



Full wwPDB X-ray Structure Validation Report

Jun 16, 2014 – 06:46 PM BST

PDB ID : 4V9H
Title : Crystal structure of the ribosome bound to elongation factor G in the guanosine triphosphatase state
Authors : Tourigny, D.S.; Fernandez, I.S.; Kelley, A.C.; Ramakrishnan, V.
Deposited on : 2013-03-25
Resolution : 2.86 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

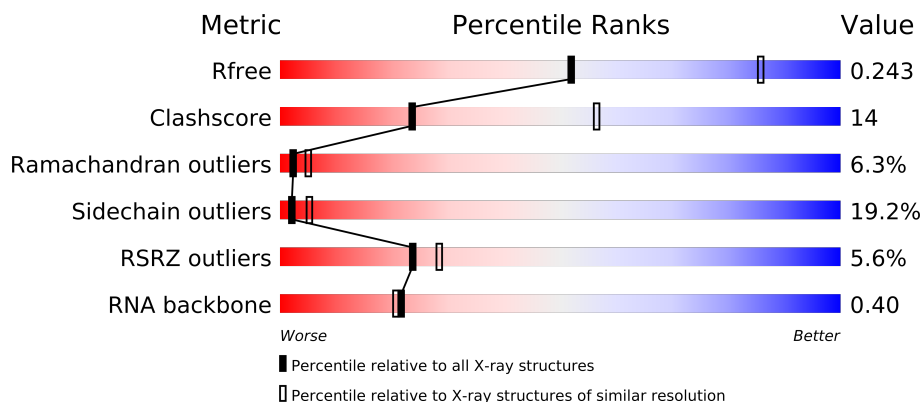
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1323
EDS : stable23397
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) : stable23397

1 Overall quality at a glance

The reported resolution of this entry is 2.86 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	1524 (2.90-2.82)
Clashscore	79885	1879 (2.90-2.82)
Ramachandran outliers	78287	1824 (2.90-2.82)
Sidechain outliers	78261	1827 (2.90-2.82)
RSRZ outliers	66119	1526 (2.90-2.82)
RNA backbone	1838	1014 (3.32-2.40)

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 ≥ 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	AA	1516	
2	AV	76	
3	AX	25	
4	AJ	98	
5	AK	119	
6	AL	124	
7	AM	124	
8	AN	60	
9	AO	88	
10	AP	83	
11	AQ	99	
12	AR	70	





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Mol	Chain	Length	Quality of chain
13	AS	78	
14	AT	99	
15	AB	234	
16	AC	206	
17	AD	208	
18	AE	150	
19	AF	101	
20	AG	155	
21	AH	138	
22	AI	127	
23	AY	680	
24	AU	24	
25	BA	2915	
26	BB	122	
27	BN	140	
28	BO	122	
29	BP	150	
30	BQ	141	
31	BR	118	
32	BS	112	
33	BT	146	
34	BU	118	
35	BV	101	
36	BW	113	
37	BX	96	
38	BY	110	
39	BZ	206	
40	B0	85	
41	B1	98	
42	B2	72	
43	BD	276	
44	B3	60	
45	B4	71	
46	B5	60	
47	B6	54	
48	B7	49	
49	B8	65	
50	B9	37	
51	BC	229	
52	BE	206	
53	BF	210	
54	BG	182	

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Mol	Chain	Length	Quality of chain
55	BH	180	
56	BK	147	
57	BJ	130	
58	BL	125	

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 151831 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 RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1514	Total	C	N	O	P	0	0	0
			32529	14480	6018	10518	1513			

- Molecule 2 is a RNA chain called PE hybrid state tRNA Phe.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AV	74	Total	C	N	O	P	0	0	0
			1579	705	285	516	73			

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AX	6	Total	C	N	O	P	0	0	0
			125	56	19	44	6			

- Molecule 4 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			

- Molecule 5 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

- Molecule 6 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			

- Molecule 7 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AM	124	Total	C	N	O	S	0	0	0
			988	611	205	170	2			

- Molecule 8 is a protein called 30S ribosomal protein S14 TYPE Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 9 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 10 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AQ	99	Total	C	N	O	S	0	0	0
			824	528	151	143	2			

- Molecule 12 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	AR	70	Total	C	N	O	0	0	0
			574	367	112	95			

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AS	78	Total	C	N	O	S	0	0	0
			630	403	114	111	2			

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AT	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

- Molecule 15 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AB	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			

- Molecule 16 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			

- Molecule 17 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 18 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	AE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			

- Molecule 19 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 20 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 21 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 22 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AI	127	Total	C	N	O		0	0	0
			1011	639	198	174				

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	58	ARG	HIS	CONFLICT	UNP P80374

- Molecule 23 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AY	622	Total	C	N	O	S	0	0	0
			4877	3097	837	924	19			

- Molecule 24 is a protein called 30S ribosomal protein THX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	AU	24	Total	C	N	O		0	0	0
			209	128	50	31				

- Molecule 25 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BA	2859	Total	C	N	O	P	0	0	0
			61580	27407	11519	19796	2858			

- Molecule 26 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 27 is a protein called 50S ribosomal protein L13.

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

- Molecule 28 is a protein called 50S ribosomal protein L14.

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

- Molecule 29 is a protein called 50S ribosomal protein L15.

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

- Molecule 30 is a protein called 50S ribosomal protein L16.

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

- Molecule 31 is a protein called 50S ribosomal protein L17.

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

- Molecule 32 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
32	BS	98	Total	C	N	O	0	0	0
			770	486	154	130			

- Molecule 33 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BT	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			

- Molecule 34 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BU	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			

- Molecule 35 is a protein called 50S ribosomal protein L21.

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

- Molecule 36 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BW	113	Total	C	N	O	S	0	0	0
			896	563	176	155	2			

- Molecule 37 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BX	92	Total	C	N	O	S	0	0	0
			725	471	131	123				

- Molecule 38 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BY	100	Total	C	N	O	S	0	0	0
			775	500	148	123	4			

- Molecule 39 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BZ	198	Total	C	N	O	S	0	0	0
			1508	960	274	272	2			

- Molecule 40 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	B0	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			

- Molecule 41 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	B1	93	Total	C	N	O	S	0	0	0
			731	460	145	125	1			

- Molecule 42 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	B2	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			

- Molecule 43 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BD	271	Total	C	N	O	S	0	0	0
			2104	1329	416	356	3			

- Molecule 44 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	B3	59	Total	C	N	O	S	0	0	0
			467	298	90	78	1			

- Molecule 45 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	B4	30	Total	C	N	O	S	0	0	0
			225	142	36	43	4			

- Molecule 46 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	B5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 47 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	B6	44	Total	C	N	O	S	0	0	0
			380	235	77	64	4			

- Molecule 48 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 49 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	B8	63	Total	C	N	O	S	0	0	0
			507	326	101	78	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B9	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	BC	225	Total	C	N	O	S	0	0	0
			1718	1085	315	316	2			

- Molecule 52 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	BE	204	Total	C	N	O	S	0	0	0
			1563	988	299	270	6			

- Molecule 53 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	BF	207	Total	C	N	O	S	0	0	0
			1623	1035	303	282	3			

- Molecule 54 is a protein called 50S ribosomal protein L5.

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

- Molecule 55 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	BH	173	Total	C	N	O	S	0	0	0
			1303	824	244	234	1			

- Molecule 56 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	BK	127	Total	C	N	O	S	0	0	0
			936	598	161	172	5			

- Molecule 57 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	BJ	130	Total	C	N	O		0	0	0
			651	390	130	131				

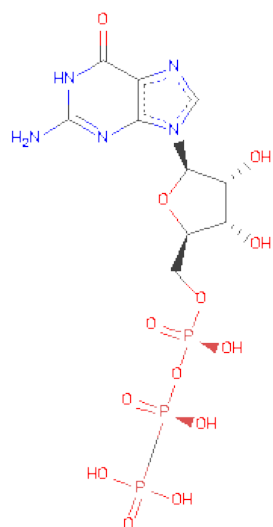
- Molecule 58 is a protein called 50S ribosomal protein L12 CTD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	BL	72	Total	C	N	O		0	0	1
			356	213	72	71				

- Molecule 59 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	BA	88	Total	Mg	0	0
			88	88		
59	BD	1	Total	Mg	0	0
			1	1		
59	BF	1	Total	Mg	0	0
			1	1		
59	B8	1	Total	Mg	0	0
			1	1		
59	BE	1	Total	Mg	0	0
			1	1		
59	AA	45	Total	Mg	0	0
			45	45		
59	AY	1	Total	Mg	0	0
			1	1		

- Molecule 60 is PHOSPHOMETHYLPHOSPHONICACID GUANYLATE ESTER (three-letter code: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
60	AY	1	Total	C	N	O	P	0	0
			32	11	5	13	3		

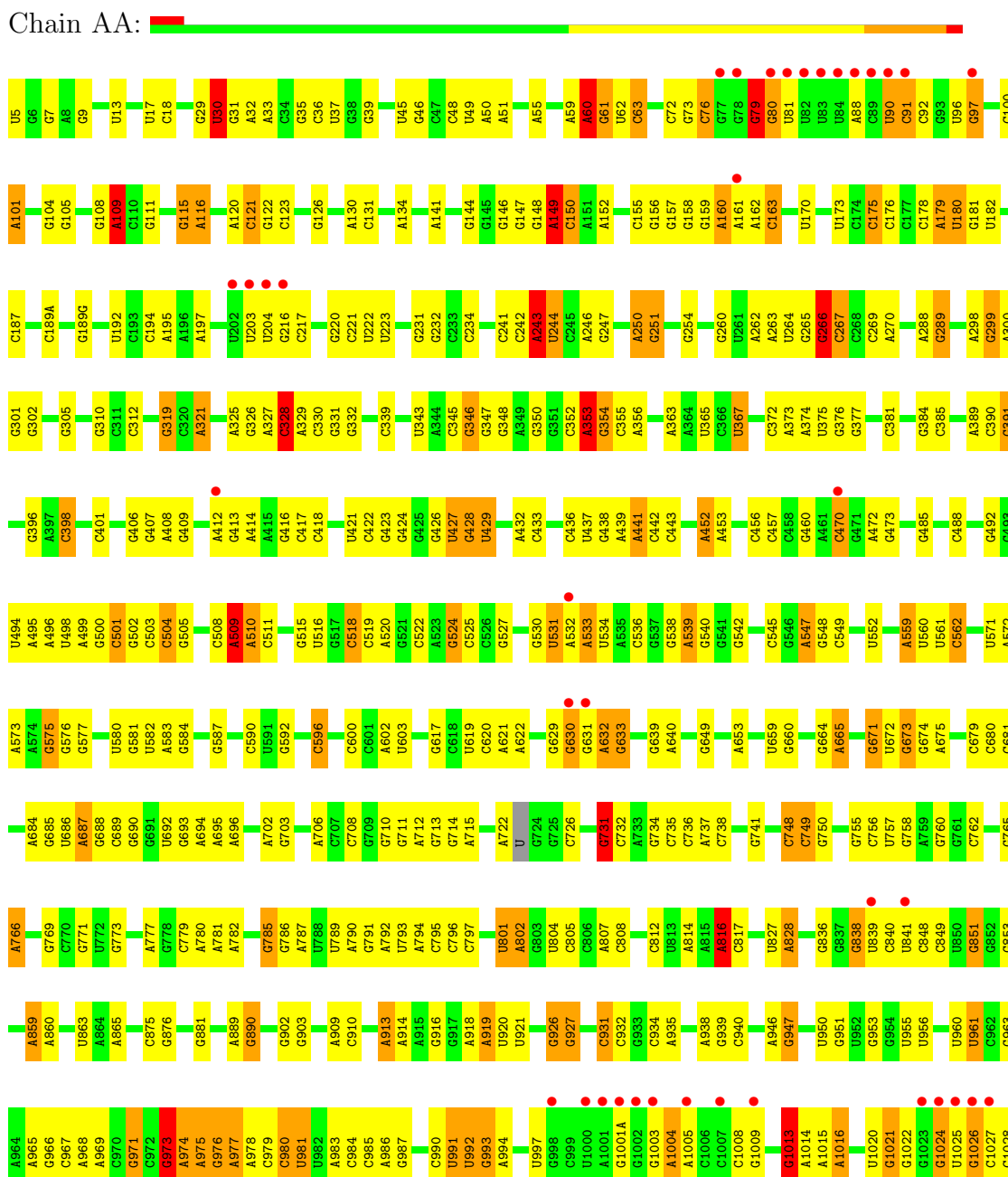
- Molecule 61 is water.

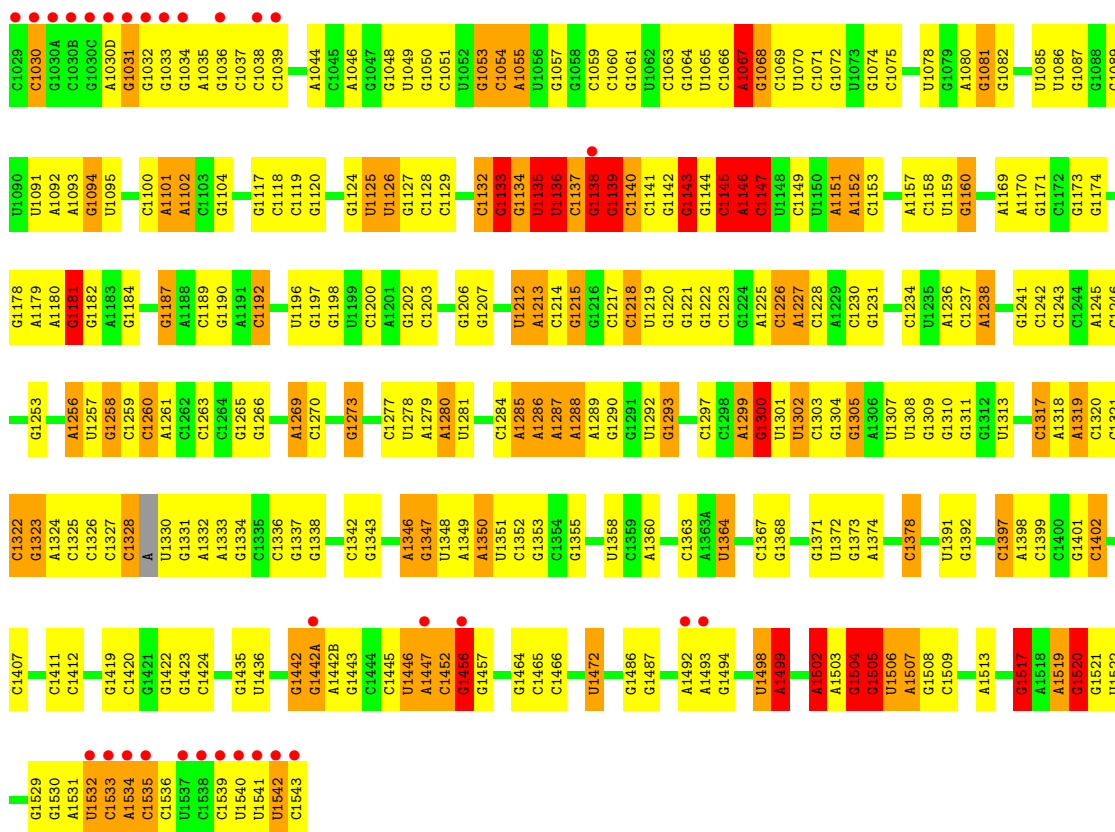
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	AY	4	Total	O	0	0
			4	4		

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.

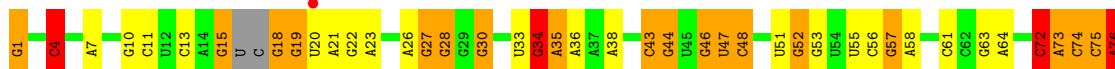
• Molecule 1: 16S ribosomal RNA





- Molecule 2: PE hybrid state tRNA Phe

Chain AV:



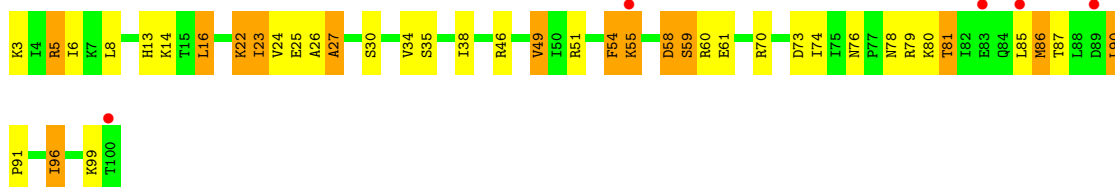
- Molecule 3: mRNA

Chain AX:



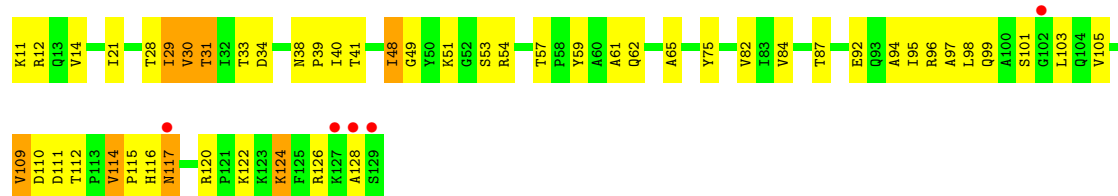
- Molecule 4: 30S ribosomal protein S10

Chain AJ:



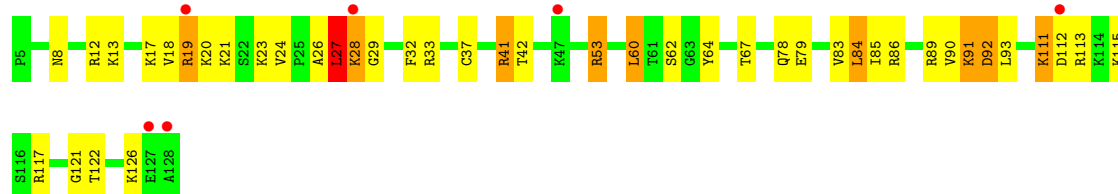
- Molecule 5: 30S ribosomal protein S11

Chain AK:



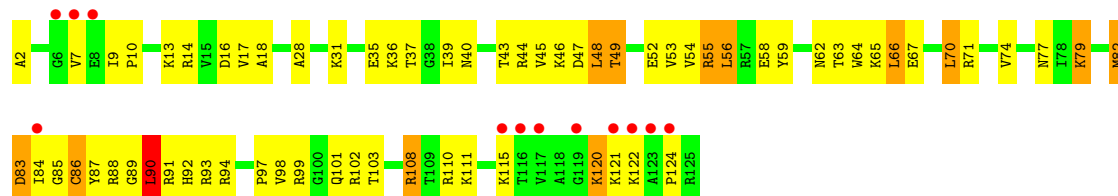
• Molecule 6: 30S ribosomal protein S12

Chain AL:



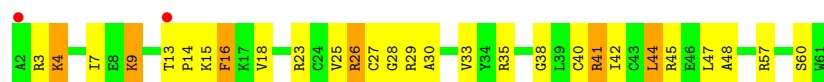
• Molecule 7: 30S ribosomal protein S13

Chain AM:



• Molecule 8: 30S ribosomal protein S14 TYPE Z

Chain AN:



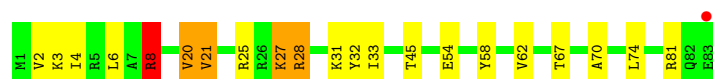
• Molecule 9: 30S ribosomal protein S15

Chain AO:



• Molecule 10: 30S ribosomal protein S16

Chain AP:



• Molecule 11: 30S ribosomal protein S17

Chain AQ:



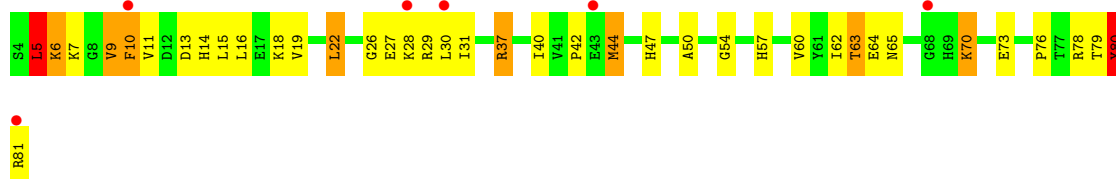
- Molecule 12: 30S ribosomal protein S18

Chain AR:



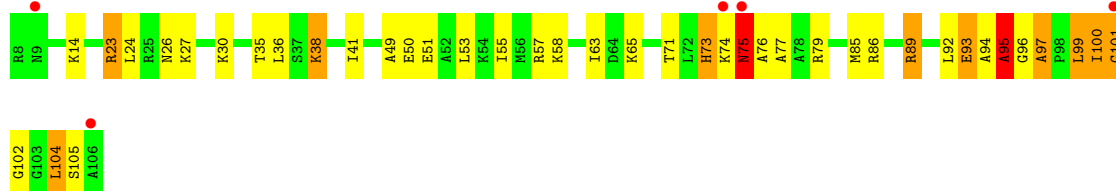
- Molecule 13: 30S ribosomal protein S19

Chain AS:



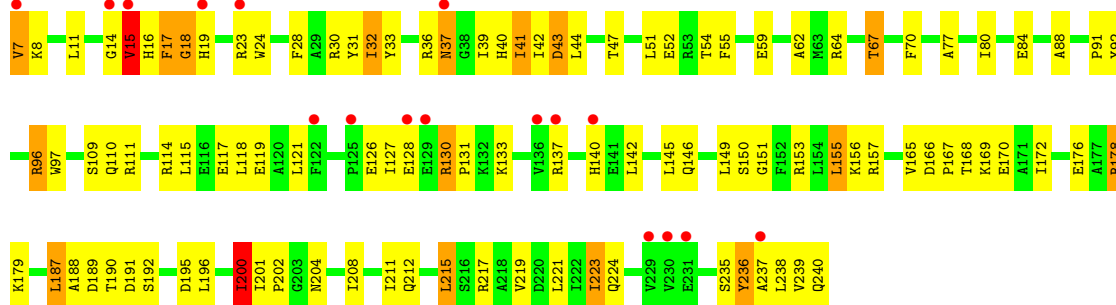
- Molecule 14: 30S ribosomal protein S20

Chain AT:



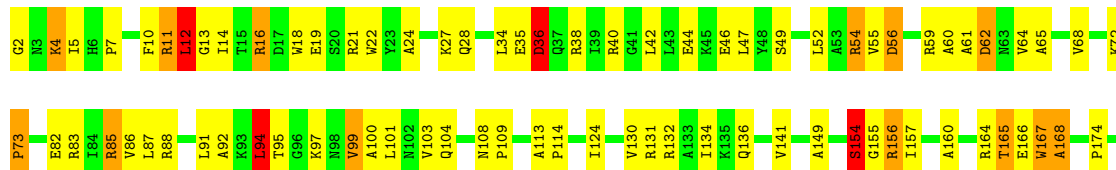
- Molecule 15: 30S ribosomal protein S2

Chain AB:



- Molecule 16: 30S ribosomal protein S3

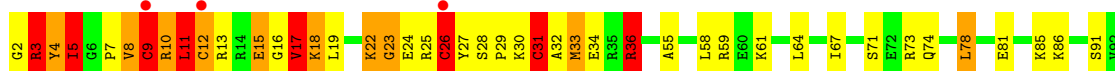
Chain AC:





- Molecule 17: 30S ribosomal protein S4

Chain AD:



- Molecule 18: 30S ribosomal protein S5

Chain AE:



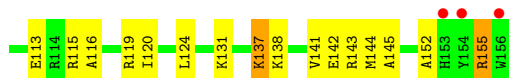
- Molecule 19: 30S ribosomal protein S6

Chain AF:



- Molecule 20: 30S ribosomal protein S7

Chain AG:



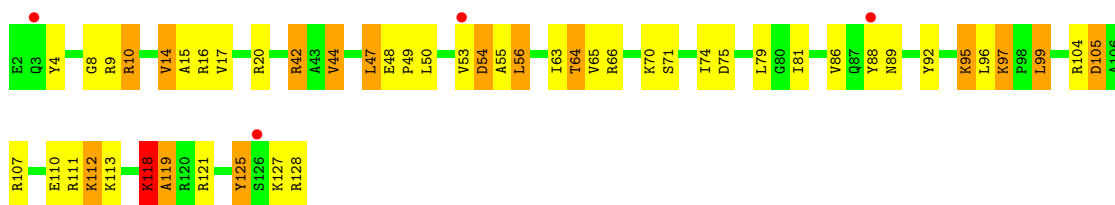
- Molecule 21: 30S ribosomal protein S8

Chain AH:



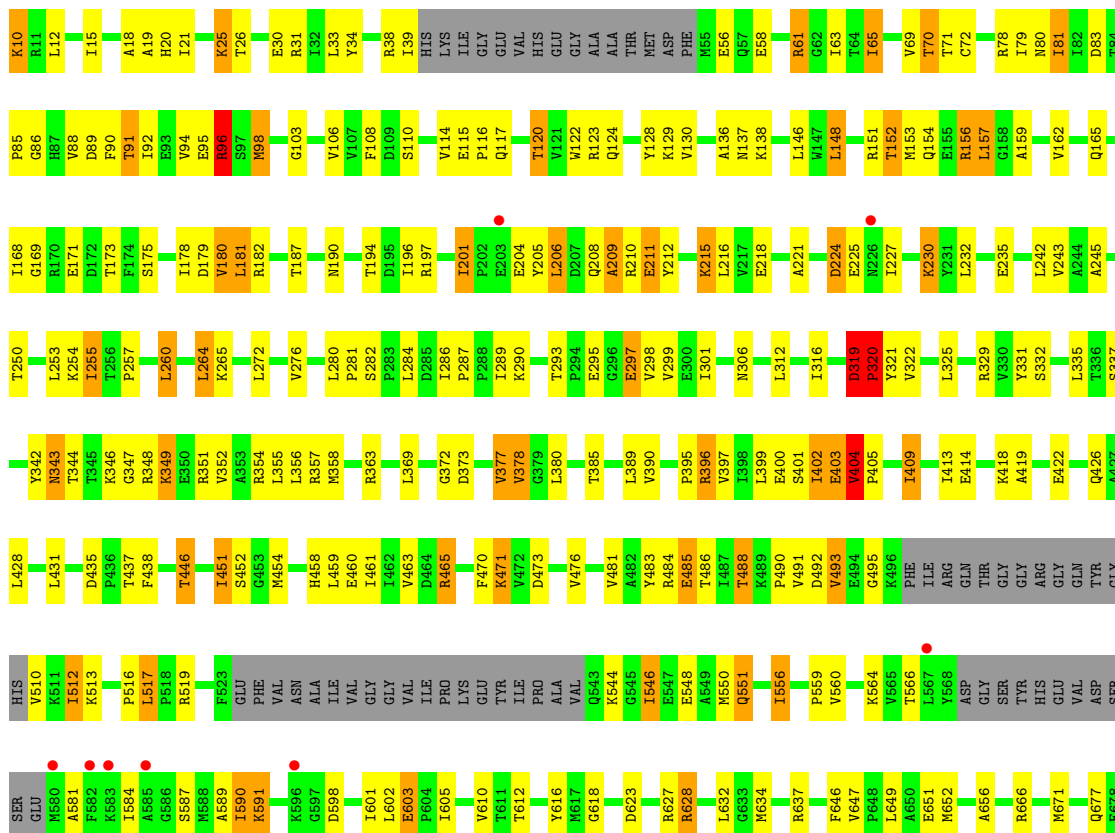
- Molecule 22: 30S ribosomal protein S9

Chain AI:



• Molecule 23: Elongation factor G

Chain AY:



• Molecule 24: 30S ribosomal protein THX

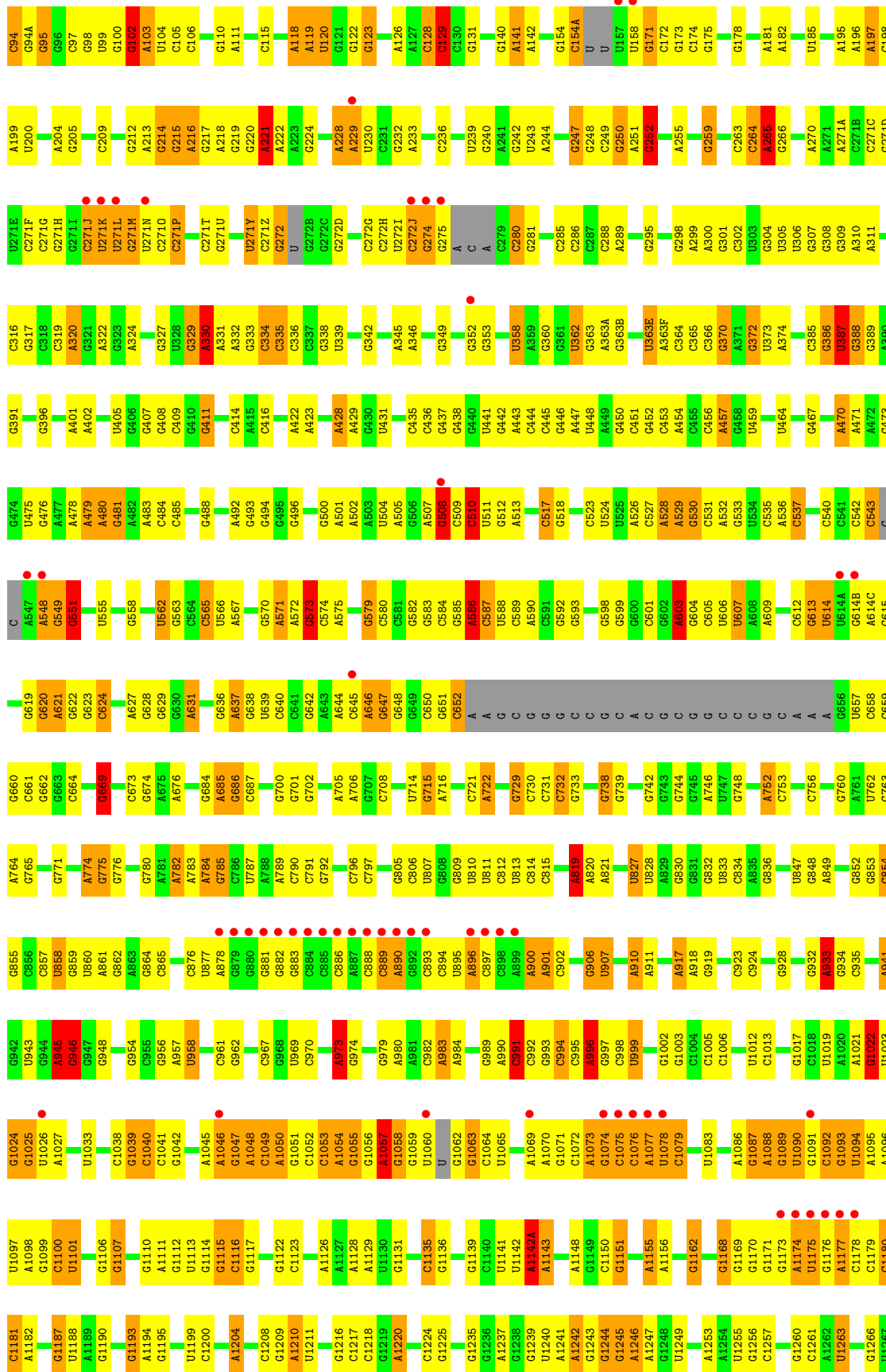
Chain AU:



• Molecule 25: 23S ribosomal RNA

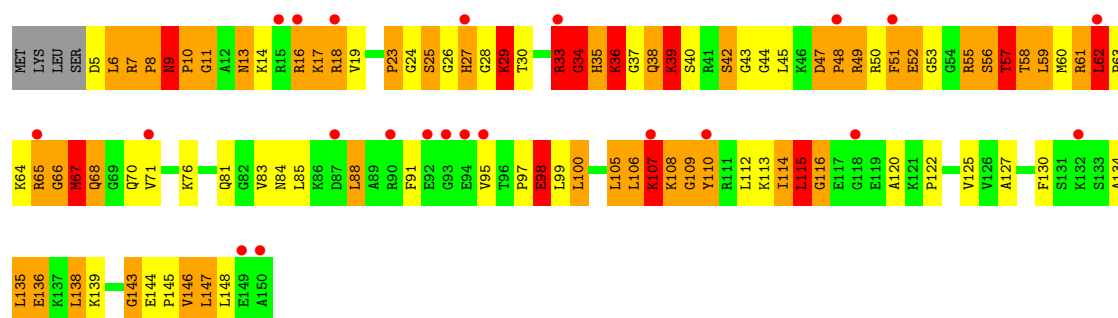
Chain BA:





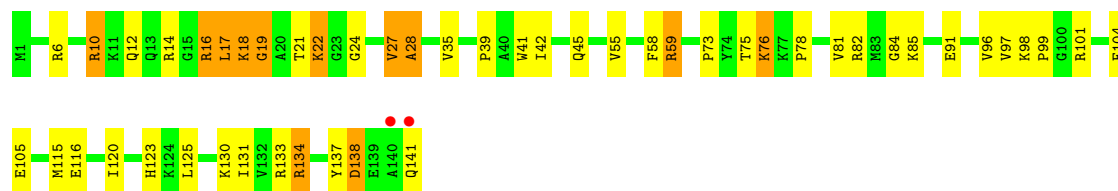
A1268	U1357	G1435	A1506	A1580	G1674	G1770	C1838	G1930	U2079	G2153	G2238	G2318	U2401
G1271	G1358	G1436	A1507	G1581	G1675	C1771	G1839	U1931	G2080	G2154	G2239	G2319	G2402
A1272	A1359	C1437	A1508	A1582	A1676	A1773	C1843	A1932	U2086	G2155	G2239	A2320	G2403
U1273	G1364	A1445	C1509	C1584	A1677	U1775	A1847	A1936	G2087	G2157	U2243	G2321	G2406
A1278	A1365	A1445A	A1509A	C1586	G1678	C1776	A1848	A1937	U2092	G2159	U2244	C2324	U2407
G1279	A1366	C1446	U1512	A1587	U1680	G1776	G1849	A1938	U2096	G2160	G2250	G2325	U2408
G1280	A1367	G1447	U1514	C1588	G1681	U1777	G1850	U1941	C2095	G2161	G2252	G2326	A2409
U1281	A1368	G1448	U1515	C1589	G1682	U1778	G1851	U1942	C2096	G2162	G2253	A2327	G2410
U1282	A1369	G1449	C1516	G1595	G1683	U1779	G1852	U1943	U2097	G2163	U2254	A2328	G2415
G1283	A1370	A1450	C1519	C1598	C1684	U1780	C1781	U1944	U2098	G2164	U2255	G2331	A2418
U1284	G1371	G1450A	U1520	C1599	G1685	A1781	A1853	U1945	U2099	G2165	U2256	G2332	U2419
G1285	U1372	C1451	G1521	C1603	G1686	A1782	A1854	U1946	U2100	G2166	U2257	G2333	G2422
A1286	C1375	A1452	U1523	A1603	G1687	A1783	U1855	U1947	G2101	G2167	U2258	G2334	U2423
A1287	C1376	U1453	U1524	U1608	A1689	A1784	A1856	U1948	G2102	G2168	U2259	G2335	U2424
U1288	C1377	C1458	U1525	A1609	U1692	A1785	A1857	A1952	G2103	G2169	U2260	A2336	U2425
C1289	A1379	C1458	G1526	A1610	U1693	A1786	A1858	U1955	C2104	A2171	U2261	G2337	G2426
C1290	G1380	A1460	G1527	A1611	U1694	C1788	A1859	U1956	G2105	U2172	U2262	G2338	U2427
C1291	G1381	G1461	A1528	C1615	C1694	A1789	G1878	U1957	G2106	A2173	A2273	C2342	G2428
G1296	G1384	C1462	A1529A	C1616	G1695	U1790	G1879	U1958	G2107	C2174	A2274	C2343	G2429
G1299	A1385	C1463	C1531	C1617	G1696	A1791	C1880	U1959	U2108	C2175	G2275	U2344	A2425
U1300	C1386	G1465	C1532	A1618	G1697	G1792	C1881	G1959	U2109	C2176	G2276	G2345	G2429
A1301	C1387	C1466	G	G1622	A1698	G1793	C1882	U1960	G2110	C2177	G2277	A2346	A2430
A1302	C1388	C1467	U	G1623	A1701	U1794	G1883	U1961	G2111	C2178	G2278	C2347	U2431
G1303	A1389	G1470	A	G1624	U1709	C1795	A1884	C1962	U2112	C2179	G2279	C2350	A2434
C1306	U1391	A1471	C	G1624	C1710	U1796	A1885	U1963	U2113	U2180	G2280	C2351	A2435
A1307	A1392	C1474	G	A1632	U1713	U1798	C1886	U1964	G2114	A2181	G2281	A2352	A2439
A1308	U1393	G1475	G1538	G1633	G1714	G1799	C1887	U1965	G2115	C2182	G2282	C2355	G2441
U1312	A1394	C1476	U1540	A1634	U1715	U1800	G1888	U1966	G2116	C2183	G2283	C2356	G2442
U1313	A1395	A1477	G1541	G1635	G1720	G1801	A1889	U1967	G2117	G2186	G2284	A2361	G2443
C1314	U1396	G1478	A1542	C1636	G1721	A1802	G1899	U1968	G2121	G2187	G2285	A2362	G2444
C1315	C1403	C1479	C1543	U1638	U1722	U1805	A1900	U1969	U2122	U2188	G2286	A2363	G2445
A1322	C1404	G1480	G1544	C1639	U1723	G1806	A1901	U1970	U2123	U2189	G2287	C2365	G2446
U1323	U1405	U1481	C1545	U1640	U1724	U1807	A1902	U1971	G2124	G2190	G2290	C2366	G2447
G1328	U1406	G1482	C1546	C1641	U1725	U1808	G1903	U1972	G2125	G2191	U2291	A2367	A2448
U1329	U1407	G1485	C1547	C1642	U1726	A1809	G1904	U1973	G2126	G2192	C2292	G2369	U2449
C1330	C1408	C1488	C1549	C1643	G1746	U1810	C	U1974	G2127	G2193	G2293	G2370	A2450
A1331	U1415	A1489	A1554	C1644	G1747	G1811	G1905	U1975	G2131	A2196	U2294	G2371	A2451
G1332	C1417	A1491	A1559	G1645	U1748	G1812	G1906	U1976	A2134	A2199	C2300	G2372	G2458
G1338	U1419	G1492	G1562	C1646	G1749	A1813	G1907	U1977	A2135	C2200	C2301	C2374	U2461
G1344	G1421	A1494	G1563	C1647	C1745	G1814	C	U1978	A2136	C2201	G2302	G2381	U2462
C1345	G1422	A1495	A1566	C1648	C1746	A1815	G1910	U1979	A2137	C2202	G2303	G2382	U2463
G1346	U1497	A1496	U1569	C1649	G1750	G1816	G1911	U1980	A2138	G2206	C2304	A2383	U2464
G1347	C1498	U1497	A1570	C1650	G1751	U1817	A1913	U1981	A2139	G2207	C2305	C2384	U2465
A1349	G1500	A1498	A1571	C1651	C1752	U1818	U1915	U1982	A2140	G2208	C2306	C2385	C2466
C1350	C1501	G1500	A1572	C1652	C1753	A1819	A1916	U1983	G2141	U2218	C2307	C2386	C2467
A1353	U1431	G1503	C1577	U1671	G1754	U1820	U1917	G1983	C2142	G2219	G2308	U2387	U2468
G1356	U1433	U1503	U1578	C1672	G1755	A1821	A1918	U1984	C2143	G2220	A2309	A2388	G2469
	A1434	C1505	U1579	U1673	U1756	U1822	C1920	U1985	C2144	G2221	U2310	G2389	G2470
					U1757	C1829	G1925	U1986	C2145	U2222	U2311	C2390	G2471
						U1830	U1926	U1987	C2146	G2223	U2312	U2391	G2472
						U1831	C1927	U1988	C2147	G2224	C2313	A2392	
						U1832	A1928	U1989	C2148	G2225	C2314	A2393	
						U1833	G1929	U1990	G2149	G2226	C2315	A2394	
								U1991	G2150	G2227	C2316	C2395	
								U1992	G2151	G2228	C2317		
								U1993	G2152	G2229			
								U1994	G2153	G2230			
								U1995	G2154	G2231			
								U1996	G2155	G2232			
								U1997	G2156				
								U1998	G2157				
								U1999	G2158				
								U2000	G2159				
								U2001	G2160				
								U2002	G2161				
								U2003	G2162				
								U2004	G2163				
								U2005	G2164				
								U2006	G2165				
								U2007	G2166				
								U2008	G2167				
								U2009	G2168				
								U2010	G2169				
								U2011	G2170				
								U2012	G2171				
								U2013	G2172				
								U2014	G2173				
								U2015	G2174				
								U2016	G2175				
								U2017	G2176				
								U2018	G2177				
								U2019	G2178				
								U2020	G2179				
								U2021	G2180				
								U2022	G2181				
								U2023	G2182				
								U2024	G2183				
								U2025	G2184				
								U2026	G2185				
								U2027	G2186				
								U2028	G2187				
								U2029	G2188				
								U2030	G2189				
								U2031	G2190				
								U2032	G2191				
								U2033	G2192				
								U2034	G2193				
								U2035	G2194				
								U2036	G2195				
								U2037	G2196				
								U2038	G2197				
								U2039	G2198				
								U2040	G2199				
								U2041	G2200				
								U2042	G2201				
								U2043	G2202				
								U2044	G2203				
								U2045	G2204				
								U2046	G2205				
								U2047	G2206				
								U2048	G2207				
								U2049	G2208				
								U2050	G2209				
								U2051	G2210				
								U2052	G2211				
								U2053	G2212				
								U2054	G2213				
								U2055	G2214				
								U2056	G2215				
								U2057	G2216				
								U2058	G2217				
								U2059	G2218				
								U2060	G2219				
								U2061	G2220				
								U2062	G2221				
								U2063	G2222				





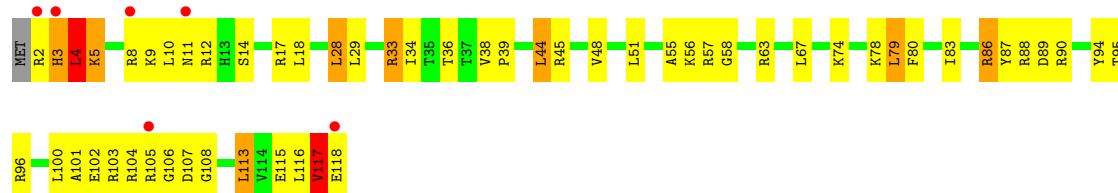
- Molecule 30: 50S ribosomal protein L16

Chain BQ:



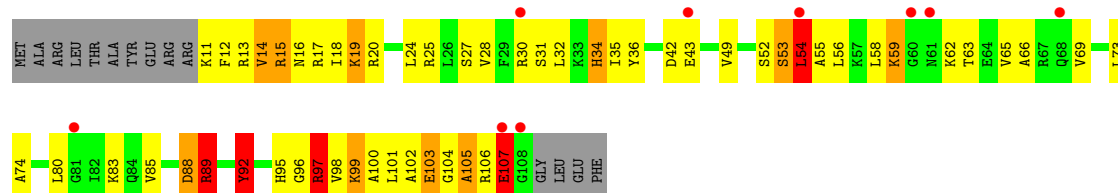
- Molecule 31: 50S ribosomal protein L17

Chain BR:



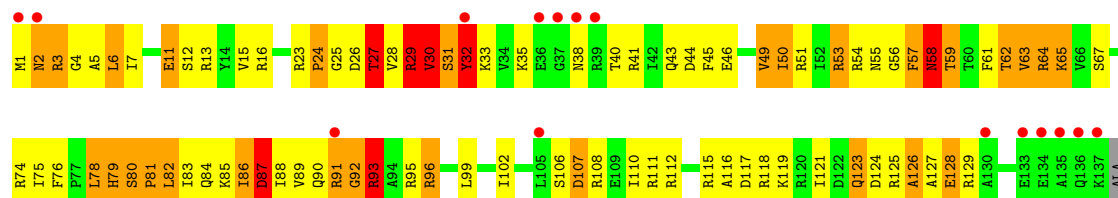
- Molecule 32: 50S ribosomal protein L18

Chain BS:



- Molecule 33: 50S ribosomal protein L19

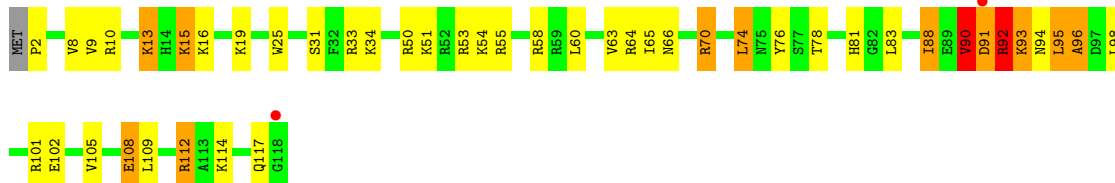
Chain BT:



GLN
GLU
PRO
LYS
ALA
SER
GLN
GLU

- Molecule 34: 50S ribosomal protein L20

Chain BU:



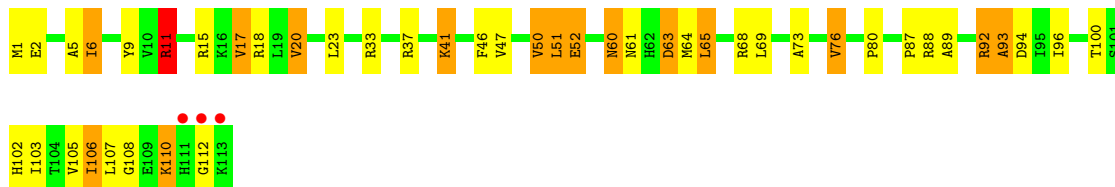
- Molecule 35: 50S ribosomal protein L21

Chain BV:



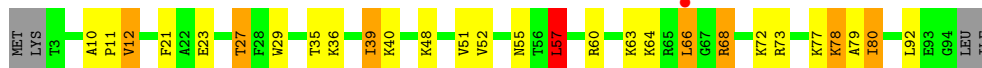
- Molecule 36: 50S ribosomal protein L22

Chain BW:



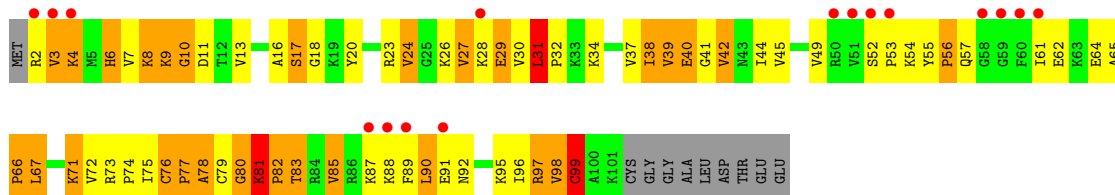
- Molecule 37: 50S ribosomal protein L23

Chain BX:



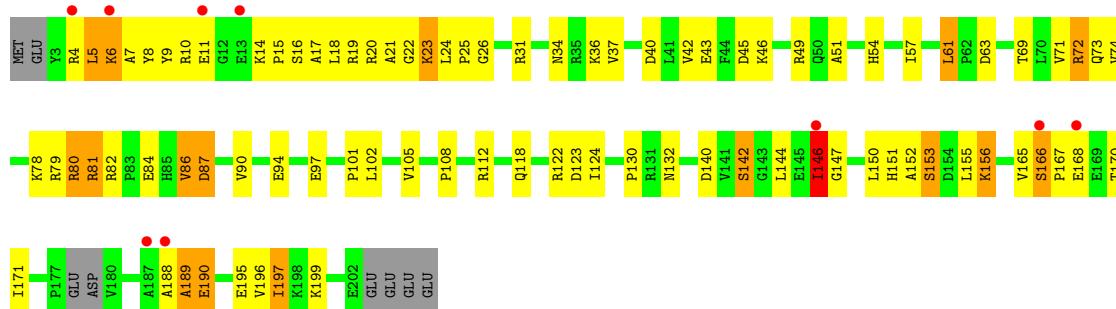
- Molecule 38: 50S ribosomal protein L24

Chain BY:



- Molecule 39: 50S ribosomal protein L25

Chain BZ:



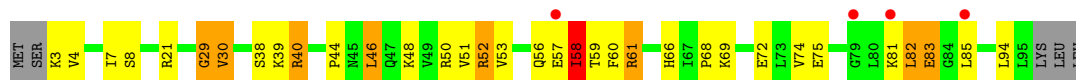
- Molecule 40: 50S ribosomal protein L27

Chain B0:



- Molecule 41: 50S ribosomal protein L28

Chain B1:



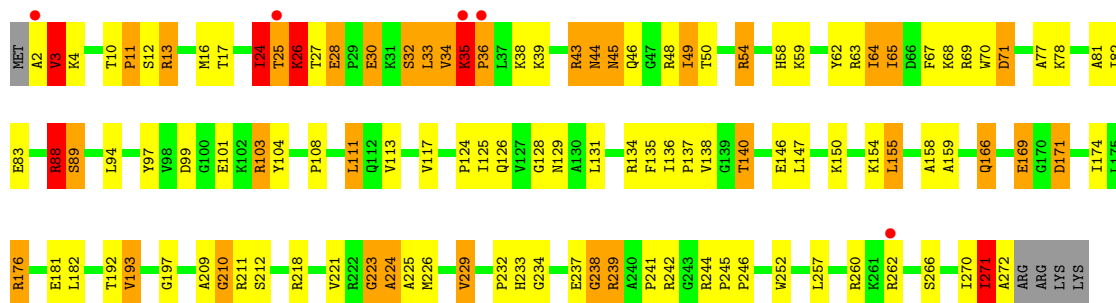
- Molecule 42: 50S ribosomal protein L29

Chain B2:



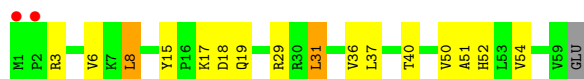
- Molecule 43: 50S ribosomal protein L2

Chain BD:



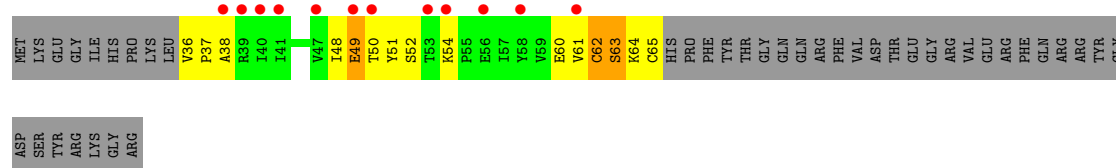
- Molecule 44: 50S ribosomal protein L30

Chain B3:



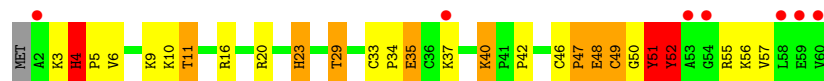
- Molecule 45: 50S ribosomal protein L31

Chain B4:



- Molecule 46: 50S ribosomal protein L32

Chain B5:



- Molecule 47: 50S ribosomal protein L33

Chain B6:



- Molecule 48: 50S ribosomal protein L34

Chain B7:



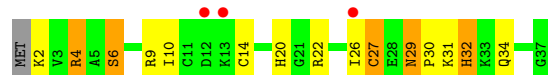
- Molecule 49: 50S ribosomal protein L35

Chain B8:



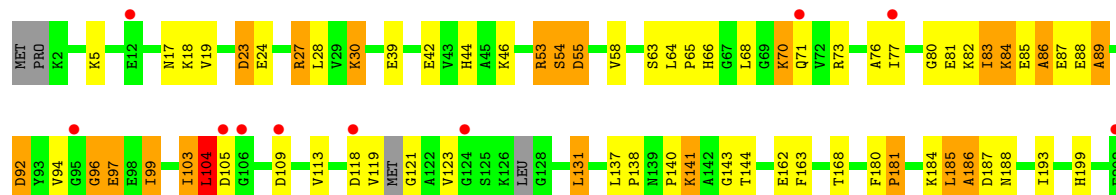
- Molecule 50: 50S ribosomal protein L36

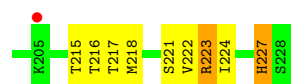
Chain B9:



- Molecule 51: 50S ribosomal protein L1

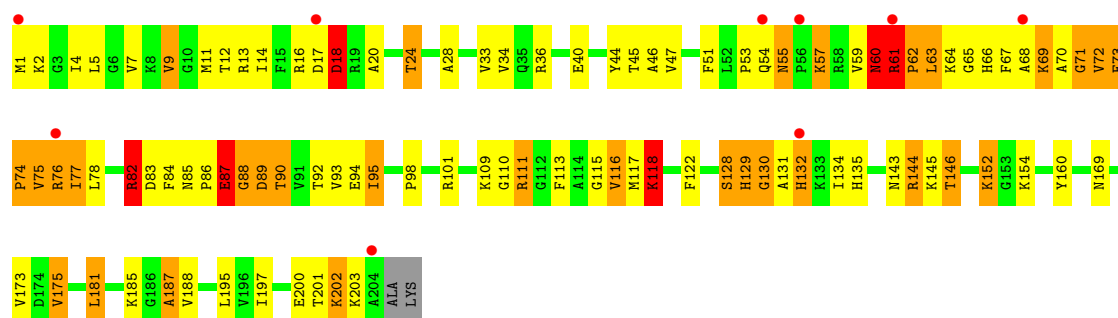
Chain BC:





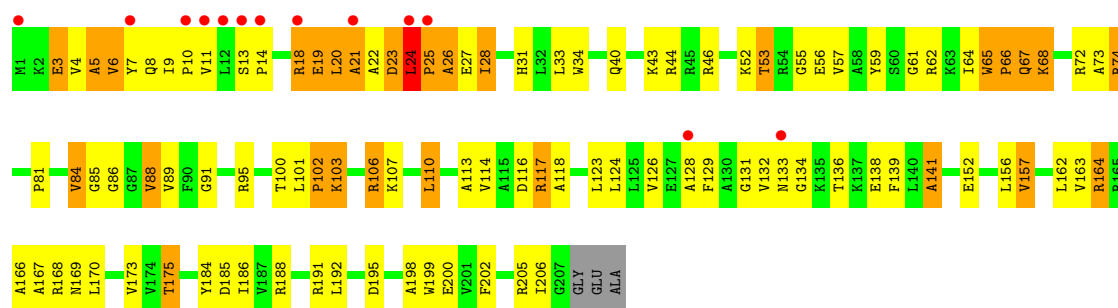
- Molecule 52: 50S ribosomal protein L3

Chain BE:



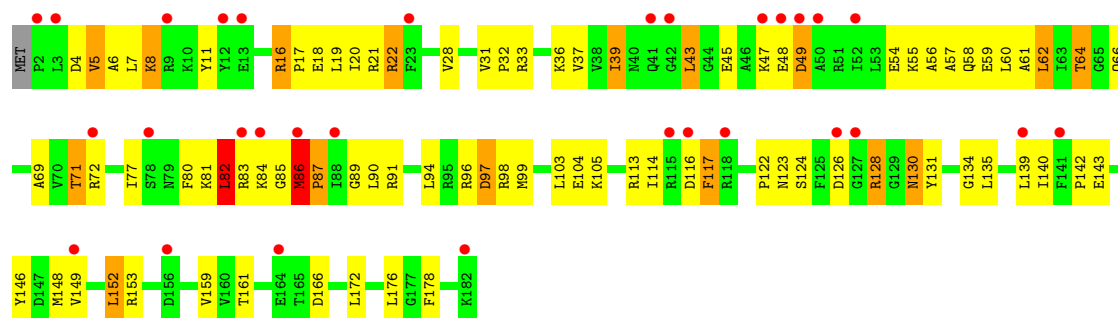
- Molecule 53: 50S ribosomal protein L4

Chain BF:



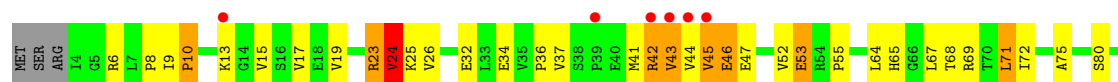
- Molecule 54: 50S ribosomal protein L5

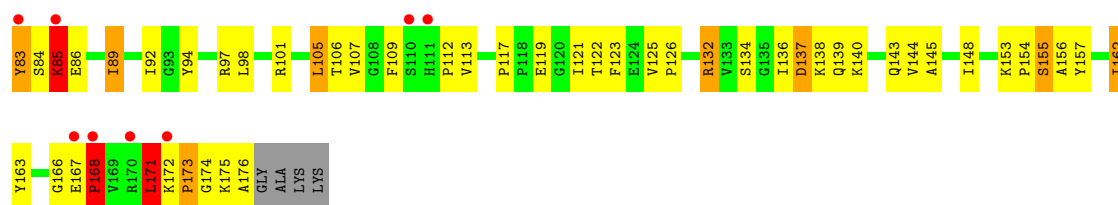
Chain BG:



- Molecule 55: 50S ribosomal protein L6

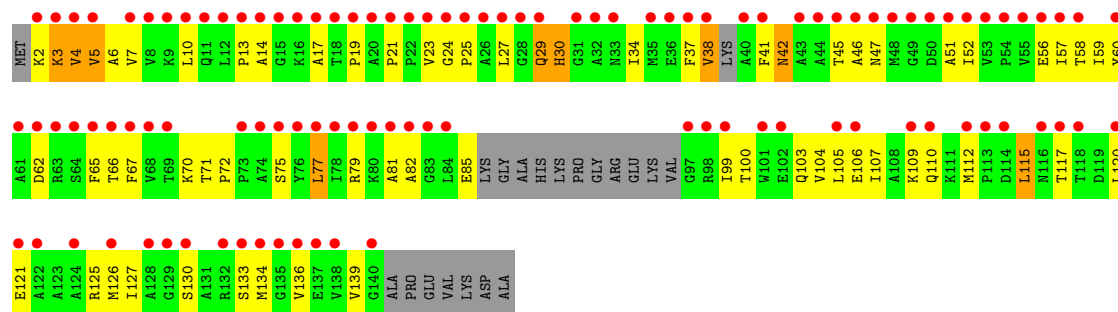
Chain BH:





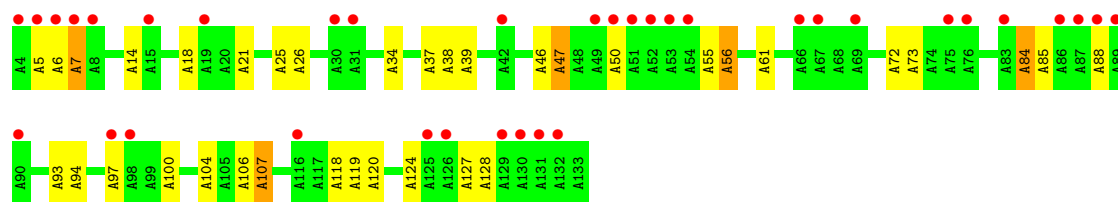
- Molecule 56: 50S ribosomal protein L11

Chain BK:



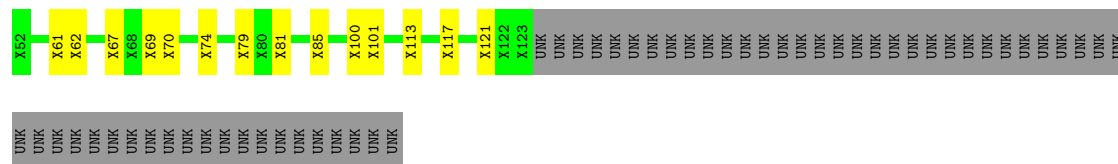
- Molecule 57: 50S ribosomal protein L10

Chain BJ:



- Molecule 58: 50S ribosomal protein L12 CTD

Chain BL:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	201.58Å 241.65Å 305.80Å 90.00° 99.48° 90.00°	Depositor
Resolution (Å)	39.60 – 2.86 39.59 – 2.86	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.60-2.86) 98.6 (39.59-2.86)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.22	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.86Å)	Xtriage
Refinement program	REFMAC5	Depositor
R, R_{free}	0.200 , 0.250 0.200 , 0.243	Depositor DCC
R_{free} test set	32790 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 5.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 655782 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	151831	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.54	8/36408 (0.0%)	0.90	98/56818 (0.2%)
2	AV	0.49	1/1764 (0.1%)	0.96	11/2747 (0.4%)
3	AX	0.50	0/138	0.79	0/212
4	AJ	0.66	0/808	0.96	0/1085
5	AK	0.59	0/900	0.86	0/1213
6	AL	0.67	0/987	1.03	1/1320 (0.1%)
7	AM	0.54	0/999	0.89	0/1336
8	AN	0.61	0/501	1.08	2/664 (0.3%)
9	AO	0.61	0/745	0.94	1/992 (0.1%)
10	AP	0.59	0/717	0.92	2/963 (0.2%)
11	AQ	0.68	0/837	0.89	1/1117 (0.1%)
12	AR	0.60	0/579	0.84	0/768
13	AS	0.58	0/643	0.91	1/865 (0.1%)
14	AT	0.61	0/765	0.90	0/1007
15	AB	0.56	0/1936	0.83	1/2609 (0.0%)
16	AC	0.64	0/1637	0.93	3/2205 (0.1%)
17	AD	0.63	2/1733 (0.1%)	0.97	8/2318 (0.3%)
18	AE	0.71	0/1163	0.93	3/1564 (0.2%)
19	AF	0.55	0/856	0.78	0/1154
20	AG	0.54	0/1276	0.82	0/1709
21	AH	0.64	0/1136	0.95	1/1527 (0.1%)
22	AI	0.57	0/1029	0.92	0/1378
23	AY	0.53	0/4961	0.81	3/6710 (0.0%)
24	AU	0.58	0/213	0.92	0/277
25	BA	0.61	43/68964 (0.1%)	0.95	224/107644 (0.2%)
26	BB	0.40	0/2853	0.84	4/4451 (0.1%)
27	BN	0.74	1/1131 (0.1%)	1.07	5/1525 (0.3%)
28	BO	0.67	0/943	0.98	2/1269 (0.2%)
29	BP	0.86	0/1131	1.29	8/1504 (0.5%)
30	BQ	0.64	0/1143	0.92	0/1527
31	BR	0.70	0/974	1.01	1/1302 (0.1%)
32	BS	0.55	0/778	0.87	0/1036

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BT	0.70	0/1155	1.15	5/1542 (0.3%)
34	BU	0.75	0/975	1.02	1/1297 (0.1%)
35	BV	0.69	0/790	0.99	1/1057 (0.1%)
36	BW	0.67	0/907	1.02	3/1216 (0.2%)
37	BX	0.69	0/739	0.90	1/993 (0.1%)
38	BY	0.81	0/788	1.08	1/1051 (0.1%)
39	BZ	0.56	0/1539	0.87	0/2093
40	B0	0.57	0/671	0.86	0/892
41	B1	0.69	0/738	0.95	0/981
42	B2	0.57	0/600	0.86	0/793
43	BD	0.87	3/2154 (0.1%)	1.08	5/2905 (0.2%)
44	B3	0.55	0/472	0.80	0/634
45	B4	0.54	0/228	0.71	0/309
46	B5	0.85	0/473	1.22	5/639 (0.8%)
47	B6	0.94	0/387	1.36	3/518 (0.6%)
48	B7	0.74	0/426	0.85	0/561
49	B8	0.79	0/515	1.22	3/679 (0.4%)
50	B9	0.69	0/302	1.05	1/397 (0.3%)
51	BC	0.56	1/1747 (0.1%)	1.01	4/2351 (0.2%)
52	BE	0.75	0/1596	1.01	3/2153 (0.1%)
53	BF	0.69	0/1658	0.93	2/2244 (0.1%)
54	BG	0.48	0/1499	0.78	2/2016 (0.1%)
55	BH	0.59	0/1327	0.93	2/1794 (0.1%)
56	BK	0.41	0/951	0.60	0/1290
57	BJ	0.51	0/650	0.62	0/907
All	All	0.61	59/163935 (0.0%)	0.93	422/244128 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
4	AJ	0	1
6	AL	0	1
8	AN	0	1
14	AT	0	2
17	AD	0	2
23	AY	0	4
27	BN	0	2
29	BP	0	15
30	BQ	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
31	BR	0	2
32	BS	0	1
33	BT	0	6
34	BU	0	3
35	BV	0	3
38	BY	0	6
41	B1	0	2
43	BD	0	4
46	B5	0	2
47	B6	0	3
51	BC	0	2
52	BE	0	5
53	BF	0	1
55	BH	0	1
58	BL	0	1
All	All	0	72

All (59) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	2506	U	O3'-P	12.63	1.76	1.61
25	BA	1695	G	O3'-P	-9.03	1.50	1.61
27	BN	127	ASP	CB-CG	8.59	1.69	1.51
25	BA	1299	G	O3'-P	-7.33	1.52	1.61
25	BA	1300	U	O3'-P	-6.92	1.52	1.61
2	AV	72	C	O3'-P	-6.78	1.53	1.61
25	BA	1779	U	O3'-P	-6.73	1.53	1.61
1	AA	1145	C	O3'-P	-6.69	1.53	1.61
25	BA	2591	C	O3'-P	-6.58	1.53	1.61
25	BA	330	A	O3'-P	-6.47	1.53	1.61
25	BA	1370	C	O3'-P	-6.37	1.53	1.61
51	BC	27	ARG	CG-CD	-6.32	1.36	1.51
25	BA	2592	G	O3'-P	-6.25	1.53	1.61
43	BD	30	GLU	CG-CD	6.08	1.61	1.51
25	BA	1694	C	O3'-P	-6.08	1.53	1.61
25	BA	126	A	O3'-P	-5.92	1.54	1.61
25	BA	1819	A	O3'-P	-5.78	1.54	1.61
1	AA	1517	G	O3'-P	-5.73	1.54	1.61
25	BA	2031	A	O3'-P	-5.72	1.54	1.61
43	BD	237	GLU	CG-CD	5.71	1.60	1.51
25	BA	2080	G	O3'-P	-5.70	1.54	1.61
25	BA	2194	G	O3'-P	-5.70	1.54	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BA	1498	C	O3'-P	-5.69	1.54	1.61
17	AD	26	CYS	CB-SG	5.67	1.91	1.82
25	BA	1216	G	O3'-P	-5.66	1.54	1.61
17	AD	26	CYS	CA-CB	5.63	1.66	1.53
25	BA	447	A	O3'-P	-5.62	1.54	1.61
1	AA	675	A	O3'-P	-5.58	1.54	1.61
25	BA	1769	G	O3'-P	-5.58	1.54	1.61
25	BA	2198	A	O3'-P	-5.58	1.54	1.61
43	BD	237	GLU	CD-OE1	5.54	1.31	1.25
25	BA	2280	G	O3'-P	-5.54	1.54	1.61
25	BA	1793	C	O3'-P	-5.51	1.54	1.61
25	BA	1332	G	O3'-P	-5.47	1.54	1.61
25	BA	973	A	P-OP2	5.42	1.58	1.49
25	BA	2068	U	O3'-P	-5.42	1.54	1.61
25	BA	1970	A	O3'-P	-5.40	1.54	1.61
1	AA	1363	C	O3'-P	-5.39	1.54	1.61
25	BA	1350	C	O3'-P	-5.36	1.54	1.61
25	BA	2072	G	O3'-P	-5.36	1.54	1.61
25	BA	1802	A	O3'-P	-5.34	1.54	1.61
1	AA	1502	A	O3'-P	5.33	1.67	1.61
25	BA	209	C	O3'-P	-5.30	1.54	1.61
25	BA	1300	U	P-OP2	-5.27	1.40	1.49
25	BA	1773	A	O3'-P	-5.21	1.54	1.61
25	BA	1432	C	O3'-P	-5.20	1.54	1.61
25	BA	1831	G	O3'-P	-5.19	1.54	1.61
25	BA	129	C	O3'-P	-5.17	1.54	1.61
25	BA	1257	C	O3'-P	-5.14	1.54	1.61
25	BA	1693	U	O3'-P	-5.14	1.54	1.61
25	BA	1963	U	O3'-P	5.14	1.67	1.61
25	BA	1978	A	O3'-P	-5.14	1.54	1.61
1	AA	932	C	O3'-P	-5.13	1.54	1.61
25	BA	2549	G	O3'-P	-5.13	1.54	1.61
25	BA	756	C	O3'-P	-5.09	1.55	1.61
25	BA	232	G	O3'-P	-5.08	1.55	1.61
25	BA	1970	A	P-OP1	5.08	1.57	1.49
1	AA	875	C	O3'-P	-5.08	1.55	1.61
1	AA	504	C	O3'-P	-5.06	1.55	1.61

All (422) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	BC	27	ARG	NE-CZ-NH2	-24.39	108.10	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	996	A	O5'-P-OP1	-17.66	89.51	110.70
1	AA	1499	A	O5'-P-OP1	-14.95	92.25	105.70
25	BA	946	G	O5'-P-OP1	-14.17	92.95	105.70
25	BA	2502	G	O5'-P-OP1	-13.94	93.15	105.70
25	BA	1647	G	O5'-P-OP1	-13.70	93.37	105.70
25	BA	1300	U	P-O3'-C3'	13.62	136.04	119.70
25	BA	1970	A	O5'-P-OP2	-13.05	93.95	105.70
1	AA	1081	G	O5'-P-OP2	-12.52	94.44	105.70
1	AA	1498	U	C2'-C3'-O3'	12.37	136.71	109.50
25	BA	1648	C	O5'-P-OP1	-12.05	94.85	105.70
25	BA	2439	A	O5'-P-OP2	-11.61	95.25	105.70
1	AA	1067	A	C2'-C3'-O3'	11.53	134.88	109.50
17	AD	9	CYS	CA-CB-SG	11.21	134.19	114.00
25	BA	2577	A	O5'-P-OP2	-11.07	95.73	105.70
17	AD	26	CYS	CA-CB-SG	11.06	133.91	114.00
1	AA	1520	G	O5'-P-OP2	-10.82	95.96	105.70
1	AA	1198	G	O5'-P-OP1	-10.62	96.14	105.70
1	AA	1499	A	O5'-P-OP2	10.62	123.44	110.70
25	BA	1617	C	O5'-P-OP1	-10.57	96.19	105.70
1	AA	328	C	C2'-C3'-O3'	10.43	132.44	109.50
25	BA	1799	G	C2'-C3'-O3'	10.32	132.21	109.50
51	BC	27	ARG	CD-NE-CZ	-10.31	109.17	123.60
25	BA	996	A	O5'-P-OP2	10.27	123.02	110.70
25	BA	2554	U	O5'-P-OP1	-10.20	96.52	105.70
25	BA	819	A	O5'-P-OP1	-10.17	96.54	105.70
25	BA	2506	U	C2'-C3'-O3'	10.15	131.84	109.50
13	AS	5	LEU	CA-CB-CG	10.00	138.30	115.30
17	AD	12	CYS	CA-CB-SG	9.92	131.86	114.00
25	BA	732	C	O5'-P-OP2	-9.76	96.92	105.70
25	BA	2430	A	O5'-P-OP1	-9.67	97.00	105.70
1	AA	1145	C	C2'-C3'-O3'	-9.66	88.25	109.50
25	BA	510	C	O5'-P-OP2	-9.65	97.01	105.70
25	BA	1784	A	O5'-P-OP1	-9.62	97.05	105.70
1	AA	353	A	O5'-P-OP2	-9.54	97.11	105.70
1	AA	299	G	O5'-P-OP1	-9.38	97.26	105.70
25	BA	1782	C	O5'-P-OP2	-9.37	97.27	105.70
25	BA	1992	G	C2'-C3'-O3'	9.32	130.00	109.50
25	BA	1647	G	O5'-P-OP2	9.30	121.86	110.70
25	BA	1622	G	O5'-P-OP2	-9.28	97.35	105.70
1	AA	828	A	O5'-P-OP2	-9.20	97.42	105.70
25	BA	2141	G	C2'-C3'-O3'	9.16	129.65	109.50
1	AA	708	C	O5'-P-OP2	-9.11	97.50	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	2577	A	O5'-P-OP1	9.06	121.57	110.70
25	BA	1786	A	N9-C1'-C2'	9.03	125.74	114.00
8	AN	40	CYS	CA-CB-SG	9.00	130.20	114.00
1	AA	30	U	C2'-C3'-O3'	8.96	129.22	109.50
25	BA	2225	A	C2'-C3'-O3'	8.92	129.13	109.50
1	AA	353	A	O5'-P-OP1	8.76	121.21	110.70
25	BA	2491	U	O5'-P-OP1	-8.71	97.86	105.70
17	AD	31	CYS	CA-CB-SG	-8.69	98.36	114.00
25	BA	1332	G	O5'-P-OP2	-8.67	97.90	105.70
2	AV	34	G	C2'-C3'-O3'	8.45	128.08	109.50
25	BA	2272	U	O5'-P-OP2	-8.43	98.12	105.70
1	AA	1181	G	O5'-P-OP2	-8.39	98.15	105.70
25	BA	752	A	C4'-C3'-O3'	-8.34	91.89	109.40
25	BA	1622	G	O5'-P-OP1	8.31	120.67	110.70
25	BA	387	U	C2'-C3'-O3'	8.21	127.56	109.50
25	BA	787	U	O5'-P-OP1	8.15	120.48	110.70
51	BC	27	ARG	CB-CG-CD	8.13	132.73	111.60
50	B9	27	CYS	CA-CB-SG	8.01	128.41	114.00
29	BP	7	ARG	NE-CZ-NH1	8.00	124.30	120.30
25	BA	1784	A	O5'-P-OP2	7.99	120.28	110.70
25	BA	752	A	C2'-C3'-O3'	7.98	127.05	109.50
25	BA	945	A	O5'-P-OP1	7.95	120.23	110.70
25	BA	2430	A	O5'-P-OP2	7.94	120.23	110.70
1	AA	1143	G	C2'-C3'-O3'	7.92	126.92	109.50
2	AV	72	C	C4'-C3'-O3'	7.91	128.82	113.00
25	BA	2479	G	O5'-P-OP2	-7.90	98.59	105.70
33	BT	93	ARG	NE-CZ-NH1	7.82	124.21	120.30
1	AA	115	G	C2'-C3'-O3'	7.79	126.65	109.50
25	BA	2439	A	O5'-P-OP1	7.79	120.04	110.70
25	BA	2444	G	O5'-P-OP2	-7.77	98.70	105.70
25	BA	1653	G	C2'-C3'-O3'	7.75	126.55	109.50
25	BA	2318	G	C2'-C3'-O3'	7.67	126.37	109.50
1	AA	1520	G	O5'-P-OP1	7.67	119.90	110.70
25	BA	1314	C	O5'-P-OP2	-7.66	98.81	105.70
1	AA	1102	A	O5'-P-OP1	-7.63	98.83	105.70
25	BA	1780	A	O5'-P-OP1	7.63	119.86	110.70
1	AA	687	A	C2'-C3'-O3'	7.59	126.19	109.50
25	BA	1541	G	C2'-C3'-O3'	7.55	126.11	109.50
1	AA	1082	G	O5'-P-OP2	-7.53	98.92	105.70
25	BA	1610	A	O5'-P-OP2	-7.50	98.95	105.70
25	BA	1693	U	P-O3'-C3'	7.50	128.70	119.70
46	B5	51	TYR	CA-CB-CG	7.50	127.65	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	B6	45	LYS	N-CA-C	7.50	131.24	111.00
1	AA	562	C	O5'-P-OP1	-7.49	98.96	105.70
25	BA	115	C	O5'-P-OP1	-7.47	98.97	105.70
25	BA	1819	A	C2'-C3'-O3'	7.45	125.89	109.50
1	AA	1133	G	N9-C1'-C2'	-7.44	103.81	112.00
1	AA	726	C	O5'-P-OP1	-7.43	99.02	105.70
9	AO	17	ARG	NE-CZ-NH1	7.40	124.00	120.30
1	AA	1145	C	C4'-C3'-O3'	-7.39	93.87	109.40
25	BA	579	G	O5'-P-OP1	-7.38	99.05	105.70
25	BA	2778	A	O5'-P-OP2	-7.38	99.06	105.70
1	AA	916	G	O5'-P-OP2	-7.37	99.06	105.70
1	AA	1138	G	O4'-C1'-N9	7.37	114.10	108.20
25	BA	2200	C	C2'-C3'-O3'	7.34	125.65	109.50
1	AA	785	G	C2'-C3'-O3'	7.33	125.63	109.50
25	BA	1671	U	O5'-P-OP1	-7.32	99.12	105.70
29	BP	59	LEU	CA-CB-CG	7.31	132.10	115.30
25	BA	2191	G	C2'-C3'-O3'	7.28	125.51	109.50
25	BA	2447	G	C4'-C3'-O3'	-7.26	94.15	109.40
36	BW	92	ARG	NE-CZ-NH1	7.25	123.92	120.30
1	AA	1133	G	C2'-C3'-O3'	7.24	125.43	109.50
25	BA	272	G	C2'-C3'-O3'	7.24	125.42	109.50
25	BA	787	U	O5'-P-OP2	-7.22	99.20	105.70
25	BA	1541	G	C4'-C3'-O3'	-7.21	94.25	109.40
25	BA	1542	A	O5'-P-OP1	-7.20	99.22	105.70
25	BA	1648	C	O5'-P-OP2	7.19	119.32	110.70
25	BA	1812	A	O5'-P-OP2	-7.18	99.24	105.70
25	BA	1022	G	C2'-C3'-O3'	7.15	125.23	109.50
36	BW	92	ARG	NE-CZ-NH2	-7.15	116.72	120.30
27	BN	127	ASP	CB-CG-OD1	7.14	124.73	118.30
1	AA	1504	G	O5'-P-OP1	-7.14	99.27	105.70
21	AH	92	ARG	NE-CZ-NH1	7.13	123.86	120.30
25	BA	1502	C	C2'-C3'-O3'	7.13	125.18	109.50
29	BP	60	MET	CG-SD-CE	7.12	111.59	100.20
25	BA	603	A	C2'-C3'-O3'	7.12	125.15	109.50
25	BA	2507	C	O5'-P-OP2	-7.10	99.31	105.70
25	BA	2581	G	O4'-C1'-N9	7.09	113.87	108.20
1	AA	266	G	P-O3'-C3'	7.08	128.20	119.70
25	BA	2199	A	C2'-C3'-O3'	7.06	125.04	109.50
25	BA	2031	A	O5'-P-OP2	-7.05	99.35	105.70
28	BO	78	ARG	NE-CZ-NH1	7.00	123.80	120.30
2	AV	28	G	C2'-C3'-O3'	6.98	124.87	113.70
10	AP	8	ARG	NE-CZ-NH1	6.97	123.78	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	299	G	O5'-P-OP2	6.97	119.06	110.70
25	BA	2036	C	O5'-P-OP1	6.96	119.05	110.70
43	BD	99	ASP	CB-CA-C	-6.92	96.55	110.40
17	AD	12	CYS	N-CA-C	-6.89	92.39	111.00
1	AA	1505	G	O5'-P-OP2	6.89	118.96	110.70
1	AA	243	A	C2'-C3'-O3'	6.88	124.70	113.70
25	BA	2585	U	C2'-C3'-O3'	6.86	124.67	113.70
1	AA	1138	G	C1'-O4'-C4'	-6.84	104.43	109.90
25	BA	990	A	C4'-C3'-O3'	-6.84	95.04	109.40
1	AA	79	G	C2'-C3'-O3'	6.81	124.60	113.70
25	BA	2541	A	C2'-C3'-O3'	6.76	124.51	113.70
1	AA	1504	G	P-O3'-C3'	6.74	127.79	119.70
43	BD	88	ARG	NE-CZ-NH2	-6.72	116.94	120.30
2	AV	72	C	N1-C1'-C2'	-6.67	104.66	112.00
25	BA	2199	A	O5'-P-OP2	6.67	118.70	110.70
25	BA	945	A	C2'-C3'-O3'	-6.67	94.83	109.50
1	AA	771	G	O5'-P-OP2	-6.64	99.72	105.70
1	AA	1519	A	O5'-P-OP2	-6.62	99.74	105.70
1	AA	913	A	C2'-C3'-O3'	6.60	124.26	113.70
1	AA	533	A	C2'-C3'-O3'	6.58	124.23	113.70
23	AY	320	PRO	N-CA-C	-6.54	95.08	112.10
25	BA	2403	C	O5'-P-OP1	-6.52	99.83	105.70
1	AA	377	G	O5'-P-OP2	-6.47	99.87	105.70
1	AA	267	C	P-O5'-C5'	-6.46	110.57	120.90
25	BA	74	A	C2'-C3'-O3'	6.44	124.00	113.70
29	BP	7	ARG	NE-CZ-NH2	-6.44	117.08	120.30
29	BP	116	GLY	N-CA-C	6.43	129.17	113.10
36	BW	11	ARG	NE-CZ-NH1	6.39	123.50	120.30
25	BA	1970	A	C4'-C3'-O3'	-6.39	95.99	109.40
1	AA	180	U	O5'-P-OP1	-6.38	99.95	105.70
25	BA	1349	A	O4'-C4'-C3'	-6.38	97.62	104.00
23	AY	260	LEU	CA-CB-CG	6.37	129.95	115.30
1	AA	1139	G	C3'-C2'-O2'	-6.37	94.83	113.30
18	AE	41	VAL	CB-CA-C	-6.37	99.30	111.40
25	BA	1970	A	C1'-O4'-C4'	-6.36	104.81	109.90
17	AD	12	CYS	CB-CA-C	6.32	123.03	110.40
27	BN	119	ARG	NE-CZ-NH1	6.30	123.45	120.30
53	BF	7	TYR	CA-CB-CG	6.29	125.35	113.40
25	BA	1698	A	O4'-C1'-C2'	-6.28	99.52	105.80
25	BA	982	C	O5'-P-OP2	-6.27	100.05	105.70
25	BA	1618	A	O5'-P-OP1	-6.26	100.07	105.70
28	BO	78	ARG	NE-CZ-NH2	-6.26	117.17	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	827	U	C2'-C3'-O3'	-6.24	95.78	109.50
25	BA	1255	U	O5'-P-OP2	-6.23	100.09	105.70
25	BA	722	A	C2'-C3'-O3'	6.22	123.66	113.70
25	BA	906	G	C2'-C3'-O3'	6.22	123.66	113.70
25	BA	2830	G	C2'-C3'-O3'	6.22	123.66	113.70
25	BA	701	G	C2'-C3'-O3'	6.22	123.65	113.70
25	BA	948	G	O5'-P-OP1	6.19	118.12	110.70
25	BA	2023	G	O5'-P-OP1	-6.18	100.13	105.70
25	BA	512	G	O4'-C1'-N9	6.18	113.14	108.20
25	BA	2579	C	O5'-P-OP2	-6.17	100.15	105.70
25	BA	1300	U	O3'-P-O5'	6.16	115.71	104.00
25	BA	732	C	O5'-P-OP1	6.15	118.08	110.70
25	BA	1516	C	O5'-P-OP1	-6.15	100.17	105.70
25	BA	2346	A	O4'-C1'-N9	6.15	113.12	108.20
1	AA	1502	A	N9-C1'-C2'	6.13	121.97	114.00
25	BA	967	C	O5'-P-OP2	-6.13	100.18	105.70
1	AA	1181	G	C4'-C3'-O3'	-6.13	96.53	109.40
1	AA	509	A	C2'-C3'-O3'	6.13	123.51	113.70
25	BA	1017	G	C2'-C3'-O3'	6.12	123.50	113.70
25	BA	1024	G	O5'-P-OP1	-6.12	100.19	105.70
16	AC	11	ARG	NE-CZ-NH1	6.12	123.36	120.30
25	BA	834	C	O5'-P-OP2	-6.12	100.19	105.70
1	AA	681	C	O5'-P-OP2	-6.11	100.20	105.70
1	AA	1300	G	O5'-P-OP2	6.10	118.03	110.70
25	BA	2722	G	O5'-P-OP1	-6.08	100.22	105.70
37	BX	57	LEU	CA-CB-CG	6.08	129.28	115.30
26	BB	75	G	C2'-C3'-O3'	6.08	123.42	113.70
25	BA	2722	G	O5'-P-OP2	6.07	117.98	110.70
1	AA	524	G	O5'-P-OP2	-6.06	100.24	105.70
43	BD	88	ARG	NE-CZ-NH1	6.04	123.32	120.30
46	B5	52	TYR	N-CA-C	-6.02	94.74	111.00
1	AA	1472	U	O5'-P-OP2	-6.01	100.29	105.70
25	BA	2163	C	C2'-C3'-O3'	6.00	123.30	113.70
23	AY	88	VAL	CB-CA-C	-5.97	100.05	111.40
25	BA	2015	A	O5'-P-OP2	-5.96	100.34	105.70
25	BA	1780	A	O5'-P-OP2	-5.95	100.34	105.70
25	BA	1962	C	C1'-C2'-O2'	-5.95	92.74	110.60
52	BE	88	GLY	N-CA-C	5.95	127.96	113.10
25	BA	54	G	C2'-C3'-O3'	5.93	123.19	113.70
51	BC	104	LEU	CA-CB-CG	5.93	128.95	115.30
1	AA	194	C	O5'-P-OP2	-5.93	100.36	105.70
25	BA	2612	C	O5'-P-OP2	-5.93	100.36	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	945	A	N9-C1'-C2'	5.91	121.68	114.00
8	AN	44	LEU	CA-CB-CG	5.89	128.85	115.30
1	AA	1147	C	C2'-C3'-O3'	5.88	123.11	113.70
25	BA	1970	A	C5'-C4'-O4'	5.87	116.15	109.10
25	BA	2600	A	O5'-P-OP2	5.86	117.73	110.70
25	BA	2031	A	C5'-C4'-C3'	-5.86	106.62	116.00
25	BA	1540	U	P-O5'-C5'	-5.85	111.54	120.90
1	AA	1330	U	O5'-P-OP2	-5.84	100.45	105.70
46	B5	3	LYS	C-N-CA	5.84	136.29	121.70
25	BA	774	A	O5'-P-OP2	-5.83	100.45	105.70
1	AA	1420	C	O5'-P-OP2	5.83	117.70	110.70
25	BA	1882	C	C2'-C3'-O3'	5.83	123.03	113.70
25	BA	1057	A	C2'-C3'-O3'	5.83	123.02	113.70
1	AA	244	U	O5'-P-OP1	-5.82	100.46	105.70
1	AA	260	G	O5'-P-OP1	-5.82	100.46	105.70
54	BG	89	GLY	N-CA-C	-5.81	98.57	113.10
55	BH	10	PRO	N-CA-CB	5.81	110.27	103.30
25	BA	1982	C	O5'-P-OP2	-5.80	100.47	105.70
2	AV	1	G	C5'-C4'-O4'	5.79	116.05	109.10
25	BA	2006	C	O5'-P-OP1	5.79	117.65	110.70
1	AA	1013	G	C2'-C3'-O3'	5.79	122.96	113.70
25	BA	2346	A	C1'-O4'-C4'	-5.79	105.27	109.90
1	AA	391	G	O5'-P-OP2	-5.79	100.49	105.70
25	BA	2506	U	C4'-C3'-O3'	-5.78	97.26	109.40
25	BA	2346	A	O4'-C1'-C2'	-5.76	100.04	105.80
2	AV	4	C	C2'-C3'-O3'	5.75	122.91	113.70
38	BY	31	LEU	C-N-CD	-5.75	107.95	120.60
25	BA	991	C	O5'-P-OP2	5.75	117.60	110.70
1	AA	762	C	O5'-P-OP1	-5.75	100.53	105.70
1	AA	828	A	O5'-P-OP1	5.74	117.59	110.70
25	BA	1959	G	C2'-C3'-O3'	5.73	122.87	113.70
17	AD	31	CYS	N-CA-CB	5.73	120.92	110.60
25	BA	252	G	O5'-P-OP2	-5.71	100.56	105.70
25	BA	1888	G	O4'-C4'-C3'	-5.71	98.29	104.00
43	BD	54	ARG	NE-CZ-NH2	-5.71	117.44	120.30
26	BB	19	G	C2'-C3'-O3'	5.70	122.83	113.70
25	BA	669	G	O5'-P-OP1	5.69	117.53	110.70
33	BT	30	VAL	N-CA-C	5.69	126.36	111.00
25	BA	739	G	C2'-C3'-O3'	-5.69	96.98	109.50
25	BA	1838	C	C4'-C3'-O3'	-5.68	97.47	109.40
25	BA	2596	U	O5'-P-OP1	-5.68	100.59	105.70
11	AQ	68	ARG	NE-CZ-NH1	5.68	123.14	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AC	94	LEU	CA-CB-CG	5.67	128.34	115.30
25	BA	2095	C	C2'-C3'-O3'	5.67	122.78	113.70
25	BA	102	G	N9-C1'-C2'	5.67	121.37	114.00
25	BA	510	C	O5'-P-OP1	5.66	117.49	110.70
29	BP	36	LYS	CD-CE-NZ	5.65	124.69	111.70
49	B8	48	PHE	CB-CA-C	-5.65	99.11	110.40
25	BA	1865	G	O5'-P-OP1	-5.64	100.62	105.70
25	BA	247	G	O5'-P-OP2	-5.64	100.62	105.70
46	B5	48	GLU	N-CA-C	-5.64	95.77	111.00
1	AA	731	G	O5'-P-OP2	-5.63	100.64	105.70
25	BA	1915	U	C2'-C3'-O3'	5.63	122.70	113.70
25	BA	1782	C	O5'-P-OP1	5.62	117.45	110.70
1	AA	1081	G	O5'-P-OP1	5.62	117.45	110.70
49	B8	46	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	AA	1498	U	P-O3'-C3'	5.60	126.42	119.70
25	BA	1485	G	C2'-C3'-O3'	5.60	122.66	113.70
25	BA	2757	A	O5'-P-OP2	-5.60	100.66	105.70
25	BA	2226	C	O5'-P-OP2	-5.59	100.67	105.70
25	BA	1969	A	O5'-P-OP2	-5.59	100.67	105.70
1	AA	1420	C	O5'-P-OP1	-5.58	100.67	105.70
29	BP	27	HIS	N-CA-C	5.57	126.05	111.00
25	BA	789	A	O5'-P-OP1	-5.57	100.69	105.70
17	AD	36	ARG	NE-CZ-NH1	5.57	123.08	120.30
25	BA	2048	G	O5'-P-OP1	5.57	117.38	110.70
31	BR	4	LEU	CB-CG-CD1	5.57	120.46	111.00
25	BA	744	G	O5'-P-OP2	-5.56	100.69	105.70
25	BA	1204	A	O4'-C1'-C2'	-5.55	100.25	105.80
25	BA	1500	G	C2'-C3'-O3'	5.55	122.58	113.70
25	BA	994	C	O5'-P-OP2	-5.55	100.71	105.70
1	AA	175	C	O5'-P-OP1	-5.54	100.71	105.70
29	BP	62	LEU	CB-CG-CD1	5.54	120.42	111.00
25	BA	586	A	O5'-P-OP2	-5.54	100.71	105.70
25	BA	1807	G	N9-C1'-C2'	-5.54	105.91	112.00
33	BT	87	ASP	CB-CG-OD1	-5.54	113.32	118.30
25	BA	1426	G	C2'-C3'-O3'	5.53	122.54	113.70
1	AA	149	A	N9-C1'-C2'	-5.51	105.93	112.00
53	BF	46	ARG	CG-CD-NE	-5.51	100.23	111.80
25	BA	2198	A	C2'-C3'-O3'	-5.50	97.40	109.50
1	AA	189(A)	C	O5'-P-OP2	-5.50	100.75	105.70
25	BA	2031	A	C2'-C3'-O3'	5.48	122.47	113.70
25	BA	1308	A	O5'-P-OP2	-5.48	100.77	105.70
25	BA	2700	C	O5'-P-OP2	-5.47	100.78	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	BN	74	ARG	NE-CZ-NH1	5.47	123.04	120.30
1	AA	1456	G	O5'-P-OP1	5.47	117.26	110.70
27	BN	114	ARG	NE-CZ-NH1	5.45	123.03	120.30
25	BA	1970	A	O4'-C1'-C2'	-5.44	100.36	105.80
25	BA	573	G	O5'-P-OP2	-5.44	100.81	105.70
27	BN	119	ARG	NE-CZ-NH2	-5.43	117.58	120.30
25	BA	551	G	C2'-C3'-O3'	5.43	122.39	113.70
1	AA	350	G	O5'-P-OP2	-5.43	100.81	105.70
25	BA	1142(A)	A	O5'-P-OP1	-5.43	100.81	105.70
1	AA	348	G	C2'-C3'-O3'	5.43	122.38	113.70
25	BA	537	C	C2'-C3'-O3'	5.43	122.38	113.70
52	BE	132	HIS	C-N-CA	-5.43	108.14	121.70
25	BA	1764	G	O5'-P-OP2	-5.42	100.82	105.70
25	BA	700	G	C2'-C3'-O3'	5.42	122.37	113.70
25	BA	738	G	O5'-P-OP2	-5.41	100.84	105.70
25	BA	1744	C	C2'-C3'-O3'	5.41	122.35	113.70
1	AA	1138	G	C5'-C4'-O4'	5.40	115.58	109.10
15	AB	200	ILE	CB-CA-C	-5.40	100.81	111.60
1	AA	149	A	C4'-C3'-O3'	5.39	123.78	113.00
25	BA	1193	G	O5'-P-OP2	-5.39	100.85	105.70
25	BA	2060	A	O5'-P-OP1	-5.38	100.86	105.70
1	AA	1151	A	O5'-P-OP2	-5.37	100.87	105.70
25	BA	1963	U	N1-C1'-C2'	5.37	120.98	114.00
25	BA	2820	A	C2'-C3'-O3'	-5.37	97.69	109.50
35	BV	39	LEU	CA-CB-CG	5.36	127.63	115.30
49	B8	62	LEU	CB-CG-CD1	5.36	120.11	111.00
1	AA	1261	A	O5'-P-OP1	-5.36	100.88	105.70
25	BA	508	G	C2'-C3'-O3'	-5.36	97.72	109.50
25	BA	1947	C	C2'-C3'-O3'	5.36	122.27	113.70
25	BA	1881	C	C2'-C3'-O3'	5.35	122.26	113.70
1	AA	971	G	O5'-P-OP2	-5.35	100.89	105.70
2	AV	1	G	C5'-C4'-C3'	5.35	124.56	116.00
25	BA	2497	A	C4'-C3'-O3'	-5.34	98.18	109.40
1	AA	1136	U	O4'-C1'-N1	5.34	112.47	108.20
1	AA	1506	U	O5'-P-OP1	5.33	117.10	110.70
25	BA	1558	A	C2'-C3'-O3'	5.33	122.23	113.70
25	BA	1653	G	P-O3'-C3'	5.33	126.09	119.70
33	BT	30	VAL	CB-CA-C	-5.32	101.28	111.40
47	B6	10	LEU	CA-CB-CG	5.32	127.53	115.30
25	BA	1917	U	O5'-P-OP1	-5.32	100.92	105.70
25	BA	1654	A	O5'-P-OP1	-5.31	100.92	105.70
25	BA	1970	A	C5'-C4'-C3'	5.31	124.49	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	B6	46	HIS	N-CA-C	5.30	125.32	111.00
25	BA	1578	U	O5'-P-OP2	-5.30	100.93	105.70
25	BA	1879	C	C2'-C3'-O3'	5.29	122.16	113.70
25	BA	1786	A	O4'-C1'-C2'	-5.28	100.52	105.80
1	AA	973	G	C2'-C3'-O3'	5.28	122.14	113.70
18	AE	126	ARG	NE-CZ-NH2	-5.28	117.66	120.30
33	BT	93	ARG	NE-CZ-NH2	-5.28	117.66	120.30
25	BA	2778	A	O5'-P-OP1	5.28	117.03	110.70
25	BA	1388	G	C2'-C3'-O3'	5.27	122.14	113.70
25	BA	2171	A	C4'-C3'-O3'	-5.27	98.33	109.40
1	AA	427	U	O5'-P-OP2	-5.27	100.96	105.70
10	AP	8	ARG	NE-CZ-NH2	-5.27	117.67	120.30
25	BA	562	U	O5'-P-OP1	-5.25	100.97	105.70
26	BB	100	A	O5'-P-OP2	-5.23	100.99	105.70
25	BA	2682	U	O5'-P-OP2	5.23	116.98	110.70
1	AA	816	A	O5'-P-OP1	5.23	116.97	110.70
1	AA	180	U	O5'-P-OP2	5.23	116.97	110.70
25	BA	2768	C	O5'-P-OP2	-5.23	101.00	105.70
1	AA	708	C	O5'-P-OP1	5.22	116.97	110.70
1	AA	1198	G	O5'-P-OP2	5.22	116.97	110.70
2	AV	72	C	C4'-C3'-C2'	-5.21	97.39	102.60
25	BA	2665	A	O4'-C4'-C3'	-5.21	98.78	104.00
1	AA	109	A	O5'-P-OP2	-5.21	101.02	105.70
25	BA	1936	A	N9-C1'-C2'	5.20	120.76	114.00
25	BA	2655	G	O5'-P-OP1	-5.20	101.02	105.70
1	AA	321	A	O5'-P-OP2	-5.20	101.02	105.70
43	BD	71	ASP	CB-CA-C	-5.19	100.01	110.40
1	AA	1145	C	C3'-C2'-O2'	-5.19	98.24	113.30
46	B5	40	LYS	CD-CE-NZ	5.19	123.64	111.70
54	BG	152	LEU	CA-CB-CG	5.19	127.24	115.30
25	BA	102	G	O4'-C1'-C2'	-5.19	100.61	105.80
25	BA	1693	U	O3'-P-O5'	5.18	113.85	104.00
25	BA	1905	C	O5'-P-OP2	-5.17	101.05	105.70
25	BA	120	U	O5'-P-OP1	-5.17	101.05	105.70
25	BA	933	A	O4'-C4'-C3'	-5.17	98.83	104.00
2	AV	76	A	C4'-C3'-C2'	-5.16	97.44	102.60
25	BA	1545	A	C2'-C3'-O3'	5.16	121.95	113.70
26	BB	15	A	C2'-C3'-O3'	5.15	121.95	113.70
6	AL	113	ARG	NE-CZ-NH2	-5.15	117.72	120.30
25	BA	2602	A	O5'-P-OP2	5.15	116.88	110.70
25	BA	1888	G	C5'-C4'-O4'	5.14	115.27	109.10
25	BA	753	C	O5'-P-OP1	-5.14	101.08	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	60	A	C2'-C3'-O3'	5.13	121.91	113.70
25	BA	2006	C	O5'-P-OP2	-5.13	101.08	105.70
25	BA	2392	A	O4'-C4'-C3'	-5.13	98.87	104.00
1	AA	1146	A	C2'-C3'-O3'	5.13	121.91	113.70
52	BE	60	ASN	N-CA-C	5.13	124.85	111.00
1	AA	1504	G	C4'-C3'-O3'	5.12	123.24	113.00
2	AV	64	A	C2'-C3'-O3'	5.12	121.89	113.70
25	BA	935	C	C2'-C3'-O3'	5.12	121.89	113.70
25	BA	2700	C	O5'-P-OP1	5.11	116.83	110.70
1	AA	319	G	O5'-P-OP2	-5.10	101.11	105.70
1	AA	762	C	O5'-P-OP2	5.10	116.82	110.70
25	BA	619	G	O5'-P-OP1	-5.10	101.11	105.70
1	AA	1261	A	O5'-P-OP2	5.09	116.81	110.70
25	BA	265	A	N9-C1'-C2'	5.08	120.61	114.00
25	BA	2444	G	O5'-P-OP1	5.08	116.80	110.70
1	AA	7	G	C2'-C3'-O3'	-5.08	98.33	109.50
25	BA	2714	G	C5'-C4'-C3'	-5.08	107.88	116.00
25	BA	221	A	C2'-C3'-O3'	5.07	121.82	113.70
25	BA	2714	G	C2'-C3'-O3'	5.07	121.82	113.70
25	BA	2075	U	O5'-P-OP2	5.07	116.79	110.70
55	BH	8	PRO	N-CA-CB	5.07	109.39	103.30
25	BA	271(Y)	U	O4'-C1'-N1	5.07	112.26	108.20
25	BA	1525	G	O5'-P-OP2	-5.07	101.14	105.70
25	BA	2074	U	O5'-P-OP2	-5.07	101.14	105.70
18	AE	14	ARG	NE-CZ-NH2	-5.07	117.77	120.30
25	BA	1245	G	C2'-C3'-O3'	5.07	121.80	113.70
25	BA	2231	C	C2'-C3'-O3'	5.07	121.81	113.70
16	AC	196	LEU	CA-CB-CG	5.06	126.93	115.30
25	BA	1204	A	C3'-C2'-C1'	-5.06	97.45	101.50
34	BU	92	ARG	NE-CZ-NH1	5.06	122.83	120.30
25	BA	2040	C	O5'-P-OP1	-5.05	101.16	105.70
25	BA	2048	G	O5'-P-OP2	-5.05	101.16	105.70
25	BA	1162	G	C2'-C3'-O3'	5.05	121.77	113.70
1	AA	1135	U	C4'-C3'-O3'	5.04	123.09	113.00
25	BA	508	G	P-O5'-C5'	5.04	128.96	120.90
2	AV	72	C	O4'-C4'-C3'	-5.04	98.97	104.00
1	AA	931	C	C2'-C3'-O3'	5.03	121.75	113.70
25	BA	1941	C	O5'-P-OP1	-5.03	101.17	105.70
25	BA	2811	G	C2'-C3'-O3'	5.03	121.75	113.70
25	BA	2620	C	O5'-P-OP2	-5.03	101.18	105.70
25	BA	2465	C	O5'-P-OP2	-5.02	101.18	105.70
25	BA	1280	G	C2'-C3'-O3'	5.01	121.72	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BA	585	G	C4'-C3'-O3'	5.01	123.02	113.00

There are no chirality outliers.

All (72) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	AD	11	LEU	Peptide
17	AD	17	VAL	Peptide
4	AJ	54	PHE	Peptide
6	AL	28	LYS	Peptide
8	AN	13	THR	Peptide
14	AT	73	HIS	Peptide
14	AT	95	ALA	Peptide
23	AY	209	ALA	Peptide
23	AY	319	ASP	Peptide
23	AY	320	PRO	Peptide
23	AY	404	VAL	Peptide
41	B1	29	GLY	Peptide
41	B1	94	LEU	Peptide
46	B5	47	PRO	Peptide
46	B5	51	TYR	Peptide
47	B6	10	LEU	Peptide
47	B6	20	ASN	Peptide
47	B6	31	PRO	Peptide
51	BC	143	GLY	Peptide
51	BC	70	LYS	Peptide
43	BD	197	GLY	Peptide
43	BD	223	GLY	Peptide
43	BD	24	ILE	Peptide
43	BD	36	PRO	Peptide
52	BE	131	ALA	Peptide
52	BE	61	ARG	Peptide
52	BE	62	PRO	Peptide
52	BE	76	ARG	Peptide
52	BE	86	PRO	Peptide
53	BF	85	GLY	Peptide
55	BH	166	GLY	Peptide
58	BL	121	UNK	Peptide
27	BN	124	ALA	Peptide
27	BN	20	GLY	Peptide
29	BP	10	PRO	Peptide
29	BP	107	LYS	Peptide

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Mol	Chain	Res	Type	Group
29	BP	115	LEU	Peptide
29	BP	143	GLY	Peptide
29	BP	29	LYS	Peptide
29	BP	33	ARG	Peptide
29	BP	34	GLY	Peptide
29	BP	37	GLY	Peptide
29	BP	40	SER	Peptide
29	BP	44	GLY	Peptide
29	BP	51	PHE	Peptide
29	BP	57	THR	Peptide
29	BP	70	GLN	Peptide
29	BP	8	PRO	Peptide
29	BP	9	ASN	Peptide
30	BQ	17	LEU	Peptide
30	BQ	19	GLY	Peptide
31	BR	117	VAL	Peptide
31	BR	5	LYS	Peptide
32	BS	11	LYS	Peptide
33	BT	29	ARG	Peptide
33	BT	30	VAL	Peptide
33	BT	58	ASN	Peptide
33	BT	79	HIS	Peptide
33	BT	92	GLY	Peptide
33	BT	93	ARG	Peptide
34	BU	90	VAL	Peptide
34	BU	95	LEU	Peptide
34	BU	96	ALA	Peptide
35	BV	1	MET	Peptide
35	BV	18	LEU	Peptide
35	BV	42	GLY	Peptide
38	BY	16	ALA	Peptide
38	BY	17	SER	Peptide
38	BY	40	GLU	Peptide
38	BY	6	HIS	Peptide
38	BY	61	ILE	Peptide
38	BY	76	CYS	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	AA	32529	0	16426	525	0
2	AV	1579	0	802	43	0
3	AX	125	0	64	2	0
4	AJ	795	0	840	29	0
5	AK	885	0	904	28	0
6	AL	971	0	1057	26	0
7	AM	988	0	1059	43	0
8	AN	492	0	529	21	0
9	AO	734	0	771	16	0
10	AP	701	0	720	14	0
11	AQ	824	0	891	19	0
12	AR	574	0	644	10	0
13	AS	630	0	652	25	0
14	AT	763	0	861	30	0
15	AB	1901	0	1951	86	0
16	AC	1613	0	1677	49	0
17	AD	1703	0	1763	64	0
18	AE	1147	0	1207	33	0
19	AF	843	0	857	19	0
20	AG	1257	0	1296	25	0
21	AH	1116	0	1177	27	0
22	AI	1011	0	1043	35	0
23	AY	4877	0	4964	166	0
24	AU	209	0	221	8	0
25	BA	61580	0	31049	1148	0
26	BB	2551	0	1295	55	0
27	BN	1104	0	1180	63	0
28	BO	933	0	996	35	0
29	BP	1114	0	1187	142	0
30	BQ	1122	0	1179	38	0
31	BR	960	0	1021	39	0
32	BS	770	0	832	42	0
33	BT	1141	0	1202	114	0
34	BU	958	0	1015	51	0
35	BV	779	0	852	50	0
36	BW	896	0	953	27	0
37	BX	725	0	778	15	0
38	BY	775	0	870	71	0
39	BZ	1508	0	1486	56	0
40	B0	662	0	688	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	B1	731	0	808	33	0
42	B2	598	0	653	31	0
43	BD	2104	0	2182	101	0
44	B3	467	0	523	5	0
45	B4	225	0	229	10	0
46	B5	459	0	477	31	0
47	B6	380	0	390	55	0
48	B7	418	0	467	12	0
49	B8	507	0	576	58	0
50	B9	299	0	323	10	0
51	BC	1718	0	1766	54	0
52	BE	1563	0	1629	81	0
53	BF	1623	0	1677	83	0
54	BG	1474	0	1535	56	0
55	BH	1303	0	1348	55	0
56	BK	936	0	970	60	0
57	BJ	651	0	649	17	0
58	BL	356	0	75	7	0
59	AA	45	0	0	0	0
59	AY	1	0	0	0	0
59	B8	1	0	0	0	0
59	BA	88	0	0	0	0
59	BD	1	0	0	0	0
59	BE	1	0	0	0	0
59	BF	1	0	0	0	0
60	AY	32	0	14	5	0
61	AY	4	0	0	1	0
All	All	151831	0	105250	3647	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 14.

All (3647) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2111:C:N3	25:BA:2147:G:N2	1.74	1.36
25:BA:1332:G:N2	25:BA:1609:A:O2'	1.62	1.26
47:B6:40:CYS:SG	47:B6:45:LYS:NZ	1.02	1.24
25:BA:90:U:O2'	25:BA:92:A:OP2	1.54	1.24
25:BA:1332:G:N2	25:BA:1609:A:HO2'	1.30	1.23
25:BA:2394:C:OP1	29:BP:63:PRO:HD2	1.41	1.20
23:AY:404:VAL:HG13	23:AY:405:PRO:HA	1.22	1.20
25:BA:1914:C:O2'	25:BA:1915:U:O5'	1.61	1.18

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:271(H):G:C5'	41:B1:81:LYS:HE2	1.72	1.17
25:BA:271(G):C:O2'	41:B1:81:LYS:CE	1.95	1.14
47:B6:48:VAL:HG23	47:B6:49:HIS:N	1.53	1.14
25:BA:271(H):G:H5'	41:B1:81:LYS:CE	1.78	1.14
25:BA:1048:A:N6	25:BA:1107:G:O6	1.81	1.12
29:BP:7:ARG:HD3	53:BF:188:ARG:HA	1.30	1.11
47:B6:40:CYS:SG	47:B6:45:LYS:CE	2.39	1.09
47:B6:48:VAL:HG23	47:B6:49:HIS:H	1.02	1.09
38:BY:79:CYS:SG	38:BY:80:GLY:N	2.20	1.08
29:BP:48:PRO:O	29:BP:50:ARG:N	1.88	1.05
29:BP:7:ARG:HA	29:BP:7:ARG:HH11	1.14	1.05
47:B6:37:ARG:O	47:B6:48:VAL:O	1.76	1.03
2:AV:76:A:H4'	2:AV:76:A:OP1	1.57	1.03
29:BP:7:ARG:HA	29:BP:7:ARG:NH1	1.72	1.02
25:BA:271(G):C:O2'	41:B1:81:LYS:HE3	1.59	1.02
25:BA:811:U:OP2	29:BP:30:THR:O	1.78	1.02
25:BA:2419:U:O4	49:B8:30:ARG:CZ	2.08	1.01
25:BA:1540:U:H6	25:BA:1540:U:H5'	1.23	1.00
35:BV:24:LYS:HA	35:BV:92:THR:HG23	1.40	0.99
29:BP:64:LYS:O	29:BP:66:GLY:N	1.95	0.99
1:AA:706:A:O4'	5:AK:29:ILE:HD11	1.63	0.99
1:AA:1054:C:O2	1:AA:1054:C:H3'	1.62	0.98
25:BA:242:G:H5''	49:B8:62:LEU:HD13	1.45	0.98
25:BA:2656:U:H3	25:BA:2665:A:H2	1.09	0.98
47:B6:48:VAL:CG2	47:B6:49:HIS:H	1.77	0.98
25:BA:676:A:H8	25:BA:2069:G:H21	1.05	0.97
25:BA:1100:C:H4'	25:BA:1100:C:OP1	1.63	0.97
17:AD:9:CYS:HA	17:AD:12:CYS:HB2	1.45	0.97
47:B6:47:THR:HG22	47:B6:48:VAL:N	1.76	0.97
1:AA:90:U:HO2'	1:AA:91:C:H5	1.09	0.96
1:AA:1502:A:H2	1:AA:1505:G:H1	1.02	0.96
25:BA:1899:G:H22	25:BA:1902:C:H41	1.09	0.96
8:AN:23:ARG:HD2	8:AN:28:GLY:O	1.63	0.96
27:BN:16:ILE:HD11	27:BN:26:LEU:HD11	1.46	0.96
46:B5:4:HIS:HB3	46:B5:5:PRO:CD	1.96	0.96
23:AY:404:VAL:HG13	23:AY:405:PRO:CA	1.95	0.96
43:BD:30:GLU:HG3	43:BD:63:ARG:NH2	1.81	0.96
47:B6:47:THR:CG2	47:B6:48:VAL:N	2.30	0.95
25:BA:250:G:OP2	49:B8:13:ARG:NH2	1.98	0.95
47:B6:48:VAL:CG2	47:B6:49:HIS:N	2.29	0.95
33:BT:85:LYS:HB3	33:BT:85:LYS:NZ	1.81	0.95
29:BP:56:SER:O	29:BP:58:THR:N	1.97	0.95

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
50:B9:29:ASN:HD21	50:B9:32:HIS:CE1	1.84	0.95
25:BA:2137:C:H3'	25:BA:2137:C:O2	1.67	0.95
29:BP:17:LYS:O	29:BP:19:VAL:N	1.99	0.95
29:BP:59:LEU:HA	29:BP:61:ARG:NH1	1.81	0.94
25:BA:1771:C:HO2'	25:BA:1786:A:H8	0.99	0.94
7:AM:65:LYS:HA	7:AM:66:LEU:HB2	1.50	0.94
52:BE:129:HIS:O	52:BE:130:GLY:O	1.86	0.94
17:AD:26:CYS:HA	17:AD:31:CYS:HB2	1.46	0.94
27:BN:58:ASP:O	27:BN:60:ILE:N	2.01	0.94
46:B5:50:GLY:O	46:B5:51:TYR:HD1	1.51	0.93
25:BA:243:U:OP1	49:B8:6:THR:HG21	1.68	0.93
39:BZ:19:ARG:NH1	39:BZ:84:GLU:O	2.01	0.93
25:BA:2200:C:OP2	41:B1:50:ARG:NH2	2.02	0.93
1:AA:159:G:N2	1:AA:162:A:OP2	2.00	0.93
23:AY:71:THR:HG22	23:AY:80:ASN:OD1	1.69	0.93
25:BA:1658:C:OP1	52:BE:132:HIS:CE1	2.22	0.93
1:AA:1277:C:HO2'	1:AA:1279:A:H8	1.16	0.93
39:BZ:18:LEU:HD12	39:BZ:18:LEU:H	1.31	0.92
25:BA:1779:U:H5	25:BA:1784:A:N7	1.66	0.92
25:BA:1494:A:N3	25:BA:1494:A:H3'	1.84	0.92
25:BA:807:U:OP2	29:BP:39:LYS:HG3	1.69	0.92
25:BA:141:A:C8	25:BA:1408:C:O2'	2.22	0.92
25:BA:271(G):C:O2'	41:B1:81:LYS:NZ	2.02	0.92
1:AA:1321:C:H3'	1:AA:1322:C:H5''	1.49	0.91
4:AJ:34:VAL:HG22	4:AJ:74:ILE:HG22	1.52	0.91
25:BA:1910:G:H1	25:BA:1920:C:H5	1.16	0.91
1:AA:1138:G:O2'	1:AA:1139:G:OP1	1.88	0.91
25:BA:1447:G:O2'	25:BA:1544:A:H8	1.52	0.91
39:BZ:9:TYR:CE1	39:BZ:61:LEU:HD12	2.04	0.91
34:BU:91:ASP:OD1	34:BU:96:ALA:N	2.04	0.91
43:BD:2:ALA:O	43:BD:3:VAL:HB	1.71	0.91
25:BA:259:G:H21	25:BA:621:A:H8	1.13	0.91
25:BA:1538:G:H2'	25:BA:1539:G:H8	1.35	0.90
25:BA:1570:A:O4'	43:BD:38:LYS:HE2	1.70	0.90
15:AB:178:ARG:HG2	15:AB:178:ARG:HH11	1.34	0.90
25:BA:2111:C:C2	25:BA:2147:G:N2	2.38	0.90
43:BD:43:ARG:NH1	43:BD:44:ASN:OD1	2.04	0.90
56:BK:77:LEU:HD12	56:BK:107:ILE:HG23	1.54	0.90
38:BY:76:CYS:SG	38:BY:77:PRO:HD2	2.12	0.90
38:BY:96:ILE:HD12	38:BY:99:CYS:SG	2.12	0.90
46:B5:4:HIS:HB3	46:B5:5:PRO:HD3	1.52	0.90
34:BU:90:VAL:O	34:BU:92:ARG:N	2.05	0.90

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
39:BZ:9:TYR:CZ	39:BZ:61:LEU:HD12	2.06	0.89
1:AA:353:A:H5'	1:AA:353:A:H8	1.34	0.89
16:AC:154:SER:OG	16:AC:155:GLY:N	1.95	0.89
25:BA:330:A:H2	25:BA:1210:A:H2'	1.37	0.89
31:BR:11:ASN:OD1	31:BR:12:ARG:N	2.05	0.89
14:AT:73:HIS:HB3	14:AT:74:LYS:HG2	1.54	0.89
55:BH:41:MET:SD	55:BH:42:ARG:N	2.45	0.89
17:AD:9:CYS:HA	17:AD:12:CYS:CB	2.02	0.89
25:BA:1496:A:H8	25:BA:1577:C:HO2'	0.92	0.89
47:B6:41:PRO:HD2	47:B6:46:HIS:H	1.36	0.89
25:BA:1155:A:OP2	34:BU:58:ARG:NH1	2.05	0.89
25:BA:2068:U:N3	25:BA:2430:A:H2	1.70	0.89
38:BY:8:LYS:HB2	38:BY:28:LYS:NZ	1.88	0.89
50:B9:27:CYS:SG	50:B9:32:HIS:CD2	2.66	0.89
46:B5:46:CYS:SG	46:B5:47:PRO:N	2.46	0.88
29:BP:64:LYS:C	29:BP:66:GLY:N	2.25	0.88
17:AD:31:CYS:O	17:AD:31:CYS:SG	2.32	0.88
47:B6:41:PRO:HD2	47:B6:46:HIS:N	1.87	0.88
25:BA:242:G:C5'	49:B8:62:LEU:HD13	2.03	0.88
25:BA:1143:A:OP1	27:BN:25:ARG:NH2	2.07	0.88
25:BA:2068:U:H3	25:BA:2430:A:H2	1.00	0.88
25:BA:2445:G:OP1	53:BF:74:ARG:NH2	2.07	0.88
33:BT:50:ILE:HD11	33:BT:102:ILE:HD11	1.56	0.88
25:BA:2139:C:O2'	25:BA:2140:C:OP2	1.92	0.87
25:BA:993:G:OP1	34:BU:50:ARG:NH2	2.08	0.87
25:BA:1899:G:H22	25:BA:1902:C:N4	1.72	0.87
1:AA:250:A:H4'	1:AA:251:G:O5'	1.74	0.87
46:B5:33:CYS:HB2	46:B5:40:LYS:HE3	1.54	0.86
27:BN:2:LYS:O	27:BN:4:TYR:CZ	2.27	0.86
6:AL:27:LEU:O	6:AL:29:GLY:N	2.07	0.86
11:AQ:66:SER:O	11:AQ:70:ARG:NH1	2.08	0.86
47:B6:47:THR:CG2	47:B6:48:VAL:H	1.88	0.86
1:AA:1004:A:O2'	1:AA:1038:C:O2	1.91	0.86
25:BA:2394:C:OP1	29:BP:63:PRO:CD	2.23	0.86
39:BZ:102:LEU:HD11	39:BZ:124:ILE:HG12	1.56	0.86
1:AA:748:C:H4'	1:AA:749:C:O5'	1.74	0.86
49:B8:61:LEU:HD12	49:B8:62:LEU:HD12	1.58	0.86
47:B6:16:CYS:O	47:B6:18:ARG:NH2	2.09	0.86
47:B6:41:PRO:CD	47:B6:46:HIS:H	1.88	0.86
43:BD:25:THR:O	43:BD:27:THR:N	2.08	0.86
25:BA:141:A:H8	25:BA:1408:C:O2'	1.59	0.85
1:AA:975:A:H4'	1:AA:976:G:H5"	1.59	0.85

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
55:BH:19:VAL:HG11	55:BH:43:VAL:O	1.77	0.85
1:AA:692:U:OP1	5:AK:124:LYS:NZ	2.08	0.85
25:BA:1689:A:H62	25:BA:1698:A:H2	1.24	0.85
42:B2:22:GLU:HG3	42:B2:64:LEU:HD11	1.57	0.85
50:B9:27:CYS:SG	50:B9:32:HIS:HD2	1.99	0.85
17:AD:2:GLY:O	17:AD:4:TYR:N	2.10	0.85
46:B5:50:GLY:O	46:B5:51:TYR:CD1	2.29	0.85
36:BW:64:MET:O	36:BW:65:LEU:HB2	1.75	0.85
25:BA:1914:C:HO2'	25:BA:1915:U:P	1.98	0.85
25:BA:1019:U:HO2'	25:BA:1021:A:H2	0.86	0.85
25:BA:271(H):G:H5'	41:B1:81:LYS:HE2	0.90	0.84
25:BA:1540:U:O2'	25:BA:1541:G:H5'	1.76	0.84
25:BA:2611:U:H6	25:BA:2611:U:H5'	1.42	0.84
29:BP:58:THR:O	29:BP:61:ARG:CZ	2.25	0.84
25:BA:528:A:C2	25:BA:2043:C:H4'	2.14	0.83
4:AJ:23:ILE:O	4:AJ:23:ILE:HG22	1.77	0.83
2:AV:27:G:H1	2:AV:43:C:H5	1.21	0.83
1:AA:508:C:OP2	17:AD:209:ARG:NH2	2.11	0.83
1:AA:1539:C:H2'	1:AA:1540:U:O4'	1.77	0.83
33:BT:78:LEU:O	33:BT:79:HIS:CG	2.30	0.83
1:AA:111:G:O6	1:AA:330:C:N4	2.12	0.83
38:BY:2:ARG:O	38:BY:4:LYS:N	2.10	0.83
33:BT:29:ARG:HB3	33:BT:30:VAL:HG22	1.59	0.83
38:BY:76:CYS:SG	38:BY:77:PRO:CD	2.67	0.83
29:BP:7:ARG:CD	53:BF:188:ARG:HA	2.08	0.82
25:BA:2187:G:H5'	25:BA:2188:C:OP2	1.79	0.82
13:AS:44:MET:N	13:AS:44:MET:SD	2.51	0.82
25:BA:1447:G:O2'	25:BA:1544:A:C8	2.30	0.82
23:AY:428:LEU:HD22	23:AY:451:ILE:HD11	1.61	0.82
1:AA:1054:C:O2'	1:AA:1055:A:H5''	1.79	0.82
17:AD:8:VAL:O	17:AD:10:ARG:N	2.13	0.82
1:AA:1189:C:OP1	4:AJ:51:ARG:NH2	2.11	0.82
17:AD:30:LYS:O	17:AD:32:ALA:N	2.13	0.82
43:BD:44:ASN:HB2	43:BD:48:ARG:O	1.79	0.81
9:AO:26:GLU:OE2	9:AO:77:ARG:NH1	2.12	0.81
25:BA:2305:A:C2	25:BA:2306:C:H1'	2.15	0.81
35:BV:64:HIS:ND1	35:BV:92:THR:HG22	1.94	0.81
25:BA:1022:G:H22	25:BA:1142(A):A:H2	1.24	0.81
25:BA:607:U:OP1	53:BF:102:PRO:HA	1.80	0.81
25:BA:714:U:O2'	25:BA:716:A:N7	2.12	0.81
38:BY:97:ARG:O	38:BY:98:VAL:HB	1.78	0.81
1:AA:1008:C:O2	1:AA:1021:G:N2	2.13	0.81

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:BP:6:LEU:HG	29:BP:8:PRO:O	1.81	0.81
29:BP:47:ASP:HB3	29:BP:48:PRO:O	1.81	0.81
25:BA:1980:G:O2'	25:BA:1982:C:OP2	1.98	0.81
25:BA:1169:G:N2	25:BA:1181:C:O2	2.14	0.81
16:AC:180:ALA:O	16:AC:205:GLY:O	1.99	0.80
38:BY:8:LYS:HB2	38:BY:28:LYS:CE	2.11	0.80
1:AA:1126:U:O2	1:AA:1280:A:H2'	1.80	0.80
1:AA:1054:C:O2	1:AA:1054:C:C3'	2.28	0.80
29:BP:58:THR:O	29:BP:61:ARG:NE	2.14	0.80
25:BA:1048:A:H4'	25:BA:1049:C:OP1	1.82	0.80
25:BA:1047:G:H4'	25:BA:1047:G:OP2	1.79	0.80
47:B6:20:ASN:O	47:B6:21:TYR:CG	2.35	0.80
25:BA:1782:C:H1'	25:BA:2609:U:H5''	1.64	0.80
38:BY:17:SER:OG	38:BY:18:GLY:N	2.09	0.80
25:BA:1093:G:H8	25:BA:1093:G:OP2	1.65	0.80
1:AA:1117:G:O3'	22:AI:104:ARG:HD3	1.82	0.80
6:AL:117:ARG:HD2	6:AL:122:THR:HG22	1.64	0.80
25:BA:1915:U:H5''	25:BA:1916:A:OP2	1.82	0.79
39:BZ:151:HIS:HB2	39:BZ:170:THR:HA	1.64	0.79
25:BA:1019:U:O2'	25:BA:1021:A:H2	1.64	0.79
26:BB:8:U:O3'	32:BS:25:ARG:NH2	2.15	0.79
25:BA:2517:C:O2'	25:BA:2542:A:N1	2.14	0.79
55:BH:41:MET:HE3	55:BH:43:VAL:HG13	1.65	0.79
29:BP:64:LYS:C	29:BP:66:GLY:H	1.85	0.79
25:BA:2808:U:O2	25:BA:2892:A:N6	2.16	0.78
57:BJ:26:ALA:HA	57:BJ:84:ALA:HA	1.65	0.78
1:AA:1134:G:C5	1:AA:1135:U:C5	2.71	0.78
15:AB:178:ARG:CG	15:AB:178:ARG:HH11	1.95	0.78
47:B6:12:GLU:HG3	47:B6:23:THR:HG22	1.64	0.78
25:BA:860:U:H5	25:BA:917:A:N7	1.82	0.78
25:BA:271(G):C:HO2'	41:B1:81:LYS:HE3	1.49	0.78
2:AV:76:A:C4'	2:AV:76:A:OP1	2.31	0.78
25:BA:662:G:OP1	29:BP:18:ARG:HD2	1.84	0.78
1:AA:1452:C:H4'	1:AA:1456:G:C2	2.19	0.78
25:BA:956:G:OP2	30:BQ:14:ARG:NH2	2.17	0.78
53:BF:24:LEU:HB3	53:BF:25:PRO:HD2	1.64	0.78
28:BO:4:PRO:O	28:BO:5:GLN:HB2	1.83	0.78
43:BD:44:ASN:HB3	43:BD:49:ILE:HA	1.66	0.77
55:BH:121:ILE:HD11	55:BH:140:LYS:HB3	1.66	0.77
25:BA:243:U:OP1	49:B8:6:THR:CG2	2.31	0.77
43:BD:44:ASN:CB	43:BD:49:ILE:HA	2.15	0.77
25:BA:1502:C:H5''	25:BA:1502:C:C6	2.20	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:AS:40:ILE:HG21	13:AS:62:ILE:HD11	1.66	0.77
25:BA:1022:G:N2	25:BA:1142(A):A:C2	2.50	0.77
23:AY:15:ILE:HA	23:AY:103:GLY:O	1.85	0.77
40:B0:23:VAL:HG22	40:B0:38:VAL:HG22	1.65	0.77
5:AK:84:VAL:HG11	5:AK:95:ILE:HD11	1.66	0.77
25:BA:881:G:N1	25:BA:895:U:O2	2.17	0.77
29:BP:84:ASN:HA	29:BP:115:LEU:O	1.84	0.77
35:BV:17:GLY:HA2	35:BV:96:ILE:O	1.84	0.77
25:BA:1539:G:C2'	25:BA:1540:U:H5''	2.15	0.77
33:BT:38:ASN:ND2	33:BT:40:THR:OG1	2.17	0.77
25:BA:2632:A:N3	52:BE:61:ARG:NH1	2.33	0.76
1:AA:1368:G:OP2	22:AI:112:LYS:HD3	1.85	0.76
1:AA:254:G:OP1	11:AQ:67:LYS:O	2.02	0.76
17:AD:8:VAL:C	17:AD:10:ARG:H	1.88	0.76
1:AA:426:G:OP1	17:AD:36:ARG:NH1	2.17	0.76
43:BD:181:GLU:HA	43:BD:272:ALA:HB3	1.68	0.76
25:BA:1300:U:H4'	25:BA:1301:A:H5'	1.68	0.76
52:BE:117:MET:O	52:BE:118:LYS:HB2	1.84	0.76
52:BE:57:LYS:HD3	52:BE:57:LYS:N	2.01	0.76
43:BD:137:PRO:O	43:BD:140:THR:OG1	2.03	0.76
25:BA:1063:G:N1	25:BA:1075:C:N4	2.34	0.76
55:BH:41:MET:CE	55:BH:43:VAL:HG13	2.16	0.76
43:BD:69:ARG:NH2	43:BD:128:GLY:O	2.19	0.76
23:AY:205:TYR:O	23:AY:209:ALA:N	2.18	0.76
35:BV:19:LYS:HG3	35:BV:20:LEU:N	1.99	0.76
33:BT:85:LYS:HB3	33:BT:85:LYS:HZ2	1.49	0.76
1:AA:353:A:C8	1:AA:353:A:H5'	2.20	0.76
46:B5:40:LYS:HE2	46:B5:46:CYS:HB3	1.66	0.75
25:BA:2287:A:N1	25:BA:2346:A:C2	2.54	0.75
25:BA:2392:A:H2	25:BA:2424:C:H42	1.31	0.75
1:AA:673:G:H2'	1:AA:674:G:C8	2.21	0.75
39:BZ:72:ARG:NH2	39:BZ:97:GLU:O	2.18	0.75
1:AA:632:A:H3'	1:AA:633:G:H5''	1.68	0.75
47:B6:48:VAL:O	47:B6:49:HIS:HB2	1.87	0.75
1:AA:1217:C:OP1	8:AN:9:LYS:NZ	2.19	0.75
25:BA:1089:G:H4'	25:BA:1090:U:OP1	1.85	0.75
15:AB:54:THR:HG21	15:AB:201:ILE:HD11	1.69	0.75
23:AY:437:THR:HB	23:AY:454:MET:HE3	1.66	0.75
25:BA:2420:C:P	49:B8:33:ASN:O	2.45	0.75
25:BA:1540:U:C6	25:BA:1540:U:H5'	2.15	0.74
15:AB:67:THR:HG21	15:AB:155:LEU:HD21	1.69	0.74
56:BK:30:HIS:HA	56:BK:59:ILE:HD12	1.69	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:AB:17:PHE:O	15:AB:18:GLY:O	2.06	0.74
11:AQ:95:TYR:HA	11:AQ:98:LEU:HD12	1.67	0.74
1:AA:1138:G:H1'	1:AA:1139:G:OP1	1.88	0.74
25:BA:2068:U:N3	25:BA:2430:A:C2	2.47	0.74
56:BK:99:ILE:HD12	56:BK:103:GLN:HB3	1.69	0.74
1:AA:390:C:O3'	10:AP:28:ARG:NH2	2.20	0.74
43:BD:210:GLY:O	43:BD:212:SER:N	2.20	0.74
49:B8:61:LEU:CD1	49:B8:62:LEU:HD12	2.17	0.74
2:AV:34:G:H2'	2:AV:35:A:H5''	1.69	0.74
25:BA:528:A:N1	25:BA:2042:A:H2'	2.03	0.74
53:BF:22:ALA:O	53:BF:26:ALA:HB2	1.87	0.74
6:AL:26:ALA:O	6:AL:27:LEU:O	2.05	0.74
25:BA:774:A:O2'	25:BA:775:G:OP2	2.04	0.74
4:AJ:8:LEU:HD23	4:AJ:96:ILE:HG22	1.70	0.74
33:BT:89:VAL:C	33:BT:91:ARG:H	1.91	0.74
55:BH:41:MET:SD	55:BH:53:GLU:O	2.46	0.74
38:BY:8:LYS:HB2	38:BY:28:LYS:HZ3	1.53	0.74
56:BK:106:GLU:HA	56:BK:109:LYS:HD3	1.68	0.74
39:BZ:151:HIS:CB	39:BZ:170:THR:HA	2.18	0.73
53:BF:167:ALA:HB1	53:BF:173:VAL:HG11	1.67	0.73
56:BK:100:THR:HA	56:BK:139:VAL:HB	1.68	0.73
9:AO:17:ARG:HH11	9:AO:17:ARG:HG3	1.54	0.73
41:B1:51:VAL:O	41:B1:57:GLU:O	2.06	0.73
23:AY:210:ARG:O	23:AY:212:TYR:N	2.18	0.73
25:BA:2849:U:OP2	33:BT:95:ARG:NH1	2.22	0.73
4:AJ:49:VAL:HG22	8:AN:41:ARG:HB2	1.69	0.73
25:BA:1091:G:O6	25:BA:1100:C:N4	2.15	0.73
31:BR:87:TYR:O	31:BR:89:ASP:N	2.22	0.73
25:BA:1899:G:N2	25:BA:1902:C:H5	1.86	0.73
6:AL:8:ASN:O	6:AL:12:ARG:HG3	1.89	0.73
52:BE:60:ASN:N	52:BE:60:ASN:HD22	1.85	0.73
25:BA:1899:G:N2	25:BA:1902:C:C5	2.57	0.72
23:AY:264:LEU:HB2	60:AY:702:GCP:C6	2.19	0.72
25:BA:1786:A:C2	25:BA:2606:C:H1'	2.24	0.72
1:AA:1446:U:O2'	1:AA:1447:A:H3'	1.89	0.72
25:BA:2079:U:OP1	41:B1:21:ARG:NH1	2.19	0.72
38:BY:74:PRO:O	38:BY:80:GLY:HA3	1.88	0.72
1:AA:1305:G:OP2	24:AU:2:GLY:N	2.22	0.72
25:BA:1064:C:H2'	25:BA:1065:U:O4'	1.89	0.72
43:BD:3:VAL:HG13	43:BD:17:THR:HB	1.70	0.72
2:AV:74:C:O2'	2:AV:75:C:OP2	2.06	0.72
25:BA:2810:A:H2'	52:BE:61:ARG:NH2	2.05	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
43:BD:10:THR:OG1	43:BD:13:ARG:HB2	1.89	0.72
33:BT:7:ILE:HG23	52:BE:181:LEU:HD21	1.72	0.72
29:BP:51:PHE:HB3	29:BP:52:GLU:OE2	1.89	0.71
27:BN:56:ASN:C	27:BN:57:ALA:O	2.27	0.71
25:BA:2137:C:C3'	25:BA:2137:C:O2	2.37	0.71
43:BD:25:THR:O	43:BD:26:LYS:C	2.28	0.71
9:AO:39:LEU:CD1	9:AO:56:LEU:HB2	2.20	0.71
23:AY:679:VAL:HB	23:AY:680:PRO:CD	2.20	0.71
15:AB:115:LEU:HD13	15:AB:145:LEU:HB3	1.71	0.71
25:BA:1899:G:N2	25:BA:1902:C:H41	1.85	0.71
33:BT:89:VAL:HG11	33:BT:91:ARG:HG3	1.72	0.71
38:BY:26:LYS:O	38:BY:27:VAL:O	2.07	0.71
39:BZ:10:ARG:NH2	39:BZ:26:GLY:O	2.23	0.71
54:BG:96:ARG:O	54:BG:99:MET:N	2.21	0.71
33:BT:23:ARG:O	33:BT:25:GLY:N	2.23	0.71
51:BC:131:LEU:HB3	51:BC:137:LEU:HD23	1.73	0.71
25:BA:2139:C:O2'	25:BA:2140:C:P	2.48	0.71
1:AA:633:G:H5''	1:AA:633:G:H8	1.56	0.71
56:BK:81:ALA:HB1	56:BK:99:ILE:HD11	1.73	0.71
56:BK:99:ILE:HG23	56:BK:103:GLN:HB2	1.72	0.71
25:BA:2180:U:C5'	25:BA:2180:U:C6	2.74	0.71
6:AL:53:ARG:HG2	6:AL:93:LEU:HD11	1.73	0.71
12:AR:22:VAL:O	12:AR:25:THR:HB	1.91	0.71
34:BU:92:ARG:NH1	34:BU:94:ASN:HD22	1.89	0.71
25:BA:1538:G:H2'	25:BA:1539:G:C8	2.25	0.71
34:BU:92:ARG:O	34:BU:94:ASN:N	2.24	0.71
25:BA:259:G:N2	25:BA:621:A:H8	1.86	0.71
53:BF:66:PRO:O	53:BF:67:GLN:CB	2.39	0.71
43:BD:13:ARG:HD2	43:BD:16:MET:HE3	1.73	0.70
25:BA:1396:U:H2'	25:BA:1396:U:O2	1.89	0.70
25:BA:1847:A:H2'	25:BA:1847:A:N3	2.06	0.70
1:AA:953:G:H5'	1:AA:965:A:H61	1.56	0.70
25:BA:1887:C:H2'	25:BA:1888:G:H5'	1.73	0.70
25:BA:613:G:H5''	25:BA:613:G:H8	1.56	0.70
25:BA:2317:C:H2'	25:BA:2318:G:H5'	1.72	0.70
25:BA:271(J):C:H5'	25:BA:271(K):U:OP2	1.90	0.70
51:BC:42:GLU:CG	51:BC:215:THR:HG23	2.21	0.70
25:BA:662:G:OP1	29:BP:18:ARG:NH1	2.24	0.70
23:AY:25:LYS:NZ	60:AY:702:GCP:O3G	2.25	0.70
42:B2:42:GLY:O	42:B2:44:LEU:N	2.25	0.70
1:AA:1144:G:O2'	1:AA:1145:C:H5'	1.92	0.70
1:AA:1533:C:H2'	1:AA:1534:A:O4'	1.92	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:330:A:C2	25:BA:1210:A:H2'	2.25	0.70
13:AS:42:PRO:O	13:AS:44:MET:SD	2.50	0.70
23:AY:212:TYR:HA	23:AY:215:LYS:HB3	1.72	0.70
25:BA:943:U:OP2	29:BP:38:GLN:CD	2.30	0.70
33:BT:16:ARG:NH2	33:BT:82:LEU:O	2.21	0.70
2:AV:33:U:H5	2:AV:36:A:OP2	1.75	0.70
25:BA:2317:C:C2'	25:BA:2318:G:H5'	2.22	0.69
1:AA:1136:U:H3'	1:AA:1137:C:H5''	1.74	0.69
47:B6:41:PRO:HD3	47:B6:46:HIS:HA	1.74	0.69
1:AA:975:A:H8	1:AA:975:A:H5'	1.56	0.69
25:BA:1079:C:H41	25:BA:1088:A:H5''	1.56	0.69
25:BA:2683:C:OP1	33:BT:53:ARG:NH2	2.25	0.69
47:B6:47:THR:HG23	47:B6:48:VAL:H	1.54	0.69
14:AT:73:HIS:O	14:AT:76:ALA:HB3	1.92	0.69
25:BA:1092:C:H2'	25:BA:1093:G:H5'	1.75	0.69
1:AA:1133:G:C8	1:AA:1133:G:H3'	2.27	0.69
1:AA:1392:G:N2	1:AA:1502:A:H8	1.90	0.69
23:AY:162:VAL:HG21	23:AY:255:ILE:HG12	1.74	0.69
51:BC:185:LEU:O	51:BC:188:ASN:N	2.25	0.69
23:AY:61:ARG:NH2	23:AY:460:GLU:OE2	2.25	0.69
29:BP:47:ASP:HB3	29:BP:48:PRO:C	2.13	0.69
10:AP:8:ARG:HG2	10:AP:8:ARG:HH11	1.58	0.69
25:BA:2646:C:OP2	25:BA:2732:G:O2'	2.08	0.69
25:BA:1100:C:C5'	25:BA:1100:C:H6	2.06	0.69
37:BX:11:PRO:HB3	37:BX:92:LEU:HD21	1.75	0.69
1:AA:460:G:O6	1:AA:470:C:H5'	1.93	0.69
45:B4:60:GLU:O	54:BG:113:ARG:NH2	2.26	0.69
1:AA:979:C:H2'	1:AA:980:C:H5'	1.73	0.69
25:BA:2167:U:H3	25:BA:2171:A:H2	1.41	0.69
23:AY:19:ALA:HB3	23:AY:25:LYS:HE3	1.75	0.69
7:AM:90:LEU:O	7:AM:92:HIS:N	2.26	0.69
29:BP:7:ARG:HB2	29:BP:8:PRO:HD2	1.75	0.69
27:BN:2:LYS:O	27:BN:4:TYR:CE1	2.45	0.69
25:BA:1918:A:HO2'	25:BA:1919:A:H2	1.38	0.69
25:BA:587:C:OP2	29:BP:33:ARG:NH2	2.26	0.69
1:AA:62:U:H2'	1:AA:63:C:H5''	1.75	0.68
1:AA:1138:G:C2'	1:AA:1139:G:OP1	2.41	0.68
46:B5:46:CYS:SG	46:B5:47:PRO:CD	2.81	0.68
25:BA:1093:G:C8	25:BA:1093:G:OP2	2.46	0.68
26:BB:50:G:OP1	32:BS:63:THR:HG23	1.93	0.68
15:AB:195:ASP:O	21:AH:68:ARG:NH2	2.26	0.68
51:BC:42:GLU:HG3	51:BC:215:THR:HG23	1.75	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2476:A:N1	25:BA:2477:C:C6	2.61	0.68
40:B0:43:THR:O	40:B0:43:THR:HG23	1.91	0.68
1:AA:1293:G:H8	1:AA:1293:G:H5''	1.58	0.68
2:AV:34:G:C2'	2:AV:35:A:H5''	2.23	0.68
15:AB:88:ALA:HB2	15:AB:219:VAL:HG13	1.75	0.68
27:BN:46:VAL:O	27:BN:47:ALA:HB3	1.92	0.68
25:BA:1496:A:H8	25:BA:1577:C:O2'	1.71	0.68
5:AK:61:ALA:HB1	5:AK:94:ALA:HB2	1.76	0.68
55:BH:175:LYS:N	55:BH:176:ALA:HB2	2.08	0.68
1:AA:1243:C:OP2	24:AU:10:ARG:NH2	2.27	0.68
52:BE:64:LYS:O	52:BE:73:GLU:OE1	2.11	0.68
25:BA:1266:G:O5'	36:BW:15:ARG:NH2	2.26	0.68
52:BE:129:HIS:O	52:BE:130:GLY:C	2.31	0.68
56:BK:4:VAL:HG12	56:BK:5:VAL:H	1.59	0.68
27:BN:3:THR:O	27:BN:5:VAL:HG12	1.93	0.68
1:AA:530:G:O2'	1:AA:531:U:OP1	2.10	0.68
25:BA:9:U:C5	25:BA:2629:A:N6	2.62	0.68
29:BP:51:PHE:CB	29:BP:52:GLU:HG2	2.24	0.68
2:AV:73:A:H2'	2:AV:74:C:H5'	1.76	0.68
25:BA:847:U:OP2	25:BA:928:G:O6	2.11	0.68
55:BH:89:ILE:C	55:BH:89:ILE:HD12	2.15	0.68
29:BP:16:ARG:HD3	29:BP:16:ARG:C	2.14	0.68
25:BA:1502:C:H5''	25:BA:1502:C:H6	1.56	0.68
14:AT:73:HIS:CB	14:AT:74:LYS:HG2	2.23	0.67
33:BT:30:VAL:HG21	33:BT:84:GLN:HG3	1.74	0.67
25:BA:684:G:OP1	48:B7:16:HIS:HD2	1.76	0.67
25:BA:271(H):G:C4'	41:B1:81:LYS:HE2	2.25	0.67
35:BV:47:VAL:O	35:BV:49:THR:O	2.12	0.67
38:BY:7:VAL:HB	38:BY:8:LYS:CE	2.24	0.67
25:BA:2287:A:N1	25:BA:2346:A:H2	1.92	0.67
56:BK:57:ILE:HA	56:BK:66:THR:O	1.94	0.67
1:AA:17:U:H2'	1:AA:18:C:C6	2.28	0.67
7:AM:97:PRO:HA	7:AM:110:ARG:HD3	1.76	0.67
25:BA:2632:A:O2'	52:BE:61:ARG:NH2	2.27	0.67
23:AY:255:ILE:HG23	23:AY:257:PRO:HD3	1.77	0.67
7:AM:89:GLY:C	7:AM:90:LEU:O	2.31	0.67
38:BY:39:VAL:HG12	38:BY:40:GLU:H	1.59	0.67
29:BP:9:ASN:HA	29:BP:11:GLY:H	1.60	0.67
25:BA:2506:U:C6	25:BA:2506:U:H5'	2.30	0.67
25:BA:517:C:OP1	46:B5:16:ARG:NH2	2.28	0.67
57:BJ:34:ALA:HA	57:BJ:37:ALA:HB3	1.75	0.67
1:AA:100:C:H2'	1:AA:101:A:C8	2.29	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AY:404:VAL:CG1	23:AY:405:PRO:HA	2.15	0.67
1:AA:1138:G:C1'	1:AA:1139:G:OP1	2.42	0.67
25:BA:2439:A:C8	25:BA:2439:A:H5'	2.29	0.67
25:BA:1076:C:O2'	25:BA:1077:A:O5'	2.12	0.67
54:BG:54:GLU:HA	54:BG:57:ALA:HB3	1.77	0.67
23:AY:94:VAL:O	23:AY:96:ARG:N	2.28	0.67
51:BC:66:HIS:CD2	51:BC:184:LYS:HG3	2.30	0.67
25:BA:1053:C:H2'	25:BA:1054:A:H5''	1.75	0.67
34:BU:65:ILE:HD11	34:BU:93:LYS:HA	1.76	0.67
35:BV:21:ARG:O	35:BV:22:VAL:HG13	1.95	0.67
36:BW:73:ALA:HB3	36:BW:106:ILE:HG12	1.75	0.67
25:BA:142:A:H8	25:BA:1595:G:H21	1.44	0.66
25:BA:1858:G:O2'	25:BA:1883:G:N2	2.26	0.66
26:BB:20:C:H2'	26:BB:21:G:H5'	1.75	0.66
56:BK:6:ALA:HB3	56:BK:59:ILE:HG22	1.77	0.66
25:BA:2850:A:OP2	25:BA:2866:U:H5	1.77	0.66
25:BA:2681:C:H5	25:BA:2725:A:H62	1.41	0.66
16:AC:154:SER:O	16:AC:157:ILE:HD11	1.95	0.66
1:AA:376:G:OP2	10:AP:67:THR:HG21	1.95	0.66
17:AD:10:ARG:CG	17:AD:10:ARG:O	2.43	0.66
39:BZ:18:LEU:CD1	39:BZ:18:LEU:H	2.08	0.66
23:AY:357:ARG:NH1	23:AY:373:ASP:OD2	2.28	0.66
25:BA:943:U:OP2	29:BP:38:GLN:NE2	2.29	0.66
55:BH:41:MET:HE2	55:BH:52:VAL:HA	1.78	0.66
53:BF:65:TRP:CZ3	53:BF:73:ALA:O	2.49	0.66
1:AA:1143:G:H5''	1:AA:1144:G:OP2	1.94	0.66
56:BK:75:SER:O	56:BK:79:ARG:HG3	1.96	0.66
1:AA:1101:A:H4'	1:AA:1102:A:O5'	1.96	0.66
25:BA:1019:U:H3	25:BA:1142(A):A:H62	1.44	0.66
30:BQ:82:ARG:HH22	40:B0:2:ALA:HB1	1.61	0.66
27:BN:126:PRO:O	27:BN:127:ASP:O	2.13	0.66
38:BY:39:VAL:C	38:BY:40:GLU:OE1	2.34	0.66
15:AB:33:TYR:HB3	15:AB:41:ILE:HG22	1.78	0.66
25:BA:1779:U:C5	25:BA:1784:A:N7	2.57	0.66
15:AB:67:THR:HG21	15:AB:155:LEU:CD2	2.26	0.66
25:BA:1887:C:C2'	25:BA:1888:G:H5'	2.25	0.66
55:BH:83:TYR:HB3	55:BH:134:SER:HA	1.78	0.66
25:BA:661:C:O2'	29:BP:16:ARG:O	2.10	0.65
33:BT:28:VAL:HG12	33:BT:29:ARG:HD3	1.77	0.65
36:BW:5:ALA:HB3	36:BW:50:VAL:HG23	1.76	0.65
56:BK:17:ALA:HB3	56:BK:38:VAL:HG22	1.78	0.65
29:BP:51:PHE:O	29:BP:52:GLU:HB2	1.95	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:B5:51:TYR:HB3	46:B5:52:TYR:O	1.97	0.65
1:AA:975:A:C8	1:AA:975:A:H5'	2.31	0.65
14:AT:100:ILE:O	14:AT:102:GLY:N	2.29	0.65
25:BA:252:G:OP2	29:BP:50:ARG:NH1	2.24	0.65
43:BD:70:TRP:CH2	43:BD:150:LYS:HA	2.31	0.65
29:BP:7:ARG:HB2	29:BP:8:PRO:CD	2.27	0.65
33:BT:50:ILE:CD1	33:BT:102:ILE:HD11	2.27	0.65
39:BZ:94:GLU:O	39:BZ:130:PRO:HD3	1.97	0.65
1:AA:328:C:O2	1:AA:328:C:H2'	1.97	0.65
25:BA:71:A:C8	25:BA:71:A:H5'	2.31	0.65
15:AB:28:PHE:CD1	15:AB:190:THR:HA	2.31	0.65
17:AD:25:ARG:C	17:AD:27:TYR:H	2.00	0.65
47:B6:41:PRO:CD	47:B6:46:HIS:N	2.55	0.65
15:AB:17:PHE:HB3	15:AB:44:LEU:HD21	1.78	0.65
33:BT:54:ARG:HA	33:BT:59:THR:HB	1.79	0.65
1:AA:1149:C:OP1	22:AI:9:ARG:NH1	2.26	0.65
49:B8:63:PRO:O	49:B8:64:TYR:O	2.12	0.65
29:BP:55:ARG:HG2	29:BP:56:SER:H	1.60	0.65
47:B6:19:ARG:HG3	47:B6:20:ASN:N	2.09	0.65
25:BA:1046:A:N7	57:BJ:5:ALA:HB3	2.11	0.65
53:BF:66:PRO:O	53:BF:67:GLN:HB3	1.97	0.65
14:AT:53:LEU:HB2	14:AT:100:ILE:CG2	2.27	0.65
25:BA:1962:C:O2'	25:BA:1964:G:OP2	2.12	0.65
47:B6:20:ASN:C	47:B6:21:TYR:CG	2.69	0.65
1:AA:1305:G:N2	1:AA:1331:G:H1'	2.12	0.65
1:AA:1307:U:OP1	7:AM:101:GLN:OE1	2.14	0.65
12:AR:32:ARG:HA	12:AR:69:THR:HG21	1.77	0.65
22:AI:17:VAL:HG22	22:AI:63:ILE:HG12	1.77	0.65
23:AY:10:LYS:N	23:AY:282:SER:HG	1.95	0.65
25:BA:2602:A:H4'	25:BA:2602:A:OP2	1.96	0.65
25:BA:1956:U:H1'	25:BA:2552:U:OP1	1.96	0.65
33:BT:13:ARG:NH1	33:BT:13:ARG:HA	2.11	0.65
4:AJ:16:LEU:HD13	4:AJ:70:ARG:HG2	1.79	0.65
25:BA:1899:G:H21	25:BA:1902:C:H5	1.45	0.65
1:AA:1004:A:OP1	1:AA:1024:G:N2	2.30	0.65
52:BE:132:HIS:CD2	52:BE:135:HIS:CE1	2.84	0.65
25:BA:1141:U:OP2	27:BN:63:THR:OG1	2.15	0.65
25:BA:2787:C:O2	52:BE:61:ARG:NH1	2.30	0.65
25:BA:2420:C:OP2	49:B8:33:ASN:O	2.15	0.65
25:BA:896:A:C8	39:BZ:146:ILE:HD13	2.32	0.65
52:BE:1:MET:HB3	52:BE:200:GLU:OE1	1.96	0.65
42:B2:47:ASN:O	42:B2:49:LYS:N	2.30	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BT:78:LEU:O	33:BT:79:HIS:ND1	2.30	0.64
23:AY:603:GLU:O	23:AY:605:ILE:HD12	1.96	0.64
12:AR:26:LEU:O	19:AF:100:ASN:ND2	2.30	0.64
53:BF:28:ILE:HD13	53:BF:28:ILE:H	1.62	0.64
47:B6:11:LEU:HD22	47:B6:12:GLU:N	2.11	0.64
25:BA:548:A:O2'	25:BA:549:G:OP1	2.13	0.64
23:AY:122:TRP:CD2	23:AY:157:LEU:HD12	2.33	0.64
43:BD:24:ILE:O	43:BD:26:LYS:N	2.31	0.64
1:AA:975:A:H4'	1:AA:976:G:C5'	2.26	0.64
33:BT:27:THR:O	33:BT:28:VAL:HG23	1.98	0.64
25:BA:9:U:C4	25:BA:2629:A:N6	2.65	0.64
25:BA:1058:G:H21	56:BK:126:MET:HE3	1.61	0.64
29:BP:85:LEU:HD23	29:BP:85:LEU:H	1.62	0.64
8:AN:23:ARG:CD	8:AN:28:GLY:O	2.43	0.64
25:BA:250:G:P	49:B8:13:ARG:HH22	2.21	0.64
25:BA:860:U:C5	25:BA:917:A:N7	2.65	0.64
23:AY:437:THR:HB	23:AY:454:MET:CE	2.27	0.64
1:AA:1464:G:OP2	33:BT:111:ARG:NH2	2.31	0.64
1:AA:1013:G:N2	1:AA:1015:A:H3'	2.12	0.64
25:BA:118:A:N3	25:BA:178:G:H1'	2.12	0.64
56:BK:42:ASN:O	56:BK:46:ALA:HB2	1.98	0.64
25:BA:1100:C:C5'	25:BA:1100:C:C6	2.81	0.64
1:AA:542:G:OP1	17:AD:10:ARG:NH2	2.29	0.64
43:BD:11:PRO:O	43:BD:13:ARG:N	2.29	0.64
1:AA:36:C:O2'	1:AA:501:C:OP1	2.12	0.64
54:BG:124:SER:HB2	54:BG:131:TYR:CE1	2.33	0.64
1:AA:737:A:H1'	19:AF:73:ASN:OD1	1.98	0.64
27:BN:3:THR:O	27:BN:5:VAL:N	2.31	0.64
28:BO:88:ASN:C	28:BO:88:ASN:HD22	2.01	0.64
51:BC:119:VAL:HB	51:BC:123:VAL:HG23	1.79	0.64
23:AY:272:LEU:O	23:AY:276:VAL:HG23	1.97	0.64
52:BE:77:ILE:HG22	52:BE:78:LEU:H	1.62	0.64
15:AB:97:TRP:CZ3	15:AB:176:GLU:OE2	2.50	0.64
25:BA:1458:C:H4'	25:BA:1459:G:O5'	1.97	0.64
30:BQ:12:GLN:HG2	30:BQ:73:PRO:HD2	1.80	0.64
29:BP:136:GLU:O	29:BP:139:LYS:N	2.31	0.64
32:BS:52:SER:HB2	32:BS:55:ALA:HB3	1.79	0.64
52:BE:70:ALA:O	52:BE:72:VAL:N	2.31	0.63
33:BT:85:LYS:HB3	33:BT:85:LYS:HZ3	1.63	0.63
4:AJ:23:ILE:O	4:AJ:23:ILE:CG2	2.46	0.63
1:AA:1323:G:H2'	1:AA:1324:A:C8	2.33	0.63
25:BA:1538:G:C4	25:BA:1539:G:C8	2.87	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BT:27:THR:HA	33:BT:87:ASP:HB2	1.81	0.63
13:AS:40:ILE:CG2	13:AS:62:ILE:HD11	2.28	0.63
25:BA:2611:U:H5'	25:BA:2611:U:C6	2.31	0.63
41:B1:52:ARG:O	41:B1:56:GLN:O	2.15	0.63
43:BD:223:GLY:C	43:BD:224:ALA:O	2.33	0.63
1:AA:472:A:H2'	1:AA:473:G:O4'	1.99	0.63
33:BT:28:VAL:O	33:BT:29:ARG:CB	2.45	0.63
1:AA:974:A:OP2	8:AN:41:ARG:NH1	2.32	0.63
47:B6:26:ASN:ND2	47:B6:32:ASN:OD1	2.32	0.63
34:BU:88:ILE:HD13	34:BU:109:LEU:HD22	1.81	0.63
14:AT:36:LEU:HD12	14:AT:55:ILE:HG23	1.80	0.63
25:BA:90:U:O2'	25:BA:92:A:P	2.57	0.63
25:BA:1407:C:C6	25:BA:1407:C:H5''	2.32	0.63
43:BD:27:THR:CG2	43:BD:83:GLU:HB3	2.28	0.63
25:BA:2517:C:O2'	25:BA:2542:A:C2	2.48	0.63
26:BB:45:A:OP2	54:BG:96:ARG:NH2	2.32	0.63
33:BT:93:ARG:HH11	33:BT:93:ARG:HG3	1.63	0.63
1:AA:1075:C:OP1	15:AB:179:LYS:NZ	2.26	0.63
47:B6:40:CYS:HG	47:B6:45:LYS:NZ	0.95	0.63
25:BA:1494:A:H2'	25:BA:1495:A:H5''	1.81	0.63
33:BT:89:VAL:CG1	33:BT:91:ARG:HG3	2.28	0.63
23:AY:616:TYR:OH	23:AY:666:ARG:NH1	2.32	0.63
1:AA:509:A:H5'	17:AD:55:ALA:HB2	1.79	0.63
17:AD:11:LEU:C	17:AD:13:ARG:N	2.51	0.63
25:BA:1539:G:C3'	25:BA:1540:U:H5''	2.29	0.62
1:AA:1452:C:H4'	1:AA:1456:G:N2	2.13	0.62
53:BF:24:LEU:O	53:BF:26:ALA:N	2.32	0.62
28:BO:4:PRO:O	28:BO:5:GLN:CB	2.47	0.62
1:AA:452:A:HO2'	1:AA:453:A:H8	1.47	0.62
43:BD:27:THR:HG21	43:BD:83:GLU:OE2	1.99	0.62
53:BF:133:ASN:HA	53:BF:162:LEU:HD23	1.80	0.62
47:B6:28:ARG:HA	47:B6:32:ASN:HB3	1.80	0.62
4:AJ:85:LEU:O	4:AJ:87:THR:N	2.32	0.62
52:BE:87:GLU:O	52:BE:89:ASP:N	2.31	0.62
25:BA:1332:G:N2	25:BA:1610:A:H8	1.96	0.62
25:BA:2849:U:O4	33:BT:23:ARG:NH2	2.30	0.62
25:BA:2850:A:OP2	25:BA:2866:U:C5	2.52	0.62
23:AY:153:MET:HA	23:AY:157:LEU:HD21	1.80	0.62
25:BA:1403:C:H5''	25:BA:1471:A:H1'	1.80	0.62
25:BA:2180:U:H5''	25:BA:2180:U:C6	2.34	0.62
51:BC:119:VAL:O	51:BC:121:GLY:N	2.33	0.62
1:AA:1401:G:C2	1:AA:1402:C:H1'	2.33	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:AP:20:VAL:HG21	10:AP:32:TYR:CD1	2.34	0.62
25:BA:1906:G:H2'	25:BA:1907:G:O4'	2.00	0.62
25:BA:252:G:P	29:BP:50:ARG:HH11	2.23	0.62
26:BB:77:U:OP1	39:BZ:19:ARG:NH2	2.32	0.62
25:BA:806:C:P	29:BP:39:LYS:HB3	2.40	0.62
13:AS:5:LEU:HG	13:AS:10:PHE:HD1	1.65	0.62
25:BA:2296:U:H4'	25:BA:2297:C:OP1	1.98	0.62
27:BN:131:GLN:HA	27:BN:131:GLN:OE1	1.99	0.62
1:AA:1305:G:H5''	24:AU:4:GLY:HA3	1.82	0.62
25:BA:140:G:N3	25:BA:142:A:N1	2.47	0.62
25:BA:27:G:O2'	25:BA:28:A:OP2	2.16	0.62
29:BP:107:LYS:O	29:BP:109:GLY:N	2.28	0.62
54:BG:57:ALA:HA	54:BG:90:LEU:HD21	1.81	0.62
25:BA:1040:C:O2'	25:BA:1041:C:OP2	2.15	0.62
38:BY:55:TYR:O	38:BY:57:GLN:O	2.17	0.62
14:AT:38:LYS:O	14:AT:41:ILE:HG12	2.00	0.62
33:BT:30:VAL:CG2	33:BT:84:GLN:O	2.48	0.62
6:AL:115:LYS:O	6:AL:117:ARG:N	2.32	0.62
23:AY:683:VAL:O	23:AY:686:LYS:N	2.32	0.62
29:BP:146:VAL:HG13	29:BP:147:LEU:N	2.14	0.62
25:BA:271(H):G:H4'	41:B1:81:LYS:HG2	1.82	0.62
29:BP:24:GLY:O	29:BP:25:SER:HB3	1.99	0.62
58:BL:67:UNK:O	58:BL:69:UNK:N	2.33	0.62
25:BA:2734:A:H5'	25:BA:2735:G:OP2	2.00	0.62
7:AM:14:ARG:NH2	7:AM:16:ASP:OD2	2.32	0.62
34:BU:90:VAL:O	34:BU:91:ASP:C	2.37	0.61
1:AA:1057:G:H5''	16:AC:154:SER:HB2	1.81	0.61
16:AC:154:SER:HG	16:AC:155:GLY:H	1.46	0.61
1:AA:460:G:C6	1:AA:470:C:H5''	2.35	0.61
2:AV:72:C:H3'	2:AV:72:C:C6	2.35	0.61
1:AA:1435:G:H2'	1:AA:1436:U:C6	2.34	0.61
1:AA:680:C:O2'	43:BD:166:GLN:HG3	2.00	0.61
17:AD:189:PRO:HB2	17:AD:194:LEU:HD21	1.80	0.61
25:BA:2419:U:O4	49:B8:30:ARG:NH2	2.32	0.61
55:BH:144:VAL:O	55:BH:148:ILE:HG12	2.00	0.61
25:BA:2801:A:N3	25:BA:2801:A:H2'	2.14	0.61
27:BN:90:MET:O	27:BN:93:THR:O	2.18	0.61
38:BY:73:ARG:NH2	38:BY:81:LYS:HA	2.14	0.61
34:BU:95:LEU:O	34:BU:98:LEU:HG	1.99	0.61
25:BA:2476:A:N1	25:BA:2477:C:C5	2.69	0.61
55:BH:89:ILE:HD11	55:BH:94:TYR:O	1.99	0.61
25:BA:2602:A:H2'	25:BA:2602:A:N3	2.15	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
53:BF:132:VAL:O	53:BF:138:GLU:OE1	2.18	0.61
36:BW:60:ASN:OD1	36:BW:61:ASN:ND2	2.33	0.61
1:AA:967:C:H4'	22:AI:125:TYR:HE1	1.65	0.61
25:BA:1246:A:OP1	29:BP:16:ARG:NH2	2.33	0.61
46:B5:46:CYS:SG	46:B5:47:PRO:HD2	2.39	0.61
33:BT:13:ARG:CZ	33:BT:13:ARG:HA	2.30	0.61
4:AJ:5:ARG:HD3	4:AJ:73:ASP:OD1	2.01	0.61
29:BP:112:LEU:CD1	29:BP:114:ILE:HG22	2.30	0.61
25:BA:2163:C:O2	25:BA:2163:C:O4'	2.15	0.61
45:B4:62:CYS:SG	45:B4:63:SER:N	2.73	0.61
23:AY:683:VAL:HG23	23:AY:684:GLN:H	1.62	0.61
1:AA:1136:U:H3'	1:AA:1137:C:C5'	2.31	0.61
25:BA:910:A:H62	30:BQ:12:GLN:HA	1.65	0.61
38:BY:97:ARG:O	38:BY:98:VAL:CB	2.47	0.61
43:BD:209:ALA:C	43:BD:210:GLY:O	2.37	0.61
2:AV:73:A:C2'	2:AV:74:C:H5'	2.30	0.61
23:AY:230:LYS:HG2	23:AY:235:GLU:O	2.00	0.61
25:BA:996:A:O2'	34:BU:92:ARG:HG3	2.01	0.61
1:AA:1158:C:O2'	1:AA:1160:G:OP1	2.17	0.61
23:AY:354:ARG:HG2	23:AY:378:VAL:HG22	1.83	0.61
47:B6:9:LEU:O	47:B6:25:LYS:HB2	2.00	0.61
25:BA:1332:G:H8	25:BA:1332:G:H5'	1.66	0.61
26:BB:105:A:H2'	26:BB:106:G:O4'	2.01	0.61
42:B2:38:GLN:HB3	42:B2:44:LEU:HB3	1.82	0.61
25:BA:1952:A:OP1	28:BO:44:LYS:NZ	2.30	0.61
18:AE:9:LYS:HB2	18:AE:112:LEU:HD11	1.83	0.61
17:AD:30:LYS:C	17:AD:32:ALA:H	2.03	0.61
42:B2:43:GLN:O	42:B2:44:LEU:HB2	2.00	0.61
25:BA:2168:G:H22	25:BA:2171:A:H5'	1.65	0.61
7:AM:88:ARG:HG3	7:AM:98:VAL:HG13	1.83	0.61
1:AA:889:A:H4'	1:AA:890:G:OP1	2.00	0.61
1:AA:580:U:H2'	1:AA:581:G:O4'	2.01	0.61
25:BA:1915:U:C5'	25:BA:1916:A:OP2	2.48	0.60
25:BA:2179:C:O2'	25:BA:2180:U:OP2	2.17	0.60
23:AY:409:ILE:HG12	23:AY:656:ALA:HB3	1.82	0.60
25:BA:1263:U:H1'	46:B5:10:LYS:HG3	1.83	0.60
39:BZ:45:ASP:OD2	39:BZ:49:ARG:HD2	2.00	0.60
20:AG:120:ILE:O	20:AG:124:LEU:HG	2.00	0.60
25:BA:607:U:N3	25:BA:621:A:C2	2.63	0.60
22:AI:118:LYS:O	22:AI:119:ALA:HB3	2.00	0.60
25:BA:2019:A:N7	46:B5:9:LYS:HE3	2.16	0.60
31:BR:102:GLU:OE1	36:BW:37:ARG:NH1	2.34	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:AM:65:LYS:HA	7:AM:66:LEU:CB	2.30	0.60
25:BA:1495:A:N3	25:BA:1495:A:H2'	2.15	0.60
35:BV:49:THR:HB	35:BV:50:PRO:CD	2.31	0.60
25:BA:860:U:O4'	25:BA:860:U:O2	2.14	0.60
30:BQ:134:ARG:HA	30:BQ:137:TYR:CD1	2.36	0.60
20:AG:5:ARG:NH1	20:AG:5:ARG:HB2	2.15	0.60
25:BA:652:C:O2	25:BA:652:C:C2'	2.48	0.60
4:AJ:58:ASP:O	4:AJ:59:SER:C	2.40	0.60
18:AE:10:MET:SD	18:AE:13:ILE:HG13	2.41	0.60
25:BA:1100:C:H5''	25:BA:1100:C:H6	1.66	0.60
1:AA:1277:C:O2'	1:AA:1279:A:H8	1.82	0.60
25:BA:996:A:H4'	34:BU:92:ARG:NE	2.16	0.60
47:B6:20:ASN:O	47:B6:21:TYR:CD2	2.53	0.60
25:BA:2140:C:O4'	25:BA:2140:C:O2	2.18	0.60
17:AD:10:ARG:HG2	17:AD:10:ARG:O	1.99	0.60
25:BA:1504:C:O2'	25:BA:1505:C:P	2.59	0.60
32:BS:14:VAL:HG12	32:BS:15:ARG:N	2.15	0.60
14:AT:104:LEU:C	14:AT:104:LEU:HD23	2.22	0.60
29:BP:51:PHE:HB2	29:BP:52:GLU:HG2	1.84	0.60
26:BB:20:C:C2'	26:BB:21:G:H5'	2.31	0.60
25:BA:2406:U:H2'	25:BA:2406:U:OP2	2.01	0.60
26:BB:2:C:H2'	26:BB:2:C:O2	2.02	0.60
49:B8:32:LEU:HB3	49:B8:36:LYS:NZ	2.17	0.60
33:BT:89:VAL:HG21	33:BT:91:ARG:NE	2.17	0.60
43:BD:224:ALA:O	43:BD:225:ALA:HB3	2.00	0.60
25:BA:2585:U:O4'	25:BA:2585:U:O2	2.19	0.60
1:AA:976:G:OP2	1:AA:1358:U:O2'	2.18	0.60
25:BA:2690:C:OP2	31:BR:14:SER:HB2	2.02	0.60
25:BA:483:A:H5''	38:BY:49:VAL:HG22	1.84	0.60
30:BQ:27:VAL:O	30:BQ:28:ALA:HB3	2.01	0.60
1:AA:1118:C:OP1	22:AI:104:ARG:HD2	2.01	0.60
25:BA:2681:C:H5	25:BA:2725:A:N6	2.00	0.60
15:AB:97:TRP:HZ3	15:AB:176:GLU:OE2	1.85	0.60
43:BD:270:ILE:C	43:BD:271:ILE:HG13	2.21	0.60
43:BD:34:VAL:O	43:BD:64:ILE:HG23	2.01	0.60
25:BA:994:C:OP1	34:BU:53:ARG:NH2	2.35	0.60
25:BA:900:A:OP1	25:BA:900:A:H4'	2.02	0.60
28:BO:76:ALA:HB3	33:BT:75:ILE:HD12	1.82	0.60
6:AL:24:VAL:O	6:AL:24:VAL:HG12	2.02	0.60
16:AC:36:ASP:OD2	16:AC:59:ARG:NH2	2.34	0.60
1:AA:149:A:O2'	1:AA:150:C:C6	2.55	0.60
25:BA:1169:G:N2	25:BA:1181:C:C2	2.70	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AY:681:LYS:C	23:AY:684:GLN:HE22	2.05	0.60
32:BS:104:GLY:O	32:BS:106:ARG:N	2.29	0.60
4:AJ:30:SER:HB2	4:AJ:81:THR:OG1	2.01	0.60
9:AO:70:LEU:HD23	9:AO:78:TYR:HA	1.84	0.60
1:AA:116:A:C8	1:AA:116:A:OP2	2.55	0.60
52:BE:128:SER:OG	52:BE:129:HIS:N	2.35	0.60
26:BB:92:C:OP1	30:BQ:19:GLY:HA2	2.01	0.60
43:BD:71:ASP:HB2	43:BD:103:ARG:HH22	1.67	0.60
17:AD:9:CYS:HA	17:AD:12:CYS:HB3	1.83	0.59
25:BA:2392:A:OP1	49:B8:32:LEU:CD2	2.50	0.59
23:AY:264:LEU:HD12	60:AY:702:GCP:C2	2.32	0.59
55:BH:171:LEU:O	55:BH:173:PRO:HD3	2.02	0.59
1:AA:1218:C:H2'	1:AA:1219:U:C6	2.37	0.59
55:BH:98:LEU:HD13	55:BH:125:VAL:HG23	1.82	0.59
36:BW:20:VAL:CG2	36:BW:47:VAL:HG21	2.32	0.59
51:BC:104:LEU:N	51:BC:105:ASP:HA	2.17	0.59
25:BA:969:U:H2'	25:BA:970:C:C6	2.37	0.59
1:AA:1346:A:O4'	1:AA:1348:U:C6	2.54	0.59
25:BA:247:G:H4'	25:BA:386:G:C5	2.37	0.59
25:BA:2590:A:OP2	43:BD:238:GLY:HA2	2.01	0.59
22:AI:42:ARG:NH1	22:AI:71:SER:OG	2.34	0.59
29:BP:47:ASP:OD2	29:BP:50:ARG:NH2	2.36	0.59
25:BA:1448:G:H1'	25:BA:1528:A:H62	1.65	0.59
39:BZ:18:LEU:HD12	39:BZ:18:LEU:N	2.12	0.59
1:AA:979:C:C3'	1:AA:980:C:H5'	2.31	0.59
23:AY:618:GLY:HA3	25:BA:1095:A:OP1	2.01	0.59
35:BV:45:THR:O	35:BV:46:VAL:HG12	2.02	0.59
25:BA:2092:U:C5	25:BA:2226:C:OP2	2.55	0.59
1:AA:263:A:OP2	14:AT:79:ARG:NH1	2.35	0.59
25:BA:2306:C:C5	25:BA:2307:G:H1'	2.37	0.59
42:B2:38:GLN:OE1	42:B2:44:LEU:HD22	2.02	0.59
26:BB:21:G:H2'	26:BB:22:U:O4'	2.02	0.59
27:BN:134:ARG:HD2	27:BN:134:ARG:O	2.01	0.59
25:BA:994:C:OP2	34:BU:54:LYS:NZ	2.36	0.59
1:AA:1442:G:O2'	1:AA:1442(A):G:OP1	2.18	0.59
25:BA:1449:A:H5'	25:BA:1450:G:OP2	2.03	0.59
23:AY:110:SER:OG	23:AY:137:ASN:O	2.14	0.59
51:BC:30:LYS:NZ	51:BC:180:PHE:O	2.27	0.59
25:BA:1539:G:C2	25:BA:1540:U:C2	2.90	0.59
1:AA:1138:G:H1'	1:AA:1139:G:P	2.42	0.59
25:BA:1063:G:H1	25:BA:1075:C:N4	1.98	0.59
25:BA:2476:A:C2	25:BA:2477:C:C6	2.90	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1217:C:OP2	34:BU:15:LYS:NZ	2.34	0.59
26:BB:71:C:H2'	26:BB:72:G:O4'	2.03	0.59
25:BA:2097:C:O2'	25:BA:2098:U:H5'	2.03	0.59
1:AA:375:U:C4	1:AA:376:G:N7	2.70	0.59
16:AC:64:VAL:HB	16:AC:99:VAL:HG12	1.84	0.59
25:BA:1239:G:H2'	25:BA:1240:U:O4'	2.03	0.59
38:BY:9:LYS:O	38:BY:11:ASP:N	2.33	0.59
1:AA:46:G:O2'	1:AA:365:U:H1'	2.02	0.59
18:AE:143:ARG:NH1	21:AH:77:GLU:OE2	2.34	0.59
9:AO:39:LEU:HD11	9:AO:56:LEU:HB2	1.84	0.59
25:BA:154(A):C:O2	25:BA:154(A):C:O4'	2.21	0.59
51:BC:70:LYS:HG2	51:BC:71:GLN:HE21	1.67	0.59
25:BA:881:G:H2'	25:BA:882:G:O4'	2.03	0.59
25:BA:2793:G:O2'	25:BA:2794:C:OP2	2.20	0.59
25:BA:2688:U:H5	25:BA:2720:U:OP2	1.86	0.59
12:AR:44:LEU:HD22	12:AR:79:LEU:HD22	1.85	0.59
31:BR:103:ARG:NH1	31:BR:108:GLY:O	2.36	0.59
53:BF:65:TRP:HZ3	53:BF:73:ALA:O	1.85	0.59
38:BY:40:GLU:HB3	38:BY:64:GLU:OE2	2.01	0.59
25:BA:1796:U:H2'	25:BA:1797:C:C6	2.37	0.59
28:BO:111:PHE:HB3	28:BO:114:ILE:HD13	1.83	0.59
14:AT:99:LEU:O	14:AT:101:GLY:N	2.36	0.59
25:BA:1742:G:H8	25:BA:1742:G:H3'	1.68	0.59
25:BA:2138:C:C5'	25:BA:2138:C:H6	2.15	0.59
1:AA:1446:U:N3	1:AA:1452:C:N3	2.51	0.59
29:BP:23:PRO:O	29:BP:33:ARG:HD2	2.03	0.59
25:BA:1054:A:C5'	25:BA:1054:A:H8	2.16	0.59
25:BA:900:A:H3'	25:BA:901:A:H8	1.68	0.59
25:BA:2319:G:OP1	25:BA:2319:G:C4'	2.51	0.59
25:BA:639:U:H2'	25:BA:640:C:C6	2.37	0.59
25:BA:662:G:P	29:BP:18:ARG:HD2	2.43	0.58
42:B2:45:SER:O	42:B2:46:GLN:NE2	2.36	0.58
25:BA:2096:U:C4'	25:BA:2096:U:OP1	2.51	0.58
29:BP:64:LYS:O	29:BP:66:GLY:CA	2.50	0.58
35:BV:18:LEU:HD22	35:BV:19:LYS:HA	1.84	0.58
56:BK:59:ILE:HG12	56:BK:60:TYR:N	2.18	0.58
2:AV:73:A:C3'	2:AV:74:C:H5'	2.33	0.58
1:AA:979:C:C2'	1:AA:980:C:H5'	2.32	0.58
1:AA:509:A:C5'	17:AD:55:ALA:HB2	2.33	0.58
29:BP:105:LEU:O	29:BP:106:LEU:CB	2.51	0.58
35:BV:29:PRO:O	35:BV:61:VAL:O	2.20	0.58
1:AA:79:G:O2'	1:AA:80:G:O5'	2.14	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
52:BE:36:ARG:NH1	52:BE:85:ASN:OD1	2.35	0.58
25:BA:1312:U:H4'	25:BA:1313:U:O5'	2.03	0.58
25:BA:1531:C:O5'	25:BA:1531:C:H6	1.86	0.58
40:B0:36:ILE:C	40:B0:36:ILE:HD12	2.22	0.58
25:BA:1528:A:C2	25:BA:1541:G:C2	2.91	0.58
1:AA:1392:G:N2	1:AA:1502:A:C8	2.69	0.58
17:AD:26:CYS:CA	17:AD:31:CYS:HB2	2.28	0.58
51:BC:185:LEU:O	51:BC:187:ASP:N	2.36	0.58
26:BB:50:G:H2'	26:BB:51:G:O4'	2.02	0.58
1:AA:1013:G:C8	1:AA:1013:G:H5''	2.39	0.58
29:BP:81:GLN:OE1	29:BP:106:LEU:HA	2.03	0.58
35:BV:2:PHE:O	35:BV:14:VAL:O	2.21	0.58
25:BA:1418:G:OP1	25:BA:1588:C:O2'	2.22	0.58
25:BA:2422:A:H4'	25:BA:2423:U:OP1	2.02	0.58
25:BA:1174:A:OP1	25:BA:1175:U:OP1	2.20	0.58
39:BZ:74:VAL:HG22	39:BZ:86:VAL:HG13	1.84	0.58
23:AY:683:VAL:O	23:AY:685:GLU:N	2.36	0.58
25:BA:2789:C:N3	25:BA:2894:G:O6	2.36	0.58
1:AA:1228:C:OP1	7:AM:108:ARG:NH2	2.36	0.58
16:AC:92:ALA:O	16:AC:95:THR:O	2.20	0.58
43:BD:77:ALA:HB2	43:BD:97:TYR:CD2	2.37	0.58
47:B6:48:VAL:O	47:B6:49:HIS:CB	2.48	0.58
43:BD:26:LYS:HD3	43:BD:113:VAL:HG21	1.85	0.58
1:AA:978:A:C5	1:AA:1319:A:C2	2.92	0.58
22:AI:42:ARG:NH2	22:AI:75:ASP:OD2	2.35	0.58
1:AA:60:A:H4'	1:AA:61:G:O5'	2.02	0.58
34:BU:92:ARG:NH1	35:BV:11:GLN:O	2.36	0.58
30:BQ:16:ARG:C	30:BQ:17:LEU:HD23	2.24	0.58
16:AC:55:VAL:HG12	16:AC:55:VAL:O	2.02	0.58
1:AA:432:A:C8	1:AA:433:C:C5	2.92	0.58
25:BA:90:U:H1'	25:BA:92:A:N7	2.19	0.58
25:BA:662:G:H5'	29:BP:18:ARG:HA	1.86	0.58
38:BY:76:CYS:O	38:BY:96:ILE:CD1	2.51	0.58
25:BA:2681:C:C5	25:BA:2725:A:N6	2.71	0.58
6:AL:37:CYS:O	6:AL:79:GLU:O	2.20	0.58
15:AB:109:SER:O	15:AB:111:ARG:N	2.36	0.58
25:BA:385:C:O2'	25:BA:388:G:N2	2.36	0.58
1:AA:158:G:N2	1:AA:163:C:O2	2.33	0.58
46:B5:40:LYS:CE	46:B5:46:CYS:HB3	2.33	0.58
55:BH:157:TYR:CE1	55:BH:171:LEU:HD22	2.38	0.58
1:AA:1442(A):G:N3	1:AA:1442(A):G:H2'	2.18	0.58
33:BT:106:SER:C	33:BT:107:ASP:OD1	2.42	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BB:1:U:O2	26:BB:1:U:H2'	2.03	0.58
28:BO:64:ARG:NH1	28:BO:81:ASP:OD2	2.37	0.58
25:BA:1210:A:H8	25:BA:1210:A:H5'	1.68	0.58
56:BK:103:GLN:O	56:BK:106:GLU:HG2	2.03	0.58
42:B2:35:LEU:HD12	42:B2:53:LEU:HD12	1.86	0.58
25:BA:1970:A:H5''	25:BA:1971:A:OP1	2.02	0.58
30:BQ:138:ASP:N	30:BQ:138:ASP:OD2	2.37	0.58
25:BA:2836:U:H2'	25:BA:2837:G:C8	2.39	0.58
25:BA:2529:G:O6	50:B9:31:LYS:NZ	2.37	0.58
25:BA:2315:G:OP1	54:BG:36:LYS:NZ	2.35	0.58
23:AY:428:LEU:CD2	23:AY:451:ILE:HD11	2.32	0.58
25:BA:2542:A:H2'	25:BA:2542:A:N3	2.19	0.58
6:AL:53:ARG:NH1	6:AL:92:ASP:OD2	2.36	0.58
25:BA:685:A:OP1	48:B7:11:LYS:NZ	2.36	0.58
8:AN:26:ARG:NH1	8:AN:47:LEU:HD21	2.19	0.58
25:BA:607:U:H3	25:BA:621:A:H2	1.44	0.57
33:BT:7:ILE:O	33:BT:11:GLU:OE1	2.21	0.57
51:BC:39:GLU:OE1	51:BC:216:THR:HB	2.04	0.57
34:BU:105:VAL:HG11	35:BV:40:LEU:HD11	1.86	0.57
33:BT:123:GLN:HA	33:BT:126:ALA:HB3	1.86	0.57
56:BK:14:ALA:HA	56:BK:41:PHE:CE2	2.39	0.57
25:BA:330:A:HO2'	25:BA:331:A:H8	1.51	0.57
25:BA:2662:A:H2'	25:BA:2663:G:O4'	2.04	0.57
40:B0:2:ALA:O	40:B0:4:LYS:N	2.34	0.57
1:AA:269:C:H2'	1:AA:270:A:C8	2.39	0.57
25:BA:705:A:H2'	25:BA:706:A:O4'	2.03	0.57
1:AA:814:A:H2'	1:AA:816:A:H5''	1.86	0.57
25:BA:1434:A:H61	25:BA:1558:A:H62	1.52	0.57
49:B8:51:ALA:N	49:B8:53:PRO:HD2	2.19	0.57
1:AA:149:A:HO2'	1:AA:150:C:H6	1.47	0.57
13:AS:47:HIS:O	13:AS:62:ILE:HG22	2.04	0.57
25:BA:2165:G:C2'	25:BA:2166:G:H5''	2.34	0.57
32:BS:15:ARG:O	32:BS:18:ILE:HG22	2.04	0.57
1:AA:59:A:H2'	1:AA:60:A:OP1	2.04	0.57
58:BL:100:UNK:O	58:BL:101:UNK:CB	2.52	0.57
1:AA:1054:C:C2'	1:AA:1055:A:H5''	2.34	0.57
35:BV:39:LEU:HA	35:BV:47:VAL:HG11	1.85	0.57
33:BT:27:THR:OG1	33:BT:28:VAL:N	2.36	0.57
15:AB:84:GLU:HB3	15:AB:219:VAL:HG21	1.86	0.57
25:BA:1058:G:C8	25:BA:1058:G:H5''	2.40	0.57
38:BY:55:TYR:O	38:BY:56:PRO:C	2.41	0.57
29:BP:97:PRO:HB3	29:BP:112:LEU:HB2	1.86	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1742:G:C8	25:BA:1743:C:C6	2.93	0.57
1:AA:986:A:H2'	1:AA:987:G:O4'	2.04	0.57
9:AO:15:PHE:CZ	9:AO:85:LEU:HD13	2.39	0.57
26:BB:76:G:O3'	39:BZ:19:ARG:NH2	2.33	0.57
2:AV:43:C:O2	2:AV:43:C:O4'	2.21	0.57
25:BA:1982:C:H5''	25:BA:1983:C:OP2	2.04	0.57
53:BF:167:ALA:O	53:BF:169:ASN:N	2.38	0.57
6:AL:41:ARG:HH11	6:AL:41:ARG:HB3	1.68	0.57
36:BW:6:ILE:HA	36:BW:103:ILE:O	2.04	0.57
57:BJ:14:ALA:O	57:BJ:18:ALA:HB3	2.05	0.57
1:AA:838:G:N2	1:AA:849:C:C2	2.72	0.57
25:BA:1496:A:C8	25:BA:1577:C:O2'	2.52	0.57
17:AD:25:ARG:O	17:AD:27:TYR:N	2.37	0.57
25:BA:2602:A:C4'	25:BA:2602:A:OP2	2.52	0.57
25:BA:2688:U:O5'	25:BA:2688:U:O2	2.23	0.57
1:AA:416:G:C5	1:AA:417:C:C4	2.93	0.57
25:BA:1688:U:H1'	25:BA:1701:A:C6	2.39	0.57
25:BA:1062:G:P	25:BA:1070:A:H4'	2.45	0.57
25:BA:2208:A:H1'	25:BA:2219:G:C5	2.39	0.57
25:BA:470:A:OP1	53:BF:59:TYR:HE2	1.87	0.57
29:BP:58:THR:O	29:BP:61:ARG:NH2	2.37	0.57
35:BV:18:LEU:HD13	35:BV:19:LYS:N	2.19	0.57
25:BA:1918:A:O2'	25:BA:1919:A:H2	1.87	0.57
1:AA:1181:G:O2'	1:AA:1182:G:H5'	2.03	0.57
49:B8:50:LEU:HA	49:B8:53:PRO:CD	2.35	0.57
11:AQ:45:HIS:HB2	11:AQ:65:ILE:HD13	1.86	0.57
56:BK:19:PRO:HB3	56:BK:34:ILE:HD12	1.87	0.57
1:AA:343:U:O2'	1:AA:346:G:O6	2.13	0.57
43:BD:30:GLU:HG3	43:BD:63:ARG:CZ	2.34	0.57
39:BZ:15:PRO:HA	39:BZ:18:LEU:HD13	1.87	0.57
27:BN:4:TYR:N	27:BN:4:TYR:CD1	2.71	0.57
33:BT:28:VAL:HG13	33:BT:46:GLU:HA	1.87	0.57
15:AB:121:LEU:HB3	15:AB:127:ILE:HD11	1.86	0.57
1:AA:1452:C:C4'	1:AA:1456:G:N2	2.67	0.57
60:AY:702:GCP:PG	61:AY:803:HOH:O	2.62	0.57
13:AS:79:THR:O	13:AS:80:TYR:O	2.22	0.57
51:BC:53:ARG:O	51:BC:54:SER:C	2.43	0.57
25:BA:2320:A:H2'	25:BA:2320:A:N3	2.20	0.57
25:BA:2845:G:O2'	25:BA:2846:G:H5'	2.05	0.57
25:BA:523:C:H4'	25:BA:540:C:O2	2.04	0.57
55:BH:106:THR:HG22	55:BH:112:PRO:HG3	1.87	0.57
38:BY:76:CYS:HB3	38:BY:96:ILE:HD11	1.87	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AV:74:C:O2'	2:AV:75:C:P	2.63	0.57
26:BB:80:U:H2'	26:BB:81:G:H21	1.68	0.57
27:BN:119:ARG:HH11	27:BN:119:ARG:HG3	1.69	0.57
12:AR:31:LEU:HD22	19:AF:97:PHE:O	2.05	0.57
16:AC:156:ARG:NE	16:AC:160:ALA:O	2.34	0.56
43:BD:136:ILE:HG22	43:BD:140:THR:OG1	2.05	0.56
52:BE:60:ASN:N	52:BE:60:ASN:ND2	2.50	0.56
23:AY:680:PRO:HD2	23:AY:683:VAL:HG22	1.87	0.56
25:BA:8:A:H2'	25:BA:9:U:C5	2.39	0.56
53:BF:23:ASP:OD1	53:BF:23:ASP:N	2.38	0.56
11:AQ:27:PHE:CZ	11:AQ:36:ILE:HD11	2.40	0.56
14:AT:96:GLY:O	14:AT:97:ALA:HB3	2.05	0.56
29:BP:6:LEU:HD12	29:BP:8:PRO:HG2	1.86	0.56
34:BU:90:VAL:HG22	35:BV:39:LEU:CB	2.36	0.56
46:B5:34:PRO:O	46:B5:35:GLU:HG2	2.04	0.56
1:AA:250:A:C4'	1:AA:251:G:O5'	2.51	0.56
42:B2:47:ASN:O	42:B2:48:HIS:C	2.43	0.56
25:BA:102:G:OP1	25:BA:102:G:C4'	2.53	0.56
27:BN:32:THR:O	27:BN:35:ARG:O	2.23	0.56
36:BW:92:ARG:O	36:BW:93:ALA:HB3	2.05	0.56
25:BA:1786:A:N1	25:BA:2606:C:H1'	2.20	0.56
25:BA:1494:A:C3'	25:BA:1494:A:N3	2.65	0.56
38:BY:76:CYS:SG	38:BY:77:PRO:HD3	2.45	0.56
25:BA:1210:A:C5'	25:BA:1210:A:H8	2.17	0.56
1:AA:975:A:C4'	1:AA:976:G:H5"	2.34	0.56
43:BD:182:LEU:O	43:BD:271:ILE:N	2.38	0.56
1:AA:432:A:N7	1:AA:433:C:C5	2.73	0.56
1:AA:1104:G:OP1	15:AB:111:ARG:NE	2.38	0.56
33:BT:106:SER:HA	33:BT:110:ILE:HG13	1.86	0.56
7:AM:79:LYS:O	7:AM:82:MET:SD	2.63	0.56
16:AC:165:THR:O	16:AC:165:THR:HG23	2.05	0.56
25:BA:272(J):C:C2'	25:BA:274:G:OP1	2.53	0.56
23:AY:418:LYS:O	23:AY:419:ALA:HB3	2.05	0.56
55:BH:167:GLU:HB3	55:BH:168:PRO:CD	2.35	0.56
15:AB:239:VAL:HG12	15:AB:239:VAL:O	2.06	0.56
28:BO:80:ASP:OD2	33:BT:64:ARG:NH2	2.37	0.56
1:AA:664:G:H22	1:AA:741:G:H1	1.52	0.56
25:BA:252:G:P	29:BP:50:ARG:NH1	2.78	0.56
6:AL:27:LEU:C	6:AL:29:GLY:H	2.07	0.56
14:AT:53:LEU:HB2	14:AT:100:ILE:HG22	1.86	0.56
34:BU:108:GLU:OE2	34:BU:112:ARG:NH1	2.38	0.56
1:AA:417:C:H2'	1:AA:418:C:H6	1.70	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AV:46:G:H3'	2:AV:47:U:C5'	2.35	0.56
25:BA:1877:A:H5''	25:BA:1878:G:OP2	2.05	0.56
39:BZ:8:TYR:O	39:BZ:37:VAL:HB	2.05	0.56
49:B8:63:PRO:O	49:B8:64:TYR:C	2.43	0.56
38:BY:17:SER:HB2	38:BY:71:LYS:HE2	1.87	0.56
25:BA:1075:C:OP1	25:BA:1075:C:H4'	2.06	0.56
51:BC:113:VAL:HG21	51:BC:131:LEU:HD11	1.88	0.56
25:BA:2180:U:H5'	25:BA:2180:U:C6	2.39	0.56
15:AB:97:TRP:HH2	15:AB:176:GLU:CD	2.09	0.56
1:AA:838:G:C2	1:AA:849:C:C2	2.94	0.56
23:AY:70:THR:HA	23:AY:358:MET:O	2.06	0.56
32:BS:89:ARG:HB3	32:BS:92:TYR:HB3	1.87	0.56
25:BA:2238:G:N3	25:BA:2238:G:H2'	2.20	0.56
25:BA:650:C:OP1	49:B8:48:PHE:CZ	2.58	0.56
25:BA:658:C:H2'	25:BA:659:C:C6	2.40	0.56
29:BP:16:ARG:HB2	29:BP:16:ARG:NH1	2.20	0.56
17:AD:8:VAL:C	17:AD:10:ARG:N	2.57	0.56
33:BT:24:PRO:HB3	33:BT:99:LEU:HD21	1.88	0.56
1:AA:1014:A:H4'	13:AS:14:HIS:CE1	2.40	0.56
38:BY:90:LEU:HG	38:BY:91:GLU:HG3	1.87	0.56
13:AS:63:THR:OG1	13:AS:65:ASN:OD1	2.23	0.56
53:BF:65:TRP:HB2	53:BF:66:PRO:HD2	1.87	0.56
23:AY:108:PHE:CE1	23:AY:114:VAL:HG22	2.41	0.56
15:AB:80:ILE:N	15:AB:80:ILE:HD12	2.20	0.56
25:BA:17:G:H4'	34:BU:25:TRP:CH2	2.41	0.56
54:BG:55:LYS:O	54:BG:59:GLU:HB2	2.06	0.56
56:BK:23:VAL:HG13	56:BK:27:LEU:HD22	1.87	0.56
29:BP:51:PHE:HB3	29:BP:52:GLU:HG2	1.87	0.56
25:BA:1022:G:N2	25:BA:1142(A):A:H2	1.97	0.56
33:BT:29:ARG:HD2	33:BT:30:VAL:HG13	1.87	0.56
23:AY:215:LYS:HA	23:AY:218:GLU:HB3	1.88	0.56
33:BT:12:SER:O	33:BT:13:ARG:NE	2.38	0.56
25:BA:821:A:H2'	25:BA:946:G:H5''	1.88	0.56
23:AY:98:MET:HG3	23:AY:130:VAL:HG21	1.88	0.56
25:BA:1448:G:H4'	25:BA:1542:A:OP1	2.06	0.56
23:AY:168:ILE:HD11	23:AY:178:ILE:CD1	2.35	0.56
25:BA:1584:C:C2'	25:BA:1584:C:O2	2.54	0.56
23:AY:493:VAL:HG23	23:AY:512:ILE:HD11	1.87	0.56
25:BA:1538:G:C5	25:BA:1539:G:N7	2.73	0.56
43:BD:24:ILE:O	43:BD:25:THR:C	2.43	0.56
25:BA:528:A:C2	25:BA:2043:C:C5'	2.89	0.56
1:AA:149:A:O2'	1:AA:150:C:H6	1.89	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1133:G:C3'	1:AA:1133:G:C8	2.89	0.56
25:BA:1504:C:HO2'	25:BA:1505:C:P	2.28	0.56
25:BA:2894:G:N3	25:BA:2894:G:H2'	2.21	0.56
7:AM:82:MET:SD	7:AM:83:ASP:N	2.79	0.56
25:BA:810:U:O5'	25:BA:810:U:H6	1.89	0.56
17:AD:17:VAL:O	17:AD:17:VAL:HG12	2.06	0.56
30:BQ:84:GLY:O	30:BQ:85:LYS:HB2	2.06	0.55
51:BC:58:VAL:HG13	51:BC:199:HIS:HB3	1.87	0.55
25:BA:762:U:H4'	25:BA:763:G:O5'	2.06	0.55
56:BK:56:GLU:O	56:BK:67:PHE:HA	2.06	0.55
42:B2:9:GLN:HE22	42:B2:56:GLN:HG2	1.72	0.55
38:BY:65:ALA:HB1	38:BY:66:PRO:CD	2.35	0.55
25:BA:1778:U:H2'	25:BA:1784:A:N6	2.20	0.55
27:BN:41:ASP:O	27:BN:42:TRP:C	2.43	0.55
25:BA:528:A:O2'	25:BA:529:A:H5'	2.06	0.55
25:BA:102:G:OP1	25:BA:102:G:O4'	2.23	0.55
38:BY:65:ALA:HB1	38:BY:66:PRO:HD3	1.88	0.55
25:BA:2444:G:OP2	53:BF:68:LYS:HE2	2.06	0.55
31:BR:104:ARG:NH1	31:BR:107:ASP:OD1	2.39	0.55
26:BB:42:C:O2'	26:BB:43:C:O5'	2.21	0.55
23:AY:404:VAL:HG22	23:AY:405:PRO:O	2.07	0.55
1:AA:1392:G:H21	1:AA:1502:A:H8	1.52	0.55
16:AC:180:ALA:O	16:AC:181:ASN:HB3	2.06	0.55
43:BD:209:ALA:O	43:BD:210:GLY:O	2.24	0.55
52:BE:77:ILE:HG22	52:BE:78:LEU:N	2.21	0.55
25:BA:456:C:O2'	37:BX:68:ARG:NH1	2.40	0.55
25:BA:2262:U:H4'	25:BA:2328:A:H2	1.71	0.55
25:BA:1754:C:OP1	33:BT:96:ARG:NH1	2.40	0.55
16:AC:7:PRO:O	16:AC:11:ARG:HG2	2.06	0.55
5:AK:54:ARG:O	5:AK:57:THR:HG22	2.06	0.55
23:AY:556:ILE:HD11	23:AY:601:ILE:HD13	1.88	0.55
38:BY:7:VAL:HB	38:BY:8:LYS:CD	2.36	0.55
38:BY:73:ARG:HH21	38:BY:81:LYS:HA	1.71	0.55
28:BO:7:TYR:CZ	28:BO:44:LYS:HG3	2.42	0.55
25:BA:1315:C:C2	25:BA:1338:G:N2	2.74	0.55
25:BA:2243:U:H2'	25:BA:2244:U:C6	2.41	0.55
44:B3:50:VAL:HG23	44:B3:54:VAL:HG21	1.88	0.55
25:BA:1188:U:H4'	35:BV:79:VAL:HG22	1.88	0.55
11:AQ:9:VAL:HG12	11:AQ:56:VAL:HG22	1.88	0.55
25:BA:1996:C:OP1	28:BO:31:LYS:HE2	2.06	0.55
56:BK:6:ALA:O	56:BK:58:THR:HG23	2.07	0.55
27:BN:5:VAL:O	27:BN:5:VAL:HG13	2.06	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1054:A:C5'	25:BA:1054:A:C8	2.89	0.55
52:BE:68:ALA:C	52:BE:70:ALA:H	2.10	0.55
35:BV:2:PHE:CB	35:BV:42:GLY:HA3	2.36	0.55
36:BW:18:ARG:NH1	36:BW:76:VAL:O	2.40	0.55
23:AY:58:GLU:HG2	23:AY:63:ILE:O	2.05	0.55
1:AA:1140:C:O2'	1:AA:1141:C:H5'	2.06	0.55
2:AV:34:G:C3'	2:AV:35:A:H5''	2.36	0.55
25:BA:2584:U:H2'	25:BA:2585:U:H2'	1.88	0.55
1:AA:694:A:N1	1:AA:787:A:O2'	2.39	0.55
11:AQ:12:SER:HB3	11:AQ:20:THR:HB	1.88	0.55
5:AK:111:ASP:HA	12:AR:84:LYS:HG3	1.87	0.55
25:BA:1054:A:H8	25:BA:1054:A:H5''	1.72	0.55
27:BN:24:GLY:HA2	27:BN:27:ALA:HB3	1.87	0.55
32:BS:96:GLY:O	32:BS:98:VAL:N	2.39	0.55
19:AF:37:VAL:HG12	19:AF:38:GLU:O	2.07	0.55
1:AA:1311:G:N2	1:AA:1327:C:C2	2.74	0.55
23:AY:652:MET:HG2	23:AY:671:MET:SD	2.47	0.55
25:BA:2365:G:O6	49:B8:39:LYS:HE3	2.07	0.55
23:AY:519:ARG:HA	23:AY:519:ARG:NE	2.21	0.55
20:AG:137:LYS:O	20:AG:141:VAL:HG23	2.07	0.55
29:BP:10:PRO:O	53:BF:34:TRP:CD1	2.60	0.55
25:BA:1300:U:O2'	25:BA:1635:G:OP1	2.22	0.55
56:BK:109:LYS:O	56:BK:112:MET:HG2	2.06	0.55
25:BA:2095:C:H6	25:BA:2095:C:H5''	1.72	0.55
7:AM:39:ILE:HD12	7:AM:56:LEU:HD23	1.88	0.55
25:BA:1272:A:H4'	25:BA:1272:A:OP1	2.05	0.55
29:BP:99:LEU:HD23	29:BP:99:LEU:O	2.07	0.55
1:AA:1178:G:N7	22:AI:97:LYS:NZ	2.48	0.55
23:AY:488:THR:OG1	23:AY:598:ASP:O	2.24	0.55
25:BA:372:G:O2'	25:BA:373:U:P	2.65	0.55
25:BA:1332:G:N2	25:BA:1610:A:C8	2.75	0.55
1:AA:1399:C:C2	1:AA:1502:A:N6	2.74	0.55
29:BP:18:ARG:O	29:BP:18:ARG:NH1	2.40	0.55
23:AY:212:TYR:O	23:AY:215:LYS:N	2.40	0.55
49:B8:32:LEU:HB2	49:B8:36:LYS:HE2	1.88	0.55
26:BB:73:A:C4	26:BB:105:A:C2	2.94	0.55
33:BT:89:VAL:C	33:BT:91:ARG:N	2.52	0.55
1:AA:1292:U:H2'	1:AA:1293:G:H5''	1.88	0.55
1:AA:1014:A:H5''	13:AS:14:HIS:CG	2.42	0.55
52:BE:89:ASP:O	52:BE:90:THR:O	2.24	0.55
31:BR:101:ALA:O	31:BR:102:GLU:HB2	2.07	0.55
7:AM:108:ARG:O	7:AM:111:LYS:O	2.25	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
51:BC:53:ARG:O	51:BC:55:ASP:OD1	2.25	0.55
54:BG:17:PRO:HA	54:BG:20:ILE:HD12	1.89	0.55
33:BT:1:MET:O	33:BT:2:ASN:C	2.44	0.55
25:BA:583:G:P	34:BU:10:ARG:HH11	2.29	0.55
25:BA:111:A:O3'	42:B2:69:ARG:NH2	2.39	0.55
25:BA:36:G:O2'	25:BA:450:G:H2'	2.07	0.55
23:AY:71:THR:CG2	23:AY:80:ASN:OD1	2.48	0.55
34:BU:98:LEU:O	34:BU:101:ARG:O	2.24	0.55
51:BC:42:GLU:HG2	51:BC:215:THR:HG23	1.87	0.55
2:AV:33:U:C5	2:AV:36:A:OP2	2.59	0.55
25:BA:2097:C:C2'	25:BA:2098:U:H5'	2.36	0.55
38:BY:42:VAL:HG12	38:BY:65:ALA:HB3	1.88	0.55
53:BF:9:ILE:O	53:BF:128:ALA:HB2	2.07	0.55
1:AA:408:A:H4'	17:AD:112:VAL:HG11	1.88	0.55
1:AA:630:G:C8	1:AA:630:G:H5''	2.42	0.55
1:AA:1036:G:H3'	1:AA:1037:C:C6	2.42	0.54
23:AY:212:TYR:HA	23:AY:215:LYS:CB	2.35	0.54
42:B2:38:GLN:O	42:B2:41:ILE:HG12	2.06	0.54
29:BP:97:PRO:O	29:BP:98:GLU:CG	2.55	0.54
25:BA:2095:C:C5'	25:BA:2095:C:H6	2.20	0.54
28:BO:18:LYS:HB2	28:BO:45:GLU:HG3	1.89	0.54
53:BF:53:THR:HG23	53:BF:55:GLY:H	1.71	0.54
25:BA:1713:U:O2'	25:BA:1714:G:H5'	2.07	0.54
25:BA:2031:A:C6	25:BA:2498:C:H1'	2.43	0.54
29:BP:8:PRO:O	29:BP:10:PRO:HD3	2.06	0.54
25:BA:1539:G:H2'	25:BA:1540:U:C5'	2.37	0.54
25:BA:2136:C:C2	25:BA:2137:C:C5	2.96	0.54
1:AA:1003:G:H2'	1:AA:1004:A:H4'	1.89	0.54
52:BE:115:GLY:C	52:BE:116:VAL:O	2.42	0.54
23:AY:679:VAL:HB	23:AY:680:PRO:HD2	1.88	0.54
52:BE:74:PRO:O	52:BE:75:VAL:O	2.26	0.54
26:BB:91:C:OP2	30:BQ:16:ARG:NH1	2.39	0.54
54:BG:116:ASP:O	54:BG:117:PHE:CB	2.55	0.54
5:AK:48:ILE:HG22	5:AK:49:GLY:N	2.23	0.54
25:BA:607:U:O2	25:BA:621:A:N1	2.40	0.54
47:B6:20:ASN:O	47:B6:21:TYR:CD1	2.60	0.54
43:BD:27:THR:HG23	43:BD:83:GLU:HB3	1.87	0.54
22:AI:118:LYS:O	22:AI:119:ALA:CB	2.55	0.54
33:BT:30:VAL:HG12	33:BT:44:ASP:OD1	2.08	0.54
27:BN:46:VAL:O	27:BN:47:ALA:CB	2.55	0.54
56:BK:37:PHE:O	56:BK:41:PHE:HB3	2.07	0.54
33:BT:3:ARG:HG3	33:BT:6:LEU:HB3	1.89	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:AS:70:LYS:HE3	13:AS:70:LYS:N	2.22	0.54
31:BR:9:LYS:O	31:BR:10:LEU:HD23	2.06	0.54
53:BF:202:PHE:O	53:BF:206:ILE:HG12	2.08	0.54
35:BV:62:LEU:CD2	35:BV:95:LEU:HB2	2.37	0.54
53:BF:81:PRO:CB	53:BF:89:VAL:HG23	2.37	0.54
25:BA:1639:U:O2'	25:BA:1640:C:H5'	2.08	0.54
25:BA:2492:U:H2'	25:BA:2493:U:C6	2.42	0.54
47:B6:41:PRO:CD	47:B6:46:HIS:HA	2.37	0.54
25:BA:528:A:C2	25:BA:2043:C:C4'	2.88	0.54
52:BE:65:GLY:O	52:BE:67:PHE:N	2.40	0.54
51:BC:84:LYS:HA	51:BC:87:GLU:HG3	1.89	0.54
16:AC:167:TRP:O	16:AC:168:ALA:HB2	2.08	0.54
25:BA:1721:G:C2	25:BA:1739:U:OP2	2.61	0.54
28:BO:1:MET:HG3	28:BO:67:LYS:HG2	1.90	0.54
25:BA:1539:G:H2'	25:BA:1540:U:H5''	1.87	0.54
25:BA:242:G:H5'	49:B8:62:LEU:HD13	1.88	0.54
27:BN:3:THR:C	27:BN:5:VAL:N	2.61	0.54
25:BA:900:A:H3'	25:BA:901:A:C8	2.42	0.54
25:BA:598:G:H2'	25:BA:599:G:O4'	2.07	0.54
1:AA:1080:A:C5'	18:AE:16:THR:HG21	2.37	0.54
25:BA:2312:U:O2'	54:BG:71:THR:HG21	2.08	0.54
29:BP:7:ARG:CZ	29:BP:7:ARG:HA	2.36	0.54
25:BA:1539:G:C3'	25:BA:1540:U:C5'	2.86	0.54
25:BA:1689:A:N7	25:BA:1698:A:N1	2.55	0.54
2:AV:33:U:O2	2:AV:33:U:O4'	2.23	0.54
29:BP:23:PRO:HB2	29:BP:33:ARG:CD	2.38	0.54
55:BH:174:GLY:C	55:BH:176:ALA:HB2	2.27	0.54
39:BZ:6:LYS:HG2	39:BZ:8:TYR:OH	2.07	0.54
1:AA:1226:C:H4'	1:AA:1227:A:OP1	2.08	0.54
25:BA:213:A:H2'	25:BA:214:G:O4'	2.07	0.54
1:AA:1504:G:OP1	1:AA:1507:A:H4'	2.08	0.54
1:AA:134:A:H1'	1:AA:325:A:C5	2.43	0.54
52:BE:4:ILE:HD13	52:BE:28:ALA:HB1	1.90	0.54
25:BA:524:U:H4'	25:BA:555:U:H4'	1.88	0.54
55:BH:117:PRO:HB3	55:BH:123:PHE:CE2	2.42	0.54
1:AA:1202:G:C2	8:AN:42:ILE:HG21	2.43	0.54
1:AA:1133:G:H2'	1:AA:1134:G:O4'	2.08	0.54
42:B2:53:LEU:O	42:B2:57:ILE:HG13	2.07	0.54
29:BP:135:LEU:HD21	29:BP:144:GLU:HG3	1.89	0.54
26:BB:66:A:O2'	26:BB:67:G:OP2	2.19	0.54
55:BH:136:ILE:HD12	55:BH:136:ILE:H	1.71	0.54
35:BV:49:THR:HB	35:BV:50:PRO:HD2	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:AV:73:A:H2'	2:AV:74:C:C5'	2.37	0.54
16:AC:60:ALA:O	16:AC:62:ASP:N	2.41	0.54
25:BA:219:G:H2'	25:BA:220:G:O4'	2.07	0.54
25:BA:1131:G:OP2	25:BA:2515:C:H4'	2.07	0.54
25:BA:2743:C:H2'	25:BA:2744:G:O5'	2.08	0.54
54:BG:7:LEU:HD22	54:BG:176:LEU:HD22	1.89	0.54
21:AH:96:GLY:N	21:AH:99:GLU:OE1	2.41	0.54
29:BP:7:ARG:CB	29:BP:8:PRO:CD	2.84	0.54
29:BP:48:PRO:O	29:BP:49:ARG:C	2.40	0.54
56:BK:77:LEU:H	56:BK:77:LEU:HD23	1.72	0.54
15:AB:77:ALA:HB2	15:AB:211:ILE:HD13	1.89	0.54
25:BA:918:A:H1'	26:BB:80:U:O2'	2.08	0.54
25:BA:2019:A:C2'	25:BA:2020:A:O5'	2.56	0.54
7:AM:10:PRO:HB2	7:AM:18:ALA:HB1	1.89	0.54
4:AJ:49:VAL:O	4:AJ:60:ARG:HB2	2.09	0.54
25:BA:2609:U:OP1	25:BA:2609:U:H4'	2.07	0.54
25:BA:2477:C:C5	50:B9:4:ARG:NH2	2.76	0.54
25:BA:684:G:OP1	48:B7:16:HIS:CD2	2.61	0.54
2:AV:57:G:H8	2:AV:57:G:H5''	1.73	0.54
1:AA:991:U:O2	1:AA:991:U:H2'	2.08	0.54
23:AY:148:LEU:O	23:AY:152:THR:OG1	2.15	0.54
25:BA:1100:C:H5'	25:BA:1100:C:C6	2.43	0.53
41:B1:57:GLU:O	41:B1:58:ILE:HG23	2.07	0.53
33:BT:56:GLY:C	33:BT:57:PHE:O	2.43	0.53
51:BC:53:ARG:O	51:BC:55:ASP:N	2.41	0.53
2:AV:18:G:O2'	2:AV:57:G:N2	2.31	0.53
15:AB:31:TYR:CE1	15:AB:200:ILE:HD12	2.42	0.53
39:BZ:11:GLU:O	39:BZ:36:LYS:NZ	2.28	0.53
25:BA:1818:U:O4	43:BD:154:LYS:HE3	2.09	0.53
25:BA:646:A:H2'	25:BA:647:G:O5'	2.08	0.53
29:BP:62:LEU:HD11	49:B8:30:ARG:HG2	1.90	0.53
25:BA:2287:A:C2	25:BA:2346:A:N1	2.76	0.53
42:B2:46:GLN:OE1	42:B2:46:GLN:HA	2.08	0.53
25:BA:1478:G:O2'	25:BA:1558:A:C2	2.60	0.53
32:BS:98:VAL:HG12	32:BS:100:ALA:N	2.23	0.53
23:AY:151:ARG:O	23:AY:154:GLN:HG2	2.08	0.53
30:BQ:21:THR:O	30:BQ:22:LYS:CB	2.55	0.53
25:BA:1763:G:OP1	25:BA:1763:G:H4'	2.07	0.53
30:BQ:6:ARG:HA	39:BZ:195:GLU:O	2.07	0.53
21:AH:38:ILE:CD1	21:AH:118:VAL:HG12	2.37	0.53
35:BV:5:VAL:HG21	35:BV:35:LEU:HD23	1.90	0.53
20:AG:144:MET:C	20:AG:145:ALA:O	2.43	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2134:A:C2	25:BA:2158:A:C5	2.95	0.53
56:BK:115:LEU:HD22	56:BK:126:MET:HE2	1.90	0.53
6:AL:23:LYS:C	6:AL:24:VAL:HG23	2.28	0.53
25:BA:2052:G:H4'	52:BE:143:ASN:O	2.07	0.53
1:AA:1360:A:H8	1:AA:1360:A:OP1	1.90	0.53
25:BA:2032:G:H21	52:BE:146:THR:HG23	1.74	0.53
23:AY:484:ARG:HB2	23:AY:602:LEU:HB2	1.89	0.53
43:BD:30:GLU:CG	43:BD:63:ARG:NH2	2.65	0.53
34:BU:91:ASP:O	34:BU:95:LEU:HB2	2.08	0.53
52:BE:116:VAL:HB	52:BE:122:PHE:CD2	2.43	0.53
56:BK:109:LYS:HA	56:BK:112:MET:HE2	1.91	0.53
14:AT:100:ILE:HG23	14:AT:100:ILE:O	2.07	0.53
1:AA:978:A:C4	1:AA:1319:A:C2	2.97	0.53
55:BH:155:SER:CB	55:BH:156:ALA:HA	2.39	0.53
51:BC:92:ASP:N	51:BC:92:ASP:OD1	2.41	0.53
1:AA:671:G:C2'	1:AA:672:U:H5'	2.39	0.53
1:AA:633:G:C5'	1:AA:633:G:C8	2.92	0.53
25:BA:2165:G:H2'	25:BA:2166:G:H5''	1.90	0.53
10:AP:3:LYS:O	10:AP:21:VAL:HA	2.08	0.53
56:BK:7:VAL:O	56:BK:7:VAL:HG13	2.08	0.53
57:BJ:55:ALA:O	57:BJ:56:ALA:C	2.46	0.53
25:BA:1570:A:H5'	43:BD:38:LYS:HG3	1.90	0.53
25:BA:661:C:H4'	29:BP:16:ARG:NH1	2.24	0.53
29:BP:16:ARG:CZ	29:BP:18:ARG:HG3	2.39	0.53
38:BY:96:ILE:CD1	38:BY:99:CYS:SG	2.92	0.53
1:AA:973:G:H2'	1:AA:974:A:OP1	2.08	0.53
25:BA:2298:A:H62	25:BA:2318:G:H8	1.55	0.53
56:BK:79:ARG:HD2	56:BK:85:GLU:O	2.09	0.53
23:AY:157:LEU:N	23:AY:157:LEU:HD23	2.23	0.53
29:BP:85:LEU:HA	29:BP:88:LEU:HD22	1.90	0.53
25:BA:1024:G:H3'	25:BA:1025:G:H5''	1.91	0.53
37:BX:27:THR:HA	37:BX:79:ALA:O	2.09	0.53
1:AA:1068:G:OP2	1:AA:1068:G:H8	1.91	0.53
25:BA:2206:G:N3	25:BA:2206:G:H5''	2.24	0.53
28:BO:104:ARG:HH21	33:BT:33:LYS:HE2	1.74	0.53
20:AG:6:ARG:O	20:AG:7:ALA:HB3	2.07	0.53
23:AY:117:GLN:HA	23:AY:120:THR:OG1	2.08	0.53
1:AA:396:G:O2'	1:AA:398:C:OP1	2.19	0.53
25:BA:1538:G:C4	25:BA:1539:G:N7	2.76	0.53
25:BA:1920:C:O2	25:BA:1920:C:O4'	2.23	0.53
1:AA:353:A:H2'	1:AA:354:G:OP2	2.09	0.53
51:BC:137:LEU:HD22	51:BC:138:PRO:HD2	1.89	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1533:C:H4'	1:AA:1533:C:OP1	2.09	0.53
23:AY:250:THR:N	23:AY:255:ILE:HG22	2.23	0.53
1:AA:518:C:H5	1:AA:530:G:O5'	1.92	0.53
25:BA:686:G:H1	48:B7:16:HIS:CE1	2.27	0.53
32:BS:52:SER:CB	32:BS:55:ALA:HB3	2.38	0.53
25:BA:2019:A:H2'	25:BA:2020:A:O5'	2.08	0.53
25:BA:1720:U:O2	25:BA:1742:G:O6	2.26	0.53
25:BA:2875:C:O2'	33:BT:3:ARG:HB2	2.09	0.53
25:BA:1204:A:N1	25:BA:1241:A:C2	2.76	0.53
20:AG:26:PHE:CE2	20:AG:30:ILE:HD11	2.43	0.53
25:BA:2109:U:H1'	25:BA:2181:G:N2	2.24	0.53
34:BU:81:HIS:NE2	34:BU:117:GLN:HG3	2.23	0.53
31:BR:4:LEU:O	31:BR:5:LYS:HG2	2.09	0.53
50:B9:29:ASN:ND2	50:B9:32:HIS:CE1	2.66	0.53
25:BA:661:C:H4'	29:BP:16:ARG:HH12	1.74	0.53
1:AA:460:G:O6	1:AA:470:C:C5'	2.55	0.53
25:BA:8:A:H2'	25:BA:9:U:C6	2.44	0.53
29:BP:100:LEU:O	29:BP:105:LEU:O	2.26	0.53
57:BJ:106:ALA:O	57:BJ:107:ALA:CB	2.57	0.53
31:BR:78:LYS:HE2	31:BR:83:ILE:HD11	1.90	0.53
25:BA:1364:G:N7	41:B1:3:LYS:HE2	2.24	0.53
4:AJ:90:LEU:N	4:AJ:91:PRO:HD3	2.24	0.53
25:BA:1833:U:O2	25:BA:1969:A:H2	1.90	0.53
54:BG:114:ILE:HG12	54:BG:140:ILE:HG21	1.90	0.53
1:AA:1118:C:H1'	1:AA:1179:A:C4	2.44	0.53
25:BA:1742:G:C8	25:BA:1742:G:H3'	2.44	0.53
1:AA:1192:C:OP2	16:AC:4:LYS:NZ	2.40	0.53
25:BA:551:G:O2'	25:BA:1220:A:N3	2.31	0.53
51:BC:76:ALA:HB3	51:BC:94:VAL:HG22	1.90	0.53
31:BR:2:ARG:CZ	52:BE:111:ARG:HG3	2.39	0.53
25:BA:2138:C:O2	25:BA:2154:G:C2	2.62	0.53
46:B5:33:CYS:HB2	46:B5:40:LYS:CE	2.34	0.53
56:BK:109:LYS:HA	56:BK:112:MET:CE	2.39	0.53
15:AB:145:LEU:CD1	15:AB:149:LEU:HD12	2.39	0.53
52:BE:1:MET:HB3	52:BE:200:GLU:CD	2.29	0.53
17:AD:11:LEU:HA	17:AD:13:ARG:O	2.09	0.53
43:BD:238:GLY:O	43:BD:239:ARG:O	2.26	0.53
17:AD:3:ARG:HG2	17:AD:118:ARG:CD	2.39	0.53
1:AA:602:A:H2'	1:AA:603:U:O4'	2.09	0.53
31:BR:117:VAL:O	31:BR:117:VAL:HG12	2.09	0.53
1:AA:1278:U:O4'	1:AA:1278:U:O2	2.26	0.53
25:BA:185:U:H4'	25:BA:218:A:H4'	1.91	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:AD:31:CYS:C	17:AD:33:MET:H	2.12	0.52
1:AA:633:G:C5'	1:AA:633:G:H8	2.19	0.52
25:BA:613:G:C5'	25:BA:613:G:H8	2.20	0.52
25:BA:2063:C:O2	25:BA:2451:A:C2	2.62	0.52
29:BP:112:LEU:HD13	29:BP:114:ILE:HG22	1.90	0.52
32:BS:66:ALA:HA	32:BS:69:VAL:HG12	1.91	0.52
1:AA:421:U:O4'	1:AA:421:U:O2	2.27	0.52
23:AY:201:ILE:H	23:AY:201:ILE:HD12	1.74	0.52
25:BA:1243:G:H2'	25:BA:1244:G:O4'	2.09	0.52
29:BP:5:ASP:N	53:BF:116:ASP:OD2	2.42	0.52
1:AA:552:U:O2'	6:AL:86:ARG:O	2.27	0.52
25:BA:2306:C:H5	25:BA:2307:G:H1'	1.71	0.52
25:BA:1858:G:H8	25:BA:1858:G:OP2	1.92	0.52
52:BE:1:MET:HG3	52:BE:83:ASP:HB2	1.92	0.52
25:BA:2096:U:OP1	25:BA:2096:U:H4'	2.09	0.52
25:BA:657:U:H2'	25:BA:658:C:C6	2.45	0.52
38:BY:42:VAL:CG1	38:BY:65:ALA:HB3	2.39	0.52
2:AV:10:G:H2'	2:AV:11:C:C6	2.43	0.52
1:AA:706:A:H2'	5:AK:31:THR:HG21	1.91	0.52
43:BD:83:GLU:OE1	43:BD:104:TYR:OH	2.27	0.52
1:AA:427:U:OP2	17:AD:36:ARG:NH2	2.42	0.52
25:BA:2305:A:H5''	54:BG:134:GLY:HA3	1.89	0.52
25:BA:715:G:H2'	25:BA:716:A:O4'	2.08	0.52
52:BE:117:MET:O	52:BE:118:LYS:CB	2.56	0.52
33:BT:24:PRO:HA	33:BT:49:VAL:O	2.08	0.52
25:BA:612:C:H2'	25:BA:613:G:H5''	1.91	0.52
1:AA:986:A:C2	1:AA:1220:G:C2	2.98	0.52
16:AC:134:ILE:CG2	16:AC:168:ALA:HB3	2.39	0.52
52:BE:24:THR:CG2	52:BE:187:ALA:H	2.22	0.52
37:BX:40:LYS:HG3	37:BX:51:VAL:HB	1.91	0.52
1:AA:539:A:H2'	1:AA:540:G:C8	2.44	0.52
25:BA:2556:C:H2'	25:BA:2557:G:O4'	2.09	0.52
1:AA:104:G:N7	14:AT:14:LYS:NZ	2.57	0.52
25:BA:2111:C:H42	25:BA:2147:G:H1	1.56	0.52
25:BA:1332:G:C8	25:BA:1332:G:H5'	2.44	0.52
29:BP:59:LEU:HA	29:BP:61:ARG:CZ	2.39	0.52
33:BT:82:LEU:N	33:BT:82:LEU:HD12	2.24	0.52
17:AD:28:SER:O	17:AD:30:LYS:N	2.36	0.52
52:BE:55:ASN:O	52:BE:57:LYS:N	2.41	0.52
27:BN:3:THR:C	27:BN:5:VAL:H	2.13	0.52
25:BA:247:G:H4'	25:BA:386:G:C6	2.45	0.52
25:BA:2492:U:H2'	25:BA:2493:U:H6	1.75	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
30:BQ:21:THR:HG23	30:BQ:101:ARG:HB2	1.90	0.52
29:BP:13:ASN:OD1	53:BF:31:HIS:HB2	2.09	0.52
52:BE:47:VAL:O	52:BE:47:VAL:HG13	2.09	0.52
25:BA:889:C:H1'	25:BA:890:A:O4'	2.10	0.52
43:BD:30:GLU:HB2	43:BD:35:LYS:HE3	1.90	0.52
29:BP:51:PHE:HB3	29:BP:52:GLU:CG	2.39	0.52
25:BA:652:C:C6	25:BA:652:C:OP2	2.62	0.52
25:BA:771:G:OP1	48:B7:10:ARG:NH1	2.42	0.52
25:BA:1506:C:O2	25:BA:1506:C:H2'	2.08	0.52
54:BG:5:VAL:HG12	54:BG:6:ALA:H	1.74	0.52
56:BK:121:GLU:H	56:BK:121:GLU:CD	2.12	0.52
55:BH:6:ARG:CB	55:BH:65:HIS:NE2	2.73	0.52
25:BA:2415:G:H4'	29:BP:67:MET:N	2.24	0.52
49:B8:6:THR:HB	49:B8:63:PRO:HG3	1.91	0.52
25:BA:528:A:H2	25:BA:2043:C:H5'	1.74	0.52
12:AR:25:THR:HG22	12:AR:26:LEU:HG	1.92	0.52
25:BA:1403:C:H5''	25:BA:1471:A:C1'	2.40	0.52
15:AB:80:ILE:HD11	15:AB:208:ILE:HG23	1.92	0.52
37:BX:35:THR:O	37:BX:39:ILE:HG13	2.10	0.52
16:AC:73:PRO:HB3	16:AC:103:VAL:HG11	1.91	0.52
52:BE:2:LYS:HA	52:BE:84:PHE:CD2	2.44	0.52
15:AB:146:GLN:O	15:AB:150:SER:OG	2.27	0.52
50:B9:10:ILE:HB	50:B9:32:HIS:CD2	2.44	0.52
47:B6:18:ARG:HG3	47:B6:19:ARG:N	2.25	0.52
49:B8:50:LEU:O	49:B8:51:ALA:CB	2.58	0.52
55:BH:85:LYS:HE3	55:BH:145:ALA:HB1	1.92	0.52
39:BZ:24:LEU:CD2	39:BZ:25:PRO:O	2.57	0.52
25:BA:1771:C:H1'	25:BA:1786:A:C8	2.44	0.52
25:BA:2141:G:H2'	25:BA:2142:C:C6	2.45	0.52
43:BD:24:ILE:O	43:BD:26:LYS:HB3	2.09	0.52
25:BA:2611:U:H6	25:BA:2611:U:C5'	2.18	0.52
25:BA:2164:C:O2	25:BA:2164:C:O4'	2.25	0.52
1:AA:187:C:O2'	14:AT:89:ARG:NH2	2.40	0.52
56:BK:41:PHE:CE1	56:BK:45:THR:HG21	2.45	0.52
32:BS:88:ASP:OD2	32:BS:89:ARG:N	2.42	0.52
18:AE:12:LEU:HB3	18:AE:31:LEU:HB2	1.92	0.52
20:AG:23:VAL:HG13	20:AG:43:PHE:CE2	2.45	0.52
32:BS:42:ASP:O	32:BS:43:GLU:HB2	2.10	0.52
25:BA:613:G:C8	25:BA:613:G:C5'	2.93	0.52
1:AA:1074:G:O2'	1:AA:1101:A:N1	2.39	0.52
25:BA:2063:C:O2	25:BA:2450:A:N1	2.43	0.52
33:BT:93:ARG:HH11	33:BT:93:ARG:CG	2.23	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1309:G:OP1	7:AM:88:ARG:NH1	2.42	0.52
15:AB:109:SER:C	15:AB:111:ARG:H	2.12	0.52
1:AA:1080:A:H5''	18:AE:16:THR:HG21	1.92	0.52
25:BA:301:G:C4	25:BA:302:C:C5	2.98	0.52
25:BA:2619:C:OP1	52:BE:152:LYS:NZ	2.39	0.52
57:BJ:21:ALA:H	57:BJ:88:ALA:HB1	1.73	0.52
39:BZ:108:PRO:HA	39:BZ:142:SER:HA	1.91	0.52
49:B8:61:LEU:HD23	49:B8:61:LEU:H	1.75	0.52
25:BA:807:U:OP2	29:BP:39:LYS:CG	2.51	0.52
39:BZ:153:SER:HA	39:BZ:155:LEU:HD23	1.91	0.52
1:AA:1020:U:H2'	1:AA:1021:G:C8	2.45	0.52
25:BA:1963:U:H4'	25:BA:1964:G:OP1	2.10	0.52
25:BA:2262:U:H4'	25:BA:2328:A:C2	2.45	0.52
29:BP:130:PHE:CB	29:BP:135:LEU:HD23	2.39	0.52
25:BA:84:A:N1	25:BA:98:G:O2'	2.35	0.52
25:BA:636:G:N7	29:BP:113:LYS:NZ	2.54	0.52
25:BA:1170:G:N2	25:BA:1180:C:N3	2.58	0.52
25:BA:195:A:H61	25:BA:198:C:H3'	1.75	0.52
31:BR:55:ALA:HB2	31:BR:79:LEU:HD13	1.91	0.52
56:BK:58:THR:O	56:BK:66:THR:HG22	2.09	0.51
56:BK:99:ILE:HG23	56:BK:103:GLN:CB	2.39	0.51
43:BD:166:GLN:HB2	43:BD:174:ILE:HG22	1.91	0.51
23:AY:493:VAL:HG23	23:AY:512:ILE:CD1	2.40	0.51
25:BA:2518:A:C8	25:BA:2518:A:H5'	2.44	0.51
18:AE:91:LEU:HG	18:AE:118:ILE:HD11	1.92	0.51
25:BA:1430:C:H2'	25:BA:1431:U:C6	2.45	0.51
43:BD:44:ASN:HB2	43:BD:49:ILE:HA	1.90	0.51
55:BH:19:VAL:HG11	55:BH:44:VAL:HA	1.93	0.51
17:AD:36:ARG:HH11	17:AD:36:ARG:HG2	1.75	0.51
25:BA:1299:G:H5'	25:BA:1301:A:O4'	2.10	0.51
1:AA:1531:A:O3'	1:AA:1532:U:H6	1.92	0.51
52:BE:75:VAL:O	52:BE:77:ILE:N	2.43	0.51
15:AB:97:TRP:CH2	15:AB:176:GLU:CD	2.83	0.51
43:BD:77:ALA:HB2	43:BD:97:TYR:CE2	2.44	0.51
33:BT:32:TYR:HD2	33:BT:81:PRO:O	1.92	0.51
25:BA:2261:C:O2'	25:BA:2262:U:H5'	2.10	0.51
1:AA:992:U:H4'	1:AA:993:G:O5'	2.09	0.51
25:BA:271(O):C:O2'	25:BA:271(P):C:P	2.68	0.51
1:AA:757:U:H2'	1:AA:758:G:O4'	2.10	0.51
25:BA:1296:G:OP1	25:BA:2709:G:O2'	2.23	0.51
32:BS:59:LYS:HB3	32:BS:65:VAL:HG22	1.92	0.51
1:AA:633:G:H5''	1:AA:633:G:C8	2.43	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AY:603:GLU:HG2	23:AY:679:VAL:HG13	1.92	0.51
25:BA:2179:C:HO2'	25:BA:2180:U:P	2.32	0.51
25:BA:1385:G:H4'	25:BA:1386:C:OP1	2.10	0.51
25:BA:2469:A:H2	25:BA:2481:G:H21	1.58	0.51
28:BO:64:ARG:HG2	28:BO:79:PHE:CG	2.45	0.51
33:BT:45:PHE:CE2	33:BT:63:VAL:HG12	2.45	0.51
5:AK:82:VAL:O	5:AK:109:VAL:HG23	2.10	0.51
25:BA:614:U:O2	25:BA:614:U:O4'	2.25	0.51
25:BA:1156:A:OP1	34:BU:55:ARG:NH1	2.43	0.51
11:AQ:40:LYS:HD3	11:AQ:42:TYR:CZ	2.46	0.51
1:AA:1151:A:HO2'	1:AA:1152:A:H8	1.56	0.51
22:AI:16:ARG:HB2	22:AI:64:THR:HG22	1.92	0.51
25:BA:2579:C:H2'	25:BA:2580:U:O4'	2.11	0.51
1:AA:1140:C:C2	1:AA:1141:C:C5	2.98	0.51
43:BD:43:ARG:HB2	43:BD:54:ARG:HB2	1.91	0.51
25:BA:958:U:O2	26:BB:90:A:H4'	2.11	0.51
23:AY:211:GLU:O	23:AY:215:LYS:HB2	2.10	0.51
25:BA:2391:G:OP1	49:B8:32:LEU:HD12	2.11	0.51
56:BK:112:MET:CE	56:BK:120:LEU:HD21	2.41	0.51
25:BA:1847:A:C5'	25:BA:1848:A:OP2	2.59	0.51
15:AB:211:ILE:HG23	15:AB:215:LEU:HD23	1.92	0.51
49:B8:50:LEU:O	49:B8:51:ALA:HB3	2.10	0.51
1:AA:552:U:H4'	6:AL:86:ARG:HG2	1.93	0.51
26:BB:78:A:C2	26:BB:100:A:C4	2.98	0.51
53:BF:64:ILE:O	53:BF:64:ILE:HD12	2.11	0.51
25:BA:2116:G:H3'	25:BA:2117:A:C8	2.45	0.51
1:AA:939:G:C6	1:AA:940:C:N4	2.78	0.51
1:AA:1391:U:H2'	1:AA:1392:G:C8	2.46	0.51
25:BA:1447:G:HO2'	25:BA:1544:A:H8	0.69	0.51
53:BF:101:LEU:O	53:BF:106:ARG:NH1	2.36	0.51
56:BK:77:LEU:HD13	56:BK:110:GLN:OE1	2.11	0.51
25:BA:1021:A:H3'	25:BA:1021:A:C8	2.45	0.51
26:BB:117:G:H5'	32:BS:55:ALA:HB1	1.92	0.51
2:AV:72:C:C6	2:AV:72:C:C3'	2.94	0.51
1:AA:680:C:O2'	43:BD:166:GLN:CG	2.59	0.51
25:BA:1478:G:O2'	25:BA:1558:A:N1	2.43	0.51
42:B2:9:GLN:NE2	42:B2:56:GLN:HG2	2.26	0.51
26:BB:40:U:H3'	26:BB:41:U:C5'	2.41	0.51
25:BA:2822:G:OP2	52:BE:110:GLY:O	2.28	0.51
15:AB:166:ASP:HB3	15:AB:169:LYS:HB3	1.93	0.51
25:BA:1789:A:C2'	25:BA:1790:C:H5'	2.39	0.51
1:AA:1371:G:C5	1:AA:1372:U:C5	2.99	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:285:C:O2'	25:BA:286:C:H5'	2.09	0.51
25:BA:479:A:H4'	25:BA:480:A:OP1	2.11	0.51
25:BA:2136:C:N3	25:BA:2137:C:H5	2.07	0.51
25:BA:2199:A:H3'	25:BA:2200:C:H6	1.76	0.51
33:BT:28:VAL:O	33:BT:29:ARG:HB2	2.10	0.51
1:AA:1293:G:H8	1:AA:1293:G:C5'	2.22	0.51
25:BA:1039:G:C2'	25:BA:1040:C:H5'	2.41	0.51
55:BH:148:ILE:O	55:BH:162:ILE:HD11	2.11	0.51
28:BO:64:ARG:HG2	28:BO:79:PHE:CD2	2.46	0.51
1:AA:685:G:O2'	1:AA:686:U:H5'	2.10	0.51
31:BR:113:LEU:HD23	31:BR:113:LEU:C	2.31	0.51
25:BA:566:U:H2'	25:BA:567:A:O4'	2.10	0.51
1:AA:438:G:O2'	1:AA:494:U:O4	2.24	0.51
25:BA:832:G:O2'	29:BP:52:GLU:HB3	2.11	0.51
39:BZ:124:ILE:HD13	39:BZ:155:LEU:HD11	1.91	0.51
38:BY:98:VAL:CG1	38:BY:98:VAL:O	2.58	0.51
39:BZ:151:HIS:HA	39:BZ:171:ILE:HG12	1.93	0.51
51:BC:66:HIS:CD2	51:BC:184:LYS:CG	2.94	0.51
10:AP:20:VAL:HG21	10:AP:32:TYR:CE1	2.45	0.51
25:BA:2098:U:O2'	25:BA:2099:U:OP2	2.22	0.51
25:BA:2887:U:H2'	25:BA:2888:C:C6	2.46	0.51
25:BA:221:A:H2'	25:BA:266:G:N7	2.26	0.51
25:BA:1281:G:H5''	25:BA:1281:G:C8	2.45	0.51
1:AA:1269:A:H5''	1:AA:1270:C:OP2	2.10	0.51
28:BO:77:ILE:CD1	33:BT:74:ARG:HD3	2.41	0.51
29:BP:57:THR:HB	29:BP:59:LEU:N	2.26	0.51
47:B6:20:ASN:CG	47:B6:21:TYR:H	2.13	0.51
25:BA:528:A:C2	25:BA:2043:C:H5'	2.46	0.51
33:BT:28:VAL:HG22	33:BT:46:GLU:HA	1.93	0.51
25:BA:1046:A:C8	57:BJ:5:ALA:HB3	2.45	0.51
33:BT:58:ASN:C	33:BT:58:ASN:HD22	2.14	0.51
7:AM:52:GLU:O	7:AM:56:LEU:HB2	2.11	0.51
5:AK:48:ILE:HD13	5:AK:48:ILE:N	2.26	0.51
41:B1:3:LYS:HB3	41:B1:61:ARG:NH2	2.26	0.51
25:BA:1281:G:H5''	25:BA:1281:G:H8	1.76	0.51
25:BA:2586:C:O5'	25:BA:2586:C:H6	1.93	0.51
17:AD:61:LYS:HA	17:AD:203:VAL:HG22	1.92	0.51
9:AO:54:ARG:O	9:AO:58:MET:HG3	2.10	0.51
28:BO:68:GLU:H	28:BO:68:GLU:CD	2.13	0.51
25:BA:1126:A:H8	25:BA:1126:A:OP1	1.93	0.51
25:BA:1678:G:H22	25:BA:1989:G:H22	1.59	0.51
6:AL:18:VAL:HG23	6:AL:19:ARG:N	2.26	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BB:75:G:H5''	26:BB:76:G:OP2	2.11	0.51
25:BA:806:C:OP1	29:BP:39:LYS:HB3	2.11	0.51
47:B6:19:ARG:CG	47:B6:20:ASN:N	2.70	0.51
38:BY:39:VAL:O	38:BY:40:GLU:OE1	2.29	0.51
25:BA:2387:U:OP1	40:B0:55:ARG:NH2	2.44	0.51
25:BA:2312:U:H4'	54:BG:71:THR:CG2	2.40	0.51
5:AK:40:ILE:HG23	5:AK:75:TYR:CD2	2.46	0.51
15:AB:7:VAL:O	15:AB:11:LEU:HD12	2.10	0.51
25:BA:319:C:H2'	25:BA:320:A:O5'	2.11	0.51
25:BA:1187:G:O5'	25:BA:1187:G:H8	1.92	0.51
15:AB:168:THR:CG2	15:AB:192:SER:HA	2.41	0.51
1:AA:1285:A:H4'	1:AA:1286:A:O5'	2.11	0.51
1:AA:1347:G:OP2	22:AI:107:ARG:HG2	2.10	0.51
28:BO:115:VAL:HG13	28:BO:121:VAL:HG21	1.93	0.51
25:BA:1464:C:HO2'	25:BA:1528:A:H8	1.56	0.51
25:BA:2134:A:H8	25:BA:2159:G:HO2'	1.57	0.51
29:BP:18:ARG:CZ	29:BP:18:ARG:HB3	2.41	0.51
25:BA:1210:A:C5'	25:BA:1210:A:C8	2.94	0.51
1:AA:1532:U:H3'	1:AA:1533:C:H5''	1.92	0.51
25:BA:537:C:H4'	27:BN:3:THR:HG21	1.92	0.51
9:AO:54:ARG:HG2	9:AO:58:MET:HE2	1.93	0.51
41:B1:82:LEU:O	41:B1:83:GLU:OE1	2.29	0.51
23:AY:204:GLU:C	23:AY:206:LEU:H	2.14	0.51
38:BY:8:LYS:HE2	38:BY:72:VAL:O	2.10	0.50
33:BT:28:VAL:CG2	33:BT:46:GLU:HG3	2.41	0.50
1:AA:148:G:O2'	1:AA:149:A:H5'	2.11	0.50
1:AA:1135:U:H2'	1:AA:1135:U:O2	2.10	0.50
27:BN:56:ASN:O	27:BN:57:ALA:O	2.29	0.50
12:AR:32:ARG:HD2	12:AR:65:ILE:CG2	2.42	0.50
1:AA:1015:A:H2'	1:AA:1016:A:C8	2.46	0.50
32:BS:34:HIS:HB3	32:BS:53:SER:HB3	1.93	0.50
4:AJ:85:LEU:C	4:AJ:87:THR:H	2.14	0.50
1:AA:1436:U:OP1	14:AT:23:ARG:NH2	2.43	0.50
31:BR:83:ILE:O	31:BR:86:ARG:HB2	2.12	0.50
23:AY:180:VAL:O	23:AY:182:ARG:N	2.44	0.50
23:AY:342:TYR:CE1	23:AY:347:GLY:HA2	2.46	0.50
25:BA:857:C:N4	25:BA:858:U:O4	2.44	0.50
56:BK:71:THR:HB	56:BK:72:PRO:HD2	1.92	0.50
25:BA:2678:C:H2'	25:BA:2679:A:O4'	2.11	0.50
25:BA:2137:C:H5'	25:BA:2138:C:OP2	2.11	0.50
2:AV:27:G:N1	2:AV:43:C:H5	2.00	0.50
40:B0:43:THR:O	40:B0:43:THR:CG2	2.57	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1293:G:C5'	1:AA:1293:G:C8	2.95	0.50
25:BA:1054:A:H4'	25:BA:1054:A:OP1	2.12	0.50
25:BA:2252:G:O6	40:B0:4:LYS:HB3	2.10	0.50
25:BA:1477:A:C2	25:BA:1515:G:C2	3.00	0.50
25:BA:1025:G:C4	25:BA:1135:C:H1'	2.47	0.50
1:AA:1352:C:O2	1:AA:1371:G:C2	2.64	0.50
25:BA:285:C:H2'	25:BA:286:C:H6	1.75	0.50
23:AY:377:VAL:CG2	23:AY:380:LEU:HD22	2.41	0.50
25:BA:1048:A:C4'	25:BA:1049:C:OP1	2.57	0.50
1:AA:706:A:C1'	5:AK:29:ILE:HD11	2.39	0.50
47:B6:18:ARG:CG	47:B6:19:ARG:N	2.74	0.50
1:AA:1125:U:O2'	1:AA:1126:U:OP2	2.20	0.50
33:BT:91:ARG:O	33:BT:117:ASP:HB2	2.11	0.50
25:BA:686:G:C4	48:B7:11:LYS:HG2	2.47	0.50
55:BH:83:TYR:HB3	55:BH:134:SER:CA	2.41	0.50
52:BE:67:PHE:O	52:BE:70:ALA:N	2.44	0.50
25:BA:1449:A:H5''	25:BA:1449:A:H8	1.75	0.50
25:BA:628:G:H4'	25:BA:651:G:O2'	2.10	0.50
26:BB:40:U:C2	26:BB:43:C:OP2	2.63	0.50
37:BX:27:THR:HB	37:BX:80:ILE:HB	1.94	0.50
1:AA:310:G:H5''	10:AP:31:LYS:HB2	1.93	0.50
1:AA:1187:G:H8	1:AA:1187:G:H5''	1.76	0.50
1:AA:1212:U:C6	1:AA:1212:U:H5'	2.46	0.50
55:BH:64:LEU:O	55:BH:68:THR:OG1	2.18	0.50
15:AB:15:VAL:H	15:AB:16:HIS:CD2	2.30	0.50
25:BA:1709:U:H2'	25:BA:1710:C:C6	2.47	0.50
25:BA:813:U:O2'	25:BA:1225:G:H1'	2.10	0.50
25:BA:2331:G:C4'	40:B0:42:GLY:HA3	2.42	0.50
33:BT:3:ARG:HG3	33:BT:6:LEU:CB	2.40	0.50
25:BA:1817:G:H2'	25:BA:1818:U:H5'	1.93	0.50
25:BA:848:G:H2'	25:BA:849:A:C8	2.46	0.50
2:AV:52:G:C2	2:AV:63:G:C2	2.99	0.50
48:B7:43:THR:O	48:B7:44:PRO:C	2.49	0.50
25:BA:590:A:OP1	53:BF:95:ARG:NH1	2.44	0.50
29:BP:17:LYS:O	29:BP:19:VAL:HG22	2.12	0.50
35:BV:39:LEU:HB3	35:BV:47:VAL:HG21	1.93	0.50
25:BA:336:C:H5''	38:BY:7:VAL:HG21	1.94	0.50
25:BA:2420:C:OP1	49:B8:34:TRP:HB2	2.11	0.50
25:BA:1858:G:HO2'	25:BA:1883:G:N2	2.08	0.50
53:BF:138:GLU:O	53:BF:141:ALA:HB3	2.12	0.50
25:BA:1504:C:O2'	25:BA:1505:C:O5'	2.30	0.50
33:BT:106:SER:O	33:BT:107:ASP:CG	2.50	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:AH:114:THR:HG21	21:AH:119:LEU:HD12	1.94	0.50
25:BA:2121:G:H2'	25:BA:2122:U:C6	2.47	0.50
54:BG:81:LYS:O	54:BG:82:LEU:O	2.28	0.50
22:AI:47:LEU:C	22:AI:49:PRO:HD2	2.32	0.50
17:AD:7:PRO:HB2	17:AD:10:ARG:HD2	1.93	0.50
1:AA:1531:A:H2'	1:AA:1532:U:C5	2.46	0.50
1:AA:979:C:H3'	1:AA:980:C:H5'	1.94	0.50
51:BC:77:ILE:HG22	51:BC:119:VAL:HG21	1.94	0.50
25:BA:910:A:C6	25:BA:911:A:C6	2.99	0.50
25:BA:2355:C:H4'	40:B0:36:ILE:HD11	1.94	0.50
1:AA:1302:U:C5	7:AM:17:VAL:HG21	2.46	0.50
1:AA:1060:C:C5	16:AC:2:GLY:HA2	2.46	0.50
30:BQ:78:PRO:HG2	30:BQ:81:VAL:HG11	1.92	0.50
25:BA:1260:G:H2'	25:BA:1261:C:O4'	2.12	0.50
23:AY:138:LYS:HE2	60:AY:702:GCP:C4	2.42	0.50
42:B2:39:ALA:HA	42:B2:45:SER:HB3	1.94	0.50
1:AA:63:C:H6	1:AA:63:C:C5'	2.24	0.50
1:AA:530:G:H3'	1:AA:531:U:C5'	2.41	0.50
33:BT:55:ASN:O	33:BT:57:PHE:O	2.29	0.50
1:AA:738:C:OP1	19:AF:2:ARG:NH1	2.45	0.50
1:AA:630:G:H5''	1:AA:630:G:H8	1.74	0.50
25:BA:1721:G:N1	25:BA:1739:U:OP2	2.45	0.50
25:BA:2206:G:H3'	25:BA:2206:G:N3	2.27	0.50
25:BA:1241:A:C2'	25:BA:1242:A:O5'	2.60	0.50
2:AV:4:C:O2'	25:BA:1850:G:H4'	2.12	0.50
13:AS:31:ILE:HG23	13:AS:31:ILE:O	2.11	0.50
25:BA:1901:A:H4'	25:BA:1901:A:OP2	2.12	0.50
1:AA:160:A:H2'	1:AA:161:A:O4'	2.12	0.50
1:AA:1169:A:H2'	1:AA:1170:A:C8	2.47	0.50
40:B0:11:ARG:O	40:B0:14:ARG:NH2	2.45	0.50
58:BL:113:UNK:HA	58:BL:117:UNK:O	2.12	0.50
25:BA:2136:C:N3	25:BA:2137:C:C5	2.80	0.50
25:BA:1658:C:OP1	52:BE:132:HIS:ND1	2.44	0.50
1:AA:1138:G:OP1	1:AA:1140:C:C1'	2.60	0.50
38:BY:96:ILE:HG21	38:BY:99:CYS:SG	2.51	0.50
30:BQ:14:ARG:HG2	30:BQ:41:TRP:HH2	1.77	0.50
6:AL:90:VAL:O	6:AL:92:ASP:N	2.41	0.50
25:BA:2789:C:OP1	25:BA:2789:C:H4'	2.12	0.50
29:BP:130:PHE:CG	29:BP:135:LEU:HD23	2.46	0.50
1:AA:1269:A:C2	1:AA:1313:U:O4'	2.64	0.50
16:AC:42:LEU:HD22	16:AC:94:LEU:HD23	1.93	0.50
1:AA:1351:U:O4'	20:AG:33:ASP:HB3	2.11	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:583:A:H2'	1:AA:584:G:O4'	2.12	0.50
38:BY:13:VAL:HG13	38:BY:72:VAL:HB	1.94	0.50
1:AA:1037:C:C4	1:AA:1038:C:N4	2.80	0.50
1:AA:1143:G:O5'	1:AA:1143:G:H8	1.94	0.50
51:BC:65:PRO:O	51:BC:188:ASN:OD1	2.30	0.50
25:BA:7:G:H2'	25:BA:8:A:O4'	2.11	0.50
25:BA:1058:G:H8	25:BA:1058:G:H5'	1.75	0.50
27:BN:131:GLN:HE22	27:BN:134:ARG:HH21	1.59	0.50
14:AT:89:ARG:CZ	14:AT:104:LEU:HD21	2.42	0.50
51:BC:180:PHE:C	51:BC:181:PRO:O	2.50	0.50
25:BA:1418:G:H8	25:BA:1418:G:O5'	1.95	0.50
1:AA:961:U:OP2	1:AA:1223:C:H1'	2.12	0.50
53:BF:18:ARG:NH2	53:BF:20:LEU:HD12	2.27	0.50
56:BK:134:MET:HG3	56:BK:136:VAL:HG12	1.94	0.50
25:BA:2824:C:H2'	25:BA:2825:C:O4'	2.12	0.50
25:BA:316:C:H2'	25:BA:317:G:O5'	2.11	0.50
26:BB:13:A:N1	26:BB:69:G:O2'	2.39	0.50
25:BA:1615:C:C2	36:BW:87:PRO:HG2	2.47	0.50
8:AN:15:LYS:O	8:AN:16:PHE:O	2.30	0.50
26:BB:77:U:P	39:BZ:19:ARG:NH2	2.85	0.49
52:BE:132:HIS:CD2	52:BE:135:HIS:NE2	2.80	0.49
35:BV:47:VAL:HB	35:BV:49:THR:O	2.12	0.49
1:AA:1367:C:OP2	22:AI:112:LYS:NZ	2.45	0.49
35:BV:19:LYS:HG3	35:BV:20:LEU:C	2.32	0.49
55:BH:89:ILE:HD13	55:BH:94:TYR:CB	2.42	0.49
55:BH:89:ILE:HD13	55:BH:94:TYR:HB3	1.93	0.49
49:B8:50:LEU:HA	49:B8:53:PRO:HD3	1.94	0.49
53:BF:53:THR:HB	53:BF:56:GLU:OE2	2.12	0.49
1:AA:1147:C:O2	22:AI:16:ARG:NH1	2.44	0.49
25:BA:2821:A:OP2	52:BE:110:GLY:O	2.30	0.49
26:BB:12:C:O2'	40:B0:74:ARG:HG2	2.12	0.49
25:BA:94:C:H5'	25:BA:94(A):G:OP2	2.11	0.49
25:BA:467:G:OP1	48:B7:33:ARG:NH1	2.44	0.49
43:BD:32:SER:O	43:BD:36:PRO:HD3	2.12	0.49
42:B2:38:GLN:CD	42:B2:44:LEU:HD13	2.33	0.49
23:AY:162:VAL:CG2	23:AY:255:ILE:HG12	2.41	0.49
26:BB:81:G:O6	26:BB:96:U:C2	2.66	0.49
31:BR:2:ARG:NE	52:BE:111:ARG:HA	2.27	0.49
25:BA:664:C:H4'	25:BA:941:A:OP1	2.11	0.49
1:AA:1263:C:C2	1:AA:1273:G:N2	2.81	0.49
35:BV:69:LYS:HA	35:BV:87:HIS:O	2.12	0.49
25:BA:907:U:OP1	30:BQ:24:GLY:N	2.42	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2814:C:O2'	46:B5:29:THR:HG21	2.12	0.49
33:BT:83:ILE:HG13	33:BT:84:GLN:H	1.76	0.49
25:BA:2420:C:OP1	49:B8:34:TRP:CB	2.60	0.49
1:AA:1293:G:H5''	1:AA:1293:G:C8	2.44	0.49
15:AB:211:ILE:CG2	15:AB:215:LEU:HD23	2.43	0.49
15:AB:32:ILE:HD11	15:AB:40:HIS:CG	2.47	0.49
26:BB:4:C:H2'	26:BB:5:C:O4'	2.11	0.49
45:B4:62:CYS:C	45:B4:64:LYS:H	2.14	0.49
20:AG:116:ALA:O	20:AG:120:ILE:HD12	2.12	0.49
23:AY:98:MET:HA	23:AY:98:MET:CE	2.42	0.49
25:BA:1204:A:N1	25:BA:1241:A:N1	2.61	0.49
7:AM:87:TYR:O	7:AM:91:ARG:HG2	2.12	0.49
7:AM:40:ASN:HB3	7:AM:43:THR:HG23	1.93	0.49
15:AB:167:PRO:HG3	15:AB:188:ALA:HB2	1.94	0.49
4:AJ:54:PHE:CZ	4:AJ:55:LYS:HE3	2.47	0.49
25:BA:2787:C:H1'	52:BE:61:ARG:HD3	1.94	0.49
15:AB:17:PHE:CB	15:AB:44:LEU:HD21	2.42	0.49
25:BA:2334:G:N3	32:BS:18:ILE:HD12	2.27	0.49
26:BB:1:U:O2	26:BB:1:U:C2'	2.61	0.49
15:AB:165:VAL:HG23	15:AB:166:ASP:N	2.27	0.49
18:AE:32:VAL:HB	18:AE:58:ALA:HB1	1.93	0.49
23:AY:546:ILE:HG12	23:AY:590:ILE:HG13	1.95	0.49
1:AA:1173:G:H2'	1:AA:1174:G:O4'	2.11	0.49
25:BA:2291:U:OP1	25:BA:2381:C:H5'	2.13	0.49
1:AA:1541:U:H2'	1:AA:1542:U:H4'	1.94	0.49
25:BA:1644:C:H2'	25:BA:1645:G:H5'	1.94	0.49
53:BF:103:LYS:HA	53:BF:106:ARG:HG3	1.94	0.49
38:BY:77:PRO:O	38:BY:78:ALA:CB	2.61	0.49
33:BT:28:VAL:O	33:BT:29:ARG:CG	2.60	0.49
25:BA:2165:G:H2'	25:BA:2166:G:C5'	2.42	0.49
15:AB:33:TYR:HB2	15:AB:43:ASP:HB2	1.94	0.49
25:BA:582:G:H2'	25:BA:583:G:C8	2.48	0.49
25:BA:2441:C:OP2	25:BA:2586:C:O2'	2.29	0.49
13:AS:19:VAL:O	13:AS:22:LEU:HB2	2.13	0.49
25:BA:2285:C:OP2	47:B6:27:LYS:HB3	2.12	0.49
52:BE:46:ALA:HA	52:BE:82:ARG:O	2.13	0.49
1:AA:1486:G:H2'	1:AA:1487:G:O4'	2.12	0.49
1:AA:706:A:C4'	5:AK:29:ILE:HD11	2.41	0.49
43:BD:24:ILE:HD13	43:BD:25:THR:N	2.27	0.49
25:BA:1058:G:OP1	25:BA:1058:G:H4'	2.11	0.49
15:AB:165:VAL:O	15:AB:187:LEU:O	2.30	0.49
54:BG:4:ASP:HB2	54:BG:8:LYS:HG2	1.95	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
57:BJ:6:ALA:O	57:BJ:7:ALA:HB3	2.13	0.49
25:BA:90:U:C2'	25:BA:92:A:OP2	2.55	0.49
29:BP:65:ARG:O	29:BP:66:GLY:C	2.51	0.49
29:BP:66:GLY:O	29:BP:67:MET:HB3	2.12	0.49
46:B5:50:GLY:O	46:B5:51:TYR:CB	2.60	0.49
27:BN:42:TRP:O	34:BU:64:ARG:NH1	2.38	0.49
47:B6:15:GLU:HG2	47:B6:18:ARG:HE	1.78	0.49
25:BA:2151:G:H5''	25:BA:2151:G:C8	2.48	0.49
23:AY:413:ILE:HG21	23:AY:451:ILE:HD12	1.95	0.49
25:BA:1299:G:H5''	25:BA:1301:A:H5''	1.94	0.49
42:B2:45:SER:O	42:B2:46:GLN:CD	2.51	0.49
29:BP:23:PRO:O	29:BP:33:ARG:NH1	2.46	0.49
26:BB:50:G:OP1	32:BS:62:LYS:HB2	2.12	0.49
56:BK:17:ALA:HB3	56:BK:38:VAL:HG13	1.93	0.49
32:BS:89:ARG:HG2	32:BS:92:TYR:HA	1.93	0.49
25:BA:1150:C:H2'	25:BA:1151:G:O4'	2.13	0.49
31:BR:2:ARG:C	31:BR:3:HIS:O	2.50	0.49
1:AA:1152:A:H2'	1:AA:1153:C:C6	2.46	0.49
57:BJ:124:ALA:HB3	57:BJ:127:ALA:HB3	1.93	0.49
28:BO:23:ARG:HG3	28:BO:24:VAL:N	2.27	0.49
31:BR:45:ARG:HA	31:BR:95:THR:HG21	1.94	0.49
13:AS:9:VAL:O	13:AS:11:VAL:N	2.45	0.49
1:AA:33:A:N3	6:AL:32:PHE:HE2	2.10	0.49
1:AA:1066:C:O2'	1:AA:1067:A:H5'	2.13	0.49
17:AD:30:LYS:C	17:AD:32:ALA:N	2.64	0.49
16:AC:180:ALA:O	16:AC:181:ASN:CB	2.56	0.49
1:AA:1118:C:H1'	1:AA:1179:A:C5	2.48	0.49
23:AY:210:ARG:C	23:AY:212:TYR:H	2.10	0.49
51:BC:138:PRO:HA	51:BC:144:THR:OG1	2.13	0.49
42:B2:45:SER:O	42:B2:45:SER:OG	2.30	0.49
25:BA:1076:C:O2	25:BA:1076:C:O2'	2.31	0.49
25:BA:1451:C:N3	25:BA:1459:G:O6	2.45	0.49
25:BA:638:G:C5	25:BA:651:G:C2	3.00	0.49
49:B8:50:LEU:HD12	49:B8:51:ALA:H	1.78	0.49
25:BA:2327:A:H2'	25:BA:2328:A:C8	2.48	0.49
39:BZ:23:LYS:HD2	39:BZ:23:LYS:N	2.27	0.49
25:BA:570:G:C6	25:BA:2030:A:C2	3.00	0.49
25:BA:492:A:H2'	25:BA:493:G:O4'	2.13	0.49
41:B1:8:SER:HB3	41:B1:66:HIS:CD2	2.48	0.49
1:AA:790:A:H2'	1:AA:791:G:C8	2.47	0.49
25:BA:263:C:O2'	25:BA:429:A:N3	2.40	0.49
25:BA:2103:C:C3'	25:BA:2104:G:H5''	2.42	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:AH:112:LEU:HD23	21:AH:112:LEU:N	2.27	0.49
1:AA:1297:C:N3	20:AG:115:ARG:NH2	2.61	0.49
25:BA:748:G:C8	36:BW:89:ALA:HB1	2.48	0.49
29:BP:62:LEU:CD1	49:B8:30:ARG:HG2	2.42	0.49
35:BV:64:HIS:CE1	35:BV:92:THR:HG22	2.47	0.49
47:B6:19:ARG:NH1	47:B6:43:CYS:SG	2.81	0.49
25:BA:674:G:O2'	53:BF:74:ARG:HD3	2.13	0.49
6:AL:60:LEU:HB2	6:AL:64:TYR:O	2.12	0.49
56:BK:57:ILE:HD12	56:BK:57:ILE:N	2.28	0.49
25:BA:637:A:H4'	25:BA:638:G:O5'	2.13	0.49
25:BA:1241:A:H2'	25:BA:1242:A:O5'	2.13	0.49
23:AY:129:LYS:HB3	23:AY:253:LEU:HD11	1.95	0.49
53:BF:185:ASP:OD1	53:BF:188:ARG:NH1	2.41	0.49
17:AD:32:ALA:O	17:AD:36:ARG:N	2.46	0.49
36:BW:5:ALA:CB	36:BW:50:VAL:HG23	2.43	0.49
1:AA:59:A:C2'	1:AA:60:A:OP1	2.61	0.49
15:AB:109:SER:C	15:AB:111:ARG:N	2.66	0.49
49:B8:51:ALA:O	49:B8:54:GLU:HB2	2.13	0.49
28:BO:1:MET:HE2	28:BO:32:TYR:CE2	2.47	0.49
52:BE:16:ARG:O	52:BE:18:ASP:N	2.46	0.49
52:BE:14:ILE:HD11	52:BE:173:VAL:HG11	1.94	0.49
30:BQ:42:ILE:HD13	30:BQ:97:VAL:HB	1.95	0.49
52:BE:201:THR:OG1	52:BE:202:LYS:N	2.46	0.49
37:BX:57:LEU:HD22	37:BX:78:LYS:HG2	1.94	0.49
1:AA:946:A:H2'	1:AA:947:G:C8	2.48	0.49
25:BA:1914:C:O2'	25:BA:1915:U:O4'	2.30	0.48
46:B5:52:TYR:CD1	46:B5:52:TYR:C	2.86	0.48
52:BE:132:HIS:ND1	52:BE:132:HIS:O	2.46	0.48
15:AB:91:PRO:HG3	15:AB:155:LEU:HB2	1.94	0.48
1:AA:45:U:H2'	1:AA:46:G:C8	2.47	0.48
25:BA:2836:U:C4	25:BA:2883:A:N6	2.81	0.48
1:AA:1226:C:OP1	13:AS:81:ARG:HD2	2.13	0.48
2:AV:56:C:H2'	2:AV:57:G:H5''	1.94	0.48
32:BS:99:LYS:C	32:BS:101:LEU:H	2.16	0.48
25:BA:1632:A:C5	25:BA:1633:G:C6	3.01	0.48
29:BP:116:GLY:H	29:BP:134:ALA:HB2	1.78	0.48
34:BU:9:VAL:O	34:BU:13:LYS:HE3	2.12	0.48
25:BA:1356:G:N2	25:BA:1376:C:C2	2.81	0.48
46:B5:4:HIS:CB	46:B5:5:PRO:HD3	2.35	0.48
2:AV:43:C:H4'	2:AV:44:G:OP1	2.13	0.48
25:BA:1952:A:OP1	28:BO:42:SER:OG	2.25	0.48
16:AC:164:ARG:O	16:AC:165:THR:HB	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
26:BB:48:A:OP1	32:BS:92:TYR:O	2.31	0.48
25:BA:1584:C:O2'	25:BA:1584:C:O2	2.28	0.48
25:BA:2875:C:O2'	33:BT:5:ALA:HB3	2.12	0.48
1:AA:791:G:C6	1:AA:792:A:N7	2.81	0.48
25:BA:1379:A:H4'	25:BA:1380:G:OP2	2.13	0.48
25:BA:2140:C:H5	25:BA:2151:G:H1	1.61	0.48
25:BA:1021:A:H8	25:BA:1021:A:H3'	1.78	0.48
33:BT:106:SER:O	33:BT:107:ASP:CB	2.61	0.48
49:B8:50:LEU:HG	49:B8:51:ALA:N	2.28	0.48
25:BA:272(J):C:H2'	25:BA:274:G:OP1	2.13	0.48
53:BF:9:ILE:HG23	53:BF:13:SER:O	2.13	0.48
53:BF:9:ILE:HG22	53:BF:9:ILE:O	2.13	0.48
16:AC:124:ILE:HG12	16:AC:130:VAL:HG22	1.95	0.48
37:BX:12:VAL:HG12	37:BX:29:TRP:CE2	2.48	0.48
25:BA:1002:G:H2'	25:BA:1003:G:O5'	2.13	0.48
1:AA:192:U:O2'	14:AT:57:ARG:HG2	2.13	0.48
25:BA:500:G:N2	25:BA:502:A:H3'	2.28	0.48
23:AY:517:LEU:HD11	23:AY:564:LYS:HB2	1.94	0.48
25:BA:330:A:H2	25:BA:1210:A:C2'	2.17	0.48
1:AA:975:A:N6	1:AA:1367:C:O4'	2.47	0.48
8:AN:41:ARG:HG2	8:AN:41:ARG:HH11	1.79	0.48
1:AA:760:G:O2'	11:AQ:98:LEU:HD23	2.12	0.48
25:BA:2849:U:P	33:BT:95:ARG:HH12	2.36	0.48
25:BA:2114:A:H2'	25:BA:2167:U:O2'	2.13	0.48
25:BA:2477:C:H1'	25:BA:2481:G:O6	2.14	0.48
1:AA:376:G:P	10:AP:67:THR:HG21	2.53	0.48
25:BA:118:A:C8	25:BA:119:A:C8	3.00	0.48
1:AA:1346:A:C8	20:AG:10:ARG:NH2	2.81	0.48
25:BA:2262:U:OP1	25:BA:2387:U:O2'	2.23	0.48
47:B6:33:LYS:HA	47:B6:33:LYS:HE2	1.94	0.48
1:AA:714:G:H2'	1:AA:715:A:C8	2.48	0.48
25:BA:244:A:C2	25:BA:255:A:C4	3.01	0.48
25:BA:1224:C:O2'	35:BV:85:LYS:HA	2.13	0.48
1:AA:29:G:O2'	1:AA:30:U:H5'	2.13	0.48
16:AC:12:LEU:HD13	16:AC:18:TRP:CE2	2.48	0.48
23:AY:301:ILE:HG22	23:AY:332:SER:HB2	1.96	0.48
25:BA:2801(A):A:H4'	25:BA:2802:G:H5'	1.95	0.48
25:BA:2467:C:H4'	30:BQ:123:HIS:CD2	2.48	0.48
1:AA:1132:C:N3	1:AA:1142:G:N2	2.59	0.48
25:BA:620:G:H4'	25:BA:621:A:H5''	1.95	0.48
1:AA:1445:C:C4	1:AA:1446:U:C4	3.01	0.48
17:AD:25:ARG:C	17:AD:27:TYR:N	2.65	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:738:C:H5''	19:AF:69:GLU:HB2	1.95	0.48
1:AA:1061:G:OP1	4:AJ:59:SER:OG	2.23	0.48
25:BA:1380:G:C2	25:BA:1381:G:C8	3.01	0.48
1:AA:299:G:H2'	1:AA:300:A:C8	2.49	0.48
22:AI:95:LYS:NZ	22:AI:96:LEU:HD13	2.29	0.48
25:BA:2600:A:O2'	25:BA:2601:C:H5'	2.13	0.48
25:BA:2155:G:C6	25:BA:2156:G:C4	3.01	0.48
58:BL:61:UNK:O	58:BL:62:UNK:CB	2.61	0.48
25:BA:2272:U:H5''	25:BA:2273:A:OP1	2.14	0.48
31:BR:33:ARG:HD2	46:B5:55:ARG:HG2	1.94	0.48
16:AC:24:ALA:HB1	16:AC:28:GLN:HB2	1.95	0.48
21:AH:83:ILE:HG13	21:AH:137:VAL:HG22	1.95	0.48
9:AO:16:ALA:HB1	9:AO:21:ASP:HB3	1.94	0.48
25:BA:1332:G:C2	25:BA:1609:A:O2'	2.54	0.48
1:AA:149:A:O2'	1:AA:150:C:P	2.71	0.48
1:AA:389:A:C6	1:AA:390:C:H1'	2.48	0.48
1:AA:986:A:H1'	13:AS:54:GLY:O	2.13	0.48
25:BA:848:G:C4	25:BA:933:A:H8	2.32	0.48
25:BA:2023:G:H4'	25:BA:2617:C:O3'	2.14	0.48
25:BA:1977:A:H2'	25:BA:1978:A:O5'	2.13	0.48
25:BA:1278:A:H4'	31:BR:34:ILE:HD12	1.96	0.48
25:BA:1329:U:H5''	25:BA:1330:C:H5	1.78	0.48
25:BA:2123:G:H2'	25:BA:2124:G:O4'	2.13	0.48
49:B8:62:LEU:N	49:B8:63:PRO:CD	2.76	0.48
38:BY:7:VAL:HB	38:BY:8:LYS:HD2	1.96	0.48
1:AA:1004:A:C8	1:AA:1036:G:O6	2.67	0.48
43:BD:176:ARG:HA	43:BD:182:LEU:HD23	1.95	0.48
14:AT:75:ASN:O	14:AT:79:ARG:HB2	2.14	0.48
25:BA:1449:A:C8	25:BA:1449:A:H5''	2.48	0.48
25:BA:518:G:H4'	36:BW:18:ARG:NH1	2.29	0.48
17:AD:23:GLY:HA3	17:AD:112:VAL:HG22	1.96	0.48
26:BB:13:A:OP2	40:B0:74:ARG:NH2	2.45	0.48
30:BQ:39:PRO:HA	30:BQ:97:VAL:O	2.13	0.48
53:BF:164:ARG:HG3	53:BF:175:THR:OG1	2.14	0.48
23:AY:458:HIS:O	23:AY:461:ILE:HG13	2.13	0.48
25:BA:1546:C:H6	25:BA:1546:C:H5''	1.78	0.48
25:BA:1199:U:H2'	25:BA:1200:C:O4'	2.14	0.48
25:BA:1528:A:H2	25:BA:1542:A:H62	1.58	0.48
47:B6:15:GLU:OE2	47:B6:41:PRO:CB	2.62	0.48
25:BA:528:A:C2	25:BA:2042:A:H2'	2.48	0.48
33:BT:28:VAL:CG1	33:BT:46:GLU:HB2	2.44	0.48
1:AA:428:G:H4'	1:AA:429:U:O5'	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1456:G:O4'	1:AA:1456:G:OP1	2.31	0.48
25:BA:958:U:OP2	30:BQ:14:ARG:HD3	2.12	0.48
52:BE:116:VAL:O	52:BE:117:MET:HB3	2.13	0.48
25:BA:2392:A:N1	25:BA:2424:C:N3	2.61	0.48
1:AA:460:G:C6	1:AA:470:C:C5'	2.96	0.48
27:BN:93:THR:OG1	27:BN:94:HIS:CD2	2.67	0.48
1:AA:345:C:H4'	1:AA:346:G:O5'	2.14	0.48
25:BA:2155:G:H2'	25:BA:2156:G:O5'	2.14	0.48
25:BA:1637:A:H5'	25:BA:1760:A:O2'	2.14	0.48
27:BN:30:ILE:HG23	27:BN:52:VAL:HG11	1.96	0.48
21:AH:107:LEU:N	21:AH:107:LEU:HD23	2.29	0.48
1:AA:520:A:N1	1:AA:536:C:H1'	2.29	0.48
27:BN:67:LEU:O	27:BN:68:GLU:HB2	2.13	0.48
25:BA:2649:U:H2'	25:BA:2650:U:C6	2.48	0.48
53:BF:107:LYS:HD2	53:BF:205:ARG:O	2.14	0.48
49:B8:23:VAL:CG1	49:B8:46:ARG:HD3	2.44	0.48
25:BA:819:A:H2'	25:BA:820:A:H5'	1.95	0.48
1:AA:155:C:H2'	1:AA:156:G:C8	2.49	0.48
52:BE:55:ASN:C	52:BE:57:LYS:H	2.16	0.48
52:BE:55:ASN:O	52:BE:57:LYS:HD3	2.14	0.48
56:BK:105:LEU:CD2	56:BK:120:LEU:HD13	2.44	0.48
53:BF:65:TRP:HB2	53:BF:66:PRO:CD	2.43	0.48
1:AA:62:U:H5''	1:AA:385:C:O2'	2.13	0.48
32:BS:106:ARG:HD2	32:BS:107:GLU:O	2.14	0.48
36:BW:20:VAL:HG22	36:BW:47:VAL:HG21	1.96	0.48
25:BA:1364:G:OP2	41:B1:61:ARG:NH2	2.45	0.48
1:AA:441:A:OP2	1:AA:441:A:H8	1.96	0.48
16:AC:174:PRO:HD2	16:AC:182:ILE:HD11	1.95	0.48
29:BP:35:HIS:C	29:BP:36:LYS:HG3	2.33	0.48
25:BA:1494:A:C2'	25:BA:1495:A:H5''	2.43	0.48
34:BU:65:ILE:HG12	34:BU:96:ALA:HB3	1.96	0.48
38:BY:13:VAL:O	38:BY:24:VAL:HA	2.14	0.48
43:BD:27:THR:CG2	43:BD:83:GLU:OE2	2.62	0.48
25:BA:2517:C:C6	25:BA:2542:A:C2	3.01	0.48
1:AA:1013:G:H22	1:AA:1015:A:H3'	1.79	0.48
52:BE:76:ARG:HA	52:BE:77:ILE:HG12	1.95	0.48
29:BP:146:VAL:O	29:BP:148:LEU:HG	2.14	0.48
20:AG:5:ARG:HH11	20:AG:5:ARG:HB2	1.77	0.48
22:AI:48:GLU:N	22:AI:49:PRO:HD2	2.28	0.48
23:AY:242:LEU:O	23:AY:245:ALA:N	2.46	0.48
25:BA:1488:G:C5	25:BA:1489:U:C5	3.02	0.48
55:BH:154:PRO:HB3	55:BH:163:TYR:CZ	2.49	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
27:BN:66:LYS:O	27:BN:70:LYS:HB3	2.14	0.48
25:BA:784:A:C6	43:BD:229:VAL:HG11	2.49	0.48
5:AK:105:VAL:O	5:AK:105:VAL:HG23	2.13	0.48
1:AA:1202:G:H1'	8:AN:29:ARG:HD2	1.96	0.47
29:BP:17:LYS:C	29:BP:19:VAL:H	2.14	0.47
25:BA:1301:A:C8	25:BA:1303:G:C8	3.02	0.47
15:AB:155:LEU:HD12	15:AB:157:ARG:O	2.14	0.47
1:AA:881:G:P	6:AL:12:ARG:HH22	2.37	0.47
17:AD:11:LEU:O	17:AD:13:ARG:O	2.32	0.47
25:BA:652:C:O2'	25:BA:652:C:O2	2.28	0.47
27:BN:115:ARG:O	27:BN:119:ARG:HG2	2.14	0.47
15:AB:142:LEU:HD21	15:AB:146:GLN:OE1	2.13	0.47
56:BK:13:PRO:HA	56:BK:52:ILE:HA	1.94	0.47
25:BA:364:C:OP2	25:BA:365:C:OP2	2.32	0.47
16:AC:40:ARG:O	16:AC:44:GLU:HB2	2.14	0.47
25:BA:2870:C:H2'	25:BA:2871:C:O4'	2.14	0.47
53:BF:3:GLU:O	53:BF:19:GLU:HA	2.14	0.47
25:BA:882:G:H2'	25:BA:883:G:C8	2.48	0.47
25:BA:883:G:N2	25:BA:893:C:O2	2.47	0.47
55:BH:173:PRO:O	55:BH:174:GLY:C	2.52	0.47
30:BQ:27:VAL:O	30:BQ:28:ALA:CB	2.62	0.47
35:BV:2:PHE:O	35:BV:3:ALA:O	2.31	0.47
28:BO:114:ILE:HD12	28:BO:114:ILE:H	1.79	0.47
25:BA:470:A:H2'	25:BA:471:A:O4'	2.14	0.47
39:BZ:22:GLY:C	39:BZ:23:LYS:HD2	2.35	0.47
15:AB:165:VAL:HG23	15:AB:166:ASP:H	1.79	0.47
54:BG:4:ASP:CB	54:BG:8:LYS:HG2	2.43	0.47
53:BF:152:GLU:OE1	53:BF:191:ARG:HD2	2.15	0.47
1:AA:1059:C:O3'	8:AN:45:ARG:NH2	2.47	0.47
32:BS:24:LEU:O	32:BS:85:VAL:HB	2.14	0.47
30:BQ:116:GLU:OE1	30:BQ:116:GLU:HA	2.13	0.47
14:AT:49:ALA:HB2	14:AT:92:LEU:HD22	1.96	0.47
1:AA:731:G:H5'	1:AA:766:A:H4'	1.96	0.47
1:AA:264:U:H2'	1:AA:265:G:O4'	2.14	0.47
25:BA:1905:C:H2'	25:BA:1930:G:C8	2.49	0.47
33:BT:30:VAL:HG23	33:BT:30:VAL:O	2.14	0.47
25:BA:714:U:H2'	25:BA:716:A:OP2	2.15	0.47
2:AV:35:A:H8	2:AV:35:A:C5'	2.27	0.47
15:AB:145:LEU:HD12	15:AB:149:LEU:HD12	1.96	0.47
25:BA:1078:U:OP1	25:BA:1078:U:H4'	2.15	0.47
23:AY:162:VAL:HG21	23:AY:255:ILE:CG1	2.42	0.47
30:BQ:27:VAL:HG12	30:BQ:28:ALA:N	2.29	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
32:BS:89:ARG:O	32:BS:92:TYR:HB3	2.14	0.47
32:BS:97:ARG:HH21	32:BS:98:VAL:HA	1.79	0.47
25:BA:2876:G:O5'	33:BT:3:ARG:HB3	2.14	0.47
1:AA:756:C:H2'	1:AA:757:U:O4'	2.15	0.47
25:BA:2023:G:H5'	25:BA:2617:C:H4'	1.95	0.47
7:AM:54:VAL:O	7:AM:55:ARG:C	2.53	0.47
25:BA:239:U:H2'	25:BA:240:G:O4'	2.14	0.47
17:AD:134:ASP:OD2	17:AD:135:LEU:HD13	2.13	0.47
53:BF:5:ALA:O	53:BF:6:VAL:CG2	2.62	0.47
23:AY:401:SER:OG	23:AY:402:ILE:N	2.47	0.47
25:BA:2316:C:O2'	54:BG:128:ARG:NH2	2.47	0.47
25:BA:1539:G:N2	25:BA:1540:U:C2	2.82	0.47
25:BA:1899:G:O2'	25:BA:1900:A:OP2	2.27	0.47
38:BY:7:VAL:HG13	38:BY:83:THR:HG21	1.97	0.47
27:BN:47:ALA:HB2	27:BN:112:LEU:HD11	1.96	0.47
25:BA:71:A:H8	25:BA:71:A:H5'	1.76	0.47
54:BG:59:GLU:HA	54:BG:62:LEU:HD22	1.95	0.47
55:BH:6:ARG:CB	55:BH:65:HIS:CD2	2.97	0.47
18:AE:6:PHE:CE1	18:AE:66:MET:HE1	2.49	0.47
1:AA:750:G:N3	9:AO:23:GLY:HA3	2.28	0.47
55:BH:17:VAL:O	55:BH:45:VAL:HG13	2.14	0.47
1:AA:1203:C:OP1	8:AN:3:ARG:HD3	2.13	0.47
18:AE:93:PRO:HG2	21:AH:105:ARG:NH2	2.29	0.47
25:BA:271(L):U:H4'	25:BA:271(M):G:C5	2.50	0.47
39:BZ:51:ALA:HB1	39:BZ:57:ILE:HD11	1.95	0.47
1:AA:659:U:O2'	1:AA:660:G:H5'	2.14	0.47
25:BA:558:G:H1'	27:BN:45:ASN:HB3	1.95	0.47
43:BD:32:SER:O	43:BD:36:PRO:CD	2.62	0.47
25:BA:9:U:O2'	25:BA:10:G:P	2.73	0.47
29:BP:146:VAL:HG13	29:BP:147:LEU:H	1.78	0.47
25:BA:2492:U:O2'	25:BA:2493:U:H5'	2.13	0.47
52:BE:111:ARG:HD2	52:BE:160:TYR:CE1	2.50	0.47
25:BA:889:C:O2	25:BA:889:C:O4'	2.29	0.47
25:BA:1429:G:H2'	25:BA:1430:C:C6	2.50	0.47
32:BS:56:LEU:HD23	32:BS:56:LEU:O	2.15	0.47
25:BA:285:C:H2'	25:BA:286:C:C6	2.50	0.47
25:BA:478:A:N1	25:BA:500:G:H4'	2.29	0.47
31:BR:34:ILE:HD13	31:BR:34:ILE:HA	1.78	0.47
1:AA:571:U:H6	1:AA:571:U:O5'	1.97	0.47
22:AI:54:ASP:O	22:AI:56:LEU:N	2.45	0.47
43:BD:147:LEU:HD12	43:BD:155:LEU:HD21	1.96	0.47
25:BA:2308:G:N7	25:BA:2310:A:H5'	2.30	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1538:G:O2'	25:BA:1539:G:O5'	2.24	0.47
25:BA:2134:A:C8	25:BA:2159:G:O2'	2.63	0.47
25:BA:1786:A:H2	25:BA:2606:C:H1'	1.76	0.47
25:BA:806:C:OP2	29:BP:39:LYS:HB3	2.15	0.47
25:BA:1406:U:H2'	25:BA:1407:C:C6	2.49	0.47
25:BA:1407:C:H5'	25:BA:1408:C:OP2	2.14	0.47
38:BY:2:ARG:O	38:BY:4:LYS:HG3	2.14	0.47
33:BT:28:VAL:HG21	33:BT:46:GLU:HG3	1.97	0.47
1:AA:673:G:OP1	19:AF:87:ARG:HD3	2.15	0.47
56:BK:59:ILE:HG12	56:BK:60:TYR:H	1.78	0.47
23:AY:250:THR:HA	23:AY:255:ILE:HG22	1.97	0.47
25:BA:71:A:OP2	25:BA:71:A:H3'	2.14	0.47
4:AJ:35:SER:OG	4:AJ:73:ASP:HB2	2.15	0.47
25:BA:2591:C:OP2	43:BD:239:ARG:HB3	2.14	0.47
35:BV:2:PHE:HB3	35:BV:42:GLY:HA3	1.96	0.47
23:AY:377:VAL:HG21	23:AY:380:LEU:HD22	1.96	0.47
55:BH:23:ARG:C	55:BH:24:VAL:HG12	2.35	0.47
25:BA:814:C:H2'	25:BA:815:C:H6	1.79	0.47
54:BG:18:GLU:O	54:BG:22:ARG:N	2.47	0.47
1:AA:779:C:H2'	1:AA:780:A:O4'	2.14	0.47
36:BW:9:TYR:H	36:BW:102:HIS:HD2	1.62	0.47
36:BW:69:LEU:HA	36:BW:108:GLY:O	2.15	0.47
1:AA:1333:A:H2'	1:AA:1334:G:O4'	2.13	0.47
1:AA:1318:A:H1'	13:AS:37:ARG:HH21	1.79	0.47
1:AA:1465:C:H2'	1:AA:1466:C:O4'	2.15	0.47
57:BJ:46:ALA:O	57:BJ:47:ALA:HB2	2.14	0.47
23:AY:319:ASP:OD1	23:AY:322:VAL:HG22	2.15	0.47
41:B1:29:GLY:O	41:B1:30:VAL:HG13	2.14	0.47
43:BD:32:SER:HA	43:BD:35:LYS:NZ	2.30	0.47
47:B6:16:CYS:O	47:B6:18:ARG:CZ	2.62	0.47
43:BD:26:LYS:HG2	43:BD:81:ALA:HA	1.97	0.47
1:AA:1368:G:OP2	22:AI:112:LYS:CD	2.61	0.47
23:AY:438:PHE:CZ	23:AY:451:ILE:HG12	2.49	0.47
1:AA:148:G:C2	1:AA:175:C:C2	3.03	0.47
23:AY:218:GLU:O	23:AY:221:ALA:HB3	2.15	0.47
42:B2:44:LEU:O	42:B2:45:SER:CB	2.62	0.47
23:AY:92:ILE:O	23:AY:96:ARG:HB2	2.15	0.47
1:AA:1307:U:H2'	1:AA:1308:U:O4'	2.13	0.47
45:B4:64:LYS:C	45:B4:65:CYS:SG	2.93	0.47
30:BQ:137:TYR:OH	39:BZ:81:ARG:HD3	2.15	0.47
25:BA:2688:U:C5	25:BA:2720:U:OP2	2.67	0.47
25:BA:647:G:O5'	25:BA:647:G:H8	1.97	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:AH:38:ILE:HD11	21:AH:118:VAL:HG12	1.96	0.47
25:BA:2181:G:H2'	25:BA:2182:G:O5'	2.15	0.47
1:AA:938:A:N6	1:AA:939:G:C6	2.83	0.47
25:BA:479:A:N3	25:BA:481:G:H5''	2.30	0.47
54:BG:82:LEU:HD23	54:BG:83:ARG:H	1.79	0.47
1:AA:298:A:H2'	1:AA:299:G:O4'	2.14	0.47
25:BA:1283:G:N2	25:BA:1285:G:H3'	2.30	0.47
49:B8:23:VAL:HA	49:B8:47:LYS:O	2.15	0.47
1:AA:264:U:O2'	11:AQ:64:PRO:O	2.32	0.47
18:AE:76:ILE:O	18:AE:93:PRO:HB3	2.15	0.47
18:AE:37:ARG:C	18:AE:38:GLN:HG2	2.34	0.47
25:BA:129:C:H5''	25:BA:129:C:H6	1.79	0.47
25:BA:295:G:C8	25:BA:295:G:H5''	2.50	0.47
17:AD:81:GLU:OE1	17:AD:139:ARG:NH2	2.46	0.47
25:BA:2370:G:H2'	25:BA:2371:G:O4'	2.14	0.47
25:BA:1809:A:H2'	25:BA:1810:A:C8	2.50	0.47
5:AK:97:ALA:O	5:AK:101:SER:HB3	2.13	0.47
1:AA:590:C:OP1	21:AH:30:ARG:N	2.46	0.47
18:AE:84:PHE:HB3	18:AE:134:ALA:HB2	1.95	0.47
1:AA:547:A:H4'	1:AA:548:G:O5'	2.14	0.47
1:AA:456:C:H2'	1:AA:457:C:C6	2.49	0.47
53:BF:129:PHE:CD2	53:BF:163:VAL:HG21	2.50	0.47
33:BT:121:ILE:O	33:BT:124:ASP:HB2	2.14	0.47
25:BA:1653:G:H4'	25:BA:1654:A:O5'	2.15	0.47
25:BA:2712:U:O2	25:BA:2712:U:H2'	2.14	0.47
38:BY:74:PRO:O	38:BY:80:GLY:CA	2.60	0.47
25:BA:1540:U:H2'	25:BA:1541:G:O4'	2.15	0.47
29:BP:61:ARG:H	29:BP:61:ARG:HD2	1.80	0.47
1:AA:1277:C:C2'	1:AA:1279:A:H8	2.27	0.47
34:BU:91:ASP:O	34:BU:92:ARG:HB3	2.13	0.47
38:BY:20:TYR:O	38:BY:23:ARG:HB2	2.15	0.47
25:BA:1053:C:H2'	25:BA:1054:A:C5'	2.45	0.47
53:BF:132:VAL:HG22	53:BF:133:ASN:H	1.80	0.47
1:AA:407:G:OP1	17:AD:3:ARG:NH1	2.48	0.47
1:AA:1152:A:H5''	4:AJ:13:HIS:CD2	2.50	0.47
23:AY:461:ILE:C	23:AY:461:ILE:HD12	2.36	0.47
25:BA:1932:A:H2'	25:BA:1933:G:O4'	2.14	0.47
1:AA:863:U:O2'	1:AA:865:A:N7	2.33	0.47
26:BB:101:G:H2'	26:BB:102:A:O4'	2.15	0.47
37:BX:55:ASN:HD22	37:BX:55:ASN:N	2.12	0.47
25:BA:669:G:C2'	25:BA:669:G:N3	2.77	0.47
15:AB:238:LEU:O	15:AB:240:GLN:N	2.47	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:AF:60:PHE:C	19:AF:61:LEU:HD12	2.34	0.47
1:AA:712:A:H2'	1:AA:713:G:O4'	2.14	0.47
1:AA:515:G:H2'	1:AA:516:U:O4'	2.15	0.47
1:AA:437:U:H5''	17:AD:155:LEU:HD21	1.97	0.47
17:AD:187:ARG:NH2	17:AD:193:ASP:OD2	2.48	0.47
25:BA:1407:C:H6	25:BA:1407:C:H5''	1.76	0.47
10:AP:8:ARG:CG	10:AP:8:ARG:HH11	2.26	0.47
26:BB:32:C:C2	26:BB:51:G:N2	2.83	0.47
19:AF:69:GLU:O	19:AF:72:VAL:HG12	2.15	0.47
32:BS:53:SER:O	32:BS:55:ALA:N	2.47	0.47
25:BA:1906:G:N7	25:BA:1929:G:C8	2.82	0.47
20:AG:116:ALA:O	20:AG:120:ILE:CD1	2.63	0.47
26:BB:2:C:O2	26:BB:2:C:C2'	2.62	0.47
1:AA:538:G:H2'	1:AA:539:A:H8	1.80	0.47
23:AY:380:LEU:HD21	23:AY:389:LEU:HD21	1.97	0.47
1:AA:997:U:H6	1:AA:997:U:O5'	1.97	0.47
1:AA:1397:C:O2	1:AA:1397:C:O4'	2.33	0.47
25:BA:1794:U:H2'	25:BA:1795:C:C6	2.50	0.47
1:AA:1063:C:H3'	1:AA:1064:G:H2'	1.96	0.47
31:BR:28:LEU:HD12	31:BR:48:VAL:HG21	1.96	0.47
8:AN:25:VAL:HB	8:AN:38:GLY:O	2.15	0.47
34:BU:92:ARG:O	34:BU:93:LYS:C	2.54	0.47
38:BY:30:VAL:HG12	38:BY:31:LEU:N	2.29	0.47
33:BT:28:VAL:HG13	33:BT:46:GLU:CA	2.45	0.47
27:BN:17:ASP:OD2	27:BN:56:ASN:ND2	2.44	0.47
56:BK:17:ALA:CB	56:BK:38:VAL:HG22	2.43	0.47
23:AY:10:LYS:HD3	23:AY:10:LYS:O	2.15	0.47
7:AM:2:ALA:N	7:AM:9:ILE:HG23	2.30	0.47
6:AL:111:LYS:O	6:AL:112:ASP:HB2	2.16	0.47
41:B1:68:PRO:O	41:B1:69:LYS:C	2.52	0.47
23:AY:21:ILE:HD13	25:BA:2661:G:H5'	1.97	0.47
34:BU:92:ARG:NH1	34:BU:94:ASN:ND2	2.61	0.46
25:BA:607:U:C2	25:BA:621:A:N1	2.83	0.46
33:BT:28:VAL:HG13	33:BT:46:GLU:HB2	1.96	0.46
25:BA:1386:C:OP2	25:BA:1396:U:H5	1.97	0.46
25:BA:1742:G:C3'	25:BA:1742:G:C8	2.98	0.46
32:BS:28:VAL:HB	32:BS:89:ARG:HB2	1.97	0.46
25:BA:1790:C:H2'	25:BA:1791:A:C5	2.50	0.46
31:BR:28:LEU:HD22	31:BR:28:LEU:O	2.15	0.46
53:BF:117:ARG:HA	53:BF:117:ARG:HD3	1.57	0.46
25:BA:1865:G:H8	25:BA:1865:G:C5'	2.29	0.46
21:AH:44:PHE:CE2	21:AH:109:ILE:HG21	2.50	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
53:BF:84:VAL:O	53:BF:86:GLY:N	2.48	0.46
29:BP:7:ARG:NH1	29:BP:7:ARG:CA	2.62	0.46
25:BA:806:C:OP2	29:BP:39:LYS:HD3	2.15	0.46
53:BF:65:TRP:CB	53:BF:66:PRO:CD	2.94	0.46
1:AA:977:A:O2'	1:AA:979:C:OP2	2.26	0.46
5:AK:99:GLN:HA	5:AK:105:VAL:HG13	1.97	0.46
25:BA:391:G:H1'	25:BA:411:G:O4'	2.14	0.46
1:AA:710:G:OP1	19:AF:54:LYS:CE	2.63	0.46
32:BS:16:ASN:O	32:BS:19:LYS:CB	2.64	0.46
25:BA:1177:A:H4'	25:BA:1178:C:C6	2.50	0.46
13:AS:50:ALA:HB1	13:AS:57:HIS:HB3	1.98	0.46
17:AD:162:LEU:HD13	17:AD:181:MET:HG2	1.97	0.46
47:B6:39:TYR:HB3	47:B6:49:HIS:CD2	2.49	0.46
43:BD:58:HIS:HD2	43:BD:59:LYS:O	1.99	0.46
1:AA:162:A:H3'	1:AA:163:C:O4'	2.16	0.46
53:BF:101:LEU:HD12	53:BF:102:PRO:HD2	1.97	0.46
38:BY:7:VAL:HB	38:BY:8:LYS:HE3	1.96	0.46
53:BF:3:GLU:HA	53:BF:24:LEU:HB3	1.96	0.46
23:AY:89:ASP:HA	23:AY:454:MET:HB3	1.96	0.46
1:AA:1305:G:H22	1:AA:1331:G:H1'	1.80	0.46
27:BN:133:GLN:HG2	27:BN:134:ARG:N	2.30	0.46
7:AM:56:LEU:O	7:AM:59:TYR:N	2.49	0.46
1:AA:538:G:H2'	1:AA:539:A:C8	2.49	0.46
25:BA:2291:U:O2'	25:BA:2374:C:O2	2.28	0.46
25:BA:2341:G:H2'	25:BA:2342:C:C6	2.50	0.46
25:BA:1959:G:H2'	25:BA:1960:A:O5'	2.15	0.46
1:AA:722:A:N3	1:AA:722:A:H3'	2.30	0.46
25:BA:2086:U:H2'	25:BA:2087:G:C8	2.49	0.46
25:BA:527:C:OP2	25:BA:2779:U:H5	1.98	0.46
35:BV:15:GLU:O	35:BV:16:PRO:C	2.53	0.46
25:BA:250:G:H2'	25:BA:251:A:C8	2.51	0.46
25:BA:528:A:N1	25:BA:2043:C:O5'	2.48	0.46
1:AA:1446:U:H4'	1:AA:1447:A:C5	2.51	0.46
23:AY:684:GLN:O	23:AY:688:ILE:N	2.41	0.46
43:BD:68:LYS:HB2	43:BD:70:TRP:CH2	2.51	0.46
33:BT:108:ARG:HB3	33:BT:111:ARG:NH1	2.31	0.46
27:BN:132:ALA:C	27:BN:133:GLN:O	2.54	0.46
1:AA:263:A:P	14:AT:79:ARG:HH11	2.38	0.46
1:AA:629:G:H2'	1:AA:630:G:O4'	2.15	0.46
1:AA:1507:A:C2	1:AA:1508:G:C4	3.03	0.46
1:AA:938:A:C6	1:AA:939:G:C5	3.04	0.46
25:BA:476:G:H4'	25:BA:502:A:N1	2.30	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
51:BC:46:LYS:NZ	51:BC:168:THR:O	2.48	0.46
25:BA:215:G:O3'	25:BA:216:A:H4'	2.15	0.46
2:AV:15:G:H8	2:AV:15:G:OP2	1.98	0.46
51:BC:222:VAL:O	51:BC:224:ILE:HG23	2.14	0.46
25:BA:2533:A:H5''	25:BA:2665:A:O2'	2.16	0.46
25:BA:1353:A:H4'	43:BD:38:LYS:HE3	1.96	0.46
38:BY:28:LYS:HE3	38:BY:30:VAL:HG22	1.98	0.46
53:BF:24:LEU:HB3	53:BF:25:PRO:CD	2.38	0.46
25:BA:2290:G:C2	25:BA:2343:C:O2	2.69	0.46
23:AY:162:VAL:HG21	23:AY:255:ILE:CD1	2.45	0.46
25:BA:2477:C:O2	25:BA:2481:G:O6	2.33	0.46
15:AB:84:GLU:HG3	15:AB:215:LEU:HB3	1.96	0.46
1:AA:328:C:C2'	1:AA:328:C:O2	2.58	0.46
25:BA:1115:G:H2'	25:BA:1116:C:C6	2.51	0.46
33:BT:106:SER:O	33:BT:107:ASP:OD1	2.34	0.46
1:AA:1226:C:H5''	13:AS:81:ARG:HB3	1.96	0.46
4:AJ:90:LEU:HG	4:AJ:90:LEU:O	2.15	0.46
54:BG:135:LEU:HD22	54:BG:140:ILE:HD11	1.97	0.46
54:BG:82:LEU:HD22	54:BG:87:PRO:HB3	1.97	0.46
25:BA:2316:C:OP2	25:BA:2316:C:H6	1.99	0.46
1:AA:1237:C:C2'	1:AA:1238:A:OP1	2.63	0.46
1:AA:499:A:C6	1:AA:547:A:C8	3.03	0.46
25:BA:1865:G:H5''	25:BA:1865:G:H8	1.80	0.46
25:BA:2612:C:H2'	25:BA:2613:U:H5'	1.98	0.46
43:BD:65:ILE:HD11	43:BD:67:PHE:CZ	2.51	0.46
16:AC:54:ARG:NH1	16:AC:56:ASP:OD1	2.35	0.46
26:BB:27:C:O3'	32:BS:36:TYR:OH	2.31	0.46
25:BA:1914:C:H2'	25:BA:1914:C:OP1	2.15	0.46
29:BP:47:ASP:HB3	29:BP:48:PRO:CA	2.46	0.46
25:BA:2134:A:H8	25:BA:2159:G:O2'	1.98	0.46
52:BE:128:SER:O	52:BE:129:HIS:C	2.53	0.46
25:BA:1021:A:OP2	27:BN:65:LYS:NZ	2.48	0.46
9:AO:56:LEU:O	9:AO:60:VAL:HG23	2.16	0.46
25:BA:651:G:H4'	49:B8:18:ALA:HB3	1.98	0.46
40:B0:24:LYS:HG3	40:B0:36:ILE:HD11	1.98	0.46
25:BA:1434:A:O2'	25:BA:1435:G:H5'	2.16	0.46
7:AM:83:ASP:OD1	7:AM:84:ILE:N	2.49	0.46
52:BE:2:LYS:HD2	52:BE:95:ILE:HG23	1.96	0.46
22:AI:50:LEU:HB3	22:AI:56:LEU:HA	1.96	0.46
25:BA:2503:A:H5'	25:BA:2503:A:N3	2.31	0.46
23:AY:463:VAL:C	23:AY:465:ARG:H	2.19	0.46
7:AM:120:LYS:HE3	7:AM:121:LYS:O	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:BR:56:LYS:NZ	31:BR:90:ARG:O	2.48	0.46
18:AE:50:GLU:CD	18:AE:51:VAL:H	2.19	0.46
25:BA:1050:A:H2'	25:BA:1051:G:H8	1.79	0.46
25:BA:1086:A:H3'	25:BA:1086:A:N3	2.31	0.46
53:BF:157:VAL:HG23	53:BF:198:ALA:HB1	1.96	0.46
1:AA:807:A:H2'	1:AA:808:C:O4'	2.16	0.46
54:BG:48:GLU:O	54:BG:49:ASP:CB	2.63	0.46
25:BA:2125:G:H5''	25:BA:2126:A:OP1	2.16	0.46
39:BZ:73:GLN:HB3	39:BZ:87:ASP:HB2	1.96	0.46
29:BP:6:LEU:H	29:BP:6:LEU:HD23	1.81	0.46
1:AA:706:A:C2'	5:AK:31:THR:HG21	2.46	0.46
1:AA:973:G:C2'	1:AA:974:A:OP1	2.64	0.46
36:BW:73:ALA:HB3	36:BW:106:ILE:CG1	2.44	0.46
56:BK:14:ALA:HA	56:BK:41:PHE:CZ	2.50	0.46
25:BA:197:A:H2'	25:BA:198:C:H5'	1.98	0.46
25:BA:2340:G:O2'	25:BA:2341:G:H5'	2.16	0.46
25:BA:1328:G:H8	25:BA:1328:G:O5'	1.98	0.46
37:BX:52:VAL:O	37:BX:52:VAL:HG12	2.16	0.46
39:BZ:166:SER:OG	39:BZ:167:PRO:HA	2.16	0.46
1:AA:1521:G:H2'	1:AA:1522:U:C6	2.50	0.46
52:BE:5:LEU:HD12	52:BE:51:PHE:HB2	1.96	0.46
54:BG:39:ILE:HD11	54:BG:94:LEU:HD11	1.96	0.46
51:BC:82:LYS:O	51:BC:83:ILE:C	2.53	0.46
23:AY:293:THR:HG22	23:AY:297:GLU:O	2.15	0.46
1:AA:1265:G:H2'	1:AA:1266:G:O4'	2.16	0.46
25:BA:586:A:H2	25:BA:809:G:N3	2.14	0.46
1:AA:1349:A:C2	1:AA:1374:A:C4	3.04	0.46
53:BF:113:ALA:HB1	53:BF:186:ILE:HG21	1.98	0.46
25:BA:2144:U:O2	25:BA:2147:G:O6	2.34	0.46
25:BA:89:G:OP2	25:BA:90:U:H2'	2.16	0.46
34:BU:90:VAL:HG12	34:BU:91:ASP:N	2.31	0.46
47:B6:11:LEU:HD21	47:B6:51:GLU:HB2	1.97	0.46
1:AA:1452:C:O4'	1:AA:1456:G:N2	2.49	0.46
1:AA:673:G:H5''	19:AF:87:ARG:CZ	2.45	0.46
25:BA:2298:A:N6	25:BA:2318:G:C8	2.82	0.46
25:BA:1741:A:N7	25:BA:1742:G:C2	2.84	0.46
2:AV:47:U:H3'	2:AV:48:C:C5'	2.46	0.46
53:BF:81:PRO:HB3	53:BF:89:VAL:HG23	1.98	0.46
25:BA:1789:A:H2'	25:BA:1790:C:H5'	1.96	0.46
28:BO:77:ILE:HD12	33:BT:74:ARG:HD3	1.97	0.46
1:AA:55:A:H1'	23:AY:321:TYR:HB3	1.97	0.46
39:BZ:166:SER:OG	39:BZ:167:PRO:CA	2.64	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
57:BJ:100:ALA:O	57:BJ:104:ALA:HB3	2.16	0.46
1:AA:120:A:O2'	1:AA:121:C:H5'	2.16	0.46
1:AA:1031:G:H2'	1:AA:1032:G:O4'	2.16	0.46
25:BA:64:A:C2	37:BX:66:LEU:HD22	2.50	0.46
1:AA:1234:C:H1'	1:AA:1364:U:O2	2.15	0.46
25:BA:991:C:H5'	25:BA:991:C:H6	1.80	0.46
33:BT:125:ARG:O	33:BT:128:GLU:HG3	2.14	0.46
21:AH:86:ILE:HB	21:AH:133:LEU:O	2.16	0.46
51:BC:215:THR:OG1	51:BC:216:THR:N	2.48	0.46
1:AA:1319:A:C8	1:AA:1323:G:C5	3.04	0.46
32:BS:97:ARG:NH2	32:BS:98:VAL:HA	2.30	0.46
1:AA:1508:G:O2'	1:AA:1509:C:H5'	2.16	0.46
1:AA:1190:G:OP1	16:AC:4:LYS:HA	2.15	0.46
25:BA:889:C:O2'	25:BA:890:A:OP2	2.32	0.46
18:AE:7:GLU:O	18:AE:8:GLU:HB3	2.16	0.46
25:BA:1051:G:H2'	25:BA:1052:C:O4'	2.16	0.46
7:AM:45:VAL:HA	7:AM:48:LEU:HD22	1.98	0.46
15:AB:114:ARG:NH1	15:AB:118:LEU:HD21	2.31	0.46
25:BA:1055:G:H5'	25:BA:1056:G:OP2	2.16	0.46
25:BA:796:C:H2'	25:BA:797:C:C6	2.51	0.46
43:BD:134:ARG:HG3	43:BD:135:PHE:CD1	2.51	0.46
14:AT:94:ALA:O	14:AT:95:ALA:CB	2.64	0.46
14:AT:26:ASN:OD1	14:AT:71:THR:OG1	2.27	0.46
45:B4:38:ALA:O	45:B4:49:GLU:HG2	2.16	0.46
15:AB:235:SER:OG	15:AB:236:TYR:CD1	2.69	0.46
34:BU:65:ILE:HG12	34:BU:96:ALA:CB	2.46	0.46
25:BA:2151:G:C6	25:BA:2152:G:C5	3.03	0.46
25:BA:309:G:O3'	38:BY:18:GLY:HA2	2.16	0.46
43:BD:13:ARG:HD2	43:BD:16:MET:CE	2.43	0.46
1:AA:1158:C:O2	1:AA:1158:C:C2'	2.64	0.46
27:BN:119:ARG:HH11	27:BN:119:ARG:CG	2.29	0.46
55:BH:64:LEU:HD23	55:BH:67:LEU:HD23	1.98	0.46
25:BA:814:C:H2'	25:BA:815:C:C6	2.51	0.46
1:AA:1128:C:C2'	1:AA:1129:C:H5'	2.45	0.46
25:BA:1208:C:C4	25:BA:1209:G:N7	2.84	0.46
1:AA:503:C:O2	1:AA:510:A:H2	1.98	0.46
43:BD:169:GLU:HA	43:BD:169:GLU:OE1	2.16	0.46
19:AF:89:MET:HG2	19:AF:91:VAL:HG23	1.98	0.46
21:AH:113:SER:O	21:AH:131:GLY:HA3	2.16	0.46
25:BA:451:C:H4'	53:BF:52:LYS:HE2	1.97	0.46
1:AA:979:C:C3'	1:AA:980:C:C5'	2.93	0.45
29:BP:23:PRO:HB2	29:BP:33:ARG:HD2	1.97	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
45:B4:64:LYS:C	45:B4:65:CYS:HG	2.19	0.45
38:BY:42:VAL:HG23	38:BY:67:LEU:HD13	1.99	0.45
26:BB:41:U:C6	54:BG:69:ALA:HB1	2.51	0.45
25:BA:35:G:C2'	25:BA:36:G:O5'	2.64	0.45
53:BF:20:LEU:HD23	53:BF:21:ALA:N	2.31	0.45
25:BA:428:A:H5'	25:BA:429:A:OP2	2.16	0.45
39:BZ:166:SER:OG	39:BZ:167:PRO:C	2.55	0.45
1:AA:503:C:H6	1:AA:503:C:O5'	1.99	0.45
25:BA:2512:C:H2'	25:BA:2513:G:O4'	2.15	0.45
18:AE:28:PHE:O	18:AE:47:LYS:HA	2.17	0.45
25:BA:2654:A:O4'	25:BA:2656:U:C6	2.69	0.45
25:BA:1499:C:O2'	25:BA:1500:G:H5'	2.16	0.45
38:BY:76:CYS:O	38:BY:96:ILE:HD13	2.16	0.45
25:BA:995:C:O2	27:BN:4:TYR:OH	2.28	0.45
1:AA:1134:G:C5	1:AA:1135:U:C6	3.04	0.45
25:BA:613:G:C8	25:BA:613:G:H5''	2.43	0.45
29:BP:33:ARG:O	29:BP:34:GLY:C	2.54	0.45
1:AA:1149:C:P	22:AI:9:ARG:HH11	2.38	0.45
25:BA:659:C:H4'	53:BF:100:THR:O	2.16	0.45
34:BU:81:HIS:CD2	34:BU:117:GLN:HG3	2.52	0.45
54:BG:72:ARG:HB3	54:BG:87:PRO:HD3	1.97	0.45
53:BF:20:LEU:HD23	53:BF:21:ALA:H	1.81	0.45
25:BA:1761:C:H2'	25:BA:1762:A:H5'	1.98	0.45
23:AY:551:GLN:O	23:AY:559:PRO:HA	2.15	0.45
7:AM:58:GLU:O	7:AM:62:ASN:ND2	2.50	0.45
25:BA:401:A:H2'	25:BA:402:A:O4'	2.16	0.45
54:BG:149:VAL:O	54:BG:149:VAL:HG13	2.17	0.45
34:BU:66:ASN:O	34:BU:70:ARG:HB2	2.16	0.45
33:BT:92:GLY:O	33:BT:115:ARG:O	2.35	0.45
43:BD:226:MET:O	43:BD:234:GLY:HA2	2.16	0.45
25:BA:2388:A:H5'	25:BA:2389:G:OP2	2.16	0.45
23:AY:78:ARG:C	23:AY:79:ILE:HD12	2.36	0.45
55:BH:105:LEU:CD2	55:BH:113:VAL:HB	2.46	0.45
25:BA:299:A:C5	25:BA:322:A:C2	3.05	0.45
20:AG:152:ALA:O	20:AG:155:ARG:NE	2.49	0.45
25:BA:2137:C:N4	25:BA:2154:G:O6	2.49	0.45
46:B5:51:TYR:CD2	46:B5:52:TYR:CE2	3.05	0.45
15:AB:178:ARG:NH1	15:AB:178:ARG:HG2	2.13	0.45
25:BA:308:G:C8	25:BA:501:A:O4'	2.69	0.45
33:BT:23:ARG:C	33:BT:25:GLY:N	2.69	0.45
2:AV:73:A:H3'	2:AV:74:C:H5'	1.97	0.45
51:BC:131:LEU:HD12	51:BC:137:LEU:HA	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1918:A:O2'	25:BA:1919:A:C2	2.64	0.45
25:BA:2506:U:H4'	25:BA:2507:C:OP1	2.14	0.45
1:AA:1013:G:H5''	1:AA:1013:G:H8	1.78	0.45
27:BN:134:ARG:CD	27:BN:134:ARG:O	2.64	0.45
23:AY:409:ILE:HD13	23:AY:409:ILE:HA	1.86	0.45
25:BA:387:U:H4'	25:BA:388:G:O5'	2.16	0.45
15:AB:7:VAL:O	15:AB:11:LEU:HB2	2.16	0.45
25:BA:1426:G:C6	25:BA:1427:A:C6	3.04	0.45
25:BA:306:U:H2'	25:BA:307:G:O4'	2.16	0.45
25:BA:1394:U:C6	25:BA:1394:U:H3'	2.52	0.45
1:AA:288:A:H2'	1:AA:289:G:H4'	1.98	0.45
30:BQ:76:LYS:HB3	30:BQ:91:GLU:HG2	1.99	0.45
25:BA:2138:C:H6	25:BA:2138:C:H5''	1.82	0.45
29:BP:38:GLN:HG3	29:BP:39:LYS:H	1.81	0.45
1:AA:353:A:C2'	1:AA:354:G:OP2	2.65	0.45
1:AA:1003:G:C2'	1:AA:1004:A:H4'	2.45	0.45
25:BA:2517:C:C2'	25:BA:2542:A:C2	2.99	0.45
1:AA:981:U:O4	1:AA:1222:G:O6	2.33	0.45
38:BY:38:ILE:CG2	38:BY:39:VAL:N	2.78	0.45
1:AA:35:G:H2'	1:AA:36:C:C6	2.51	0.45
1:AA:501:C:H1'	1:AA:549:C:H1'	1.98	0.45
4:AJ:30:SER:CB	4:AJ:81:THR:OG1	2.65	0.45
41:B1:4:VAL:O	41:B1:4:VAL:HG13	2.15	0.45
25:BA:2757:A:N1	55:BH:67:LEU:HD22	2.31	0.45
25:BA:94:C:H2'	25:BA:94:C:O2	2.17	0.45
1:AA:33:A:O2'	1:AA:363:A:H1'	2.16	0.45
18:AE:41:VAL:HG23	18:AE:67:VAL:HG13	1.99	0.45
1:AA:695:A:H2'	1:AA:696:A:C8	2.51	0.45
1:AA:141:A:H1'	1:AA:182:U:O2	2.17	0.45
51:BC:99:ILE:H	51:BC:99:ILE:HD13	1.81	0.45
25:BA:2461:C:H2'	25:BA:2462:U:C6	2.51	0.45
39:BZ:188:ALA:O	39:BZ:189:ALA:C	2.55	0.45
25:BA:2746:U:H2'	25:BA:2747:G:H5'	1.99	0.45
23:AY:72:CYS:SG	23:AY:81:ILE:HD11	2.56	0.45
31:BR:38:VAL:HB	31:BR:39:PRO:CD	2.45	0.45
25:BA:271(A):A:N1	25:BA:272(D):G:O2'	2.46	0.45
25:BA:30:G:H2'	25:BA:31:C:C6	2.51	0.45
23:AY:289:ILE:HD11	23:AY:331:TYR:CD2	2.51	0.45
25:BA:1910:G:N1	25:BA:1920:C:H5	1.98	0.45
38:BY:28:LYS:HB3	38:BY:37:VAL:HB	1.97	0.45
38:BY:17:SER:HB2	38:BY:71:LYS:HB3	1.97	0.45
23:AY:212:TYR:O	23:AY:216:LEU:N	2.40	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
49:B8:33:ASN:HA	49:B8:36:LYS:CG	2.47	0.45
42:B2:38:GLN:HB3	42:B2:44:LEU:CB	2.45	0.45
25:BA:2506:U:H6	25:BA:2506:U:H5'	1.79	0.45
1:AA:737:A:O2'	19:AF:72:VAL:CG1	2.65	0.45
35:BV:40:LEU:HD23	35:BV:46:VAL:HG23	1.98	0.45
35:BV:79:VAL:HG13	35:BV:79:VAL:O	2.16	0.45
53:BF:114:VAL:HG21	53:BF:202:PHE:CE1	2.51	0.45
16:AC:40:ARG:NH1	16:AC:40:ARG:HG3	2.30	0.45
25:BA:2371:G:C6	25:BA:2372:G:N7	2.85	0.45
51:BC:193:ILE:H	51:BC:193:ILE:HD12	1.80	0.45
25:BA:1421:G:C2	25:BA:1422:G:C8	3.05	0.45
48:B7:5:TRP:CD1	48:B7:7:PRO:HD3	2.51	0.45
25:BA:2302:G:C3'	25:BA:2303:G:H5'	2.47	0.45
25:BA:2302:G:H2'	25:BA:2303:G:H5'	1.99	0.45
25:BA:1562:A:H2'	25:BA:1563:G:O4'	2.17	0.45
47:B6:15:GLU:OE2	47:B6:41:PRO:HB2	2.16	0.45
25:BA:2142:C:H5''	25:BA:2143:C:OP2	2.16	0.45
43:BD:24:ILE:O	43:BD:26:LYS:CB	2.65	0.45
54:BG:96:ARG:O	54:BG:97:ASP:C	2.55	0.45
25:BA:2164:C:C4	25:BA:2165:G:C8	3.05	0.45
17:AD:22:LYS:O	17:AD:24:GLU:N	2.49	0.45
19:AF:72:VAL:HG13	19:AF:73:ASN:N	2.31	0.45
1:AA:262:A:C6	1:AA:263:A:C6	3.04	0.45
31:BR:4:LEU:O	31:BR:5:LYS:HD3	2.17	0.45
55:BH:85:LYS:NZ	55:BH:85:LYS:O	2.42	0.45
21:AH:83:ILE:HG23	21:AH:83:ILE:O	2.17	0.45
1:AA:1349:A:H2'	1:AA:1350:A:O5'	2.16	0.45
1:AA:1230:C:O2'	1:AA:1231:G:H5'	2.17	0.45
1:AA:769:G:H4'	1:AA:1513:A:H4'	1.98	0.45
25:BA:338:G:C5	25:BA:339:U:C5	3.05	0.45
25:BA:780:G:H2'	25:BA:782:A:N7	2.31	0.45
2:AV:19:G:C5	25:BA:2169:A:H1'	2.52	0.45
53:BF:88:VAL:HG11	53:BF:91:GLY:HA3	1.98	0.45
38:BY:85:VAL:HG13	38:BY:92:ASN:OD1	2.16	0.45
25:BA:833:U:H5''	29:BP:48:PRO:HB3	1.97	0.45
6:AL:27:LEU:HB2	6:AL:62:SER:HB2	1.98	0.45
22:AI:112:LYS:HG2	22:AI:118:LYS:HA	1.98	0.45
25:BA:529:A:O4'	25:BA:529:A:N3	2.50	0.45
41:B1:44:PRO:HB2	41:B1:46:LEU:HD13	1.98	0.45
1:AA:1371:G:C6	1:AA:1372:U:C4	3.04	0.45
23:AY:20:HIS:CG	23:AY:21:ILE:N	2.85	0.45
52:BE:98:PRO:HD3	52:BE:175:VAL:CG1	2.47	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AY:627:ARG:NH1	23:AY:651:GLU:O	2.50	0.45
58:BL:79:UNK:C	58:BL:81:UNK:N	2.78	0.45
45:B4:37:PRO:HA	45:B4:51:TYR:CD2	2.52	0.45
25:BA:2592:G:H2'	25:BA:2593:U:O4'	2.17	0.45
23:AY:490:PRO:O	23:AY:491:VAL:HG23	2.17	0.45
25:BA:1569:A:O2'	43:BD:38:LYS:HG2	2.17	0.45
25:BA:1063:G:C6	25:BA:1075:C:N4	2.84	0.45
14:AT:100:ILE:C	14:AT:102:GLY:N	2.70	0.45
23:AY:114:VAL:HG11	23:AY:157:LEU:HD22	1.98	0.45
25:BA:26:G:C6	25:BA:27:G:N1	2.85	0.45
25:BA:27:G:O2'	25:BA:28:A:P	2.73	0.45
38:BY:55:TYR:O	38:BY:57:GLN:N	2.50	0.45
9:AO:78:TYR:O	9:AO:82:ILE:HG22	2.17	0.45
25:BA:1449:A:C4	25:BA:1528(A):A:C2	3.05	0.45
16:AC:95:THR:C	16:AC:97:LYS:H	2.19	0.45
15:AB:31:TYR:CZ	15:AB:200:ILE:HD12	2.52	0.45
25:BA:864:G:N7	30:BQ:22:LYS:NZ	2.62	0.45
18:AE:51:VAL:O	18:AE:55:VAL:HG23	2.16	0.45
39:BZ:188:ALA:O	39:BZ:190:GLU:N	2.50	0.45
25:BA:2575:C:H6	25:BA:2575:C:O5'	1.99	0.45
51:BC:28:LEU:O	51:BC:28:LEU:HD12	2.17	0.45
23:AY:286:ILE:O	23:AY:287:PRO:C	2.55	0.45
34:BU:74:LEU:HD23	34:BU:78:THR:HG22	1.98	0.45
25:BA:2645:G:N2	25:BA:2767:C:OP2	2.49	0.45
25:BA:363(E):U:H5'	25:BA:363(F):A:OP2	2.17	0.45
43:BD:125:ILE:HD11	43:BD:131:LEU:HD22	1.98	0.45
25:BA:1089:G:C4'	25:BA:1090:U:OP1	2.63	0.45
25:BA:1078:U:O2	25:BA:1088:A:H5'	2.17	0.45
26:BB:82:G:H2'	26:BB:83:G:O5'	2.16	0.45
52:BE:67:PHE:O	52:BE:68:ALA:C	2.55	0.45
30:BQ:35:VAL:HG11	30:BQ:130:LYS:HE3	1.99	0.45
16:AC:91:LEU:HD11	16:AC:101:LEU:HD12	1.99	0.45
6:AL:41:ARG:NH1	6:AL:41:ARG:HB3	2.32	0.45
25:BA:2208:A:O2'	25:BA:2219:G:C8	2.70	0.45
33:BT:32:TYR:O	33:BT:41:ARG:O	2.35	0.45
25:BA:1204:A:C2	25:BA:1241:A:N1	2.85	0.45
25:BA:571:A:H5'	25:BA:2030:A:N7	2.32	0.45
25:BA:1057:A:C6	25:BA:1086:A:C2	3.05	0.45
39:BZ:152:ALA:HB1	39:BZ:167:PRO:HB2	1.98	0.45
25:BA:2447:G:N7	25:BA:2501:C:O4'	2.50	0.45
25:BA:1775:U:H2'	25:BA:1776:G:O5'	2.16	0.45
37:BX:21:PHE:O	37:BX:23:GLU:O	2.35	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
54:BG:60:LEU:HD13	54:BG:60:LEU:C	2.37	0.45
20:AG:44:TYR:O	20:AG:45:ASP:C	2.55	0.45
25:BA:1805:U:O2	43:BD:50:THR:HB	2.16	0.45
23:AY:470:PHE:O	23:AY:471:LYS:HG3	2.17	0.45
20:AG:113:GLU:HG2	20:AG:119:ARG:HG2	1.99	0.45
1:AA:918:A:H2'	1:AA:919:A:C8	2.51	0.45
25:BA:270:A:N1	25:BA:366:C:O2'	2.43	0.45
1:AA:1100:C:OP2	15:AB:96:ARG:NE	2.50	0.45
1:AA:1028:C:N4	1:AA:1033:G:O6	2.49	0.45
25:BA:1914:C:C2'	25:BA:1915:U:O5'	2.59	0.45
1:AA:927:G:OP2	1:AA:927:G:H4'	2.17	0.45
25:BA:251:A:H5''	29:BP:51:PHE:HZ	1.82	0.45
29:BP:57:THR:HB	29:BP:59:LEU:HB2	1.99	0.45
15:AB:178:ARG:NH1	15:AB:178:ARG:CG	2.65	0.45
23:AY:685:GLU:HA	23:AY:688:ILE:HG22	1.99	0.45
1:AA:62:U:C2'	1:AA:63:C:H5''	2.45	0.45
25:BA:1076:C:O2'	25:BA:1077:A:O4'	2.34	0.45
52:BE:68:ALA:O	52:BE:70:ALA:N	2.50	0.45
23:AY:58:GLU:HG3	23:AY:65:ILE:HG22	1.98	0.45
25:BA:301:G:H1'	25:BA:302:C:C6	2.52	0.45
57:BJ:21:ALA:HB3	57:BJ:88:ALA:HA	1.98	0.45
15:AB:166:ASP:HB3	15:AB:169:LYS:CB	2.46	0.45
23:AY:180:VAL:HG23	23:AY:181:LEU:N	2.31	0.45
25:BA:854:G:H5''	25:BA:855:G:OP2	2.17	0.45
25:BA:2637:U:C2'	25:BA:2638:G:H5'	2.46	0.45
54:BG:28:VAL:O	54:BG:31:VAL:HG12	2.17	0.45
27:BN:15:LEU:O	27:BN:136:GLU:HA	2.17	0.45
18:AE:148:VAL:O	18:AE:152:ARG:HG3	2.17	0.45
7:AM:13:LYS:O	7:AM:44:ARG:HA	2.16	0.45
23:AY:224:ASP:HB2	23:AY:227:ILE:HD12	1.98	0.45
25:BA:1246:A:P	29:BP:16:ARG:NH2	2.90	0.44
1:AA:1138:G:O2'	1:AA:1139:G:P	2.75	0.44
25:BA:1527:G:H2'	25:BA:1544:A:C2	2.52	0.44
33:BT:82:LEU:H	33:BT:82:LEU:HD12	1.80	0.44
25:BA:2179:C:O2	25:BA:2179:C:O4'	2.35	0.44
25:BA:2166:G:O2'	25:BA:2167:U:H5'	2.17	0.44
25:BA:1458:C:C4'	25:BA:1459:G:O5'	2.64	0.44
29:BP:120:ALA:HB1	29:BP:138:LEU:HD12	1.99	0.44
42:B2:35:LEU:CD1	42:B2:53:LEU:HD12	2.46	0.44
51:BC:84:LYS:C	51:BC:86:ALA:H	2.20	0.44
25:BA:1817:G:C6	25:BA:1818:U:C4	3.04	0.44
41:B1:3:LYS:HG2	41:B1:4:VAL:H	1.82	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
23:AY:343:ASN:C	23:AY:343:ASN:HD22	2.20	0.44
25:BA:316:C:C2'	25:BA:317:G:O5'	2.65	0.44
1:AA:711:G:O2'	1:AA:712:A:H5'	2.17	0.44
31:BR:44:LEU:HD22	31:BR:48:VAL:HG23	1.98	0.44
37:BX:66:LEU:HD23	37:BX:66:LEU:O	2.16	0.44
25:BA:1943:U:H4'	25:BA:1944:U:OP1	2.17	0.44
2:AV:55:U:O4'	2:AV:55:U:O2	2.35	0.44
25:BA:861:A:H2'	25:BA:862:G:O4'	2.17	0.44
15:AB:223:ILE:O	15:AB:224:GLN:C	2.55	0.44
25:BA:1462:C:H4'	25:BA:2703:C:H5'	1.98	0.44
25:BA:1367:A:H5''	25:BA:1368:G:OP2	2.17	0.44
51:BC:23:ASP:O	51:BC:24:GLU:C	2.56	0.44
47:B6:41:PRO:O	47:B6:42:TRP:C	2.55	0.44
1:AA:1037:C:H2'	1:AA:1038:C:C6	2.52	0.44
53:BF:22:ALA:HB1	53:BF:26:ALA:CB	2.47	0.44
25:BA:2343:C:O2'	25:BA:2344:U:H5'	2.17	0.44
1:AA:1533:C:H3'	1:AA:1534:A:H5''	1.98	0.44
15:AB:215:LEU:HD13	15:AB:215:LEU:HA	1.76	0.44
17:AD:22:LYS:HE2	17:AD:25:ARG:HD2	1.98	0.44
49:B8:54:GLU:O	49:B8:58:ILE:HG13	2.17	0.44
28:BO:104:ARG:HH11	28:BO:107:ARG:HH12	1.63	0.44
31:BR:78:LYS:CE	31:BR:83:ILE:HD11	2.47	0.44
25:BA:332:A:O2'	25:BA:334:C:OP2	2.29	0.44
23:AY:79:ILE:N	23:AY:79:ILE:HD12	2.32	0.44
25:BA:852:G:O2'	25:BA:853:G:H5'	2.17	0.44
54:BG:32:PRO:HB2	54:BG:172:LEU:HD13	1.99	0.44
1:AA:180:U:H2'	1:AA:181:G:H5'	1.99	0.44
25:BA:1903:G:OP1	43:BD:241:PRO:HB2	2.17	0.44
25:BA:2685:G:P	33:BT:51:ARG:HH12	2.40	0.44
25:BA:1899:G:HO2'	25:BA:1900:A:P	2.38	0.44
7:AM:65:LYS:O	7:AM:65:LYS:CG	2.65	0.44
38:BY:28:LYS:O	38:BY:29:GLU:C	2.56	0.44
49:B8:33:ASN:HA	49:B8:36:LYS:HG2	2.00	0.44
49:B8:32:LEU:CB	49:B8:36:LYS:NZ	2.80	0.44
56:BK:3:LYS:HD3	56:BK:29:GLN:HG2	2.00	0.44
25:BA:2469:A:H2'	25:BA:2470:G:O4'	2.18	0.44
15:AB:19:HIS:HB2	15:AB:204:ASN:HD22	1.83	0.44
1:AA:501:C:H2'	1:AA:502:G:C8	2.53	0.44
34:BU:88:ILE:HD13	34:BU:109:LEU:CD2	2.44	0.44
8:AN:47:LEU:O	8:AN:48:ALA:C	2.56	0.44
23:AY:325:LEU:HD21	23:AY:358:MET:CE	2.47	0.44
55:BH:23:ARG:O	55:BH:24:VAL:HG12	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:AE:7:GLU:OE1	18:AE:37:ARG:NE	2.49	0.44
26:BB:84:C:OP1	44:B3:15:TYR:OH	2.35	0.44
23:AY:632:LEU:HD11	23:AY:646:PHE:CD2	2.52	0.44
25:BA:370:G:O5'	25:BA:370:G:C8	2.70	0.44
28:BO:9:GLU:O	28:BO:83:ALA:HA	2.18	0.44
38:BY:52:SER:O	38:BY:54:LYS:N	2.50	0.44
25:BA:1268:A:C2	25:BA:2013:A:C4	3.05	0.44
5:AK:38:ASN:HA	5:AK:39:PRO:HD3	1.91	0.44
23:AY:26:THR:HA	23:AY:83:ASP:OD2	2.16	0.44
25:BA:92:A:C2	25:BA:93:G:H1'	2.52	0.44
25:BA:1491:G:OP2	25:BA:1494:A:C6	2.71	0.44
39:BZ:151:HIS:HB3	39:BZ:170:THR:HA	1.99	0.44
53:BF:24:LEU:HD13	53:BF:118:ALA:HB1	1.98	0.44
35:BV:19:LYS:CG	35:BV:20:LEU:O	2.65	0.44
25:BA:2287:A:N1	25:BA:2346:A:N1	2.65	0.44
41:B1:51:VAL:HG21	41:B1:74:VAL:HG21	2.00	0.44
32:BS:53:SER:OG	32:BS:54:LEU:N	2.50	0.44
27:BN:134:ARG:N	27:BN:134:ARG:HD2	2.32	0.44
33:BT:80:SER:HB3	33:BT:81:PRO:HD3	1.98	0.44
29:BP:143:GLY:HA3	29:BP:145:PRO:HD3	1.99	0.44
25:BA:2743:C:C2'	25:BA:2744:G:O5'	2.65	0.44
23:AY:86:GLY:O	23:AY:117:GLN:CG	2.66	0.44
1:AA:684:A:C6	1:AA:685:G:C6	3.05	0.44
54:BG:48:GLU:O	54:BG:49:ASP:HB3	2.17	0.44
23:AY:281:PRO:HB2	23:AY:286:ILE:HD11	2.00	0.44
25:BA:484:C:H2'	25:BA:485:C:C6	2.52	0.44
15:AB:126:GLU:O	15:AB:130:ARG:HG3	2.18	0.44
1:AA:702:A:H4'	1:AA:703:G:OP2	2.17	0.44
25:BA:358:U:O2	25:BA:358:U:H2'	2.18	0.44
15:AB:92:TYR:O	15:AB:151:GLY:HA3	2.18	0.44
28:BO:63:VAL:HG11	28:BO:85:VAL:HG23	1.99	0.44
15:AB:51:LEU:O	15:AB:55:PHE:HB2	2.17	0.44
23:AY:495:GLY:O	23:AY:510:VAL:N	2.51	0.44
56:BK:77:LEU:N	56:BK:77:LEU:HD23	2.32	0.44
25:BA:2151:G:C2	25:BA:2152:G:C4	3.05	0.44
25:BA:2392:A:OP1	49:B8:32:LEU:HD21	2.16	0.44
55:BH:157:TYR:CE1	55:BH:173:PRO:HB3	2.53	0.44
56:BK:19:PRO:CB	56:BK:34:ILE:HD12	2.47	0.44
27:BN:35:ARG:O	27:BN:37:LYS:N	2.50	0.44
33:BT:96:ARG:CZ	33:BT:96:ARG:HB3	2.47	0.44
33:BT:5:ALA:O	33:BT:6:LEU:C	2.55	0.44
25:BA:2557:G:H2'	25:BA:2558:C:C6	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:685:G:C2	1:AA:686:U:C4	3.05	0.44
7:AM:86:CYS:HA	13:AS:73:GLU:O	2.18	0.44
32:BS:99:LYS:HD3	32:BS:99:LYS:N	2.27	0.44
25:BA:1835:G:H1'	25:BA:1931:U:C2	2.53	0.44
25:BA:603:A:O4'	25:BA:603:A:N3	2.50	0.44
41:B1:40:ARG:HD3	41:B1:40:ARG:C	2.38	0.44
25:BA:510:C:OP1	25:BA:511:U:OP2	2.36	0.44
25:BA:1692:U:O2'	25:BA:1693:U:H2'	2.18	0.44
25:BA:2025:C:H2'	25:BA:2026:C:C6	2.52	0.44
25:BA:2401:U:O2'	25:BA:2402:C:H5''	2.17	0.44
47:B6:14:THR:O	47:B6:49:HIS:HA	2.17	0.44
49:B8:61:LEU:H	49:B8:61:LEU:CD2	2.22	0.44
29:BP:55:ARG:CG	29:BP:56:SER:H	2.30	0.44
4:AJ:24:VAL:O	4:AJ:25:GLU:C	2.56	0.44
38:BY:23:ARG:O	38:BY:24:VAL:O	2.35	0.44
33:BT:83:ILE:HG13	33:BT:84:GLN:N	2.33	0.44
25:BA:774:A:HO2'	25:BA:775:G:P	2.32	0.44
25:BA:2165:G:C5	25:BA:2166:G:C6	3.05	0.44
54:BG:37:VAL:HG22	54:BG:159:VAL:HA	2.00	0.44
19:AF:72:VAL:CG2	19:AF:90:VAL:HG11	2.48	0.44
25:BA:2689:U:O2	25:BA:2713:A:O5'	2.36	0.44
35:BV:3:ALA:HA	35:BV:40:LEU:O	2.18	0.44
56:BK:21:PRO:HA	56:BK:23:VAL:N	2.33	0.44
23:AY:512:ILE:CD1	23:AY:589:ALA:HB1	2.47	0.44
25:BA:271(O):C:O2'	25:BA:271(P):C:OP2	2.31	0.44
25:BA:614:U:O5'	25:BA:614:U:O2	2.35	0.44
25:BA:2115:G:H2'	25:BA:2117:A:N7	2.33	0.44
23:AY:179:ASP:C	23:AY:180:VAL:O	2.56	0.44
22:AI:48:GLU:N	22:AI:49:PRO:CD	2.80	0.44
23:AY:491:VAL:O	23:AY:513:LYS:HA	2.17	0.44
54:BG:16:ARG:NE	54:BG:31:VAL:HG11	2.33	0.44
25:BA:104:U:C5	25:BA:105:C:C5	3.05	0.44
1:AA:96:U:O2'	1:AA:97:G:P	2.76	0.44
25:BA:445:C:OP1	34:BU:2:PRO:HA	2.18	0.44
25:BA:2266:A:H4'	25:BA:2267:A:O5'	2.18	0.44
29:BP:68:GLN:HE21	29:BP:68:GLN:HB2	1.61	0.44
54:BG:130:ASN:OD1	54:BG:130:ASN:N	2.50	0.44
28:BO:43:VAL:HG21	28:BO:52:VAL:CG1	2.47	0.44
1:AA:909:A:H2'	1:AA:910:C:O4'	2.18	0.44
25:BA:264:C:O2'	25:BA:265:A:H2'	2.18	0.44
25:BA:2667:C:H1'	55:BH:109:PHE:CD1	2.52	0.44
22:AI:10:ARG:CZ	22:AI:105:ASP:OD2	2.65	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:926:G:H5''	1:AA:927:G:O5'	2.17	0.44
31:BR:11:ASN:CG	31:BR:12:ARG:H	2.12	0.44
43:BD:27:THR:CG2	43:BD:81:ALA:HB1	2.47	0.44
2:AV:35:A:H8	2:AV:35:A:H5''	1.82	0.44
25:BA:2681:C:H2'	25:BA:2681:C:O2	2.17	0.44
1:AA:1119:C:OP2	22:AI:9:ARG:NH2	2.50	0.44
1:AA:452:A:O2'	1:AA:453:A:H8	2.00	0.44
25:BA:2097:C:H2'	25:BA:2098:U:H5'	1.99	0.44
54:BG:116:ASP:O	54:BG:117:PHE:HB3	2.18	0.44
32:BS:35:ILE:HG23	32:BS:69:VAL:HG11	1.98	0.44
15:AB:15:VAL:O	15:AB:16:HIS:ND1	2.51	0.44
25:BA:1375:C:H2'	25:BA:1376:C:H6	1.83	0.44
25:BA:2648:C:H2'	25:BA:2649:U:C6	2.52	0.44
25:BA:2712:U:O2'	25:BA:2712(A):A:OP2	2.29	0.44
23:AY:321:TYR:N	23:AY:321:TYR:CD1	2.86	0.44
23:AY:627:ARG:O	23:AY:628:ARG:CB	2.66	0.44
21:AH:31:PHE:O	21:AH:35:ILE:HG13	2.18	0.44
1:AA:804:U:H5''	1:AA:805:C:OP2	2.17	0.44
1:AA:1085:U:C2	1:AA:1094:G:O6	2.71	0.44
25:BA:1667:G:O2'	25:BA:1991:U:O4	2.26	0.44
54:BG:64:THR:HG23	54:BG:66:GLN:H	1.83	0.44
25:BA:2769:C:H2'	25:BA:2770:G:O4'	2.17	0.44
27:BN:58:ASP:O	27:BN:60:ILE:HG13	2.17	0.44
25:BA:2451:A:H5'	40:B0:2:ALA:HB2	1.99	0.44
16:AC:91:LEU:CB	16:AC:99:VAL:HG21	2.48	0.44
26:BB:40:U:H3'	26:BB:41:U:H5'	1.98	0.44
31:BR:94:TYR:O	31:BR:117:VAL:HB	2.18	0.44
18:AE:84:PHE:CB	18:AE:134:ALA:HB2	2.48	0.44
21:AH:44:PHE:HE2	21:AH:109:ILE:HG21	1.82	0.44
25:BA:2302:G:C2'	25:BA:2303:G:H5'	2.47	0.44
25:BA:485:C:C2	25:BA:496:G:N2	2.86	0.44
25:BA:508:G:H2'	25:BA:508:G:N3	2.32	0.44
25:BA:1599:C:OP1	37:BX:36:LYS:N	2.45	0.44
25:BA:2189:U:O5'	25:BA:2189:U:H6	2.00	0.44
15:AB:191:ASP:O	15:AB:191:ASP:OD1	2.35	0.44
34:BU:102:GLU:OE2	35:BV:13:ARG:NH2	2.51	0.44
1:AA:72:C:H2'	1:AA:73:G:C8	2.53	0.44
1:AA:926:G:H2'	1:AA:1505:G:N3	2.33	0.44
50:B9:29:ASN:HA	50:B9:30:PRO:HD3	1.77	0.44
11:AQ:66:SER:OG	11:AQ:69:LYS:HB2	2.17	0.44
4:AJ:51:ARG:HG3	4:AJ:60:ARG:HA	1.99	0.44
53:BF:65:TRP:CH2	53:BF:73:ALA:O	2.70	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1859:A:C2	25:BA:1884:A:H1'	2.52	0.44
25:BA:171:G:H2'	25:BA:172:C:O4'	2.18	0.44
25:BA:2789:C:O2'	25:BA:2790:A:H1'	2.17	0.44
29:BP:143:GLY:CA	29:BP:145:PRO:HD3	2.48	0.44
17:AD:61:LYS:HD2	17:AD:207:TYR:OH	2.17	0.44
1:AA:1499:A:H1'	1:AA:1520:G:H5'	2.00	0.44
5:AK:114:VAL:HA	5:AK:115:PRO:HD2	1.88	0.44
25:BA:1676:A:H2'	25:BA:1677:A:O4'	2.18	0.44
35:BV:36:PRO:HA	35:BV:56:SER:CB	2.48	0.44
1:AA:786:G:C2	1:AA:797:C:C2	3.06	0.44
21:AH:9:MET:O	21:AH:13:ILE:HG12	2.18	0.44
25:BA:1881:C:H5''	25:BA:1881:C:C6	2.53	0.44
38:BY:3:VAL:O	38:BY:3:VAL:HG12	2.18	0.44
25:BA:2762:G:H5''	25:BA:2762:G:H8	1.82	0.44
25:BA:236:C:O2'	25:BA:431:U:H4'	2.17	0.44
25:BA:2193:G:C4	25:BA:2194:G:C8	3.06	0.44
52:BE:69:LYS:C	52:BE:71:GLY:H	2.20	0.44
39:BZ:40:ASP:HB3	39:BZ:43:GLU:HB2	1.99	0.44
1:AA:241:C:O2'	1:AA:242:C:H5'	2.18	0.44
36:BW:88:ARG:HG3	36:BW:94:ASP:OD1	2.17	0.44
29:BP:57:THR:CB	29:BP:59:LEU:HB2	2.47	0.43
35:BV:47:VAL:O	35:BV:48:GLY:C	2.56	0.43
43:BD:2:ALA:O	43:BD:3:VAL:CB	2.54	0.43
25:BA:1168:G:H2'	25:BA:1169:G:O4'	2.17	0.43
47:B6:12:GLU:HB2	47:B6:52:VAL:HG13	1.99	0.43
25:BA:2180:U:OP2	25:BA:2180:U:H3'	2.18	0.43
1:AA:1531:A:O3'	1:AA:1532:U:C6	2.70	0.43
54:BG:54:GLU:HA	54:BG:57:ALA:CB	2.44	0.43
25:BA:1058:G:C5'	25:BA:1058:G:C8	3.01	0.43
33:BT:93:ARG:HD2	33:BT:93:ARG:HA	1.83	0.43
1:AA:116:A:H8	1:AA:116:A:OP2	2.01	0.43
1:AA:1442:G:C8	1:AA:1442(B):A:C2	3.06	0.43
39:BZ:8:TYR:CD1	39:BZ:8:TYR:N	2.86	0.43
1:AA:693:G:C8	3:AX:15:A:H1'	2.52	0.43
1:AA:325:A:H2'	1:AA:326:G:O4'	2.18	0.43
25:BA:2821:A:OP1	52:BE:110:GLY:N	2.47	0.43
1:AA:1317:C:C2	8:AN:16:PHE:CE1	3.06	0.43
53:BF:157:VAL:O	53:BF:157:VAL:CG2	2.65	0.43
5:AK:33:THR:HG22	5:AK:39:PRO:HA	2.01	0.43
25:BA:105:C:H2'	25:BA:106:C:C6	2.53	0.43
25:BA:445:C:H2'	25:BA:446:G:O4'	2.18	0.43
1:AA:243:A:C2	1:AA:246:A:C8	3.06	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:2077:A:C2'	25:BA:2434:A:O2'	2.66	0.43
1:AA:1423:G:H2'	1:AA:1424:C:O4'	2.19	0.43
25:BA:601:C:O2	25:BA:605:C:H4'	2.17	0.43
25:BA:1344:G:H4'	25:BA:1384:A:C5	2.53	0.43
11:AQ:50:LYS:HG3	11:AQ:51:TYR:CE1	2.53	0.43
16:AC:10:PHE:CE2	16:AC:178:LEU:HD13	2.52	0.43
17:AD:176:LEU:HD12	17:AD:182:LYS:O	2.18	0.43
1:AA:706:A:O2'	5:AK:31:THR:CG2	2.67	0.43
25:BA:1569:A:O4'	43:BD:59:LYS:NZ	2.51	0.43
16:AC:155:GLY:O	16:AC:156:ARG:HB2	2.18	0.43
25:BA:1210:A:H5'	25:BA:1210:A:C8	2.50	0.43
25:BA:336:C:O3'	38:BY:7:VAL:CG2	2.66	0.43
25:BA:2810:A:C2'	52:BE:61:ARG:NH2	2.79	0.43
51:BC:131:LEU:CB	51:BC:137:LEU:HD23	2.46	0.43
25:BA:2113:U:H5''	25:BA:2114:A:OP2	2.18	0.43
1:AA:1158:C:O2	1:AA:1158:C:H2'	2.17	0.43
33:BT:107:ASP:N	33:BT:107:ASP:OD1	2.51	0.43
1:AA:416:G:C6	1:AA:417:C:C4	3.06	0.43
39:BZ:7:ALA:C	39:BZ:8:TYR:CD1	2.91	0.43
25:BA:2876:G:H4'	33:BT:3:ARG:HE	1.83	0.43
25:BA:2103:C:H3'	25:BA:2104:G:H5''	2.00	0.43
25:BA:2746:U:C2'	25:BA:2747:G:H5'	2.48	0.43
1:AA:985:C:C2	1:AA:1221:G:N2	2.86	0.43
25:BA:1684:C:O2'	25:BA:1685:C:H5'	2.18	0.43
11:AQ:100:LYS:HD3	11:AQ:100:LYS:N	2.33	0.43
33:BT:26:ASP:O	33:BT:26:ASP:OD2	2.35	0.43
23:AY:190:ASN:ND2	23:AY:194:THR:OG1	2.44	0.43
43:BD:108:PRO:HD2	43:BD:111:LEU:HD12	2.00	0.43
25:BA:998:C:H2'	25:BA:999:U:O5'	2.18	0.43
1:AA:1288:A:H2'	1:AA:1289:A:O4'	2.17	0.43
1:AA:1069:C:C2'	1:AA:1070:U:O5'	2.66	0.43
42:B2:12:GLU:HA	42:B2:15:LYS:HE2	2.01	0.43
29:BP:7:ARG:NH1	29:BP:7:ARG:O	2.52	0.43
25:BA:2419:U:O4	49:B8:30:ARG:NH1	2.48	0.43
1:AA:1053:G:H4'	1:AA:1054:C:H5'	2.00	0.43
25:BA:2137:C:H3'	25:BA:2138:C:H5''	2.00	0.43
47:B6:41:PRO:HG2	47:B6:44:ARG:O	2.18	0.43
1:AA:1034:G:H2'	1:AA:1035:A:C8	2.53	0.43
33:BT:16:ARG:HG2	33:BT:79:HIS:HA	1.99	0.43
1:AA:1534:A:H2'	1:AA:1535:C:C6	2.53	0.43
26:BB:81:G:O6	26:BB:96:U:O2	2.36	0.43
39:BZ:71:VAL:HG11	39:BZ:74:VAL:HG23	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:BT:31:SER:HB2	33:BT:32:TYR:CD2	2.54	0.43
22:AI:49:PRO:HG2	22:AI:81:ILE:HG22	2.01	0.43
25:BA:2291:U:H2'	25:BA:2292:C:C6	2.53	0.43
25:BA:128:C:H3'	25:BA:128:C:C6	2.53	0.43
20:AG:15:ASP:O	20:AG:19:GLY:HA2	2.18	0.43
57:BJ:118:ALA:O	57:BJ:119:ALA:HB3	2.18	0.43
1:AA:795:C:H5''	1:AA:796:C:OP2	2.18	0.43
19:AF:16:GLN:HB3	19:AF:16:GLN:HE21	1.64	0.43
36:BW:33:ARG:NH2	36:BW:52:GLU:OE1	2.42	0.43
23:AY:485:GLU:O	23:AY:560:VAL:HA	2.18	0.43
16:AC:141:VAL:HG11	16:AC:149:ALA:HB2	2.00	0.43
1:AA:178:C:C2	1:AA:179:A:C8	3.06	0.43
1:AA:1245:A:H2'	1:AA:1246:C:O4'	2.18	0.43
25:BA:2577:A:H5''	25:BA:2578:G:H5'	1.99	0.43
1:AA:1328:C:H5''	7:AM:28:ALA:CB	2.48	0.43
1:AA:1206:G:H2'	1:AA:1207:G:O4'	2.17	0.43
29:BP:16:ARG:HD3	29:BP:17:LYS:N	2.33	0.43
25:BA:607:U:C5'	53:BF:103:LYS:HE2	2.48	0.43
25:BA:336:C:H4'	38:BY:7:VAL:HG21	2.00	0.43
25:BA:1021:A:O2'	25:BA:1123:C:OP1	2.33	0.43
33:BT:29:ARG:HE	33:BT:86:ILE:HG22	1.83	0.43
52:BE:61:ARG:HA	52:BE:63:LEU:HB2	1.99	0.43
25:BA:2392:A:H2	25:BA:2424:C:N4	2.06	0.43
2:AV:35:A:C5'	2:AV:35:A:C8	3.01	0.43
23:AY:605:ILE:HD13	23:AY:677:GLN:HB3	1.99	0.43
35:BV:28:GLU:HG3	35:BV:29:PRO:HD3	2.00	0.43
51:BC:84:LYS:O	51:BC:86:ALA:N	2.43	0.43
25:BA:1430:C:H2'	25:BA:1431:U:H6	1.83	0.43
25:BA:1644:C:C2'	25:BA:1645:G:H5'	2.48	0.43
25:BA:128:C:H4'	25:BA:129:C:OP1	2.19	0.43
25:BA:1762:A:O5'	25:BA:1762:A:H8	2.01	0.43
28:BO:43:VAL:HG12	28:BO:54:GLU:HA	2.01	0.43
25:BA:742:G:H4'	25:BA:1676:A:H5'	2.00	0.43
25:BA:2740:A:C6	25:BA:2741:A:C6	3.06	0.43
25:BA:1820:U:H4'	25:BA:1821:A:OP2	2.18	0.43
25:BA:2774:C:H2'	25:BA:2775:A:O4'	2.17	0.43
43:BD:43:ARG:CB	43:BD:54:ARG:HB2	2.47	0.43
51:BC:84:LYS:C	51:BC:86:ALA:N	2.72	0.43
13:AS:78:ARG:HD2	13:AS:81:ARG:HH12	1.83	0.43
1:AA:1378:C:OP1	20:AG:6:ARG:O	2.36	0.43
41:B1:3:LYS:CG	41:B1:4:VAL:N	2.80	0.43
18:AE:11:ILE:HG22	18:AE:31:LEU:HB3	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:AL:18:VAL:CG2	6:AL:19:ARG:N	2.82	0.43
18:AE:36:ASP:O	18:AE:37:ARG:HB2	2.17	0.43
25:BA:1881:C:H6	25:BA:1881:C:H5'	1.83	0.43
33:BT:65:LYS:HE3	33:BT:67:SER:HB2	2.01	0.43
23:AY:169:GLY:HA3	23:AY:173:THR:O	2.18	0.43
8:AN:57:ARG:NH2	16:AC:13:GLY:HA3	2.33	0.43
25:BA:543:C:H6	25:BA:543:C:C5'	2.32	0.43
25:BA:623:G:H2'	25:BA:624:C:C6	2.53	0.43
49:B8:62:LEU:O	49:B8:64:TYR:N	2.49	0.43
27:BN:39:ARG:HD3	27:BN:41:ASP:OD1	2.18	0.43
47:B6:51:GLU:HG3	47:B6:52:VAL:N	2.32	0.43
23:AY:205:TYR:HA	23:AY:208:GLN:HB3	2.00	0.43
23:AY:264:LEU:HD13	23:AY:265:LYS:HE3	2.01	0.43
23:AY:684:GLN:N	23:AY:687:LEU:HB2	2.33	0.43
1:AA:1157:A:H4'	1:AA:1158:C:O5'	2.19	0.43
9:AO:82:ILE:HG13	9:AO:88:ARG:HB2	2.01	0.43
11:AQ:45:HIS:CB	11:AQ:65:ILE:HD13	2.46	0.43
7:AM:59:TYR:O	7:AM:63:THR:OG1	2.15	0.43
25:BA:1131:G:N2	27:BN:73:THR:HG23	2.33	0.43
15:AB:200:ILE:HB	15:AB:202:PRO:HD3	2.01	0.43
23:AY:181:LEU:HD23	23:AY:182:ARG:NH1	2.34	0.43
1:AA:310:G:OP2	10:AP:27:LYS:HE2	2.18	0.43
27:BN:67:LEU:O	27:BN:68:GLU:CB	2.65	0.43
26:BB:84:C:H2'	26:BB:85:G:O5'	2.18	0.43
25:BA:1674:G:H1'	25:BA:1676:A:N6	2.33	0.43
1:AA:689:C:H2'	1:AA:690:G:O4'	2.18	0.43
25:BA:2352:A:C4	25:BA:2366:A:C2	3.06	0.43
25:BA:579:G:H2'	25:BA:580:C:C6	2.54	0.43
11:AQ:59:ILE:HD13	11:AQ:59:ILE:HA	1.75	0.43
25:BA:228:A:H3'	25:BA:229:A:C5'	2.48	0.43
25:BA:876:C:H2'	25:BA:877:U:O4'	2.19	0.43
1:AA:812:C:OP1	1:AA:903:G:H1'	2.19	0.43
25:BA:1073:A:H2'	25:BA:1074:G:O4'	2.18	0.43
25:BA:2009:G:OP1	36:BW:41:LYS:HE2	2.19	0.43
25:BA:1538:G:C2'	25:BA:1539:G:O5'	2.66	0.43
25:BA:2056:G:N2	46:B5:5:PRO:HA	2.34	0.43
4:AJ:22:LYS:C	4:AJ:24:VAL:H	2.21	0.43
17:AD:28:SER:HB3	17:AD:30:LYS:HG3	2.01	0.43
25:BA:1181:C:C2'	25:BA:1182:A:H5'	2.48	0.43
1:AA:1134:G:C4	1:AA:1135:U:C6	3.06	0.43
56:BK:29:GLN:O	56:BK:59:ILE:HD12	2.19	0.43
2:AV:1:G:C2	2:AV:73:A:C8	3.07	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
43:BD:10:THR:C	43:BD:11:PRO:O	2.55	0.43
2:AV:36:A:C2	3:AX:19:U:C2	3.06	0.43
54:BG:131:TYR:HB3	54:BG:159:VAL:CG1	2.49	0.43
25:BA:1722:A:C6	25:BA:1741:A:N1	2.87	0.43
30:BQ:16:ARG:O	30:BQ:17:LEU:HD23	2.18	0.43
25:BA:385:C:O2	29:BP:71:VAL:HG21	2.18	0.43
26:BB:42:C:C5'	54:BG:69:ALA:HB2	2.49	0.43
23:AY:86:GLY:O	23:AY:117:GLN:HG2	2.19	0.43
29:BP:13:ASN:OD1	53:BF:31:HIS:CB	2.67	0.43
39:BZ:23:LYS:O	39:BZ:25:PRO:HD3	2.19	0.43
55:BH:37:VAL:HG13	55:BH:68:THR:HG21	2.00	0.43
25:BA:2712:U:O2	25:BA:2712:U:H5'	2.19	0.43
18:AE:50:GLU:OE1	18:AE:50:GLU:HA	2.18	0.43
15:AB:62:ALA:C	15:AB:64:ARG:H	2.21	0.43
19:AF:3:ARG:HB2	19:AF:3:ARG:CZ	2.49	0.43
15:AB:23:ARG:O	15:AB:23:ARG:HG3	2.18	0.43
25:BA:2815:C:O2'	46:B5:42:PRO:HG2	2.19	0.43
25:BA:983:A:C6	25:BA:984:A:N1	2.87	0.43
55:BH:26:VAL:O	55:BH:32:GLU:HA	2.18	0.43
39:BZ:196:VAL:O	39:BZ:197:ILE:C	2.56	0.43
18:AE:107:ARG:O	18:AE:108:ALA:C	2.56	0.43
1:AA:504:C:C2	1:AA:542:G:N2	2.87	0.43
25:BA:2305:A:C2	25:BA:2306:C:C1'	2.95	0.43
25:BA:2298:A:H2'	25:BA:2299:G:O4'	2.17	0.43
54:BG:37:VAL:HG22	54:BG:159:VAL:HG23	2.01	0.43
29:BP:136:GLU:O	29:BP:138:LEU:N	2.51	0.43
43:BD:224:ALA:N	43:BD:233:HIS:HB2	2.32	0.43
25:BA:2734:A:C5'	25:BA:2735:G:OP2	2.65	0.43
28:BO:66:LYS:HD2	28:BO:80:ASP:O	2.18	0.43
25:BA:422:A:C6	25:BA:423:A:C6	3.06	0.43
25:BA:702:G:C2	25:BA:731:C:C2	3.06	0.43
23:AY:395:PRO:O	23:AY:397:VAL:N	2.51	0.43
21:AH:50:ARG:O	21:AH:51:VAL:CG1	2.67	0.43
49:B8:26:LYS:HB2	49:B8:44:LYS:HG3	2.00	0.43
25:BA:2035:G:H4'	25:BA:2036:C:OP2	2.18	0.43
25:BA:2151:G:H5''	25:BA:2151:G:H8	1.84	0.43
52:BE:61:ARG:H	52:BE:62:PRO:CD	2.32	0.43
52:BE:59:VAL:C	52:BE:60:ASN:HD22	2.21	0.43
33:BT:12:SER:O	33:BT:13:ARG:CZ	2.67	0.43
23:AY:122:TRP:CZ2	23:AY:159:ALA:HB2	2.53	0.43
25:BA:27:G:HO2'	25:BA:28:A:P	2.41	0.43
25:BA:1504:C:H1'	25:BA:1505:C:H5''	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1174:A:OP1	25:BA:1175:U:H5''	2.17	0.43
32:BS:89:ARG:HG2	32:BS:92:TYR:CA	2.49	0.43
15:AB:80:ILE:H	15:AB:80:ILE:HD12	1.84	0.43
1:AA:1326:C:OP1	24:AU:12:LYS:NZ	2.25	0.43
29:BP:144:GLU:N	29:BP:145:PRO:HD3	2.33	0.43
1:AA:1030:C:N4	1:AA:1032:G:C2	2.86	0.43
25:BA:760:G:H4'	25:BA:1776:G:OP1	2.19	0.43
25:BA:508:G:C5'	25:BA:509:C:OP1	2.67	0.43
1:AA:1303:C:H2'	1:AA:1304:G:H5'	2.01	0.43
25:BA:1322:A:C5	25:BA:1323:U:C5	3.06	0.43
25:BA:1975:G:H2'	25:BA:1976:U:O4'	2.19	0.43
42:B2:63:VAL:O	42:B2:66:GLU:HG2	2.18	0.43
25:BA:1512:U:H2'	25:BA:1513:C:C6	2.53	0.43
54:BG:56:ALA:CB	54:BG:153:ARG:NH1	2.82	0.43
52:BE:144:ARG:HB3	52:BE:145:LYS:H	1.62	0.43
25:BA:1786:A:N1	25:BA:2606:C:C1'	2.82	0.43
4:AJ:24:VAL:HG22	4:AJ:34:VAL:HG11	2.00	0.43
1:AA:428:G:C4'	1:AA:429:U:O5'	2.66	0.43
56:BK:57:ILE:HD12	56:BK:57:ILE:H	1.84	0.43
51:BC:215:THR:HB	51:BC:221:SER:HA	2.01	0.43
51:BC:185:LEU:O	51:BC:186:ALA:C	2.57	0.43
25:BA:464:U:O2'	48:B7:16:HIS:CE1	2.72	0.43
25:BA:1039:G:H1'	25:BA:1117:G:N2	2.34	0.43
27:BN:89:LYS:O	27:BN:93:THR:HG22	2.18	0.43
29:BP:83:VAL:CG1	29:BP:112:LEU:HD21	2.49	0.43
2:AV:47:U:H3'	2:AV:48:C:H5''	2.01	0.43
53:BF:114:VAL:HG21	53:BF:202:PHE:CZ	2.53	0.43
54:BG:72:ARG:HA	54:BG:87:PRO:HD2	2.00	0.43
25:BA:2623:G:H4'	25:BA:2825:C:O2	2.19	0.43
1:AA:1237:C:H2'	1:AA:1238:A:OP1	2.18	0.43
43:BD:221:VAL:HG22	43:BD:226:MET:HE2	2.01	0.43
25:BA:2741:A:H2'	25:BA:2742:C:O4'	2.18	0.43
33:BT:61:PHE:CE2	33:BT:76:PHE:HB2	2.54	0.43
25:BA:362:U:H6	25:BA:362:U:H5''	1.84	0.43
25:BA:1799:G:H5'	25:BA:1819:A:N6	2.34	0.43
36:BW:68:ARG:O	36:BW:110:LYS:HB3	2.19	0.43
25:BA:459:U:H5''	48:B7:40:TRP:CD2	2.54	0.43
7:AM:31:LYS:O	7:AM:35:GLU:HG2	2.18	0.43
26:BB:46:A:C5	26:BB:47:C:C4	3.07	0.43
25:BA:832:G:H21	29:BP:53:GLY:HA3	1.83	0.42
25:BA:2134:A:C8	25:BA:2135:A:C8	3.06	0.42
46:B5:52:TYR:CG	46:B5:52:TYR:O	2.72	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
34:BU:64:ARG:O	34:BU:65:ILE:C	2.57	0.42
55:BH:41:MET:HE3	55:BH:43:VAL:N	2.34	0.42
46:B5:33:CYS:SG	46:B5:34:PRO:O	2.76	0.42
25:BA:2139:C:O2'	25:BA:2140:C:O2	2.36	0.42
6:AL:60:LEU:HB3	6:AL:62:SER:H	1.84	0.42
5:AK:84:VAL:HG22	5:AK:110:ASP:HA	2.01	0.42
1:AA:1013:G:H5'	1:AA:1014:A:OP2	2.19	0.42
25:BA:638:G:H2'	25:BA:639:U:O4'	2.19	0.42
25:BA:387:U:H6	25:BA:387:U:O5'	2.01	0.42
25:BA:1876:A:H2'	25:BA:1877:A:C8	2.54	0.42
25:BA:2261:C:H3'	40:B0:16:SER:OG	2.19	0.42
25:BA:973:A:O4'	25:BA:1188:U:C6	2.72	0.42
33:BT:1:MET:O	33:BT:3:ARG:N	2.52	0.42
26:BB:65:C:H2'	26:BB:66:A:H5'	2.01	0.42
25:BA:1817:G:H5''	43:BD:88:ARG:NH2	2.34	0.42
54:BG:6:ALA:HB3	54:BG:104:GLU:OE2	2.19	0.42
1:AA:155:C:H2'	1:AA:156:G:O4'	2.19	0.42
33:BT:125:ARG:C	33:BT:127:ALA:H	2.22	0.42
21:AH:13:ILE:O	21:AH:17:THR:HG23	2.19	0.42
57:BJ:94:ALA:O	57:BJ:97:ALA:HB3	2.19	0.42
16:AC:179:ARG:HG3	16:AC:207:VAL:H	1.84	0.42
25:BA:2174:C:O2	51:BC:218:MET:SD	2.77	0.42
25:BA:1445:A:N3	25:BA:1445:A:C2'	2.82	0.42
25:BA:1094:U:C5'	25:BA:1094:U:H6	2.32	0.42
22:AI:4:TYR:CD2	22:AI:88:TYR:HB2	2.54	0.42
25:BA:2864:G:H2'	25:BA:2865:U:O4'	2.19	0.42
27:BN:16:ILE:HD11	27:BN:26:LEU:CD1	2.34	0.42
25:BA:1777:U:O2'	25:BA:1778:U:H5'	2.19	0.42
25:BA:1494:A:O2'	25:BA:1495:A:OP1	2.19	0.42
25:BA:642:G:O3'	47:B6:42:TRP:CZ2	2.72	0.42
46:B5:34:PRO:O	46:B5:35:GLU:CB	2.67	0.42
35:BV:18:LEU:O	35:BV:19:LYS:O	2.37	0.42
25:BA:2392:A:OP1	49:B8:32:LEU:HD22	2.19	0.42
25:BA:1847:A:H5'	25:BA:1848:A:OP2	2.19	0.42
37:BX:10:ALA:HB1	37:BX:11:PRO:HD2	2.01	0.42
27:BN:132:ALA:O	27:BN:133:GLN:O	2.37	0.42
29:BP:146:VAL:HG22	29:BP:147:LEU:H	1.83	0.42
25:BA:1313:U:O2	25:BA:1313:U:C2'	2.66	0.42
1:AA:269:C:H2'	1:AA:270:A:H8	1.81	0.42
25:BA:2219:G:H8	25:BA:2219:G:O5'	2.02	0.42
24:AU:12:LYS:O	24:AU:13:ILE:C	2.58	0.42
30:BQ:98:LYS:HB3	30:BQ:99:PRO:HD2	2.00	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:AC:12:LEU:O	16:AC:16:ARG:O	2.37	0.42
25:BA:2273:A:H2'	25:BA:2274:A:C8	2.54	0.42
25:BA:1050:A:H2'	25:BA:1051:G:C8	2.54	0.42
25:BA:370:G:H8	25:BA:370:G:O5'	2.02	0.42
36:BW:1:MET:HE3	36:BW:2:GLU:H	1.84	0.42
34:BU:92:ARG:HD2	35:BV:11:GLN:HB2	2.01	0.42
35:BV:47:VAL:C	35:BV:49:THR:O	2.58	0.42
38:BY:2:ARG:C	38:BY:4:LYS:H	2.11	0.42
25:BA:2287:A:H62	25:BA:2344:U:H3	1.67	0.42
25:BA:2078:C:C4	25:BA:2079:U:C4	3.07	0.42
23:AY:483:TYR:CE1	23:AY:603:GLU:HB3	2.54	0.42
23:AY:94:VAL:C	23:AY:96:ARG:N	2.72	0.42
16:AC:87:LEU:O	16:AC:91:LEU:HG	2.18	0.42
4:AJ:61:GLU:OE2	8:AN:45:ARG:NH1	2.47	0.42
18:AE:100:VAL:O	18:AE:107:ARG:NH2	2.50	0.42
16:AC:108:ASN:HA	16:AC:109:PRO:HD2	1.88	0.42
25:BA:1945:G:H2'	25:BA:1946:U:C6	2.55	0.42
25:BA:437:G:H8	25:BA:437:G:O5'	2.01	0.42
2:AV:30:G:H5''	2:AV:30:G:H8	1.84	0.42
22:AI:99:LEU:N	22:AI:99:LEU:HD13	2.33	0.42
1:AA:1051:C:O5'	1:AA:1051:C:H6	2.02	0.42
53:BF:40:GLN:O	53:BF:44:ARG:HG2	2.19	0.42
25:BA:2001:A:H2'	25:BA:2002:G:C8	2.54	0.42
29:BP:108:LYS:C	29:BP:110:TYR:H	2.20	0.42
53:BF:139:PHE:CZ	53:BF:156:LEU:HD22	2.54	0.42
15:AB:59:GLU:HB2	15:AB:221:LEU:HD11	2.00	0.42
27:BN:42:TRP:CD1	34:BU:63:VAL:HG11	2.55	0.42
33:BT:89:VAL:HG21	33:BT:91:ARG:CZ	2.49	0.42
42:B2:42:GLY:O	42:B2:44:LEU:O	2.37	0.42
26:BB:33:G:N3	26:BB:50:G:C2	2.88	0.42
1:AA:679:C:H2'	1:AA:680:C:C6	2.54	0.42
25:BA:1952:A:C4	28:BO:22:ILE:HG13	2.55	0.42
25:BA:2095:C:H2'	25:BA:2096:U:O4'	2.19	0.42
1:AA:417:C:H2'	1:AA:418:C:C6	2.51	0.42
7:AM:84:ILE:HG22	7:AM:84:ILE:O	2.20	0.42
25:BA:1833:U:O2	25:BA:1969:A:C2	2.71	0.42
25:BA:185:U:C2	25:BA:212:G:N2	2.87	0.42
25:BA:300:A:H2'	25:BA:334:C:H1'	2.01	0.42
1:AA:1286:A:C8	1:AA:1287:A:H4'	2.55	0.42
23:AY:181:LEU:HD23	23:AY:182:ARG:HG3	2.00	0.42
25:BA:2331:G:O4'	40:B0:42:GLY:HA3	2.19	0.42
25:BA:954:G:N3	25:BA:2274:A:C2	2.88	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1977:A:C2'	25:BA:1978:A:O5'	2.67	0.42
1:AA:120:A:C6	1:AA:122:G:C2	3.07	0.42
1:AA:1128:C:O2'	1:AA:1129:C:H5'	2.19	0.42
25:BA:1578:U:C2'	25:BA:1579:A:H5'	2.49	0.42
1:AA:222:U:H2'	1:AA:223:U:C6	2.54	0.42
25:BA:1532:C:O2	25:BA:1532:C:H2'	2.17	0.42
18:AE:102:ALA:HB2	18:AE:120:THR:HG21	2.01	0.42
20:AG:138:LYS:O	20:AG:142:GLU:HG3	2.19	0.42
35:BV:8:GLY:O	35:BV:10:LYS:HE3	2.19	0.42
39:BZ:61:LEU:CD2	39:BZ:61:LEU:N	2.82	0.42
47:B6:15:GLU:OE1	47:B6:18:ARG:HD2	2.19	0.42
1:AA:427:U:C4	1:AA:428:G:C6	3.08	0.42
56:BK:99:ILE:O	56:BK:139:VAL:N	2.52	0.42
43:BD:270:ILE:HD12	43:BD:270:ILE:O	2.20	0.42
34:BU:112:ARG:NH2	35:BV:46:VAL:CG1	2.82	0.42
1:AA:990:C:C4	1:AA:991:U:C5	3.07	0.42
41:B1:44:PRO:HB2	41:B1:46:LEU:CD1	2.48	0.42
25:BA:300:A:H1'	25:BA:319:C:O4'	2.20	0.42
15:AB:15:VAL:C	15:AB:16:HIS:CG	2.92	0.42
32:BS:16:ASN:OD1	32:BS:17:ARG:N	2.52	0.42
43:BD:65:ILE:HD11	43:BD:67:PHE:CE1	2.55	0.42
25:BA:586:A:C2	25:BA:809:G:N3	2.87	0.42
30:BQ:76:LYS:HB3	30:BQ:91:GLU:CG	2.50	0.42
25:BA:562:U:C4	25:BA:2036:C:O4'	2.72	0.42
44:B3:19:GLN:NE2	44:B3:52:HIS:NE2	2.67	0.42
52:BE:13:ARG:HD2	52:BE:20:ALA:HB1	2.01	0.42
25:BA:588:U:H2'	25:BA:589:C:C6	2.54	0.42
42:B2:21:LEU:HA	42:B2:21:LEU:HD23	1.83	0.42
43:BD:171:ASP:OD2	43:BD:171:ASP:N	2.53	0.42
1:AA:1342:C:H2'	1:AA:1343:G:C8	2.54	0.42
25:BA:2820:A:C8	52:BE:109:LYS:HE2	2.54	0.42
25:BA:1006:C:O2'	27:BN:106:MET:HB3	2.20	0.42
25:BA:2754:U:H2'	25:BA:2756:U:OP1	2.18	0.42
29:BP:18:ARG:HB3	29:BP:18:ARG:NH1	2.35	0.42
47:B6:42:TRP:HA	47:B6:42:TRP:CE3	2.55	0.42
49:B8:36:LYS:HD2	49:B8:41:ILE:HG22	2.02	0.42
55:BH:157:TYR:HD1	55:BH:173:PRO:HG3	1.84	0.42
26:BB:81:G:C6	26:BB:82:G:C5	3.07	0.42
27:BN:93:THR:HG1	27:BN:94:HIS:CD2	2.38	0.42
11:AQ:45:HIS:HB2	11:AQ:65:ILE:CD1	2.49	0.42
14:AT:96:GLY:O	14:AT:97:ALA:CB	2.68	0.42
25:BA:334:C:H2'	25:BA:335:C:OP1	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1273:G:H5''	1:AA:1273:G:H8	1.83	0.42
1:AA:620:C:C2	17:AD:135:LEU:HG	2.55	0.42
31:BR:44:LEU:CD2	31:BR:48:VAL:HG23	2.49	0.42
25:BA:1394:U:H4'	25:BA:1603:A:H4'	2.00	0.42
40:B0:50:ASN:HB3	40:B0:63:VAL:HG22	2.02	0.42
25:BA:304:G:H2'	25:BA:305:U:C6	2.55	0.42
55:BH:15:VAL:HG23	55:BH:15:VAL:O	2.18	0.42
18:AE:131:ILE:HD13	18:AE:131:ILE:HA	1.93	0.42
27:BN:108:PRO:O	27:BN:113:GLY:HA3	2.19	0.42
1:AA:1078:U:H1'	18:AE:130:ASN:OD1	2.20	0.42
23:AY:115:GLU:HB3	23:AY:116:PRO:CD	2.49	0.42
1:AA:559:A:OP1	18:AE:126:ARG:NH2	2.48	0.42
5:AK:21:ILE:HG12	5:AK:30:VAL:CG1	2.50	0.42
27:BN:36:GLY:CA	27:BN:49:GLY:HA2	2.48	0.42
35:BV:64:HIS:HD1	35:BV:92:THR:HG22	1.78	0.42
8:AN:23:ARG:NH1	8:AN:30:ALA:HB2	2.34	0.42
17:AD:31:CYS:O	17:AD:33:MET:N	2.47	0.42
25:BA:2151:G:N1	25:BA:2152:G:C5	2.88	0.42
43:BD:27:THR:HG22	43:BD:81:ALA:HB1	2.01	0.42
1:AA:1118:C:C1'	1:AA:1179:A:C4	3.02	0.42
1:AA:1179:A:H2'	1:AA:1180:A:O4'	2.18	0.42
8:AN:9:LYS:O	8:AN:9:LYS:HG2	2.19	0.42
25:BA:1090:U:H3	25:BA:1101:U:H3	1.67	0.42
56:BK:105:LEU:HD21	56:BK:120:LEU:HD13	2.01	0.42
25:BA:2811:G:H2'	25:BA:2812:G:O4'	2.20	0.42
15:AB:39:ILE:HG22	15:AB:41:ILE:CD1	2.50	0.42
25:BA:548:A:O2'	25:BA:549:G:P	2.77	0.42
29:BP:97:PRO:O	29:BP:98:GLU:CB	2.68	0.42
25:BA:1416:G:C4	25:BA:1417:C:C5	3.07	0.42
1:AA:346:G:H5'	33:BT:41:ARG:CZ	2.50	0.42
33:BT:32:TYR:CD2	33:BT:81:PRO:O	2.72	0.42
44:B3:50:VAL:CG2	44:B3:54:VAL:HG21	2.50	0.42
16:AC:167:TRP:O	16:AC:168:ALA:CB	2.68	0.42
25:BA:1721:G:N2	25:BA:1739:U:OP2	2.53	0.42
33:BT:62:THR:HA	33:BT:74:ARG:O	2.20	0.42
56:BK:136:VAL:HG13	56:BK:136:VAL:O	2.20	0.42
25:BA:1329:U:H3'	25:BA:1330:C:H6	1.84	0.42
15:AB:47:THR:HG22	15:AB:51:LEU:HD12	2.00	0.42
25:BA:572:A:OP2	35:BV:78:LYS:HE2	2.19	0.42
23:AY:335:LEU:HD11	23:AY:352:VAL:HG11	2.00	0.42
43:BD:45:ASN:ND2	43:BD:46:GLN:N	2.68	0.42
15:AB:8:LYS:HD3	15:AB:8:LYS:HA	1.92	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:979:G:H3'	25:BA:980:A:H5''	2.02	0.42
1:AA:1241:G:H2'	1:AA:1242:C:C6	2.55	0.42
1:AA:1092:A:C6	1:AA:1093:A:C6	3.08	0.42
23:AY:587:SER:O	23:AY:591:LYS:HB2	2.20	0.42
25:BA:271(F):C:H2'	25:BA:271(G):C:C6	2.55	0.42
25:BA:832:G:N3	29:BP:53:GLY:HA2	2.35	0.42
25:BA:2135:A:H2'	25:BA:2136:C:O4'	2.19	0.42
34:BU:92:ARG:HD3	34:BU:94:ASN:HB3	2.02	0.42
35:BV:39:LEU:HD13	35:BV:39:LEU:N	2.34	0.42
46:B5:40:LYS:HE2	46:B5:40:LYS:HB3	1.70	0.42
25:BA:309:G:N3	25:BA:329:G:O2'	2.48	0.42
25:BA:1299:G:O5'	25:BA:1299:G:H8	2.02	0.42
23:AY:209:ALA:O	23:AY:210:ARG:HB2	2.20	0.42
15:AB:155:LEU:HD22	15:AB:155:LEU:HA	1.87	0.42
7:AM:99:ARG:HB2	7:AM:101:GLN:HE21	1.84	0.42
30:BQ:27:VAL:O	30:BQ:105:GLU:OE1	2.37	0.42
31:BR:10:LEU:HD22	31:BR:17:ARG:CD	2.50	0.42
41:B1:3:LYS:HG2	41:B1:4:VAL:N	2.34	0.42
25:BA:1959:G:C2'	25:BA:1960:A:O5'	2.68	0.42
25:BA:2702:U:H4'	25:BA:2703:C:OP1	2.20	0.42
1:AA:73:G:H2'	1:AA:76:C:O4'	2.19	0.42
25:BA:1005:C:H2'	25:BA:1006:C:C6	2.54	0.42
19:AF:23:LYS:O	19:AF:27:GLN:HG2	2.19	0.42
25:BA:1816:G:H8	43:BD:62:TYR:OH	2.02	0.42
25:BA:122:G:H2'	25:BA:123:G:O5'	2.20	0.42
1:AA:355:C:H2'	1:AA:356:A:O4'	2.20	0.42
23:AY:344:THR:HG23	23:AY:390:VAL:HG22	2.02	0.42
1:AA:339:C:OP2	28:BO:97:ARG:NH1	2.52	0.42
1:AA:920:U:H2'	1:AA:921:U:C6	2.54	0.42
17:AD:71:SER:OG	17:AD:74:GLN:HB2	2.20	0.42
25:BA:962:G:H4'	25:BA:2496:C:O2'	2.19	0.42
53:BF:184:TYR:O	53:BF:188:ARG:HG2	2.19	0.42
35:BV:23:GLU:O	35:BV:24:LYS:C	2.57	0.42
25:BA:996:A:OP2	34:BU:92:ARG:NH2	2.53	0.42
33:BT:29:ARG:HE	33:BT:86:ILE:CG2	2.32	0.42
25:BA:2420:C:O5'	25:BA:2420:C:H6	2.01	0.42
56:BK:99:ILE:HD12	56:BK:103:GLN:CB	2.45	0.42
55:BH:171:LEU:O	55:BH:173:PRO:CD	2.67	0.42
25:BA:1857:G:C6	25:BA:1858:G:N1	2.88	0.42
25:BA:26:G:OP1	36:BW:80:PRO:HB3	2.20	0.42
25:BA:2690:C:OP2	31:BR:14:SER:CB	2.67	0.42
22:AI:71:SER:HA	22:AI:74:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
49:B8:52:LYS:N	49:B8:53:PRO:CD	2.82	0.42
7:AM:83:ASP:OD1	7:AM:85:GLY:N	2.48	0.42
23:AY:418:LYS:O	23:AY:419:ALA:CB	2.67	0.42
36:BW:17:VAL:O	36:BW:18:ARG:C	2.55	0.42
1:AA:684:A:N6	1:AA:685:G:C6	2.88	0.42
25:BA:813:U:H2'	25:BA:814:C:C6	2.54	0.42
25:BA:97:C:H5''	42:B2:2:LYS:HB2	2.02	0.42
25:BA:2230:G:C6	25:BA:2231:C:C4	3.07	0.42
27:BN:28:THR:HG22	27:BN:29:LYS:N	2.34	0.42
23:AY:689:LYS:HG3	23:AY:689:LYS:O	2.19	0.42
25:BA:2795:G:H2'	25:BA:2795:G:N3	2.35	0.42
51:BC:88:GLU:O	51:BC:89:ALA:CB	2.68	0.42
43:BD:129:ASN:O	43:BD:193:VAL:HG12	2.19	0.42
25:BA:453:C:O2	25:BA:457:A:O2'	2.35	0.42
1:AA:836:G:C6	1:AA:851:G:C6	3.08	0.42
50:B9:32:HIS:O	50:B9:34:GLN:HG3	2.20	0.42
25:BA:785:G:O2'	25:BA:1779:U:H5'	2.19	0.42
43:BD:26:LYS:CD	43:BD:113:VAL:HG21	2.50	0.42
12:AR:61:LYS:O	12:AR:65:ILE:HG12	2.20	0.42
25:BA:1470:G:H5''	25:BA:1471:A:OP1	2.20	0.42
29:BP:106:LEU:O	29:BP:107:LYS:O	2.38	0.42
25:BA:2801:A:H2'	25:BA:2895:U:H4'	2.01	0.42
25:BA:2584:U:O2	25:BA:2584:U:O4'	2.37	0.42
43:BD:33:LEU:HD23	43:BD:34:VAL:HG13	2.02	0.42
1:AA:346:G:OP1	33:BT:35:LYS:NZ	2.52	0.42
42:B2:65:ASN:HB3	42:B2:69:ARG:NH2	2.35	0.42
25:BA:864:G:C6	25:BA:865:C:N4	2.88	0.42
25:BA:1364:G:P	41:B1:61:ARG:HH22	2.43	0.42
17:AD:3:ARG:NE	17:AD:5:ILE:HG13	2.35	0.42
32:BS:56:LEU:HD23	32:BS:58:LEU:HB2	2.01	0.42
34:BU:74:LEU:CD2	34:BU:78:THR:HG22	2.50	0.42
20:AG:108:ALA:O	20:AG:119:ARG:HD2	2.19	0.42
5:AK:59:TYR:O	5:AK:62:GLN:HB3	2.19	0.42
25:BA:2324:C:H5''	25:BA:2325:G:H5'	2.01	0.42
33:BT:4:GLY:HA2	52:BE:9:VAL:HG23	2.02	0.42
25:BA:530:G:N3	25:BA:530:G:O4'	2.52	0.42
15:AB:37:ASN:HA	15:AB:37:ASN:HD22	1.68	0.42
1:AA:1146:A:N3	1:AA:1146:A:H2'	2.33	0.42
1:AA:302:G:O3'	6:AL:17:LYS:HE2	2.20	0.42
23:AY:85:PRO:HG2	23:AY:90:PHE:HB2	2.02	0.42
25:BA:280:C:N4	25:BA:281:G:C6	2.88	0.42
1:AA:90:U:O2'	1:AA:91:C:H5	1.86	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
46:B5:4:HIS:CB	46:B5:5:PRO:CD	2.82	0.41
29:BP:16:ARG:HB2	29:BP:16:ARG:CZ	2.50	0.41
25:BA:1019:U:C2'	25:BA:1021:A:C2	3.03	0.41
33:BT:29:ARG:CB	33:BT:30:VAL:HG22	2.41	0.41
25:BA:1168:G:C2	25:BA:1182:A:C2	3.08	0.41
25:BA:881:G:C2	25:BA:882:G:H1'	2.55	0.41
35:BV:18:LEU:HD13	35:BV:19:LYS:H	1.85	0.41
25:BA:2287:A:C2	25:BA:2346:A:C2	3.08	0.41
1:AA:126:G:H5'	1:AA:633:G:N2	2.35	0.41
33:BT:23:ARG:O	33:BT:24:PRO:C	2.58	0.41
27:BN:56:ASN:H	27:BN:125:GLY:HA3	1.85	0.41
1:AA:1517:G:H1'	25:BA:1919:A:O3'	2.20	0.41
1:AA:1319:A:OP2	13:AS:5:LEU:HD23	2.19	0.41
4:AJ:85:LEU:C	4:AJ:87:THR:N	2.74	0.41
17:AD:194:LEU:HD22	17:AD:194:LEU:N	2.35	0.41
25:BA:1417:C:H2'	25:BA:1418:G:O4'	2.20	0.41
1:AA:1226:C:H2'	7:AM:103:THR:OG1	2.20	0.41
29:BP:127:ALA:HB3	29:BP:130:PHE:CE2	2.55	0.41
23:AY:343:ASN:O	23:AY:347:GLY:N	2.53	0.41
22:AI:53:VAL:HG13	22:AI:95:LYS:NZ	2.35	0.41
1:AA:264:U:H4'	11:AQ:63:ARG:HD3	2.02	0.41
21:AH:17:THR:OG1	21:AH:18:ARG:NH1	2.53	0.41
1:AA:950:U:H2'	1:AA:951:G:C8	2.55	0.41
1:AA:1325:C:P	24:AU:6:ARG:HH12	2.43	0.41
16:AC:113:ALA:HB3	16:AC:114:PRO:HD3	2.01	0.41
20:AG:13:GLN:O	20:AG:24:THR:HG21	2.20	0.41
23:AY:320:PRO:O	23:AY:320:PRO:CD	2.67	0.41
25:BA:1475:G:C8	25:BA:1475:G:H5''	2.54	0.41
23:AY:349:LYS:HD3	23:AY:349:LYS:H	1.85	0.41
39:BZ:17:ALA:O	39:BZ:20:ARG:HB3	2.19	0.41
25:BA:435:C:C2'	25:BA:436:C:H5'	2.50	0.41
1:AA:640:A:N3	21:AH:115:SER:HB3	2.35	0.41
25:BA:1370:C:HO2'	25:BA:1811:G:HO2'	1.67	0.41
39:BZ:54:HIS:CE1	39:BZ:123:ASP:OD1	2.73	0.41
17:AD:78:LEU:HB3	17:AD:93:PHE:HE2	1.85	0.41
17:AD:31:CYS:C	17:AD:33:MET:N	2.73	0.41
17:AD:26:CYS:CB	17:AD:31:CYS:HB2	2.50	0.41
25:BA:2430:A:H8	25:BA:2431:U:H5	1.68	0.41
25:BA:2286:A:H4'	25:BA:2287:A:O4'	2.20	0.41
25:BA:2468:G:HO2'	25:BA:2476:A:H8	1.63	0.41
33:BT:56:GLY:O	33:BT:59:THR:HG23	2.19	0.41
33:BT:57:PHE:O	33:BT:58:ASN:C	2.59	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:AI:9:ARG:CG	22:AI:14:VAL:HG13	2.50	0.41
1:AA:232:G:H1'	1:AA:262:A:N1	2.34	0.41
23:AY:120:THR:O	23:AY:124:GLN:HG3	2.20	0.41
25:BA:1156:A:C8	34:BU:51:LYS:HD2	2.54	0.41
1:AA:1187:G:C8	1:AA:1187:G:C5'	3.03	0.41
55:BH:105:LEU:H	55:BH:105:LEU:HD22	1.84	0.41
25:BA:228:A:H2'	25:BA:230:U:O4'	2.21	0.41
25:BA:414:C:OP1	25:BA:1879:C:O2'	2.38	0.41
26:BB:39:A:N3	26:BB:39:A:H2'	2.35	0.41
1:AA:782:A:C6	1:AA:801:U:C2	3.08	0.41
10:AP:58:TYR:O	10:AP:62:VAL:HG22	2.20	0.41
1:AA:367:U:H4'	23:AY:351:ARG:NE	2.35	0.41
49:B8:14:VAL:CG2	49:B8:22:VAL:HG13	2.50	0.41
22:AI:110:GLU:OE2	22:AI:113:LYS:NZ	2.48	0.41
8:AN:28:GLY:O	8:AN:29:ARG:C	2.58	0.41
25:BA:2055:C:H5'	25:BA:2056:G:O5'	2.19	0.41
1:AA:390:C:H2'	1:AA:391:G:C8	2.55	0.41
2:AV:73:A:C2'	2:AV:74:C:C5'	2.98	0.41
33:BT:11:GLU:CD	33:BT:11:GLU:N	2.74	0.41
33:BT:57:PHE:O	33:BT:59:THR:N	2.54	0.41
25:BA:896:A:N7	39:BZ:146:ILE:HD13	2.36	0.41
25:BA:2219:G:C2	25:BA:2220:G:C8	3.08	0.41
25:BA:629:G:OP1	25:BA:650:C:O2'	2.36	0.41
31:BR:2:ARG:HD2	52:BE:111:ARG:HG3	2.02	0.41
25:BA:1286:A:N1	25:BA:1329:U:O2'	2.46	0.41
1:AA:665:A:N3	1:AA:732:C:H2'	2.35	0.41
14:AT:63:ILE:HG22	14:AT:77:ALA:HB1	2.02	0.41
25:BA:945:A:C4	25:BA:2448:A:C2	3.08	0.41
29:BP:28:GLY:HA3	29:BP:29:LYS:HD2	2.02	0.41
32:BS:12:PHE:CD1	32:BS:12:PHE:O	2.74	0.41
25:BA:2016:U:O5'	25:BA:2016:U:H6	2.03	0.41
16:AC:196:LEU:CD2	16:AC:196:LEU:N	2.84	0.41
36:BW:51:LEU:HD23	36:BW:105:VAL:HG11	2.02	0.41
1:AA:1260:C:OP1	1:AA:1284:C:H4'	2.20	0.41
19:AF:76:ALA:HB1	19:AF:80:ARG:NH2	2.35	0.41
48:B7:34:ARG:HB3	48:B7:39:ARG:HG3	2.02	0.41
53:BF:123:LEU:HD12	53:BF:124:LEU:N	2.35	0.41
25:BA:1570:A:OP1	43:BD:36:PRO:HB2	2.20	0.41
25:BA:259:G:C2'	25:BA:621:A:O2'	2.68	0.41
43:BD:26:LYS:HG2	43:BD:113:VAL:HG21	2.02	0.41
1:AA:1135:U:C2'	1:AA:1135:U:O2	2.67	0.41
49:B8:32:LEU:HB3	49:B8:36:LYS:HZ1	1.81	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
49:B8:32:LEU:HB2	49:B8:36:LYS:CE	2.48	0.41
25:BA:535:C:O2'	25:BA:536:A:H5'	2.20	0.41
25:BA:95:G:O2'	42:B2:48:HIS:ND1	2.40	0.41
13:AS:5:LEU:HG	13:AS:10:PHE:CD1	2.51	0.41
25:BA:1151:G:H5'	34:BU:81:HIS:CE1	2.54	0.41
31:BR:55:ALA:HA	31:BR:80:PHE:CZ	2.55	0.41
31:BR:58:GLY:HA2	31:BR:80:PHE:CE1	2.56	0.41
15:AB:169:LYS:O	15:AB:169:LYS:HD3	2.20	0.41
25:BA:319:C:C2'	25:BA:320:A:O5'	2.68	0.41
17:AD:191:ARG:NH1	17:AD:200:GLU:OE1	2.54	0.41
56:BK:130:SER:HA	56:BK:133:SER:OG	2.21	0.41
18:AE:80:ILE:CD1	18:AE:138:ALA:HB1	2.50	0.41
57:BJ:25:ALA:O	57:BJ:85:ALA:N	2.53	0.41
21:AH:75:ARG:HA	21:AH:76:PRO:HD2	1.88	0.41
51:BC:17:ASN:O	51:BC:18:LYS:C	2.59	0.41
25:BA:923:C:H2'	25:BA:924:C:C6	2.56	0.41
25:BA:1839:G:H1'	25:BA:1927:A:O5'	2.20	0.41
25:BA:1290:C:O2'	25:BA:1291:C:H5'	2.20	0.41
46:B5:20:ARG:HG2	46:B5:23:HIS:CD2	2.56	0.41
49:B8:2:PRO:O	49:B8:3:LYS:CB	2.68	0.41
21:AH:97:VAL:HG13	21:AH:98:LYS:N	2.35	0.41
25:BA:2419:U:O4	49:B8:30:ARG:NE	2.52	0.41
25:BA:2154:G:C8	25:BA:2154:G:C5'	3.04	0.41
25:BA:660:G:C6	25:BA:661:C:C4	3.08	0.41
25:BA:2141:G:N2	25:BA:2151:G:H1'	2.36	0.41
25:BA:1021:A:H62	25:BA:1141:U:H3	1.67	0.41
1:AA:266:G:O3'	11:AQ:67:LYS:HB2	2.20	0.41
23:AY:250:THR:CA	23:AY:255:ILE:HG22	2.50	0.41
15:AB:19:HIS:CD2	15:AB:189:ASP:OD2	2.73	0.41
15:AB:40:HIS:HB3	15:AB:190:THR:HG21	2.01	0.41
25:BA:1039:G:O6	25:BA:1116:C:N3	2.53	0.41
14:AT:89:ARG:NH1	14:AT:105:SER:O	2.49	0.41
1:AA:1228:C:P	7:AM:108:ARG:NH2	2.94	0.41
27:BN:119:ARG:HG3	27:BN:119:ARG:NH1	2.34	0.41
25:BA:1876:A:H2'	25:BA:1877:A:H8	1.85	0.41
1:AA:1326:C:O2'	1:AA:1327:C:H5'	2.20	0.41
49:B8:39:LYS:O	49:B8:43:GLN:HB2	2.20	0.41
25:BA:475:U:C4	25:BA:481:G:O6	2.73	0.41
15:AB:11:LEU:HD13	15:AB:217:ARG:NH2	2.36	0.41
54:BG:19:LEU:HA	54:BG:22:ARG:HB2	2.03	0.41
25:BA:30:G:H2'	25:BA:31:C:O4'	2.21	0.41
25:BA:2592:G:C5	25:BA:2593:U:C4	3.09	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
31:BR:96:ARG:NH1	31:BR:115:GLU:OE1	2.46	0.41
25:BA:2695:C:H2'	25:BA:2696:U:C6	2.55	0.41
1:AA:1213:A:C8	1:AA:1215:G:C5	3.08	0.41
51:BC:64:LEU:HD23	51:BC:64:LEU:HA	1.95	0.41
25:BA:783:A:C8	25:BA:783:A:H3'	2.55	0.41
25:BA:103:A:H8	25:BA:103:A:O5'	2.03	0.41
23:AY:156:ARG:HB3	23:AY:156:ARG:HH11	1.85	0.41
25:BA:1446:C:C2	25:BA:1466:G:N2	2.87	0.41
55:BH:72:ILE:O	55:BH:75:ALA:HB3	2.19	0.41
1:AA:859:A:H2	21:AH:19:VAL:HG11	1.83	0.41
25:BA:631:A:O2'	29:BP:67:MET:HB3	2.20	0.41
34:BU:65:ILE:CG1	34:BU:96:ALA:HB3	2.49	0.41
27:BN:47:ALA:HB2	27:BN:112:LEU:CD1	2.50	0.41
1:AA:1119:C:O2'	1:AA:1120:G:H5'	2.21	0.41
56:BK:115:LEU:HD13	56:BK:126:MET:SD	2.59	0.41
27:BN:93:THR:OG1	27:BN:94:HIS:NE2	2.53	0.41
25:BA:2689:U:H5''	25:BA:2690:C:H5'	2.03	0.41
25:BA:83:G:H22	25:BA:102:G:H2'	1.84	0.41
2:AV:46:G:H3'	2:AV:47:U:H5''	2.02	0.41
54:BG:7:LEU:O	54:BG:11:TYR:HB3	2.20	0.41
1:AA:1347:G:C6	22:AI:107:ARG:NH2	2.89	0.41
40:B0:14:ARG:NH1	40:B0:14:ARG:HB2	2.36	0.41
25:BA:2123:G:O6	25:BA:2175:C:N3	2.53	0.41
23:AY:79:ILE:CD1	23:AY:79:ILE:N	2.83	0.41
25:BA:2637:U:O2'	25:BA:2638:G:H5'	2.20	0.41
1:AA:242:C:H2'	1:AA:243:A:H5'	2.03	0.41
25:BA:2173:A:H5''	25:BA:2174:C:OP2	2.19	0.41
25:BA:122:G:C2'	25:BA:123:G:O5'	2.69	0.41
32:BS:74:ALA:HB1	32:BS:103:GLU:CB	2.51	0.41
23:AY:18:ALA:O	23:AY:106:VAL:HA	2.20	0.41
1:AA:1048:G:OP1	8:AN:4:LYS:HB2	2.20	0.41
1:AA:130:A:N6	1:AA:234:C:O4'	2.53	0.41
14:AT:93:GLU:OE1	14:AT:93:GLU:C	2.59	0.41
25:BA:1437:C:H5''	25:BA:1437:C:H6	1.86	0.41
20:AG:143:ARG:O	20:AG:143:ARG:HG2	2.21	0.41
23:AY:435:ASP:C	23:AY:435:ASP:OD1	2.58	0.41
1:AA:1256:A:H4'	1:AA:1258:G:C4	2.56	0.41
52:BE:101:ARG:NH1	52:BE:169:ASN:O	2.49	0.41
43:BD:124:PRO:HB2	43:BD:126:GLN:HG2	2.02	0.41
20:AG:66:VAL:HG12	20:AG:70:LYS:HE3	2.03	0.41
10:AP:70:ALA:O	10:AP:74:LEU:HD12	2.21	0.41
20:AG:74:GLU:HG2	20:AG:91:VAL:HG22	2.01	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
25:BA:1655:A:H3'	25:BA:1656:C:H6	1.86	0.41
2:AV:76:A:H2'	25:BA:2395:C:C2	2.56	0.41
55:BH:43:VAL:HG12	55:BH:46:GLU:OE2	2.20	0.41
1:AA:1134:G:C6	1:AA:1135:U:C5	3.09	0.41
1:AA:1144:G:C2'	1:AA:1145:C:H5'	2.50	0.41
1:AA:979:C:OP1	1:AA:981:U:O4	2.38	0.41
25:BA:685:A:C4'	25:BA:686:G:O5'	2.69	0.41
57:BJ:37:ALA:C	57:BJ:39:ALA:H	2.23	0.41
25:BA:1054:A:H5'	25:BA:1054:A:C8	2.56	0.41
14:AT:50:GLU:HG3	14:AT:100:ILE:HB	2.03	0.41
25:BA:1477:A:H2'	25:BA:1478:G:O4'	2.21	0.41
15:AB:239:VAL:O	15:AB:239:VAL:CG1	2.69	0.41
1:AA:789:U:O2'	1:AA:791:G:N7	2.46	0.41
25:BA:1190:G:H5''	29:BP:35:HIS:H	1.84	0.41
1:AA:620:C:H2'	1:AA:621:A:O4'	2.19	0.41
45:B4:36:VAL:HB	45:B4:37:PRO:HD2	2.03	0.41
15:AB:62:ALA:O	15:AB:64:ARG:N	2.54	0.41
39:BZ:54:HIS:HB3	39:BZ:101:PRO:HD3	2.02	0.41
1:AA:781:A:H5'	1:AA:782:A:OP2	2.20	0.41
25:BA:1668:A:N3	25:BA:1670:C:C4	2.89	0.41
1:AA:401:C:H1'	1:AA:622:A:H1'	2.03	0.41
1:AA:1411:C:O2'	1:AA:1412:C:H5'	2.20	0.41
25:BA:1682:G:C5	25:BA:1683:C:C4	3.09	0.41
25:BA:2176:A:N3	51:BC:44:HIS:HE1	2.18	0.41
15:AB:172:ILE:HD12	15:AB:172:ILE:H	1.85	0.41
25:BA:2100:G:H2'	25:BA:2100:G:N3	2.35	0.41
1:AA:1071:C:H2'	1:AA:1072:G:C8	2.55	0.41
25:BA:957:A:N1	25:BA:2458:G:H4'	2.35	0.41
1:AA:600:C:C2	1:AA:639:G:C2	3.09	0.41
5:AK:65:ALA:HB1	5:AK:98:LEU:CD2	2.50	0.41
56:BK:24:GLY:H	56:BK:25:PRO:HD2	1.86	0.41
43:BD:158:ALA:O	43:BD:159:ALA:C	2.59	0.41
26:BB:31:C:N4	32:BS:32:LEU:HD22	2.36	0.41
25:BA:1538:G:H5'	25:BA:1538:G:H8	1.85	0.41
35:BV:64:HIS:CE1	35:BV:92:THR:CG2	3.04	0.41
29:BP:64:LYS:O	29:BP:65:ARG:C	2.56	0.41
38:BY:82:PRO:HD2	38:BY:97:ARG:HD3	2.03	0.41
1:AA:1021:G:H2'	1:AA:1022:G:O4'	2.20	0.41
41:B1:58:ILE:HD11	41:B1:60:PHE:CZ	2.56	0.41
25:BA:1396:U:O2	25:BA:1396:U:C2'	2.60	0.41
25:BA:2167:U:H2'	25:BA:2168:G:O4'	2.20	0.41
1:AA:693:G:H2'	1:AA:694:A:O4'	2.19	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
24:AU:12:LYS:HG2	24:AU:22:ARG:HB3	2.01	0.41
55:BH:24:VAL:CG1	55:BH:37:VAL:HG21	2.51	0.41
55:BH:67:LEU:HD12	55:BH:71:LEU:HD13	2.03	0.41
4:AJ:54:PHE:CE2	4:AJ:55:LYS:HE3	2.56	0.41
25:BA:2061:G:H5''	25:BA:2503:A:C2	2.55	0.41
15:AB:235:SER:OG	15:AB:236:TYR:N	2.54	0.41
25:BA:729:G:H2'	25:BA:1775:U:H1'	2.02	0.41
42:B2:11:GLU:O	42:B2:15:LYS:HG3	2.21	0.41
25:BA:1069:A:N7	25:BA:1073:A:N6	2.68	0.41
1:AA:801:U:H2'	1:AA:802:A:O5'	2.21	0.41
1:AA:859:A:H2'	1:AA:860:A:O4'	2.20	0.41
32:BS:83:LYS:HB3	32:BS:105:ALA:HB3	2.03	0.41
1:AA:596:C:H2'	1:AA:596:C:O2	2.20	0.41
1:AA:1253:G:H1'	1:AA:1355:G:O2'	2.20	0.41
25:BA:2466:C:H5''	50:B9:6:SER:HB3	2.02	0.41
7:AM:36:LYS:O	7:AM:37:THR:HG23	2.21	0.41
25:BA:2135:A:H4'	25:BA:2160:G:H4'	2.03	0.41
25:BA:1245:G:OP1	29:BP:16:ARG:HG2	2.20	0.41
25:BA:1405:U:H2'	25:BA:1406:U:C6	2.55	0.41
1:AA:1140:C:H2'	1:AA:1141:C:H6	1.86	0.41
38:BY:95:LYS:HD3	38:BY:99:CYS:O	2.21	0.41
38:BY:8:LYS:C	38:BY:28:LYS:HE2	2.41	0.41
1:AA:1003:G:N2	1:AA:1039:C:N4	2.69	0.41
25:BA:893:C:H2'	25:BA:894:C:C6	2.55	0.41
25:BA:1299:G:H4'	25:BA:1300:U:H5''	2.02	0.41
25:BA:2346:A:H5'	25:BA:2383:G:O4'	2.21	0.41
26:BB:105:A:OP1	39:BZ:72:ARG:NH1	2.54	0.41
25:BA:2811:G:OP1	52:BE:60:ASN:CB	2.68	0.41
9:AO:39:LEU:HD12	9:AO:56:LEU:HB2	2.01	0.41
25:BA:1848:A:H2'	25:BA:1849:G:O4'	2.21	0.41
25:BA:2164:C:C4	25:BA:2165:G:H8	2.39	0.41
25:BA:536:A:H2'	25:BA:537:C:C6	2.55	0.41
25:BA:2505:G:HO2'	25:BA:2506:U:H6	1.67	0.41
25:BA:2680:C:O2'	25:BA:2681:C:H5'	2.21	0.41
15:AB:19:HIS:O	15:AB:39:ILE:HG23	2.21	0.41
43:BD:70:TRP:HZ3	43:BD:146:GLU:CD	2.24	0.41
29:BP:85:LEU:H	29:BP:85:LEU:CD2	2.33	0.41
25:BA:901:A:H2'	25:BA:902:C:O4'	2.21	0.41
16:AC:35:GLU:O	16:AC:36:ASP:C	2.59	0.41
51:BC:103:ILE:HG23	51:BC:105:ASP:OD2	2.21	0.41
25:BA:1742:G:N7	25:BA:1743:C:C6	2.89	0.41
25:BA:673:C:H5''	53:BF:81:PRO:HD2	2.03	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
29:BP:144:GLU:N	29:BP:145:PRO:CD	2.84	0.41
30:BQ:21:THR:OG1	30:BQ:99:PRO:O	2.35	0.41
41:B1:3:LYS:C	41:B1:46:LEU:HD21	2.41	0.41
32:BS:58:LEU:O	32:BS:59:LYS:O	2.38	0.41
5:AK:12:ARG:NH2	5:AK:34:ASP:OD1	2.53	0.41
54:BG:83:ARG:O	54:BG:85:GLY:N	2.54	0.41
1:AA:192:U:H4'	14:AT:57:ARG:HD2	2.03	0.41
25:BA:2155:G:C2'	25:BA:2156:G:O5'	2.69	0.41
1:AA:731:G:N2	1:AA:732:C:C2	2.89	0.41
25:BA:991:C:O2'	25:BA:992:C:H5'	2.21	0.41
45:B4:36:VAL:HG22	45:B4:52:SER:O	2.21	0.41
2:AV:55:U:H5	2:AV:58:A:OP2	2.04	0.41
43:BD:89:SER:HB2	43:BD:159:ALA:HB2	2.02	0.41
25:BA:408:G:O2'	25:BA:409:C:H5'	2.21	0.41
53:BF:33:LEU:HA	53:BF:33:LEU:HD12	1.89	0.41
25:BA:2766:G:N3	25:BA:2766:G:H2'	2.36	0.41
1:AA:575:G:OP1	1:AA:575:G:H4'	2.21	0.41
51:BC:96:GLY:O	51:BC:97:GLU:HG3	2.20	0.41
28:BO:35:VAL:CG2	28:BO:69:ILE:HD11	2.51	0.41
7:AM:70:LEU:O	7:AM:71:ARG:C	2.59	0.41
25:BA:57:C:H2'	25:BA:58:G:O4'	2.21	0.41
9:AO:18:PHE:O	9:AO:19:PRO:C	2.58	0.41
35:BV:55:ALA:HA	35:BV:100:ARG:O	2.20	0.41
1:AA:123:C:OP1	1:AA:312:C:H5'	2.21	0.41
26:BB:104:U:C5'	30:BQ:141:GLN:HB3	2.50	0.41
28:BO:10:VAL:HG22	28:BO:10:VAL:O	2.21	0.41
20:AG:50:ILE:O	20:AG:54:THR:HG23	2.21	0.41
7:AM:74:VAL:O	7:AM:77:ASN:HB2	2.20	0.41
47:B6:22:ALA:HB2	47:B6:39:TYR:CZ	2.56	0.41
5:AK:29:ILE:HG21	5:AK:29:ILE:HD13	1.75	0.41
1:AA:1053:G:N7	1:AA:1200:C:H5''	2.36	0.41
34:BU:91:ASP:OD1	34:BU:96:ALA:HB2	2.20	0.41
55:BH:41:MET:HE3	55:BH:43:VAL:CG1	2.42	0.41
17:AD:28:SER:C	17:AD:30:LYS:N	2.75	0.41
55:BH:137:ASP:HB3	55:BH:140:LYS:HB2	2.02	0.41
40:B0:23:VAL:HG22	40:B0:38:VAL:CG2	2.44	0.41
29:BP:23:PRO:O	29:BP:33:ARG:CZ	2.69	0.41
1:AA:1181:G:H5''	1:AA:1181:G:H8	1.86	0.41
53:BF:28:ILE:H	53:BF:28:ILE:CD1	2.31	0.41
1:AA:500:G:H2'	1:AA:501:C:C6	2.56	0.41
25:BA:1451:C:H4'	25:BA:1452:A:C8	2.55	0.41
51:BC:30:LYS:NZ	51:BC:30:LYS:HB3	2.36	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
17:AD:16:GLY:C	17:AD:17:VAL:HG23	2.41	0.41
31:BR:4:LEU:O	31:BR:5:LYS:CG	2.68	0.41
56:BK:121:GLU:O	56:BK:125:ARG:NE	2.53	0.41
1:AA:684:A:O3'	5:AK:12:ARG:NH1	2.54	0.41
25:BA:507:A:H5''	25:BA:508:G:H5'	2.02	0.41
25:BA:572:A:H3'	25:BA:573:G:O4'	2.21	0.41
1:AA:955:U:H2'	1:AA:956:U:O4'	2.21	0.41
55:BH:86:GLU:HB3	55:BH:132:ARG:HB2	2.01	0.41
44:B3:8:LEU:HD13	44:B3:31:LEU:HD23	2.03	0.41
6:AL:84:LEU:HA	6:AL:84:LEU:HD23	1.95	0.41
28:BO:87:ILE:HA	28:BO:87:ILE:HD13	1.82	0.41
38:BY:77:PRO:O	38:BY:78:ALA:HB2	2.20	0.40
17:AD:2:GLY:C	17:AD:4:TYR:N	2.73	0.40
25:BA:1046:A:O5'	25:BA:1047:G:OP1	2.39	0.40
53:BF:3:GLU:HA	53:BF:24:LEU:CB	2.51	0.40
33:BT:91:ARG:HG2	33:BT:116:ALA:HA	2.03	0.40
38:BY:10:GLY:HA2	38:BY:27:VAL:HG13	2.03	0.40
12:AR:22:VAL:O	12:AR:23:LYS:C	2.58	0.40
51:BC:39:GLU:OE1	51:BC:216:THR:CB	2.69	0.40
23:AY:61:ARG:NH1	25:BA:2663:G:OP1	2.54	0.40
27:BN:5:VAL:O	27:BN:5:VAL:CG1	2.68	0.40
54:BG:54:GLU:O	54:BG:58:GLN:HG3	2.21	0.40
1:AA:109:A:C6	1:AA:327:A:C6	3.09	0.40
1:AA:36:C:H2'	1:AA:37:U:O4'	2.21	0.40
16:AC:91:LEU:HB2	16:AC:99:VAL:HG21	2.03	0.40
38:BY:41:GLY:O	38:BY:42:VAL:C	2.59	0.40
53:BF:13:SER:HB2	53:BF:14:PRO:CD	2.50	0.40
25:BA:1680:U:O2	25:BA:1763:G:H3'	2.21	0.40
18:AE:11:ILE:HD12	18:AE:33:VAL:CG2	2.51	0.40
1:AA:963:G:H21	4:AJ:55:LYS:HE3	1.86	0.40
27:BN:30:ILE:HG22	27:BN:34:LEU:HD22	2.03	0.40
25:BA:1086:A:C5'	25:BA:1087:G:OP1	2.69	0.40
25:BA:1461:G:C6	25:BA:1462:C:C4	3.10	0.40
23:AY:90:PHE:O	23:AY:91:THR:C	2.59	0.40
25:BA:1668:A:H4'	25:BA:1669:A:O5'	2.20	0.40
25:BA:2313:C:H4'	54:BG:91:ARG:HG3	2.02	0.40
25:BA:2356:C:O3'	40:B0:20:ARG:HD3	2.21	0.40
16:AC:65:ALA:HA	16:AC:100:ALA:HB3	2.02	0.40
47:B6:10:LEU:CD2	47:B6:10:LEU:H	2.34	0.40
53:BF:110:LEU:HA	53:BF:110:LEU:HD23	1.86	0.40
25:BA:2472:G:H3'	25:BA:2475:C:H42	1.86	0.40
1:AA:735:C:O2'	1:AA:736:C:H5'	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:AC:85:ARG:HH12	16:AC:88:ARG:NH1	2.18	0.40
22:AI:8:GLY:O	22:AI:15:ALA:N	2.46	0.40
25:BA:41:C:H2'	25:BA:42:G:O4'	2.21	0.40
25:BA:52:A:O2'	25:BA:53:A:H5'	2.21	0.40
25:BA:1491:G:C6	25:BA:1500:G:C2	3.09	0.40
56:BK:58:THR:HB	56:BK:66:THR:CG2	2.52	0.40
53:BF:167:ALA:CB	53:BF:173:VAL:HG11	2.43	0.40
1:AA:375:U:O3'	10:AP:6:LEU:HB2	2.21	0.40
36:BW:46:PHE:O	36:BW:50:VAL:HG12	2.20	0.40
25:BA:1338:G:N3	25:BA:1393:A:H2	2.19	0.40
24:AU:9:ARG:HH21	24:AU:22:ARG:HA	1.86	0.40
18:AE:91:LEU:HD12	18:AE:91:LEU:HA	1.86	0.40
25:BA:565:C:H2'	25:BA:566:U:O4'	2.21	0.40
54:BG:85:GLY:O	54:BG:86:MET:C	2.59	0.40
13:AS:22:LEU:HD13	13:AS:27:GLU:HB2	2.02	0.40
25:BA:570:G:C5	25:BA:2030:A:C2	3.09	0.40
25:BA:1285:G:C5	25:BA:1329:U:C4	3.09	0.40
23:AY:128:TYR:OH	23:AY:402:ILE:O	2.36	0.40
7:AM:121:LYS:O	7:AM:122:LYS:HG2	2.21	0.40
34:BU:66:ASN:CG	34:BU:76:TYR:HB2	2.41	0.40
45:B4:51:TYR:O	54:BG:105:LYS:NZ	2.52	0.40
43:BD:39:LYS:HB2	43:BD:62:TYR:HB2	2.03	0.40
7:AM:49:THR:O	7:AM:53:VAL:HG23	2.20	0.40
53:BF:136:THR:HA	53:BF:166:ALA:O	2.22	0.40
25:BA:2519:U:C5	25:BA:2541:A:C6	3.09	0.40
52:BE:134:ILE:C	52:BE:134:ILE:HD12	2.42	0.40
1:AA:488:C:O5'	1:AA:488:C:H6	2.04	0.40
1:AA:1026:G:N3	1:AA:1026:G:H2'	2.36	0.40
23:AY:446:THR:O	23:AY:446:THR:HG23	2.21	0.40
1:AA:524:G:H2'	1:AA:525:C:C6	2.56	0.40
17:AD:15:GLU:OE1	17:AD:59:ARG:NE	2.43	0.40
43:BD:32:SER:HA	43:BD:35:LYS:HZ2	1.85	0.40
43:BD:26:LYS:HG2	43:BD:82:ILE:H	1.86	0.40
25:BA:2810:A:H2'	52:BE:61:ARG:HH21	1.81	0.40
41:B1:58:ILE:HD11	41:B1:60:PHE:CE2	2.56	0.40
25:BA:2468:G:H5'	30:BQ:120:ILE:HD12	2.03	0.40
25:BA:535:C:C2'	25:BA:536:A:H5'	2.52	0.40
39:BZ:24:LEU:HD23	39:BZ:25:PRO:O	2.21	0.40
25:BA:2279:G:N7	40:B0:14:ARG:NH1	2.64	0.40
7:AM:87:TYR:N	13:AS:73:GLU:O	2.54	0.40
25:BA:1645:G:OP1	25:BA:1646:C:H5'	2.20	0.40
21:AH:10:LEU:HD22	21:AH:83:ILE:HD11	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:441:A:H3'	1:AA:442:C:H6	1.87	0.40
58:BL:81:UNK:O	58:BL:85:UNK:C	2.69	0.40
1:AA:1236:A:H4'	1:AA:1304:G:H4'	2.02	0.40
1:AA:1373:G:O5'	1:AA:1373:G:H8	2.04	0.40
25:BA:687:C:O2'	25:BA:1780:A:N1	2.47	0.40
4:AJ:26:ALA:O	4:AJ:27:ALA:HB2	2.22	0.40
53:BF:61:GLY:O	53:BF:62:ARG:C	2.59	0.40
25:BA:1814:G:OP2	25:BA:1815:A:O2'	2.32	0.40
30:BQ:104:PHE:HE1	30:BQ:125:LEU:HD11	1.86	0.40
51:BC:19:VAL:HG22	51:BC:223:ARG:HG3	2.02	0.40
25:BA:644:A:C2	25:BA:2369:A:H1'	2.56	0.40
39:BZ:69:THR:HG22	39:BZ:90:VAL:HA	2.04	0.40
25:BA:2408:U:H2'	25:BA:2409:G:C8	2.56	0.40
1:AA:157:G:C6	1:AA:158:G:C5	3.10	0.40
25:BA:2139:C:C2'	25:BA:2140:C:OP2	2.68	0.40
43:BD:131:LEU:HB2	43:BD:136:ILE:HD11	2.03	0.40
25:BA:2392:A:OP1	49:B8:32:LEU:CD1	2.70	0.40
25:BA:774:A:O2'	25:BA:775:G:P	2.78	0.40
1:AA:327:A:O3'	1:AA:328:C:H4'	2.21	0.40
28:BO:88:ASN:C	28:BO:88:ASN:ND2	2.73	0.40
52:BE:72:VAL:O	52:BE:74:PRO:N	2.53	0.40
25:BA:1263:U:O3'	46:B5:11:THR:OG1	2.39	0.40
11:AQ:26:GLN:HA	11:AQ:36:ILE:O	2.22	0.40
23:AY:486:THR:HG21	23:AY:519:ARG:HH12	1.86	0.40
25:BA:647:G:H2'	25:BA:648:G:O4'	2.21	0.40
31:BR:2:ARG:CD	52:BE:111:ARG:HG3	2.52	0.40
21:AH:111:ILE:C	21:AH:112:LEU:HD23	2.42	0.40
53:BF:5:ALA:O	53:BF:6:VAL:HG23	2.20	0.40
16:AC:19:GLU:O	16:AC:56:ASP:HA	2.22	0.40
25:BA:1684:C:H2'	25:BA:1685:C:C6	2.57	0.40
25:BA:2250:G:C8	25:BA:2496:C:H5"	2.57	0.40
26:BB:24:G:N7	26:BB:56:G:H2'	2.37	0.40
17:AD:64:LEU:O	17:AD:67:ILE:HB	2.22	0.40
58:BL:70:UNK:O	58:BL:74:UNK:N	2.54	0.40
1:AA:619:U:O2	17:AD:133:VAL:HA	2.21	0.40
25:BA:1787:A:O4'	25:BA:2589:A:H4'	2.21	0.40
25:BA:526:A:N3	25:BA:2044:C:H1'	2.36	0.40
56:BK:104:VAL:CG2	56:BK:127:ILE:HB	2.51	0.40
43:BD:245:PRO:HA	43:BD:246:PRO:HD3	1.87	0.40
23:AY:329:ARG:HH21	23:AY:372:GLY:HA2	1.86	0.40
25:BA:1771:C:C1'	25:BA:1786:A:C8	3.05	0.40
1:AA:1141:C:C2	1:AA:1142:G:C8	3.09	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:AA:1003:G:N2	1:AA:1038:C:C4	2.89	0.40
1:AA:175:C:H2'	1:AA:176:C:C6	2.57	0.40
30:BQ:35:VAL:HG21	39:BZ:81:ARG:HH21	1.86	0.40
25:BA:2092:U:C6	25:BA:2225:A:O2'	2.75	0.40
51:BC:53:ARG:HG3	51:BC:55:ASP:OD1	2.21	0.40
23:AY:168:ILE:HD11	23:AY:178:ILE:HD12	2.03	0.40
54:BG:77:ILE:O	54:BG:81:LYS:O	2.39	0.40
25:BA:2285:C:C5	47:B6:27:LYS:HE3	2.57	0.40
25:BA:1002:G:H2'	25:BA:1003:G:O4'	2.21	0.40
25:BA:2310:A:H2'	25:BA:2310:A:N3	2.36	0.40
1:AA:1237:C:C4'	1:AA:1334:G:N2	2.84	0.40
15:AB:70:PHE:O	15:AB:92:TYR:HA	2.21	0.40
42:B2:12:GLU:O	42:B2:15:LYS:HE3	2.22	0.40
1:AA:1091:U:O2	1:AA:1093:A:C8	2.74	0.40
25:BA:435:C:H2'	25:BA:436:C:H5'	2.04	0.40
53:BF:123:LEU:HD12	53:BF:124:LEU:H	1.86	0.40
25:BA:2731:G:OP1	52:BE:169:ASN:ND2	2.37	0.40
1:AA:1299:A:O3'	1:AA:1300:G:H4'	2.21	0.40
9:AO:27:VAL:HG12	9:AO:31:LEU:HD22	2.04	0.40
10:AP:33:ILE:N	10:AP:33:ILE:HD13	2.36	0.40
30:BQ:10:ARG:O	30:BQ:10:ARG:HG3	2.21	0.40
25:BA:2550:G:C2'	25:BA:2551:C:H5'	2.51	0.40
54:BG:103:LEU:HD22	54:BG:178:PHE:HZ	1.87	0.40
1:AA:152:A:N6	1:AA:170:U:C2	2.89	0.40
39:BZ:4:ARG:O	39:BZ:5:LEU:HB2	2.21	0.40
51:BC:162:GLU:HG2	51:BC:163:PHE:N	2.37	0.40
25:BA:732:C:H2'	25:BA:733:G:O4'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
4	AJ	96/98 (98%)	80 (83%)	10 (10%)	6 (6%)	2	5
5	AK	117/119 (98%)	105 (90%)	9 (8%)	3 (3%)	8	29
6	AL	122/124 (98%)	107 (88%)	10 (8%)	5 (4%)	4	14
7	AM	122/124 (98%)	82 (67%)	32 (26%)	8 (7%)	2	4
8	AN	58/60 (97%)	48 (83%)	8 (14%)	2 (3%)	6	21
9	AO	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	19	54
10	AP	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
11	AQ	97/99 (98%)	92 (95%)	4 (4%)	1 (1%)	22	59
12	AR	68/70 (97%)	60 (88%)	5 (7%)	3 (4%)	4	13
13	AS	76/78 (97%)	60 (79%)	8 (10%)	8 (10%)	1	2
14	AT	97/99 (98%)	86 (89%)	5 (5%)	6 (6%)	2	5
15	AB	232/234 (99%)	191 (82%)	32 (14%)	9 (4%)	5	16
16	AC	204/206 (99%)	173 (85%)	22 (11%)	9 (4%)	4	13
17	AD	206/208 (99%)	171 (83%)	25 (12%)	10 (5%)	3	10
18	AE	148/150 (99%)	141 (95%)	5 (3%)	2 (1%)	16	49
19	AF	99/101 (98%)	91 (92%)	8 (8%)	0	100	100
20	AG	153/155 (99%)	132 (86%)	17 (11%)	4 (3%)	8	29
21	AH	136/138 (99%)	127 (93%)	6 (4%)	3 (2%)	10	34
22	AI	125/127 (98%)	99 (79%)	17 (14%)	9 (7%)	2	3
23	AY	612/680 (90%)	520 (85%)	72 (12%)	20 (3%)	6	22
24	AU	22/24 (92%)	17 (77%)	5 (23%)	0	100	100
27	BN	136/140 (97%)	113 (83%)	17 (12%)	6 (4%)	4	13
28	BO	120/122 (98%)	113 (94%)	3 (2%)	4 (3%)	6	22
29	BP	144/150 (96%)	90 (62%)	21 (15%)	33 (23%)	0	0
30	BQ	139/141 (99%)	117 (84%)	17 (12%)	5 (4%)	5	19
31	BR	115/118 (98%)	101 (88%)	9 (8%)	5 (4%)	4	13
32	BS	96/112 (86%)	61 (64%)	20 (21%)	15 (16%)	0	0
33	BT	135/146 (92%)	96 (71%)	24 (18%)	15 (11%)	1	1
34	BU	115/118 (98%)	101 (88%)	10 (9%)	4 (4%)	6	20
35	BV	99/101 (98%)	75 (76%)	9 (9%)	15 (15%)	0	0
36	BW	111/113 (98%)	101 (91%)	4 (4%)	6 (5%)	3	8
37	BX	90/96 (94%)	83 (92%)	7 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	BY	98/110 (89%)	58 (59%)	18 (18%)	22 (22%)	0	0
39	BZ	194/206 (94%)	146 (75%)	32 (16%)	16 (8%)	1	3
40	B0	82/85 (96%)	71 (87%)	8 (10%)	3 (4%)	5	18
41	B1	91/98 (93%)	76 (84%)	12 (13%)	3 (3%)	6	22
42	B2	69/72 (96%)	58 (84%)	4 (6%)	7 (10%)	1	2
43	BD	269/276 (98%)	231 (86%)	24 (9%)	14 (5%)	3	8
44	B3	57/60 (95%)	54 (95%)	2 (4%)	1 (2%)	13	41
45	B4	28/71 (39%)	21 (75%)	4 (14%)	3 (11%)	1	1
46	B5	57/60 (95%)	47 (82%)	4 (7%)	6 (10%)	1	2
47	B6	42/54 (78%)	20 (48%)	15 (36%)	7 (17%)	0	0
48	B7	46/49 (94%)	43 (94%)	2 (4%)	1 (2%)	10	34
49	B8	61/65 (94%)	45 (74%)	11 (18%)	5 (8%)	1	3
50	B9	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
51	BC	219/229 (96%)	166 (76%)	35 (16%)	18 (8%)	1	3
52	BE	202/206 (98%)	145 (72%)	30 (15%)	27 (13%)	0	1
53	BF	205/210 (98%)	165 (80%)	24 (12%)	16 (8%)	1	3
54	BG	179/182 (98%)	123 (69%)	44 (25%)	12 (7%)	2	4
55	BH	171/180 (95%)	128 (75%)	26 (15%)	17 (10%)	1	2
56	BK	121/147 (82%)	84 (69%)	30 (25%)	7 (6%)	3	6
57	BJ	128/130 (98%)	84 (66%)	31 (24%)	13 (10%)	1	2
All	All	6610/6949 (95%)	5383 (81%)	812 (12%)	415 (6%)	2	5

All (415) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AJ	23	ILE
4	AJ	59	SER
4	AJ	86	MET
5	AK	117	ASN
5	AK	128	ALA
6	AL	27	LEU
7	AM	46	LYS
7	AM	83	ASP
7	AM	90	LEU
8	AN	16	PHE

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Mol	Chain	Res	Type
11	AQ	49	GLU
12	AR	25	THR
13	AS	5	LEU
13	AS	10	PHE
13	AS	26	GLY
13	AS	28	LYS
13	AS	80	TYR
14	AT	95	ALA
15	AB	18	GLY
15	AB	237	ALA
16	AC	154	SER
16	AC	165	THR
16	AC	168	ALA
17	AD	3	ARG
17	AD	31	CYS
20	AG	155	ARG
22	AI	55	ALA
22	AI	89	ASN
22	AI	118	LYS
22	AI	119	ALA
23	AY	34	TYR
23	AY	95	GLU
23	AY	171	GLU
23	AY	180	VAL
23	AY	215	LYS
23	AY	683	VAL
23	AY	684	GLN
27	BN	4	TYR
27	BN	57	ALA
27	BN	59	LYS
27	BN	127	ASP
27	BN	133	GLN
29	BP	14	LYS
29	BP	18	ARG
29	BP	23	PRO
29	BP	25	SER
29	BP	47	ASP
29	BP	49	ARG
29	BP	52	GLU
29	BP	57	THR
29	BP	65	ARG
29	BP	106	LEU

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Mol	Chain	Res	Type
29	BP	107	LYS
30	BQ	18	LYS
30	BQ	22	LYS
31	BR	4	LEU
32	BS	59	LYS
32	BS	89	ARG
32	BS	97	ARG
32	BS	105	ALA
33	BT	24	PRO
33	BT	30	VAL
33	BT	80	SER
33	BT	91	ARG
33	BT	107	ASP
34	BU	91	ASP
34	BU	93	LYS
35	BV	3	ALA
35	BV	16	PRO
35	BV	19	LYS
35	BV	22	VAL
35	BV	24	LYS
35	BV	46	VAL
36	BW	63	ASP
38	BY	3	VAL
38	BY	10	GLY
38	BY	24	VAL
38	BY	27	VAL
38	BY	31	LEU
38	BY	42	VAL
38	BY	56	PRO
38	BY	62	GLU
38	BY	77	PRO
38	BY	78	ALA
38	BY	98	VAL
39	BZ	21	ALA
39	BZ	146	ILE
39	BZ	189	ALA
40	B0	3	HIS
41	B1	53	VAL
42	B2	43	GLN
42	B2	44	LEU
42	B2	70	GLN
43	BD	3	VAL

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Mol	Chain	Res	Type
43	BD	12	SER
43	BD	26	LYS
46	B5	4	HIS
46	B5	35	GLU
46	B5	49	CYS
46	B5	51	TYR
46	B5	52	TYR
46	B5	57	VAL
47	B6	19	ARG
47	B6	31	PRO
47	B6	46	HIS
49	B8	34	TRP
49	B8	61	LEU
51	BC	54	SER
51	BC	55	ASP
51	BC	80	GLY
51	BC	83	ILE
51	BC	109	ASP
51	BC	186	ALA
52	BE	60	ASN
52	BE	66	HIS
52	BE	69	LYS
52	BE	72	VAL
52	BE	75	VAL
52	BE	77	ILE
52	BE	82	ARG
52	BE	87	GLU
52	BE	88	GLY
52	BE	90	THR
52	BE	118	LYS
53	BF	21	ALA
53	BF	67	GLN
53	BF	168	ARG
53	BF	195	ASP
54	BG	82	LEU
54	BG	87	PRO
54	BG	97	ASP
55	BH	9	ILE
55	BH	10	PRO
55	BH	13	LYS
55	BH	45	VAL
55	BH	83	TYR

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Mol	Chain	Res	Type
55	BH	85	LYS
55	BH	92	ILE
55	BH	138	LYS
56	BK	115	LEU
57	BJ	47	ALA
57	BJ	50	ALA
57	BJ	56	ALA
57	BJ	61	ALA
57	BJ	73	ALA
57	BJ	107	ALA
57	BJ	128	ALA
4	AJ	27	ALA
6	AL	91	LYS
7	AM	66	LEU
8	AN	14	PRO
12	AR	28	GLU
14	AT	75	ASN
14	AT	101	GLY
15	AB	14	GLY
15	AB	110	GLN
16	AC	12	LEU
16	AC	61	ALA
16	AC	156	ARG
17	AD	9	CYS
17	AD	17	VAL
17	AD	23	GLY
17	AD	26	CYS
22	AI	105	ASP
23	AY	196	ILE
23	AY	211	GLU
23	AY	396	ARG
23	AY	551	GLN
28	BO	5	GLN
29	BP	11	GLY
29	BP	26	GLY
29	BP	33	ARG
29	BP	34	GLY
29	BP	66	GLY
29	BP	67	MET
29	BP	98	GLU
29	BP	109	GLY
30	BQ	27	VAL

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Mol	Chain	Res	Type
30	BQ	28	ALA
32	BS	14	VAL
32	BS	102	ALA
33	BT	2	ASN
33	BT	81	PRO
33	BT	126	ALA
33	BT	129	ARG
35	BV	37	VAL
35	BV	40	LEU
36	BW	65	LEU
38	BY	29	GLU
38	BY	39	VAL
39	BZ	142	SER
39	BZ	165	VAL
39	BZ	168	GLU
39	BZ	190	GLU
41	B1	58	ILE
42	B2	9	GLN
43	BD	11	PRO
43	BD	25	THR
43	BD	210	GLY
43	BD	224	ALA
43	BD	238	GLY
43	BD	239	ARG
45	B4	61	VAL
47	B6	23	THR
51	BC	85	GLU
51	BC	86	ALA
51	BC	89	ALA
51	BC	97	GLU
52	BE	45	THR
52	BE	63	LEU
52	BE	71	GLY
52	BE	74	PRO
52	BE	95	ILE
52	BE	130	GLY
53	BF	3	GLU
53	BF	5	ALA
53	BF	6	VAL
53	BF	11	VAL
53	BF	25	PRO
53	BF	134	GLY

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Mol	Chain	Res	Type
54	BG	61	ALA
54	BG	84	LYS
54	BG	117	PHE
55	BH	55	PRO
55	BH	84	SER
55	BH	172	LYS
56	BK	82	ALA
57	BJ	7	ALA
57	BJ	72	ALA
57	BJ	120	ALA
4	AJ	58	ASP
6	AL	28	LYS
7	AM	124	PRO
12	AR	87	ARG
13	AS	6	LYS
13	AS	76	PRO
14	AT	99	LEU
15	AB	153	ARG
15	AB	236	TYR
16	AC	4	LYS
16	AC	181	ASN
17	AD	18	LYS
18	AE	68	GLU
23	AY	96	ARG
23	AY	181	LEU
23	AY	403	GLU
23	AY	404	VAL
23	AY	581	ALA
27	BN	47	ALA
28	BO	29	ASN
29	BP	17	LYS
29	BP	35	HIS
29	BP	36	LYS
29	BP	39	LYS
29	BP	42	SER
29	BP	108	LYS
29	BP	136	GLU
29	BP	146	VAL
32	BS	19	LYS
32	BS	53	SER
32	BS	88	ASP
32	BS	92	TYR

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Mol	Chain	Res	Type
32	BS	103	GLU
33	BT	27	THR
33	BT	58	ASN
35	BV	2	PHE
35	BV	20	LEU
35	BV	23	GLU
35	BV	47	VAL
35	BV	48	GLY
38	BY	67	LEU
38	BY	82	PRO
38	BY	90	LEU
39	BZ	140	ASP
42	B2	45	SER
42	B2	48	HIS
43	BD	32	SER
43	BD	101	GLU
44	B3	51	ALA
45	B4	63	SER
47	B6	22	ALA
47	B6	28	ARG
49	B8	51	ALA
51	BC	141	LYS
52	BE	17	ASP
52	BE	61	ARG
52	BE	128	SER
53	BF	10	PRO
53	BF	141	ALA
54	BG	49	ASP
54	BG	64	THR
54	BG	142	PRO
55	BH	126	PRO
56	BK	51	ALA
57	BJ	84	ALA
6	AL	19	ARG
7	AM	67	GLU
14	AT	97	ALA
15	AB	15	VAL
15	AB	130	ARG
15	AB	131	PRO
16	AC	36	ASP
17	AD	4	TYR
20	AG	81	GLY

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Mol	Chain	Res	Type
21	AH	2	LEU
22	AI	92	TYR
28	BO	26	LYS
29	BP	43	GLY
29	BP	48	PRO
29	BP	122	PRO
29	BP	147	LEU
30	BQ	59	ARG
31	BR	3	HIS
31	BR	106	GLY
32	BS	54	LEU
33	BT	31	SER
33	BT	32	TYR
34	BU	33	ARG
36	BW	6	ILE
38	BY	32	PRO
38	BY	99	CYS
39	BZ	14	LYS
39	BZ	80	ARG
39	BZ	199	LYS
40	B0	6	GLY
40	B0	9	SER
41	B1	85	LEU
48	B7	47	ARG
49	B8	33	ASN
49	B8	53	PRO
51	BC	185	LEU
52	BE	18	ASP
52	BE	187	ALA
53	BF	131	GLY
54	BG	122	PRO
55	BH	168	PRO
56	BK	42	ASN
57	BJ	93	ALA
7	AM	7	VAL
7	AM	55	ARG
9	AO	24	SER
14	AT	100	ILE
17	AD	5	ILE
18	AE	8	GLU
20	AG	54	THR
22	AI	54	ASP

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Mol	Chain	Res	Type
22	AI	127	LYS
23	AY	136	ALA
29	BP	38	GLN
31	BR	86	ARG
31	BR	117	VAL
32	BS	13	ARG
33	BT	57	PHE
35	BV	44	LYS
39	BZ	156	LYS
47	B6	44	ARG
51	BC	140	PRO
51	BC	227	HIS
52	BE	44	TYR
53	BF	26	ALA
54	BG	43	LEU
55	BH	24	VAL
55	BH	137	ASP
55	BH	171	LEU
56	BK	62	ASP
57	BJ	38	ALA
4	AJ	90	LEU
13	AS	29	ARG
20	AG	7	ALA
21	AH	51	VAL
29	BP	9	ASN
32	BS	95	HIS
32	BS	107	GLU
35	BV	79	VAL
36	BW	11	ARG
36	BW	93	ALA
38	BY	81	LYS
39	BZ	78	LYS
39	BZ	147	GLY
42	B2	17	SER
43	BD	35	LYS
45	B4	54	LYS
51	BC	118	ASP
51	BC	181	PRO
52	BE	129	HIS
54	BG	86	MET
55	BH	47	GLU
56	BK	10	LEU

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Mol	Chain	Res	Type
22	AI	44	VAL
6	AL	121	GLY
17	AD	29	PRO
23	AY	243	VAL
23	AY	299	VAL
28	BO	48	PRO
34	BU	90	VAL
38	BY	53	PRO
38	BY	66	PRO
39	BZ	197	ILE
51	BC	96	GLY
52	BE	73	GLU
53	BF	84	VAL
5	AK	48	ILE
23	AY	516	PRO
43	BD	271	ILE
21	AH	73	ASP
33	BT	88	ILE
36	BW	112	GLY
38	BY	80	GLY
43	BD	28	GLU
51	BC	103	ILE
52	BE	116	VAL
53	BF	24	LEU
39	BZ	166	SER
52	BE	53	PRO
56	BK	4	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	
4	AJ	88/88 (100%)	70 (80%)	18 (20%)	2	4
5	AK	90/90 (100%)	68 (76%)	22 (24%)	1	2
6	AL	104/104 (100%)	85 (82%)	19 (18%)	2	6
7	AM	99/99 (100%)	83 (84%)	16 (16%)	3	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	AN	49/49 (100%)	38 (78%)	11 (22%)	1	3
9	AO	79/79 (100%)	67 (85%)	12 (15%)	4	10
10	AP	72/72 (100%)	61 (85%)	11 (15%)	4	10
11	AQ	94/94 (100%)	79 (84%)	15 (16%)	3	9
12	AR	61/61 (100%)	52 (85%)	9 (15%)	4	11
13	AS	69/69 (100%)	52 (75%)	17 (25%)	1	2
14	AT	76/76 (100%)	61 (80%)	15 (20%)	2	5
15	AB	202/202 (100%)	172 (85%)	30 (15%)	4	11
16	AC	160/160 (100%)	125 (78%)	35 (22%)	1	3
17	AD	180/180 (100%)	144 (80%)	36 (20%)	2	5
18	AE	115/115 (100%)	104 (90%)	11 (10%)	12	32
19	AF	90/90 (100%)	76 (84%)	14 (16%)	4	10
20	AG	126/126 (100%)	110 (87%)	16 (13%)	6	16
21	AH	119/119 (100%)	96 (81%)	23 (19%)	2	5
22	AI	98/98 (100%)	76 (78%)	22 (22%)	1	3
23	AY	528/573 (92%)	420 (80%)	108 (20%)	2	4
24	AU	19/19 (100%)	14 (74%)	5 (26%)	1	2
27	BN	117/119 (98%)	84 (72%)	33 (28%)	0	1
28	BO	100/100 (100%)	84 (84%)	16 (16%)	3	9
29	BP	112/116 (97%)	82 (73%)	30 (27%)	1	2
30	BQ	111/111 (100%)	96 (86%)	15 (14%)	6	14
31	BR	100/101 (99%)	80 (80%)	20 (20%)	2	5
32	BS	77/88 (88%)	62 (80%)	15 (20%)	2	5
33	BT	120/127 (94%)	91 (76%)	29 (24%)	1	2
34	BU	92/94 (98%)	76 (83%)	16 (17%)	3	7
35	BV	82/82 (100%)	56 (68%)	26 (32%)	0	0
36	BW	91/92 (99%)	75 (82%)	16 (18%)	3	7
37	BX	74/78 (95%)	59 (80%)	15 (20%)	2	4
38	BY	84/91 (92%)	65 (77%)	19 (23%)	1	3
39	BZ	154/179 (86%)	127 (82%)	27 (18%)	3	7
40	B0	66/67 (98%)	56 (85%)	10 (15%)	4	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	B1	78/83 (94%)	63 (81%)	15 (19%)	2	5
42	B2	66/67 (98%)	51 (77%)	15 (23%)	1	3
43	BD	213/218 (98%)	170 (80%)	43 (20%)	2	4
44	B3	51/52 (98%)	41 (80%)	10 (20%)	2	5
45	B4	27/63 (43%)	23 (85%)	4 (15%)	4	11
46	B5	51/52 (98%)	42 (82%)	9 (18%)	3	7
47	B6	43/52 (83%)	31 (72%)	12 (28%)	0	1
48	B7	41/42 (98%)	35 (85%)	6 (15%)	5	12
49	B8	53/55 (96%)	33 (62%)	20 (38%)	0	0
50	B9	33/34 (97%)	23 (70%)	10 (30%)	0	1
51	BC	177/181 (98%)	159 (90%)	18 (10%)	11	28
52	BE	165/166 (99%)	131 (79%)	34 (21%)	2	4
53	BF	165/166 (99%)	134 (81%)	31 (19%)	2	5
54	BG	155/156 (99%)	128 (83%)	27 (17%)	3	7
55	BH	136/148 (92%)	107 (79%)	29 (21%)	1	4
56	BK	96/111 (86%)	85 (88%)	11 (12%)	8	22
All	All	5448/5654 (96%)	4402 (81%)	1046 (19%)	2	5

All (1046) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	AJ	3	LYS
4	AJ	5	ARG
4	AJ	6	ILE
4	AJ	14	LYS
4	AJ	16	LEU
4	AJ	22	LYS
4	AJ	38	ILE
4	AJ	46	ARG
4	AJ	49	VAL
4	AJ	55	LYS
4	AJ	76	ASN
4	AJ	78	ASN
4	AJ	79	ARG
4	AJ	80	LYS
4	AJ	81	THR

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Mol	Chain	Res	Type
4	AJ	86	MET
4	AJ	96	ILE
4	AJ	99	LYS
5	AK	11	LYS
5	AK	14	VAL
5	AK	28	THR
5	AK	29	ILE
5	AK	30	VAL
5	AK	31	THR
5	AK	41	THR
5	AK	51	LYS
5	AK	53	SER
5	AK	87	THR
5	AK	92	GLU
5	AK	96	ARG
5	AK	103	LEU
5	AK	109	VAL
5	AK	112	THR
5	AK	114	VAL
5	AK	116	HIS
5	AK	117	ASN
5	AK	120	ARG
5	AK	122	LYS
5	AK	124	LYS
5	AK	126	ARG
6	AL	13	LYS
6	AL	20	LYS
6	AL	21	LYS
6	AL	27	LEU
6	AL	33	ARG
6	AL	41	ARG
6	AL	42	THR
6	AL	53	ARG
6	AL	60	LEU
6	AL	67	THR
6	AL	78	GLN
6	AL	83	VAL
6	AL	84	LEU
6	AL	85	ILE
6	AL	89	ARG
6	AL	91	LYS
6	AL	92	ASP

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Mol	Chain	Res	Type
6	AL	111	LYS
6	AL	126	LYS
7	AM	47	ASP
7	AM	48	LEU
7	AM	49	THR
7	AM	56	LEU
7	AM	64	TRP
7	AM	70	LEU
7	AM	79	LYS
7	AM	82	MET
7	AM	86	CYS
7	AM	90	LEU
7	AM	93	ARG
7	AM	94	ARG
7	AM	102	ARG
7	AM	108	ARG
7	AM	115	LYS
7	AM	120	LYS
8	AN	4	LYS
8	AN	7	ILE
8	AN	9	LYS
8	AN	18	VAL
8	AN	26	ARG
8	AN	27	CYS
8	AN	33	VAL
8	AN	35	ARG
8	AN	41	ARG
8	AN	44	LEU
8	AN	60	SER
9	AO	10	LYS
9	AO	17	ARG
9	AO	24	SER
9	AO	26	GLU
9	AO	31	LEU
9	AO	38	ARG
9	AO	39	LEU
9	AO	45	VAL
9	AO	65	ARG
9	AO	66	LEU
9	AO	82	ILE
9	AO	83	GLU
10	AP	2	VAL

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Mol	Chain	Res	Type
10	AP	4	ILE
10	AP	8	ARG
10	AP	20	VAL
10	AP	21	VAL
10	AP	25	ARG
10	AP	27	LYS
10	AP	28	ARG
10	AP	45	THR
10	AP	54	GLU
10	AP	81	ARG
11	AQ	7	THR
11	AQ	14	LYS
11	AQ	36	ILE
11	AQ	37	LYS
11	AQ	38	ARG
11	AQ	48	GLU
11	AQ	50	LYS
11	AQ	52	LYS
11	AQ	59	ILE
11	AQ	74	LEU
11	AQ	87	LYS
11	AQ	92	ARG
11	AQ	93	GLN
11	AQ	97	SER
11	AQ	100	LYS
12	AR	31	LEU
12	AR	32	ARG
12	AR	37	VAL
12	AR	45	SER
12	AR	47	THR
12	AR	54	ARG
12	AR	65	ILE
12	AR	76	LEU
12	AR	85	LEU
13	AS	5	LEU
13	AS	6	LYS
13	AS	7	LYS
13	AS	9	VAL
13	AS	13	ASP
13	AS	15	LEU
13	AS	16	LEU
13	AS	18	LYS

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Mol	Chain	Res	Type
13	AS	22	LEU
13	AS	30	LEU
13	AS	37	ARG
13	AS	44	MET
13	AS	60	VAL
13	AS	63	THR
13	AS	64	GLU
13	AS	70	LYS
13	AS	80	TYR
14	AT	23	ARG
14	AT	24	LEU
14	AT	27	LYS
14	AT	30	LYS
14	AT	35	THR
14	AT	38	LYS
14	AT	51	GLU
14	AT	58	LYS
14	AT	65	LYS
14	AT	75	ASN
14	AT	85	MET
14	AT	86	ARG
14	AT	89	ARG
14	AT	93	GLU
14	AT	104	LEU
15	AB	7	VAL
15	AB	15	VAL
15	AB	17	PHE
15	AB	24	TRP
15	AB	30	ARG
15	AB	32	ILE
15	AB	36	ARG
15	AB	37	ASN
15	AB	41	ILE
15	AB	42	ILE
15	AB	43	ASP
15	AB	52	GLU
15	AB	67	THR
15	AB	96	ARG
15	AB	117	GLU
15	AB	119	GLU
15	AB	128	GLU
15	AB	133	LYS

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Mol	Chain	Res	Type
15	AB	137	ARG
15	AB	140	HIS
15	AB	155	LEU
15	AB	156	LYS
15	AB	170	GLU
15	AB	178	ARG
15	AB	187	LEU
15	AB	196	LEU
15	AB	200	ILE
15	AB	212	GLN
15	AB	215	LEU
15	AB	223	ILE
16	AC	5	ILE
16	AC	12	LEU
16	AC	14	ILE
16	AC	16	ARG
16	AC	21	ARG
16	AC	22	TRP
16	AC	27	LYS
16	AC	34	LEU
16	AC	36	ASP
16	AC	38	ARG
16	AC	46	GLU
16	AC	47	LEU
16	AC	49	SER
16	AC	52	LEU
16	AC	54	ARG
16	AC	56	ASP
16	AC	62	ASP
16	AC	68	VAL
16	AC	72	LYS
16	AC	73	PRO
16	AC	82	GLU
16	AC	83	ARG
16	AC	85	ARG
16	AC	86	VAL
16	AC	94	LEU
16	AC	99	VAL
16	AC	104	GLN
16	AC	131	ARG
16	AC	132	ARG
16	AC	136	GLN

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Mol	Chain	Res	Type
16	AC	154	SER
16	AC	166	GLU
16	AC	167	TRP
16	AC	179	ARG
16	AC	196	LEU
17	AD	3	ARG
17	AD	5	ILE
17	AD	8	VAL
17	AD	9	CYS
17	AD	10	ARG
17	AD	11	LEU
17	AD	15	GLU
17	AD	18	LYS
17	AD	19	LEU
17	AD	22	LYS
17	AD	33	MET
17	AD	34	GLU
17	AD	36	ARG
17	AD	58	LEU
17	AD	73	ARG
17	AD	78	LEU
17	AD	85	LYS
17	AD	86	LYS
17	AD	91	SER
17	AD	96	LEU
17	AD	108	LEU
17	AD	115	ARG
17	AD	127	THR
17	AD	131	ARG
17	AD	132	ARG
17	AD	135	LEU
17	AD	139	ARG
17	AD	145	GLU
17	AD	150	GLU
17	AD	155	LEU
17	AD	162	LEU
17	AD	175	SER
17	AD	184	LYS
17	AD	187	ARG
17	AD	194	LEU
17	AD	201	GLN
18	AE	11	ILE

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Mol	Chain	Res	Type
18	AE	31	LEU
18	AE	34	VAL
18	AE	41	VAL
18	AE	47	LYS
18	AE	66	MET
18	AE	67	VAL
18	AE	76	ILE
18	AE	80	ILE
18	AE	100	VAL
18	AE	152	ARG
19	AF	3	ARG
19	AF	10	LEU
19	AF	16	GLN
19	AF	17	SER
19	AF	24	GLU
19	AF	25	ILE
19	AF	28	ARG
19	AF	43	LEU
19	AF	46	ARG
19	AF	54	LYS
19	AF	69	GLU
19	AF	78	GLU
19	AF	83	ASP
19	AF	92	LYS
20	AG	5	ARG
20	AG	8	GLU
20	AG	13	GLN
20	AG	22	LEU
20	AG	30	ILE
20	AG	32	ARG
20	AG	45	ASP
20	AG	54	THR
20	AG	61	VAL
20	AG	63	LYS
20	AG	67	GLU
20	AG	72	ARG
20	AG	84	ASN
20	AG	90	GLU
20	AG	131	LYS
20	AG	137	LYS
21	AH	1	MET
21	AH	6	ILE

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Mol	Chain	Res	Type
21	AH	18	ARG
21	AH	21	LYS
21	AH	24	THR
21	AH	30	ARG
21	AH	39	LEU
21	AH	41	ARG
21	AH	52	ASP
21	AH	56	LYS
21	AH	88	LYS
21	AH	91	ARG
21	AH	92	ARG
21	AH	99	GLU
21	AH	102	ARG
21	AH	104	ARG
21	AH	107	LEU
21	AH	109	ILE
21	AH	112	LEU
21	AH	115	SER
21	AH	125	ARG
21	AH	126	LYS
21	AH	127	LEU
22	AI	10	ARG
22	AI	14	VAL
22	AI	20	ARG
22	AI	42	ARG
22	AI	44	VAL
22	AI	47	LEU
22	AI	56	LEU
22	AI	64	THR
22	AI	65	VAL
22	AI	66	ARG
22	AI	70	LYS
22	AI	79	LEU
22	AI	86	VAL
22	AI	95	LYS
22	AI	97	LYS
22	AI	99	LEU
22	AI	111	ARG
22	AI	112	LYS
22	AI	118	LYS
22	AI	121	ARG
22	AI	125	TYR

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Mol	Chain	Res	Type
22	AI	128	ARG
23	AY	10	LYS
23	AY	12	LEU
23	AY	25	LYS
23	AY	30	GLU
23	AY	31	ARG
23	AY	33	LEU
23	AY	38	ARG
23	AY	39	ILE
23	AY	56	GLU
23	AY	61	ARG
23	AY	65	ILE
23	AY	69	VAL
23	AY	70	THR
23	AY	81	ILE
23	AY	91	THR
23	AY	96	ARG
23	AY	98	MET
23	AY	120	THR
23	AY	123	ARG
23	AY	146	LEU
23	AY	148	LEU
23	AY	152	THR
23	AY	156	ARG
23	AY	157	LEU
23	AY	165	GLN
23	AY	175	SER
23	AY	187	THR
23	AY	197	ARG
23	AY	201	ILE
23	AY	206	LEU
23	AY	224	ASP
23	AY	225	GLU
23	AY	230	LYS
23	AY	232	LEU
23	AY	254	LYS
23	AY	255	ILE
23	AY	260	LEU
23	AY	264	LEU
23	AY	280	LEU
23	AY	284	LEU
23	AY	290	LYS

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Mol	Chain	Res	Type
23	AY	295	GLU
23	AY	297	GLU
23	AY	298	VAL
23	AY	306	ASN
23	AY	312	LEU
23	AY	316	ILE
23	AY	319	ASP
23	AY	337	SER
23	AY	343	ASN
23	AY	346	LYS
23	AY	348	ARG
23	AY	349	LYS
23	AY	355	LEU
23	AY	356	LEU
23	AY	363	ARG
23	AY	369	LEU
23	AY	377	VAL
23	AY	378	VAL
23	AY	385	THR
23	AY	396	ARG
23	AY	399	LEU
23	AY	400	GLU
23	AY	402	ILE
23	AY	403	GLU
23	AY	409	ILE
23	AY	414	GLU
23	AY	422	GLU
23	AY	426	GLN
23	AY	431	LEU
23	AY	446	THR
23	AY	451	ILE
23	AY	452	SER
23	AY	459	LEU
23	AY	465	ARG
23	AY	471	LYS
23	AY	473	ASP
23	AY	476	VAL
23	AY	481	VAL
23	AY	485	GLU
23	AY	488	THR
23	AY	492	ASP
23	AY	493	VAL

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Mol	Chain	Res	Type
23	AY	512	ILE
23	AY	517	LEU
23	AY	544	LYS
23	AY	546	ILE
23	AY	548	GLU
23	AY	550	MET
23	AY	556	ILE
23	AY	566	THR
23	AY	584	ILE
23	AY	590	ILE
23	AY	591	LYS
23	AY	603	GLU
23	AY	610	VAL
23	AY	612	THR
23	AY	623	ASP
23	AY	628	ARG
23	AY	634	MET
23	AY	637	ARG
23	AY	647	VAL
23	AY	649	LEU
23	AY	679	VAL
23	AY	681	LYS
23	AY	684	GLN
23	AY	686	LYS
23	AY	687	LEU
24	AU	7	ARG
24	AU	9	ARG
24	AU	12	LYS
24	AU	15	ARG
24	AU	25	LYS
27	BN	1	MET
27	BN	3	THR
27	BN	4	TYR
27	BN	8	GLN
27	BN	9	VAL
27	BN	16	ILE
27	BN	19	GLU
27	BN	28	THR
27	BN	33	LEU
27	BN	34	LEU
27	BN	39	ARG
27	BN	41	ASP

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Mol	Chain	Res	Type
27	BN	43	THR
27	BN	48	MET
27	BN	55	VAL
27	BN	58	ASP
27	BN	60	ILE
27	BN	62	VAL
27	BN	63	THR
27	BN	65	LYS
27	BN	67	LEU
27	BN	68	GLU
27	BN	73	THR
27	BN	87	LEU
27	BN	93	THR
27	BN	99	LEU
27	BN	109	LYS
27	BN	119	ARG
27	BN	120	LEU
27	BN	121	LYS
27	BN	133	GLN
27	BN	134	ARG
27	BN	136	GLU
28	BO	3	GLN
28	BO	8	LEU
28	BO	10	VAL
28	BO	22	ILE
28	BO	23	ARG
28	BO	24	VAL
28	BO	47	ILE
28	BO	49	ARG
28	BO	66	LYS
28	BO	70	LYS
28	BO	88	ASN
28	BO	91	LEU
28	BO	94	ARG
28	BO	98	VAL
28	BO	104	ARG
28	BO	113	LYS
29	BP	6	LEU
29	BP	13	ASN
29	BP	16	ARG
29	BP	27	HIS
29	BP	29	LYS

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Mol	Chain	Res	Type
29	BP	39	LYS
29	BP	42	SER
29	BP	45	LEU
29	BP	55	ARG
29	BP	56	SER
29	BP	57	THR
29	BP	58	THR
29	BP	61	ARG
29	BP	62	LEU
29	BP	67	MET
29	BP	68	GLN
29	BP	76	LYS
29	BP	88	LEU
29	BP	91	PHE
29	BP	95	VAL
29	BP	98	GLU
29	BP	100	LEU
29	BP	105	LEU
29	BP	107	LYS
29	BP	110	TYR
29	BP	114	ILE
29	BP	115	LEU
29	BP	125	VAL
29	BP	135	LEU
29	BP	138	LEU
30	BQ	10	ARG
30	BQ	16	ARG
30	BQ	18	LYS
30	BQ	45	GLN
30	BQ	55	VAL
30	BQ	58	PHE
30	BQ	59	ARG
30	BQ	75	THR
30	BQ	76	LYS
30	BQ	96	VAL
30	BQ	115	MET
30	BQ	131	ILE
30	BQ	133	ARG
30	BQ	134	ARG
30	BQ	138	ASP
31	BR	4	LEU
31	BR	8	ARG

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Mol	Chain	Res	Type
31	BR	18	LEU
31	BR	28	LEU
31	BR	29	LEU
31	BR	33	ARG
31	BR	36	THR
31	BR	44	LEU
31	BR	51	LEU
31	BR	57	ARG
31	BR	63	ARG
31	BR	67	LEU
31	BR	74	LYS
31	BR	79	LEU
31	BR	88	ARG
31	BR	100	LEU
31	BR	105	ARG
31	BR	113	LEU
31	BR	116	LEU
31	BR	118	GLU
32	BS	15	ARG
32	BS	20	ARG
32	BS	27	SER
32	BS	30	ARG
32	BS	31	SER
32	BS	34	HIS
32	BS	49	VAL
32	BS	54	LEU
32	BS	73	LEU
32	BS	80	LEU
32	BS	89	ARG
32	BS	92	TYR
32	BS	97	ARG
32	BS	99	LYS
32	BS	107	GLU
33	BT	3	ARG
33	BT	6	LEU
33	BT	11	GLU
33	BT	15	VAL
33	BT	27	THR
33	BT	29	ARG
33	BT	32	TYR
33	BT	43	GLN
33	BT	49	VAL

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Mol	Chain	Res	Type
33	BT	50	ILE
33	BT	53	ARG
33	BT	58	ASN
33	BT	59	THR
33	BT	62	THR
33	BT	63	VAL
33	BT	64	ARG
33	BT	65	LYS
33	BT	78	LEU
33	BT	82	LEU
33	BT	86	ILE
33	BT	87	ASP
33	BT	90	GLN
33	BT	93	ARG
33	BT	96	ARG
33	BT	112	ARG
33	BT	118	ARG
33	BT	119	LYS
33	BT	123	GLN
33	BT	128	GLU
34	BU	8	VAL
34	BU	13	LYS
34	BU	15	LYS
34	BU	16	LYS
34	BU	19	LYS
34	BU	31	SER
34	BU	34	LYS
34	BU	60	LEU
34	BU	70	ARG
34	BU	74	LEU
34	BU	83	LEU
34	BU	88	ILE
34	BU	92	ARG
34	BU	108	GLU
34	BU	112	ARG
34	BU	114	LYS
35	BV	5	VAL
35	BV	6	LYS
35	BV	13	ARG
35	BV	16	PRO
35	BV	18	LEU
35	BV	19	LYS

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Mol	Chain	Res	Type
35	BV	20	LEU
35	BV	21	ARG
35	BV	28	GLU
35	BV	32	THR
35	BV	33	VAL
35	BV	35	LEU
35	BV	39	LEU
35	BV	40	LEU
35	BV	46	VAL
35	BV	47	VAL
35	BV	57	VAL
35	BV	61	VAL
35	BV	62	LEU
35	BV	66	ARG
35	BV	72	VAL
35	BV	73	SER
35	BV	79	VAL
35	BV	85	LYS
35	BV	95	LEU
35	BV	99	ILE
36	BW	11	ARG
36	BW	17	VAL
36	BW	20	VAL
36	BW	23	LEU
36	BW	41	LYS
36	BW	50	VAL
36	BW	51	LEU
36	BW	52	GLU
36	BW	60	ASN
36	BW	63	ASP
36	BW	76	VAL
36	BW	96	ILE
36	BW	100	THR
36	BW	106	ILE
36	BW	107	LEU
36	BW	110	LYS
37	BX	12	VAL
37	BX	27	THR
37	BX	39	ILE
37	BX	48	LYS
37	BX	57	LEU
37	BX	60	ARG

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Mol	Chain	Res	Type
37	BX	63	LYS
37	BX	64	LYS
37	BX	66	LEU
37	BX	68	ARG
37	BX	72	LYS
37	BX	73	ARG
37	BX	77	LYS
37	BX	78	LYS
37	BX	80	ILE
38	BY	4	LYS
38	BY	6	HIS
38	BY	8	LYS
38	BY	9	LYS
38	BY	31	LEU
38	BY	34	LYS
38	BY	38	ILE
38	BY	44	ILE
38	BY	45	VAL
38	BY	71	LYS
38	BY	75	ILE
38	BY	81	LYS
38	BY	83	THR
38	BY	85	VAL
38	BY	87	LYS
38	BY	88	LYS
38	BY	89	PHE
38	BY	97	ARG
38	BY	99	CYS
39	BZ	5	LEU
39	BZ	6	LYS
39	BZ	16	SER
39	BZ	23	LYS
39	BZ	31	ARG
39	BZ	34	ASN
39	BZ	42	VAL
39	BZ	46	LYS
39	BZ	61	LEU
39	BZ	63	ASP
39	BZ	72	ARG
39	BZ	79	ARG
39	BZ	80	ARG
39	BZ	81	ARG

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Mol	Chain	Res	Type
39	BZ	82	ARG
39	BZ	86	VAL
39	BZ	87	ASP
39	BZ	105	VAL
39	BZ	112	ARG
39	BZ	118	GLN
39	BZ	122	ARG
39	BZ	132	ASN
39	BZ	144	LEU
39	BZ	146	ILE
39	BZ	150	LEU
39	BZ	153	SER
39	BZ	156	LYS
40	B0	11	ARG
40	B0	19	LYS
40	B0	20	ARG
40	B0	30	VAL
40	B0	41	ARG
40	B0	43	THR
40	B0	49	LYS
40	B0	64	ASP
40	B0	68	GLU
40	B0	84	LEU
41	B1	7	ILE
41	B1	30	VAL
41	B1	38	SER
41	B1	39	LYS
41	B1	40	ARG
41	B1	46	LEU
41	B1	48	LYS
41	B1	52	ARG
41	B1	58	ILE
41	B1	59	THR
41	B1	61	ARG
41	B1	72	GLU
41	B1	75	GLU
41	B1	82	LEU
41	B1	83	GLU
42	B2	2	LYS
42	B2	3	LEU
42	B2	8	LYS
42	B2	15	LYS

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Mol	Chain	Res	Type
42	B2	16	LEU
42	B2	17	SER
42	B2	30	ARG
42	B2	32	LEU
42	B2	44	LEU
42	B2	47	ASN
42	B2	51	ARG
42	B2	52	ASP
42	B2	53	LEU
42	B2	64	LEU
42	B2	68	ARG
43	BD	3	VAL
43	BD	4	LYS
43	BD	13	ARG
43	BD	24	ILE
43	BD	26	LYS
43	BD	28	GLU
43	BD	33	LEU
43	BD	34	VAL
43	BD	35	LYS
43	BD	43	ARG
43	BD	44	ASN
43	BD	45	ASN
43	BD	49	ILE
43	BD	64	ILE
43	BD	65	ILE
43	BD	78	LYS
43	BD	88	ARG
43	BD	89	SER
43	BD	94	LEU
43	BD	103	ARG
43	BD	111	LEU
43	BD	117	VAL
43	BD	138	VAL
43	BD	140	THR
43	BD	155	LEU
43	BD	166	GLN
43	BD	169	GLU
43	BD	171	ASP
43	BD	176	ARG
43	BD	192	THR
43	BD	193	VAL

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Mol	Chain	Res	Type
43	BD	211	ARG
43	BD	218	ARG
43	BD	229	VAL
43	BD	232	PRO
43	BD	242	ARG
43	BD	244	ARG
43	BD	252	TRP
43	BD	257	LEU
43	BD	260	ARG
43	BD	262	ARG
43	BD	266	SER
43	BD	271	ILE
44	B3	3	ARG
44	B3	6	VAL
44	B3	8	LEU
44	B3	17	LYS
44	B3	18	ASP
44	B3	29	ARG
44	B3	31	LEU
44	B3	36	VAL
44	B3	37	LEU
44	B3	40	THR
45	B4	48	ILE
45	B4	49	GLU
45	B4	50	THR
45	B4	62	CYS
46	B5	4	HIS
46	B5	6	VAL
46	B5	11	THR
46	B5	23	HIS
46	B5	29	THR
46	B5	37	LYS
46	B5	48	GLU
46	B5	49	CYS
46	B5	56	LYS
47	B6	10	LEU
47	B6	11	LEU
47	B6	17	LYS
47	B6	18	ARG
47	B6	26	ASN
47	B6	32	ASN
47	B6	33	LYS

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Mol	Chain	Res	Type
47	B6	42	TRP
47	B6	44	ARG
47	B6	46	HIS
47	B6	50	ARG
47	B6	51	GLU
48	B7	11	LYS
48	B7	23	ARG
48	B7	24	THR
48	B7	41	ARG
48	B7	43	THR
48	B7	48	LYS
49	B8	6	THR
49	B8	8	LYS
49	B8	13	ARG
49	B8	14	VAL
49	B8	15	LYS
49	B8	23	VAL
49	B8	30	ARG
49	B8	31	HIS
49	B8	32	LEU
49	B8	33	ASN
49	B8	34	TRP
49	B8	35	GLN
49	B8	36	LYS
49	B8	44	LYS
49	B8	47	LYS
49	B8	49	VAL
49	B8	52	LYS
49	B8	56	GLU
49	B8	61	LEU
49	B8	64	TYR
50	B9	2	LYS
50	B9	4	ARG
50	B9	6	SER
50	B9	9	ARG
50	B9	14	CYS
50	B9	20	HIS
50	B9	22	ARG
50	B9	26	ILE
50	B9	29	ASN
50	B9	32	HIS
51	BC	5	LYS

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Mol	Chain	Res	Type
51	BC	23	ASP
51	BC	27	ARG
51	BC	30	LYS
51	BC	53	ARG
51	BC	63	SER
51	BC	68	LEU
51	BC	73	ARG
51	BC	81	GLU
51	BC	84	LYS
51	BC	92	ASP
51	BC	99	ILE
51	BC	104	LEU
51	BC	131	LEU
51	BC	141	LYS
51	BC	217	THR
51	BC	223	ARG
51	BC	227	HIS
52	BE	7	VAL
52	BE	9	VAL
52	BE	11	MET
52	BE	12	THR
52	BE	18	ASP
52	BE	24	THR
52	BE	33	VAL
52	BE	34	VAL
52	BE	40	GLU
52	BE	54	GLN
52	BE	55	ASN
52	BE	57	LYS
52	BE	60	ASN
52	BE	82	ARG
52	BE	87	GLU
52	BE	89	ASP
52	BE	92	THR
52	BE	93	VAL
52	BE	94	GLU
52	BE	111	ARG
52	BE	113	PHE
52	BE	118	LYS
52	BE	144	ARG
52	BE	146	THR
52	BE	152	LYS

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Mol	Chain	Res	Type
52	BE	154	LYS
52	BE	175	VAL
52	BE	181	LEU
52	BE	185	LYS
52	BE	188	VAL
52	BE	195	LEU
52	BE	197	ILE
52	BE	202	LYS
52	BE	203	LYS
53	BF	4	VAL
53	BF	8	GLN
53	BF	18	ARG
53	BF	19	GLU
53	BF	20	LEU
53	BF	23	ASP
53	BF	24	LEU
53	BF	27	GLU
53	BF	28	ILE
53	BF	43	LYS
53	BF	53	THR
53	BF	57	VAL
53	BF	65	TRP
53	BF	66	PRO
53	BF	68	LYS
53	BF	72	ARG
53	BF	74	ARG
53	BF	88	VAL
53	BF	102	PRO
53	BF	103	LYS
53	BF	106	ARG
53	BF	110	LEU
53	BF	117	ARG
53	BF	126	VAL
53	BF	157	VAL
53	BF	164	ARG
53	BF	170	LEU
53	BF	175	THR
53	BF	192	LEU
53	BF	199	TRP
53	BF	200	GLU
54	BG	5	VAL
54	BG	8	LYS

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Mol	Chain	Res	Type
54	BG	16	ARG
54	BG	21	ARG
54	BG	22	ARG
54	BG	33	ARG
54	BG	39	ILE
54	BG	43	LEU
54	BG	45	GLU
54	BG	47	LYS
54	BG	62	LEU
54	BG	71	THR
54	BG	80	PHE
54	BG	82	LEU
54	BG	86	MET
54	BG	98	ARG
54	BG	123	ASN
54	BG	126	ASP
54	BG	128	ARG
54	BG	130	ASN
54	BG	139	LEU
54	BG	143	GLU
54	BG	146	TYR
54	BG	148	MET
54	BG	152	LEU
54	BG	161	THR
54	BG	166	ASP
55	BH	23	ARG
55	BH	24	VAL
55	BH	25	LYS
55	BH	34	GLU
55	BH	36	PRO
55	BH	42	ARG
55	BH	43	VAL
55	BH	46	GLU
55	BH	53	GLU
55	BH	69	ARG
55	BH	71	LEU
55	BH	80	SER
55	BH	85	LYS
55	BH	89	ILE
55	BH	97	ARG
55	BH	101	ARG
55	BH	105	LEU

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Mol	Chain	Res	Type
55	BH	107	VAL
55	BH	119	GLU
55	BH	122	THR
55	BH	132	ARG
55	BH	139	GLN
55	BH	143	GLN
55	BH	153	LYS
55	BH	155	SER
55	BH	162	ILE
55	BH	168	PRO
55	BH	171	LEU
55	BH	173	PRO
56	BK	2	LYS
56	BK	3	LYS
56	BK	5	VAL
56	BK	29	GLN
56	BK	30	HIS
56	BK	38	VAL
56	BK	47	ASN
56	BK	65	PHE
56	BK	70	LYS
56	BK	77	LEU
56	BK	117	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
4	AJ	13	HIS
5	AK	93	GLN
5	AK	117	ASN
7	AM	62	ASN
7	AM	101	GLN
9	AO	9	GLN
13	AS	23	ASN
15	AB	37	ASN
15	AB	76	GLN
15	AB	95	GLN
15	AB	135	GLN
17	AD	42	GLN
17	AD	62	GLN
19	AF	16	GLN
19	AF	64	GLN

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Mol	Chain	Res	Type
20	AG	86	GLN
23	AY	124	GLN
23	AY	154	GLN
23	AY	343	ASN
23	AY	664	GLN
28	BO	3	GLN
28	BO	88	ASN
29	BP	38	GLN
29	BP	70	GLN
30	BQ	12	GLN
30	BQ	123	HIS
31	BR	13	HIS
31	BR	23	ASN
32	BS	95	HIS
33	BT	38	ASN
33	BT	90	GLN
34	BU	94	ASN
36	BW	61	ASN
36	BW	102	HIS
37	BX	55	ASN
39	BZ	34	ASN
40	B0	70	GLN
42	B2	70	GLN
43	BD	45	ASN
43	BD	58	HIS
43	BD	96	HIS
43	BD	227	ASN
44	B3	19	GLN
47	B6	26	ASN
47	B6	49	HIS
48	B7	16	HIS
49	B8	43	GLN
50	B9	29	ASN
50	B9	32	HIS
51	BC	66	HIS
51	BC	71	GLN
51	BC	188	ASN
52	BE	60	ASN
52	BE	132	HIS
52	BE	180	ASN
53	BF	31	HIS
53	BF	169	ASN

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Mol	Chain	Res	Type
55	BH	61	HIS
56	BK	29	GLN
56	BK	47	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1512/1516 (99%)	315 (20%)	65 (4%)
2	AV	73/76 (96%)	28 (38%)	9 (12%)
25	BA	2849/2915 (97%)	756 (26%)	130 (4%)
26	BB	119/122 (97%)	34 (28%)	4 (3%)
3	AX	5/25 (20%)	0	0
All	All	4558/4654 (97%)	1133 (24%)	208 (4%)

All (1133) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	G
1	AA	13	U
1	AA	30	U
1	AA	31	G
1	AA	32	A
1	AA	39	G
1	AA	48	C
1	AA	49	U
1	AA	50	A
1	AA	51	A
1	AA	60	A
1	AA	61	G
1	AA	63	C
1	AA	76	C
1	AA	79	G
1	AA	80	G
1	AA	81	U
1	AA	88	A
1	AA	90	U
1	AA	91	C
1	AA	92	C
1	AA	97	G
1	AA	101	A
1	AA	105	G

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Mol	Chain	Res	Type
1	AA	108	G
1	AA	116	A
1	AA	121	C
1	AA	131	C
1	AA	144	G
1	AA	146	G
1	AA	147	G
1	AA	150	C
1	AA	160	A
1	AA	163	C
1	AA	179	A
1	AA	189(G)	G
1	AA	195	A
1	AA	197	A
1	AA	203	U
1	AA	204	U
1	AA	216	G
1	AA	217	C
1	AA	220	G
1	AA	221	C
1	AA	231	G
1	AA	244	U
1	AA	247	G
1	AA	251	G
1	AA	266	G
1	AA	267	C
1	AA	289	G
1	AA	301	G
1	AA	319	G
1	AA	321	A
1	AA	328	C
1	AA	329	A
1	AA	331	G
1	AA	332	G
1	AA	346	G
1	AA	347	G
1	AA	352	C
1	AA	353	A
1	AA	354	G
1	AA	367	U
1	AA	372	C
1	AA	373	A

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Mol	Chain	Res	Type
1	AA	374	A
1	AA	381	C
1	AA	384	G
1	AA	398	C
1	AA	406	G
1	AA	409	G
1	AA	412	A
1	AA	413	G
1	AA	414	A
1	AA	422	C
1	AA	423	G
1	AA	424	G
1	AA	429	U
1	AA	436	C
1	AA	439	A
1	AA	441	A
1	AA	443	C
1	AA	452	A
1	AA	470	C
1	AA	485	G
1	AA	492	G
1	AA	495	A
1	AA	496	A
1	AA	498	U
1	AA	501	C
1	AA	505	G
1	AA	509	A
1	AA	510	A
1	AA	511	C
1	AA	518	C
1	AA	519	C
1	AA	522	C
1	AA	527	G
1	AA	531	U
1	AA	532	A
1	AA	533	A
1	AA	534	U
1	AA	539	A
1	AA	545	C
1	AA	547	A
1	AA	559	A
1	AA	561	U

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Mol	Chain	Res	Type
1	AA	562	C
1	AA	572	A
1	AA	573	A
1	AA	576	G
1	AA	577	G
1	AA	582	U
1	AA	592	G
1	AA	596	C
1	AA	617	G
1	AA	630	G
1	AA	631	G
1	AA	632	A
1	AA	633	G
1	AA	649	G
1	AA	653	A
1	AA	665	A
1	AA	671	G
1	AA	673	G
1	AA	688	G
1	AA	731	G
1	AA	734	G
1	AA	749	C
1	AA	755	G
1	AA	765	G
1	AA	773	G
1	AA	777	A
1	AA	785	G
1	AA	794	A
1	AA	801	U
1	AA	802	A
1	AA	816	A
1	AA	817	C
1	AA	827	U
1	AA	828	A
1	AA	838	G
1	AA	839	U
1	AA	840	C
1	AA	841	U
1	AA	848	C
1	AA	851	G
1	AA	853	G
1	AA	859	A

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Mol	Chain	Res	Type
1	AA	876	G
1	AA	890	G
1	AA	902	G
1	AA	913	A
1	AA	914	A
1	AA	919	A
1	AA	926	G
1	AA	927	G
1	AA	934	C
1	AA	935	A
1	AA	947	G
1	AA	960	U
1	AA	961	U
1	AA	966	G
1	AA	968	A
1	AA	969	A
1	AA	973	G
1	AA	974	A
1	AA	975	A
1	AA	976	G
1	AA	977	A
1	AA	980	C
1	AA	981	U
1	AA	984	C
1	AA	991	U
1	AA	992	U
1	AA	993	G
1	AA	994	A
1	AA	1001(A)	G
1	AA	1004	A
1	AA	1005	A
1	AA	1009	G
1	AA	1013	G
1	AA	1016	A
1	AA	1021	G
1	AA	1024	G
1	AA	1025	U
1	AA	1026	G
1	AA	1027	C
1	AA	1030	C
1	AA	1030(D)	A
1	AA	1031	G

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Mol	Chain	Res	Type
1	AA	1044	A
1	AA	1046	A
1	AA	1050	G
1	AA	1053	G
1	AA	1054	C
1	AA	1055	A
1	AA	1065	U
1	AA	1067	A
1	AA	1068	G
1	AA	1081	G
1	AA	1086	U
1	AA	1087	G
1	AA	1089	G
1	AA	1094	G
1	AA	1095	U
1	AA	1101	A
1	AA	1124	G
1	AA	1125	U
1	AA	1126	U
1	AA	1127	G
1	AA	1132	C
1	AA	1133	G
1	AA	1134	G
1	AA	1135	U
1	AA	1136	U
1	AA	1137	C
1	AA	1138	G
1	AA	1139	G
1	AA	1140	C
1	AA	1143	G
1	AA	1146	A
1	AA	1147	C
1	AA	1152	A
1	AA	1159	U
1	AA	1160	G
1	AA	1171	G
1	AA	1181	G
1	AA	1184	G
1	AA	1187	G
1	AA	1192	C
1	AA	1196	U
1	AA	1197	G

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Mol	Chain	Res	Type
1	AA	1212	U
1	AA	1213	A
1	AA	1214	C
1	AA	1215	G
1	AA	1218	C
1	AA	1225	A
1	AA	1226	C
1	AA	1227	A
1	AA	1238	A
1	AA	1256	A
1	AA	1257	U
1	AA	1258	G
1	AA	1259	C
1	AA	1260	C
1	AA	1269	A
1	AA	1273	G
1	AA	1281	U
1	AA	1285	A
1	AA	1286	A
1	AA	1287	A
1	AA	1288	A
1	AA	1290	G
1	AA	1293	G
1	AA	1299	A
1	AA	1300	G
1	AA	1301	U
1	AA	1302	U
1	AA	1305	G
1	AA	1310	G
1	AA	1317	C
1	AA	1319	A
1	AA	1320	C
1	AA	1322	C
1	AA	1323	G
1	AA	1328	C
1	AA	1332	A
1	AA	1336	C
1	AA	1337	G
1	AA	1338	G
1	AA	1346	A
1	AA	1347	G
1	AA	1350	A

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Mol	Chain	Res	Type
1	AA	1353	G
1	AA	1364	U
1	AA	1378	C
1	AA	1397	C
1	AA	1398	A
1	AA	1402	C
1	AA	1407	C
1	AA	1419	G
1	AA	1422	G
1	AA	1442	G
1	AA	1442(A)	G
1	AA	1443	G
1	AA	1446	U
1	AA	1447	A
1	AA	1452	C
1	AA	1456	G
1	AA	1457	G
1	AA	1472	U
1	AA	1492	A
1	AA	1493	A
1	AA	1494	G
1	AA	1499	A
1	AA	1502	A
1	AA	1504	G
1	AA	1505	G
1	AA	1506	U
1	AA	1507	A
1	AA	1517	G
1	AA	1519	A
1	AA	1520	G
1	AA	1529	G
1	AA	1530	G
1	AA	1532	U
1	AA	1533	C
1	AA	1534	A
1	AA	1535	C
1	AA	1536	C
1	AA	1542	U
1	AA	1543	C
2	AV	4	C
2	AV	13	C
2	AV	15	G

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Mol	Chain	Res	Type
2	AV	19	G
2	AV	20	U
2	AV	21	A
2	AV	22	G
2	AV	23	A
2	AV	26	A
2	AV	27	G
2	AV	30	G
2	AV	34	G
2	AV	35	A
2	AV	38	A
2	AV	44	G
2	AV	46	G
2	AV	47	U
2	AV	48	C
2	AV	51	U
2	AV	52	G
2	AV	53	G
2	AV	57	G
2	AV	61	C
2	AV	72	C
2	AV	73	A
2	AV	74	C
2	AV	75	C
2	AV	76	A
25	BA	9	U
25	BA	10	G
25	BA	34	C
25	BA	35	G
25	BA	36	G
25	BA	41	C
25	BA	45	C
25	BA	49	A
25	BA	50	U
25	BA	55	G
25	BA	63	U
25	BA	71	A
25	BA	72	U
25	BA	74	A
25	BA	75	G
25	BA	86	C
25	BA	88	G

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Mol	Chain	Res	Type
25	BA	90	U
25	BA	92	A
25	BA	94	C
25	BA	95	G
25	BA	99	U
25	BA	100	G
25	BA	102	G
25	BA	103	A
25	BA	110	G
25	BA	118	A
25	BA	119	A
25	BA	120	U
25	BA	123	G
25	BA	128	C
25	BA	129	C
25	BA	131	G
25	BA	141	A
25	BA	154	G
25	BA	154(A)	C
25	BA	158	U
25	BA	171	G
25	BA	173	G
25	BA	174	C
25	BA	175	G
25	BA	181	A
25	BA	182	A
25	BA	196	A
25	BA	197	A
25	BA	199	A
25	BA	200	U
25	BA	204	A
25	BA	205	G
25	BA	214	G
25	BA	215	G
25	BA	216	A
25	BA	217	G
25	BA	221	A
25	BA	222	A
25	BA	224	G
25	BA	228	A
25	BA	229	A
25	BA	233	A

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Mol	Chain	Res	Type
25	BA	248	G
25	BA	250	G
25	BA	252	G
25	BA	259	G
25	BA	264	C
25	BA	265	A
25	BA	271(C)	C
25	BA	271(D)	G
25	BA	271(J)	C
25	BA	271(K)	U
25	BA	271(L)	U
25	BA	271(M)	G
25	BA	271(N)	U
25	BA	271(P)	C
25	BA	271(T)	C
25	BA	271(U)	G
25	BA	271(Y)	U
25	BA	271(Z)	C
25	BA	272	G
25	BA	272(G)	C
25	BA	272(H)	C
25	BA	272(I)	U
25	BA	272(J)	C
25	BA	274	G
25	BA	275	G
25	BA	280	C
25	BA	288	C
25	BA	289	A
25	BA	298	G
25	BA	310	A
25	BA	311	A
25	BA	320	A
25	BA	324	A
25	BA	327	G
25	BA	329	G
25	BA	330	A
25	BA	333	G
25	BA	334	C
25	BA	335	C
25	BA	342	G
25	BA	345	A
25	BA	346	A

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Mol	Chain	Res	Type
25	BA	349	G
25	BA	352	G
25	BA	353	G
25	BA	358	U
25	BA	360	G
25	BA	362	U
25	BA	363	G
25	BA	363(A)	A
25	BA	363(B)	G
25	BA	363(E)	U
25	BA	372	G
25	BA	374	A
25	BA	386	G
25	BA	387	U
25	BA	388	G
25	BA	389	G
25	BA	396	G
25	BA	405	U
25	BA	407	G
25	BA	411	G
25	BA	416	C
25	BA	428	A
25	BA	438	G
25	BA	441	U
25	BA	442	G
25	BA	443	A
25	BA	444	C
25	BA	448	U
25	BA	452	G
25	BA	454	A
25	BA	457	A
25	BA	470	A
25	BA	473	G
25	BA	479	A
25	BA	480	A
25	BA	481	G
25	BA	488	G
25	BA	494	G
25	BA	504	U
25	BA	505	A
25	BA	508	G
25	BA	510	C

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Mol	Chain	Res	Type
25	BA	513	A
25	BA	517	C
25	BA	528	A
25	BA	529	A
25	BA	530	G
25	BA	531	C
25	BA	532	A
25	BA	533	G
25	BA	543	C
25	BA	548	A
25	BA	549	G
25	BA	551	G
25	BA	563	G
25	BA	565	C
25	BA	571	A
25	BA	573	G
25	BA	574	C
25	BA	575	A
25	BA	584	C
25	BA	586	A
25	BA	587	C
25	BA	592	G
25	BA	593	G
25	BA	604	G
25	BA	606	U
25	BA	607	U
25	BA	609	A
25	BA	613	G
25	BA	614	U
25	BA	614(B)	G
25	BA	615	G
25	BA	620	G
25	BA	621	A
25	BA	622	G
25	BA	624	C
25	BA	627	A
25	BA	631	A
25	BA	637	A
25	BA	645	C
25	BA	646	A
25	BA	647	G
25	BA	652	C

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Mol	Chain	Res	Type
25	BA	669	G
25	BA	685	A
25	BA	686	G
25	BA	708	C
25	BA	715	G
25	BA	721	C
25	BA	722	A
25	BA	729	G
25	BA	730	C
25	BA	738	G
25	BA	764	A
25	BA	765	G
25	BA	775	G
25	BA	776	G
25	BA	782	A
25	BA	784	A
25	BA	785	G
25	BA	790	C
25	BA	791	C
25	BA	792	G
25	BA	805	G
25	BA	812	C
25	BA	819	A
25	BA	827	U
25	BA	828	U
25	BA	830	G
25	BA	836	G
25	BA	854	G
25	BA	858	U
25	BA	859	G
25	BA	878	A
25	BA	886	C
25	BA	888	C
25	BA	890	A
25	BA	896	A
25	BA	897	C
25	BA	900	A
25	BA	901	A
25	BA	906	G
25	BA	907	U
25	BA	910	A
25	BA	917	A

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Mol	Chain	Res	Type
25	BA	919	G
25	BA	932	G
25	BA	933	A
25	BA	934	G
25	BA	941	A
25	BA	945	A
25	BA	946	G
25	BA	958	U
25	BA	961	C
25	BA	973	A
25	BA	974	G
25	BA	983	A
25	BA	991	C
25	BA	996	A
25	BA	997	G
25	BA	999	U
25	BA	1012	U
25	BA	1013	C
25	BA	1022	G
25	BA	1023	U
25	BA	1025	G
25	BA	1026	U
25	BA	1027	A
25	BA	1033	U
25	BA	1038	C
25	BA	1039	G
25	BA	1040	C
25	BA	1042	G
25	BA	1045	A
25	BA	1046	A
25	BA	1047	G
25	BA	1048	A
25	BA	1049	C
25	BA	1050	A
25	BA	1053	C
25	BA	1054	A
25	BA	1055	G
25	BA	1057	A
25	BA	1058	G
25	BA	1059	G
25	BA	1060	U
25	BA	1063	G

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Mol	Chain	Res	Type
25	BA	1071	G
25	BA	1072	C
25	BA	1073	A
25	BA	1074	G
25	BA	1075	C
25	BA	1076	C
25	BA	1077	A
25	BA	1078	U
25	BA	1079	C
25	BA	1083	U
25	BA	1087	G
25	BA	1088	A
25	BA	1089	G
25	BA	1090	U
25	BA	1092	C
25	BA	1093	G
25	BA	1094	U
25	BA	1096	A
25	BA	1097	U
25	BA	1098	A
25	BA	1099	G
25	BA	1100	C
25	BA	1101	U
25	BA	1106	G
25	BA	1107	G
25	BA	1110	G
25	BA	1111	A
25	BA	1112	G
25	BA	1113	U
25	BA	1114	G
25	BA	1115	G
25	BA	1116	C
25	BA	1122	G
25	BA	1128	A
25	BA	1129	A
25	BA	1135	C
25	BA	1136	G
25	BA	1139	G
25	BA	1142	U
25	BA	1143	A
25	BA	1148	A
25	BA	1151	G

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Mol	Chain	Res	Type
25	BA	1155	A
25	BA	1168	G
25	BA	1171	G
25	BA	1173	G
25	BA	1174	A
25	BA	1175	U
25	BA	1176	G
25	BA	1177	A
25	BA	1179	C
25	BA	1180	C
25	BA	1187	G
25	BA	1193	G
25	BA	1194	A
25	BA	1195	G
25	BA	1210	A
25	BA	1211	U
25	BA	1218	C
25	BA	1220	A
25	BA	1235	G
25	BA	1237	A
25	BA	1242	A
25	BA	1244	G
25	BA	1246	A
25	BA	1247	A
25	BA	1249	U
25	BA	1253	A
25	BA	1256	G
25	BA	1263	U
25	BA	1271	G
25	BA	1272	A
25	BA	1273	U
25	BA	1281	G
25	BA	1284	A
25	BA	1288	U
25	BA	1289	C
25	BA	1300	U
25	BA	1301	A
25	BA	1302	A
25	BA	1306	C
25	BA	1308	A
25	BA	1329	U
25	BA	1338	G

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Mol	Chain	Res	Type
25	BA	1344	G
25	BA	1345	C
25	BA	1347	G
25	BA	1350	C
25	BA	1358	G
25	BA	1359	A
25	BA	1365	A
25	BA	1372	U
25	BA	1380	G
25	BA	1384	A
25	BA	1385	G
25	BA	1390	U
25	BA	1392	A
25	BA	1406	U
25	BA	1407	C
25	BA	1415	U
25	BA	1416	G
25	BA	1420	U
25	BA	1428	C
25	BA	1437	C
25	BA	1445	A
25	BA	1449	A
25	BA	1450	G
25	BA	1453	U
25	BA	1459	G
25	BA	1467	C
25	BA	1471	A
25	BA	1474	C
25	BA	1475	G
25	BA	1478	G
25	BA	1480	G
25	BA	1482	G
25	BA	1485	G
25	BA	1488	G
25	BA	1490	A
25	BA	1491	G
25	BA	1493	C
25	BA	1494	A
25	BA	1495	A
25	BA	1496	A
25	BA	1497	U
25	BA	1502	C

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Mol	Chain	Res	Type
25	BA	1503	U
25	BA	1505	C
25	BA	1506	C
25	BA	1508	A
25	BA	1509	C
25	BA	1509(A)	A
25	BA	1512	U
25	BA	1514	U
25	BA	1519	G
25	BA	1523	U
25	BA	1525	G
25	BA	1532	C
25	BA	1539	G
25	BA	1540	U
25	BA	1541	G
25	BA	1542	A
25	BA	1543	C
25	BA	1544	A
25	BA	1545	A
25	BA	1547	C
25	BA	1549	C
25	BA	1554	A
25	BA	1558	A
25	BA	1559	G
25	BA	1566	A
25	BA	1569	A
25	BA	1572	A
25	BA	1578	U
25	BA	1579	A
25	BA	1580	A
25	BA	1581	G
25	BA	1582	C
25	BA	1584	C
25	BA	1587	A
25	BA	1588	C
25	BA	1598	C
25	BA	1608	A
25	BA	1609	A
25	BA	1610	A
25	BA	1616	A
25	BA	1617	C
25	BA	1618	A

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Mol	Chain	Res	Type
25	BA	1622	G
25	BA	1624	G
25	BA	1647	G
25	BA	1648	C
25	BA	1652	A
25	BA	1653	G
25	BA	1654	A
25	BA	1655	A
25	BA	1672	C
25	BA	1674	G
25	BA	1678	G
25	BA	1681	G
25	BA	1686	C
25	BA	1695	G
25	BA	1696	G
25	BA	1701	A
25	BA	1722	A
25	BA	1739	U
25	BA	1740	G
25	BA	1741	A
25	BA	1742	G
25	BA	1744	C
25	BA	1745	C
25	BA	1745(A)	C
25	BA	1747	G
25	BA	1750	G
25	BA	1756	G
25	BA	1762	A
25	BA	1763	G
25	BA	1764	G
25	BA	1769	G
25	BA	1773	A
25	BA	1780	A
25	BA	1786	A
25	BA	1791	A
25	BA	1799	G
25	BA	1800	C
25	BA	1801	G
25	BA	1802	A
25	BA	1810	A
25	BA	1816	G
25	BA	1820	U

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Mol	Chain	Res	Type
25	BA	1829	A
25	BA	1834	U
25	BA	1835	G
25	BA	1838	C
25	BA	1839	G
25	BA	1843	C
25	BA	1847	A
25	BA	1848	A
25	BA	1858	G
25	BA	1859	A
25	BA	1864	U
25	BA	1865	G
25	BA	1876	A
25	BA	1877	A
25	BA	1878	G
25	BA	1880	C
25	BA	1881	C
25	BA	1882	C
25	BA	1885	A
25	BA	1888	G
25	BA	1889	A
25	BA	1900	A
25	BA	1907	G
25	BA	1913	A
25	BA	1914	C
25	BA	1915	U
25	BA	1919	A
25	BA	1924	C
25	BA	1925	C
25	BA	1930	G
25	BA	1936	A
25	BA	1938	A
25	BA	1944	U
25	BA	1947	C
25	BA	1955	U
25	BA	1963	U
25	BA	1964	G
25	BA	1965	C
25	BA	1967	C
25	BA	1969	A
25	BA	1970	A
25	BA	1971	A

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Mol	Chain	Res	Type
25	BA	1972	A
25	BA	1978	A
25	BA	1982	C
25	BA	1987	G
25	BA	1991	U
25	BA	1992	G
25	BA	1993	U
25	BA	1996	C
25	BA	1997	G
25	BA	2020	A
25	BA	2021	C
25	BA	2023	G
25	BA	2026	C
25	BA	2027	G
25	BA	2031	A
25	BA	2032	G
25	BA	2033	A
25	BA	2036	C
25	BA	2039	C
25	BA	2043	C
25	BA	2049	G
25	BA	2051	A
25	BA	2055	C
25	BA	2056	G
25	BA	2060	A
25	BA	2061	G
25	BA	2062	A
25	BA	2069	G
25	BA	2070	G
25	BA	2095	C
25	BA	2096	U
25	BA	2100	G
25	BA	2101	G
25	BA	2102	U
25	BA	2103	C
25	BA	2104	G
25	BA	2106	G
25	BA	2107	C
25	BA	2108	C
25	BA	2113	U
25	BA	2115	G
25	BA	2116	G

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Mol	Chain	Res	Type
25	BA	2122	U
25	BA	2123	G
25	BA	2126	A
25	BA	2127	G
25	BA	2131	G
25	BA	2137	C
25	BA	2138	C
25	BA	2140	C
25	BA	2141	G
25	BA	2142	C
25	BA	2145	C
25	BA	2146	C
25	BA	2147	G
25	BA	2148	G
25	BA	2151	G
25	BA	2152	G
25	BA	2153	G
25	BA	2154	G
25	BA	2156	G
25	BA	2158	A
25	BA	2159	G
25	BA	2163	C
25	BA	2172	U
25	BA	2173	A
25	BA	2178	C
25	BA	2179	C
25	BA	2180	U
25	BA	2182	G
25	BA	2183	C
25	BA	2186	G
25	BA	2187	G
25	BA	2191	G
25	BA	2192	G
25	BA	2193	G
25	BA	2194	G
25	BA	2198	A
25	BA	2199	A
25	BA	2201	C
25	BA	2202	C
25	BA	2206	G
25	BA	2207	G
25	BA	2208	A

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Mol	Chain	Res	Type
25	BA	2218	U
25	BA	2219	G
25	BA	2225	A
25	BA	2226	C
25	BA	2232	U
25	BA	2238	G
25	BA	2239	G
25	BA	2243	U
25	BA	2267	A
25	BA	2268	A
25	BA	2275	C
25	BA	2276	G
25	BA	2283	C
25	BA	2287	A
25	BA	2297	C
25	BA	2301	C
25	BA	2302	G
25	BA	2303	G
25	BA	2305	A
25	BA	2307	G
25	BA	2308	G
25	BA	2309	A
25	BA	2310	A
25	BA	2312	U
25	BA	2316	C
25	BA	2318	G
25	BA	2319	G
25	BA	2320	A
25	BA	2321	G
25	BA	2324	C
25	BA	2325	G
25	BA	2334	G
25	BA	2336	A
25	BA	2342	C
25	BA	2347	C
25	BA	2350	C
25	BA	2361	A
25	BA	2372	G
25	BA	2383	G
25	BA	2385	C
25	BA	2386	C
25	BA	2393	A

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Mol	Chain	Res	Type
25	BA	2394	C
25	BA	2402	C
25	BA	2406	U
25	BA	2410	G
25	BA	2418	A
25	BA	2423	U
25	BA	2424	C
25	BA	2425	A
25	BA	2429	G
25	BA	2430	A
25	BA	2431	U
25	BA	2434	A
25	BA	2435	A
25	BA	2439	A
25	BA	2440	C
25	BA	2441	C
25	BA	2442	C
25	BA	2447	G
25	BA	2448	A
25	BA	2469	A
25	BA	2470	G
25	BA	2471	C
25	BA	2472	G
25	BA	2476	A
25	BA	2477	C
25	BA	2478	A
25	BA	2491	U
25	BA	2496	C
25	BA	2502	G
25	BA	2505	G
25	BA	2508	G
25	BA	2515	C
25	BA	2518	A
25	BA	2520	C
25	BA	2529	G
25	BA	2542	A
25	BA	2543	G
25	BA	2552	U
25	BA	2554	U
25	BA	2556	C
25	BA	2564	A
25	BA	2566	A

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Mol	Chain	Res	Type
25	BA	2567	G
25	BA	2572	A
25	BA	2573	C
25	BA	2576	G
25	BA	2581	G
25	BA	2582	G
25	BA	2585	U
25	BA	2586	C
25	BA	2602	A
25	BA	2603	G
25	BA	2604	U
25	BA	2609	U
25	BA	2611	U
25	BA	2612	C
25	BA	2615	U
25	BA	2630	G
25	BA	2634	G
25	BA	2655	G
25	BA	2656	U
25	BA	2669	G
25	BA	2670	A
25	BA	2673	G
25	BA	2690	C
25	BA	2691	C
25	BA	2712	U
25	BA	2712(A)	A
25	BA	2713	A
25	BA	2726	U
25	BA	2730	C
25	BA	2733	A
25	BA	2748	A
25	BA	2755	C
25	BA	2757	A
25	BA	2758	A
25	BA	2760	C
25	BA	2762	G
25	BA	2764	A
25	BA	2765	A
25	BA	2766	G
25	BA	2778	A
25	BA	2779	U
25	BA	2780	G

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Mol	Chain	Res	Type
25	BA	2789	C
25	BA	2790	A
25	BA	2791	C
25	BA	2793	G
25	BA	2794	C
25	BA	2795	G
25	BA	2801(A)	A
25	BA	2802	G
25	BA	2803	C
25	BA	2804	C
25	BA	2808	U
25	BA	2820	A
25	BA	2821	A
25	BA	2835	A
25	BA	2842	G
25	BA	2843	G
25	BA	2854	G
25	BA	2863	C
25	BA	2872	G
25	BA	2880	C
25	BA	2883	A
25	BA	2889	C
25	BA	2893	G
25	BA	2894	G
25	BA	2896	C
26	BB	2	C
26	BB	3	C
26	BB	5	C
26	BB	9	G
26	BB	12	C
26	BB	13	A
26	BB	15	A
26	BB	16	G
26	BB	17	C
26	BB	25	A
26	BB	26	A
26	BB	29	A
26	BB	32	C
26	BB	34	U
26	BB	40	U
26	BB	41	U
26	BB	42	C

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Mol	Chain	Res	Type
26	BB	43	C
26	BB	44	G
26	BB	47	C
26	BB	50	G
26	BB	53	A
26	BB	56	G
26	BB	67	G
26	BB	73	A
26	BB	75	G
26	BB	81	G
26	BB	99	G
26	BB	102	A
26	BB	106	G
26	BB	109	C
26	BB	110	G
26	BB	116	G
26	BB	118	G

All (208) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	30	U
1	AA	49	U
1	AA	60	A
1	AA	79	G
1	AA	108	G
1	AA	109	A
1	AA	115	G
1	AA	121	C
1	AA	149	A
1	AA	173	U
1	AA	243	A
1	AA	250	A
1	AA	251	G
1	AA	266	G
1	AA	305	G
1	AA	328	C
1	AA	353	A
1	AA	428	G
1	AA	496	A
1	AA	509	A

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Mol	Chain	Res	Type
1	AA	533	A
1	AA	560	U
1	AA	575	G
1	AA	576	G
1	AA	587	G
1	AA	687	A
1	AA	748	C
1	AA	766	A
1	AA	785	G
1	AA	793	U
1	AA	913	A
1	AA	931	C
1	AA	971	G
1	AA	973	G
1	AA	983	A
1	AA	992	U
1	AA	1049	U
1	AA	1067	A
1	AA	1086	U
1	AA	1124	G
1	AA	1133	G
1	AA	1135	U
1	AA	1136	U
1	AA	1138	G
1	AA	1139	G
1	AA	1145	C
1	AA	1181	G
1	AA	1212	U
1	AA	1225	A
1	AA	1257	U
1	AA	1280	A
1	AA	1285	A
1	AA	1300	G
1	AA	1319	A
1	AA	1332	A
1	AA	1337	G
1	AA	1397	C
1	AA	1442	G
1	AA	1447	A
1	AA	1498	U
1	AA	1503	A
1	AA	1504	G

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Mol	Chain	Res	Type
1	AA	1505	G
1	AA	1533	C
2	AV	7	A
2	AV	18	G
2	AV	19	G
2	AV	28	G
2	AV	34	G
2	AV	35	A
2	AV	43	C
2	AV	57	G
2	AV	72	C
25	BA	27	G
25	BA	49	A
25	BA	71	A
25	BA	74	A
25	BA	102	G
25	BA	119	A
25	BA	128	C
25	BA	196	A
25	BA	199	A
25	BA	221	A
25	BA	249	C
25	BA	271(U)	G
25	BA	271(Y)	U
25	BA	272(J)	C
25	BA	310	A
25	BA	311	A
25	BA	333	G
25	BA	370	G
25	BA	372	G
25	BA	387	U
25	BA	405	U
25	BA	479	A
25	BA	542	C
25	BA	549	G
25	BA	551	G
25	BA	603	A
25	BA	614(C)	A
25	BA	615	G
25	BA	627	A
25	BA	685	A
25	BA	686	G

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Mol	Chain	Res	Type
25	BA	746	A
25	BA	752	A
25	BA	764	A
25	BA	776	G
25	BA	790	C
25	BA	805	G
25	BA	827	U
25	BA	858	U
25	BA	889	C
25	BA	906	G
25	BA	933	A
25	BA	974	G
25	BA	989	G
25	BA	1022	G
25	BA	1026	U
25	BA	1033	U
25	BA	1048	A
25	BA	1053	C
25	BA	1054	A
25	BA	1057	A
25	BA	1058	G
25	BA	1076	C
25	BA	1087	G
25	BA	1089	G
25	BA	1100	C
25	BA	1128	A
25	BA	1142(A)	A
25	BA	1151	G
25	BA	1162	G
25	BA	1181	C
25	BA	1210	A
25	BA	1237	A
25	BA	1253	A
25	BA	1286	A
25	BA	1300	U
25	BA	1301	A
25	BA	1349	A
25	BA	1379	A
25	BA	1396	U
25	BA	1403	C
25	BA	1494	A
25	BA	1497	U

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Mol	Chain	Res	Type
25	BA	1540	U
25	BA	1543	C
25	BA	1558	A
25	BA	1559	G
25	BA	1608	A
25	BA	1609	A
25	BA	1610	A
25	BA	1617	C
25	BA	1653	G
25	BA	1740	G
25	BA	1763	G
25	BA	1780	A
25	BA	1784	A
25	BA	1786	A
25	BA	1799	G
25	BA	1819	A
25	BA	1847	A
25	BA	1858	G
25	BA	1888	G
25	BA	1913	A
25	BA	1914	C
25	BA	1943	U
25	BA	1962	C
25	BA	1963	U
25	BA	1970	A
25	BA	1992	G
25	BA	2019	A
25	BA	2031	A
25	BA	2141	G
25	BA	2146	C
25	BA	2179	C
25	BA	2180	U
25	BA	2191	G
25	BA	2207	G
25	BA	2225	A
25	BA	2275	C
25	BA	2282	G
25	BA	2296	U
25	BA	2311	A
25	BA	2318	G
25	BA	2319	G
25	BA	2320	A

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Mol	Chain	Res	Type
25	BA	2402	C
25	BA	2422	A
25	BA	2439	A
25	BA	2497	A
25	BA	2542	A
25	BA	2566	A
25	BA	2581	G
25	BA	2602	A
25	BA	2609	U
25	BA	2611	U
25	BA	2655	G
25	BA	2665	A
25	BA	2689	U
25	BA	2778	A
25	BA	2802	G
26	BB	1	U
26	BB	44	G
26	BB	66	A
26	BB	109	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 ⓘ

Of 139 ligands modelled in this entry, 138 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
60	GCP	AY	702	59	34,34,34	2.23	12 (35%)	52,54,54	3.45	21 (40%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	GCP	AY	702	59	-	0/20/38/38	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	AY	702	GCP	PG-O2G	-4.06	1.46	1.54
60	AY	702	GCP	C2'-C3'	-3.96	1.42	1.53
60	AY	702	GCP	C5-N7	-3.93	1.33	1.38
60	AY	702	GCP	PB-O2B	-3.87	1.46	1.56
60	AY	702	GCP	PG-O3G	-3.64	1.47	1.54
60	AY	702	GCP	C4-N9	-3.55	1.32	1.37
60	AY	702	GCP	C2-N1	3.37	1.41	1.36
60	AY	702	GCP	C6-N1	3.33	1.41	1.36
60	AY	702	GCP	PB-O3A	2.96	1.61	1.58
60	AY	702	GCP	C5-C4	-2.65	1.34	1.40
60	AY	702	GCP	PB-C3B	2.50	1.82	1.79
60	AY	702	GCP	PA-O3A	2.30	1.64	1.59

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	AY	702	GCP	C6-C5-N7	-19.03	131.58	134.14
60	AY	702	GCP	N2-C2-N1	4.85	123.02	117.82
60	AY	702	GCP	C1'-N9-C4	-4.75	118.43	126.64
60	AY	702	GCP	O4'-C4'-C5'	-4.38	93.80	109.37
60	AY	702	GCP	C2-N3-C4	4.38	120.56	115.30
60	AY	702	GCP	C8-N9-C1'	4.06	133.80	126.15
60	AY	702	GCP	O1G-PG-C3B	-3.83	103.03	110.77
60	AY	702	GCP	PB-C3B-PG	-3.72	111.85	118.95
60	AY	702	GCP	C2'-C3'-C4'	-3.56	95.53	102.64
60	AY	702	GCP	O4'-C1'-C2'	-3.12	102.14	106.69
60	AY	702	GCP	C5-C4-N3	-3.05	122.55	126.07
60	AY	702	GCP	C4'-O4'-C1'	-3.04	106.38	109.72
60	AY	702	GCP	O2B-PB-O1B	2.98	119.68	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	AY	702	GCP	O4'-C1'-N9	2.91	114.43	108.10
60	AY	702	GCP	O2'-C2'-C3'	-2.66	103.24	111.83
60	AY	702	GCP	N1-C2-N3	-2.59	118.28	121.78
60	AY	702	GCP	O3A-PB-O1B	-2.51	106.18	111.51
60	AY	702	GCP	O3'-C3'-C2'	-2.45	103.92	111.83
60	AY	702	GCP	C6-C5-C4	2.30	120.86	117.53
60	AY	702	GCP	O3G-PG-O2G	2.19	115.20	108.34
60	AY	702	GCP	PA-O3A-PB	-2.16	125.52	132.02

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 95th 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 ²)	Q<0.9
1	AA	1514/1516 (99%)	0.01	68 (4%) 32 38	9, 32, 113, 247	0
2	AV	74/76 (97%)	0.29	1 (1%) 72 80	23, 54, 91, 134	0
3	AX	6/25 (24%)	0.40	1 (16%) 2 3	18, 22, 53, 75	0
4	AJ	98/98 (100%)	0.27	5 (5%) 27 32	22, 49, 98, 108	0
5	AK	119/119 (100%)	-0.01	5 (4%) 35 41	18, 41, 65, 104	0
6	AL	124/124 (100%)	-0.10	6 (4%) 29 35	16, 32, 64, 107	0
7	AM	124/124 (100%)	0.81	12 (9%) 8 10	31, 69, 118, 161	0
8	AN	60/60 (100%)	-0.07	2 (3%) 44 53	21, 33, 69, 83	0
9	AO	88/88 (100%)	-0.22	0 100 100	24, 41, 67, 73	0
10	AP	83/83 (100%)	-0.23	1 (1%) 75 83	29, 40, 60, 112	0
11	AQ	99/99 (100%)	-0.38	0 100 100	20, 34, 53, 59	0
12	AR	70/70 (100%)	-0.20	1 (1%) 72 80	23, 41, 75, 92	0
13	AS	78/78 (100%)	0.55	6 (7%) 13 16	39, 69, 107, 121	0
14	AT	99/99 (100%)	-0.08	5 (5%) 27 32	24, 39, 78, 90	0
15	AB	234/234 (100%)	0.10	17 (7%) 15 17	21, 55, 117, 134	0
16	AC	206/206 (100%)	-0.33	0 100 100	22, 41, 67, 103	0
17	AD	208/208 (100%)	-0.05	5 (2%) 56 65	26, 49, 75, 90	0
18	AE	150/150 (100%)	-0.41	1 (0%) 84 90	19, 30, 54, 81	0
19	AF	101/101 (100%)	-0.10	2 (1%) 62 71	28, 52, 75, 87	0
20	AG	155/155 (100%)	0.10	10 (6%) 18 21	31, 53, 104, 148	0
21	AH	138/138 (100%)	-0.43	1 (0%) 84 90	19, 32, 55, 84	0
22	AI	127/127 (100%)	-0.02	4 (3%) 47 56	21, 51, 82, 108	0
23	AY	622/680 (91%)	-0.06	10 (1%) 68 77	30, 55, 97, 131	0
24	AU	24/24 (100%)	0.46	1 (4%) 35 41	33, 48, 65, 83	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	BA	2859/2915 (98%)	-0.04	92 (3%) 45 54	7, 27, 90, 267	0
26	BB	119/122 (97%)	0.29	1 (0%) 83 89	26, 63, 95, 134	0
27	BN	138/140 (98%)	-0.15	4 (2%) 49 59	18, 35, 66, 80	0
28	BO	122/122 (100%)	-0.53	0 100 100	18, 31, 49, 60	0
29	BP	146/150 (97%)	0.69	22 (15%) 3 3	18, 55, 94, 127	0
30	BQ	141/141 (100%)	-0.20	2 (1%) 72 80	23, 35, 64, 112	0
31	BR	117/118 (99%)	-0.21	6 (5%) 27 32	15, 33, 58, 75	0
32	BS	98/112 (87%)	0.82	9 (9%) 9 11	50, 80, 106, 125	0
33	BT	137/146 (93%)	0.58	15 (10%) 6 8	23, 50, 135, 151	0
34	BU	117/118 (99%)	-0.24	2 (1%) 67 76	16, 29, 58, 85	0
35	BV	101/101 (100%)	0.10	5 (4%) 28 33	15, 49, 77, 97	0
36	BW	113/113 (100%)	-0.15	3 (2%) 52 61	18, 29, 67, 122	0
37	BX	92/96 (95%)	-0.31	1 (1%) 77 84	20, 34, 54, 61	0
38	BY	100/110 (90%)	1.09	16 (16%) 3 3	29, 56, 122, 168	0
39	BZ	198/206 (96%)	0.12	9 (4%) 32 38	33, 59, 92, 103	0
40	B0	84/85 (98%)	0.40	9 (10%) 6 8	26, 41, 96, 133	0
41	B1	93/98 (94%)	0.13	4 (4%) 34 40	18, 33, 72, 121	0
42	B2	71/72 (98%)	0.07	2 (2%) 50 60	30, 49, 82, 100	0
43	BD	271/276 (98%)	-0.38	5 (1%) 65 74	9, 20, 46, 89	0
44	B3	59/60 (98%)	0.20	2 (3%) 43 52	24, 40, 76, 137	0
45	B4	30/71 (42%)	1.93	12 (40%) 1 0	102, 130, 156, 174	0
46	B5	59/60 (98%)	0.49	7 (11%) 5 6	10, 35, 98, 134	0
47	B6	44/54 (81%)	1.21	9 (20%) 1 2	34, 59, 99, 109	0
48	B7	48/49 (97%)	-0.30	2 (4%) 35 41	10, 19, 59, 101	0
49	B8	63/65 (96%)	0.28	5 (7%) 13 15	22, 37, 61, 118	0
50	B9	36/37 (97%)	0.25	3 (8%) 11 13	26, 44, 69, 77	0
51	BC	225/229 (98%)	0.14	11 (4%) 28 34	36, 64, 111, 132	0
52	BE	204/206 (99%)	-0.12	9 (4%) 33 39	14, 32, 85, 109	0
53	BF	207/210 (98%)	0.06	13 (6%) 19 22	15, 37, 103, 187	0
54	BG	181/182 (99%)	1.11	30 (16%) 2 3	67, 101, 130, 147	0
55	BH	173/180 (96%)	0.45	14 (8%) 12 14	35, 60, 95, 159	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
56	BK	127/147 (86%)	4.89	105 (82%) 0 0	127, 181, 237, 263	0
57	BJ	130/130 (100%)	1.48	36 (27%) 1 1	74, 106, 140, 195	0
58	BL	0/125	-	-	-	-
All	All	11304/11728 (96%)	0.11	629 (5%) 24 28	7, 40, 108, 267	0

All (629) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
55	BH	44	VAL	21.9
7	AM	123	ALA	17.5
56	BK	136	VAL	15.3
56	BK	83	GLY	14.4
53	BF	11	VAL	13.6
38	BY	52	SER	12.1
38	BY	51	VAL	12.1
1	AA	89	C	11.3
7	AM	122	LYS	11.1
25	BA	889	C	10.9
55	BH	45	VAL	10.6
56	BK	105	LEU	10.5
56	BK	135	GLY	10.5
56	BK	7	VAL	10.4
56	BK	10	LEU	10.4
56	BK	13	PRO	10.1
7	AM	124	PRO	10.0
25	BA	2803	C	9.9
46	B5	58	LEU	9.9
38	BY	50	ARG	9.6
57	BJ	88	ALA	9.6
56	BK	134	MET	9.6
25	BA	887	A	9.5
57	BJ	87	ALA	9.5
56	BK	66	THR	9.3
38	BY	3	VAL	9.0
56	BK	76	TYR	8.9
32	BS	54	LEU	8.8
56	BK	52	ILE	8.6
56	BK	132	ARG	8.5
1	AA	82	U	8.5
56	BK	53	VAL	8.5
56	BK	12	LEU	8.4

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Mol	Chain	Res	Type	RSRZ
25	BA	2802	G	8.3
56	BK	140	GLY	8.3
25	BA	2801(A)	A	8.2
25	BA	2801	A	8.2
25	BA	1509	C	8.2
56	BK	27	LEU	8.2
53	BF	12	LEU	8.2
56	BK	63	ARG	8.1
36	BW	112	GLY	8.1
7	AM	7	VAL	8.0
56	BK	51	ALA	8.0
56	BK	64	SER	8.0
56	BK	67	PHE	7.8
5	AK	129	SER	7.8
40	B0	3	HIS	7.8
56	BK	77	LEU	7.7
33	BT	36	GLU	7.7
56	BK	65	PHE	7.6
1	AA	81	U	7.6
56	BK	17	ALA	7.4
56	BK	20	ALA	7.3
35	BV	36	PRO	7.3
56	BK	28	GLY	7.3
56	BK	68	VAL	7.3
56	BK	61	ALA	7.3
56	BK	106	GLU	7.2
56	BK	84	LEU	7.2
57	BJ	49	ALA	7.1
54	BG	2	PRO	7.1
57	BJ	50	ALA	7.0
5	AK	128	ALA	7.0
6	AL	128	ALA	7.0
40	B0	5	LYS	7.0
1	AA	88	A	7.0
56	BK	56	GLU	7.0
56	BK	26	ALA	6.9
33	BT	134	GLU	6.9
56	BK	137	GLU	6.9
33	BT	37	GLY	6.9
40	B0	6	GLY	6.9
25	BA	2795	G	6.8
41	B1	85	LEU	6.8

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Mol	Chain	Res	Type	RSRZ
56	BK	74	ALA	6.8
46	B5	54	GLY	6.8
36	BW	113	LYS	6.8
56	BK	29	GLN	6.7
56	BK	22	PRO	6.7
25	BA	888	C	6.6
56	BK	15	GLY	6.6
7	AM	84	ILE	6.5
57	BJ	4	ALA	6.4
56	BK	82	ALA	6.4
33	BT	135	ALA	6.4
25	BA	1174	A	6.4
57	BJ	7	ALA	6.3
38	BY	58	GLY	6.3
56	BK	50	ASP	6.1
46	B5	59	GLU	6.1
44	B3	1	MET	6.0
53	BF	1	MET	6.0
53	BF	24	LEU	6.0
56	BK	21	PRO	6.0
56	BK	16	LYS	6.0
56	BK	3	LYS	6.0
56	BK	4	VAL	5.9
47	B6	42	TRP	5.9
1	AA	1030(C)	G	5.9
25	BA	886	C	5.8
56	BK	110	GLN	5.8
33	BT	136	GLN	5.8
56	BK	8	VAL	5.7
56	BK	33	ASN	5.7
40	B0	7	LEU	5.7
33	BT	39	ARG	5.7
54	BG	86	MET	5.6
54	BG	48	GLU	5.6
57	BJ	132	ALA	5.6
42	B2	72	ALA	5.5
56	BK	133	SER	5.5
54	BG	126	ASP	5.5
52	BE	76	ARG	5.4
56	BK	31	GLY	5.4
57	BJ	89	ALA	5.4
56	BK	11	GLN	5.4

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Mol	Chain	Res	Type	RSRZ
53	BF	133	ASN	5.4
25	BA	884	C	5.4
1	AA	90	U	5.3
46	B5	2	ALA	5.3
1	AA	1543	C	5.2
29	BP	110	TYR	5.2
1	AA	841	U	5.2
56	BK	18	THR	5.2
56	BK	80	LYS	5.2
56	BK	19	PRO	5.2
25	BA	2896	C	5.1
33	BT	130	ALA	5.1
56	BK	35	MET	5.1
56	BK	126	MET	5.1
54	BG	42	GLY	5.1
4	AJ	100	THR	5.1
25	BA	1847	A	5.1
1	AA	1001(A)	G	5.1
17	AD	9	CYS	5.0
13	AS	43	GLU	5.0
56	BK	49	GLY	5.0
56	BK	14	ALA	4.9
25	BA	2207	G	4.9
34	BU	118	GLY	4.9
25	BA	899	A	4.9
56	BK	98	ARG	4.8
56	BK	81	ALA	4.8
1	AA	839	U	4.8
38	BY	28	LYS	4.8
2	AV	20	U	4.8
54	BG	84	LYS	4.8
1	AA	83	U	4.8
1	AA	1542	U	4.8
7	AM	6	GLY	4.8
45	B4	61	VAL	4.8
56	BK	2	LYS	4.8
1	AA	204	U	4.7
45	B4	39	ARG	4.7
54	BG	50	ALA	4.7
25	BA	2310	A	4.7
25	BA	890	A	4.6
56	BK	47	ASN	4.6

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Mol	Chain	Res	Type	RSRZ
30	BQ	140	ALA	4.6
25	BA	880	G	4.6
56	BK	36	GLU	4.6
40	B0	2	ALA	4.6
55	BH	43	VAL	4.5
1	AA	1030(D)	A	4.5
45	B4	58	TYR	4.5
1	AA	1541	U	4.5
20	AG	81	GLY	4.5
25	BA	2792	G	4.5
56	BK	112	MET	4.5
57	BJ	8	ALA	4.5
30	BQ	141	GLN	4.5
1	AA	1138	G	4.4
56	BK	122	ALA	4.4
1	AA	1493	A	4.4
1	AA	1442(A)	G	4.4
25	BA	645	C	4.4
53	BF	7	TYR	4.4
56	BK	138	VAL	4.4
1	AA	1492	A	4.4
56	BK	46	ALA	4.3
56	BK	101	TRP	4.3
1	AA	1027	C	4.3
25	BA	2793	G	4.3
56	BK	5	VAL	4.3
56	BK	24	GLY	4.2
56	BK	62	ASP	4.2
53	BF	21	ALA	4.2
45	B4	54	LYS	4.2
56	BK	60	TYR	4.2
25	BA	2602	A	4.2
56	BK	113	PRO	4.2
1	AA	470	C	4.2
6	AL	28	LYS	4.2
54	BG	182	LYS	4.2
46	B5	53	ALA	4.2
25	BA	2892	A	4.2
1	AA	78	G	4.1
56	BK	58	THR	4.1
25	BA	881	G	4.1
54	BG	47	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
56	BK	117	THR	4.1
25	BA	883	G	4.1
25	BA	1173	G	4.1
25	BA	2794	C	4.1
13	AS	10	PHE	4.1
25	BA	508	G	4.0
49	B8	64	TYR	4.0
25	BA	2833	G	4.0
15	AB	237	ALA	4.0
57	BJ	86	ALA	4.0
38	BY	61	ILE	4.0
39	BZ	146	ILE	4.0
56	BK	23	VAL	4.0
43	BD	25	THR	4.0
56	BK	43	ALA	4.0
1	AA	1533	C	4.0
8	AN	2	ALA	4.0
53	BF	25	PRO	4.0
5	AK	127	LYS	3.9
40	B0	4	LYS	3.9
51	BC	105	ASP	3.9
25	BA	352	G	3.9
25	BA	892	G	3.9
1	AA	1039	C	3.9
54	BG	3	LEU	3.9
57	BJ	6	ALA	3.9
38	BY	2	ARG	3.9
8	AN	13	THR	3.9
25	BA	2790	A	3.9
45	B4	53	THR	3.8
22	AI	88	TYR	3.8
56	BK	48	MET	3.8
23	AY	582	PHE	3.8
56	BK	73	PRO	3.8
20	AG	82	GLY	3.8
56	BK	130	SER	3.8
15	AB	128	GLU	3.8
25	BA	896	A	3.8
56	BK	9	LYS	3.8
25	BA	885	C	3.8
25	BA	271(K)	U	3.8
33	BT	137	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
38	BY	89	PHE	3.7
29	BP	27	HIS	3.7
56	BK	54	PRO	3.7
46	B5	60	VAL	3.7
56	BK	45	THR	3.7
25	BA	229	A	3.7
1	AA	80	G	3.7
25	BA	2897	U	3.7
56	BK	78	ILE	3.7
56	BK	121	GLU	3.6
54	BG	127	GLY	3.6
38	BY	53	PRO	3.6
57	BJ	131	ALA	3.6
1	AA	1030(B)	C	3.6
56	BK	37	PHE	3.6
56	BK	38	VAL	3.6
1	AA	91	C	3.6
17	AD	12	CYS	3.6
25	BA	1076	C	3.5
39	BZ	6	LYS	3.5
21	AH	1	MET	3.5
44	B3	2	PRO	3.5
27	BN	68	GLU	3.5
51	BC	95	GLY	3.5
57	BJ	51	ALA	3.5
1	AA	1002	G	3.5
25	BA	275	G	3.5
25	BA	2894	G	3.5
1	AA	77	G	3.5
25	BA	2402	C	3.5
54	BG	49	ASP	3.5
13	AS	28	LYS	3.4
33	BT	91	ARG	3.4
47	B6	44	ARG	3.4
29	BP	65	ARG	3.4
48	B7	47	ARG	3.4
56	BK	75	SER	3.4
25	BA	1176	G	3.4
1	AA	1031	G	3.4
25	BA	882	G	3.4
10	AP	83	GLU	3.4
15	AB	129	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
7	AM	121	LYS	3.4
1	AA	1026	G	3.4
53	BF	10	PRO	3.4
52	BE	54	GLN	3.4
38	BY	60	PHE	3.3
54	BG	72	ARG	3.3
25	BA	2895	U	3.3
45	B4	40	ILE	3.3
56	BK	102	GLU	3.3
52	BE	204	ALA	3.3
57	BJ	66	ALA	3.3
27	BN	3	THR	3.3
14	AT	9	ASN	3.3
33	BT	2	ASN	3.3
51	BC	202	GLU	3.3
57	BJ	31	ALA	3.3
1	AA	1456	G	3.3
31	BR	3	HIS	3.3
56	BK	128	ALA	3.3
7	AM	119	GLY	3.3
35	BV	101	GLY	3.3
25	BA	897	C	3.3
33	BT	38	ASN	3.3
54	BG	52	ILE	3.3
33	BT	32	TYR	3.3
1	AA	1534	A	3.3
33	BT	105	LEU	3.3
57	BJ	98	ALA	3.2
25	BA	1177	A	3.2
25	BA	1742	G	3.2
56	BK	57	ILE	3.2
13	AS	30	LEU	3.2
54	BG	139	LEU	3.2
54	BG	118	ARG	3.2
57	BJ	53	ALA	3.2
25	BA	11	G	3.2
25	BA	271(N)	U	3.2
1	AA	161	A	3.2
47	B6	43	CYS	3.2
54	BG	156	ASP	3.2
17	AD	26	CYS	3.2
7	AM	117	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
33	BT	1	MET	3.2
56	BK	55	VAL	3.2
32	BS	68	GLN	3.2
25	BA	2179	C	3.2
56	BK	120	LEU	3.2
15	AB	19	HIS	3.1
45	B4	49	GLU	3.1
22	AI	3	GLN	3.1
57	BJ	52	ALA	3.1
1	AA	1538	C	3.1
25	BA	1848	A	3.1
15	AB	136	VAL	3.1
1	AA	203	U	3.1
1	AA	1032	G	3.1
25	BA	893	C	3.1
56	BK	40	ALA	3.1
43	BD	262	ARG	3.1
54	BG	115	ARG	3.1
1	AA	84	U	3.1
54	BG	78	SER	3.1
47	B6	17	LYS	3.1
57	BJ	30	ALA	3.1
25	BA	1740	G	3.0
55	BH	170	ARG	3.0
25	BA	1091	G	3.0
25	BA	2893	G	3.0
47	B6	23	THR	3.0
25	BA	614(A)	U	3.0
56	BK	79	ARG	3.0
15	AB	122	PHE	3.0
23	AY	580	MET	3.0
55	BH	111	HIS	3.0
29	BP	149	GLU	3.0
33	BT	133	GLU	3.0
20	AG	156	TRP	3.0
20	AG	83	ALA	3.0
32	BS	60	GLY	3.0
56	BK	129	GLY	3.0
25	BA	547	A	3.0
4	AJ	83	GLU	3.0
32	BS	107	GLU	3.0
29	BP	107	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
36	BW	111	HIS	3.0
1	AA	1447	A	2.9
43	BD	35	LYS	2.9
20	AG	79	ARG	2.9
49	B8	63	PRO	2.9
22	AI	53	VAL	2.9
43	BD	2	ALA	2.9
49	B8	34	TRP	2.9
29	BP	118	GLY	2.9
51	BC	124	GLY	2.9
48	B7	48	LYS	2.9
3	AX	15	A	2.9
29	BP	15	ARG	2.9
1	AA	998	G	2.9
1	AA	1030	C	2.9
1	AA	1030(A)	G	2.9
1	AA	1000	U	2.9
31	BR	105	ARG	2.9
23	AY	585	ALA	2.9
7	AM	115	LYS	2.9
23	AY	596	LYS	2.9
29	BP	33	ARG	2.9
51	BC	106	GLY	2.8
25	BA	1175	U	2.8
54	BG	13	GLU	2.8
38	BY	59	GLY	2.8
1	AA	1023	G	2.8
23	AY	583	LYS	2.8
56	BK	41	PHE	2.8
56	BK	114	ASP	2.8
1	AA	1038	C	2.8
15	AB	230	VAL	2.8
1	AA	1003	G	2.8
25	BA	879	G	2.8
29	BP	18	ARG	2.8
54	BG	12	TYR	2.8
56	BK	99	ILE	2.8
1	AA	1029	C	2.8
25	BA	898	C	2.8
25	BA	878	A	2.8
25	BA	2309	A	2.8
1	AA	631	G	2.8

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Mol	Chain	Res	Type	RSRZ
39	BZ	188	ALA	2.8
38	BY	91	GLU	2.7
15	AB	125	PRO	2.7
20	AG	85	TYR	2.7
1	AA	1036	G	2.7
51	BC	71	GLN	2.7
15	AB	7	VAL	2.7
55	BH	42	ARG	2.7
56	BK	109	LYS	2.7
54	BG	88	ILE	2.7
52	BE	61	ARG	2.7
54	BG	149	VAL	2.7
1	AA	1034	G	2.7
39	BZ	13	GLU	2.7
41	B1	81	LYS	2.7
27	BN	8	GLN	2.7
45	B4	56	GLU	2.7
49	B8	48	PHE	2.7
51	BC	205	LYS	2.6
57	BJ	116	ALA	2.6
23	AY	567	LEU	2.6
15	AB	15	VAL	2.6
38	BY	87	LYS	2.6
52	BE	1	MET	2.6
38	BY	4	LYS	2.6
25	BA	1060	U	2.6
25	BA	6	A	2.6
20	AG	154	TYR	2.6
47	B6	22	ALA	2.6
54	BG	41	GLN	2.6
39	BZ	4	ARG	2.6
43	BD	36	PRO	2.6
25	BA	2805	G	2.6
45	B4	41	ILE	2.6
19	AF	101	ALA	2.6
29	BP	94	GLU	2.6
1	AA	532	A	2.6
35	BV	20	LEU	2.6
25	BA	614(B)	G	2.6
56	BK	116	ASN	2.6
40	B0	74	ARG	2.6
1	AA	630	G	2.5

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Mol	Chain	Res	Type	RSRZ
1	AA	1009	G	2.5
45	B4	50	THR	2.5
38	BY	88	LYS	2.5
56	BK	25	PRO	2.5
56	BK	32	ALA	2.5
39	BZ	11	GLU	2.5
42	B2	71	ASN	2.5
50	B9	12	ASP	2.5
32	BS	43	GLU	2.5
53	BF	128	ALA	2.5
57	BJ	54	ALA	2.5
57	BJ	130	ALA	2.5
47	B6	31	PRO	2.5
57	BJ	75	ALA	2.5
25	BA	1508	A	2.5
41	B1	79	GLY	2.5
1	AA	1025	U	2.5
1	AA	1539	C	2.5
45	B4	47	VAL	2.5
6	AL	47	LYS	2.5
55	BH	110	SER	2.5
14	AT	106	ALA	2.5
29	BP	150	ALA	2.5
25	BA	2791	C	2.5
18	AE	154	GLY	2.5
50	B9	13	LYS	2.5
1	AA	1532	U	2.4
52	BE	56	PRO	2.4
57	BJ	19	ALA	2.4
31	BR	118	GLU	2.4
55	BH	172	LYS	2.4
1	AA	1024	G	2.4
1	AA	1033	G	2.4
46	B5	37	LYS	2.4
51	BC	12	GLU	2.4
57	BJ	15	ALA	2.4
25	BA	157	U	2.4
53	BF	14	PRO	2.4
52	BE	68	ALA	2.4
34	BU	91	ASP	2.4
23	AY	203	GLU	2.4
25	BA	1075	C	2.4

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Mol	Chain	Res	Type	RSRZ
15	AB	137	ARG	2.4
15	AB	229	VAL	2.4
37	BX	66	LEU	2.4
57	BJ	129	ALA	2.4
4	AJ	55	LYS	2.4
29	BP	132	LYS	2.4
14	AT	75	ASN	2.4
29	BP	92	GLU	2.4
1	AA	412	A	2.4
52	BE	17	ASP	2.4
55	BH	168	PRO	2.4
4	AJ	85	LEU	2.4
24	AU	25	LYS	2.4
31	BR	2	ARG	2.4
1	AA	1537	U	2.4
25	BA	1460	A	2.4
14	AT	101	GLY	2.3
39	BZ	187	ALA	2.3
5	AK	117	ASN	2.3
53	BF	18	ARG	2.3
1	AA	202	U	2.3
1	AA	1540	U	2.3
25	BA	1505	C	2.3
25	BA	2804	C	2.3
40	B0	85	ALA	2.3
5	AK	102	GLY	2.3
54	BG	141	PHE	2.3
56	BK	69	THR	2.3
1	AA	1535	C	2.3
12	AR	88	LYS	2.3
25	BA	1494	A	2.3
54	BG	164	GLU	2.3
56	BK	44	ALA	2.3
56	BK	118	THR	2.3
57	BJ	97	ALA	2.3
15	AB	14	GLY	2.3
35	BV	48	GLY	2.3
6	AL	127	GLU	2.3
7	AM	8	GLU	2.3
55	BH	13	LYS	2.3
55	BH	85	LYS	2.3
45	B4	38	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
27	BN	4	TYR	2.3
52	BE	132	HIS	2.3
1	AA	1005	A	2.3
57	BJ	90	ALA	2.3
53	BF	13	SER	2.3
1	AA	216	G	2.3
56	BK	124	ALA	2.3
29	BP	16	ARG	2.3
47	B6	39	TYR	2.3
54	BG	9	ARG	2.3
32	BS	61	ASN	2.2
4	AJ	89	ASP	2.2
25	BA	158	U	2.2
32	BS	30	ARG	2.2
57	BJ	83	ALA	2.2
1	AA	1007	C	2.2
20	AG	86	GLN	2.2
40	B0	84	LEU	2.2
51	BC	109	ASP	2.2
51	BC	118	ASP	2.2
15	AB	23	ARG	2.2
39	BZ	166	SER	2.2
29	BP	71	VAL	2.2
7	AM	116	THR	2.2
15	AB	140	HIS	2.2
1	AA	1001	A	2.2
25	BA	2218	U	2.2
57	BJ	76	ALA	2.2
13	AS	81	ARG	2.2
29	BP	87	ASP	2.2
25	BA	34	C	2.2
25	BA	1078	U	2.2
6	AL	19	ARG	2.2
25	BA	10	G	2.2
25	BA	274	G	2.2
32	BS	81	GLY	2.2
29	BP	51	PHE	2.2
29	BP	95	VAL	2.2
25	BA	548	A	2.2
50	B9	26	ILE	2.2
56	BK	97	GLY	2.2
47	B6	30	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	AA	97	G	2.2
22	AI	126	SER	2.2
54	BG	23	PHE	2.2
54	BG	83	ARG	2.2
17	AD	150	GLU	2.2
57	BJ	5	ALA	2.2
54	BG	116	ASP	2.2
25	BA	1046	A	2.1
41	B1	57	GLU	2.1
55	BH	167	GLU	2.1
57	BJ	125	ALA	2.1
29	BP	90	ARG	2.1
25	BA	1077	A	2.1
17	AD	167	GLY	2.1
20	AG	84	ASN	2.1
25	BA	2308	G	2.1
31	BR	8	ARG	2.1
25	BA	1178	C	2.1
29	BP	62	LEU	2.1
35	BV	19	LYS	2.1
25	BA	271(J)	C	2.1
55	BH	83	TYR	2.1
25	BA	271(L)	U	2.1
57	BJ	67	ALA	2.1
57	BJ	69	ALA	2.1
20	AG	153	HIS	2.1
25	BA	1069	A	2.1
13	AS	68	GLY	2.1
29	BP	93	GLY	2.1
6	AL	112	ASP	2.1
51	BC	77	ILE	2.1
49	B8	35	GLN	2.1
23	AY	681	LYS	2.1
55	BH	39	PRO	2.1
57	BJ	42	ALA	2.1
14	AT	74	LYS	2.1
15	AB	37	ASN	2.1
23	AY	226	ASN	2.1
31	BR	11	ASN	2.1
15	AB	231	GLU	2.1
25	BA	272(J)	C	2.1
25	BA	1074	G	2.1

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Mol	Chain	Res	Type	RSRZ
25	BA	1026	U	2.0
39	BZ	168	GLU	2.0
29	BP	48	PRO	2.0
32	BS	108	GLY	2.0
23	AY	682	GLN	2.0
19	AF	28	ARG	2.0
26	BB	25	A	2.0
57	BJ	126	ALA	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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
59	MG	BA	3014	1/1	0.28	-	27,27,27,27	0
59	MG	AA	1639	1/1	0.18	-	20,20,20,20	0
59	MG	AA	1621	1/1	0.17	-	14,14,14,14	0
59	MG	BA	3073	1/1	0.26	-	14,14,14,14	0
59	MG	BA	3054	1/1	0.27	-	9,9,9,9	0
59	MG	BA	3070	1/1	0.28	-	24,24,24,24	0
59	MG	BA	3013	1/1	0.20	-	26,26,26,26	0
59	MG	AA	1623	1/1	0.21	-	15,15,15,15	0
59	MG	AA	1624	1/1	0.17	-	14,14,14,14	0
59	MG	AA	1604	1/1	0.09	-	3,3,3,3	0
59	MG	BA	3027	1/1	0.35	-	30,30,30,30	0
59	MG	BA	3030	1/1	0.32	-	12,12,12,12	0
59	MG	BA	3077	1/1	0.14	-	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	BA	3074	1/1	0.15	-	16,16,16,16	0
59	MG	BA	3017	1/1	0.20	-	16,16,16,16	0
59	MG	BA	3019	1/1	0.27	-	16,16,16,16	0
60	GCP	AY	702	32/32	0.13	-	27,42,47,49	0
59	MG	BA	3045	1/1	0.20	-	16,16,16,16	0
59	MG	AA	1603	1/1	0.22	-	23,23,23,23	0
59	MG	AA	1632	1/1	0.21	-	22,22,22,22	0
59	MG	BA	3060	1/1	0.30	-	22,22,22,22	0
59	MG	AA	1631	1/1	0.19	-	13,13,13,13	0
59	MG	BA	3004	1/1	0.14	-	46,46,46,46	0
59	MG	AA	1637	1/1	0.13	-	34,34,34,34	0
59	MG	AA	1613	1/1	0.17	-	6,6,6,6	0
59	MG	BA	3024	1/1	0.29	-	2,2,2,2	0
59	MG	BA	3064	1/1	0.17	-	22,22,22,22	0
59	MG	BA	3068	1/1	0.25	-	7,7,7,7	0
59	MG	BA	3083	1/1	0.13	-	37,37,37,37	0
59	MG	BA	3051	1/1	0.28	-	24,24,24,24	0
59	MG	AA	1611	1/1	0.22	-	7,7,7,7	0
59	MG	AA	1643	1/1	0.14	-	31,31,31,31	0
59	MG	BA	3032	1/1	0.27	-	21,21,21,21	0
59	MG	AA	1617	1/1	0.31	-	21,21,21,21	0
59	MG	AA	1635	1/1	0.21	-	24,24,24,24	0
59	MG	AA	1644	1/1	0.34	-	33,33,33,33	0
59	MG	BA	3039	1/1	0.19	-	24,24,24,24	0
59	MG	BA	3035	1/1	0.37	-	18,18,18,18	0
59	MG	AA	1609	1/1	0.24	-	16,16,16,16	0
59	MG	BA	3085	1/1	0.25	-	18,18,18,18	0
59	MG	AA	1615	1/1	0.17	-	24,24,24,24	0
59	MG	BA	3081	1/1	0.16	-	17,17,17,17	0
59	MG	BA	3075	1/1	0.20	-	12,12,12,12	0
59	MG	BA	3011	1/1	0.24	-	30,30,30,30	0
59	MG	BA	3015	1/1	0.22	-	10,10,10,10	0
59	MG	BA	3080	1/1	0.23	-	16,16,16,16	0
59	MG	BA	3087	1/1	0.23	-	26,26,26,26	0
59	MG	AA	1638	1/1	0.17	-	22,22,22,22	0
59	MG	BA	3055	1/1	0.20	-	5,5,5,5	0
59	MG	BA	3031	1/1	0.30	-	16,16,16,16	0
59	MG	BA	3088	1/1	0.29	-	26,26,26,26	0
59	MG	BA	3021	1/1	0.19	-	25,25,25,25	0
59	MG	BA	3008	1/1	0.27	-	13,13,13,13	0
59	MG	AA	1640	1/1	0.14	-	21,21,21,21	0
59	MG	BA	3006	1/1	0.29	-	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	BA	3065	1/1	0.31	-	24,24,24,24	0
59	MG	B8	101	1/1	0.12	-	15,15,15,15	0
59	MG	BA	3049	1/1	0.28	-	2,2,2,2	0
59	MG	BA	3026	1/1	0.19	-	19,19,19,19	0
59	MG	BA	3018	1/1	0.23	-	12,12,12,12	0
59	MG	AA	1628	1/1	0.06	-	18,18,18,18	0
59	MG	AA	1619	1/1	0.22	-	27,27,27,27	0
59	MG	AA	1620	1/1	0.36	-	18,18,18,18	0
59	MG	BA	3072	1/1	0.23	-	19,19,19,19	0
59	MG	AA	1612	1/1	0.15	-	14,14,14,14	0
59	MG	BA	3002	1/1	0.17	-	17,17,17,17	0
59	MG	AA	1601	1/1	0.25	-	13,13,13,13	0
59	MG	AA	1641	1/1	0.14	-	25,25,25,25	0
59	MG	BA	3022	1/1	0.32	-	13,13,13,13	0
59	MG	BA	3056	1/1	0.14	-	18,18,18,18	0
59	MG	BA	3025	1/1	0.21	-	16,16,16,16	0
59	MG	AA	1625	1/1	0.32	-	25,25,25,25	0
59	MG	BA	3084	1/1	0.19	-	22,22,22,22	0
59	MG	AY	701	1/1	0.13	-	41,41,41,41	0
59	MG	BA	3058	1/1	0.16	-	3,3,3,3	0
59	MG	AA	1622	1/1	0.23	-	25,25,25,25	0
59	MG	BA	3028	1/1	0.20	-	23,23,23,23	0
59	MG	BA	3037	1/1	0.20	-	7,7,7,7	0
59	MG	AA	1633	1/1	0.13	-	27,27,27,27	0
59	MG	BA	3033	1/1	0.26	-	12,12,12,12	0
59	MG	BA	3061	1/1	0.30	-	8,8,8,8	0
59	MG	AA	1616	1/1	0.17	-	5,5,5,5	0
59	MG	AA	1606	1/1	0.24	-	15,15,15,15	0
59	MG	BA	3041	1/1	0.32	-	11,11,11,11	0
59	MG	BA	3029	1/1	0.24	-	28,28,28,28	0
59	MG	BA	3009	1/1	0.32	-	31,31,31,31	0
59	MG	BA	3010	1/1	0.30	-	14,14,14,14	0
59	MG	AA	1636	1/1	0.10	-	24,24,24,24	0
59	MG	AA	1626	1/1	0.19	-	19,19,19,19	0
59	MG	BA	3003	1/1	0.35	-	2,2,2,2	0
59	MG	BA	3043	1/1	0.28	-	7,7,7,7	0
59	MG	BE	301	1/1	0.25	-	16,16,16,16	0
59	MG	BA	3063	1/1	0.19	-	22,22,22,22	0
59	MG	BA	3086	1/1	0.26	-	26,26,26,26	0
59	MG	BA	3050	1/1	0.27	-	10,10,10,10	0
59	MG	AA	1630	1/1	0.29	-	29,29,29,29	0
59	MG	AA	1602	1/1	0.31	-	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	BA	3048	1/1	0.25	-	9,9,9,9	0
59	MG	BA	3057	1/1	0.21	-	8,8,8,8	0
59	MG	BA	3038	1/1	0.37	-	19,19,19,19	0
59	MG	BA	3020	1/1	0.31	-	6,6,6,6	0
59	MG	BA	3012	1/1	0.13	-	10,10,10,10	0
59	MG	BF	301	1/1	0.14	-	27,27,27,27	0
59	MG	BA	3023	1/1	0.25	-	9,9,9,9	0
59	MG	AA	1627	1/1	0.24	-	15,15,15,15	0
59	MG	BA	3067	1/1	0.19	-	16,16,16,16	0
59	MG	BA	3078	1/1	0.18	-	15,15,15,15	0
59	MG	AA	1614	1/1	0.24	-	11,11,11,11	0
59	MG	BA	3053	1/1	0.22	-	7,7,7,7	0
59	MG	BA	3076	1/1	0.22	-	8,8,8,8	0
59	MG	AA	1608	1/1	0.41	-	23,23,23,23	0
59	MG	BA	3047	1/1	0.32	-	27,27,27,27	0
59	MG	BA	3082	1/1	0.24	-	21,21,21,21	0
59	MG	AA	1645	1/1	0.37	-	35,35,35,35	0
59	MG	AA	1607	1/1	0.16	-	24,24,24,24	0
59	MG	BA	3071	1/1	0.32	-	29,29,29,29	0
59	MG	AA	1642	1/1	0.19	-	30,30,30,30	0
59	MG	BA	3040	1/1	0.25	-	10,10,10,10	0
59	MG	BA	3007	1/1	0.29	-	4,4,4,4	0
59	MG	AA	1605	1/1	0.11	-	25,25,25,25	0
59	MG	BA	3016	1/1	0.07	-	15,15,15,15	0
59	MG	BA	3059	1/1	0.22	-	9,9,9,9	0
59	MG	AA	1634	1/1	0.07	-	6,6,6,6	0
59	MG	BA	3046	1/1	0.19	-	14,14,14,14	0
59	MG	AA	1629	1/1	0.13	-	38,38,38,38	0
59	MG	BA	3036	1/1	0.26	-	20,20,20,20	0
59	MG	AA	1618	1/1	0.19	-	22,22,22,22	0
59	MG	BA	3044	1/1	0.16	-	15,15,15,15	0
59	MG	BA	3069	1/1	0.33	-	14,14,14,14	0
59	MG	BA	3005	1/1	0.33	-	12,12,12,12	0
59	MG	AA	1610	1/1	0.23	-	14,14,14,14	0
59	MG	BA	3062	1/1	0.22	-	18,18,18,18	0
59	MG	BA	3066	1/1	0.25	-	15,15,15,15	0
59	MG	BA	3079	1/1	0.22	-	14,14,14,14	0
59	MG	BD	301	1/1	0.26	-	7,7,7,7	0
59	MG	BA	3034	1/1	0.26	-	5,5,5,5	0
59	MG	BA	3042	1/1	0.32	-	11,11,11,11	0
59	MG	BA	3001	1/1	0.32	-	32,32,32,32	0
59	MG	BA	3052	1/1	0.23	-	19,19,19,19	0

6.5 Other polymers ⓘ

There are no such residues in this entry.