A5	333	ASN
19	A5	527	HIS
20	A8	553	GLN
20	A8	609	ASN
20	A8	636	GLN
21	A9	474	HIS
21	A9	478	ASN
21	A9	509	GLN
22	AE	14	ASN
22	AE	96	ASN
22	AE	141	ASN
22	AE	166	ASN
22	AE	219	ASN
22	AE	224	ASN
22	AE	258	HIS
22	AE	304	GLN
22	AE	477	ASN
22	AE	480	ASN
22	AE	545	ASN
22	AE	673	ASN
23	AF	18	GLN
23	AF	48	ASN
23	AF	125	HIS
23	AF	133	HIS
23	AF	135	GLN
23	AF	156	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
23	AF	217	ASN
23	AF	250	ASN
23	AF	269	GLN
23	AF	289	ASN
23	AF	419	GLN
23	AF	481	GLN
23	AF	496	HIS
24	AG	50	ASN
24	AG	105	HIS
24	AG	131	HIS
24	AG	166	ASN
24	AG	184	GLN
24	AG	190	GLN
24	AG	266	ASN
24	AG	269	GLN
24	AG	289	GLN
24	AG	325	GLN
24	AG	332	GLN
24	AG	370	GLN
24	AG	393	ASN
24	AG	407	ASN
24	AG	410	ASN
24	AG	418	ASN
24	AG	453	HIS
24	AG	467	GLN
24	AG	535	ASN
24	AG	568	ASN
24	AG	579	ASN
24	AG	603	ASN
24	AG	706	HIS
24	AG	719	ASN
24	AG	880	GLN
25	B1	57	ASN
25	B1	92	HIS
25	B1	142	HIS
25	B1	188	ASN
25	B1	201	HIS
25	B1	254	HIS
25	B1	297	GLN
25	B1	303	ASN
25	B1	349	ASN
25	B1	386	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
25	B1	432	GLN
25	B1	452	ASN
25	B1	456	HIS
25	B1	461	GLN
25	B1	483	GLN
25	B1	549	GLN
25	B1	552	ASN
25	B1	650	ASN
25	B1	707	ASN
25	B1	734	GLN
25	B1	752	ASN
25	B1	813	HIS
25	B1	837	ASN
25	B1	842	ASN
26	B2	172	GLN
26	B2	327	HIS
26	B2	390	GLN
26	B2	455	GLN
26	B2	523	HIS
26	B2	524	HIS
26	B2	656	HIS
26	B2	657	GLN
26	B2	770	ASN
26	B2	798	ASN
26	B2	856	ASN
26	B2	871	GLN
26	B2	881	ASN
26	B2	916	HIS
27	B3	13	ASN
27	B3	81	GLN
27	B3	138	HIS
27	B3	157	ASN
27	B3	187	GLN
27	B3	189	HIS
27	B3	240	ASN
27	B3	282	ASN
27	B3	309	GLN
27	B3	315	ASN
27	B3	433	HIS
27	B3	459	ASN
27	B3	478	GLN
27	B3	585	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	B3	667	GLN
27	B3	670	GLN
27	B3	690	HIS
27	B3	696	ASN
27	B3	767	HIS
27	B3	802	GLN
28	B8	151	ASN
28	B8	162	ASN
28	B8	167	GLN
28	B8	224	ASN
28	B8	276	HIS
28	B8	282	ASN
28	B8	308	ASN
28	B8	322	HIS
28	B8	352	GLN
28	B8	472	GLN
28	B8	492	ASN
28	B8	498	ASN
28	B8	528	GLN
28	B8	592	ASN
28	B8	593	HIS
29	BE	32	ASN
29	BE	64	ASN
29	BE	120	HIS
29	BE	163	GLN
29	BE	248	GLN
29	BE	289	ASN
29	BE	305	ASN
29	BE	349	HIS
29	BE	362	GLN
29	BE	447	ASN
29	BE	481	ASN
29	BE	501	HIS
29	BE	514	ASN
29	BE	627	ASN
29	BE	708	ASN
29	BE	736	HIS
29	BE	826	GLN
29	BE	877	ASN
29	BE	911	ASN
30	B6	62	ASN
30	B6	64	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	B6	90	GLN
30	B6	115	ASN
30	B6	166	ASN
30	B6	169	GLN
30	B6	287	ASN
30	B6	289	HIS
31	5B	207	ASN
32	5C	101	ASN
32	5C	133	HIS
32	5C	143	GLN
32	5C	151	ASN
32	5C	155	HIS
32	5C	164	GLN
32	5C	170	GLN
32	5C	371	HIS
32	5C	394	HIS
32	5C	468	GLN
32	5C	517	GLN
32	5C	525	ASN
33	5D	42	HIS
33	5D	144	ASN
33	5D	153	ASN
34	5E	303	GLN
34	5E	316	ASN
34	5E	526	ASN
35	5F	7	HIS
35	5F	10	GLN
35	5F	99	ASN
35	5F	125	GLN
35	5F	135	HIS
36	5G	102	GLN
36	5G	121	ASN
36	5G	143	HIS
36	5G	159	HIS
36	5G	168	HIS
36	5G	236	HIS
37	5H	499	GLN
37	5H	515	ASN
37	5H	560	ASN
38	5I	20	GLN
38	5I	46	ASN
38	5I	81	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
38	5I	109	HIS
38	5I	260	GLN
38	5I	276	ASN
38	5I	281	ASN
38	5I	336	HIS
38	5I	371	ASN
38	5I	406	HIS
38	5I	418	HIS
38	5I	421	GLN
39	5J	53	GLN
39	5J	135	HIS
39	5J	139	GLN
39	5J	184	ASN
39	5J	192	ASN
39	5J	195	GLN
40	5K	29	GLN
41	RC	112	GLN
41	RC	149	ASN
41	RC	151	ASN
41	RC	195	HIS
43	RE	120	HIS
43	RE	170	GLN
43	RE	226	HIS
43	RE	261	ASN
43	RE	333	ASN
43	RE	409	ASN
43	RE	582	GLN
43	RE	588	GLN
43	RE	602	ASN
43	RE	634	HIS
43	RE	767	GLN
43	RE	834	ASN
43	RE	841	ASN
43	RE	901	ASN
43	RE	907	GLN
43	RE	928	HIS
43	RE	1073	ASN
43	RE	1086	ASN
43	RE	1172	ASN
43	RE	1194	HIS
43	RE	1215	ASN
43	RE	1233	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
44	RF	23	HIS
44	RF	63	ASN
44	RF	66	HIS
44	RF	96	HIS
44	RF	136	ASN
44	RF	148	HIS
45	RG	105	ASN
45	RG	125	ASN
45	RH	69	ASN
45	RH	74	GLN
45	RH	105	ASN
45	RH	125	ASN
45	RH	250	ASN
46	RI	52	ASN
46	RI	117	GLN
46	RI	186	ASN
46	RI	193	ASN
46	RI	215	ASN
46	RI	221	ASN
47	RJ	126	ASN
47	RJ	157	ASN
47	RJ	289	HIS
47	RJ	761	GLN
47	RJ	778	GLN
47	RJ	909	ASN
47	RJ	944	ASN
47	RJ	1082	GLN
48	RK	16	ASN
48	RK	61	ASN
48	RK	317	GLN
48	RK	334	ASN
49	RN	8	ASN
49	RN	56	ASN
49	RN	432	HIS
49	RN	495	ASN
49	RN	531	GLN
49	RN	683	ASN
49	RN	686	ASN
49	RN	703	GLN
49	RN	705	HIS
49	RN	713	HIS
49	RN	771	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	RN	797	ASN
50	RO	192	GLN
50	RO	249	ASN
50	RO	266	ASN
50	RO	268	GLN
50	RO	273	GLN
50	RO	290	HIS
50	RO	304	ASN
50	RO	306	GLN
50	RO	343	GLN
50	RO	434	ASN
50	RO	449	HIS
50	RO	472	HIS
50	RO	474	HIS
51	RQ	344	GLN
51	RQ	836	ASN
51	RQ	867	GLN
52	RS	241	ASN
52	RS	276	GLN
52	RS	300	ASN
53	RT	127	GLN
53	RT	218	ASN
53	RT	232	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	44 (26%)	2 (1%)
2	5A	518/700 (74%)	161 (31%)	11 (2%)
3	SA	848/1808 (46%)	301 (35%)	20 (2%)
All	All	1535/2841 (54%)	506 (32%)	33 (2%)

All (506) 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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	3A	28	A
1	3A	30	A
1	3A	33	A
1	3A	35	U
1	3A	38	U
1	3A	56	A
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	101	G
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	305	G
1	3A	309	G
1	3A	310	G
1	3A	311	G
1	3A	313	A
1	3A	314	C
1	3A	322	A
1	3A	324	U
1	3A	325	C
1	3A	328	A
1	3A	329	C
1	3A	332	G
2	5A	5	G
2	5A	6	A
2	5A	7	A
2	5A	8	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	82	A
2	5A	83	U
2	5A	86	C
2	5A	87	C
2	5A	90	G
2	5A	102	A
2	5A	103	G
2	5A	104	A
2	5A	109	C
2	5A	110	G
2	5A	114	G
2	5A	124	A
2	5A	125	G
2	5A	127	U
2	5A	128	C
2	5A	129	U
2	5A	130	G
2	5A	141	A
2	5A	142	U
2	5A	143	A
2	5A	144	C
2	5A	150	G
2	5A	151	U
2	5A	152	U
2	5A	156	U
2	5A	159	A
2	5A	161	A
2	5A	162	U
2	5A	163	G
2	5A	167	U
2	5A	168	G
2	5A	169	A
2	5A	170	U
2	5A	171	G
2	5A	172	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	5A	173	G
2	5A	174	U
2	5A	175	A
2	5A	176	U
2	5A	177	U
2	5A	178	G
2	5A	179	A
2	5A	182	G
2	5A	185	A
2	5A	190	U
2	5A	200	A
2	5A	201	U
2	5A	206	A
2	5A	207	G
2	5A	211	G
2	5A	213	G
2	5A	219	U
2	5A	220	U
2	5A	222	G
2	5A	223	C
2	5A	224	G
2	5A	225	U
2	5A	227	U
2	5A	235	A
2	5A	240	C
2	5A	254	C
2	5A	256	U
2	5A	259	G
2	5A	260	A
2	5A	261	U
2	5A	263	C
2	5A	267	U
2	5A	268	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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	5A	311	C
2	5A	312	U
2	5A	313	A
2	5A	321	G
2	5A	322	A
2	5A	325	U
2	5A	326	C
2	5A	328	A
2	5A	337	G
2	5A	339	A
2	5A	346	G
2	5A	350	A
2	5A	353	A
2	5A	354	G
2	5A	355	C
2	5A	359	U
2	5A	361	G
2	5A	363	A
2	5A	364	A
2	5A	368	U
2	5A	369	G
2	5A	370	U
2	5A	371	G
2	5A	372	A
2	5A	373	U
2	5A	381	G
2	5A	385	A
2	5A	386	A
2	5A	391	C
2	5A	393	C
2	5A	395	C
2	5A	407	A
2	5A	419	A
2	5A	427	A
2	5A	428	A
2	5A	429	A
2	5A	430	C
2	5A	431	A
2	5A	432	C
2	5A	433	C
2	5A	440	U
2	5A	443	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	5A	444	U
2	5A	461	A
2	5A	462	G
2	5A	464	G
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	436	A
3	SA	437	A
3	SA	439	U
3	SA	440	U
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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
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	873	U
3	SA	876	G
3	SA	877	G
3	SA	894	U
3	SA	898	A
3	SA	899	G
3	SA	900	A
3	SA	901	G
3	SA	906	A
3	SA	909	U
3	SA	910	C
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	928	U
3	SA	932	U
3	SA	933	A
3	SA	935	U
3	SA	944	A
3	SA	945	U
3	SA	951	A
3	SA	960	U
3	SA	964	U
3	SA	966	A
3	SA	969	C
3	SA	970	A
3	SA	971	A
3	SA	972	G
3	SA	975	C
3	SA	976	G
3	SA	980	G
3	SA	987	G
3	SA	988	A
3	SA	992	A
3	SA	993	A
3	SA	996	U
3	SA	998	A
3	SA	1000	C
3	SA	1004	U
3	SA	1005	A
3	SA	1009	U
3	SA	1012	U
3	SA	1019	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	1147	A
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	1255	G
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	1488	G
3	SA	1492	A
3	SA	1493	A
3	SA	1496	U
3	SA	1498	G
3	SA	1506	G
3	SA	1517	U
3	SA	1518	C
3	SA	1520	U
3	SA	1521	G
3	SA	1522	U
3	SA	1523	G
3	SA	1524	A
3	SA	1527	C
3	SA	1533	C

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	1539	G
3	SA	1541	G
3	SA	1543	A
3	SA	1544	U
3	SA	1567	U
3	SA	1568	C
3	SA	1569	A
3	SA	1570	A
3	SA	1573	A
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	1643	U
3	SA	1644	C
3	SA	1645	G
3	SA	1649	G
3	SA	1651	A
3	SA	1654	G
3	SA	1655	A
3	SA	1657	U
3	SA	1658	G
3	SA	1659	A
3	SA	1660	A
3	SA	1670	G
3	SA	1678	A
3	SA	1680	G
3	SA	1681	A
3	SA	1682	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	SA	1683	C
3	SA	1688	U
3	SA	1689	A
3	SA	1697	G
3	SA	1709	C
3	SA	1711	C
3	SA	1712	A
3	SA	1713	G
3	SA	1715	G
3	SA	1717	G
3	SA	1724	U
3	SA	1727	G
3	SA	1736	G
3	SA	1737	G
3	SA	1739	C
3	SA	1742	U
3	SA	1743	U
3	SA	1744	A
3	SA	1745	G
3	SA	1747	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	1759	C
3	SA	1761	U
3	SA	1764	C
3	SA	1766	A
3	SA	1767	G
3	SA	1768	G
3	SA	1769	U
3	SA	1779	U
3	SA	1780	G
3	SA	1781	A
3	SA	1782	A
3	SA	1789	G

All (33) RNA pucker outliers are listed below:

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	3A	198	U
1	3A	248	G
2	5A	169	A
2	5A	172	C
2	5A	173	G
2	5A	224	G
2	5A	312	U
2	5A	358	G
2	5A	363	A
2	5A	368	U
2	5A	487	A
2	5A	492	G
2	5A	536	A
3	SA	-7	A
3	SA	0	U
3	SA	538	A
3	SA	542	A
3	SA	579	A
3	SA	602	U
3	SA	899	G
3	SA	909	U
3	SA	913	G
3	SA	970	A
3	SA	971	A
3	SA	1146	G
3	SA	1197	C
3	SA	1521	G
3	SA	1594	G
3	SA	1632	C
3	SA	1654	G
3	SA	1743	U
3	SA	1744	A
3	SA	1749	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	GTP	RJ	1201	58	33,34,34	0.56	0	50,54,54	0.72	1 (2%)

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
57	GTP	RJ	1201	58	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	RJ	1201	GTP	C4'-O4'-C1'	-2.14	104.73	109.47

There are no chirality outliers.

All (3) torsion outliers are listed below:

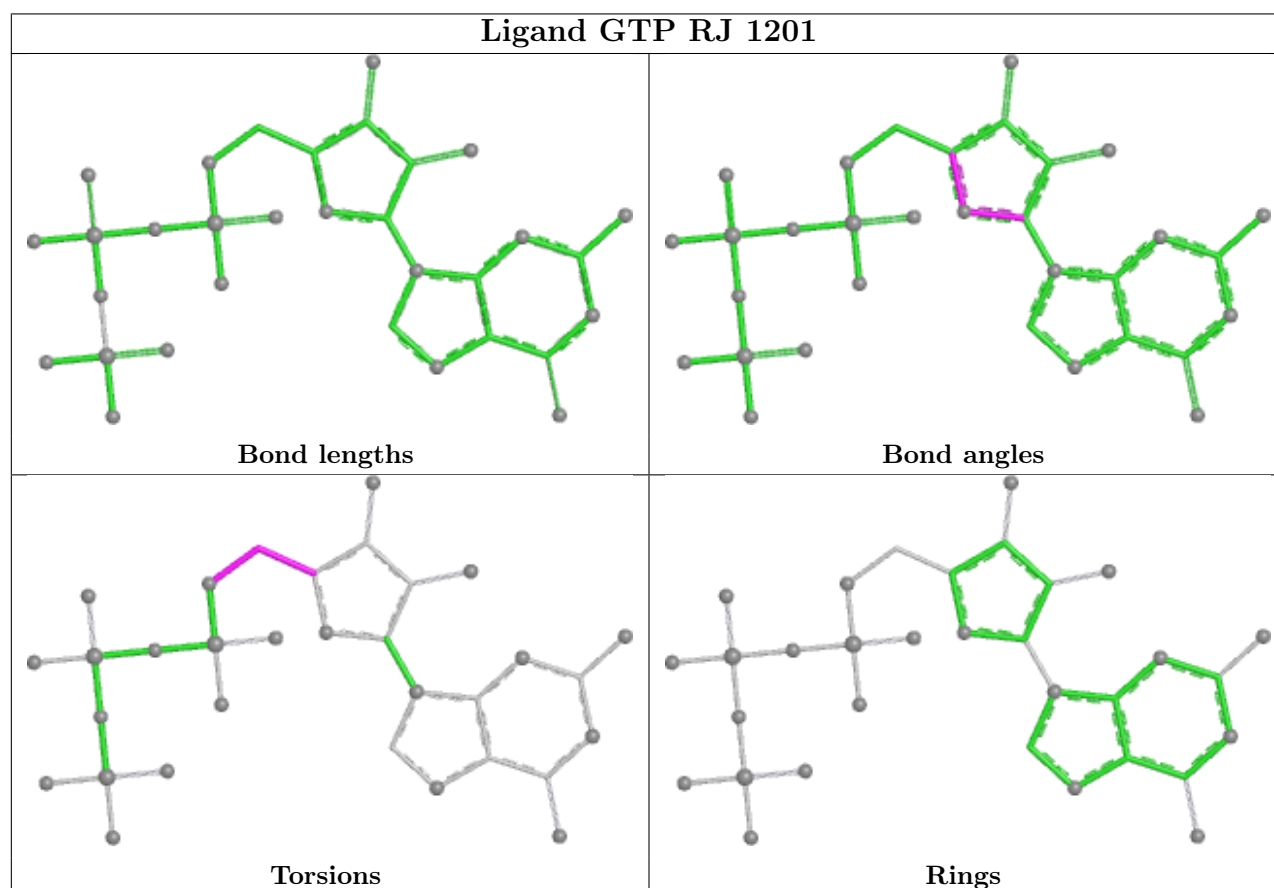
Mol	Chain	Res	Type	Atoms
57	RJ	1201	GTP	O4'-C4'-C5'-O5'
57	RJ	1201	GTP	C3'-C4'-C5'-O5'
57	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	RJ	1201	GTP	2	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

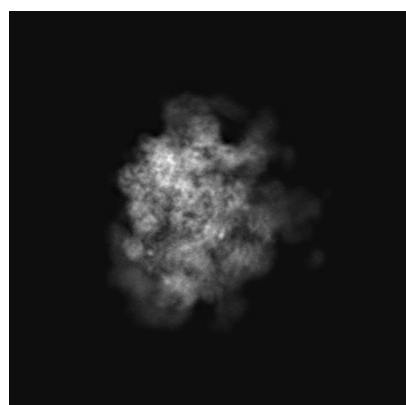
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30584. These allow visual inspection of the internal detail of the map and identification of artifacts.

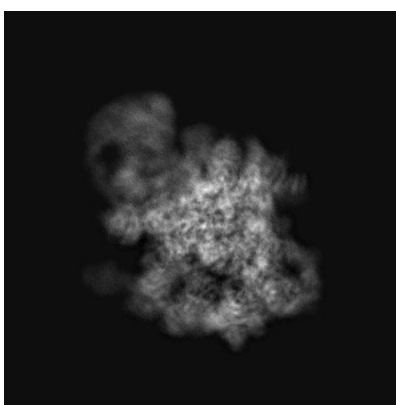
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

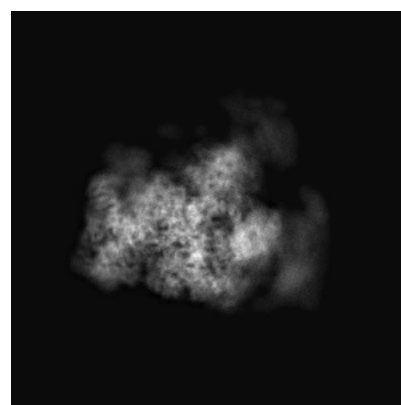
6.1.1 Primary map



X



Y

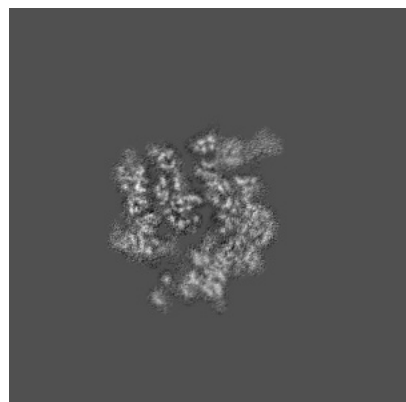


Z

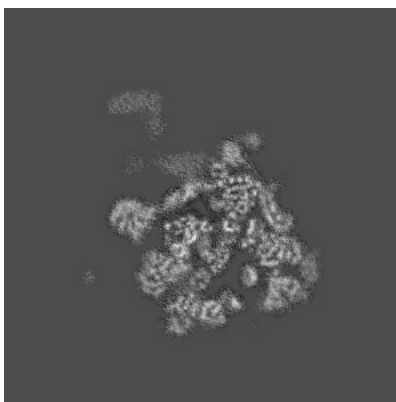
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

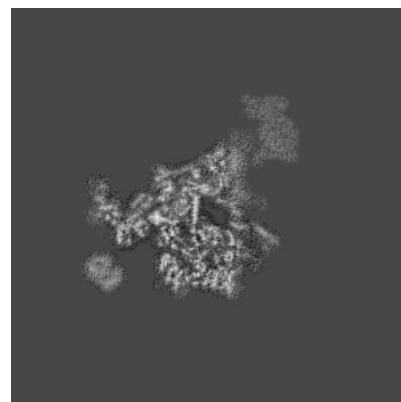
6.2.1 Primary map



X Index: 200



Y Index: 200

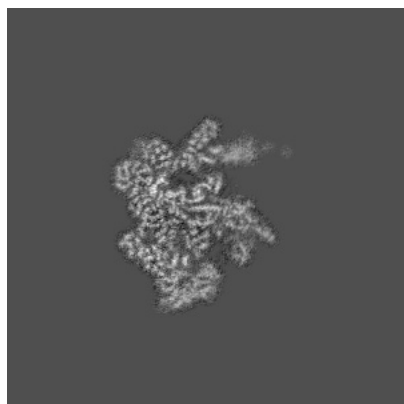


Z Index: 200

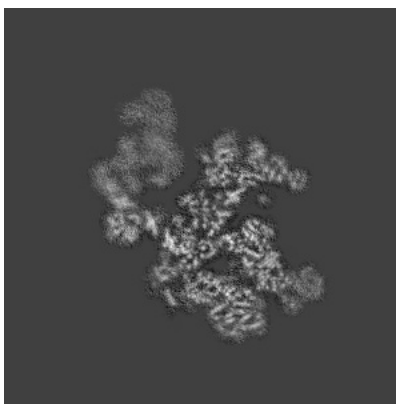
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

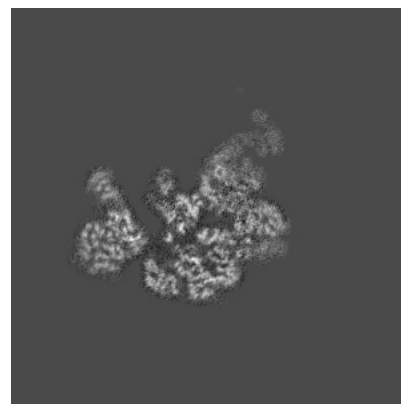
6.3.1 Primary map



X Index: 184



Y Index: 177

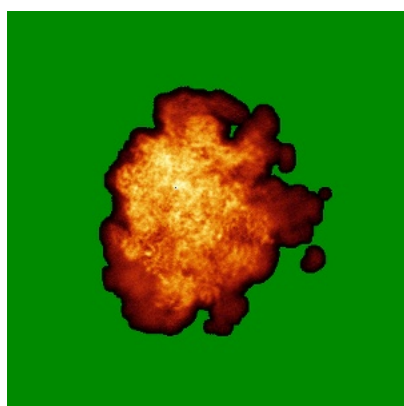


Z Index: 222

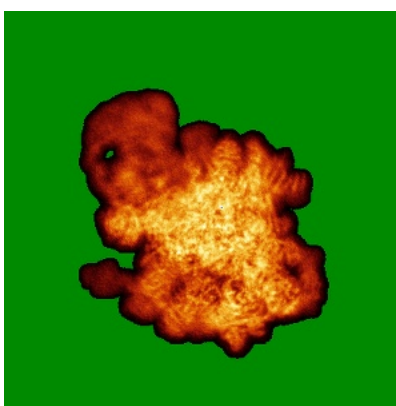
The images above show the largest variance slices of the map in three orthogonal directions.

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

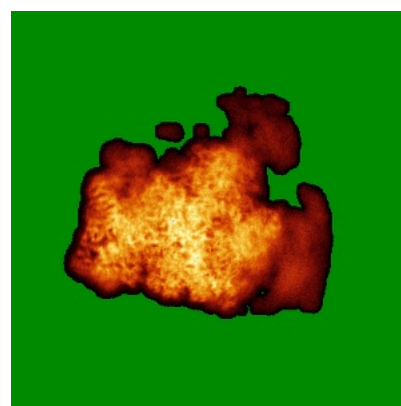
6.4.1 Primary map



X



Y

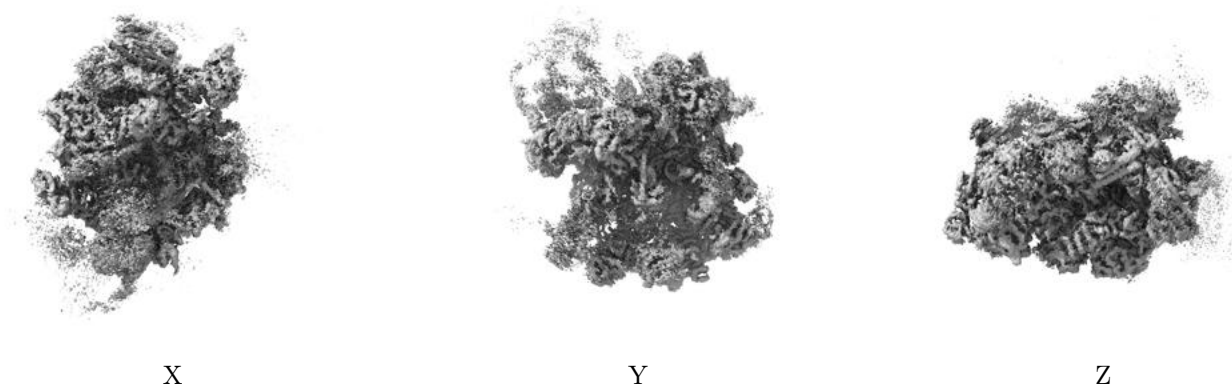


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

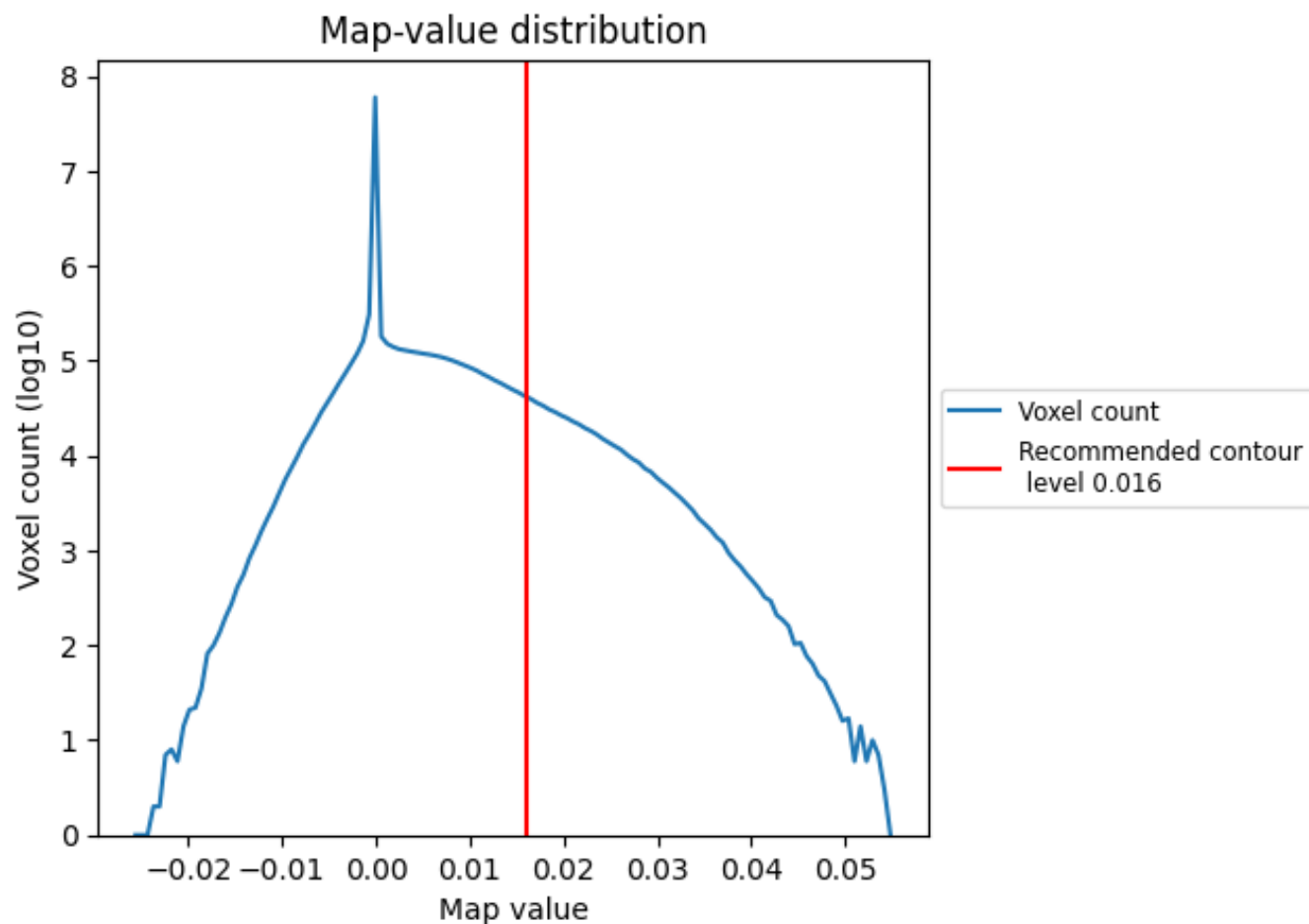
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

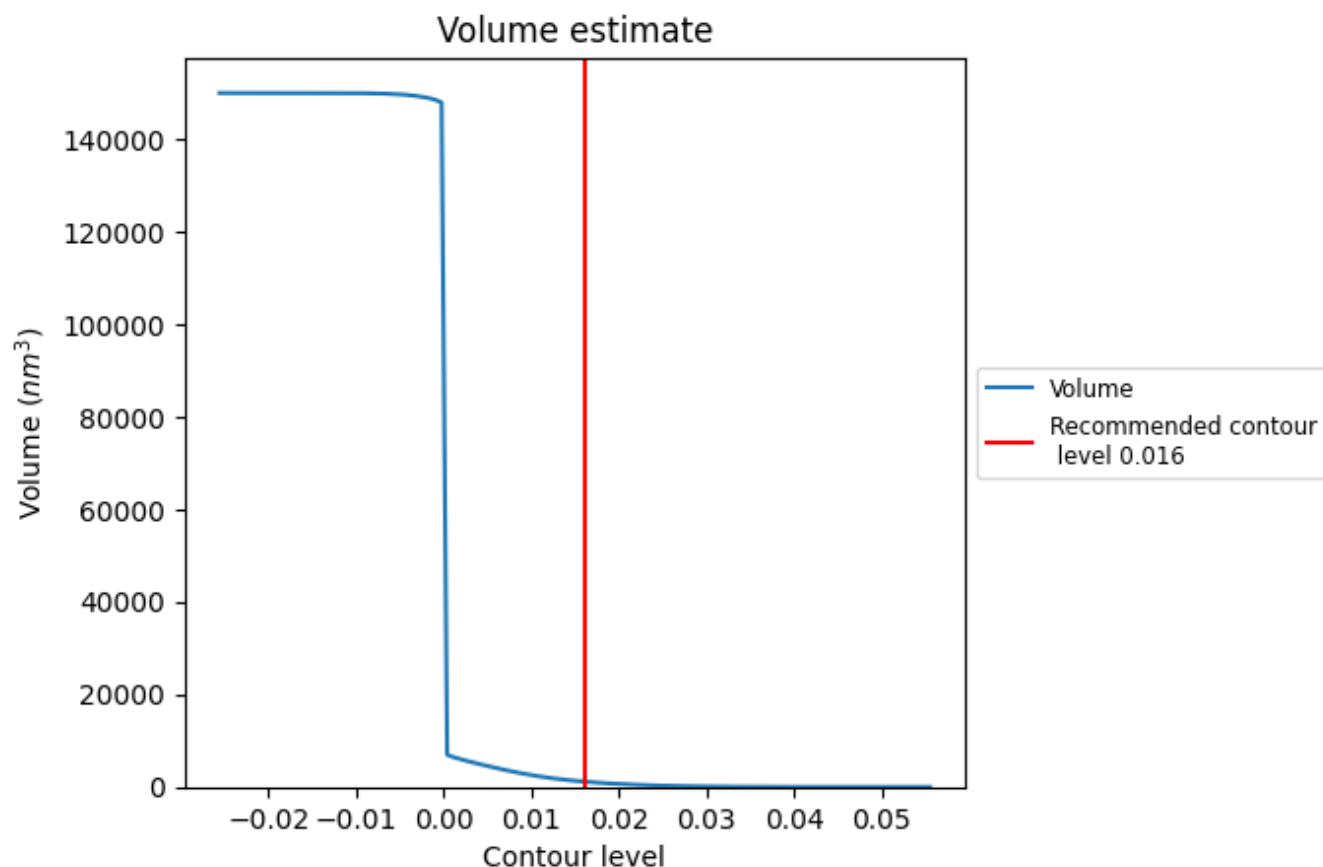
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

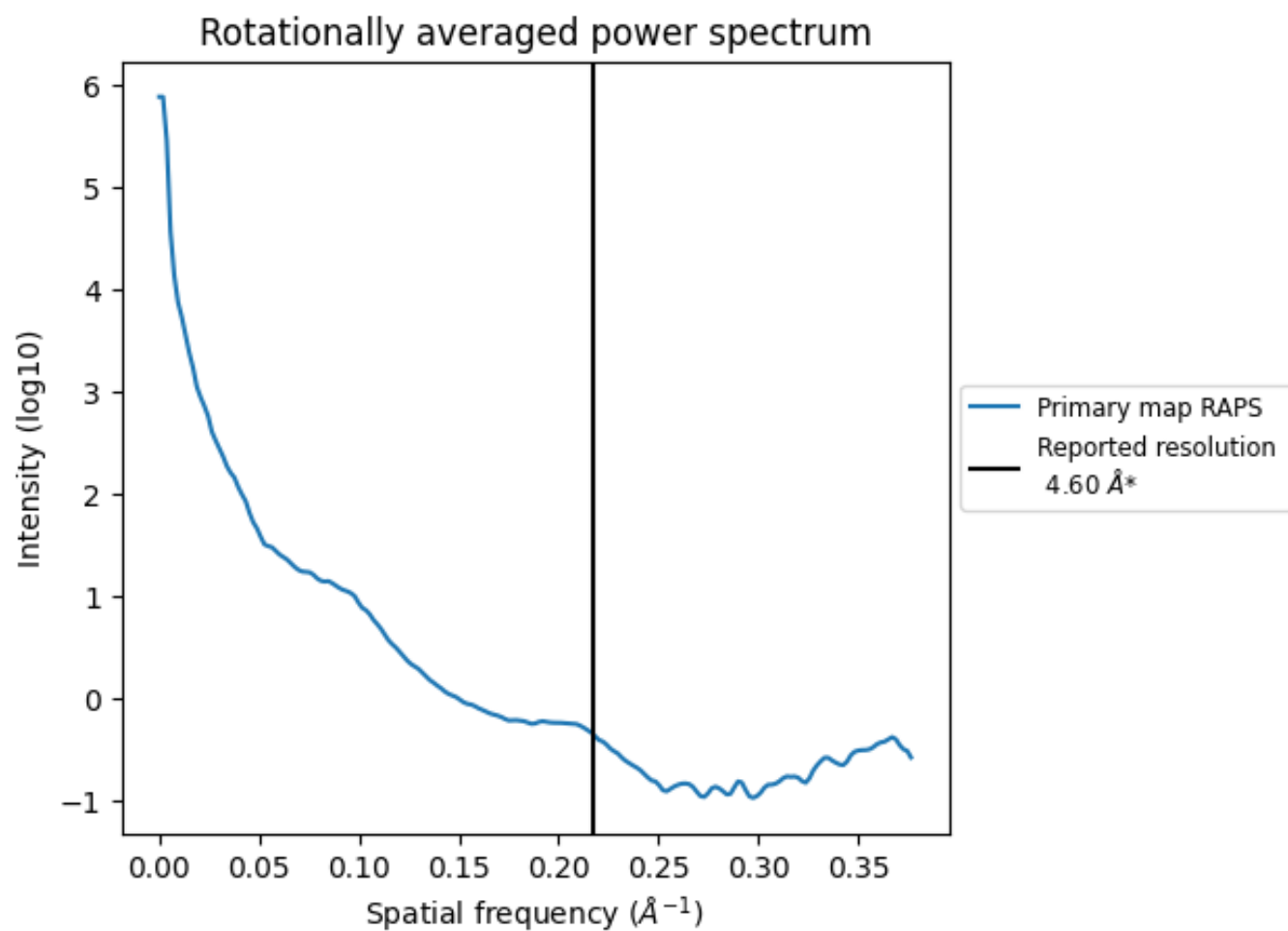
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1155 nm^3 ; this corresponds to an approximate mass of 1044 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.217 $\text{\AA}^{-1}$

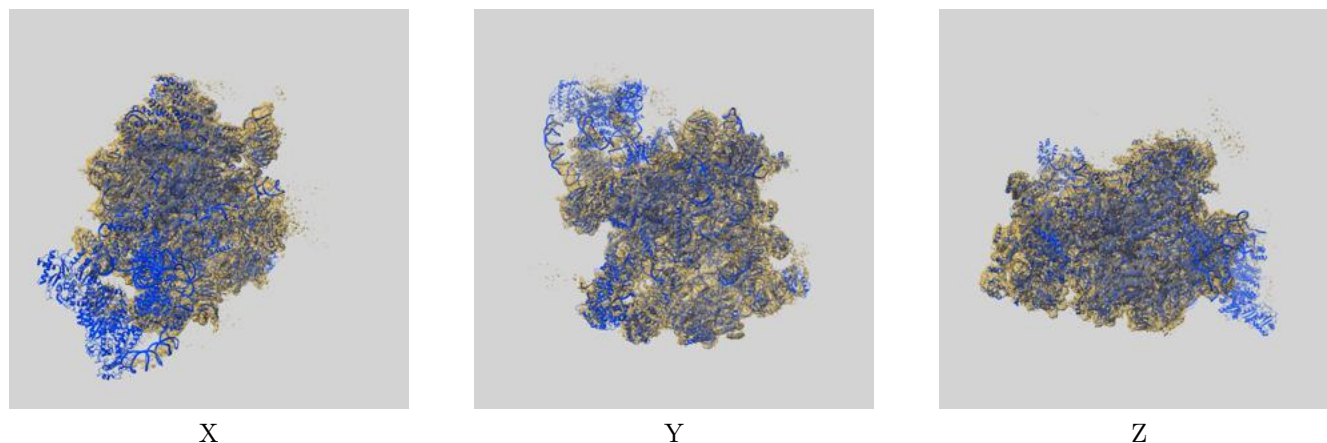
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

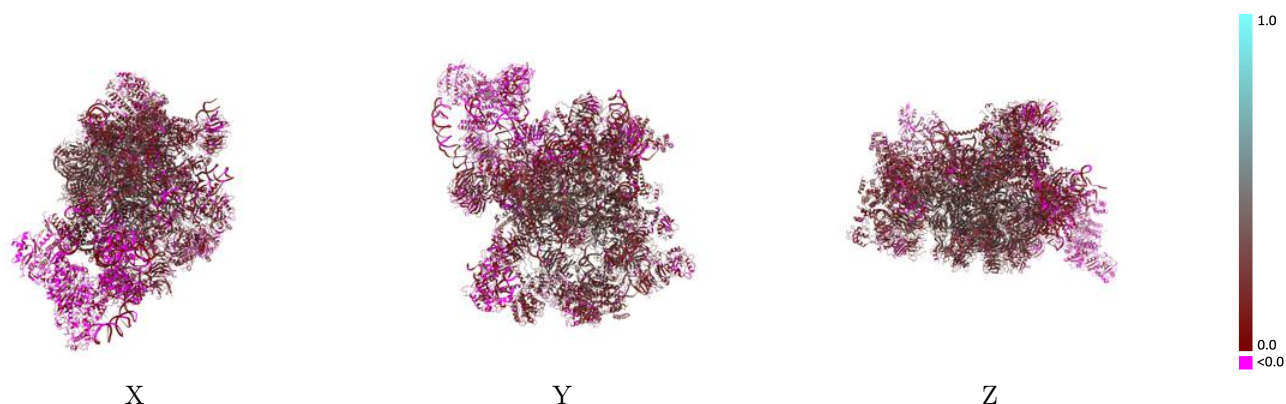
This section contains information regarding the fit between EMDB map EMD-30584 and PDB model 7D5S. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



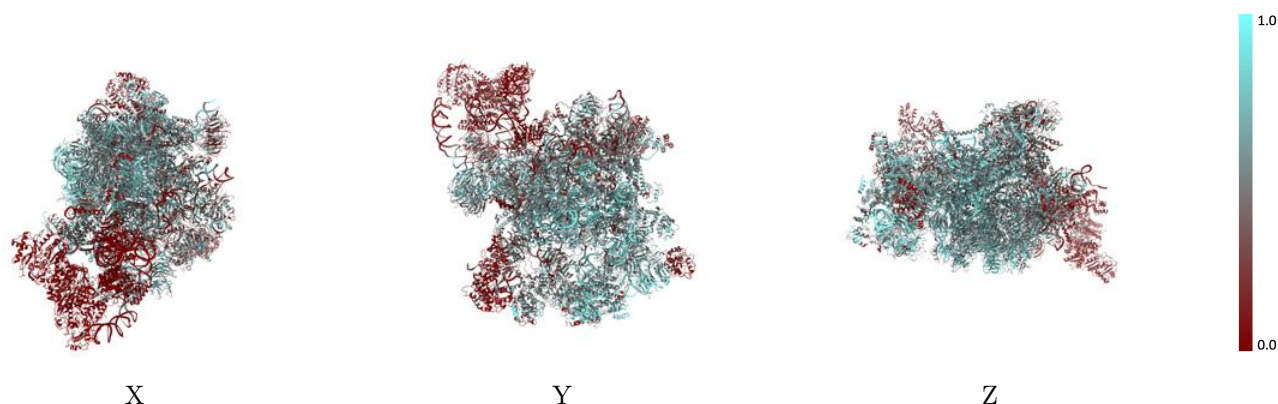
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



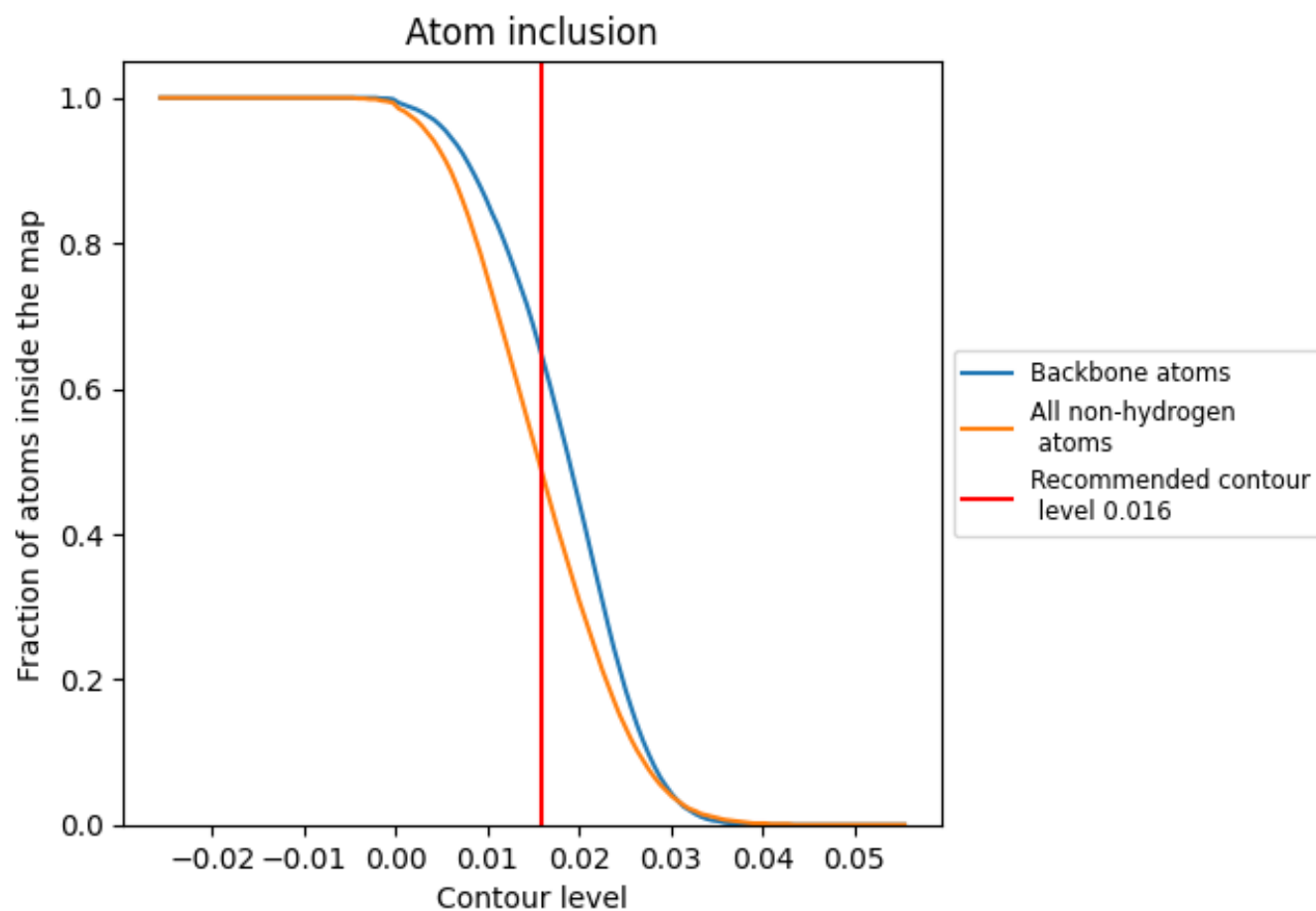
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.016).

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 48% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4820	 0.1810
3A	 0.7750	 0.2400
3B	 0.5190	 0.2300
3C	 0.5630	 0.2000
3D	 0.5420	 0.1850
3E	 0.5950	 0.2150
3F	 0.3600	 0.1270
3G	 0.6170	 0.2850
3H	 0.4440	 0.2030
5A	 0.7380	 0.2250
5B	 0.5020	 0.1960
5C	 0.5190	 0.2300
5D	 0.5620	 0.2480
5E	 0.4920	 0.2040
5F	 0.5780	 0.2600
5G	 0.4710	 0.2230
5H	 0.4360	 0.1930
5I	 0.5640	 0.1830
5J	 0.3770	 0.1950
5K	 0.4330	 0.1940
A4	 0.6490	 0.2330
A5	 0.6400	 0.2520
A8	 0.4600	 0.1310
A9	 0.6130	 0.2000
AE	 0.3960	 0.1900
AF	 0.6420	 0.2690
AG	 0.6370	 0.2400
B1	 0.6170	 0.2730
B2	 0.5790	 0.1620
B3	 0.2620	 0.0760
B6	 0.4860	 0.1650
B8	 0.6630	 0.2900
BE	 0.6510	 0.2670
RC	 0.0180	 0.0130
RD	 0.0380	 0.0320



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
RE	 0.0030	 0.0090
RF	 0.0000	 -0.0230
RG	 0.3780	 0.1680
RH	 0.4420	 0.2090
RI	 0.5760	 0.2190
RJ	 0.5170	 0.1940
RK	 0.4680	 0.1600
RN	 0.3660	 0.1580
RO	 0.5490	 0.1940
RQ	 0.2300	 0.1500
RS	 0.1150	 0.0550
RT	 0.4890	 0.1240
RW	 0.2090	 0.1480
SA	 0.4460	 0.1350
SG	 0.5980	 0.2850
SK	 0.3330	 0.1550
SN	 0.0090	 0.0370
SO	 0.0060	 -0.0110
SP	 0.0110	 0.0160
SR	 0.5680	 0.3000
ST	 0.2810	 0.1720
SY	 0.2990	 0.1390
Sd	 0.5740	 0.2920
X1	 0.3110	 0.1720