



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2014 – 03:56 PM GMT

PDB ID : 4KD2

Title : 70S RIBOSOME TRANSLOCATION INTERMEDIATE GDPNP-I CONTAINING ELONGATION FACTOR EFG/GDPNP, MRNA, AND TRNA BOUND IN THE  $pe^*/E$  STATE. THIS ENTRY CONTAINS THE 50S RIBOSOMAL SUBUNIT B. THE 30S SUBUNIT B CAN BE FOUND IN 4KD0. MOLECULE A IN THE SAME ASYMMETRIC UNIT IS DEPOSITED AS 4KCY (30S) AND 4KCZ (50S).

Authors : Zhou, J.; Lancaster, L.; Donohue, J.P.; Noller, H.F.

Deposited on : 2013-04-24

Resolution : 3.50 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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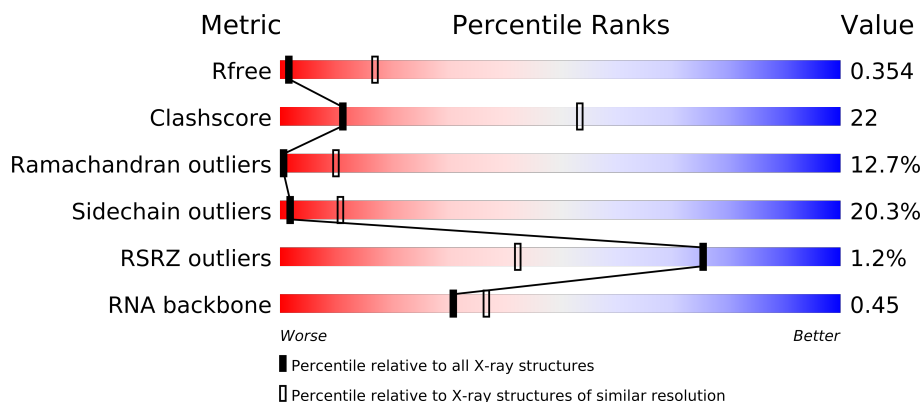
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.50 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1243 (3.70-3.30)
Clashscore	79885	1039 (3.66-3.34)
Ramachandran outliers	78287	1000 (3.66-3.34)
Sidechain outliers	78261	1000 (3.66-3.34)
RSRZ outliers	66119	1243 (3.70-3.30)
RNA backbone	1838	1007 (4.22-2.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	C	228	
2	D	275	
3	E	205	
4	F	208	
5	G	181	
6	H	167	
7	J	170	
8	K	140	
9	N	138	
10	O	122	
11	P	146	
12	Q	141	

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Mol	Chain	Length	Quality of chain
13	R	117	
14	S	99	
15	T	138	
16	U	117	
17	V	101	
18	W	113	
19	X	93	
20	Y	107	
21	Z	185	
22	0	84	
23	2	71	
24	3	60	
25	5	59	
26	6	50	
27	7	49	
28	8	64	
29	9	37	
30	f	31	
30	g	31	
31	h	30	
32	1	93	
33	4	35	
34	e	102	
35	A	2879	
36	B	119	

## 2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 95124 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	228	Total	C	N	O	S	0	0	0
			1742	1101	319	319	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	20	VAL	ILE	CONFLICT	UNP Q72GV9
C	28	ARG	HIS	CONFLICT	UNP Q72GV9

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	275	Total	C	N	O	S	0	0	0
			2145	1353	428	361	3			

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	205	Total	C	N	O	S	0	0	0
			1569	991	300	272	6			

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	208	Total	C	N	O	S	0	0	0
			1628	1037	304	284	3			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	2	LYS	-	INSERTION	UNP Q72I05
F	3	GLU	-	INSERTION	UNP Q72I05

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Chain	Residue	Modelled	Actual	Comment	Reference
F	4	VAL	-	INSERTION	UNP Q72I05
F	5	ALA	-	INSERTION	UNP Q72I05
F	6	VAL	-	INSERTION	UNP Q72I05

- Molecule 5 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	5	VAL	LEU	CONFLICT	UNP Q72I16

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	167	Total	C	N	O	S	0	0	0
			1274	806	238	229	1			

- Molecule 7 is a protein called 50S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	J	170	Total	C	N	O		0	0	0
			851	510	170	171				

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	K	140	Total	C	N	O	S	0	0	0
			1035	659	183	188	5			

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	N	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	69	ILE	VAL	CONFLICT	UNP Q72I14

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	P	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	Q	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	32	TYR	PHE	CONFLICT	UNP Q72I11

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	R	117	Total	C	N	O		0	0	0
			960	599	202	159				

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	S	99	Total	C	N	O		0	0	0
			775	488	155	132				

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	T	138	Total	C	N	O	S	0	0	0
			1147	713	235	198	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	123	GLN	LYS	CONFLICT	UNP Q72JU9
T	135	ALA	VAL	CONFLICT	UNP Q72JU9

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	U	117	Total	C	N	O	S	0	0	0
			964	610	202	151	1			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	V	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	W	113	Total	C	N	O	S	0	0	0
			900	566	177	155	2			

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	X	93	Total	C	N	O	S	0	0	0
			734	477	132	125				

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	Y	107	Total	C	N	O	S	0	0	0
			818	524	155	134	5			

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	Z	185	Total	C	N	O	S	0	0	0
			1473	939	262	270	2			

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	0	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	11	ARG	LYS	CONFLICT	UNP Q72HR3

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	2	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	3	60	Total	C	N	O	S	0	0	0
			477	303	91	82	1			

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	29	THR	ILE	CONFLICT	UNP P62652

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	6	50	Total	C	N	O	S	0	0	0
			433	270	88	71	4			

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	7	49	Total	C	N	O	S	0	0	0
			430	263	108	57	2			



- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 30 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
30	f	31	Total	C	N	O	0	0	0
			156	93	31	32			
30	g	31	Total	C	N	O	0	0	0
			156	93	31	32			

- Molecule 31 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
31	h	30	Total	C	N	O	0	0	0
			151	90	30	31			

- Molecule 32 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	1	93	Total	C	N	O	S	0	0	0
			732	460	145	126	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	81	LYS	ARG	CONFLICT	UNP Q72G84

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	4	35	Total	C	N	O	S	0	0	0
			271	174	44	50	3			

- Molecule 34 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
34	e	102	Total	C	N	O	0	0	0
			686	430	119	137			

- Molecule 35 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	A	2879	Total	C	N	O	P	0	0	0
			61997	27594	11582	19943	2878			

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

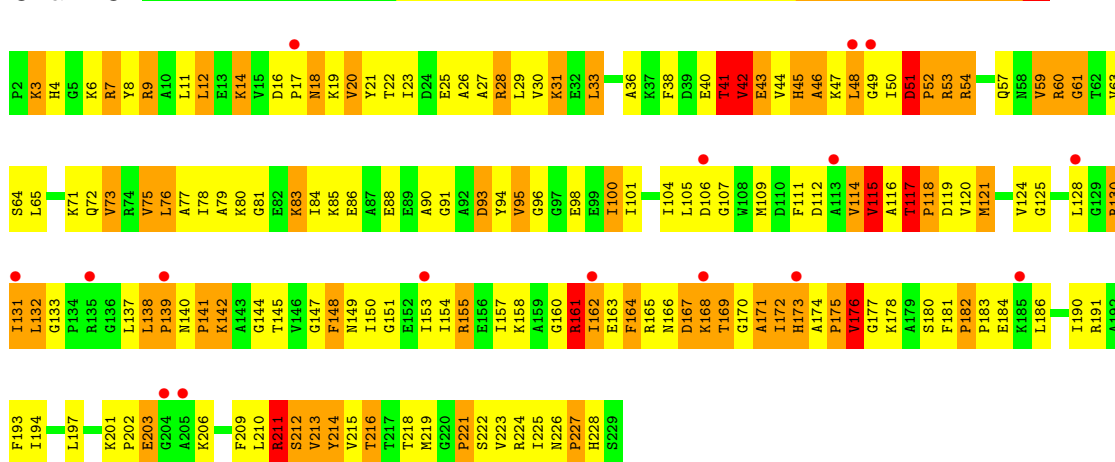
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	B	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

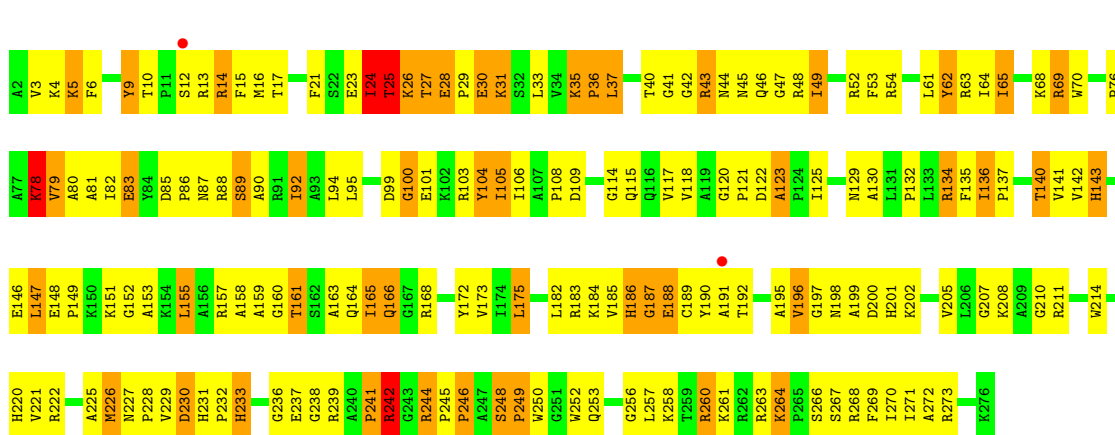
- Molecule 1: 50S ribosomal protein L1

Chain C:



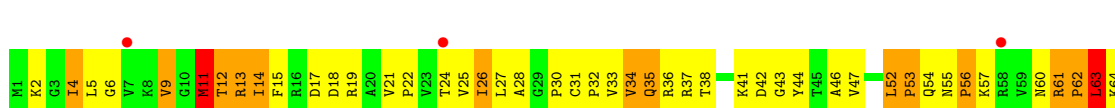
- Molecule 2: 50S ribosomal protein L2

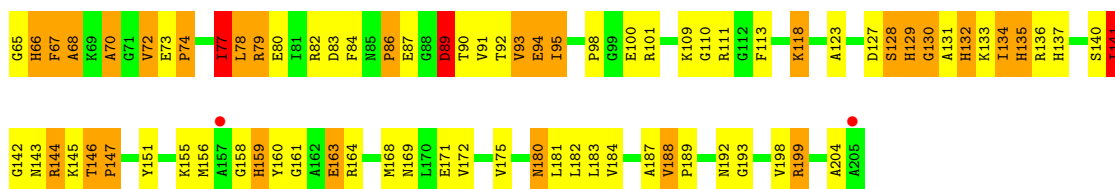
Chain D:



- Molecule 3: 50S ribosomal protein L3

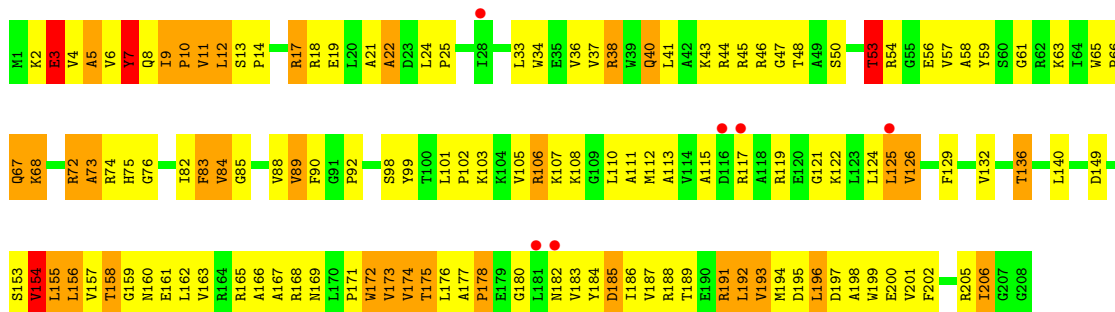
Chain E:





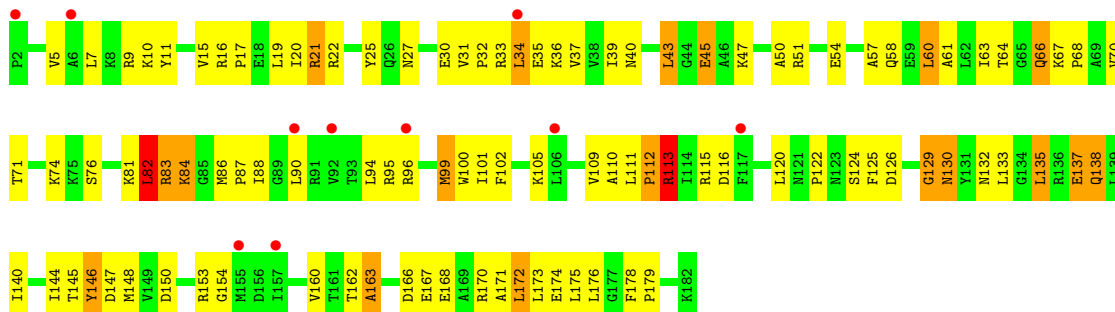
• Molecule 4: 50S ribosomal protein L4

Chain F:



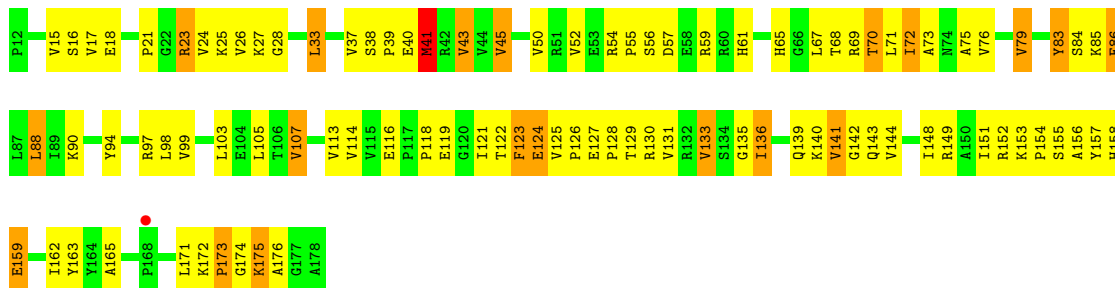
• Molecule 5: 50S ribosomal protein L5

Chain G:



• Molecule 6: 50S ribosomal protein L6

Chain H:

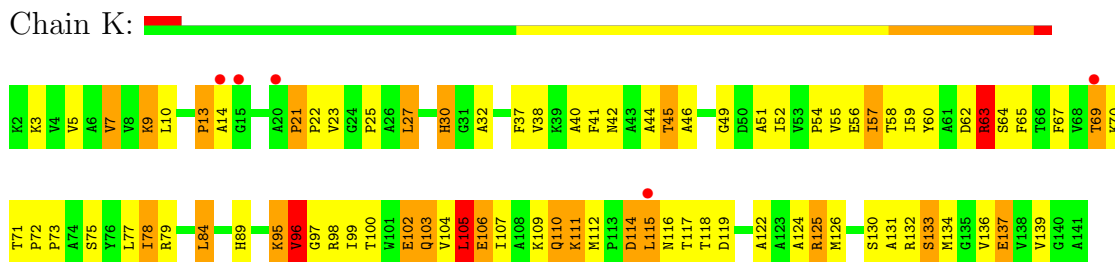


• Molecule 7: 50S RIBOSOMAL PROTEIN L10

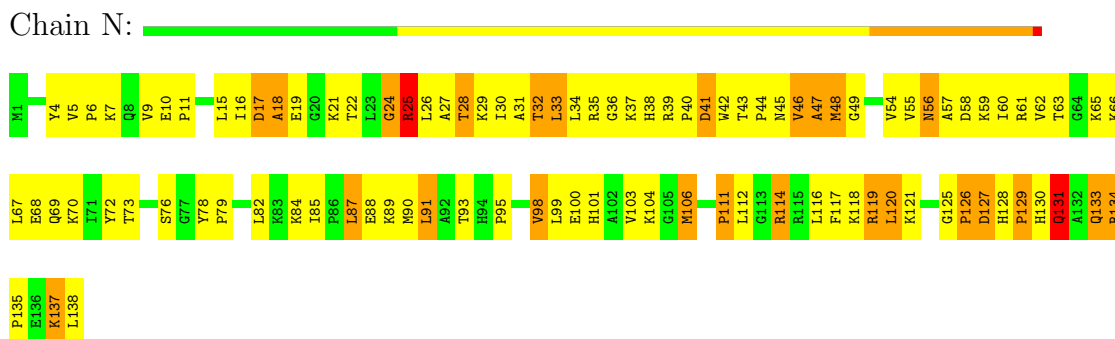
Chain J:



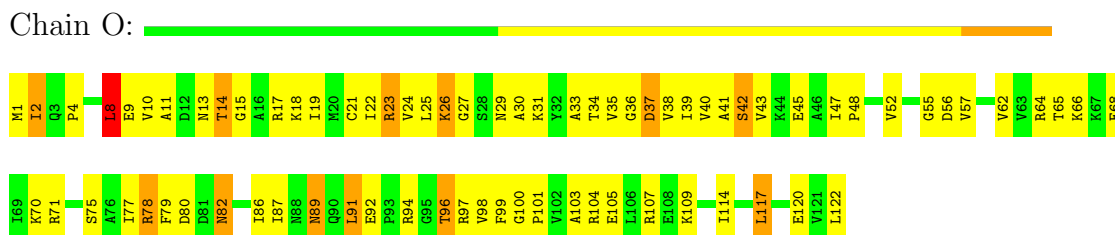
- Molecule 8: 50S ribosomal protein L11



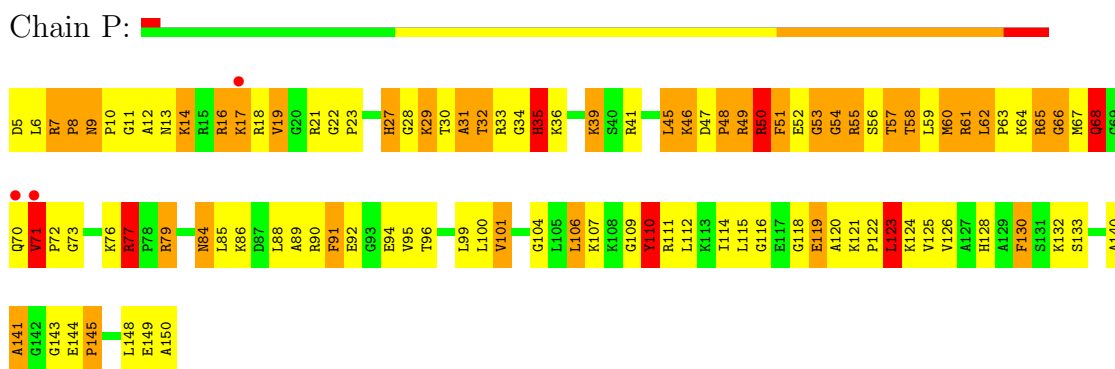
- Molecule 9: 50S ribosomal protein L13



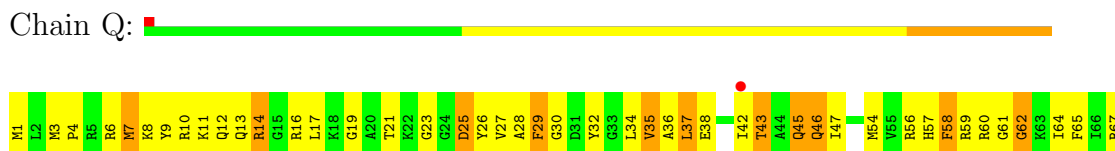
- Molecule 10: 50S ribosomal protein L14

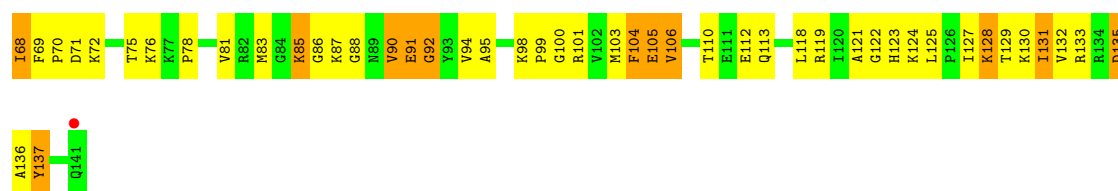


- Molecule 11: 50S ribosomal protein L15



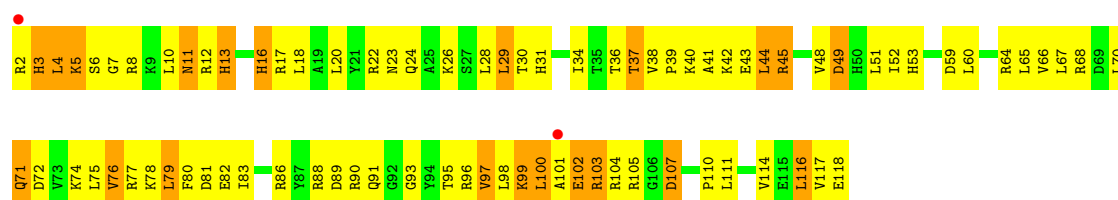
- Molecule 12: 50S ribosomal protein L16





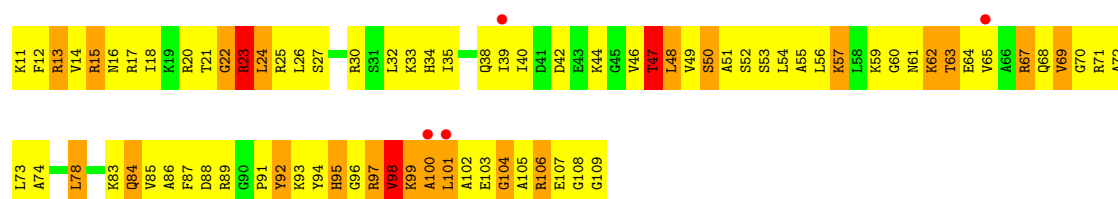
• Molecule 13: 50S ribosomal protein L17

Chain R:



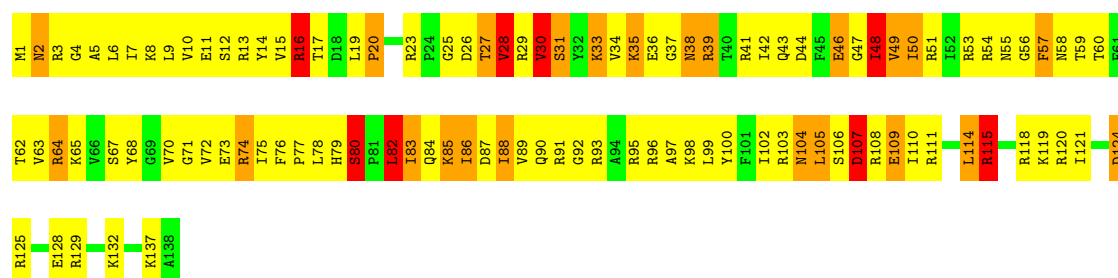
• Molecule 14: 50S ribosomal protein L18

Chain S:



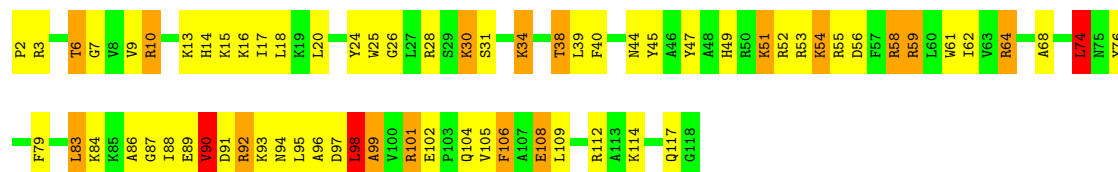
• Molecule 15: 50S ribosomal protein L19

Chain T:



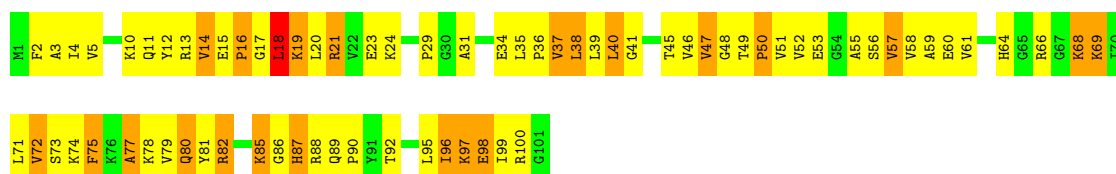
• Molecule 16: 50S ribosomal protein L20

Chain U:



• Molecule 17: 50S ribosomal protein L21

Chain V:



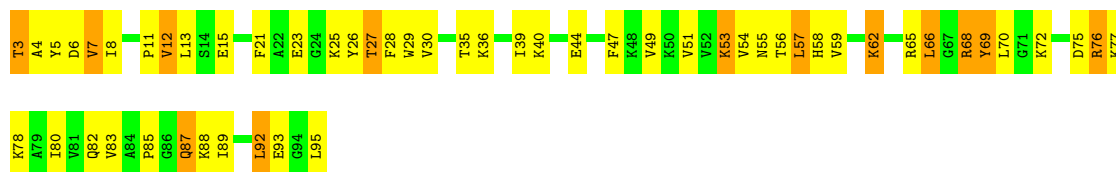
- Molecule 18: 50S ribosomal protein L22

Chain W:



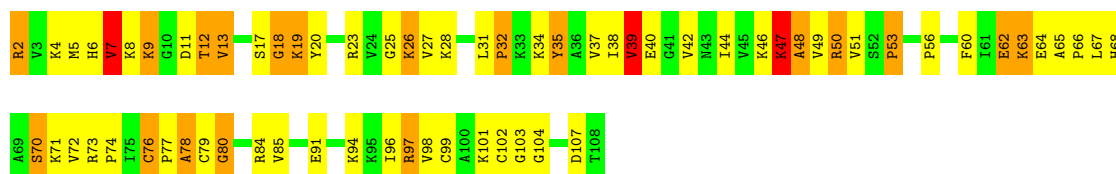
- Molecule 19: 50S ribosomal protein L23

Chain X:



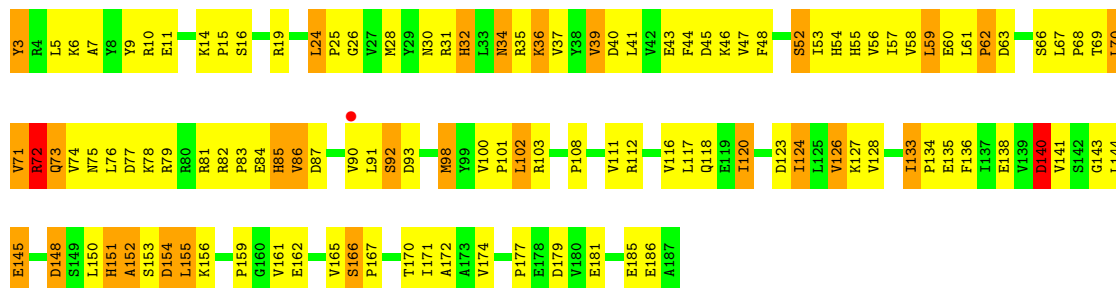
- Molecule 20: 50S ribosomal protein L24

Chain Y:



- Molecule 21: 50S ribosomal protein L25

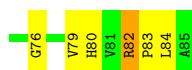
Chain Z:



- Molecule 22: 50S ribosomal protein L27

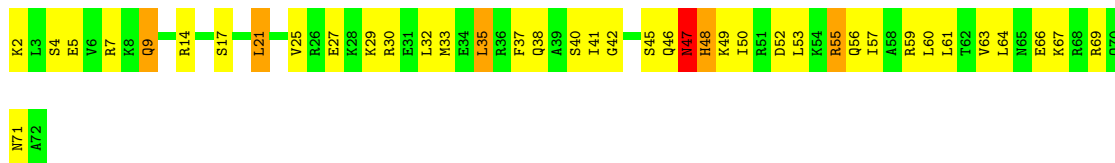
Chain 0:





- Molecule 23: 50S ribosomal protein L29

Chain 2:



- Molecule 24: 50S ribosomal protein L30

Chain 3:



- Molecule 25: 50S ribosomal protein L32

Chain 5:



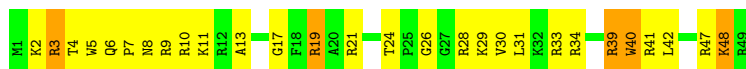
- Molecule 26: 50S ribosomal protein L33

Chain 6:



- Molecule 27: 50S ribosomal protein L34

Chain 7:



- Molecule 28: 50S ribosomal protein L35

Chain 8:



- Molecule 29: 50S ribosomal protein L36

Chain 9:



- Molecule 30: 50S ribosomal protein L7/L12



Chain f: \_\_\_\_\_

There are no outlier residues recorded for this chain.

- Molecule 30: 50S ribosomal protein L7/L12

Chain g: 

There are no outlier residues recorded for this chain.

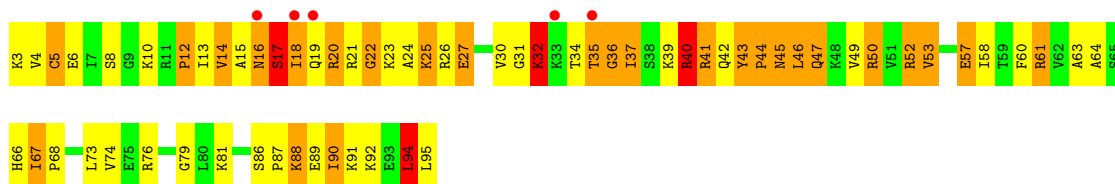
- Molecule 31: 50S ribosomal protein L7/L12

Chain h: 

There are no outlier residues recorded for this chain.

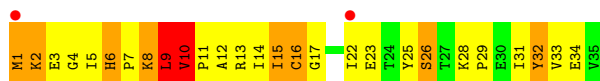
- Molecule 32: 50S ribosomal protein L28

Chain 1: 



- Molecule 33: 50S ribosomal protein L31

Chain 4:



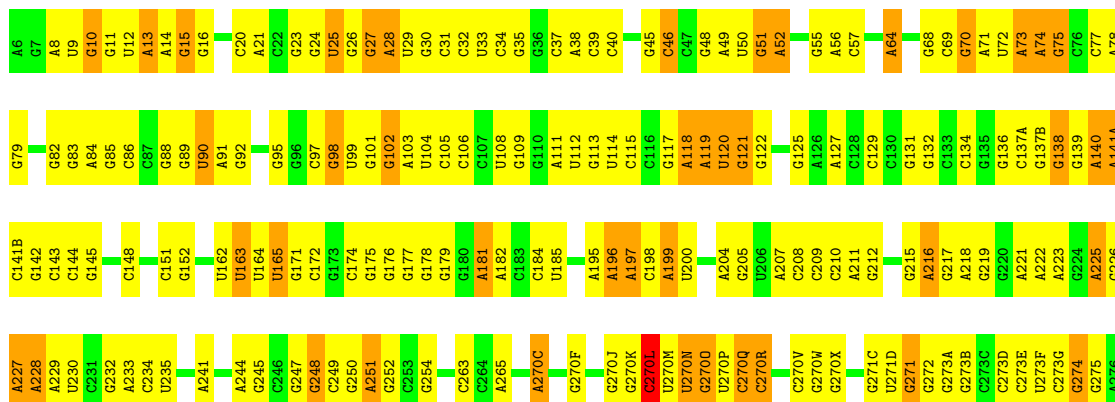
- Molecule 34: 50S ribosomal protein L7/L12

Chain e: 



- Molecule 35: 23S ribosomal RNA

Chain A: 



A1349	A1278	A1213	U1142	C1072	A1000	G938	A872	A804	G729	C661	U594	C517	G446	G363D	C277
A1352	G1279	A1214	A114B	C1076	A1001	G939	G873	G805	G729	G662	C595	G518	A447	G363E	A278
A1353	A1286	G1216	G1144	A1077	G1002	G940	G874	C906	C730	G663	G600	U519	U448	U363F	C279
A1354	A1287	C1217	A1148	U1078	C1005	G942	A878	U807	G731	G664	G601	G520	A449	A363G	C280
G1355	U1288	C1221	G1149	C1079	C1006	G943	A879	G808	G732	G665	G602	U525	G450	C364	G281
G1356	C1291	C1221	G1149	C1080	C1007	G944	G879	G812	A734	A670	A603	A526	A371	A371	U284
U1357	U1292	C1224	C1152	U1081	C1008	A945	G880	U813	G738	A671	G604	C527	G372	G372	C285
G1358	C1293	G1225	G1153	U1082	A1009	G946	G881	C915	C671	C671	G605	A528	U373	U373	C286
A1359	U1294	A1226	G1154	U1083	A1010	G947	G882	C916	G672	G672	U606	A529	A374	A374	C287
A1360	G1295	G1227	G1155	U1084	A1011	G948	G883	C917	U740	C673	U607	G530	A457	A457	C288
G1361	U1296	C1227	A1156	U1085	A1012	G949	G884	C918	G741	G674	A608	C531	G458	G458	A289
G1362	C1296	C1227	A1156	U1086	C1013	G950	G885	C919	G742	A675	A609A	A532	U459	U459	G290
G1363	U1300	G1230	G1157	U1087	U1014	C951	C886	G818	G743	A676	G609B	G533	A460	U380	
A1364	A1301	G1231	U1158	A1088	G1015	G952	A887	A919	U747	A677	C811	U534	G381	G381	U293
A1365	A1302	G1232	U1159	U1089	G1016	A953	C888	A820	G748	C678	G612	C535	C462	C462	A294
G1366	G1303	C1233	G1160	U1090	G1017	G954	C889	A821	G749	C679	U613	A536	U383	U383	C295
G1367	C1306	U1234	G1161	U1091	C1018	C955	A890	U822	C749	C680	U614	C537	U464	U464	C296
U1372	G1309	G1235	G1162	U1092	U1019	G956	G892	U826	U757	G682	G615	G539	C465	C465	C297
A1373	G1310	G1236	G1163	U1094	A1020	A957	C893	U827	C758	G682	A616	C540	A466	A466	G298
G1374	U1311	G1237	U1164	A1095	A1021	U958	C894	U828	C759	G683	G617	C541	U387	U387	A299
G1375	G1312	G1238	G1165	A1096	G1022	A959	U895	U828	A761	G686	G618A	C542	G388	G388	A300
G1376	U1313	G1239	U1166	U1097	U1023	A960	A896	A829	G763	C687	C618B	C546	G469	G469	G301
G1377	U1314	U1240	U1167	U1101	G1024	C961	C897	G830	G764	U688	G619	A547	A470	A470	C302
A1378	U1315	A1241	G1170	C1102	G1025	C964	A900	G831	G765	U689	G620	A548	G473	G473	U303
G1379	G1316	G1242	G1171	A1103	U1026	G965	A901	G836	G766	G690	A621	G549	G474	G474	G304
G1380	A1317	G1243	G1172	C1104	A1027	G966	C902	C937	G767	C691	G627	G556	G475	G475	U305
G1381	U1318	G1244	G1173	U1105	A1028	G967	C903	C938	G768	C692	G628	G557	U306	U306	G307
G1382	G1320	G1245	G1174	U1106	G1030	G968	C904	U839	G769	G695	G629	G558	A401	A401	A310
G1383	U1321	G1246	G1175	U1107	U1033	U969	U905	C840	G771	G696	G630	G559	A402	A402	
G1384	G1322	G1247	G1176	U1108	U1034	C970	G906	A841	G772	G697	A631	C560	U403	U403	
G1385	U1323	U1248	G1177	C1109	G1035	C971	C907	G842	A774	C698	G632	G561	A404	A404	A314
G1386	A1324	G1249	G1178	U1110	U1036	G972	C908	G843	G775	C699	A633	U562	A482	A482	A322
G1387	G1325	C1250	C1179	A1111	G1037	A973	A909	G844	G776	G700	C634	G563	C484	C484	G323
U1394	G1326	G1251	G1184	G1112	A1045	G974A	A910	C846	A777	G701	C635	A571	C485	C485	A324
A1395	A1327	A1252	C1185	U1113	A1046	G974B	A911	U847	G778	G702	G636	A572	G408	G408	G325
U1396	U1328	A1253	G1186	U1114	A1047	G975	C912	G848	G779	U703	G637	A573	C409	C409	G329
U1397	G1329	U1254	G1187	G1115	A1048	C976	U913	G849	G780	G704	G638	C574	G411	G411	A330
G1398	U1330	G1255	G1190	C1116	A1049	G977	C914	G852	A781	A705	U639	G575	A412	A412	
G1399	G1331	C1256	G1191	U1119	A1050	G978	C915	G853	A782	A706	A643	U576	G495	G495	C335
G1400	U1332	U1257	G1192	C1120	G1051	A980	A917	G854	A783	G707	A644	G577	G496	G496	C336
G1401	G1333	G1260	G1193	C1121	G1055	A983	A918	G855	G785	G710	G645	A578	G498	G498	
G1402	C1333	C1261	C1196	G1122	G1056	A984	G919	C856	G786	G711	A646	C580	A503	A503	A340
G1403	U1334	A1262	U1197	C1123	A1057	A985	G920	C857	U787	G712	G647	C581	A422	A422	
G1404	U1335	U1263	U1198	C1124	G1058	C985	G921	U858	G788	G713	G648	C582	A504	A504	A347
U1405	A1336	G1264	U1199	G1125	G1059	C986	U922	G859	A789	U714	G649	G583	A505	A505	
U1406	G1337	A1265	C1200	A1126	U1060	G987	C923	U860	C790	G717	C650	G584	A429	A429	G352
U1407	U1338	G1266	C1201	A1127	U1061	A990	C924	A861	G791	G718	G651	C585	C435	C435	
U1408	G1339	U1267	C1202	C1132	U1062	C991	G925	G862	G792	A719	U652	G586	C436	C436	G355
C1409	U1340	A1268	U1203	A1133	G1063	C992	G929	G864	A793	C719	C653	A586	G438	G438	
G1410	U1341	A1269	U1204	U1135	C1064	G993	U930	C965	G794	C720	U854	C587	C439	C439	A359
C1411	A1342	C1270	U1205	C1136	U1065	C994	G931	A866	C795	C721	A655	U588	G440	G440	G360
A1412	G1343	G1271	G1206	U1137	U1066	C995	G932	C867	C796	A722	G656	C589	U441	U441	G361
G1413	U1344	A1272	C1207	G1138	A1067	A996	A933	U868	G799	G723	U857	A590	G442	G442	U362
G1414	C1345	C1272	U1207	C1139	A1070	G997	G934	G869	A800	G724	C658	C591	A513	A513	G363A
U1415	A1275	A1275	A1210	G1139	A1070	C998	G935	A870	G799	G725	C659	G592	A514	A514	G363B
G1416	G1347	A1276	G1211	C1140	G1071	U999	C936	A871	A800	G726	G660	G593	C443	C443	A363C
G1417	G1348	G1277	G1212	U1141				U871					C516	C516	G363C

C2467	G2468	C2469	G2470	C2471	C2472	C2473	C2474	C2475	A2476	C2477	A2478	C2479	C2480	G2481	C2482	C2483	C2484	C2485	C2486	G2487	A2488	U2489	G2494	C2495	C2496	C2497	C2498	C2499	U2500	C2501	C2502	A2503	U2504	C2505	U2506	C2507	C2508	C2509	C2510	U2511	C2512	C2513	C2514	C2515	C2516	C2517	A2518	U2519	C2520	U2521	U2522	C2523	C2524	C2525	C2526	C2529				
G2397	U2398	G2399	G2400	U2401	C2402	C2403	C2404	C2405	A2406	C2407	G2410	A2411	A2412	G2415	C2416	C2417	A2418	U2419	C2420	C2421	A2422	C2423	C2424	A2425	C2426	C2427	C2428	C2429	A2430	U2431	C2432	A2435	U2436	U2437	U2438	A2439	C2440	C2441	C2442	C2443	G2446	G2447	A2448	U2449	A2450	G2454	U2457	G2458	C2461	U2462	C2466									
G2325	C2326	A2327	A2328	G2329	C2330	G2331	C2334	A2335	A2336	G2339	G2340	U2344	G2345	A2346	C2347	U2348	G2349	C2350	G2351	C2355	C2356	U2357	C2358	A2361	A2366	C2369	G2370	G2373	C2374	G2375	A2376	A2377	A2378	C2379	C2380	C2381	G2382	C2383	C2384	C2385	C2386	U2387	A2388	U2389	U2390	U2457	G2458	C2461	U2462	C2466										
C2176	C2177	C2178	C2179	G2184	C2185	G2190	G2191	C2192	G2193	G2194	C2195	C2196	U2197	A2198	A2199	C2205	U2208	C2209	G2210	C2211	C2282	C2283	C2284	C2285	C2286	C2287	A2288	C2289	C2290	U2291	C2292	C2293	C2294	C2295	C2229	G2230	C2231	U2232	U2233	G2234	C2235	C2236	G2237	C2238	C2239	C2240	A2241	C2242	U2243	U2244	U2245	U2246	C2247	U2248	U2249	G2250	C2251	C2252	C2253	C2254
C2108	U2109	G2110	C2111	C2112	U2113	A2114	G2115	C2116	A2117	U2118	A2119	C2120	G2121	U2122	C2123	G2124	C2125	A2126	G2127	G2131	U2132	C2133	A2134	A2135	C2136	C2137	C2138	C2142	C2143	U2144	G2147	U2150	C2151	G2152	C2153	G2154	C2155	C2156	C2157	A2158	C2159	C2160	C2163	C2164	C2165	C2166	U2167	C2168	A2171	U2172	A2173	C2174	C2175							
A2042	C2043	C2044	C2045	G2046	U2047	G2048	G2049	A2051	G2052	C2053	C2055	G2056	A2060	C2061	A2062	C2065	C2066	G2067	U2068	C2069	C2070	A2071	G2072	C2073	U2074	U2075	C2078	U2079	G2080	C2081	C2084	C2085	U2086	U2089	C2090	U2091	U2092	C2093	G2094	C2095	U2096	C2097	U2098	U2099	G2100	C2101	U2102	C2103	C2104	C2105	C2106	C2107								
A1972	G1973	C1974	G1975	U1976	A1981	C1982	G1985	A1986	C1990	U1991	G1992	C1994	U1995	C1996	G1997	C1998	C1999	A2001	G2002	G2003	A2004	A2005	C2008	G2009	G2010	U2011	G2012	A2013	G2018	A2019	C2020	C2021	U2022	G2023	C2024	C2025	C2026	G2027	U2028	G2029	A2030	C2031	G2032	A2033	U2034	G2035	C2036	G2037	C2038	C2039	U2041									
C1806	A1810	G1811	A1812	G1813	A1814	A1815	G1816	A1817	U1818	A1819	U1820	A1821	A1825	G1826	C1827	U1828	A1829	C1830	U1833	U1834	C1837	C1838	G1839	A1840	U1841	G1842	C1843	C1844	G1845	U1846	A1847	A1854	C1858	A1859	G1860	C1861	G1862	C1863	U1864	G1865	U1866	C1867	U1868	C1869	U1870	A1871	A1872	C1882	G1883	A1884	C1885	C1886	C1887	G1888	A1889	A1890				
C1551	C1556	C1557	A1558	G1559	C1565	A1566	A1567	C1568	A1569	A1570	C1577	U1578	G1581	C1582	A1583	C1585	A1586	A1587	C1588	C1589	U1590	G1591	C1592	G1593	G1594	G1595	A1596	C1599	C1600	C1601	U1602	A1603	C1604	C1605	G1606	C1607	A1608	U1609	A1610	C1611	C1612	C1615	A1616	C1617	A1618	G1619	U1621	C1622	G1623	G1624	A1631									
A1632	G1633	A1634	G1635	C1636	A1637	C1638	U1639	C1640	A1641	G1642	C1643	G1644	G1645	C1646	C1647	C1648	G1651	A1652	C1653	A1654	A1655	C1656	C1657	C1658	U1659	C1663	A1664	A1665	C1666	G1667	A1668	C1669	C1670	U1671	G1674	A1675	A1676	A1677	C1678	U1679	U1680	G1681	C1682	C1683	A1689	A1690	C1691	U1692	G1693	C1694	G1695	G1696	G1697	A1698						
G1707	C1708	U1709	G1710	C1711	C1712	U1727	G1728	A1729	A1732	G1733	G1750	C1751	A1755	G1756	U1757	A1762	G1763	G1764	G1770	C1771	G1772	A1773	C1774	U1775	G1776	U1779	A1780	C1781	G1782	A1783	A1784	A1785	A1786	A1787	C1788	A1789	C1790	G1792	C1793	U1794	C1795	U1796	U1797	U1798	G1799	C1800	G1801	A1802	A1803	C1804	U1805									
C1485	A1486	G1487	G1488	G1491	G1492	C1493	A1494	A1495	C1496	U1497	C1498	C1499	G1500	C1501	C1502	G1505	C1506	A1510	A1511	G1512	C1513	U1514	C1515	U1516	G1517	G1522	U1523	G1525	G1526	G1527	A1528	A1529	G1530	C1531	C1532	C1533	G1534	U1535	A1536	G1537	G1538	C1539	G1540	U1541	G1542	A1543	C1544	U1545	A1546	G1547	C1548	C1550								
C1419	U1420	G1421	G1422	G1423	G1424	A1427	C1428	G1429	C1430	U1431	C1432	U1433	U1434	G1435	G1436	C1437	U1438	A1439	G1440	G1441	C1442	G1443	G1444	A1445	C1446	G1447	C1448	A1498	G1449	A1453	U1454	G1455	G1458	G1459	A1460	G1461	C1462	C1463	C1464	G1465	G1466	C1467	C1468	A1469	G1470	A1471	C1476	A1477	C1478	G1479	C1480	U1481	G1483	C1484						



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	306.01Å 673.49Å 351.98Å 90.00° 92.69° 90.00°	Depositor
Resolution (Å)	40.00 – 3.50 131.34 – 3.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.50) 74.9 (131.34-3.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.30 (at 3.49Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.262 , 0.309 0.352 , 0.354	Depositor DCC
$R_{free}$ test set	38207 reflections (4.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	80.5	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 278.0	EDS
Estimated twinning fraction	0.247 for h,-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.26$ , $\langle L^2 \rangle = 0.11$	Xtriage
Outliers	0 of 765681 reflections	Xtriage
$F_o, F_c$ correlation	0.64	EDS
Total number of atoms	95124	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	C	0.50	1/1774 (0.1%)	0.76	0/2391
2	D	0.38	0/2195	0.67	0/2955
3	E	0.35	0/1602	0.67	1/2160 (0.0%)
4	F	0.41	0/1663	0.79	4/2249 (0.2%)
5	G	0.59	1/1499 (0.1%)	0.67	3/2016 (0.1%)
6	H	0.34	0/1298	0.62	0/1751
8	K	0.34	0/1054	0.56	1/1427 (0.1%)
9	N	0.54	0/1131	0.80	0/1525
10	O	0.36	0/943	0.64	1/1269 (0.1%)
11	P	0.34	0/1131	0.71	0/1504
12	Q	0.36	0/1143	0.60	0/1527
13	R	0.34	0/974	0.62	1/1302 (0.1%)
14	S	0.40	0/783	0.75	0/1041
15	T	0.37	0/1161	0.67	0/1549
16	U	0.42	0/982	0.68	1/1306 (0.1%)
17	V	0.38	0/790	0.71	0/1057
18	W	0.37	0/911	0.65	0/1220
19	X	0.35	0/748	0.60	0/1004
20	Y	0.34	0/831	0.60	0/1108
21	Z	0.32	0/1505	0.59	0/2042
22	0	0.31	0/671	0.56	0/892
23	2	0.34	0/600	0.60	0/793
24	3	0.31	0/482	0.58	0/646
25	5	0.34	0/473	0.60	0/639
26	6	0.35	0/440	0.79	1/586 (0.2%)
27	7	0.48	0/438	0.69	0/575
28	8	0.36	0/525	0.64	0/691
29	9	0.29	0/310	0.55	0/407
32	1	0.54	0/739	0.84	2/981 (0.2%)
33	4	0.45	0/276	0.66	0/372
34	e	0.35	0/538	0.61	0/715
35	A	0.40	1/69437 (0.0%)	0.97	72/108401 (0.1%)
36	B	0.34	0/2853	0.90	1/4451 (0.0%)
All	All	0.40	3/101900 (0.0%)	0.90	88/152552 (0.1%)

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
1	C	0	2
2	D	0	1
4	F	0	2
5	G	0	1
7	J	0	1
14	S	0	2
15	T	0	1
18	W	0	1
32	1	0	3
All	All	0	14

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	112	PRO	CA-C	17.59	1.88	1.52
1	C	46	ALA	CA-CB	6.31	1.65	1.52
35	A	2780	G	N7-C5	-6.19	1.35	1.39

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	116	ASP	O-C-N	-10.28	106.25	122.70
4	F	193	VAL	N-CA-C	-10.27	83.28	111.00
35	A	645	C	C2-N1-C1'	9.76	129.54	118.80
35	A	645	C	N1-C2-O2	8.29	123.88	118.90
35	A	270(L)	C	N1-C2-O2	7.29	123.28	118.90
35	A	645	C	C6-N1-C1'	-7.26	112.08	120.80
35	A	1022	G	N3-C4-C5	-7.15	125.02	128.60
35	A	163	U	C2-N1-C1'	7.05	126.16	117.70
5	G	116	ASP	CA-C-N	7.01	132.63	117.20
35	A	1963	U	C2-N1-C1'	6.94	126.03	117.70
4	F	155	LEU	N-CA-C	-6.90	92.38	111.00
35	A	1963	U	N1-C2-O2	6.79	127.56	122.80
35	A	2780	G	O5'-P-OP1	-6.55	99.80	105.70
35	A	448	U	N1-C2-O2	6.55	127.38	122.80
35	A	2780	G	C4-C5-C6	6.51	122.71	118.80
35	A	1396	U	C2-N1-C1'	6.44	125.43	117.70
35	A	2780	G	N1-C6-O6	6.35	123.71	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	U	98	LEU	CA-CB-CG	6.35	129.90	115.30
35	A	1420	U	C2-N1-C1'	6.21	125.15	117.70
35	A	448	U	N3-C2-O2	-6.21	117.85	122.20
35	A	1314	C	C2-N1-C1'	6.20	125.62	118.80
35	A	676	A	O4'-C1'-N9	6.16	113.13	108.20
35	A	1909	C	C2-N1-C1'	6.12	125.54	118.80
35	A	2585	U	C2-N1-C1'	6.11	125.03	117.70
35	A	1313	U	C2-N1-C1'	6.09	125.00	117.70
35	A	270(L)	C	N3-C2-O2	-6.00	117.70	121.90
35	A	2780	G	C6-C5-N7	-5.96	126.82	130.40
35	A	2780	G	N3-C4-N9	5.86	129.52	126.00
35	A	645	C	N3-C2-O2	-5.86	117.80	121.90
3	E	63	LEU	CA-CB-CG	5.84	128.74	115.30
35	A	2585	U	N1-C2-O2	5.82	126.87	122.80
35	A	2779	U	OP2-P-O3'	5.77	117.89	105.20
26	6	9	LEU	CA-CB-CG	5.76	128.56	115.30
35	A	2779	U	OP1-P-O3'	-5.68	92.70	105.20
35	A	270(L)	C	C2-N1-C1'	5.68	125.04	118.80
35	A	1315	C	N1-C2-O2	5.64	122.29	118.90
32	1	40	ARG	N-CA-C	5.62	126.17	111.00
35	A	90	U	C2-N1-C1'	5.60	124.42	117.70
35	A	2895	U	C2-N1-C1'	5.59	124.41	117.70
35	A	1396	U	N1-C2-O2	5.57	126.70	122.80
4	F	156	LEU	CA-CB-CG	5.52	128.00	115.30
35	A	2111	C	C6-N1-C2	-5.51	118.09	120.30
35	A	2710	C	C6-N1-C2	-5.48	118.11	120.30
35	A	645	C	C5-C6-N1	5.46	123.73	121.00
36	B	31	C	C6-N1-C2	-5.45	118.12	120.30
35	A	2804	C	C6-N1-C2	-5.41	118.14	120.30
35	A	448	U	C2-N1-C1'	5.40	124.18	117.70
35	A	1396	U	N3-C2-O2	-5.38	118.43	122.20
35	A	2033	A	N9-C4-C5	5.36	107.94	105.80
35	A	2033	A	C8-N9-C4	-5.35	103.66	105.80
10	O	8	LEU	CA-CB-CG	5.34	127.58	115.30
4	F	174	VAL	N-CA-C	-5.31	96.65	111.00
35	A	2118	U	C2-N1-C1'	5.31	124.07	117.70
35	A	1680	U	C2-N1-C1'	-5.29	111.35	117.70
35	A	1664	A	C8-N9-C4	-5.28	103.69	105.80
35	A	933	A	O4'-C1'-N9	5.28	112.42	108.20
35	A	165	U	O4'-C1'-N1	5.26	112.41	108.20
35	A	935	C	C2-N1-C1'	5.25	124.57	118.80
35	A	2032	G	C8-N9-C4	-5.23	104.31	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	A	1963	U	N3-C2-O2	-5.23	118.54	122.20
35	A	2598	A	N1-C6-N6	5.22	121.73	118.60
35	A	1139	G	O5'-P-OP2	-5.22	101.00	105.70
35	A	840	C	C6-N1-C2	-5.21	118.22	120.30
35	A	1776	G	C6-C5-N7	-5.21	127.28	130.40
35	A	2730	C	C2-N1-C1'	5.20	124.52	118.80
35	A	2055	C	C6-N1-C2	-5.20	118.22	120.30
35	A	165	U	C2-N1-C1'	5.19	123.93	117.70
32	1	17	SER	N-CA-C	-5.18	97.02	111.00
35	A	1909	C	C6-N1-C1'	-5.17	114.59	120.80
35	A	1314	C	C6-N1-C2	-5.16	118.23	120.30
13	R	116	LEU	CA-CB-CG	5.15	127.15	115.30
35	A	2780	G	C5-N7-C8	5.15	106.88	104.30
35	A	1776	G	C4-N9-C1'	5.11	133.15	126.50
8	K	105	LEU	CA-CB-CG	5.10	127.04	115.30
35	A	1313	U	C5-C6-N1	5.09	125.25	122.70
35	A	270(L)	C	C6-N1-C2	-5.08	118.27	120.30
35	A	1378	A	O4'-C1'-N9	5.07	112.25	108.20
35	A	1776	G	C4-C5-N7	5.06	112.83	110.80
35	A	1909	C	N1-C2-O2	5.06	121.94	118.90
35	A	897	C	C2-N1-C1'	5.06	124.37	118.80
35	A	691	C	C6-N1-C2	-5.04	118.28	120.30
35	A	302	C	O4'-C1'-N1	5.03	112.23	108.20
35	A	2389	G	N3-C4-N9	-5.03	122.98	126.00
5	G	116	ASP	C-N-CA	5.03	134.27	121.70
35	A	2473	U	C2-N1-C1'	5.03	123.73	117.70
35	A	506	G	O4'-C1'-N9	5.02	112.22	108.20
35	A	2422	A	P-O3'-C3'	5.02	125.72	119.70
35	A	935	C	C6-N1-C2	-5.00	118.30	120.30

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
32	1	16	ASN	Peptide
32	1	17	SER	Peptide
32	1	18	ILE	Peptide
1	C	171	ALA	Peptide
1	C	211	ARG	Peptide
2	D	78	LYS	Peptide
4	F	154	VAL	Peptide
4	F	173	VAL	Peptide

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Mol	Chain	Res	Type	Group
5	G	113	ARG	Peptide
7	J	83	UNK	Peptide
14	S	100	ALA	Peptide
14	S	46	VAL	Peptide
15	T	28	VAL	Peptide
18	W	75	TYR	Peptide

## 5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1742	0	1798	147	0
2	D	2145	0	2234	164	0
3	E	1569	0	1634	122	0
4	F	1628	0	1680	141	0
5	G	1474	0	1535	82	0
6	H	1274	0	1342	72	0
7	J	851	0	196	25	0
8	K	1035	0	1082	57	0
9	N	1104	0	1180	115	0
10	O	933	0	996	68	0
11	P	1114	0	1187	111	0
12	Q	1122	0	1179	65	0
13	R	960	0	1021	71	0
14	S	775	0	835	76	0
15	T	1147	0	1207	109	0
16	U	964	0	1022	76	0
17	V	779	0	852	62	0
18	W	900	0	964	57	0
19	X	734	0	789	42	0
20	Y	818	0	908	58	0
21	Z	1473	0	1497	81	0
22	0	662	0	688	40	0
23	2	598	0	653	28	0
24	3	477	0	529	25	0
25	5	459	0	477	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	6	433	0	461	36	0
27	7	430	0	480	32	0
28	8	517	0	582	50	0
29	9	307	0	335	20	0
30	f	156	0	41	0	0
30	g	156	0	39	0	0
31	h	151	0	37	0	0
32	1	732	0	808	75	0
33	4	271	0	284	20	0
34	e	686	0	619	0	0
35	A	61997	0	31250	1726	0
36	B	2551	0	1295	70	0
All	All	95124	0	63716	3497	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 22.

All (3497) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:G:112:PRO:C	5:G:112:PRO:CA	1.88	1.41
35:A:2133:G:H21	35:A:2158:A:N6	1.39	1.19
35:A:2133:G:N2	35:A:2158:A:H62	1.42	1.17
35:A:1170:G:H1	35:A:1179:C:N4	1.46	1.12
35:A:281:G:H21	35:A:359:A:N6	1.48	1.11
35:A:281:G:N2	35:A:359:A:H62	1.49	1.09
35:A:1436:G:H1	35:A:1556:C:N4	1.50	1.08
35:A:2093:G:H1	35:A:2196:C:N4	1.51	1.07
35:A:814:C:N4	35:A:1193:G:H1	1.53	1.07
9:N:70:LYS:NZ	35:A:1139:G:OP2	1.91	1.02
35:A:122:G:H1	35:A:129:C:H42	1.05	1.00
35:A:270(J):G:H1	35:A:270(R):C:N4	1.61	0.99
35:A:1346:G:H1	35:A:1600:C:N4	1.58	0.99
35:A:949:C:H42	35:A:968:G:H1	1.08	0.98
35:A:947:G:H1	35:A:970:C:N4	1.62	0.98
35:A:852:G:H1	35:A:925:C:H42	1.05	0.98
35:A:1663:C:H42	35:A:1997:G:H1	1.06	0.98
35:A:2121:G:H1	35:A:2177:C:H42	0.99	0.98
35:A:2138:C:N4	35:A:2153:G:H1	1.62	0.98
35:A:1347:G:H1	35:A:1599:C:H42	1.08	0.97
35:A:1417:C:H42	35:A:1581:G:H1	1.04	0.97
35:A:2466:C:H42	35:A:2484:G:H1	1.10	0.96
35:A:273(G):C:H42	35:A:363(A):G:H1	0.99	0.95

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:1013:C:H42	35:A:1149:G:H1	1.10	0.94
1:C:47:LYS:HB3	1:C:212:SER:HB2	1.48	0.94
35:A:1002:G:H1	35:A:1153:C:H42	1.05	0.94
35:A:678:C:H42	35:A:799:G:H1	0.94	0.94
9:N:49:GLY:O	9:N:119:ARG:NH1	2.01	0.94
2:D:44:ASN:HB2	2:D:49:ILE:HA	1.48	0.94
7:J:54:UNK:HA	7:J:79:UNK:HA	1.47	0.93
35:A:1840:G:H1	35:A:1902:C:H42	0.94	0.93
35:A:286:C:H42	35:A:355:G:H1	1.03	0.93
32:1:25:LYS:HG2	32:1:34:THR:HA	1.49	0.93
35:A:20:C:H42	35:A:520:G:H1	1.15	0.93
35:A:949:C:N3	35:A:968:G:N2	2.17	0.92
35:A:610:C:H42	35:A:618(A):G:H1	1.14	0.92
35:A:704:G:HO2'	35:A:726:G:H1	1.15	0.92
35:A:854:G:H1	35:A:923:C:H42	0.92	0.92
35:A:2642:G:H1	35:A:2772:C:H42	1.17	0.91
35:A:270(F):G:H1	35:A:270(V):C:H42	0.95	0.91
35:A:1324:G:H1	35:A:1330:C:H42	1.16	0.91
35:A:1906:G:H1	35:A:1924:C:H42	1.18	0.91
35:A:852:G:N2	35:A:925:C:N3	2.19	0.90
35:A:882:G:N2	35:A:894:C:N3	2.19	0.90
35:A:884:C:H42	35:A:892:G:H1	1.20	0.90
35:A:882:G:H1	35:A:894:C:H42	1.19	0.89
35:A:681:G:H1	35:A:796:C:H42	0.99	0.89
27:7:34:ARG:HD3	27:7:42:LEU:HB3	1.54	0.88
1:C:169:THR:HB	35:A:2178:C:H1'	1.56	0.88
35:A:854:G:H1	35:A:923:C:N4	1.70	0.88
35:A:1411:C:H42	35:A:1591:G:H1	0.88	0.88
20:Y:46:LYS:H	20:Y:62:GLU:HB2	1.39	0.88
35:A:678:C:N4	35:A:799:G:H1	1.72	0.88
35:A:1411:C:N4	35:A:1591:G:H1	1.71	0.87
35:A:2093:G:N2	35:A:2196:C:N3	2.23	0.87
35:A:1782:C:H42	35:A:2586:C:H42	1.18	0.87
35:A:783:A:H2'	35:A:784:A:H4'	1.56	0.87
35:A:1345:C:H42	35:A:1601:G:H1	1.20	0.87
35:A:884:C:N3	35:A:892:G:N2	2.23	0.87
35:A:852:G:H1	35:A:925:C:N4	1.73	0.87
35:A:1207:C:H42	35:A:1239:G:H1	1.19	0.86
35:A:2794:C:H42	35:A:2802:G:H1	1.23	0.86
21:Z:151:HIS:HB3	21:Z:170:THR:HA	1.57	0.86
14:S:86:ALA:O	14:S:106:ARG:NH1	2.09	0.86
35:A:1059:G:N1	35:A:1079:C:N4	2.22	0.86

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:273(G):C:N4	35:A:363(A):G:H1	1.74	0.86
35:A:882:G:H1	35:A:894:C:N4	1.73	0.86
35:A:1436:G:N2	35:A:1556:C:N3	2.22	0.86
35:A:1840:G:H1	35:A:1902:C:N4	1.71	0.86
35:A:817:C:H42	35:A:1190:G:H1	1.24	0.86
35:A:2121:G:H1	35:A:2177:C:N4	1.73	0.86
9:N:9:VAL:HG21	9:N:39:ARG:HH12	1.39	0.86
35:A:1411:C:N3	35:A:1591:G:N2	2.23	0.85
35:A:671:C:N4	35:A:809:G:H1	1.73	0.85
7:J:25:UNK:HA	7:J:80:UNK:HA	1.57	0.85
29:9:22:ARG:HH11	29:9:35:ARG:HH12	1.20	0.85
5:G:112:PRO:C	5:G:112:PRO:HA	1.95	0.85
25:5:3:LYS:HG2	25:5:5:PRO:HD2	1.57	0.85
1:C:40:GLU:O	1:C:42:VAL:N	2.09	0.85
18:W:18:ARG:HH11	18:W:76:VAL:HG13	1.41	0.85
17:V:24:LYS:HB3	35:A:1162:G:H4'	1.58	0.84
35:A:2293:C:H42	35:A:2339:G:H1	1.25	0.84
35:A:2701:C:H42	35:A:2706:G:H1	1.22	0.84
35:A:360:G:H2'	35:A:361:G:H8	1.43	0.84
4:F:38:ARG:HH22	35:A:661:C:H5'	1.41	0.84
35:A:671:C:H42	35:A:809:G:H1	0.88	0.84
3:E:61:ARG:HH21	35:A:2810:A:H2'	1.43	0.84
15:T:106:SER:HB2	15:T:110:ILE:HG12	1.60	0.84
35:A:1646:C:H5''	35:A:1647:G:H5''	1.58	0.83
35:A:1018:C:H42	35:A:1144:G:H1	1.25	0.83
35:A:2020:A:N1	35:A:2034:U:O4	2.10	0.83
14:S:101:LEU:HD22	14:S:104:GLY:HA3	1.60	0.83
6:H:41:MET:HE1	6:H:43:VAL:HG13	1.60	0.83
35:A:8:A:N1	35:A:2895:U:O4	2.12	0.83
1:C:43:GLU:HB2	1:C:216:THR:HG23	1.61	0.82
2:D:260:ARG:NH1	35:A:1799:G:OP1	2.12	0.82
11:P:45:LEU:HG	11:P:46:LYS:HD2	1.61	0.82
23:2:14:ARG:HG2	23:2:63:VAL:HG11	1.59	0.82
36:B:5:C:O2'	36:B:27:C:O2	1.98	0.82
1:C:138:LEU:HD22	1:C:139:PRO:HD2	1.61	0.82
35:A:1436:G:H1	35:A:1556:C:H42	0.87	0.82
35:A:270(J):G:H1	35:A:270(R):C:H42	1.24	0.82
4:F:103:LYS:HE2	4:F:107:LYS:HE3	1.62	0.82
35:A:273(A):G:H1	35:A:364:C:H42	1.23	0.82
3:E:13:ARG:HA	3:E:21:VAL:O	1.80	0.82
35:A:1530:G:O6	35:A:1541:U:O2	1.98	0.82
9:N:9:VAL:HG21	9:N:39:ARG:NH1	1.95	0.81

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:W:84:ARG:NH2	35:A:1322:A:O2'	2.13	0.81
1:C:46:ALA:HA	1:C:212:SER:O	1.81	0.81
35:A:270(F):G:H1	35:A:270(V):C:N4	1.77	0.81
32:1:46:LEU:O	32:1:47:GLN:NE2	2.14	0.81
35:A:293:U:H3	35:A:347:A:H61	1.27	0.81
25:5:15:ARG:NH1	35:A:2046:G:OP1	2.13	0.81
13:R:90:ARG:NH1	35:A:2880:C:O2'	2.12	0.81
35:A:2265:U:H3'	35:A:2266:A:H8	1.45	0.81
35:A:1830:C:H42	35:A:1975:G:H1	1.26	0.81
35:A:2287:A:H62	35:A:2344:U:H3	1.28	0.81
13:R:31:HIS:HB2	13:R:34:ILE:HD11	1.62	0.81
35:A:884:C:N4	35:A:892:G:H1	1.77	0.81
12:Q:12:GLN:HA	35:A:910:A:H62	1.46	0.81
35:A:681:G:H1	35:A:796:C:N4	1.78	0.80
28:8:14:VAL:HG23	28:8:24:ALA:HB2	1.63	0.80
9:N:101:HIS:ND1	9:N:101:HIS:O	2.13	0.80
35:A:1311:G:H21	35:A:1603:A:H62	1.26	0.80
21:Z:102:LEU:HD11	21:Z:124:ILE:HG23	1.63	0.80
18:W:11:ARG:HH12	18:W:12:ILE:HD13	1.47	0.80
35:A:15:G:H1	35:A:525:U:H3	1.30	0.80
35:A:1992:G:N2	35:A:1996:C:O2'	2.15	0.79
14:S:106:ARG:HE	14:S:108:GLY:HA2	1.48	0.79
35:A:978:G:H1	35:A:985:C:H42	1.29	0.79
1:C:118:PRO:HD3	1:C:147:GLY:HA2	1.63	0.79
17:V:77:ALA:O	17:V:79:VAL:N	2.16	0.79
35:A:610:C:N4	35:A:618(A):G:H1	1.80	0.79
15:T:25:GLY:HA3	15:T:92:GLY:HA2	1.65	0.79
2:D:13:ARG:NH1	35:A:729:G:OP2	2.16	0.79
35:A:136:G:H1	35:A:143:C:H42	1.31	0.79
35:A:2576:G:O2'	35:A:2579:C:OP2	2.01	0.79
20:Y:102:CYS:SG	20:Y:103:GLY:N	2.56	0.79
35:A:1417:C:N4	35:A:1581:G:H1	1.81	0.79
35:A:1449:G:O6	35:A:1462:C:N3	2.17	0.78
1:C:51:ASP:O	1:C:53:ARG:N	2.16	0.78
20:Y:51:VAL:HG12	20:Y:53:PRO:HD2	1.62	0.78
3:E:168:MET:O	35:A:2730:C:O2'	2.02	0.78
35:A:1248:G:H3'	35:A:1249:U:H5"	1.65	0.78
4:F:4:VAL:HA	4:F:22:ALA:HB3	1.65	0.78
1:C:23:ILE:HD13	1:C:191:ARG:HG2	1.65	0.78
35:A:1347:G:H1	35:A:1599:C:N4	1.82	0.78
35:A:1002:G:H1	35:A:1153:C:N4	1.81	0.78
14:S:27:SER:HA	14:S:88:ASP:HB3	1.64	0.78

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:P:88:LEU:HD11	11:P:123:LEU:HD21	1.66	0.78
35:A:1387:C:H42	35:A:1400:G:H1	1.30	0.78
6:H:149:ARG:HE	6:H:163:TYR:HA	1.47	0.77
21:Z:52:SER:OG	21:Z:53:ILE:N	2.15	0.77
2:D:21:PHE:O	2:D:25:THR:OG1	2.02	0.77
35:A:1536:A:OP2	35:A:1537:C:N4	2.17	0.77
1:C:150:ILE:HA	1:C:153:ILE:HB	1.66	0.77
35:A:949:C:N4	35:A:968:G:H1	1.83	0.77
35:A:1013:C:N4	35:A:1149:G:H1	1.82	0.77
35:A:883:G:N2	35:A:893:C:N3	2.32	0.77
35:A:2503:A:O2'	35:A:2505:G:OP2	2.03	0.77
1:C:45:HIS:ND1	1:C:171:ALA:O	2.17	0.77
9:N:48:MET:N	9:N:48:MET:SD	2.57	0.77
15:T:64:ARG:HH12	15:T:103:ARG:HG2	1.48	0.77
10:O:66:LYS:HG2	35:A:1665:A:H5''	1.67	0.77
35:A:883:G:N2	35:A:893:C:C2	2.53	0.76
19:X:29:TRP:HA	19:X:78:LYS:HA	1.65	0.76
13:R:12:ARG:HB3	13:R:16:HIS:HB3	1.67	0.76
11:P:18:ARG:NH1	35:A:662:G:OP1	2.18	0.76
32:1:19:GLN:NE2	35:A:2233:U:OP2	2.17	0.76
19:X:5:TYR:HA	19:X:7:VAL:HG23	1.67	0.76
12:Q:43:THR:HA	12:Q:94:VAL:HG12	1.67	0.76
1:C:48:LEU:HD13	1:C:50:ILE:HG13	1.68	0.76
17:V:4:ILE:HB	17:V:40:LEU:HB2	1.67	0.76
35:A:784:A:N6	35:A:2072:G:O2'	2.19	0.76
35:A:2791:C:OP1	35:A:2893:G:N2	2.18	0.76
2:D:78:LYS:HD3	2:D:114:GLY:HA2	1.66	0.76
35:A:1541:U:H3'	35:A:1542:G:H3'	1.68	0.76
4:F:122:LYS:HD2	4:F:191:ARG:HH21	1.50	0.76
14:S:17:ARG:O	14:S:21:THR:N	2.17	0.76
4:F:191:ARG:O	4:F:193:VAL:N	2.19	0.76
2:D:222:ARG:NH2	35:A:1828:G:OP2	2.18	0.76
35:A:1315:C:H42	35:A:1337:G:H1	1.32	0.76
5:G:36:LYS:HB3	5:G:95:ARG:HH12	1.50	0.76
3:E:37:ARG:NH1	3:E:42:ASP:OD1	2.18	0.75
12:Q:42:ILE:HD11	12:Q:95:ALA:HB3	1.68	0.75
35:A:1825:A:H2'	35:A:1826:G:H8	1.52	0.75
11:P:124:LYS:HD3	11:P:143:GLY:HA3	1.68	0.75
25:5:46:CYS:HB3	25:5:49:CYS:HB2	1.68	0.75
1:C:213:VAL:HG11	1:C:225:ILE:HG12	1.68	0.75
9:N:5:VAL:O	9:N:7:LYS:NZ	2.19	0.75
35:A:2282:G:H1	35:A:2427:C:H42	1.32	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:E:189:PRO:HA	35:A:2680:C:H5'	1.69	0.75
35:A:1275:A:OP2	35:A:1646:C:N4	2.20	0.75
12:Q:34:LEU:HD23	12:Q:104:PHE:HE1	1.51	0.75
6:H:83:TYR:HB2	6:H:135:GLY:H	1.51	0.75
9:N:25:ARG:HH22	35:A:114(B):A:H4'	1.51	0.75
6:H:113:VAL:HG11	6:H:151:ILE:HD13	1.69	0.75
35:A:1854:A:H62	35:A:1888:G:H8	1.34	0.75
13:R:45:ARG:HG2	13:R:97:VAL:HG21	1.68	0.75
35:A:1000:A:OP2	35:A:1154:G:N1	2.20	0.74
18:W:81:ALA:HB1	18:W:98:LYS:O	1.87	0.74
4:F:63:LYS:HE3	4:F:67:GLN:HB2	1.69	0.74
9:N:41:ASP:HA	16:U:64:ARG:HH11	1.51	0.74
35:A:1483:G:H1	35:A:1506:C:H42	1.35	0.74
5:G:173:LEU:HB3	5:G:178:PHE:HB2	1.67	0.74
35:A:2689:U:OP2	35:A:2872:G:N2	2.21	0.74
35:A:1800:C:H42	35:A:1817:G:N2	1.84	0.74
36:B:24:G:C6	36:B:56:G:N3	2.55	0.74
29:9:25:VAL:HB	29:9:34:GLN:HB2	1.69	0.74
6:H:23:ARG:HD2	6:H:25:LYS:HE2	1.69	0.74
19:X:53:LYS:HB3	19:X:82:GLN:HB3	1.68	0.74
35:A:884:C:C2	35:A:892:G:N2	2.55	0.74
35:A:1059:G:C6	35:A:1079:C:N4	2.55	0.74
17:V:87:HIS:HE1	35:A:1163:G:H21	1.33	0.74
10:O:14:THR:HG21	10:O:86:ILE:HD12	1.69	0.74
35:A:2514:U:H3	35:A:2570:G:H1	1.36	0.74
1:C:61:GLY:O	1:C:163:GLU:HA	1.86	0.74
32:1:19:GLN:HB3	32:1:40:ARG:HD3	1.69	0.74
35:A:273(A):G:H1	35:A:364:C:N4	1.86	0.74
20:Y:7:VAL:HG21	35:A:336:C:H4'	1.68	0.73
24:3:22:ALA:HB2	24:3:49:LYS:HD3	1.70	0.73
11:P:23:PRO:HD2	11:P:33:ARG:HE	1.53	0.73
12:Q:124:LYS:NZ	35:A:2467:C:O2	2.22	0.73
35:A:270(J):G:N1	35:A:270(R):C:N4	2.32	0.73
35:A:1059:G:N2	35:A:1079:C:N3	2.36	0.73
4:F:53:THR:OG1	4:F:54:ARG:N	2.20	0.73
1:C:214:TYR:HB3	1:C:222:SER:HB2	1.70	0.73
19:X:12:VAL:HA	19:X:29:TRP:HE1	1.54	0.73
9:N:27:ALA:HA	9:N:30:ILE:HB	1.69	0.73
35:A:1324:G:H1	35:A:1330:C:N4	1.87	0.73
4:F:9:ILE:HG21	4:F:124:LEU:HA	1.68	0.73
35:A:1487:G:H1	35:A:1502:C:H42	1.35	0.73
20:Y:13:VAL:HG21	20:Y:74:PRO:HA	1.69	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:3:8:LEU:HD12	24:3:28:LEU:HD12	1.69	0.73
35:A:1782:C:N4	35:A:2586:C:H42	1.86	0.73
21:Z:72:ARG:HH12	36:B:103:U:H4'	1.53	0.73
35:A:2089:U:H3	35:A:2230:G:H1	1.37	0.73
35:A:947:G:H1	35:A:970:C:H42	0.82	0.73
15:T:49:VAL:HA	15:T:63:VAL:HA	1.70	0.73
15:T:95:ARG:NH1	35:A:2849:U:OP2	2.20	0.73
35:A:404:C:H4'	35:A:405:U:H5'	1.70	0.72
35:A:131:G:H2'	35:A:132:G:H8	1.54	0.72
35:A:1024:G:H3'	35:A:1025:G:H5''	1.71	0.72
9:N:63:THR:OG1	35:A:1141:U:OP2	2.06	0.72
17:V:66:ARG:HA	17:V:90:PRO:HA	1.71	0.72
35:A:1899:G:N2	35:A:1902:C:H41	1.88	0.72
2:D:136:ILE:O	2:D:168:ARG:NH2	2.22	0.72
4:F:101:LEU:HD12	4:F:102:PRO:HD2	1.71	0.72
3:E:111:ARG:HG2	13:R:2:ARG:HE	1.54	0.72
29:9:22:ARG:HH12	35:A:2741:A:H5''	1.54	0.72
5:G:122:PRO:HB3	5:G:170:ARG:HH21	1.53	0.72
35:A:976:C:H2'	35:A:977:G:H8	1.53	0.72
26:6:30:THR:O	26:6:32:ASN:N	2.20	0.72
35:A:1346:G:H1	35:A:1600:C:H42	0.79	0.72
1:C:121:MET:O	1:C:125:GLY:N	2.22	0.72
4:F:197:ASP:OD2	4:F:198:ALA:N	2.23	0.72
2:D:222:ARG:N	35:A:1789:A:OP1	2.14	0.72
35:A:86:C:HO2'	35:A:104:U:HO2'	1.28	0.72
12:Q:135:ASP:O	12:Q:137:TYR:N	2.22	0.72
35:A:1317:A:H61	35:A:1335:U:H3	1.38	0.72
26:6:15:GLU:HB2	26:6:20:ASN:HB2	1.70	0.72
35:A:144:C:H2'	35:A:145:G:H8	1.54	0.72
15:T:50:ILE:HA	15:T:99:LEU:HD12	1.72	0.72
35:A:994:C:H42	35:A:1160:G:H1	1.38	0.72
35:A:270(J):G:N2	35:A:270(R):C:N3	2.36	0.71
26:6:15:GLU:HG3	26:6:47:THR:HG21	1.71	0.71
35:A:573:G:N1	35:A:2031:A:OP2	2.21	0.71
35:A:382:G:H1	35:A:392:C:H42	1.38	0.71
14:S:15:ARG:HB3	14:S:18:ILE:HB	1.71	0.71
16:U:6:THR:HG21	16:U:10:ARG:HH21	1.54	0.71
1:C:16:ASP:O	1:C:18:ASN:N	2.23	0.71
12:Q:14:ARG:NH1	35:A:958:U:OP2	2.24	0.71
13:R:76:VAL:HA	13:R:79:LEU:HB2	1.73	0.71
1:C:52:PRO:HG3	1:C:168:LYS:HA	1.71	0.71
4:F:125:LEU:HA	4:F:194:MET:HB2	1.73	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:1083:U:O2'	35:A:1085:A:N7	2.18	0.71
14:S:35:ILE:H	14:S:53:SER:HB3	1.55	0.71
27:7:21:ARG:HB3	27:7:31:LEU:HD11	1.73	0.71
1:C:162:ILE:HG21	1:C:193:PHE:HE1	1.55	0.70
26:6:19:ARG:O	26:6:20:ASN:ND2	2.23	0.70
4:F:2:LYS:O	4:F:4:VAL:N	2.23	0.70
14:S:70:GLY:HA3	14:S:99:LYS:HG3	1.73	0.70
9:N:56:ASN:HA	9:N:125:GLY:H	1.56	0.70
22:0:25:ARG:HH12	35:A:2355:C:H5'	1.56	0.70
35:A:2454:G:H1	35:A:2498:C:H42	1.39	0.70
14:S:38:GLN:HG2	14:S:50:SER:HB2	1.72	0.70
10:O:43:VAL:HB	10:O:55:GLY:H	1.55	0.70
35:A:1014:U:O4	35:A:1148:A:N1	2.24	0.70
9:N:41:ASP:CA	16:U:64:ARG:HH11	2.05	0.70
35:A:2119:A:H61	35:A:2168:G:H21	1.39	0.70
35:A:1782:C:H42	35:A:2586:C:N4	1.89	0.70
16:U:92:ARG:HD3	16:U:95:LEU:HG	1.74	0.70
35:A:2780:G:H4'	35:A:2781:A:OP2	1.92	0.70
35:A:2133:G:N2	35:A:2158:A:N6	2.15	0.70
35:A:1336:A:H2'	35:A:1337:G:C8	2.26	0.70
11:P:56:SER:O	11:P:58:THR:N	2.24	0.70
33:4:10:VAL:HG22	33:4:11:PRO:HD2	1.74	0.70
35:A:2304:G:H22	35:A:2312:U:H3	1.38	0.70
35:A:2641:G:O6	35:A:2773:C:N3	2.24	0.70
2:D:268:ARG:NH1	35:A:2224:G:OP1	2.24	0.70
1:C:30:VAL:HG13	1:C:33:LEU:HB2	1.74	0.70
35:A:307:G:N2	35:A:310:A:OP2	2.21	0.70
36:B:81:G:H1	36:B:95:U:H3	1.40	0.70
36:B:85:G:O6	36:B:91:C:N3	2.24	0.70
35:A:273(B):G:H1	35:A:363(F):U:H3	1.40	0.70
32:1:52:ARG:HA	32:1:57:GLU:HA	1.74	0.70
2:D:263:ARG:NH1	35:A:2227:A:OP1	2.22	0.70
25:5:22:HIS:NE2	35:A:2045:C:O2	2.25	0.70
8:K:116:ASN:HB2	35:A:1058:G:H1'	1.72	0.70
35:A:1825:A:H2'	35:A:1826:G:C8	2.27	0.70
35:A:2886:G:H2'	35:A:2887:U:C6	2.27	0.70
2:D:118:VAL:N	2:D:129:ASN:OD1	2.22	0.69
22:0:20:ARG:HD2	22:0:20:ARG:H	1.56	0.69
35:A:854:G:N2	35:A:923:C:N3	2.35	0.69
4:F:191:ARG:HB3	4:F:193:VAL:HG23	1.73	0.69
22:0:23:VAL:HG12	22:0:38:VAL:HG22	1.74	0.69
35:A:1051:G:H1	35:A:1108:U:H3	1.39	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:R:23:ASN:HD21	35:A:1277:G:H1'	1.56	0.69
35:A:2466:C:N4	35:A:2484:G:H1	1.89	0.69
35:A:2642:G:H1	35:A:2772:C:N4	1.89	0.69
15:T:91:ARG:O	15:T:120:ARG:NH2	2.21	0.69
20:Y:85:VAL:HG21	35:A:297:C:H5''	1.73	0.69
4:F:63:LYS:HG3	4:F:76:GLY:HA2	1.75	0.69
35:A:1019:U:H2'	35:A:1020:A:C8	2.28	0.69
35:A:1806:C:H42	35:A:1811:G:H1	1.38	0.69
5:G:150:ASP:OD2	5:G:153:ARG:NH2	2.24	0.69
35:A:2068:U:H3	35:A:2430:A:H2	1.41	0.69
3:E:9:VAL:HG12	15:T:8:LYS:HE3	1.75	0.69
35:A:873:G:H1	35:A:904:C:H42	1.39	0.69
35:A:2008:C:H2'	35:A:2009:G:C8	2.28	0.69
32:1:86:SER:HB2	32:1:89:GLU:HB2	1.74	0.69
35:A:1358:G:N1	35:A:1372:U:OP2	2.23	0.69
36:B:18:G:H1	36:B:65:C:H42	1.40	0.69
2:D:256:GLY:O	35:A:1843:C:O2'	2.11	0.69
4:F:182:ASN:HD21	4:F:184:TYR:HB3	1.57	0.68
2:D:165:ILE:O	2:D:166:GLN:HB2	1.93	0.68
35:A:244:A:H62	35:A:254:G:H21	1.40	0.68
4:F:44:ARG:HB3	35:A:615:G:H21	1.56	0.68
7:J:50:UNK:H	7:J:82:UNK:HA	1.58	0.68
35:A:2133:G:H21	35:A:2158:A:H62	0.74	0.68
35:A:1516:U:H2'	35:A:1517:G:C8	2.29	0.68
20:Y:85:VAL:HA	20:Y:94:LYS:HA	1.73	0.68
35:A:1049:C:H1'	35:A:1113:U:H4'	1.75	0.68
35:A:578:A:OP1	35:A:1255:U:O2'	2.10	0.68
35:A:286:C:N4	35:A:355:G:H1	1.86	0.68
35:A:273(G):C:H3'	35:A:274:G:H5''	1.74	0.68
1:C:101:ILE:HD12	1:C:104:ILE:HD12	1.76	0.68
26:6:53:LYS:HG3	26:6:54:ILE:HG12	1.75	0.68
3:E:134:ILE:HB	3:E:137:HIS:HB2	1.75	0.68
35:A:2080:G:H1	35:A:2240:C:H42	1.40	0.68
6:H:85:LYS:HD2	6:H:133:VAL:HB	1.75	0.68
11:P:79:ARG:HH22	11:P:109:GLY:HA2	1.58	0.68
2:D:134:ARG:HG3	2:D:135:PHE:HD1	1.58	0.68
21:Z:69:THR:HA	21:Z:91:LEU:HG	1.76	0.68
20:Y:32:PRO:HD2	20:Y:34:LYS:H	1.58	0.68
35:A:2250:G:O2'	35:A:2496:C:OP1	2.10	0.68
27:7:10:ARG:NH1	35:A:771:G:OP1	2.27	0.68
10:O:14:THR:HG22	10:O:52:VAL:HG21	1.74	0.68
8:K:106:GLU:HA	8:K:109:LYS:HD3	1.76	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:1270:C:H5''	35:A:1271:G:H5''	1.76	0.68
28:8:53:PRO:HA	28:8:56:GLU:HB2	1.74	0.68
11:P:67:MET:H	35:A:2415:G:H4'	1.58	0.68
10:O:68:GLU:HB3	10:O:78:ARG:HB3	1.76	0.68
2:D:148:GLU:HB3	2:D:151:LYS:HG3	1.76	0.68
27:7:30:VAL:O	27:7:34:ARG:HG2	1.94	0.67
15:T:49:VAL:HG23	15:T:63:VAL:HG12	1.75	0.67
24:3:9:VAL:HG23	24:3:10:LYS:H	1.58	0.67
15:T:55:ASN:H	15:T:59:THR:HB	1.60	0.67
9:N:40:PRO:HB3	16:U:68:ALA:HB2	1.73	0.67
14:S:105:ALA:O	14:S:107:GLU:N	2.27	0.67
4:F:7:TYR:HD2	4:F:19:GLU:HG3	1.59	0.67
35:A:1207:C:N4	35:A:1239:G:H1	1.91	0.67
35:A:1800:C:H42	35:A:1817:G:H22	1.42	0.67
28:8:16:ILE:HG22	28:8:22:VAL:HG22	1.77	0.67
19:X:59:VAL:O	19:X:76:ARG:NH1	2.26	0.67
35:A:2115:G:O2'	35:A:2171:A:N6	2.28	0.67
35:A:1497:U:H5'	35:A:1498:C:C5	2.29	0.67
36:B:14:U:O3'	36:B:107:U:O2'	2.12	0.67
1:C:61:GLY:HA3	1:C:164:PHE:CD1	2.30	0.67
35:A:2123:G:H1	35:A:2175:C:H42	1.43	0.67
1:C:47:LYS:HG3	1:C:47:LYS:O	1.95	0.67
33:4:28:LYS:HB3	33:4:31:ILE:HD11	1.77	0.67
5:G:47:LYS:HA	5:G:82:LEU:HG	1.75	0.67
35:A:20:C:N4	35:A:520:G:H1	1.89	0.67
1:C:30:VAL:HG22	1:C:33:LEU:HD12	1.76	0.67
22:0:44:ARG:NH1	35:A:2330:G:O2'	2.28	0.67
18:W:38:TYR:HD2	25:5:30:LEU:HD21	1.60	0.67
15:T:33:LYS:HG2	15:T:43:GLN:HB3	1.77	0.67
3:E:61:ARG:HG3	35:A:2811:G:OP1	1.95	0.67
35:A:380:U:H2'	35:A:381:G:H8	1.59	0.67
35:A:872:A:H61	35:A:905:U:H3	1.42	0.67
5:G:43:LEU:HB3	5:G:45:GLU:HG2	1.77	0.67
35:A:1214:A:H2'	35:A:1215:G:H8	1.60	0.67
19:X:62:LYS:NZ	35:A:1338:G:N7	2.42	0.67
11:P:66:GLY:HA3	35:A:631:A:H1'	1.77	0.67
35:A:528:A:H2	35:A:2043:C:H4'	1.60	0.67
8:K:13:PRO:HA	8:K:52:ILE:HA	1.76	0.67
35:A:1030:G:H1	35:A:1124:C:H42	1.43	0.67
11:P:32:THR:OG1	11:P:35:HIS:O	2.13	0.67
35:A:740:U:H2'	35:A:741:G:H8	1.58	0.66
10:O:23:ARG:HH22	10:O:31:LYS:HG2	1.57	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:S:22:GLY:O	14:S:23:ARG:NE	2.28	0.66
13:R:90:ARG:HH12	35:A:2881:C:H5'	1.61	0.66
35:A:2526:G:H5'	35:A:2743:C:H5'	1.76	0.66
32:1:26:ARG:O	32:1:32:LYS:N	2.25	0.66
3:E:127:ASP:HA	3:E:135:HIS:NE2	2.11	0.66
2:D:134:ARG:HE	2:D:135:PHE:HE1	1.41	0.66
35:A:700:G:H1	35:A:732:C:H42	1.44	0.66
26:6:5:VAL:HB	35:A:2283:C:H5'	1.76	0.66
19:X:36:LYS:N	35:A:1599:C:OP1	2.28	0.66
21:Z:140:ASP:OD2	21:Z:140:ASP:N	2.27	0.66
35:A:2047:U:H2'	35:A:2048:G:C8	2.30	0.66
35:A:2138:C:H42	35:A:2153:G:H1	0.79	0.66
35:A:2633:G:H1	35:A:2785:C:H42	1.41	0.66
35:A:884:C:N3	35:A:892:G:C2	2.64	0.66
27:7:33:ARG:HB2	27:7:34:ARG:HH12	1.60	0.66
15:T:107:ASP:N	15:T:109:GLU:OE1	2.28	0.66
2:D:264:LYS:HD3	2:D:266:SER:H	1.59	0.66
35:A:681:G:H2'	35:A:682:G:C8	2.31	0.66
35:A:2293:C:N4	35:A:2339:G:H1	1.94	0.66
35:A:392:C:H5''	35:A:409:C:H5''	1.78	0.66
35:A:2047:U:H2'	35:A:2048:G:H8	1.61	0.66
15:T:29:ARG:HA	15:T:46:GLU:HB3	1.78	0.66
5:G:27:ASN:HB3	5:G:30:GLU:HB3	1.78	0.66
25:5:11:THR:HG21	35:A:1264:G:H5'	1.77	0.66
35:A:2698:U:H2'	35:A:2699:C:C6	2.30	0.66
1:C:64:SER:HA	1:C:160:GLY:HA3	1.78	0.66
23:2:27:GLU:HA	23:2:30:ARG:HD3	1.78	0.66
35:A:1434:A:H2'	35:A:1435:G:C8	2.30	0.66
1:C:60:ARG:HE	1:C:142:LYS:HB3	1.61	0.66
35:A:864:G:H1'	35:A:914:C:H42	1.60	0.66
11:P:17:LYS:NZ	11:P:19:VAL:O	2.29	0.66
35:A:2892:A:H2'	35:A:2893:G:H5'	1.78	0.66
25:5:33:CYS:HA	25:5:40:LYS:HE3	1.77	0.66
17:V:56:SER:H	17:V:100:ARG:HG3	1.60	0.66
14:S:89:ARG:HG2	14:S:92:TYR:HB3	1.78	0.66
35:A:1286:A:O2'	35:A:1288:U:OP2	2.14	0.65
21:Z:145:GLU:HB3	21:Z:148:ASP:HB2	1.76	0.65
35:A:1906:G:H1	35:A:1924:C:N4	1.90	0.65
35:A:1538:G:H2'	35:A:1539:G:C8	2.31	0.65
4:F:185:ASP:OD2	4:F:188:ARG:NH2	2.27	0.65
35:A:2089:U:O2	35:A:2230:G:N2	2.29	0.65
16:U:90:VAL:HG11	17:V:39:LEU:HG	1.77	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:83:G:N2	35:A:103:A:OP2	2.24	0.65
10:O:64:ARG:HH21	10:O:101:PRO:HD2	1.60	0.65
3:E:159:HIS:HB3	35:A:2621:A:H4'	1.76	0.65
35:A:813:U:H2'	35:A:814:C:H6	1.61	0.65
16:U:87:GLY:O	16:U:89:GLU:N	2.28	0.65
35:A:151:C:H42	35:A:175:G:H1	1.44	0.65
35:A:947:G:N2	35:A:970:C:N3	2.37	0.65
14:S:99:LYS:HG2	14:S:101:LEU:H	1.60	0.65
35:A:812:C:HO2'	35:A:1226:A:HO2'	1.43	0.65
6:H:98:LEU:HD13	6:H:125:VAL:HG23	1.77	0.65
35:A:1345:C:N4	35:A:1601:G:H1	1.94	0.65
27:7:29:LYS:HD2	35:A:210:C:OP1	1.97	0.65
35:A:2690:C:N4	35:A:2713:A:O2'	2.29	0.65
35:A:1639:U:H2'	35:A:1640:C:H5''	1.78	0.65
35:A:1095:A:H2'	35:A:1096:A:C8	2.32	0.65
4:F:90:PHE:HB3	35:A:588:U:H1'	1.78	0.65
35:A:1019:U:H2'	35:A:1020:A:H8	1.60	0.65
16:U:55:ARG:HD3	35:A:1155:A:H5'	1.77	0.65
18:W:72:LYS:H	18:W:107:LEU:HA	1.62	0.65
35:A:2816:C:H42	35:A:2830:G:H1	1.45	0.65
3:E:2:LYS:NZ	3:E:95:ILE:O	2.29	0.65
35:A:122:G:H1	35:A:129:C:N4	1.87	0.65
35:A:1608:A:O2'	35:A:1610:A:OP2	2.15	0.65
35:A:1776:G:H1	35:A:1788:C:H42	1.45	0.65
35:A:1497:U:H5'	35:A:1498:C:H5	1.59	0.65
35:A:717:G:H2'	35:A:718:A:O4'	1.95	0.65
2:D:54:ARG:NH1	35:A:1815:A:OP2	2.24	0.65
35:A:1899:G:H21	35:A:1902:C:H41	1.45	0.65
35:A:26:G:N2	35:A:513:A:OP2	2.30	0.65
35:A:2707:G:H2'	35:A:2708:G:H8	1.62	0.65
22:0:82:ARG:HG2	22:0:83:PRO:HD2	1.79	0.65
3:E:98:PRO:HA	3:E:172:VAL:HG13	1.77	0.64
9:N:15:LEU:HD21	9:N:55:VAL:HG13	1.79	0.64
19:X:57:LEU:HB3	35:A:1341:U:H4'	1.79	0.64
3:E:65:GLY:HA2	3:E:70:ALA:HA	1.79	0.64
14:S:84:GLN:HA	14:S:106:ARG:HG2	1.79	0.64
10:O:34:THR:OG1	10:O:35:VAL:N	2.30	0.64
9:N:24:GLY:O	9:N:26:LEU:N	2.30	0.64
32:1:3:LYS:HG3	32:1:4:VAL:HG12	1.79	0.64
32:1:63:ALA:HB3	32:1:66:HIS:HB2	1.79	0.64
35:A:702:G:H1	35:A:730:C:H42	1.45	0.64
36:B:40:U:H3'	36:B:41:U:H5''	1.78	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:Q:110:THR:HB	12:Q:113:GLN:HB2	1.79	0.64
4:F:111:ALA:HB2	4:F:206:ILE:HG21	1.79	0.64
17:V:89:GLN:HE22	35:A:1162:G:H1'	1.62	0.64
13:R:41:ALA:HB1	13:R:97:VAL:HG11	1.79	0.64
35:A:1484:G:O6	35:A:1505:C:N3	2.31	0.64
2:D:35:LYS:HD3	2:D:61:LEU:HG	1.80	0.64
35:A:1526:G:H1	35:A:154(B):C:H42	1.46	0.64
4:F:157:VAL:O	4:F:193:VAL:O	2.15	0.64
13:R:45:ARG:HB2	13:R:95:THR:HG21	1.78	0.64
11:P:59:LEU:O	28:8:13:ARG:NH1	2.30	0.64
6:H:98:LEU:HD22	6:H:125:VAL:H	1.63	0.64
35:A:2263:C:H42	35:A:2277:G:H1	1.45	0.64
9:N:41:ASP:C	16:U:64:ARG:HH11	2.02	0.64
1:C:81:GLY:O	1:C:84:ILE:HB	1.97	0.64
1:C:26:ALA:HA	1:C:30:VAL:HG23	1.80	0.64
35:A:2711:A:H5''	35:A:2712:U:H5'	1.79	0.64
1:C:73:VAL:HG23	1:C:112:ASP:HB3	1.79	0.64
35:A:2265:U:H3'	35:A:2266:A:C8	2.31	0.64
23:2:21:LEU:O	23:2:25:VAL:HG23	1.96	0.64
6:H:157:TYR:CZ	35:A:2531:A:H5''	2.31	0.64
35:A:882:G:N2	35:A:894:C:C2	2.66	0.64
9:N:41:ASP:HA	16:U:64:ARG:NH1	2.12	0.64
35:A:659:C:H2'	35:A:660:G:H8	1.63	0.64
28:8:22:VAL:HB	28:8:53:PRO:HB3	1.79	0.64
24:3:7:LYS:HE2	24:3:32:GLN:HA	1.80	0.64
35:A:2829:C:H2'	35:A:2830:G:C8	2.33	0.64
5:G:76:SER:HA	5:G:83:ARG:HB3	1.80	0.64
20:Y:42:VAL:HG21	20:Y:67:LEU:HD22	1.79	0.63
19:X:12:VAL:HA	19:X:29:TRP:NE1	2.12	0.63
9:N:137:LYS:HZ2	9:N:137:LYS:HB3	1.63	0.63
26:6:16:CYS:HB3	26:6:17:LYS:HD2	1.80	0.63
35:A:2508:G:H1	35:A:2580:U:H3	1.45	0.63
35:A:1663:C:N4	35:A:1997:G:H1	1.88	0.63
10:O:68:GLU:OE2	10:O:78:ARG:NH1	2.30	0.63
20:Y:97:ARG:NE	35:A:300:A:OP1	2.29	0.63
8:K:44:ALA:O	8:K:46:ALA:N	2.31	0.63
15:T:119:LYS:NZ	35:A:2867:G:OP2	2.20	0.63
11:P:66:GLY:HA2	35:A:2415:G:H4'	1.79	0.63
20:Y:76:CYS:SG	20:Y:99:CYS:HB3	2.39	0.63
5:G:124:SER:OG	5:G:132:ASN:O	2.16	0.63
35:A:78:A:H2'	35:A:79:G:H8	1.63	0.63
35:A:1203:G:H21	35:A:1242:A:H62	1.46	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:G:105:LYS:HE3	33:4:26:SER:HB3	1.80	0.63
35:A:1347:G:H2'	35:A:1348:G:H8	1.64	0.63
4:F:3:GLU:HA	4:F:24:LEU:HB2	1.80	0.63
32:1:17:SER:HG	32:1:42:GLN:H	1.46	0.63
3:E:93:VAL:HB	3:E:175:VAL:HG23	1.79	0.63
2:D:143:HIS:CD2	2:D:196:VAL:HG13	2.34	0.63
17:V:59:ALA:HA	17:V:96:ILE:HA	1.81	0.63
35:A:373:U:H2'	35:A:374:A:C8	2.33	0.63
35:A:1755:A:H61	35:A:2694:G:H21	1.45	0.63
7:J:25:UNK:N	7:J:112:UNK:N	2.47	0.63
6:H:41:MET:HE2	6:H:52:VAL:HG13	1.80	0.63
32:1:16:ASN:HB3	35:A:381:G:H5'	1.81	0.63
13:R:97:VAL:HG13	13:R:114:VAL:HG22	1.79	0.63
11:P:59:LEU:HA	11:P:61:ARG:CZ	2.28	0.63
20:Y:31:LEU:HD22	20:Y:32:PRO:HB3	1.79	0.63
35:A:1771:C:H2'	35:A:1772:G:C8	2.34	0.63
32:1:12:PRO:HA	32:1:44:PRO:HD3	1.81	0.63
35:A:1434:A:H2'	35:A:1435:G:H8	1.63	0.63
2:D:85:ASP:HB2	2:D:92:ILE:HG12	1.80	0.63
35:A:2793:G:H1	35:A:2803:C:H42	1.47	0.63
25:5:7:PRO:HA	35:A:2615:U:C2	2.34	0.63
13:R:105:ARG:HH12	18:W:40:ASN:HA	1.63	0.63
35:A:828:U:H4'	35:A:831:G:C2	2.34	0.63
2:D:210:GLY:HA2	35:A:764:A:H5'	1.80	0.63
20:Y:49:VAL:HA	35:A:483:A:H4'	1.81	0.63
11:P:41:ARG:HE	11:P:45:LEU:HD22	1.64	0.63
35:A:2691:C:H5'	35:A:2872:G:H5''	1.80	0.63
8:K:79:ARG:HA	8:K:84:LEU:HB3	1.81	0.63
35:A:814:C:H42	35:A:1193:G:H1	0.75	0.62
27:7:39:ARG:HH12	27:7:42:LEU:HB2	1.64	0.62
12:Q:70:PRO:HA	12:Q:95:ALA:HB2	1.80	0.62
9:N:125:GLY:HA3	9:N:126:PRO:O	1.99	0.62
12:Q:37:LEU:HD21	12:Q:130:LYS:HB2	1.81	0.62
35:A:1090:U:H2'	35:A:1091:G:C8	2.34	0.62
1:C:139:PRO:HA	1:C:145:THR:HG21	1.80	0.62
35:A:1340:U:H4'	35:A:1394:U:H1'	1.81	0.62
16:U:106:PHE:O	16:U:109:LEU:N	2.32	0.62
6:H:118:PRO:HG2	6:H:121:ILE:HD11	1.80	0.62
35:A:863:A:H2'	35:A:864:G:H8	1.63	0.62
28:8:33:ASN:ND2	35:A:2420:C:OP2	2.24	0.62
11:P:65:ARG:NH2	28:8:15:LYS:HB2	2.14	0.62
18:W:18:ARG:NH1	18:W:76:VAL:HG13	2.13	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:740:U:H2'	35:A:741:G:C8	2.34	0.62
35:A:2135:A:H4'	35:A:2160:G:H4'	1.81	0.62
35:A:2448:A:H3'	35:A:2449:U:H2'	1.80	0.62
35:A:506:G:H5'	35:A:509:C:H1'	1.81	0.62
35:A:216:A:H2'	35:A:217:G:O4'	1.99	0.62
27:7:33:ARG:HB2	27:7:34:ARG:NH1	2.15	0.62
11:P:58:THR:O	11:P:61:ARG:NE	2.31	0.62
11:P:54:GLY:HA3	35:A:826:U:O2'	2.00	0.62
35:A:371:A:H61	35:A:401:A:H3'	1.64	0.62
35:A:2692:C:H2'	35:A:2693:A:H8	1.65	0.62
15:T:129:ARG:HE	15:T:129:ARG:HA	1.64	0.62
16:U:15:LYS:NZ	35:A:1217:C:OP2	2.23	0.62
22:0:39:ARG:NH1	22:0:56:ASP:OD1	2.33	0.62
15:T:35:LYS:HD2	15:T:41:ARG:HD2	1.81	0.62
32:1:34:THR:HG23	32:1:35:THR:H	1.63	0.62
35:A:1058:G:H2'	35:A:1059:G:H8	1.64	0.62
35:A:1310:G:O2'	35:A:1611:C:OP1	2.17	0.62
35:A:1315:C:N4	35:A:1337:G:H1	1.97	0.62
35:A:1214:A:H2'	35:A:1215:G:C8	2.35	0.62
3:E:172:VAL:HA	3:E:184:VAL:HG12	1.82	0.62
35:A:401:A:H2'	35:A:402:A:H8	1.64	0.62
32:1:30:VAL:HG12	35:A:2396:G:H1'	1.79	0.62
9:N:103:VAL:O	9:N:106:MET:N	2.32	0.62
19:X:11:PRO:HG3	23:2:41:ILE:HG22	1.80	0.62
21:Z:40:ASP:HB3	21:Z:43:GLU:HG2	1.81	0.62
35:A:1487:G:H1	35:A:1502:C:N4	1.98	0.62
13:R:20:LEU:HD11	35:A:1277:G:H4'	1.82	0.62
2:D:186:HIS:O	2:D:188:GLU:N	2.32	0.62
35:A:1802:A:OP1	35:A:1814:G:N1	2.33	0.62
32:1:76:ARG:NH2	32:1:94:LEU:O	2.33	0.62
14:S:40:ILE:HA	14:S:47:THR:HA	1.82	0.62
28:8:42:ARG:NH2	35:A:2348:U:OP2	2.32	0.62
12:Q:10:ARG:HB3	12:Q:90:VAL:HG11	1.79	0.62
35:A:681:G:N2	35:A:796:C:N3	2.34	0.62
5:G:36:LYS:HB3	5:G:95:ARG:NH1	2.14	0.62
22:0:12:ASN:ND2	35:A:2277:G:OP2	2.30	0.62
11:P:9:ASN:H	11:P:10:PRO:HD3	1.65	0.62
3:E:4:ILE:HD12	3:E:28:ALA:HB1	1.82	0.62
35:A:88:G:H2'	35:A:89:G:H8	1.65	0.62
22:0:4:LYS:HE2	22:0:7:LEU:HD12	1.81	0.62
35:A:852:G:H2'	35:A:853:G:C8	2.34	0.61
21:Z:7:ALA:O	21:Z:62:PRO:HD2	1.99	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:141(A):A:H8	35:A:1595:G:H21	1.47	0.61
35:A:918:A:N3	36:B:80:U:O2'	2.31	0.61
13:R:26:LYS:HZ3	35:A:1294:U:H4'	1.65	0.61
6:H:139:GLN:NE2	35:A:2745:C:O2	2.32	0.61
35:A:868:U:H3	35:A:909:A:H61	1.48	0.61
1:C:182:PRO:O	1:C:186:LEU:HD12	2.00	0.61
14:S:67:ARG:HA	14:S:99:LYS:HB3	1.80	0.61
3:E:109:LYS:NZ	35:A:2681:C:OP2	2.27	0.61
36:B:24:G:N1	36:B:56:G:N2	2.49	0.61
2:D:220:HIS:N	35:A:1790:C:OP1	2.34	0.61
11:P:94:GLU:HG2	11:P:124:LYS:HB2	1.81	0.61
20:Y:2:ARG:CZ	35:A:106:C:H1'	2.31	0.61
35:A:2328:A:H2'	35:A:2329:G:C8	2.35	0.61
35:A:689:A:H2'	35:A:690:G:C8	2.35	0.61
4:F:168:ARG:HA	4:F:175:THR:HG21	1.82	0.61
35:A:2084:C:H42	35:A:2235:G:H1	1.46	0.61
35:A:922:U:H2'	35:A:923:C:C6	2.35	0.61
35:A:2437:U:H2'	35:A:2438:U:H6	1.65	0.61
32:1:27:GLU:HA	32:1:31:GLY:HA2	1.81	0.61
1:C:47:LYS:HE3	1:C:211:ARG:HH21	1.65	0.61
35:A:1018:C:N4	35:A:1144:G:H1	1.98	0.61
35:A:1538:G:H2'	35:A:1539:G:H8	1.64	0.61
32:1:18:ILE:HG21	35:A:380:U:H4'	1.82	0.61
4:F:193:VAL:O	4:F:194:MET:HG2	2.00	0.61
15:T:56:GLY:H	15:T:59:THR:HB	1.64	0.61
21:Z:54:HIS:HB3	21:Z:101:PRO:HG3	1.82	0.61
2:D:231:HIS:O	2:D:233:HIS:N	2.34	0.61
35:A:2643:G:H1	35:A:2771:C:H42	1.47	0.61
19:X:40:LYS:HG3	19:X:51:VAL:HB	1.83	0.61
35:A:2093:G:H1	35:A:2196:C:H42	0.73	0.61
14:S:97:ARG:O	14:S:99:LYS:N	2.34	0.61
2:D:157:ARG:NH2	35:A:1817:G:H3'	2.16	0.61
5:G:19:LEU:HD11	5:G:172:LEU:HB2	1.81	0.61
35:A:1326:U:H2'	35:A:1327:C:O4'	2.01	0.61
27:7:40:TRP:CE3	35:A:459:U:H5''	2.36	0.61
35:A:1400:G:H2'	35:A:1401:G:C8	2.36	0.61
16:U:91:ASP:O	16:U:95:LEU:HB2	2.00	0.61
35:A:2789:C:H2'	35:A:2790:A:H4'	1.82	0.61
26:6:8:LYS:HZ2	26:6:27:LYS:HB2	1.66	0.61
27:7:40:TRP:CE3	35:A:459:U:H3'	2.36	0.61
35:A:1817:G:H2'	35:A:1818:U:H5'	1.83	0.61
35:A:1603:A:H5'	35:A:1604:C:OP2	2.00	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:1999:C:H5''	35:A:2723:C:O2'	2.00	0.61
12:Q:26:TYR:O	12:Q:67:ARG:NH1	2.34	0.61
25:5:19:ARG:NH1	35:A:1266:G:OP2	2.33	0.61
3:E:61:ARG:O	3:E:63:LEU:N	2.34	0.61
21:Z:61:LEU:O	21:Z:63:ASP:N	2.33	0.61
35:A:1800:C:N4	35:A:1817:G:H22	1.99	0.60
35:A:603:A:N6	35:A:655:A:H1'	2.16	0.60
35:A:2224:G:H4'	35:A:2226:C:C2	2.35	0.60
28:8:5:LYS:NZ	35:A:254:G:N7	2.43	0.60
35:A:742:G:H2'	35:A:743:G:H8	1.66	0.60
35:A:862:G:H2'	35:A:863:A:O4'	2.00	0.60
11:P:62:LEU:HB3	35:A:2393:A:H5''	1.83	0.60
17:V:4:ILE:HG22	17:V:39:LEU:HB2	1.83	0.60
5:G:30:GLU:HB2	36:B:57:A:H1'	1.83	0.60
22:0:72:ARG:O	22:0:76:GLY:N	2.28	0.60
35:A:1796:U:H2'	35:A:1797:C:C6	2.36	0.60
35:A:532:A:OP1	35:A:561:G:N2	2.34	0.60
35:A:978:G:H1	35:A:985:C:N4	1.98	0.60
12:Q:43:THR:HB	12:Q:46:GLN:HB2	1.83	0.60
25:5:40:LYS:HB3	25:5:46:CYS:HB2	1.82	0.60
26:6:27:LYS:NZ	26:6:30:THR:H	1.99	0.60
35:A:137(B):G:H1	35:A:141(B):C:N4	1.99	0.60
35:A:85:G:N1	35:A:97:C:O2	2.27	0.60
8:K:56:GLU:O	8:K:67:PHE:HA	2.01	0.60
3:E:110:GLY:N	35:A:2821:A:OP1	2.26	0.60
5:G:25:TYR:OH	5:G:168:GLU:OE1	2.18	0.60
12:Q:62:GLY:HA2	21:Z:116:VAL:HG21	1.82	0.60
35:A:670:A:H4'	35:A:671:C:H5'	1.83	0.60
14:S:70:GLY:C	14:S:101:LEU:HD21	2.21	0.60
22:0:82:ARG:HH21	22:0:84:LEU:HA	1.66	0.60
11:P:64:LYS:HZ1	35:A:2417:C:P	2.24	0.60
35:A:575:A:OP2	35:A:2499:C:O2'	2.18	0.60
35:A:2629:A:O2'	35:A:2895:U:O4	2.19	0.60
35:A:1948:G:H1	35:A:1958:C:H42	1.50	0.60
14:S:63:THR:OG1	36:B:50:G:OP1	2.16	0.60
2:D:208:LYS:NZ	35:A:729:G:O5'	2.33	0.60
9:N:118:LYS:NZ	35:A:2780:G:OP1	2.22	0.60
22:0:11:ARG:O	22:0:14:ARG:NH2	2.34	0.60
20:Y:73:ARG:HD2	35:A:335:C:H4'	1.82	0.60
5:G:145:THR:OG1	5:G:146:TYR:N	2.27	0.60
16:U:34:LYS:NZ	35:A:2018:G:N3	2.50	0.60
14:S:51:ALA:HB1	14:S:69:VAL:HG22	1.82	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:119:A:H4'	35:A:120:U:H5'	1.83	0.60
35:A:1059:G:H1	35:A:1079:C:N4	2.00	0.60
9:N:61:ARG:HH11	9:N:61:ARG:HG2	1.67	0.60
35:A:2557:G:H2'	35:A:2558:C:C6	2.36	0.60
35:A:37:C:H2'	35:A:38:A:C8	2.37	0.60
3:E:131:ALA:HB1	3:E:133:LYS:HG3	1.84	0.60
4:F:105:VAL:HG22	35:A:600:G:H1'	1.82	0.60
35:A:2817:G:H21	35:A:2836:U:H1'	1.67	0.60
35:A:299:A:N1	35:A:322:A:O2'	2.30	0.60
35:A:1972:A:H2'	35:A:1973:G:H8	1.67	0.60
21:Z:144:LEU:HD21	21:Z:150:LEU:HD22	1.84	0.60
6:H:175:LYS:HD3	6:H:176:ALA:H	1.66	0.60
10:O:25:LEU:HB3	10:O:38:VAL:HG23	1.84	0.60
35:A:1844:C:H42	35:A:1896:G:H1	1.48	0.60
2:D:244:ARG:NH1	35:A:1841:U:O2'	2.34	0.60
18:W:19:LEU:HD12	25:5:25:LEU:H	1.66	0.60
28:8:56:GLU:HA	28:8:59:LYS:HE2	1.84	0.60
18:W:11:ARG:NH2	18:W:99:ARG:O	2.34	0.60
35:A:655:A:H2'	35:A:656:G:O4'	2.02	0.60
10:O:104:ARG:NE	10:O:122:LEU:O	2.34	0.60
35:A:1230:C:H2'	35:A:1231:G:C8	2.37	0.60
35:A:1102:C:H2'	35:A:1103:A:H8	1.67	0.60
20:Y:9:LYS:O	20:Y:28:LYS:NZ	2.23	0.59
35:A:1536:A:H3'	35:A:1537:C:C6	2.37	0.59
3:E:91:VAL:HB	3:E:95:ILE:HD12	1.84	0.59
9:N:73:THR:HB	9:N:82:LEU:HD11	1.82	0.59
23:2:45:SER:O	23:2:46:GLN:NE2	2.35	0.59
35:A:1268:A:H2'	35:A:1269:A:O4'	2.01	0.59
35:A:814:C:N3	35:A:1193:G:N2	2.39	0.59
35:A:1346:G:N2	35:A:1600:C:N3	2.42	0.59
2:D:157:ARG:NH2	35:A:1818:U:H6	1.99	0.59
35:A:401:A:H2'	35:A:402:A:C8	2.37	0.59
8:K:30:HIS:CE1	8:K:32:ALA:HB2	2.37	0.59
35:A:2136:C:N3	35:A:2155:G:N2	2.44	0.59
35:A:819:A:OP2	35:A:1187:G:N2	2.31	0.59
35:A:1417:C:O2'	35:A:1587:A:N3	2.29	0.59
15:T:49:VAL:HG22	15:T:50:ILE:H	1.67	0.59
35:A:900:A:H2'	35:A:901:A:O4'	2.01	0.59
35:A:1707:G:H1	35:A:1751:C:H42	1.48	0.59
3:E:66:HIS:O	3:E:68:ALA:N	2.35	0.59
20:Y:94:LYS:HG3	20:Y:102:CYS:HB2	1.84	0.59
32:1:88:LYS:NZ	35:A:1361:G:OP1	2.34	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:7:8:ASN:HB3	27:7:11:LYS:HB3	1.83	0.59
10:O:2:ILE:HB	10:O:33:ALA:HB3	1.83	0.59
1:C:132:LEU:O	1:C:137:LEU:N	2.33	0.59
35:A:137(B):G:H1	35:A:141(B):C:H42	1.51	0.59
9:N:103:VAL:HG11	9:N:120:LEU:HD13	1.84	0.59
6:H:97:ARG:HD3	6:H:99:VAL:HB	1.84	0.59
35:A:2853:C:H2'	35:A:2854:G:H8	1.68	0.59
27:7:13:ALA:O	27:7:17:GLY:N	2.35	0.59
1:C:41:THR:O	1:C:176:VAL:N	2.36	0.59
13:R:64:ARG:NH2	35:A:2851:A:O2'	2.35	0.59
4:F:10:PRO:HG3	4:F:19:GLU:HA	1.85	0.59
4:F:117:ARG:HB2	4:F:186:ILE:HD11	1.85	0.59
15:T:89:VAL:HG12	15:T:91:ARG:HG3	1.85	0.59
10:O:77:ILE:HD13	15:T:74:ARG:HG2	1.84	0.59
20:Y:76:CYS:O	20:Y:78:ALA:N	2.36	0.59
11:P:92:GLU:OE1	11:P:121:LYS:NZ	2.27	0.59
35:A:1094:U:N3	35:A:1097:U:OP2	2.34	0.59
1:C:44:VAL:HB	1:C:174:ALA:HB3	1.85	0.59
35:A:1324:G:H1'	35:A:1616:A:N6	2.18	0.59
35:A:307:G:H21	35:A:330:A:H62	1.51	0.59
35:A:2818:G:O6	35:A:2828:C:N3	2.35	0.59
35:A:1231:G:H2'	35:A:1232:G:C8	2.36	0.59
2:D:17:THR:HG1	2:D:205:VAL:H	1.51	0.59
2:D:226:MET:HG2	35:A:782:A:C2	2.38	0.59
35:A:1468:C:H2'	35:A:1469:A:C8	2.38	0.59
35:A:2134:A:H2	35:A:2159:G:HO2'	1.51	0.59
2:D:88:ARG:NH2	35:A:1817:G:OP1	2.34	0.59
36:B:66:A:N6	36:B:108:C:OP2	2.35	0.59
1:C:59:VAL:HG13	1:C:202:PRO:HD3	1.84	0.59
35:A:828:U:H4'	35:A:831:G:N1	2.17	0.59
35:A:1861:G:H2'	35:A:1862:G:H8	1.67	0.59
35:A:2023:G:H5'	35:A:2617:C:H4'	1.85	0.59
6:H:16:SER:N	6:H:27:LYS:O	2.34	0.59
35:A:848:G:C2	35:A:933:A:H1'	2.37	0.59
35:A:855:G:H1	35:A:922:U:H3	1.51	0.59
9:N:39:ARG:HH21	9:N:41:ASP:HB3	1.68	0.59
1:C:216:THR:HA	1:C:221:PRO:O	2.03	0.59
1:C:63:VAL:HG12	1:C:162:ILE:HB	1.84	0.59
36:B:18:G:H2'	36:B:19:G:C8	2.37	0.59
1:C:28:ARG:HE	1:C:183:PRO:HB2	1.68	0.59
4:F:89:VAL:HG21	35:A:586:A:H5'	1.85	0.59
35:A:1674:G:H21	35:A:1677:A:H61	1.50	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:U:56:ASP:O	16:U:59:ARG:HB3	2.03	0.59
10:O:37:ASP:N	10:O:37:ASP:OD1	2.36	0.59
35:A:2669:G:H2'	35:A:2670:A:H8	1.67	0.59
32:1:81:LYS:HE2	35:A:270(J):G:H5''	1.85	0.59
35:A:134:C:H42	35:A:145:G:H1	1.50	0.59
35:A:77:C:H42	35:A:109:G:H1	1.51	0.59
25:5:16:ARG:NH1	35:A:1263:U:OP1	2.32	0.59
14:S:47:THR:O	14:S:48:LEU:HB2	2.03	0.58
35:A:137(B):G:O2'	35:A:138:G:N2	2.36	0.58
10:O:64:ARG:HG2	10:O:79:PHE:CD2	2.37	0.58
21:Z:73:GLN:OE1	36:B:102:G:N2	2.33	0.58
6:H:103:LEU:HG	6:H:105:LEU:HD22	1.84	0.58
21:Z:5:LEU:HD12	21:Z:47:VAL:HG11	1.84	0.58
35:A:136:G:H1	35:A:143:C:N4	1.99	0.58
35:A:528:A:C2	35:A:2043:C:H4'	2.38	0.58
16:U:61:TRP:CE2	16:U:94:ASN:HB2	2.38	0.58
35:A:1429:G:H2'	35:A:1430:C:C6	2.37	0.58
35:A:1937:A:N7	35:A:1939:U:H2'	2.18	0.58
35:A:1347:G:H2'	35:A:1348:G:C8	2.37	0.58
17:V:87:HIS:HE1	35:A:1163:G:N2	2.01	0.58
22:0:27:GLU:HB3	22:0:68:GLU:HA	1.85	0.58
11:P:62:LEU:H	11:P:62:LEU:HD23	1.67	0.58
35:A:11:G:N2	35:A:2628:C:OP1	2.35	0.58
3:E:25:VAL:HG22	3:E:183:LEU:HG	1.84	0.58
35:A:1258:C:H2'	35:A:1259:G:H8	1.68	0.58
23:2:9:GLN:HE22	23:2:56:GLN:HG2	1.68	0.58
22:0:23:VAL:HG21	35:A:857:C:H4'	1.86	0.58
21:Z:10:ARG:HG2	21:Z:11:GLU:H	1.68	0.58
2:D:147:LEU:HD13	2:D:155:LEU:HD11	1.85	0.58
5:G:112:PRO:CA	5:G:113:ARG:N	2.62	0.58
35:A:1148:A:H2'	35:A:1149:G:C8	2.38	0.58
18:W:18:ARG:NH2	35:A:517:C:O2'	2.35	0.58
35:A:1207:C:N3	35:A:1239:G:N2	2.45	0.58
13:R:96:ARG:N	13:R:117:VAL:HG21	2.19	0.58
35:A:329:G:H8	35:A:329:G:P	2.26	0.58
35:A:2125:G:H21	35:A:2173:A:H62	1.51	0.58
35:A:836:G:H2'	35:A:837:C:C6	2.38	0.58
35:A:1655:A:C2	35:A:2049:G:H5''	2.38	0.58
35:A:270(J):G:C6	35:A:270(R):C:N4	2.72	0.58
32:1:35:THR:OG1	32:1:36:GLY:N	2.36	0.58
9:N:41:ASP:HA	16:U:64:ARG:HE	1.69	0.58
6:H:55:PRO:HG2	6:H:61:HIS:CE1	2.38	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:1871:A:H2'	35:A:1872:A:C8	2.39	0.58
35:A:1403:C:H5''	35:A:1471:A:H1'	1.86	0.58
35:A:576:U:H2'	35:A:577:G:C8	2.39	0.58
32:1:37:ILE:HG12	35:A:200:U:H4'	1.86	0.58
15:T:5:ALA:O	15:T:9:LEU:HG	2.03	0.58
4:F:82:ILE:HD13	35:A:673:C:H4'	1.86	0.58
2:D:44:ASN:CB	2:D:49:ILE:HA	2.30	0.58
3:E:66:HIS:CD2	35:A:2786:U:H4'	2.38	0.58
4:F:154:VAL:HG23	4:F:173:VAL:HG22	1.86	0.58
21:Z:15:PRO:HG3	36:B:76:G:H5''	1.86	0.58
23:2:4:SER:HA	23:2:7:ARG:HD2	1.85	0.58
35:A:2011:U:H2'	35:A:2012:G:O4'	2.04	0.58
35:A:270(W):G:H2'	35:A:270(X):G:H8	1.68	0.58
35:A:516:C:H2'	35:A:517:C:C6	2.39	0.58
9:N:56:ASN:HA	9:N:125:GLY:N	2.19	0.58
2:D:63:ARG:HB3	2:D:104:TYR:CE1	2.39	0.58
27:7:40:TRP:CZ2	35:A:458:G:H1'	2.39	0.58
35:A:2136:C:H42	35:A:2155:G:H1	1.52	0.58
35:A:1588:C:H2'	35:A:1589:C:C6	2.38	0.58
35:A:270(K):G:C2	35:A:270(L):C:H1'	2.39	0.58
32:1:16:ASN:HB3	35:A:381:G:C5'	2.34	0.58
2:D:14:ARG:NH2	35:A:1693:U:O2'	2.37	0.58
5:G:15:VAL:HG22	5:G:175:LEU:HB2	1.85	0.58
35:A:2105:C:H2'	35:A:2106:G:C8	2.39	0.58
1:C:46:ALA:HA	1:C:212:SER:C	2.23	0.57
35:A:712(B):A:H5''	35:A:2713:A:OP2	2.04	0.57
9:N:106:MET:CE	35:A:1006:C:H1'	2.34	0.57
35:A:688:U:H2'	35:A:689:A:H8	1.68	0.57
5:G:171:ALA:O	5:G:175:LEU:HG	2.03	0.57
35:A:1793:C:H2'	35:A:1794:U:C6	2.39	0.57
9:N:67:LEU:HD12	9:N:87:LEU:HD13	1.86	0.57
35:A:20:C:H2'	35:A:21:A:C8	2.40	0.57
6:H:68:THR:HA	6:H:71:LEU:HD12	1.85	0.57
35:A:28:A:H1'	35:A:513:A:C2	2.39	0.57
35:A:1791:A:N6	35:A:1828:G:O2'	2.34	0.57
35:A:2678:C:H2'	35:A:2679:A:C8	2.39	0.57
5:G:43:LEU:HD23	5:G:88:ILE:HD13	1.86	0.57
35:A:863:A:H2'	35:A:864:G:C8	2.39	0.57
35:A:2830:G:O2'	35:A:2883:A:N1	2.31	0.57
36:B:60:C:H2'	36:B:61:G:C8	2.38	0.57
22:0:46:LYS:HG2	22:0:47:PRO:HD2	1.86	0.57
35:A:911:A:H5''	35:A:912:C:H5''	1.85	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:2104:G:O6	35:A:2185:C:N3	2.37	0.57
12:Q:119:ARG:O	12:Q:123:HIS:HB2	2.04	0.57
2:D:105:ILE:HD13	2:D:106:ILE:N	2.19	0.57
13:R:26:LYS:O	13:R:30:THR:OG1	2.15	0.57
9:N:61:ARG:NH1	9:N:61:ARG:HG2	2.20	0.57
2:D:258:LYS:NZ	35:A:1844:C:O3'	2.23	0.57
35:A:1258:C:H2'	35:A:1259:G:C8	2.40	0.57
3:E:46:ALA:HB2	3:E:82:ARG:HA	1.86	0.57
35:A:1623:G:H2'	35:A:1624:G:H8	1.69	0.57
2:D:125:ILE:HG21	2:D:137:PRO:HG2	1.85	0.57
35:A:1357:U:H3	35:A:1374:G:H1	1.52	0.57
27:7:30:VAL:O	27:7:34:ARG:NH1	2.38	0.57
27:7:34:ARG:NH1	35:A:467:G:OP1	2.37	0.57
12:Q:14:ARG:NH2	35:A:956:G:OP2	2.36	0.57
35:A:1775:U:H2'	35:A:1776:G:O4'	2.05	0.57
35:A:379:G:O2'	35:A:2232:U:OP1	2.22	0.57
25:5:30:LEU:HD13	25:5:39:MET:HB3	1.84	0.57
35:A:2425:A:H4'	35:A:2426:A:H5'	1.85	0.57
10:O:9:GLU:HB3	10:O:18:LYS:HE3	1.85	0.57
36:B:24:G:O2'	36:B:27:C:N4	2.38	0.57
3:E:4:ILE:HD13	3:E:5:LEU:N	2.19	0.57
35:A:628:G:H2'	35:A:629:G:C8	2.39	0.57
15:T:83:ILE:HD12	15:T:84:GLN:HG2	1.87	0.57
35:A:541:C:H2'	35:A:542:C:C6	2.39	0.57
35:A:882:G:C2	35:A:894:C:N3	2.72	0.57
35:A:149(B):A:O2'	35:A:1530:G:N2	2.38	0.57
13:R:45:ARG:O	13:R:49:ASP:HB2	2.04	0.57
35:A:1090:U:H2'	35:A:1091:G:H8	1.68	0.57
4:F:48:THR:O	35:A:442:G:N2	2.34	0.57
5:G:57:ALA:HB1	5:G:90:LEU:HD22	1.86	0.57
20:Y:17:SER:HB3	20:Y:71:LYS:HB3	1.85	0.57
35:A:1535:U:H2'	35:A:1536:A:H5'	1.85	0.57
13:R:49:ASP:HB3	35:A:2839:G:H4'	1.87	0.57
36:B:81:G:O6	36:B:95:U:O2	2.22	0.57
18:W:69:LEU:HD13	18:W:107:LEU:HD21	1.85	0.57
32:1:76:ARG:HH22	32:1:95:LEU:HD13	1.70	0.57
4:F:167:ALA:HB1	4:F:173:VAL:HG11	1.87	0.57
12:Q:7:MET:HG2	35:A:870:A:H4'	1.86	0.57
35:A:1636:C:H2'	35:A:1637:A:C8	2.40	0.57
35:A:2391:G:O2'	35:A:2424:C:N4	2.37	0.57
35:A:1159:U:H2'	35:A:1160:G:H8	1.69	0.57
7:J:50:UNK:O	7:J:82:UNK:N	2.37	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:F:172:TRP:CD1	4:F:173:VAL:HG23	2.40	0.57
35:A:2437:U:H2'	35:A:2438:U:C6	2.40	0.57
5:G:166:ASP:OD2	5:G:167:GLU:N	2.37	0.57
35:A:2794:C:N4	35:A:2802:G:H1	1.99	0.57
36:B:43:C:H2'	36:B:44:G:H5''	1.87	0.57
1:C:128:LEU:HD13	1:C:132:LEU:HD11	1.86	0.57
1:C:128:LEU:HB3	1:C:132:LEU:HG	1.87	0.57
2:D:207:GLY:H	2:D:211:ARG:HD3	1.70	0.57
35:A:2283:C:N3	35:A:2325:G:O6	2.38	0.57
3:E:4:ILE:HD13	3:E:5:LEU:H	1.69	0.57
2:D:37:LEU:HB3	2:D:62:TYR:HB3	1.87	0.57
35:A:2692:C:H2'	35:A:2693:A:C8	2.39	0.57
35:A:1320:C:H42	35:A:1331:A:H62	1.52	0.57
35:A:33:U:O4	35:A:446:G:O2'	2.23	0.57
9:N:127:ASP:OD1	9:N:127:ASP:N	2.36	0.57
35:A:2446:G:N7	35:A:2501:C:O2'	2.36	0.57
17:V:85:LYS:NZ	35:A:815:C:OP1	2.27	0.57
12:Q:19:GLY:HA2	12:Q:98:LYS:HB3	1.86	0.57
20:Y:46:LYS:HE3	20:Y:48:ALA:HB2	1.86	0.57
4:F:157:VAL:HG12	4:F:192:LEU:HA	1.86	0.57
35:A:2678:C:H2'	35:A:2679:A:H8	1.70	0.57
3:E:111:ARG:HG2	13:R:2:ARG:NE	2.20	0.57
35:A:2210:G:H3'	35:A:2210:G:N3	2.19	0.57
35:A:1076:C:H2'	35:A:1077:A:H4'	1.86	0.57
14:S:30:ARG:HH21	14:S:33:LYS:HA	1.69	0.57
16:U:62:ILE:HD12	16:U:76:TYR:CE1	2.40	0.56
15:T:53:ARG:HH21	35:A:2683:C:H5''	1.70	0.56
17:V:31:ALA:O	17:V:61:VAL:HG12	2.05	0.56
13:R:100:LEU:HD13	13:R:101:ALA:H	1.70	0.56
32:1:25:LYS:HB3	35:A:388:G:OP2	2.04	0.56
4:F:107:LYS:NZ	35:A:618(A):G:H5''	2.20	0.56
35:A:2144:U:H2'	35:A:2147:G:H1	1.71	0.56
7:J:23:UNK:O	7:J:85:UNK:N	2.38	0.56
35:A:108:U:H2'	35:A:109:G:H8	1.69	0.56
11:P:8:PRO:HG3	35:A:1242:A:N1	2.20	0.56
35:A:1201:C:H42	35:A:1244:G:H1	1.53	0.56
35:A:1547:C:H2'	35:A:1548:C:C6	2.39	0.56
35:A:2889:C:H2'	35:A:2891:G:O4'	2.05	0.56
17:V:24:LYS:HA	17:V:92:THR:HG23	1.86	0.56
35:A:360:G:H2'	35:A:361:G:C8	2.32	0.56
2:D:78:LYS:O	2:D:78:LYS:NZ	2.31	0.56
32:1:45:ASN:HB3	35:A:397:G:H5''	1.88	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:6:28:ARG:O	26:6:30:THR:N	2.38	0.56
33:4:11:PRO:O	33:4:29:PRO:HA	2.05	0.56
13:R:23:ASN:ND2	35:A:1277:G:H1'	2.20	0.56
35:A:1278:A:H2'	35:A:1279:G:C8	2.40	0.56
35:A:1513:C:H2'	35:A:1514:U:O4'	2.05	0.56
19:X:11:PRO:O	19:X:13:LEU:N	2.35	0.56
11:P:119:GLU:O	11:P:121:LYS:N	2.39	0.56
21:Z:36:LYS:HD3	21:Z:36:LYS:H	1.69	0.56
23:2:32:LEU:HD13	23:2:53:LEU:HB3	1.86	0.56
17:V:35:LEU:HB2	17:V:57:VAL:O	2.05	0.56
35:A:1213:A:H62	35:A:1236:G:H1'	1.70	0.56
35:A:829:A:C8	35:A:2248:C:H5'	2.41	0.56
35:A:1750:G:O2'	35:A:2860:A:N1	2.33	0.56
16:U:25:TRP:HD1	16:U:26:GLY:N	2.04	0.56
35:A:286:C:N3	35:A:355:G:N2	2.45	0.56
36:B:24:G:N1	36:B:56:G:C2	2.74	0.56
32:1:39:LYS:NZ	32:1:40:ARG:O	2.38	0.56
26:6:27:LYS:HZ1	26:6:29:ASN:HB3	1.70	0.56
16:U:6:THR:HG21	16:U:10:ARG:NH2	2.21	0.56
11:P:8:PRO:O	11:P:9:ASN:ND2	2.38	0.56
15:T:121:ILE:O	15:T:125:ARG:HG2	2.05	0.56
15:T:93:ARG:HD2	15:T:115:ARG:HG3	1.87	0.56
18:W:36:LEU:HD13	18:W:48:ALA:HA	1.86	0.56
11:P:86:LYS:HD3	11:P:118:GLY:HA2	1.88	0.56
35:A:2601:C:N4	35:A:2603:G:O6	2.38	0.56
1:C:153:ILE:O	1:C:157:ILE:HG13	2.05	0.56
35:A:131:G:H2'	35:A:132:G:C8	2.37	0.56
8:K:130:SER:O	8:K:133:SER:OG	2.22	0.56
9:N:42:TRP:N	16:U:64:ARG:HE	2.04	0.56
18:W:80:PRO:O	18:W:100:THR:HG22	2.06	0.56
26:6:15:GLU:OE2	26:6:20:ASN:ND2	2.39	0.56
35:A:1565:C:O2'	35:A:1567:A:N7	2.29	0.56
8:K:30:HIS:CD2	8:K:59:ILE:HB	2.41	0.56
13:R:100:LEU:HB3	13:R:111:LEU:HB2	1.88	0.56
36:B:9:G:H1	36:B:111:U:H3	1.53	0.56
35:A:55:G:O2'	35:A:127:A:N1	2.36	0.56
16:U:92:ARG:NH1	17:V:11:GLN:O	2.35	0.56
10:O:103:ALA:HB1	10:O:105:GLU:OE1	2.06	0.56
35:A:1861:G:H2'	35:A:1862:G:C8	2.41	0.56
3:E:11:MET:HA	3:E:24:THR:HA	1.88	0.56
35:A:1405:U:H2'	35:A:1406:U:C6	2.40	0.56
35:A:558:G:H2'	35:A:559:G:H8	1.70	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:X:36:LYS:HA	19:X:39:ILE:HD12	1.88	0.56
35:A:248:G:C2	35:A:2431:U:H4'	2.40	0.56
17:V:18:LEU:H	17:V:96:ILE:HD11	1.70	0.56
10:O:98:VAL:HG22	10:O:117:LEU:HB3	1.88	0.56
33:4:14:ILE:O	33:4:16:CYS:N	2.39	0.56
35:A:2440:C:H5''	35:A:2587:A:H4'	1.88	0.56
14:S:68:GLN:O	14:S:72:ALA:N	2.35	0.56
14:S:25:ARG:HA	14:S:86:ALA:HB3	1.87	0.56
10:O:105:GLU:N	10:O:105:GLU:OE1	2.35	0.56
2:D:125:ILE:HG12	2:D:137:PRO:HG2	1.87	0.56
35:A:594:U:H2'	35:A:595:C:C6	2.41	0.56
35:A:1138:G:H2'	35:A:1139:G:O4'	2.06	0.56
1:C:20:VAL:HG13	1:C:226:ASN:HB2	1.87	0.56
2:D:157:ARG:NH2	35:A:1818:U:O5'	2.39	0.56
35:A:1335:U:H2'	35:A:1336:A:C8	2.41	0.56
35:A:1811:G:H2'	35:A:1812:A:H8	1.71	0.56
10:O:68:GLU:OE1	35:A:2684:U:O2'	2.24	0.56
35:A:1327:C:H3'	35:A:1328:G:C8	2.41	0.56
35:A:679:C:H2'	35:A:680:G:H8	1.71	0.56
35:A:2604:U:H2'	35:A:2605:U:H6	1.70	0.56
8:K:124:ALA:HB3	8:K:125:ARG:CZ	2.36	0.56
35:A:1412:A:H61	35:A:1590:U:H3	1.53	0.56
11:P:53:GLY:C	11:P:55:ARG:H	2.09	0.55
35:A:1638:C:H2'	35:A:1639:U:O4'	2.05	0.55
22:0:49:LYS:HB2	22:0:80:HIS:HB3	1.87	0.55
28:8:4:MET:HE1	35:A:592:G:H21	1.71	0.55
35:A:2133:G:O2'	35:A:2157:G:N1	2.40	0.55
9:N:39:ARG:NH2	9:N:41:ASP:HB3	2.21	0.55
2:D:88:ARG:HE	35:A:1817:G:H5''	1.71	0.55
1:C:133:GLY:N	1:C:138:LEU:HB2	2.22	0.55
32:1:18:ILE:H	32:1:42:GLN:HB2	1.71	0.55
35:A:1278:A:H2'	35:A:1279:G:H8	1.71	0.55
15:T:53:ARG:NH1	15:T:60:THR:OG1	2.38	0.55
10:O:15:GLY:O	10:O:47:ILE:N	2.34	0.55
5:G:31:VAL:O	5:G:33:ARG:HG3	2.07	0.55
12:Q:76:LYS:NZ	35:A:957:A:OP1	2.39	0.55
35:A:1127:A:N7	35:A:2488:A:O2'	2.37	0.55
35:A:2178:C:H2'	35:A:2179:C:H6	1.71	0.55
26:6:27:LYS:HZ1	26:6:30:THR:H	1.53	0.55
5:G:138:GLN:HB2	5:G:153:ARG:O	2.07	0.55
3:E:34:VAL:HG22	3:E:35:GLN:H	1.70	0.55
35:A:1028:A:N3	35:A:2486:G:O2'	2.30	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:817:C:O2'	35:A:839:U:OP1	2.20	0.55
35:A:27:G:N2	35:A:512:G:O2'	2.30	0.55
1:C:63:VAL:HB	1:C:164:PHE:HZ	1.71	0.55
28:8:18:ALA:HB3	35:A:651:G:H5''	1.88	0.55
35:A:380:U:H2'	35:A:381:G:C8	2.40	0.55
26:6:28:ARG:HD3	26:6:29:ASN:N	2.21	0.55
21:Z:30:ASN:HB2	21:Z:90:VAL:HB	1.87	0.55
19:X:49:VAL:HG12	19:X:87:GLN:HB3	1.88	0.55
16:U:25:TRP:HD1	16:U:26:GLY:H	1.54	0.55
11:P:47:ASP:HB3	11:P:51:PHE:HB2	1.89	0.55
9:N:39:ARG:C	9:N:41:ASP:H	2.09	0.55
29:9:22:ARG:NH2	35:A:2741:A:OP1	2.39	0.55
35:A:1800:C:N3	35:A:1817:G:N1	2.53	0.55
2:D:88:ARG:HB3	35:A:1817:G:H5''	1.88	0.55
20:Y:85:VAL:HG12	20:Y:94:LYS:HB3	1.88	0.55
4:F:194:MET:HE3	4:F:198:ALA:HB3	1.88	0.55
35:A:1486:A:H2'	35:A:1487:G:C8	2.42	0.55
21:Z:30:ASN:O	21:Z:32:HIS:N	2.34	0.55
5:G:51:ARG:HH12	5:G:88:ILE:HD12	1.71	0.55
35:A:465:G:H2'	35:A:466:A:C8	2.42	0.55
35:A:1086:A:H4'	35:A:1103:A:H2	1.72	0.55
23:2:42:GLY:O	23:2:45:SER:OG	2.22	0.55
35:A:2593:U:H2'	35:A:2594:C:C6	2.42	0.55
24:3:35:ARG:HB3	24:3:37:LEU:HD13	1.89	0.55
26:6:23:THR:HG21	35:A:2419:U:OP1	2.07	0.55
11:P:122:PRO:HG3	11:P:141:ALA:HB3	1.87	0.55
13:R:13:HIS:O	13:R:16:HIS:N	2.39	0.55
35:A:1336:A:H2'	35:A:1337:G:H8	1.72	0.55
35:A:860:U:H2'	35:A:861:A:C8	2.42	0.55
2:D:130:ALA:HB1	2:D:190:TYR:HD2	1.71	0.55
35:A:676:A:H8	35:A:2069:G:H21	1.54	0.55
2:D:244:ARG:HB2	35:A:1902:C:O2'	2.06	0.55
8:K:133:SER:HB3	35:A:1088:A:H62	1.71	0.55
35:A:1542:G:OP2	35:A:1543:A:H5'	2.07	0.55
18:W:80:PRO:O	18:W:81:ALA:HB2	2.07	0.55
35:A:2788:C:H2'	35:A:2789:C:C6	2.42	0.55
35:A:198:C:H4'	35:A:2243:U:H4'	1.87	0.55
21:Z:30:ASN:ND2	21:Z:90:VAL:O	2.40	0.55
12:Q:19:GLY:O	21:Z:79:ARG:HD3	2.07	0.55
2:D:172:TYR:CD1	2:D:184:LYS:HB3	2.42	0.55
27:7:5:TRP:HD1	35:A:1612:C:H5''	1.71	0.55
2:D:160:GLY:HA3	2:D:199:ALA:HB2	1.88	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:1:6:GLU:HG3	32:1:61:ARG:HB2	1.89	0.55
11:P:95:VAL:HA	11:P:99:LEU:HD23	1.88	0.55
1:C:11:LEU:HD13	1:C:221:PRO:HD3	1.89	0.55
35:A:2241:A:H2'	35:A:2242:G:C8	2.42	0.55
4:F:155:LEU:HD12	4:F:176:LEU:HB3	1.89	0.55
35:A:1434:A:H61	35:A:1558:A:H62	1.55	0.55
16:U:25:TRP:CD1	16:U:26:GLY:N	2.74	0.55
6:H:127:GLU:O	6:H:129:THR:N	2.31	0.55
28:8:61:LEU:HD11	35:A:593:G:O2'	2.07	0.55
14:S:109:GLY:OXT	35:A:2376:A:O2'	2.20	0.55
13:R:88:ARG:NH2	13:R:89:ASP:OD2	2.40	0.55
5:G:60:LEU:O	5:G:63:ILE:HG12	2.07	0.55
16:U:62:ILE:HD12	16:U:76:TYR:HE1	1.70	0.54
1:C:88:GLU:HG3	1:C:95:VAL:HG21	1.88	0.54
4:F:188:ARG:HG3	4:F:189:THR:HG23	1.90	0.54
10:O:64:ARG:O	10:O:82:ASN:HA	2.07	0.54
35:A:2853:C:H2'	35:A:2854:G:C8	2.42	0.54
9:N:85:ILE:HG21	9:N:90:MET:HE3	1.89	0.54
26:6:37:ARG:NH2	35:A:2286:A:N7	2.55	0.54
3:E:72:VAL:HG12	3:E:73:GLU:H	1.71	0.54
9:N:41:ASP:OD2	16:U:64:ARG:NH1	2.40	0.54
15:T:27:THR:O	15:T:87:ASP:HB2	2.06	0.54
16:U:95:LEU:O	16:U:98:LEU:HB3	2.07	0.54
13:R:42:LYS:O	13:R:45:ARG:HG3	2.08	0.54
35:A:2230:G:H2'	35:A:2231:C:C6	2.42	0.54
2:D:109:ASP:HB2	2:D:197:GLY:HA2	1.90	0.54
28:8:26:LYS:HG2	28:8:47:LYS:HG3	1.89	0.54
2:D:140:THR:HG22	2:D:141:VAL:H	1.71	0.54
35:A:938:G:H2'	35:A:939:G:C8	2.42	0.54
36:B:81:G:H3'	36:B:82:G:H8	1.71	0.54
35:A:1677:A:H2'	35:A:1678:G:C8	2.43	0.54
28:8:28:GLY:N	28:8:44:LYS:HZ1	2.05	0.54
35:A:2461:C:H2'	35:A:2462:U:C6	2.43	0.54
18:W:14:PRO:O	18:W:16:LYS:N	2.40	0.54
20:Y:17:SER:OG	20:Y:18:GLY:N	2.38	0.54
4:F:183:VAL:O	4:F:187:VAL:HG23	2.07	0.54
32:1:45:ASN:OD1	32:1:64:ALA:HB2	2.08	0.54
35:A:1690:A:H2'	35:A:1691:C:O4'	2.07	0.54
15:T:2:ASN:O	15:T:4:GLY:N	2.40	0.54
18:W:20:VAL:HA	25:5:25:LEU:HD22	1.88	0.54
14:S:95:HIS:O	14:S:97:ARG:N	2.33	0.54
32:1:21:ARG:HG3	35:A:2080:G:H5''	1.89	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:2283:C:H2'	35:A:2284:C:O4'	2.08	0.54
35:A:270(W):G:H2'	35:A:270(X):G:C8	2.42	0.54
5:G:94:LEU:HB3	5:G:99:MET:HB2	1.90	0.54
35:A:1659:U:H3	35:A:2001:A:H61	1.55	0.54
11:P:84:ASN:HA	11:P:116:GLY:HA3	1.90	0.54
35:A:1139:G:O2'	35:A:1143:A:N1	2.36	0.54
8:K:115:LEU:HD21	8:K:126:MET:SD	2.48	0.54
1:C:40:GLU:N	1:C:218:THR:OG1	2.41	0.54
36:B:24:G:C2	36:B:56:G:N2	2.76	0.54
20:Y:28:LYS:HD3	20:Y:37:VAL:HB	1.90	0.54
12:Q:68:ILE:H	12:Q:68:ILE:HD13	1.72	0.54
35:A:2350:C:H2'	35:A:2351:G:O4'	2.08	0.54
35:A:1407:C:H42	35:A:1595:G:H1	1.54	0.54
6:H:56:SER:OG	6:H:57:ASP:N	2.40	0.54
1:C:76:LEU:HA	1:C:93:ASP:O	2.07	0.54
2:D:146:GLU:HA	2:D:153:ALA:HA	1.88	0.54
8:K:99:ILE:HG13	8:K:136:VAL:HG21	1.88	0.54
3:E:61:ARG:CG	3:E:62:PRO:HD2	2.37	0.54
3:E:12:THR:O	35:A:2682:U:H1'	2.08	0.54
35:A:15:G:H2'	35:A:16:G:H8	1.73	0.54
4:F:8:GLN:HB2	4:F:22:ALA:HB2	1.90	0.54
35:A:1006:C:H2'	35:A:1007:C:C6	2.43	0.54
16:U:74:LEU:H	16:U:74:LEU:HD13	1.71	0.54
21:Z:34:ASN:ND2	21:Z:34:ASN:O	2.32	0.54
35:A:2522:U:H3	35:A:2543:G:H1	1.56	0.54
4:F:43:LYS:HA	4:F:98:SER:HB3	1.90	0.54
3:E:36:ARG:HH22	3:E:86:PRO:HG2	1.73	0.54
11:P:101:VAL:HG12	11:P:106:LEU:HD22	1.89	0.54
35:A:720:C:H2'	35:A:721:C:H6	1.72	0.54
35:A:468:G:H2'	35:A:469:G:O4'	2.08	0.54
11:P:27:HIS:CG	11:P:28:GLY:N	2.76	0.54
35:A:2176:A:H2'	35:A:2177:C:C6	2.43	0.54
35:A:681:G:H2'	35:A:682:G:H8	1.69	0.54
4:F:113:ALA:HB1	4:F:186:ILE:HG21	1.90	0.54
4:F:176:LEU:HG	4:F:177:ALA:H	1.72	0.54
35:A:2111:C:H41	35:A:2147:G:N2	2.06	0.54
4:F:25:PRO:HG2	4:F:119:ARG:HE	1.73	0.54
35:A:1123:C:H2'	35:A:1124:C:H6	1.71	0.54
9:N:137:LYS:NZ	9:N:137:LYS:HB3	2.23	0.54
8:K:9:LYS:HD3	8:K:9:LYS:H	1.72	0.54
2:D:147:LEU:HB2	2:D:155:LEU:HD21	1.90	0.54
5:G:11:TYR:OH	5:G:16:ARG:NH2	2.37	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:P:47:ASP:O	35:A:666:G:H5'	2.07	0.54
8:K:71:THR:HG21	8:K:114:ASP:HB3	1.89	0.54
35:A:2025:C:H2'	35:A:2026:C:C6	2.42	0.54
35:A:949:C:C2	35:A:968:G:N2	2.69	0.54
35:A:2121:G:N2	35:A:2177:C:N3	2.47	0.54
1:C:45:HIS:CG	1:C:173:HIS:CD2	2.96	0.54
35:A:1782:C:O2	35:A:2609:U:H5'	2.08	0.54
25:5:5:PRO:HB2	35:A:2614:A:H5'	1.90	0.54
6:H:40:GLU:O	6:H:41:MET:HB3	2.08	0.54
1:C:144:GLY:HA3	1:C:161:ARG:NH2	2.22	0.54
3:E:143:ASN:HB3	3:E:147:PRO:HD2	1.88	0.54
22:0:27:GLU:HA	22:0:67:VAL:HB	1.90	0.54
35:A:198:C:H2'	35:A:199:A:H5''	1.89	0.54
35:A:872:A:N1	35:A:905:U:O2	2.41	0.54
10:O:64:ARG:NH2	10:O:100:GLY:HA3	2.23	0.54
6:H:119:GLU:O	6:H:140:LYS:NZ	2.29	0.54
35:A:964:C:O2'	35:A:2273:A:N3	2.41	0.54
6:H:158:HIS:CG	6:H:159:GLU:H	2.26	0.54
35:A:1165:U:H2'	35:A:1166:C:C6	2.43	0.54
35:A:883:G:H2'	35:A:884:C:C6	2.43	0.54
35:A:2212:A:H1'	35:A:2215:G:C4	2.43	0.54
2:D:134:ARG:HG3	2:D:135:PHE:CD1	2.42	0.54
35:A:2712:U:H1'	35:A:712(B):A:C8	2.43	0.54
12:Q:36:ALA:HA	12:Q:129:THR:HG22	1.90	0.54
4:F:72:ARG:HD2	4:F:73:ALA:H	1.73	0.54
36:B:60:C:H2'	36:B:61:G:H8	1.73	0.54
8:K:100:THR:HG22	8:K:139:VAL:HB	1.89	0.54
12:Q:69:PHE:CE2	12:Q:71:ASP:HB3	2.42	0.54
9:N:67:LEU:HA	9:N:87:LEU:HD12	1.89	0.53
9:N:42:TRP:N	16:U:64:ARG:NE	2.56	0.53
35:A:26:G:H1'	35:A:515:A:H61	1.74	0.53
2:D:79:VAL:HG12	2:D:80:ALA:N	2.23	0.53
1:C:162:ILE:HG21	1:C:193:PHE:CE1	2.39	0.53
3:E:5:LEU:HB2	3:E:31:CYS:SG	2.47	0.53
2:D:227:ASN:OD1	2:D:230:ASP:HB2	2.08	0.53
35:A:176:G:H3'	35:A:177:G:N2	2.23	0.53
35:A:20:C:H2'	35:A:21:A:H8	1.71	0.53
35:A:1784:A:H4'	35:A:1785:A:H5''	1.88	0.53
1:C:131:ILE:HG12	1:C:132:LEU:HD23	1.90	0.53
35:A:1337:G:H2'	35:A:1338:G:O4'	2.08	0.53
15:T:23:ARG:HH11	15:T:120:ARG:HH11	1.57	0.53
11:P:111:ARG:HB3	11:P:128:HIS:CG	2.43	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:P:65:ARG:HH22	28:8:15:LYS:HB2	1.73	0.53
35:A:88:G:H2'	35:A:89:G:C8	2.43	0.53
22:0:47:PRO:HG3	22:0:53:MET:HB2	1.90	0.53
17:V:58:VAL:HB	17:V:98:GLU:HG3	1.89	0.53
4:F:7:TYR:CZ	4:F:10:PRO:HD3	2.44	0.53
35:A:1487:G:H2'	35:A:1488:G:H8	1.73	0.53
35:A:2784:C:H2'	35:A:2785:C:C6	2.44	0.53
35:A:2708:G:H2'	35:A:2709:G:C8	2.43	0.53
35:A:322:A:O4'	35:A:340:A:H1'	2.07	0.53
28:8:32:LEU:HD12	28:8:36:LYS:HG2	1.90	0.53
35:A:2604:U:H2'	35:A:2605:U:C6	2.43	0.53
12:Q:32:TYR:HB2	12:Q:106:VAL:HG23	1.91	0.53
35:A:2471:C:N4	35:A:2476:A:O2'	2.40	0.53
35:A:2208:U:H3	35:A:2216:G:H1	1.56	0.53
25:5:40:LYS:HE2	25:5:46:CYS:HB2	1.91	0.53
22:0:11:ARG:HH22	35:A:2278:A:H3'	1.73	0.53
2:D:63:ARG:NH2	35:A:1568:G:OP2	2.40	0.53
22:0:36:ILE:HA	22:0:60:PHE:HA	1.89	0.53
35:A:2529:G:OP2	35:A:2530:A:H8	1.91	0.53
35:A:813:U:H2'	35:A:814:C:C6	2.42	0.53
35:A:1058:G:H2'	35:A:1059:G:C8	2.43	0.53
8:K:130:SER:OG	35:A:1059:G:N2	2.24	0.53
35:A:817:C:N4	35:A:1190:G:H1	2.01	0.53
12:Q:135:ASP:C	12:Q:137:TYR:H	2.11	0.53
35:A:628:G:H2'	35:A:629:G:H8	1.73	0.53
36:B:8:U:H2'	36:B:9:G:H8	1.73	0.53
35:A:1494:A:O2'	35:A:1496:A:OP2	2.25	0.53
15:T:38:ASN:OD1	15:T:38:ASN:N	2.41	0.53
14:S:59:LYS:HB3	14:S:65:VAL:HG22	1.89	0.53
35:A:2505:G:O6	35:A:2610:C:O2	2.26	0.53
35:A:2773:C:H2'	35:A:2774:C:H6	1.72	0.53
35:A:2886:G:H2'	35:A:2887:U:H6	1.73	0.53
1:C:186:LEU:O	1:C:190:ILE:HG12	2.08	0.53
19:X:49:VAL:HB	19:X:83:VAL:HG11	1.91	0.53
21:Z:75:ASN:OD1	36:B:75:G:N2	2.41	0.53
2:D:155:LEU:H	2:D:155:LEU:HD22	1.74	0.53
32:1:49:VAL:O	32:1:60:PHE:HB2	2.08	0.53
5:G:130:ASN:ND2	5:G:160:VAL:HG13	2.23	0.53
2:D:42:GLY:O	2:D:43:ARG:HG3	2.08	0.53
35:A:1669:A:C2	35:A:1994:C:H1'	2.42	0.53
1:C:11:LEU:HD23	1:C:14:LYS:HG3	1.91	0.53
4:F:108:LYS:NZ	35:A:601:C:OP1	2.41	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:1806:C:N4	35:A:1811:G:H1	2.05	0.53
2:D:257:LEU:O	35:A:1797:C:H4'	2.08	0.53
3:E:47:VAL:HG21	3:E:86:PRO:HD3	1.90	0.53
35:A:443:A:H2	35:A:1245:G:N3	2.06	0.53
13:R:4:LEU:HD22	13:R:7:GLY:HA2	1.90	0.53
1:C:144:GLY:HA2	1:C:153:ILE:HG21	1.90	0.53
32:1:20:ARG:O	32:1:22:GLY:N	2.37	0.53
17:V:47:VAL:HG23	17:V:48:GLY:O	2.09	0.53
4:F:182:ASN:OD1	4:F:183:VAL:N	2.42	0.53
29:9:16:VAL:HG22	29:9:25:VAL:HG22	1.89	0.53
11:P:32:THR:O	11:P:32:THR:OG1	2.26	0.53
16:U:16:LYS:NZ	35:A:1226:A:OP1	2.35	0.53
35:A:589:C:H2'	35:A:590:A:C8	2.44	0.53
27:7:11:LYS:NZ	35:A:685:A:OP1	2.42	0.53
35:A:849:A:N6	35:A:929:G:H1'	2.24	0.53
35:A:2649:U:H2'	35:A:2650:U:H6	1.74	0.53
35:A:1728:G:H1'	35:A:1732:A:N6	2.23	0.53
32:1:41:ARG:HH22	32:1:43:TYR:HB2	1.73	0.53
4:F:158:THR:O	4:F:178:PRO:HD3	2.09	0.53
35:A:1788:C:H2'	35:A:1789:A:O4'	2.09	0.53
35:A:139:G:N2	35:A:1596:A:H4'	2.24	0.53
35:A:1123:C:H2'	35:A:1124:C:C6	2.44	0.53
35:A:1405:U:H2'	35:A:1406:U:H6	1.74	0.53
35:A:2622:C:H2'	35:A:2623:G:O4'	2.08	0.53
35:A:2004:G:H2'	35:A:2005:A:O4'	2.09	0.53
35:A:2100:G:H2'	35:A:2101:G:H8	1.73	0.53
4:F:107:LYS:HZ1	35:A:618(A):G:H5''	1.73	0.52
1:C:21:TYR:O	1:C:25:GLU:HB2	2.09	0.52
35:A:2531:A:N3	35:A:2658:C:O2'	2.35	0.52
35:A:373:U:H2'	35:A:374:A:H8	1.74	0.52
35:A:2163:C:H2'	35:A:2164:C:C6	2.44	0.52
35:A:2246:G:H1'	35:A:2426:A:C2	2.44	0.52
27:7:7:PRO:HA	35:A:686:G:C8	2.44	0.52
7:J:122:UNK:O	7:J:124:UNK:N	2.42	0.52
35:A:1641:A:H2'	35:A:1642:G:O4'	2.09	0.52
1:C:47:LYS:HB3	1:C:212:SER:CB	2.30	0.52
35:A:2649:U:H2'	35:A:2650:U:C6	2.44	0.52
36:B:29:A:H1'	36:B:59:A:C2	2.45	0.52
17:V:51:VAL:O	17:V:53:GLU:N	2.42	0.52
24:3:41:PRO:HA	24:3:44:ARG:HG3	1.92	0.52
5:G:67:LYS:HE2	33:4:5:ILE:HD11	1.91	0.52
35:A:948:G:C6	35:A:949:C:C4	2.98	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:6:24:GLU:OE1	35:A:2346:A:O2'	2.27	0.52
13:R:2:ARG:HD3	35:A:2723:C:H5''	1.92	0.52
32:1:52:ARG:HH12	35:A:2213:U:H4'	1.74	0.52
11:P:62:LEU:H	11:P:62:LEU:CD2	2.22	0.52
35:A:780:G:H2'	35:A:782:A:C5	2.44	0.52
6:H:158:HIS:CD2	6:H:159:GLU:H	2.28	0.52
2:D:101:GLU:OE2	35:A:1491:G:O2'	2.25	0.52
15:T:132:LYS:HD3	15:T:132:LYS:O	2.09	0.52
2:D:68:LYS:HG2	2:D:152:GLY:HA2	1.91	0.52
1:C:4:HIS:HB3	1:C:8:TYR:HD2	1.75	0.52
15:T:25:GLY:O	15:T:114:LEU:HD11	2.10	0.52
33:4:3:GLU:HG2	36:B:43:C:OP1	2.08	0.52
7:J:24:UNK:HA	7:J:84:UNK:C	2.40	0.52
17:V:55:ALA:HB1	17:V:100:ARG:O	2.09	0.52
2:D:108:PRO:HB3	2:D:143:HIS:NE2	2.25	0.52
2:D:226:MET:HE2	2:D:230:ASP:HB3	1.91	0.52
5:G:33:ARG:NH2	5:G:162:THR:OG1	2.43	0.52
4:F:161:GLU:O	4:F:165:ARG:HG2	2.09	0.52
35:A:950:G:H2'	35:A:951:C:C6	2.44	0.52
35:A:284:U:H2'	35:A:285:C:C6	2.45	0.52
35:A:2306:C:H5''	35:A:2307:G:N7	2.24	0.52
29:9:22:ARG:HB2	29:9:24:TYR:HE1	1.74	0.52
36:B:24:G:C6	36:B:56:G:C2	2.97	0.52
21:Z:72:ARG:HH22	36:B:104:A:P	2.32	0.52
13:R:67:LEU:HD21	13:R:76:VAL:HG11	1.90	0.52
2:D:165:ILE:O	2:D:175:LEU:HA	2.09	0.52
36:B:14:U:OP2	36:B:70:C:O2'	2.26	0.52
1:C:60:ARG:HE	1:C:142:LYS:CB	2.22	0.52
1:C:44:VAL:O	1:C:172:ILE:O	2.28	0.52
17:V:69:LYS:HE3	17:V:86:GLY:HA3	1.90	0.52
35:A:2667:C:H2'	35:A:2668:G:O4'	2.10	0.52
35:A:1170:G:H2'	35:A:1171:G:H8	1.74	0.52
35:A:968:G:H2'	35:A:969:U:C6	2.45	0.52
35:A:853:G:H1	35:A:924:C:H42	1.57	0.52
35:A:532:A:N1	35:A:2020:A:H1'	2.25	0.52
32:1:17:SER:HG	32:1:42:GLN:N	2.08	0.52
3:E:147:PRO:HG3	3:E:151:TYR:OH	2.10	0.52
35:A:2304:G:N2	35:A:2312:U:H3	2.06	0.52
17:V:56:SER:HB2	17:V:100:ARG:HE	1.75	0.52
35:A:1728:G:H1'	35:A:1732:A:H61	1.74	0.52
3:E:129:HIS:NE2	35:A:1675:C:N3	2.58	0.52
3:E:199:ARG:HH11	3:E:199:ARG:HB2	1.75	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
36:B:15:A:H3'	36:B:16:G:H8	1.74	0.52
24:3:40:THR:O	24:3:42:ALA:N	2.42	0.52
27:7:48:LYS:HG2	35:A:125:G:N2	2.23	0.52
18:W:21:VAL:C	18:W:23:LEU:H	2.13	0.52
35:A:817:C:H2'	35:A:818:G:O4'	2.10	0.52
17:V:64:HIS:ND1	17:V:92:THR:HG22	2.24	0.52
32:1:15:ALA:H	32:1:41:ARG:HG2	1.74	0.52
16:U:95:LEU:HD22	17:V:13:ARG:HB2	1.90	0.52
4:F:12:LEU:HD22	4:F:17:ARG:HB3	1.91	0.52
26:6:47:THR:OG1	26:6:48:VAL:N	2.39	0.52
35:A:1159:U:H2'	35:A:1160:G:C8	2.44	0.52
22:0:31:VAL:HG11	22:0:37:LEU:HD21	1.91	0.52
35:A:1049:C:O2	35:A:2751:G:N1	2.38	0.52
15:T:129:ARG:NE	15:T:129:ARG:HA	2.25	0.52
4:F:75:HIS:NE2	35:A:1256:G:O2'	2.39	0.52
17:V:35:LEU:HB2	17:V:57:VAL:HG13	1.92	0.52
35:A:464:U:C4	35:A:465:G:C6	2.97	0.52
5:G:110:ALA:O	5:G:140:ILE:HD12	2.10	0.52
35:A:45:G:H2'	35:A:215:G:C8	2.45	0.52
35:A:1476:C:H2'	35:A:1477:A:C8	2.44	0.52
1:C:11:LEU:HA	1:C:14:LYS:HG3	1.91	0.52
35:A:1536:A:H5''	35:A:1537:C:OP2	2.10	0.52
36:B:18:G:H1	36:B:65:C:N4	2.07	0.52
11:P:8:PRO:HG3	35:A:1242:A:C2	2.45	0.52
35:A:1496:A:H1'	35:A:1577:C:O2'	2.10	0.52
13:R:18:LEU:HB3	13:R:22:ARG:HE	1.74	0.52
35:A:476:G:N1	35:A:479:A:OP2	2.35	0.52
10:O:75:SER:HB2	15:T:75:ILE:O	2.10	0.52
4:F:158:THR:OG1	4:F:159:GLY:N	2.43	0.52
26:6:13:CYS:SG	26:6:22:ALA:HB3	2.49	0.52
35:A:861:A:H2'	35:A:862:G:O4'	2.10	0.52
21:Z:60:GLU:HA	21:Z:66:SER:HA	1.92	0.52
35:A:271:G:H2'	35:A:272:G:C8	2.44	0.52
2:D:161:THR:HG21	35:A:1819:A:OP1	2.10	0.52
35:A:883:G:H1	35:A:893:C:H42	1.58	0.52
1:C:7:ARG:O	1:C:11:LEU:HG	2.10	0.52
35:A:1604:C:H2'	35:A:1605:C:C6	2.45	0.52
35:A:450:G:OP1	35:A:1248:G:N2	2.42	0.52
3:E:136:ARG:NH2	35:A:1998:G:OP2	2.43	0.52
9:N:34:LEU:HD21	9:N:120:LEU:HD12	1.92	0.52
4:F:171:PRO:C	4:F:173:VAL:H	2.14	0.52
16:U:61:TRP:CD2	16:U:94:ASN:HB2	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:55:G:N2	35:A:115:C:N3	2.48	0.52
35:A:938:G:H2'	35:A:939:G:H8	1.75	0.52
35:A:1224:C:H5	35:A:1225:G:C4	2.28	0.52
32:1:17:SER:OG	32:1:42:GLN:N	2.43	0.51
35:A:2789:C:H1'	35:A:2892:A:N1	2.25	0.51
17:V:66:ARG:HG2	17:V:88:ARG:HB2	1.92	0.51
35:A:857:C:N4	35:A:858:U:O4	2.43	0.51
23:2:38:GLN:HA	23:2:41:ILE:HG23	1.91	0.51
35:A:1056:G:H4'	35:A:1086:A:H8	1.75	0.51
2:D:142:VAL:HG13	2:D:163:ALA:HB3	1.92	0.51
16:U:49:HIS:ND1	35:A:534:U:O2'	2.35	0.51
35:A:747:U:C4	35:A:2613:U:C4	2.98	0.51
20:Y:11:ASP:O	20:Y:27:VAL:HA	2.10	0.51
8:K:103:GLN:O	8:K:107:ILE:HG12	2.10	0.51
35:A:2135:A:N6	35:A:2156:G:O2'	2.41	0.51
4:F:46:ARG:NH1	35:A:441:U:O2'	2.44	0.51
35:A:2261:C:H2'	35:A:2262:U:H6	1.74	0.51
35:A:1441:G:H2'	35:A:1442:G:H8	1.75	0.51
12:Q:14:ARG:HA	12:Q:72:LYS:HE3	1.91	0.51
2:D:24:ILE:HG23	2:D:25:THR:H	1.75	0.51
15:T:50:ILE:HG22	15:T:51:ARG:HB3	1.92	0.51
9:N:4:TYR:CZ	9:N:6:PRO:HA	2.45	0.51
10:O:14:THR:CG2	10:O:52:VAL:HG21	2.41	0.51
4:F:102:PRO:HB3	35:A:606:U:H5''	1.93	0.51
5:G:27:ASN:HD21	36:B:57:A:H8	1.59	0.51
35:A:72:U:C4	35:A:112:U:H4'	2.45	0.51
4:F:169:ASN:ND2	35:A:322:A:H3'	2.25	0.51
4:F:156:LEU:O	4:F:156:LEU:HG	2.11	0.51
3:E:53:PRO:HA	3:E:74:PRO:HA	1.92	0.51
12:Q:9:TYR:OH	35:A:911:A:H2'	2.10	0.51
26:6:12:GLU:OE1	35:A:2419:U:O2'	2.17	0.51
35:A:1111:A:N3	35:A:1112:G:H1'	2.25	0.51
29:9:10:ILE:HG13	29:9:11:CYS:N	2.26	0.51
3:E:118:LYS:NZ	35:A:2724:C:OP1	2.29	0.51
15:T:6:LEU:O	15:T:10:VAL:HG23	2.10	0.51
35:A:1830:C:N4	35:A:1975:G:H1	2.04	0.51
1:C:157:ILE:HA	1:C:160:GLY:O	2.11	0.51
32:1:44:PRO:HA	35:A:396:G:O2'	2.09	0.51
26:6:19:ARG:HG2	35:A:2400:G:H4'	1.91	0.51
35:A:2454:G:H1	35:A:2498:C:N4	2.07	0.51
35:A:2115:G:H4'	35:A:2167:U:H1'	1.93	0.51
35:A:1480:G:H1	35:A:1513:C:H42	1.57	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:W:3:ALA:O	18:W:106:ILE:HA	2.10	0.51
4:F:154:VAL:HG12	4:F:156:LEU:HA	1.92	0.51
11:P:106:LEU:HD12	11:P:112:LEU:HD23	1.91	0.51
35:A:70:G:H1'	35:A:73:A:N3	2.25	0.51
21:Z:19:ARG:HD3	21:Z:84:GLU:HG3	1.90	0.51
32:1:25:LYS:HB3	35:A:388:G:P	2.50	0.51
35:A:2701:C:N4	35:A:2706:G:H1	2.02	0.51
6:H:37:VAL:HG12	6:H:38:SER:O	2.10	0.51
1:C:132:LEU:HB3	1:C:138:LEU:N	2.25	0.51
28:8:14:VAL:HG21	28:8:22:VAL:HG12	1.92	0.51
35:A:1019:U:C2	35:A:1020:A:N7	2.79	0.51
4:F:33:LEU:O	4:F:37:VAL:HG23	2.10	0.51
15:T:36:GLU:HB3	15:T:39:ARG:O	2.11	0.51
17:V:17:GLY:HA2	17:V:96:ILE:HG13	1.92	0.51
35:A:577:G:O2'	35:A:1254:A:OP1	2.28	0.51
35:A:1727:U:H2'	35:A:1728:G:O4'	2.10	0.51
35:A:2100:G:H2'	35:A:2101:G:C8	2.45	0.51
35:A:1819:A:H4'	35:A:1820:U:H5''	1.91	0.51
35:A:1440:G:H2'	35:A:1441:G:H8	1.76	0.51
35:A:1059:G:N1	35:A:1079:C:C4	2.77	0.51
1:C:41:THR:HB	1:C:43:GLU:HG3	1.92	0.51
35:A:2629:A:H8	35:A:2895:U:O4	1.92	0.51
1:C:53:ARG:N	1:C:53:ARG:HD3	2.24	0.51
35:A:914:C:H2'	35:A:915:C:H5'	1.92	0.51
3:E:4:ILE:HG22	3:E:198:VAL:HB	1.93	0.51
35:A:1440:G:H2'	35:A:1441:G:C8	2.46	0.51
35:A:1176:G:H3'	35:A:1177:A:H8	1.74	0.51
18:W:75:TYR:O	18:W:104:THR:N	2.41	0.51
25:5:4:HIS:HB3	35:A:2577:A:H1'	1.93	0.51
1:C:131:ILE:HG12	1:C:132:LEU:N	2.25	0.51
21:Z:102:LEU:H	21:Z:102:LEU:HD12	1.74	0.51
35:A:2243:U:H2'	35:A:2244:U:C6	2.45	0.51
36:B:18:G:H2'	36:B:19:G:H8	1.75	0.51
21:Z:3:TYR:N	21:Z:56:VAL:O	2.44	0.51
15:T:33:LYS:NZ	15:T:74:ARG:HH22	2.08	0.51
35:A:2047:U:O2'	35:A:2823:A:N1	2.44	0.51
29:9:10:ILE:HD11	29:9:32:HIS:NE2	2.26	0.51
35:A:2884:U:H2'	35:A:2885:C:O4'	2.11	0.51
35:A:1119:C:H2'	35:A:1120:G:H8	1.75	0.51
21:Z:166:SER:H	21:Z:167:PRO:HA	1.75	0.51
3:E:61:ARG:NH1	35:A:2632:A:O2'	2.42	0.51
11:P:36:LYS:HG2	11:P:41:ARG:HB3	1.93	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:R:90:ARG:NH1	35:A:2881:C:H5'	2.24	0.51
20:Y:68:HIS:HB3	20:Y:71:LYS:HE2	1.92	0.51
1:C:150:ILE:O	1:C:154:ILE:HG13	2.10	0.51
15:T:49:VAL:O	15:T:50:ILE:HG13	2.10	0.51
17:V:39:LEU:HD12	17:V:47:VAL:HG21	1.92	0.51
26:6:41:PRO:HD3	26:6:47:THR:HG22	1.91	0.51
35:A:573:G:H1	35:A:2031:A:P	2.34	0.51
2:D:117:VAL:HG12	2:D:129:ASN:HD21	1.74	0.51
35:A:2329:G:H2'	35:A:2330:G:H8	1.75	0.51
35:A:1670:C:H2'	35:A:1671:U:O4'	2.09	0.51
3:E:123:ALA:HB3	35:A:2511:U:H5''	1.92	0.51
20:Y:8:LYS:HB3	20:Y:28:LYS:HZ1	1.75	0.51
4:F:187:VAL:HG12	11:P:7:ARG:HH22	1.76	0.51
35:A:2389:G:H5''	35:A:2390:U:O4'	2.10	0.51
9:N:27:ALA:O	9:N:31:ALA:N	2.38	0.51
18:W:37:ARG:HG3	18:W:38:TYR:CD1	2.46	0.51
29:9:33:LYS:NZ	35:A:2526:G:O3'	2.44	0.51
35:A:2834:G:H1'	35:A:2883:A:N6	2.26	0.51
35:A:826:U:H5''	35:A:2429:G:P	2.51	0.51
3:E:34:VAL:HG11	3:E:78:LEU:HD22	1.92	0.51
21:Z:10:ARG:NH2	21:Z:26:GLY:O	2.43	0.51
4:F:46:ARG:O	4:F:48:THR:N	2.44	0.51
20:Y:62:GLU:CD	20:Y:63:LYS:H	2.14	0.51
9:N:42:TRP:H	16:U:64:ARG:HE	1.59	0.51
6:H:54:ARG:HB3	6:H:65:HIS:HB2	1.93	0.51
20:Y:27:VAL:O	20:Y:28:LYS:HB3	2.11	0.51
32:1:15:ALA:HA	32:1:40:ARG:O	2.10	0.51
35:A:307:G:H21	35:A:330:A:N6	2.08	0.51
35:A:198:C:H42	35:A:248:G:H1	1.59	0.51
7:J:24:UNK:HA	7:J:84:UNK:O	2.11	0.51
35:A:2784:C:H2'	35:A:2785:C:H6	1.76	0.51
3:E:93:VAL:HG12	3:E:182:LEU:HD13	1.92	0.51
3:E:82:ARG:NE	35:A:2637:U:OP1	2.43	0.51
10:O:9:GLU:HA	10:O:18:LYS:HA	1.92	0.51
32:1:67:ILE:N	32:1:68:PRO:HD2	2.26	0.51
10:O:71:ARG:HB3	10:O:71:ARG:HH11	1.76	0.51
35:A:697:C:H2'	35:A:698:C:C6	2.46	0.51
23:2:29:LYS:HG2	23:2:57:ILE:HD12	1.93	0.51
8:K:41:PHE:HB2	8:K:69:THR:HG21	1.92	0.51
12:Q:11:LYS:NZ	12:Q:88:GLY:H	2.09	0.51
35:A:852:G:N2	35:A:925:C:C2	2.75	0.50
35:A:1448:G:H2'	35:A:149(B):A:C8	2.46	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:1:22:GLY:O	32:1:37:ILE:N	2.43	0.50
35:A:2781:A:H5'	35:A:2782:G:H5'	1.93	0.50
9:N:56:ASN:H	9:N:126:PRO:HA	1.76	0.50
35:A:919:G:H4'	36:B:81:G:O2'	2.11	0.50
10:O:77:ILE:HB	15:T:74:ARG:HG2	1.92	0.50
11:P:6:LEU:HG	11:P:8:PRO:HD2	1.93	0.50
9:N:106:MET:HE1	35:A:1006:C:H1'	1.93	0.50
35:A:1844:C:H2'	35:A:1845:G:O4'	2.11	0.50
3:E:183:LEU:HD21	15:T:11:GLU:HG2	1.93	0.50
14:S:54:LEU:HD13	14:S:60:GLY:HA2	1.93	0.50
35:A:55:G:H1	35:A:115:C:H42	1.58	0.50
35:A:2471:C:H2'	35:A:2472:G:O4'	2.12	0.50
35:A:2208:U:H2'	35:A:2209:C:C6	2.46	0.50
5:G:144:ILE:HG13	5:G:148:MET:HG3	1.92	0.50
35:A:1234:U:H2'	35:A:1235:G:O4'	2.10	0.50
35:A:784:A:O2'	35:A:785:G:H5''	2.12	0.50
4:F:182:ASN:ND2	4:F:185:ASP:OD1	2.30	0.50
2:D:207:GLY:O	35:A:1791:A:O2'	2.23	0.50
10:O:104:ARG:HH21	15:T:33:LYS:HE3	1.75	0.50
2:D:86:PRO:HB3	35:A:1567:A:P	2.50	0.50
35:A:1165:U:H2'	35:A:1166:C:H6	1.76	0.50
5:G:130:ASN:HD21	5:G:160:VAL:HG13	1.76	0.50
9:N:100:GLU:HB3	9:N:117:PHE:HZ	1.77	0.50
9:N:38:HIS:CG	9:N:39:ARG:N	2.79	0.50
1:C:42:VAL:O	1:C:43:GLU:C	2.50	0.50
36:B:49:C:H2'	36:B:50:G:C8	2.45	0.50
28:8:10:ALA:O	28:8:14:VAL:HG12	2.11	0.50
32:1:91:LYS:HA	32:1:94:LEU:HD22	1.93	0.50
5:G:67:LYS:NZ	5:G:68:PRO:HD2	2.26	0.50
12:Q:11:LYS:HZ3	12:Q:88:GLY:H	1.59	0.50
24:3:12:PRO:C	24:3:20:LYS:HZ1	2.12	0.50
35:A:460:A:H2'	35:A:461:C:O4'	2.11	0.50
35:A:1935:G:H3'	35:A:1962:C:H42	1.76	0.50
9:N:41:ASP:HA	16:U:64:ARG:NE	2.27	0.50
35:A:1533:C:H42	35:A:1538:G:H1	1.57	0.50
15:T:27:THR:HG22	15:T:49:VAL:HB	1.92	0.50
35:A:1483:G:H1	35:A:1506:C:N4	2.08	0.50
2:D:187:GLY:C	2:D:189:CYS:H	2.14	0.50
35:A:860:U:H2'	35:A:861:A:H8	1.75	0.50
22:0:36:ILE:HD13	22:0:39:ARG:HG2	1.94	0.50
24:3:11:SER:OG	24:3:13:ILE:HG12	2.12	0.50
9:N:133:GLN:HG2	9:N:135:PRO:HD3	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:998:C:H2'	35:A:999:U:O4'	2.10	0.50
13:R:51:LEU:HD11	13:R:66:VAL:HG13	1.92	0.50
35:A:2861:G:H2'	35:A:2862:G:H8	1.76	0.50
35:A:1916:A:H2'	35:A:1917:U:O4'	2.11	0.50
2:D:90:ALA:HB2	2:D:159:ALA:HA	1.93	0.50
35:A:1139:G:H8	35:A:1139:G:O5'	1.95	0.50
35:A:2642:G:N2	35:A:2772:C:N3	2.46	0.50
3:E:61:ARG:CB	3:E:62:PRO:HD2	2.42	0.50
35:A:1409:C:H2'	35:A:1410:G:C8	2.47	0.50
14:S:13:ARG:O	14:S:15:ARG:N	2.43	0.50
20:Y:8:LYS:HZ3	20:Y:70:SER:HA	1.77	0.50
35:A:1462:C:H4'	35:A:2703:C:H5'	1.94	0.50
35:A:1533:C:H2'	35:A:1534:G:O4'	2.11	0.50
3:E:143:ASN:ND2	3:E:146:THR:O	2.45	0.50
3:E:146:THR:O	35:A:2571:C:O2'	2.28	0.50
35:A:994:C:N4	35:A:1160:G:H1	2.07	0.50
14:S:34:HIS:ND1	14:S:54:LEU:O	2.44	0.50
35:A:592:G:H1	35:A:665:C:H42	1.59	0.50
35:A:485:C:H42	35:A:495:G:H1	1.59	0.50
35:A:2524:G:H1	35:A:2539:C:H42	1.58	0.50
14:S:32:LEU:HD11	36:B:30:C:H5	1.76	0.50
35:A:778:G:C5	35:A:779:U:C4	2.99	0.50
16:U:54:LYS:HB3	16:U:58:ARG:HH21	1.76	0.50
1:C:213:VAL:HG11	1:C:225:ILE:CG1	2.41	0.50
26:6:39:TYR:HB3	26:6:49:HIS:CD2	2.46	0.50
4:F:33:LEU:HD11	4:F:112:MET:HG2	1.94	0.50
35:A:2658:C:H2'	35:A:2659:G:O4'	2.11	0.50
35:A:676:A:C8	35:A:2443:C:H1'	2.46	0.50
7:J:58:UNK:O	7:J:60:UNK:N	2.44	0.50
35:A:1985:G:C2	35:A:1986:A:C8	3.00	0.50
35:A:2133:G:C2	35:A:2158:A:N6	2.80	0.50
6:H:18:GLU:HB3	6:H:25:LYS:O	2.12	0.50
35:A:873:G:H1	35:A:904:C:N4	2.09	0.50
15:T:53:ARG:NH1	35:A:2684:U:OP1	2.45	0.50
15:T:46:GLU:HG3	15:T:65:LYS:HZ1	1.76	0.50
35:A:1288:U:C2	35:A:1327:C:C2	3.00	0.50
35:A:2018:G:H2'	35:A:2019:A:O4'	2.11	0.50
36:B:22:U:O2	36:B:61:G:N2	2.40	0.50
35:A:2306:C:H3'	35:A:2307:G:H8	1.76	0.50
7:J:33:UNK:O	7:J:37:UNK:N	2.45	0.50
35:A:906:G:C2	35:A:907:U:H1'	2.47	0.50
35:A:1582:C:O2'	35:A:1586:A:N3	2.45	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:211:ARG:HB3	1:C:211:ARG:CZ	2.41	0.50
16:U:76:TYR:HE2	35:A:1152:C:HO2'	1.59	0.50
35:A:516:C:H2'	35:A:517:C:H6	1.74	0.50
3:E:63:LEU:C	3:E:65:GLY:H	2.14	0.50
35:A:795:C:H2'	35:A:796:C:C6	2.46	0.50
35:A:1410:G:H2'	35:A:1411:C:C6	2.47	0.50
1:C:84:ILE:O	1:C:88:GLU:N	2.42	0.50
4:F:157:VAL:HG13	4:F:194:MET:HG2	1.93	0.50
35:A:1651:G:H2'	35:A:1652:A:C8	2.46	0.50
4:F:67:GLN:NE2	35:A:674:G:O2'	2.40	0.50
10:O:8:LEU:HB2	10:O:82:ASN:O	2.11	0.50
35:A:2829:C:H2'	35:A:2830:G:H8	1.74	0.50
36:B:40:U:H3'	36:B:41:U:C5'	2.40	0.50
35:A:971:C:O2'	35:A:983:A:N3	2.40	0.50
16:U:40:PHE:HZ	17:V:82:ARG:HH21	1.59	0.50
15:T:15:VAL:O	15:T:17:THR:N	2.45	0.50
35:A:2747:G:H21	35:A:2757:A:H62	1.59	0.50
35:A:846:C:H4'	35:A:847:U:H5'	1.93	0.50
2:D:208:LYS:HG3	2:D:210:GLY:H	1.77	0.50
35:A:1386:C:H2'	35:A:1387:C:C6	2.47	0.50
9:N:31:ALA:O	9:N:33:LEU:N	2.45	0.50
9:N:16:ILE:HG22	9:N:17:ASP:H	1.77	0.50
22:O:43:THR:H	35:A:2331:G:H4'	1.77	0.50
2:D:106:ILE:O	2:D:108:PRO:HD3	2.12	0.50
6:H:142:GLY:C	35:A:2745:C:H4'	2.33	0.50
3:E:55:ASN:HB2	3:E:74:PRO:O	2.12	0.50
35:A:1230:C:H2'	35:A:1231:G:H8	1.75	0.50
10:O:96:THR:HG23	10:O:97:ARG:HG3	1.92	0.50
35:A:46:C:H42	35:A:179:G:H1	1.58	0.50
21:Z:100:VAL:O	21:Z:123:ASP:HA	2.12	0.50
35:A:2792:G:H1	35:A:2804:C:H42	1.59	0.50
35:A:2085:C:H2'	35:A:2086:U:O4'	2.12	0.50
35:A:2314:C:H2'	35:A:2315:G:H8	1.76	0.50
3:E:13:ARG:HA	3:E:21:VAL:C	2.31	0.49
35:A:296:C:H2'	35:A:297:C:C6	2.47	0.49
35:A:2243:U:H2'	35:A:2244:U:H6	1.77	0.49
11:P:68:GLN:NE2	28:8:12:LYS:HG2	2.26	0.49
1:C:140:ASN:O	1:C:142:LYS:N	2.45	0.49
9:N:24:GLY:C	9:N:26:LEU:H	2.14	0.49
3:E:78:LEU:O	3:E:79:ARG:HD2	2.12	0.49
35:A:2669:G:H2'	35:A:2670:A:C8	2.46	0.49
23:2:56:GLN:O	23:2:60:LEU:HG	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:O:13:ASN:O	10:O:15:GLY:N	2.45	0.49
7:J:18:UNK:O	7:J:20:UNK:N	2.45	0.49
35:A:705:A:H2'	35:A:706:A:O4'	2.12	0.49
5:G:101:ILE:HG12	33:4:25:TYR:O	2.13	0.49
12:Q:58:PHE:CZ	12:Q:64:ILE:HD11	2.47	0.49
8:K:117:THR:HB	35:A:1081:U:O2'	2.11	0.49
35:A:2660:A:H2'	35:A:2661:G:O4'	2.12	0.49
11:P:77:ARG:CZ	11:P:77:ARG:HB3	2.42	0.49
35:A:1292:U:H2'	35:A:1293:C:C6	2.47	0.49
35:A:1839:G:H2'	35:A:1840:G:H8	1.76	0.49
1:C:45:HIS:N	1:C:213:VAL:O	2.43	0.49
11:P:88:LEU:O	11:P:91:PHE:N	2.45	0.49
21:Z:48:PHE:CZ	21:Z:71:VAL:HG11	2.46	0.49
15:T:88:ILE:HG22	15:T:89:VAL:N	2.27	0.49
1:C:78:ILE:HG13	1:C:101:ILE:HD13	1.93	0.49
35:A:174:C:H2'	35:A:175:G:O4'	2.12	0.49
35:A:1056:G:H4'	35:A:1086:A:C8	2.48	0.49
35:A:2591:C:H2'	35:A:2592:G:C8	2.46	0.49
11:P:96:THR:HA	11:P:126:VAL:HB	1.93	0.49
3:E:33:VAL:HG21	3:E:36:ARG:NH2	2.27	0.49
4:F:136:THR:HA	4:F:166:ALA:HB1	1.94	0.49
6:H:28:GLY:HA3	6:H:79:VAL:HB	1.93	0.49
13:R:36:THR:OG1	13:R:37:THR:N	2.44	0.49
35:A:1955:U:O2'	35:A:1956:U:H5'	2.13	0.49
2:D:246:PRO:HD3	35:A:1902:C:H5'	1.94	0.49
1:C:22:THR:HA	1:C:225:ILE:O	2.12	0.49
25:5:15:ARG:HG2	35:A:2021:C:OP1	2.13	0.49
35:A:1799:G:N2	35:A:1818:U:O2'	2.46	0.49
17:V:4:ILE:HD11	17:V:13:ARG:HG3	1.93	0.49
35:A:2282:G:H1	35:A:2427:C:N4	2.05	0.49
26:6:27:LYS:NZ	26:6:29:ASN:HB3	2.26	0.49
35:A:2270:G:H2'	35:A:2271:G:O4'	2.12	0.49
2:D:261:LYS:HD2	2:D:264:LYS:HG2	1.94	0.49
3:E:113:PHE:CE1	35:A:1655:A:H1'	2.47	0.49
2:D:172:TYR:HD1	2:D:184:LYS:HB3	1.77	0.49
2:D:202:LYS:HB3	35:A:1820:U:C2	2.48	0.49
12:Q:21:THR:OG1	12:Q:99:PRO:O	2.29	0.49
35:A:303:U:O4	35:A:314:A:N1	2.45	0.49
29:9:19:ARG:HD3	35:A:2756:U:OP2	2.11	0.49
27:7:41:ARG:HB3	35:A:463:G:O6	2.12	0.49
18:W:14:PRO:O	18:W:17:VAL:N	2.46	0.49
33:4:1:MET:HA	36:B:43:C:H5''	1.95	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:F:63:LYS:NZ	4:F:65:TRP:O	2.38	0.49
35:A:1029:A:N6	35:A:1125:G:O2'	2.41	0.49
35:A:211:A:H2'	35:A:212:G:O4'	2.11	0.49
2:D:92:ILE:HG22	2:D:106:ILE:HA	1.93	0.49
4:F:75:HIS:HD2	4:F:82:ILE:HD12	1.77	0.49
35:A:1165:U:H3	35:A:1184:G:H1	1.61	0.49
35:A:699:A:N3	35:A:1633:G:O2'	2.37	0.49
35:A:1531:C:H2'	35:A:1532:C:C6	2.48	0.49
24:3:24:LYS:NZ	35:A:931:G:O2'	2.45	0.49
1:C:46:ALA:CA	1:C:212:SER:O	2.57	0.49
19:X:8:ILE:HG23	19:X:28:PHE:HB3	1.94	0.49
4:F:187:VAL:HG13	11:P:5:ASP:N	2.28	0.49
7:J:51:UNK:O	35:A:1084:A:H5'	2.12	0.49
4:F:112:MET:HA	4:F:115:ALA:HB3	1.95	0.49
5:G:43:LEU:HB2	5:G:88:ILE:HG21	1.95	0.49
4:F:202:PHE:CE1	4:F:206:ILE:HG13	2.48	0.49
4:F:154:VAL:HB	4:F:173:VAL:HG13	1.94	0.49
35:A:2049:G:N2	35:A:2619:C:O2	2.41	0.49
35:A:957:A:N1	35:A:2458:G:H4'	2.27	0.49
35:A:2079:U:H2'	35:A:2080:G:O4'	2.13	0.49
4:F:63:LYS:HA	4:F:76:GLY:O	2.13	0.49
2:D:168:ARG:HA	2:D:173:VAL:HA	1.94	0.49
11:P:55:ARG:HG3	11:P:56:SER:O	2.12	0.49
18:W:38:TYR:CD2	25:5:30:LEU:HD21	2.46	0.49
2:D:105:ILE:HD13	2:D:106:ILE:HG22	1.93	0.49
12:Q:37:LEU:HG	12:Q:129:THR:HA	1.95	0.49
32:1:88:LYS:HA	32:1:91:LYS:HB3	1.93	0.49
21:Z:77:ASP:O	21:Z:79:ARG:N	2.44	0.49
4:F:41:LEU:HB3	35:A:443:A:N6	2.28	0.49
35:A:1918:A:O2'	35:A:1920:C:N4	2.45	0.49
35:A:207:A:H2'	35:A:208:C:O4'	2.12	0.49
1:C:114:VAL:C	1:C:116:ALA:H	2.15	0.49
35:A:1210:A:H4'	35:A:1211:U:O5'	2.12	0.49
35:A:1667:G:O2'	35:A:1991:U:O4	2.29	0.49
2:D:149:PRO:HG2	35:A:2218:G:C4'	2.43	0.49
35:A:1416:G:H2'	35:A:1417:C:C6	2.48	0.49
35:A:793:A:OP2	35:A:2071:A:O2'	2.28	0.49
9:N:9:VAL:CG2	9:N:39:ARG:HH12	2.17	0.49
35:A:270(C):A:O2'	35:A:364:C:O2	2.24	0.49
15:T:124:ASP:HB3	15:T:125:ARG:HH21	1.78	0.49
35:A:2592:G:H2'	35:A:2593:U:O4'	2.12	0.49
35:A:1494:A:H4'	35:A:1496:A:N1	2.28	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:K:21:PRO:HG3	8:K:25:PRO:HD3	1.93	0.49
35:A:2740:A:OP2	35:A:2763:G:N2	2.37	0.49
35:A:2671:A:H2'	35:A:2672:G:C8	2.48	0.49
19:X:66:LEU:HD11	35:A:64:A:N3	2.28	0.49
35:A:842:G:H2'	35:A:843:G:H8	1.77	0.49
35:A:1417:C:N3	35:A:1581:G:N2	2.48	0.49
18:W:17:VAL:O	18:W:21:VAL:HG23	2.13	0.49
1:C:214:TYR:O	1:C:216:THR:HG22	2.13	0.49
4:F:124:LEU:O	4:F:194:MET:HB2	2.13	0.49
4:F:201:VAL:HG13	4:F:205:ARG:CZ	2.43	0.49
11:P:66:GLY:C	11:P:68:GLN:H	2.15	0.49
35:A:137(B):G:H2'	35:A:139:G:N7	2.27	0.49
35:A:2828:C:H2'	35:A:2829:C:C6	2.47	0.49
17:V:95:LEU:O	17:V:96:ILE:O	2.30	0.49
4:F:154:VAL:O	4:F:156:LEU:N	2.46	0.49
4:F:68:LYS:HG2	35:A:2443:C:OP1	2.13	0.49
35:A:2306:C:H3'	35:A:2307:G:C8	2.47	0.49
7:J:58:UNK:HA	35:A:1107:G:OP1	2.12	0.49
36:B:89(A):G:H2'	36:B:89(B):A:C8	2.48	0.49
23:2:55:ARG:HB3	23:2:59:ARG:NH2	2.27	0.49
1:C:169:THR:O	1:C:171:ALA:N	2.46	0.49
20:Y:8:LYS:NZ	20:Y:70:SER:HA	2.27	0.49
32:1:42:GLN:OE1	35:A:396:G:H1'	2.13	0.49
19:X:28:PHE:HE1	19:X:92:LEU:HD21	1.78	0.49
35:A:1864:U:OP1	35:A:2410:G:O2'	2.17	0.49
35:A:1213:A:N6	35:A:1236:G:H1'	2.27	0.49
4:F:41:LEU:HB3	35:A:443:A:H61	1.76	0.49
35:A:1224:C:H5	35:A:1225:G:C5	2.30	0.49
35:A:68:G:H2'	35:A:69:C:C6	2.47	0.49
2:D:53:PHE:HZ	2:D:221:VAL:HG12	1.78	0.49
4:F:34:TRP:CE2	11:P:12:ALA:HB2	2.47	0.49
35:A:799:G:H2'	35:A:800:A:C8	2.48	0.49
8:K:133:SER:HB3	35:A:1088:A:N6	2.27	0.49
35:A:1310:G:O6	35:A:1311:G:N2	2.46	0.49
4:F:155:LEU:HD13	4:F:185:ASP:HB3	1.95	0.49
35:A:248:G:N3	35:A:2431:U:H4'	2.27	0.49
36:B:78:A:H2'	36:B:79:C:O4'	2.13	0.49
1:C:28:ARG:HE	1:C:183:PRO:CB	2.25	0.49
35:A:1707:G:H1	35:A:1751:C:N4	2.11	0.49
5:G:99:MET:O	5:G:102:PHE:HB3	2.13	0.49
8:K:131:ALA:HB1	8:K:136:VAL:HG13	1.94	0.49
1:C:114:VAL:O	1:C:116:ALA:N	2.45	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:Z:133:ILE:O	21:Z:135:GLU:N	2.45	0.49
35:A:52:A:OP2	35:A:117:G:N1	2.38	0.49
1:C:40:GLU:HA	1:C:218:THR:H	1.78	0.48
11:P:122:PRO:HA	11:P:141:ALA:O	2.13	0.48
16:U:98:LEU:HD13	16:U:99:ALA:N	2.27	0.48
32:1:45:ASN:HB3	35:A:397:G:OP1	2.12	0.48
14:S:78:LEU:HG	14:S:105:ALA:CB	2.43	0.48
35:A:1479:G:H2'	35:A:1480:G:H8	1.77	0.48
35:A:108:U:H2'	35:A:109:G:C8	2.46	0.48
35:A:1403:C:H5''	35:A:1471:A:C1'	2.43	0.48
33:4:14:ILE:HG13	33:4:22:ILE:HB	1.95	0.48
35:A:2376:A:H2'	35:A:2377:A:O4'	2.13	0.48
35:A:2305:A:N1	35:A:2306:C:H1'	2.28	0.48
11:P:21:ARG:HG3	35:A:663:G:H5''	1.93	0.48
35:A:389:G:H1'	35:A:2412:A:N3	2.28	0.48
19:X:35:THR:O	19:X:39:ILE:HG13	2.14	0.48
35:A:1316:U:H2'	35:A:1317:A:C8	2.48	0.48
5:G:51:ARG:NE	5:G:51:ARG:HA	2.28	0.48
35:A:141(A):A:N6	35:A:1595:G:O2'	2.47	0.48
28:8:46:ARG:NH2	35:A:630:G:OP1	2.46	0.48
35:A:766:C:H2'	35:A:767:U:O4'	2.13	0.48
8:K:54:PRO:HB2	8:K:70:LYS:HD3	1.94	0.48
21:Z:120:ILE:H	21:Z:172:ALA:HA	1.78	0.48
13:R:86:ARG:HD2	13:R:118:GLU:HG2	1.94	0.48
35:A:247:G:H4'	35:A:386:G:C4	2.49	0.48
14:S:106:ARG:NE	14:S:108:GLY:HA2	2.23	0.48
18:W:12:ILE:HA	18:W:12:ILE:HD13	1.63	0.48
35:A:2399:G:H2'	35:A:2400:G:O4'	2.12	0.48
16:U:10:ARG:NH1	35:A:583:G:OP2	2.47	0.48
4:F:110:LEU:HD23	4:F:206:ILE:HD11	1.95	0.48
15:T:16:ARG:NH2	15:T:83:ILE:O	2.44	0.48
9:N:111:PRO:O	9:N:114:ARG:HG3	2.13	0.48
9:N:57:ALA:O	9:N:60:ILE:HG13	2.13	0.48
35:A:1657:C:H2'	35:A:1658:C:C6	2.48	0.48
3:E:63:LEU:C	3:E:65:GLY:N	2.66	0.48
35:A:1800:C:O2'	35:A:1818:U:O4	2.31	0.48
35:A:27:G:H1'	35:A:513:A:H62	1.79	0.48
18:W:8:ARG:NH2	35:A:24:G:O3'	2.46	0.48
15:T:34:VAL:HG13	15:T:39:ARG:HA	1.96	0.48
17:V:81:TYR:CE2	35:A:1187:G:H5''	2.49	0.48
13:R:98:LEU:HD23	13:R:99:LYS:HE3	1.96	0.48
35:A:1510:A:H2'	35:A:1511:A:O4'	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:2583:G:H2'	35:A:2584:U:O4'	2.13	0.48
35:A:49:A:H5''	35:A:51:G:O4'	2.12	0.48
10:O:27:GLY:H	10:O:30:ALA:HB2	1.79	0.48
7:J:112:UNK:O	7:J:114:UNK:N	2.46	0.48
1:C:91:GLY:H	1:C:154:ILE:HG21	1.78	0.48
35:A:2115:G:N1	35:A:2118:U:OP1	2.46	0.48
11:P:61:ARG:O	28:8:13:ARG:HD3	2.13	0.48
35:A:1811:G:H2'	35:A:1812:A:C8	2.48	0.48
21:Z:69:THR:HG22	21:Z:90:VAL:HA	1.95	0.48
5:G:84:LYS:H	5:G:84:LYS:HD2	1.78	0.48
16:U:31:SER:OG	35:A:581:C:OP1	2.23	0.48
35:A:548:A:C2	35:A:549:G:H1'	2.48	0.48
12:Q:13:GLN:HG2	35:A:954:G:O3'	2.13	0.48
35:A:1036:G:H2'	35:A:1037:G:H8	1.79	0.48
35:A:1015:G:H2'	35:A:1016:G:C8	2.49	0.48
4:F:125:LEU:CA	4:F:194:MET:HB2	2.41	0.48
13:R:95:THR:C	13:R:117:VAL:HG21	2.33	0.48
3:E:134:ILE:HG12	3:E:135:HIS:H	1.77	0.48
35:A:702:G:H1	35:A:730:C:N4	2.12	0.48
2:D:227:ASN:HB2	2:D:228:PRO:HD2	1.95	0.48
35:A:848:G:N2	35:A:933:A:H1'	2.28	0.48
2:D:43:ARG:HG2	35:A:691:C:O2'	2.14	0.48
17:V:86:GLY:H	35:A:1224:C:HO2'	1.58	0.48
2:D:52:ARG:HE	2:D:53:PHE:HE1	1.62	0.48
13:R:29:LEU:HB3	13:R:75:LEU:HD12	1.95	0.48
35:A:2567:G:H2'	35:A:2568:C:C6	2.49	0.48
35:A:1464:C:H2'	35:A:1465:G:C8	2.49	0.48
35:A:289:A:H2'	35:A:290:G:O4'	2.13	0.48
35:A:1139:G:H2'	35:A:1140:C:H6	1.79	0.48
18:W:41:LYS:HB3	18:W:42:ARG:H	1.55	0.48
11:P:59:LEU:HG	28:8:13:ARG:NH1	2.28	0.48
11:P:109:GLY:O	11:P:111:ARG:N	2.46	0.48
6:H:142:GLY:HA3	35:A:2745:C:H4'	1.95	0.48
4:F:153:SER:HA	4:F:172:TRP:O	2.14	0.48
9:N:61:ARG:HA	9:N:61:ARG:NE	2.29	0.48
35:A:56:A:H2'	35:A:57:C:O4'	2.13	0.48
28:8:4:MET:CE	35:A:592:G:H21	2.26	0.48
35:A:719:C:H2'	35:A:720:C:C6	2.49	0.48
35:A:2074:U:H2'	35:A:2075:U:C6	2.48	0.48
9:N:54:VAL:N	9:N:121:LYS:O	2.40	0.48
9:N:91:LEU:HD23	9:N:98:VAL:HG11	1.96	0.48
35:A:184:C:H2'	35:A:185:U:C6	2.49	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:775:G:C4	35:A:794:G:C8	3.01	0.48
35:A:1005:C:H42	35:A:1138:G:H1	1.62	0.48
35:A:2627:G:O2'	35:A:2781:A:N1	2.42	0.48
9:N:31:ALA:C	9:N:33:LEU:H	2.16	0.48
35:A:378:C:H2'	35:A:379:G:C8	2.49	0.48
20:Y:19:LYS:HB2	35:A:329:G:O6	2.13	0.48
35:A:138:G:N1	35:A:139:G:O6	2.47	0.48
17:V:49:THR:OG1	17:V:50:PRO:HD3	2.13	0.48
35:A:974(B):C:OP2	35:A:975:G:H5''	2.13	0.48
35:A:1259:G:H2'	35:A:1260:G:H8	1.78	0.48
35:A:2306:C:H5''	35:A:2307:G:C8	2.49	0.48
35:A:271:G:H2'	35:A:272:G:H8	1.78	0.48
14:S:71:ARG:O	14:S:74:ALA:HB3	2.13	0.48
10:O:36:GLY:HA3	10:O:109:LYS:HG3	1.95	0.48
4:F:50:SER:HA	4:F:92:PRO:HB2	1.95	0.48
35:A:98:G:H5'	35:A:99:U:OP2	2.13	0.48
35:A:1710:C:H4'	35:A:2858:C:N3	2.29	0.48
35:A:649:G:H2'	35:A:650:C:C6	2.49	0.48
1:C:27:ALA:O	1:C:31:LYS:HB2	2.14	0.48
35:A:882:G:N1	35:A:894:C:N4	2.45	0.48
14:S:13:ARG:HE	14:S:13:ARG:H	1.61	0.48
1:C:8:TYR:CD1	1:C:11:LEU:HB2	2.48	0.48
5:G:66:GLN:HB3	33:4:6:HIS:NE2	2.29	0.48
3:E:12:THR:HG22	15:T:58:ASN:HD21	1.78	0.48
18:W:82:LEU:HD13	18:W:84:ARG:NE	2.29	0.48
15:T:64:ARG:HH22	15:T:103:ARG:HA	1.78	0.48
35:A:605:C:H1'	35:A:657:U:O2'	2.14	0.48
11:P:60:MET:HB3	35:A:2392:A:H8	1.79	0.48
5:G:51:ARG:NH1	5:G:54:GLU:HB2	2.29	0.48
6:H:98:LEU:HB2	6:H:125:VAL:HB	1.96	0.48
35:A:1669:A:H4'	35:A:2549:G:H4'	1.95	0.48
17:V:10:LYS:NZ	17:V:23:GLU:OE1	2.45	0.48
11:P:132:LYS:HD2	11:P:132:LYS:N	2.29	0.48
21:Z:9:TYR:CE1	21:Z:35:ARG:HD3	2.48	0.48
35:A:120:U:H4'	35:A:122:G:OP2	2.13	0.48
35:A:1591:G:H2'	35:A:1592:C:C6	2.49	0.48
14:S:21:THR:O	14:S:23:ARG:N	2.47	0.48
8:K:115:LEU:HB3	8:K:116:ASN:H	1.54	0.48
35:A:839:U:H2'	35:A:840:C:C6	2.48	0.48
35:A:2706:G:H5''	35:A:2851:A:H5''	1.96	0.48
35:A:2851:A:O5'	35:A:2851:A:H8	1.97	0.48
5:G:66:GLN:HG2	33:4:1:MET:HG3	1.95	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:H:85:LYS:HG2	6:H:141:VAL:HG13	1.95	0.48
13:R:39:PRO:HA	13:R:42:LYS:HD2	1.95	0.48
24:3:18:ASP:HB2	24:3:49:LYS:HE3	1.96	0.48
10:O:23:ARG:NH2	10:O:31:LYS:HG2	2.27	0.48
12:Q:36:ALA:HB2	12:Q:103:MET:SD	2.54	0.48
35:A:1007:C:H5''	35:A:1008:C:P	2.54	0.48
19:X:11:PRO:HB3	23:2:37:PHE:HE2	1.79	0.48
15:T:16:ARG:HA	15:T:16:ARG:HD2	1.54	0.48
10:O:13:ASN:OD1	10:O:96:THR:HG22	2.14	0.48
35:A:679:C:H2'	35:A:680:G:C8	2.47	0.48
2:D:158:ALA:N	2:D:161:THR:OG1	2.47	0.48
35:A:1935:G:H3'	35:A:1962:C:N4	2.28	0.48
35:A:165:U:H2'	35:A:171:G:O4'	2.13	0.48
21:Z:25:PRO:HG2	21:Z:85:HIS:HB2	1.95	0.48
4:F:117:ARG:O	4:F:121:GLY:N	2.46	0.47
4:F:12:LEU:HD13	4:F:17:ARG:HG2	1.95	0.47
4:F:193:VAL:O	4:F:194:MET:CG	2.62	0.47
17:V:87:HIS:CE1	35:A:1163:G:H21	2.23	0.47
32:1:45:ASN:HB2	35:A:2230:G:O2'	2.14	0.47
26:6:8:LYS:HD2	26:6:27:LYS:HA	1.96	0.47
26:6:20:ASN:OD1	26:6:42:TRP:N	2.42	0.47
13:R:48:VAL:O	13:R:52:ILE:HG12	2.14	0.47
35:A:2525:G:H2'	35:A:2526:G:H8	1.79	0.47
35:A:2742:C:H2'	35:A:2743:C:H6	1.79	0.47
35:A:140:A:H2'	35:A:141(A):A:H5''	1.96	0.47
35:A:2605:U:H2'	35:A:2606:C:C6	2.49	0.47
24:3:5:LYS:HA	24:3:35:ARG:O	2.14	0.47
3:E:27:LEU:HA	3:E:181:LEU:HD13	1.95	0.47
35:A:941:A:H3'	35:A:942:G:H8	1.79	0.47
35:A:2795:G:H3'	35:A:2797:U:C5'	2.44	0.47
35:A:1681:G:N3	35:A:1762:A:H2'	2.29	0.47
29:9:13:LYS:O	29:9:15:LYS:HD2	2.14	0.47
35:A:1786:A:H4'	35:A:1787:A:OP2	2.12	0.47
4:F:83:PHE:CD2	35:A:1257:C:H4'	2.49	0.47
35:A:2561:A:H2'	35:A:2562:U:O4'	2.14	0.47
17:V:15:GLU:HB3	17:V:16:PRO:HD2	1.96	0.47
9:N:116:LEU:HD23	9:N:119:ARG:HG3	1.96	0.47
20:Y:68:HIS:CE1	20:Y:70:SER:H	2.32	0.47
21:Z:72:ARG:NH2	36:B:104:A:OP1	2.47	0.47
35:A:1999:C:H4'	35:A:2723:C:O2	2.14	0.47
25:5:22:HIS:NE2	35:A:2045:C:H1'	2.29	0.47
35:A:151:C:N4	35:A:175:G:H1	2.11	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:1407:C:N3	35:A:1595:G:N2	2.49	0.47
5:G:67:LYS:HZ2	5:G:68:PRO:HD2	1.79	0.47
27:7:19:ARG:HD2	35:A:125:G:OP2	2.14	0.47
35:A:1709:U:H2'	35:A:1710:C:C6	2.49	0.47
35:A:2237:G:O2'	35:A:2239:G:N7	2.39	0.47
20:Y:39:VAL:HB	20:Y:40:GLU:H	1.44	0.47
16:U:17:ILE:O	16:U:20:LEU:HB2	2.13	0.47
5:G:61:ALA:HA	5:G:64:THR:HG22	1.96	0.47
8:K:134:MET:HG2	35:A:1063:G:H5'	1.96	0.47
3:E:144:ARG:HD3	35:A:2572:A:C8	2.49	0.47
24:3:32:GLN:HB2	35:A:1158:C:H4'	1.96	0.47
36:B:61:G:H2'	36:B:62:C:C6	2.49	0.47
28:8:47:LYS:HE2	35:A:2361:A:P	2.54	0.47
35:A:2165:G:N3	35:A:2165:G:H2'	2.29	0.47
9:N:129:PRO:O	9:N:131:GLN:N	2.44	0.47
35:A:2037:G:H2'	35:A:2038:G:H8	1.80	0.47
5:G:34:LEU:HD22	5:G:100:TRP:CZ2	2.49	0.47
18:W:79:GLY:HA2	35:A:25:U:H5'	1.96	0.47
35:A:27:G:H1'	35:A:513:A:N6	2.30	0.47
35:A:2080:G:H2'	35:A:2081:C:C6	2.50	0.47
2:D:168:ARG:HG2	2:D:173:VAL:HG12	1.97	0.47
35:A:856:C:H2'	35:A:857:C:C6	2.49	0.47
35:A:915:C:H2'	35:A:916:G:O4'	2.15	0.47
9:N:35:ARG:NH1	35:A:1007:C:H5'	2.29	0.47
21:Z:7:ALA:HA	21:Z:39:VAL:HG13	1.97	0.47
4:F:88:VAL:HG13	4:F:89:VAL:O	2.14	0.47
8:K:117:THR:OG1	8:K:119:ASP:OD1	2.20	0.47
12:Q:21:THR:C	12:Q:23:GLY:H	2.17	0.47
3:E:156:MET:HE1	35:A:2050:C:H1'	1.95	0.47
35:A:234:C:H2'	35:A:235:U:C6	2.49	0.47
7:J:54:UNK:CA	7:J:79:UNK:HA	2.34	0.47
9:N:42:TRP:O	16:U:64:ARG:CZ	2.63	0.47
14:S:95:HIS:CE1	36:B:48:A:H4'	2.50	0.47
35:A:1975:G:H2'	35:A:1976:U:O4'	2.15	0.47
35:A:959:A:O2'	35:A:2457:U:O3'	2.30	0.47
12:Q:12:GLN:HE21	12:Q:72:LYS:HG3	1.79	0.47
35:A:601:C:O2'	35:A:605:C:H5''	2.15	0.47
35:A:210:C:H2'	35:A:211:A:C8	2.49	0.47
3:E:100:GLU:O	3:E:172:VAL:HG12	2.14	0.47
35:A:223:A:C8	35:A:422:A:H1'	2.50	0.47
35:A:454:A:H3'	35:A:455:C:H6	1.79	0.47
35:A:1259:G:H2'	35:A:1260:G:C8	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:1793:C:H2'	35:A:1794:U:H6	1.76	0.47
35:A:627:A:O4'	35:A:637:A:N6	2.48	0.47
12:Q:11:LYS:HZ3	12:Q:87:LYS:HB3	1.80	0.47
21:Z:123:ASP:OD1	21:Z:123:ASP:N	2.48	0.47
8:K:21:PRO:HA	8:K:23:VAL:H	1.79	0.47
2:D:45:ASN:O	2:D:47:GLY:N	2.47	0.47
10:O:10:VAL:HG22	10:O:17:ARG:O	2.15	0.47
11:P:16:ARG:HH12	35:A:661:C:H4'	1.80	0.47
4:F:195:ASP:OD2	4:F:196:LEU:N	2.48	0.47
35:A:447:A:O2'	35:A:473:G:N7	2.40	0.47
22:O:27:GLU:HG3	22:O:69:PHE:HD1	1.79	0.47
13:R:24:GLN:OE1	35:A:1278:A:H5'	2.14	0.47
21:Z:3:TYR:O	21:Z:58:VAL:N	2.47	0.47
1:C:59:VAL:HG12	1:C:60:ARG:H	1.79	0.47
35:A:2531:A:H3'	35:A:2532:G:H8	1.80	0.47
21:Z:10:ARG:HH21	21:Z:26:GLY:N	2.13	0.47
35:A:1201:C:H2'	35:A:1202:C:H6	1.80	0.47
11:P:49:ARG:O	11:P:50:ARG:HB3	2.15	0.47
3:E:36:ARG:NH2	3:E:86:PRO:HG2	2.30	0.47
27:7:3:ARG:HB3	27:7:4:THR:H	1.55	0.47
16:U:102:GLU:HG2	17:V:2:PHE:HE1	1.79	0.47
35:A:1524:G:H2'	35:A:1525:G:O4'	2.14	0.47
12:Q:54:MET:HG3	12:Q:121:ALA:HB2	1.96	0.47
9:N:78:TYR:CE1	35:A:2642:G:H5'	2.49	0.47
27:7:39:ARG:HA	27:7:39:ARG:NH1	2.30	0.47
35:A:808:G:C6	35:A:809:G:C6	3.02	0.47
35:A:1394:U:H2'	35:A:1395:A:O4'	2.15	0.47
24:3:18:ASP:OD1	24:3:19:GLN:HG2	2.15	0.47
11:P:23:PRO:HB3	11:P:29:LYS:HB2	1.96	0.47
35:A:105:C:H2'	35:A:106:C:C6	2.49	0.47
9:N:17:ASP:OD2	9:N:18:ALA:N	2.48	0.47
15:T:36:GLU:HG3	15:T:37:GLY:N	2.29	0.47
35:A:1479:G:H2'	35:A:1480:G:C8	2.49	0.47
35:A:1558:A:H4'	35:A:1559:G:H21	1.79	0.47
35:A:2712:U:O2'	35:A:712(B):A:O5'	2.31	0.47
35:A:2707:G:H2'	35:A:2708:G:C8	2.46	0.47
13:R:26:LYS:HZ2	13:R:71:GLN:HB2	1.80	0.47
17:V:74:LYS:HE3	17:V:81:TYR:OH	2.14	0.47
35:A:1674:G:H21	35:A:1677:A:N6	2.11	0.47
2:D:125:ILE:HG12	2:D:137:PRO:CG	2.44	0.47
29:9:3:VAL:HG21	35:A:2539:C:H4'	1.97	0.47
35:A:2630:G:H2'	35:A:2631:G:C8	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:2379:G:H2'	35:A:2380:C:C6	2.50	0.47
14:S:56:LEU:O	14:S:57:LYS:HB2	2.14	0.47
35:A:761:A:H8	35:A:761:A:O5'	1.97	0.47
14:S:85:VAL:HG23	14:S:106:ARG:HH11	1.80	0.47
35:A:2061:G:H1'	35:A:2503:A:N7	2.30	0.47
32:1:41:ARG:HE	32:1:41:ARG:HB3	1.41	0.47
11:P:63:PRO:HB3	28:8:13:ARG:HG2	1.96	0.47
5:G:81:LYS:HB3	5:G:82:LEU:H	1.52	0.47
18:W:69:LEU:HD22	18:W:107:LEU:HD22	1.97	0.47
23:2:21:LEU:HB3	23:2:64:LEU:HD23	1.96	0.47
9:N:99:LEU:O	9:N:103:VAL:HG23	2.15	0.47
5:G:37:VAL:HB	5:G:94:LEU:HB2	1.97	0.47
35:A:208:C:H2'	35:A:209:C:H6	1.80	0.47
35:A:263:C:O2'	35:A:429:A:N3	2.41	0.47
16:U:53:ARG:NH1	35:A:536:A:OP1	2.48	0.47
35:A:273(D):C:H42	35:A:363(D):G:H1	1.63	0.47
8:K:75:SER:HA	8:K:134:MET:SD	2.55	0.47
10:O:1:MET:HB2	35:A:1665:A:O2'	2.14	0.47
19:X:92:LEU:HD22	19:X:92:LEU:HA	1.69	0.47
11:P:30:THR:HG22	11:P:31:ALA:N	2.30	0.47
35:A:2029:G:H2'	35:A:2031:A:OP2	2.15	0.47
3:E:164:ARG:HG2	35:A:2773:C:H5''	1.96	0.47
1:C:101:ILE:HD11	1:C:124:VAL:HG13	1.97	0.47
21:Z:70:LEU:HB2	21:Z:91:LEU:HD21	1.97	0.47
3:E:182:LEU:HD23	3:E:198:VAL:HG21	1.97	0.47
21:Z:143:GLY:O	21:Z:144:LEU:HD22	2.15	0.47
10:O:26:LYS:HB3	10:O:27:GLY:H	1.50	0.47
35:A:2564:A:OP1	35:A:2564:A:H8	1.97	0.47
3:E:14:ILE:HG23	15:T:14:TYR:CE1	2.50	0.47
1:C:6:LYS:HA	1:C:9:ARG:HD3	1.97	0.47
35:A:2095:C:H2'	35:A:2096:U:H6	1.80	0.47
28:8:63:PRO:O	28:8:65:GLU:HG2	2.14	0.47
35:A:2695:C:H2'	35:A:2696:U:C6	2.49	0.47
29:9:9:ARG:NH2	29:9:16:VAL:HB	2.30	0.47
35:A:2144:U:C2'	35:A:2147:G:H1	2.28	0.47
5:G:27:ASN:ND2	36:B:57:A:O4'	2.47	0.47
16:U:13:LYS:O	16:U:16:LYS:HB3	2.15	0.47
18:W:70:TYR:OH	18:W:72:LYS:HG3	2.15	0.47
15:T:82:LEU:O	15:T:83:ILE:HG13	2.14	0.47
15:T:84:GLN:C	15:T:86:ILE:H	2.17	0.47
35:A:2471:C:N3	35:A:2479:G:O6	2.48	0.47
35:A:2037:G:H2'	35:A:2038:G:C8	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:H:33:LEU:HD11	6:H:75:ALA:HA	1.97	0.47
15:T:20:PRO:HD2	15:T:85:LYS:NZ	2.30	0.47
35:A:2731:G:H2'	35:A:2732:G:C8	2.50	0.47
35:A:162:U:H2'	35:A:164:U:C4	2.50	0.47
35:A:2157:G:H8	35:A:2157:G:O5'	1.99	0.46
16:U:76:TYR:HE2	35:A:1152:C:O2'	1.98	0.46
14:S:101:LEU:HD23	14:S:101:LEU:HA	1.51	0.46
12:Q:43:THR:HG22	12:Q:45:GLN:HG2	1.96	0.46
35:A:2398:U:H2'	35:A:2399:G:C8	2.49	0.46
35:A:2270:G:H3'	35:A:2271:G:C8	2.50	0.46
35:A:868:U:H3	35:A:909:A:N6	2.13	0.46
3:E:128:SER:O	3:E:130:GLY:N	2.48	0.46
21:Z:76:LEU:HD22	21:Z:83:PRO:HA	1.97	0.46
32:1:50:ARG:NH1	35:A:2205:C:OP2	2.48	0.46
21:Z:117:LEU:HA	21:Z:174:VAL:HG22	1.97	0.46
9:N:67:LEU:O	9:N:88:GLU:HB2	2.15	0.46
3:E:60:ASN:OD1	3:E:61:ARG:N	2.48	0.46
15:T:110:ILE:O	15:T:114:LEU:N	2.49	0.46
20:Y:8:LYS:HG2	20:Y:72:VAL:HG23	1.97	0.46
16:U:3:ARG:HB2	35:A:445:C:H5''	1.98	0.46
35:A:450:G:P	35:A:1248:G:H22	2.37	0.46
4:F:12:LEU:HB3	4:F:126:VAL:HG12	1.98	0.46
4:F:178:PRO:HB2	4:F:201:VAL:HG11	1.97	0.46
2:D:117:VAL:HG12	2:D:129:ASN:ND2	2.31	0.46
35:A:83:G:N2	35:A:102:G:H2'	2.30	0.46
35:A:140:A:H62	35:A:141(A):A:N6	2.13	0.46
35:A:2084:C:N4	35:A:2235:G:H1	2.12	0.46
35:A:32:C:N4	35:A:33:U:O4	2.48	0.46
14:S:52:SER:C	14:S:69:VAL:HG21	2.36	0.46
9:N:45:ASN:N	9:N:45:ASN:OD1	2.48	0.46
11:P:47:ASP:HB3	11:P:48:PRO:O	2.15	0.46
9:N:114:ARG:O	9:N:117:PHE:N	2.48	0.46
16:U:54:LYS:HE2	35:A:995:C:OP2	2.15	0.46
35:A:1291:C:H2'	35:A:1292:U:C6	2.50	0.46
35:A:482:A:H1'	35:A:498:G:N2	2.30	0.46
35:A:1810:A:H8	35:A:1810:A:O5'	1.98	0.46
35:A:608:A:H2'	35:A:609(A):A:C8	2.49	0.46
35:A:1352:U:O2'	35:A:1570:A:N3	2.47	0.46
32:1:79:GLY:O	35:A:270(J):G:H1'	2.15	0.46
1:C:47:LYS:O	1:C:211:ARG:O	2.33	0.46
9:N:39:ARG:HB3	9:N:41:ASP:H	1.79	0.46
1:C:115:VAL:HG11	1:C:154:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:U:98:LEU:O	16:U:101:ARG:N	2.38	0.46
8:K:107:ILE:HA	8:K:110:GLN:NE2	2.31	0.46
20:Y:84:ARG:HE	20:Y:97:ARG:HD2	1.80	0.46
11:P:11:GLY:HA2	35:A:1244:G:H4'	1.98	0.46
28:8:60:LEU:HD12	28:8:61:LEU:N	2.29	0.46
28:8:46:ARG:HG2	28:8:47:LYS:H	1.80	0.46
23:2:33:MET:HE2	23:2:33:MET:HB2	1.81	0.46
23:2:48:HIS:ND1	35:A:95:G:O2'	2.47	0.46
35:A:2150:U:H2'	35:A:2151:G:C8	2.51	0.46
35:A:2294:C:H2'	35:A:2295:C:H6	1.80	0.46
14:S:42:ASP:O	14:S:44:LYS:N	2.47	0.46
9:N:70:LYS:HB3	9:N:87:LEU:HB2	1.96	0.46
3:E:63:LEU:HB2	3:E:65:GLY:H	1.80	0.46
1:C:41:THR:HG21	35:A:2124:G:H4'	1.96	0.46
35:A:1448:G:O2'	35:A:1528:A:N6	2.48	0.46
1:C:79:ALA:O	1:C:81:GLY:N	2.49	0.46
3:E:144:ARG:O	35:A:2052:G:O2'	2.33	0.46
4:F:25:PRO:HD3	4:F:115:ALA:HB1	1.97	0.46
3:E:82:ARG:HG3	3:E:83:ASP:N	2.31	0.46
13:R:102:GLU:O	13:R:103:ARG:HB2	2.15	0.46
16:U:52:ARG:HD2	16:U:52:ARG:HA	1.72	0.46
35:A:1711:C:H2'	35:A:1712:C:C6	2.50	0.46
9:N:131:GLN:HE21	9:N:131:GLN:HB3	1.60	0.46
35:A:886:C:O2	35:A:889:C:H5	1.99	0.46
2:D:250:TRP:HB2	2:D:252:TRP:CD1	2.50	0.46
35:A:1930:G:HO2'	35:A:1931:U:P	2.39	0.46
35:A:1152:C:H2'	35:A:1153:C:H6	1.79	0.46
35:A:519:U:H2'	35:A:520:G:C8	2.50	0.46
18:W:21:VAL:HG12	18:W:25:ARG:HH12	1.81	0.46
3:E:12:THR:O	3:E:22:PRO:HA	2.15	0.46
4:F:10:PRO:HB2	4:F:11:VAL:H	1.61	0.46
1:C:164:PHE:CD2	1:C:164:PHE:N	2.83	0.46
26:6:11:LEU:HD12	26:6:26:ASN:HB2	1.97	0.46
11:P:79:ARG:HG3	11:P:110:TYR:CD1	2.50	0.46
35:A:1558:A:O2'	35:A:1559:G:OP2	2.27	0.46
3:E:2:LYS:HA	3:E:84:PHE:CD2	2.51	0.46
35:A:299:A:N7	35:A:300:A:N6	2.64	0.46
15:T:35:LYS:HG3	15:T:41:ARG:HH11	1.80	0.46
12:Q:85:LYS:HD2	22:0:7:LEU:HD22	1.98	0.46
35:A:2023:G:H4'	35:A:2617:C:O3'	2.16	0.46
35:A:74:A:H5''	35:A:75:G:O4'	2.16	0.46
20:Y:79:CYS:SG	20:Y:80:GLY:N	2.89	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:612:G:N2	35:A:616:A:O2'	2.48	0.46
35:A:14:A:H2	35:A:2624:G:N2	2.14	0.46
23:2:66:GLU:O	23:2:69:ARG:HG2	2.15	0.46
18:W:65:LEU:HG	18:W:67:ASP:H	1.81	0.46
19:X:55:ASN:ND2	35:A:1342:A:H5'	2.31	0.46
3:E:89:ASP:HB3	3:E:90:THR:H	1.59	0.46
35:A:783:A:C4	35:A:785:G:H1'	2.51	0.46
25:5:4:HIS:HA	35:A:2056:G:H22	1.80	0.46
16:U:99:ALA:HB1	16:U:106:PHE:CG	2.51	0.46
2:D:78:LYS:O	2:D:79:VAL:O	2.34	0.46
22:0:24:LYS:O	22:0:25:ARG:HD3	2.16	0.46
33:4:8:LYS:HB3	33:4:9:LEU:H	1.58	0.46
35:A:2211:G:C2'	35:A:2212:A:H5''	2.45	0.46
2:D:63:ARG:H	2:D:87:ASN:HD21	1.62	0.46
22:0:39:ARG:HD3	22:0:58:THR:OG1	2.15	0.46
35:A:690:G:O5'	35:A:690:G:H8	1.99	0.46
35:A:734:A:O2'	35:A:1635:G:H5'	2.16	0.46
35:A:698:C:O2'	35:A:734:A:N6	2.49	0.46
35:A:2861:G:H2'	35:A:2862:G:C8	2.50	0.46
16:U:40:PHE:HB3	17:V:75:PHE:CE1	2.51	0.46
35:A:842:G:H2'	35:A:843:G:C8	2.51	0.46
26:6:25:LYS:HE3	26:6:25:LYS:HB2	1.66	0.46
35:A:2837:G:H2'	35:A:2838:G:H8	1.81	0.46
35:A:2652:C:C4	35:A:2653:U:C4	3.04	0.46
35:A:2345:G:N3	35:A:2381:C:H2'	2.30	0.46
35:A:2291:U:H2'	35:A:2292:C:C6	2.51	0.46
35:A:1378:A:H2'	35:A:1380:G:N7	2.31	0.46
17:V:19:LYS:NZ	17:V:21:ARG:O	2.48	0.46
35:A:1324:G:H3'	35:A:1325:G:C5'	2.45	0.46
14:S:25:ARG:HB2	14:S:40:ILE:HG23	1.97	0.46
22:0:2:ALA:N	35:A:2494:G:OP1	2.49	0.46
15:T:49:VAL:HA	15:T:63:VAL:CA	2.43	0.46
35:A:1776:G:H1	35:A:1788:C:N4	2.10	0.46
2:D:211:ARG:HA	2:D:214:TRP:CD2	2.50	0.46
5:G:170:ARG:O	5:G:174:GLU:HG2	2.16	0.46
12:Q:27:VAL:O	12:Q:29:PHE:N	2.36	0.46
13:R:52:ILE:HD12	13:R:79:LEU:HD11	1.96	0.46
35:A:2114:A:H2'	35:A:2115:G:O4'	2.15	0.46
35:A:741:G:H2'	35:A:742:G:C8	2.51	0.46
10:O:101:PRO:HB3	10:O:120:GLU:HG2	1.97	0.46
22:0:12:ASN:O	22:0:14:ARG:N	2.48	0.46
21:Z:43:GLU:HG3	21:Z:44:PHE:N	2.30	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:141(A):A:C8	35:A:1408:C:H1'	2.50	0.46
35:A:2745:C:H2'	35:A:2746:U:C6	2.51	0.46
35:A:688:U:H2'	35:A:689:A:C8	2.50	0.46
35:A:2643:G:H2'	35:A:2644:G:O4'	2.16	0.46
35:A:685:A:C5	35:A:774:A:C2	3.04	0.46
35:A:1438:U:H2'	35:A:1439:A:C8	2.50	0.46
35:A:208:C:H2'	35:A:209:C:C6	2.50	0.46
6:H:123:PHE:O	6:H:124:GLU:HB2	2.16	0.46
35:A:1139:G:H2'	35:A:1140:C:C6	2.51	0.46
35:A:1324:G:H3'	35:A:1325:G:H4'	1.97	0.46
35:A:2702:U:H1'	35:A:2703:C:H5	1.80	0.46
35:A:2390:U:O2'	35:A:2391:G:H5'	2.16	0.46
35:A:2231:C:H2'	35:A:2232:U:O4'	2.16	0.46
35:A:144:C:H2'	35:A:145:G:C8	2.43	0.46
9:N:17:ASP:O	9:N:18:ALA:HB2	2.14	0.46
35:A:2329:G:H2'	35:A:2330:G:C8	2.50	0.46
15:T:16:ARG:HB2	15:T:79:HIS:ND1	2.31	0.46
22:O:48:GLY:HA3	22:O:80:HIS:CD2	2.50	0.46
2:D:248:SER:O	2:D:250:TRP:N	2.49	0.46
35:A:618(B):C:H2'	35:A:619:G:O4'	2.16	0.46
35:A:1105:U:H2'	35:A:1106:G:C8	2.51	0.46
35:A:1014:U:H3	35:A:1148:A:H2	1.64	0.46
9:N:41:ASP:CA	16:U:64:ARG:HE	2.29	0.46
11:P:16:ARG:O	35:A:661:C:O2'	2.33	0.46
15:T:106:SER:HB2	15:T:110:ILE:CG1	2.41	0.46
1:C:115:VAL:HA	1:C:144:GLY:O	2.16	0.46
35:A:1516:U:H2'	35:A:1517:G:H8	1.75	0.46
21:Z:30:ASN:CB	21:Z:90:VAL:HB	2.46	0.46
8:K:106:GLU:O	8:K:110:GLN:HG3	2.16	0.46
5:G:47:LYS:HE2	5:G:81:LYS:HB2	1.98	0.46
8:K:40:ALA:O	8:K:44:ALA:HB2	2.15	0.46
28:8:32:LEU:HB3	28:8:33:ASN:H	1.46	0.46
13:R:103:ARG:HG2	13:R:110:PRO:HA	1.98	0.46
35:A:548:A:H8	35:A:548:A:OP2	1.99	0.46
17:V:10:LYS:HE3	17:V:10:LYS:HB2	1.82	0.46
19:X:55:ASN:HD22	35:A:1342:A:H5'	1.81	0.46
21:Z:103:ARG:HB3	21:Z:138:GLU:HG2	1.98	0.46
35:A:1199:U:H2'	35:A:1200:C:C6	2.51	0.46
15:T:97:ALA:C	15:T:98:LYS:HD2	2.36	0.46
13:R:53:HIS:CD2	35:A:2840:C:H5''	2.50	0.46
35:A:1059:G:C2	35:A:1079:C:N3	2.84	0.46
1:C:148:PHE:C	1:C:150:ILE:H	2.20	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:1:13:ILE:HG13	32:1:17:SER:HB3	1.98	0.46
35:A:605:C:H2'	35:A:606:U:C6	2.51	0.46
24:3:9:VAL:O	24:3:31:LEU:HD21	2.16	0.46
36:B:13:A:N1	36:B:70:C:H5'	2.30	0.46
35:A:588:U:H2'	35:A:589:C:C6	2.51	0.46
18:W:3:ALA:HB3	18:W:107:LEU:HD13	1.97	0.46
3:E:2:LYS:HA	3:E:84:PHE:HD2	1.78	0.46
12:Q:68:ILE:HG23	12:Q:103:MET:HA	1.97	0.46
2:D:248:SER:C	2:D:250:TRP:H	2.20	0.46
35:A:2837:G:H2'	35:A:2838:G:C8	2.51	0.46
1:C:203:GLU:N	1:C:203:GLU:OE1	2.48	0.46
5:G:135:LEU:HD11	5:G:137:GLU:O	2.16	0.46
1:C:90:ALA:HB1	1:C:155:ARG:HD3	1.98	0.46
25:5:44:THR:HG22	25:5:45:VAL:H	1.79	0.46
35:A:2310:A:O2'	35:A:2311:A:H5'	2.16	0.46
2:D:244:ARG:NH2	35:A:1902:C:O2	2.49	0.45
6:H:37:VAL:HG21	6:H:68:THR:HG23	1.96	0.45
35:A:15:G:H2'	35:A:16:G:C8	2.50	0.45
35:A:2078:C:H2'	35:A:2079:U:C6	2.51	0.45
35:A:2240:C:H2'	35:A:2241:A:H8	1.81	0.45
35:A:2790:A:H2'	35:A:2790:A:N3	2.31	0.45
35:A:131:G:H1	35:A:148:C:H42	1.64	0.45
22:0:27:GLU:HG3	22:0:69:PHE:CD1	2.51	0.45
11:P:111:ARG:HD3	11:P:128:HIS:CD2	2.50	0.45
35:A:2415:G:H2'	35:A:2416:C:C6	2.51	0.45
35:A:2043:C:C4	35:A:2777:G:C2	3.04	0.45
18:W:66:GLU:HA	18:W:69:LEU:HG	1.97	0.45
32:1:3:LYS:HB2	35:A:1364:G:P	2.57	0.45
2:D:105:ILE:HG23	2:D:106:ILE:O	2.16	0.45
35:A:2393:A:H62	35:A:2422:A:H61	1.64	0.45
35:A:2662:A:H2'	35:A:2663:G:O4'	2.16	0.45
19:X:65:ARG:HG2	19:X:66:LEU:N	2.31	0.45
1:C:155:ARG:HD2	1:C:155:ARG:HA	1.63	0.45
35:A:579:G:O6	35:A:1261:C:N3	2.49	0.45
35:A:503:A:H4'	35:A:504:U:H5''	1.97	0.45
35:A:510:C:H2'	35:A:511:U:O4'	2.17	0.45
28:8:52:LYS:HE2	35:A:2358:G:H21	1.82	0.45
35:A:2197:U:H1'	35:A:2198:A:C8	2.52	0.45
35:A:273(E):C:H2'	35:A:273(F):U:C6	2.51	0.45
35:A:39:C:H2'	35:A:40:C:C6	2.51	0.45
35:A:1581:G:H2'	35:A:1582:C:C6	2.51	0.45
1:C:219:MET:SD	35:A:2174:C:O2'	2.73	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:S:97:ARG:O	14:S:100:ALA:N	2.44	0.45
35:A:1607:C:H4'	35:A:1608:A:O5'	2.16	0.45
20:Y:12:THR:HG23	20:Y:25:GLY:O	2.15	0.45
35:A:2789:C:C2'	35:A:2790:A:H4'	2.44	0.45
13:R:38:VAL:O	13:R:41:ALA:HB3	2.16	0.45
7:J:50:UNK:N	7:J:82:UNK:HA	2.26	0.45
5:G:47:LYS:HD3	5:G:81:LYS:HD2	1.98	0.45
35:A:2526:G:H1	35:A:2537:U:H3	1.62	0.45
2:D:35:LYS:HZ1	2:D:36:PRO:HA	1.81	0.45
8:K:55:VAL:HG22	8:K:56:GLU:H	1.81	0.45
35:A:836:G:H2'	35:A:837:C:H6	1.81	0.45
6:H:156:ALA:O	6:H:158:HIS:ND1	2.49	0.45
27:7:7:PRO:HG2	35:A:1309:G:H4'	1.98	0.45
35:A:1477:A:H2'	35:A:1478:G:O4'	2.16	0.45
21:Z:9:TYR:HE1	21:Z:35:ARG:HD3	1.81	0.45
35:A:363(D):G:H2'	35:A:363(E):G:C8	2.52	0.45
35:A:2095:C:H2'	35:A:2096:U:C6	2.51	0.45
15:T:98:LYS:HE2	35:A:2719:G:OP1	2.16	0.45
35:A:952:G:C6	35:A:966:G:C6	3.04	0.45
19:X:21:PHE:CE2	19:X:26:TYR:HA	2.52	0.45
35:A:1423:G:C2	35:A:1424:G:C8	3.04	0.45
5:G:129:GLY:HA3	5:G:163:ALA:O	2.16	0.45
35:A:1306:C:N3	35:A:1622:G:O6	2.49	0.45
35:A:2515:C:H42	35:A:2569:G:H1	1.64	0.45
27:7:34:ARG:CD	27:7:42:LEU:HB3	2.37	0.45
14:S:64:GLU:HA	14:S:67:ARG:HG3	1.99	0.45
11:P:122:PRO:O	11:P:123:LEU:HB3	2.17	0.45
11:P:31:ALA:C	11:P:33:ARG:H	2.20	0.45
26:6:22:ALA:HB2	26:6:39:TYR:CZ	2.51	0.45
35:A:447:A:H4'	35:A:448:U:H5'	1.97	0.45
9:N:18:ALA:HB3	9:N:56:ASN:OD1	2.16	0.45
35:A:1113:U:H2'	35:A:1114:G:H8	1.81	0.45
35:A:812:C:OP1	35:A:1251:C:H5'	2.16	0.45
16:U:13:LYS:HD3	35:A:1227:G:OP1	2.16	0.45
18:W:106:ILE:O	18:W:107:LEU:HB3	2.16	0.45
32:1:90:ILE:O	32:1:94:LEU:HD13	2.16	0.45
11:P:85:LEU:H	11:P:85:LEU:HD23	1.82	0.45
11:P:126:VAL:HA	11:P:145:PRO:CD	2.46	0.45
1:C:9:ARG:HB2	1:C:9:ARG:CZ	2.46	0.45
1:C:117:THR:HG1	1:C:120:VAL:HG13	1.82	0.45
23:2:2:LYS:HD2	23:2:5:GLU:OE1	2.16	0.45
12:Q:25:ASP:HB3	12:Q:100:GLY:O	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:270(N):U:H4'	35:A:270(O):G:H5'	1.98	0.45
10:O:22:ILE:HD11	10:O:42:SER:HB2	1.98	0.45
35:A:704:G:O2'	35:A:726:G:N1	2.27	0.45
35:A:1385:G:H1'	35:A:1386:C:C6	2.51	0.45
35:A:2781:A:H5'	35:A:2782:G:C5'	2.47	0.45
5:G:122:PRO:O	5:G:125:PHE:HD1	1.99	0.45
8:K:72:PRO:HG2	8:K:111:LYS:HZ1	1.80	0.45
15:T:56:GLY:O	15:T:59:THR:HG22	2.17	0.45
29:9:36:GLN:HA	29:9:36:GLN:HE21	1.81	0.45
2:D:183:ARG:HB2	2:D:270:ILE:HG22	1.98	0.45
35:A:410:G:OP1	35:A:411:G:H5'	2.17	0.45
32:1:5:CYS:SG	32:1:8:SER:N	2.72	0.45
16:U:79:PHE:CE2	16:U:83:LEU:HD21	2.52	0.45
9:N:66:LYS:O	9:N:69:GLN:N	2.49	0.45
9:N:19:GLU:HB3	9:N:59:LYS:HB3	1.98	0.45
35:A:2175:C:H2'	35:A:2176:A:C8	2.52	0.45
3:E:61:ARG:NH2	35:A:2810:A:H2'	2.23	0.45
1:C:167:ASP:OD1	1:C:169:THR:HG23	2.16	0.45
14:S:93:LYS:HB2	36:B:47:C:O2'	2.17	0.45
3:E:111:ARG:H	3:E:161:GLY:HA3	1.81	0.45
35:A:382:G:H1	35:A:392:C:N4	2.12	0.45
2:D:76:PRO:HA	2:D:118:VAL:HB	1.99	0.45
2:D:165:ILE:HG22	2:D:166:GLN:N	2.31	0.45
4:F:37:VAL:O	4:F:40:GLN:NE2	2.48	0.45
35:A:1557:C:H5''	35:A:1558:A:OP2	2.17	0.45
35:A:77:C:H2'	35:A:78:A:C8	2.51	0.45
8:K:27:LEU:O	8:K:30:HIS:HB3	2.16	0.45
35:A:465:G:C6	35:A:466:A:C6	3.04	0.45
35:A:2142:C:H2'	35:A:2143:C:C6	2.51	0.45
35:A:2116:G:N7	35:A:2166:G:N2	2.64	0.45
35:A:71:A:N7	35:A:114:U:H1'	2.32	0.45
35:A:1173:G:H5''	35:A:1174:A:OP2	2.16	0.45
35:A:2133:G:O2'	35:A:2157:G:N2	2.49	0.45
9:N:43:THR:HB	9:N:46:VAL:HG11	1.97	0.45
6:H:41:MET:CB	6:H:54:ARG:HA	2.46	0.45
28:8:53:PRO:HA	28:8:56:GLU:CB	2.46	0.45
32:1:16:ASN:O	35:A:380:U:O2'	2.19	0.45
19:X:3:THR:O	19:X:5:TYR:N	2.49	0.45
35:A:986:C:H2'	35:A:987:G:O4'	2.16	0.45
35:A:2115:G:H4'	35:A:2167:U:C1'	2.46	0.45
11:P:59:LEU:HG	28:8:13:ARG:HH12	1.82	0.45
3:E:134:ILE:HG12	3:E:135:HIS:N	2.30	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:K:72:PRO:HG2	8:K:111:LYS:NZ	2.31	0.45
35:A:2818:G:H2'	35:A:2819:G:H8	1.82	0.45
5:G:71:THR:HA	36:B:41:U:O4	2.16	0.45
35:A:225:A:H2'	35:A:226:G:H5'	1.98	0.45
32:1:76:ARG:NH1	32:1:95:LEU:HD22	2.31	0.45
13:R:89:ASP:HA	13:R:91:GLN:HE22	1.81	0.45
3:E:128:SER:HG	3:E:129:HIS:CE1	2.35	0.45
35:A:2661:G:C6	35:A:2662:A:C2	3.04	0.45
35:A:1569:A:H2'	35:A:1570:A:C8	2.52	0.45
28:8:52:LYS:CE	35:A:2358:G:H21	2.29	0.45
10:O:114:ILE:HG12	10:O:114:ILE:H	1.51	0.45
2:D:41:GLY:HA3	35:A:692:C:H4'	1.99	0.45
35:A:1444:G:HO2'	35:A:144(B):A:H8	1.64	0.45
1:C:71:LYS:HG3	1:C:72:GLN:H	1.82	0.45
3:E:44:TYR:HE2	3:E:80:GLU:OE1	2.00	0.45
35:A:1431:U:H2'	35:A:1432:C:C6	2.52	0.45
17:V:72:VAL:HG11	35:A:992:C:O3'	2.16	0.45
35:A:1914:C:H2'	35:A:1915:U:O4'	2.16	0.45
35:A:1540:G:C2	35:A:1541:U:H1'	2.52	0.45
2:D:132:PRO:HB2	2:D:135:PHE:HB2	1.98	0.45
35:A:83:G:H22	35:A:102:G:H2'	1.81	0.45
35:A:2395:C:H2'	35:A:2396:G:O4'	2.17	0.45
35:A:848:G:N7	35:A:929:G:N2	2.65	0.45
5:G:11:TYR:OH	5:G:33:ARG:HG2	2.17	0.45
24:3:12:PRO:HB2	24:3:20:LYS:HZ3	1.82	0.45
10:O:56:ASP:OD2	10:O:56:ASP:N	2.50	0.45
10:O:87:ILE:HD12	10:O:91:LEU:HA	1.98	0.45
35:A:920:G:H2'	35:A:921:G:O4'	2.17	0.45
35:A:1932:A:H2'	35:A:1933:G:O4'	2.16	0.45
4:F:103:LYS:HA	4:F:106:ARG:CZ	2.47	0.45
35:A:1270:C:O2'	35:A:1325:G:H2'	2.16	0.45
35:A:2811:G:N2	35:A:2891:G:H1'	2.32	0.45
9:N:25:ARG:HA	9:N:28:THR:OG1	2.16	0.45
35:A:2033:A:O2'	35:A:2034:U:H5''	2.17	0.45
35:A:871:U:H2'	35:A:872:A:C8	2.51	0.45
21:Z:67:LEU:HD12	21:Z:68:PRO:HD2	1.97	0.45
11:P:67:MET:H	35:A:2415:G:C4'	2.27	0.45
35:A:2643:G:H1	35:A:2771:C:N4	2.13	0.45
12:Q:7:MET:O	12:Q:9:TYR:N	2.49	0.45
35:A:2104:G:N1	35:A:2185:C:O2	2.36	0.45
33:4:14:ILE:HA	33:4:32:TYR:HA	1.98	0.45
35:A:1732:A:H2'	35:A:1733:G:O4'	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:476:G:H1'	35:A:480:A:N6	2.32	0.45
17:V:19:LYS:HG3	17:V:20:LEU:N	2.31	0.45
35:A:1199:U:H3	35:A:1246:A:H61	1.64	0.45
6:H:86:GLU:CD	6:H:86:GLU:H	2.21	0.45
6:H:144:VAL:O	6:H:148:ILE:HG12	2.17	0.45
16:U:2:PRO:HD3	35:A:444:C:OP2	2.17	0.45
18:W:80:PRO:HB3	35:A:26:G:OP1	2.17	0.45
35:A:607:U:O4	35:A:620:G:H5''	2.17	0.45
26:6:26:ASN:HD22	26:6:27:LYS:H	1.64	0.45
26:6:15:GLU:OE2	26:6:44:ARG:NH2	2.50	0.45
35:A:248:G:O5'	35:A:249:C:H5''	2.17	0.45
35:A:137(A):C:H2'	35:A:137(B):G:C8	2.52	0.45
5:G:50:ALA:O	5:G:51:ARG:NH2	2.49	0.45
35:A:557:U:H2'	35:A:558:G:C8	2.52	0.45
8:K:71:THR:HG21	8:K:114:ASP:CB	2.46	0.45
12:Q:87:LYS:NZ	35:A:955:C:OP1	2.43	0.45
35:A:906:G:N2	35:A:907:U:H1'	2.31	0.45
11:P:77:ARG:NH1	35:A:633:A:OP1	2.50	0.45
19:X:65:ARG:HD3	19:X:70:LEU:HG	1.98	0.45
35:A:2718:G:O2'	35:A:2847:U:H5''	2.16	0.45
35:A:270(O):G:H1'	35:A:270(Q):C:O5'	2.17	0.45
35:A:2798:C:H5''	35:A:2799:A:OP2	2.17	0.45
18:W:1:MET:HG3	18:W:2:GLU:H	1.81	0.45
1:C:210:LEU:HD13	1:C:227:PRO:O	2.17	0.45
3:E:64:LYS:O	3:E:67:PHE:HB3	2.17	0.45
4:F:162:LEU:H	4:F:162:LEU:HD12	1.81	0.45
9:N:42:TRP:H	16:U:64:ARG:NE	2.15	0.45
6:H:41:MET:HA	6:H:55:PRO:HD3	1.99	0.45
6:H:43:VAL:HG11	6:H:72:ILE:HD12	1.99	0.45
12:Q:12:GLN:HG3	12:Q:72:LYS:HZ2	1.82	0.45
18:W:8:ARG:HA	18:W:102:HIS:ND1	2.32	0.45
1:C:53:ARG:HG2	1:C:54:ARG:N	2.32	0.45
35:A:1827:C:H2'	35:A:1828:G:O4'	2.16	0.45
4:F:66:PRO:O	4:F:67:GLN:HB3	2.17	0.45
35:A:977:G:C6	35:A:987:G:C6	3.05	0.45
35:A:473:G:H5''	35:A:508:G:N2	2.32	0.45
35:A:1084:A:H2'	35:A:1085:A:C8	2.52	0.45
1:C:25:GLU:O	1:C:29:LEU:HB2	2.16	0.45
35:A:227:A:C2	35:A:2407:G:H1'	2.51	0.45
35:A:414:C:H2'	35:A:415:A:C8	2.52	0.45
35:A:2601:C:H5''	35:A:2602:A:OP1	2.17	0.45
35:A:558:G:H2'	35:A:559:G:C8	2.51	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:E:129:HIS:CE1	35:A:1675:C:N3	2.85	0.45
35:A:1120:G:C6	35:A:1121:C:N4	2.85	0.45
2:D:89:SER:OG	2:D:90:ALA:N	2.50	0.45
2:D:248:SER:OG	2:D:250:TRP:HE3	2.00	0.45
19:X:93:GLU:O	19:X:95:LEU:HD12	2.16	0.45
27:7:2:LYS:HG3	35:A:1620:G:O2'	2.17	0.45
35:A:2193:G:H2'	35:A:2194:G:C8	2.52	0.45
35:A:1663:C:H1'	35:A:2686:G:H4'	2.00	0.44
35:A:854:G:H2'	35:A:855:G:C8	2.52	0.44
9:N:78:TYR:CD1	35:A:2642:G:H5'	2.52	0.44
1:C:20:VAL:O	1:C:225:ILE:HA	2.17	0.44
9:N:39:ARG:C	9:N:41:ASP:N	2.71	0.44
3:E:21:VAL:HA	3:E:22:PRO:HD2	1.74	0.44
35:A:2287:A:N1	35:A:2346:A:H2	2.16	0.44
2:D:210:GLY:HA2	35:A:764:A:C5'	2.44	0.44
15:T:64:ARG:NH2	15:T:103:ARG:HA	2.32	0.44
32:1:14:VAL:HA	32:1:41:ARG:HD2	1.98	0.44
32:1:21:ARG:HD2	32:1:22:GLY:N	2.32	0.44
35:A:1316:U:H2'	35:A:1317:A:H8	1.82	0.44
13:R:40:LYS:O	13:R:44:LEU:HB2	2.17	0.44
35:A:2008:C:H2'	35:A:2009:G:H8	1.79	0.44
18:W:4:LYS:HA	18:W:106:ILE:HG12	2.00	0.44
28:8:42:ARG:HH11	35:A:2350:C:H5	1.65	0.44
1:C:182:PRO:HB3	1:C:183:PRO:HD2	1.98	0.44
35:A:1669:A:O3'	35:A:2549:G:H5'	2.16	0.44
21:Z:152:ALA:HA	21:Z:167:PRO:O	2.16	0.44
13:R:29:LEU:HD23	13:R:70:LEU:HD11	1.98	0.44
2:D:241:PRO:HB3	35:A:1971:A:C4	2.51	0.44
7:J:111:UNK:H	7:J:116:UNK:HA	1.82	0.44
10:O:11:ALA:HB1	10:O:99:PHE:H	1.82	0.44
12:Q:86:GLY:HA2	22:O:10:THR:HG23	1.99	0.44
2:D:242:ARG:NE	35:A:1902:C:OP1	2.50	0.44
18:W:25:ARG:HH21	35:A:519:U:H4'	1.81	0.44
35:A:1785:A:H4'	35:A:1982:C:H1'	1.98	0.44
32:1:43:TYR:CD2	32:1:44:PRO:HD2	2.52	0.44
4:F:125:LEU:HD22	4:F:194:MET:SD	2.57	0.44
20:Y:2:ARG:NH2	35:A:106:C:O2	2.50	0.44
35:A:473:G:H5''	35:A:508:G:H22	1.82	0.44
13:R:79:LEU:HB3	13:R:80:PHE:CD2	2.53	0.44
11:P:57:THR:O	11:P:57:THR:OG1	2.29	0.44
2:D:165:ILE:HA	2:D:175:LEU:HD22	1.99	0.44
3:E:134:ILE:O	3:E:136:ARG:N	2.43	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:O:68:GLU:OE2	10:O:68:GLU:N	2.51	0.44
2:D:92:ILE:H	2:D:92:ILE:HG13	1.65	0.44
35:A:637:A:N1	35:A:651:G:O2'	2.45	0.44
10:O:22:ILE:HD12	35:A:1952:A:C4	2.52	0.44
4:F:160:ASN:OD1	4:F:163:VAL:HG23	2.17	0.44
16:U:108:GLU:O	16:U:112:ARG:HG2	2.17	0.44
35:A:2737:G:H2'	35:A:2738:A:C8	2.52	0.44
35:A:439:G:H2'	35:A:440:G:C8	2.52	0.44
11:P:39:LYS:HB3	35:A:806:C:OP2	2.16	0.44
24:3:50:VAL:O	24:3:54:VAL:HG22	2.17	0.44
19:X:69:TYR:N	19:X:69:TYR:CD1	2.85	0.44
10:O:4:PRO:HA	10:O:21:CYS:SG	2.57	0.44
35:A:2870:C:H2'	35:A:2871:C:O4'	2.17	0.44
14:S:67:ARG:NH1	14:S:98:VAL:HB	2.33	0.44
6:H:85:LYS:HE2	6:H:141:VAL:HG22	1.99	0.44
35:A:571:A:H1'	35:A:573:G:C8	2.52	0.44
2:D:253:GLN:OE1	35:A:1843:C:H5'	2.18	0.44
35:A:757:U:H2'	35:A:758:C:O4'	2.17	0.44
3:E:79:ARG:HE	8:K:63:ARG:HD2	101.60	0.44
16:U:45:TYR:O	16:U:49:HIS:ND1	2.51	0.44
27:7:3:ARG:HA	27:7:3:ARG:HD3	1.70	0.44
35:A:1682:G:C5	35:A:1683:C:C4	3.05	0.44
23:2:48:HIS:CG	23:2:49:LYS:H	2.35	0.44
4:F:160:ASN:OD1	4:F:162:LEU:HB2	2.17	0.44
36:B:25:A:H2'	36:B:25:A:N3	2.32	0.44
13:R:74:LYS:H	13:R:74:LYS:HG2	1.50	0.44
14:S:12:PHE:CD1	14:S:91:PRO:HB3	2.52	0.44
1:C:178:LYS:O	1:C:180:SER:N	2.46	0.44
3:E:141:ILE:HB	3:E:142:GLY:H	1.45	0.44
9:N:47:ALA:HB1	9:N:116:LEU:HD21	1.98	0.44
1:C:20:VAL:CG1	1:C:226:ASN:HB2	2.47	0.44
35:A:2056:G:H2'	35:A:2056:G:N3	2.32	0.44
20:Y:9:LYS:NZ	20:Y:103:GLY:HA3	2.32	0.44
15:T:50:ILE:HG22	15:T:51:ARG:N	2.32	0.44
3:E:188:VAL:HA	3:E:189:PRO:HD2	1.84	0.44
4:F:36:VAL:HG22	4:F:101:LEU:HD21	1.99	0.44
15:T:28:VAL:HB	15:T:88:ILE:HB	1.99	0.44
35:A:197:A:H61	35:A:2431:U:H5'	1.83	0.44
35:A:873:G:N2	35:A:904:C:N3	2.55	0.44
21:Z:58:VAL:HA	21:Z:68:PRO:HA	1.98	0.44
4:F:5:ALA:HB2	4:F:24:LEU:HD21	1.98	0.44
2:D:105:ILE:HD13	2:D:106:ILE:H	1.83	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
28:8:33:ASN:O	28:8:35:GLN:N	2.50	0.44
4:F:175:THR:OG1	4:F:175:THR:O	2.26	0.44
8:K:57:ILE:HG23	8:K:67:PHE:HB3	1.98	0.44
14:S:102:ALA:HA	14:S:109:GLY:H	1.83	0.44
35:A:1166:C:H2'	35:A:1167:U:C6	2.52	0.44
14:S:59:LYS:HE2	14:S:61:ASN:HB3	2.00	0.44
7:J:58:UNK:C	7:J:60:UNK:N	2.80	0.44
15:T:20:PRO:HD2	15:T:85:LYS:HZ3	1.82	0.44
35:A:616:A:H4'	35:A:617:G:OP1	2.18	0.44
21:Z:103:ARG:HB3	21:Z:138:GLU:HA	2.00	0.44
35:A:584:C:H2'	35:A:585:G:O4'	2.17	0.44
3:E:19:ARG:HB3	3:E:19:ARG:NH1	2.32	0.44
32:1:53:VAL:HG13	32:1:74:VAL:HG13	1.99	0.44
35:A:539:G:H2'	35:A:540:G:H8	1.82	0.44
6:H:24:VAL:O	6:H:26:VAL:HG23	2.17	0.44
13:R:78:LYS:HG2	13:R:83:ILE:HD13	2.00	0.44
35:A:2851:A:H2'	35:A:2852:G:C8	2.52	0.44
35:A:2020:A:O2'	35:A:2021:C:H5'	2.17	0.44
2:D:65:ILE:H	2:D:65:ILE:HD13	1.82	0.44
15:T:26:ASP:OD2	15:T:48:ILE:HA	2.18	0.44
19:X:59:VAL:HG21	19:X:78:LYS:HG2	1.99	0.44
4:F:126:VAL:O	4:F:195:ASP:HA	2.18	0.44
4:F:57:VAL:C	4:F:59:TYR:H	2.21	0.44
4:F:54:ARG:HA	4:F:57:VAL:HG23	1.99	0.44
3:E:134:ILE:CG1	3:E:135:HIS:H	2.30	0.44
20:Y:32:PRO:HD2	20:Y:34:LYS:N	2.30	0.44
15:T:74:ARG:HD2	15:T:76:PHE:CZ	2.53	0.44
35:A:151:C:H2'	35:A:152:G:O4'	2.17	0.44
20:Y:96:ILE:HB	20:Y:99:CYS:HB2	2.00	0.44
17:V:96:ILE:O	17:V:97:LYS:HB2	2.17	0.44
35:A:1890:A:O5'	35:A:1890:A:H8	2.01	0.44
3:E:74:PRO:HG3	3:E:77:ILE:O	2.18	0.44
35:A:2101:G:H2'	35:A:2102:U:C6	2.51	0.44
2:D:5:LYS:HD3	2:D:6:PHE:O	2.18	0.44
9:N:37:LYS:HE2	9:N:37:LYS:HB3	1.78	0.44
35:A:2541:A:O5'	35:A:2541:A:H8	1.99	0.44
35:A:713:G:H2'	35:A:714:U:C6	2.53	0.44
2:D:122:ASP:OD2	2:D:123:ALA:N	2.50	0.44
35:A:2574:G:H2'	35:A:2575:C:O4'	2.17	0.44
20:Y:65:ALA:HA	20:Y:66:PRO:HD3	1.87	0.44
1:C:216:THR:HB	1:C:222:SER:HB3	1.99	0.44
19:X:12:VAL:HA	19:X:29:TRP:CD1	2.51	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:7:28:ARG:HA	27:7:31:LEU:HD12	1.99	0.44
35:A:2742:C:H2'	35:A:2743:C:C6	2.52	0.44
17:V:59:ALA:CA	17:V:96:ILE:HA	2.47	0.44
14:S:34:HIS:CG	14:S:54:LEU:HB3	2.51	0.44
12:Q:21:THR:HG23	12:Q:101:ARG:HB2	1.99	0.44
2:D:249:PRO:HG2	2:D:250:TRP:CZ3	2.53	0.44
9:N:58:ASP:OD1	9:N:58:ASP:N	2.43	0.44
11:P:27:HIS:HB3	35:A:813:U:OP2	2.17	0.44
20:Y:7:VAL:HG23	20:Y:8:LYS:HD2	1.99	0.44
15:T:26:ASP:CG	15:T:27:THR:H	2.20	0.44
32:1:21:ARG:NH1	32:1:37:ILE:H	2.16	0.44
35:A:571:A:H5'	35:A:2030:A:N7	2.33	0.44
27:7:21:ARG:HD3	27:7:21:ARG:HA	1.71	0.44
35:A:1030:G:H1	35:A:1124:C:N4	2.13	0.44
5:G:83:ARG:HB2	5:G:84:LYS:NZ	2.32	0.44
2:D:94:LEU:HB2	2:D:104:TYR:HE2	1.82	0.44
28:8:33:ASN:HA	28:8:36:LYS:HB2	1.98	0.44
35:A:1407:C:H2'	35:A:1408:C:H6	1.83	0.44
2:D:70:TRP:HH2	2:D:152:GLY:H	1.65	0.44
23:2:67:LYS:HA	23:2:67:LYS:HD3	1.84	0.44
10:O:41:ALA:O	10:O:57:VAL:HA	2.18	0.44
23:2:35:LEU:HD22	23:2:50:ILE:HG12	2.00	0.44
35:A:181:A:H1'	35:A:435:C:H5'	1.99	0.44
35:A:2768:C:H2'	35:A:2769:C:O4'	2.18	0.44
18:W:19:LEU:HB3	25:5:25:LEU:HB2	2.00	0.44
35:A:2632:A:HO2'	35:A:2811:G:HO2'	1.64	0.44
35:A:2789:C:H1'	35:A:2892:A:C2	2.53	0.44
5:G:19:LEU:HD13	5:G:32:PRO:HG2	2.00	0.44
11:P:23:PRO:HB2	11:P:33:ARG:HG3	2.00	0.44
35:A:244:A:H62	35:A:254:G:N2	2.13	0.44
35:A:1948:G:N2	35:A:1958:C:N3	2.51	0.44
35:A:1057:A:N7	35:A:1086:A:H2'	2.33	0.44
35:A:1186:G:H2'	35:A:1187:G:O4'	2.17	0.44
29:9:1:MET:N	29:9:1:MET:SD	2.74	0.44
13:R:10:LEU:HD22	13:R:17:ARG:NH2	2.33	0.44
35:A:2546:U:H5''	35:A:2547:U:H5'	2.00	0.44
35:A:1376:C:H2'	35:A:1377:G:O4'	2.18	0.44
8:K:95:LYS:HG2	8:K:137:GLU:N	2.33	0.44
15:T:12:SER:HA	15:T:57:PHE:CZ	2.53	0.44
32:1:35:THR:HG21	35:A:2432:A:C8	2.53	0.44
28:8:16:ILE:CG2	28:8:22:VAL:HG22	2.47	0.44
17:V:4:ILE:O	17:V:39:LEU:N	2.37	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:2626:C:H2'	35:A:2627:G:O4'	2.17	0.44
4:F:155:LEU:O	4:F:191:ARG:O	2.35	0.44
35:A:1790:C:H2'	35:A:1791:A:C8	2.52	0.44
11:P:53:GLY:C	11:P:55:ARG:N	2.71	0.44
7:J:23:UNK:O	7:J:84:UNK:C	2.66	0.44
36:B:54:G:H2'	36:B:55:U:O4'	2.18	0.44
5:G:82:LEU:HA	5:G:82:LEU:HD22	1.76	0.44
35:A:700:G:H2'	35:A:701:G:O4'	2.18	0.44
17:V:56:SER:O	17:V:100:ARG:HG2	2.17	0.44
35:A:103:A:O5'	35:A:103:A:H8	2.01	0.44
6:H:88:LEU:HB3	6:H:130:ARG:HG2	2.00	0.44
35:A:413:C:H2'	35:A:414:C:C6	2.52	0.44
4:F:171:PRO:HA	35:A:1205:U:N3	2.32	0.44
10:O:24:VAL:HA	10:O:39:ILE:HG22	2.00	0.44
13:R:3:HIS:CE1	35:A:1654:A:H4'	2.53	0.44
14:S:34:HIS:CD2	14:S:34:HIS:N	2.85	0.44
35:A:1466:G:H2'	35:A:1547:C:N4	2.33	0.44
35:A:1917:U:O4	35:A:1918:A:C6	2.71	0.44
35:A:68:G:H21	35:A:74:A:H5'	1.83	0.44
35:A:608:A:H2'	35:A:609(A):A:H8	1.82	0.44
21:Z:155:LEU:H	21:Z:155:LEU:HD23	1.82	0.44
35:A:2094:G:H1	35:A:2195:C:H42	1.66	0.44
35:A:646:A:H2'	35:A:647:G:O4'	2.18	0.44
14:S:48:LEU:HB3	14:S:49:VAL:HG23	2.00	0.43
14:S:99:LYS:HD3	14:S:100:ALA:H	1.81	0.43
28:8:22:VAL:HG21	28:8:56:GLU:HB3	2.00	0.43
13:R:40:LYS:HE3	35:A:1651:G:OP1	2.17	0.43
15:T:33:LYS:CD	15:T:34:VAL:H	2.31	0.43
19:X:44:GLU:HG3	19:X:49:VAL:O	2.18	0.43
8:K:7:VAL:HA	8:K:57:ILE:O	2.18	0.43
35:A:1429:G:H2'	35:A:1430:C:H6	1.80	0.43
15:T:84:GLN:O	15:T:86:ILE:N	2.37	0.43
35:A:55:G:H2'	35:A:56:A:C8	2.53	0.43
2:D:130:ALA:HA	2:D:191:ALA:O	2.18	0.43
28:8:58:ILE:O	28:8:61:LEU:HD22	2.18	0.43
2:D:248:SER:OG	2:D:252:TRP:NE1	2.39	0.43
35:A:2585:U:O2	35:A:2585:U:H2'	2.18	0.43
2:D:31:LYS:HE2	2:D:33:LEU:HD12	1.99	0.43
1:C:94:TYR:HB3	1:C:100:ILE:HD12	2.00	0.43
19:X:23:GLU:HB3	19:X:25:LYS:HG3	2.00	0.43
14:S:23:ARG:HD3	14:S:23:ARG:HA	1.54	0.43
6:H:43:VAL:HG12	6:H:50:VAL:HG12	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:T:63:VAL:O	15:T:73:GLU:HA	2.17	0.43
17:V:4:ILE:HA	17:V:12:TYR:O	2.18	0.43
4:F:155:LEU:HD22	4:F:186:ILE:HA	1.99	0.43
35:A:2282:G:H4'	35:A:2389:G:O2'	2.18	0.43
26:6:8:LYS:HZ2	26:6:27:LYS:HD3	1.83	0.43
11:P:60:MET:HB3	35:A:2392:A:C8	2.53	0.43
15:T:74:ARG:HB3	15:T:76:PHE:CE1	2.53	0.43
1:C:60:ARG:HG2	1:C:142:LYS:HD3	2.00	0.43
35:A:78:A:H2'	35:A:79:G:C8	2.49	0.43
28:8:33:ASN:CA	28:8:36:LYS:HB2	2.48	0.43
19:X:40:LYS:O	19:X:44:GLU:HB2	2.17	0.43
8:K:62:ASP:HB2	8:K:63:ARG:H	1.55	0.43
21:Z:5:LEU:HD23	21:Z:6:LYS:N	2.34	0.43
36:B:61:G:H2'	36:B:62:C:H6	1.84	0.43
35:A:720:C:H2'	35:A:721:C:C6	2.51	0.43
6:H:158:HIS:CG	6:H:159:GLU:N	2.85	0.43
35:A:2476:A:H2'	35:A:2477:C:H5'	2.00	0.43
36:B:15:A:C8	36:B:109:G:C6	3.06	0.43
35:A:2280:G:O2'	35:A:2388:A:N1	2.34	0.43
21:Z:28:MET:SD	21:Z:35:ARG:N	2.81	0.43
35:A:941:A:H2'	35:A:942:G:O4'	2.17	0.43
35:A:2502:G:OP1	35:A:2502:G:H8	2.02	0.43
35:A:2356:C:H2'	35:A:2357:U:O4'	2.18	0.43
2:D:26:LYS:O	2:D:81:ALA:HB1	2.18	0.43
3:E:30:PRO:O	3:E:32:PRO:HD3	2.18	0.43
35:A:195:A:H4'	35:A:251:A:H4'	2.00	0.43
11:P:71:VAL:H	11:P:72:PRO:CD	2.30	0.43
6:H:153:LYS:HG2	6:H:154:PRO:HD2	1.99	0.43
35:A:363(B):A:H2'	35:A:363(C):G:H8	1.83	0.43
8:K:96:VAL:HB	8:K:97:GLY:H	1.55	0.43
35:A:948:G:H1	35:A:969:U:H3	1.65	0.43
18:W:19:LEU:HB3	25:5:25:LEU:HD13	2.00	0.43
35:A:1247:A:O2'	35:A:1248:G:H5''	2.18	0.43
6:H:90:LYS:HB2	6:H:163:TYR:CE1	2.53	0.43
1:C:83:LYS:HD2	1:C:148:PHE:CE1	2.54	0.43
35:A:2679:A:H2'	35:A:2680:C:C6	2.53	0.43
6:H:83:TYR:O	6:H:85:LYS:HG3	2.18	0.43
35:A:2570:G:H2'	35:A:2571:C:O4'	2.17	0.43
1:C:29:LEU:O	1:C:33:LEU:HG	2.19	0.43
35:A:740:U:N3	35:A:758:C:H1'	2.33	0.43
18:W:70:TYR:CZ	18:W:72:LYS:HG3	2.54	0.43
32:1:3:LYS:HB2	35:A:1364:G:OP2	2.17	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:Q:81:VAL:HB	22:O:7:LEU:HD21	1.99	0.43
35:A:848:G:C4	35:A:933:A:H8	2.36	0.43
5:G:16:ARG:O	5:G:20:ILE:HG12	2.17	0.43
28:8:19:SER:OG	35:A:651:G:OP1	2.35	0.43
8:K:78:ILE:HD11	8:K:136:VAL:HB	1.99	0.43
2:D:159:ALA:HB1	2:D:198:ASN:O	2.17	0.43
35:A:1081:U:H2'	35:A:1082:U:C6	2.54	0.43
4:F:180:GLY:HA3	35:A:616:A:N3	2.33	0.43
35:A:181:A:H2'	35:A:182:A:C8	2.53	0.43
4:F:18:ARG:HD3	4:F:18:ARG:O	2.17	0.43
35:A:2238:G:N3	35:A:2238:G:H5'	2.33	0.43
20:Y:20:TYR:HB3	20:Y:23:ARG:HG3	2.00	0.43
35:A:305:U:H2'	35:A:306:U:C6	2.53	0.43
5:G:120:LEU:HG	5:G:179:PRO:O	2.19	0.43
2:D:120:GLY:HA2	2:D:121:PRO:HD3	1.85	0.43
33:4:2:LYS:NZ	36:B:39:A:H61	2.15	0.43
35:A:1436:G:N1	35:A:1556:C:N4	2.29	0.43
25:5:3:LYS:HD3	35:A:747:U:C5	2.52	0.43
25:5:17:ASP:HB2	35:A:16:G:H5''	1.99	0.43
1:C:118:PRO:O	1:C:121:MET:HB2	2.19	0.43
32:1:20:ARG:HH12	32:1:24:ALA:HB2	1.84	0.43
35:A:1114:G:H2'	35:A:1115:G:C8	2.53	0.43
8:K:106:GLU:O	8:K:109:LYS:HB2	2.19	0.43
14:S:103:GLU:O	14:S:105:ALA:N	2.51	0.43
2:D:63:ARG:CZ	2:D:86:PRO:HD2	2.47	0.43
20:Y:47:LYS:HG3	20:Y:60:PHE:CE2	2.53	0.43
4:F:154:VAL:O	4:F:174:VAL:O	2.36	0.43
8:K:9:LYS:HB2	8:K:55:VAL:O	2.17	0.43
12:Q:76:LYS:HA	12:Q:76:LYS:HD2	1.85	0.43
23:2:47:ASN:HB2	23:2:48:HIS:H	1.52	0.43
25:5:48:GLU:H	25:5:48:GLU:CD	2.21	0.43
17:V:41:GLY:HA3	17:V:45:THR:OG1	2.17	0.43
21:Z:118:GLN:HE22	35:A:874:G:H5'	1.83	0.43
2:D:69:ARG:NH2	2:D:192:THR:HG21	2.33	0.43
35:A:710:G:C4	35:A:711:G:C8	3.06	0.43
17:V:34:GLU:HG3	17:V:36:PRO:HD3	2.01	0.43
35:A:218:A:H2'	35:A:219:G:O4'	2.17	0.43
1:C:166:ASN:HA	1:C:170:GLY:HA2	2.00	0.43
3:E:92:THR:OG1	3:E:94:GLU:OE1	2.26	0.43
3:E:140:SER:HB2	35:A:2578:G:C5	2.54	0.43
35:A:947:G:O2'	35:A:984:A:N1	2.43	0.43
28:8:22:VAL:HG11	28:8:56:GLU:HG2	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:79:VAL:CG1	2:D:80:ALA:N	2.81	0.43
4:F:155:LEU:HD22	4:F:186:ILE:HB	2.00	0.43
13:R:107:ASP:HB2	35:A:2009:G:H21	1.83	0.43
15:T:53:ARG:NH1	15:T:53:ARG:HB3	2.33	0.43
10:O:34:THR:O	10:O:62:VAL:HB	2.18	0.43
13:R:26:LYS:NZ	35:A:1294:U:H4'	2.32	0.43
2:D:231:HIS:CD2	2:D:233:HIS:HB2	2.53	0.43
3:E:52:LEU:HA	3:E:53:PRO:HD3	1.57	0.43
35:A:1101:U:H2'	35:A:1102:C:C6	2.53	0.43
35:A:1094:U:H1'	35:A:1097:U:H5	1.84	0.43
35:A:1344:G:H4'	35:A:1384:A:C5	2.54	0.43
35:A:1510:A:C2	35:A:1511:A:H1'	2.54	0.43
35:A:940:G:H2'	35:A:941:A:O4'	2.18	0.43
1:C:165:ARG:CG	1:C:166:ASN:H	2.31	0.43
35:A:2469:A:H5'	35:A:2469:A:N3	2.33	0.43
25:5:18:ALA:O	25:5:21:SER:N	2.52	0.43
9:N:39:ARG:HE	9:N:41:ASP:HB3	1.83	0.43
9:N:43:THR:HG23	9:N:44:PRO:HD2	2.00	0.43
4:F:99:TYR:CE2	35:A:660:G:H5'	2.54	0.43
6:H:38:SER:C	6:H:40:GLU:H	2.22	0.43
35:A:1332:G:H5'	35:A:1333:C:OP2	2.19	0.43
35:A:2704:C:H2'	35:A:2705:A:C8	2.54	0.43
12:Q:34:LEU:HB2	12:Q:118:LEU:HD22	2.01	0.43
16:U:87:GLY:O	17:V:49:THR:HA	2.18	0.43
32:1:3:LYS:HD2	32:1:3:LYS:HA	1.82	0.43
4:F:171:PRO:HB3	35:A:1205:U:C2	2.53	0.43
35:A:974(A):G:O5'	35:A:1186:G:N2	2.48	0.43
6:H:105:LEU:H	6:H:105:LEU:HD23	1.84	0.43
35:A:1413:G:H2'	35:A:1414:G:C8	2.53	0.43
35:A:1077:A:N3	35:A:1077:A:H2'	2.34	0.43
35:A:594:U:H2'	35:A:595:C:H6	1.83	0.43
35:A:1633:G:C6	35:A:1635:G:C2	3.07	0.43
35:A:2792:G:C2	35:A:2805:G:N1	2.87	0.43
35:A:1710:C:H2'	35:A:1711:C:C6	2.53	0.43
35:A:2294:C:H2'	35:A:2295:C:C6	2.53	0.43
4:F:84:VAL:HB	4:F:85:GLY:H	1.56	0.43
18:W:60:ASN:O	18:W:61:ASN:HB2	2.18	0.43
21:Z:128:VAL:HG21	21:Z:161:VAL:HG22	1.99	0.43
14:S:26:LEU:HA	14:S:39:ILE:HA	2.01	0.43
13:R:6:SER:HB2	35:A:2873:A:H1'	1.98	0.43
21:Z:41:LEU:O	21:Z:45:ASP:N	2.28	0.43
35:A:785:G:O2'	35:A:1779:U:H4'	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:P:46:LYS:HZ2	11:P:46:LYS:HA	1.83	0.43
13:R:28:LEU:HA	13:R:34:ILE:CD1	2.49	0.43
20:Y:67:LEU:HG	20:Y:68:HIS:H	1.84	0.43
16:U:98:LEU:O	16:U:101:ARG:HG3	2.19	0.43
24:3:7:LYS:NZ	24:3:8:LEU:O	2.50	0.43
35:A:600:G:H2'	35:A:601:C:C6	2.54	0.43
35:A:872:A:N6	35:A:905:U:H3	2.10	0.43
2:D:264:LYS:HD2	2:D:266:SER:OG	2.19	0.43
3:E:95:ILE:H	3:E:95:ILE:HD13	1.84	0.43
35:A:414:C:H1'	35:A:1864:U:H1'	1.99	0.43
9:N:137:LYS:NZ	9:N:137:LYS:CB	2.81	0.43
35:A:1770:G:C5	35:A:1771:C:C4	3.06	0.43
14:S:52:SER:O	14:S:69:VAL:HG21	2.18	0.43
35:A:901:A:H2'	35:A:902:C:H6	1.84	0.43
10:O:2:ILE:HD11	10:O:65:THR:HG22	1.99	0.43
15:T:16:ARG:HH12	15:T:19:LEU:HG	1.83	0.43
28:8:26:LYS:HB3	28:8:44:LYS:HE2	1.99	0.43
10:O:89:ASN:N	10:O:89:ASN:OD1	2.52	0.43
35:A:2544:G:H1'	35:A:2646:C:H4'	2.00	0.43
35:A:2066:C:H2'	35:A:2067:G:C8	2.53	0.43
35:A:1148:A:H2'	35:A:1149:G:H8	1.83	0.43
35:A:587:C:C2	35:A:671:C:H1'	2.54	0.43
1:C:154:ILE:O	1:C:157:ILE:HB	2.19	0.43
35:A:2061:G:O2'	35:A:2062:A:H5''	2.18	0.43
35:A:121:G:H4'	35:A:148:C:H2'	2.01	0.43
35:A:329:G:H4'	35:A:330:A:OP2	2.17	0.43
33:4:12:ALA:HB2	33:4:28:LYS:O	2.19	0.43
35:A:864:G:H2'	35:A:865:C:C6	2.52	0.43
2:D:17:THR:OG1	2:D:205:VAL:N	2.30	0.43
11:P:95:VAL:HG23	11:P:125:VAL:HA	1.99	0.43
4:F:45:ARG:HD2	35:A:443:A:C5	2.54	0.43
24:3:40:THR:O	24:3:43:ILE:HG12	2.18	0.43
35:A:2261:C:H5'	35:A:2388:A:H4'	2.00	0.43
21:Z:98:MET:SD	21:Z:100:VAL:HG23	2.59	0.43
12:Q:21:THR:O	12:Q:23:GLY:N	2.50	0.43
35:A:1210:A:N6	35:A:1237:A:C5	2.87	0.43
2:D:149:PRO:HG2	35:A:2218:G:H4'	2.01	0.43
10:O:26:LYS:HD2	10:O:26:LYS:HA	1.86	0.43
13:R:53:HIS:CG	35:A:2840:C:H5''	2.54	0.43
22:0:59:LEU:HD13	22:0:79:VAL:HB	2.01	0.43
3:E:101:ARG:HG2	3:E:171:GLU:HA	2.01	0.43
11:P:148:LEU:O	11:P:150:ALA:N	2.51	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:E:145:LYS:NZ	35:A:2054:A:OP1	2.51	0.43
11:P:27:HIS:NE2	35:A:814:C:H5	2.16	0.43
35:A:1153:C:H2'	35:A:1154:G:O4'	2.19	0.43
3:E:61:ARG:NH2	35:A:2632:A:O2'	2.50	0.43
18:W:78:GLU:HG2	18:W:79:GLY:O	2.19	0.43
25:5:17:ASP:CB	35:A:16:G:H5''	2.49	0.43
1:C:151:GLY:O	1:C:154:ILE:HB	2.18	0.43
1:C:79:ALA:HB1	1:C:83:LYS:HB2	2.00	0.43
35:A:675:A:C8	35:A:804:A:C6	3.07	0.43
13:R:2:ARG:HB3	35:A:2723:C:H4'	2.01	0.43
35:A:2212:A:H4'	35:A:2213:U:C4	2.53	0.43
21:Z:67:LEU:HD11	21:Z:90:VAL:HG13	2.01	0.43
35:A:2525:G:C2	35:A:2526:G:C5	3.07	0.43
28:8:34:TRP:CG	28:8:35:GLN:N	2.87	0.43
2:D:109:ASP:N	2:D:195:ALA:O	2.51	0.43
35:A:1120:G:C6	35:A:1121:C:C4	3.07	0.43
35:A:971:C:H2'	35:A:972:G:O4'	2.18	0.43
20:Y:35:TYR:HA	20:Y:35:TYR:HD1	1.73	0.43
25:5:42:PRO:HB2	35:A:2815:C:O2'	2.18	0.43
20:Y:38:ILE:HG12	20:Y:64:GLU:HB3	2.01	0.43
3:E:62:PRO:HD3	35:A:2787:C:O4'	2.19	0.43
35:A:2178:C:H2'	35:A:2179:C:C6	2.52	0.43
14:S:15:ARG:NE	35:A:2334:G:N3	2.67	0.43
35:A:1062:G:H2'	35:A:1063:G:H8	1.84	0.43
1:C:4:HIS:O	1:C:8:TYR:HB3	2.19	0.43
35:A:1400:G:H2'	35:A:1401:G:H8	1.81	0.43
1:C:64:SER:O	1:C:64:SER:OG	2.29	0.43
12:Q:43:THR:CB	12:Q:46:GLN:HB2	2.46	0.43
6:H:85:LYS:HB2	6:H:133:VAL:HB	2.01	0.43
29:9:33:LYS:HE3	29:9:33:LYS:HB2	1.70	0.43
10:O:101:PRO:HA	10:O:120:GLU:O	2.19	0.43
35:A:2508:G:H2'	35:A:2509:G:H8	1.83	0.43
2:D:63:ARG:HD2	2:D:85:ASP:CG	2.39	0.43
3:E:79:ARG:HD3	8:K:3:LYS:HZ2	96.00	0.43
3:E:110:GLY:H	35:A:2821:A:P	2.37	0.43
23:2:32:LEU:HB2	23:2:53:LEU:HD22	2.01	0.43
1:C:9:ARG:HG3	1:C:9:ARG:H	1.60	0.43
35:A:1174:A:H3'	35:A:1175:U:C5'	2.48	0.43
35:A:695:G:C4	35:A:696:G:C8	3.07	0.43
18:W:31:GLU:O	18:W:35:ILE:HG13	2.19	0.43
25:5:56:LYS:HB3	25:5:57:VAL:H	1.66	0.43
35:A:2123:G:H1	35:A:2175:C:N4	2.13	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:9:U:N3	35:A:2629:A:N7	2.67	0.42
35:A:82:G:H5''	35:A:296:C:C5'	2.49	0.42
20:Y:8:LYS:HB3	20:Y:28:LYS:NZ	2.34	0.42
35:A:2703:C:H2'	35:A:2704:C:C6	2.54	0.42
24:3:7:LYS:HA	24:3:33:GLN:O	2.19	0.42
26:6:47:THR:HG23	26:6:49:HIS:CD2	2.54	0.42
35:A:2030:A:H4'	35:A:2031:A:C8	2.54	0.42
11:P:17:LYS:NZ	11:P:19:VAL:HG23	2.35	0.42
20:Y:73:ARG:CD	35:A:335:C:H4'	2.49	0.42
1:C:174:ALA:HA	1:C:175:PRO:HD3	1.63	0.42
2:D:52:ARG:HB3	2:D:53:PHE:CD1	2.54	0.42
35:A:2193:G:H2'	35:A:2194:G:H8	1.83	0.42
21:Z:74:VAL:HG13	21:Z:86:VAL:HG13	2.01	0.42
15:T:104:ASN:HB3	15:T:105:LEU:H	1.55	0.42
27:7:9:ARG:H	27:7:9:ARG:HG2	1.69	0.42
35:A:1803:A:H2'	35:A:1804:C:O4'	2.19	0.42
5:G:21:ARG:HG3	5:G:22:ARG:HG3	2.00	0.42
35:A:1025:G:H1	35:A:1139:G:H1	1.65	0.42
9:N:68:GLU:HG2	9:N:88:GLU:OE1	2.19	0.42
16:U:30:LYS:HD2	35:A:516:C:OP2	2.19	0.42
35:A:1270:C:H5''	35:A:1271:G:C5'	2.48	0.42
14:S:85:VAL:H	14:S:106:ARG:CG	2.32	0.42
25:5:3:LYS:HG2	25:5:4:HIS:N	2.34	0.42
1:C:176:VAL:HB	1:C:177:GLY:H	1.47	0.42
1:C:42:VAL:HG22	1:C:215:VAL:HG13	2.00	0.42
6:H:45:VAL:HA	6:H:50:VAL:HG22	2.01	0.42
16:U:96:ALA:O	16:U:99:ALA:HB3	2.19	0.42
2:D:134:ARG:HG2	2:D:187:GLY:O	2.18	0.42
35:A:1498:C:H2'	35:A:1499:C:C6	2.54	0.42
10:O:35:VAL:HG11	10:O:105:GLU:HB2	2.02	0.42
5:G:76:SER:CA	5:G:83:ARG:HB3	2.46	0.42
11:P:64:LYS:HG3	11:P:64:LYS:HZ2	1.55	0.42
5:G:15:VAL:HA	5:G:175:LEU:HD13	2.00	0.42
35:A:829:A:H8	35:A:2248:C:H5'	1.81	0.42
26:6:23:THR:O	26:6:23:THR:OG1	2.36	0.42
35:A:2208:U:H2'	35:A:2209:C:H6	1.84	0.42
35:A:1491:G:H5''	35:A:1494:A:N7	2.34	0.42
35:A:273(E):C:H2'	35:A:273(F):U:H6	1.82	0.42
35:A:2540:C:H2'	35:A:2541:A:O4'	2.19	0.42
12:Q:38:GLU:OE2	12:Q:128:LYS:HG2	2.19	0.42
35:A:1882:C:H2'	35:A:1883:G:O4'	2.19	0.42
35:A:2090:G:H1	35:A:2229:C:H42	1.66	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:Z:14:LYS:HD2	21:Z:16:SER:HB3	2.01	0.42
35:A:30:G:H2'	35:A:31:C:C6	2.54	0.42
35:A:1833:U:H2'	35:A:1834:U:C6	2.55	0.42
35:A:2134:A:N6	35:A:2157:G:H1'	2.34	0.42
35:A:1583:A:O2'	35:A:1586:A:N6	2.51	0.42
9:N:25:ARG:NH2	35:A:114(B):A:H4'	2.27	0.42
1:C:151:GLY:HA2	1:C:154:ILE:HD12	2.01	0.42
10:O:75:SER:HB3	15:T:77:PRO:HD3	2.01	0.42
12:Q:46:GLN:NE2	35:A:2485:G:OP1	2.51	0.42
13:R:39:PRO:HG2	35:A:1651:G:H5'	2.00	0.42
35:A:2773:C:H2'	35:A:2774:C:C6	2.52	0.42
35:A:1050:A:H2'	35:A:1051:G:O4'	2.20	0.42
3:E:134:ILE:H	3:E:134:ILE:HD13	1.84	0.42
35:A:1479:G:H1'	35:A:1558:A:OP1	2.19	0.42
32:1:30:VAL:HA	35:A:2396:G:H4'	2.01	0.42
35:A:2126:A:N6	35:A:2163:C:H4'	2.35	0.42
9:N:72:TYR:HB2	9:N:85:ILE:O	2.19	0.42
1:C:77:ALA:HA	1:C:114:VAL:O	2.19	0.42
35:A:767:U:H2'	35:A:768:G:H8	1.84	0.42
20:Y:38:ILE:CG1	20:Y:64:GLU:HB3	2.49	0.42
35:A:29:U:H2'	35:A:30:G:C8	2.53	0.42
3:E:158:GLY:HA3	35:A:2620:C:O2'	2.18	0.42
35:A:1196:C:H2'	35:A:1197:G:H8	1.84	0.42
35:A:2175:C:H2'	35:A:2176:A:H8	1.85	0.42
14:S:83:LYS:O	14:S:106:ARG:HA	2.19	0.42
9:N:39:ARG:NH2	9:N:41:ASP:O	2.47	0.42
17:V:89:GLN:NE2	35:A:1162:G:N3	2.66	0.42
35:A:1541:U:H3'	35:A:1542:G:C3'	2.44	0.42
2:D:208:LYS:HG3	2:D:210:GLY:N	2.34	0.42
35:A:1461:G:H2'	35:A:1462:C:H6	1.85	0.42
10:O:19:ILE:HG22	10:O:43:VAL:HA	2.01	0.42
26:6:53:LYS:HD2	26:6:53:LYS:HA	1.55	0.42
35:A:141(B):C:H2'	35:A:142:G:O4'	2.19	0.42
23:2:61:LEU:O	23:2:64:LEU:HB3	2.20	0.42
14:S:51:ALA:HB3	14:S:73:LEU:HD12	2.02	0.42
35:A:849:A:H61	35:A:929:G:H1'	1.82	0.42
25:5:16:ARG:O	25:5:20:ARG:HB2	2.19	0.42
35:A:836:G:H1	35:A:943:U:H3	1.66	0.42
8:K:99:ILE:CG2	8:K:104:VAL:HB	2.49	0.42
3:E:6:GLY:HA2	3:E:27:LEU:O	2.19	0.42
29:9:19:ARG:HG2	29:9:20:HIS:ND1	2.34	0.42
9:N:95:PRO:HA	9:N:98:VAL:HG13	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:Z:154:ASP:N	21:Z:154:ASP:OD2	2.51	0.42
11:P:14:LYS:HA	11:P:14:LYS:HD3	1.90	0.42
6:H:70:THR:HA	6:H:73:ALA:HB3	2.01	0.42
35:A:879:G:H2'	35:A:880:G:H8	1.84	0.42
35:A:2404:C:H2'	35:A:2405:G:O4'	2.18	0.42
36:B:42:C:H2'	36:B:43:C:H6	1.85	0.42
36:B:47:C:H2'	36:B:48:A:H5'	2.01	0.42
35:A:1529:A:H62	35:A:1542:G:N2	2.17	0.42
13:R:28:LEU:HA	13:R:34:ILE:HD13	2.01	0.42
28:8:16:ILE:HG21	28:8:57:ARG:HG2	2.01	0.42
35:A:2703:C:H2'	35:A:2704:C:H6	1.83	0.42
10:O:66:LYS:HB3	35:A:1665:A:H4'	2.00	0.42
35:A:2391:G:C6	35:A:2427:C:H1'	2.54	0.42
35:A:976:C:H2'	35:A:977:G:C8	2.43	0.42
35:A:2111:C:H1'	35:A:2118:U:H4'	2.00	0.42
35:A:702:G:C2	35:A:703:U:C2	3.08	0.42
10:O:97:ARG:HA	10:O:117:LEU:HD22	2.01	0.42
28:8:60:LEU:HD13	28:8:64:TYR:O	2.20	0.42
2:D:6:PHE:HD2	2:D:9:TYR:OH	2.03	0.42
35:A:536:A:H2'	35:A:537:C:C6	2.53	0.42
35:A:579:G:H2'	35:A:580:C:C6	2.54	0.42
19:X:68:ARG:HH21	19:X:69:TYR:HA	1.83	0.42
22:0:70:GLN:HG2	22:0:71:ASP:N	2.33	0.42
35:A:2109:U:H2'	35:A:2110:G:C8	2.55	0.42
35:A:1631:A:C6	35:A:1632:A:C6	3.08	0.42
35:A:638:G:H2'	35:A:639:U:C6	2.55	0.42
16:U:84:LYS:NZ	35:A:1152:C:OP1	2.42	0.42
18:W:16:LYS:O	18:W:20:VAL:HG23	2.19	0.42
13:R:60:LEU:HD21	13:R:64:ARG:CZ	2.50	0.42
35:A:9:U:C2	35:A:2629:A:N7	2.87	0.42
18:W:81:ALA:CB	18:W:99:ARG:HA	2.48	0.42
15:T:64:ARG:HA	15:T:64:ARG:HD3	1.78	0.42
35:A:2625:G:H2'	35:A:2626:C:C6	2.54	0.42
12:Q:34:LEU:HD13	12:Q:131:ILE:HG23	2.00	0.42
4:F:102:PRO:HA	35:A:607:U:OP1	2.19	0.42
11:P:56:SER:OG	11:P:60:MET:SD	2.76	0.42
15:T:47:GLY:N	15:T:65:LYS:HZ3	2.17	0.42
10:O:79:PHE:HA	15:T:72:VAL:HG12	2.01	0.42
2:D:106:ILE:HD12	2:D:106:ILE:HA	1.90	0.42
35:A:2820:A:H5'	35:A:2821:A:N7	2.34	0.42
35:A:1794:U:H2'	35:A:1795:C:O4'	2.19	0.42
35:A:46:C:OP2	35:A:215:G:H8	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:485:C:N4	35:A:496:G:O6	2.53	0.42
3:E:15:PHE:CD1	15:T:80:SER:HB2	2.54	0.42
22:0:41:ARG:NH2	35:A:2387:U:O2'	2.53	0.42
24:3:4:LEU:HD23	24:3:58:VAL:HG13	2.01	0.42
2:D:201:HIS:NE2	35:A:1821:A:OP1	2.46	0.42
1:C:47:LYS:HE3	1:C:211:ARG:NH2	2.32	0.42
14:S:47:THR:O	14:S:48:LEU:CB	2.66	0.42
18:W:77:ASP:O	18:W:102:HIS:N	2.52	0.42
15:T:27:THR:CG2	15:T:49:VAL:HB	2.50	0.42
2:D:16:MET:HG3	2:D:207:GLY:HA3	2.02	0.42
35:A:372:G:O2'	35:A:400:G:O6	2.30	0.42
35:A:2235:G:H2'	35:A:2236:C:C6	2.54	0.42
16:U:34:LYS:HZ3	35:A:2018:G:H21	1.66	0.42
35:A:2127:G:N2	35:A:2173:A:H1'	2.35	0.42
2:D:12:SER:C	2:D:14:ARG:H	2.22	0.42
4:F:46:ARG:HH21	4:F:48:THR:HG21	1.84	0.42
35:A:2592:G:N1	35:A:2603:G:C6	2.87	0.42
36:B:8:U:H2'	36:B:9:G:C8	2.54	0.42
1:C:76:LEU:HD12	1:C:93:ASP:O	2.20	0.42
16:U:47:TYR:OH	35:A:992:C:OP1	2.31	0.42
13:R:10:LEU:HD22	13:R:17:ARG:CZ	2.50	0.42
7:J:86:UNK:O	7:J:87:UNK:C	2.67	0.42
35:A:2027:G:C2	35:A:2028:U:H1'	2.55	0.42
35:A:287:C:H2'	35:A:288:C:O4'	2.20	0.42
35:A:1938:A:N1	35:A:2590:A:H1'	2.34	0.42
16:U:28:ARG:HH11	16:U:38:THR:HG23	1.85	0.42
35:A:1135:C:H42	35:A:1138:G:H8	1.67	0.42
35:A:1348:G:H2'	35:A:1349:A:H5''	2.00	0.42
4:F:107:LYS:HA	4:F:107:LYS:HD3	1.90	0.42
35:A:1906:G:H2'	35:A:1907:G:H8	1.85	0.42
9:N:36:GLY:HA3	9:N:48:MET:HE2	2.02	0.42
9:N:46:VAL:HG13	9:N:48:MET:HG3	2.01	0.42
35:A:807:U:H2'	35:A:808:G:H8	1.85	0.42
1:C:11:LEU:HA	1:C:14:LYS:HB2	2.00	0.42
35:A:1394:U:C4	35:A:1395:A:C5	3.07	0.42
35:A:1605:C:H2'	35:A:1606:G:O4'	2.20	0.42
35:A:1313:U:C2	35:A:1610:A:H2	2.37	0.42
21:Z:102:LEU:HD21	21:Z:124:ILE:HD12	2.00	0.42
1:C:79:ALA:O	1:C:84:ILE:HG13	2.20	0.42
32:1:18:ILE:HA	32:1:41:ARG:H	1.84	0.42
5:G:172:LEU:HD23	5:G:173:LEU:HG	2.02	0.42
24:3:30:ARG:NH1	35:A:1159:U:OP1	2.32	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:1326:U:C2	35:A:1327:C:C6	3.08	0.42
35:A:1638:C:H4'	35:A:2710:C:O2	2.20	0.42
20:Y:97:ARG:HD2	20:Y:97:ARG:HA	1.84	0.42
35:A:1770:G:H2'	35:A:1771:C:C6	2.55	0.42
8:K:32:ALA:HB1	8:K:57:ILE:HD12	2.02	0.42
16:U:61:TRP:HE3	16:U:93:LYS:HB2	1.84	0.42
2:D:14:ARG:NH1	35:A:1693:U:O3'	2.52	0.42
17:V:51:VAL:HG23	17:V:53:GLU:HA	2.01	0.42
4:F:136:THR:O	4:F:140:LEU:HD13	2.19	0.42
5:G:34:LEU:HG	5:G:34:LEU:H	1.56	0.42
1:C:9:ARG:O	1:C:12:LEU:HB3	2.19	0.42
35:A:1378:A:O2'	35:A:1379:A:H2'	2.20	0.42
35:A:2450:A:OP1	35:A:2497:A:O2'	2.33	0.42
35:A:2369:A:H2'	35:A:2370:G:C8	2.55	0.42
12:Q:65:PHE:HB2	12:Q:105:GLU:HG2	2.02	0.42
6:H:173:PRO:HB2	6:H:174:GLY:H	1.58	0.42
35:A:118:A:C8	35:A:119:A:C8	3.08	0.42
14:S:17:ARG:HH11	14:S:25:ARG:NH2	2.18	0.42
36:B:36:C:N3	36:B:49:C:O2'	2.49	0.42
35:A:2287:A:HO2'	35:A:2288:A:P	2.43	0.42
11:P:88:LEU:O	11:P:90:ARG:N	2.53	0.42
15:T:50:ILE:HG13	15:T:64:ARG:HB2	2.01	0.42
32:1:18:ILE:HG12	32:1:20:ARG:HB3	2.01	0.42
16:U:92:ARG:HB2	17:V:11:GLN:CD	2.40	0.42
35:A:104:U:H3'	35:A:105:C:H6	1.85	0.42
35:A:448:U:H3	35:A:583:G:H1'	1.85	0.42
22:0:25:ARG:HB2	22:0:37:LEU:HD22	2.02	0.42
1:C:30:VAL:HA	1:C:33:LEU:H	1.84	0.42
35:A:197:A:H2'	35:A:198:C:H6	1.85	0.42
35:A:2828:C:H2'	35:A:2829:C:H6	1.83	0.42
9:N:21:LYS:HG3	9:N:26:LEU:HD13	2.00	0.42
6:H:157:TYR:HD1	6:H:171:LEU:HD22	1.84	0.42
35:A:1344:G:H4'	35:A:1384:A:C8	2.54	0.42
35:A:2461:C:C2	35:A:2462:U:C5	3.08	0.42
35:A:2461:C:H2'	35:A:2462:U:H6	1.82	0.42
35:A:2003:G:C6	35:A:2004:G:N7	2.87	0.42
35:A:1657:C:H2'	35:A:1658:C:H6	1.85	0.42
3:E:132:HIS:ND1	35:A:1658:C:OP1	2.53	0.42
35:A:1427:A:H4'	35:A:1428:C:O4'	2.18	0.42
35:A:195:A:H5''	35:A:196:A:OP2	2.20	0.42
35:A:1067:A:H8	35:A:1067:A:OP1	2.02	0.42
2:D:269:PHE:CZ	35:A:2219:G:H5''	2.54	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:V:3:ALA:O	17:V:14:VAL:HG22	2.20	0.42
35:A:587:C:C6	35:A:671:C:H1'	2.55	0.42
36:B:46:A:C5	36:B:47:C:C4	3.08	0.42
14:S:97:ARG:O	14:S:99:LYS:HD3	2.20	0.42
6:H:41:MET:HB2	6:H:54:ARG:HA	2.00	0.42
36:B:24:G:C2	36:B:56:G:C2	3.08	0.42
16:U:3:ARG:HD2	35:A:1248:G:C6	2.55	0.42
32:1:21:ARG:O	32:1:23:LYS:N	2.50	0.42
35:A:573:G:O2'	35:A:574:C:H3'	2.20	0.42
6:H:125:VAL:HA	6:H:126:PRO:HD2	1.88	0.42
22:O:11:ARG:NE	22:O:12:ASN:OD1	2.52	0.42
2:D:62:TYR:HA	2:D:87:ASN:HD21	1.84	0.42
21:Z:7:ALA:HB2	21:Z:59:LEU:HB2	2.02	0.42
14:S:34:HIS:CD2	14:S:54:LEU:HB3	2.55	0.42
5:G:154:GLY:HA3	35:A:2305:A:N3	2.34	0.42
35:A:2795:G:H3'	35:A:2797:U:H5''	2.02	0.42
21:Z:111:VAL:O	21:Z:112:ARG:HB3	2.20	0.42
35:A:2720:U:H2'	35:A:2721:A:C8	2.55	0.42
35:A:2720:U:H2'	35:A:2721:A:H8	1.84	0.42
35:A:2725:A:H1'	35:A:2726:U:H2'	2.02	0.42
35:A:2825:U:H2'	35:A:2826:A:O4'	2.19	0.42
5:G:109:VAL:C	5:G:112:PRO:HD2	2.40	0.41
14:S:15:ARG:C	14:S:17:ARG:N	2.74	0.41
9:N:43:THR:HB	9:N:46:VAL:CG1	2.50	0.41
35:A:1295:C:H2'	35:A:1296:G:C8	2.55	0.41
2:D:65:ILE:HD12	2:D:88:ARG:CZ	2.50	0.41
20:Y:102:CYS:SG	20:Y:104:GLY:N	2.93	0.41
15:T:62:THR:OG1	15:T:75:ILE:HG12	2.19	0.41
4:F:155:LEU:O	4:F:191:ARG:C	2.58	0.41
35:A:657:U:C4	35:A:658:C:N4	2.88	0.41
35:A:872:A:N1	35:A:905:U:C2	2.88	0.41
21:Z:55:HIS:HB3	21:Z:56:VAL:H	1.63	0.41
15:T:33:LYS:CG	15:T:43:GLN:HB3	2.47	0.41
20:Y:47:LYS:HD2	35:A:481:G:OP2	2.20	0.41
35:A:216:A:C2	35:A:217:G:H1'	2.55	0.41
35:A:820:A:N3	35:A:943:U:O2'	2.52	0.41
18:W:96:ILE:HD11	35:A:2012:G:H5''	2.01	0.41
10:O:47:ILE:HA	10:O:48:PRO:HD3	1.78	0.41
11:P:125:VAL:O	11:P:145:PRO:HD3	2.20	0.41
35:A:2001:A:H2'	35:A:2002:G:O4'	2.19	0.41
16:U:49:HIS:HA	16:U:52:ARG:HB3	2.02	0.41
11:P:71:VAL:C	11:P:73:GLY:H	2.22	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:J:32:UNK:O	35:A:1055:G:H4'	2.19	0.41
3:E:38:THR:HG23	3:E:41:LYS:H	1.85	0.41
18:W:14:PRO:HB3	18:W:18:ARG:CZ	2.49	0.41
35:A:793:A:OP2	35:A:2072:G:H5'	2.20	0.41
14:S:85:VAL:HG23	14:S:106:ARG:NH1	2.35	0.41
9:N:39:ARG:NE	9:N:41:ASP:HB3	2.35	0.41
1:C:3:LYS:HB3	1:C:4:HIS:H	1.64	0.41
15:T:25:GLY:HA2	15:T:114:LEU:HD21	2.02	0.41
35:A:1312:U:H5'	35:A:1313:U:C5	2.55	0.41
21:Z:124:ILE:HG12	21:Z:126:VAL:HG22	2.02	0.41
13:R:116:LEU:C	13:R:117:VAL:HG23	2.40	0.41
3:E:143:ASN:CG	3:E:144:ARG:N	2.74	0.41
4:F:40:GLN:O	4:F:44:ARG:HD3	2.20	0.41
7:J:82:UNK:O	7:J:84:UNK:N	2.54	0.41
5:G:43:LEU:HB2	5:G:88:ILE:CG2	2.50	0.41
35:A:223:A:N6	35:A:374:A:H4'	2.36	0.41
16:U:59:ARG:HA	16:U:59:ARG:NH1	2.34	0.41
13:R:103:ARG:HA	13:R:111:LEU:HG	2.01	0.41
11:P:115:LEU:HB2	11:P:116:GLY:H	1.67	0.41
35:A:686:G:N2	35:A:788:A:H61	2.18	0.41
24:3:20:LYS:HG2	24:3:20:LYS:H	1.58	0.41
35:A:1954:G:H1'	35:A:1956:U:O4	2.19	0.41
12:Q:35:VAL:HG23	12:Q:101:ARG:N	2.35	0.41
35:A:775:G:O5'	35:A:777:A:H1'	2.21	0.41
19:X:55:ASN:HB2	19:X:80:ILE:HG13	2.03	0.41
5:G:176:LEU:HA	5:G:176:LEU:HD23	1.80	0.41
35:A:1132:A:N1	35:A:2039:C:O2'	2.47	0.41
12:Q:122:GLY:HA2	12:Q:125:LEU:HG	2.01	0.41
24:3:14:GLY:HA2	35:A:970:C:OP1	2.19	0.41
35:A:519:U:H2'	35:A:520:G:H8	1.85	0.41
18:W:41:LYS:HD3	35:A:2010:G:OP1	2.20	0.41
9:N:41:ASP:HA	16:U:64:ARG:CZ	2.49	0.41
4:F:38:ARG:NH2	35:A:660:G:O2'	2.52	0.41
35:A:1275:A:N6	35:A:1296:G:H4'	2.36	0.41
14:S:95:HIS:H	14:S:97:ARG:NH2	2.18	0.41
35:A:1528:A:H62	35:A:1543:A:H2	1.68	0.41
35:A:2287:A:N1	35:A:2346:A:C2	2.89	0.41
18:W:80:PRO:HB2	18:W:81:ALA:H	1.64	0.41
32:1:18:ILE:HG12	32:1:20:ARG:N	2.35	0.41
32:1:37:ILE:CG1	35:A:200:U:H4'	2.51	0.41
19:X:7:VAL:HB	19:X:8:ILE:H	1.59	0.41
17:V:38:LEU:C	17:V:39:LEU:HD22	2.40	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:2513:G:H5'	35:A:2514:U:OP2	2.20	0.41
3:E:151:TYR:HB3	9:N:79:PRO:HG3	2.02	0.41
21:Z:72:ARG:HB3	21:Z:72:ARG:HH11	1.85	0.41
35:A:2031:A:H8	35:A:2031:A:OP1	2.03	0.41
3:E:9:VAL:HG23	3:E:26:ILE:HA	2.02	0.41
35:A:2330:G:H1	35:A:2385:C:H42	1.68	0.41
5:G:70:VAL:CG1	5:G:88:ILE:HG13	2.50	0.41
35:A:864:G:H2'	35:A:865:C:H6	1.84	0.41
17:V:18:LEU:O	17:V:95:LEU:HA	2.20	0.41
9:N:106:MET:HE3	35:A:1006:C:H1'	2.01	0.41
35:A:1407:C:H2'	35:A:1408:C:C6	2.55	0.41
35:A:2556:C:H2'	35:A:2557:G:O4'	2.20	0.41
21:Z:150:LEU:O	21:Z:171:ILE:HG13	2.19	0.41
35:A:1102:C:H2'	35:A:1103:A:C8	2.50	0.41
35:A:1654:A:H2'	35:A:1655:A:H8	1.85	0.41
33:4:13:ARG:O	33:4:14:ILE:HG12	2.20	0.41
5:G:94:LEU:HB3	5:G:99:MET:CB	2.50	0.41
35:A:1494:A:O2'	35:A:1495:A:H5''	2.20	0.41
35:A:2648:C:H2'	35:A:2649:U:H6	1.85	0.41
2:D:9:TYR:CE1	35:A:705:A:H1'	2.55	0.41
23:2:49:LYS:O	23:2:52:ASP:HB2	2.20	0.41
15:T:98:LYS:NZ	35:A:2847:U:OP1	2.33	0.41
15:T:98:LYS:HD3	35:A:2718:G:O2'	2.20	0.41
9:N:19:GLU:HA	9:N:59:LYS:O	2.20	0.41
35:A:2737:G:H2'	35:A:2738:A:H8	1.85	0.41
35:A:695:G:H2'	35:A:696:G:O4'	2.19	0.41
16:U:51:LYS:H	16:U:51:LYS:HD2	1.86	0.41
22:0:50:ASN:HB3	22:0:63:VAL:HG22	2.03	0.41
11:P:70:GLN:H	35:A:245:G:H5'	1.85	0.41
35:A:1859:A:H3'	35:A:1860:G:H8	1.85	0.41
35:A:2040:C:H2'	35:A:2041:U:H6	1.86	0.41
4:F:38:ARG:HH21	11:P:16:ARG:NH2	2.18	0.41
9:N:25:ARG:HH22	35:A:114(B):A:C4'	2.26	0.41
35:A:24:G:C6	35:A:25:U:C4	3.09	0.41
15:T:51:ARG:HG2	15:T:62:THR:HG22	2.03	0.41
35:A:1486:A:H2'	35:A:1487:G:H8	1.83	0.41
33:4:9:LEU:HB3	33:4:10:VAL:H	1.60	0.41
35:A:197:A:H2'	35:A:198:C:C6	2.56	0.41
35:A:1115:G:H2'	35:A:1116:C:H6	1.86	0.41
15:T:33:LYS:HZ3	15:T:74:ARG:HH22	1.66	0.41
35:A:373:U:OP2	35:A:400:G:N1	2.41	0.41
32:1:73:LEU:HD11	32:1:95:LEU:HB3	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:2462:U:H1'	35:A:2491:U:O4	2.20	0.41
36:B:15:A:H3'	36:B:16:G:C8	2.54	0.41
7:J:151:UNK:C	7:J:153:UNK:H	2.33	0.41
35:A:2688:U:H6	35:A:2721:A:H62	1.66	0.41
35:A:2322:A:H2'	35:A:2323:G:O4'	2.19	0.41
35:A:2516:G:H2'	35:A:2517:C:C6	2.56	0.41
19:X:47:PHE:HB3	19:X:89:ILE:HG12	2.03	0.41
12:Q:91:GLU:CD	12:Q:92:GLY:H	2.23	0.41
35:A:1024:G:OP2	35:A:1025:G:H3'	2.20	0.41
35:A:1062:G:H2'	35:A:1063:G:C8	2.55	0.41
36:B:44:G:H21	36:B:47:C:H42	1.68	0.41
32:1:20:ARG:H	32:1:40:ARG:HB2	1.84	0.41
12:Q:45:GLN:HG2	12:Q:45:GLN:H	1.58	0.41
3:E:189:PRO:HB3	35:A:2679:A:H4'	2.03	0.41
35:A:2849:U:O2'	35:A:2866:U:O2	2.38	0.41
35:A:1021:A:H62	35:A:1141:U:H3	1.69	0.41
35:A:329:G:H8	35:A:329:G:OP2	2.03	0.41
35:A:872:A:H2'	35:A:873:G:H8	1.85	0.41
35:A:1115:G:H2'	35:A:1116:C:C6	2.56	0.41
35:A:2525:G:H2'	35:A:2526:G:C8	2.54	0.41
35:A:2712:U:O2'	35:A:712(B):A:H3'	2.20	0.41
23:2:61:LEU:HD12	35:A:72:U:O4'	2.20	0.41
21:Z:10:ARG:HD2	21:Z:36:LYS:HB2	2.03	0.41
21:Z:77:ASP:OD2	21:Z:77:ASP:N	2.51	0.41
35:A:1384:A:N3	35:A:1405:U:H1'	2.35	0.41
35:A:2024:G:C6	35:A:2025:C:C4	3.09	0.41
35:A:2857:G:N1	35:A:2861:G:C6	2.89	0.41
29:9:17:ILE:HD12	29:9:19:ARG:HB2	2.01	0.41
10:O:27:GLY:HA3	35:A:2674:G:O2'	2.21	0.41
35:A:1709:U:H2'	35:A:1710:C:H6	1.85	0.41
10:O:40:VAL:HG21	35:A:2561:A:O2'	2.20	0.41
35:A:144(B):A:H5''	35:A:1445:C:H5	1.86	0.41
35:A:30:G:H2'	35:A:31:C:O4'	2.20	0.41
6:H:94:TYR:CD2	6:H:107:VAL:HG12	2.55	0.41
15:T:67:SER:H	15:T:71:GLY:HA2	1.85	0.41
2:D:28:GLU:H	2:D:29:PRO:HD2	1.86	0.41
9:N:10:GLU:CG	9:N:11:PRO:HD2	2.50	0.41
15:T:54:ARG:O	35:A:2845:G:H5''	2.20	0.41
18:W:21:VAL:CG1	18:W:74:ALA:HB1	2.51	0.41
35:A:114(B):A:C5	35:A:1144:G:C5	3.08	0.41
36:B:48:A:H2'	36:B:49:C:C6	2.55	0.41
35:A:956:G:HO2'	35:A:959:A:H62	1.67	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:Y:49:VAL:C	20:Y:51:VAL:H	2.24	0.41
4:F:188:ARG:HA	11:P:7:ARG:HH21	1.85	0.41
12:Q:42:ILE:CD1	12:Q:95:ALA:HB3	2.44	0.41
35:A:2330:G:H2'	35:A:2331:G:O4'	2.21	0.41
35:A:700:G:N2	35:A:732:C:N3	2.56	0.41
35:A:2817:G:O2'	35:A:2836:U:O2	2.30	0.41
2:D:35:LYS:HB3	2:D:35:LYS:HE3	1.83	0.41
35:A:111:A:H2'	35:A:112:U:O4'	2.21	0.41
35:A:415:A:O2'	35:A:1869:G:H4'	2.21	0.41
6:H:97:ARG:HG2	6:H:99:VAL:H	1.86	0.41
35:A:1413:G:H1	35:A:1589:C:H42	1.69	0.41
11:P:85:LEU:C	11:P:118:GLY:HA3	2.41	0.41
35:A:1668:A:H4'	35:A:1669:A:O5'	2.21	0.41
35:A:2847:U:H2'	35:A:2848:G:H5'	2.02	0.41
19:X:21:PHE:HE2	19:X:26:TYR:HA	1.85	0.41
35:A:539:G:H2'	35:A:540:G:C8	2.56	0.41
35:A:638:G:H2'	35:A:639:U:O4'	2.21	0.41
35:A:1689:A:H62	35:A:1698:A:H2	1.69	0.41
35:A:1301:A:C8	35:A:1303:G:C8	3.09	0.41
35:A:1470:G:O2'	35:A:1522:G:O6	2.38	0.41
11:P:27:HIS:CE1	35:A:813:U:C4	3.08	0.41
3:E:61:ARG:CZ	35:A:2811:G:H4'	2.50	0.41
9:N:42:TRP:CZ2	9:N:44:PRO:HA	2.56	0.41
32:1:18:ILE:CG2	35:A:380:U:H4'	2.50	0.41
6:H:85:LYS:HZ1	6:H:121:ILE:CG2	2.34	0.41
20:Y:2:ARG:HD2	35:A:295:G:OP1	2.20	0.41
15:T:88:ILE:HG22	15:T:89:VAL:HG23	2.02	0.41
8:K:110:GLN:OE1	8:K:111:LYS:HG2	2.20	0.41
2:D:151:LYS:HZ1	35:A:2217:G:H21	1.67	0.41
35:A:1514:U:H2'	35:A:1515:C:C6	2.55	0.41
27:7:40:TRP:CZ3	35:A:459:U:H3'	2.54	0.41
35:A:481:G:H2'	35:A:507:A:N1	2.36	0.41
36:B:79:C:H2'	36:B:80:U:O4'	2.21	0.41
10:O:24:VAL:HG13	10:O:33:ALA:HB2	2.02	0.41
35:A:91:A:H3'	35:A:92:G:H8	1.86	0.41
35:A:659:C:H2'	35:A:660:G:C8	2.49	0.41
35:A:1313:U:H4'	35:A:1332:G:H4'	2.03	0.41
35:A:449:A:C5	35:A:450:G:C5	3.09	0.41
15:T:100:TYR:HD1	15:T:103:ARG:HD3	1.86	0.41
4:F:155:LEU:HB2	4:F:189:THR:OG1	2.21	0.41
22:0:20:ARG:HG3	35:A:2271:G:H5'	2.02	0.41
4:F:25:PRO:HB3	4:F:115:ALA:HB1	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:101:ILE:HA	1:C:101:ILE:HD12	1.94	0.41
21:Z:91:LEU:O	21:Z:92:SER:OG	2.38	0.41
15:T:53:ARG:NH2	35:A:2683:C:H5''	2.35	0.41
35:A:702:G:H2'	35:A:703:U:C6	2.56	0.41
35:A:2531:A:H3'	35:A:2532:G:C8	2.56	0.41
35:A:2018:G:H2'	35:A:2019:A:C8	2.56	0.41
5:G:16:ARG:HB2	5:G:17:PRO:HD3	2.03	0.41
32:1:49:VAL:HG21	32:1:67:ILE:HG23	2.02	0.41
35:A:1669:A:C6	35:A:1994:C:O2	2.74	0.41
9:N:133:GLN:CG	9:N:135:PRO:HD3	2.50	0.41
35:A:2792:G:H2'	35:A:2792:G:N3	2.35	0.41
35:A:48:G:H2'	35:A:49:A:H2	1.86	0.41
35:A:1016:G:C2	35:A:1017:G:N7	2.88	0.41
35:A:2150:U:H2'	35:A:2151:G:H8	1.85	0.41
21:Z:24:LEU:HB2	21:Z:41:LEU:HD21	2.03	0.41
36:B:113:C:H2'	36:B:114:G:C8	2.56	0.41
35:A:1885:A:H2'	35:A:1886:C:O4'	2.20	0.41
12:Q:61:GLY:O	21:Z:177:PRO:HB3	2.20	0.41
35:A:1779:U:OP2	35:A:1784:A:N6	2.43	0.41
35:A:10:G:N2	35:A:2802:G:OP1	2.52	0.41
14:S:13:ARG:C	14:S:15:ARG:N	2.74	0.41
14:S:17:ARG:HA	14:S:20:ARG:HG2	2.03	0.41
35:A:587:C:C4	35:A:671:C:C2	3.09	0.41
35:A:2339:G:H2'	35:A:2340:G:C8	2.55	0.41
35:A:531:C:OP1	35:A:561:G:N2	2.49	0.41
5:G:66:GLN:HB3	33:4:6:HIS:CD2	2.56	0.41
6:H:52:VAL:HG21	6:H:69:ARG:HA	2.02	0.41
1:C:132:LEU:HD22	1:C:137:LEU:HD12	2.03	0.41
35:A:2879:C:H4'	35:A:2880:C:OP1	2.20	0.41
35:A:136:G:N2	35:A:143:C:N3	2.62	0.41
20:Y:11:ASP:OD2	20:Y:12:THR:N	2.53	0.41
11:P:140:ALA:O	11:P:141:ALA:HB2	2.21	0.41
19:X:12:VAL:HG21	19:X:27:THR:HG23	2.02	0.41
35:A:2849:U:O2'	35:A:2866:U:C2	2.73	0.41
3:E:161:GLY:O	3:E:163:GLU:N	2.52	0.41
22:0:37:LEU:HD13	22:0:67:VAL:HG13	2.03	0.41
35:A:2641:G:C2	35:A:2774:C:C2	3.08	0.41
36:B:95:U:H2'	36:B:96:G:C8	2.56	0.41
35:A:1108:U:H2'	35:A:1109:C:O4'	2.21	0.41
4:F:44:ARG:HB3	35:A:615:G:N2	2.29	0.41
8:K:105:LEU:HD23	8:K:106:GLU:N	2.36	0.41
5:G:51:ARG:CZ	5:G:54:GLU:HB2	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:700:G:H1	35:A:732:C:N4	2.12	0.41
1:C:141:PRO:O	1:C:142:LYS:HB2	2.21	0.41
35:A:2818:G:H1'	35:A:2836:U:O2'	2.21	0.41
35:A:1203:G:C6	35:A:1204:A:N6	2.88	0.41
19:X:87:GLN:NE2	19:X:88:LYS:O	2.53	0.41
3:E:55:ASN:HA	3:E:56:PRO:HD3	1.79	0.41
35:A:900:A:C6	35:A:901:A:C4	3.08	0.41
21:Z:73:GLN:NE2	21:Z:75:ASN:HD21	2.19	0.41
4:F:72:ARG:NH2	35:A:1258:C:OP2	2.52	0.41
35:A:1213:A:N3	35:A:1238:G:O2'	2.52	0.41
9:N:45:ASN:ND2	35:A:557:U:O2	2.48	0.41
11:P:133:SER:OG	35:A:637:A:OP1	2.35	0.41
11:P:48:PRO:O	11:P:49:ARG:C	2.59	0.41
6:H:127:GLU:OE2	6:H:129:THR:HB	2.21	0.41
1:C:76:LEU:HB2	1:C:111:PHE:HB3	2.03	0.41
24:3:29:ARG:HD3	35:A:1184:G:OP1	2.21	0.41
17:V:68:LYS:HE2	17:V:69:LYS:O	2.20	0.41
35:A:1107:G:O5'	35:A:1107:G:H8	2.03	0.41
35:A:1510:A:C6	35:A:1511:A:C4	3.09	0.41
35:A:171:G:H2'	35:A:172:C:C6	2.56	0.41
35:A:1524:G:C2	35:A:1525:G:H1'	2.55	0.41
35:A:2695:C:H2'	35:A:2696:U:C5	2.56	0.41
4:F:129:PHE:CE2	4:F:163:VAL:HG21	2.56	0.41
1:C:100:ILE:HG12	1:C:100:ILE:H	1.73	0.41
35:A:2646:C:H2'	35:A:2647:U:O4'	2.20	0.41
35:A:324:A:N6	35:A:325:G:C2	2.89	0.41
35:A:1353:A:H2'	35:A:1354:A:C8	2.56	0.41
2:D:182:LEU:HB2	2:D:271:ILE:O	2.21	0.41
35:A:1858:G:H1'	35:A:1884:A:N6	2.36	0.41
35:A:634:C:H2'	35:A:635:C:O4'	2.21	0.41
2:D:27:THR:HG23	2:D:83:GLU:HB3	2.02	0.41
35:A:2301:C:H2'	35:A:2302:G:H8	1.85	0.41
35:A:2595:G:N2	35:A:2598:A:OP2	2.50	0.41
5:G:111:LEU:HB2	5:G:112:PRO:HD3	2.02	0.41
35:A:1838:C:H4'	35:A:1839:G:C8	2.56	0.41
18:W:19:LEU:HD13	18:W:19:LEU:HA	1.83	0.41
35:A:2888:C:H2'	35:A:2889:C:C6	2.56	0.41
8:K:133:SER:HB2	35:A:1062:G:O2'	2.21	0.41
35:A:1605:C:H1'	35:A:1610:A:C5	2.56	0.41
4:F:9:ILE:HA	4:F:10:PRO:HD3	1.82	0.41
6:H:121:ILE:HG22	6:H:135:GLY:HA3	2.02	0.41
2:D:173:VAL:HG23	2:D:185:VAL:HB	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:604:G:C6	35:A:605:C:C4	3.09	0.41
11:P:57:THR:C	11:P:59:LEU:N	2.73	0.41
33:4:28:LYS:HA	33:4:28:LYS:HD2	1.72	0.41
6:H:125:VAL:HG13	6:H:130:ARG:O	2.21	0.41
2:D:30:GLU:CD	2:D:63:ARG:HE	2.25	0.41
35:A:481:G:H1'	35:A:506:G:N2	2.36	0.41
35:A:2643:G:C2	35:A:2644:G:H1'	2.56	0.41
35:A:32:C:C4	35:A:33:U:C4	3.09	0.41
8:K:30:HIS:CD2	8:K:30:HIS:C	2.94	0.41
14:S:33:LYS:HB2	14:S:34:HIS:HD2	1.84	0.41
28:8:40:GLU:O	28:8:44:LYS:HB2	2.21	0.41
35:A:2529:G:OP2	35:A:2530:A:H5''	2.21	0.41
13:R:86:ARG:HB3	13:R:118:GLU:CD	2.42	0.41
35:A:1036:G:H2'	35:A:1037:G:C8	2.56	0.41
35:A:2858:C:H2'	35:A:2859:G:O4'	2.21	0.41
2:D:31:LYS:HA	2:D:31:LYS:HD2	1.97	0.41
9:N:89:LYS:HB3	9:N:89:LYS:HZ2	1.86	0.41
14:S:11:LYS:HE3	14:S:11:LYS:HB2	1.90	0.41
6:H:15:VAL:HG11	6:H:76:VAL:HG13	2.02	0.41
1:C:194:ILE:O	1:C:197:LEU:HB2	2.20	0.41
11:P:114:ILE:HG13	11:P:130:PHE:HA	2.03	0.41
35:A:384:U:H2'	35:A:385:C:H6	1.85	0.41
35:A:270(J):G:C2	35:A:270(R):C:N3	2.89	0.40
2:D:244:ARG:HA	2:D:245:PRO:HA	1.62	0.40
14:S:85:VAL:H	14:S:106:ARG:HG2	1.85	0.40
35:A:25:U:H3	35:A:515:A:N6	2.19	0.40
4:F:177:ALA:HB1	4:F:178:PRO:CD	2.51	0.40
2:D:211:ARG:HA	2:D:214:TRP:CE3	2.57	0.40
6:H:83:TYR:HD2	6:H:84:SER:N	2.18	0.40
35:A:674:G:H2'	35:A:804:A:H61	1.86	0.40
21:Z:71:VAL:HB	21:Z:72:ARG:H	1.63	0.40
3:E:161:GLY:O	3:E:163:GLU:HG2	2.21	0.40
26:6:8:LYS:NZ	26:6:27:LYS:HD3	2.34	0.40
11:P:17:LYS:HG3	11:P:17:LYS:O	2.21	0.40
35:A:826:U:H5''	35:A:2429:G:OP1	2.22	0.40
4:F:154:VAL:O	4:F:175:THR:HA	2.20	0.40
35:A:2126:A:H4'	35:A:2127:G:O5'	2.20	0.40
15:T:115:ARG:H	15:T:115:ARG:HG2	1.61	0.40
9:N:90:MET:CE	9:N:90:MET:HA	2.51	0.40
28:8:40:GLU:O	28:8:44:LYS:N	2.54	0.40
5:G:35:GLU:OE2	5:G:160:VAL:HG12	2.21	0.40
35:A:1635:G:H8	35:A:1635:G:O5'	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:9:3:VAL:HG13	29:9:37:GLY:HA3	2.02	0.40
2:D:53:PHE:CZ	2:D:221:VAL:HG12	2.56	0.40
35:A:13:A:OP2	35:A:13:A:H2'	2.21	0.40
8:K:77:LEU:HA	8:K:77:LEU:HD13	1.97	0.40
4:F:13:SER:HB3	4:F:14:PRO:HD2	2.03	0.40
35:A:2098:U:H3	35:A:2191:G:H1	1.67	0.40
2:D:100:GLY:O	35:A:1500:G:O2'	2.27	0.40
35:A:1446:C:H2'	35:A:1447:G:C8	2.56	0.40
17:V:5:VAL:HG23	17:V:37:VAL:O	2.21	0.40
7:J:159:UNK:C	7:J:161:UNK:N	2.82	0.40
35:A:2686:G:H2'	35:A:2687:U:C6	2.56	0.40
35:A:1586:A:H2'	35:A:1586:A:N3	2.36	0.40
35:A:2851:A:H2'	35:A:2852:G:H8	1.85	0.40
36:B:42:C:H2'	36:B:43:C:C6	2.56	0.40
35:A:2457:U:H3	35:A:2494:G:H1	1.69	0.40
35:A:1537:C:N4	35:A:1538:G:N3	2.69	0.40
35:A:1664:A:H1'	35:A:2685:G:O2'	2.22	0.40
1:C:48:LEU:H	1:C:48:LEU:HD12	1.86	0.40
35:A:656:G:H2'	35:A:657:U:O4'	2.21	0.40
12:Q:27:VAL:HB	12:Q:137:TYR:HE2	1.86	0.40
35:A:2114:A:C2	35:A:2168:G:H1'	2.56	0.40
35:A:2327:A:H2'	35:A:2328:A:C8	2.56	0.40
8:K:13:PRO:HB3	8:K:52:ILE:HG12	2.03	0.40
35:A:414:C:O2	35:A:1864:U:O2'	2.30	0.40
28:8:42:ARG:HG3	35:A:2349:G:OP2	2.21	0.40
11:P:62:LEU:N	11:P:62:LEU:HD23	2.34	0.40
14:S:52:SER:HB3	14:S:55:ALA:HB3	2.03	0.40
13:R:3:HIS:C	13:R:5:LYS:H	2.24	0.40
35:A:1439:A:H2'	35:A:1440:G:H5'	2.02	0.40
35:A:2695:C:N3	35:A:2714:G:O6	2.55	0.40
35:A:1431:U:H2'	35:A:1432:C:H6	1.85	0.40
2:D:69:ARG:HH22	2:D:192:THR:HG21	1.86	0.40
15:T:54:ARG:HB2	35:A:2846:G:P	2.61	0.40
35:A:2254:C:H2'	35:A:2255:G:O4'	2.22	0.40
35:A:2373:G:H2'	35:A:2374:C:O4'	2.21	0.40
5:G:7:LEU:HA	5:G:10:LYS:HB2	2.04	0.40
29:9:4:ARG:O	29:9:6:SER:N	2.53	0.40
19:X:30:VAL:HG22	19:X:77:LYS:O	2.22	0.40
3:E:62:PRO:HG3	35:A:2786:U:O2	2.21	0.40
35:A:2265:U:O5'	35:A:2266:A:H2'	2.22	0.40
35:A:296:C:H2'	35:A:297:C:H6	1.85	0.40
16:U:3:ARG:NH2	35:A:449:A:H4'	2.37	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:T:48:ILE:HB	15:T:49:VAL:H	1.58	0.40
9:N:6:PRO:C	9:N:7:LYS:NZ	2.75	0.40
4:F:57:VAL:HG12	4:F:59:TYR:H	1.86	0.40
35:A:1277:G:H2'	35:A:1278:A:C8	2.55	0.40
35:A:197:A:N6	35:A:2430:A:H2'	2.36	0.40
35:A:827:U:O2'	35:A:2068:U:N3	2.54	0.40
6:H:125:VAL:HG22	6:H:131:VAL:HG13	2.03	0.40
35:A:1755:A:N6	35:A:2694:G:H21	2.15	0.40
35:A:826:U:H3	35:A:831:G:H1	1.68	0.40
3:E:79:ARG:NH2	8:K:30:HIS:O	103.06	0.40
35:A:1086:A:H3'	35:A:1086:A:N3	2.37	0.40
35:A:1186:G:H3'	35:A:1187:G:H8	1.87	0.40
35:A:1468:C:H2'	35:A:1469:A:H8	1.84	0.40
35:A:1356:G:H2'	35:A:1357:U:O4'	2.21	0.40
11:P:144:GLU:HA	11:P:145:PRO:HD3	1.87	0.40
35:A:2307:G:H5''	35:A:2308:G:OP2	2.21	0.40
9:N:133:GLN:HB3	9:N:134:ARG:H	1.68	0.40
35:A:547:A:H3'	35:A:548:A:C8	2.56	0.40
20:Y:26:LYS:H	20:Y:40:GLU:CG	2.34	0.40
35:A:1428:C:C5	35:A:1569:A:H5''	2.56	0.40
23:2:48:HIS:CD2	23:2:49:LYS:H	2.38	0.40
10:O:87:ILE:HD13	10:O:91:LEU:HD23	2.03	0.40
9:N:89:LYS:NZ	9:N:89:LYS:HB3	2.36	0.40
35:A:723:G:H2'	35:A:724:U:O4'	2.21	0.40
35:A:1550:C:H2'	35:A:1551:C:C6	2.56	0.40
2:D:48:ARG:O	2:D:49:ILE:HG13	2.22	0.40
25:5:3:LYS:HE2	25:5:3:LYS:N	2.36	0.40
13:R:64:ARG:O	13:R:68:ARG:HB2	2.22	0.40
15:T:51:ARG:NH1	35:A:2685:G:OP1	2.54	0.40
15:T:48:ILE:HD12	15:T:48:ILE:H	1.87	0.40
4:F:195:ASP:HB3	4:F:197:ASP:CG	2.42	0.40
36:B:81:G:C2	36:B:82:G:C5	3.09	0.40
35:A:1029:A:H2'	35:A:1030:G:O4'	2.22	0.40
11:P:76:LYS:NZ	35:A:228:A:OP1	2.55	0.40
9:N:34:LEU:HD11	9:N:120:LEU:HB2	2.04	0.40
35:A:1895:C:H2'	35:A:1896:G:C8	2.57	0.40
35:A:1086:A:O2'	35:A:1087:G:N7	2.55	0.40
15:T:7:ILE:O	15:T:10:VAL:N	2.52	0.40
35:A:1917:U:C4	35:A:1918:A:C6	3.09	0.40
35:A:1990:C:H2'	35:A:1991:U:C6	2.56	0.40
35:A:733:G:C8	35:A:761:A:N6	2.90	0.40
35:A:613:U:H4'	35:A:616:A:C5	2.57	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:H:152:ARG:HB3	6:H:162:ILE:HG13	2.04	0.40
35:A:763:G:H2'	35:A:765:G:OP2	2.22	0.40
12:Q:47:ILE:HA	12:Q:47:ILE:HD13	1.69	0.40
35:A:2758:A:C2	35:A:2759:G:H1'	2.57	0.40
13:R:77:ARG:O	13:R:81:ASP:HB2	2.22	0.40
11:P:27:HIS:NE2	35:A:814:C:C5	2.89	0.40
35:A:270(K):G:H2'	35:A:270(L):C:O4'	2.22	0.40
35:A:2319:G:N2	35:A:2334:G:OP1	2.49	0.40
14:S:85:VAL:H	14:S:106:ARG:HD3	1.87	0.40
35:A:531:C:H5''	35:A:532:A:C5	2.56	0.40
1:C:161:ARG:HA	1:C:161:ARG:HH11	1.87	0.40
15:T:102:ILE:HG13	15:T:103:ARG:N	2.36	0.40
17:V:66:ARG:HG3	17:V:90:PRO:HG3	2.03	0.40
35:A:528:A:C8	35:A:528:A:H3'	2.57	0.40
35:A:528:A:H8	35:A:528:A:H3'	1.87	0.40
27:7:26:GLY:HA2	27:7:29:LYS:HG3	2.03	0.40
35:A:226:G:O2'	35:A:227:A:C8	2.74	0.40
35:A:2532:G:C6	35:A:2533:A:C6	3.10	0.40
10:O:107:ARG:NH2	15:T:35:LYS:HE2	2.36	0.40
35:A:1407:C:N4	35:A:1595:G:H1	2.19	0.40
6:H:139:GLN:HB3	6:H:143:GLN:OE1	2.22	0.40
10:O:13:ASN:CG	10:O:96:THR:HG22	2.41	0.40
6:H:123:PHE:O	6:H:124:GLU:CB	2.70	0.40
6:H:107:VAL:HG21	6:H:152:ARG:HB2	2.03	0.40
9:N:10:GLU:HG3	9:N:11:PRO:HD2	2.04	0.40
8:K:38:VAL:HA	8:K:42:ASN:HB3	2.03	0.40
35:A:1065:U:H3'	35:A:1066:U:H6	1.87	0.40
18:W:26:GLY:HA2	18:W:71:VAL:O	2.20	0.40
35:A:1362:C:H42	35:A:1369:G:H1	1.70	0.40
15:T:30:VAL:HG22	15:T:31:SER:H	1.86	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. 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	
1	C	226/228 (99%)	105 (46%)	75 (33%)	46 (20%)	0	2
2	D	273/275 (99%)	188 (69%)	47 (17%)	38 (14%)	0	8
3	E	203/205 (99%)	133 (66%)	36 (18%)	34 (17%)	0	5
4	F	206/208 (99%)	137 (66%)	47 (23%)	22 (11%)	1	13
5	G	179/181 (99%)	127 (71%)	44 (25%)	8 (4%)	4	40
6	H	165/167 (99%)	118 (72%)	32 (19%)	15 (9%)	1	18
8	K	138/140 (99%)	86 (62%)	33 (24%)	19 (14%)	0	8
9	N	136/138 (99%)	91 (67%)	27 (20%)	18 (13%)	0	9
10	O	120/122 (98%)	95 (79%)	20 (17%)	5 (4%)	4	43
11	P	144/146 (99%)	76 (53%)	35 (24%)	33 (23%)	0	1
12	Q	139/141 (99%)	91 (66%)	31 (22%)	17 (12%)	1	11
13	R	115/117 (98%)	91 (79%)	17 (15%)	7 (6%)	2	30
14	S	97/99 (98%)	57 (59%)	25 (26%)	15 (16%)	0	5
15	T	136/138 (99%)	82 (60%)	28 (21%)	26 (19%)	0	3
16	U	115/117 (98%)	80 (70%)	23 (20%)	12 (10%)	1	14
17	V	99/101 (98%)	64 (65%)	22 (22%)	13 (13%)	0	9
18	W	111/113 (98%)	81 (73%)	16 (14%)	14 (13%)	0	10
19	X	91/93 (98%)	70 (77%)	16 (18%)	5 (6%)	3	34
20	Y	105/107 (98%)	50 (48%)	34 (32%)	21 (20%)	0	2
21	Z	183/185 (99%)	121 (66%)	44 (24%)	18 (10%)	1	16
22	0	82/84 (98%)	65 (79%)	13 (16%)	4 (5%)	3	37
23	2	69/71 (97%)	50 (72%)	17 (25%)	2 (3%)	7	54
24	3	58/60 (97%)	44 (76%)	9 (16%)	5 (9%)	1	19
25	5	57/59 (97%)	42 (74%)	11 (19%)	4 (7%)	2	26
26	6	48/50 (96%)	27 (56%)	8 (17%)	13 (27%)	0	1
27	7	47/49 (96%)	34 (72%)	11 (23%)	2 (4%)	4	42
28	8	62/64 (97%)	40 (64%)	11 (18%)	11 (18%)	0	4
29	9	35/37 (95%)	29 (83%)	4 (11%)	2 (6%)	3	33
32	1	91/93 (98%)	59 (65%)	18 (20%)	14 (15%)	0	6
33	4	33/35 (94%)	15 (46%)	9 (27%)	9 (27%)	0	1
34	e	70/102 (69%)	40 (57%)	22 (31%)	8 (11%)	1	12
All	All	3633/3725 (98%)	2388 (66%)	785 (22%)	460 (13%)	0	10

All (460) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	17	PRO
1	C	41	THR
1	C	42	VAL
1	C	43	GLU
1	C	52	PRO
1	C	80	LYS
1	C	96	GLY
1	C	115	VAL
1	C	141	PRO
1	C	142	LYS
1	C	162	ILE
1	C	176	VAL
1	C	182	PRO
1	C	184	GLU
1	C	212	SER
1	C	223	VAL
1	C	227	PRO
1	C	228	HIS
2	D	3	VAL
2	D	27	THR
2	D	36	PRO
2	D	46	GLN
2	D	49	ILE
2	D	79	VAL
2	D	89	SER
2	D	165	ILE
2	D	166	GLN
2	D	187	GLY
2	D	200	ASP
2	D	273	ARG
3	E	11	MET
3	E	12	THR
3	E	13	ARG
3	E	56	PRO
3	E	62	PRO
3	E	63	LEU
3	E	67	PHE
3	E	68	ALA
3	E	72	VAL
3	E	77	ILE
3	E	128	SER
3	E	129	HIS

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Mol	Chain	Res	Type
3	E	144	ARG
3	E	187	ALA
4	F	3	GLU
4	F	7	TYR
4	F	10	PRO
4	F	21	ALA
4	F	84	VAL
4	F	89	VAL
4	F	192	LEU
5	G	87	PRO
5	G	130	ASN
5	G	137	GLU
6	H	124	GLU
6	H	141	VAL
6	H	155	SER
6	H	165	ALA
6	H	172	LYS
6	H	173	PRO
8	K	45	THR
8	K	96	VAL
8	K	137	GLU
9	N	17	ASP
9	N	18	ALA
9	N	25	ARG
9	N	126	PRO
9	N	128	HIS
9	N	130	HIS
9	N	133	GLN
10	O	14	THR
10	O	23	ARG
11	P	9	ASN
11	P	22	GLY
11	P	45	LEU
11	P	57	THR
11	P	71	VAL
11	P	110	TYR
11	P	120	ALA
11	P	141	ALA
11	P	149	GLU
12	Q	29	PHE
12	Q	83	MET
12	Q	85	LYS

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Mol	Chain	Res	Type
12	Q	92	GLY
12	Q	133	ARG
12	Q	136	ALA
13	R	103	ARG
14	S	22	GLY
14	S	47	THR
14	S	48	LEU
14	S	62	LYS
14	S	98	VAL
14	S	101	LEU
14	S	104	GLY
14	S	106	ARG
15	T	3	ARG
15	T	30	VAL
15	T	49	VAL
15	T	80	SER
15	T	86	ILE
15	T	104	ASN
15	T	137	LYS
16	U	24	TYR
16	U	88	ILE
16	U	90	VAL
17	V	29	PRO
17	V	46	VAL
17	V	50	PRO
17	V	78	LYS
17	V	96	ILE
17	V	97	LYS
18	W	12	ILE
18	W	14	PRO
18	W	15	ARG
18	W	61	ASN
18	W	74	ALA
18	W	75	TYR
18	W	77	ASP
18	W	81	ALA
19	X	7	VAL
19	X	12	VAL
20	Y	32	PRO
20	Y	39	VAL
20	Y	53	PRO
20	Y	56	PRO

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Mol	Chain	Res	Type
20	Y	77	PRO
21	Z	71	VAL
21	Z	72	ARG
21	Z	92	SER
21	Z	140	ASP
21	Z	152	ALA
22	0	15	ASP
23	2	47	ASN
23	2	48	HIS
24	3	41	PRO
26	6	8	LYS
26	6	9	LEU
26	6	15	GLU
26	6	20	ASN
26	6	27	LYS
26	6	29	ASN
28	8	32	LEU
28	8	49	VAL
32	1	12	PRO
32	1	35	THR
32	1	87	PRO
32	1	94	LEU
33	4	16	CYS
34	e	52	ALA
1	C	3	LYS
1	C	38	PHE
1	C	59	VAL
1	C	60	ARG
1	C	61	GLY
1	C	106	ASP
1	C	114	VAL
1	C	161	ARG
2	D	43	ARG
2	D	99	ASP
2	D	236	GLY
2	D	239	ARG
2	D	249	PRO
3	E	14	ILE
3	E	74	PRO
3	E	86	PRO
3	E	130	GLY
3	E	180	ASN

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Mol	Chain	Res	Type
4	F	47	GLY
4	F	67	GLN
4	F	158	THR
5	G	82	LEU
5	G	163	ALA
6	H	41	MET
8	K	5	VAL
8	K	13	PRO
8	K	30	HIS
8	K	102	GLU
8	K	103	GLN
9	N	24	GLY
9	N	111	PRO
10	O	26	LYS
10	O	29	ASN
10	O	96	THR
11	P	13	ASN
11	P	14	LYS
11	P	17	LYS
11	P	48	PRO
11	P	50	ARG
11	P	58	THR
11	P	66	GLY
11	P	89	ALA
11	P	106	LEU
11	P	107	LYS
11	P	145	PRO
12	Q	4	PRO
12	Q	8	LYS
12	Q	30	GLY
12	Q	75	THR
14	S	96	GLY
15	T	2	ASN
15	T	16	ARG
15	T	28	VAL
15	T	48	ILE
15	T	50	ILE
15	T	90	GLN
15	T	128	GLU
16	U	9	VAL
18	W	25	ARG
18	W	65	LEU

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Mol	Chain	Res	Type
18	W	80	PRO
19	X	4	ALA
19	X	62	LYS
20	Y	26	LYS
20	Y	78	ALA
20	Y	80	GLY
20	Y	97	ARG
20	Y	101	LYS
20	Y	107	ASP
21	Z	62	PRO
21	Z	73	GLN
21	Z	166	SER
22	0	13	GLY
24	3	52	HIS
25	5	24	ALA
25	5	53	ALA
26	6	16	CYS
26	6	28	ARG
26	6	31	PRO
26	6	49	HIS
28	8	30	ARG
28	8	45	GLY
28	8	51	ALA
32	1	32	LYS
32	1	36	GLY
32	1	53	VAL
33	4	15	ILE
33	4	33	VAL
34	e	81	ILE
1	C	18	ASN
1	C	33	LEU
1	C	167	ASP
1	C	214	TYR
2	D	147	LEU
2	D	186	HIS
2	D	188	GLU
2	D	225	ALA
2	D	232	PRO
2	D	233	HIS
2	D	241	PRO
2	D	260	ARG
2	D	272	ALA

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Mol	Chain	Res	Type
3	E	155	LYS
3	E	169	ASN
3	E	188	VAL
3	E	204	ALA
4	F	22	ALA
4	F	58	ALA
4	F	73	ALA
6	H	123	PHE
6	H	128	PRO
8	K	51	ALA
8	K	63	ARG
9	N	56	ASN
9	N	62	VAL
9	N	91	LEU
9	N	131	GLN
11	P	35	HIS
11	P	53	GLY
11	P	119	GLU
11	P	123	LEU
12	Q	6	ARG
12	Q	62	GLY
14	S	14	VAL
14	S	57	LYS
15	T	68	TYR
15	T	78	LEU
15	T	85	LYS
15	T	107	ASP
16	U	92	ARG
16	U	99	ALA
16	U	106	PHE
17	V	68	LYS
17	V	77	ALA
18	W	22	ASP
20	Y	7	VAL
20	Y	12	THR
20	Y	48	ALA
20	Y	50	ARG
20	Y	63	LYS
20	Y	91	GLU
21	Z	32	HIS
21	Z	78	LYS
21	Z	159	PRO

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Mol	Chain	Res	Type
22	0	11	ARG
22	0	33	ALA
25	5	47	PRO
26	6	44	ARG
28	8	3	LYS
28	8	6	THR
28	8	34	TRP
29	9	5	ALA
32	1	37	ILE
32	1	40	ARG
32	1	52	ARG
32	1	92	LYS
33	4	2	LYS
33	4	9	LEU
1	C	51	ASP
1	C	117	THR
1	C	130	ARG
2	D	28	GLU
2	D	40	THR
2	D	164	GLN
2	D	238	GLY
3	E	17	ASP
3	E	53	PRO
3	E	70	ALA
3	E	89	ASP
3	E	147	PRO
4	F	61	GLY
4	F	68	LYS
4	F	83	PHE
5	G	74	LYS
6	H	175	LYS
8	K	89	HIS
9	N	47	ALA
9	N	129	PRO
11	P	31	ALA
11	P	68	GLN
11	P	104	GLY
12	Q	28	ALA
12	Q	135	ASP
13	R	5	LYS
13	R	8	ARG
13	R	11	ASN

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Mol	Chain	Res	Type
13	R	102	GLU
13	R	104	ARG
14	S	23	ARG
14	S	94	TYR
15	T	31	SER
15	T	35	LYS
15	T	39	ARG
15	T	82	LEU
15	T	83	ILE
15	T	115	ARG
16	U	30	LYS
16	U	74	LEU
17	V	18	LEU
17	V	80	GLN
19	X	85	PRO
20	Y	47	LYS
21	Z	93	ASP
27	7	3	ARG
28	8	48	PHE
32	1	10	LYS
32	1	44	PRO
33	4	4	GLY
33	4	10	VAL
34	e	62	VAL
34	e	108	ALA
1	C	36	ALA
1	C	49	GLY
1	C	65	LEU
1	C	107	GLY
1	C	118	PRO
1	C	221	PRO
1	C	224	ARG
2	D	24	ILE
2	D	123	ALA
2	D	226	MET
2	D	244	ARG
2	D	246	PRO
3	E	34	VAL
3	E	118	LYS
4	F	5	ALA
4	F	11	VAL
4	F	172	TRP

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Mol	Chain	Res	Type
4	F	178	PRO
5	G	96	ARG
6	H	45	VAL
6	H	59	ARG
8	K	14	ALA
8	K	21	PRO
8	K	73	PRO
8	K	112	MET
8	K	122	ALA
9	N	32	THR
9	N	104	LYS
11	P	49	ARG
11	P	52	GLU
11	P	77	ARG
12	Q	90	VAL
14	S	24	LEU
14	S	63	THR
16	U	10	ARG
16	U	86	ALA
17	V	16	PRO
17	V	52	VAL
18	W	63	ASP
21	Z	134	PRO
21	Z	162	GLU
24	3	13	ILE
24	3	32	GLN
25	5	57	VAL
26	6	18	ARG
26	6	33	LYS
28	8	10	ALA
32	1	22	GLY
33	4	7	PRO
1	C	20	VAL
1	C	76	LEU
1	C	139	PRO
1	C	175	PRO
2	D	25	THR
2	D	242	ARG
3	E	66	HIS
4	F	9	ILE
4	F	53	THR
15	T	88	ILE

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Mol	Chain	Res	Type
18	W	31	GLU
20	Y	70	SER
21	Z	85	HIS
21	Z	108	PRO
21	Z	120	ILE
27	7	48	LYS
28	8	64	TYR
34	e	99	VAL
34	e	117	ALA
2	D	100	GLY
3	E	141	ILE
5	G	129	GLY
6	H	21	PRO
12	Q	127	ILE
15	T	20	PRO
16	U	7	GLY
20	Y	18	GLY
20	Y	98	VAL
1	C	181	PHE
3	E	193	GLY
6	H	39	PRO
8	K	7	VAL
8	K	49	GLY
11	P	34	GLY
11	P	54	GLY
12	Q	78	PRO
3	E	43	GLY
11	P	8	PRO
24	3	2	PRO
29	9	3	VAL
1	C	75	VAL
6	H	136	ILE
9	N	46	VAL
13	R	93	GLY
17	V	72	VAL
21	Z	141	VAL
33	4	17	GLY
34	e	83	GLY
34	e	118	VAL
8	K	22	PRO

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. 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	
1	C	180/180 (100%)	128 (71%)	52 (29%)	0	4
2	D	217/217 (100%)	175 (81%)	42 (19%)	2	12
3	E	165/165 (100%)	136 (82%)	29 (18%)	3	16
4	F	165/165 (100%)	140 (85%)	25 (15%)	4	25
5	G	155/155 (100%)	130 (84%)	25 (16%)	3	22
6	H	136/136 (100%)	117 (86%)	19 (14%)	5	28
8	K	105/105 (100%)	77 (73%)	28 (27%)	1	5
9	N	117/117 (100%)	93 (80%)	24 (20%)	2	10
10	O	100/100 (100%)	86 (86%)	14 (14%)	5	28
11	P	112/112 (100%)	85 (76%)	27 (24%)	1	6
12	Q	111/111 (100%)	84 (76%)	27 (24%)	1	6
13	R	100/100 (100%)	78 (78%)	22 (22%)	1	8
14	S	77/77 (100%)	59 (77%)	18 (23%)	1	7
15	T	120/120 (100%)	93 (78%)	27 (22%)	1	8
16	U	93/93 (100%)	70 (75%)	23 (25%)	1	6
17	V	82/82 (100%)	62 (76%)	20 (24%)	1	6
18	W	92/92 (100%)	76 (83%)	16 (17%)	3	17
19	X	75/75 (100%)	58 (77%)	17 (23%)	1	7
20	Y	88/88 (100%)	73 (83%)	15 (17%)	3	18
21	Z	162/162 (100%)	125 (77%)	37 (23%)	1	7
22	0	66/66 (100%)	56 (85%)	10 (15%)	4	25
23	2	66/66 (100%)	58 (88%)	8 (12%)	7	36
24	3	52/52 (100%)	45 (86%)	7 (14%)	6	30
25	5	51/51 (100%)	41 (80%)	10 (20%)	2	11
26	6	49/49 (100%)	34 (69%)	15 (31%)	0	4
27	7	42/42 (100%)	36 (86%)	6 (14%)	5	28
28	8	54/54 (100%)	44 (82%)	10 (18%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	9	34/34 (100%)	30 (88%)	4 (12%)	8	38
32	1	78/78 (100%)	58 (74%)	20 (26%)	1	5
33	4	31/31 (100%)	21 (68%)	10 (32%)	0	3
34	e	54/54 (100%)	46 (85%)	8 (15%)	4	26
All	All	3029/3029 (100%)	2414 (80%)	615 (20%)	2	11

All (615) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	7	ARG
1	C	9	ARG
1	C	12	LEU
1	C	14	LYS
1	C	19	LYS
1	C	28	ARG
1	C	31	LYS
1	C	41	THR
1	C	42	VAL
1	C	45	HIS
1	C	48	LEU
1	C	51	ASP
1	C	53	ARG
1	C	54	ARG
1	C	57	GLN
1	C	73	VAL
1	C	75	VAL
1	C	83	LYS
1	C	85	LYS
1	C	86	GLU
1	C	93	ASP
1	C	95	VAL
1	C	98	GLU
1	C	100	ILE
1	C	105	LEU
1	C	109	MET
1	C	115	VAL
1	C	117	THR
1	C	119	ASP
1	C	121	MET
1	C	130	ARG
1	C	131	ILE

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Mol	Chain	Res	Type
1	C	132	LEU
1	C	138	LEU
1	C	148	PHE
1	C	149	ASN
1	C	155	ARG
1	C	158	LYS
1	C	161	ARG
1	C	164	PHE
1	C	168	LYS
1	C	169	THR
1	C	172	ILE
1	C	173	HIS
1	C	176	VAL
1	C	201	LYS
1	C	203	GLU
1	C	206	LYS
1	C	209	PHE
1	C	211	ARG
1	C	213	VAL
1	C	216	THR
2	D	4	LYS
2	D	5	LYS
2	D	9	TYR
2	D	10	THR
2	D	14	ARG
2	D	15	PHE
2	D	23	GLU
2	D	24	ILE
2	D	25	THR
2	D	26	LYS
2	D	30	GLU
2	D	31	LYS
2	D	35	LYS
2	D	37	LEU
2	D	62	TYR
2	D	64	ILE
2	D	65	ILE
2	D	69	ARG
2	D	78	LYS
2	D	82	ILE
2	D	83	GLU
2	D	92	ILE

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Mol	Chain	Res	Type
2	D	95	LEU
2	D	103	ARG
2	D	104	TYR
2	D	105	ILE
2	D	115	GLN
2	D	134	ARG
2	D	136	ILE
2	D	140	THR
2	D	143	HIS
2	D	155	LEU
2	D	161	THR
2	D	175	LEU
2	D	196	VAL
2	D	229	VAL
2	D	230	ASP
2	D	237	GLU
2	D	242	ARG
2	D	248	SER
2	D	264	LYS
2	D	267	SER
3	E	4	ILE
3	E	9	VAL
3	E	11	MET
3	E	18	ASP
3	E	26	ILE
3	E	35	GLN
3	E	52	LEU
3	E	54	GLN
3	E	57	LYS
3	E	61	ARG
3	E	77	ILE
3	E	78	LEU
3	E	79	ARG
3	E	87	GLU
3	E	89	ASP
3	E	93	VAL
3	E	94	GLU
3	E	95	ILE
3	E	132	HIS
3	E	134	ILE
3	E	135	HIS
3	E	141	ILE

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Mol	Chain	Res	Type
3	E	146	THR
3	E	159	HIS
3	E	160	TYR
3	E	163	GLU
3	E	180	ASN
3	E	192	ASN
3	E	199	ARG
4	F	3	GLU
4	F	6	VAL
4	F	7	TYR
4	F	12	LEU
4	F	17	ARG
4	F	38	ARG
4	F	40	GLN
4	F	53	THR
4	F	56	GLU
4	F	72	ARG
4	F	74	ARG
4	F	106	ARG
4	F	125	LEU
4	F	126	VAL
4	F	132	VAL
4	F	136	THR
4	F	149	ASP
4	F	154	VAL
4	F	175	THR
4	F	185	ASP
4	F	191	ARG
4	F	196	LEU
4	F	199	TRP
4	F	200	GLU
4	F	206	ILE
5	G	5	VAL
5	G	9	ARG
5	G	21	ARG
5	G	34	LEU
5	G	39	ILE
5	G	40	ASN
5	G	43	LEU
5	G	45	GLU
5	G	58	GLN
5	G	60	LEU

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Mol	Chain	Res	Type
5	G	66	GLN
5	G	82	LEU
5	G	83	ARG
5	G	84	LYS
5	G	86	MET
5	G	99	MET
5	G	113	ARG
5	G	115	ARG
5	G	126	ASP
5	G	133	LEU
5	G	135	LEU
5	G	138	GLN
5	G	146	TYR
5	G	147	ASP
5	G	172	LEU
6	H	17	VAL
6	H	23	ARG
6	H	33	LEU
6	H	41	MET
6	H	43	VAL
6	H	67	LEU
6	H	70	THR
6	H	72	ILE
6	H	79	VAL
6	H	83	TYR
6	H	86	GLU
6	H	88	LEU
6	H	107	VAL
6	H	114	VAL
6	H	116	GLU
6	H	122	THR
6	H	133	VAL
6	H	136	ILE
6	H	159	GLU
8	K	9	LYS
8	K	10	LEU
8	K	27	LEU
8	K	37	PHE
8	K	45	THR
8	K	57	ILE
8	K	58	THR
8	K	60	TYR

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Mol	Chain	Res	Type
8	K	63	ARG
8	K	64	SER
8	K	65	PHE
8	K	69	THR
8	K	78	ILE
8	K	84	LEU
8	K	95	LYS
8	K	96	VAL
8	K	98	ARG
8	K	102	GLU
8	K	105	LEU
8	K	106	GLU
8	K	110	GLN
8	K	111	LYS
8	K	114	ASP
8	K	115	LEU
8	K	118	THR
8	K	125	ARG
8	K	132	ARG
8	K	133	SER
9	N	22	THR
9	N	25	ARG
9	N	28	THR
9	N	29	LYS
9	N	32	THR
9	N	33	LEU
9	N	41	ASP
9	N	48	MET
9	N	65	LYS
9	N	76	SER
9	N	84	LYS
9	N	87	LEU
9	N	93	THR
9	N	98	VAL
9	N	106	MET
9	N	112	LEU
9	N	114	ARG
9	N	119	ARG
9	N	120	LEU
9	N	127	ASP
9	N	131	GLN
9	N	134	ARG

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Mol	Chain	Res	Type
9	N	137	LYS
9	N	138	LEU
10	O	2	ILE
10	O	8	LEU
10	O	37	ASP
10	O	42	SER
10	O	45	GLU
10	O	70	LYS
10	O	78	ARG
10	O	80	ASP
10	O	82	ASN
10	O	89	ASN
10	O	91	LEU
10	O	92	GLU
10	O	94	ARG
10	O	117	LEU
11	P	7	ARG
11	P	16	ARG
11	P	19	VAL
11	P	27	HIS
11	P	29	LYS
11	P	32	THR
11	P	35	HIS
11	P	39	LYS
11	P	46	LYS
11	P	50	ARG
11	P	51	PHE
11	P	55	ARG
11	P	60	MET
11	P	61	ARG
11	P	62	LEU
11	P	65	ARG
11	P	68	GLN
11	P	71	VAL
11	P	77	ARG
11	P	79	ARG
11	P	84	ASN
11	P	91	PHE
11	P	100	LEU
11	P	101	VAL
11	P	110	TYR
11	P	123	LEU

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Mol	Chain	Res	Type
11	P	130	PHE
12	Q	1	MET
12	Q	3	MET
12	Q	7	MET
12	Q	14	ARG
12	Q	16	ARG
12	Q	17	LEU
12	Q	25	ASP
12	Q	35	VAL
12	Q	37	LEU
12	Q	43	THR
12	Q	45	GLN
12	Q	46	GLN
12	Q	56	ARG
12	Q	57	HIS
12	Q	58	PHE
12	Q	59	ARG
12	Q	60	ARG
12	Q	68	ILE
12	Q	91	GLU
12	Q	104	PHE
12	Q	105	GLU
12	Q	106	VAL
12	Q	112	GLU
12	Q	128	LYS
12	Q	131	ILE
12	Q	132	VAL
12	Q	137	TYR
13	R	3	HIS
13	R	4	LEU
13	R	11	ASN
13	R	13	HIS
13	R	16	HIS
13	R	29	LEU
13	R	37	THR
13	R	43	GLU
13	R	44	LEU
13	R	45	ARG
13	R	49	ASP
13	R	59	ASP
13	R	65	LEU
13	R	71	GLN

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Mol	Chain	Res	Type
13	R	72	ASP
13	R	76	VAL
13	R	79	LEU
13	R	82	GLU
13	R	97	VAL
13	R	99	LYS
13	R	100	LEU
13	R	107	ASP
14	S	13	ARG
14	S	15	ARG
14	S	16	ASN
14	S	23	ARG
14	S	24	LEU
14	S	47	THR
14	S	50	SER
14	S	62	LYS
14	S	67	ARG
14	S	69	VAL
14	S	78	LEU
14	S	84	GLN
14	S	87	PHE
14	S	92	TYR
14	S	95	HIS
14	S	97	ARG
14	S	98	VAL
14	S	99	LYS
15	T	1	MET
15	T	13	ARG
15	T	16	ARG
15	T	27	THR
15	T	30	VAL
15	T	33	LYS
15	T	38	ASN
15	T	42	ILE
15	T	44	ASP
15	T	46	GLU
15	T	48	ILE
15	T	57	PHE
15	T	64	ARG
15	T	70	VAL
15	T	74	ARG
15	T	80	SER

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Mol	Chain	Res	Type
15	T	82	LEU
15	T	96	ARG
15	T	105	LEU
15	T	107	ASP
15	T	108	ARG
15	T	109	GLU
15	T	111	ARG
15	T	114	LEU
15	T	115	ARG
15	T	118	ARG
15	T	124	ASP
16	U	6	THR
16	U	14	HIS
16	U	18	LEU
16	U	34	LYS
16	U	38	THR
16	U	39	LEU
16	U	44	ASN
16	U	51	LYS
16	U	54	LYS
16	U	58	ARG
16	U	59	ARG
16	U	64	ARG
16	U	74	LEU
16	U	83	LEU
16	U	90	VAL
16	U	97	ASP
16	U	98	LEU
16	U	101	ARG
16	U	104	GLN
16	U	105	VAL
16	U	108	GLU
16	U	114	LYS
16	U	117	GLN
17	V	14	VAL
17	V	18	LEU
17	V	19	LYS
17	V	21	ARG
17	V	37	VAL
17	V	38	LEU
17	V	40	LEU
17	V	47	VAL

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Mol	Chain	Res	Type
17	V	57	VAL
17	V	60	GLU
17	V	69	LYS
17	V	71	LEU
17	V	73	SER
17	V	75	PHE
17	V	80	GLN
17	V	82	ARG
17	V	85	LYS
17	V	87	HIS
17	V	98	GLU
17	V	99	ILE
18	W	11	ARG
18	W	12	ILE
18	W	17	VAL
18	W	19	LEU
18	W	27	LYS
18	W	37	ARG
18	W	39	THR
18	W	61	ASN
18	W	64	MET
18	W	66	GLU
18	W	70	TYR
18	W	88	ARG
18	W	95	ILE
18	W	96	ILE
18	W	99	ARG
18	W	107	LEU
19	X	3	THR
19	X	6	ASP
19	X	15	GLU
19	X	27	THR
19	X	53	LYS
19	X	54	VAL
19	X	56	THR
19	X	57	LEU
19	X	58	HIS
19	X	66	LEU
19	X	68	ARG
19	X	69	TYR
19	X	72	LYS
19	X	75	ASP

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Mol	Chain	Res	Type
19	X	76	ARG
19	X	87	GLN
19	X	92	LEU
20	Y	2	ARG
20	Y	4	LYS
20	Y	5	MET
20	Y	6	HIS
20	Y	7	VAL
20	Y	9	LYS
20	Y	13	VAL
20	Y	19	LYS
20	Y	35	TYR
20	Y	39	VAL
20	Y	44	ILE
20	Y	47	LYS
20	Y	50	ARG
20	Y	62	GLU
20	Y	76	CYS
21	Z	3	TYR
21	Z	24	LEU
21	Z	31	ARG
21	Z	34	ASN
21	Z	36	LYS
21	Z	37	VAL
21	Z	39	VAL
21	Z	46	LYS
21	Z	52	SER
21	Z	57	ILE
21	Z	59	LEU
21	Z	70	LEU
21	Z	72	ARG
21	Z	81	ARG
21	Z	82	ARG
21	Z	86	VAL
21	Z	87	ASP
21	Z	98	MET
21	Z	102	LEU
21	Z	124	ILE
21	Z	126	VAL
21	Z	127	LYS
21	Z	133	ILE
21	Z	136	PHE

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Mol	Chain	Res	Type
21	Z	140	ASP
21	Z	145	GLU
21	Z	148	ASP
21	Z	151	HIS
21	Z	153	SER
21	Z	154	ASP
21	Z	155	LEU
21	Z	156	LYS
21	Z	165	VAL
21	Z	179	ASP
21	Z	181	GLU
21	Z	185	GLU
21	Z	186	GLU
22	0	11	ARG
22	0	21	LEU
22	0	27	GLU
22	0	30	VAL
22	0	35	ASN
22	0	36	ILE
22	0	41	ARG
22	0	43	THR
22	0	57	PHE
22	0	82	ARG
23	2	9	GLN
23	2	17	SER
23	2	21	LEU
23	2	35	LEU
23	2	40	SER
23	2	47	ASN
23	2	55	ARG
23	2	71	ASN
24	3	8	LEU
24	3	17	LYS
24	3	19	GLN
24	3	29	ARG
24	3	36	VAL
24	3	48	GLU
24	3	60	GLU
25	5	3	LYS
25	5	20	ARG
25	5	25	LEU
25	5	26	THR

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Mol	Chain	Res	Type
25	5	31	VAL
25	5	44	THR
25	5	48	GLU
25	5	51	TYR
25	5	52	TYR
25	5	58	LEU
26	6	6	ARG
26	6	9	LEU
26	6	10	LEU
26	6	11	LEU
26	6	18	ARG
26	6	19	ARG
26	6	23	THR
26	6	25	LYS
26	6	28	ARG
26	6	34	LEU
26	6	43	CYS
26	6	46	HIS
26	6	47	THR
26	6	53	LYS
26	6	54	ILE
27	7	6	GLN
27	7	19	ARG
27	7	24	THR
27	7	39	ARG
27	7	40	TRP
27	7	47	ARG
28	8	33	ASN
28	8	34	TRP
28	8	36	LYS
28	8	40	GLU
28	8	44	LYS
28	8	49	VAL
28	8	53	PRO
28	8	59	LYS
28	8	61	LEU
28	8	64	TYR
29	9	11	CYS
29	9	17	ILE
29	9	27	CYS
29	9	35	ARG
32	1	5	CYS

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Mol	Chain	Res	Type
32	1	14	VAL
32	1	20	ARG
32	1	25	LYS
32	1	27	GLU
32	1	32	LYS
32	1	40	ARG
32	1	41	ARG
32	1	43	TYR
32	1	45	ASN
32	1	46	LEU
32	1	47	GLN
32	1	50	ARG
32	1	57	GLU
32	1	58	ILE
32	1	61	ARG
32	1	67	ILE
32	1	88	LYS
32	1	90	ILE
32	1	94	LEU
33	4	1	MET
33	4	6	HIS
33	4	8	LYS
33	4	9	LEU
33	4	10	VAL
33	4	15	ILE
33	4	23	GLU
33	4	26	SER
33	4	32	TYR
33	4	34	GLU
34	e	61	ASP
34	e	70	LYS
34	e	73	GLU
34	e	78	LEU
34	e	90	LYS
34	e	94	GLU
34	e	95	LYS
34	e	101	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	87	ASN

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Mol	Chain	Res	Type
2	D	126	GLN
2	D	231	HIS
3	E	180	ASN
4	F	40	GLN
4	F	169	ASN
5	G	27	ASN
8	K	30	HIS
9	N	131	GLN
11	P	9	ASN
11	P	68	GLN
12	Q	12	GLN
12	Q	89	ASN
12	Q	123	HIS
13	R	23	ASN
14	S	34	HIS
14	S	38	GLN
15	T	84	GLN
17	V	87	HIS
17	V	89	GLN
19	X	58	HIS
19	X	87	GLN
21	Z	118	GLN
22	0	80	HIS
26	6	26	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	A	2878/2879 (99%)	629 (21%)	17 (0%)
36	B	118/119 (99%)	19 (16%)	3 (2%)
All	All	2996/2998 (99%)	648 (21%)	20 (0%)

All (648) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	A	10	G
35	A	12	U
35	A	13	A
35	A	15	G
35	A	23	G
35	A	25	U

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Mol	Chain	Res	Type
35	A	27	G
35	A	28	A
35	A	34	C
35	A	35	G
35	A	46	C
35	A	50	U
35	A	51	G
35	A	52	A
35	A	64	A
35	A	70	G
35	A	73	A
35	A	74	A
35	A	75	G
35	A	84	A
35	A	90	U
35	A	98	G
35	A	101	G
35	A	102	G
35	A	113	G
35	A	118	A
35	A	119	A
35	A	120	U
35	A	121	G
35	A	138	G
35	A	140	A
35	A	141(A)	A
35	A	163	U
35	A	178	G
35	A	181	A
35	A	196	A
35	A	197	A
35	A	199	A
35	A	204	A
35	A	205	G
35	A	216	A
35	A	221	A
35	A	222	A
35	A	225	A
35	A	227	A
35	A	228	A
35	A	229	A
35	A	230	U

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Mol	Chain	Res	Type
35	A	232	G
35	A	233	A
35	A	241	A
35	A	248	G
35	A	250	G
35	A	251	A
35	A	252	G
35	A	265	A
35	A	270(C)	A
35	A	270(L)	C
35	A	270(M)	U
35	A	270(N)	U
35	A	270(O)	G
35	A	270(P)	U
35	A	270(Q)	C
35	A	270(R)	C
35	A	271(D)	U
35	A	271	G
35	A	274	G
35	A	275	G
35	A	277	C
35	A	279	C
35	A	294	A
35	A	301	G
35	A	302	C
35	A	310	A
35	A	322	A
35	A	324	A
35	A	329	G
35	A	330	A
35	A	352	G
35	A	360	G
35	A	363(A)	G
35	A	363(B)	A
35	A	363(D)	G
35	A	363(G)	A
35	A	384	U
35	A	386	G
35	A	387	U
35	A	389	G
35	A	396	G
35	A	405	U

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Mol	Chain	Res	Type
35	A	407	G
35	A	411	G
35	A	422	A
35	A	438	G
35	A	444	C
35	A	446	G
35	A	447	A
35	A	448	U
35	A	449	A
35	A	451	C
35	A	455	C
35	A	456	C
35	A	457	A
35	A	458	G
35	A	459	U
35	A	464	U
35	A	470	A
35	A	473	G
35	A	474	G
35	A	475	U
35	A	480	A
35	A	481	G
35	A	489	G
35	A	491	G
35	A	505	A
35	A	506	G
35	A	507	A
35	A	508	G
35	A	509	C
35	A	513	A
35	A	527	C
35	A	528	A
35	A	530	G
35	A	531	C
35	A	532	A
35	A	542	C
35	A	546	C
35	A	548	A
35	A	556	G
35	A	563	G
35	A	572	A
35	A	573	G

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Mol	Chain	Res	Type
35	A	575	A
35	A	586	A
35	A	587	C
35	A	603	A
35	A	614	U
35	A	615	G
35	A	616	A
35	A	617	G
35	A	620	G
35	A	621	A
35	A	627	A
35	A	637	A
35	A	643	A
35	A	645	C
35	A	646	A
35	A	653	C
35	A	654	U
35	A	671	C
35	A	686	G
35	A	695	G
35	A	701	G
35	A	707	G
35	A	730	C
35	A	738	G
35	A	747	U
35	A	749	C
35	A	764	A
35	A	771	G
35	A	776	G
35	A	778	G
35	A	779	U
35	A	781	A
35	A	782	A
35	A	783	A
35	A	784	A
35	A	785	G
35	A	786	C
35	A	788	A
35	A	789	A
35	A	790	C
35	A	792	G
35	A	794	G

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Mol	Chain	Res	Type
35	A	799	G
35	A	800	A
35	A	805	G
35	A	812	C
35	A	819	A
35	A	822	U
35	A	827	U
35	A	829	A
35	A	838	C
35	A	846	C
35	A	847	U
35	A	852	G
35	A	859	G
35	A	866	A
35	A	869	G
35	A	877	U
35	A	878	A
35	A	879	G
35	A	881	G
35	A	882	G
35	A	886	C
35	A	887	A
35	A	890	A
35	A	896	A
35	A	897	C
35	A	906	G
35	A	907	U
35	A	910	A
35	A	917	A
35	A	932	G
35	A	933	A
35	A	941	A
35	A	943	U
35	A	945	A
35	A	946	G
35	A	959	A
35	A	961	C
35	A	970	C
35	A	972	G
35	A	974(A)	G
35	A	974(B)	C
35	A	980	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
35	A	983	A
35	A	990	A
35	A	991	C
35	A	996	A
35	A	1007	C
35	A	1008	C
35	A	1009	A
35	A	1010	A
35	A	1011	G
35	A	1012	U
35	A	1013	C
35	A	1017	G
35	A	1022	G
35	A	1023	U
35	A	1024	G
35	A	1025	G
35	A	1026	U
35	A	1033	U
35	A	1045	A
35	A	1046	A
35	A	1047	G
35	A	1048	A
35	A	1056	G
35	A	1057	A
35	A	1060	U
35	A	1065	U
35	A	1070	A
35	A	1072	C
35	A	1078	U
35	A	1079	C
35	A	1086	A
35	A	1087	G
35	A	1088	A
35	A	1090	U
35	A	1105	U
35	A	1106	G
35	A	1107	G
35	A	1110	G
35	A	1112	G
35	A	1123	C
35	A	1126	A
35	A	1132	A

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Mol	Chain	Res	Type
35	A	1136	G
35	A	1139	G
35	A	1141	U
35	A	114(B)	A
35	A	1144	G
35	A	1155	A
35	A	1156	A
35	A	1157	G
35	A	1173	G
35	A	1175	U
35	A	1176	G
35	A	1179	C
35	A	1186	G
35	A	1204	A
35	A	1205	U
35	A	1206	G
35	A	1210	A
35	A	1211	U
35	A	1212	G
35	A	1221	C
35	A	1241	A
35	A	1248	G
35	A	1249	U
35	A	1253	A
35	A	1256	G
35	A	1265	A
35	A	1271	G
35	A	1272	A
35	A	1286	A
35	A	1300	U
35	A	1301	A
35	A	1302	A
35	A	1312	U
35	A	1314	C
35	A	1321	A
35	A	1322	A
35	A	1325	G
35	A	1329	U
35	A	1330	C
35	A	1332	G
35	A	1333	C
35	A	1349	A

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Mol	Chain	Res	Type
35	A	1359	A
35	A	1365	A
35	A	1368	G
35	A	1378	A
35	A	1379	A
35	A	1380	G
35	A	1384	A
35	A	1385	G
35	A	1395	A
35	A	1396	U
35	A	1398	C
35	A	1416	G
35	A	1417	C
35	A	1418	G
35	A	1420	U
35	A	1421	G
35	A	1428	C
35	A	144(B)	A
35	A	149(B)	A
35	A	1449	G
35	A	1453	A
35	A	1454	U
35	A	1455	G
35	A	1458	C
35	A	1460	A
35	A	1467	C
35	A	1478	G
35	A	1483	G
35	A	1491	G
35	A	1493	C
35	A	1495	A
35	A	1497	U
35	A	1498	C
35	A	1510	A
35	A	1523	U
35	A	1531	C
35	A	1535	U
35	A	1536	A
35	A	1538	G
35	A	1539	G
35	A	1540	G
35	A	1541	U

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Mol	Chain	Res	Type
35	A	1542	G
35	A	1543	A
35	A	1545	A
35	A	1547	C
35	A	1558	A
35	A	1559	G
35	A	1566	A
35	A	1569	A
35	A	1578	U
35	A	1583	A
35	A	1585	C
35	A	1593	G
35	A	1602	U
35	A	1603	A
35	A	1608	A
35	A	1609	A
35	A	1615	C
35	A	1616	A
35	A	1617	C
35	A	1618	A
35	A	1619	G
35	A	1631	A
35	A	1640	C
35	A	1641	A
35	A	1644	C
35	A	1646	C
35	A	1648	C
35	A	1665	A
35	A	1674	G
35	A	1677	A
35	A	1678	G
35	A	1694	C
35	A	1695	G
35	A	1696	G
35	A	1729	A
35	A	1732	A
35	A	1755	A
35	A	1757	U
35	A	1762	A
35	A	1763	G
35	A	1764	G
35	A	1773	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
35	A	1781	C
35	A	1782	C
35	A	1784	A
35	A	1785	A
35	A	1786	A
35	A	1787	A
35	A	1800	C
35	A	1802	A
35	A	1815	A
35	A	1816	G
35	A	1820	U
35	A	1821	A
35	A	1829	A
35	A	1833	U
35	A	1837	C
35	A	1847	A
35	A	1858	G
35	A	1870	C
35	A	1872	A
35	A	1888	G
35	A	1889	A
35	A	1900	A
35	A	1902	C
35	A	1903	G
35	A	1906	G
35	A	1909	C
35	A	1912	A
35	A	1913	A
35	A	1914	C
35	A	1929	G
35	A	1936	A
35	A	1937	A
35	A	1939	U
35	A	1940	U
35	A	1944	U
35	A	1955	U
35	A	1963	U
35	A	1964	G
35	A	1967	C
35	A	1970	A
35	A	1971	A
35	A	1972	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
35	A	1981	A
35	A	1982	C
35	A	1991	U
35	A	1992	G
35	A	1993	U
35	A	2005	A
35	A	2013	A
35	A	2023	G
35	A	2030	A
35	A	2031	A
35	A	2032	G
35	A	2033	A
35	A	2034	U
35	A	2036	C
35	A	2043	C
35	A	2051	A
35	A	2052	G
35	A	2055	C
35	A	2056	G
35	A	2060	A
35	A	2061	G
35	A	2062	A
35	A	2065	C
35	A	2069	G
35	A	2078	C
35	A	2093	G
35	A	2108	C
35	A	2110	G
35	A	2112	G
35	A	2113	U
35	A	2116	G
35	A	2117	A
35	A	2118	U
35	A	2126	A
35	A	2131	G
35	A	2133	G
35	A	2134	A
35	A	2144	U
35	A	2159	G
35	A	2165	G
35	A	2167	U
35	A	2168	G

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Mol	Chain	Res	Type
35	A	2171	A
35	A	2173	A
35	A	2184	G
35	A	2190	G
35	A	2199	A
35	A	2210	G
35	A	2211	G
35	A	2212	A
35	A	2213	U
35	A	2225	A
35	A	2239	G
35	A	2246	G
35	A	2266	A
35	A	2267	A
35	A	2268	A
35	A	2274	A
35	A	2275	C
35	A	2280	G
35	A	2283	C
35	A	2287	A
35	A	2289	G
35	A	2305	A
35	A	2308	G
35	A	2310	A
35	A	2311	A
35	A	2320	A
35	A	2322	A
35	A	2325	G
35	A	2327	A
35	A	2334	G
35	A	2336	A
35	A	2345	G
35	A	2346	A
35	A	2347	C
35	A	2350	C
35	A	2366	A
35	A	2377	A
35	A	2383	G
35	A	2385	C
35	A	2389	G
35	A	2401	U
35	A	2402	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
35	A	2405	G
35	A	2406	U
35	A	2422	A
35	A	2423	U
35	A	2425	A
35	A	2426	A
35	A	2427	C
35	A	2428	G
35	A	2429	G
35	A	2430	A
35	A	2435	A
35	A	2439	A
35	A	2441	C
35	A	2448	A
35	A	2450	A
35	A	2469	A
35	A	2470	G
35	A	2474	C
35	A	2476	A
35	A	2477	C
35	A	2478	A
35	A	2480	C
35	A	2482	G
35	A	2497	A
35	A	2502	G
35	A	2503	A
35	A	2505	G
35	A	2513	G
35	A	2514	U
35	A	2518	A
35	A	2520	C
35	A	2526	G
35	A	2529	G
35	A	2530	A
35	A	2532	G
35	A	2533	A
35	A	2542	A
35	A	2543	G
35	A	2546	U
35	A	2554	U
35	A	2563	U
35	A	2564	A

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Mol	Chain	Res	Type
35	A	2566	A
35	A	2567	G
35	A	2572	A
35	A	2573	C
35	A	2578	G
35	A	2586	C
35	A	2593	U
35	A	2602	A
35	A	2603	G
35	A	2609	U
35	A	2610	C
35	A	2612	C
35	A	2615	U
35	A	2623	G
35	A	2630	G
35	A	2633	G
35	A	2638	G
35	A	2641	G
35	A	2645	G
35	A	2646	C
35	A	2657	A
35	A	2663	G
35	A	2665	A
35	A	2667	C
35	A	2681	C
35	A	2682	U
35	A	2689	U
35	A	2691	C
35	A	2702	U
35	A	2703	C
35	A	2706	G
35	A	2711	A
35	A	2712	U
35	A	712(B)	A
35	A	2713	A
35	A	2714	G
35	A	2718	G
35	A	2720	U
35	A	2721	A
35	A	2726	U
35	A	2733	A
35	A	2748	A

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Mol	Chain	Res	Type
35	A	2760	C
35	A	2764	A
35	A	2765	A
35	A	2766	G
35	A	2770	G
35	A	2778	A
35	A	2779	U
35	A	2780	G
35	A	2781	A
35	A	2782	G
35	A	2786	U
35	A	2790	A
35	A	2791	C
35	A	2797	U
35	A	2798	C
35	A	2811	G
35	A	2820	A
35	A	2821	A
35	A	2823	A
35	A	2825	U
35	A	2832	U
35	A	2833	G
35	A	2834	G
35	A	2835	A
35	A	2849	U
35	A	2866	U
35	A	2871	C
35	A	2872	G
35	A	2876	G
35	A	2879	C
35	A	2880	C
35	A	2892	A
35	A	2893	G
35	A	2894	G
35	A	2895	U
36	B	7	G
36	B	13	A
36	B	15	A
36	B	16	G
36	B	25	A
36	B	35	U
36	B	41	U

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Mol	Chain	Res	Type
36	B	42	C
36	B	45	A
36	B	47	C
36	B	50	G
36	B	53	A
36	B	55	U
36	B	65	C
36	B	67	G
36	B	73	A
36	B	87	G
36	B	109	G
36	B	115	G

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	A	221	A
35	A	271(C)	G
35	A	474	G
35	A	479	A
35	A	586	A
35	A	1012	U
35	A	1022	G
35	A	1210	A
35	A	1240	U
35	A	1377	G
35	A	1558	A
35	A	1786	A
35	A	1899	G
35	A	2092	U
35	A	2422	A
35	A	2447	G
35	A	2780	G
36	B	41	U
36	B	66	A
36	B	108	C

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	C	228/228 (100%)	0.34	16 (7%) 16 7	102, 162, 214, 247	0
2	D	275/275 (100%)	-0.12	2 (0%) 84 56	23, 54, 107, 147	0
3	E	205/205 (100%)	0.07	5 (2%) 56 26	12, 60, 120, 175	0
4	F	208/208 (100%)	0.16	6 (2%) 49 23	34, 83, 176, 205	0
5	G	181/181 (100%)	0.32	10 (5%) 24 10	44, 104, 159, 196	0
6	H	167/167 (100%)	-0.18	1 (0%) 86 59	36, 73, 140, 192	0
7	J	0/170	-	-	-	-
8	K	140/140 (100%)	-0.01	5 (3%) 41 18	72, 142, 197, 229	0
9	N	138/138 (100%)	-0.14	0 100 100	61, 89, 110, 118	0
10	O	122/122 (100%)	-0.05	0 100 100	26, 47, 96, 121	0
11	P	146/146 (100%)	-0.09	3 (2%) 60 29	19, 88, 140, 212	0
12	Q	141/141 (100%)	-0.28	2 (1%) 72 38	34, 58, 126, 178	0
13	R	117/117 (100%)	-0.02	2 (1%) 67 34	34, 67, 108, 138	0
14	S	99/99 (100%)	0.24	4 (4%) 36 16	44, 114, 168, 203	0
15	T	138/138 (100%)	-0.44	0 100 100	25, 71, 133, 177	0
16	U	117/117 (100%)	-0.13	0 100 100	29, 54, 89, 222	0
17	V	101/101 (100%)	-0.28	0 100 100	28, 60, 114, 177	0
18	W	113/113 (100%)	-0.16	0 100 100	11, 60, 133, 215	0
19	X	93/93 (100%)	-0.29	0 100 100	16, 66, 134, 180	0
20	Y	107/107 (100%)	-0.23	0 100 100	45, 96, 167, 200	0
21	Z	185/185 (100%)	-0.32	1 (0%) 88 64	48, 82, 136, 193	0
22	0	84/84 (100%)	-0.13	0 100 100	47, 77, 140, 162	0
23	2	71/71 (100%)	-0.31	0 100 100	33, 85, 127, 141	0
24	3	60/60 (100%)	-0.10	1 (1%) 67 34	32, 73, 137, 160	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	5	59/59 (100%)	-0.04	0 100 100	29, 75, 130, 161	0
26	6	50/50 (100%)	-0.13	0 100 100	49, 81, 143, 164	0
27	7	49/49 (100%)	0.07	0 100 100	34, 61, 112, 165	0
28	8	64/64 (100%)	-0.00	1 (1%) 68 35	33, 70, 118, 139	0
29	9	37/37 (100%)	-0.06	0 100 100	46, 60, 134, 159	0
30	f	0/31	-	-	-	-
30	g	0/31	-	-	-	-
31	h	0/30	-	-	-	-
32	1	93/93 (100%)	0.11	5 (5%) 25 10	41, 89, 159, 194	0
33	4	35/35 (100%)	0.36	2 (5%) 23 10	73, 136, 168, 196	0
34	e	72/102 (70%)	0.29	6 (8%) 11 6	87, 141, 192, 236	0
35	A	2879/2879 (100%)	-0.27	5 (0%) 93 80	5, 63, 160, 308	0
36	B	119/119 (100%)	-0.33	1 (0%) 83 53	33, 108, 159, 193	0
All	All	6693/6985 (95%)	-0.15	78 (1%) 75 42	5, 73, 168, 308	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
34	e	59	GLU	6.2
34	e	58	THR	5.9
5	G	90	LEU	5.4
3	E	58	ARG	5.1
8	K	115	LEU	5.0
35	A	2164	C	4.7
35	A	2125	G	4.2
11	P	17	LYS	4.1
12	Q	141	GLN	4.0
1	C	205	ALA	3.8
4	F	116	ASP	3.7
5	G	34	LEU	3.6
1	C	17	PRO	3.6
1	C	113	ALA	3.5
14	S	101	LEU	3.4
1	C	135	ARG	3.4
1	C	131	ILE	3.4
33	4	1	MET	3.4
35	A	2506	U	3.4
1	C	128	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
32	1	18	ILE	3.3
1	C	204	GLY	3.1
4	F	182	ASN	3.1
5	G	157	ILE	3.0
13	R	101	ALA	3.0
4	F	125	LEU	3.0
8	K	20	ALA	2.9
3	E	7	VAL	2.9
32	1	33	LYS	2.8
5	G	106	LEU	2.8
3	E	205	ALA	2.8
34	e	51	ALA	2.7
35	A	2585	U	2.7
34	e	55	GLU	2.6
34	e	57	LYS	2.6
14	S	39	ILE	2.6
32	1	16	ASN	2.6
13	R	2	ARG	2.6
3	E	24	THR	2.6
4	F	28	ILE	2.6
4	F	117	ARG	2.5
6	H	168	PRO	2.5
1	C	49	GLY	2.5
5	G	2	PRO	2.5
1	C	173	HIS	2.4
4	F	181	LEU	2.4
5	G	6	ALA	2.4
1	C	139	PRO	2.4
5	G	96	ARG	2.4
1	C	162	ILE	2.4
5	G	155	MET	2.4
2	D	191	ALA	2.3
8	K	15	GLY	2.3
5	G	92	VAL	2.3
21	Z	90	VAL	2.3
8	K	14	ALA	2.3
5	G	117	PHE	2.3
28	8	25	MET	2.2
32	1	19	GLN	2.2
2	D	12	SER	2.2
24	3	21	ALA	2.2
12	Q	42	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
32	1	35	THR	2.2
1	C	168	LYS	2.2
3	E	157	ALA	2.1
33	4	22	ILE	2.1
36	B	43	C	2.1
1	C	48	LEU	2.1
8	K	69	THR	2.1
11	P	70	GLN	2.1
14	S	100	ALA	2.1
1	C	185	LYS	2.0
11	P	71	VAL	2.0
1	C	153	ILE	2.0
34	e	108	ALA	2.0
1	C	106	ASP	2.0
14	S	65	VAL	2.0
35	A	2070	G	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.