



Full wwPDB EM Validation Report ⓘ

Mar 26, 2026 – 06:03 AM UTC

PDB ID : 6LQR / pdb_00006lqr
EMDB ID : EMD-0951
Title : Cryo-EM structure of 90S small subunit preribosomes in transition states (State C)
Authors : Du, Y.; Ye, K.
Deposited on : 2020-01-14
Resolution : 8.60 Å(reported)
Based on initial model : 6LQP

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:

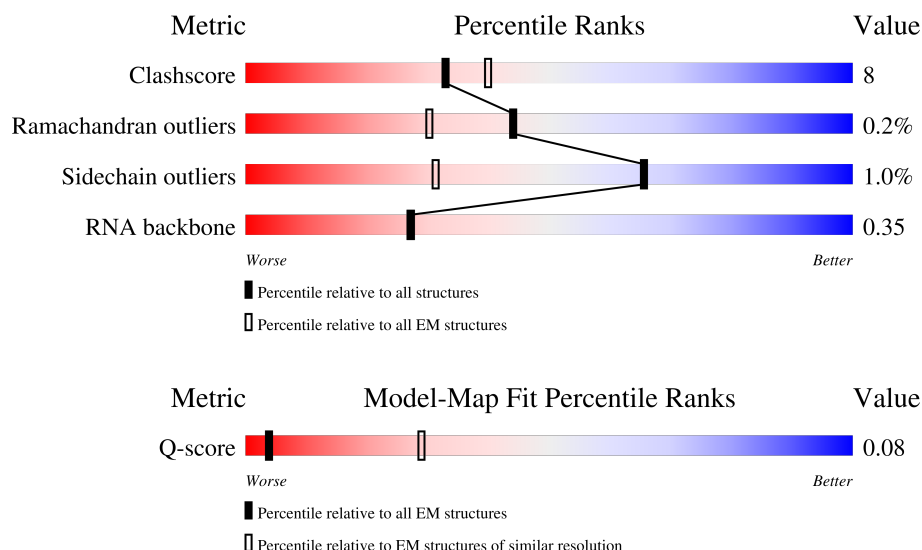
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 8.60 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	292 (8.10 - 9.10)

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	1809	

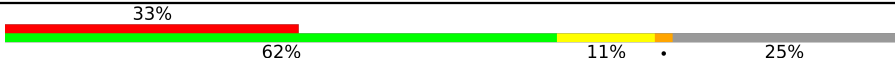
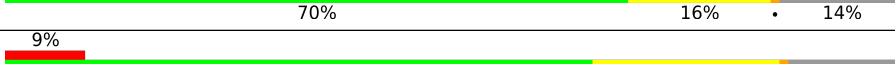
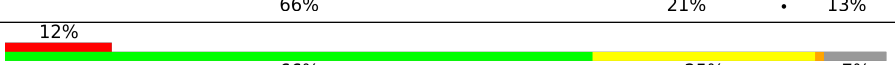
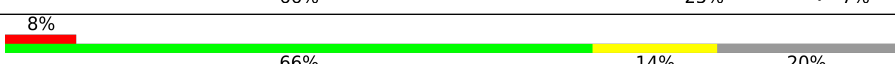
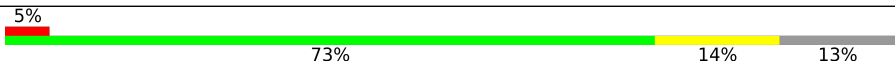
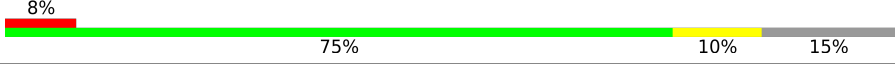
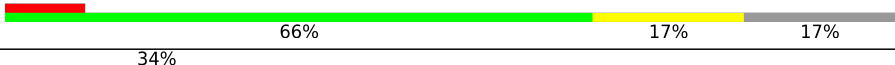
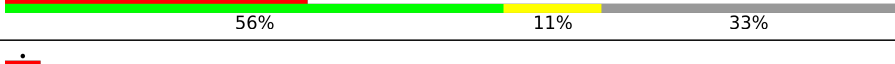
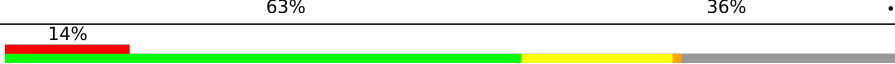
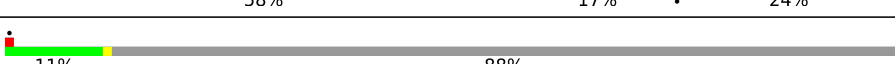
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Mol	Chain	Length	Quality of chain
4	SC	255	
5	SF	261	
6	SG	225	
7	SH	236	
8	SI	190	
9	SJ	200	
10	SK	197	
11	SM	156	
12	SO	151	
13	SP	137	
14	SR	143	
15	SX	130	
16	SY	145	
17	SZ	135	
18	Sc	82	
19	Sd	67	
20	3B	327	
20	3C	327	
21	3D	504	
22	3E	511	
23	3F	573	
24	3G	126	
24	3H	126	
25	A4	776	
26	A5	643	

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Mol	Chain	Length	Quality of chain
27	A8	713	
28	A9	575	
29	AE	1769	
30	AF	513	
31	AG	896	
32	B1	923	
33	B2	943	
34	B3	817	
35	B8	594	
36	BE	939	
37	B6	440	
38	5B	214	
39	5C	554	
40	5D	250	
41	5E	593	
42	5F	183	
43	5G	290	
44	5H	610	
45	5I	489	
46	5J	217	
47	5K	189	
48	RA	707	
49	RB	357	
50	RD	1729	
51	RE	1237	

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Mol	Chain	Length	Quality of chain
52	RF	297	
53	RG	252	
53	RH	252	
54	RJ	1183	
55	RK	367	
56	RL	1056	
56	RM	1056	
57	RN	810	
58	RO	552	
59	RP	2493	
60	RQ	899	
61	RS	483	
62	RT	326	
63	RY	534	
64	X1	347	

2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 215267 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called U3 snoRNA.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	1283	Total	C	N	O	P	0	0
			27362	12228	4872	8979	1283		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 21 is a protein called Nucleolar protein 56.

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

- Molecule 22 is a protein called Nucleolar protein 58.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 45 is a protein called Protein SOF1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	5J	151	Total	C	N	O	S	0	0
			1280	807	240	228	5		

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

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

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

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

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

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

- Molecule 50 is a protein called rRNA biogenesis protein RRP5.

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

- Molecule 51 is a protein called U3 small nucleolar RNA-associated protein 22.

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

- Molecule 52 is a protein called Ribosomal RNA-processing protein 7.

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

- Molecule 53 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

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

- Molecule 54 is a protein called Ribosome biogenesis protein BMS1.

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

- Molecule 55 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 56 is a protein called RNA cytidine acetyltransferase.

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

- Molecule 57 is a protein called Nucleolar complex protein 14.

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

- Molecule 58 is a protein called Nucleolar complex protein 4.

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

- Molecule 59 is a protein called U3 small nucleolar RNA-associated protein 20.

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

- Molecule 60 is a protein called U3 small nucleolar RNA-associated protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	RQ	226	Total	C	N	O	S	0	0
			1651	1023	313	313	2		

- Molecule 61 is a protein called Essential nuclear protein 1.

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

- Molecule 62 is a protein called Pno1.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	RT	169	Total	C	N	O	S	0	0
			1334	849	244	237	4		

- Molecule 63 is a protein called Protein BFR2.

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

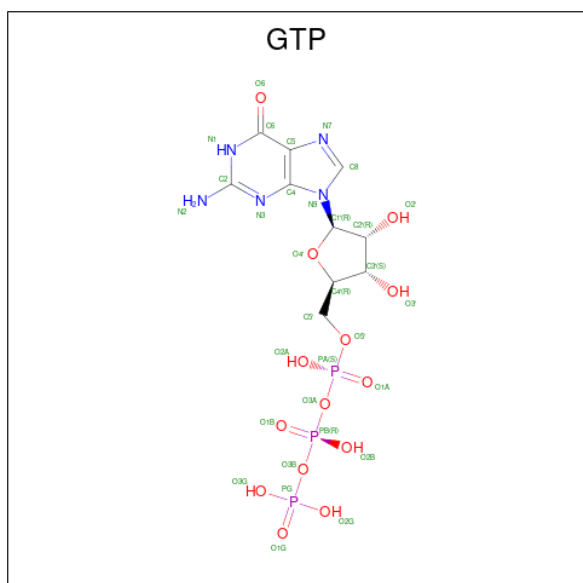
- Molecule 64 is a protein called Unassigned helices.

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

- Molecule 65 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
65	Sc	1	Total	Zn	0
			1	1	
65	5K	1	Total	Zn	0
			1	1	

- Molecule 66 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

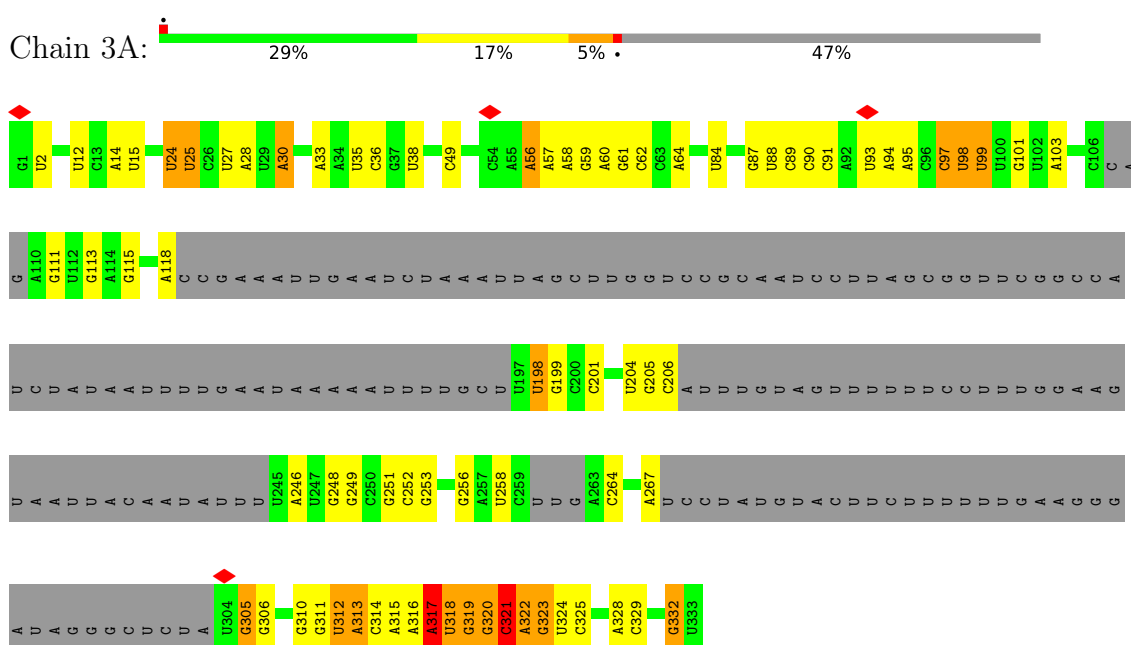
- Molecule 67 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

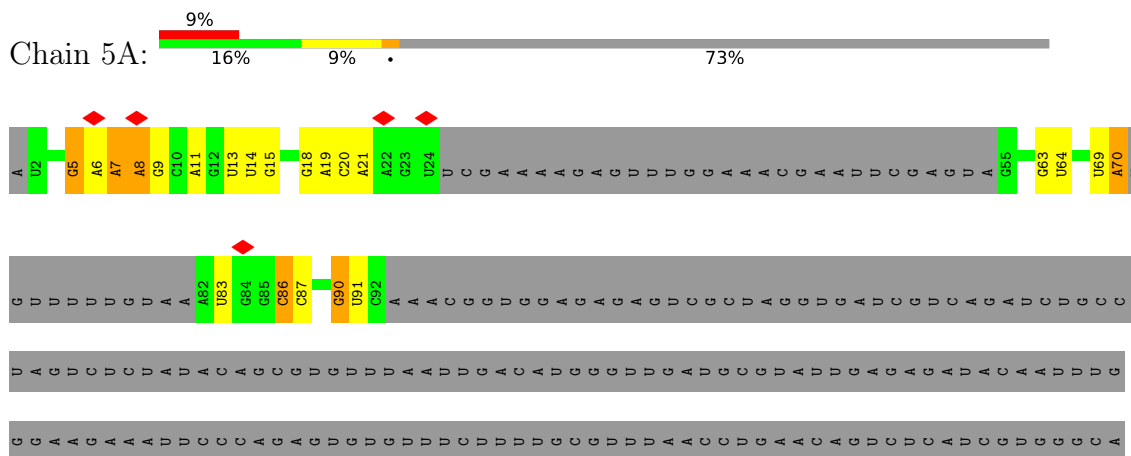
3 Residue-property plots [i](#)

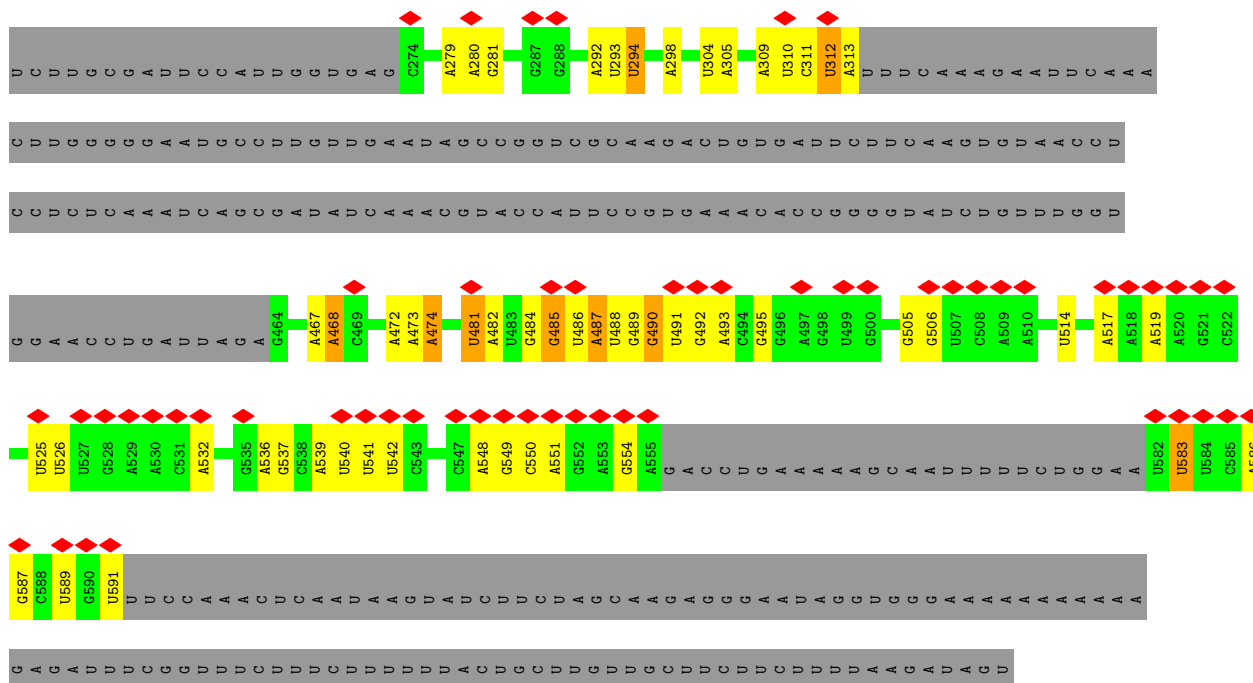
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: U3 snoRNA

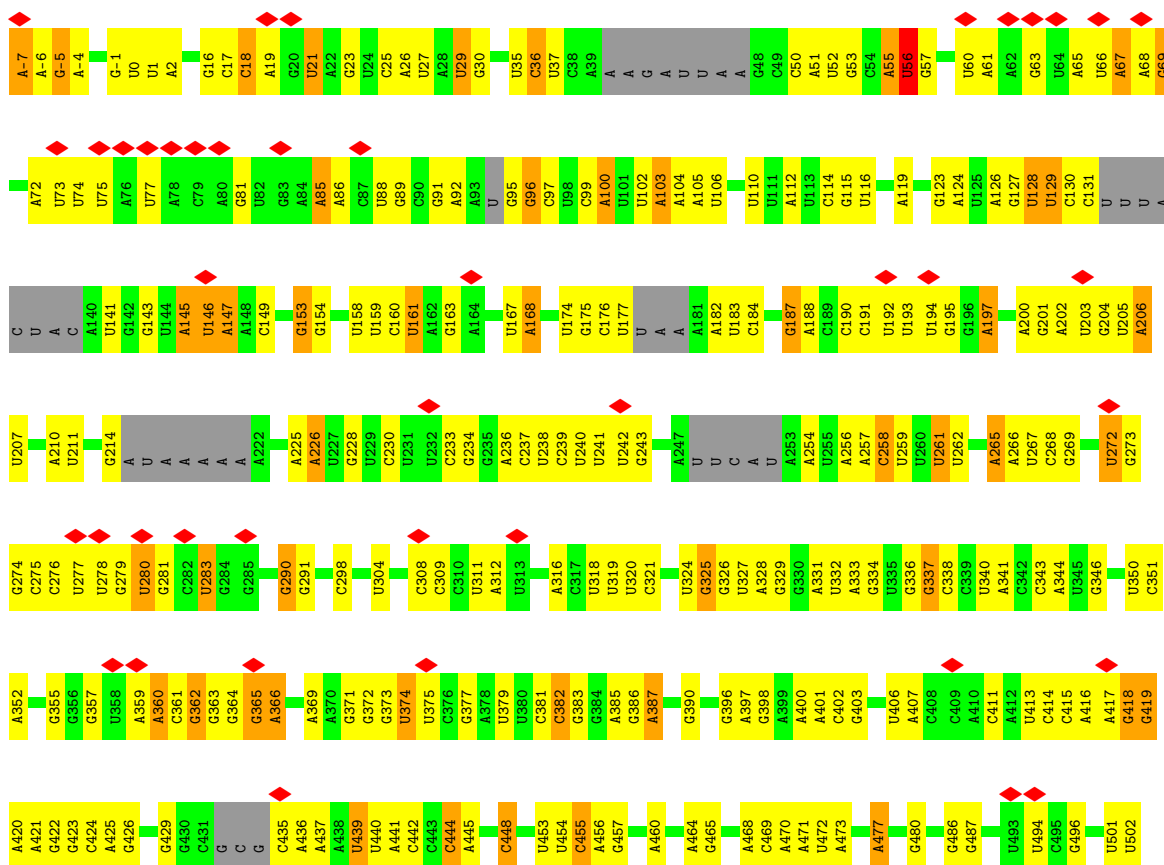


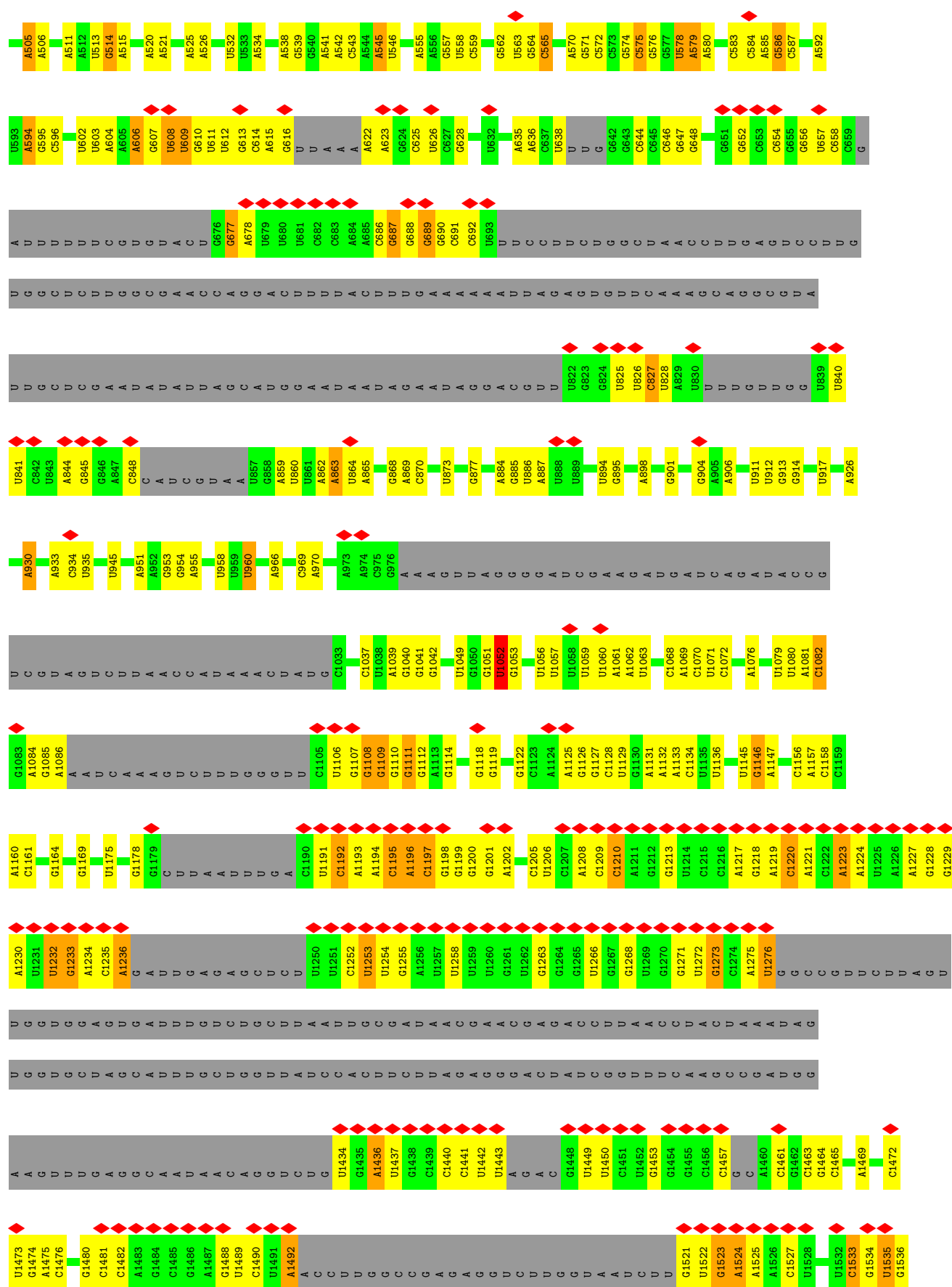
• Molecule 2: 5' ETS

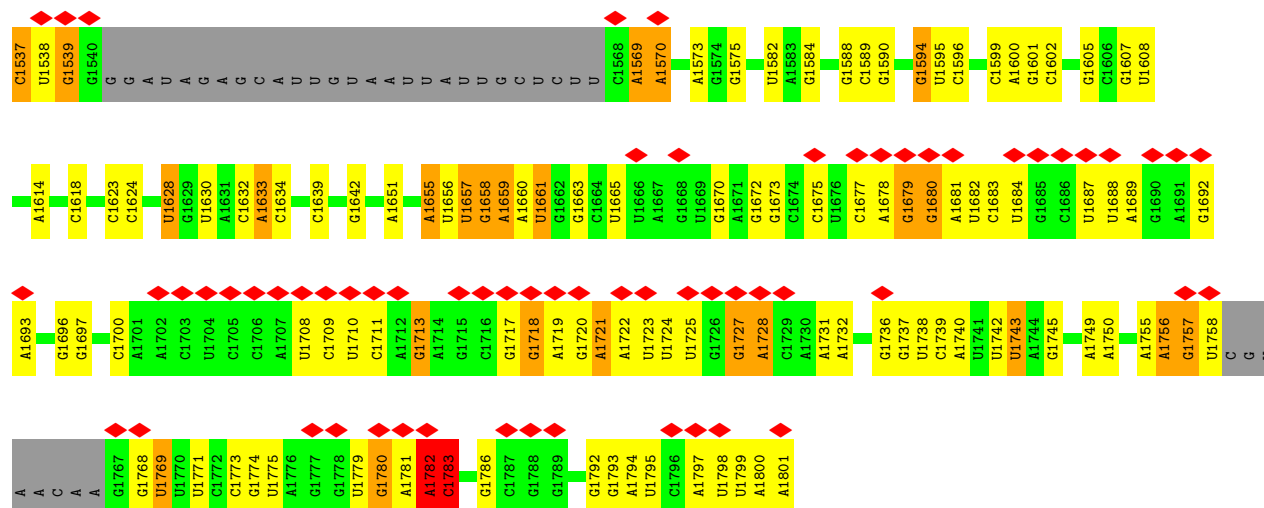




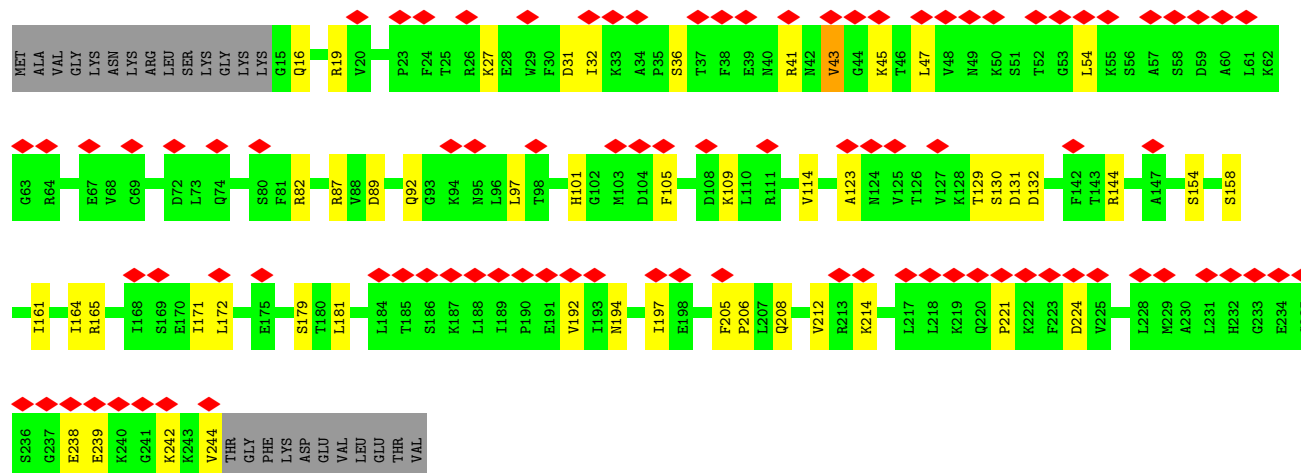
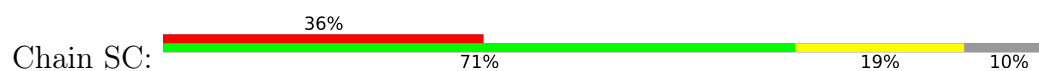
• Molecule 3: 18S pre-rRNA



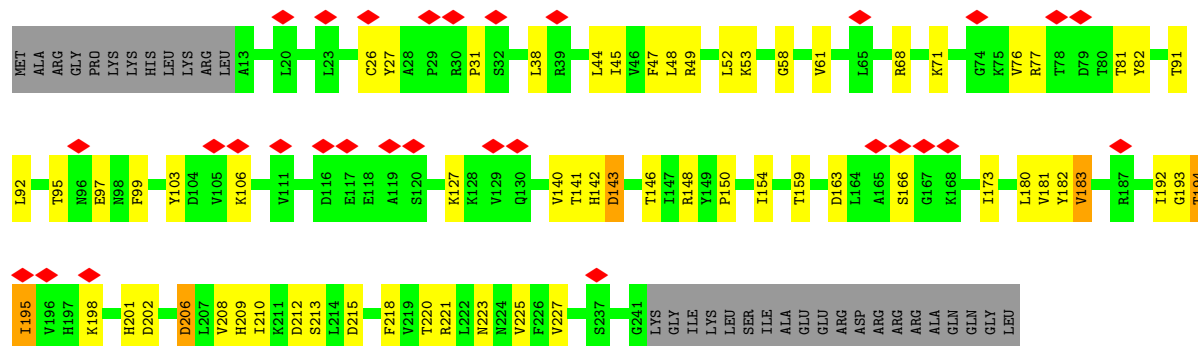




• Molecule 4: 40S ribosomal protein S1-A

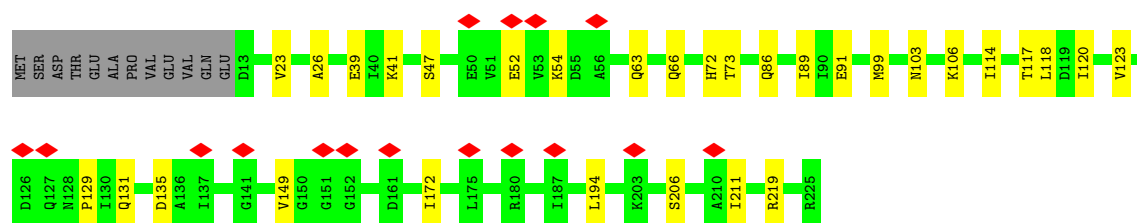


• Molecule 5: 40S ribosomal protein S4-A



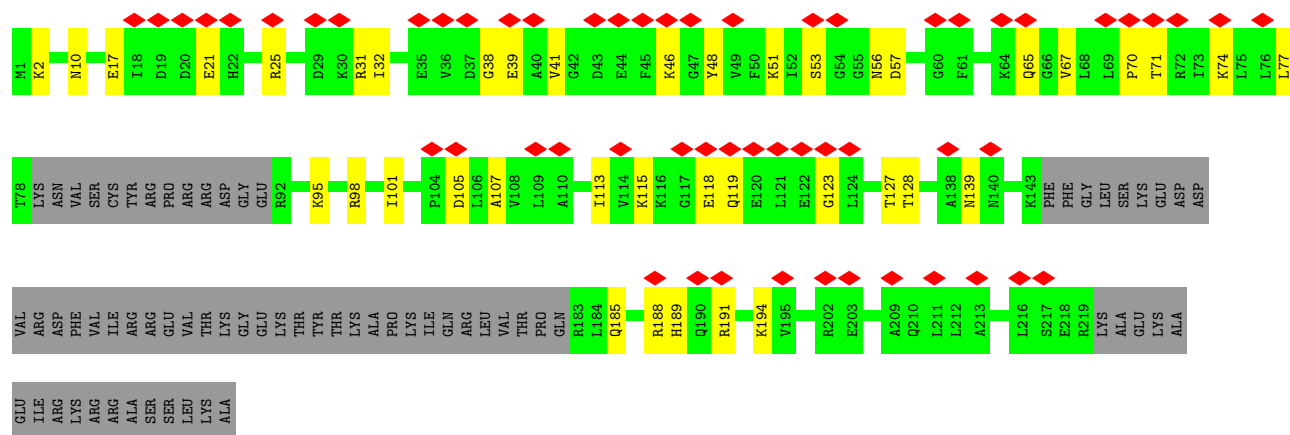
• Molecule 6: 40S ribosomal protein S5

Chain SG: 



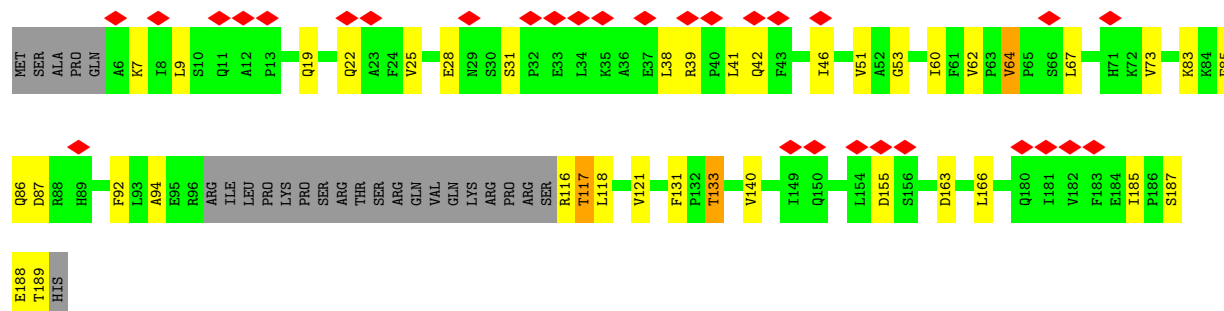
• Molecule 7: 40S ribosomal protein S6-A

Chain SH: 



• Molecule 8: 40S ribosomal protein S7-A

Chain SI: 



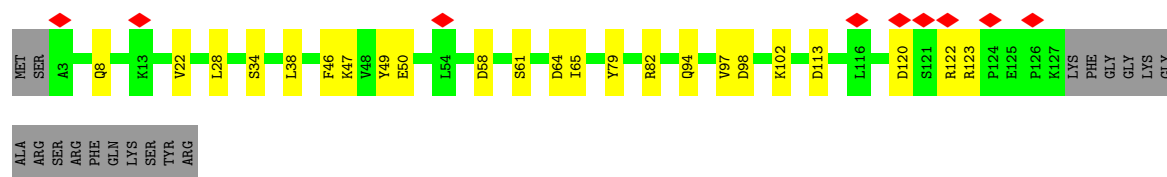
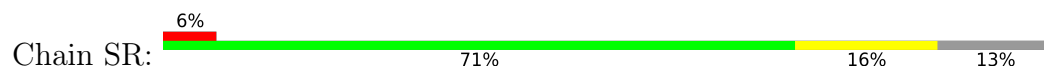
• Molecule 9: 40S ribosomal protein S8-A

Chain SJ: 

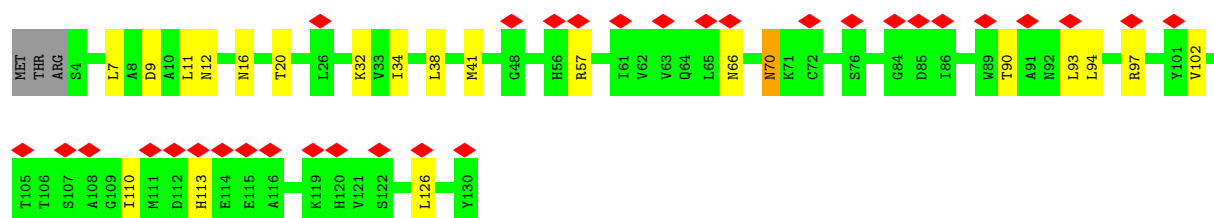
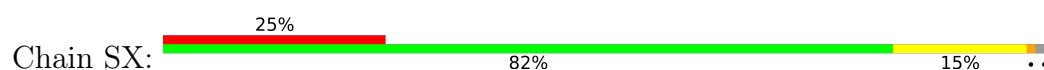




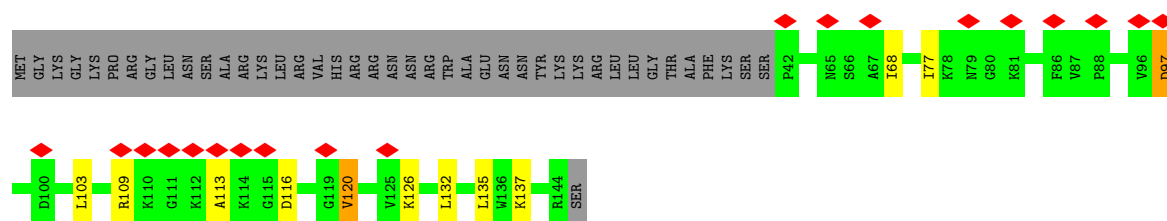
- Molecule 14: 40S ribosomal protein S16-A



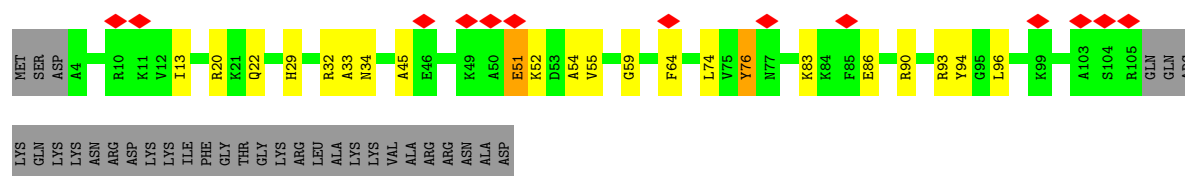
- Molecule 15: 40S ribosomal protein S22-B



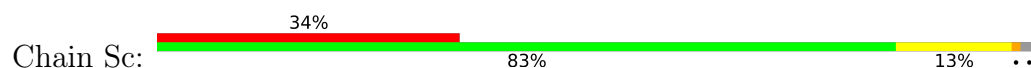
- Molecule 16: 40S ribosomal protein S23-A



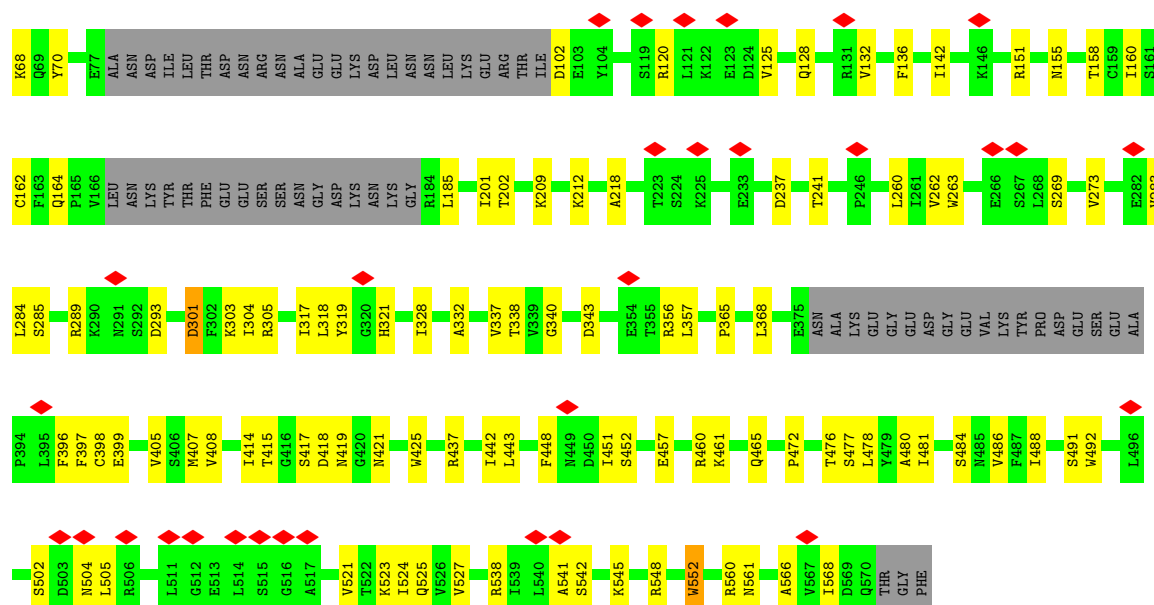
- Molecule 17: 40S ribosomal protein S24-A



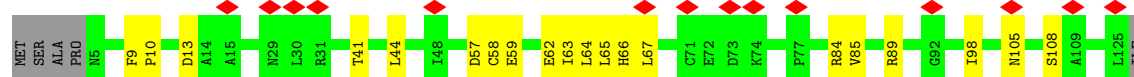
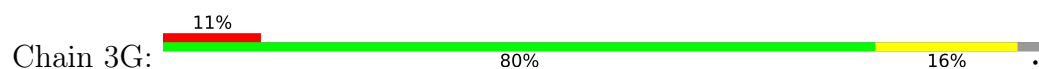
- Molecule 18: 40S ribosomal protein S27-A



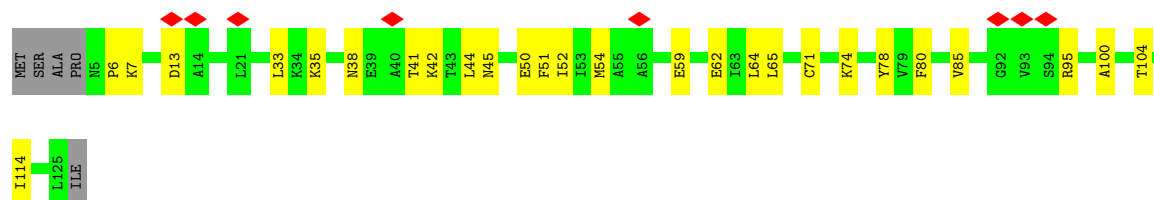
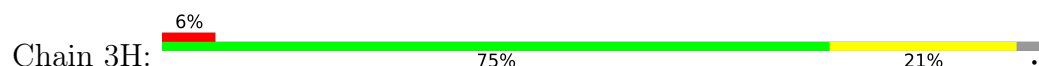




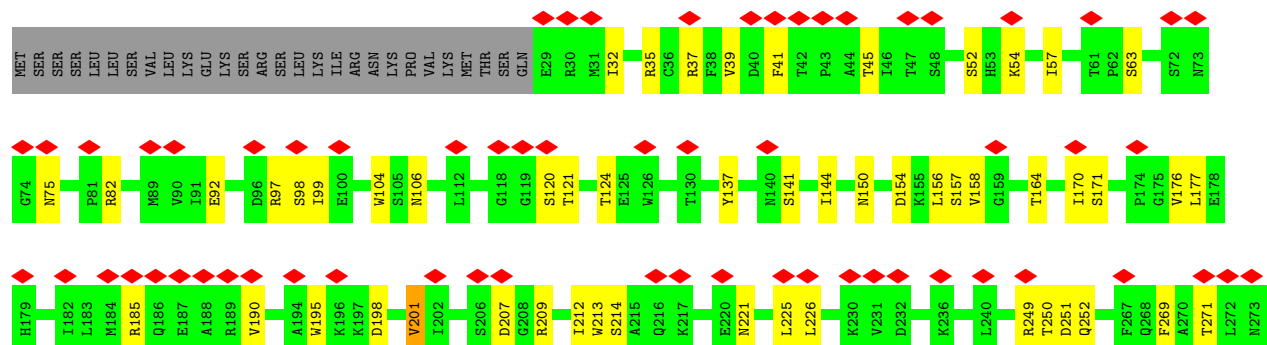
- Molecule 24: 13 kDa ribonucleoprotein-associated protein

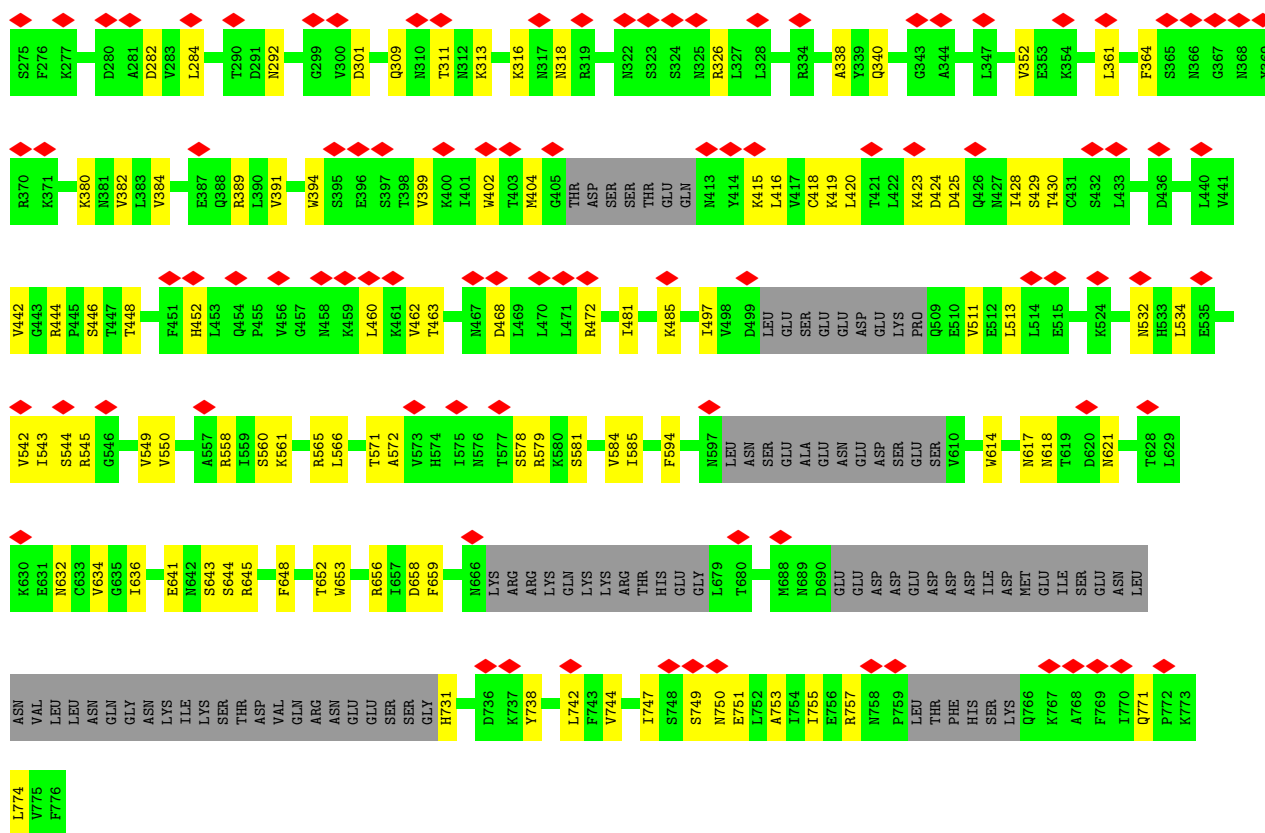


- Molecule 24: 13 kDa ribonucleoprotein-associated protein

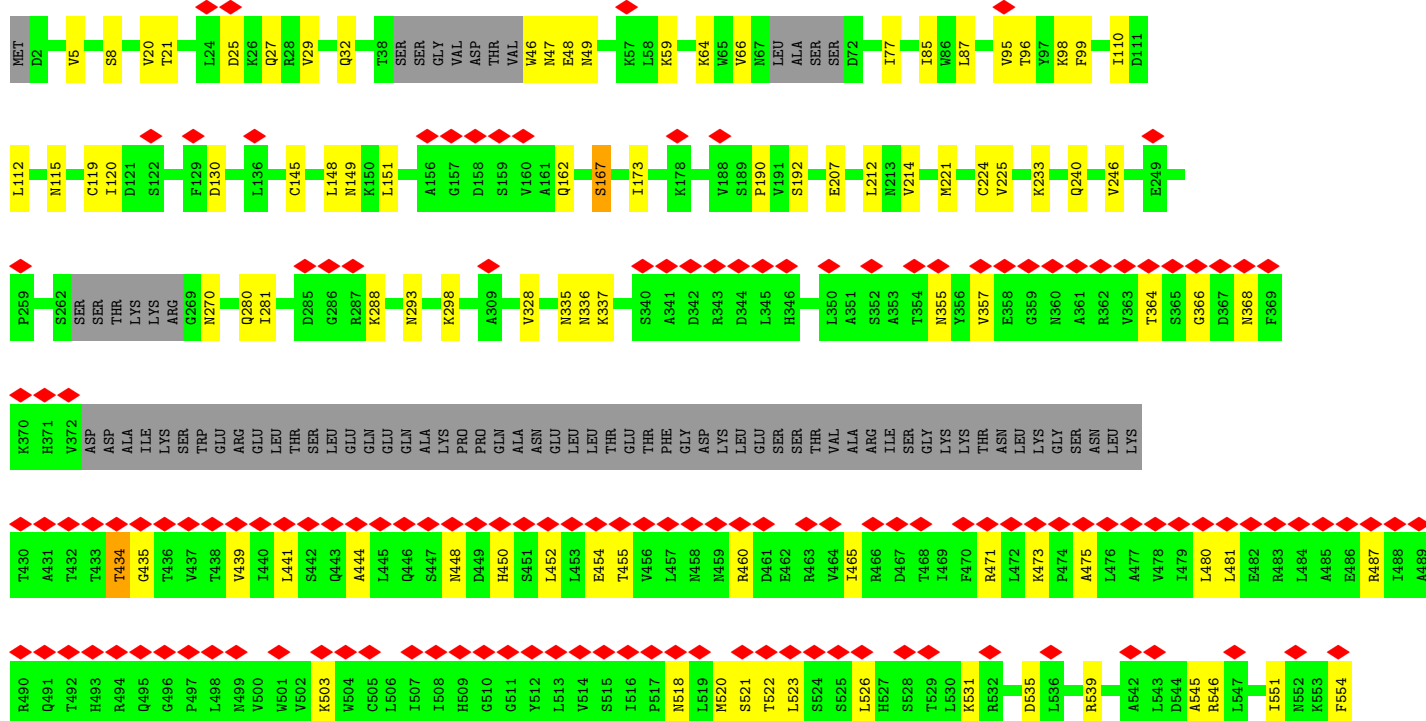


- Molecule 25: U3 small nucleolar RNA-associated protein 4

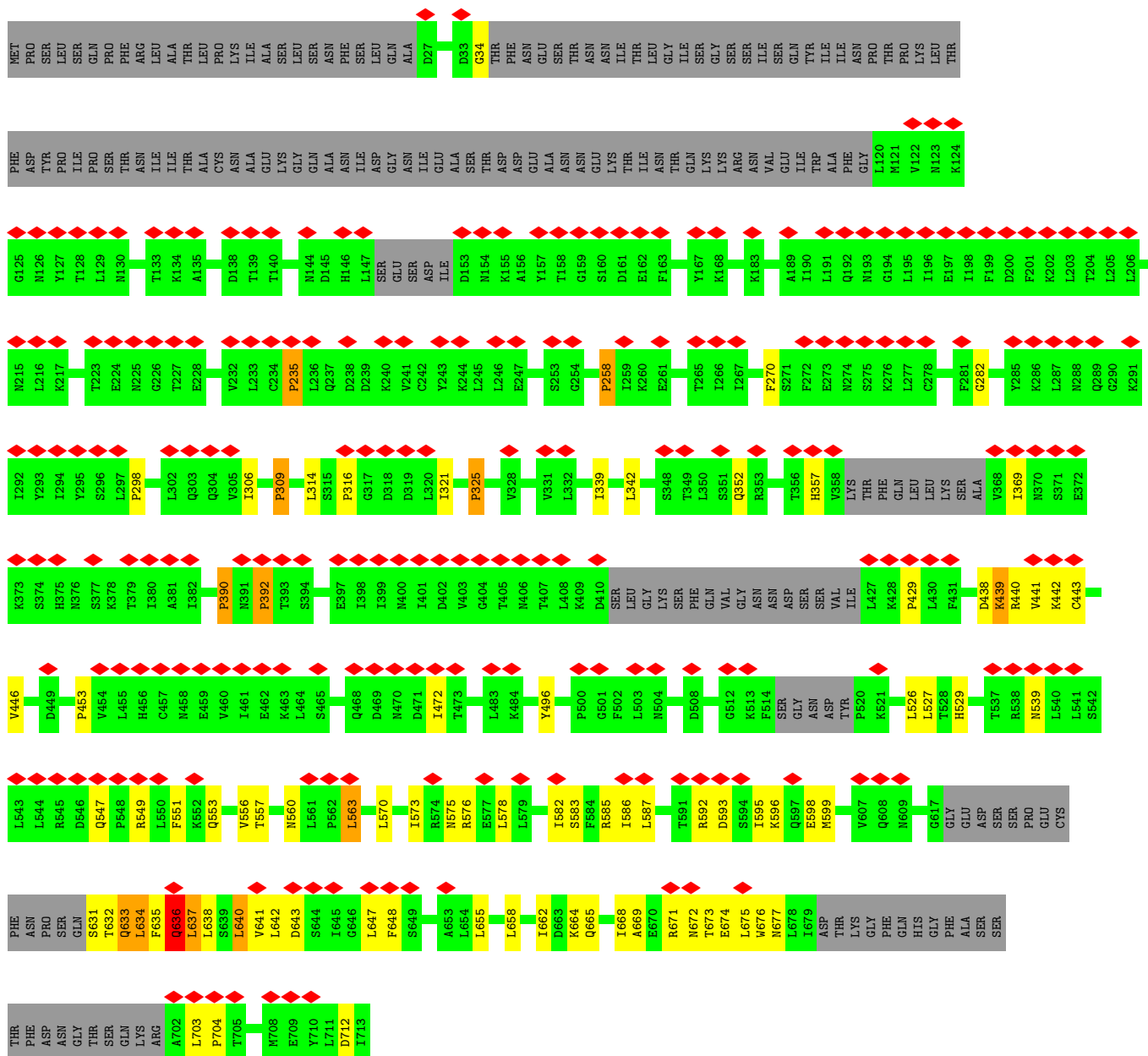




• Molecule 26: U3 small nucleolar RNA-associated protein 5



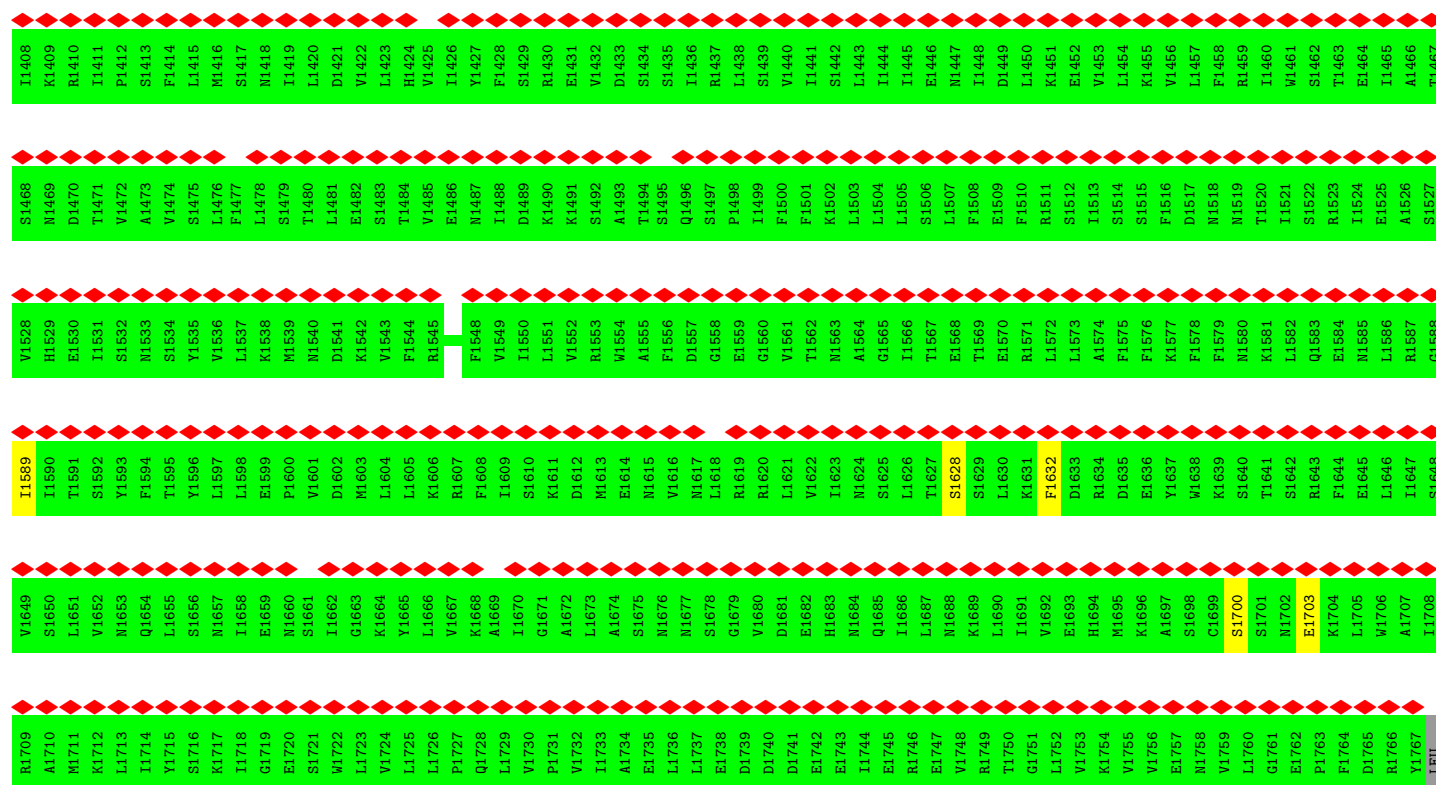
- Molecule 27: U3 small nucleolar RNA-associated protein 8



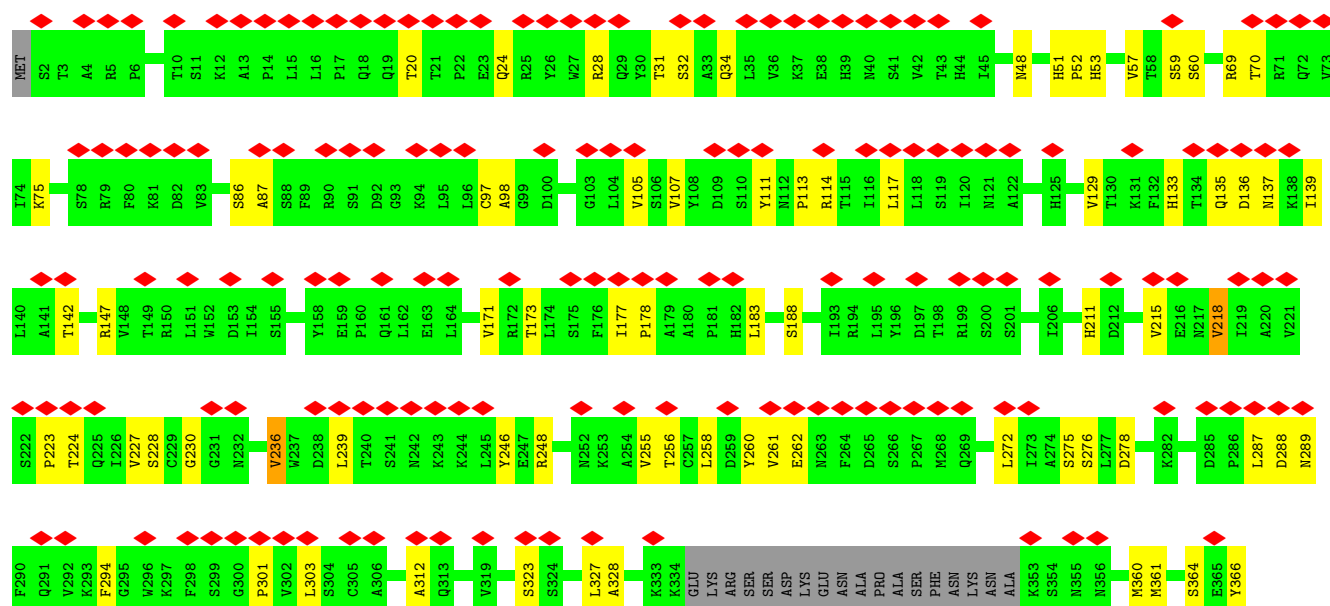
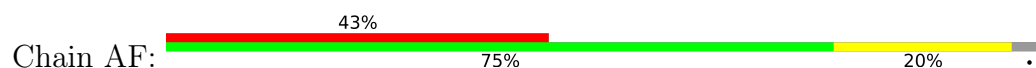
- Molecule 28: U3 small nucleolar RNA-associated protein 9

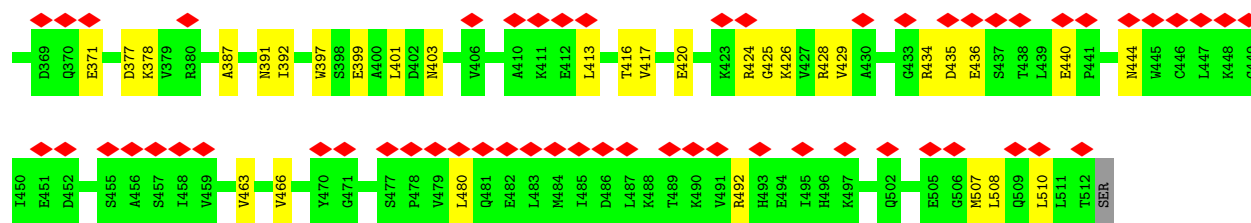


K1348	I1349	S1350	S1351	L1352	A1353	L1354	I1355	T1356	N1357	C1358	V1359	S1360	V1361	L1362	G1363	V1364	K1365	S1366	I1367	A1368	F1369	V1370	P1371	K1372	I1373	V1374	P1375	P1376	S1377	I1378	K1379	L1380	F1381	D1382	A1383	S1384	L1385	A1386	D1387	S1388	S1389	N1390	P1391	L1392	K1393	E1394	Q1395	L1396	Q1397	V1398	A1399	I1400	L1401	L1402	L1403	F1404	A1405	G1406	L1407																																																																																																																																																																																																																																																																																																																																																																																																																																													
V1288	M1289	K1290	V1291	L1292	L1293	D1294	L1295	M1296	P1297	L1298	E1299	S1300	K1301	S1302	V1303	V1304	I1305	S1306	Q1307	V1308	F1309	V1310	M1311	T1312	M1313	T1314	A1315	L1316	V1317	S1318	K1319	Y1320	GLY	LYS	LYS	LEU	GLU	G1326	S1327	L1328	L1329	T1330	Q1331	A1332	L1333	T1334	L1335	A1336	T1337	E1338	K1339	V1340	I1341	S1342	D1343	M1344	T1345	E1346	V1347																																																																																																																																																																																																																																																																																																																																																																																																																																													
E1228	I1229	L1230	F1231	K1232	V1233	L1234	G1235	N1236	V1237	LEU	GLN	ILE	LEU	PRO	V1243	D1244	E1245	F1246	V1247	N1248	A1249	V1250	L1251	P1252	L1253	L1254	S1255	T1256	S1257	T1258	N1259	E1260	D1261	I1262	R1263	Y1264	H1265	L1266	T1267	L1268	V1269	I1270	G1271	S1272	K1273	F1274	L1275	E1276	E1277	G1278	S1279	E1280	A1281	I1282	P1283	I1284	V1285	N1286	N1287																																																																																																																																																																																																																																																																																																																																																																																																																																													
LEU	ASP	GLU	THR	SER	D1172	K1173	K1174	L1175	T1176	R1177	N1178	I1179	L1180	GLU	GLU	PHE	THR	LEU	GLY	THR	LEU	GLY	VAL	PHE	THR	THR	V1197	E1198	L1199	T1200	F1201	S1202	C1203	I1204	T1205	E1208	N1209	E1210	E1211	A1212	S1213	D1214	S1215	E1216	T1217	SER	LEU	SER	ASP	H1222	T1223	T1224	E1225	I1226	K1227																																																																																																																																																																																																																																																																																																																																																																																																																																																	
E1106	K1107	K1108	K1109	S1110	L1111	E1112	S1113	R1114	VAL	L1057	V1058	N1059	F1060	K1061	I1062	ASN	PHE	SER	GLY	THR	LEU	GLY	VAL	PHE	THR	THR	LYS	ALA	LEU	PHE	ILE	ASN	LYS	ILE	THR	V1081	M1082	E1083	E1084	L1085	S1086	G1087	L1088	N1089	D1090	L1091	L1092	D1093	I1094	I1095	K1096	L1097	L1098	T1099	S1100	S1101	K1102	S1103	S1104	S1105																																																																																																																																																																																																																																																																																																																																																																																																																																												
A1041	L1042	I1049	ALA	GLN	TYR	SER	SER	ALA	L1057	V1058	N1059	F1060	K1061	I1062	ASN	G1063	E1064	A1065	R1066	I1067	L1068	I1069	PHE	E1070	F1071	ILE	LYS	ALA	LEU	PHE	LEU	VAL	ASP	ASN	LYS	H1080	V1081	M1082	E1083	E1084	L1085	S1086	G1087	L1088	N1089	D1090	L1091	L1092	D1093	I1094	I1095	K1096	L1097	L1098	T1099	S1100	S1101	K1102	S1103	S1104	S1105																																																																																																																																																																																																																																																																																																																																																																																																																																											
THR	THR	VAL	VAL	GLU	ARG	THR	ILE	ALA	ASP	ILE	LEU	VAL	ALA	ASP	ASN	A933	S934	P935	K940	L941	L942	L943	V944	I945	L948	ALA	THR	LEU	LEU	THR	SER	SER	THR	THR	ALA	LEU	GLN	H1019	V1020	R1024	R1025	V1026	K1027	L1028	F1029	S1030	T1031	L1032	ILE	LYS	THR	LEU	ASP	PRO	V1039	K1040																																																																																																																																																																																																																																																																																																																																																																																																																																																
E916	L917	T918	N919	V920	R921	ALA	ASP	ILE	ASP	LEU	VAL	SER	ALA	ILE	ARG	ASN	A933	S934	P935	K940	L941	L942	L943	V944	I945	L948	ALA	THR	LEU	LEU	THR	SER	SER	THR	THR	ALA	LEU	GLN	H1019	V1020	R1024	R1025	V1026	K1027	L1028	F1029	S1030	T1031	L1032	ILE	LYS	THR	LEU	ASP	PRO	V1039	K1040																																																																																																																																																																																																																																																																																																																																																																																																																																															
HIS	LEU	ARG	LYS	THR	THR	ILE	ILE	GLU	A857	L858	D859	V864	G865	K868	LEU	LEU	PHE	THR	LEU	LEU	LEU	THR	THR	THR	THR	ILE	ASP	GLN	ASP	GLU	THR	THR	THR	THR	GLN	ASP	GLU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

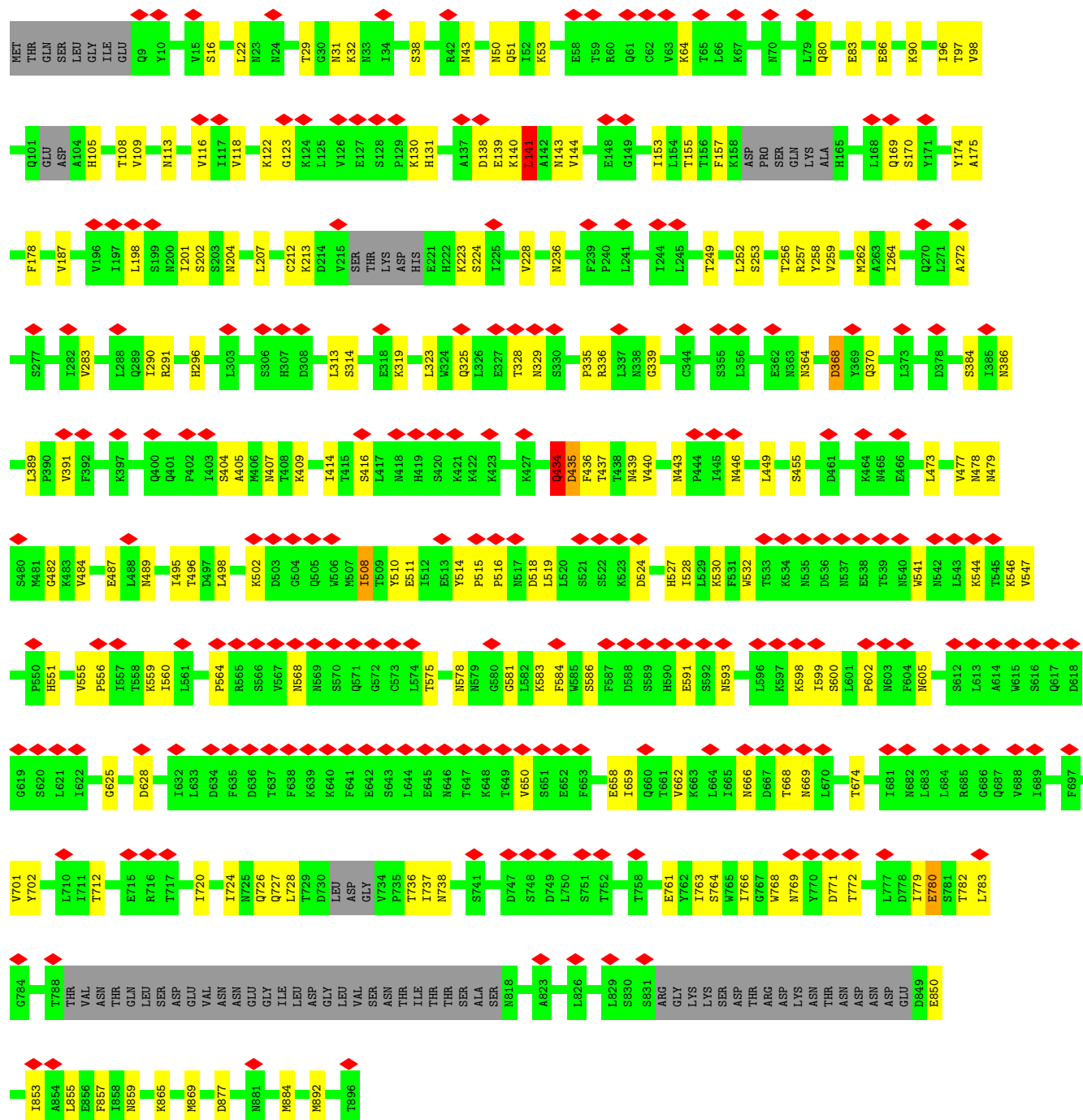
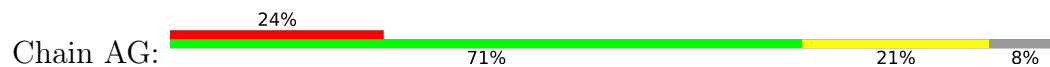


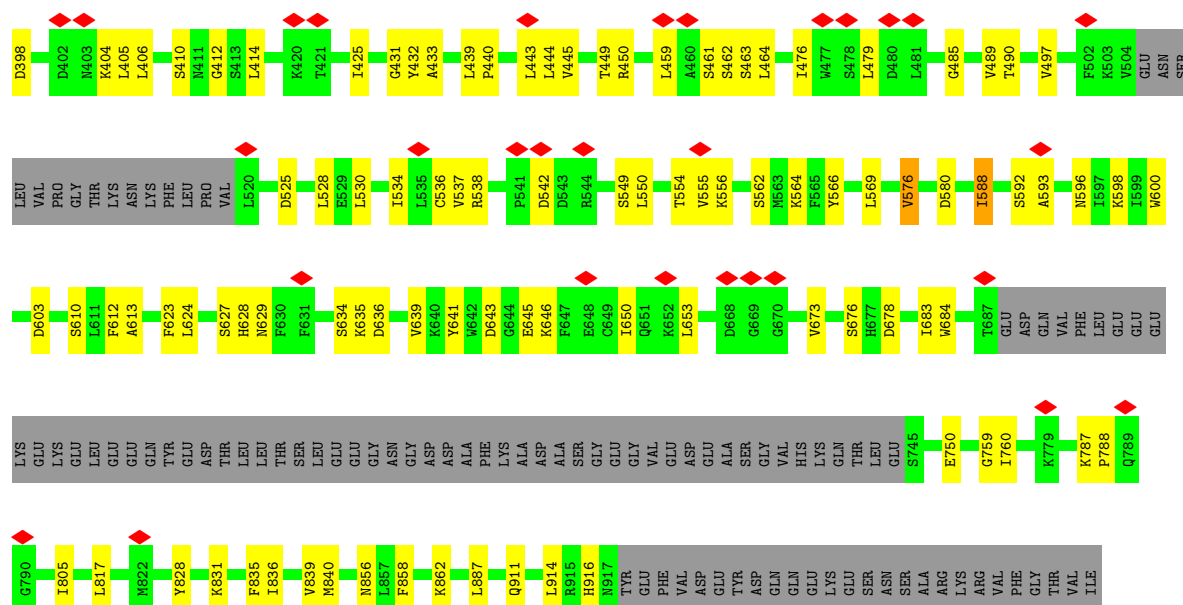
- Molecule 30: U3 small nucleolar RNA-associated protein 15



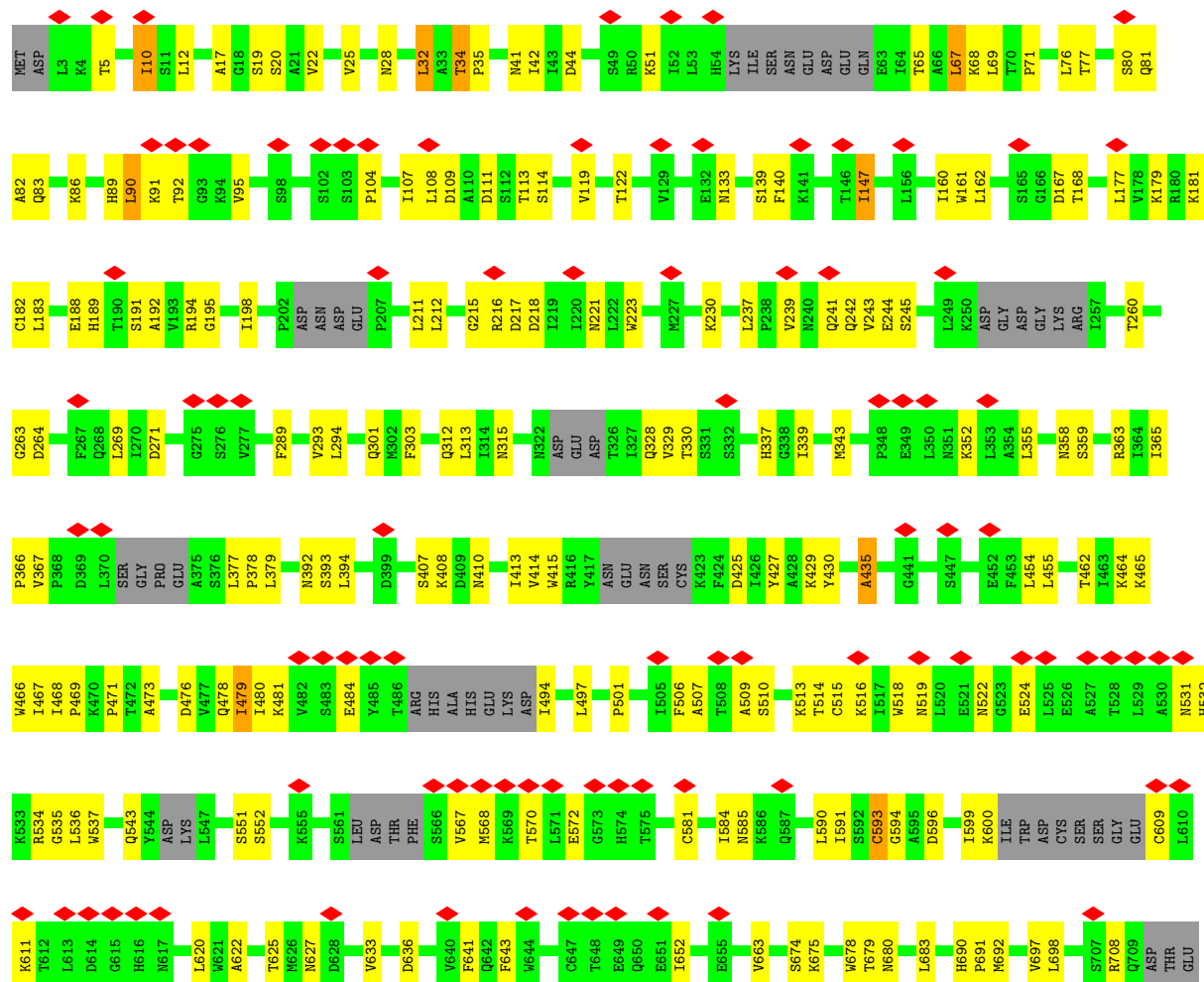


• Molecule 31: NET1-associated nuclear protein 1



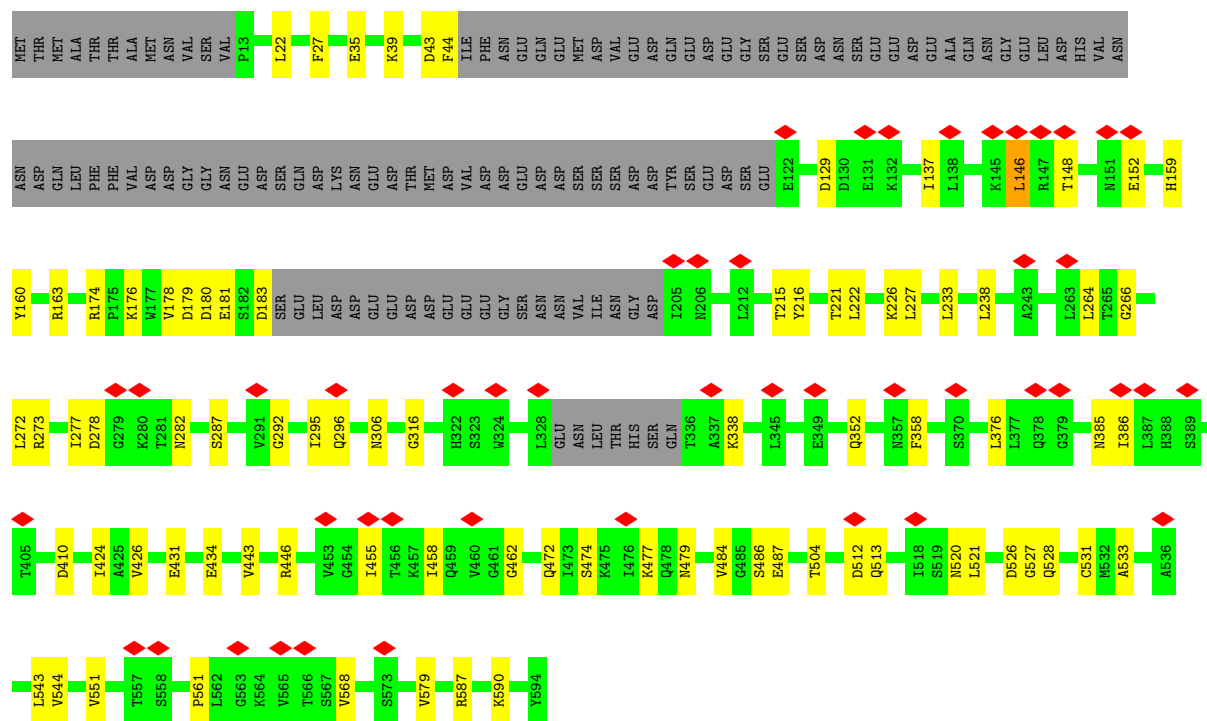


• Molecule 34: U3 small nucleolar RNA-associated protein 13

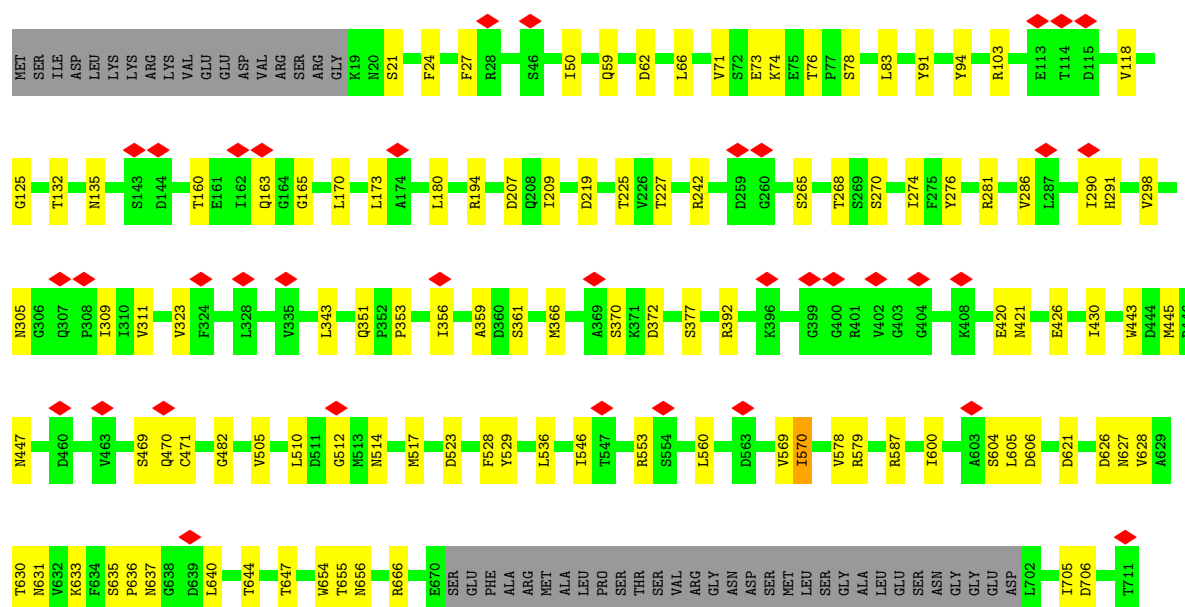
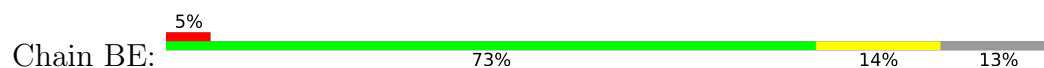


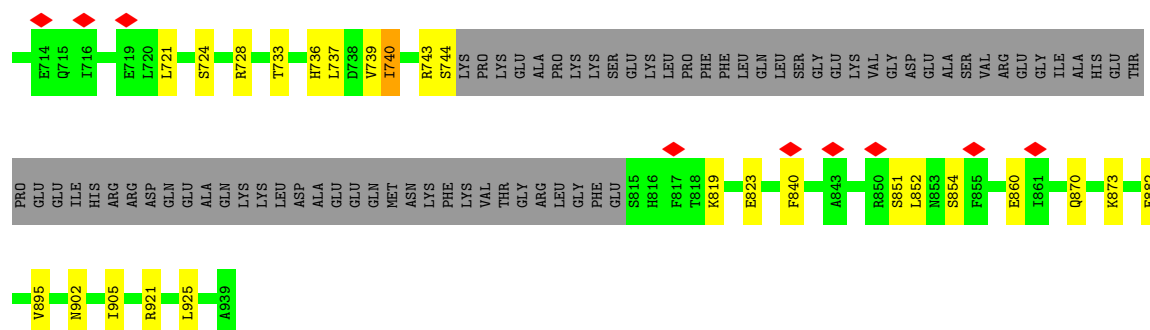


- Molecule 35: U3 small nucleolar RNA-associated protein 18

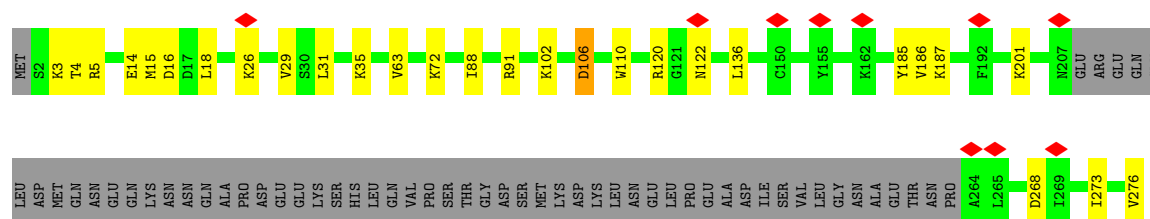


- Molecule 36: U3 small nucleolar RNA-associated protein 21

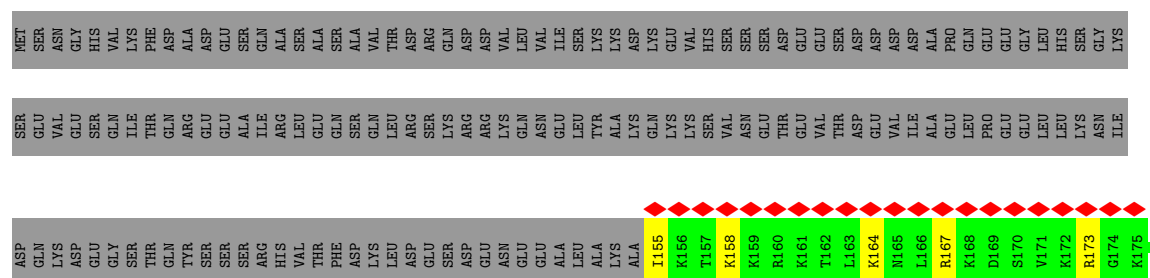




• Molecule 37: U3 small nucleolar RNA-associated protein 6



• Molecule 38: Bud site selection protein 21

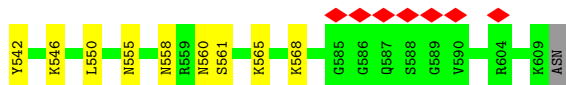


• Molecule 39: U3 small nucleolar RNA-associated protein 7

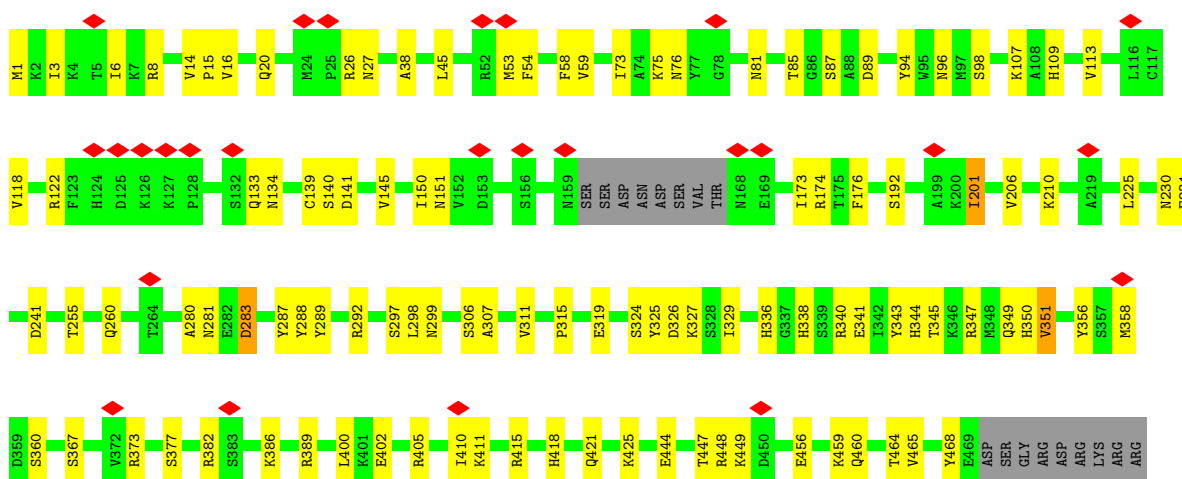




Chain 5H: 11% 88%

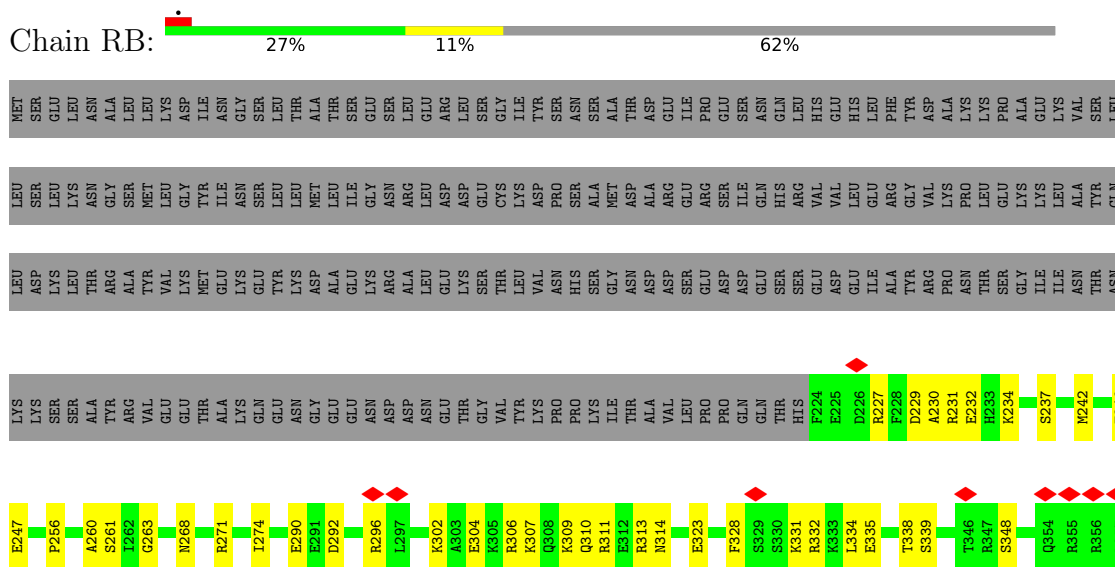


Chain 5I: 5% 72% 22% 6%

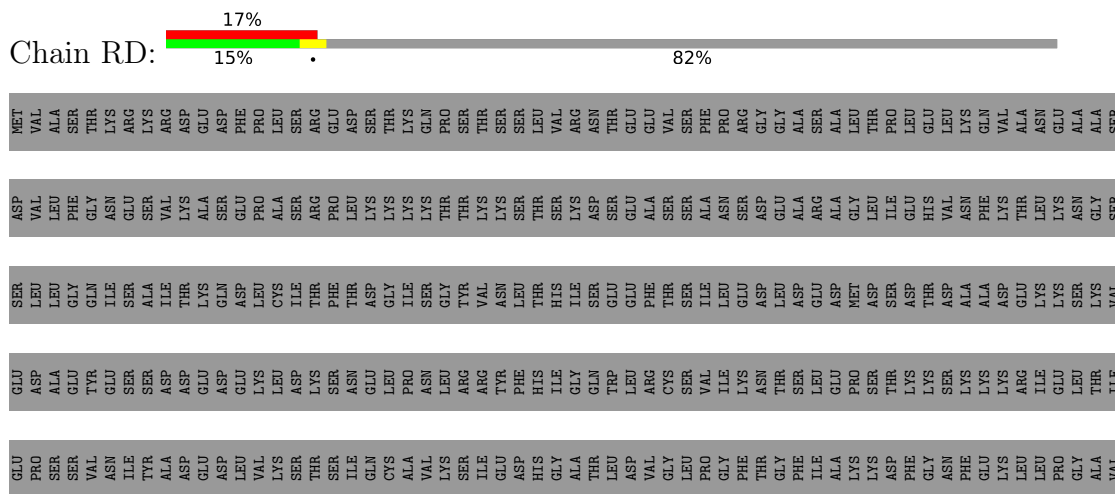


[illegible]

- Molecule 49: U3 small nucleolar ribonucleoprotein protein LCP5

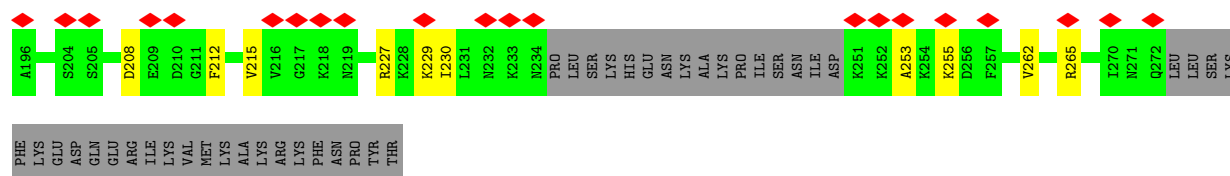


- Molecule 50: rRNA biogenesis protein RRP5

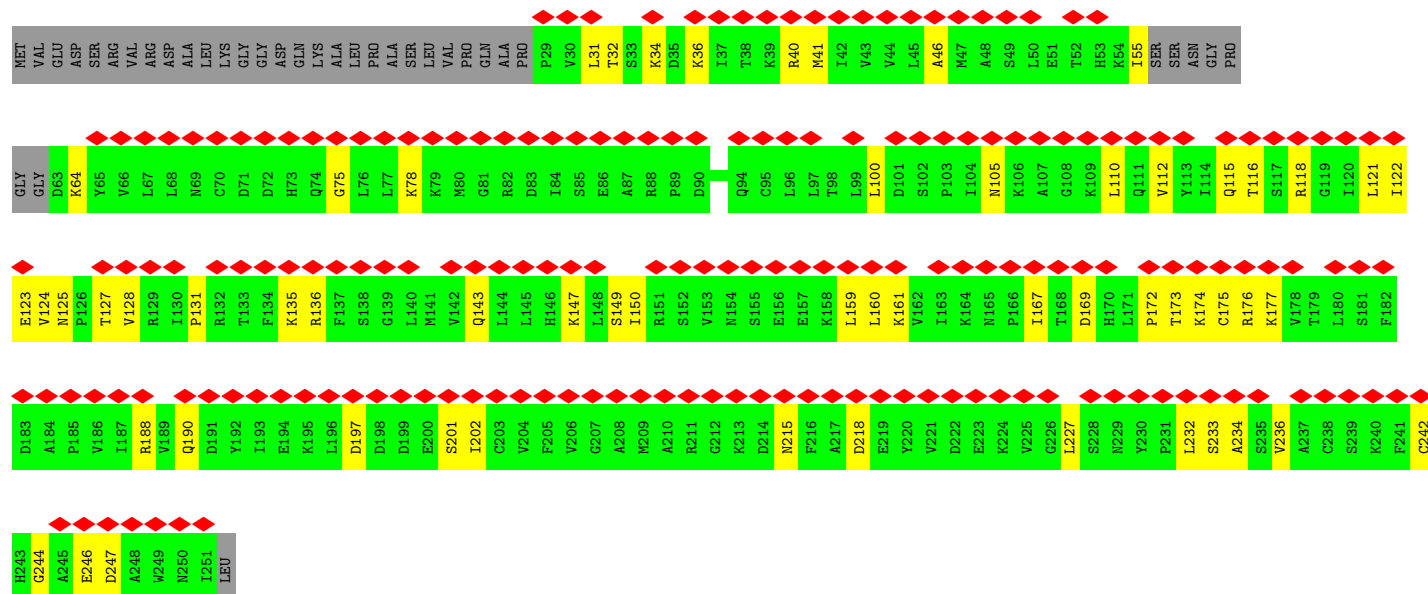
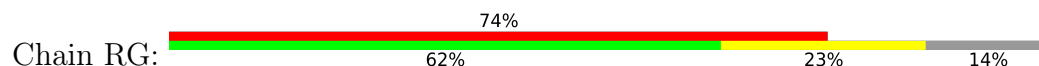




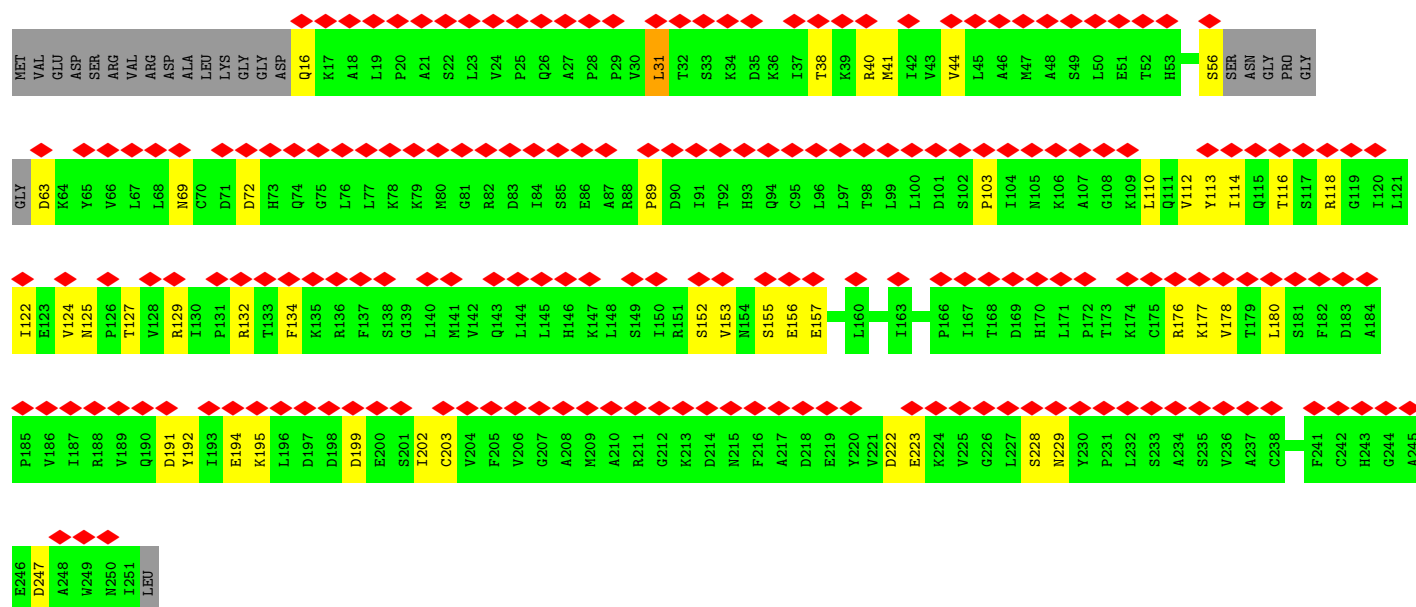
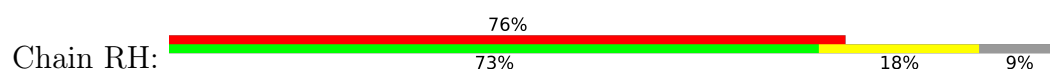




• Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

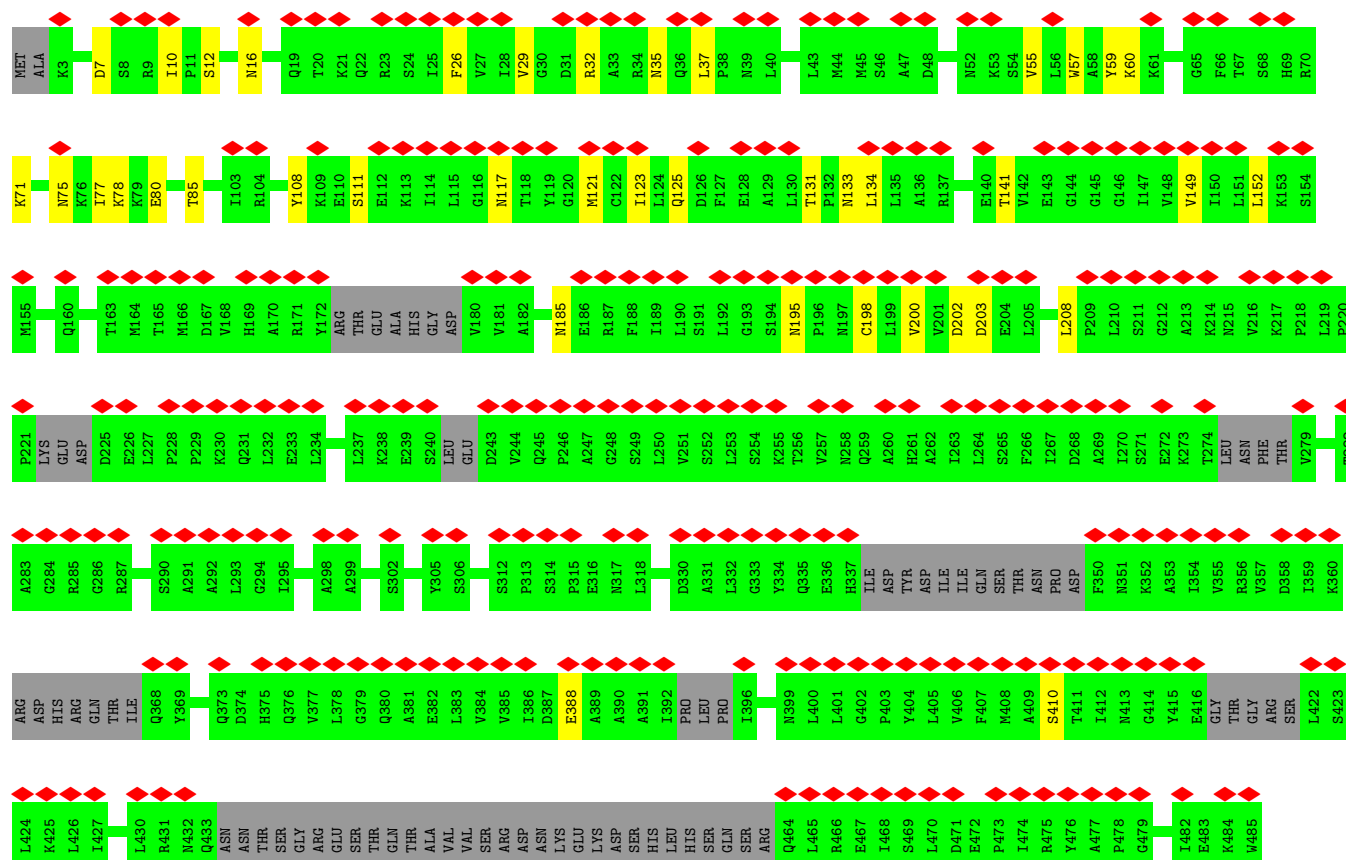


• Molecule 53: Ribosomal RNA small subunit methyltransferase NEP1

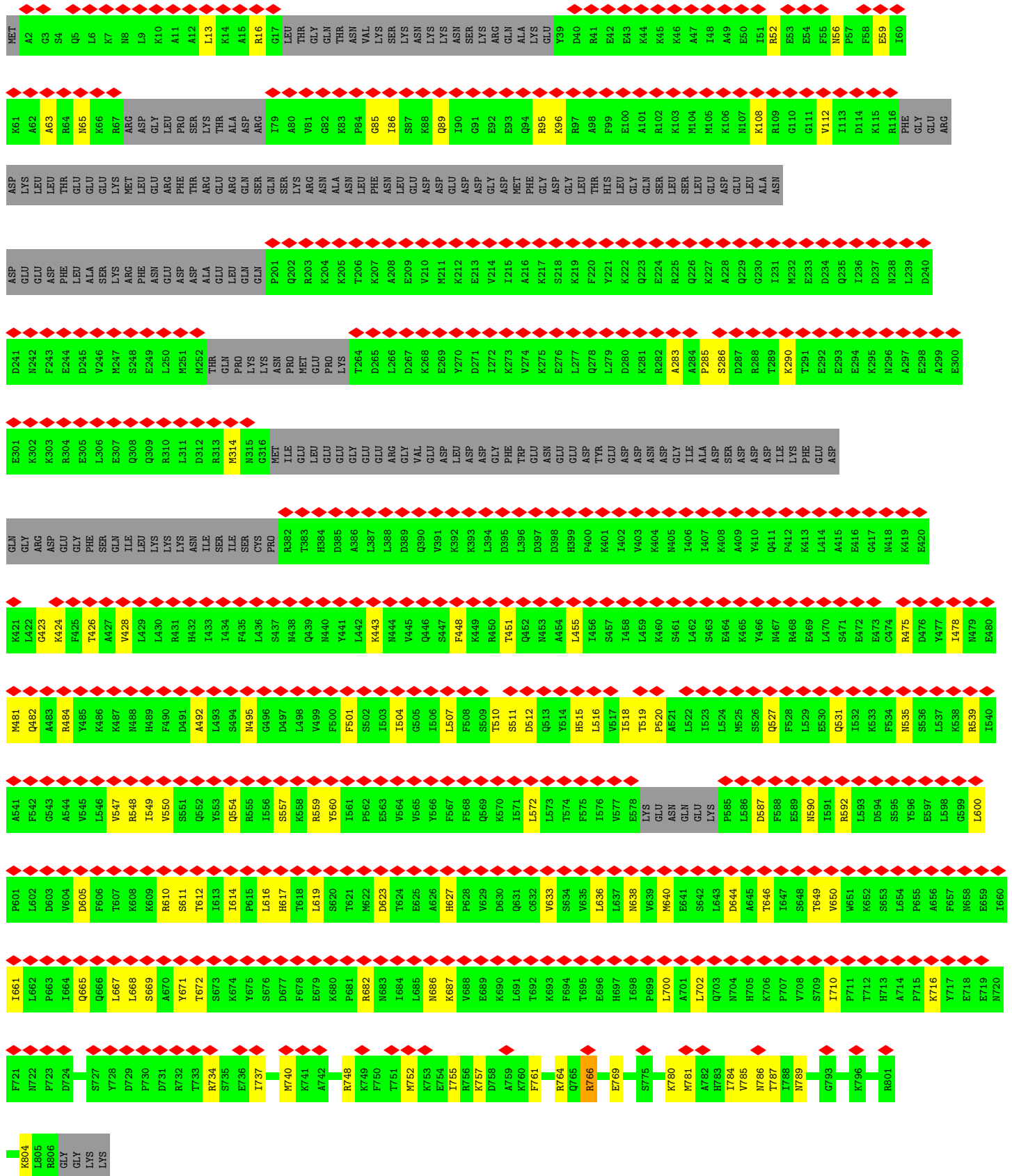


Chain RJ:

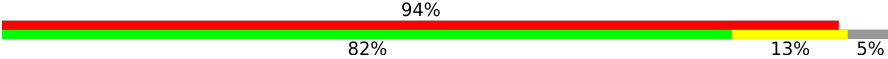


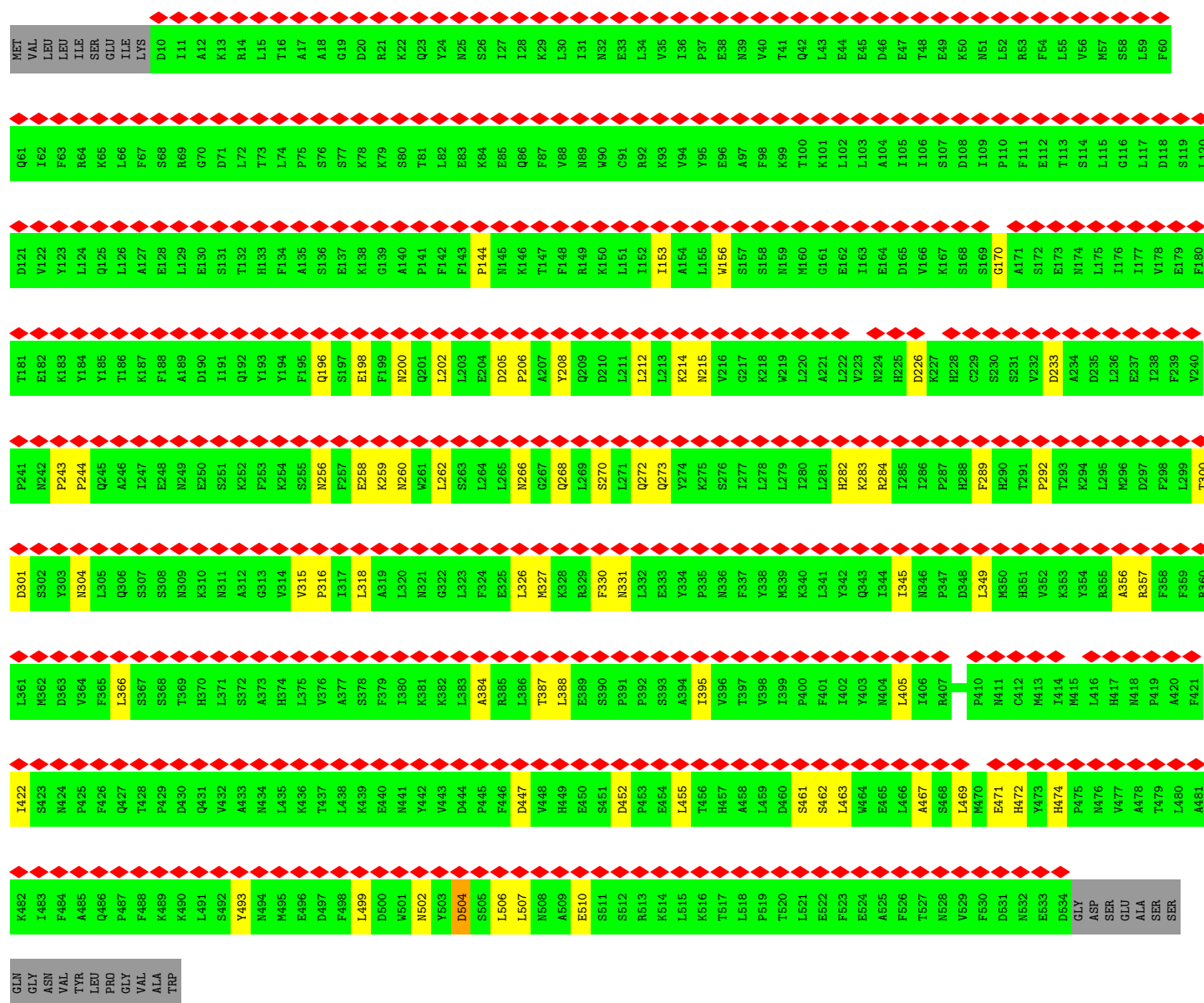






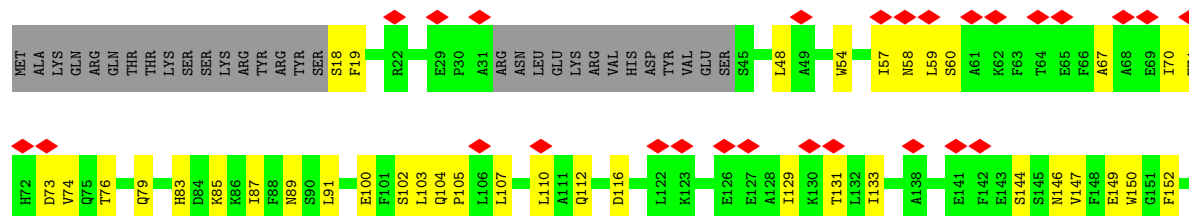
- Molecule 58: Nucleolar complex protein 4

Chain RO: 



• Molecule 59: U3 small nucleolar RNA-associated protein 20

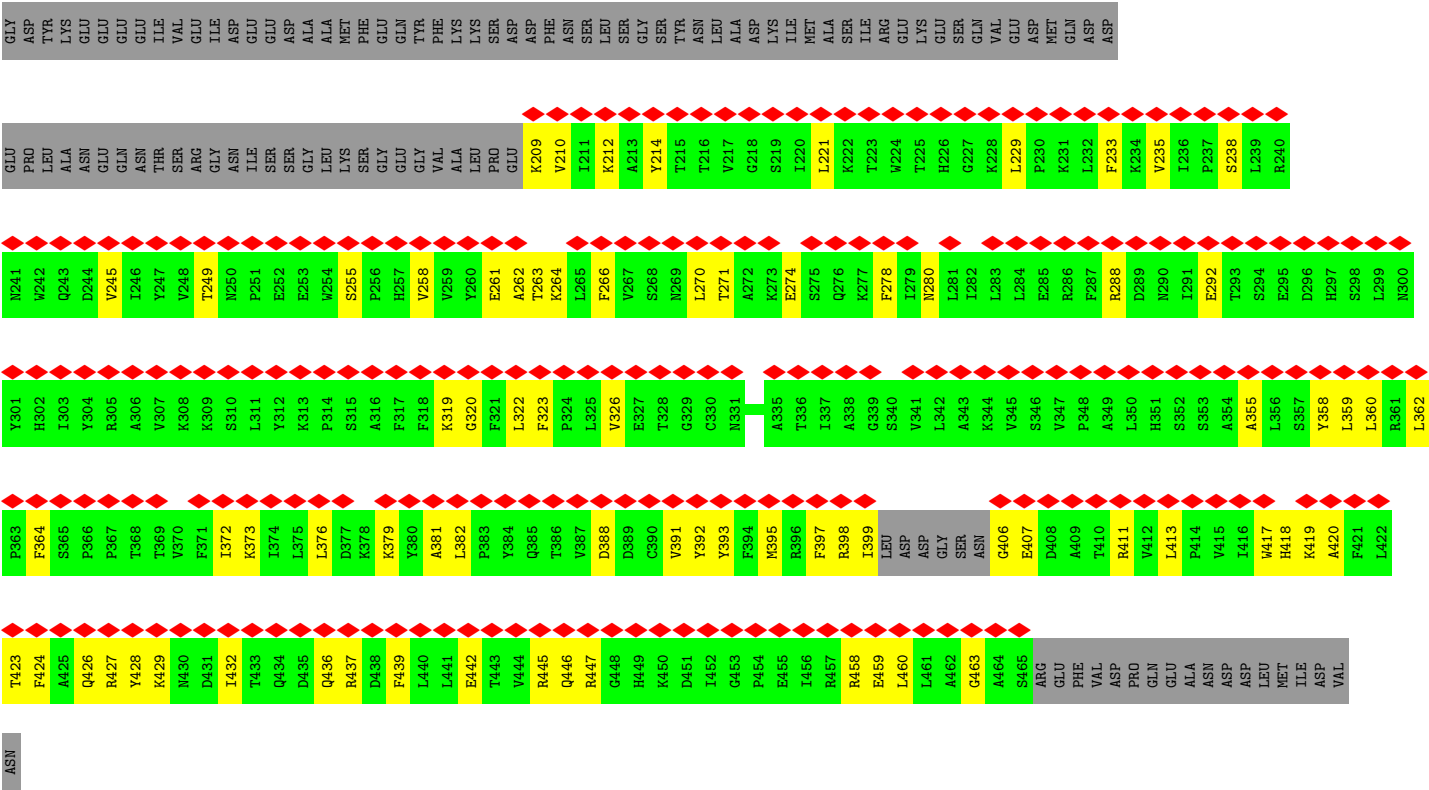
Chain RP: 



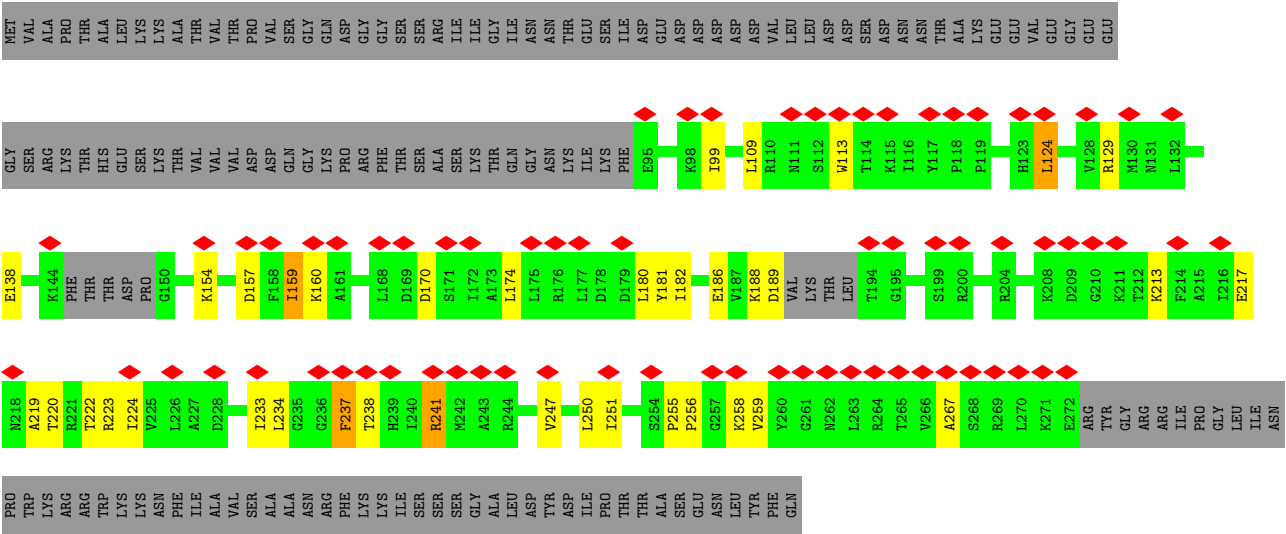
GLY	TYR	LYS	SER	TYR	SER	GLU	LEU	GLU	TRP	PRO	LEU	LEU	PHE	THR	PHE	HIS	PHE	ILE	ASN	ASN	LYS	GLU	GLU	LEU	ALA	ALA	ARG	THR	ASN	ALA	HIS	ALA	ILE	MET	LYS	PHE	ILE	D1376	N1379	E1380	I1391	K1395	D1396	V1413	GLN	SER	GLU	TYR	VAL	SER	V1420				
S1222	S1223	K1233	K1234	N1238	D1239	T1240	Q1241	K1242	I1243	L1247	M1255	C1256	S1257	W1258	L1264	Y1265	T1266	T1267	I1268	S1269	F1272	K1273	R1278	N1279	L1280	R1281	V1282	I1289	E1299	V1305	A1306	H1317	D1320	F1321	P1322	ARG	ILE	LEU	SER	THR	PHE	LYS	GLY	LEU	ILE	GLU	ASP								
A251	T264	K265	P268	S287	L288	L292	P293	V294	Y295	F302	N303	D304	S305	LEU	ASP	ALA	THR	ASN	ILE	ASP	R313	T319	T320	F323	S324	E325	SER	GLY	ARG	LYS	T330	P331	D332	W333	N334	K335	L336	T337	I338	E341	M344	SER	GLN	SER	GLU	ASN	CYS	ALA	SER	L353					
R367	N368	S369	D370	V371	K372	T375	H378	F382	N383	I389	S390	F393	L394	E395	F396	F397	Q398	F399	A400	Y405	E406	R407	F411	ASN	GLY	LEU	PHE	LYS	LEU	GLN	L419	N424	W425	Q426	S427	Q428	G429	K430	K431	I432	A433	L434	F435	F436	L437	E438	V439	D441	K442						
P443	E444	L445	Q446	N452	F453	P454	E455	E456	F457	I458	L459	S460	I461	R462	D463	F464	F465	A468	E469	I470	N474	I479	TYR	TRP	ARG	ALA	ILE	I485	F486	K487	Y488	S489	K490	L491	Q492	I496	I497	ILE	PRO	D593	LEU	LEU	E502	R503	T515	K516	ASP	MET	VAL	G520	T521	D531	A532		
S533	GLY	ASN	ASN	LEU	K539	D543	N544	Y545	E546	K549	E550	S551	L552	ASN	PHE	LEU	ARG	G557	W558	N559	K560	L561	V562	S563	N564	L565	H566	P567	I485	F486	K487	Y488	S489	K490	L491	Q492	I496	I497	ILE	PRO	D593	LEU	LEU	E502	R503	T515	K516	ASP	MET	VAL	G520	T521	D531	A532	
L610	Q611	G612	M613	Q614	V615	P616	D617	L618	L619	S620	S621	C622	M623	L630	T631	N634	A635	L638	T639	I640	R641	I642	K643	ASN	VAL	GLY	ALA	GLU	PHE	GLY	LYS	T652	K653	T654	D655	K656	S659	S660	F661	K664	F667	G668	L669	L670	R673	F674	V677	G680	V681	F682					
D683	T684	L685	P686	N687	V688	T689	K691	V694	D692	E693	V700	L706	P707	D708	E709	N710	D714	Y715	P718	L719	N725	S732	R735	L736	T739	F743	Y750	S751	T752	Q753	S756	I757	T758	S759	Y770	P771	L772	L773	I774	R775	N776	Q777	A778	L779	K780										
V781	M782	L783	F786	A789	F793	V794	V800	D803	E810	E811	D812	M813	E814	N815	T820	G821	L835	S836	K837	F838	E849	H853	L854	L857	L858	G859	S860	T863	D864	A869	L870	D871	A872	L873	L874	A875	Y876	K877	N878	P879	T880	N882	K883	Y884											
L891	T895	K898	D899	E900	I901	T902	T903	T906	E907	S910	Q911	E916	D917	E918	M922	P923	Y924	T938	Q941	K942	R943	S944	R945	V949	A968	S969	E970	R971	L972	D973	Y974	N975	Y976	N980	S981	H982	Q983	I984	N985	S986	S987	H1018	S1021	V1022	P1025										
Y1028	S1029	I1030	A1031	M1032	A1033	Y1034	Y1035	V1036	L1037	H1046	Q1057	K1060	C1061	L1062	E1067	D1074	W1075	S1076	T1077	S1078	M1079	V1085	V1086	V1087	M1098	L1099	Q1100	Q1101	S1104	Y1119	Q1120	F1121	L1122	Y1123	Y1124	F1127	T1131	Q1140	H1141	V1142	K1143	E1144	A1145	V1146	P1149										
I1150	I1151	E1152	A1153	A1154	D1155	S1156	I1157	D1164	D1165	H1166	Y1167	V1168	D1169	L1170	V1171	T1172	L1173	L1174	C1175	T1176	S1177	C1178	L1179	K1180	I1181	L1182	P1183	S1184	L1185	Y1186	V1187	L1188	L1189	S1190	Q1191	S1192	N1193	S1194	I1195	S1196	T1197	F1198	L1199	N1200	L1201	L1202	V1203	S1204	I1205	M1208	G1209	D1214	H1215	V1216	R1217
S1222	S1223	K1233	K1234	N1238	D1239	T1240	Q1241	K1242	I1243	L1247	M1255	C1256	S1257	W1258	L1264	Y1265	T1266	T1267	I1268	S1269	F1272	K1273	R1278	N1279	L1280	R1281	V1282	I1289	E1299	V1305	A1306	H1317	D1320	F1321	P1322	ARG	ILE	LEU	SER	THR	PHE	LYS	GLY	LEU	ILE	GLU	ASP								



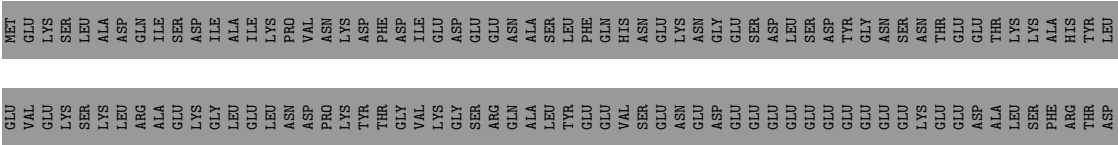




• Molecule 62: Pno1



• Molecule 63: Protein BFR2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3050	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	0.062	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	597.632, 597.632, 597.632	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	3A	0.46	0/4141	0.62	3/6433 (0.0%)
2	5A	0.40	0/4605	0.46	1/7168 (0.0%)
3	SA	0.35	0/30585	0.47	8/47611 (0.0%)
4	SC	0.44	0/1856	0.77	3/2490 (0.1%)
5	SF	0.29	0/1854	0.66	0/2504
6	SG	0.49	0/1690	0.67	2/2285 (0.1%)
7	SH	0.24	0/1341	0.61	1/1789 (0.1%)
8	SI	0.32	0/1341	0.69	2/1806 (0.1%)
9	SJ	0.26	0/1347	0.60	0/1801
10	SK	0.44	0/1410	0.63	0/1888
11	SM	0.26	0/1020	0.64	0/1374
12	SO	0.39	0/1109	0.63	0/1495
13	SP	0.47	0/879	0.80	0/1186
14	SR	0.52	0/990	0.77	3/1335 (0.2%)
15	SX	0.46	0/1020	0.63	0/1371
16	SY	0.48	0/798	0.65	0/1065
17	SZ	0.36	0/822	0.73	0/1103
18	Sc	0.40	0/613	0.63	0/828
19	Sd	0.50	0/499	0.72	2/670 (0.3%)
20	3B	0.51	0/1901	0.66	1/2567 (0.0%)
20	3C	0.37	0/1796	0.67	0/2424
21	3D	0.40	0/2891	0.62	0/3895
22	3E	0.38	0/3059	0.62	0/4153
23	3F	0.36	0/3715	0.64	0/5001
24	3G	0.51	0/928	0.72	1/1262 (0.1%)
24	3H	0.45	0/928	0.70	0/1262
25	A4	0.43	0/5321	0.66	0/7207
26	A5	0.44	0/4044	0.65	0/5493
27	A8	0.38	0/3249	0.86	12/4454 (0.3%)
28	A9	0.29	0/951	0.61	0/1287
29	AE	0.32	1/10049 (0.0%)	0.56	1/13737 (0.0%)
30	AF	0.48	0/3993	0.68	0/5413

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	AG	0.42	0/6699	0.64	3/9077 (0.0%)
32	B1	0.59	0/6474	0.70	3/8763 (0.0%)
33	B2	0.39	0/6628	0.69	2/8954 (0.0%)
34	B3	0.35	0/6014	0.70	2/8137 (0.0%)
35	B8	0.55	0/3848	0.63	0/5218
36	BE	0.54	0/6580	0.65	2/8901 (0.0%)
37	B6	0.37	0/2849	0.60	0/3853
38	5B	0.31	0/499	0.62	0/659
39	5C	0.58	0/3690	0.67	2/4991 (0.0%)
40	5D	0.47	0/1417	0.74	0/1885
41	5E	0.42	0/1580	0.87	1/2115 (0.0%)
42	5F	0.37	0/1559	0.81	2/2097 (0.1%)
43	5G	0.34	0/1792	0.76	3/2425 (0.1%)
44	5H	0.47	0/601	0.59	0/789
45	5I	0.56	0/3844	0.68	0/5174
46	5J	0.37	0/1302	0.59	0/1728
47	5K	0.51	0/1426	0.66	0/1917
48	RA	0.27	0/2769	0.66	2/3753 (0.1%)
49	RB	0.37	0/1121	0.79	0/1487
50	RD	0.26	0/2453	0.67	2/3308 (0.1%)
51	RE	0.33	0/8924	0.64	4/12070 (0.0%)
52	RF	0.28	0/2004	0.66	1/2697 (0.0%)
53	RG	0.32	0/1727	0.70	0/2329
53	RH	0.37	0/1828	0.59	0/2470
54	RJ	0.44	0/6514	0.62	0/8768
55	RK	0.39	0/2832	0.64	0/3825
56	RL	0.21	0/4549	0.51	1/6241 (0.0%)
56	RM	0.15	0/3765	0.44	1/5218 (0.0%)
57	RN	0.31	0/4591	0.63	1/6187 (0.0%)
58	RO	0.32	0/3849	0.63	0/5261
59	RP	0.21	0/12225	0.54	4/16812 (0.0%)
60	RQ	0.41	0/1678	0.63	1/2282 (0.0%)
61	RS	0.30	0/2104	0.70	0/2854
62	RT	0.37	0/1355	0.74	0/1821
63	RY	0.23	0/307	0.53	0/415
All	All	0.39	1/222142 (0.0%)	0.62	77/308838 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	SC	0	1
5	SF	0	2
8	SI	0	3
9	SJ	0	1
11	SM	0	1
12	SO	0	1
13	SP	0	1
17	SZ	0	1
18	Sc	0	1
21	3D	0	3
22	3E	0	1
23	3F	0	1
24	3G	0	2
24	3H	0	1
25	A4	0	1
26	A5	0	1
27	A8	0	2
31	AG	0	2
32	B1	0	2
33	B2	0	8
34	B3	0	11
36	BE	0	1
39	5C	0	1
40	5D	0	1
43	5G	0	2
45	5I	0	2
48	RA	0	2
49	RB	0	1
51	RE	0	1
52	RF	0	1
54	RJ	0	2
55	RK	0	1
56	RL	0	1
56	RM	0	1
57	RN	0	1
58	RO	0	1
59	RP	0	3
60	RQ	0	1
62	RT	0	1
All	All	0	71

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	AE	564	VAL	C-N	5.39	1.40	1.34

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	SA	1783	C	C4'-C3'-O3'	10.71	129.07	113.00
27	A8	316	PRO	N-CA-CB	10.46	109.82	102.81
1	3A	99	U	C4'-C3'-O3'	8.84	126.25	113.00
1	3A	317	A	C4'-C3'-O3'	8.46	125.68	113.00
27	A8	258	PRO	N-CA-CB	8.38	112.05	103.25
50	RD	1223	PRO	N-CA-CB	8.04	111.69	103.25
1	3A	321	C	N1-C1'-C2'	-8.02	99.96	112.00
27	A8	325	PRO	N-CA-CB	7.91	111.55	103.25
51	RE	1105	PRO	O-C-N	-7.87	112.02	122.64
50	RD	1205	PRO	N-CA-CB	7.68	110.60	103.15
27	A8	453	PRO	N-CA-CB	7.63	110.43	103.34
27	A8	392	PRO	N-CA-CB	7.62	111.25	103.25
27	A8	429	PRO	N-CA-CB	7.45	110.27	103.19
27	A8	309	PRO	N-CA-CB	7.14	110.75	103.25
33	B2	267	ASP	CA-C-N	6.86	134.65	121.54
33	B2	267	ASP	C-N-CA	6.86	134.65	121.54
2	5A	312	U	P-O3'-C3'	6.82	130.43	120.20
27	A8	390	PRO	N-CA-CB	6.71	110.29	103.25
59	RP	2033	LYS	CA-C-N	6.64	134.22	121.54
59	RP	2033	LYS	C-N-CA	6.64	134.22	121.54
27	A8	235	PRO	N-CA-CB	6.58	110.16	103.25
32	B1	339	LEU	CA-C-N	6.48	132.06	122.86
32	B1	339	LEU	C-N-CA	6.48	132.06	122.86
27	A8	298	PRO	N-CA-CB	6.35	110.25	103.52
32	B1	339	LEU	O-C-N	6.28	130.42	123.33
52	RF	157	GLU	N-CA-C	6.11	116.34	108.34
56	RL	744	PRO	N-CA-C	6.07	124.97	112.47
56	RM	744	PRO	N-CA-C	5.99	124.81	112.47
31	AG	141	LEU	N-CA-C	5.92	117.83	110.91
24	3G	67	LEU	CA-CB-CG	5.86	136.82	116.30
59	RP	1745	ILE	CA-C-N	5.82	132.66	121.54
59	RP	1745	ILE	C-N-CA	5.82	132.66	121.54
8	SI	117	THR	CA-C-N	5.82	132.65	121.54
8	SI	117	THR	C-N-CA	5.82	132.65	121.54
43	5G	192	ASP	CA-C-N	5.76	132.54	121.54
43	5G	192	ASP	C-N-CA	5.76	132.54	121.54
36	BE	840	PHE	CA-C-N	5.67	130.10	121.03
36	BE	840	PHE	C-N-CA	5.67	130.10	121.03

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	SA	1052	U	O3'-P-O5'	5.66	112.49	104.00
43	5G	157	PHE	N-CA-C	5.60	122.18	109.81
14	SR	123	ARG	CA-C-N	5.59	140.41	127.00
14	SR	123	ARG	C-N-CA	5.59	140.41	127.00
4	SC	54	LEU	CA-CB-CG	5.58	135.85	116.30
27	A8	640	LEU	CA-C-O	-5.51	115.03	120.70
27	A8	636	GLN	N-CA-C	-5.49	105.39	111.71
51	RE	924	LEU	CA-CB-CG	5.49	135.50	116.30
48	RA	286	GLU	CA-C-N	5.46	131.98	121.54
48	RA	286	GLU	C-N-CA	5.46	131.98	121.54
3	SA	1782	A	C4'-C3'-O3'	5.44	121.17	113.00
60	RQ	313	PHE	N-CA-C	5.43	121.82	109.81
3	SA	579	A	P-O3'-C3'	5.38	128.27	120.20
29	AE	1589	ILE	N-CA-C	-5.35	107.61	112.96
4	SC	54	LEU	CA-C-N	5.31	131.68	121.54
4	SC	54	LEU	C-N-CA	5.31	131.68	121.54
3	SA	272	U	P-O3'-C3'	5.30	128.16	120.20
7	SH	41	VAL	N-CA-C	-5.24	107.72	112.96
51	RE	1105	PRO	CA-C-N	5.22	130.68	122.33
51	RE	1105	PRO	C-N-CA	5.22	130.68	122.33
42	5F	174	ARG	CA-C-N	5.11	131.29	121.54
42	5F	174	ARG	C-N-CA	5.11	131.29	121.54
3	SA	1782	A	N9-C1'-C2'	-5.10	104.35	112.00
41	5E	448	LEU	CA-CB-CG	5.08	134.10	116.30
14	SR	123	ARG	C-N-CD	-5.07	109.46	120.60
19	Sd	50	GLU	CA-C-N	5.05	131.19	121.54
19	Sd	50	GLU	C-N-CA	5.05	131.19	121.54
39	5C	456	SER	CA-C-N	5.04	128.82	121.31
39	5C	456	SER	C-N-CA	5.04	128.82	121.31
3	SA	1594	G	C4'-C3'-O3'	5.04	116.95	109.40
31	AG	138	ASP	CA-C-N	5.03	128.22	120.82
31	AG	138	ASP	C-N-CA	5.03	128.22	120.82
3	SA	56	U	P-O3'-C3'	5.03	127.74	120.20
6	SG	99	MET	CA-C-N	5.01	131.12	121.54
6	SG	99	MET	C-N-CA	5.01	131.12	121.54
20	3B	306	LEU	CA-CB-CG	5.01	133.82	116.30
34	B3	471	PRO	CA-C-N	5.01	135.31	126.45
34	B3	471	PRO	C-N-CA	5.01	135.31	126.45
57	RN	592	ARG	CA-CB-CG	5.00	124.10	114.10

There are no chirality outliers.

All (71) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	3D	142	LEU	Peptide
21	3D	202	HIS	Peptide
21	3D	286	ARG	Peptide
22	3E	331	LYS	Peptide
23	3F	237	ASP	Peptide
24	3G	59	GLU	Peptide
24	3G	9	PHE	Peptide
24	3H	59	GLU	Peptide
39	5C	551	SER	Peptide
40	5D	138	ASP	Peptide
43	5G	254	PHE	Peptide
43	5G	74	ASP	Peptide
45	5I	230	ASN	Peptide
45	5I	283	ASP	Peptide
25	A4	54	LYS	Peptide
26	A5	167	SER	Peptide
27	A8	496	TYR	Peptide
27	A8	529	HIS	Peptide
31	AG	178	PHE	Peptide
31	AG	780	GLU	Peptide
32	B1	288	ASP	Peptide
32	B1	690	ALA	Peptide
33	B2	131	GLY	Peptide
33	B2	213	LYS	Peptide
33	B2	266	SER	Peptide
33	B2	267	ASP	Peptide
33	B2	278	ASP	Peptide
33	B2	44	SER	Peptide
33	B2	613	ALA	Peptide
33	B2	916	HIS	Peptide
34	B3	34	THR	Peptide
34	B3	435	ALA	Peptide
34	B3	473	ALA	Peptide
34	B3	479	ILE	Peptide
34	B3	480	ILE	Peptide
34	B3	585	ASN	Peptide
34	B3	593	CYS	Peptide
34	B3	594	GLY	Peptide
34	B3	627	ASN	Peptide
34	B3	89	HIS	Peptide
34	B3	90	LEU	Peptide
36	BE	94	TYR	Peptide
48	RA	111	TRP	Peptide

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Mol	Chain	Res	Type	Group
48	RA	173	LEU	Peptide
49	RB	261	SER	Peptide
51	RE	767	GLN	Peptide
52	RF	253	ALA	Peptide
54	RJ	1026	LYS	Peptide
54	RJ	868	ARG	Peptide
55	RK	333	PHE	Peptide
56	RL	743	VAL	Peptide
56	RM	743	VAL	Peptide
57	RN	286	SER	Peptide
58	RO	144	PRO	Peptide
59	RP	1746	LYS	Peptide
59	RP	2051	ASP	Peptide
59	RP	835	LEU	Peptide
60	RQ	313	PHE	Peptide
62	RT	124	LEU	Peptide
4	SC	238	GLU	Peptide
5	SF	193	GLY	Peptide
5	SF	195	ILE	Peptide
8	SI	133	THR	Peptide
8	SI	31	SER	Peptide
8	SI	64	VAL	Peptide
9	SJ	85	PRO	Peptide
11	SM	128	CYS	Peptide
12	SO	58	HIS	Peptide
13	SP	90	ARG	Peptide
17	SZ	76	TYR	Peptide
18	Sc	49	HIS	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	3711	0	1882	58	0
2	5A	4117	0	2068	38	0
3	SA	27362	0	13798	266	0
4	SC	1830	0	1914	33	0
5	SF	1815	0	1870	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	SG	1669	0	1724	18	0
7	SH	1327	0	1403	30	0
8	SI	1321	0	1387	23	0
9	SJ	1324	0	1344	48	0
10	SK	1388	0	1467	32	0
11	SM	997	0	1048	34	0
12	SO	1087	0	1152	10	0
13	SP	868	0	894	32	0
14	SR	973	0	1029	19	0
15	SX	1003	0	1040	16	0
16	SY	786	0	843	8	0
17	SZ	809	0	842	15	0
18	Sc	603	0	623	9	0
19	Sd	497	0	535	3	0
20	3B	1865	0	1910	30	0
20	3C	1763	0	1805	43	0
21	3D	2848	0	2815	46	0
22	3E	3028	0	2813	62	0
23	3F	3643	0	3654	79	0
24	3G	916	0	964	11	0
24	3H	916	0	964	26	0
25	A4	5226	0	5199	96	0
26	A5	3976	0	3919	60	0
27	A8	3229	0	2281	133	0
28	A9	939	0	898	47	0
29	AE	9955	0	7968	103	0
30	AF	3911	0	3906	75	0
31	AG	6570	0	6473	143	0
32	B1	6331	0	6236	151	0
33	B2	6502	0	6493	122	0
34	B3	5919	0	6007	139	0
35	B8	3764	0	3757	58	0
36	BE	6450	0	6420	97	0
37	B6	2800	0	2517	35	0
38	5B	495	0	561	13	0
39	5C	3612	0	3578	65	0
40	5D	1396	0	1407	46	0
41	5E	1564	0	1592	165	0
42	5F	1530	0	1572	82	0
43	5G	1756	0	1765	57	0
44	5H	596	0	661	8	0
45	5I	3765	0	3714	76	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	5J	1280	0	1331	24	0
47	5K	1403	0	1484	17	0
48	RA	2709	0	2622	64	0
49	RB	1108	0	1087	27	0
50	RD	2412	0	2263	40	0
51	RE	8716	0	8828	239	0
52	RF	1963	0	1942	45	0
53	RG	1701	0	1767	40	0
53	RH	1799	0	1872	29	0
54	RJ	6379	0	6506	147	0
55	RK	2781	0	2878	51	0
56	RL	4539	0	2874	29	0
56	RM	3779	0	1650	8	0
57	RN	4529	0	4262	86	0
58	RO	3766	0	3269	47	0
59	RP	12171	0	7749	76	0
60	RQ	1651	0	1450	28	0
61	RS	2051	0	2096	53	0
62	RT	1334	0	1404	58	0
63	RY	299	0	275	6	0
64	X1	110	0	29	4	0
65	5K	1	0	0	0	0
65	Sc	1	0	0	0	0
66	RJ	32	0	12	2	0
67	RJ	1	0	0	0	0
All	All	215267	0	186362	3316	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 8.

All (3316) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A8:596:LYS:HE3	27:A8:637:LEU:CD2	1.25	1.58
51:RE:1203:ASN:HD22	51:RE:1219:ILE:CG2	1.50	1.22
32:B1:382:THR:O	41:5E:481:PRO:HB3	1.40	1.22
62:RT:174:LEU:CG	62:RT:180:LEU:HD21	1.69	1.22
27:A8:596:LYS:HE3	27:A8:637:LEU:HD23	1.23	1.21
51:RE:1102:LEU:HD23	51:RE:1180:ASN:O	1.40	1.20
41:5E:366:GLU:OE2	43:5G:247:ILE:HG21	1.40	1.19
27:A8:443:CYS:HA	31:AG:728:LEU:HD13	1.25	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A8:563:LEU:HB2	27:A8:598:GLU:OE1	1.41	1.17
27:A8:596:LYS:CE	27:A8:637:LEU:CD2	2.21	1.17
27:A8:596:LYS:CE	27:A8:637:LEU:HD22	1.75	1.17
39:5C:430:VAL:HG21	42:5F:3:ARG:HD3	1.25	1.16
41:5E:520:LEU:HD11	41:5E:525:LYS:CG	1.74	1.16
42:5F:8:HIS:HA	45:5I:53:MET:HE1	1.26	1.16
27:A8:673:THR:HG22	28:A9:490:GLU:HB2	1.20	1.16
27:A8:633:GLN:O	27:A8:637:LEU:HG	1.44	1.14
40:5D:78:LEU:HB2	54:RJ:1082:GLN:HE21	1.10	1.14
27:A8:673:THR:HG22	28:A9:490:GLU:CB	1.80	1.12
41:5E:520:LEU:CD1	41:5E:525:LYS:HG3	1.80	1.11
41:5E:520:LEU:HD11	41:5E:525:LYS:HG3	1.29	1.10
62:RT:182:ILE:HG22	62:RT:234:LEU:HD13	1.30	1.08
36:BE:737:LEU:HA	36:BE:740:ILE:CG2	1.82	1.08
62:RT:174:LEU:HA	62:RT:180:LEU:HD23	1.35	1.08
62:RT:174:LEU:HG	62:RT:180:LEU:CD2	1.85	1.07
27:A8:631:SER:O	27:A8:634:LEU:HG	1.56	1.06
32:B1:298:LEU:HD12	41:5E:476:MET:SD	1.95	1.06
62:RT:174:LEU:HA	62:RT:180:LEU:CD2	1.83	1.06
27:A8:443:CYS:N	31:AG:728:LEU:HD22	1.70	1.05
51:RE:518:PHE:CZ	51:RE:1075:LEU:HG	1.92	1.05
27:A8:443:CYS:CB	31:AG:728:LEU:HB3	1.86	1.05
51:RE:1203:ASN:HD22	51:RE:1219:ILE:HG21	1.18	1.04
51:RE:1204:VAL:HB	51:RE:1212:VAL:HG11	1.35	1.04
32:B1:341:GLN:NE2	32:B1:378:PHE:HB3	1.73	1.03
34:B3:690:HIS:CG	41:5E:519:GLU:HB2	1.94	1.03
32:B1:298:LEU:CD1	41:5E:476:MET:SD	2.47	1.02
36:BE:740:ILE:HG13	41:5E:483:TYR:OH	1.58	1.02
42:5F:19:LEU:HG	47:5K:25:LEU:HB3	1.41	1.02
27:A8:592:ARG:HB2	27:A8:596:LYS:HZ1	0.88	1.01
32:B1:418:ARG:HD2	41:5E:489:SER:O	1.59	1.01
33:B2:17:ILE:HG22	33:B2:52:TRP:CZ2	1.94	1.01
57:RN:527:GLN:O	57:RN:531:GLN:HB2	1.60	1.01
27:A8:631:SER:HA	27:A8:634:LEU:HD11	1.43	1.01
62:RT:181:TYR:CZ	62:RT:237:PHE:CE2	2.49	1.01
60:RQ:298:TRP:NE1	60:RQ:899:LYS:HG3	1.76	1.00
27:A8:592:ARG:HB2	27:A8:596:LYS:NZ	1.76	1.00
41:5E:384:ARG:HD2	43:5G:83:ILE:HD12	1.42	1.00
32:B1:337:TYR:OH	41:5E:474:ILE:HD13	1.61	1.00
41:5E:343:GLU:OE2	54:RJ:1007:TYR:HE1	1.43	1.00
62:RT:174:LEU:HG	62:RT:180:LEU:HD21	1.01	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:36:C:H42	3:SA:472:U:H3	1.00	0.99
57:RN:86:ILE:HA	57:RN:89:GLN:HE21	1.26	0.98
39:5C:430:VAL:HG21	42:5F:3:ARG:CD	1.94	0.97
27:A8:593:ASP:HA	27:A8:596:LYS:HD2	1.43	0.97
51:RE:1203:ASN:ND2	51:RE:1219:ILE:CG2	2.28	0.96
10:SK:65:LYS:HZ2	23:3F:59:PRO:CD	1.77	0.96
51:RE:518:PHE:HZ	51:RE:1075:LEU:HG	1.28	0.96
10:SK:65:LYS:HZ2	23:3F:59:PRO:CG	1.78	0.94
51:RE:1204:VAL:HB	51:RE:1212:VAL:CG1	1.97	0.94
1:3A:319:G:H5'	20:3C:121:LYS:NZ	1.82	0.94
27:A8:443:CYS:CA	31:AG:728:LEU:HD22	1.96	0.94
51:RE:918:ARG:HE	51:RE:1089:PHE:HE2	1.12	0.94
41:5E:319:VAL:HG21	54:RJ:1038:ILE:CG2	1.97	0.93
27:A8:596:LYS:HE2	27:A8:637:LEU:HA	1.48	0.93
51:RE:1203:ASN:ND2	51:RE:1219:ILE:HG21	1.83	0.93
36:BE:739:VAL:HG21	41:5E:487:ALA:HB2	1.51	0.92
62:RT:174:LEU:CB	62:RT:180:LEU:HD21	1.98	0.92
10:SK:65:LYS:HZ2	23:3F:59:PRO:CB	1.82	0.92
27:A8:443:CYS:HA	31:AG:728:LEU:CD1	2.00	0.92
2:5A:9:G:H5'	28:A9:483:LYS:NZ	1.85	0.92
32:B1:418:ARG:HH21	32:B1:418:ARG:HG3	1.33	0.91
36:BE:737:LEU:HA	36:BE:740:ILE:HG21	1.50	0.91
51:RE:1098:PHE:HD2	51:RE:1184:GLY:H	1.12	0.91
51:RE:918:ARG:NE	51:RE:1089:PHE:HE2	1.68	0.91
27:A8:596:LYS:CE	27:A8:637:LEU:HD23	1.91	0.90
57:RN:86:ILE:HA	57:RN:89:GLN:NE2	1.87	0.90
3:SA:36:C:N4	3:SA:472:U:H3	1.70	0.89
41:5E:343:GLU:OE2	54:RJ:1007:TYR:CE1	2.25	0.89
10:SK:65:LYS:NZ	23:3F:59:PRO:CG	2.35	0.89
51:RE:1157:TYR:HE1	51:RE:1203:ASN:HD21	1.17	0.88
1:3A:318:U:H3	20:3C:119:GLY:HA3	1.36	0.88
27:A8:673:THR:HG22	28:A9:490:GLU:CA	2.02	0.88
45:5I:231:GLU:OE2	60:RQ:899:LYS:HD3	1.74	0.87
50:RD:1473:ASN:HB3	50:RD:1509:GLU:OE2	1.72	0.87
27:A8:592:ARG:CB	27:A8:596:LYS:HZ1	1.82	0.87
32:B1:418:ARG:CD	41:5E:489:SER:O	2.21	0.87
34:B3:494:ILE:N	34:B3:510:SER:HG	1.71	0.87
51:RE:1203:ASN:HD22	51:RE:1219:ILE:HG22	1.37	0.87
41:5E:493:GLN:NE2	41:5E:497:ASN:HB3	1.88	0.86
27:A8:673:THR:CG2	28:A9:490:GLU:CA	2.54	0.86
40:5D:78:LEU:HD22	54:RJ:1082:GLN:CG	2.05	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:RE:1065:THR:O	51:RE:1069:LYS:HG3	1.75	0.86
40:5D:78:LEU:HB2	54:RJ:1082:GLN:NE2	1.91	0.85
10:SK:65:LYS:NZ	23:3F:59:PRO:CD	2.38	0.85
27:A8:596:LYS:HE3	27:A8:637:LEU:HD22	0.88	0.85
41:5E:384:ARG:HE	43:5G:82:GLY:H	1.22	0.85
39:5C:430:VAL:CG2	42:5F:3:ARG:HD3	2.07	0.85
56:RM:313:PRO:O	56:RM:372:PRO:HA	1.77	0.84
41:5E:319:VAL:HG21	54:RJ:1038:ILE:HG22	1.57	0.84
27:A8:673:THR:CG2	28:A9:490:GLU:HA	2.07	0.84
57:RN:86:ILE:CA	57:RN:89:GLN:HE21	1.89	0.84
27:A8:643:ASP:HA	30:AF:510:LEU:CD1	2.06	0.84
51:RE:1216:LYS:HE3	51:RE:1236:THR:HG23	1.60	0.84
61:RS:424:PHE:O	61:RS:428:TYR:HB2	1.78	0.84
51:RE:919:TRP:CZ2	51:RE:1067:LEU:HD22	2.12	0.84
62:RT:174:LEU:CA	62:RT:180:LEU:CD2	2.55	0.84
1:3A:24:U:O2	42:5F:13:LEU:HB2	1.77	0.84
5:SF:213:SER:HG	23:3F:102:ASP:N	1.75	0.84
13:SP:99:GLN:HE22	62:RT:188:LYS:HD3	1.42	0.83
1:3A:94:A:H61	1:3A:322:A:H61	1.27	0.83
58:RO:502:ASN:O	58:RO:506:LEU:HB2	1.77	0.83
34:B3:691:PRO:HD2	41:5E:516:SER:HB3	1.60	0.83
32:B1:382:THR:O	41:5E:481:PRO:CB	2.26	0.82
41:5E:384:ARG:HD2	43:5G:83:ILE:CD1	2.10	0.82
36:BE:736:HIS:O	36:BE:740:ILE:HG22	1.78	0.82
41:5E:532:LEU:O	41:5E:536:ARG:HG2	1.78	0.82
41:5E:520:LEU:HD11	41:5E:525:LYS:HG2	1.61	0.82
1:3A:319:G:C5'	20:3C:121:LYS:NZ	2.42	0.82
40:5D:68:HIS:CE1	42:5F:169:THR:HG21	2.14	0.82
50:RD:1509:GLU:HB3	50:RD:1512:GLU:HB2	1.60	0.82
41:5E:384:ARG:HH21	43:5G:81:SER:HB3	1.45	0.81
1:3A:318:U:OP1	1:3A:318:U:H3'	1.80	0.81
60:RQ:346:LEU:O	60:RQ:350:ASN:HA	1.80	0.81
41:5E:384:ARG:CD	43:5G:83:ILE:HD12	2.09	0.81
62:RT:174:LEU:CG	62:RT:180:LEU:CD2	2.53	0.81
24:3H:44:LEU:HD22	24:3H:52:ILE:CD1	2.10	0.81
29:AE:151:ILE:O	29:AE:155:ILE:HB	1.81	0.81
40:5D:58:ARG:HD2	42:5F:174:ARG:NH2	1.96	0.81
32:B1:14:VAL:HG21	32:B1:341:GLN:O	1.81	0.80
32:B1:678:GLU:OE2	41:5E:455:HIS:CE1	2.34	0.80
32:B1:298:LEU:HA	41:5E:472:PRO:HB2	1.62	0.80
41:5E:345:LEU:O	41:5E:345:LEU:HD23	1.81	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:RJ:871:MET:HE2	54:RJ:930:LYS:HZ2	1.45	0.80
56:RM:746:TYR:O	56:RM:765:VAL:HA	1.81	0.80
60:RQ:298:TRP:HE1	60:RQ:899:LYS:HG3	1.44	0.80
51:RE:1174:GLY:HA3	51:RE:1179:LYS:HE2	1.62	0.80
41:5E:533:LYS:HA	41:5E:536:ARG:NE	1.97	0.80
62:RT:180:LEU:HD12	62:RT:180:LEU:O	1.82	0.80
27:A8:596:LYS:HD3	27:A8:640:LEU:HD22	1.62	0.79
36:BE:737:LEU:HA	36:BE:740:ILE:HG22	1.63	0.79
51:RE:1157:TYR:HE1	51:RE:1203:ASN:ND2	1.79	0.79
34:B3:690:HIS:CD2	41:5E:519:GLU:HB2	2.18	0.79
27:A8:633:GLN:O	27:A8:637:LEU:CG	2.29	0.79
1:3A:323:G:N3	1:3A:323:G:H2'	1.96	0.79
37:B6:319:TYR:O	37:B6:323:PHE:HB2	1.81	0.79
62:RT:182:ILE:CG2	62:RT:234:LEU:HD13	2.12	0.79
9:SJ:48:THR:O	9:SJ:52:ASN:HB2	1.83	0.79
41:5E:319:VAL:CG2	54:RJ:1038:ILE:CG2	2.60	0.79
27:A8:631:SER:CA	27:A8:634:LEU:HD21	2.13	0.78
50:RD:1470:GLY:O	51:RE:1189:LEU:HA	1.82	0.78
3:SA:825:U:H3	3:SA:845:G:H1	1.32	0.78
2:5A:9:G:H5'	28:A9:483:LYS:HZ2	1.46	0.78
10:SK:65:LYS:NZ	23:3F:59:PRO:HD3	1.97	0.78
27:A8:672:ASN:HB2	28:A9:489:SER:OG	1.83	0.78
57:RN:86:ILE:O	57:RN:89:GLN:HG3	1.84	0.78
3:SA:1663:G:H1	3:SA:1738:U:H3	1.31	0.78
57:RN:86:ILE:HA	57:RN:89:GLN:HG2	1.66	0.78
27:A8:665:GLN:HB3	28:A9:496:LEU:HD21	1.64	0.78
30:AF:224:THR:O	30:AF:239:LEU:HB2	1.83	0.78
3:SA:868:G:H1	3:SA:960:U:H3	1.30	0.78
13:SP:107:ARG:NE	13:SP:107:ARG:HA	2.00	0.77
51:RE:1169:ILE:HD12	51:RE:1177:GLY:O	1.84	0.77
43:5G:239:VAL:HG21	57:RN:13:LEU:HD12	1.65	0.77
51:RE:1216:LYS:HG2	51:RE:1220:PHE:CE2	2.19	0.77
41:5E:319:VAL:CG2	54:RJ:1038:ILE:HG21	2.14	0.77
51:RE:1098:PHE:HD2	51:RE:1184:GLY:N	1.80	0.77
62:RT:174:LEU:CB	62:RT:180:LEU:CD2	2.62	0.77
3:SA:153:G:H1	3:SA:161:U:H3	1.33	0.77
27:A8:673:THR:HG21	28:A9:490:GLU:HA	1.66	0.77
27:A8:631:SER:HA	27:A8:634:LEU:HD21	1.66	0.77
54:RJ:871:MET:HE2	54:RJ:930:LYS:NZ	2.00	0.77
62:RT:174:LEU:CA	62:RT:180:LEU:HD21	2.14	0.76
41:5E:533:LYS:HA	41:5E:536:ARG:HE	1.47	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A8:647:LEU:HB3	28:A9:509:GLN:HE22	1.50	0.76
3:SA:1688:U:H3	3:SA:1713:G:H1	1.34	0.76
40:5D:78:LEU:HD22	54:RJ:1082:GLN:HG3	1.68	0.76
42:5F:6:LYS:O	42:5F:9:GLU:HB2	1.85	0.76
32:B1:299:SER:O	41:5E:476:MET:HG2	1.87	0.75
41:5E:319:VAL:HG21	54:RJ:1038:ILE:HG21	1.69	0.75
40:5D:78:LEU:HD22	54:RJ:1082:GLN:HG2	1.68	0.75
10:SK:138:LYS:H	49:RB:263:GLY:HA3	1.51	0.75
41:5E:493:GLN:HE22	41:5E:497:ASN:ND2	1.84	0.75
3:SA:415:C:H1'	3:SA:419:G:H22	1.50	0.75
42:5F:5:LEU:HB3	42:5F:9:GLU:HB3	1.67	0.75
41:5E:345:LEU:HD22	54:RJ:961:PHE:CZ	2.22	0.74
32:B1:680:ARG:NH1	41:5E:455:HIS:CD2	2.56	0.74
51:RE:1203:ASN:ND2	51:RE:1219:ILE:HG22	1.98	0.74
41:5E:533:LYS:HA	41:5E:536:ARG:HG2	1.68	0.74
25:A4:614:TRP:O	25:A4:618:ASN:HB2	1.87	0.74
14:SR:94:GLN:OE1	42:5F:182:PHE:CD1	2.39	0.74
1:3A:319:G:H5'	20:3C:121:LYS:HZ2	1.50	0.74
32:B1:419:TYR:HE2	41:5E:486:ASN:ND2	1.86	0.74
41:5E:384:ARG:CD	43:5G:83:ILE:CD1	2.65	0.74
62:RT:181:TYR:CZ	62:RT:237:PHE:HE2	2.03	0.74
32:B1:298:LEU:HD11	41:5E:476:MET:HE1	1.69	0.74
54:RJ:871:MET:HE1	54:RJ:930:LYS:CE	2.17	0.74
46:5J:114:ARG:O	46:5J:118:GLN:HB3	1.88	0.74
51:RE:1102:LEU:CD2	51:RE:1180:ASN:O	2.30	0.74
39:5C:188:LYS:HE2	42:5F:23:GLN:OE1	1.87	0.74
14:SR:94:GLN:OE1	42:5F:182:PHE:HD1	1.69	0.73
32:B1:420:ARG:HH22	41:5E:494:GLU:CD	1.96	0.73
1:3A:319:G:C5'	20:3C:121:LYS:HZ2	2.01	0.73
3:SA:1779:U:H1'	32:B1:257:TYR:HE1	1.53	0.73
36:BE:737:LEU:CA	36:BE:740:ILE:CG2	2.64	0.73
3:SA:1051:G:H21	45:5I:447:THR:HG21	1.54	0.73
41:5E:517:LYS:HD2	41:5E:517:LYS:C	2.14	0.73
62:RT:181:TYR:CE2	62:RT:237:PHE:CD2	2.77	0.73
2:5A:9:G:C5'	28:A9:483:LYS:NZ	2.51	0.72
27:A8:643:ASP:HA	30:AF:510:LEU:HD13	1.69	0.72
27:A8:669:ALA:HA	28:A9:489:SER:HB2	1.69	0.72
51:RE:919:TRP:CH2	51:RE:1067:LEU:HD22	2.24	0.72
41:5E:384:ARG:NE	43:5G:82:GLY:H	1.87	0.72
34:B3:216:ARG:HH11	34:B3:241:GLN:HE22	1.36	0.72
3:SA:1756:A:H5'	41:5E:536:ARG:HB2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:SK:65:LYS:HZ1	23:3F:59:PRO:HD3	1.55	0.72
27:A8:642:LEU:HD12	28:A9:499:ILE:HG23	1.70	0.72
54:RJ:871:MET:CE	54:RJ:930:LYS:NZ	2.53	0.72
32:B1:341:GLN:HE21	32:B1:378:PHE:HB3	1.55	0.72
10:SK:65:LYS:NZ	23:3F:59:PRO:CB	2.52	0.72
27:A8:596:LYS:CG	27:A8:637:LEU:HB3	2.20	0.71
1:3A:318:U:H3'	1:3A:318:U:P	2.30	0.71
3:SA:505:A:H61	3:SA:586:G:H8	1.38	0.71
22:3E:397:ARG:HH21	22:3E:400:GLN:HE21	1.38	0.71
32:B1:298:LEU:HD11	41:5E:476:MET:SD	2.30	0.71
56:RL:29:VAL:HG12	56:RL:152:LEU:HD12	1.72	0.71
41:5E:493:GLN:HE21	41:5E:497:ASN:HB3	1.52	0.71
57:RN:86:ILE:HA	57:RN:89:GLN:CG	2.21	0.71
26:A5:545:ALA:CB	27:A8:674:GLU:HG3	2.20	0.71
27:A8:631:SER:HA	27:A8:634:LEU:CD1	2.18	0.71
31:AG:435:ASP:HB2	31:AG:702:TYR:CD1	2.26	0.71
62:RT:238:THR:O	62:RT:241:ARG:HG3	1.91	0.71
13:SP:99:GLN:OE1	62:RT:188:LYS:HD2	1.91	0.70
50:RD:1508:ARG:NH1	52:RF:97:GLU:HG2	2.06	0.70
50:RD:1518:ILE:HG12	50:RD:1552:LYS:HG2	1.73	0.70
42:5F:8:HIS:HA	45:5I:53:MET:CE	2.14	0.70
36:BE:740:ILE:HG13	41:5E:483:TYR:HH	1.52	0.70
41:5E:493:GLN:HE22	41:5E:497:ASN:HD22	1.37	0.70
3:SA:1756:A:N7	41:5E:532:LEU:HB2	2.07	0.70
51:RE:1189:LEU:HD23	51:RE:1189:LEU:C	2.16	0.70
5:SF:92:LEU:HB2	5:SF:97:GLU:HB2	1.74	0.70
27:A8:596:LYS:CE	27:A8:637:LEU:HA	2.22	0.70
41:5E:340:LEU:HB2	54:RJ:957:GLU:OE2	1.92	0.70
6:SG:206:SER:H	6:SG:211:ILE:HD11	1.55	0.70
13:SP:107:ARG:HB2	13:SP:107:ARG:NH2	2.07	0.70
51:RE:1174:GLY:CA	51:RE:1179:LYS:HE2	2.22	0.70
1:3A:323:G:OP2	40:5D:116:LYS:HB3	1.92	0.69
41:5E:345:LEU:HD23	41:5E:345:LEU:C	2.17	0.69
32:B1:337:TYR:CD2	32:B1:340:LYS:HD3	2.27	0.69
51:RE:1108:LEU:O	51:RE:1112:CYS:HB2	1.91	0.69
32:B1:58:ILE:HA	32:B1:74:ASP:HA	1.74	0.69
41:5E:533:LYS:HA	41:5E:536:ARG:CG	2.22	0.69
51:RE:1204:VAL:CB	51:RE:1212:VAL:HG11	2.19	0.69
57:RN:86:ILE:HG23	57:RN:89:GLN:NE2	2.07	0.69
62:RT:180:LEU:HD12	62:RT:180:LEU:C	2.17	0.69
51:RE:441:GLN:O	51:RE:455:SER:HA	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A8:643:ASP:HA	30:AF:510:LEU:HD12	1.75	0.68
32:B1:678:GLU:CD	41:5E:455:HIS:ND1	2.51	0.68
17:SZ:29:HIS:HB2	17:SZ:32:ARG:HB2	1.76	0.68
41:5E:517:LYS:NZ	41:5E:517:LYS:HB3	2.09	0.68
10:SK:65:LYS:NZ	23:3F:59:PRO:HB3	2.08	0.68
27:A8:664:LYS:O	27:A8:668:ILE:HG13	1.92	0.68
28:A9:480:LYS:O	28:A9:483:LYS:HG3	1.93	0.68
27:A8:596:LYS:HG3	27:A8:637:LEU:HB3	1.74	0.68
45:5I:345:THR:HG22	45:5I:347:ARG:H	1.58	0.68
50:RD:1512:GLU:HG2	51:RE:1199:ASN:HD21	1.57	0.68
27:A8:443:CYS:CB	31:AG:728:LEU:HD22	2.23	0.68
41:5E:315:GLU:HB3	54:RJ:1032:LEU:HD11	1.74	0.68
3:SA:646:C:H2'	3:SA:647:G:H8	1.59	0.68
60:RQ:297:LYS:HB2	60:RQ:899:LYS:HB3	1.76	0.68
41:5E:538:LYS:HD3	41:5E:538:LYS:C	2.19	0.68
55:RK:192:THR:HA	55:RK:224:ASN:O	1.92	0.68
29:AE:692:ILE:HA	29:AE:695:TYR:HB3	1.76	0.68
59:RP:173:THR:O	59:RP:177:LEU:HB2	1.94	0.68
30:AF:86:SER:O	30:AF:98:ALA:HA	1.93	0.68
41:5E:366:GLU:OE2	43:5G:247:ILE:CG2	2.33	0.68
30:AF:211:HIS:HD1	30:AF:228:SER:HG	1.42	0.67
33:B2:17:ILE:HG22	33:B2:52:TRP:CH2	2.28	0.67
10:SK:65:LYS:NZ	23:3F:59:PRO:HG3	2.08	0.67
51:RE:918:ARG:NE	51:RE:1089:PHE:CE2	2.59	0.67
3:SA:1679:G:H1'	3:SA:1722:A:H61	1.59	0.67
23:3F:443:LEU:HD21	23:3F:492:TRP:HE1	1.59	0.67
51:RE:1069:LYS:O	51:RE:1072:VAL:HG12	1.94	0.67
57:RN:86:ILE:CB	57:RN:89:GLN:HE21	2.07	0.67
41:5E:520:LEU:CG	41:5E:525:LYS:HG3	2.24	0.67
51:RE:1096:TYR:CZ	51:RE:1183:THR:OG1	2.46	0.67
51:RE:1216:LYS:CE	51:RE:1236:THR:HG23	2.24	0.67
36:BE:209:ILE:HG22	36:BE:225:THR:HG22	1.76	0.67
41:5E:384:ARG:HH21	43:5G:81:SER:CB	2.08	0.67
41:5E:384:ARG:NH2	43:5G:81:SER:HB3	2.09	0.67
57:RN:85:GLY:O	57:RN:89:GLN:HG2	1.95	0.67
23:3F:185:LEU:H	23:3F:202:THR:HB	1.59	0.67
25:A4:645:ARG:HD2	25:A4:656:ARG:HD3	1.76	0.67
27:A8:648:PHE:CE1	28:A9:510:ALA:HA	2.29	0.67
42:5F:11:LYS:HA	42:5F:14:LYS:HE3	1.75	0.67
43:5G:123:VAL:HG12	43:5G:125:PRO:HD2	1.77	0.67
35:B8:513:GLN:HG3	35:B8:551:VAL:HG21	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B2:536:CYS:HB3	33:B2:549:SER:HB3	1.77	0.67
3:SA:187:G:N2	3:SA:197:A:N7	2.43	0.66
13:SP:103:ARG:NH2	62:RT:188:LYS:HG3	2.09	0.66
17:SZ:51:GLU:HB2	17:SZ:54:ALA:HB3	1.76	0.66
32:B1:20:ILE:H	32:B1:307:THR:HG21	1.58	0.66
41:5E:490:LEU:HD22	41:5E:494:GLU:OE1	1.95	0.66
51:RE:235:LEU:O	51:RE:239:LEU:HB2	1.95	0.66
27:A8:631:SER:C	27:A8:634:LEU:HG	2.19	0.66
27:A8:648:PHE:HE1	28:A9:510:ALA:HA	1.59	0.66
31:AG:435:ASP:HB3	31:AG:701:VAL:O	1.96	0.66
36:BE:209:ILE:HA	36:BE:225:THR:HA	1.76	0.66
16:SY:103:LEU:HB3	16:SY:126:LYS:HB2	1.76	0.66
20:3B:103:GLU:HG3	46:5J:134:ARG:HH12	1.60	0.66
11:SM:67:ARG:HH21	11:SM:129:ARG:H	1.44	0.66
32:B1:337:TYR:CD2	36:BE:744:SER:O	2.48	0.66
1:3A:323:G:H5'	40:5D:116:LYS:HG3	1.76	0.66
13:SP:107:ARG:HG2	13:SP:107:ARG:HH21	1.60	0.66
54:RJ:248:ARG:HB3	54:RJ:272:TYR:HB2	1.78	0.66
31:AG:16:SER:HB2	31:AG:783:LEU:HB2	1.77	0.66
62:RT:181:TYR:CE1	62:RT:237:PHE:CE2	2.83	0.66
51:RE:756:VAL:HA	51:RE:896:THR:HG21	1.78	0.66
30:AF:52:PRO:HG2	30:AF:312:ALA:HA	1.77	0.65
34:B3:462:THR:HA	34:B3:484:GLU:HG2	1.77	0.65
27:A8:665:GLN:HB3	28:A9:496:LEU:CD2	2.26	0.65
42:5F:5:LEU:HB3	42:5F:9:GLU:CB	2.25	0.65
27:A8:443:CYS:N	31:AG:728:LEU:CD2	2.56	0.65
56:RM:283:ALA:HA	56:RM:411:THR:O	1.96	0.65
3:SA:207:U:H3	3:SA:258:C:H42	1.45	0.65
51:RE:518:PHE:HE2	51:RE:1075:LEU:HB3	1.62	0.65
56:RM:311:THR:O	56:RM:370:ILE:HA	1.97	0.65
27:A8:643:ASP:OD1	30:AF:510:LEU:HA	1.96	0.65
25:A4:497:ILE:HD11	25:A4:511:VAL:HG23	1.78	0.65
33:B2:262:ILE:O	33:B2:270:SER:HA	1.97	0.65
40:5D:61:ASP:O	42:5F:160:TRP:CH2	2.50	0.65
1:3A:84:U:OP2	22:3E:361:ARG:NH2	2.30	0.65
39:5C:170:GLN:NE2	39:5C:177:TYR:OH	2.30	0.64
51:RE:1101:ASP:HB3	51:RE:1233:ASN:HB2	1.78	0.64
4:SC:132:ASP:HB2	4:SC:221:PRO:HB3	1.79	0.64
11:SM:87:ARG:HE	11:SM:104:HIS:HB2	1.62	0.64
13:SP:107:ARG:HH21	13:SP:107:ARG:CG	2.10	0.64
23:3F:125:VAL:O	23:3F:128:GLN:NE2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RD:1525:ASN:HD22	50:RD:1556:ILE:HG22	1.62	0.64
53:RG:122:ILE:HA	53:RG:161:LYS:O	1.97	0.64
54:RJ:263:LEU:HD23	54:RJ:267:ARG:HH22	1.63	0.64
58:RO:472:HIS:HD2	58:RO:474:HIS:H	1.46	0.64
1:3A:319:G:C5'	20:3C:121:LYS:HZ1	2.08	0.64
3:SA:1052:U:H5''	45:5I:449:LYS:HG2	1.78	0.64
10:SK:57:ARG:HE	47:5K:88:ASP:HB3	1.60	0.64
41:5E:493:GLN:NE2	41:5E:497:ASN:CB	2.61	0.64
2:5A:487:A:H62	60:RQ:876:GLN:HE22	1.45	0.64
3:SA:415:C:H1'	3:SA:419:G:N2	2.12	0.64
3:SA:1727:G:N2	3:SA:1728:A:N7	2.46	0.64
27:A8:576:ARG:HG2	27:A8:578:LEU:H	1.63	0.64
32:B1:438:VAL:HG12	32:B1:445:VAL:HG23	1.79	0.64
27:A8:672:ASN:HB2	28:A9:489:SER:HG	1.63	0.64
33:B2:439:LEU:HB2	33:B2:444:LEU:HB3	1.79	0.64
34:B3:719:ILE:HD11	34:B3:762:CYS:HB3	1.78	0.64
36:BE:631:ASN:HB2	36:BE:644:THR:HB	1.80	0.64
57:RN:86:ILE:HG23	57:RN:89:GLN:HE21	1.63	0.64
16:SY:97:ASP:OD1	16:SY:97:ASP:N	2.31	0.64
35:B8:521:LEU:HA	35:B8:531:CYS:O	1.98	0.64
27:A8:664:LYS:HD2	28:A9:448:GLU:OE1	1.98	0.64
9:SJ:5:ARG:NH2	9:SJ:29:LEU:O	2.31	0.63
26:A5:145:CYS:HB2	26:A5:148:LEU:HD21	1.80	0.63
42:5F:8:HIS:CA	45:5I:53:MET:HE1	2.17	0.63
58:RO:318:LEU:HA	58:RO:357:ARG:HH12	1.62	0.63
24:3H:44:LEU:HD22	24:3H:52:ILE:HD11	1.80	0.63
40:5D:78:LEU:CB	54:RJ:1082:GLN:HE21	2.01	0.63
41:5E:381:LEU:HB2	43:5G:212:ALA:HA	1.80	0.63
48:RA:18:GLY:HA2	48:RA:339:HIS:HD2	1.62	0.63
41:5E:340:LEU:HD13	54:RJ:957:GLU:OE2	1.98	0.63
3:SA:343:C:H2'	3:SA:344:A:H8	1.63	0.63
9:SJ:42:ARG:HD3	48:RA:57:GLU:HB3	1.80	0.63
17:SZ:20:ARG:HD2	17:SZ:74:LEU:HD12	1.79	0.63
54:RJ:831:ARG:NH2	54:RJ:835:HIS:O	2.30	0.63
3:SA:576:G:H4'	41:5E:327:LYS:HE2	1.81	0.63
25:A4:578:SER:HG	25:A4:643:SER:HG	1.46	0.63
41:5E:370:ARG:NH1	57:RN:52:ARG:NH1	2.47	0.63
23:3F:538:ARG:HA	23:3F:566:ALA:O	1.97	0.63
39:5C:386:PHE:O	45:5I:8:ARG:NH2	2.31	0.63
53:RH:192:TYR:HA	53:RH:195:LYS:HD2	1.81	0.63
34:B3:244:GLU:HG2	34:B3:293:VAL:H	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:SR:94:GLN:HB2	14:SR:102:LYS:HG3	1.80	0.63
10:SK:65:LYS:HZ2	23:3F:59:PRO:HB3	1.64	0.63
25:A4:399:VAL:HG22	25:A4:420:LEU:HB2	1.80	0.63
29:AE:638:SER:HA	29:AE:641:LEU:HD12	1.80	0.63
34:B3:531:ASN:HD21	34:B3:568:MET:HE2	1.63	0.63
41:5E:533:LYS:CA	41:5E:536:ARG:HG2	2.29	0.63
48:RA:247:THR:HG23	48:RA:249:ASN:H	1.64	0.63
1:3A:319:G:O5'	20:3C:121:LYS:NZ	2.32	0.62
8:SI:9:LEU:HD22	8:SI:42:GLN:HE22	1.63	0.62
53:RH:129:ARG:HH11	53:RH:132:ARG:HD3	1.63	0.62
22:3E:384:GLY:O	22:3E:388:LEU:HB2	1.99	0.62
41:5E:517:LYS:HB3	41:5E:517:LYS:HZ2	1.64	0.62
48:RA:287:ASN:HB2	48:RA:302:ARG:HB2	1.80	0.62
54:RJ:932:LEU:HD22	54:RJ:1007:TYR:HB2	1.80	0.62
3:SA:1775:U:H3	3:SA:1786:G:H1	1.46	0.62
32:B1:298:LEU:HD11	41:5E:476:MET:CE	2.28	0.62
40:5D:29:GLU:OE2	40:5D:37:ARG:NH1	2.31	0.62
58:RO:300:THR:O	58:RO:304:ASN:ND2	2.32	0.62
61:RS:379:LYS:HD2	61:RS:427:ARG:HE	1.64	0.62
27:A8:672:ASN:CB	28:A9:489:SER:OG	2.46	0.62
34:B3:691:PRO:CD	41:5E:516:SER:HB3	2.29	0.62
37:B6:285:TYR:HD2	37:B6:308:THR:HG22	1.63	0.62
3:SA:146:U:H3	3:SA:168:A:N6	1.97	0.62
57:RN:482:GLN:HG2	58:RO:507:LEU:HD11	1.80	0.62
3:SA:1220:C:H2'	3:SA:1221:A:H8	1.64	0.62
3:SA:1655:A:N6	3:SA:1743:U:O4	2.32	0.62
26:A5:120:ILE:HB	26:A5:151:LEU:HD23	1.82	0.62
28:A9:432:LYS:HB3	28:A9:435:LEU:HB3	1.81	0.62
36:BE:733:THR:O	36:BE:737:LEU:HB3	2.00	0.62
42:5F:153:ASN:O	42:5F:153:ASN:ND2	2.32	0.62
54:RJ:871:MET:CE	54:RJ:930:LYS:HD2	2.30	0.62
3:SA:477:A:H5'	44:5H:560:ASN:HD22	1.64	0.62
61:RS:214:TYR:HB3	61:RS:249:THR:HG22	1.80	0.62
27:A8:592:ARG:HH11	31:AG:605:ASN:ND2	1.98	0.61
32:B1:303:ASN:ND2	32:B1:323:LYS:HD3	2.15	0.61
3:SA:1538:U:H2'	3:SA:1569:A:H61	1.65	0.61
30:AF:440:GLU:O	30:AF:444:ASN:HB2	2.00	0.61
41:5E:345:LEU:CD2	54:RJ:961:PHE:CZ	2.82	0.61
51:RE:1096:TYR:OH	51:RE:1183:THR:HG21	2.00	0.61
57:RN:95:ARG:HH12	57:RN:757:LYS:HG3	1.64	0.61
24:3H:50:GLU:HG3	24:3H:104:THR:HG22	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A8:631:SER:CA	27:A8:634:LEU:HD11	2.25	0.61
36:BE:471:CYS:SG	36:BE:514:ASN:ND2	2.74	0.61
3:SA:362:G:H22	3:SA:382:C:H1'	1.66	0.61
30:AF:428:ARG:NH2	31:AG:518:ASP:O	2.34	0.61
55:RK:155:LYS:HG2	55:RK:165:GLU:HG2	1.82	0.61
61:RS:423:THR:HA	61:RS:426:GLN:HG2	1.81	0.61
3:SA:521:A:N3	17:SZ:34:ASN:ND2	2.48	0.61
5:SF:95:THR:HG22	59:RP:59:LEU:HB3	1.83	0.61
27:A8:443:CYS:HA	31:AG:728:LEU:CG	2.30	0.61
3:SA:1779:U:H1'	32:B1:257:TYR:CE1	2.35	0.61
5:SF:212:ASP:H	5:SF:215:ASP:HA	1.65	0.61
13:SP:16:VAL:HG12	13:SP:80:HIS:HB2	1.82	0.61
35:B8:424:ILE:HG12	35:B8:434:GLU:HG2	1.83	0.61
26:A5:162:GLN:HA	26:A5:173:ILE:O	2.01	0.61
27:A8:671:ARG:NH2	28:A9:453:PRO:HG2	2.16	0.61
30:AF:51:HIS:O	30:AF:53:HIS:ND1	2.30	0.61
53:RG:36:LYS:HB3	53:RG:172:PRO:HA	1.82	0.61
31:AG:335:PRO:HB2	31:AG:336:ARG:HD3	1.82	0.61
31:AG:769:ASN:ND2	31:AG:771:ASP:OD1	2.33	0.61
37:B6:286:ILE:HG22	37:B6:308:THR:HG21	1.83	0.61
51:RE:398:ALA:HA	51:RE:401:LEU:HD12	1.82	0.61
51:RE:779:PHE:HB3	51:RE:851:LYS:HG3	1.82	0.61
41:5E:371:ARG:NH1	41:5E:375:ASP:OD2	2.34	0.61
57:RN:511:SER:HA	57:RN:557:SER:HB2	1.82	0.61
13:SP:80:HIS:HA	13:SP:113:GLY:O	2.01	0.60
13:SP:103:ARG:HH22	62:RT:188:LYS:CG	2.14	0.60
20:3B:142:ARG:NH1	20:3B:186:ASP:OD2	2.34	0.60
23:3F:356:ARG:NH1	49:RB:260:ALA:O	2.34	0.60
26:A5:481:LEU:HD21	26:A5:526:LEU:HD22	1.82	0.60
59:RP:91:LEU:HD21	59:RP:110:LEU:HD12	1.83	0.60
1:3A:319:G:H5'	20:3C:121:LYS:HZ1	1.59	0.60
20:3C:186:ASP:OD1	20:3C:214:ARG:NH1	2.34	0.60
54:RJ:60:ASP:O	54:RJ:239:ASN:ND2	2.34	0.60
3:SA:374:U:H5''	49:RB:331:LYS:HE3	1.83	0.60
32:B1:14:VAL:HG11	32:B1:341:GLN:HB3	1.84	0.60
34:B3:160:ILE:HG22	34:B3:162:LEU:HD13	1.82	0.60
37:B6:201:LYS:HZ1	46:5J:55:ILE:HG21	1.67	0.60
45:5I:260:GLN:NE2	45:5I:289:TYR:OH	2.35	0.60
51:RE:923:HIS:CD2	51:RE:1067:LEU:HD11	2.35	0.60
53:RG:147:LYS:HD3	53:RG:150:ILE:HG22	1.83	0.60
53:RH:156:GLU:HG2	53:RH:157:GLU:HG2	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RO:461:SER:OG	58:RO:462:SER:N	2.33	0.60
13:SP:99:GLN:HE22	62:RT:188:LYS:CD	2.15	0.60
40:5D:68:HIS:HE1	42:5F:169:THR:HG21	1.67	0.60
3:SA:435:C:H42	54:RJ:166:ARG:HH12	1.47	0.60
23:3F:328:ILE:HG13	23:3F:338:THR:HG22	1.82	0.60
25:A4:429:SER:HB3	25:A4:444:ARG:HA	1.83	0.60
26:A5:545:ALA:HB2	27:A8:674:GLU:HG3	1.82	0.60
57:RN:548:ARG:NH1	57:RN:638:ASN:OD1	2.34	0.60
58:RO:452:ASP:HB3	58:RO:455:LEU:HB2	1.84	0.60
3:SA:606:A:N3	3:SA:607:G:N1	2.50	0.60
5:SF:194:THR:HG23	5:SF:195:ILE:HG12	1.83	0.60
27:A8:638:LEU:HD21	27:A8:658:LEU:HD11	1.83	0.60
57:RN:649:THR:HG23	57:RN:650:VAL:HG23	1.82	0.60
10:SK:65:LYS:HZ2	23:3F:59:PRO:N	1.98	0.60
21:3D:29:SER:O	21:3D:35:GLN:NE2	2.34	0.60
33:B2:54:ILE:HD13	33:B2:364:TYR:HD2	1.66	0.60
34:B3:581:CYS:HA	34:B3:590:LEU:O	2.02	0.60
51:RE:363:THR:HG22	51:RE:394:THR:HG21	1.83	0.60
40:5D:22:ARG:NH1	54:RJ:997:MET:O	2.35	0.60
3:SA:85:A:H2'	3:SA:86:A:H8	1.65	0.60
13:SP:99:GLN:NE2	62:RT:188:LYS:HD3	2.14	0.60
48:RA:333:ASN:HD21	48:RA:338:MET:HA	1.67	0.60
3:SA:870:C:O2	18:Sc:51:GLN:NE2	2.35	0.59
27:A8:593:ASP:CA	27:A8:596:LYS:HD2	2.26	0.59
29:AE:699:ARG:NH1	29:AE:702:TRP:O	2.35	0.59
30:AF:248:ARG:NH1	30:AF:289:ASN:O	2.35	0.59
42:5F:69:PRO:HA	42:5F:72:ARG:HG2	1.83	0.59
43:5G:239:VAL:HG21	57:RN:13:LEU:CD1	2.30	0.59
51:RE:345:TYR:O	51:RE:349:LEU:HB3	2.02	0.59
55:RK:14:SER:HB2	55:RK:36:ILE:HG23	1.83	0.59
8:SI:118:LEU:HA	8:SI:121:VAL:HB	1.82	0.59
13:SP:40:ALA:HB2	13:SP:70:LYS:HD2	1.84	0.59
30:AF:301:PRO:HG2	30:AF:323:SER:HB3	1.84	0.59
34:B3:189:HIS:NE2	34:B3:217:ASP:OD1	2.35	0.59
51:RE:1100:VAL:O	51:RE:1181:VAL:HG12	2.01	0.59
6:SG:131:GLN:NE2	6:SG:135:ASP:OD1	2.35	0.59
7:SH:70:PRO:HB3	7:SH:101:ILE:HB	1.84	0.59
21:3D:382:LYS:HD2	21:3D:404:LEU:HD22	1.83	0.59
30:AF:133:HIS:HD2	30:AF:135:GLN:H	1.50	0.59
51:RE:383:GLY:HA3	51:RE:585:MET:HG2	1.82	0.59
31:AG:90:LYS:HG2	31:AG:144:VAL:HG22	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:RN:614:ILE:HG22	57:RN:616:LEU:HB2	1.85	0.59
9:SJ:32:GLN:HG2	48:RA:79:PRO:HD2	1.84	0.59
14:SR:122:ARG:NH2	43:5G:133:LYS:HD2	2.17	0.59
18:Sc:73:LEU:HB2	52:RF:215:VAL:HG21	1.85	0.59
36:BE:737:LEU:CA	36:BE:740:ILE:HG22	2.28	0.59
42:5F:109:ARG:NH2	42:5F:155:GLU:OE2	2.36	0.59
51:RE:344:ASN:HA	51:RE:347:LYS:HD2	1.84	0.59
59:RP:112:GLN:NE2	59:RP:116:ASP:OD2	2.36	0.59
51:RE:1111:SER:HA	51:RE:1129:PRO:HG3	1.85	0.59
59:RP:54:TRP:O	59:RP:58:ASN:ND2	2.35	0.59
21:3D:286:ARG:HA	21:3D:289:TYR:HB3	1.85	0.59
22:3E:210:LEU:HD23	22:3E:256:ASN:HD22	1.68	0.59
27:A8:673:THR:CG2	28:A9:490:GLU:CB	2.68	0.59
32:B1:497:ILE:HG23	32:B1:512:ILE:HB	1.84	0.59
37:B6:15:MET:HA	37:B6:18:LEU:HB3	1.85	0.59
43:5G:233:VAL:HG21	43:5G:256:MET:HE3	1.83	0.59
57:RN:86:ILE:CG2	57:RN:89:GLN:HE21	2.16	0.59
39:5C:257:SER:OG	39:5C:259:TRP:NE1	2.36	0.59
5:SF:180:LEU:HA	5:SF:194:THR:HG21	1.85	0.59
15:SX:90:THR:O	15:SX:94:LEU:HB2	2.03	0.59
41:5E:384:ARG:HE	43:5G:82:GLY:N	1.97	0.59
41:5E:493:GLN:NE2	41:5E:497:ASN:HD22	2.01	0.59
51:RE:525:LEU:HB2	51:RE:617:LEU:HB2	1.84	0.59
53:RG:125:ASN:ND2	53:RG:127:THR:OG1	2.36	0.59
57:RN:535:ASN:OD1	57:RN:539:ARG:NH1	2.36	0.59
20:3C:114:GLY:O	20:3C:122:ARG:NH1	2.35	0.58
31:AG:510:TYR:HH	31:AG:527:HIS:HD1	1.49	0.58
39:5C:190:HIS:HB3	39:5C:207:THR:HG21	1.84	0.58
51:RE:1096:TYR:OH	51:RE:1183:THR:CG2	2.51	0.58
19:Sd:65:ARG:NH2	33:B2:750:GLU:OE2	2.36	0.58
27:A8:647:LEU:C	28:A9:509:GLN:NE2	2.62	0.58
31:AG:153:ILE:HG22	31:AG:174:TYR:HB2	1.85	0.58
40:5D:58:ARG:NH2	42:5F:174:ARG:NE	2.51	0.58
51:RE:381:HIS:NE2	51:RE:478:THR:O	2.36	0.58
15:SX:97:ARG:HH11	47:5K:84:ARG:HH12	1.51	0.58
32:B1:300:MET:HE3	32:B1:328:LEU:HD13	1.85	0.58
43:5G:144:GLU:HA	43:5G:149:PRO:HA	1.84	0.58
51:RE:834:ASN:ND2	51:RE:863:TYR:OH	2.36	0.58
59:RP:1904:LEU:HD12	59:RP:1940:LYS:HE2	1.85	0.58
62:RT:99:ILE:HG12	62:RT:159:ILE:HD13	1.85	0.58
1:3A:58:A:OP1	42:5F:165:LYS:HE3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:92:GLN:HE21	4:SC:97:LEU:HD21	1.68	0.58
25:A4:380:LYS:NZ	25:A4:634:VAL:O	2.35	0.58
39:5C:76:PRO:HA	45:5I:1:MET:HE2	1.86	0.58
52:RF:91:ASP:O	52:RF:121:ARG:NH2	2.36	0.58
59:RP:144:SER:HB3	59:RP:147:VAL:HG12	1.86	0.58
25:A4:565:ARG:HD3	29:AE:633:GLU:HB2	1.86	0.58
31:AG:568:ASN:ND2	31:AG:586:SER:OG	2.35	0.58
33:B2:97:GLY:HA3	33:B2:124:ILE:HD11	1.84	0.58
34:B3:237:LEU:HD21	51:RE:663:ILE:HG21	1.86	0.58
40:5D:113:ILE:HG23	40:5D:117:LYS:HE3	1.86	0.58
42:5F:54:ILE:HD11	42:5F:101:VAL:HG21	1.84	0.58
45:5I:411:LYS:O	45:5I:415:ARG:HB2	2.02	0.58
51:RE:520:ASN:HD22	51:RE:959:LEU:HD12	1.68	0.58
1:3A:30:A:N6	45:5I:341:GLU:OE2	2.36	0.58
22:3E:11:GLY:HA2	22:3E:143:LEU:HD22	1.86	0.58
40:5D:37:ARG:NH2	54:RJ:994:LYS:O	2.36	0.58
59:RP:2030:ASN:O	59:RP:2036:ARG:NH2	2.35	0.58
59:RP:2036:ARG:HH12	59:RP:2074:SER:HB2	1.69	0.58
42:5F:9:GLU:HA	42:5F:9:GLU:OE2	2.04	0.58
50:RD:1583:SER:HA	50:RD:1586:VAL:HG12	1.85	0.58
5:SF:44:LEU:HD13	5:SF:82:TYR:HB3	1.85	0.58
25:A4:269:PHE:O	35:B8:446:ARG:NH2	2.36	0.58
27:A8:631:SER:HA	27:A8:634:LEU:CD2	2.34	0.58
29:AE:248:SER:OG	29:AE:253:CYS:SG	2.62	0.58
31:AG:118:VAL:HB	31:AG:130:LYS:HB2	1.85	0.58
34:B3:494:ILE:N	34:B3:510:SER:OG	2.35	0.58
34:B3:742:ARG:NH1	41:5E:506:GLU:OE1	2.36	0.58
57:RN:86:ILE:CA	57:RN:89:GLN:HG2	2.33	0.58
58:RO:202:LEU:HD22	58:RO:212:LEU:HD22	1.86	0.58
1:3A:251:G:H2'	23:3F:155:ASN:HD21	1.67	0.58
3:SA:126:A:N6	3:SA:291:G:O2'	2.37	0.58
26:A5:546:ARG:NH1	27:A8:677:ASN:O	2.36	0.58
27:A8:632:THR:O	27:A8:636:GLN:HG3	2.04	0.58
31:AG:435:ASP:CB	31:AG:702:TYR:HA	2.34	0.58
33:B2:259:ILE:HA	33:B2:273:TYR:O	2.03	0.58
48:RA:75:GLY:HA3	48:RA:80:GLN:H	1.68	0.58
51:RE:412:LEU:HD21	51:RE:424:GLY:HA3	1.84	0.58
53:RH:44:VAL:HA	53:RH:113:TYR:O	2.03	0.58
20:3B:236:MET:HG3	21:3D:133:LEU:HA	1.84	0.58
26:A5:545:ALA:HB1	27:A8:674:GLU:HG3	1.86	0.58
31:AG:144:VAL:HG12	31:AG:153:ILE:HG13	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:157:PHE:HB2	31:AG:170:SER:HB3	1.86	0.58
32:B1:501:SER:HB2	32:B1:508:GLN:HB2	1.84	0.58
43:5G:183:SER:HB3	43:5G:220:ARG:HD2	1.86	0.58
50:RD:1530:GLU:HA	50:RD:1533:LEU:HB2	1.85	0.58
34:B3:584:ILE:HD11	34:B3:599:ILE:HD11	1.85	0.57
51:RE:373:ARG:NH2	51:RE:510:ILE:O	2.37	0.57
58:RO:270:SER:H	58:RO:273:GLN:HE21	1.50	0.57
1:3A:323:G:OP2	40:5D:116:LYS:CB	2.51	0.57
23:3F:241:THR:HG21	23:3F:285:SER:HA	1.86	0.57
24:3H:44:LEU:HD13	24:3H:52:ILE:HD11	1.86	0.57
29:AE:671:LEU:O	29:AE:675:ASN:HB3	2.04	0.57
30:AF:303:LEU:HD13	30:AF:323:SER:HB2	1.86	0.57
35:B8:221:THR:OG1	35:B8:222:LEU:N	2.38	0.57
36:BE:482:GLY:HA2	36:BE:505:VAL:HG23	1.86	0.57
39:5C:317:THR:HG23	39:5C:334:ARG:HB3	1.86	0.57
51:RE:443:HIS:HB3	51:RE:470:LYS:HB2	1.85	0.57
54:RJ:773:THR:HA	54:RJ:777:ARG:HH11	1.69	0.57
55:RK:114:PHE:HB2	55:RK:170:VAL:HG22	1.86	0.57
3:SA:1196:A:N3	53:RG:136:ARG:NH2	2.52	0.57
16:SY:109:ARG:NH2	16:SY:120:VAL:O	2.37	0.57
29:AE:186:MET:HE1	29:AE:234:LEU:HD12	1.86	0.57
33:B2:365:TYR:HA	33:B2:381:LYS:HA	1.85	0.57
38:5B:194:LYS:HD2	38:5B:199:ILE:HG13	1.86	0.57
41:5E:384:ARG:HE	43:5G:81:SER:HB3	1.69	0.57
53:RH:31:LEU:HD13	53:RH:40:ARG:HE	1.69	0.57
17:SZ:83:LYS:HD2	17:SZ:96:LEU:HD21	1.86	0.57
20:3C:267:VAL:HG21	20:3C:298:ILE:HD12	1.87	0.57
34:B3:744:ARG:HA	34:B3:785:ILE:HG21	1.86	0.57
35:B8:227:LEU:HB2	35:B8:528:GLN:HE22	1.67	0.57
36:BE:359:ALA:O	36:BE:421:ASN:ND2	2.38	0.57
40:5D:113:ILE:CG2	40:5D:117:LYS:HE3	2.34	0.57
1:3A:318:U:H3	20:3C:119:GLY:CA	2.12	0.57
22:3E:339:TYR:HB3	22:3E:343:TYR:HB2	1.85	0.57
29:AE:559:ASN:HA	29:AE:592:ARG:HD3	1.85	0.57
39:5C:450:GLY:O	60:RQ:857:TYR:OH	2.21	0.57
56:RL:29:VAL:HG22	56:RL:202:ASP:HA	1.86	0.57
5:SF:206:ASP:OD1	5:SF:206:ASP:N	2.38	0.57
9:SJ:167:ALA:HB2	9:SJ:183:ILE:HD12	1.87	0.57
26:A5:148:LEU:HD23	26:A5:167:SER:HB3	1.86	0.57
30:AF:24:GLN:O	30:AF:28:ARG:HB3	2.05	0.57
32:B1:264:LYS:HD3	32:B1:280:THR:HG22	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B1:405:SER:HB3	32:B1:436:LEU:HD23	1.85	0.57
34:B3:392:ASN:H	34:B3:407:SER:HA	1.69	0.57
39:5C:430:VAL:HG21	42:5F:3:ARG:NE	2.18	0.57
45:5I:87:SER:OG	45:5I:89:ASP:OD1	2.22	0.57
52:RF:134:ILE:O	52:RF:138:TRP:HB3	2.05	0.57
59:RP:2073:GLU:OE2	59:RP:2076:ARG:NH1	2.36	0.57
1:3A:57:A:H5''	42:5F:165:LYS:HG3	1.87	0.57
3:SA:205:U:H2'	3:SA:206:A:H8	1.68	0.57
3:SA:1684:U:H3	3:SA:1718:G:H1	1.52	0.57
23:3F:442:ILE:HA	23:3F:472:PRO:HA	1.86	0.57
35:B8:146:LEU:O	35:B8:163:ARG:NH1	2.37	0.57
51:RE:440:LEU:HA	51:RE:456:LYS:O	2.05	0.57
51:RE:919:TRP:CZ2	51:RE:1067:LEU:CD2	2.87	0.57
20:3C:142:ARG:NH1	20:3C:186:ASP:OD2	2.36	0.57
27:A8:596:LYS:HG2	27:A8:637:LEU:HB3	1.86	0.57
32:B1:418:ARG:HH21	32:B1:418:ARG:CG	2.09	0.57
48:RA:152:ASP:HA	48:RA:166:ASN:HA	1.86	0.57
54:RJ:1042:MET:HG3	54:RJ:1044:LEU:HD13	1.86	0.57
2:5A:481:U:O2'	37:B6:102:LYS:NZ	2.37	0.57
3:SA:146:U:N3	3:SA:168:A:N6	2.51	0.57
3:SA:559:C:OP1	54:RJ:868:ARG:NH2	2.37	0.57
21:3D:264:SER:OG	21:3D:265:GLU:N	2.37	0.57
23:3F:142:ILE:HA	23:3F:568:ILE:HD11	1.86	0.57
26:A5:434:THR:HG23	58:RO:266:ASN:HD21	1.68	0.57
31:AG:86:GLU:OE1	31:AG:113:ASN:ND2	2.36	0.57
35:B8:129:ASP:OD1	36:BE:194:ARG:NH2	2.36	0.57
45:5I:81:ASN:ND2	45:5I:96:ASN:OD1	2.38	0.57
51:RE:1160:SER:O	51:RE:1187:LYS:HG2	2.04	0.57
56:RL:32:ARG:HE	56:RL:35:ASN:HD21	1.53	0.57
3:SA:112:A:O2'	11:SM:67:ARG:NH1	2.37	0.57
8:SI:187:SER:OG	8:SI:188:GLU:N	2.38	0.57
36:BE:666:ARG:NH1	36:BE:706:ASP:OD2	2.38	0.57
45:5I:45:LEU:HD13	45:5I:410:ILE:HG22	1.86	0.57
51:RE:1170:GLY:HA3	51:RE:1177:GLY:HA2	1.87	0.57
59:RP:54:TRP:HA	59:RP:57:ILE:HG22	1.87	0.57
61:RS:209:LYS:HE3	61:RS:212:LYS:HG3	1.87	0.57
3:SA:1197:C:OP1	53:RG:136:ARG:NH1	2.38	0.56
23:3F:545:LYS:HG2	23:3F:561:ASN:HD21	1.70	0.56
26:A5:212:LEU:HD11	26:A5:246:VAL:HG11	1.87	0.56
27:A8:655:LEU:HD23	28:A9:507:ARG:HB3	1.86	0.56
32:B1:373:ASP:HB2	32:B1:380:LEU:HD21	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5E:310:GLN:HA	41:5E:313:GLN:HG2	1.86	0.56
41:5E:350:THR:OG1	54:RJ:975:GLU:CD	2.48	0.56
47:5K:26:LYS:HD3	47:5K:29:GLN:HG3	1.87	0.56
1:3A:94:A:H61	1:3A:322:A:N6	2.01	0.56
13:SP:103:ARG:NH2	62:RT:188:LYS:CG	2.68	0.56
31:AG:473:LEU:HB2	31:AG:495:ILE:HD11	1.87	0.56
32:B1:54:HIS:NE2	32:B1:72:SER:OG	2.32	0.56
32:B1:479:LEU:HD12	32:B1:488:LEU:HD11	1.87	0.56
34:B3:690:HIS:ND1	41:5E:519:GLU:HB2	2.20	0.56
45:5I:15:PRO:HB3	45:5I:20:GLN:HE21	1.70	0.56
56:RL:12:SER:O	56:RL:16:ASN:ND2	2.38	0.56
3:SA:439:U:H4'	3:SA:465:G:H22	1.69	0.56
3:SA:1680:G:N2	3:SA:1720:G:O6	2.38	0.56
30:AF:147:ARG:NH2	53:RH:16:GLN:O	2.39	0.56
32:B1:298:LEU:HA	41:5E:472:PRO:CB	2.33	0.56
33:B2:598:LYS:NZ	33:B2:610:SER:OG	2.38	0.56
41:5E:507:ILE:HD11	41:5E:528:LEU:HD23	1.86	0.56
48:RA:227:ARG:NH2	48:RA:248:SER:O	2.34	0.56
49:RB:230:ALA:O	49:RB:234:LYS:HB2	2.05	0.56
53:RG:41:MET:HG3	53:RG:202:ILE:HG23	1.88	0.56
55:RK:221:CYS:SG	55:RK:222:GLU:N	2.71	0.56
3:SA:337:G:N2	3:SA:340:U:OP2	2.39	0.56
22:3E:414:ARG:NH1	29:AE:187:ASP:OD2	2.36	0.56
28:A9:473:LYS:O	28:A9:477:LYS:NZ	2.39	0.56
16:SY:132:LEU:HA	16:SY:135:LEU:HB2	1.87	0.56
25:A4:32:ILE:O	25:A4:751:GLU:HA	2.06	0.56
25:A4:37:ARG:NH1	27:A8:704:PRO:O	2.38	0.56
32:B1:329:VAL:HG12	32:B1:339:LEU:HG	1.87	0.56
50:RD:1509:GLU:HG2	51:RE:1199:ASN:HB2	1.87	0.56
10:SK:78:ARG:NH2	49:RB:247:GLU:OE1	2.33	0.56
25:A4:301:ASP:O	25:A4:771:GLN:NE2	2.38	0.56
33:B2:145:ILE:HG23	33:B2:159:LEU:HB2	1.88	0.56
51:RE:228:ARG:HE	51:RE:296:ILE:HG12	1.71	0.56
51:RE:606:ASN:ND2	51:RE:608:PHE:O	2.39	0.56
51:RE:822:ARG:HE	51:RE:1136:LEU:HD21	1.71	0.56
56:RL:71:LYS:O	56:RL:75:ASN:ND2	2.38	0.56
2:5A:484:G:OP2	37:B6:3:LYS:NZ	2.39	0.56
4:SC:87:ARG:HH21	4:SC:101:HIS:HD2	1.52	0.56
41:5E:474:ILE:HG23	41:5E:476:MET:H	1.71	0.56
51:RE:223:ARG:HA	51:RE:226:HIS:HB2	1.86	0.56
58:RO:170:GLY:O	58:RO:272:GLN:NE2	2.32	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5A:5:G:N2	2:5A:8:A:OP2	2.39	0.56
20:3C:160:ASP:OD1	20:3C:160:ASP:N	2.37	0.56
26:A5:435:GLY:HA3	58:RO:262:LEU:HD11	1.88	0.56
32:B1:419:TYR:CE2	41:5E:486:ASN:ND2	2.73	0.56
33:B2:347:SER:O	33:B2:371:LYS:NZ	2.39	0.56
33:B2:461:SER:OG	33:B2:462:SER:N	2.38	0.56
52:RF:262:VAL:HA	52:RF:265:ARG:HG2	1.88	0.56
56:RL:7:ASP:HB2	56:RL:10:ILE:HG12	1.88	0.56
3:SA:143:G:OP2	7:SH:139:ASN:ND2	2.38	0.56
3:SA:1657:U:OP1	3:SA:1658:G:O2'	2.23	0.56
9:SJ:104:ILE:O	9:SJ:164:ARG:HA	2.06	0.56
21:3D:389:ILE:HA	24:3H:62:GLU:HB2	1.87	0.56
26:A5:25:ASP:OD2	35:B8:590:LYS:NZ	2.37	0.56
26:A5:471:ARG:NH2	58:RO:301:ASP:OD2	2.39	0.56
43:5G:76:GLU:OE2	43:5G:201:ARG:NH2	2.36	0.56
47:5K:123:PRO:O	47:5K:126:LYS:NZ	2.39	0.56
48:RA:175:PRO:O	48:RA:177:LYS:NZ	2.36	0.56
51:RE:241:ILE:HA	51:RE:244:LYS:HD2	1.88	0.56
22:3E:136:LEU:HG	22:3E:139:MET:HE2	1.88	0.56
29:AE:272:LYS:NZ	29:AE:310:GLY:O	2.39	0.56
45:5I:73:ILE:HG12	45:5I:85:THR:HG22	1.88	0.56
51:RE:560:ASN:OD1	51:RE:560:ASN:N	2.39	0.56
55:RK:34:GLU:HG3	55:RK:35:LYS:HG2	1.88	0.56
55:RK:154:LEU:HB2	55:RK:165:GLU:HG3	1.88	0.56
57:RN:478:ILE:HD13	57:RN:520:PRO:HB2	1.88	0.56
57:RN:512:ASP:OD1	57:RN:512:ASP:N	2.38	0.56
63:RY:487:ASP:N	63:RY:487:ASP:OD1	2.36	0.56
3:SA:1490:C:OP1	54:RJ:1062:ARG:NH2	2.38	0.55
20:3C:320:TYR:OH	20:3C:322:ARG:NH2	2.39	0.55
23:3F:417:SER:OG	23:3F:418:ASP:N	2.37	0.55
26:A5:364:THR:OG1	26:A5:368:ASN:ND2	2.38	0.55
29:AE:95:ASP:HB2	29:AE:131:ASN:HD21	1.71	0.55
31:AG:435:ASP:HB3	31:AG:702:TYR:HA	1.88	0.55
34:B3:12:LEU:HG	34:B3:641:PHE:HB2	1.87	0.55
35:B8:181:GLU:HB3	36:BE:281:ARG:HH12	1.71	0.55
59:RP:67:ALA:O	59:RP:71:GLU:HB2	2.07	0.55
1:3A:94:A:N6	1:3A:322:A:H61	2.00	0.55
3:SA:448:C:OP2	5:SF:49:ARG:NH2	2.38	0.55
7:SH:46:LYS:HB3	7:SH:118:GLU:HG2	1.88	0.55
17:SZ:54:ALA:HB1	17:SZ:76:TYR:HB2	1.88	0.55
24:3H:41:THR:O	24:3H:45:ASN:ND2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:A5:5:VAL:HA	26:A5:21:THR:HG22	1.89	0.55
33:B2:463:SER:OG	33:B2:464:LEU:N	2.39	0.55
33:B2:858:PHE:O	33:B2:862:LYS:HB2	2.06	0.55
46:5J:129:ALA:HB1	54:RJ:1119:ILE:HG22	1.89	0.55
48:RA:101:ASN:HA	48:RA:118:GLN:HA	1.88	0.55
3:SA:128:U:H3	59:RP:906:THR:H	1.53	0.55
32:B1:341:GLN:HG3	32:B1:378:PHE:CD1	2.41	0.55
40:5D:58:ARG:NH2	42:5F:174:ARG:CZ	2.69	0.55
51:RE:578:ILE:HG22	51:RE:619:VAL:HG12	1.88	0.55
57:RN:86:ILE:O	57:RN:89:GLN:CG	2.54	0.55
59:RP:1760:ASN:ND2	59:RP:1805:ASP:OD2	2.39	0.55
3:SA:396:G:O6	9:SJ:26:LYS:NZ	2.37	0.55
3:SA:1678:A:N6	3:SA:1723:U:O4	2.39	0.55
9:SJ:195:ARG:NH2	11:SM:11:ARG:O	2.39	0.55
33:B2:124:ILE:HA	33:B2:140:SER:HA	1.89	0.55
33:B2:142:ASP:OD2	33:B2:144:ASN:ND2	2.39	0.55
33:B2:267:ASP:OD1	33:B2:267:ASP:N	2.36	0.55
40:5D:61:ASP:HA	42:5F:160:TRP:HZ3	1.71	0.55
42:5F:4:LYS:O	42:5F:4:LYS:HG2	2.07	0.55
45:5I:26:ARG:NH1	60:RQ:867:GLN:O	2.40	0.55
45:5I:340:ARG:NH2	45:5I:377:SER:O	2.39	0.55
50:RD:1674:LEU:HD23	50:RD:1677:ARG:HD3	1.88	0.55
51:RE:707:PHE:O	51:RE:918:ARG:NH1	2.39	0.55
54:RJ:939:TYR:HA	54:RJ:997:MET:HE1	1.88	0.55
55:RK:139:PRO:HA	55:RK:142:GLU:HB2	1.89	0.55
57:RN:682:ARG:O	57:RN:686:ASN:ND2	2.40	0.55
59:RP:1981:TYR:OH	59:RP:1985:ARG:NH1	2.39	0.55
3:SA:207:U:H3	3:SA:258:C:N4	2.04	0.55
3:SA:444:C:O2	3:SA:460:A:N6	2.39	0.55
3:SA:453:U:O2'	3:SA:455:C:OP2	2.24	0.55
3:SA:862:A:OP2	12:SO:64:ARG:NH2	2.40	0.55
4:SC:192:VAL:HG21	51:RE:751:LYS:HA	1.88	0.55
20:3B:225:ARG:NH1	20:3B:248:ASP:OD2	2.38	0.55
20:3C:189:GLY:O	20:3C:216:ASN:ND2	2.39	0.55
20:3C:225:ARG:NH2	20:3C:246:GLN:OE1	2.38	0.55
23:3F:289:ARG:NH2	23:3F:332:ALA:O	2.39	0.55
23:3F:337:VAL:HG23	23:3F:407:MET:HE2	1.88	0.55
23:3F:552:TRP:HB3	24:3H:85:VAL:HG13	1.88	0.55
31:AG:262:MET:HA	31:AG:272:ALA:O	2.07	0.55
34:B3:366:PRO:HG2	34:B3:378:PRO:HB3	1.88	0.55
39:5C:162:ASN:HB3	39:5C:164:GLN:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5C:369:MET:HE1	39:5C:404:PRO:HD2	1.88	0.55
42:5F:13:LEU:CD1	42:5F:16:VAL:HG11	2.37	0.55
45:5I:173:ILE:HG13	45:5I:174:ARG:HG2	1.87	0.55
45:5I:329:ILE:HG12	45:5I:343:TYR:HB2	1.89	0.55
51:RE:412:LEU:HD13	51:RE:421:LEU:HD12	1.89	0.55
54:RJ:279:PRO:HB3	54:RJ:784:LYS:HA	1.88	0.55
54:RJ:360:ASP:OD1	54:RJ:360:ASP:N	2.35	0.55
54:RJ:608:LEU:HB2	55:RK:16:ASN:HD22	1.72	0.55
54:RJ:921:GLU:HB2	55:RK:365:LYS:HG3	1.88	0.55
60:RQ:896:ALA:HB1	60:RQ:897:PRO:HD2	1.89	0.55
9:SJ:41:LYS:HE2	9:SJ:43:ILE:HD11	1.89	0.55
9:SJ:98:LYS:NZ	9:SJ:170:SER:O	2.36	0.55
25:A4:57:ILE:HD13	25:A4:340:GLN:HG2	1.89	0.55
31:AG:583:LYS:HE2	31:AG:599:ILE:HD13	1.88	0.55
35:B8:526:ASP:OD1	35:B8:526:ASP:N	2.38	0.55
35:B8:561:PRO:O	35:B8:587:ARG:NH1	2.39	0.55
37:B6:278:MET:HA	37:B6:312:LEU:HD11	1.89	0.55
49:RB:304:GLU:OE1	49:RB:309:LYS:NZ	2.40	0.55
51:RE:1174:GLY:N	51:RE:1179:LYS:CE	2.70	0.55
54:RJ:871:MET:SD	54:RJ:930:LYS:HD2	2.47	0.55
60:RQ:898:PHE:N	60:RQ:898:PHE:CD1	2.73	0.55
3:SA:365:G:N7	49:RB:231:ARG:NH1	2.55	0.55
3:SA:545:A:O2'	3:SA:546:U:O4'	2.22	0.55
3:SA:1232:U:O4	3:SA:1234:A:N6	2.39	0.55
23:3F:293:ASP:N	23:3F:293:ASP:OD1	2.37	0.55
29:AE:1172:ASP:N	29:AE:1236:ASN:O	2.40	0.55
33:B2:163:LYS:HG2	41:5E:522:ARG:HH22	1.71	0.55
33:B2:592:SER:OG	33:B2:593:ALA:N	2.40	0.55
34:B3:179:LYS:O	34:B3:181:LYS:NZ	2.38	0.55
51:RE:691:SER:OG	51:RE:692:LYS:N	2.40	0.55
61:RS:445:ARG:NH1	61:RS:445:ARG:O	2.40	0.55
10:SK:139:GLN:NE2	17:SZ:64:PHE:O	2.39	0.55
21:3D:21:LYS:HE2	21:3D:49:GLU:HB2	1.88	0.55
24:3G:57:ASP:O	24:3G:84:ARG:NH1	2.40	0.55
25:A4:641:GLU:OE2	25:A4:645:ARG:NH1	2.40	0.55
27:A8:596:LYS:HE2	27:A8:637:LEU:CA	2.29	0.55
31:AG:51:GLN:HE21	31:AG:53:LYS:HD3	1.72	0.55
32:B1:356:ASP:HB2	32:B1:826:ARG:HG3	1.89	0.55
33:B2:787:LYS:NZ	33:B2:788:PRO:O	2.38	0.55
34:B3:5:THR:O	34:B3:611:LYS:NZ	2.39	0.55
45:5I:75:LYS:NZ	45:5I:356:TYR:O	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:RA:166:ASN:ND2	48:RA:168:GLU:O	2.40	0.55
51:RE:356:THR:HB	51:RE:414:HIS:HB2	1.89	0.55
54:RJ:130:ASP:OD2	54:RJ:853:ARG:NH2	2.40	0.55
55:RK:171:ASP:N	55:RK:171:ASP:OD1	2.39	0.55
1:3A:58:A:P	42:5F:165:LYS:HE3	2.47	0.55
3:SA:96:G:N2	3:SA:387:A:N1	2.55	0.55
3:SA:258:C:O2	9:SJ:178:ARG:NH2	2.40	0.55
5:SF:45:ILE:HG13	5:SF:61:VAL:HG11	1.88	0.55
12:SO:60:VAL:HG23	12:SO:66:ILE:HD12	1.88	0.55
26:A5:454:GLU:OE2	26:A5:487:ARG:NH1	2.40	0.55
29:AE:196:LEU:HD11	29:AE:213:THR:HG21	1.88	0.55
29:AE:636:ASP:OD1	29:AE:639:ARG:NH1	2.40	0.55
34:B3:107:ILE:HD11	34:B3:147:ILE:HG22	1.88	0.55
51:RE:508:SER:HA	51:RE:512:LEU:HB2	1.89	0.55
55:RK:155:LYS:HG3	55:RK:164:GLY:HA2	1.89	0.55
57:RN:290:LYS:O	61:RS:458:ARG:NH1	2.40	0.55
3:SA:1684:U:O2	3:SA:1718:G:N2	2.40	0.55
7:SH:10:ASN:O	7:SH:128:THR:OG1	2.25	0.55
11:SM:125:VAL:HB	11:SM:137:PHE:HB3	1.89	0.55
13:SP:122:PRO:HB2	13:SP:125:SER:HB3	1.89	0.55
14:SR:122:ARG:CZ	43:5G:133:LYS:HD2	2.37	0.55
22:3E:280:MET:HG3	22:3E:288:THR:HG22	1.89	0.55
26:A5:531:LYS:O	26:A5:535:ASP:HB2	2.07	0.55
29:AE:12:ALA:HB2	39:5C:142:GLY:HA3	1.89	0.55
29:AE:558:VAL:O	29:AE:592:ARG:NH1	2.40	0.55
29:AE:652:MET:HE3	29:AE:683:SER:HB3	1.89	0.55
44:5H:565:LYS:HA	44:5H:568:LYS:HG2	1.89	0.55
51:RE:190:ALA:O	51:RE:350:TYR:OH	2.25	0.55
51:RE:267:ILE:HD12	51:RE:293:ASN:HB3	1.89	0.55
54:RJ:289:HIS:HB2	54:RJ:815:LEU:HD21	1.89	0.55
3:SA:332:U:OP1	9:SJ:31:ARG:NH2	2.37	0.54
9:SJ:8:ARG:HD2	9:SJ:22:ARG:HH11	1.72	0.54
21:3D:379:LEU:O	21:3D:383:CYS:HB2	2.07	0.54
27:A8:638:LEU:HA	27:A8:641:VAL:HG12	1.89	0.54
30:AF:75:LYS:HD3	30:AF:113:PRO:HD3	1.89	0.54
30:AF:420:GLU:O	30:AF:424:ARG:HB3	2.07	0.54
35:B8:176:LYS:O	35:B8:180:ASP:CB	2.55	0.54
39:5C:96:ASP:OD1	39:5C:96:ASP:N	2.35	0.54
51:RE:536:TYR:OH	51:RE:552:ARG:NH1	2.40	0.54
51:RE:1189:LEU:HD23	51:RE:1189:LEU:O	2.07	0.54
54:RJ:551:LYS:O	54:RJ:555:MET:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1628:U:OP2	41:5E:534:ARG:NH1	2.40	0.54
27:A8:563:LEU:HB2	27:A8:598:GLU:CD	2.27	0.54
31:AG:727:GLN:OE1	31:AG:738:ASN:ND2	2.39	0.54
32:B1:375:THR:OG1	32:B1:376:SER:N	2.41	0.54
35:B8:176:LYS:O	35:B8:180:ASP:HB3	2.07	0.54
37:B6:187:LYS:HE3	46:5J:63:PRO:HB2	1.89	0.54
45:5I:402:GLU:O	45:5I:405:ARG:NH2	2.40	0.54
54:RJ:966:ILE:HD13	54:RJ:976:ILE:HG22	1.88	0.54
58:RO:345:ILE:HA	58:RO:349:LEU:HD13	1.89	0.54
3:SA:562:G:H8	43:5G:283:THR:HB	1.72	0.54
27:A8:441:VAL:C	31:AG:728:LEU:HD21	2.33	0.54
29:AE:205:THR:HB	29:AE:210:LEU:HD21	1.89	0.54
31:AG:850:GLU:HA	31:AG:853:ILE:HD12	1.89	0.54
39:5C:186:ARG:NH1	42:5F:42:GLU:OE2	2.40	0.54
45:5I:133:GLN:NE2	45:5I:151:ASN:OD1	2.40	0.54
49:RB:335:GLU:HA	49:RB:339:SER:HB2	1.89	0.54
55:RK:37:ARG:NH2	55:RK:49:GLU:OE2	2.36	0.54
61:RS:319:LYS:HA	61:RS:323:PHE:HB2	1.89	0.54
3:SA:576:G:C5'	41:5E:327:LYS:HE2	2.37	0.54
14:SR:22:VAL:HG22	14:SR:65:ILE:HG23	1.89	0.54
21:3D:63:LEU:O	21:3D:67:ASN:ND2	2.40	0.54
25:A4:534:LEU:HA	25:A4:542:VAL:O	2.07	0.54
27:A8:441:VAL:C	31:AG:728:LEU:CD2	2.80	0.54
27:A8:527:LEU:HD11	27:A8:549:ARG:HH22	1.72	0.54
32:B1:202:ASP:N	32:B1:202:ASP:OD1	2.40	0.54
34:B3:537:TRP:N	34:B3:551:SER:O	2.37	0.54
40:5D:61:ASP:C	42:5F:160:TRP:CH2	2.86	0.54
48:RA:78:LYS:O	48:RA:80:GLN:NE2	2.41	0.54
49:RB:242:MET:HE2	49:RB:332:ARG:HE	1.73	0.54
54:RJ:1018:VAL:O	54:RJ:1029:TRP:NE1	2.41	0.54
58:RO:156:TRP:O	58:RO:215:ASN:ND2	2.40	0.54
62:RT:181:TYR:CE2	62:RT:237:PHE:CE2	2.94	0.54
25:A4:252:GLN:NE2	25:A4:318:ASN:OD1	2.40	0.54
30:AF:215:VAL:HA	30:AF:230:GLY:HA3	1.90	0.54
34:B3:328:GLN:NE2	34:B3:329:VAL:O	2.41	0.54
35:B8:352:GLN:HE21	35:B8:385:ASN:HD22	1.54	0.54
36:BE:73:GLU:OE2	36:BE:74:LYS:NZ	2.40	0.54
36:BE:626:ASP:N	36:BE:626:ASP:OD1	2.35	0.54
53:RH:114:ILE:HG12	53:RH:122:ILE:HB	1.89	0.54
3:SA:103:A:OP1	9:SJ:18:ARG:NH1	2.40	0.54
21:3D:392:TYR:HB3	24:3H:65:LEU:HD22	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AE:274:ILE:HD11	35:B8:215:THR:HG21	1.90	0.54
30:AF:360:MET:HE3	30:AF:361:MET:HE3	1.89	0.54
31:AG:64:LYS:NZ	31:AG:123:GLY:O	2.39	0.54
54:RJ:73:ALA:HB1	54:RJ:131:ILE:HD12	1.90	0.54
3:SA:511:A:OP2	10:SK:176:ASN:ND2	2.40	0.54
3:SA:1175:U:OP1	57:RN:748:ARG:NH1	2.41	0.54
5:SF:198:LYS:HG3	5:SF:208:VAL:HG23	1.89	0.54
6:SG:26:ALA:HB3	14:SR:28:LEU:HB3	1.89	0.54
14:SR:34:SER:HB2	14:SR:38:LEU:HD12	1.90	0.54
23:3F:398:CYS:O	23:3F:419:ASN:ND2	2.40	0.54
23:3F:414:ILE:HD11	23:3F:480:ALA:HB2	1.90	0.54
24:3G:13:ASP:OD1	24:3G:13:ASP:N	2.39	0.54
32:B1:396:ALA:HB2	32:B1:438:VAL:HG21	1.90	0.54
33:B2:287:ARG:NH1	33:B2:324:PHE:O	2.41	0.54
35:B8:486:SER:OG	35:B8:487:GLU:N	2.41	0.54
41:5E:437:ILE:HD11	42:5F:70:PHE:HE2	1.73	0.54
47:5K:145:VAL:HG23	47:5K:151:TYR:HB2	1.89	0.54
49:RB:310:GLN:O	49:RB:314:ASN:ND2	2.40	0.54
51:RE:1216:LYS:HG2	51:RE:1220:PHE:HE2	1.68	0.54
55:RK:347:ASN:ND2	55:RK:349:ASP:OD2	2.40	0.54
57:RN:515:HIS:HB3	57:RN:518:ILE:HG22	1.90	0.54
57:RN:780:LYS:HG2	57:RN:781:MET:HE2	1.90	0.54
20:3B:90:PRO:HD3	46:5J:106:LEU:HD12	1.90	0.54
20:3C:268:VAL:HG22	20:3C:317:VAL:HG12	1.89	0.54
23:3F:481:ILE:HD12	23:3F:486:VAL:HG13	1.90	0.54
31:AG:325:GLN:NE2	31:AG:328:THR:OG1	2.41	0.54
31:AG:368:ASP:OD1	31:AG:368:ASP:N	2.38	0.54
33:B2:317:ILE:O	33:B2:321:TYR:N	2.41	0.54
34:B3:510:SER:O	34:B3:514:THR:OG1	2.26	0.54
48:RA:64:VAL:HG21	48:RA:323:VAL:HG12	1.90	0.54
48:RA:121:ARG:HH22	63:RY:462:ARG:HD2	1.72	0.54
48:RA:250:GLY:HA2	48:RA:274:ILE:HG23	1.88	0.54
51:RE:174:TYR:HE2	51:RE:227:LYS:HB3	1.73	0.54
51:RE:578:ILE:HG21	51:RE:617:LEU:HD12	1.90	0.54
1:3A:258:U:O4	21:3D:377:ARG:NH2	2.41	0.54
3:SA:146:U:O4	3:SA:168:A:N7	2.41	0.54
3:SA:265:A:OP2	7:SH:194:LYS:NZ	2.37	0.54
3:SA:1605:G:OP1	43:5G:119:ARG:NH2	2.40	0.54
20:3B:124:SER:HB3	46:5J:153:ILE:HD11	1.90	0.54
26:A5:20:VAL:HG22	26:A5:29:VAL:HG22	1.89	0.54
29:AE:519:LEU:HD23	29:AE:523:ILE:HD13	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:AF:387:ALA:O	30:AF:391:ASN:ND2	2.40	0.54
31:AG:510:TYR:OH	31:AG:527:HIS:ND1	2.35	0.54
31:AG:724:ILE:HD11	31:AG:763:ILE:HG22	1.90	0.54
33:B2:260:GLU:O	33:B2:272:PHE:HA	2.08	0.54
36:BE:430:ILE:HB	36:BE:443:TRP:HB2	1.89	0.54
36:BE:604:SER:OG	36:BE:606:ASP:OD1	2.25	0.54
51:RE:931:ASP:OD1	51:RE:931:ASP:N	2.37	0.54
54:RJ:954:SER:HA	54:RJ:984:GLU:HG3	1.89	0.54
57:RN:86:ILE:HA	57:RN:89:GLN:CD	2.33	0.54
3:SA:325:G:H2'	3:SA:326:G:H8	1.73	0.54
3:SA:1539:G:N1	3:SA:1569:A:OP2	2.41	0.54
21:3D:392:TYR:HB2	24:3H:62:GLU:HB3	1.90	0.54
22:3E:380:ARG:NH1	22:3E:382:ASP:OD1	2.40	0.54
23:3F:399:GLU:OE2	23:3F:417:SER:OG	2.26	0.54
24:3H:38:ASN:HA	24:3H:41:THR:HG22	1.90	0.54
25:A4:207:ASP:OD2	25:A4:209:ARG:NH1	2.37	0.54
25:A4:641:GLU:HB3	25:A4:749:SER:HB3	1.90	0.54
34:B3:745:ASP:O	41:5E:512:GLY:O	2.26	0.54
36:BE:160:THR:OG1	36:BE:163:GLN:NE2	2.41	0.54
39:5C:449:ILE:HD11	45:5I:38:ALA:HA	1.89	0.54
51:RE:375:PHE:HZ	51:RE:487:ILE:HG23	1.73	0.54
54:RJ:871:MET:CE	54:RJ:930:LYS:CE	2.86	0.54
54:RJ:1027:THR:HG23	54:RJ:1028:GLU:HG2	1.89	0.54
55:RK:214:LYS:O	55:RK:217:LYS:NZ	2.40	0.54
57:RN:605:ASP:OD1	57:RN:610:ARG:NH1	2.41	0.54
59:RP:1939:ARG:HG3	59:RP:1974:LEU:HD11	1.88	0.54
3:SA:1738:U:OP1	33:B2:279:LYS:NZ	2.40	0.53
8:SI:155:ASP:OD1	8:SI:155:ASP:N	2.41	0.53
9:SJ:184:LEU:HD23	9:SJ:189:LEU:HA	1.90	0.53
18:Sc:67:THR:OG1	18:Sc:70:LYS:O	2.26	0.53
25:A4:271:THR:HG21	35:B8:443:VAL:HG21	1.91	0.53
31:AG:157:PHE:O	31:AG:169:GLN:NE2	2.40	0.53
33:B2:525:ASP:OD1	33:B2:525:ASP:N	2.41	0.53
42:5F:136:VAL:HA	42:5F:160:TRP:HA	1.90	0.53
45:5I:192:SER:HB2	45:5I:206:VAL:HG22	1.89	0.53
51:RE:227:LYS:HA	51:RE:230:VAL:HG12	1.90	0.53
10:SK:76:LEU:HB2	49:RB:328:PHE:CE1	2.43	0.53
31:AG:404:SER:OG	31:AG:405:ALA:N	2.40	0.53
36:BE:743:ARG:O	36:BE:743:ARG:HD3	2.08	0.53
51:RE:1183:THR:HG23	51:RE:1183:THR:O	2.07	0.53
53:RH:125:ASN:ND2	53:RH:127:THR:OG1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:RN:96:LYS:HD2	57:RN:761:PHE:HZ	1.73	0.53
1:3A:318:U:N3	20:3C:119:GLY:HA3	2.16	0.53
3:SA:396:G:N7	9:SJ:47:ARG:NH1	2.56	0.53
6:SG:73:THR:OG1	6:SG:91:GLU:OE1	2.27	0.53
25:A4:311:THR:HG22	25:A4:313:LYS:H	1.74	0.53
29:AE:651:LEU:HD21	29:AE:680:TYR:HB2	1.90	0.53
30:AF:173:THR:HG21	30:AF:218:VAL:H	1.74	0.53
32:B1:283:GLU:OE2	32:B1:297:GLN:NE2	2.42	0.53
1:3A:25:U:H5'	42:5F:11:LYS:O	2.07	0.53
4:SC:32:ILE:HB	4:SC:43:VAL:HG22	1.90	0.53
20:3B:230:TYR:OH	20:3B:256:ASN:OD1	2.25	0.53
29:AE:626:PHE:HB3	29:AE:629:GLU:HB2	1.90	0.53
32:B1:418:ARG:HG3	32:B1:418:ARG:NH2	2.12	0.53
32:B1:419:TYR:CD2	41:5E:482:LEU:HD12	2.44	0.53
34:B3:596:ASP:OD1	34:B3:596:ASP:N	2.42	0.53
36:BE:737:LEU:O	36:BE:740:ILE:HG23	2.09	0.53
39:5C:312:VAL:HG21	39:5C:353:PRO:HG2	1.90	0.53
50:RD:1473:ASN:CB	50:RD:1509:GLU:OE2	2.51	0.53
52:RF:107:LEU:HD12	52:RF:194:ARG:HG3	1.89	0.53
23:3F:357:LEU:HD22	49:RB:256:PRO:HB2	1.90	0.53
24:3H:45:ASN:HA	24:3H:74:LYS:HE2	1.90	0.53
31:AG:291:ARG:HD2	31:AG:329:ASN:HD21	1.73	0.53
33:B2:412:GLY:HA2	33:B2:431:GLY:H	1.73	0.53
41:5E:315:GLU:HB3	54:RJ:1032:LEU:CD1	2.37	0.53
45:5I:349:GLN:O	45:5I:367:SER:OG	2.24	0.53
51:RE:179:LYS:HB2	51:RE:210:PRO:HG2	1.90	0.53
51:RE:1098:PHE:HE2	51:RE:1182:ILE:HG22	1.72	0.53
62:RT:189:ASP:OD2	62:RT:251:ILE:CD1	2.57	0.53
7:SH:48:TYR:OH	7:SH:119:GLN:O	2.27	0.53
11:SM:82:ARG:HA	11:SM:111:VAL:HG13	1.91	0.53
31:AG:213:LYS:HA	31:AG:223:LYS:HA	1.91	0.53
51:RE:687:GLN:NE2	51:RE:694:ALA:O	2.41	0.53
53:RG:36:LYS:NZ	53:RG:169:ASP:O	2.40	0.53
55:RK:289:VAL:HG21	55:RK:294:LEU:HD13	1.90	0.53
56:RL:37:LEU:HD13	56:RL:123:ILE:HD13	1.90	0.53
1:3A:98:U:OP2	1:3A:98:U:H6	1.92	0.53
3:SA:1108:G:O2'	3:SA:1109:G:N7	2.37	0.53
51:RE:969:ASN:ND2	51:RE:972:ASP:OD1	2.41	0.53
1:3A:256:G:OP1	21:3D:382:LYS:NZ	2.37	0.53
3:SA:513:U:H2'	3:SA:514:G:C8	2.44	0.53
3:SA:1209:C:N3	3:SA:1210:C:N4	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:SF:209:HIS:ND1	5:SF:218:PHE:O	2.41	0.53
22:3E:289:GLN:HE21	22:3E:388:LEU:HD13	1.74	0.53
26:A5:46:TRP:HD1	26:A5:48:GLU:HG3	1.74	0.53
31:AG:283:VAL:HG12	31:AG:290:ILE:HG22	1.91	0.53
33:B2:554:THR:OG1	33:B2:556:LYS:NZ	2.39	0.53
53:RG:188:ARG:NH2	53:RH:247:ASP:OD2	2.41	0.53
54:RJ:374:ASP:OD1	54:RJ:374:ASP:N	2.40	0.53
61:RS:437:ARG:NH2	61:RS:459:GLU:O	2.42	0.53
3:SA:647:G:H22	3:SA:687:G:H22	1.56	0.53
25:A4:35:ARG:HH11	25:A4:738:TYR:HD1	1.57	0.53
25:A4:420:LEU:HD23	26:A5:581:ASN:HA	1.91	0.53
28:A9:513:ARG:HH21	28:A9:515:ASP:HA	1.72	0.53
41:5E:322:LYS:HD2	41:5E:327:LYS:HB2	1.90	0.53
48:RA:202:ASN:ND2	48:RA:229:PHE:O	2.41	0.53
51:RE:417:SER:OG	51:RE:418:SER:N	2.42	0.53
53:RG:121:LEU:HD21	53:RG:167:ILE:HG13	1.89	0.53
54:RJ:844:PRO:HA	54:RJ:856:THR:O	2.08	0.53
58:RO:233:ASP:N	58:RO:233:ASP:OD1	2.42	0.53
1:3A:323:G:N3	1:3A:323:G:C2'	2.71	0.53
3:SA:1633:A:O3'	32:B1:418:ARG:NH2	2.38	0.53
21:3D:102:ASP:HB3	21:3D:105:LEU:HB3	1.91	0.53
27:A8:443:CYS:CB	31:AG:728:LEU:CB	2.76	0.53
29:AE:40:ALA:HB1	29:AE:123:ARG:HH12	1.73	0.53
32:B1:812:GLU:HG3	32:B1:813:HIS:HD2	1.74	0.53
3:SA:1136:U:O2'	33:B2:596:ASN:ND2	2.43	0.52
11:SM:97:TYR:O	11:SM:99:ARG:NH1	2.42	0.52
29:AE:571:LEU:HD11	29:AE:582:VAL:HG11	1.91	0.52
32:B1:418:ARG:NH1	41:5E:492:PRO:HD3	2.24	0.52
35:B8:216:TYR:OH	36:BE:276:TYR:OH	2.27	0.52
41:5E:493:GLN:HE21	41:5E:497:ASN:CB	2.20	0.52
41:5E:500:LYS:O	41:5E:508:ARG:NH2	2.42	0.52
42:5F:123:THR:HG23	42:5F:126:ASP:H	1.74	0.52
48:RA:13:VAL:HG12	48:RA:343:ILE:HG12	1.89	0.52
51:RE:526:CYS:O	51:RE:698:ASN:ND2	2.42	0.52
54:RJ:871:MET:HE1	54:RJ:930:LYS:HE2	1.88	0.52
59:RP:18:SER:OG	59:RP:19:PHE:N	2.42	0.52
1:3A:97:C:O2	1:3A:320:G:C2	2.62	0.52
3:SA:153:G:H2'	3:SA:154:G:H8	1.74	0.52
3:SA:1782:A:C6	32:B1:257:TYR:CD2	2.97	0.52
21:3D:157:ALA:O	37:B6:293:TYR:OH	2.26	0.52
22:3E:251:ASP:OD1	22:3E:251:ASP:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3F:162:CYS:SG	23:3F:525:GLN:NE2	2.78	0.52
27:A8:443:CYS:CA	31:AG:728:LEU:CD2	2.79	0.52
27:A8:647:LEU:O	28:A9:509:GLN:NE2	2.41	0.52
30:AF:87:ALA:HA	30:AF:97:CYS:O	2.08	0.52
51:RE:398:ALA:O	51:RE:402:ASN:ND2	2.43	0.52
51:RE:596:LYS:HZ2	51:RE:600:TYR:HD1	1.56	0.52
51:RE:1108:LEU:HB2	51:RE:1169:ILE:HD11	1.91	0.52
54:RJ:135:ALA:O	54:RJ:238:ARG:NH2	2.42	0.52
54:RJ:982:LYS:HG3	54:RJ:983:PRO:HD3	1.92	0.52
56:RL:131:THR:OG1	56:RL:133:ASN:ND2	2.42	0.52
60:RQ:298:TRP:HE1	60:RQ:899:LYS:CG	2.19	0.52
3:SA:258:C:H4'	9:SJ:75:LYS:HD2	1.91	0.52
29:AE:502:ILE:HG23	29:AE:542:ILE:HG13	1.90	0.52
51:RE:443:HIS:HB3	51:RE:470:LYS:HE2	1.91	0.52
54:RJ:90:VAL:HG23	54:RJ:107:VAL:HG11	1.92	0.52
55:RK:97:GLY:HA2	55:RK:100:VAL:HG12	1.92	0.52
55:RK:180:MET:HE3	55:RK:181:HIS:H	1.75	0.52
57:RN:587:ASP:OD1	57:RN:587:ASP:N	2.42	0.52
62:RT:109:LEU:O	62:RT:113:TRP:HB2	2.08	0.52
3:SA:153:G:N2	7:SH:56:ASN:OD1	2.42	0.52
10:SK:67:PRO:HB2	49:RB:334:LEU:HD23	1.91	0.52
24:3H:54:MET:HE1	24:3H:78:TYR:HB2	1.90	0.52
25:A4:39:VAL:H	25:A4:755:ILE:HD11	1.75	0.52
25:A4:658:ASP:OD2	25:A4:731:HIS:N	2.42	0.52
26:A5:481:LEU:HD22	26:A5:523:LEU:HD22	1.92	0.52
33:B2:398:ASP:HB2	33:B2:406:LEU:HB3	1.92	0.52
36:BE:470:GLN:NE2	36:BE:512:GLY:O	2.42	0.52
51:RE:437:ASP:N	51:RE:437:ASP:OD1	2.42	0.52
5:SF:53:LYS:O	23:3F:120:ARG:NH2	2.42	0.52
9:SJ:191:PHE:O	9:SJ:195:ARG:NH1	2.41	0.52
34:B3:337:HIS:HD2	34:B3:363:ARG:HD3	1.74	0.52
36:BE:268:THR:HG22	36:BE:270:SER:H	1.75	0.52
41:5E:384:ARG:HD3	43:5G:83:ILE:CD1	2.38	0.52
50:RD:1547:TYR:OH	50:RD:1583:SER:OG	2.27	0.52
51:RE:270:ILE:HB	51:RE:292:ILE:HG23	1.91	0.52
51:RE:518:PHE:CE2	51:RE:1075:LEU:HG	2.43	0.52
53:RH:116:THR:HG22	53:RH:118:ARG:H	1.73	0.52
3:SA:494:U:OP1	54:RJ:1138:ARG:NH2	2.32	0.52
3:SA:594:A:OP1	10:SK:38:ASN:ND2	2.43	0.52
20:3B:281:ASP:OD1	20:3B:281:ASP:N	2.41	0.52
21:3D:169:LYS:HA	21:3D:299:VAL:HG22	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3F:284:LEU:O	23:3F:548:ARG:NH2	2.38	0.52
29:AE:556:LYS:O	29:AE:592:ARG:NH2	2.42	0.52
51:RE:596:LYS:HG3	51:RE:598:LYS:H	1.74	0.52
52:RF:51:ASP:HB2	52:RF:134:ILE:HG21	1.91	0.52
53:RG:169:ASP:N	53:RG:169:ASP:OD1	2.40	0.52
55:RK:30:PRO:HB3	55:RK:77:ARG:HG3	1.90	0.52
59:RP:452:ASN:O	59:RP:456:GLU:N	2.43	0.52
3:SA:331:A:N3	9:SJ:5:ARG:NH1	2.57	0.52
3:SA:1436:A:H1'	61:RS:419:LYS:HD2	1.91	0.52
7:SH:105:ASP:OD1	7:SH:105:ASP:N	2.43	0.52
9:SJ:110:ARG:NH1	9:SJ:161:SER:O	2.43	0.52
28:A9:504:GLU:OE2	28:A9:507:ARG:NH1	2.43	0.52
31:AG:319:LYS:HD2	31:AG:339:GLY:H	1.74	0.52
36:BE:578:VAL:O	36:BE:579:ARG:NH1	2.42	0.52
36:BE:605:LEU:HD23	36:BE:628:VAL:HG11	1.92	0.52
42:5F:66:PRO:O	42:5F:72:ARG:NH2	2.43	0.52
51:RE:186:ILE:HD11	51:RE:206:LEU:HB2	1.91	0.52
52:RF:44:SER:H	52:RF:50:SER:HA	1.75	0.52
58:RO:258:GLU:HG3	58:RO:289:PHE:HD1	1.74	0.52
59:RP:1892:LEU:HA	59:RP:1895:PHE:HB2	1.92	0.52
61:RS:397:PHE:HD1	61:RS:407:GLU:HG2	1.75	0.52
2:5A:7:A:N7	31:AG:578:ASN:ND2	2.55	0.52
3:SA:862:A:H4'	15:SX:57:ARG:HG3	1.90	0.52
22:3E:426:ALA:HB2	36:BE:305:ASN:HD21	1.75	0.52
32:B1:420:ARG:NH2	41:5E:494:GLU:CD	2.66	0.52
32:B1:678:GLU:OE2	41:5E:455:HIS:ND1	2.43	0.52
34:B3:680:ASN:N	34:B3:680:ASN:OD1	2.42	0.52
36:BE:819:LYS:NZ	36:BE:823:GLU:OE2	2.40	0.52
46:5J:58:ASN:HA	46:5J:61:LYS:HG2	1.92	0.52
48:RA:147:ASN:ND2	48:RA:154:TYR:OH	2.43	0.52
51:RE:315:ILE:HG13	51:RE:329:THR:HG21	1.92	0.52
51:RE:529:VAL:HB	51:RE:613:VAL:HB	1.91	0.52
1:3A:198:U:O4	23:3F:151:ARG:NE	2.38	0.52
1:3A:312:U:H5''	46:5J:167:LYS:HG2	1.91	0.52
7:SH:39:GLU:HG3	7:SH:46:LYS:HG3	1.91	0.52
8:SI:163:ASP:HA	8:SI:166:LEU:HG	1.90	0.52
20:3C:297:ARG:HD3	20:3C:322:ARG:HA	1.92	0.52
26:A5:503:LYS:HD3	28:A9:508:ARG:HH22	1.75	0.52
27:A8:596:LYS:CD	27:A8:637:LEU:HD22	2.38	0.52
30:AF:256:THR:N	30:AF:275:SER:O	2.39	0.52
32:B1:678:GLU:OE2	41:5E:455:HIS:HE1	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:B2:634:SER:OG	33:B2:635:LYS:N	2.41	0.52
36:BE:377:SER:HB2	36:BE:445:MET:HE1	1.92	0.52
54:RJ:72:VAL:HG22	54:RJ:137:LEU:HB3	1.91	0.52
54:RJ:246:ALA:HB3	54:RJ:810:ILE:HB	1.91	0.52
54:RJ:776:GLN:NE2	54:RJ:781:GLU:OE2	2.40	0.52
58:RO:356:ALA:HA	58:RO:499:LEU:HD22	1.91	0.52
59:RP:1880:ILE:HD11	59:RP:1892:LEU:HD21	1.91	0.52
2:5A:9:G:H5'	28:A9:483:LYS:HZ1	1.73	0.52
3:SA:1533:C:OP2	30:AF:114:ARG:NH2	2.43	0.52
3:SA:1720:G:N7	3:SA:1721:A:N6	2.58	0.52
4:SC:164:ILE:HD11	4:SC:205:PHE:HB2	1.91	0.52
22:3E:3:TYR:N	22:3E:21:LYS:O	2.43	0.52
22:3E:359:ILE:HA	22:3E:362:VAL:HG12	1.92	0.52
33:B2:53:ASP:OD2	33:B2:58:ASP:OD1	2.27	0.52
37:B6:296:SER:HB3	37:B6:300:MET:HB2	1.91	0.52
54:RJ:193:ARG:NH2	54:RJ:196:THR:OG1	2.43	0.52
56:RL:589:ALA:HB3	56:RL:593:GLU:H	1.75	0.52
60:RQ:298:TRP:NE1	60:RQ:899:LYS:CG	2.62	0.52
61:RS:360:LEU:HD21	61:RS:393:TYR:HB2	1.92	0.52
3:SA:532:U:O2'	17:SZ:33:ALA:O	2.27	0.51
6:SG:120:ILE:HA	6:SG:123:VAL:HG12	1.92	0.51
22:3E:385:ASP:OD1	22:3E:385:ASP:N	2.42	0.51
33:B2:54:ILE:CD1	33:B2:364:TYR:CD2	2.93	0.51
39:5C:130:ARG:NH2	39:5C:379:GLU:OE2	2.42	0.51
45:5I:319:GLU:OE2	45:5I:356:TYR:OH	2.27	0.51
45:5I:324:SER:OG	45:5I:326:ASP:OD1	2.23	0.51
51:RE:634:HIS:HB2	51:RE:655:LEU:HD11	1.91	0.51
52:RF:128:PHE:HD2	52:RF:134:ILE:HG22	1.76	0.51
54:RJ:871:MET:HE1	54:RJ:930:LYS:HD2	1.91	0.51
58:RO:200:ASN:ND2	58:RO:256:ASN:O	2.43	0.51
60:RQ:298:TRP:CD1	60:RQ:899:LYS:HG3	2.44	0.51
2:5A:294:U:OP1	32:B1:631:ASN:ND2	2.43	0.51
3:SA:-5:G:N1	39:5C:39:ASP:OD1	2.36	0.51
3:SA:419:G:H5''	3:SA:419:G:H8	1.75	0.51
3:SA:1599:C:H4'	43:5G:145:HIS:CD2	2.45	0.51
7:SH:74:LYS:HB2	48:RA:88:ASN:HD21	1.75	0.51
8:SI:83:LYS:O	8:SI:86:GLN:NE2	2.43	0.51
20:3B:277:ASP:N	20:3B:277:ASP:OD1	2.43	0.51
24:3H:44:LEU:HD22	24:3H:52:ILE:HD12	1.90	0.51
25:A4:63:SER:HA	25:A4:82:ARG:HH12	1.75	0.51
27:A8:443:CYS:CA	31:AG:728:LEU:HD13	2.17	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AE:659:LEU:HD13	29:AE:690:GLU:HB3	1.92	0.51
31:AG:736:THR:HG23	31:AG:738:ASN:H	1.74	0.51
32:B1:506:SER:OG	32:B1:507:GLN:N	2.43	0.51
33:B2:281:ILE:HB	33:B2:332:ILE:HG23	1.91	0.51
33:B2:362:ILE:HG12	33:B2:385:ILE:HB	1.92	0.51
39:5C:410:ASN:O	45:5I:27:ASN:ND2	2.43	0.51
43:5G:108:LYS:HD2	43:5G:116:ARG:HB2	1.92	0.51
51:RE:469:ASP:OD2	51:RE:472:THR:OG1	2.27	0.51
51:RE:1215:ASN:HD21	52:RF:35:HIS:HA	1.75	0.51
52:RF:227:ARG:HA	52:RF:230:ILE:HD12	1.91	0.51
54:RJ:864:ASP:OD1	54:RJ:864:ASP:N	2.44	0.51
62:RT:256:PRO:HA	62:RT:259:VAL:HG22	1.91	0.51
20:3B:120:GLU:OE2	20:3B:142:ARG:NE	2.41	0.51
25:A4:481:ILE:HB	25:A4:485:LYS:HB2	1.91	0.51
27:A8:587:LEU:HD23	27:A8:587:LEU:O	2.10	0.51
31:AG:407:ASN:ND2	31:AG:416:SER:OG	2.44	0.51
33:B2:759:GLY:HA3	33:B2:805:ILE:HD11	1.91	0.51
34:B3:679:THR:HG21	34:B3:723:GLU:HB2	1.93	0.51
43:5G:143:HIS:HB2	43:5G:151:SER:HB2	1.91	0.51
49:RB:348:SER:HB2	59:RP:1728:PHE:HB3	1.93	0.51
51:RE:261:ASN:HB3	51:RE:379:MET:HB2	1.91	0.51
52:RF:71:VAL:HA	52:RF:74:LEU:HD12	1.92	0.51
54:RJ:616:ASP:HB2	54:RJ:621:LEU:HG	1.90	0.51
58:RO:214:LYS:O	58:RO:268:GLN:NE2	2.43	0.51
5:SF:201:HIS:H	5:SF:206:ASP:HB3	1.75	0.51
9:SJ:171:SER:HB3	9:SJ:180:ASP:H	1.74	0.51
21:3D:126:ASP:HA	21:3D:129:ARG:HG2	1.93	0.51
23:3F:136:PHE:HE1	23:3F:484:SER:HB2	1.74	0.51
27:A8:631:SER:O	27:A8:634:LEU:CG	2.45	0.51
43:5G:185:VAL:O	43:5G:220:ARG:NH1	2.39	0.51
56:RL:117:ASN:O	56:RL:141:THR:OG1	2.26	0.51
59:RP:85:LYS:NZ	59:RP:89:ASN:OD1	2.40	0.51
59:RP:1746:LYS:O	59:RP:1748:ASN:ND2	2.41	0.51
62:RT:238:THR:HA	62:RT:241:ARG:HG2	1.91	0.51
2:5A:473:A:H5"	39:5C:164:GLN:HE22	1.76	0.51
8:SI:67:LEU:HD13	8:SI:94:ALA:HB2	1.93	0.51
21:3D:26:ASP:OD1	45:5I:98:SER:OG	2.29	0.51
22:3E:218:ALA:O	22:3E:236:LYS:NZ	2.41	0.51
25:A4:402:TRP:HB3	25:A4:416:LEU:HA	1.91	0.51
32:B1:329:VAL:HG13	32:B1:338:ILE:HB	1.92	0.51
36:BE:59:GLN:HG2	36:BE:71:VAL:HG22	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5E:350:THR:HG21	54:RJ:975:GLU:HB2	1.92	0.51
45:5I:329:ILE:HG22	45:5I:351:VAL:HG11	1.93	0.51
51:RE:111:LEU:HA	51:RE:114:VAL:HG12	1.93	0.51
53:RG:105:ASN:HD21	53:RG:110:LEU:HD22	1.75	0.51
55:RK:315:LYS:HB2	55:RK:348:GLU:HB3	1.92	0.51
57:RN:661:ILE:HG22	57:RN:665:GLN:HG3	1.92	0.51
6:SG:118:LEU:HG	6:SG:129:PRO:HB2	1.92	0.51
9:SJ:100:ALA:O	9:SJ:168:CYS:HA	2.10	0.51
11:SM:18:HIS:HB2	11:SM:63:LEU:HD21	1.91	0.51
13:SP:103:ARG:NH2	62:RT:186:GLU:OE1	2.44	0.51
13:SP:107:ARG:NH2	13:SP:107:ARG:CB	2.73	0.51
20:3B:91:HIS:HD2	20:3B:93:HIS:H	1.57	0.51
27:A8:712:ASP:OD1	27:A8:712:ASP:N	2.40	0.51
29:AE:558:VAL:HG13	29:AE:615:ASN:HA	1.93	0.51
32:B1:588:ASP:OD1	32:B1:588:ASP:N	2.43	0.51
32:B1:680:ARG:HH11	41:5E:455:HIS:CD2	2.27	0.51
34:B3:501:PRO:HG3	34:B3:543:GLN:HG3	1.91	0.51
36:BE:854:SER:HB2	36:BE:895:VAL:HG21	1.93	0.51
42:5F:6:LYS:HB2	42:5F:9:GLU:HG2	1.91	0.51
45:5I:122:ARG:HB2	45:5I:192:SER:HB3	1.93	0.51
45:5I:327:LYS:HG2	45:5I:350:HIS:H	1.76	0.51
48:RA:101:ASN:HD21	48:RA:116:HIS:HB3	1.76	0.51
51:RE:1202:CYS:SG	51:RE:1203:ASN:N	2.83	0.51
59:RP:1896:ILE:HG13	59:RP:1897:PRO:HD3	1.92	0.51
61:RS:229:LEU:HD11	61:RS:233:PHE:HD2	1.74	0.51
7:SH:70:PRO:HD3	7:SH:101:ILE:HD12	1.93	0.51
25:A4:420:LEU:HD11	25:A4:462:VAL:HG21	1.92	0.51
31:AG:434:GLN:OE1	31:AG:434:GLN:N	2.43	0.51
32:B1:722:THR:HG22	32:B1:724:HIS:H	1.75	0.51
33:B2:201:ILE:HG13	34:B3:663:VAL:HG11	1.92	0.51
34:B3:497:LEU:HA	34:B3:507:ALA:O	2.11	0.51
61:RS:263:THR:HA	61:RS:266:PHE:HB2	1.93	0.51
62:RT:182:ILE:HG22	62:RT:234:LEU:CD1	2.21	0.51
3:SA:898:A:N1	3:SA:911:U:O2'	2.41	0.51
3:SA:1780:G:N1	32:B1:252:LYS:HE2	2.25	0.51
9:SJ:67:TRP:NE1	9:SJ:70:GLU:OE1	2.42	0.51
13:SP:99:GLN:NE2	62:RT:188:LYS:CD	2.73	0.51
20:3C:94:ALA:HB3	20:3C:166:PRO:HG3	1.92	0.51
27:A8:647:LEU:CB	28:A9:509:GLN:HE22	2.23	0.51
30:AF:258:LEU:HD22	30:AF:272:LEU:HD21	1.93	0.51
32:B1:392:ALA:O	32:B1:404:SER:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B3:414:VAL:HG23	34:B3:427:TYR:HB3	1.92	0.51
39:5C:74:LEU:HD23	39:5C:404:PRO:HG2	1.93	0.51
46:5J:120:ASP:HB2	46:5J:173:ILE:HD12	1.92	0.51
51:RE:298:PHE:HB2	51:RE:340:SER:HA	1.93	0.51
51:RE:1162:ILE:HG23	51:RE:1187:LYS:NZ	2.26	0.51
52:RF:178:ASP:OD1	52:RF:178:ASP:N	2.43	0.51
53:RG:150:ILE:HD11	53:RG:160:LEU:HD23	1.92	0.51
56:RL:539:ALA:O	56:RL:543:SER:CB	2.59	0.51
2:5A:293:U:H3	32:B1:632:SER:HB3	1.75	0.51
3:SA:283:U:OP1	7:SH:191:ARG:NH1	2.40	0.51
3:SA:340:U:H2'	3:SA:341:A:H8	1.75	0.51
3:SA:647:G:H1	3:SA:687:G:H1	1.59	0.51
3:SA:1634:C:P	32:B1:418:ARG:HH22	2.32	0.51
13:SP:12:GLN:HE21	13:SP:78:ALA:HB2	1.76	0.51
20:3C:171:LEU:HD23	20:3C:240:VAL:HG12	1.92	0.51
27:A8:441:VAL:CA	31:AG:728:LEU:HD21	2.41	0.51
28:A9:471:LYS:HZ3	28:A9:474:HIS:H	1.59	0.51
29:AE:522:ARG:HH12	29:AE:561:PHE:HB2	1.76	0.51
34:B3:17:ALA:HB3	34:B3:35:PRO:HA	1.91	0.51
48:RA:282:ASN:HD21	48:RA:325:GLY:H	1.58	0.51
51:RE:777:ASP:O	51:RE:780:GLN:NE2	2.43	0.51
53:RH:178:VAL:HG12	53:RH:223:GLU:HB2	1.93	0.51
1:3A:59:G:H5'	32:B1:570:THR:HG23	1.92	0.51
1:3A:305:G:H2'	1:3A:306:G:H8	1.75	0.51
3:SA:29:U:H2'	3:SA:30:G:H8	1.74	0.51
3:SA:123:G:OP1	5:SF:77:ARG:NH2	2.40	0.51
3:SA:826:U:O2'	3:SA:827:C:O2	2.23	0.51
4:SC:36:SER:HA	4:SC:41:ARG:HD3	1.91	0.51
9:SJ:104:ILE:HD13	9:SJ:167:ALA:HB3	1.91	0.51
12:SO:63:ALA:O	12:SO:67:THR:OG1	2.24	0.51
17:SZ:86:GLU:OE2	17:SZ:90:ARG:NH1	2.43	0.51
22:3E:355:ASN:HB2	22:3E:401:LEU:HD13	1.93	0.51
26:A5:8:SER:OG	26:A5:293:ASN:ND2	2.43	0.51
26:A5:439:VAL:HG11	58:RO:300:THR:HG21	1.92	0.51
29:AE:586:LEU:O	29:AE:590:ALA:CB	2.58	0.51
32:B1:732:GLU:HG2	32:B1:734:GLN:HE22	1.76	0.51
36:BE:135:ASN:ND2	36:BE:165:GLY:O	2.42	0.51
41:5E:336:PRO:HB2	41:5E:339:ALA:HB2	1.93	0.51
51:RE:1107:GLY:HA3	51:RE:1176:LYS:HG2	1.93	0.51
51:RE:1189:LEU:HD22	51:RE:1190:PHE:CD2	2.46	0.51
54:RJ:776:GLN:HA	54:RJ:780:ILE:HG22	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:27:LYS:HB3	4:SC:47:LEU:HD22	1.93	0.50
7:SH:21:GLU:OE2	7:SH:25:ARG:NH2	2.44	0.50
20:3B:142:ARG:NH2	20:3B:182:SER:OG	2.44	0.50
27:A8:587:LEU:HD23	27:A8:587:LEU:C	2.35	0.50
31:AG:668:THR:OG1	31:AG:669:ASN:OD1	2.30	0.50
33:B2:562:SER:HB2	33:B2:564:LYS:HB2	1.93	0.50
33:B2:627:SER:OG	33:B2:628:HIS:N	2.45	0.50
39:5C:91:ILE:HG23	45:5I:3:ILE:HD11	1.92	0.50
40:5D:61:ASP:HB3	42:5F:160:TRP:CZ3	2.46	0.50
51:RE:404:GLY:H	51:RE:455:SER:HB3	1.76	0.50
53:RG:150:ILE:HG12	53:RG:160:LEU:HB2	1.93	0.50
56:RL:80:GLU:OE2	56:RL:85:THR:OG1	2.29	0.50
3:SA:290:G:H3'	3:SA:291:G:H8	1.76	0.50
3:SA:442:C:O2'	3:SA:525:A:N1	2.35	0.50
26:A5:192:SER:HB3	26:A5:207:GLU:HG3	1.93	0.50
27:A8:34:GLY:HA2	27:A8:352:GLN:HA	1.92	0.50
31:AG:855:LEU:HD23	35:B8:477:LYS:HE3	1.93	0.50
32:B1:328:LEU:HD21	41:5E:476:MET:HG3	1.93	0.50
34:B3:413:ILE:HG22	34:B3:429:LYS:HA	1.92	0.50
45:5I:54:PHE:O	45:5I:382:ARG:NH2	2.44	0.50
3:SA:304:U:OP1	11:SM:136:ARG:NH2	2.45	0.50
3:SA:340:U:H2'	3:SA:341:A:C8	2.47	0.50
3:SA:420:A:H8	3:SA:420:A:H3'	1.76	0.50
20:3C:223:ASP:OD2	20:3C:225:ARG:NH1	2.44	0.50
30:AF:401:LEU:HB3	30:AF:434:ARG:HH22	1.77	0.50
31:AG:207:LEU:HG	31:AG:264:ILE:HD12	1.93	0.50
36:BE:225:THR:OG1	36:BE:227:THR:O	2.29	0.50
36:BE:370:SER:OG	36:BE:372:ASP:OD1	2.20	0.50
37:B6:297:ASP:OD1	37:B6:297:ASP:N	2.44	0.50
39:5C:238:MET:HE3	39:5C:247:MET:HE2	1.92	0.50
51:RE:261:ASN:OD1	51:RE:588:GLN:NE2	2.42	0.50
53:RH:228:SER:OG	53:RH:229:ASN:N	2.44	0.50
1:3A:93:U:OP2	22:3E:302:HIS:ND1	2.42	0.50
1:3A:316:A:H2'	1:3A:317:A:H8	1.76	0.50
2:5A:90:G:O2'	2:5A:91:U:O4'	2.25	0.50
3:SA:413:U:H2'	3:SA:414:C:H6	1.77	0.50
30:AF:224:THR:O	30:AF:239:LEU:CB	2.57	0.50
30:AF:378:LYS:NZ	35:B8:292:GLY:O	2.44	0.50
50:RD:1674:LEU:HA	50:RD:1677:ARG:HG2	1.93	0.50
54:RJ:634:ARG:HD2	55:RK:185:ARG:HH21	1.77	0.50
54:RJ:772:MET:HE3	54:RJ:773:THR:H	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:RK:65:ILE:HB	57:RN:112:VAL:HG12	1.94	0.50
55:RK:183:ILE:HG22	55:RK:351:ILE:HD13	1.94	0.50
59:RP:1873:LEU:HD22	59:RP:1917:ILE:HG13	1.93	0.50
5:SF:26:CYS:SG	5:SF:27:TYR:N	2.84	0.50
13:SP:85:ALA:H	13:SP:119:THR:HB	1.76	0.50
20:3B:111:MET:HB2	20:3B:186:ASP:HB3	1.92	0.50
22:3E:430:ASP:HA	36:BE:125:GLY:HA2	1.93	0.50
25:A4:382:VAL:HG11	25:A4:755:ILE:HG21	1.92	0.50
26:A5:355:ASN:OD1	31:AG:479:ASN:ND2	2.44	0.50
30:AF:399:GLU:O	30:AF:403:ASN:ND2	2.42	0.50
31:AG:249:THR:HG22	31:AG:256:THR:HB	1.93	0.50
41:5E:345:LEU:HD21	54:RJ:961:PHE:CE2	2.46	0.50
51:RE:1096:TYR:CD2	51:RE:1185:LEU:HD12	2.47	0.50
53:RH:41:MET:O	53:RH:110:LEU:HA	2.11	0.50
53:RH:41:MET:HG3	53:RH:202:ILE:HG23	1.92	0.50
61:RS:322:LEU:HD21	61:RS:359:LEU:HD11	1.92	0.50
3:SA:420:A:H3'	3:SA:420:A:C8	2.47	0.50
3:SA:1134:C:H1'	33:B2:610:SER:HB2	1.94	0.50
11:SM:109:VAL:HG11	11:SM:139:VAL:HG13	1.94	0.50
20:3C:170:VAL:HG23	20:3C:194:VAL:HG13	1.93	0.50
29:AE:558:VAL:HG22	29:AE:615:ASN:HD22	1.76	0.50
30:AF:59:SER:OG	30:AF:60:SER:N	2.43	0.50
33:B2:102:VAL:HA	33:B2:118:ASN:HA	1.94	0.50
34:B3:182:CYS:SG	34:B3:183:LEU:N	2.84	0.50
38:5B:173:ARG:HE	40:5D:146:PHE:HA	1.76	0.50
51:RE:177:ASN:ND2	51:RE:213:LEU:O	2.44	0.50
62:RT:157:ASP:HA	62:RT:160:LYS:HB3	1.93	0.50
2:5A:20:C:H2'	2:5A:21:A:H8	1.77	0.50
2:5A:505:G:H2'	2:5A:506:G:C8	2.47	0.50
3:SA:1192:C:H1'	53:RG:131:PRO:HA	1.92	0.50
3:SA:1194:A:OP2	3:SA:1195:C:N4	2.40	0.50
20:3B:228:GLN:O	20:3B:231:ARG:NH2	2.43	0.50
27:A8:539:ASN:ND2	27:A8:560:ASN:O	2.44	0.50
31:AG:80:GLN:NE2	31:AG:83:GLU:OE1	2.44	0.50
43:5G:287:LYS:HE2	43:5G:290:LEU:HA	1.94	0.50
51:RE:1062:THR:HG21	64:X1:310:UNK:HA	1.94	0.50
55:RK:114:PHE:O	55:RK:169:VAL:HA	2.12	0.50
59:RP:1769:LEU:HD21	59:RP:1797:LEU:HD22	1.94	0.50
3:SA:1782:A:C5	32:B1:257:TYR:CE2	3.00	0.50
5:SF:181:VAL:HA	5:SF:227:VAL:HA	1.94	0.50
25:A4:415:LYS:NZ	25:A4:416:LEU:O	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:AG:139:GLU:HB3	31:AG:155:THR:HB	1.94	0.50
34:B3:407:SER:OG	34:B3:408:LYS:N	2.45	0.50
34:B3:455:LEU:HA	34:B3:464:LYS:O	2.12	0.50
39:5C:37:THR:O	39:5C:43:ARG:NH2	2.44	0.50
41:5E:533:LYS:HA	41:5E:536:ARG:CD	2.42	0.50
53:RG:175:CYS:SG	53:RG:201:SER:OG	2.67	0.50
58:RO:327:MET:O	58:RO:331:ASN:HA	2.11	0.50
61:RS:439:PHE:HA	61:RS:442:GLU:HG3	1.94	0.50
63:RY:472:ILE:HA	63:RY:475:TYR:HB2	1.93	0.50
1:3A:321:C:H2'	1:3A:322:A:C8	2.47	0.50
2:5A:293:U:H2'	32:B1:631:ASN:HA	1.93	0.50
2:5A:484:G:O6	60:RQ:872:ARG:NH1	2.45	0.50
3:SA:1588:G:H1	3:SA:1608:U:H3	1.60	0.50
8:SI:28:GLU:OE2	8:SI:39:ARG:NH2	2.45	0.50
9:SJ:80:GLY:O	9:SJ:103:GLN:NE2	2.45	0.50
18:Sc:78:SER:HB3	52:RF:212:PHE:HB3	1.94	0.50
25:A4:156:LEU:HD22	25:A4:170:ILE:HD11	1.93	0.50
25:A4:418:CYS:SG	25:A4:419:LYS:N	2.85	0.50
30:AF:48:ASN:ND2	30:AF:111:TYR:OH	2.45	0.50
30:AF:260:TYR:OH	30:AF:262:GLU:OE1	2.30	0.50
31:AG:370:GLN:NE2	31:AG:384:SER:OG	2.44	0.50
31:AG:877:ASP:N	31:AG:877:ASP:OD1	2.43	0.50
36:BE:587:ARG:HB3	36:BE:605:LEU:HD12	1.92	0.50
38:5B:186:ASP:HA	38:5B:189:THR:HG22	1.94	0.50
40:5D:113:ILE:O	40:5D:117:LYS:HG3	2.12	0.50
51:RE:345:TYR:O	51:RE:349:LEU:CB	2.59	0.50
54:RJ:852:ARG:HD2	54:RJ:888:PRO:HG3	1.94	0.50
3:SA:55:A:OP2	56:RL:78:LYS:NZ	2.43	0.49
4:SC:144:ARG:HB3	4:SC:206:PRO:HB2	1.93	0.49
11:SM:109:VAL:HG13	11:SM:138:ASN:HA	1.94	0.49
26:A5:115:ASN:ND2	26:A5:130:ASP:OD1	2.45	0.49
29:AE:306:LEU:HD22	29:AE:311:ASN:HA	1.94	0.49
33:B2:828:TYR:HA	33:B2:831:LYS:HG2	1.93	0.49
35:B8:410:ASP:OD1	35:B8:479:ASN:ND2	2.45	0.49
43:5G:202:VAL:HA	43:5G:205:ILE:HG22	1.94	0.49
51:RE:138:ILE:HD11	51:RE:238:HIS:HB3	1.94	0.49
54:RJ:106:THR:HG23	54:RJ:355:TYR:HB3	1.94	0.49
54:RJ:138:VAL:HB	54:RJ:167:VAL:HG22	1.93	0.49
54:RJ:274:TYR:OH	54:RJ:306:ASP:OD1	2.29	0.49
59:RP:73:ASP:OD2	59:RP:83:HIS:ND1	2.45	0.49
2:5A:485:G:H4'	2:5A:486:U:H5'	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:123:G:H21	5:SF:146:THR:HG21	1.76	0.49
23:3F:365:PRO:HB3	23:3F:397:PHE:HA	1.93	0.49
25:A4:452:HIS:HB3	25:A4:463:THR:HG23	1.94	0.49
25:A4:566:LEU:HD11	25:A4:584:VAL:HG21	1.94	0.49
31:AG:435:ASP:HB2	31:AG:702:TYR:HD1	1.75	0.49
34:B3:65:THR:HA	34:B3:80:SER:HA	1.94	0.49
35:B8:520:ASN:HB2	35:B8:533:ALA:HB3	1.94	0.49
40:5D:67:MET:SD	42:5F:170:LEU:HB3	2.52	0.49
42:5F:96:ASP:HB3	42:5F:100:LYS:HE2	1.94	0.49
48:RA:281:ASP:OD1	48:RA:281:ASP:N	2.45	0.49
51:RE:566:ILE:HD13	51:RE:690:VAL:HG21	1.94	0.49
51:RE:711:PRO:HG3	51:RE:767:GLN:HE21	1.76	0.49
54:RJ:1069:VAL:HG11	54:RJ:1083:ILE:HD13	1.93	0.49
62:RT:180:LEU:C	62:RT:180:LEU:CD1	2.85	0.49
62:RT:181:TYR:OH	62:RT:237:PHE:HE2	1.94	0.49
3:SA:268:C:H2'	3:SA:269:G:H8	1.76	0.49
27:A8:673:THR:CG2	28:A9:490:GLU:N	2.74	0.49
32:B1:839:THR:HG22	36:BE:882:GLU:HG3	1.95	0.49
33:B2:90:ASP:N	33:B2:90:ASP:OD1	2.39	0.49
33:B2:476:ILE:HD11	33:B2:490:THR:HB	1.93	0.49
34:B3:22:VAL:O	34:B3:68:LYS:NZ	2.45	0.49
36:BE:118:VAL:HA	36:BE:132:THR:HA	1.94	0.49
39:5C:340:LEU:O	39:5C:368:TYR:N	2.43	0.49
40:5D:149:GLU:HB3	40:5D:153:ASN:HA	1.94	0.49
48:RA:300:TRP:HB3	48:RA:307:ALA:HA	1.95	0.49
51:RE:606:ASN:ND2	51:RE:610:PHE:O	2.45	0.49
54:RJ:1094:TYR:HA	54:RJ:1097:LYS:HG2	1.94	0.49
59:RP:1473:ALA:O	59:RP:1477:LYS:CB	2.61	0.49
29:AE:387:LEU:HD21	29:AE:403:LEU:HD13	1.93	0.49
30:AF:133:HIS:HB2	30:AF:139:ILE:HG13	1.94	0.49
31:AG:584:PHE:HB3	31:AG:598:LYS:HB2	1.94	0.49
34:B3:83:GLN:HG3	62:RT:181:TYR:HE2	1.78	0.49
39:5C:84:PHE:HA	39:5C:369:MET:HA	1.95	0.49
41:5E:319:VAL:HG23	54:RJ:1038:ILE:HG21	1.91	0.49
48:RA:252:SER:HB2	48:RA:266:LYS:HB3	1.94	0.49
54:RJ:777:ARG:O	54:RJ:778:GLN:NE2	2.46	0.49
54:RJ:951:MET:SD	54:RJ:987:TYR:OH	2.63	0.49
55:RK:107:ALA:HB1	55:RK:170:VAL:HG21	1.94	0.49
57:RN:600:LEU:HD21	57:RN:636:LEU:HD13	1.94	0.49
57:RN:623:ASP:O	57:RN:627:HIS:HB3	2.13	0.49
3:SA:562:G:C8	43:5G:283:THR:HB	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:SJ:70:GLU:OE2	9:SJ:117:TYR:OH	2.30	0.49
14:SR:58:ASP:OD1	14:SR:58:ASP:N	2.43	0.49
22:3E:164:ILE:HG12	22:3E:301:ALA:HA	1.93	0.49
24:3H:52:ILE:HG22	24:3H:54:MET:SD	2.52	0.49
27:A8:631:SER:HA	27:A8:634:LEU:CG	2.43	0.49
33:B2:180:THR:OG1	33:B2:207:CYS:SG	2.62	0.49
33:B2:624:LEU:HD12	33:B2:629:ASN:HB2	1.93	0.49
34:B3:513:LYS:HG3	34:B3:532:HIS:HB2	1.95	0.49
45:5I:76:ASN:HA	45:5I:118:VAL:HG21	1.93	0.49
45:5I:140:SER:OG	45:5I:141:ASP:N	2.44	0.49
50:RD:1519:ALA:HA	50:RD:1522:ASN:HD22	1.78	0.49
51:RE:803:LYS:NZ	51:RE:859:ASP:OD2	2.43	0.49
51:RE:972:ASP:OD1	51:RE:972:ASP:N	2.45	0.49
53:RG:46:ALA:HA	53:RG:115:GLN:HG3	1.93	0.49
54:RJ:871:MET:HE1	54:RJ:930:LYS:CD	2.43	0.49
55:RK:180:MET:O	55:RK:181:HIS:ND1	2.45	0.49
57:RN:752:MET:HA	57:RN:755:ILE:HG12	1.93	0.49
59:RP:752:THR:O	59:RP:756:SER:CB	2.59	0.49
3:SA:622:A:HI1'	3:SA:623:A:C8	2.48	0.49
22:3E:24:LYS:O	22:3E:28:LEU:CB	2.60	0.49
24:3H:7:LYS:HB3	24:3H:65:LEU:HD11	1.95	0.49
24:3H:54:MET:O	24:3H:80:PHE:HA	2.12	0.49
31:AG:96:ILE:HG12	31:AG:108:THR:HG21	1.95	0.49
31:AG:628:ASP:H	31:AG:658:GLU:HA	1.77	0.49
31:AG:736:THR:OG1	31:AG:737:ILE:N	2.45	0.49
32:B1:286:LEU:HD12	32:B1:295:ILE:HB	1.94	0.49
32:B1:406:SER:OG	32:B1:407:LEU:N	2.46	0.49
32:B1:567:ASP:HB3	42:5F:144:ASN:ND2	2.28	0.49
33:B2:337:LYS:O	33:B2:357:THR:OG1	2.25	0.49
33:B2:549:SER:OG	33:B2:576:VAL:O	2.28	0.49
33:B2:817:LEU:HD11	33:B2:856:ASN:HD21	1.77	0.49
34:B3:466:TRP:HZ3	34:B3:478:GLN:HA	1.77	0.49
37:B6:63:VAL:HG13	37:B6:88:ILE:HD11	1.94	0.49
39:5C:183:GLU:HB3	47:5K:16:THR:HG22	1.94	0.49
49:RB:268:ASN:HB3	49:RB:271:ARG:HB3	1.94	0.49
50:RD:1633:ASP:OD2	50:RD:1636:ARG:NH1	2.42	0.49
53:RH:38:THR:O	53:RH:40:ARG:NH1	2.45	0.49
53:RH:69:ASN:HD22	53:RH:72:ASP:HB3	1.77	0.49
54:RJ:176:LEU:HD12	54:RJ:183:LEU:HA	1.94	0.49
59:RP:1794:ARG:HH22	59:RP:1870:LYS:HD2	1.77	0.49
1:3A:57:A:N3	42:5F:133:GLN:NE2	2.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:158:SER:HA	4:SC:161:ILE:HB	1.94	0.49
7:SH:57:ASP:HA	7:SH:107:ALA:H	1.78	0.49
25:A4:338:ALA:HB1	25:A4:361:LEU:HD11	1.95	0.49
27:A8:593:ASP:OD1	27:A8:596:LYS:NZ	2.34	0.49
29:AE:637:ILE:HA	29:AE:640:ILE:HG22	1.94	0.49
33:B2:397:ILE:HD11	33:B2:405:LEU:HD21	1.94	0.49
33:B2:862:LYS:HE2	34:B3:805:ILE:HD13	1.93	0.49
34:B3:80:SER:OG	34:B3:81:GLN:N	2.46	0.49
35:B8:43:ASP:N	35:B8:43:ASP:OD1	2.40	0.49
36:BE:737:LEU:C	36:BE:740:ILE:CG2	2.85	0.49
40:5D:67:MET:SD	42:5F:170:LEU:CB	3.01	0.49
53:RH:112:VAL:O	53:RH:124:VAL:HB	2.12	0.49
1:3A:64:A:OP2	36:BE:392:ARG:NH2	2.46	0.49
24:3G:105:ASN:HB3	24:3G:108:SER:HB2	1.94	0.49
30:AF:276:SER:OG	30:AF:278:ASP:OD1	2.30	0.49
31:AG:31:ASN:HD21	31:AG:201:ILE:HB	1.78	0.49
31:AG:116:VAL:O	31:AG:131:HIS:HA	2.13	0.49
32:B1:569:PHE:CZ	42:5F:142:LEU:HD21	2.48	0.49
34:B3:343:MET:HE2	34:B3:622:ALA:HB1	1.95	0.49
35:B8:183:ASP:OD1	36:BE:281:ARG:NH2	2.45	0.49
36:BE:528:PHE:HZ	36:BE:570:ILE:HD11	1.78	0.49
45:5I:315:PRO:HG2	45:5I:360:SER:HB3	1.93	0.49
45:5I:421:GLN:HG3	45:5I:425:LYS:HD2	1.95	0.49
47:5K:65:VAL:HG22	47:5K:152:ILE:HB	1.94	0.49
54:RJ:262:GLY:O	54:RJ:264:GLN:NE2	2.44	0.49
57:RN:646:THR:HA	57:RN:649:THR:HG22	1.95	0.49
60:RQ:853:ASN:OD1	60:RQ:853:ASN:N	2.45	0.49
61:RS:388:ASP:HA	61:RS:391:VAL:HG22	1.93	0.49
5:SF:202:ASP:OD1	5:SF:202:ASP:N	2.41	0.49
20:3B:269:ILE:O	20:3B:315:ILE:HA	2.13	0.49
25:A4:389:ARG:HE	25:A4:404:MET:HB2	1.78	0.49
29:AE:1628:SER:O	29:AE:1632:PHE:CB	2.60	0.49
33:B2:440:PRO:HG3	33:B2:485:GLY:HA3	1.94	0.49
34:B3:198:ILE:HG12	34:B3:211:LEU:HD13	1.95	0.49
35:B8:233:LEU:HD11	35:B8:543:LEU:HD12	1.95	0.49
36:BE:274:ILE:HG23	36:BE:286:VAL:HG22	1.94	0.49
49:RB:230:ALA:O	49:RB:234:LYS:CB	2.61	0.49
54:RJ:309:PRO:HD2	54:RJ:353:LEU:HD22	1.95	0.49
3:SA:895:G:H1	3:SA:917:U:H3	1.61	0.49
6:SG:219:ARG:NH2	53:RH:222:ASP:OD2	2.45	0.49
11:SM:109:VAL:HG21	11:SM:125:VAL:HG11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:3D:297:HIS:NE2	21:3D:309:GLU:OE2	2.46	0.49
23:3F:305:ARG:HG2	23:3F:317:ILE:HD13	1.94	0.49
27:A8:635:PHE:HD2	28:A9:492:ILE:CD1	2.26	0.49
32:B1:441:SER:O	32:B1:443:GLU:N	2.43	0.49
34:B3:749:ASN:ND2	41:5E:511:ASN:OD1	2.45	0.49
36:BE:173:LEU:HD13	36:BE:219:ASP:HA	1.95	0.49
36:BE:469:SER:HB3	36:BE:510:LEU:HD23	1.95	0.49
36:BE:902:ASN:HB3	36:BE:905:ILE:HG22	1.95	0.49
45:5I:145:VAL:HB	45:5I:176:PHE:HB2	1.94	0.49
51:RE:858:ARG:HD2	51:RE:861:ILE:HD11	1.95	0.49
52:RF:23:HIS:HD2	52:RF:26:LEU:HG	1.78	0.49
53:RG:197:ASP:OD1	53:RG:197:ASP:N	2.45	0.49
3:SA:158:U:H3	3:SA:420:A:HO2'	1.59	0.48
10:SK:82:ARG:NH1	49:RB:323:GLU:OE2	2.46	0.48
22:3E:214:ILE:HD11	22:3E:252:LEU:HD22	1.94	0.48
24:3H:51:PHE:HE1	24:3H:114:ILE:HG23	1.78	0.48
26:A5:280:GLN:HB2	26:A5:288:LYS:HE2	1.95	0.48
30:AF:75:LYS:HD2	30:AF:111:TYR:HA	1.95	0.48
30:AF:428:ARG:HH21	31:AG:518:ASP:HB3	1.76	0.48
33:B2:263:THR:HA	33:B2:269:THR:O	2.13	0.48
34:B3:454:LEU:O	34:B3:465:LYS:HA	2.12	0.48
35:B8:462:GLY:HA2	35:B8:527:GLY:HA3	1.95	0.48
40:5D:78:LEU:HD13	54:RJ:1082:GLN:HG2	1.95	0.48
51:RE:1189:LEU:C	51:RE:1189:LEU:CD2	2.85	0.48
53:RG:190:GLN:HE22	53:RG:247:ASP:HB2	1.78	0.48
57:RN:786:ASN:HA	57:RN:789:ASN:HB2	1.95	0.48
3:SA:129:U:O2'	59:RP:903:THR:O	2.30	0.48
3:SA:1133:A:OP1	55:RK:231:ARG:NE	2.42	0.48
4:SC:129:THR:OG1	4:SC:179:SER:O	2.31	0.48
24:3H:54:MET:HB3	24:3H:64:LEU:HD13	1.93	0.48
26:A5:149:ASN:HD21	26:A5:190:PRO:HB3	1.77	0.48
31:AG:249:THR:O	31:AG:257:ARG:NH1	2.41	0.48
33:B2:291:GLU:HA	33:B2:294:ARG:HG2	1.94	0.48
38:5B:155:ILE:HD12	38:5B:158:LYS:HE3	1.95	0.48
39:5C:112:GLY:HA3	39:5C:130:ARG:HB3	1.94	0.48
39:5C:284:ARG:NH1	39:5C:408:GLU:OE1	2.39	0.48
47:5K:149:LYS:HD3	47:5K:170:ILE:HD11	1.95	0.48
52:RF:56:VAL:HG22	52:RF:123:THR:HG22	1.93	0.48
59:RP:393:PHE:O	59:RP:397:PHE:CB	2.60	0.48
59:RP:1802:HIS:HE1	59:RP:1882:ARG:HB2	1.77	0.48
17:SZ:52:LYS:O	17:SZ:94:TYR:OH	2.23	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:3D:225:ASP:OD1	21:3D:226:LYS:N	2.46	0.48
23:3F:421:ASN:HD22	23:3F:437:ARG:HA	1.78	0.48
29:AE:8:LEU:HD12	39:5C:144:LEU:HD23	1.96	0.48
29:AE:395:GLU:OE2	29:AE:397:LYS:NZ	2.44	0.48
29:AE:482:SER:HB2	29:AE:484:LEU:HG	1.94	0.48
33:B2:392:THR:HG21	33:B2:410:SER:HB3	1.93	0.48
36:BE:656:ASN:N	36:BE:656:ASN:OD1	2.46	0.48
37:B6:16:ASP:OD2	39:5C:15:ARG:NH2	2.46	0.48
37:B6:273:ILE:HA	37:B6:276:VAL:HG22	1.95	0.48
43:5G:85:ASP:OD1	43:5G:211:ASN:ND2	2.42	0.48
45:5I:260:GLN:NE2	45:5I:460:GLN:OE1	2.47	0.48
51:RE:146:LEU:HA	51:RE:149:VAL:HG12	1.94	0.48
51:RE:592:PHE:HB3	51:RE:599:VAL:HG22	1.95	0.48
55:RK:103:MET:O	55:RK:107:ALA:HB2	2.13	0.48
62:RT:247:VAL:HA	62:RT:250:LEU:HD23	1.95	0.48
11:SM:132:SER:OG	11:SM:133:LYS:N	2.46	0.48
15:SX:70:ASN:N	15:SX:70:ASN:OD1	2.43	0.48
18:Sc:58:SER:OG	18:Sc:59:CYS:N	2.46	0.48
20:3C:170:VAL:HG12	20:3C:239:CYS:HB3	1.96	0.48
27:A8:596:LYS:CE	27:A8:640:LEU:HD13	2.43	0.48
31:AG:771:ASP:OD1	31:AG:771:ASP:N	2.46	0.48
34:B3:536:LEU:HA	34:B3:552:SER:HA	1.96	0.48
34:B3:600:LYS:HA	34:B3:609:CYS:HA	1.95	0.48
47:5K:67:ILE:HD11	47:5K:96:PRO:HB2	1.95	0.48
51:RE:264:LEU:HD12	51:RE:265:LEU:HG	1.94	0.48
54:RJ:863:THR:O	54:RJ:863:THR:OG1	2.30	0.48
54:RJ:951:MET:HE1	54:RJ:1003:LEU:HB2	1.94	0.48
55:RK:130:ILE:HG23	55:RK:151:LEU:HD23	1.95	0.48
56:RM:716:PRO:O	56:RM:720:LEU:CB	2.61	0.48
58:RO:447:ASP:OD1	58:RO:447:ASP:N	2.46	0.48
3:SA:163:G:O2'	7:SH:53:SER:OG	2.30	0.48
3:SA:886:U:H2'	3:SA:887:A:H8	1.78	0.48
24:3H:13:ASP:OD1	24:3H:13:ASP:N	2.42	0.48
25:A4:150:ASN:ND2	25:A4:198:ASP:OD1	2.37	0.48
27:A8:583:SER:HA	27:A8:586:ILE:HG22	1.94	0.48
27:A8:668:ILE:O	27:A8:671:ARG:HG3	2.14	0.48
32:B1:680:ARG:HH11	41:5E:455:HIS:CG	2.31	0.48
32:B1:717:LEU:HD12	36:BE:578:VAL:HB	1.94	0.48
33:B2:643:ASP:HB3	33:B2:650:ILE:HD11	1.95	0.48
34:B3:44:ASP:OD1	34:B3:44:ASP:N	2.46	0.48
35:B8:148:THR:OG1	35:B8:152:GLU:OE2	2.31	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B8:266:GLY:HA3	35:B8:295:ILE:HD11	1.95	0.48
35:B8:458:ILE:HG13	35:B8:484:VAL:HG22	1.95	0.48
36:BE:529:TYR:HA	36:BE:536:LEU:HA	1.95	0.48
36:BE:630:THR:N	36:BE:644:THR:O	2.44	0.48
51:RE:132:TYR:HA	51:RE:135:LEU:HG	1.95	0.48
54:RJ:634:ARG:NH2	55:RK:186:PRO:O	2.42	0.48
3:SA:364:G:N7	3:SA:366:A:N6	2.62	0.48
3:SA:1642:G:OP2	41:5E:530:ARG:NH2	2.47	0.48
5:SF:223:ASN:OD1	5:SF:223:ASN:N	2.47	0.48
9:SJ:72:ILE:HG22	9:SJ:74:LYS:HG2	1.96	0.48
25:A4:424:ASP:N	25:A4:424:ASP:OD1	2.45	0.48
37:B6:426:ASP:O	37:B6:430:TYR:N	2.47	0.48
41:5E:475:SER:C	41:5E:477:GLU:H	2.21	0.48
41:5E:520:LEU:HG	41:5E:525:LYS:HG3	1.96	0.48
50:RD:1508:ARG:HH12	52:RF:97:GLU:HB3	1.78	0.48
51:RE:886:THR:HG23	51:RE:890:LEU:HD12	1.96	0.48
52:RF:97:GLU:OE2	52:RF:121:ARG:NH1	2.45	0.48
3:SA:647:G:H22	3:SA:687:G:H1	1.60	0.48
11:SM:90:TYR:H	11:SM:103:ARG:HB3	1.79	0.48
17:SZ:20:ARG:NH1	17:SZ:22:GLN:OE1	2.47	0.48
22:3E:225:GLU:HG2	22:3E:226:ILE:HG13	1.96	0.48
23:3F:448:PHE:HA	23:3F:451:ILE:HG22	1.95	0.48
25:A4:579:ARG:NH2	25:A4:644:SER:OG	2.47	0.48
30:AF:420:GLU:O	30:AF:424:ARG:CB	2.61	0.48
31:AG:105:HIS:HB2	31:AG:122:LYS:HG3	1.95	0.48
34:B3:167:ASP:OD1	34:B3:168:THR:N	2.47	0.48
49:RB:237:SER:O	49:RB:237:SER:OG	2.32	0.48
50:RD:1662:GLU:HG3	50:RD:1671:VAL:HG22	1.95	0.48
51:RE:373:ARG:HA	51:RE:515:ILE:HG12	1.96	0.48
51:RE:1174:GLY:N	51:RE:1179:LYS:HE2	2.28	0.48
54:RJ:298:VAL:HG23	54:RJ:791:ILE:HG23	1.94	0.48
56:RM:507:THR:H	63:RY:495:ALA:HB3	1.77	0.48
57:RN:734:ARG:HA	57:RN:737:ILE:HG12	1.95	0.48
58:RO:507:LEU:HA	58:RO:510:GLU:HB3	1.95	0.48
3:SA:895:G:H21	13:SP:38:THR:HG21	1.79	0.48
14:SR:120:ASP:OD1	14:SR:120:ASP:N	2.40	0.48
23:3F:477:SER:OG	23:3F:521:VAL:O	2.27	0.48
29:AE:684:TYR:HB2	29:AE:687:LEU:HD23	1.95	0.48
34:B3:161:TRP:HB3	34:B3:177:LEU:HG	1.96	0.48
35:B8:183:ASP:HB2	36:BE:242:ARG:HA	1.96	0.48
41:5E:517:LYS:NZ	41:5E:518:GLU:HG3	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:RA:313:PRO:HG3	48:RA:317:ILE:HD11	1.94	0.48
50:RD:1644:LEU:HD13	50:RD:1654:LEU:HD22	1.96	0.48
51:RE:1108:LEU:O	51:RE:1112:CYS:CB	2.60	0.48
58:RO:153:ILE:HD13	58:RO:202:LEU:HD21	1.94	0.48
59:RP:48:LEU:HG	59:RP:74:VAL:HG22	1.95	0.48
1:3A:332:G:H21	31:AG:869:MET:HE3	1.79	0.48
3:SA:153:G:N2	3:SA:161:U:O2	2.43	0.48
3:SA:464:A:H2'	3:SA:465:G:H8	1.78	0.48
7:SH:31:ARG:HE	48:RA:359:ILE:HD13	1.78	0.48
10:SK:136:VAL:HG12	10:SK:156:ILE:HG12	1.96	0.48
25:A4:560:SER:OG	25:A4:561:LYS:N	2.47	0.48
29:AE:336:LEU:HD22	29:AE:373:ILE:HG21	1.96	0.48
29:AE:484:LEU:HD13	29:AE:663:SER:HB3	1.95	0.48
30:AF:435:ASP:OD1	30:AF:435:ASP:N	2.45	0.48
33:B2:479:LEU:HA	33:B2:489:VAL:O	2.14	0.48
34:B3:271:ASP:OD1	34:B3:271:ASP:N	2.47	0.48
34:B3:301:GLN:HG2	34:B3:315:ASN:HA	1.95	0.48
39:5C:137:MET:HA	39:5C:144:LEU:HA	1.96	0.48
41:5E:384:ARG:NE	43:5G:81:SER:HB3	2.28	0.48
52:RF:66:HIS:HA	52:RF:69:LYS:HG3	1.94	0.48
56:RL:55:VAL:HG23	56:RL:121:MET:HB3	1.95	0.48
56:RL:388:GLU:HA	56:RL:410:SER:O	2.14	0.48
57:RN:560:TYR:OH	58:RO:388:LEU:O	2.30	0.48
59:RP:190:ARG:NH1	59:RP:194:GLU:OE2	2.46	0.48
3:SA:1041:G:H2'	3:SA:1042:G:C8	2.49	0.48
3:SA:1082:C:H5''	15:SX:20:THR:HA	1.96	0.48
3:SA:1624:C:H5''	43:5G:185:VAL:HG22	1.96	0.48
21:3D:160:ARG:NH2	22:3E:243:MET:O	2.43	0.48
22:3E:207:ARG:HH11	22:3E:226:ILE:HG12	1.78	0.48
23:3F:523:LYS:O	23:3F:541:ALA:HA	2.13	0.48
27:A8:570:LEU:HD23	27:A8:582:ILE:HD11	1.95	0.48
31:AG:141:LEU:HD11	31:AG:153:ILE:HD11	1.96	0.48
41:5E:477:GLU:HG2	41:5E:477:GLU:O	2.14	0.48
48:RA:164:ARG:NH2	48:RA:174:ASN:OD1	2.46	0.48
51:RE:209:MET:HB2	51:RE:299:PRO:HD3	1.96	0.48
52:RF:9:MET:HB2	52:RF:13:PHE:HB2	1.96	0.48
52:RF:176:ASP:OD1	52:RF:176:ASP:N	2.37	0.48
53:RG:173:THR:OG1	53:RG:174:LYS:N	2.47	0.48
59:RP:1709:ASP:HA	59:RP:1758:ALA:HA	1.94	0.48
60:RQ:322:ASN:OD1	60:RQ:322:ASN:N	2.46	0.48
62:RT:124:LEU:HD11	62:RT:154:LYS:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:94:A:H2'	1:3A:95:A:H8	1.79	0.47
3:SA:124:A:O2'	5:SF:148:ARG:NH2	2.33	0.47
3:SA:336:G:H1	9:SJ:5:ARG:HB2	1.79	0.47
3:SA:351:C:N3	11:SM:102:LYS:NZ	2.52	0.47
11:SM:124:THR:HG22	11:SM:141:LYS:HB3	1.96	0.47
15:SX:9:ASP:OD1	15:SX:9:ASP:N	2.45	0.47
25:A4:284:LEU:HD21	38:5B:206:LEU:HD21	1.95	0.47
25:A4:747:ILE:HD11	25:A4:753:ALA:HB2	1.96	0.47
26:A5:335:ASN:O	26:A5:337:LYS:NZ	2.47	0.47
29:AE:329:THR:HG21	29:AE:365:ILE:HG21	1.95	0.47
31:AG:440:VAL:HG11	31:AG:449:LEU:HD12	1.95	0.47
32:B1:205:LYS:HG2	32:B1:219:GLU:HG2	1.96	0.47
33:B2:118:ASN:OD1	33:B2:118:ASN:N	2.46	0.47
33:B2:404:LYS:HZ1	33:B2:425:ILE:HD11	1.78	0.47
34:B3:77:THR:HG22	34:B3:86:LYS:HB3	1.96	0.47
51:RE:1063:ARG:HD2	64:X1:305:UNK:CB	2.44	0.47
51:RE:1216:LYS:HE3	51:RE:1236:THR:CG2	2.39	0.47
53:RG:232:LEU:HD21	53:RH:103:PRO:HG3	1.96	0.47
54:RJ:1105:ASP:N	54:RJ:1105:ASP:OD1	2.47	0.47
55:RK:282:GLU:O	55:RK:286:SER:HB3	2.14	0.47
56:RL:57:TRP:NE1	56:RL:125:GLN:OE1	2.39	0.47
59:RP:1778:MET:HG2	59:RP:1864:LEU:HD22	1.96	0.47
62:RT:170:ASP:OD1	62:RT:223:ARG:NH2	2.47	0.47
2:5A:517:A:OP2	59:RP:1939:ARG:NH1	2.46	0.47
3:SA:954:G:H2'	3:SA:955:A:C8	2.49	0.47
13:SP:16:VAL:O	13:SP:30:VAL:HA	2.14	0.47
25:A4:97:ARG:NE	38:5B:191:PRO:O	2.39	0.47
26:A5:460:ARG:HA	26:A5:465:ILE:HD11	1.96	0.47
29:AE:376:GLU:H	29:AE:379:GLU:HG3	1.79	0.47
30:AF:246:TYR:OH	30:AF:289:ASN:ND2	2.44	0.47
33:B2:54:ILE:CD1	33:B2:364:TYR:HD2	2.27	0.47
48:RA:250:GLY:HA3	48:RA:271:GLY:HA2	1.96	0.47
48:RA:273:ASP:O	48:RA:275:LYS:NZ	2.47	0.47
3:SA:1757:G:H2'	41:5E:500:LYS:HD2	1.96	0.47
5:SF:143:ASP:OD1	5:SF:143:ASP:N	2.35	0.47
11:SM:112:SER:HB3	11:SM:139:VAL:HG23	1.95	0.47
25:A4:214:SER:OG	25:A4:221:ASN:O	2.28	0.47
26:A5:473:LYS:HE3	26:A5:475:ALA:HB3	1.96	0.47
30:AF:135:GLN:HE22	30:AF:178:PRO:HA	1.79	0.47
33:B2:137:ILE:HG22	33:B2:147:VAL:HG22	1.97	0.47
33:B2:530:LEU:HD13	33:B2:550:LEU:HD11	1.94	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5C:333:SER:HB3	39:5C:381:LEU:HD11	1.95	0.47
40:5D:58:ARG:HH21	42:5F:174:ARG:CZ	2.28	0.47
51:RE:400:LEU:HB3	51:RE:412:LEU:HD12	1.95	0.47
51:RE:627:LEU:HD12	51:RE:628:VAL:HG23	1.96	0.47
51:RE:1025:THR:O	51:RE:1029:ASN:ND2	2.47	0.47
54:RJ:92:ARG:HH21	54:RJ:221:LEU:HG	1.79	0.47
54:RJ:111:LYS:O	54:RJ:310:THR:OG1	2.32	0.47
1:3A:315:A:H2'	1:3A:316:A:C8	2.49	0.47
3:SA:280:U:H2'	7:SH:188:ARG:HH22	1.80	0.47
3:SA:1061:A:OP1	52:RF:229:LYS:NZ	2.46	0.47
6:SG:52:GLU:OE2	6:SG:54:LYS:NZ	2.48	0.47
10:SK:87:SER:OG	10:SK:89:ASP:OD1	2.33	0.47
31:AG:581:GLY:HA2	31:AG:602:PRO:HD2	1.97	0.47
33:B2:214:ASP:OD1	33:B2:214:ASP:N	2.45	0.47
39:5C:133:HIS:HE1	39:5C:147:GLU:HG3	1.79	0.47
47:5K:152:ILE:HG12	47:5K:171:PRO:HG2	1.95	0.47
56:RL:200:VAL:HG12	56:RL:208:LEU:HD13	1.97	0.47
4:SC:16:GLN:HB2	34:B3:358:ASN:HD22	1.80	0.47
5:SF:103:TYR:O	5:SF:182:TYR:OH	2.32	0.47
8:SI:64:VAL:HG23	8:SI:67:LEU:HB3	1.96	0.47
29:AE:141:ASN:ND2	29:AE:206:TYR:OH	2.46	0.47
31:AG:498:LEU:HA	31:AG:508:ILE:O	2.14	0.47
31:AG:855:LEU:O	31:AG:859:ASN:HB2	2.13	0.47
33:B2:9:GLU:O	33:B2:684:TRP:HA	2.14	0.47
33:B2:414:LEU:HD11	33:B2:445:VAL:HG11	1.94	0.47
34:B3:223:TRP:CD1	34:B3:230:LYS:HZ1	2.33	0.47
40:5D:58:ARG:HD2	42:5F:174:ARG:CZ	2.45	0.47
49:RB:290:GLU:OE2	49:RB:296:ARG:NH1	2.47	0.47
52:RF:17:PRO:HB2	52:RF:34:LEU:HD11	1.96	0.47
54:RJ:631:ILE:HG13	54:RJ:634:ARG:HB2	1.97	0.47
58:RO:198:GLU:O	58:RO:202:LEU:HB2	2.13	0.47
59:RP:1278:ARG:O	59:RP:1282:VAL:HA	2.15	0.47
60:RQ:835:VAL:HG13	60:RQ:837:LYS:HG3	1.96	0.47
3:SA:869:A:H61	3:SA:958:U:H3	1.62	0.47
22:3E:355:ASN:HA	22:3E:358:LYS:HB2	1.97	0.47
25:A4:157:SER:OG	25:A4:195:TRP:NE1	2.47	0.47
25:A4:744:VAL:HA	25:A4:753:ALA:O	2.15	0.47
32:B1:150:THR:N	32:B1:164:THR:O	2.45	0.47
51:RE:1103:ARG:HA	51:RE:1178:ASP:HB2	1.96	0.47
51:RE:1157:TYR:HE1	51:RE:1203:ASN:CG	2.22	0.47
53:RH:153:VAL:HA	57:RN:716:LYS:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:RS:258:VAL:HA	61:RS:261:GLU:HG2	1.97	0.47
3:SA:406:U:H2'	3:SA:407:A:C8	2.50	0.47
3:SA:576:G:OP2	54:RJ:873:LYS:NZ	2.36	0.47
3:SA:1779:U:HO2'	32:B1:257:TYR:HH	1.63	0.47
7:SH:32:ILE:HD12	7:SH:65:GLN:HA	1.96	0.47
13:SP:53:ASP:O	13:SP:56:SER:OG	2.28	0.47
20:3C:173:LEU:HA	20:3C:197:VAL:HG13	1.97	0.47
22:3E:262:ILE:HA	22:3E:265:PHE:HB2	1.96	0.47
25:A4:534:LEU:HB3	25:A4:543:ILE:HG22	1.95	0.47
27:A8:635:PHE:HD2	28:A9:492:ILE:HD12	1.79	0.47
31:AG:175:ALA:O	31:AG:187:VAL:HA	2.15	0.47
32:B1:156:GLN:HB2	32:B1:203:GLN:HE21	1.79	0.47
32:B1:165:SER:OG	32:B1:166:LYS:N	2.48	0.47
32:B1:537:GLY:HA3	32:B1:556:ARG:HB3	1.96	0.47
33:B2:183:ASP:OD1	33:B2:183:ASP:N	2.42	0.47
34:B3:10:ILE:HG23	34:B3:643:PHE:HB2	1.95	0.47
34:B3:108:LEU:HG	34:B3:119:VAL:HG12	1.97	0.47
35:B8:238:LEU:HD11	35:B8:590:LYS:HB2	1.97	0.47
36:BE:207:ASP:N	36:BE:207:ASP:OD1	2.47	0.47
40:5D:52:ARG:NH2	43:5G:270:ASP:OD1	2.43	0.47
42:5F:163:ASN:N	42:5F:183:SER:OG	2.45	0.47
48:RA:80:GLN:HB2	48:RA:82:HIS:HD2	1.78	0.47
51:RE:159:SER:O	51:RE:256:TYR:OH	2.27	0.47
51:RE:253:GLN:NE2	51:RE:254:LEU:O	2.48	0.47
51:RE:348:TYR:HA	51:RE:351:LYS:HD3	1.97	0.47
52:RF:69:LYS:NZ	52:RF:159:THR:H	2.12	0.47
54:RJ:879:THR:OG1	54:RJ:880:TYR:N	2.48	0.47
60:RQ:341:LYS:HA	60:RQ:344:GLN:HE21	1.79	0.47
62:RT:129:ARG:HB2	62:RT:138:GLU:HB3	1.96	0.47
3:SA:1769:U:O2	62:RT:213:LYS:NZ	2.47	0.47
14:SR:50:GLU:OE2	14:SR:82:ARG:NH2	2.47	0.47
17:SZ:59:GLY:O	49:RB:296:ARG:NH2	2.44	0.47
22:3E:176:GLU:HA	22:3E:179:THR:HG22	1.97	0.47
22:3E:191:HIS:HD2	22:3E:246:GLU:HA	1.80	0.47
31:AG:22:LEU:HD12	31:AG:32:LYS:HB2	1.97	0.47
33:B2:235:ASN:ND2	33:B2:240:GLY:O	2.40	0.47
33:B2:367:ILE:HD12	33:B2:368:PRO:HD2	1.97	0.47
34:B3:19:SER:OG	34:B3:20:SER:N	2.48	0.47
34:B3:113:THR:OG1	34:B3:114:SER:N	2.48	0.47
34:B3:339:ILE:HG13	34:B3:358:ASN:HD21	1.80	0.47
34:B3:481:LYS:HE2	34:B3:522:ASN:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B8:568:VAL:HG23	35:B8:579:VAL:HG22	1.96	0.47
37:B6:14:GLU:OE2	37:B6:91:ARG:NH2	2.38	0.47
37:B6:122:ASN:OD1	37:B6:122:ASN:N	2.48	0.47
51:RE:1087:LEU:HA	51:RE:1090:THR:HG23	1.97	0.47
51:RE:1159:ASN:O	51:RE:1187:LYS:HG3	2.14	0.47
54:RJ:80:THR:O	66:RJ:1201:GTP:O2B	2.31	0.47
2:5A:69:U:O4	2:5A:70:A:N6	2.48	0.47
3:SA:158:U:N3	3:SA:420:A:O2'	2.46	0.47
3:SA:677:G:O2'	59:RP:1884:ARG:NH2	2.48	0.47
13:SP:123:SER:O	13:SP:123:SER:OG	2.29	0.47
23:3F:70:TYR:OH	49:RB:246:GLU:OE2	2.29	0.47
24:3G:57:ASP:HB3	24:3G:84:ARG:HG2	1.97	0.47
26:A5:366:GLY:O	31:AG:583:LYS:NZ	2.48	0.47
29:AE:136:LEU:HD21	29:AE:155:ILE:HG12	1.97	0.47
33:B2:393:ASP:OD1	33:B2:393:ASP:N	2.46	0.47
34:B3:139:SER:OG	34:B3:140:PHE:N	2.48	0.47
34:B3:245:SER:O	34:B3:245:SER:OG	2.32	0.47
45:5I:201:ILE:HD12	45:5I:225:LEU:HD21	1.97	0.47
51:RE:578:ILE:HA	51:RE:619:VAL:HA	1.96	0.47
52:RF:46:ASN:OD1	52:RF:46:ASN:N	2.39	0.47
54:RJ:347:LEU:O	54:RJ:352:LYS:NZ	2.48	0.47
57:RN:510:THR:HB	57:RN:518:ILE:HD13	1.96	0.47
2:5A:18:G:H2'	2:5A:19:A:C8	2.50	0.47
2:5A:485:G:H2'	21:3D:22:LEU:HD21	1.97	0.47
3:SA:1779:U:HO2'	32:B1:257:TYR:HE1	1.62	0.47
25:A4:511:VAL:HA	25:A4:558:ARG:HB3	1.96	0.47
31:AG:443:ASN:ND2	31:AG:446:ASN:OD1	2.48	0.47
32:B1:115:SER:O	32:B1:115:SER:OG	2.33	0.47
32:B1:299:SER:O	41:5E:475:SER:HA	2.15	0.47
33:B2:542:ASP:N	33:B2:542:ASP:OD1	2.45	0.47
33:B2:588:ILE:HG12	33:B2:600:TRP:HB2	1.97	0.47
34:B3:593:CYS:HB2	34:B3:620:LEU:HB3	1.95	0.47
34:B3:622:ALA:HB3	34:B3:636:ASP:H	1.78	0.47
36:BE:170:LEU:HG	36:BE:180:LEU:HD21	1.97	0.47
36:BE:430:ILE:HD11	36:BE:445:MET:HB2	1.97	0.47
36:BE:737:LEU:C	36:BE:740:ILE:HG22	2.41	0.47
42:5F:103:VAL:HA	42:5F:106:ILE:HG22	1.96	0.47
50:RD:1592:LEU:HB3	50:RD:1597:GLU:HB2	1.97	0.47
51:RE:1174:GLY:CA	51:RE:1179:LYS:CE	2.91	0.47
61:RS:271:THR:OG1	61:RS:274:GLU:OE1	2.31	0.47
4:SC:19:ARG:HH21	34:B3:359:SER:HA	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:SP:107:ARG:NH2	13:SP:107:ARG:CG	2.73	0.46
32:B1:515:TYR:CE2	42:5F:180:PHE:HZ	2.33	0.46
33:B2:360:ASN:OD1	33:B2:360:ASN:N	2.47	0.46
34:B3:352:LYS:HA	34:B3:365:ILE:O	2.15	0.46
34:B3:680:ASN:HA	34:B3:683:LEU:HG	1.96	0.46
34:B3:749:ASN:HB3	34:B3:751:LYS:H	1.81	0.46
51:RE:1063:ARG:CD	64:X1:305:UNK:CB	2.93	0.46
57:RN:451:THR:O	57:RN:455:LEU:HB2	2.15	0.46
59:RP:1721:ILE:HD11	59:RP:1751:TYR:HB2	1.96	0.46
3:SA:545:A:OP2	44:5H:542:TYR:OH	2.33	0.46
3:SA:1160:A:H2'	3:SA:1161:C:H6	1.80	0.46
5:SF:52:LEU:O	23:3F:120:ARG:NH1	2.48	0.46
5:SF:53:LYS:NZ	49:RB:292:ASP:OD2	2.38	0.46
29:AE:262:VAL:HG21	31:AG:892:MET:HE1	1.96	0.46
33:B2:676:SER:OG	33:B2:678:ASP:OD1	2.22	0.46
34:B3:476:ASP:N	34:B3:476:ASP:OD1	2.48	0.46
37:B6:185:TYR:HE2	60:RQ:338:LEU:HD21	1.81	0.46
38:5B:173:ARG:NH2	40:5D:144:ASN:O	2.48	0.46
40:5D:25:TYR:HD1	46:5J:213:ARG:HE	1.62	0.46
41:5E:493:GLN:NE2	41:5E:497:ASN:ND2	2.58	0.46
48:RA:245:CYS:HB3	48:RA:253:TYR:HB2	1.96	0.46
48:RA:251:TYR:HA	48:RA:266:LYS:O	2.16	0.46
49:RB:309:LYS:HB3	49:RB:313:ARG:HH11	1.80	0.46
50:RD:1183:ILE:CB	51:RE:718:LYS:NZ	2.78	0.46
51:RE:793:PRO:HG2	51:RE:799:LEU:HA	1.96	0.46
56:RL:729:LEU:HA	56:RL:764:ASN:HA	1.97	0.46
59:RP:1725:ILE:HD11	59:RP:1793:LEU:HD22	1.98	0.46
20:3C:194:VAL:HB	20:3C:217:ILE:HD13	1.97	0.46
25:A4:418:CYS:HB2	25:A4:460:LEU:HB2	1.97	0.46
25:A4:742:LEU:HD12	25:A4:757:ARG:HG3	1.96	0.46
29:AE:509:SER:HA	29:AE:512:LEU:HD12	1.98	0.46
31:AG:204:ASN:OD1	31:AG:204:ASN:N	2.47	0.46
31:AG:530:LYS:HG2	31:AG:546:LYS:HB3	1.97	0.46
33:B2:163:LYS:HG2	41:5E:522:ARG:NH2	2.30	0.46
33:B2:236:ASP:OD1	33:B2:236:ASP:N	2.46	0.46
34:B3:69:LEU:HD13	34:B3:109:ASP:HA	1.96	0.46
41:5E:521:THR:HG23	41:5E:524:ASP:H	1.80	0.46
48:RA:286:GLU:HG3	48:RA:287:ASN:H	1.80	0.46
51:RE:209:MET:HB3	51:RE:213:LEU:HD21	1.98	0.46
51:RE:1189:LEU:HD22	51:RE:1190:PHE:CE2	2.51	0.46
52:RF:69:LYS:HZ1	52:RF:158:TRP:HA	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:RJ:187:LYS:HE3	54:RJ:187:LYS:HB2	1.75	0.46
55:RK:337:VAL:HG23	55:RK:354:ILE:HG12	1.98	0.46
57:RN:56:ASN:HD21	57:RN:59:GLU:HG3	1.81	0.46
58:RO:202:LEU:HD23	58:RO:208:TYR:HB3	1.98	0.46
59:RP:1756:ILE:HD13	59:RP:1800:LEU:HB3	1.98	0.46
2:5A:485:G:OP2	21:3D:46:LYS:NZ	2.39	0.46
13:SP:32:ASP:OD1	13:SP:32:ASP:N	2.47	0.46
17:SZ:45:ALA:HB2	17:SZ:55:VAL:HG11	1.97	0.46
23:3F:417:SER:HB3	23:3F:421:ASN:HB2	1.96	0.46
26:A5:518:ASN:O	26:A5:522:THR:OG1	2.32	0.46
28:A9:505:MET:HB2	30:AF:507:MET:HE3	1.98	0.46
29:AE:374:ARG:NH1	29:AE:375:LEU:O	2.49	0.46
32:B1:32:PRO:HG3	32:B1:61:ILE:HG13	1.97	0.46
34:B3:189:HIS:HD2	34:B3:191:SER:H	1.62	0.46
35:B8:306:ASN:OD1	35:B8:306:ASN:N	2.43	0.46
51:RE:218:ASP:N	51:RE:218:ASP:OD1	2.46	0.46
53:RH:152:SER:OG	53:RH:155:SER:N	2.49	0.46
54:RJ:819:GLU:O	54:RJ:852:ARG:NH2	2.47	0.46
54:RJ:1082:GLN:OE1	54:RJ:1082:GLN:HA	2.15	0.46
55:RK:282:GLU:O	55:RK:286:SER:CB	2.64	0.46
58:RO:196:GLN:OE1	58:RO:260:ASN:ND2	2.37	0.46
3:SA:1276:U:H3	3:SA:1434:U:H3	1.64	0.46
8:SI:62:VAL:HG12	8:SI:64:VAL:H	1.80	0.46
12:SO:16:ILE:HG23	12:SO:62:GLN:HE22	1.79	0.46
20:3C:308:PRO:HG3	40:5D:129:SER:HA	1.96	0.46
25:A4:326:ARG:NH2	25:A4:364:PHE:O	2.49	0.46
26:A5:85:ILE:HB	26:A5:99:PHE:HB2	1.98	0.46
31:AG:212:CYS:HB2	31:AG:224:SER:HB3	1.98	0.46
31:AG:446:ASN:OD1	31:AG:446:ASN:N	2.46	0.46
32:B1:29:LEU:HD22	32:B1:42:LEU:HD11	1.96	0.46
32:B1:557:LYS:NZ	36:BE:426:GLU:OE1	2.44	0.46
32:B1:680:ARG:HH12	41:5E:455:HIS:CD2	2.29	0.46
34:B3:67:LEU:HD23	34:B3:68:LYS:H	1.80	0.46
34:B3:534:ARG:HH11	34:B3:535:GLY:H	1.63	0.46
34:B3:708:ARG:NH2	34:B3:720:PHE:O	2.49	0.46
35:B8:278:ASP:N	35:B8:278:ASP:OD1	2.46	0.46
38:5B:211:LEU:HD13	38:5B:213:LYS:HE3	1.96	0.46
41:5E:384:ARG:HD3	43:5G:83:ILE:HD11	1.97	0.46
41:5E:448:LEU:HD12	42:5F:85:MET:SD	2.55	0.46
42:5F:61:LEU:O	42:5F:71:ARG:NE	2.47	0.46
51:RE:333:ASN:HA	51:RE:336:VAL:HG22	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:RG:112:VAL:HB	53:RG:124:VAL:HG22	1.97	0.46
54:RJ:360:ASP:HB3	54:RJ:365:LEU:HB2	1.98	0.46
58:RO:462:SER:OG	58:RO:463:LEU:N	2.48	0.46
61:RS:270:LEU:HB3	61:RS:278:PHE:HZ	1.80	0.46
3:SA:328:A:H2'	3:SA:329:G:C8	2.50	0.46
14:SR:113:ASP:N	14:SR:113:ASP:OD1	2.48	0.46
16:SY:113:ALA:HB3	16:SY:116:ASP:HB2	1.96	0.46
27:A8:638:LEU:HD12	27:A8:641:VAL:CG1	2.46	0.46
29:AE:568:ILE:HD11	29:AE:673:ASN:HD21	1.80	0.46
34:B3:591:ILE:HG23	34:B3:600:LYS:HZ1	1.81	0.46
35:B8:472:GLN:NE2	35:B8:474:SER:OG	2.49	0.46
42:5F:115:MET:HG3	42:5F:120:MET:HB3	1.98	0.46
43:5G:119:ARG:HG3	43:5G:122:TYR:HB2	1.98	0.46
45:5I:288:TYR:O	45:5I:298:LEU:N	2.42	0.46
51:RE:822:ARG:HB2	51:RE:843:LEU:HB2	1.96	0.46
53:RG:55:ILE:O	53:RG:64:LYS:HB2	2.16	0.46
55:RK:104:LEU:O	55:RK:300:TYR:OH	2.33	0.46
59:RP:104:GLN:HG3	59:RP:105:PRO:HD3	1.97	0.46
59:RP:1691:SER:HA	59:RP:1724:ASN:HD21	1.81	0.46
1:3A:56:A:O2'	40:5D:63:TYR:OH	2.34	0.46
2:5A:486:U:H4'	2:5A:487:A:H5''	1.98	0.46
3:SA:1111:G:C8	54:RJ:1162:ALA:HA	2.51	0.46
7:SH:17:GLU:N	56:RL:604:SER:O	2.47	0.46
9:SJ:48:THR:O	9:SJ:52:ASN:CB	2.58	0.46
25:A4:164:THR:HG22	25:A4:185:ARG:HG2	1.98	0.46
29:AE:583:LYS:HE2	29:AE:627:LEU:HA	1.98	0.46
30:AF:436:GLU:HG2	30:AF:480:LEU:HD23	1.98	0.46
33:B2:63:LEU:HD21	33:B2:106:TRP:CD2	2.50	0.46
33:B2:341:ALA:HB1	33:B2:353:LEU:HD11	1.96	0.46
36:BE:640:LEU:HD23	36:BE:655:THR:HG22	1.98	0.46
40:5D:61:ASP:CA	42:5F:160:TRP:CZ3	2.99	0.46
45:5I:255:THR:HG22	60:RQ:288:TYR:HD1	1.81	0.46
47:5K:83:VAL:HG12	47:5K:96:PRO:HG3	1.98	0.46
57:RN:547:VAL:HA	57:RN:550:VAL:HG12	1.97	0.46
57:RN:554:GLN:HE21	57:RN:559:ARG:H	1.63	0.46
57:RN:804:LYS:HD3	57:RN:804:LYS:HA	1.75	0.46
58:RO:395:ILE:HG23	58:RO:469:LEU:HD21	1.98	0.46
61:RS:379:LYS:HA	61:RS:379:LYS:HD3	1.72	0.46
61:RS:392:TYR:HA	61:RS:395:MET:HB2	1.96	0.46
61:RS:413:LEU:O	61:RS:418:HIS:NE2	2.49	0.46
62:RT:219:ALA:HB1	62:RT:267:ALA:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:129:THR:OG1	4:SC:130:SER:N	2.47	0.46
8:SI:7:LYS:O	8:SI:42:GLN:NE2	2.49	0.46
9:SJ:32:GLN:HE21	48:RA:78:LYS:HG2	1.81	0.46
21:3D:175:ILE:HD12	21:3D:317:SER:HA	1.98	0.46
21:3D:371:ASN:OD1	21:3D:374:ARG:NH1	2.48	0.46
27:A8:631:SER:C	27:A8:634:LEU:CG	2.86	0.46
32:B1:280:THR:HA	32:B1:304:PRO:HB3	1.98	0.46
34:B3:32:LEU:HD12	34:B3:68:LYS:HE2	1.97	0.46
36:BE:323:VAL:HB	36:BE:343:LEU:HD22	1.98	0.46
41:5E:330:VAL:HG21	54:RJ:932:LEU:HD12	1.97	0.46
41:5E:384:ARG:HD2	43:5G:83:ILE:N	2.30	0.46
48:RA:164:ARG:HH12	48:RA:176:PHE:H	1.64	0.46
50:RD:1512:GLU:HG2	51:RE:1199:ASN:ND2	2.28	0.46
50:RD:1520:MET:HE3	50:RD:1536:VAL:HB	1.98	0.46
51:RE:377:SER:HB3	51:RE:389:GLY:HA3	1.97	0.46
56:RM:249:SER:O	56:RM:253:LEU:CB	2.63	0.46
2:5A:86:C:N4	31:AG:482:GLY:O	2.45	0.46
3:SA:1273:G:H1	3:SA:1437:U:H2'	1.80	0.46
4:SC:144:ARG:HG3	4:SC:208:GLN:HB3	1.98	0.46
16:SY:137:LYS:HE2	16:SY:137:LYS:HB3	1.80	0.46
20:3B:261:LEU:O	21:3D:129:ARG:NH1	2.49	0.46
22:3E:392:ALA:O	22:3E:396:ASN:ND2	2.49	0.46
31:AG:143:ASN:OD1	31:AG:143:ASN:N	2.47	0.46
31:AG:253:SER:O	31:AG:256:THR:OG1	2.33	0.46
31:AG:296:HIS:NE2	31:AG:314:SER:OG	2.37	0.46
34:B3:195:GLY:O	34:B3:245:SER:OG	2.29	0.46
34:B3:625:THR:HG22	34:B3:633:VAL:HG13	1.97	0.46
38:5B:200:ARG:O	38:5B:204:ARG:HB3	2.15	0.46
45:5I:280:ALA:HB2	45:5I:311:VAL:HB	1.97	0.46
45:5I:281:ASN:ND2	45:5I:283:ASP:OD1	2.49	0.46
48:RA:300:TRP:HA	48:RA:308:TYR:H	1.80	0.46
51:RE:501:ASN:OD1	51:RE:501:ASN:N	2.49	0.46
61:RS:280:ASN:ND2	61:RS:320:GLY:O	2.46	0.46
61:RS:359:LEU:HB2	61:RS:372:ILE:HD11	1.97	0.46
62:RT:181:TYR:O	62:RT:234:LEU:HD12	2.15	0.46
3:SA:225:A:H2'	3:SA:226:A:H8	1.79	0.46
25:A4:124:THR:HG21	38:5B:191:PRO:HG3	1.97	0.46
29:AE:495:LEU:HA	29:AE:498:PHE:HB2	1.97	0.46
30:AF:117:LEU:HD12	30:AF:117:LEU:HA	1.79	0.46
39:5C:335:GLY:HA2	39:5C:377:LYS:HG3	1.98	0.46
42:5F:5:LEU:HD23	42:5F:9:GLU:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:5I:283:ASP:OD2	45:5I:287:TYR:OH	2.30	0.46
55:RK:199:ARG:HB2	55:RK:239:PRO:HA	1.97	0.46
57:RN:495:ASN:HD22	57:RN:617:HIS:HB2	1.80	0.46
58:RO:366:LEU:HD13	58:RO:405:LEU:HD11	1.96	0.46
59:RP:1948:SER:O	59:RP:1985:ARG:NH2	2.48	0.46
3:SA:689:G:C6	3:SA:690:G:O6	2.69	0.45
9:SJ:83:TYR:HB3	9:SJ:101:ILE:HD11	1.98	0.45
9:SJ:103:GLN:HB3	9:SJ:164:ARG:HG2	1.98	0.45
19:Sd:35:ASP:N	19:Sd:35:ASP:OD1	2.45	0.45
22:3E:381:ASP:OD1	22:3E:381:ASP:N	2.49	0.45
25:A4:444:ARG:HG3	25:A4:446:SER:H	1.81	0.45
25:A4:545:ARG:HG3	25:A4:549:VAL:HB	1.98	0.45
25:A4:652:THR:HG23	25:A4:653:TRP:HD1	1.81	0.45
41:5E:437:ILE:HD11	42:5F:70:PHE:CE2	2.51	0.45
51:RE:521:LEU:HD22	51:RE:960:LYS:HG3	1.97	0.45
51:RE:928:HIS:HE1	51:RE:1164:SER:HB2	1.80	0.45
54:RJ:65:ASP:OD1	54:RJ:65:ASP:N	2.46	0.45
54:RJ:772:MET:HG3	54:RJ:774:PRO:HD2	1.98	0.45
62:RT:224:ILE:HG22	62:RT:233:ILE:HG12	1.98	0.45
1:3A:36:C:O2'	45:5I:389:ARG:NH1	2.48	0.45
2:5A:485:G:N2	45:5I:386:LYS:O	2.41	0.45
3:SA:381:C:H2'	3:SA:382:C:H4'	1.97	0.45
3:SA:420:A:C8	3:SA:420:A:C3'	2.98	0.45
5:SF:58:GLY:HA2	5:SF:61:VAL:HG12	1.99	0.45
5:SF:127:LYS:HB2	5:SF:140:VAL:HG23	1.99	0.45
11:SM:76:VAL:HG21	11:SM:87:ARG:HH11	1.81	0.45
27:A8:633:GLN:H	27:A8:633:GLN:HG3	1.41	0.45
36:BE:351:GLN:HG3	36:BE:372:ASP:HB3	1.97	0.45
36:BE:420:GLU:HG2	36:BE:470:GLN:HA	1.97	0.45
39:5C:15:ARG:HB2	39:5C:18:GLN:HG3	1.98	0.45
40:5D:48:LEU:HG	54:RJ:1067:LEU:HD11	1.98	0.45
42:5F:29:ASP:OD2	42:5F:41:ARG:NH1	2.49	0.45
43:5G:100:LEU:HD22	43:5G:144:GLU:HB3	1.97	0.45
45:5I:306:SER:HB3	45:5I:326:ASP:H	1.81	0.45
48:RA:60:ASN:ND2	48:RA:100:GLU:OE2	2.50	0.45
49:RB:229:ASP:HB3	49:RB:232:GLU:HG2	1.97	0.45
51:RE:380:SER:HB2	51:RE:481:THR:HG22	1.98	0.45
51:RE:626:LYS:HA	51:RE:626:LYS:HD3	1.80	0.45
3:SA:397:A:H5''	9:SJ:50:GLY:HA2	1.98	0.45
3:SA:895:G:H22	3:SA:917:U:H3	1.64	0.45
3:SA:1463:C:H4'	57:RN:63:ALA:HB1	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:SA:1639:C:H41	34:B3:692:MET:HE1	1.82	0.45
26:A5:66:VAL:HG12	26:A5:112:LEU:HD21	1.97	0.45
27:A8:631:SER:N	27:A8:634:LEU:HD21	2.31	0.45
29:AE:11:VAL:HA	29:AE:14:ASN:HD22	1.80	0.45
29:AE:255:ILE:HD11	31:AG:884:MET:HB3	1.98	0.45
29:AE:1700:SER:O	29:AE:1703:GLU:N	2.49	0.45
30:AF:69:ARG:HG3	30:AF:70:THR:HG23	1.97	0.45
33:B2:760:ILE:HD11	33:B2:835:PHE:HB2	1.98	0.45
34:B3:343:MET:HB3	34:B3:355:LEU:HD23	1.98	0.45
39:5C:39:ASP:HB3	39:5C:42:LEU:HB3	1.97	0.45
39:5C:243:TRP:NE1	39:5C:304:ARG:HH22	2.15	0.45
41:5E:520:LEU:HD11	41:5E:525:LYS:CA	2.45	0.45
42:5F:13:LEU:HG	42:5F:13:LEU:O	2.16	0.45
51:RE:1157:TYR:CE1	51:RE:1203:ASN:ND2	2.59	0.45
53:RG:143:GLN:HE22	53:RG:149:SER:HA	1.81	0.45
57:RN:13:LEU:HD22	57:RN:16:ARG:HE	1.81	0.45
59:RP:971:ARG:O	59:RP:975:ASN:HA	2.16	0.45
61:RS:271:THR:H	61:RS:274:GLU:HB2	1.82	0.45
62:RT:189:ASP:OD2	62:RT:251:ILE:HD11	2.16	0.45
4:SC:224:ASP:OD2	51:RE:981:LYS:NZ	2.43	0.45
4:SC:242:LYS:N	51:RE:655:LEU:O	2.48	0.45
21:3D:379:LEU:HD13	21:3D:408:VAL:HG21	1.98	0.45
25:A4:137:TYR:HB2	25:A4:177:LEU:HD12	1.99	0.45
26:A5:452:LEU:HA	26:A5:455:THR:HG22	1.98	0.45
26:A5:518:ASN:HB2	26:A5:521:SER:HB3	1.98	0.45
26:A5:539:ARG:NH1	31:AG:524:ASP:OD2	2.49	0.45
27:A8:440:ARG:O	31:AG:728:LEU:HD21	2.16	0.45
30:AF:171:VAL:HG22	30:AF:188:SER:HB3	1.99	0.45
33:B2:49:VAL:HG22	33:B2:63:LEU:HD22	1.98	0.45
50:RD:1675:PHE:HE1	50:RD:1691:PHE:HB3	1.82	0.45
52:RF:255:LYS:O	52:RF:265:ARG:NH1	2.45	0.45
53:RH:191:ASP:HA	53:RH:194:GLU:HG2	1.98	0.45
57:RN:600:LEU:HD22	57:RN:633:VAL:HG22	1.98	0.45
61:RS:399:ILE:O	61:RS:406:GLY:N	2.50	0.45
3:SA:385:A:OP1	9:SJ:25:ARG:NH2	2.46	0.45
6:SG:117:THR:HG21	6:SG:194:LEU:HD23	1.98	0.45
12:SO:69:ASN:OD1	12:SO:69:ASN:N	2.47	0.45
21:3D:195:VAL:HG12	21:3D:216:PHE:HE2	1.81	0.45
24:3G:58:CYS:HB3	24:3G:98:ILE:HD12	1.99	0.45
25:A4:249:ARG:HB2	25:A4:292:ASN:HD22	1.81	0.45
27:A8:547:GLN:O	27:A8:551:PHE:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:AE:718:ARG:HA	29:AE:721:VAL:HG12	1.99	0.45
31:AG:364:ASN:OD1	31:AG:364:ASN:N	2.42	0.45
32:B1:418:ARG:HD3	41:5E:489:SER:O	2.10	0.45
33:B2:103:ILE:HB	33:B2:117:PHE:HB2	1.99	0.45
33:B2:220:THR:HG22	33:B2:259:ILE:HD11	1.96	0.45
35:B8:264:LEU:HD11	35:B8:272:LEU:HD12	1.97	0.45
37:B6:186:VAL:HG12	37:B6:273:ILE:HG13	1.98	0.45
42:5F:111:LEU:HD13	42:5F:143:ILE:HG21	1.97	0.45
48:RA:21:VAL:HG12	48:RA:46:ARG:HH12	1.81	0.45
51:RE:308:LEU:HG	51:RE:337:LEU:HD21	1.99	0.45
53:RH:56:SER:HA	53:RH:63:ASP:HB2	1.99	0.45
2:5A:550:C:H2'	2:5A:551:A:C8	2.52	0.45
3:SA:1537:C:N4	53:RH:155:SER:O	2.37	0.45
5:SF:150:PRO:HB2	5:SF:154:ILE:HG13	1.98	0.45
6:SG:39:GLU:OE2	6:SG:47:SER:OG	2.33	0.45
23:3F:164:GLN:HE21	23:3F:527:VAL:HG13	1.81	0.45
23:3F:452:SER:HB3	23:3F:460:ARG:HG2	1.99	0.45
29:AE:864:VAL:O	29:AE:868:LYS:CB	2.65	0.45
30:AF:31:THR:OG1	30:AF:32:SER:N	2.46	0.45
31:AG:726:GLN:NE2	31:AG:736:THR:O	2.42	0.45
31:AG:761:GLU:HG3	31:AG:779:ILE:HG22	1.99	0.45
36:BE:851:SER:O	36:BE:851:SER:OG	2.31	0.45
41:5E:325:SER:OG	54:RJ:1007:TYR:CE1	2.69	0.45
48:RA:14:TYR:HE2	48:RA:344:PRO:HG3	1.81	0.45
48:RA:164:ARG:HH12	48:RA:176:PHE:N	2.15	0.45
51:RE:151:SER:HA	51:RE:154:LYS:HB2	1.98	0.45
51:RE:1155:LEU:HD23	52:RF:93:PHE:HB3	1.98	0.45
59:RP:378:HIS:O	59:RP:382:PHE:CB	2.65	0.45
3:SA:67:A:H2'	3:SA:69:G:C8	2.52	0.45
3:SA:420:A:C8	3:SA:420:A:O5'	2.70	0.45
11:SM:92:HIS:HD2	11:SM:94:ILE:HG13	1.82	0.45
12:SO:49:GLN:HA	12:SO:52:VAL:HG12	1.99	0.45
21:3D:120:SER:O	21:3D:120:SER:OG	2.33	0.45
25:A4:468:ASP:OD2	25:A4:472:ARG:NH1	2.44	0.45
25:A4:636:ILE:HG23	25:A4:648:PHE:HD2	1.82	0.45
29:AE:583:LYS:HD3	29:AE:631:VAL:HG21	1.99	0.45
31:AG:600:SER:O	31:AG:600:SER:OG	2.33	0.45
33:B2:54:ILE:HD13	33:B2:364:TYR:CD2	2.48	0.45
33:B2:140:SER:OG	33:B2:142:ASP:OD1	2.31	0.45
34:B3:42:ILE:HD11	34:B3:379:LEU:HD13	1.97	0.45
35:B8:512:ASP:OD1	35:B8:512:ASP:N	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5C:104:LEU:HD21	39:5C:139:TRP:HB2	1.99	0.45
50:RD:1628:GLU:HG3	50:RD:1640:LEU:HD22	1.99	0.45
54:RJ:871:MET:CE	54:RJ:930:LYS:CD	2.95	0.45
56:RL:77:ILE:HD12	56:RL:77:ILE:HA	1.82	0.45
56:RL:846:SER:O	56:RL:850:LEU:CB	2.65	0.45
57:RN:423:GLY:O	57:RN:426:THR:OG1	2.31	0.45
59:RP:2006:LEU:HG	59:RP:2011:ILE:HD12	1.97	0.45
1:3A:316:A:H2'	1:3A:317:A:C8	2.51	0.45
2:5A:514:U:OP2	59:RP:1975:LYS:NZ	2.37	0.45
3:SA:145:A:O2'	3:SA:146:U:O5'	2.33	0.45
3:SA:326:G:H4'	11:SM:82:ARG:HD2	1.98	0.45
3:SA:884:A:H2'	3:SA:885:G:C8	2.52	0.45
3:SA:1070:C:H5''	18:Sc:17:ARG:HH21	1.82	0.45
5:SF:159:THR:HB	5:SF:173:ILE:HB	1.99	0.45
11:SM:57:LYS:O	11:SM:138:ASN:ND2	2.50	0.45
20:3C:253:ILE:HD11	20:3C:293:LEU:HD21	1.99	0.45
27:A8:635:PHE:CD2	28:A9:492:ILE:HD12	2.51	0.45
29:AE:65:LYS:HB3	29:AE:104:LEU:HD11	1.99	0.45
30:AF:227:VAL:HG22	30:AF:236:VAL:HG12	1.99	0.45
31:AG:38:SER:OG	31:AG:43:ASN:O	2.35	0.45
32:B1:25:ASP:O	32:B1:27:LYS:N	2.49	0.45
32:B1:369:ILE:HD11	32:B1:390:VAL:HG11	1.99	0.45
34:B3:217:ASP:OD1	34:B3:217:ASP:N	2.48	0.45
34:B3:509:ALA:HB1	34:B3:515:CYS:HA	1.98	0.45
39:5C:311:SER:OG	39:5C:313:GLU:OE2	2.33	0.45
43:5G:104:ALA:HB3	43:5G:116:ARG:HE	1.82	0.45
45:5I:94:TYR:OH	45:5I:134:ASN:ND2	2.41	0.45
48:RA:247:THR:HG21	48:RA:251:TYR:HB2	1.99	0.45
1:3A:12:U:H3	3:SA:1112:G:H1	1.65	0.45
3:SA:1223:A:H2'	3:SA:1224:A:C8	2.52	0.45
3:SA:1782:A:N3	3:SA:1782:A:H2'	2.32	0.45
4:SC:242:LYS:HD2	4:SC:244:VAL:H	1.82	0.45
20:3B:88:ILE:HD11	20:3B:123:ILE:HG21	1.98	0.45
24:3H:33:LEU:HD23	24:3H:35:LYS:HE3	1.98	0.45
29:AE:348:ILE:HD13	29:AE:348:ILE:HA	1.87	0.45
32:B1:300:MET:HE2	32:B1:300:MET:HB3	1.78	0.45
32:B1:475:PRO:HD2	32:B1:493:TRP:HB2	1.99	0.45
45:5I:297:SER:OG	45:5I:299:ASN:O	2.33	0.45
46:5J:110:ASP:OD1	46:5J:110:ASP:N	2.36	0.45
50:RD:1670:LYS:HG2	50:RD:1674:LEU:HG	1.99	0.45
54:RJ:617:THR:HG23	54:RJ:620:LYS:HE2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:RP:465:PHE:HA	59:RP:468:ALA:HB3	1.98	0.45
61:RS:235:VAL:HG12	61:RS:238:SER:HB3	1.98	0.45
61:RS:429:LYS:HD2	61:RS:437:ARG:HH22	1.82	0.45
3:SA:1634:C:O2	32:B1:397:LYS:NZ	2.50	0.45
20:3C:175:ALA:N	20:3C:198:GLU:OE2	2.48	0.45
26:A5:582:GLU:O	26:A5:586:ASP:N	2.50	0.45
27:A8:633:GLN:O	27:A8:637:LEU:CD2	2.65	0.45
29:AE:659:LEU:HD21	29:AE:691:PHE:HA	1.98	0.45
30:AF:371:GLU:OE2	35:B8:273:ARG:NH2	2.50	0.45
39:5C:214:LEU:HD23	39:5C:228:LEU:HD12	1.99	0.45
39:5C:269:LYS:HB2	60:RQ:830:ILE:HG23	1.98	0.45
39:5C:460:ARG:HB3	60:RQ:847:VAL:HB	1.99	0.45
42:5F:5:LEU:CD2	42:5F:13:LEU:HD21	2.47	0.45
48:RA:231:VAL:HA	48:RA:247:THR:HA	1.98	0.45
50:RD:1708:ILE:HA	50:RD:1711:VAL:HG22	1.99	0.45
51:RE:173:ASN:O	51:RE:175:LYS:NZ	2.37	0.45
52:RF:71:VAL:HG21	52:RF:84:VAL:HB	1.98	0.45
55:RK:143:LYS:HE3	55:RK:143:LYS:HB2	1.75	0.45
61:RS:373:LYS:HG3	61:RS:420:ALA:HA	1.99	0.45
3:SA:930:A:H2'	4:SC:114:VAL:HG11	1.99	0.44
4:SC:31:ASP:HB3	4:SC:45:LYS:HG2	1.99	0.44
11:SM:46:LYS:HD3	11:SM:49:ILE:HD12	1.98	0.44
26:A5:87:LEU:O	26:A5:96:THR:N	2.50	0.44
29:AE:109:TRP:HA	29:AE:114:THR:HG21	2.00	0.44
31:AG:43:ASN:OD1	31:AG:43:ASN:N	2.48	0.44
33:B2:129:PHE:HE1	33:B2:150:LEU:HD11	1.82	0.44
33:B2:292:ILE:HG23	33:B2:324:PHE:HE2	1.83	0.44
33:B2:641:TYR:O	33:B2:650:ILE:N	2.49	0.44
36:BE:546:ILE:HG21	36:BE:560:LEU:HD22	1.99	0.44
45:5I:210:LYS:HA	45:5I:210:LYS:HD3	1.69	0.44
50:RD:1483:ALA:HA	50:RD:1486:LEU:HB2	1.99	0.44
53:RG:135:LYS:HD3	53:RG:135:LYS:HA	1.87	0.44
54:RJ:1148:GLU:OE2	54:RJ:1152:ARG:NH1	2.49	0.44
59:RP:60:SER:HB3	59:RP:102:SER:HB3	1.99	0.44
62:RT:174:LEU:HG	62:RT:180:LEU:HD11	1.99	0.44
3:SA:406:U:H2'	3:SA:407:A:H8	1.82	0.44
11:SM:94:ILE:HD12	11:SM:101:GLU:H	1.81	0.44
18:Sc:48:SER:OG	18:Sc:49:HIS:ND1	2.50	0.44
20:3B:104:ASP:OD1	20:3B:104:ASP:N	2.38	0.44
50:RD:1670:LYS:HA	50:RD:1673:ASP:HB2	1.98	0.44
51:RE:585:MET:HB3	51:RE:610:PHE:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:RJ:889:LEU:HD22	54:RJ:922:ILE:HB	2.00	0.44
56:RL:111:SER:HB3	56:RL:134:LEU:HD12	1.99	0.44
57:RN:737:ILE:HA	57:RN:740:MET:HG2	2.00	0.44
58:RO:282:HIS:CD2	58:RO:283:LYS:HG2	2.52	0.44
3:SA:1080:U:H5'	45:5I:425:LYS:HE2	1.99	0.44
8:SI:163:ASP:O	60:RQ:277:ARG:NH2	2.50	0.44
22:3E:372:ARG:HG3	24:3G:63:ILE:HA	2.00	0.44
23:3F:405:VAL:HG12	23:3F:415:THR:HG22	2.00	0.44
29:AE:763:LEU:HD12	29:AE:768:LYS:HD3	2.00	0.44
30:AF:51:HIS:O	30:AF:53:HIS:N	2.49	0.44
33:B2:566:TYR:OH	33:B2:603:ASP:O	2.33	0.44
33:B2:580:ASP:OD2	33:B2:623:PHE:N	2.40	0.44
34:B3:32:LEU:HD22	34:B3:76:LEU:HD12	2.00	0.44
34:B3:104:PRO:O	34:B3:122:THR:OG1	2.35	0.44
36:BE:921:ARG:O	36:BE:925:LEU:HB2	2.17	0.44
54:RJ:288:VAL:HG11	54:RJ:812:MET:HE2	1.98	0.44
59:RP:107:LEU:HD21	59:RP:150:TRP:HB3	1.98	0.44
3:SA:362:G:H2'	3:SA:363:G:C8	2.52	0.44
3:SA:608:U:O2'	3:SA:609:U:O4'	2.34	0.44
3:SA:863:A:H4'	15:5X:57:ARG:HG2	1.99	0.44
3:SA:1146:G:H2'	3:SA:1147:A:H8	1.83	0.44
3:SA:1660:A:H2'	3:SA:1661:U:C6	2.52	0.44
3:SA:1773:C:H2'	3:SA:1774:G:H8	1.83	0.44
11:SM:84:ILE:N	11:SM:109:VAL:O	2.47	0.44
20:3B:210:MET:HE2	20:3B:210:MET:HB3	1.79	0.44
21:3D:31:LEU:HD21	45:5I:59:VAL:HG13	1.99	0.44
25:A4:579:ARG:HH12	25:A4:659:PHE:HD1	1.65	0.44
32:B1:157:ASP:N	32:B1:157:ASP:OD1	2.50	0.44
34:B3:430:TYR:HD2	34:B3:454:LEU:HD23	1.82	0.44
34:B3:531:ASN:OD1	34:B3:531:ASN:N	2.49	0.44
41:5E:319:VAL:CG1	54:RJ:1044:LEU:HD22	2.47	0.44
42:5F:43:ASP:HA	42:5F:46:LYS:HG2	1.99	0.44
43:5G:234:ARG:NH1	43:5G:254:PHE:O	2.51	0.44
44:5H:555:ASN:HB3	44:5H:558:ASN:HB2	1.98	0.44
49:RB:302:LYS:HB3	49:RB:306:ARG:HH22	1.81	0.44
51:RE:165:PRO:HD2	51:RE:222:PHE:HZ	1.83	0.44
51:RE:174:TYR:CE2	51:RE:227:LYS:HB3	2.53	0.44
51:RE:804:THR:HG21	51:RE:838:VAL:HB	1.99	0.44
52:RF:15:VAL:HG12	52:RF:17:PRO:HD3	1.98	0.44
52:RF:84:VAL:HG13	52:RF:126:LEU:HD11	1.99	0.44
55:RK:187:ILE:HB	55:RK:251:GLN:HE22	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:RN:443:LYS:HG3	57:RN:448:PHE:HE2	1.81	0.44
2:5A:554:G:H1	2:5A:583:U:H3	1.64	0.44
6:SG:63:GLN:HE22	6:SG:66:GLN:HB3	1.82	0.44
12:SO:93:LYS:HA	12:SO:96:VAL:HG12	1.99	0.44
13:SP:107:ARG:CB	13:SP:107:ARG:CZ	2.93	0.44
20:3C:92:ARG:HH12	40:5D:151:PHE:HB2	1.81	0.44
21:3D:281:LEU:HD23	22:3E:261:GLN:HE21	1.82	0.44
25:A4:75:ASN:HB3	25:A4:92:GLU:HA	2.00	0.44
25:A4:201:VAL:HG13	25:A4:213:TRP:HB2	1.99	0.44
29:AE:488:GLY:HA2	29:AE:491:TYR:HB3	1.98	0.44
29:AE:729:LYS:HA	29:AE:733:MET:HG3	2.00	0.44
31:AG:414:ILE:HA	31:AG:414:ILE:HD12	1.80	0.44
32:B1:418:ARG:CZ	41:5E:491:ALA:HA	2.47	0.44
33:B2:443:LEU:HG	33:B2:459:LEU:HD13	2.00	0.44
34:B3:467:ILE:H	34:B3:479:ILE:HD11	1.83	0.44
34:B3:749:ASN:OD1	41:5E:511:ASN:OD1	2.36	0.44
35:B8:358:PHE:HA	35:B8:376:LEU:O	2.17	0.44
36:BE:356:ILE:HG22	36:BE:633:LYS:HG3	2.00	0.44
39:5C:122:GLY:O	39:5C:139:TRP:NE1	2.34	0.44
41:5E:325:SER:OG	54:RJ:1007:TYR:CD1	2.71	0.44
42:5F:85:MET:HE3	42:5F:149:LEU:HD11	1.98	0.44
43:5G:138:ASP:N	43:5G:138:ASP:OD1	2.48	0.44
48:RA:60:ASN:HB3	48:RA:74:THR:HB	2.00	0.44
51:RE:554:LYS:HA	51:RE:554:LYS:HD2	1.82	0.44
53:RG:242:CYS:O	53:RG:246:GLU:HG3	2.18	0.44
59:RP:70:ILE:HG21	59:RP:87:ILE:HG22	1.98	0.44
62:RT:213:LYS:HG3	62:RT:224:ILE:HD11	2.00	0.44
2:5A:20:C:H2'	2:5A:21:A:C8	2.52	0.44
3:SA:592:A:O2'	3:SA:596:C:OP1	2.35	0.44
3:SA:1234:A:O2'	3:SA:1236:A:N6	2.50	0.44
3:SA:1782:A:N6	32:B1:257:TYR:CD1	2.86	0.44
6:SG:86:GLN:HE22	32:B1:546:ASP:HB3	1.83	0.44
14:SR:8:GLN:OE1	42:5F:177:ILE:HG23	2.18	0.44
16:SY:77:ILE:HG22	54:RJ:751:TYR:HB2	1.99	0.44
20:3B:125:VAL:HG12	46:5J:150:GLY:HA3	2.00	0.44
20:3B:169:LYS:HA	20:3B:193:VAL:O	2.18	0.44
25:A4:120:SER:OG	25:A4:121:THR:N	2.50	0.44
31:AG:484:VAL:O	31:AG:487:GLU:N	2.51	0.44
32:B1:476:VAL:HA	32:B1:492:SER:HB3	1.98	0.44
32:B1:743:PHE:HZ	32:B1:778:ILE:HD13	1.83	0.44
35:B8:27:PHE:HB3	37:B6:31:LEU:HD23	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:5E:447:LYS:HA	41:5E:450:VAL:HG12	1.98	0.44
50:RD:1181:ASP:HA	50:RD:1191:GLY:HA2	1.98	0.44
51:RE:655:LEU:HD12	51:RE:655:LEU:HA	1.90	0.44
51:RE:1098:PHE:CD2	51:RE:1184:GLY:N	2.72	0.44
53:RH:199:ASP:OD1	53:RH:199:ASP:N	2.49	0.44
58:RO:259:LYS:HB3	58:RO:259:LYS:HE2	1.72	0.44
3:SA:398:G:OP2	9:SJ:47:ARG:NH2	2.40	0.44
5:SF:140:VAL:HG12	5:SF:146:THR:HG22	2.00	0.44
10:SK:38:ASN:HA	44:5H:565:LYS:HE2	1.99	0.44
11:SM:57:LYS:HG3	11:SM:110:HIS:CE1	2.53	0.44
14:SR:64:ASP:OD1	14:SR:64:ASP:N	2.50	0.44
20:3B:218:ILE:HD11	21:3D:152:LEU:HD22	1.98	0.44
22:3E:227:LEU:HG	22:3E:231:ILE:HB	2.00	0.44
27:A8:675:LEU:CB	28:A9:486:LEU:HD13	2.47	0.44
29:AE:396:ASP:OD1	29:AE:396:ASP:N	2.47	0.44
30:AF:20:THR:HA	30:AF:24:GLN:HE21	1.83	0.44
31:AG:768:TRP:HE1	31:AG:772:THR:HA	1.83	0.44
34:B3:111:ASP:N	34:B3:111:ASP:OD1	2.48	0.44
45:5I:241:ASP:OD1	45:5I:241:ASP:N	2.39	0.44
48:RA:152:ASP:OD1	48:RA:152:ASP:N	2.51	0.44
52:RF:150:LYS:HG3	52:RF:151:HIS:ND1	2.33	0.44
52:RF:208:ASP:N	52:RF:212:PHE:O	2.41	0.44
54:RJ:841:THR:HB	54:RJ:859:ILE:HA	1.99	0.44
57:RN:314:MET:HA	57:RN:512:ASP:HA	2.00	0.44
59:RP:1183:PRO:O	59:RP:1187:VAL:CB	2.65	0.44
63:RY:489:GLN:O	63:RY:493:PHE:CB	2.66	0.44
3:SA:1782:A:C6	3:SA:1783:C:H1'	2.53	0.44
4:SC:36:SER:OG	4:SC:41:ARG:NH1	2.50	0.44
9:SJ:66:SER:HA	9:SJ:73:SER:HA	1.99	0.44
21:3D:206:LEU:HD11	21:3D:219:LEU:HD11	2.00	0.44
25:A4:214:SER:HB3	25:A4:226:LEU:HD13	1.99	0.44
29:AE:63:GLU:HA	29:AE:64:PRO:HD3	1.88	0.44
33:B2:107:ASP:OD1	33:B2:107:ASP:N	2.46	0.44
41:5E:538:LYS:C	41:5E:538:LYS:CD	2.86	0.44
45:5I:444:GLU:OE2	45:5I:448:ARG:NH2	2.37	0.44
48:RA:184:ASN:OD1	48:RA:230:GLN:NE2	2.51	0.44
51:RE:822:ARG:NH1	51:RE:1133:PRO:O	2.50	0.44
52:RF:131:ALA:HA	52:RF:134:ILE:HG12	1.99	0.44
53:RG:227:LEU:HA	53:RG:227:LEU:HD23	1.79	0.44
3:SA:1599:C:H2'	3:SA:1600:A:C8	2.53	0.44
3:SA:1623:C:O2'	43:5G:184:GLU:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:SC:129:THR:HG23	4:SC:131:ASP:H	1.82	0.44
4:SC:194:ASN:HD21	4:SC:212:VAL:HG23	1.82	0.44
7:SH:65:GLN:NE2	48:RA:43:TYR:O	2.51	0.44
8:SI:38:LEU:HD12	8:SI:41:LEU:HD12	2.00	0.44
9:SJ:67:TRP:HD1	9:SJ:70:GLU:H	1.66	0.44
11:SM:36:LYS:HD2	11:SM:36:LYS:HA	1.74	0.44
15:SX:66:ASN:O	45:5I:325:TYR:OH	2.27	0.44
25:A4:45:THR:HB	25:A4:352:VAL:HA	1.99	0.44
25:A4:774:LEU:HD12	25:A4:774:LEU:HA	1.83	0.44
27:A8:676:TRP:CE3	27:A8:676:TRP:O	2.70	0.44
29:AE:238:LEU:HA	29:AE:241:ILE:HG22	1.99	0.44
29:AE:538:ALA:HA	29:AE:541:LEU:HB2	2.00	0.44
31:AG:228:VAL:HG23	31:AG:236:ASN:HB3	2.00	0.44
31:AG:510:TYR:HE1	31:AG:527:HIS:HB3	1.83	0.44
31:AG:532:TRP:HB3	31:AG:541:TRP:HB3	1.99	0.44
32:B1:35:ASN:HA	32:B1:58:ILE:HG23	1.99	0.44
32:B1:157:ASP:OD1	32:B1:203:GLN:NE2	2.38	0.44
33:B2:59:LEU:HD21	33:B2:62:LYS:HE2	1.99	0.44
34:B3:188:GLU:O	34:B3:221:ASN:ND2	2.50	0.44
35:B8:277:ILE:HA	35:B8:282:ASN:HD22	1.83	0.44
36:BE:852:LEU:HD22	36:BE:860:GLU:HG2	2.00	0.44
39:5C:162:ASN:ND2	39:5C:429:GLU:OE1	2.51	0.44
41:5E:384:ARG:CD	43:5G:82:GLY:H	2.30	0.44
51:RE:1160:SER:C	51:RE:1187:LYS:HG2	2.43	0.44
51:RE:1188:PRO:HG3	64:X1:308:UNK:CB	2.48	0.44
51:RE:1222:GLU:HG2	52:RF:60:LEU:HB2	2.00	0.44
53:RH:89:PRO:HG2	53:RH:134:PHE:HZ	1.83	0.44
56:RL:195:ASN:HB3	56:RL:198:CYS:HB3	1.99	0.44
60:RQ:284:ARG:HE	60:RQ:284:ARG:HB3	1.51	0.44
62:RT:220:THR:HG23	62:RT:222:THR:HG22	1.99	0.44
3:SA:257:A:O2'	9:SJ:73:SER:O	2.34	0.43
3:SA:415:C:O2'	3:SA:418:G:O6	2.36	0.43
3:SA:1775:U:O2	3:SA:1786:G:N2	2.40	0.43
26:A5:233:LYS:HA	26:A5:233:LYS:HD3	1.82	0.43
26:A5:520:MET:H	26:A5:520:MET:HG3	1.60	0.43
27:A8:573:ILE:HG22	27:A8:575:ASN:H	1.83	0.43
27:A8:634:LEU:HD23	27:A8:634:LEU:H	1.83	0.43
27:A8:642:LEU:HD12	28:A9:499:ILE:CG2	2.44	0.43
29:AE:100:ALA:HB1	35:B8:44:PHE:HZ	1.82	0.43
30:AF:288:ASP:OD1	30:AF:288:ASP:N	2.48	0.43
32:B1:356:ASP:OD1	32:B1:356:ASP:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:B3:652:ILE:HD12	34:B3:652:ILE:HA	1.92	0.43
36:BE:76:THR:OG1	36:BE:78:SER:O	2.29	0.43
39:5C:228:LEU:HD22	39:5C:264:PRO:HA	1.99	0.43
41:5E:533:LYS:CA	41:5E:536:ARG:HE	2.25	0.43
42:5F:29:ASP:OD1	42:5F:29:ASP:N	2.50	0.43
45:5I:139:CYS:HB3	45:5I:145:VAL:HG22	1.99	0.43
52:RF:50:SER:O	52:RF:127:LYS:NZ	2.51	0.43
53:RG:177:LYS:HE2	53:RG:177:LYS:HB3	1.68	0.43
54:RJ:203:LYS:HA	54:RJ:203:LYS:HD2	1.78	0.43
59:RP:103:LEU:HD11	59:RP:147:VAL:HG23	1.99	0.43
3:SA:328:A:H2'	3:SA:329:G:H8	1.83	0.43
4:SC:123:ALA:HB2	4:SC:165:ARG:HG3	2.00	0.43
4:SC:171:ILE:HD11	4:SC:197:ILE:HA	1.99	0.43
8:SI:87:ASP:OD1	59:RP:2031:HIS:NE2	2.49	0.43
11:SM:123:VAL:HG12	11:SM:142:VAL:HA	1.99	0.43
20:3B:221:ILE:HD13	21:3D:163:VAL:HB	2.00	0.43
25:A4:212:ILE:O	25:A4:226:LEU:N	2.50	0.43
25:A4:571:THR:HG21	25:A4:632:ASN:HB3	2.00	0.43
26:A5:240:GLN:HE22	26:A5:298:LYS:HB3	1.83	0.43
27:A8:439:LYS:HA	27:A8:442:LYS:CB	2.48	0.43
27:A8:635:PHE:CD2	28:A9:492:ILE:CD1	3.01	0.43
31:AG:712:THR:HG23	31:AG:720:ILE:HD13	1.99	0.43
37:B6:5:ARG:HA	37:B6:5:ARG:HD2	1.80	0.43
50:RD:1479:MET:HE2	50:RD:1519:ALA:HB2	1.99	0.43
51:RE:518:PHE:HD1	51:RE:520:ASN:H	1.67	0.43
51:RE:976:ILE:HG22	51:RE:1042:ALA:HB3	2.00	0.43
51:RE:1221:HIS:CE1	52:RF:20:LEU:HB3	2.53	0.43
54:RJ:625:TRP:HZ2	55:RK:284:SER:HB3	1.83	0.43
56:RM:281:LEU:HA	56:RM:409:ALA:HB3	1.99	0.43
58:RO:292:PRO:HG2	58:RO:330:PHE:HE2	1.82	0.43
58:RO:315:VAL:HG23	58:RO:316:PRO:HD3	1.98	0.43
58:RO:472:HIS:CD2	58:RO:474:HIS:H	2.31	0.43
59:RP:1941:VAL:HA	59:RP:1944:ILE:HD12	1.99	0.43
3:SA:153:G:O3'	7:SH:2:LYS:NZ	2.41	0.43
3:SA:513:U:H2'	3:SA:514:G:H8	1.82	0.43
3:SA:1146:G:H2'	3:SA:1147:A:C8	2.53	0.43
5:SF:183:VAL:HB	5:SF:225:VAL:HG23	2.00	0.43
5:SF:194:THR:H	5:SF:210:ILE:HG23	1.82	0.43
8:SI:19:GLN:HB3	8:SI:85:PHE:HZ	1.83	0.43
9:SJ:74:LYS:HD3	9:SJ:74:LYS:HA	1.68	0.43
22:3E:330:LEU:HD13	40:5D:109:THR:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:A4:144:ILE:HD12	25:A4:158:VAL:HB	2.00	0.43
27:A8:633:GLN:HE21	27:A8:633:GLN:HB2	1.55	0.43
29:AE:641:LEU:O	29:AE:644:LYS:NZ	2.42	0.43
31:AG:516:PRO:HG2	31:AG:519:LEU:HD21	2.00	0.43
32:B1:605:ASP:OD1	32:B1:605:ASP:N	2.40	0.43
34:B3:28:ASN:OD1	34:B3:28:ASN:N	2.48	0.43
34:B3:34:THR:HG23	34:B3:68:LYS:HE3	2.00	0.43
40:5D:78:LEU:HA	40:5D:78:LEU:HD12	1.82	0.43
45:5I:306:SER:OG	45:5I:307:ALA:N	2.50	0.43
47:5K:171:PRO:HA	47:5K:184:LYS:HB2	2.00	0.43
59:RP:1756:ILE:HG21	59:RP:1800:LEU:HB3	2.01	0.43
59:RP:1782:ASN:OD1	59:RP:1782:ASN:N	2.44	0.43
5:SF:141:THR:OG1	5:SF:142:HIS:N	2.52	0.43
22:3E:206:ALA:HB2	22:3E:262:ILE:HD11	2.00	0.43
25:A4:572:ALA:HB3	25:A4:585:ILE:HD11	2.00	0.43
25:A4:750:ASN:N	25:A4:750:ASN:OD1	2.50	0.43
29:AE:655:ALA:O	29:AE:659:LEU:HB2	2.18	0.43
30:AF:24:GLN:HB2	30:AF:294:PHE:HD1	1.83	0.43
32:B1:369:ILE:HB	32:B1:383:PHE:HB2	1.99	0.43
34:B3:194:ARG:HD3	34:B3:243:VAL:HG13	1.99	0.43
43:5G:164:GLN:HE21	43:5G:260:GLU:HB3	1.84	0.43
45:5I:358:MET:HB3	60:RQ:890:VAL:HG23	2.00	0.43
46:5J:207:LYS:HE2	46:5J:207:LYS:HB3	1.88	0.43
51:RE:527:TYR:HB2	51:RE:615:VAL:HG13	2.00	0.43
51:RE:870:ALA:O	51:RE:875:LYS:NZ	2.51	0.43
54:RJ:904:ASN:HA	54:RJ:907:THR:HB	2.00	0.43
55:RK:68:SER:OG	55:RK:69:TYR:N	2.52	0.43
61:RS:221:LEU:HD22	61:RS:258:VAL:HG11	2.00	0.43
61:RS:373:LYS:HE2	61:RS:373:LYS:HB3	1.84	0.43
62:RT:238:THR:HA	62:RT:241:ARG:CG	2.49	0.43
2:5A:467:A:N1	2:5A:468:A:N6	2.66	0.43
2:5A:489:G:O6	37:B6:120:ARG:NH1	2.51	0.43
3:SA:18:C:O2'	3:SA:21:U:O4'	2.37	0.43
3:SA:578:U:OP2	54:RJ:874:TYR:OH	2.29	0.43
8:SI:22:GLN:HA	8:SI:25:VAL:HG22	1.99	0.43
9:SJ:76:THR:OG1	9:SJ:77:ARG:N	2.52	0.43
10:SK:65:LYS:HZ2	23:3F:59:PRO:CA	2.27	0.43
15:SX:32:LYS:HB2	15:SX:32:LYS:HE3	1.81	0.43
16:SY:68:ILE:HD12	57:RN:785:VAL:HG23	2.00	0.43
20:3C:185:SER:HB3	20:3C:217:ILE:HD11	2.00	0.43
22:3E:191:HIS:HB2	22:3E:247:ILE:HG23	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:3G:62:GLU:HA	24:3G:65:LEU:HG	2.00	0.43
24:3H:95:ARG:HD2	24:3H:95:ARG:HA	1.87	0.43
27:A8:443:CYS:CA	31:AG:728:LEU:HB3	2.47	0.43
31:AG:50:ASN:HD21	31:AG:782:THR:HG22	1.84	0.43
31:AG:252:LEU:HD23	31:AG:256:THR:HG21	2.00	0.43
32:B1:829:VAL:HG23	32:B1:830:ARG:HG2	2.01	0.43
33:B2:276:ASN:ND2	33:B2:280:THR:O	2.47	0.43
34:B3:41:ASN:OD1	34:B3:41:ASN:N	2.49	0.43
36:BE:606:ASP:OD1	36:BE:606:ASP:N	2.41	0.43
41:5E:323:LYS:HG2	41:5E:325:SER:H	1.84	0.43
45:5I:8:ARG:HD3	45:5I:8:ARG:HA	1.80	0.43
47:5K:52:PHE:HB3	47:5K:55:TYR:HB3	2.01	0.43
47:5K:161:LYS:HG2	47:5K:172:LEU:HD21	1.99	0.43
50:RD:1472:PRO:HG2	51:RE:1189:LEU:HD12	2.00	0.43
51:RE:207:LEU:HB2	51:RE:296:ILE:HA	2.00	0.43
51:RE:1109:LYS:HZ1	51:RE:1170:GLY:H	1.66	0.43
54:RJ:80:THR:C	66:RJ:1201:GTP:O2B	2.61	0.43
57:RN:640:MET:HE2	57:RN:640:MET:HB3	1.81	0.43
59:RP:1610:MET:O	59:RP:1614:GLU:CB	2.67	0.43
61:RS:359:LEU:HD23	61:RS:362:LEU:HD12	2.00	0.43
3:SA:526:A:OP1	17:SZ:93:ARG:NE	2.48	0.43
10:SK:155:HIS:NE2	23:3F:321:HIS:O	2.50	0.43
15:SX:38:LEU:HA	15:SX:41:MET:HG2	2.01	0.43
20:3C:261:LEU:O	22:3E:118:ARG:NH2	2.34	0.43
22:3E:372:ARG:O	22:3E:376:LEU:HB2	2.19	0.43
23:3F:303:LYS:HB3	23:3F:317:ILE:HD11	2.01	0.43
24:3H:52:ILE:HD12	24:3H:71:CYS:SG	2.58	0.43
26:A5:336:ASN:OD1	26:A5:336:ASN:N	2.49	0.43
27:A8:270:PHE:HA	27:A8:282:GLY:HA2	2.00	0.43
27:A8:547:GLN:O	27:A8:551:PHE:CB	2.66	0.43
32:B1:341:GLN:OE1	32:B1:341:GLN:HA	2.19	0.43
33:B2:645:GLU:HG2	33:B2:646:LYS:HG3	1.99	0.43
36:BE:569:VAL:HB	36:BE:579:ARG:HB2	2.01	0.43
41:5E:384:ARG:CZ	43:5G:81:SER:HB3	2.49	0.43
45:5I:6:ILE:HG21	45:5I:8:ARG:HH21	1.84	0.43
48:RA:155:VAL:HG13	48:RA:163:TYR:HB2	2.00	0.43
50:RD:1544:MET:HB2	50:RD:1544:MET:HE2	1.67	0.43
51:RE:257:SER:O	51:RE:266:PRO:HA	2.18	0.43
51:RE:611:ASP:OD1	51:RE:611:ASP:N	2.51	0.43
51:RE:745:LYS:HA	51:RE:745:LYS:HD2	1.83	0.43
55:RK:36:ILE:HB	55:RK:72:THR:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:RN:590:ASN:OD1	57:RN:590:ASN:N	2.50	0.43
3:SA:646:C:H2'	3:SA:647:G:C8	2.47	0.43
4:SC:239:GLU:HG2	51:RE:658:PHE:HA	2.00	0.43
6:SG:89:ILE:HD11	6:SG:172:ILE:HD11	2.00	0.43
8:SI:46:ILE:HD12	8:SI:60:ILE:HG13	2.01	0.43
8:SI:185:ILE:HG13	8:SI:187:SER:HB3	2.01	0.43
20:3C:185:SER:HA	20:3C:188:VAL:HG12	2.01	0.43
27:A8:643:ASP:OD1	30:AF:510:LEU:O	2.37	0.43
29:AE:348:ILE:HG21	29:AE:373:ILE:HD11	2.00	0.43
29:AE:715:HIS:HA	29:AE:718:ARG:HG2	2.00	0.43
31:AG:140:LYS:HA	31:AG:140:LYS:HD3	1.78	0.43
34:B3:377:LEU:HA	34:B3:378:PRO:HD3	1.85	0.43
34:B3:519:ASN:HD22	34:B3:524:GLU:H	1.67	0.43
34:B3:678:TRP:HE3	34:B3:697:VAL:HG23	1.84	0.43
35:B8:35:GLU:O	35:B8:39:LYS:HB2	2.18	0.43
39:5C:64:ASP:HA	39:5C:67:LEU:HG	1.99	0.43
45:5I:133:GLN:HA	45:5I:150:ILE:O	2.18	0.43
54:RJ:280:LEU:HD12	54:RJ:281:PRO:HD2	2.01	0.43
57:RN:616:LEU:HB3	57:RN:619:LEU:HD13	2.01	0.43
57:RN:644:ASP:OD1	57:RN:687:LYS:NZ	2.51	0.43
5:SF:163:ASP:OD2	5:SF:166:SER:N	2.51	0.43
6:SG:72:HIS:O	14:SR:79:TYR:OH	2.37	0.43
23:3F:209:LYS:HA	23:3F:209:LYS:HD2	1.82	0.43
23:3F:343:ASP:OD1	23:3F:343:ASP:N	2.46	0.43
23:3F:415:THR:OG1	23:3F:425:TRP:NE1	2.39	0.43
26:A5:281:ILE:HG12	26:A5:328:VAL:HB	2.01	0.43
28:A9:475:THR:HA	28:A9:478:ASN:HB2	1.99	0.43
30:AF:377:ASP:OD1	30:AF:377:ASP:N	2.51	0.43
30:AF:463:VAL:HA	30:AF:466:VAL:HG12	2.01	0.43
32:B1:847:ARG:O	32:B1:851:SER:OG	2.30	0.43
33:B2:596:ASN:HB3	33:B2:612:PHE:HA	1.99	0.43
35:B8:376:LEU:HG	35:B8:386:ILE:HG12	1.99	0.43
36:BE:24:PHE:HB3	36:BE:654:TRP:HB3	2.01	0.43
40:5D:145:GLU:OE1	40:5D:146:PHE:N	2.52	0.43
41:5E:316:ASN:O	41:5E:320:ALA:CB	2.66	0.43
45:5I:344:HIS:NE2	45:5I:418:HIS:O	2.51	0.43
51:RE:911:PRO:HB2	51:RE:954:LEU:HD13	2.01	0.43
51:RE:1206:PRO:HB3	51:RE:1212:VAL:HG22	2.01	0.43
51:RE:1216:LYS:HA	51:RE:1219:ILE:HG12	2.00	0.43
57:RN:700:LEU:HD21	58:RO:467:ALA:HB2	2.00	0.43
63:RY:489:GLN:O	63:RY:493:PHE:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3A:97:C:C2	1:3A:320:G:N2	2.86	0.43
2:5A:474:A:OP2	39:5C:425:ARG:NH2	2.37	0.43
3:SA:1233:G:H1	3:SA:1253:U:H2'	1.83	0.43
4:SC:154:SER:O	4:SC:154:SER:OG	2.32	0.43
5:SF:182:TYR:CD2	5:SF:192:ILE:HD11	2.54	0.43
6:SG:103:ASN:HA	6:SG:106:LYS:HD2	2.01	0.43
8:SI:131:PHE:O	8:SI:133:THR:N	2.52	0.43
9:SJ:67:TRP:O	9:SJ:71:GLY:HA2	2.18	0.43
21:3D:52:SER:HB2	21:3D:85:ASN:HD21	1.84	0.43
22:3E:218:ALA:HA	22:3E:221:THR:HG22	2.00	0.43
22:3E:319:ILE:HD12	22:3E:326:LEU:HD22	2.01	0.43
23:3F:201:ILE:HG12	23:3F:538:ARG:HD3	2.00	0.43
25:A4:617:ASN:O	25:A4:621:ASN:HB2	2.19	0.43
31:AG:478:ASN:OD1	31:AG:478:ASN:N	2.51	0.43
32:B1:76:ASP:OD1	32:B1:76:ASP:N	2.51	0.43
33:B2:178:ILE:HD11	33:B2:186:ILE:HD11	2.01	0.43
34:B3:192:ALA:HB3	34:B3:216:ARG:HG3	2.00	0.43
35:B8:426:VAL:HG11	35:B8:455:ILE:HG21	2.01	0.43
36:BE:50:ILE:HD13	36:BE:311:VAL:HG11	2.01	0.43
51:RE:208:THR:OG1	51:RE:209:MET:N	2.52	0.43
54:RJ:831:ARG:HD3	54:RJ:838:ILE:HD12	2.01	0.43
57:RN:484:ARG:HB3	57:RN:492:ALA:HB1	2.01	0.43
57:RN:669:SER:HA	57:RN:672:THR:HG22	2.01	0.43
59:RP:1741:LYS:HD3	59:RP:1741:LYS:HA	1.90	0.43
1:3A:94:A:H2'	1:3A:95:A:C8	2.53	0.43
3:SA:200:A:H2'	3:SA:201:G:H8	1.84	0.43
3:SA:555:A:N6	3:SA:571:G:O2'	2.50	0.43
3:SA:628:G:OP1	12:SO:120:SER:OG	2.37	0.43
3:SA:1169:G:N1	3:SA:1575:G:OP2	2.44	0.43
9:SJ:31:ARG:HH12	9:SJ:48:THR:HB	1.84	0.43
15:SX:12:ASN:O	15:SX:16:ASN:ND2	2.52	0.43
25:A4:313:LYS:HA	25:A4:316:LYS:HG2	2.01	0.43
26:A5:110:ILE:HG22	26:A5:119:CYS:HB2	2.00	0.43
26:A5:448:ASN:OD1	26:A5:450:HIS:NE2	2.52	0.43
27:A8:314:LEU:HA	27:A8:321:ILE:HA	2.00	0.43
27:A8:595:ILE:O	27:A8:599:MET:HB2	2.19	0.43
29:AE:586:LEU:O	29:AE:590:ALA:HB2	2.18	0.43
30:AF:413:LEU:HA	30:AF:416:THR:HG22	2.00	0.43
31:AG:202:SER:OG	31:AG:204:ASN:OD1	2.30	0.43
32:B1:493:TRP:HA	32:B1:517:ASP:HB2	2.01	0.43
34:B3:133:ASN:OD1	34:B3:133:ASN:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BE:627:ASN:ND2	36:BE:647:THR:OG1	2.52	0.43
36:BE:739:VAL:CG2	41:5E:487:ALA:HB2	2.37	0.43
38:5B:164:LYS:HB3	38:5B:164:LYS:HE3	1.76	0.43
39:5C:268:VAL:HG13	60:RQ:831:ILE:HG12	2.00	0.43
39:5C:544:ASP:HB3	39:5C:547:GLU:HB3	2.00	0.43
40:5D:102:GLN:HE21	54:RJ:1098:ARG:NH1	2.17	0.43
41:5E:493:GLN:C	41:5E:493:GLN:CD	2.86	0.43
42:5F:169:THR:HA	42:5F:172:ARG:HG2	2.01	0.43
43:5G:119:ARG:HA	43:5G:122:TYR:HD2	1.84	0.43
47:5K:61:PRO:HB3	47:5K:92:ALA:HB1	2.01	0.43
51:RE:224:CYS:O	51:RE:227:LYS:HG3	2.19	0.43
52:RF:130:ASP:HB2	52:RF:133:SER:HB2	2.01	0.43
53:RG:75:GLY:HA2	53:RG:78:LYS:HE3	2.01	0.43
54:RJ:1080:LYS:HA	54:RJ:1080:LYS:HD2	1.80	0.43
57:RN:475:ARG:HH22	57:RN:516:LEU:HB3	1.84	0.43
1:3A:62:C:O2'	36:BE:447:ASN:O	2.35	0.42
3:SA:200:A:O2'	59:RP:1061:CYS:O	2.36	0.42
3:SA:327:U:OP2	11:SM:57:LYS:NZ	2.38	0.42
3:SA:1782:A:H5''	3:SA:1783:C:H5	1.84	0.42
5:SF:45:ILE:O	5:SF:49:ARG:HB3	2.19	0.42
15:SX:93:LEU:HD11	15:SX:102:VAL:HG22	2.01	0.42
22:3E:283:ILE:HD13	22:3E:283:ILE:HA	1.88	0.42
23:3F:414:ILE:HG13	23:3F:478:LEU:HD21	2.00	0.42
26:A5:441:LEU:HD11	26:A5:480:LEU:HD13	2.01	0.42
29:AE:476:ILE:HG23	29:AE:515:PHE:HE2	1.84	0.42
33:B2:351:LEU:HB2	33:B2:367:ILE:HG23	2.00	0.42
33:B2:369:TYR:HA	33:B2:374:PRO:HA	2.01	0.42
36:BE:470:GLN:HB3	36:BE:553:ARG:NH1	2.34	0.42
39:5C:230:THR:HG22	39:5C:232:ALA:H	1.83	0.42
48:RA:95:ARG:NH2	48:RA:128:LYS:O	2.51	0.42
48:RA:254:ILE:HD12	48:RA:254:ILE:HA	1.84	0.42
50:RD:1592:LEU:HB2	50:RD:1601:ALA:HB2	2.01	0.42
54:RJ:1019:THR:HB	54:RJ:1022:LEU:HD12	2.01	0.42
54:RJ:1075:LYS:HE3	54:RJ:1075:LYS:HB2	1.84	0.42
58:RO:504:ASP:OD1	58:RO:504:ASP:N	2.48	0.42
61:RS:266:PHE:O	61:RS:270:LEU:HB3	2.18	0.42
61:RS:398:ARG:H	61:RS:406:GLY:HA3	1.83	0.42
61:RS:437:ARG:HH21	61:RS:463:GLY:HA3	1.84	0.42
3:SA:1779:U:O2'	32:B1:257:TYR:OH	2.31	0.42
6:SG:39:GLU:OE1	6:SG:41:LYS:NZ	2.45	0.42
22:3E:132:SER:OG	22:3E:134:ASN:OD1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3F:160:ILE:HG12	23:3F:542:SER:HB2	2.00	0.42
25:A4:106:ASN:OD1	25:A4:106:ASN:N	2.51	0.42
26:A5:270:ASN:OD1	26:A5:270:ASN:N	2.49	0.42
27:A8:556:VAL:O	27:A8:585:ARG:NH1	2.52	0.42
30:AF:424:ARG:HA	31:AG:477:VAL:HG11	2.01	0.42
31:AG:555:VAL:HA	31:AG:556:PRO:HD3	1.89	0.42
31:AG:857:PHE:HE2	35:B8:226:LYS:HB3	1.84	0.42
33:B2:123:ALA:HB3	33:B2:141:LYS:HD3	2.00	0.42
34:B3:260:THR:HG22	34:B3:269:LEU:HD13	2.01	0.42
36:BE:353:PRO:HA	36:BE:370:SER:HA	2.01	0.42
37:B6:72:LYS:HD2	37:B6:72:LYS:HA	1.78	0.42
44:5H:550:LEU:HD23	44:5H:550:LEU:HA	1.88	0.42
48:RA:217:LYS:HE2	48:RA:217:LYS:HB3	1.87	0.42
48:RA:277:ILE:HA	48:RA:290:VAL:O	2.19	0.42
53:RG:34:LYS:HD3	53:RG:34:LYS:HA	1.84	0.42
57:RN:65:ASN:OD1	57:RN:65:ASN:N	2.50	0.42
58:RO:208:TYR:O	58:RO:212:LEU:HB2	2.19	0.42
61:RS:382:LEU:HD11	61:RS:428:TYR:CG	2.55	0.42
3:SA:274:G:N1	3:SA:283:U:O2'	2.50	0.42
3:SA:1739:C:H2'	3:SA:1740:A:C8	2.53	0.42
3:SA:1782:A:N1	32:B1:257:TYR:CD2	2.88	0.42
20:3B:198:GLU:O	20:3B:221:ILE:HA	2.18	0.42
22:3E:160:ASP:HB3	22:3E:283:ILE:HG21	2.01	0.42
25:A4:532:ASN:N	25:A4:544:SER:O	2.50	0.42
25:A4:566:LEU:HA	25:A4:566:LEU:HD23	1.83	0.42
29:AE:323:PHE:CZ	29:AE:332:ILE:HD11	2.54	0.42
29:AE:354:SER:O	29:AE:358:TYR:HB2	2.20	0.42
29:AE:422:LEU:HD12	29:AE:422:LEU:HA	1.87	0.42
31:AG:437:THR:OG1	31:AG:764:SER:O	2.31	0.42
31:AG:551:HIS:HA	31:AG:583:LYS:HE3	2.00	0.42
32:B1:749:TYR:HE2	36:BE:705:ILE:HG13	1.84	0.42
33:B2:297:LYS:HA	33:B2:300:GLU:HB2	2.02	0.42
33:B2:636:ASP:OD1	33:B2:636:ASP:N	2.52	0.42
33:B2:673:VAL:HG23	33:B2:683:ILE:HD13	2.01	0.42
33:B2:840:MET:HE1	33:B2:887:LEU:HD13	2.02	0.42
34:B3:188:GLU:HB2	34:B3:223:TRP:HZ2	1.83	0.42
34:B3:572:GLU:HG3	34:B3:600:LYS:HD2	2.01	0.42
38:5B:213:LYS:HZ2	38:5B:213:LYS:HG3	1.69	0.42
43:5G:153:THR:HG23	43:5G:164:GLN:HB3	2.02	0.42
48:RA:306:LYS:HA	48:RA:306:LYS:HD2	1.83	0.42
50:RD:1472:PRO:CG	51:RE:1189:LEU:HD12	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:RD:1695:TRP:HE1	50:RD:1711:VAL:HG11	1.84	0.42
51:RE:902:ILE:HD13	51:RE:902:ILE:HA	1.90	0.42
51:RE:1151:LYS:HE3	51:RE:1151:LYS:HB2	1.92	0.42
57:RN:86:ILE:HG13	57:RN:89:GLN:NE2	2.34	0.42
62:RT:217:GLU:HG2	62:RT:223:ARG:HA	2.00	0.42
3:SA:-7:A:N7	45:5I:292:ARG:NH1	2.68	0.42
7:SH:74:LYS:O	48:RA:88:ASN:ND2	2.52	0.42
10:SK:163:PRO:HB3	10:SK:169:PRO:HA	2.01	0.42
20:3B:272:LYS:HD3	20:3B:275:CYS:HB3	2.01	0.42
27:A8:596:LYS:CE	27:A8:637:LEU:CA	2.95	0.42
27:A8:638:LEU:HA	27:A8:641:VAL:CG1	2.48	0.42
31:AG:780:GLU:O	31:AG:782:THR:N	2.49	0.42
32:B1:515:TYR:HE2	42:5F:180:PHE:HZ	1.67	0.42
33:B2:39:GLY:O	33:B2:54:ILE:HG13	2.20	0.42
33:B2:294:ARG:O	33:B2:298:LYS:NZ	2.44	0.42
33:B2:432:TYR:O	33:B2:450:ARG:N	2.48	0.42
33:B2:497:VAL:HG12	33:B2:528:LEU:HB3	2.01	0.42
39:5C:215:LYS:HG2	39:5C:227:GLU:HG2	2.00	0.42
42:5F:94:ILE:HG23	42:5F:97:LEU:HD12	2.02	0.42
45:5I:456:GLU:HA	45:5I:459:LYS:HE2	2.01	0.42
46:5J:106:LEU:O	46:5J:146:ARG:NH1	2.44	0.42
49:RB:307:LYS:O	49:RB:311:ARG:HB3	2.19	0.42
51:RE:713:LEU:HB2	51:RE:716:SER:HB2	2.01	0.42
55:RK:81:ILE:HG22	55:RK:110:SER:HB3	2.01	0.42
56:RL:203:ASP:OD1	56:RL:203:ASP:N	2.52	0.42
57:RN:108:LYS:HA	57:RN:108:LYS:HD2	1.85	0.42
1:3A:58:A:OP2	42:5F:165:LYS:CE	2.68	0.42
3:SA:99:C:H2'	3:SA:100:A:C8	2.54	0.42
3:SA:147:A:N7	3:SA:167:U:O2	2.52	0.42
3:SA:1659:A:H2'	3:SA:1660:A:C8	2.53	0.42
8:SI:51:VAL:HG23	8:SI:53:GLY:H	1.84	0.42
8:SI:188:GLU:HG3	45:5I:465:VAL:HG22	2.00	0.42
21:3D:4:ILE:HG23	21:3D:20:VAL:HG21	2.01	0.42
32:B1:25:ASP:OD1	32:B1:25:ASP:N	2.50	0.42
32:B1:46:LYS:HE2	32:B1:46:LYS:HB3	1.87	0.42
32:B1:275:LEU:HD22	32:B1:289:LEU:HD13	2.02	0.42
33:B2:534:ILE:HD11	33:B2:537:VAL:HG12	2.01	0.42
33:B2:836:ILE:HA	33:B2:839:VAL:HG12	2.00	0.42
36:BE:27:PHE:HB2	36:BE:655:THR:HG23	2.00	0.42
43:5G:164:GLN:NE2	43:5G:260:GLU:OE1	2.52	0.42
46:5J:216:ARG:HA	46:5J:216:ARG:HD3	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:RE:919:TRP:HE3	51:RE:920:LEU:HD12	1.85	0.42
51:RE:976:ILE:HA	51:RE:1042:ALA:O	2.19	0.42
58:RO:395:ILE:HD12	58:RO:469:LEU:HD11	2.02	0.42
61:RS:210:VAL:HG23	61:RS:212:LYS:HG2	2.00	0.42
2:5A:532:A:O2'	60:RQ:332:ASP:OD2	2.37	0.42
5:SF:68:ARG:HH21	5:SF:76:VAL:HG11	1.85	0.42
6:SG:23:VAL:HG23	14:SR:61:SER:HB3	2.00	0.42
21:3D:61:GLU:OE2	21:3D:77:SER:OG	2.36	0.42
26:A5:221:MET:HE3	26:A5:221:MET:HB3	1.75	0.42
31:AG:511:GLU:HG2	31:AG:528:ILE:HB	2.00	0.42
34:B3:82:ALA:HB3	62:RT:181:TYR:OH	2.19	0.42
36:BE:21:SER:OG	36:BE:621:ASP:OD2	2.28	0.42
36:BE:523:ASP:OD1	36:BE:523:ASP:N	2.38	0.42
42:5F:124:ILE:H	42:5F:124:ILE:HG13	1.47	0.42
43:5G:154:ILE:O	43:5G:162:THR:HA	2.20	0.42
45:5I:464:THR:HG21	45:5I:468:TYR:HE1	1.85	0.42
52:RF:153:ASN:HD22	52:RF:154:GLU:HG2	1.84	0.42
54:RJ:217:ASP:O	54:RJ:221:LEU:HB2	2.20	0.42
54:RJ:940:LYS:HB2	54:RJ:940:LYS:HE2	1.73	0.42
55:RK:310:ARG:HB3	55:RK:353:THR:HG22	2.01	0.42
57:RN:501:PHE:HB3	57:RN:549:ILE:HG21	2.02	0.42
59:RP:1945:ILE:HA	59:RP:1948:SER:HB2	2.01	0.42
61:RS:432:ILE:HG23	61:RS:436:GLN:HB2	2.00	0.42
3:SA:341:A:OP1	48:RA:121:ARG:NH2	2.48	0.42
3:SA:1068:C:H2'	3:SA:1069:A:C8	2.55	0.42
4:SC:181:LEU:HA	4:SC:181:LEU:HD23	1.86	0.42
5:SF:71:LYS:N	5:SF:91:THR:O	2.52	0.42
6:SG:114:ILE:HA	6:SG:117:THR:HG22	2.02	0.42
11:SM:92:HIS:NE2	11:SM:101:GLU:O	2.52	0.42
22:3E:172:ASP:O	22:3E:176:GLU:HG2	2.20	0.42
27:A8:596:LYS:HG3	27:A8:637:LEU:HD22	2.00	0.42
29:AE:487:THR:HG22	29:AE:488:GLY:H	1.85	0.42
29:AE:539:LEU:HD12	29:AE:540:LYS:HG3	2.01	0.42
32:B1:60:ALA:HB1	32:B1:102:VAL:HG12	2.02	0.42
34:B3:674:SER:OG	34:B3:675:LYS:N	2.52	0.42
36:BE:62:ASP:O	36:BE:66:LEU:N	2.48	0.42
41:5E:508:ARG:HG2	41:5E:514:ALA:HB2	2.02	0.42
42:5F:166:ILE:H	42:5F:166:ILE:HG13	1.68	0.42
50:RD:1597:GLU:HB3	50:RD:1600:GLU:HB3	2.00	0.42
51:RE:379:MET:HE3	51:RE:381:HIS:HB2	2.02	0.42
51:RE:918:ARG:HD3	51:RE:1089:PHE:CZ	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:RF:73:GLN:HE21	52:RF:156:PHE:HD2	1.65	0.42
53:RG:190:GLN:NE2	53:RG:244:GLY:HA2	2.34	0.42
62:RT:255:PRO:HD2	62:RT:258:LYS:HD3	2.00	0.42
1:3A:118:A:C5	23:3F:218:ALA:HB2	2.55	0.42
3:SA:1773:C:H2'	3:SA:1774:G:C8	2.54	0.42
9:SJ:67:TRP:O	9:SJ:71:GLY:CA	2.68	0.42
10:SK:45:ILE:HD12	10:SK:48:GLN:HE21	1.84	0.42
11:SM:70:ILE:HA	11:SM:125:VAL:O	2.20	0.42
11:SM:115:PHE:CG	11:SM:142:VAL:HG21	2.55	0.42
20:3C:124:SER:HA	20:3C:139:VAL:O	2.19	0.42
23:3F:560:ARG:HE	23:3F:560:ARG:HB3	1.75	0.42
26:A5:27:GLN:HG3	26:A5:59:LYS:HA	2.02	0.42
29:AE:25:ARG:HH21	45:5I:16:VAL:HG22	1.83	0.42
31:AG:313:LEU:HD23	31:AG:323:LEU:HB3	2.01	0.42
31:AG:559:LYS:HE2	31:AG:559:LYS:HB2	1.79	0.42
34:B3:367:VAL:HG12	34:B3:643:PHE:HE2	1.85	0.42
35:B8:504:THR:O	35:B8:504:THR:OG1	2.35	0.42
42:5F:60:LYS:HZ2	42:5F:63:LEU:HD22	1.85	0.42
51:RE:486:GLN:HE22	51:RE:571:ARG:HH22	1.68	0.42
51:RE:1178:ASP:OD1	51:RE:1178:ASP:N	2.52	0.42
55:RK:56:ILE:HD13	55:RK:56:ILE:HA	1.89	0.42
55:RK:216:LEU:HB3	55:RK:223:VAL:HG21	2.01	0.42
56:RL:37:LEU:HD22	56:RL:149:VAL:HG11	2.01	0.42
56:RL:59:TYR:O	56:RL:108:TYR:N	2.53	0.42
59:RP:1877:ARG:NH2	59:RP:1913:SER:O	2.51	0.42
61:RS:364:PHE:HE1	61:RS:417:TRP:HE1	1.67	0.42
61:RS:373:LYS:HA	61:RS:376:LEU:HG	2.02	0.42
61:RS:382:LEU:HD21	61:RS:428:TYR:CZ	2.53	0.42
62:RT:159:ILE:H	62:RT:159:ILE:HG13	1.68	0.42
3:SA:565:C:N4	54:RJ:993:ASP:HB3	2.35	0.42
3:SA:1656:U:H3	3:SA:1743:U:H3	1.67	0.42
5:SF:47:PHE:HD2	5:SF:48:LEU:HD12	1.84	0.42
5:SF:220:THR:OG1	5:SF:221:ARG:N	2.53	0.42
8:SI:116:ARG:HB3	8:SI:117:THR:H	1.55	0.42
12:SO:58:HIS:O	12:SO:60:VAL:N	2.49	0.42
18:Sc:50:ALA:O	18:Sc:52:THR:N	2.53	0.42
25:A4:313:LYS:HA	25:A4:316:LYS:HZ3	1.84	0.42
26:A5:98:LYS:HE3	26:A5:98:LYS:HB2	1.88	0.42
32:B1:274:LEU:HD11	32:B1:286:LEU:HD13	2.02	0.42
34:B3:516:LYS:HE2	34:B3:516:LYS:HB2	1.89	0.42
36:BE:361:SER:HA	36:BE:636:PRO:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:5F:7:HIS:C	42:5F:9:GLU:H	2.28	0.42
43:5G:157:PHE:O	43:5G:159:HIS:N	2.51	0.42
48:RA:164:ARG:NH2	48:RA:174:ASN:O	2.51	0.42
51:RE:209:MET:HE3	51:RE:213:LEU:HD11	2.02	0.42
53:RG:128:VAL:HG22	53:RG:159:LEU:HD22	2.01	0.42
53:RH:176:ARG:NH2	53:RH:192:TYR:OH	2.52	0.42
54:RJ:773:THR:HG23	54:RJ:777:ARG:HD3	2.02	0.42
55:RK:190:SER:OG	55:RK:191:ILE:N	2.51	0.42
57:RN:700:LEU:HD23	57:RN:702:LEU:HG	2.01	0.42
61:RS:437:ARG:HD2	61:RS:460:LEU:HG	2.02	0.42
3:SA:575:C:O2	54:RJ:1052:SER:OG	2.28	0.42
4:SC:109:LYS:HA	4:SC:109:LYS:HD2	1.88	0.42
5:SF:31:PRO:HA	5:SF:81:THR:HB	2.01	0.42
7:SH:77:LEU:HD12	7:SH:95:LYS:HD3	2.00	0.42
7:SH:101:ILE:H	7:SH:101:ILE:HG13	1.72	0.42
15:SX:7:LEU:HD13	15:SX:34:ILE:HG12	2.02	0.42
20:3B:107:VAL:HG13	20:3B:141:TYR:HB3	2.01	0.42
22:3E:117:TYR:HA	22:3E:120:ILE:HG12	2.01	0.42
23:3F:303:LYS:HE3	23:3F:319:TYR:HE2	1.85	0.42
25:A4:98:SER:OG	25:A4:99:ILE:N	2.53	0.42
25:A4:213:TRP:HA	25:A4:225:LEU:HA	2.02	0.42
26:A5:224:CYS:SG	26:A5:225:VAL:N	2.93	0.42
27:A8:443:CYS:CB	31:AG:728:LEU:CD2	2.97	0.42
29:AE:91:ILE:HD13	29:AE:91:ILE:HA	1.90	0.42
29:AE:420:LYS:HB2	29:AE:420:LYS:HE2	1.91	0.42
31:AG:502:LYS:HD2	31:AG:564:PRO:HA	2.02	0.42
32:B1:147:GLN:HB2	32:B1:167:ASP:H	1.85	0.42
33:B2:26:ILE:HA	33:B2:27:PRO:HD3	1.94	0.42
33:B2:405:LEU:HD11	33:B2:673:VAL:HG21	2.02	0.42
33:B2:555:VAL:HG22	33:B2:569:LEU:HB2	2.02	0.42
34:B3:303:PHE:HA	34:B3:312:GLN:O	2.20	0.42
39:5C:191:ILE:HD13	39:5C:191:ILE:HA	1.87	0.42
39:5C:369:MET:HB3	39:5C:369:MET:HE2	1.79	0.42
46:5J:134:ARG:HD2	46:5J:134:ARG:HA	1.83	0.42
2:5A:490:G:H1'	2:5A:495:G:H5'	2.01	0.41
3:SA:318:U:O2	3:SA:346:G:O6	2.37	0.41
3:SA:576:G:C4'	41:5E:327:LYS:HE2	2.48	0.41
3:SA:1489:U:N3	46:5J:202:ARG:O	2.53	0.41
20:3C:149:SER:OG	20:3C:150:LYS:N	2.52	0.41
20:3C:291:GLN:HA	20:3C:294:ARG:HG2	2.01	0.41
22:3E:333:LYS:HD3	40:5D:103:ASP:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3F:301:ASP:OD1	23:3F:301:ASP:N	2.51	0.41
23:3F:368:LEU:HB3	23:3F:396:PHE:HE2	1.83	0.41
24:3G:44:LEU:HD23	24:3G:44:LEU:HA	1.87	0.41
25:A4:423:LYS:NZ	38:5B:167:ARG:HH11	2.18	0.41
27:A8:662:ILE:HA	27:A8:665:GLN:HB2	2.01	0.41
29:AE:755:ARG:O	29:AE:759:ILE:HG12	2.20	0.41
30:AF:105:VAL:HG21	30:AF:142:THR:HG21	2.02	0.41
45:5I:336:HIS:CE1	45:5I:338:HIS:HB2	2.55	0.41
51:RE:501:ASN:HD21	51:RE:506:GLN:HE22	1.66	0.41
51:RE:974:PRO:HB2	51:RE:976:ILE:HG23	2.02	0.41
51:RE:1072:VAL:HA	51:RE:1075:LEU:HB2	2.02	0.41
53:RG:215:ASN:HB2	53:RG:218:ASP:HB2	2.01	0.41
57:RN:611:SER:OG	57:RN:612:THR:N	2.52	0.41
57:RN:616:LEU:HD13	57:RN:619:LEU:HD22	2.01	0.41
59:RP:129:ILE:O	59:RP:133:ILE:HG12	2.20	0.41
59:RP:1975:LYS:HA	59:RP:1975:LYS:HD2	1.80	0.41
2:5A:298:A:OP2	36:BE:103:ARG:NH2	2.45	0.41
12:SO:140:LYS:HA	12:SO:140:LYS:HD3	1.88	0.41
21:3D:268:MET:HA	21:3D:271:VAL:HG12	2.02	0.41
23:3F:421:ASN:ND2	23:3F:437:ARG:HA	2.34	0.41
23:3F:476:THR:HG22	23:3F:491:SER:HA	2.02	0.41
29:AE:35:TYR:O	29:AE:150:ARG:NH1	2.53	0.41
29:AE:664:PRO:HB2	29:AE:716:PHE:HE2	1.85	0.41
30:AF:366:TYR:OH	30:AF:371:GLU:OE1	2.23	0.41
31:AG:625:GLY:HA3	31:AG:662:VAL:HG11	2.02	0.41
31:AG:659:ILE:HG22	31:AG:674:THR:HB	2.01	0.41
32:B1:300:MET:HG2	32:B1:328:LEU:HD22	2.02	0.41
32:B1:498:ARG:HH11	32:B1:498:ARG:HD3	1.72	0.41
33:B2:538:ARG:HD3	33:B2:580:ASP:HA	2.02	0.41
34:B3:506:PHE:CE1	34:B3:518:TRP:HB2	2.55	0.41
34:B3:745:ASP:OD2	41:5E:508:ARG:HD2	2.20	0.41
36:BE:517:MET:HE3	36:BE:517:MET:HB2	1.85	0.41
36:BE:635:SER:OG	36:BE:637:ASN:OD1	2.30	0.41
39:5C:201:TYR:OH	39:5C:415:GLU:OE1	2.29	0.41
41:5E:352:LYS:HE2	57:RN:764:ARG:HE	1.85	0.41
41:5E:533:LYS:HG3	41:5E:536:ARG:HE	1.83	0.41
58:RO:243:PRO:HA	58:RO:244:PRO:HD3	1.81	0.41
59:RP:1756:ILE:HG22	59:RP:1760:ASN:HD21	1.85	0.41
61:RS:255:SER:HB3	61:RS:258:VAL:HG22	2.01	0.41
3:SA:360:A:O2'	3:SA:362:G:N2	2.45	0.41
3:SA:1782:A:C6	32:B1:257:TYR:CG	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:SH:123:GLY:O	7:SH:127:THR:OG1	2.39	0.41
10:SK:154:LYS:HE2	10:SK:154:LYS:HB3	1.88	0.41
19:Sd:43:ASN:OD1	19:Sd:43:ASN:N	2.53	0.41
20:3B:150:LYS:NZ	20:3B:310:GLU:OE2	2.44	0.41
20:3C:242:ALA:HB3	20:3C:269:ILE:HA	2.01	0.41
21:3D:206:LEU:HB3	21:3D:216:PHE:HE1	1.84	0.41
28:A9:451:LEU:HA	28:A9:451:LEU:HD13	1.83	0.41
29:AE:148:PHE:HA	29:AE:151:ILE:HG12	2.01	0.41
29:AE:480:ASN:HA	29:AE:518:THR:HG21	2.02	0.41
30:AF:177:ILE:HA	30:AF:178:PRO:HD3	1.84	0.41
32:B1:275:LEU:HB2	32:B1:289:LEU:HD22	2.02	0.41
32:B1:363:ALA:HB2	32:B1:393:VAL:HG13	2.01	0.41
32:B1:381:ALA:HA	41:5E:481:PRO:HA	2.01	0.41
32:B1:501:SER:O	32:B1:506:SER:OG	2.38	0.41
32:B1:721:VAL:O	36:BE:579:ARG:NH2	2.53	0.41
37:B6:106:ASP:OD1	37:B6:106:ASP:N	2.38	0.41
39:5C:357:SER:O	39:5C:357:SER:OG	2.39	0.41
42:5F:6:LYS:O	42:5F:10:GLN:N	2.52	0.41
43:5G:73:VAL:HG23	43:5G:208:HIS:HE1	1.85	0.41
50:RD:1695:TRP:HD1	50:RD:1696:LEU:HD22	1.86	0.41
51:RE:1010:GLU:HG2	51:RE:1011:ARG:HG2	2.01	0.41
55:RK:80:ILE:HD13	55:RK:80:ILE:HA	1.90	0.41
1:3A:49:C:H42	2:5A:467:A:H61	1.67	0.41
1:3A:312:U:O4	1:3A:313:A:N6	2.53	0.41
3:SA:647:G:N2	3:SA:687:G:H22	2.17	0.41
3:SA:886:U:OP1	4:SC:214:LYS:NZ	2.54	0.41
3:SA:1049:U:H5"	18:Sc:70:LYS:HG3	2.01	0.41
7:SH:51:LYS:HE2	7:SH:51:LYS:HB3	1.91	0.41
13:SP:107:ARG:NE	13:SP:107:ARG:CA	2.73	0.41
14:SR:97:VAL:HG12	14:SR:98:ASP:H	1.83	0.41
22:3E:388:LEU:HD12	22:3E:388:LEU:HA	1.89	0.41
23:3F:132:VAL:HG21	23:3F:505:LEU:HD21	2.02	0.41
23:3F:260:LEU:HD21	23:3F:283:VAL:HG11	2.02	0.41
23:3F:304:ILE:HB	23:3F:318:LEU:HG	2.03	0.41
24:3G:64:LEU:O	24:3G:66:HIS:N	2.43	0.41
29:AE:559:ASN:HB2	29:AE:614:LEU:HD12	2.02	0.41
29:AE:682:SER:O	29:AE:682:SER:OG	2.33	0.41
30:AF:34:GLN:O	30:AF:328:ALA:HA	2.21	0.41
31:AG:258:TYR:CD1	31:AG:414:ILE:HD11	2.55	0.41
31:AG:386:ASN:HD21	31:AG:389:LEU:HD11	1.86	0.41
32:B1:347:SER:HB2	32:B1:365:GLU:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B1:559:ILE:HG21	32:B1:578:LYS:HA	2.03	0.41
33:B2:50:ASN:HB3	33:B2:62:LYS:HG3	2.02	0.41
34:B3:195:GLY:HA3	34:B3:245:SER:H	1.85	0.41
34:B3:242:GLN:HA	34:B3:263:GLY:HA3	2.01	0.41
34:B3:264:ASP:HA	34:B3:289:PHE:HB2	2.03	0.41
34:B3:690:HIS:CE1	41:5E:519:GLU:HB2	2.55	0.41
35:B8:174:ARG:NE	35:B8:179:ASP:OD2	2.44	0.41
35:B8:278:ASP:H	35:B8:282:ASN:HD22	1.67	0.41
35:B8:296:GLN:HB3	35:B8:316:GLY:HA2	2.03	0.41
42:5F:7:HIS:C	42:5F:9:GLU:N	2.77	0.41
45:5I:58:PHE:HE1	45:5I:373:ARG:HB3	1.85	0.41
45:5I:107:LYS:NZ	45:5I:109:HIS:O	2.45	0.41
51:RE:477:LEU:HD23	51:RE:477:LEU:HA	1.94	0.41
51:RE:975:LEU:HG	51:RE:1041:VAL:HG23	2.01	0.41
51:RE:978:ASP:HB3	51:RE:1012:LEU:HG	2.02	0.41
54:RJ:244:MET:HE2	54:RJ:271:ILE:HG22	2.02	0.41
54:RJ:1042:MET:HE2	54:RJ:1042:MET:HB3	1.87	0.41
55:RK:32:LYS:HG2	55:RK:75:ILE:HG13	2.02	0.41
56:RL:26:PHE:O	56:RL:149:VAL:HA	2.20	0.41
57:RN:481:MET:HE3	57:RN:481:MET:HB2	1.92	0.41
59:RP:1752:ASP:HA	59:RP:1755:GLU:HG2	2.03	0.41
61:RS:355:ALA:HA	61:RS:358:TYR:CE2	2.55	0.41
5:SF:181:VAL:HG23	5:SF:227:VAL:HG22	2.02	0.41
14:SR:46:PHE:HA	14:SR:49:TYR:HB2	2.02	0.41
20:3C:151:LEU:HD13	20:3C:241:PHE:HE1	1.86	0.41
22:3E:163:ILE:HD13	22:3E:163:ILE:HA	1.86	0.41
23:3F:488:ILE:HG22	23:3F:524:ILE:HD13	2.02	0.41
25:A4:39:VAL:HG12	25:A4:41:PHE:H	1.85	0.41
25:A4:171:SER:O	25:A4:171:SER:OG	2.32	0.41
26:A5:32:GLN:HE22	26:A5:47:ASN:HB3	1.85	0.41
29:AE:526:LEU:HA	29:AE:529:VAL:HG12	2.01	0.41
30:AF:392:ILE:HD11	30:AF:417:VAL:HG23	2.03	0.41
31:AG:97:THR:OG1	31:AG:98:VAL:N	2.54	0.41
31:AG:544:LYS:HD3	31:AG:544:LYS:HA	1.88	0.41
32:B1:14:VAL:CG2	32:B1:341:GLN:O	2.62	0.41
33:B2:433:ALA:HA	33:B2:449:THR:HA	2.03	0.41
42:5F:6:LYS:N	42:5F:9:GLU:HB2	2.36	0.41
48:RA:164:ARG:HB2	48:RA:173:LEU:HB2	2.03	0.41
51:RE:708:LEU:HA	51:RE:709:PRO:HD3	1.96	0.41
54:RJ:552:LEU:HD23	54:RJ:552:LEU:HA	1.92	0.41
55:RK:286:SER:OG	55:RK:289:VAL:O	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:RN:515:HIS:O	57:RN:519:THR:OG1	2.32	0.41
59:RP:1923:ARG:HA	59:RP:1923:ARG:HD3	1.71	0.41
60:RQ:313:PHE:HE2	60:RQ:883:ILE:HD12	1.84	0.41
3:SA:88:U:H2'	3:SA:89:G:H8	1.85	0.41
3:SA:110:U:OP1	49:RB:227:ARG:NH1	2.53	0.41
3:SA:1156:C:H2'	3:SA:1157:A:C8	2.54	0.41
3:SA:1523:G:H1'	3:SA:1524:A:H5'	2.02	0.41
3:SA:1534:G:O2'	3:SA:1535:U:O2	2.29	0.41
20:3C:89:GLU:HG2	20:3C:98:ILE:HB	2.03	0.41
25:A4:154:ASP:OD1	25:A4:154:ASP:N	2.49	0.41
25:A4:394:TRP:HB3	25:A4:399:VAL:HG12	2.03	0.41
26:A5:551:ILE:HA	26:A5:554:PHE:CE2	2.56	0.41
29:AE:109:TRP:HB2	29:AE:142:TYR:CZ	2.56	0.41
31:AG:31:ASN:OD1	31:AG:31:ASN:N	2.52	0.41
31:AG:712:THR:HG22	31:AG:766:ILE:HG23	2.01	0.41
32:B1:150:THR:OG1	32:B1:164:THR:OG1	2.31	0.41
32:B1:298:LEU:HD12	41:5E:474:ILE:CG2	2.51	0.41
33:B2:164:ASP:HB3	33:B2:182:LYS:HB3	2.02	0.41
34:B3:218:ASP:OD1	34:B3:218:ASP:N	2.52	0.41
35:B8:137:ILE:HD13	35:B8:137:ILE:HA	1.86	0.41
35:B8:159:HIS:O	35:B8:163:ARG:HG2	2.21	0.41
35:B8:278:ASP:H	35:B8:282:ASN:ND2	2.18	0.41
37:B6:35:LYS:HE3	37:B6:35:LYS:HB3	1.88	0.41
37:B6:268:ASP:OD1	37:B6:268:ASP:N	2.53	0.41
37:B6:311:TYR:O	37:B6:315:GLU:HG2	2.21	0.41
39:5C:244:ASN:HB3	39:5C:446:PRO:HG3	2.02	0.41
40:5D:61:ASP:O	42:5F:160:TRP:HH2	2.03	0.41
41:5E:314:LEU:HA	41:5E:317:GLU:HB2	2.03	0.41
41:5E:350:THR:CG2	54:RJ:975:GLU:HB2	2.51	0.41
43:5G:260:GLU:OE2	43:5G:262:ARG:NH2	2.33	0.41
44:5H:542:TYR:CZ	44:5H:546:LYS:HG3	2.56	0.41
51:RE:518:PHE:CE2	51:RE:1075:LEU:HB3	2.48	0.41
51:RE:1094:LYS:HB3	51:RE:1096:TYR:HD1	1.85	0.41
52:RF:9:MET:HE1	52:RF:15:VAL:HG23	2.02	0.41
53:RH:180:LEU:HD23	53:RH:180:LEU:HA	1.88	0.41
1:3A:113:G:O6	24:3H:42:LYS:NZ	2.44	0.41
3:SA:1782:A:N3	3:SA:1782:A:C2'	2.83	0.41
7:SH:70:PRO:O	7:SH:98:ARG:NH2	2.54	0.41
7:SH:115:LYS:HB2	7:SH:115:LYS:HE3	1.76	0.41
11:SM:82:ARG:HD3	11:SM:110:HIS:CD2	2.55	0.41
11:SM:115:PHE:HB2	11:SM:142:VAL:HG11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:3C:210:MET:HE2	20:3C:210:MET:HB2	1.97	0.41
22:3E:192:PHE:CD2	22:3E:195:LEU:HB2	2.56	0.41
23:3F:158:THR:HG23	23:3F:548:ARG:HB2	2.02	0.41
23:3F:321:HIS:CE1	23:3F:340:GLY:H	2.39	0.41
23:3F:502:SER:OG	23:3F:504:ASN:OD1	2.32	0.41
26:A5:64:LYS:HB3	26:A5:77:ILE:HG13	2.02	0.41
28:A9:416:ILE:O	28:A9:420:ILE:CB	2.69	0.41
29:AE:549:LYS:HD3	29:AE:549:LYS:HA	1.91	0.41
30:AF:255:VAL:HA	30:AF:276:SER:HA	2.03	0.41
32:B1:410:THR:HG22	32:B1:426:THR:HG22	2.01	0.41
34:B3:468:ILE:HA	34:B3:469:PRO:HD3	1.83	0.41
41:5E:522:ARG:HA	41:5E:525:LYS:HE3	2.02	0.41
46:5J:117:VAL:HG11	46:5J:149:ILE:HG13	2.02	0.41
48:RA:94:ASP:OD1	48:RA:94:ASP:N	2.54	0.41
51:RE:356:THR:HG23	51:RE:359:PHE:HB2	2.02	0.41
51:RE:841:ASN:ND2	51:RE:851:LYS:HG2	2.35	0.41
53:RG:232:LEU:HB3	53:RG:236:VAL:HG13	2.02	0.41
57:RN:283:ALA:HA	61:RS:381:ALA:HB1	2.03	0.41
57:RN:784:ILE:HA	57:RN:787:THR:HG22	2.03	0.41
61:RS:264:LYS:HB2	61:RS:264:LYS:HE3	1.81	0.41
3:SA:200:A:H2'	3:SA:201:G:C8	2.56	0.41
9:SJ:35:ASN:HD21	48:RA:119:ASN:HD22	1.69	0.41
9:SJ:58:LEU:HD21	48:RA:77:TYR:HB2	2.02	0.41
10:SK:63:ASP:OD1	10:SK:63:ASP:N	2.46	0.41
13:SP:103:ARG:HH21	62:RT:188:LYS:HG3	1.85	0.41
21:3D:24:GLN:NE2	21:3D:126:ASP:OD1	2.48	0.41
25:A4:389:ARG:HG2	25:A4:747:ILE:HG21	2.02	0.41
25:A4:428:ILE:HD12	25:A4:444:ARG:HH21	1.85	0.41
26:A5:49:ASN:OD1	26:A5:49:ASN:N	2.49	0.41
27:A8:438:ASP:C	27:A8:440:ARG:N	2.79	0.41
27:A8:563:LEU:H	27:A8:563:LEU:HG	1.51	0.41
27:A8:703:LEU:HA	27:A8:704:PRO:HD3	1.96	0.41
29:AE:32:SER:OG	29:AE:33:LEU:N	2.54	0.41
29:AE:33:LEU:HD11	29:AE:151:ILE:HG22	2.03	0.41
29:AE:69:PHE:HE2	29:AE:104:LEU:HD13	1.85	0.41
29:AE:572:ARG:NH2	29:AE:632:THR:O	2.40	0.41
29:AE:597:HIS:HB3	29:AE:615:ASN:HB3	2.03	0.41
31:AG:439:ASN:ND2	31:AG:496:THR:O	2.54	0.41
31:AG:514:TYR:HA	31:AG:515:PRO:HD3	1.94	0.41
32:B1:419:TYR:HB2	41:5E:482:LEU:CD1	2.50	0.41
34:B3:90:LEU:O	34:B3:92:THR:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BE:870:GLN:HA	36:BE:873:LYS:HE3	2.03	0.41
43:5G:260:GLU:HG3	43:5G:276:GLN:HB3	2.03	0.41
48:RA:237:ARG:NE	48:RA:239:ASP:OD2	2.46	0.41
51:RE:217:LYS:HD3	51:RE:217:LYS:HA	1.83	0.41
51:RE:360:VAL:O	51:RE:363:THR:OG1	2.30	0.41
52:RF:153:ASN:ND2	52:RF:154:GLU:HG2	2.36	0.41
53:RG:40:ARG:O	53:RG:201:SER:HA	2.20	0.41
56:RL:185:ASN:OD1	56:RL:185:ASN:N	2.52	0.41
57:RN:766:ARG:NH2	57:RN:769:GLU:OE2	2.54	0.41
58:RO:226:ASP:OD1	58:RO:284:ARG:NE	2.54	0.41
59:RP:2073:GLU:HA	59:RP:2076:ARG:HG2	2.03	0.41
61:RS:238:SER:O	61:RS:238:SER:OG	2.33	0.41
2:5A:18:G:H2'	2:5A:19:A:H8	1.85	0.41
3:SA:153:G:O6	3:SA:161:U:O4	2.39	0.41
3:SA:406:U:O2'	48:RA:92:LYS:O	2.38	0.41
3:SA:1538:U:H1'	3:SA:1570:A:H61	1.84	0.41
4:SC:82:ARG:HD3	4:SC:105:PHE:HE1	1.86	0.41
7:SH:185:GLN:O	7:SH:189:HIS:ND1	2.44	0.41
9:SJ:36:THR:O	9:SJ:96:LEU:N	2.52	0.41
9:SJ:49:ARG:HA	9:SJ:49:ARG:HD3	1.83	0.41
13:SP:125:SER:HB2	13:SP:126:THR:H	1.73	0.41
20:3B:116:SER:OG	20:3B:120:GLU:OE1	2.28	0.41
21:3D:7:LEU:HD12	21:3D:99:ALA:HB3	2.02	0.41
21:3D:157:ALA:HB2	37:B6:292:TYR:CZ	2.56	0.41
22:3E:311:LYS:HB3	22:3E:311:LYS:HE2	1.84	0.41
23:3F:457:GLU:HG3	23:3F:461:LYS:HE2	2.02	0.41
24:3G:85:VAL:O	24:3G:89:ARG:HG2	2.21	0.41
25:A4:52:SER:HA	25:A4:104:TRP:CG	2.56	0.41
25:A4:249:ARG:NH2	25:A4:309:GLN:OE1	2.49	0.41
25:A4:513:LEU:HD12	25:A4:513:LEU:HA	1.89	0.41
25:A4:581:SER:HA	25:A4:594:PHE:O	2.21	0.41
27:A8:342:LEU:HA	27:A8:357:HIS:HA	2.02	0.41
27:A8:443:CYS:HA	31:AG:728:LEU:CD2	2.47	0.41
27:A8:553:GLN:O	27:A8:557:THR:OG1	2.31	0.41
28:A9:475:THR:HA	28:A9:478:ASN:HD22	1.86	0.41
29:AE:214:THR:HG23	29:AE:260:ILE:HG13	2.03	0.41
29:AE:227:ASN:OD1	29:AE:227:ASN:N	2.53	0.41
30:AF:287:LEU:HD13	30:AF:287:LEU:HA	1.96	0.41
31:AG:455:SER:O	31:AG:455:SER:OG	2.34	0.41
31:AG:591:GLU:O	31:AG:593:ASN:N	2.54	0.41
31:AG:666:ASN:OD1	31:AG:666:ASN:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:B1:492:SER:OG	32:B1:494:ASP:OD1	2.28	0.41
33:B2:17:ILE:CG2	33:B2:52:TRP:CH2	3.01	0.41
34:B3:567:VAL:HG22	34:B3:568:MET:HG2	2.02	0.41
35:B8:338:LYS:HE3	35:B8:338:LYS:HB2	1.89	0.41
36:BE:724:SER:O	36:BE:728:ARG:NH2	2.39	0.41
37:B6:15:MET:HE2	37:B6:15:MET:HB3	1.67	0.41
39:5C:117:LYS:HD2	39:5C:117:LYS:HA	1.85	0.41
45:5I:400:LEU:HD12	45:5I:400:LEU:HA	1.89	0.41
46:5J:119:ARG:HD3	54:RJ:1113:ILE:HG13	2.02	0.41
48:RA:139:LYS:HA	48:RA:139:LYS:HD2	1.89	0.41
50:RD:1457:ALA:HA	50:RD:1458:PRO:HD3	1.95	0.41
51:RE:566:ILE:HD11	51:RE:686:LEU:HD21	2.03	0.41
51:RE:970:TRP:HB2	51:RE:971:LYS:HD3	2.02	0.41
53:RG:31:LEU:HD23	53:RG:31:LEU:HA	1.86	0.41
53:RG:116:THR:HG22	53:RG:118:ARG:H	1.86	0.41
53:RG:123:GLU:HB2	53:RG:161:LYS:HB2	2.03	0.41
53:RG:233:SER:OG	53:RG:234:ALA:N	2.54	0.41
53:RH:177:LYS:HG2	53:RH:203:CYS:HB3	2.03	0.41
54:RJ:43:MET:N	54:RJ:43:MET:SD	2.94	0.41
54:RJ:906:ASP:OD1	54:RJ:906:ASP:N	2.45	0.41
54:RJ:926:ILE:HG12	54:RJ:928:ILE:HG23	2.01	0.41
55:RK:117:LEU:HA	55:RK:166:VAL:O	2.21	0.41
59:RP:76:THR:O	59:RP:79:GLN:N	2.54	0.41
59:RP:879:PRO:O	59:RP:882:ASN:C	2.64	0.41
61:RS:288:ARG:O	61:RS:292:GLU:HG2	2.21	0.41
61:RS:407:GLU:HB2	61:RS:411:ARG:HD2	2.03	0.41
62:RT:182:ILE:O	62:RT:182:ILE:HG13	2.21	0.41
3:SA:27:U:H4'	54:RJ:45:ARG:HG3	2.02	0.41
3:SA:1492:A:N6	54:RJ:941:ILE:O	2.46	0.41
3:SA:1655:A:O2'	33:B2:395:ARG:NH1	2.53	0.41
4:SC:31:ASP:HA	4:SC:45:LYS:HA	2.03	0.41
13:SP:29:HIS:CD2	13:SP:41:ARG:HB2	2.56	0.41
22:3E:201:ASP:HB3	22:3E:204:ALA:HB3	2.03	0.41
25:A4:425:ASP:OD2	25:A4:444:ARG:NH2	2.53	0.41
30:AF:136:ASP:OD1	30:AF:137:ASN:N	2.54	0.41
30:AF:364:SER:O	30:AF:364:SER:OG	2.26	0.41
30:AF:492:ARG:HD3	30:AF:492:ARG:HA	1.80	0.41
32:B1:263:VAL:HG13	32:B1:277:VAL:HG13	2.03	0.41
33:B2:241:LYS:HB2	33:B2:241:LYS:HE3	1.89	0.41
33:B2:911:GLN:HA	33:B2:914:LEU:HG	2.02	0.41
34:B3:410:ASN:OD1	34:B3:435:ALA:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:BE:83:LEU:HA	36:BE:91:TYR:O	2.21	0.41
37:B6:26:LYS:HA	37:B6:29:VAL:HG12	2.03	0.41
37:B6:306:LYS:HE3	37:B6:306:LYS:HB2	1.77	0.41
41:5E:533:LYS:O	41:5E:537:SER:HB2	2.21	0.41
45:5I:225:LEU:HA	45:5I:225:LEU:HD23	1.87	0.41
50:RD:1622:ARG:NH1	50:RD:1626:GLN:HE21	2.19	0.41
51:RE:177:ASN:HB2	51:RE:213:LEU:HB2	2.03	0.41
57:RN:668:LEU:HD23	57:RN:671:TYR:HD2	1.86	0.41
59:RP:149:GLU:HA	59:RP:152:PHE:CD2	2.56	0.41
3:SA:304:U:H5''	11:SM:136:ARG:HH21	1.86	0.40
7:SH:38:GLY:N	7:SH:48:TYR:O	2.54	0.40
8:SI:60:ILE:HB	8:SI:92:PHE:HD1	1.86	0.40
15:SX:102:VAL:O	15:SX:113:HIS:N	2.54	0.40
22:3E:162:MET:HB3	22:3E:162:MET:HE2	1.86	0.40
23:3F:212:LYS:HB2	23:3F:212:LYS:HE3	1.88	0.40
25:A4:250:THR:OG1	25:A4:251:ASP:N	2.53	0.40
28:A9:432:LYS:HA	28:A9:432:LYS:HD3	1.85	0.40
29:AE:688:PHE:HB3	29:AE:730:GLN:HE21	1.86	0.40
30:AF:183:LEU:HD12	30:AF:183:LEU:HA	1.85	0.40
30:AF:397:TRP:CZ3	30:AF:425:GLY:HA3	2.56	0.40
32:B1:519:LEU:HD13	32:B1:581:THR:HG22	2.03	0.40
32:B1:523:MET:HE2	32:B1:523:MET:HB2	1.76	0.40
34:B3:678:TRP:CE3	34:B3:697:VAL:HG23	2.56	0.40
34:B3:745:ASP:OD2	41:5E:508:ARG:CD	2.70	0.40
40:5D:70:ARG:HD3	40:5D:78:LEU:HD11	2.02	0.40
46:5J:77:LYS:HA	46:5J:77:LYS:HD2	1.84	0.40
51:RE:110:LEU:HD21	51:RE:368:LEU:HD23	2.03	0.40
51:RE:202:SER:OG	51:RE:203:ILE:N	2.54	0.40
51:RE:676:PRO:HB2	51:RE:678:ILE:HG22	2.03	0.40
51:RE:1173:GLY:CA	51:RE:1179:LYS:HB2	2.52	0.40
52:RF:62:SER:HA	52:RF:66:HIS:NE2	2.36	0.40
53:RG:176:ARG:HA	53:RG:176:ARG:HD2	1.91	0.40
55:RK:184:ASP:OD1	55:RK:185:ARG:N	2.53	0.40
57:RN:504:ILE:HA	57:RN:507:LEU:HG	2.03	0.40
3:SA:844:A:H2'	3:SA:845:G:C8	2.57	0.40
3:SA:1525:A:N3	3:SA:1589:C:O2'	2.53	0.40
3:SA:1672:G:H2'	3:SA:1673:G:C8	2.55	0.40
5:SF:97:GLU:HB3	5:SF:99:PHE:CE2	2.56	0.40
15:SX:110:ILE:HD12	15:SX:126:LEU:HD22	2.02	0.40
20:3B:248:ASP:OD1	20:3B:248:ASP:N	2.37	0.40
20:3C:202:ARG:HA	20:3C:202:ARG:HD2	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:3E:88:ILE:HA	22:3E:106:ASN:O	2.22	0.40
24:3G:41:THR:HG21	24:3G:66:HIS:CE1	2.55	0.40
24:3H:33:LEU:HD11	24:3H:100:ALA:HB1	2.02	0.40
25:A4:141:SER:O	25:A4:141:SER:OG	2.34	0.40
30:AF:57:VAL:HG21	30:AF:327:LEU:HD11	2.04	0.40
30:AF:426:LYS:HB3	30:AF:429:VAL:HB	2.03	0.40
33:B2:639:VAL:HG22	33:B2:653:LEU:HB2	2.03	0.40
34:B3:25:VAL:HG22	34:B3:294:LEU:HD13	2.03	0.40
34:B3:313:LEU:O	34:B3:330:THR:OG1	2.33	0.40
36:BE:265:SER:O	36:BE:265:SER:OG	2.39	0.40
36:BE:290:ILE:HG23	36:BE:291:HIS:CD2	2.56	0.40
37:B6:304:LEU:O	37:B6:308:THR:HG23	2.21	0.40
39:5C:340:LEU:HD22	39:5C:403:VAL:HG11	2.03	0.40
41:5E:362:THR:HA	41:5E:365:LEU:HD23	2.03	0.40
41:5E:445:VAL:HG13	42:5F:81:LYS:HE2	2.03	0.40
46:5J:106:LEU:HD23	46:5J:106:LEU:HA	1.95	0.40
46:5J:195:GLN:O	46:5J:199:THR:HG22	2.22	0.40
58:RO:422:ILE:HD13	58:RO:422:ILE:HA	1.93	0.40
59:RP:100:GLU:OE2	59:RP:146:ASN:ND2	2.54	0.40
61:RS:245:VAL:O	61:RS:249:THR:HG23	2.22	0.40
3:SA:16:G:H4'	47:5K:159:GLY:HA2	2.03	0.40
3:SA:268:C:H2'	3:SA:269:G:C8	2.56	0.40
3:SA:298:C:H5''	5:SF:38:LEU:HG	2.02	0.40
3:SA:625:C:H2'	3:SA:626:U:C6	2.57	0.40
5:SF:106:LYS:HE3	5:SF:106:LYS:HB3	1.88	0.40
10:SK:79:ARG:HE	10:SK:79:ARG:HB3	1.78	0.40
13:SP:107:ARG:HB2	13:SP:107:ARG:CZ	2.51	0.40
20:3C:165:ALA:HB3	20:3C:168:LYS:HD3	2.04	0.40
21:3D:182:ASP:OD1	21:3D:314:ARG:NH2	2.39	0.40
22:3E:248:THR:OG1	22:3E:251:ASP:OD1	2.29	0.40
22:3E:367:ALA:O	22:3E:371:LEU:HB3	2.22	0.40
22:3E:431:ALA:O	35:B8:160:TYR:OH	2.28	0.40
23:3F:263:TRP:HA	23:3F:269:SER:O	2.22	0.40
23:3F:465:GLN:HG2	24:3H:6:PRO:HG3	2.03	0.40
25:A4:429:SER:OG	25:A4:430:THR:N	2.52	0.40
31:AG:29:THR:HB	31:AG:198:LEU:HD11	2.03	0.40
31:AG:560:ILE:HG22	31:AG:575:THR:HG22	2.03	0.40
34:B3:415:TRP:HA	34:B3:425:ASP:O	2.20	0.40
34:B3:690:HIS:CE1	41:5E:519:GLU:HA	2.57	0.40
35:B8:431:GLU:H	35:B8:431:GLU:HG2	1.71	0.40
37:B6:110:TRP:CD2	37:B6:136:LEU:HD13	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:5C:114:TYR:HA	39:5C:128:THR:O	2.22	0.40
48:RA:343:ILE:HG22	48:RA:346:LEU:H	1.87	0.40
51:RE:310:PRO:HA	51:RE:333:ASN:HD21	1.87	0.40
51:RE:1204:VAL:HG23	51:RE:1204:VAL:O	2.21	0.40
54:RJ:60:ASP:OD2	54:RJ:62:THR:OG1	2.32	0.40
54:RJ:74:VAL:HG11	54:RJ:82:LYS:HA	2.03	0.40
54:RJ:563:CYS:SG	55:RK:327:ARG:NH2	2.95	0.40
56:RL:60:LYS:HB3	56:RL:108:TYR:CD2	2.56	0.40
57:RN:424:LYS:O	57:RN:428:VAL:HG23	2.20	0.40
61:RS:446:GLN:HG2	61:RS:447:ARG:HE	1.86	0.40
1:3A:253:G:OP2	24:3H:95:ARG:NH1	2.54	0.40
3:SA:259:U:O2'	3:SA:261:U:OP2	2.32	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
3:SA:1464:G:H2'	3:SA:1465:C:C6	2.57	0.40
3:SA:1480:G:H2'	3:SA:1481:C:O4'	2.22	0.40
4:SC:87:ARG:NH1	4:SC:89:ASP:OD2	2.47	0.40
15:SX:66:ASN:OD1	15:SX:66:ASN:N	2.50	0.40
20:3B:227:PRO:HG2	20:3B:255:LEU:HB3	2.02	0.40
21:3D:86:LEU:HD21	21:3D:98:LEU:HD13	2.03	0.40
21:3D:315:LEU:HD12	21:3D:315:LEU:HA	1.90	0.40
22:3E:215:ARG:NH1	22:3E:244:GLY:O	2.54	0.40
22:3E:299:LEU:HD22	22:3E:320:LEU:HD23	2.03	0.40
22:3E:306:LEU:HG	22:3E:375:ALA:HB2	2.04	0.40
22:3E:359:ILE:HD13	22:3E:398:LEU:HD13	2.03	0.40
25:A4:442:VAL:O	25:A4:448:THR:OG1	2.26	0.40
30:AF:371:GLU:HG3	35:B8:287:SER:OG	2.21	0.40
31:AG:409:LYS:HG2	31:AG:489:ASN:HA	2.03	0.40
32:B1:382:THR:H	41:5E:481:PRO:HB3	1.87	0.40
32:B1:423:ARG:HD3	32:B1:423:ARG:HA	1.88	0.40
34:B3:189:HIS:NE2	34:B3:215:GLY:HA3	2.37	0.40
34:B3:393:SER:OG	34:B3:394:LEU:N	2.53	0.40
36:BE:366:MET:HE3	36:BE:366:MET:HB2	1.80	0.40
41:5E:448:LEU:HA	41:5E:451:LEU:HD23	2.02	0.40
42:5F:41:ARG:HA	42:5F:41:ARG:HD2	1.89	0.40
42:5F:102:THR:HG22	42:5F:104:SER:H	1.87	0.40
52:RF:47:SER:OG	52:RF:48:ASN:N	2.54	0.40
52:RF:71:VAL:HG11	52:RF:84:VAL:HG21	2.03	0.40
57:RN:572:LEU:HB3	57:RN:667:LEU:HD13	2.04	0.40
57:RN:710:ILE:HD13	57:RN:710:ILE:HA	1.91	0.40
58:RO:205:ASP:HA	58:RO:206:PRO:HD3	1.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:RO:326:LEU:HA	58:RO:326:LEU:HD12	1.90	0.40
58:RO:384:ALA:HA	58:RO:387:THR:HG22	2.03	0.40
1:3A:59:G:OP1	32:B1:573:ASN:ND2	2.43	0.40
3:SA:56:U:O2	3:SA:91:G:N2	2.54	0.40
3:SA:1071:U:H2'	3:SA:1072:C:C6	2.56	0.40
9:SJ:191:PHE:HA	9:SJ:194:ARG:HE	1.85	0.40
10:SK:37:LYS:O	44:5H:561:SER:OG	2.39	0.40
14:SR:47:LYS:HD2	14:SR:47:LYS:HA	1.93	0.40
17:SZ:13:ILE:HD11	17:SZ:22:GLN:HE21	1.85	0.40
21:3D:59:ALA:HB1	37:B6:292:TYR:HE1	1.87	0.40
23:3F:68:LYS:HE3	23:3F:68:LYS:HB2	1.93	0.40
26:A5:444:ALA:HB2	26:A5:452:LEU:HD12	2.03	0.40
29:AE:677:SER:HA	29:AE:678:PRO:HD3	1.98	0.40
30:AF:178:PRO:HD2	30:AF:223:PRO:HA	2.02	0.40
31:AG:865:LYS:HE2	31:AG:865:LYS:HB3	1.81	0.40
32:B1:103:LYS:HB3	32:B1:103:LYS:HE3	1.92	0.40
32:B1:298:LEU:HD12	41:5E:474:ILE:HG22	2.04	0.40
33:B2:85:LEU:HD12	33:B2:94:LEU:HD11	2.04	0.40
34:B3:51:LYS:H	34:B3:51:LYS:HG2	1.66	0.40
34:B3:698:LEU:HD23	34:B3:698:LEU:HA	1.92	0.40
39:5C:258:LEU:O	39:5C:267:LEU:N	2.54	0.40
39:5C:307:LYS:HA	39:5C:307:LYS:HD3	1.89	0.40
41:5E:384:ARG:HD2	43:5G:83:ILE:CG1	2.51	0.40
46:5J:121:LEU:HD22	46:5J:141:TRP:HH2	1.87	0.40
51:RE:883:LEU:HD22	51:RE:1051:LEU:HA	2.03	0.40
54:RJ:286:THR:H	54:RJ:298:VAL:HG12	1.86	0.40
59:RP:2009:LYS:HD3	59:RP:2009:LYS:HA	1.88	0.40
61:RS:258:VAL:O	61:RS:262:ALA:CB	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SC	228/255 (89%)	196 (86%)	32 (14%)	0	100	100
5	SF	227/261 (87%)	197 (87%)	29 (13%)	1 (0%)	30	67
6	SG	211/225 (94%)	195 (92%)	16 (8%)	0	100	100
7	SH	161/236 (68%)	143 (89%)	18 (11%)	0	100	100
8	SI	161/190 (85%)	143 (89%)	18 (11%)	0	100	100
9	SJ	162/200 (81%)	140 (86%)	22 (14%)	0	100	100
10	SK	169/197 (86%)	163 (96%)	6 (4%)	0	100	100
11	SM	119/156 (76%)	103 (87%)	16 (13%)	0	100	100
12	SO	132/151 (87%)	123 (93%)	9 (7%)	0	100	100
13	SP	116/137 (85%)	100 (86%)	15 (13%)	1 (1%)	14	51
14	SR	123/143 (86%)	112 (91%)	11 (9%)	0	100	100
15	SX	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
16	SY	101/145 (70%)	90 (89%)	11 (11%)	0	100	100
17	SZ	100/135 (74%)	87 (87%)	12 (12%)	1 (1%)	12	49
18	Sc	78/82 (95%)	69 (88%)	9 (12%)	0	100	100
19	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
20	3B	236/327 (72%)	222 (94%)	14 (6%)	0	100	100
20	3C	221/327 (68%)	207 (94%)	14 (6%)	0	100	100
21	3D	359/504 (71%)	346 (96%)	13 (4%)	0	100	100
22	3E	427/511 (84%)	387 (91%)	40 (9%)	0	100	100
23	3F	446/573 (78%)	403 (90%)	42 (9%)	1 (0%)	43	78
24	3G	119/126 (94%)	107 (90%)	11 (9%)	1 (1%)	16	54
24	3H	119/126 (94%)	111 (93%)	8 (7%)	0	100	100
25	A4	648/776 (84%)	590 (91%)	58 (9%)	0	100	100
26	A5	504/643 (78%)	465 (92%)	39 (8%)	0	100	100
27	A8	516/713 (72%)	397 (77%)	107 (21%)	12 (2%)	5	28
28	A9	126/575 (22%)	115 (91%)	11 (9%)	0	100	100
29	AE	1496/1769 (85%)	1367 (91%)	129 (9%)	0	100	100
30	AF	489/513 (95%)	442 (90%)	47 (10%)	0	100	100
31	AG	812/896 (91%)	731 (90%)	80 (10%)	1 (0%)	48	83
32	B1	787/923 (85%)	732 (93%)	55 (7%)	0	100	100
33	B2	813/943 (86%)	724 (89%)	87 (11%)	2 (0%)	43	78

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	B3	733/817 (90%)	606 (83%)	125 (17%)	2 (0%)	36	72
35	B8	469/594 (79%)	439 (94%)	30 (6%)	0	100	100
36	BE	814/939 (87%)	765 (94%)	49 (6%)	0	100	100
37	B6	368/440 (84%)	341 (93%)	27 (7%)	0	100	100
38	5B	58/214 (27%)	55 (95%)	3 (5%)	0	100	100
39	5C	452/554 (82%)	419 (93%)	32 (7%)	1 (0%)	43	78
40	5D	165/250 (66%)	145 (88%)	20 (12%)	0	100	100
41	5E	187/593 (32%)	175 (94%)	10 (5%)	2 (1%)	11	46
42	5F	180/183 (98%)	164 (91%)	16 (9%)	0	100	100
43	5G	217/290 (75%)	203 (94%)	14 (6%)	0	100	100
44	5H	72/610 (12%)	65 (90%)	7 (10%)	0	100	100
45	5I	457/489 (94%)	421 (92%)	36 (8%)	0	100	100
46	5J	147/217 (68%)	136 (92%)	11 (8%)	0	100	100
47	5K	171/189 (90%)	166 (97%)	5 (3%)	0	100	100
48	RA	332/707 (47%)	276 (83%)	56 (17%)	0	100	100
49	RB	132/357 (37%)	117 (89%)	14 (11%)	1 (1%)	16	54
50	RD	310/1729 (18%)	284 (92%)	23 (7%)	3 (1%)	12	49
51	RE	1067/1237 (86%)	999 (94%)	68 (6%)	0	100	100
52	RF	233/297 (78%)	203 (87%)	30 (13%)	0	100	100
53	RG	212/252 (84%)	182 (86%)	30 (14%)	0	100	100
53	RH	226/252 (90%)	219 (97%)	7 (3%)	0	100	100
54	RJ	784/1183 (66%)	721 (92%)	62 (8%)	1 (0%)	48	83
55	RK	358/367 (98%)	341 (95%)	17 (5%)	0	100	100
56	RL	781/1056 (74%)	664 (85%)	115 (15%)	2 (0%)	36	72
56	RM	738/1056 (70%)	625 (85%)	109 (15%)	4 (0%)	24	63
57	RN	593/810 (73%)	545 (92%)	47 (8%)	1 (0%)	43	78
58	RO	523/552 (95%)	455 (87%)	68 (13%)	0	100	100
59	RP	2042/2493 (82%)	1815 (89%)	226 (11%)	1 (0%)	100	100
60	RQ	220/899 (24%)	199 (90%)	21 (10%)	0	100	100
61	RS	247/483 (51%)	225 (91%)	22 (9%)	0	100	100
62	RT	163/326 (50%)	147 (90%)	16 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	RY	35/534 (7%)	29 (83%)	6 (17%)	0	100	100
All	All	23878/33924 (70%)	21529 (90%)	2311 (10%)	38 (0%)	44	78

All (38) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
27	A8	258	PRO
27	A8	309	PRO
27	A8	325	PRO
27	A8	390	PRO
27	A8	392	PRO
27	A8	446	VAL
27	A8	472	ILE
50	RD	1223	PRO
56	RL	744	PRO
56	RM	744	PRO
56	RM	905	PRO
17	SZ	51	GLU
54	RJ	82	LYS
27	A8	235	PRO
31	AG	434	GLN
33	B2	132	THR
34	B3	91	LYS
56	RM	904	LEU
57	RN	285	PRO
23	3F	552	TRP
27	A8	369	ILE
41	5E	476	MET
5	SF	194	THR
33	B2	118	ASN
41	5E	481	PRO
49	RB	274	ILE
50	RD	1204	VAL
50	RD	1222	LYS
56	RL	743	VAL
56	RM	743	VAL
13	SP	123	SER
27	A8	439	LYS
34	B3	71	PRO
39	5C	16	GLU
59	RP	2052	GLN
24	3G	10	PRO

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Mol	Chain	Res	Type
27	A8	306	ILE
27	A8	339	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	SC	203/224 (91%)	201 (99%)	2 (1%)	68	78
5	SF	196/222 (88%)	193 (98%)	3 (2%)	57	72
6	SG	180/191 (94%)	179 (99%)	1 (1%)	78	83
7	SH	139/201 (69%)	136 (98%)	3 (2%)	45	64
8	SI	146/170 (86%)	143 (98%)	3 (2%)	47	65
9	SJ	136/161 (84%)	134 (98%)	2 (2%)	57	72
10	SK	147/166 (89%)	147 (100%)	0	100	100
11	SM	110/137 (80%)	108 (98%)	2 (2%)	51	68
12	SO	117/128 (91%)	116 (99%)	1 (1%)	70	79
13	SP	90/105 (86%)	88 (98%)	2 (2%)	45	64
14	SR	105/119 (88%)	105 (100%)	0	100	100
15	SX	108/111 (97%)	106 (98%)	2 (2%)	50	67
16	SY	85/120 (71%)	83 (98%)	2 (2%)	43	64
17	SZ	85/113 (75%)	85 (100%)	0	100	100
18	Sc	69/71 (97%)	69 (100%)	0	100	100
19	Sd	56/60 (93%)	56 (100%)	0	100	100
20	3B	201/240 (84%)	201 (100%)	0	100	100
20	3C	190/240 (79%)	188 (99%)	2 (1%)	65	76
21	3D	296/435 (68%)	295 (100%)	1 (0%)	86	86
22	3E	262/433 (60%)	261 (100%)	1 (0%)	84	84
23	3F	396/503 (79%)	392 (99%)	4 (1%)	68	78
24	3G	100/104 (96%)	100 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	3H	100/104 (96%)	100 (100%)	0	100	100
25	A4	591/713 (83%)	584 (99%)	7 (1%)	63	75
26	A5	433/574 (75%)	429 (99%)	4 (1%)	70	79
27	A8	174/657 (26%)	168 (97%)	6 (3%)	32	54
28	A9	89/533 (17%)	89 (100%)	0	100	100
29	AE	708/1633 (43%)	705 (100%)	3 (0%)	84	84
30	AF	437/454 (96%)	431 (99%)	6 (1%)	59	72
31	AG	750/826 (91%)	739 (98%)	11 (2%)	57	72
32	B1	696/812 (86%)	685 (98%)	11 (2%)	55	70
33	B2	712/832 (86%)	705 (99%)	7 (1%)	68	78
34	B3	665/719 (92%)	656 (99%)	9 (1%)	59	72
35	B8	421/529 (80%)	417 (99%)	4 (1%)	68	78
36	BE	718/819 (88%)	712 (99%)	6 (1%)	73	80
37	B6	251/414 (61%)	249 (99%)	2 (1%)	73	80
38	5B	57/196 (29%)	56 (98%)	1 (2%)	51	68
39	5C	394/480 (82%)	392 (100%)	2 (0%)	81	83
40	5D	156/234 (67%)	156 (100%)	0	100	100
41	5E	175/535 (33%)	162 (93%)	13 (7%)	13	33
42	5F	171/172 (99%)	169 (99%)	2 (1%)	63	75
43	5G	194/258 (75%)	194 (100%)	0	100	100
44	5H	63/538 (12%)	63 (100%)	0	100	100
45	5I	416/443 (94%)	412 (99%)	4 (1%)	68	78
46	5J	140/200 (70%)	140 (100%)	0	100	100
47	5K	157/169 (93%)	157 (100%)	0	100	100
48	RA	303/636 (48%)	299 (99%)	4 (1%)	61	74
49	RB	117/315 (37%)	116 (99%)	1 (1%)	70	79
50	RD	226/1544 (15%)	224 (99%)	2 (1%)	70	79
51	RE	984/1125 (88%)	976 (99%)	8 (1%)	73	80
52	RF	221/274 (81%)	221 (100%)	0	100	100
53	RG	195/222 (88%)	193 (99%)	2 (1%)	68	78
53	RH	206/222 (93%)	205 (100%)	1 (0%)	81	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	RJ	683/1039 (66%)	678 (99%)	5 (1%)	76	81
55	RK	307/312 (98%)	304 (99%)	3 (1%)	68	78
56	RL	164/934 (18%)	164 (100%)	0	100	100
57	RN	422/732 (58%)	421 (100%)	1 (0%)	87	87
58	RO	329/506 (65%)	326 (99%)	3 (1%)	70	79
59	RP	499/2307 (22%)	496 (99%)	3 (1%)	78	83
60	RQ	148/808 (18%)	145 (98%)	3 (2%)	48	66
61	RS	225/424 (53%)	224 (100%)	1 (0%)	84	84
62	RT	146/282 (52%)	143 (98%)	3 (2%)	47	65
63	RY	31/482 (6%)	31 (100%)	0	100	100
All	All	17291/29262 (59%)	17122 (99%)	169 (1%)	65	78

All (169) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	SC	43	VAL
4	SC	172	LEU
5	SF	143	ASP
5	SF	183	VAL
5	SF	206	ASP
6	SG	149	VAL
7	SH	67	VAL
7	SH	71	THR
7	SH	113	ILE
8	SI	73	VAL
8	SI	140	VAL
8	SI	189	THR
9	SJ	104	ILE
9	SJ	165	LEU
11	SM	107	VAL
11	SM	135	VAL
12	SO	60	VAL
13	SP	42	VAL
13	SP	107	ARG
15	SX	11	LEU
15	SX	70	ASN
16	SY	97	ASP
16	SY	120	VAL

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Mol	Chain	Res	Type
20	3C	197	VAL
20	3C	237	VAL
21	3D	219	LEU
22	3E	371	LEU
23	3F	262	VAL
23	3F	273	VAL
23	3F	301	ASP
23	3F	408	VAL
25	A4	176	VAL
25	A4	190	VAL
25	A4	201	VAL
25	A4	282	ASP
25	A4	384	VAL
25	A4	391	VAL
25	A4	550	VAL
26	A5	95	VAL
26	A5	214	VAL
26	A5	357	VAL
26	A5	434	THR
27	A8	526	LEU
27	A8	563	LEU
27	A8	633	GLN
27	A8	634	LEU
27	A8	636	GLN
27	A8	637	LEU
29	AE	210	LEU
29	AE	227	ASN
29	AE	734	ILE
30	AF	107	VAL
30	AF	129	VAL
30	AF	218	VAL
30	AF	236	VAL
30	AF	261	VAL
30	AF	508	LEU
31	AG	109	VAL
31	AG	141	LEU
31	AG	259	VAL
31	AG	368	ASP
31	AG	391	VAL
31	AG	434	GLN
31	AG	435	ASP
31	AG	436	PHE

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Mol	Chain	Res	Type
31	AG	508	ILE
31	AG	547	VAL
31	AG	650	VAL
32	B1	89	VAL
32	B1	141	VAL
32	B1	164	THR
32	B1	215	VAL
32	B1	337	TYR
32	B1	351	LEU
32	B1	418	ARG
32	B1	497	ILE
32	B1	519	LEU
32	B1	530	VAL
32	B1	745	LEU
33	B2	47	GLU
33	B2	49	VAL
33	B2	144	ASN
33	B2	212	VAL
33	B2	332	ILE
33	B2	576	VAL
33	B2	588	ILE
34	B3	10	ILE
34	B3	32	LEU
34	B3	67	LEU
34	B3	95	VAL
34	B3	147	ILE
34	B3	212	LEU
34	B3	239	VAL
34	B3	570	THR
34	B3	731	LEU
35	B8	22	LEU
35	B8	146	LEU
35	B8	178	VAL
35	B8	544	VAL
36	BE	298	VAL
36	BE	309	ILE
36	BE	570	ILE
36	BE	600	ILE
36	BE	721	LEU
36	BE	740	ILE
37	B6	4	THR
37	B6	106	ASP

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Mol	Chain	Res	Type
38	5B	211	LEU
39	5C	153	THR
39	5C	392	VAL
41	5E	345	LEU
41	5E	365	LEU
41	5E	428	GLU
41	5E	439	GLU
41	5E	448	LEU
41	5E	451	LEU
41	5E	494	GLU
41	5E	515	MET
41	5E	516	SER
41	5E	517	LYS
41	5E	520	LEU
41	5E	537	SER
41	5E	538	LYS
42	5F	75	GLU
42	5F	124	ILE
45	5I	14	VAL
45	5I	113	VAL
45	5I	201	ILE
45	5I	351	VAL
48	RA	76	THR
48	RA	155	VAL
48	RA	231	VAL
48	RA	264	ILE
49	RB	338	THR
50	RD	1521	LEU
50	RD	1670	LYS
51	RE	102	ILE
51	RE	292	ILE
51	RE	560	ASN
51	RE	742	PHE
51	RE	753	ILE
51	RE	929	ILE
51	RE	1075	LEU
51	RE	1189	LEU
53	RG	32	THR
53	RG	100	LEU
53	RH	31	LEU
54	RJ	288	VAL
54	RJ	859	ILE

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Mol	Chain	Res	Type
54	RJ	869	THR
54	RJ	976	ILE
54	RJ	1069	VAL
55	RK	26	LEU
55	RK	90	CYS
55	RK	335	THR
57	RN	766	ARG
58	RO	471	GLU
58	RO	493	TYR
58	RO	504	ASP
59	RP	131	THR
59	RP	1770	LEU
59	RP	1896	ILE
60	RQ	330	THR
60	RQ	898	PHE
60	RQ	899	LYS
61	RS	326	VAL
62	RT	159	ILE
62	RT	237	PHE
62	RT	241	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (417) such sidechains are listed below:

Mol	Chain	Res	Type
4	SC	74	GLN
4	SC	92	GLN
4	SC	101	HIS
4	SC	194	ASN
6	SG	63	GLN
6	SG	66	GLN
6	SG	131	GLN
6	SG	169	ASN
7	SH	119	GLN
7	SH	140	ASN
8	SI	29	ASN
8	SI	42	GLN
8	SI	74	GLN
8	SI	122	HIS
8	SI	170	GLN
8	SI	174	ASN
8	SI	180	GLN
9	SJ	32	GLN

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Mol	Chain	Res	Type
9	SJ	103	GLN
9	SJ	159	GLN
10	SK	48	GLN
10	SK	142	ASN
11	SM	8	GLN
11	SM	81	HIS
11	SM	98	ASN
11	SM	106	ASN
12	SO	36	GLN
12	SO	58	HIS
13	SP	12	GLN
13	SP	24	ASN
14	SR	74	HIS
15	SX	12	ASN
15	SX	16	ASN
15	SX	120	HIS
16	SY	48	HIS
18	Sc	5	GLN
18	Sc	19	HIS
18	Sc	42	ASN
20	3B	91	HIS
20	3B	228	GLN
20	3C	264	GLN
21	3D	39	ASN
21	3D	85	ASN
21	3D	168	GLN
21	3D	172	ASN
21	3D	183	GLN
21	3D	213	ASN
21	3D	324	ASN
21	3D	398	ASN
22	3E	191	HIS
22	3E	256	ASN
22	3E	286	ASN
22	3E	289	GLN
22	3E	396	ASN
22	3E	400	GLN
23	3F	129	GLN
23	3F	155	ASN
23	3F	156	ASN
23	3F	164	GLN
23	3F	195	GLN

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Mol	Chain	Res	Type
23	3F	226	HIS
23	3F	525	GLN
23	3F	561	ASN
24	3G	29	ASN
24	3H	5	ASN
24	3H	18	GLN
24	3H	45	ASN
25	A4	140	ASN
25	A4	279	HIS
25	A4	292	ASN
25	A4	317	ASN
25	A4	331	ASN
25	A4	438	GLN
25	A4	467	ASN
25	A4	483	ASN
25	A4	529	ASN
25	A4	574	HIS
25	A4	589	ASN
25	A4	621	ASN
25	A4	731	HIS
26	A5	32	GLN
26	A5	67	ASN
26	A5	103	ASN
26	A5	133	GLN
26	A5	139	HIS
26	A5	302	ASN
26	A5	308	ASN
26	A5	316	ASN
26	A5	333	ASN
26	A5	527	HIS
27	A8	588	GLN
27	A8	677	ASN
28	A9	478	ASN
28	A9	509	GLN
29	AE	14	ASN
29	AE	96	ASN
29	AE	141	ASN
29	AE	166	ASN
29	AE	224	ASN
29	AE	258	HIS
29	AE	304	GLN
29	AE	477	ASN

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Mol	Chain	Res	Type
29	AE	480	ASN
29	AE	545	ASN
29	AE	673	ASN
29	AE	698	ASN
29	AE	730	GLN
30	AF	18	GLN
30	AF	48	ASN
30	AF	125	HIS
30	AF	133	HIS
30	AF	135	GLN
30	AF	137	ASN
30	AF	156	ASN
30	AF	217	ASN
30	AF	250	ASN
30	AF	269	GLN
30	AF	289	ASN
30	AF	419	GLN
30	AF	481	GLN
30	AF	496	HIS
31	AG	50	ASN
31	AG	105	HIS
31	AG	131	HIS
31	AG	166	ASN
31	AG	184	GLN
31	AG	190	GLN
31	AG	266	ASN
31	AG	269	GLN
31	AG	289	GLN
31	AG	325	GLN
31	AG	332	GLN
31	AG	370	GLN
31	AG	393	ASN
31	AG	407	ASN
31	AG	410	ASN
31	AG	418	ASN
31	AG	453	HIS
31	AG	467	GLN
31	AG	489	ASN
31	AG	568	ASN
31	AG	579	ASN
31	AG	603	ASN
31	AG	605	ASN

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Mol	Chain	Res	Type
31	AG	669	ASN
31	AG	706	HIS
31	AG	719	ASN
31	AG	880	GLN
32	B1	57	ASN
32	B1	92	HIS
32	B1	142	HIS
32	B1	201	HIS
32	B1	254	HIS
32	B1	297	GLN
32	B1	303	ASN
32	B1	349	ASN
32	B1	386	HIS
32	B1	452	ASN
32	B1	456	HIS
32	B1	461	GLN
32	B1	483	GLN
32	B1	549	GLN
32	B1	552	ASN
32	B1	707	ASN
32	B1	734	GLN
32	B1	752	ASN
32	B1	813	HIS
32	B1	837	ASN
32	B1	842	ASN
33	B2	172	GLN
33	B2	327	HIS
33	B2	390	GLN
33	B2	455	GLN
33	B2	523	HIS
33	B2	524	HIS
33	B2	656	HIS
33	B2	657	GLN
33	B2	770	ASN
33	B2	856	ASN
33	B2	871	GLN
33	B2	881	ASN
34	B3	81	GLN
34	B3	187	GLN
34	B3	241	GLN
34	B3	309	GLN
34	B3	312	GLN

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Mol	Chain	Res	Type
34	B3	337	HIS
34	B3	358	ASN
34	B3	387	HIS
34	B3	478	GLN
34	B3	495	ASN
34	B3	519	ASN
34	B3	522	ASN
34	B3	642	GLN
34	B3	667	GLN
34	B3	735	GLN
34	B3	747	ASN
34	B3	749	ASN
34	B3	753	HIS
34	B3	767	HIS
34	B3	792	HIS
35	B8	151	ASN
35	B8	162	ASN
35	B8	167	GLN
35	B8	224	ASN
35	B8	276	HIS
35	B8	282	ASN
35	B8	308	ASN
35	B8	322	HIS
35	B8	352	GLN
35	B8	472	GLN
35	B8	492	ASN
35	B8	498	ASN
35	B8	528	GLN
35	B8	592	ASN
35	B8	593	HIS
36	BE	32	ASN
36	BE	64	ASN
36	BE	120	HIS
36	BE	163	GLN
36	BE	248	GLN
36	BE	289	ASN
36	BE	305	ASN
36	BE	349	HIS
36	BE	362	GLN
36	BE	447	ASN
36	BE	481	ASN
36	BE	501	HIS

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Mol	Chain	Res	Type
36	BE	514	ASN
36	BE	627	ASN
36	BE	708	ASN
36	BE	736	HIS
36	BE	826	GLN
36	BE	877	ASN
36	BE	911	ASN
37	B6	62	ASN
37	B6	64	ASN
37	B6	90	GLN
37	B6	115	ASN
37	B6	166	ASN
37	B6	169	GLN
37	B6	287	ASN
37	B6	289	HIS
38	5B	207	ASN
39	5C	101	ASN
39	5C	124	HIS
39	5C	133	HIS
39	5C	143	GLN
39	5C	151	ASN
39	5C	155	HIS
39	5C	164	GLN
39	5C	170	GLN
39	5C	185	HIS
39	5C	308	GLN
39	5C	371	HIS
39	5C	394	HIS
40	5D	42	HIS
40	5D	68	HIS
40	5D	144	ASN
40	5D	153	ASN
41	5E	303	GLN
41	5E	434	HIS
41	5E	455	HIS
41	5E	493	GLN
42	5F	7	HIS
42	5F	27	HIS
42	5F	48	ASN
42	5F	144	ASN
42	5F	153	ASN
43	5G	118	ASN

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Mol	Chain	Res	Type
43	5G	145	HIS
43	5G	164	GLN
43	5G	182	GLN
43	5G	188	HIS
43	5G	211	ASN
43	5G	235	GLN
44	5H	560	ASN
45	5I	20	GLN
45	5I	46	ASN
45	5I	81	ASN
45	5I	109	HIS
45	5I	242	ASN
45	5I	260	GLN
45	5I	276	ASN
45	5I	281	ASN
45	5I	336	HIS
45	5I	371	ASN
45	5I	406	HIS
45	5I	418	HIS
45	5I	421	GLN
45	5I	427	GLN
46	5J	53	GLN
46	5J	135	HIS
46	5J	184	ASN
46	5J	192	ASN
46	5J	195	GLN
47	5K	29	GLN
48	RA	60	ASN
48	RA	82	HIS
48	RA	96	HIS
48	RA	118	GLN
48	RA	119	ASN
48	RA	147	ASN
48	RA	230	GLN
48	RA	268	GLN
48	RA	282	ASN
49	RB	314	ASN
49	RB	318	ASN
50	RD	1473	ASN
50	RD	1522	ASN
50	RD	1525	ASN
50	RD	1626	GLN

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Mol	Chain	Res	Type
51	RE	136	GLN
51	RE	170	GLN
51	RE	237	HIS
51	RE	293	ASN
51	RE	342	HIS
51	RE	344	ASN
51	RE	402	ASN
51	RE	409	ASN
51	RE	506	GLN
51	RE	520	ASN
51	RE	537	ASN
51	RE	568	ASN
51	RE	602	ASN
51	RE	683	ASN
51	RE	729	ASN
51	RE	767	GLN
51	RE	834	ASN
51	RE	841	ASN
51	RE	869	ASN
51	RE	872	ASN
51	RE	956	ASN
51	RE	969	ASN
51	RE	1029	ASN
51	RE	1073	ASN
51	RE	1078	HIS
51	RE	1086	ASN
51	RE	1194	HIS
51	RE	1199	ASN
51	RE	1203	ASN
51	RE	1215	ASN
51	RE	1228	ASN
52	RF	23	HIS
52	RF	73	GLN
52	RF	135	ASN
52	RF	136	ASN
52	RF	187	HIS
52	RF	197	GLN
52	RF	261	GLN
53	RG	105	ASN
53	RG	125	ASN
53	RH	69	ASN
53	RH	74	GLN

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Mol	Chain	Res	Type
53	RH	105	ASN
53	RH	125	ASN
53	RH	250	ASN
54	RJ	126	ASN
54	RJ	157	ASN
54	RJ	254	HIS
54	RJ	289	HIS
54	RJ	761	GLN
54	RJ	778	GLN
54	RJ	944	ASN
54	RJ	1082	GLN
54	RJ	1151	GLN
55	RK	16	ASN
55	RK	61	ASN
55	RK	317	GLN
55	RK	334	ASN
56	RL	16	ASN
56	RL	75	ASN
56	RL	117	ASN
56	RL	133	ASN
57	RN	8	ASN
57	RN	56	ASN
57	RN	89	GLN
57	RN	432	HIS
57	RN	495	ASN
57	RN	683	ASN
57	RN	686	ASN
57	RN	703	GLN
57	RN	705	HIS
57	RN	713	HIS
57	RN	771	ASN
57	RN	797	ASN
58	RO	192	GLN
58	RO	249	ASN
58	RO	266	ASN
58	RO	268	GLN
58	RO	273	GLN
58	RO	304	ASN
58	RO	306	GLN
58	RO	343	GLN
58	RO	370	HIS
58	RO	434	ASN

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Mol	Chain	Res	Type
58	RO	449	HIS
58	RO	472	HIS
58	RO	474	HIS
59	RP	58	ASN
59	RP	153	ASN
59	RP	1686	GLN
59	RP	1702	HIS
59	RP	1707	HIS
59	RP	1785	ASN
59	RP	1802	HIS
59	RP	1803	ASN
59	RP	1816	HIS
59	RP	2045	GLN
60	RQ	344	GLN
60	RQ	836	ASN
60	RQ	867	GLN
61	RS	241	ASN
61	RS	276	GLN
61	RS	300	ASN
62	RT	218	ASN
63	RY	469	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	169/333 (50%)	55 (32%)	8 (4%)
2	5A	186/700 (26%)	54 (29%)	4 (2%)
3	SA	1262/1809 (69%)	483 (38%)	19 (1%)
All	All	1617/2842 (56%)	592 (36%)	31 (1%)

All (592) RNA backbone outliers are listed below:

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

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Mol	Chain	Res	Type
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	97	C
1	3A	98	U
1	3A	99	U
1	3A	101	G
1	3A	103	A
1	3A	111	G
1	3A	115	G
1	3A	198	U
1	3A	199	G
1	3A	201	C
1	3A	204	U
1	3A	205	G
1	3A	206	C
1	3A	246	A
1	3A	248	G
1	3A	249	G
1	3A	252	C
1	3A	264	C
1	3A	267	A
1	3A	305	G
1	3A	310	G
1	3A	311	G
1	3A	313	A
1	3A	314	C
1	3A	317	A
1	3A	318	U
1	3A	319	G
1	3A	320	G
1	3A	321	C
1	3A	322	A
1	3A	323	G

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

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Mol	Chain	Res	Type
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
3	SA	23	G
3	SA	25	C
3	SA	26	A
3	SA	29	U
3	SA	35	U
3	SA	36	C
3	SA	37	U
3	SA	50	C
3	SA	51	A
3	SA	52	U
3	SA	53	G
3	SA	55	A
3	SA	56	U
3	SA	57	G

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Mol	Chain	Res	Type
3	SA	60	U
3	SA	61	A
3	SA	63	G
3	SA	65	A
3	SA	66	U
3	SA	67	A
3	SA	68	A
3	SA	69	G
3	SA	72	A
3	SA	73	U
3	SA	74	U
3	SA	75	U
3	SA	77	U
3	SA	81	G
3	SA	85	A
3	SA	92	A
3	SA	95	G
3	SA	96	G
3	SA	97	C
3	SA	100	A
3	SA	102	U
3	SA	103	A
3	SA	104	A
3	SA	105	A
3	SA	106	U
3	SA	114	C
3	SA	115	G
3	SA	116	U
3	SA	119	A
3	SA	127	G
3	SA	128	U
3	SA	129	U
3	SA	130	C
3	SA	131	C
3	SA	141	U
3	SA	145	A
3	SA	146	U
3	SA	147	A
3	SA	149	C
3	SA	153	G
3	SA	159	U
3	SA	160	C

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Mol	Chain	Res	Type
3	SA	161	U
3	SA	168	A
3	SA	174	U
3	SA	175	G
3	SA	176	C
3	SA	177	U
3	SA	182	A
3	SA	183	U
3	SA	184	C
3	SA	187	G
3	SA	188	A
3	SA	190	C
3	SA	191	C
3	SA	192	U
3	SA	193	U
3	SA	194	U
3	SA	195	G
3	SA	197	A
3	SA	202	A
3	SA	203	U
3	SA	204	G
3	SA	206	A
3	SA	210	A
3	SA	211	U
3	SA	214	G
3	SA	226	A
3	SA	228	G
3	SA	230	C
3	SA	233	C
3	SA	234	G
3	SA	236	A
3	SA	237	C
3	SA	238	U
3	SA	239	C
3	SA	240	U
3	SA	241	U
3	SA	242	U
3	SA	243	G
3	SA	254	A
3	SA	256	A
3	SA	258	C
3	SA	261	U

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Mol	Chain	Res	Type
3	SA	262	U
3	SA	265	A
3	SA	266	A
3	SA	267	U
3	SA	272	U
3	SA	273	G
3	SA	275	C
3	SA	276	C
3	SA	277	U
3	SA	278	U
3	SA	279	G
3	SA	280	U
3	SA	281	G
3	SA	283	U
3	SA	290	G
3	SA	308	C
3	SA	309	C
3	SA	311	U
3	SA	312	A
3	SA	316	A
3	SA	319	U
3	SA	320	U
3	SA	321	C
3	SA	324	U
3	SA	325	G
3	SA	333	A
3	SA	334	G
3	SA	337	G
3	SA	338	C
3	SA	350	U
3	SA	352	A
3	SA	355	G
3	SA	357	G
3	SA	359	A
3	SA	360	A
3	SA	361	C
3	SA	362	G
3	SA	365	G
3	SA	366	A
3	SA	369	A
3	SA	371	G
3	SA	373	G

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Mol	Chain	Res	Type
3	SA	374	U
3	SA	375	U
3	SA	377	G
3	SA	379	U
3	SA	382	C
3	SA	383	G
3	SA	386	G
3	SA	387	A
3	SA	390	G
3	SA	400	A
3	SA	401	A
3	SA	402	C
3	SA	403	G
3	SA	411	C
3	SA	416	A
3	SA	417	A
3	SA	418	G
3	SA	419	G
3	SA	421	A
3	SA	422	G
3	SA	423	G
3	SA	424	C
3	SA	425	A
3	SA	426	G
3	SA	429	G
3	SA	436	A
3	SA	437	A
3	SA	439	U
3	SA	440	U
3	SA	441	A
3	SA	444	C
3	SA	445	A
3	SA	448	C
3	SA	454	U
3	SA	455	C
3	SA	456	A
3	SA	457	G
3	SA	468	A
3	SA	469	C
3	SA	470	A
3	SA	471	A
3	SA	473	A

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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	644	C
3	SA	648	G
3	SA	652	G
3	SA	654	C
3	SA	656	G
3	SA	657	U
3	SA	658	C
3	SA	677	G
3	SA	678	A
3	SA	686	C
3	SA	687	G
3	SA	688	G
3	SA	689	G
3	SA	691	C
3	SA	692	C
3	SA	827	C
3	SA	828	U
3	SA	840	U
3	SA	841	U
3	SA	848	C
3	SA	859	A
3	SA	860	U
3	SA	863	A
3	SA	864	U
3	SA	865	A
3	SA	873	U
3	SA	877	G
3	SA	894	U
3	SA	901	G
3	SA	904	G
3	SA	906	A

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Mol	Chain	Res	Type
3	SA	912	U
3	SA	913	G
3	SA	914	G
3	SA	926	A
3	SA	930	A
3	SA	933	A
3	SA	934	C
3	SA	935	U
3	SA	945	U
3	SA	951	A
3	SA	953	G
3	SA	960	U
3	SA	966	A
3	SA	969	C
3	SA	970	A
3	SA	1037	C
3	SA	1039	A
3	SA	1040	G
3	SA	1052	U
3	SA	1053	G
3	SA	1056	U
3	SA	1057	U
3	SA	1059	U
3	SA	1060	U
3	SA	1062	A
3	SA	1063	U
3	SA	1076	A
3	SA	1079	U
3	SA	1081	A
3	SA	1082	C
3	SA	1084	A
3	SA	1085	G
3	SA	1086	A
3	SA	1106	U
3	SA	1107	G
3	SA	1108	G
3	SA	1109	G
3	SA	1110	G
3	SA	1111	G
3	SA	1114	G
3	SA	1118	G
3	SA	1119	G

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Mol	Chain	Res	Type
3	SA	1122	G
3	SA	1125	A
3	SA	1126	G
3	SA	1127	G
3	SA	1128	C
3	SA	1129	U
3	SA	1131	A
3	SA	1132	A
3	SA	1145	U
3	SA	1146	G
3	SA	1158	C
3	SA	1164	G
3	SA	1178	G
3	SA	1191	U
3	SA	1192	C
3	SA	1193	A
3	SA	1195	C
3	SA	1196	A
3	SA	1197	C
3	SA	1198	G
3	SA	1199	G
3	SA	1200	G
3	SA	1201	G
3	SA	1202	A
3	SA	1205	C
3	SA	1206	U
3	SA	1208	A
3	SA	1210	C
3	SA	1213	G
3	SA	1217	A
3	SA	1218	G
3	SA	1219	A
3	SA	1220	C
3	SA	1223	A
3	SA	1227	A
3	SA	1228	G
3	SA	1229	G
3	SA	1230	A
3	SA	1232	U
3	SA	1233	G
3	SA	1235	C
3	SA	1236	A

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Mol	Chain	Res	Type
3	SA	1252	C
3	SA	1253	U
3	SA	1254	U
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	1522	U
3	SA	1523	G
3	SA	1524	A
3	SA	1527	C
3	SA	1533	C
3	SA	1535	U
3	SA	1536	G
3	SA	1537	C
3	SA	1539	G
3	SA	1569	A

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Mol	Chain	Res	Type
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	1651	A
3	SA	1655	A
3	SA	1657	U
3	SA	1658	G
3	SA	1659	A
3	SA	1661	U
3	SA	1665	U
3	SA	1670	G
3	SA	1675	C
3	SA	1677	C
3	SA	1679	G
3	SA	1680	G
3	SA	1681	A
3	SA	1682	U
3	SA	1683	C
3	SA	1687	U
3	SA	1689	A
3	SA	1692	G
3	SA	1693	A
3	SA	1696	G
3	SA	1697	G
3	SA	1700	C
3	SA	1708	U
3	SA	1709	C
3	SA	1710	U
3	SA	1711	C

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Mol	Chain	Res	Type
3	SA	1713	G
3	SA	1717	G
3	SA	1718	G
3	SA	1719	A
3	SA	1721	A
3	SA	1724	U
3	SA	1725	U
3	SA	1727	G
3	SA	1728	A
3	SA	1731	A
3	SA	1732	A
3	SA	1736	G
3	SA	1737	G
3	SA	1742	U
3	SA	1743	U
3	SA	1745	G
3	SA	1749	A
3	SA	1750	A
3	SA	1755	A
3	SA	1756	A
3	SA	1757	G
3	SA	1758	U
3	SA	1768	G
3	SA	1769	U
3	SA	1771	U
3	SA	1780	G
3	SA	1781	A
3	SA	1782	A
3	SA	1783	C
3	SA	1792	G
3	SA	1793	G
3	SA	1794	A
3	SA	1795	U
3	SA	1797	A
3	SA	1798	U
3	SA	1799	U
3	SA	1800	A
3	SA	1801	A

All (31) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
1	3A	97	C
1	3A	98	U
1	3A	198	U
1	3A	248	G
1	3A	312	U
1	3A	318	U
1	3A	322	A
1	3A	323	G
2	5A	312	U
2	5A	487	A
2	5A	492	G
2	5A	536	A
3	SA	-7	A
3	SA	0	U
3	SA	56	U
3	SA	68	A
3	SA	272	U
3	SA	372	G
3	SA	401	A
3	SA	417	A
3	SA	538	A
3	SA	542	A
3	SA	579	A
3	SA	602	U
3	SA	1052	U
3	SA	1084	A
3	SA	1197	C
3	SA	1521	G
3	SA	1594	G
3	SA	1632	C
3	SA	1781	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
66	GTP	RJ	1201	67	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
66	GTP	RJ	1201	67	-	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(°)
66	RJ	1201	GTP	C4'-O4'-C1'	-2.15	104.72	109.47

There are no chirality outliers.

All (3) torsion outliers are listed below:

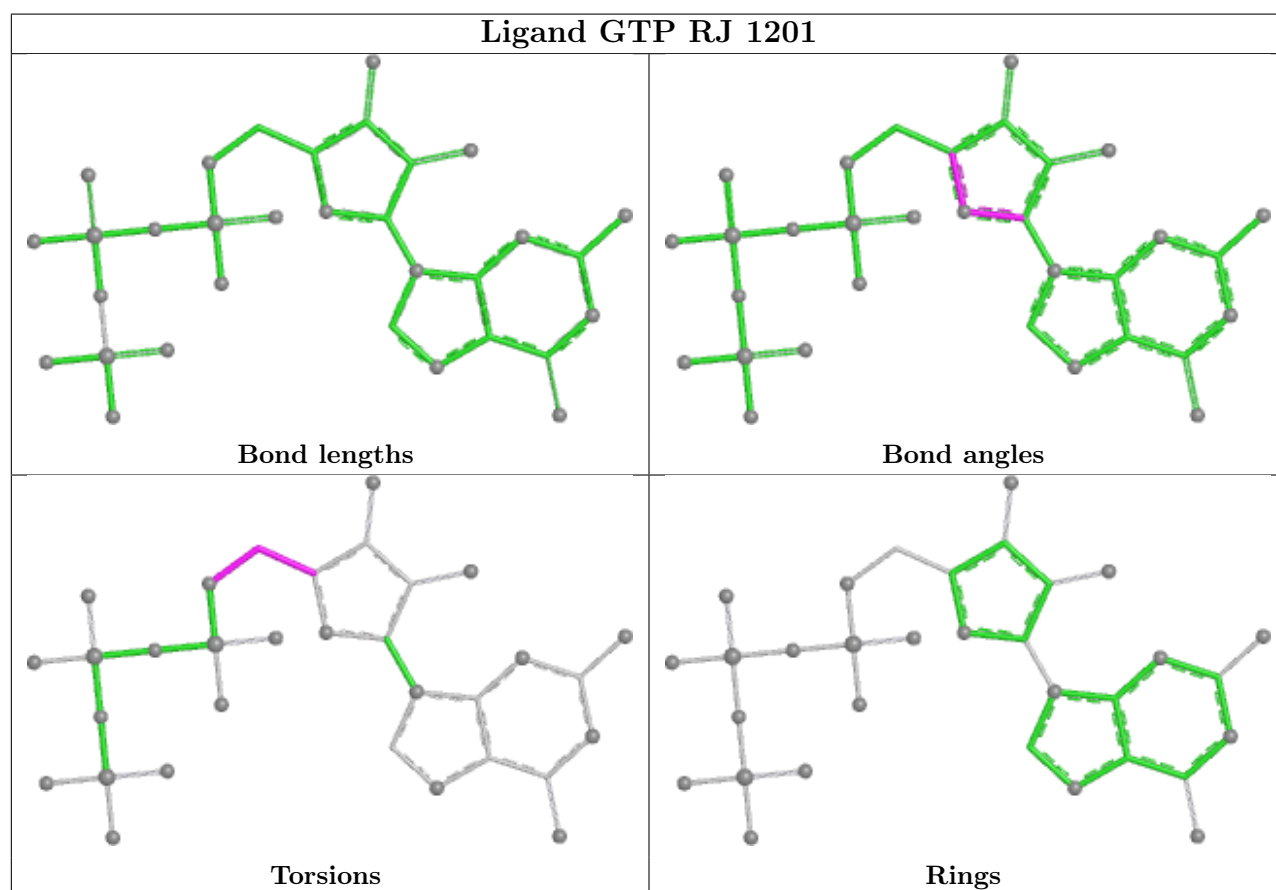
Mol	Chain	Res	Type	Atoms
66	RJ	1201	GTP	O4'-C4'-C5'-O5'
66	RJ	1201	GTP	C3'-C4'-C5'-O5'
66	RJ	1201	GTP	C4'-C5'-O5'-PA

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	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 [i](#)

There are no chain breaks in this entry.

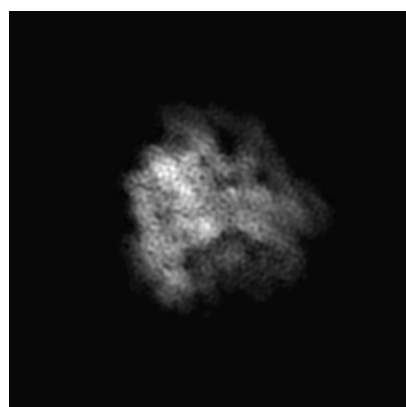
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0951. These allow visual inspection of the internal detail of the map and identification of artifacts.

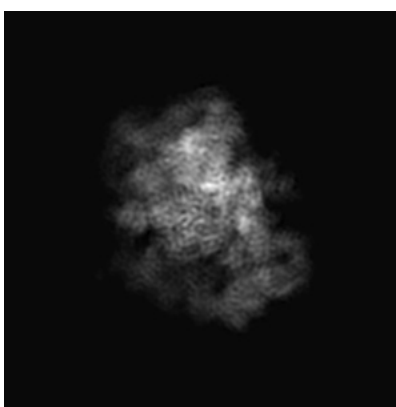
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

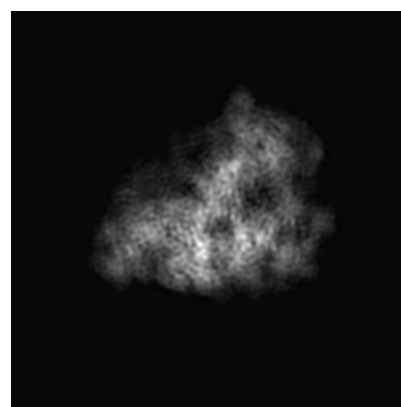
6.1.1 Primary map



X



Y

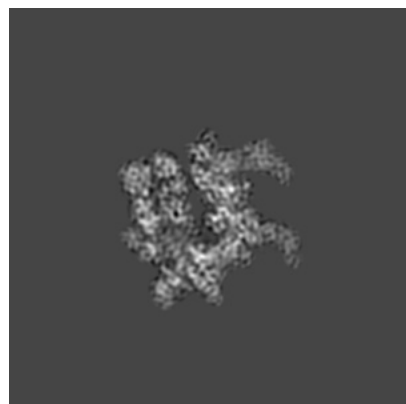


Z

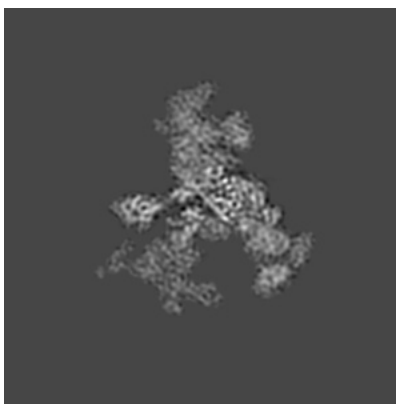
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

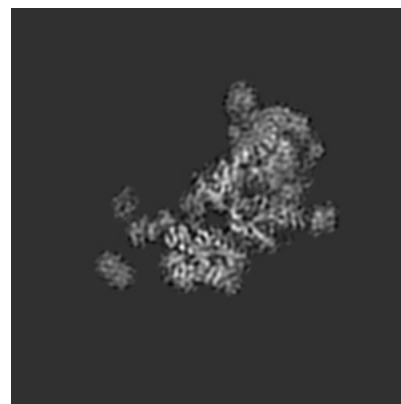
6.2.1 Primary map



X Index: 224



Y Index: 224

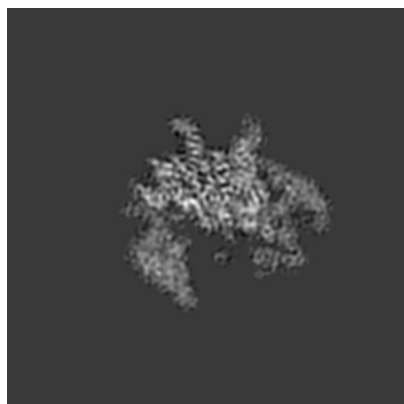


Z Index: 224

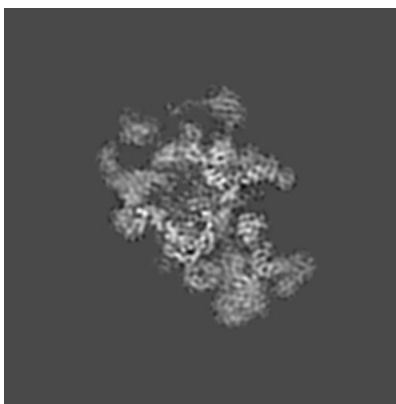
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

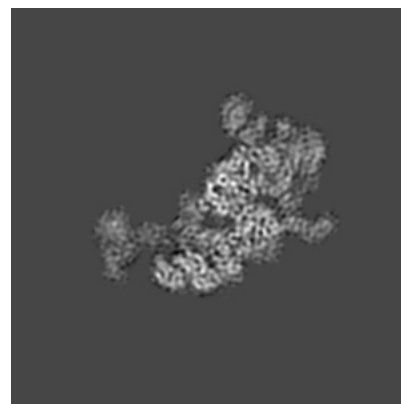
6.3.1 Primary map



X Index: 252



Y Index: 194

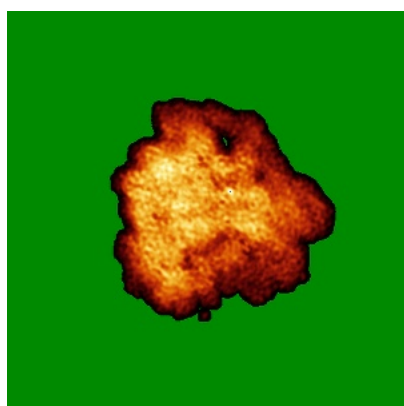


Z Index: 243

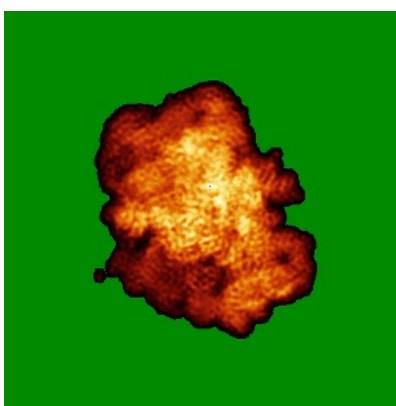
The images above show the largest variance slices of the map in three orthogonal directions.

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

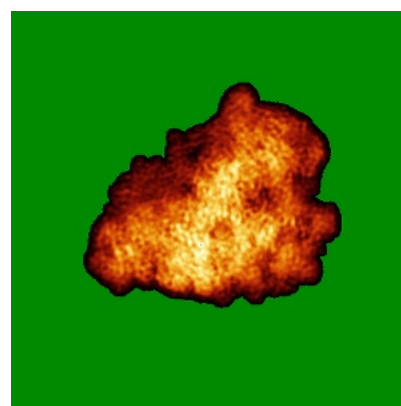
6.4.1 Primary map



X



Y

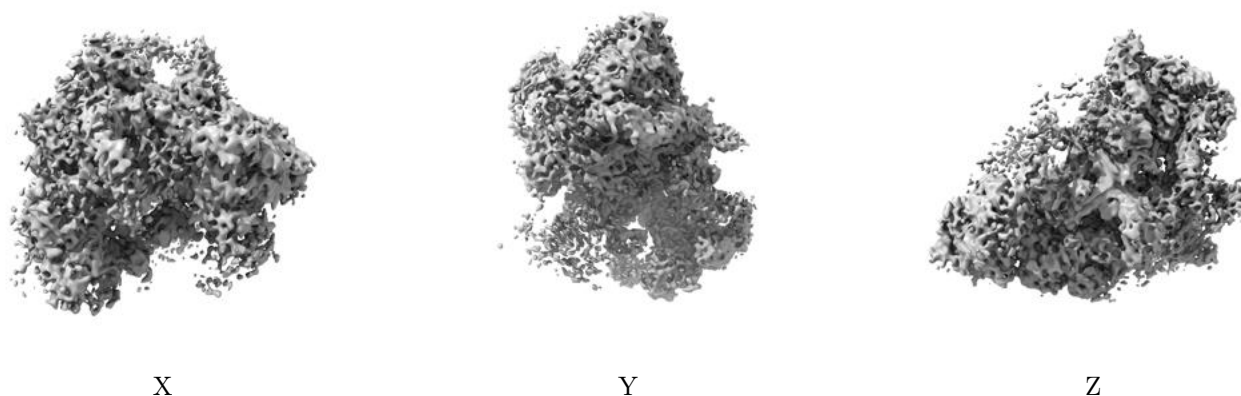


Z

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 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

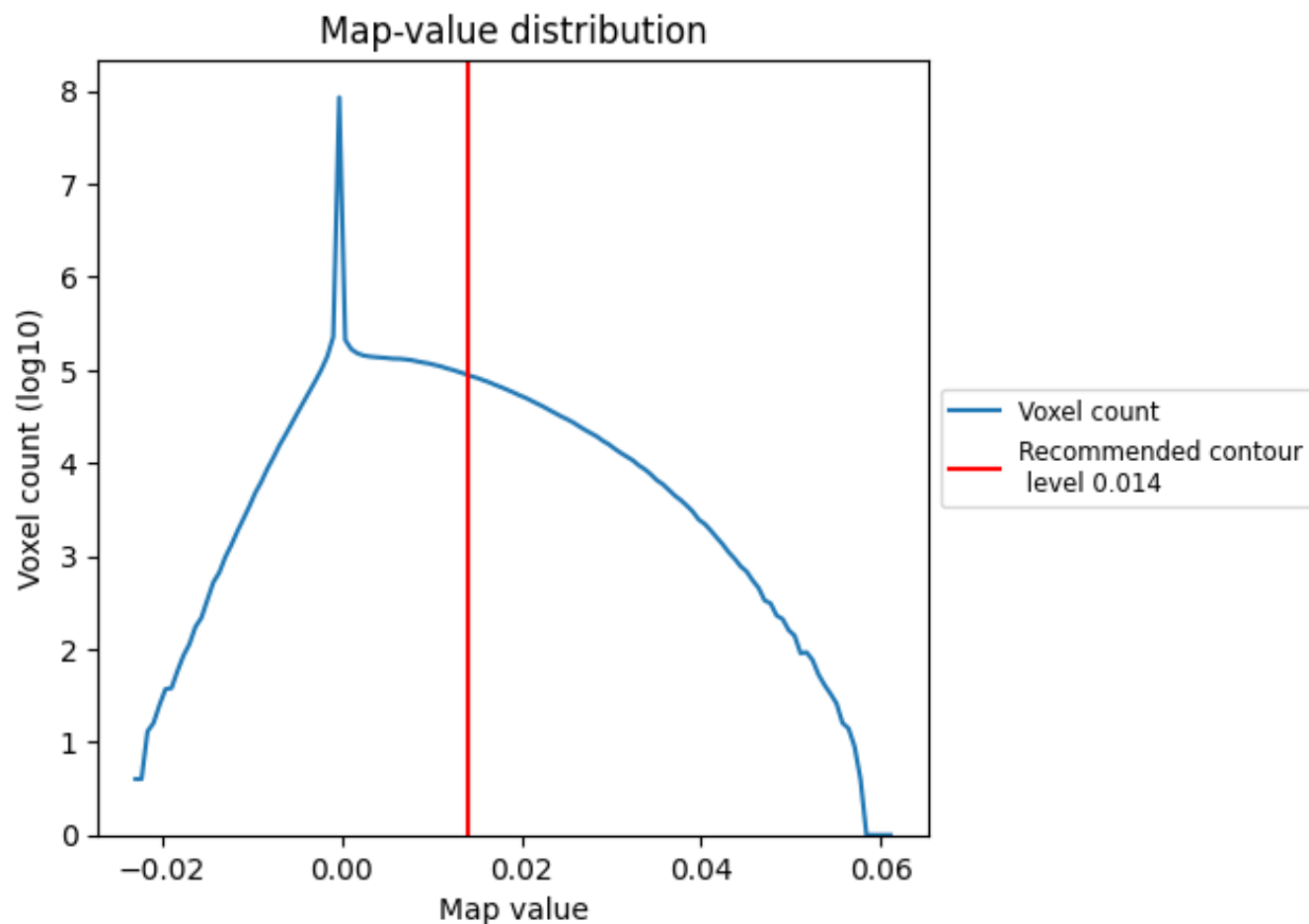
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

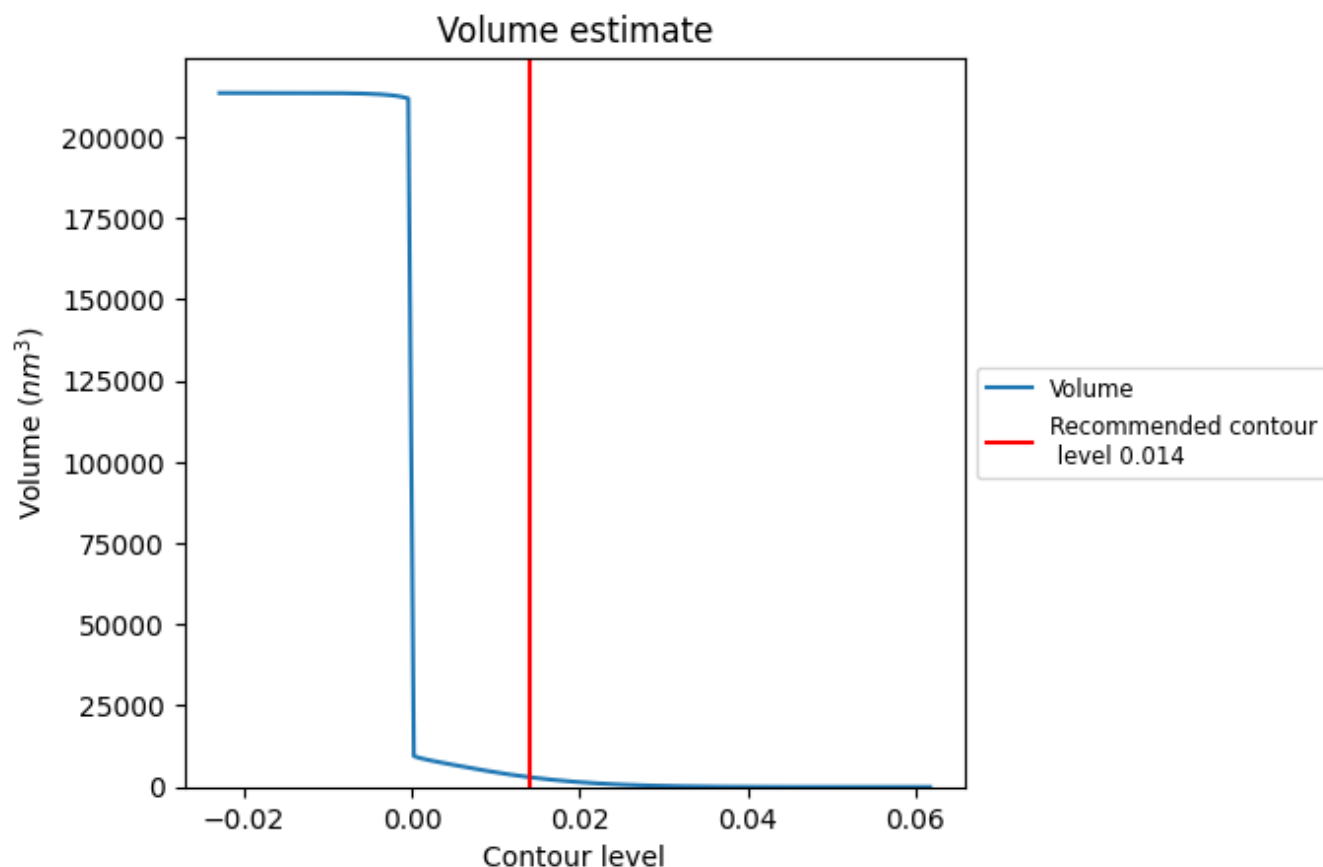
This section contains the results of statistical analysis of the map.

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.

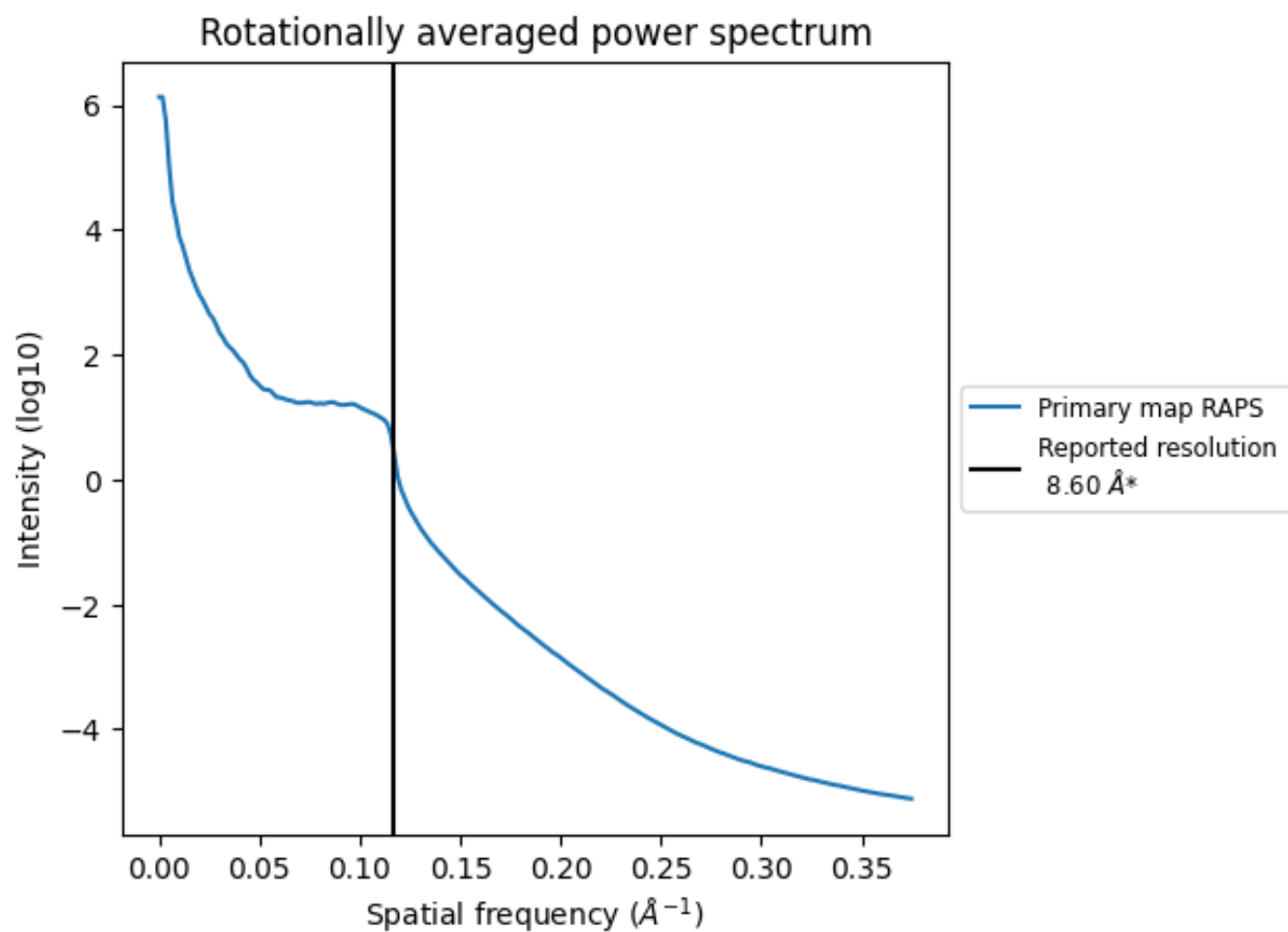
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3008 nm³; this corresponds to an approximate mass of 2717 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.116 Å⁻¹

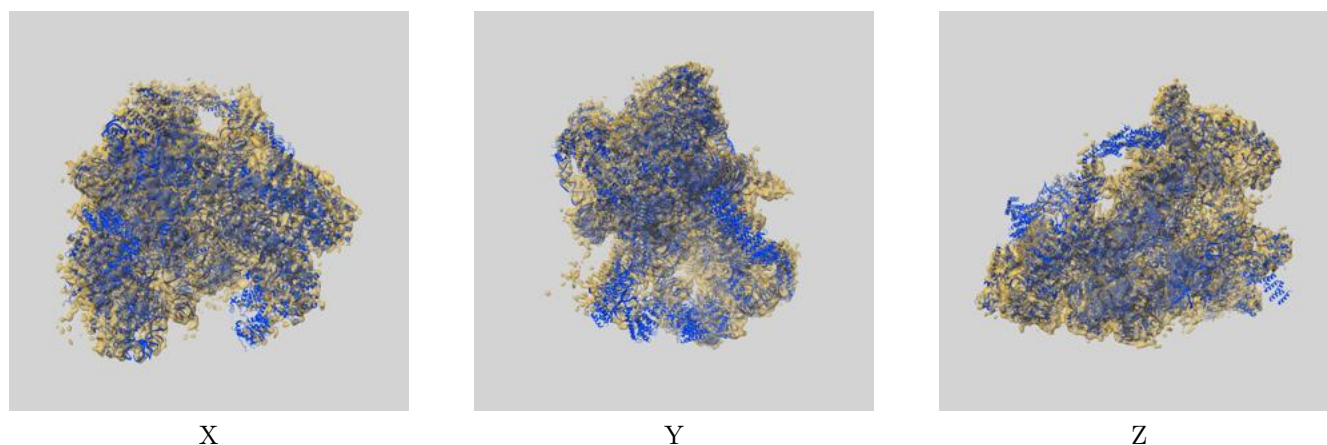
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

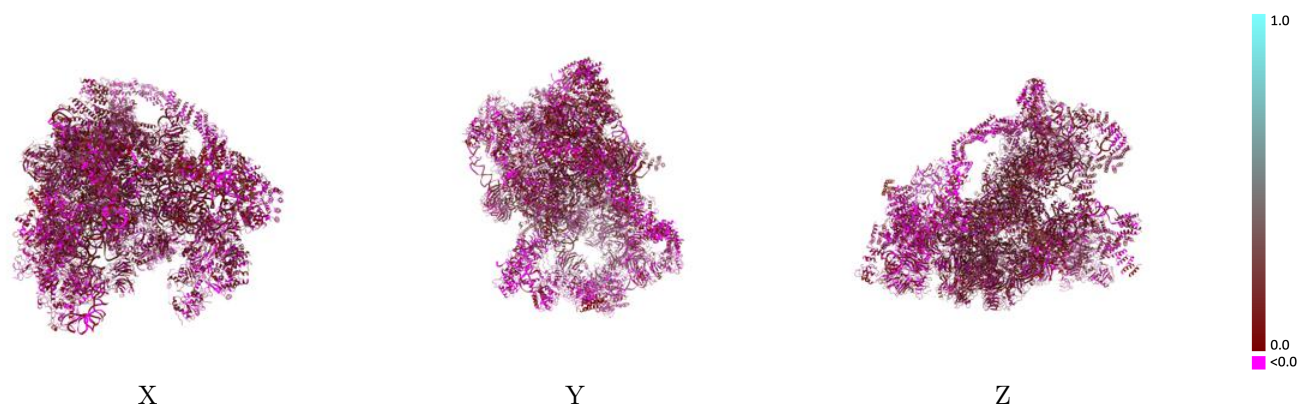
This section contains information regarding the fit between EMDB map EMD-0951 and PDB model 6LQR. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



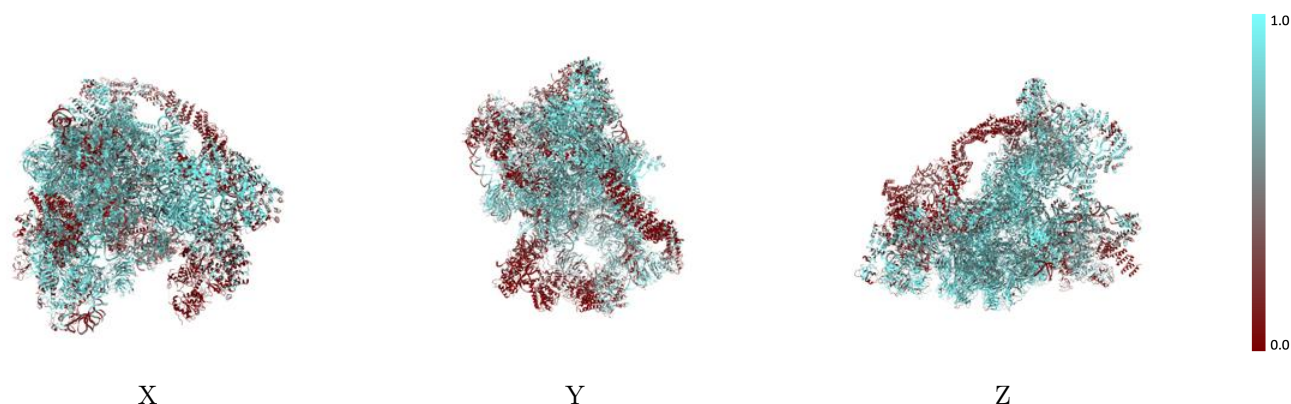
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



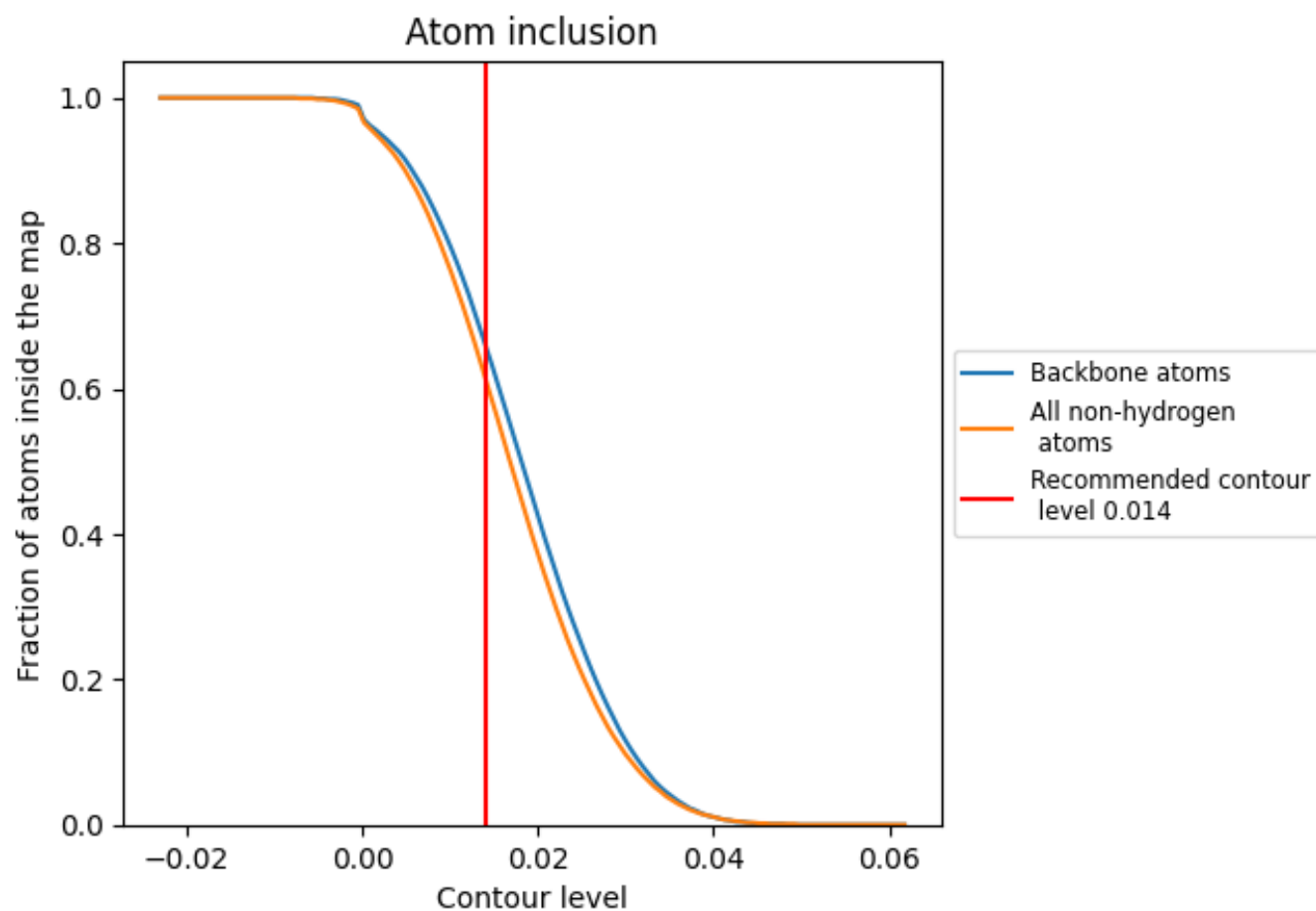
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 62% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6160	 0.0800
3A	 0.9100	 0.1510
3B	 0.7970	 0.1140
3C	 0.6800	 0.0660
3D	 0.8060	 0.1300
3E	 0.6940	 0.0930
3F	 0.8070	 0.1120
3G	 0.7630	 0.1090
3H	 0.7880	 0.1290
5A	 0.5880	 0.0630
5B	 0.1210	 0.0310
5C	 0.7700	 0.1040
5D	 0.4060	 0.0490
5E	 0.7420	 0.1350
5F	 0.7360	 0.1260
5G	 0.6730	 0.0950
5H	 0.7540	 0.1070
5I	 0.8410	 0.1040
5J	 0.5670	 0.0960
5K	 0.7420	 0.1100
A4	 0.6850	 0.0470
A5	 0.6060	 0.0740
A8	 0.5480	 0.0590
A9	 0.4820	 0.0400
AE	 0.3840	 0.0540
AF	 0.4860	 0.0490
AG	 0.6670	 0.0340
B1	 0.8250	 0.1060
B2	 0.7950	 0.0960
B3	 0.7850	 0.0710
B6	 0.7680	 0.1260
B8	 0.7800	 0.0970
BE	 0.8310	 0.1070
RA	 0.5970	 0.0600
RB	 0.7440	 0.1240



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Chain	Atom inclusion	Q-score
RD	 0.0800	 0.0120
RE	 0.5560	 0.0610
RF	 0.3930	 0.0800
RG	 0.1280	 0.0160
RH	 0.1390	 0.0120
RJ	 0.7030	 0.1020
RK	 0.7460	 0.1140
RL	 0.3280	 0.0860
RM	 0.1560	 0.0450
RN	 0.1110	 0.0080
RO	 0.0220	 -0.0030
RP	 0.6090	 0.0830
RQ	 0.5520	 0.0900
RS	 0.0450	 -0.0100
RT	 0.4820	 0.0510
RY	 0.3750	 0.0560
SA	 0.7140	 0.1010
SC	 0.5150	 0.0690
SF	 0.7690	 0.0950
SG	 0.7890	 0.1220
SH	 0.5730	 0.0710
SI	 0.6500	 0.1140
SJ	 0.7190	 0.0430
SK	 0.7950	 0.1150
SM	 0.8200	 0.0610
SO	 0.6930	 0.0860
SP	 0.6230	 0.0520
SR	 0.7910	 0.1080
SX	 0.5930	 0.1030
SY	 0.6430	 0.0990
SZ	 0.7610	 0.1050
Sc	 0.5460	 0.0810
Sd	 0.7760	 0.1250
X1	 0.5360	 0.0930