



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 12:31 AM UTC

PDB ID : 6HIY / pdb_00006hiy
EMDB ID : EMD-0232
Title : Cryo-EM structure of the Trypanosoma brucei mitochondrial ribosome - This entry contains the body of the small mitoribosomal subunit in complex with mt-IF-3
Authors : Ramrath, D.J.F.; Niemann, M.; Leibundgut, M.; Bieri, P.; Prange, C.; Horn, E.K.; Leitner, A.; Boehringer, D.; Schneider, A.; Ban, N.
Deposited on : 2018-08-31
Resolution : 3.27 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

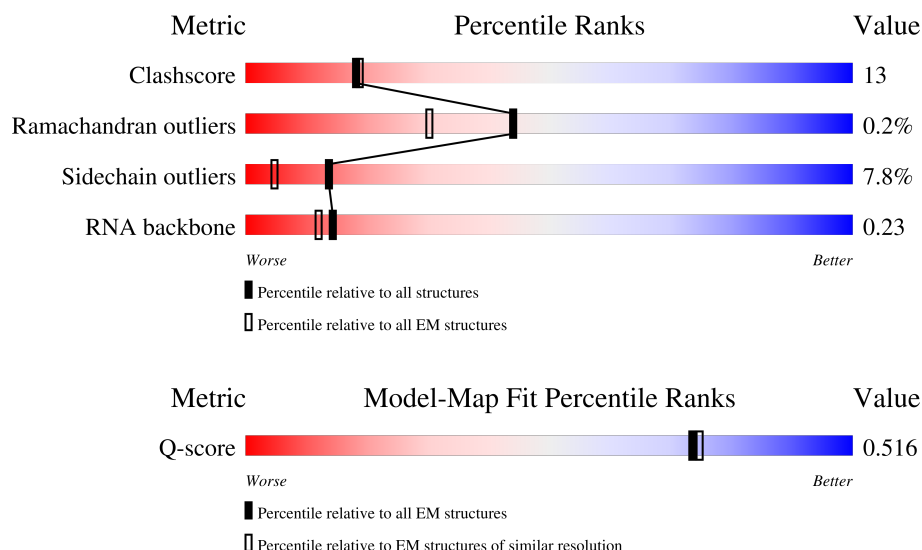
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.27 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



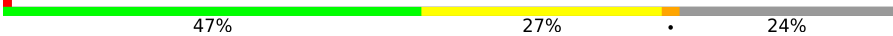
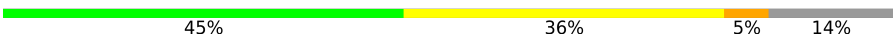
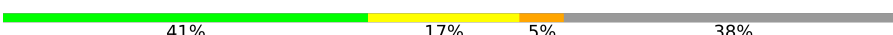
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14508 (2.77 - 3.77)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	DA	1788	
2	DD	812	
3	DI	407	

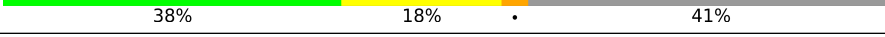
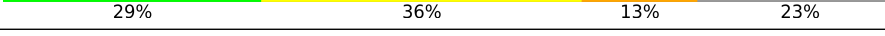
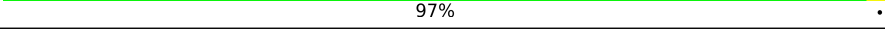
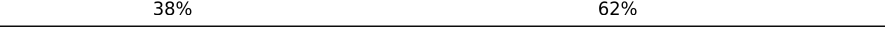
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Mol	Chain	Length	Quality of chain
4	DL	307	
5	DM	294	
6	DN	293	
7	DO	282	
8	DP	274	
9	DQ	268	
10	DR	270	
11	DS	261	
12	DU	228	
13	DZ	94	
14	Da	64	
15	CE	435	
16	CF	160	
17	CH	282	
18	CI	443	
19	CK	326	
20	CL	87	
21	CO	429	
22	CP	188	
23	CQ	307	
24	CR	320	
25	CU	193	
26	CZ	360	
27	Ca	602	
28	Cb	324	

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Mol	Chain	Length	Quality of chain
29	Cd	440	
30	Cj	257	
31	Cm	215	
32	Cn	250	
33	Cp	187	
34	Cq	263	
35	Cr	439	
36	Cv	1211	
37	CA	621	
38	UQ	32	
39	UR	8	
40	US	54	
41	UT	44	

2 Entry composition [i](#)

There are 45 unique types of molecules in this entry. The entry contains 100780 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called mS48.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	DA	1426	Total	C	N	O	S	0	0
			11489	7252	2052	2151	34		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DA	894	HIS	ASN	conflict	UNP Q57UJ2
DA	1181	THR	ILE	conflict	UNP Q57UJ2
DA	1333	ALA	VAL	conflict	UNP Q57UJ2
DA	1700	ARG	HIS	conflict	UNP Q57UJ2
DA	1761	LYS	ARG	conflict	UNP Q57UJ2

- Molecule 2 is a protein called mS51.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	DD	791	Total	C	N	O	S	0	0
			6523	4127	1184	1171	41		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DD	371	PRO	SER	conflict	UNP Q385L8
DD	599	ALA	VAL	conflict	UNP Q385L8

- Molecule 3 is a protein called mS56.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	DI	390	Total	C	N	O	S	0	0
			3182	2020	554	594	14		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DI	92	GLU	GLY	conflict	UNP Q587C2
DI	116	ASP	GLU	conflict	UNP Q587C2

- Molecule 4 is a protein called mS59.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DL	140	Total	C	N	O	S	0	0
			1134	718	208	199	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DL	274	THR	ALA	conflict	UNP Q38BS2

- Molecule 5 is a protein called mS60.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	DM	294	Total	C	N	O	S	0	0
			2430	1533	459	426	12		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DM	69	PHE	TYR	conflict	UNP Q57XL2
DM	97	ASN	SER	conflict	UNP Q57XL2
DM	138	SER	PRO	conflict	UNP Q57XL2
DM	173	ALA	THR	conflict	UNP Q57XL2
DM	206	ALA	THR	conflict	UNP Q57XL2

- Molecule 6 is a protein called mS61.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	DN	257	Total	C	N	O	S	0	0
			2091	1331	379	371	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DN	51	GLY	SER	conflict	UNP Q38D60

- Molecule 7 is a protein called mS62.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	DO	222	Total	C	N	O	S	0	0
			1804	1127	327	340	10		

- Molecule 8 is a protein called mS63.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	DP	207	Total	C	N	O	S	0	0
			1760	1132	312	307	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DP	3	HIS	ARG	conflict	UNP Q38F25

- Molecule 9 is a protein called mS64.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	DQ	256	Total	C	N	O	S	0	0
			2061	1293	389	370	9		

- Molecule 10 is a protein called mS65.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	DR	251	Total	C	N	O	S	0	0
			2025	1304	369	342	10		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DR	65	GLY	SER	conflict	UNP Q57UA2
DR	94	GLY	GLU	conflict	UNP Q57UA2
DR	128	PRO	SER	conflict	UNP Q57UA2
DR	229	ARG	GLN	conflict	UNP Q57UA2

- Molecule 11 is a protein called mS66.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	DS	238	Total	C	N	O	S	0	0
			1904	1185	356	348	15		

- Molecule 12 is a protein called mS68.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	DU	213	Total	C	N	O	S	0	0
			1754	1103	310	335	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DU	119	ILE	LEU	conflict	UNP Q582T9
DU	152	ILE	VAL	conflict	UNP Q582T9

- Molecule 13 is a protein called mS73.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	DZ	82	Total	C	N	O	S	0	0
			697	457	113	123	4		

- Molecule 14 is a protein called mS74.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Da	55	Total	C	N	O	S	0	0
			501	315	109	74	3		

- Molecule 15 is a protein called mS55m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CE	417	Total	C	N	O	S	0	0
			3399	2151	632	600	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	341	ARG	LYS	conflict	UNP Q38AX6

- Molecule 16 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CF	159	Total	C	N	O	S	0	0
			1292	821	228	237	6		

- Molecule 17 is a protein called uS8m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CH	273	Total	C	N	O	S	0	0
			2228	1387	432	398	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CH	74	ASN	SER	conflict	UNP Q388R7

- Molecule 18 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CI	202	Total	C	N	O	S	0	0
			1632	1035	281	309	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CI	370	ALA	VAL	conflict	UNP Q57W62

- Molecule 19 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CK	241	Total	C	N	O	S	0	0
			1980	1234	368	363	15		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CK	3	ARG	GLN	conflict	UNP Q389T7
CK	138	UNK	ILE	conflict	UNP Q389T7

- Molecule 20 is a protein called uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CL	87	Total	C	N	O	S	0	0
			733	503	113	107	10		

- Molecule 21 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CO	361	Total	C	N	O	S	0	0
			3003	1907	560	520	16		

- Molecule 22 is a protein called bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CP	180	Total	C	N	O	S	0	0
			1489	956	274	250	9		

- Molecule 23 is a protein called uS17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CQ	190	Total	C	N	O	S	0	0
			1584	1015	302	259	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CQ	138	ALA	VAL	conflict	UNP Q38DP8

- Molecule 24 is a protein called bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	CR	314	Total	C	N	O	S	0	0
			2567	1623	471	465	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CR	8	ILE	VAL	conflict	UNP Q38AS2

- Molecule 25 is a protein called uS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	CU	184	Total	C	N	O	S	0	0
			1538	965	307	254	12		

- Molecule 26 is a protein called mt-IF-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	CZ	151	Total	C	N	O	S	0	0
			1212	759	231	215	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CZ	6	SER	GLY	conflict	UNP Q57WU2
CZ	30	THR	ILE	conflict	UNP Q57WU2
CZ	172	THR	ALA	conflict	UNP Q57WU2

- Molecule 27 is a protein called mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ca	592	Total	C	N	O	S	0	0
			5004	3201	898	882	23		

- Molecule 28 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Cb	252	Total	C	N	O	S	0	0
			2056	1300	368	380	8		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cb	244	SER	ASN	conflict	UNP Q57VB2
Cb	?	-	GLU	deletion	UNP Q57VB2
Cb	312	CYS	-	expression tag	UNP Q57VB2
Cb	313	SER	-	expression tag	UNP Q57VB2
Cb	314	ARG	-	expression tag	UNP Q57VB2
Cb	315	ASP	-	expression tag	UNP Q57VB2
Cb	316	GLY	-	expression tag	UNP Q57VB2
Cb	317	PHE	-	expression tag	UNP Q57VB2
Cb	318	ALA	-	expression tag	UNP Q57VB2
Cb	319	LEU	-	expression tag	UNP Q57VB2
Cb	320	MET	-	expression tag	UNP Q57VB2
Cb	321	LYS	-	expression tag	UNP Q57VB2
Cb	322	ALA	-	expression tag	UNP Q57VB2
Cb	323	ASN	-	expression tag	UNP Q57VB2
Cb	324	LYS	-	expression tag	UNP Q57VB2

- Molecule 29 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Cd	291	Total	C	N	O	S	0	0
			2389	1491	442	446	10		

- Molecule 30 is a protein called mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Cj	226	Total	C	N	O	S	0	0
			1792	1138	310	340	4		

- Molecule 31 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Cm	196	Total	C	N	O	S	0	0
			1577	975	304	289	9		

- Molecule 32 is a protein called mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Cn	110	Total	C	N	O	S	0	0
			912	585	181	143	3		

- Molecule 33 is a protein called mS41.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Cp	175	Total	C	N	O	S	0	0
			1483	937	268	273	5		

- Molecule 34 is a protein called mS42.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Cq	252	Total	C	N	O	S	0	0
			2005	1285	342	369	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cq	48	THR	ALA	conflict	UNP Q586A1
Cq	167	MET	VAL	conflict	UNP Q586A1

- Molecule 35 is a protein called mS43.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Cr	257	Total	C	N	O	S	0	0
			1999	1261	368	356	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cr	351	LYS	GLU	conflict	UNP Q585I1

- Molecule 36 is a protein called mS47.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Cv	1059	Total	C	N	O	S	0	0
			8557	5387	1535	1596	39		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cv	16	CYS	PRO	conflict	UNP Q383R4
Cv	718	THR	ALA	conflict	UNP Q383R4
Cv	1179	GLU	GLY	conflict	UNP Q383R4

- Molecule 37 is a RNA chain called 9S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	CA	478	Total	C	N	O	P	0	0
			10092	4542	1705	3367	478		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CA	298	U	C	conflict	GB 343546
CA	614	U	-	insertion	GB 343546
CA	615	U	-	insertion	GB 343546
CA	616	U	-	insertion	GB 343546
CA	617	U	-	insertion	GB 343546
CA	618	U	-	insertion	GB 343546
CA	619	U	-	insertion	GB 343546
CA	620	U	-	insertion	GB 343546
CA	621	U	-	insertion	GB 343546

- Molecule 38 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	UQ	32	Total	C	N	O	0	0
			192	128	32	32		

- Molecule 39 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	UR	8	Total	C	N	O	0	0
			48	32	8	8		

- Molecule 40 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	US	54	Total	C	N	O	0	0
			324	216	54	54		

- Molecule 41 is a protein called Unknown protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	UT	44	Total	C	N	O	0	0
			264	176	44	44		

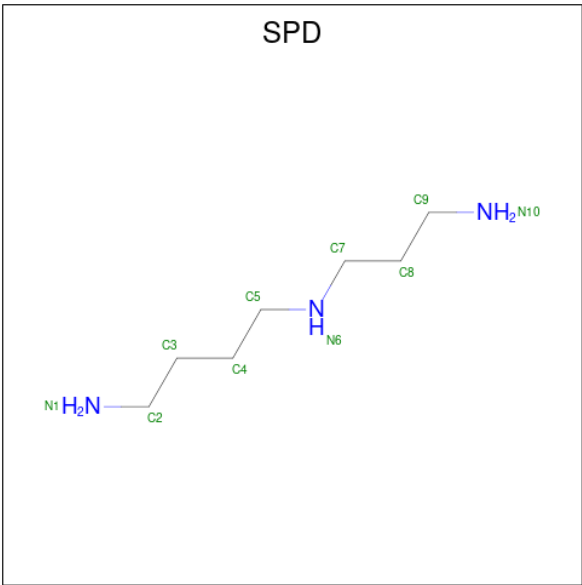
- Molecule 42 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
42	DA	1	Total	Zn	0
			1	1	
42	DS	2	Total	Zn	0
			2	2	
42	Cr	1	Total	Zn	0
			1	1	

- Molecule 43 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

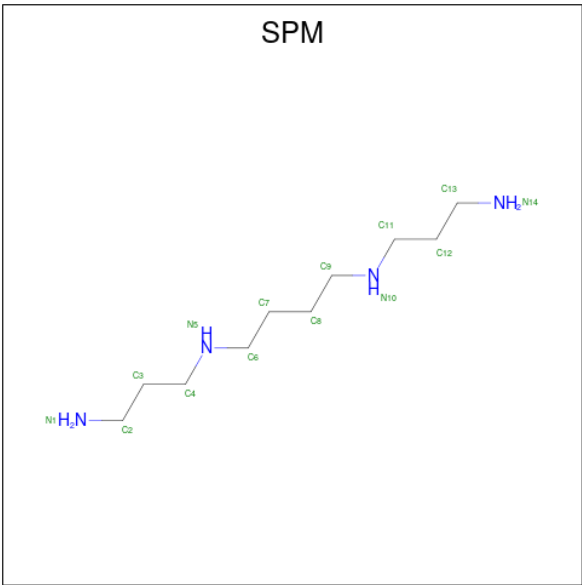
Mol	Chain	Residues	Atoms		AltConf
43	CO	1	Total	Mg	0
			1	1	
43	CQ	1	Total	Mg	0
			1	1	
43	Ca	1	Total	Mg	0
			1	1	
43	Cv	1	Total	Mg	0
			1	1	
43	CA	32	Total	Mg	0
			32	32	

- Molecule 44 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
44	CA	1	Total	C	N	0
			10	7	3	
44	CA	1	Total	C	N	0
			10	7	3	

- Molecule 45 is SPERMINE (CCD ID: SPM) (formula: C₁₀H₂₆N₄).



Mol	Chain	Residues	Atoms			AltConf
45	CA	1	Total	C	N	0
			14	10	4	

LYS	GLY	Q1562	ARG	SER
SER	ASP	R1566	SER	GLN
ARG	ARG	N1570	VAL	GLN
GLU	ARG	N1580	GLN	CYS
LEU	ASN	L1583	VAL	VAL
SER	THR	Q1584	VAL	HIS
ARG	THR	L1587	VAL	SER
LEU	ALA	K1588	LEU	ARG
LEU	ALA	L1589	ALA	GLY
GLU	ALA	R1590	GLY	GLY
ARG	ARG	R1591	GLY	GLU
GLU	ASN	G1592	GLU	GLU
MET	ASN	A1593	THR	VAL
GLY	GLN	V1596	GLY	SER
LEU	GLN	E1597	GLY	PRO
THR	GLN	T1598	GLY	ARG
THR	ARG	F1599	ALA	ARG
GLY	ARG	N1600	GLY	VAL
ILE	SER	R1601	GLU	THR
ALA	ALA	L1492	GLN	SER
ALA	ALA	K1493	LEU	ARG
ILE	LEU	L1494	LEU	GLY
THR	ALA	L1498	GLN	ARG
ARG	ARG	F1502	GLY	ASP
GLY	GLY	D1505	ASN	THR
LEU	GLN	N1506	LEU	LYS
ALA	GLN	V1507	LEU	LEU
ASP	GLY	E1510	ASP	VAL
ASP	SER	R1517	THR	PRO
PHE	ALA	R1524	LYS	LYS
ALA	SER	A1525	THR	THR
VAL	GLY	G1526	PHE	THR
PRO	ARG	A1530	GLY	SER
VAL	VAL	P1531	GLY	GLY
SER	TRP	F1535	THR	THR
LEU	Q1368	R1654	ALA	ALA
ILE	L1381	R1655	LYS	LYS
LEU	L1381	S1542	ASN	ASN
SER	R1384	L1543	THR	THR
TRP	N1385	N1544	GLY	GLY
ASP	D1386	E1552	ASN	ASN
GLY	N1399	V1553	GLN	GLN
GLY	R1404	V1556	HIS	ARG
SER	L1414	T1557	ASN	ARG
GLY	P1415	I1664	GLN	GLY
GLY	V1416	G1667	PRO	PRO
SER	F1417		LYS	LYS

• Molecule 2: mS51

Chain DD:  68% 26%

MET	D107	Y215	A344	R448	R595	R694	R794
LEU	T108	E221	P345	L449	V602	D700	F797
ARG	E115	E226	Y345	L452	R605	E701	F798
THR	R118	T227	E347	N453	R606	G703	D799
VAL	Y119	K228	K350	T454	Q607	D704	Q803
VAL	Q122	H229	S351	L457	D608	Q707	Y812
GLY	Y124	H230	V352	F465	D609	R708	
HIS	R123	N233	H354	G469	D611	R709	
	S12	N237	S355	K470	M612	G713	
	G13	L242	P356	E471	M613	P721	
	K14	E243	R357	A475	L616	GLY	
	A15	P244	L359	R479	A620	TYR	
	A17	G245	N361	R486	L621	ALA	
	F20	V247	L366	R497	M622	PRO	
	R21	D248	A367	R497	M623	ALA	
	D22	K250	L368	R504	A625	PRO	
	P23	S24	P371	F518	R626	MET	
	S24	V255	E377	N521	G627	GLY	
	R25	P256	M378	N527	N628	GLY	
	L26	L284	Q379	T527	A629	HIS	
	K27	K271	Q387	R631	P630	GLN	
	M28	K272	V390	L635	L635	GLY	
	L37	K273	H391	R636	R637	GLY	
	R38	D274	S392	R642	R642	GLY	
	M42	R164	K393	L646	L646	GLY	
	Y46	M165	E395	R647	R647	GLY	
	G47	N171	P172	T538	R651	GLY	
	M48	P173	R398	R541	R654	GLY	
	K52	Y177	H408	L543	L656	GLY	
	Q63	M181	R414	V546	E655	GLY	
	S70	E189	T417	V547	E665	GLY	
	Q79	L190	E418	A419	R668	GLY	
	T83	M192	F420	F421	H669	GLY	
	R84	A193	T424	T575	N679	GLY	
	M87	R194	L431	M576	D883	GLY	
	Y88	K198	L323	K577	Y684	GLY	
	Y91	I199	E201	E439	V685	GLY	
	N92	M200	P326	R440	A686	GLY	
	P93	E201	R339	L441	H687	GLY	
	K94	C208	R340	F442	F691	GLY	
	R95	I212	C213	A443	M692	GLY	
	T99	A214	W343	S594	R786	GLY	
	A106				R787	GLY	

• Molecule 3: mS56

Response	Percentage
Used	70%
Not used	22%
Don't know	•
Refused	•



Category	Percentage
Very good	34%
Good	11%
Not good	54%
Very bad	1%



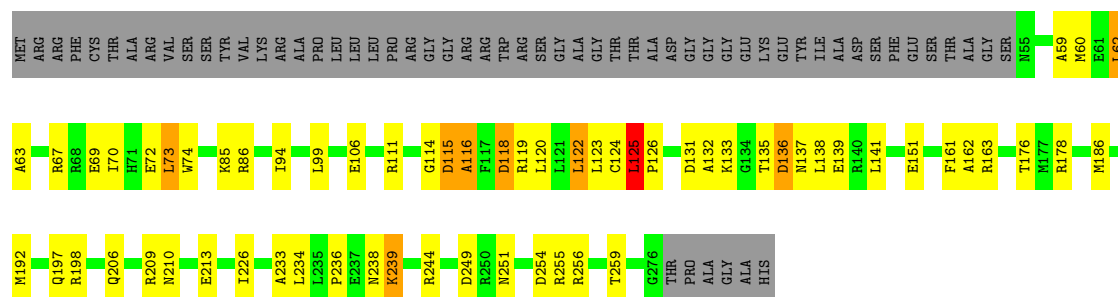
Response	Percentage
Yes, the U.S. should take action to protect the environment	65%
No, the U.S. should not take action to protect the environment	30%
Don't know	5%



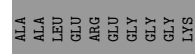
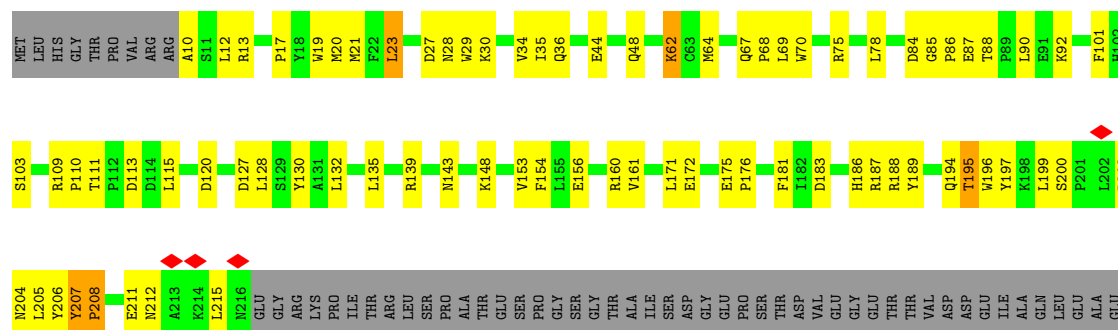
Age Group	Percentage
18-24	53%
25-34	29%
35-44	6%
45-54	12%



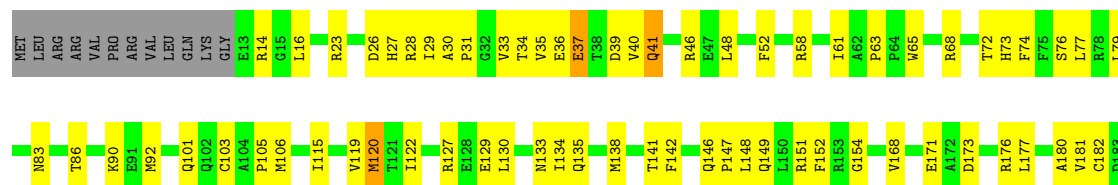
- Molecule 7: mS62

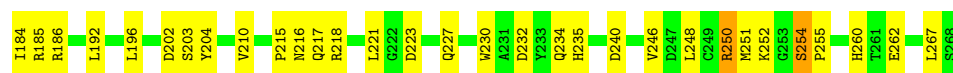


- Molecule 8: mS63



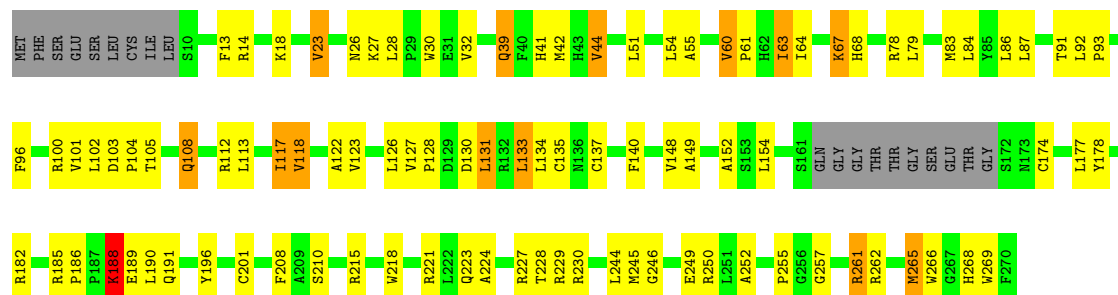
- Molecule 9: mS64





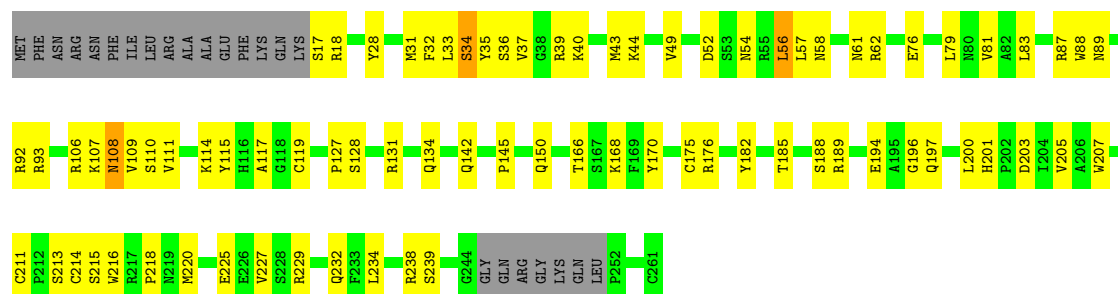
• Molecule 10: mS65

Chain DR: 57% 30% 5% 7%



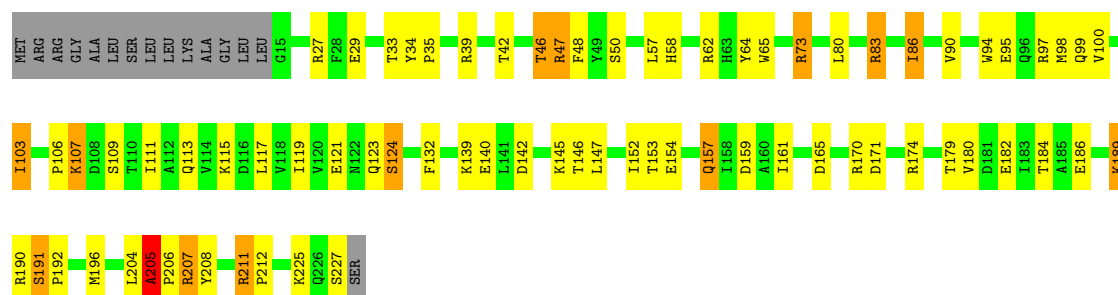
• Molecule 11: mS66

Chain DS: 61% 29% 9%



• Molecule 12: mS68

Chain DU: 61% 27% 6% 7%

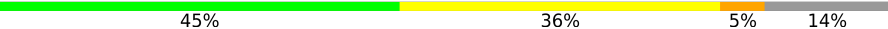


• Molecule 13: mS73

Chain DZ: 64% 20% 13%



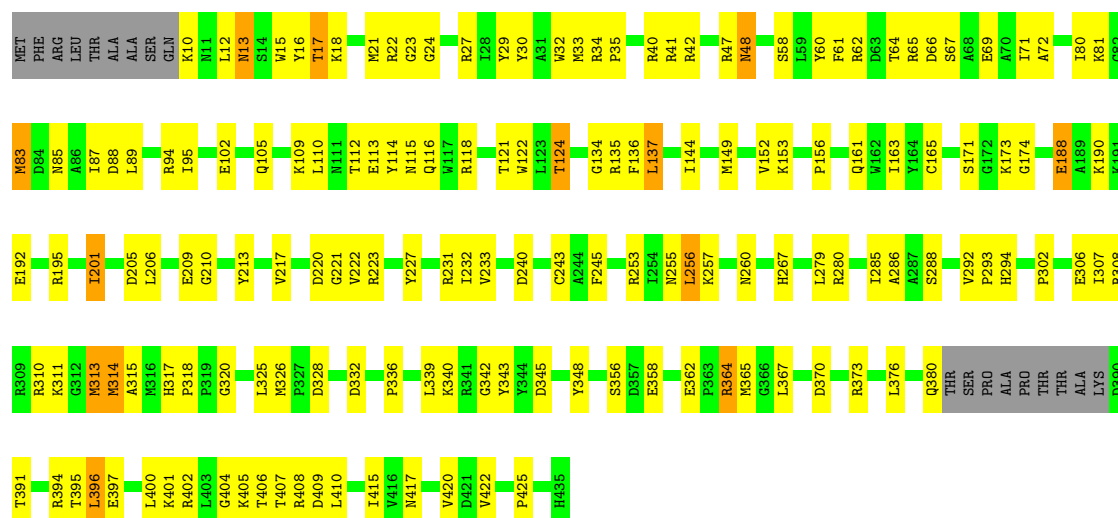
• Molecule 14: mS74

Chain Da:  45% 36% 5% 14%



• Molecule 15: mS55m

Chain CE:  59% 34%



• Molecule 16: bS6m

Chain CF:  74% 22%



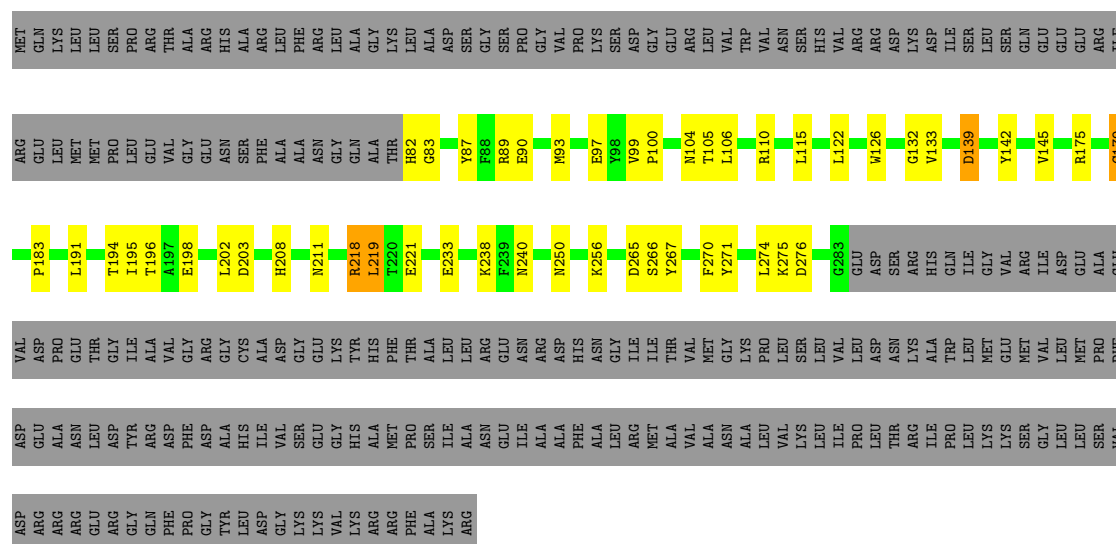
• Molecule 17: uS8m

Chain CH:  68% 25%



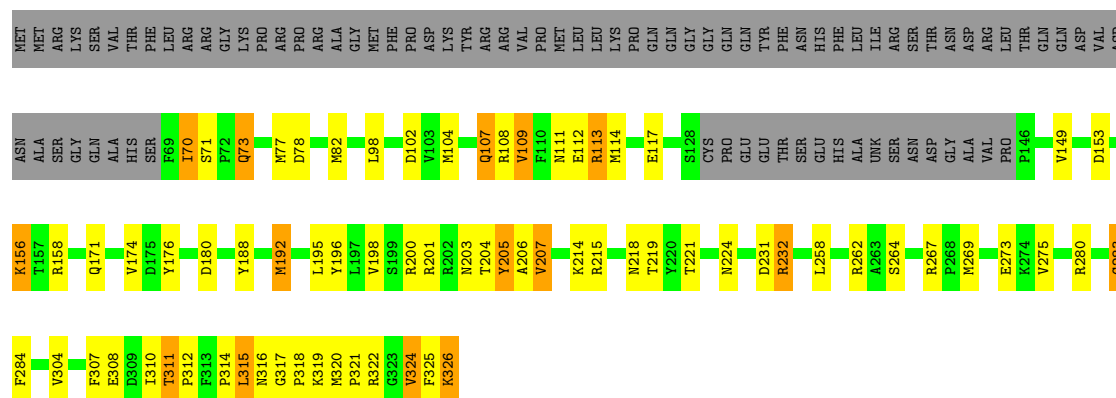
• Molecule 18: uS9m

Chain CI:  35% 10% 54%



• Molecule 19: uS11m

Chain CK:  52% 18% 5% 26%



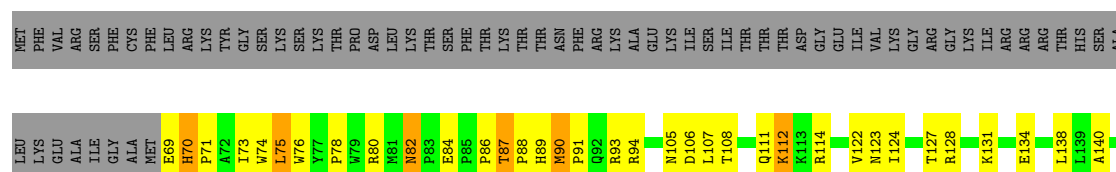
• Molecule 20: uS12m

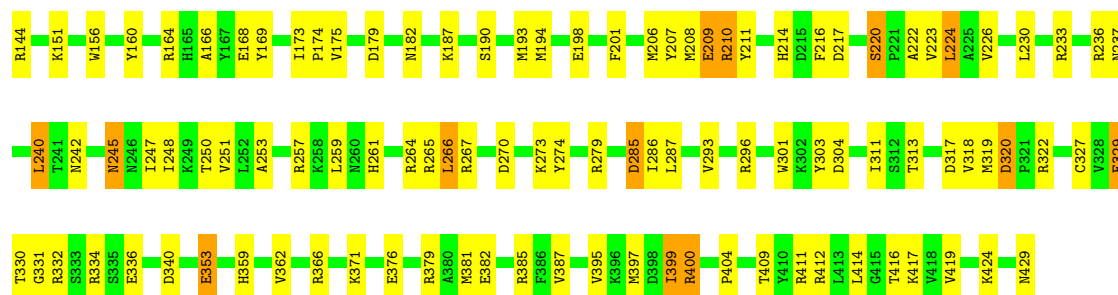
Chain CL:  59% 37% 5%



• Molecule 21: uS15m

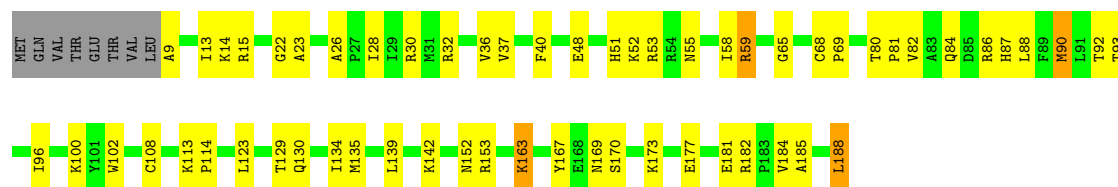
Chain CO:  52% 28% 16%





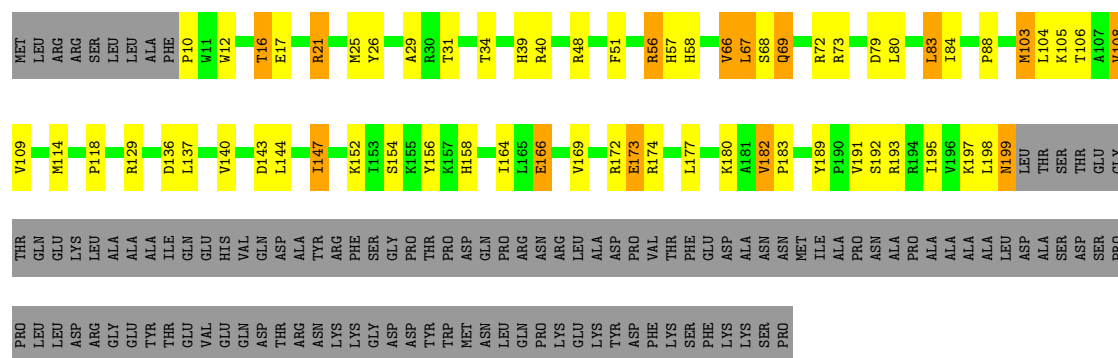
• Molecule 22: bS16m

Chain CP: 64% 29%



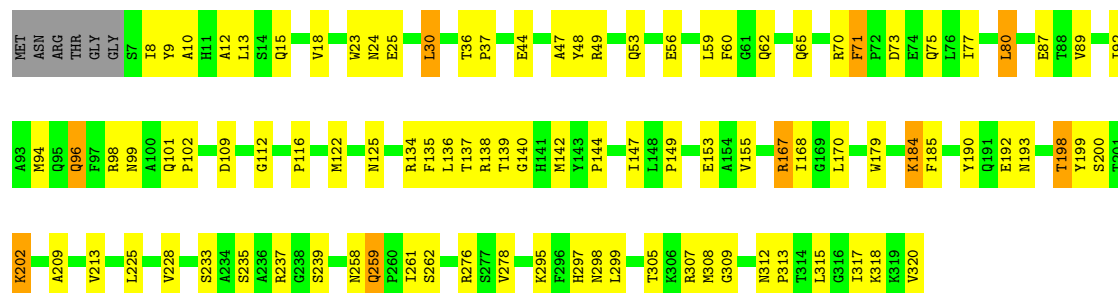
• Molecule 23: uS17m

Chain CQ: 41% 17% 5% 38%



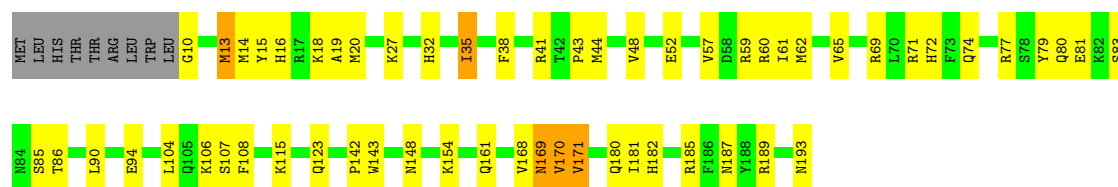
• Molecule 24: bS18m

Chain CR: 68% 28%



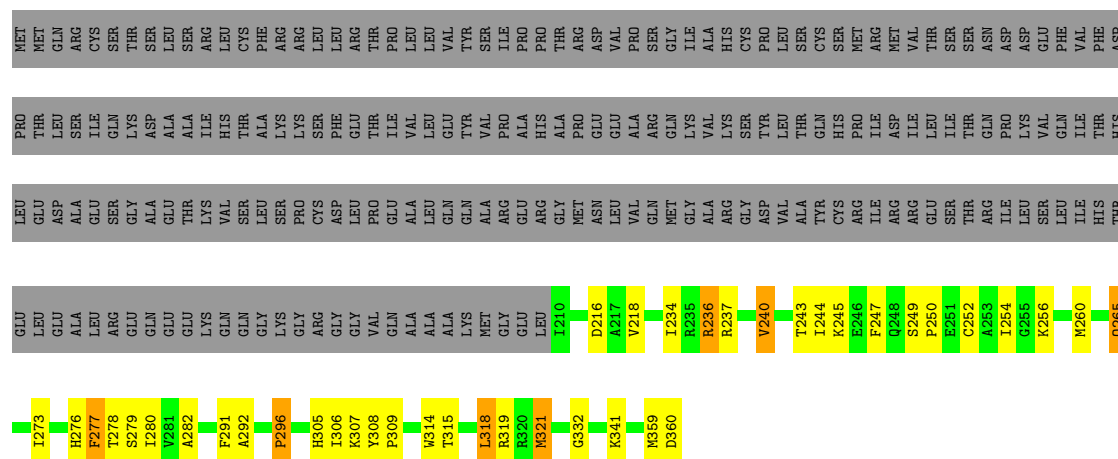
• Molecule 25: uS21m

Chain CU:  65% 27% 5%



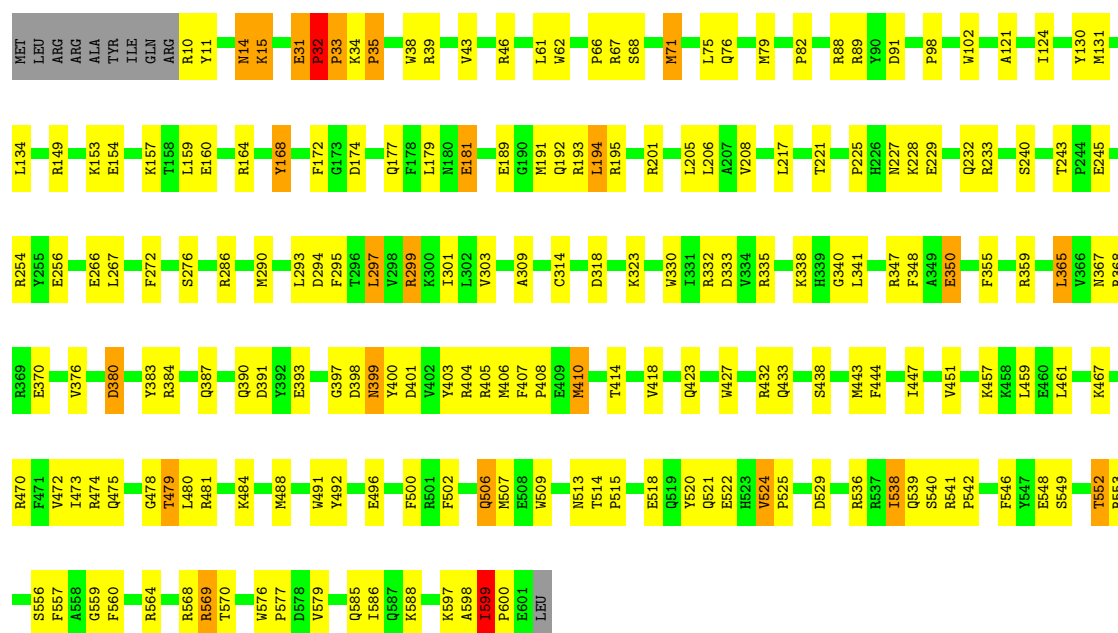
• Molecule 26: mt-IF-3

Chain CZ:  31% 9% 58%



• Molecule 27: mS22

Chain Ca:  66% 28% 5%



• Molecule 28: mS23

Device Type	Percentage
Smartphones	56%
Tablets	20%
Feature phones	2%
Other devices	22%



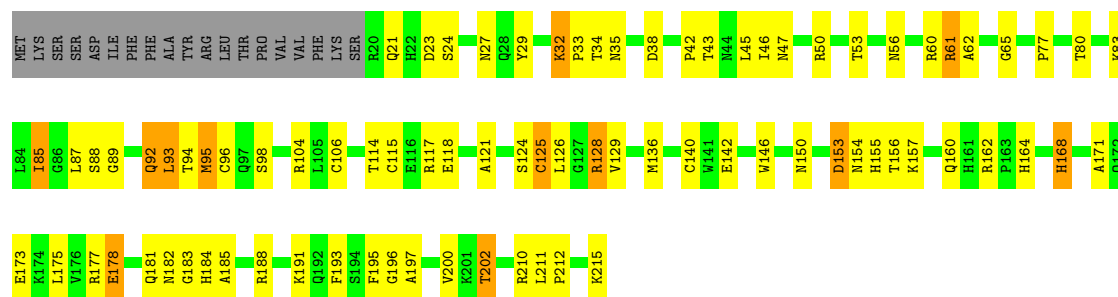
Response	Percentage
Yes	48%
No	15%
Don't know	34%



Category	Percentage
Very good	65%
Good	19%
Not good	12%
Very bad	4%

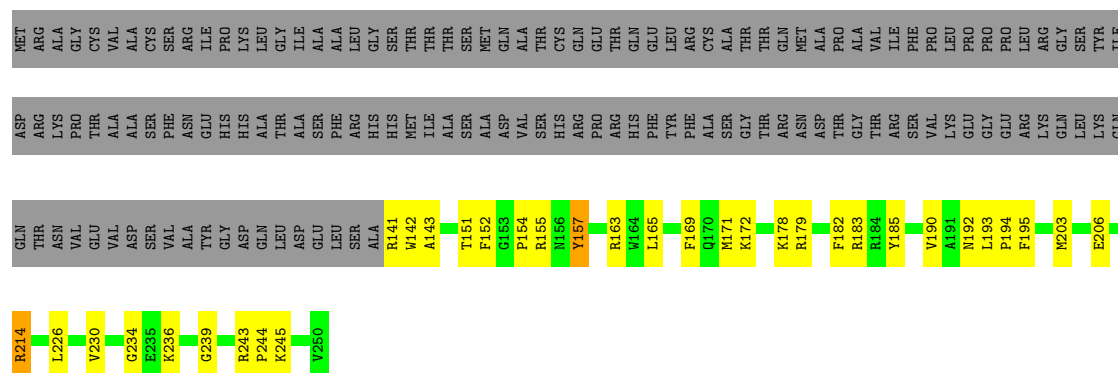


Category	Percentage
Very bad	53%
Bad	33%
Good	6%
Very good	9%



• Molecule 32: mS38

Chain Cn: 30% 13% 56%



• Molecule 33: mS41

Chain Cp: 53% 39% 6%

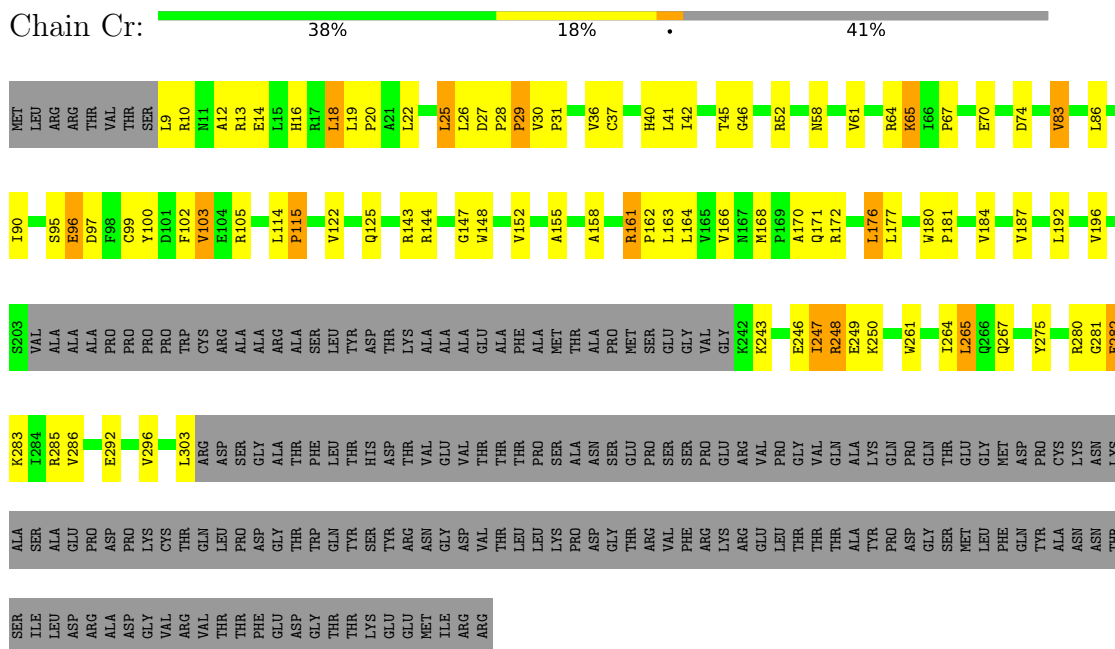


• Molecule 34: mS42

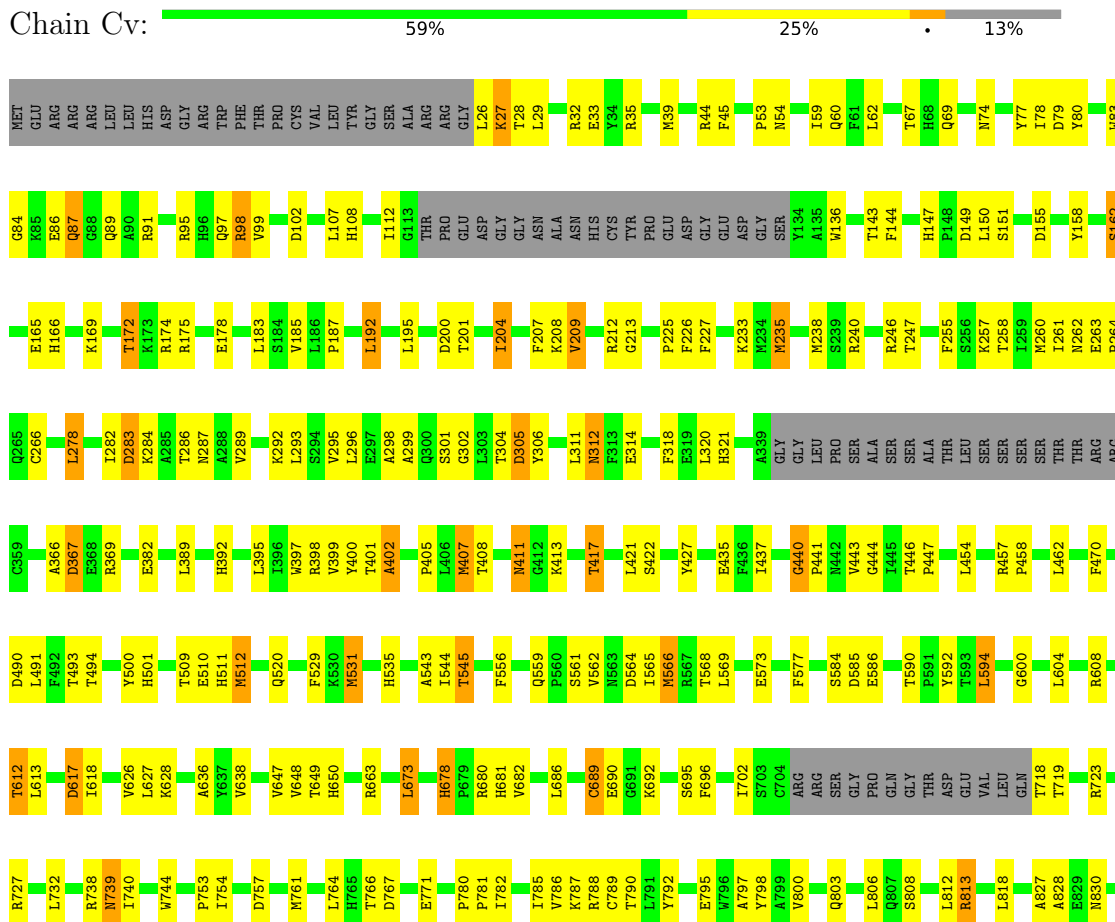
Chain Cq: 68% 25% 7%

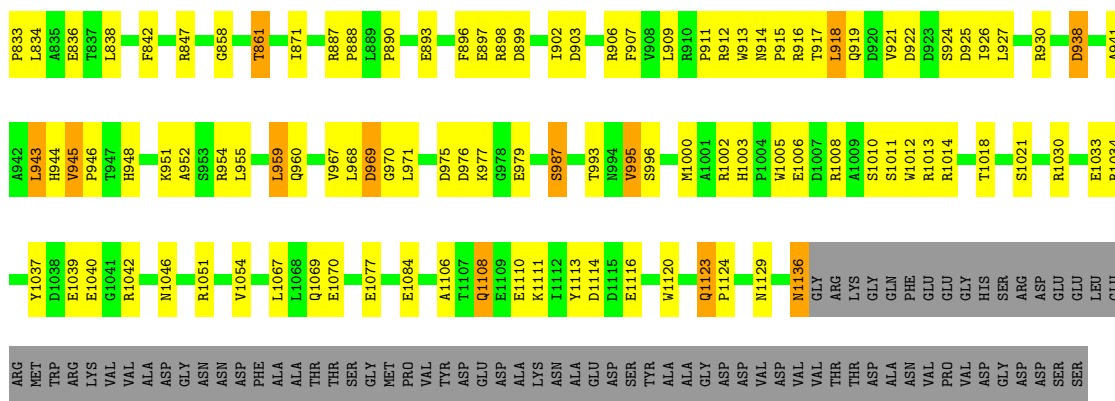


- Molecule 35: mS43



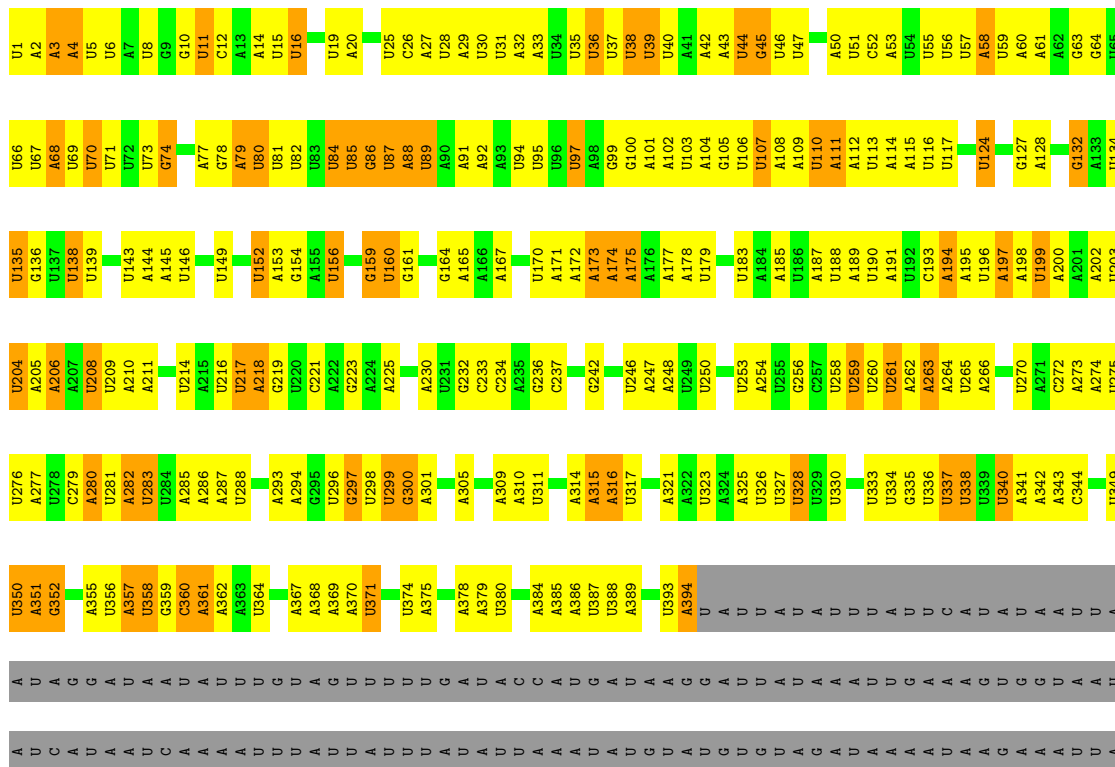
- Molecule 36: mS47





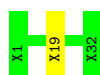
• Molecule 37: 9S rRNA

Chain CA: 29% 36% 13% 23%

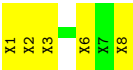
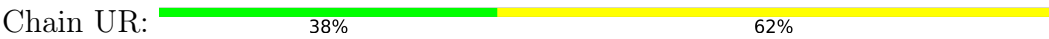


• Molecule 38: Unknown protein

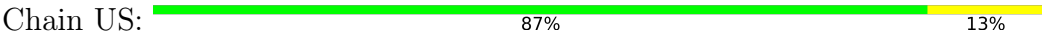
Chain UQ: 97%



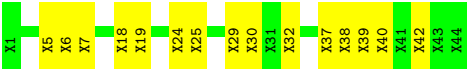
• Molecule 39: Unknown protein



● Molecule 40: Unknown protein



● Molecule 41: Unknown protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31911	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.514	Depositor
Minimum map value	-0.265	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.0115	Depositor
Map size ($\text{\AA}$)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.39, 1.39, 1.39	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	DA	0.48	4/11769 (0.0%)	0.88	29/15925 (0.2%)
2	DD	0.48	0/6710	0.91	11/9087 (0.1%)
3	DI	0.46	0/3248	0.88	3/4401 (0.1%)
4	DL	0.50	0/1160	0.90	6/1560 (0.4%)
5	DM	0.49	0/2488	0.88	7/3362 (0.2%)
6	DN	0.53	0/2148	0.99	8/2916 (0.3%)
7	DO	0.46	0/1840	0.89	5/2482 (0.2%)
8	DP	0.57	0/1813	0.89	2/2457 (0.1%)
9	DQ	0.47	0/2111	0.92	0/2863
10	DR	0.48	0/2090	0.92	4/2849 (0.1%)
11	DS	0.43	0/1950	0.82	0/2633
12	DU	0.46	0/1799	0.86	4/2438 (0.2%)
13	DZ	0.45	0/725	0.87	2/984 (0.2%)
14	Da	0.45	0/520	0.83	0/694
15	CE	0.53	0/3484	0.90	4/4708 (0.1%)
16	CF	0.46	0/1319	0.81	0/1783
17	CH	0.52	0/2276	0.95	6/3071 (0.2%)
18	CI	0.44	0/1670	0.77	0/2260
19	CK	0.43	0/2024	0.88	1/2715 (0.0%)
20	CL	0.46	0/759	0.87	2/1026 (0.2%)
21	CO	0.48	0/3085	0.89	2/4165 (0.0%)
22	CP	0.55	0/1533	0.93	5/2074 (0.2%)
23	CQ	0.56	0/1631	0.98	4/2203 (0.2%)
24	CR	0.49	0/2640	0.88	3/3572 (0.1%)
25	CU	0.45	0/1576	0.80	0/2115
26	CZ	0.51	0/1237	0.88	1/1659 (0.1%)
27	Ca	0.49	0/5159	0.90	13/6980 (0.2%)
28	Cb	0.49	0/2105	0.88	0/2842
29	Cd	0.50	0/2446	0.81	0/3299
30	Cj	0.44	0/1842	0.87	2/2511 (0.1%)
31	Cm	0.53	0/1616	0.97	5/2175 (0.2%)
32	Cn	0.49	0/934	0.91	3/1248 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Cp	0.44	0/1528	0.85	3/2072 (0.1%)
34	Cq	0.48	0/2066	0.85	3/2815 (0.1%)
35	Cr	0.45	0/2038	0.90	7/2759 (0.3%)
36	Cv	0.46	0/8780	0.90	15/11901 (0.1%)
37	CA	0.28	0/11286	0.45	0/17548
All	All	0.47	4/103405 (0.0%)	0.85	160/142152 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	DA	0	1
2	DD	0	2
6	DN	0	2
7	DO	0	2
10	DR	0	1
17	CH	0	1
27	Ca	0	1
30	Cj	0	1
36	Cv	0	2
All	All	0	13

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	DA	323	HIS	CG-CD2	10.30	1.47	1.35
1	DA	529	ILE	C-O	5.88	1.30	1.24
1	DA	323	HIS	CD2-NE2	-5.66	1.31	1.37
1	DA	323	HIS	CB-CG	-5.29	1.42	1.50

All (160) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	CK	283	GLY	N-CA-C	14.42	132.53	114.37
2	DD	255	VAL	CA-C-N	12.41	135.36	119.84
2	DD	255	VAL	C-N-CA	12.41	135.36	119.84
27	Ca	32	PRO	N-CA-CB	8.14	110.98	103.08
7	DO	125	LEU	CA-C-N	-7.86	110.57	120.23
7	DO	125	LEU	C-N-CA	-7.86	110.57	120.23
1	DA	311	THR	CA-C-N	7.84	127.48	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DA	311	THR	C-N-CA	7.84	127.48	119.56
35	Cr	28	PRO	N-CA-CB	7.76	110.60	103.08
10	DR	257	GLY	N-CA-C	-7.63	103.33	115.08
27	Ca	35	PRO	N-CA-CB	7.51	111.13	103.25
27	Ca	33	PRO	N-CA-CB	7.37	110.99	103.25
17	CH	17	PRO	CA-C-N	7.35	127.39	119.90
17	CH	17	PRO	C-N-CA	7.35	127.39	119.90
31	Cm	43	THR	N-CA-C	-7.32	104.15	113.23
36	Cv	1123	GLN	CA-C-N	7.24	127.58	119.32
36	Cv	1123	GLN	C-N-CA	7.24	127.58	119.32
6	DN	225	GLY	CA-C-N	7.24	127.40	120.31
6	DN	225	GLY	C-N-CA	7.24	127.40	120.31
31	Cm	32	LYS	CA-C-N	7.02	128.61	119.84
31	Cm	32	LYS	C-N-CA	7.02	128.61	119.84
4	DL	229	THR	CA-C-N	7.01	126.49	118.85
4	DL	229	THR	C-N-CA	7.01	126.49	118.85
36	Cv	545	THR	CA-C-N	6.93	128.50	119.84
36	Cv	545	THR	C-N-CA	6.93	128.50	119.84
17	CH	16	VAL	CA-C-N	-6.88	113.29	120.38
17	CH	16	VAL	C-N-CA	-6.88	113.29	120.38
35	Cr	31	PRO	N-CA-CB	6.83	110.43	103.25
36	Cv	213	GLY	N-CA-C	-6.69	101.72	110.29
2	DD	355	SER	CA-C-N	6.63	126.32	119.82
2	DD	355	SER	C-N-CA	6.63	126.32	119.82
36	Cv	440	GLY	CA-C-N	-6.55	113.06	119.87
36	Cv	440	GLY	C-N-CA	-6.55	113.06	119.87
26	CZ	296	PRO	N-CA-CB	6.54	110.11	103.25
23	CQ	166	GLU	CA-C-N	-6.52	114.06	120.52
23	CQ	166	GLU	C-N-CA	-6.52	114.06	120.52
21	CO	320	ASP	CA-C-N	6.52	126.21	119.82
21	CO	320	ASP	C-N-CA	6.52	126.21	119.82
1	DA	1592	GLY	N-CA-C	-6.41	107.37	115.31
1	DA	224	VAL	N-CA-C	6.37	121.06	113.22
1	DA	1484	PRO	N-CA-CB	6.33	109.90	103.25
5	DM	122	LYS	CA-C-N	-6.25	112.56	119.19
5	DM	122	LYS	C-N-CA	-6.25	112.56	119.19
3	DI	66	ARG	N-CA-C	6.23	118.87	111.71
4	DL	132	ASN	CA-C-N	-6.20	115.38	121.65
4	DL	132	ASN	C-N-CA	-6.20	115.38	121.65
8	DP	207	TYR	C-N-CD	6.17	134.17	120.60
22	CP	182	ARG	CA-C-N	6.16	126.18	119.90
22	CP	182	ARG	C-N-CA	6.16	126.18	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	CL	79	SER	CA-C-N	6.14	126.11	120.21
20	CL	79	SER	C-N-CA	6.14	126.11	120.21
36	Cv	402	ALA	CA-C-N	6.14	125.36	118.97
36	Cv	402	ALA	C-N-CA	6.14	125.36	118.97
1	DA	1457	HIS	CA-C-N	6.14	125.76	119.56
1	DA	1457	HIS	C-N-CA	6.14	125.76	119.56
23	CQ	68	SER	N-CA-C	-6.12	105.46	113.17
1	DA	1134	ILE	N-CA-C	6.11	114.70	109.02
36	Cv	59	ILE	N-CA-C	6.06	117.99	112.29
27	Ca	340	GLY	N-CA-C	-6.04	102.16	111.64
7	DO	239	LYS	CA-C-N	6.04	125.66	119.56
7	DO	239	LYS	C-N-CA	6.04	125.66	119.56
15	CE	256	LEU	CB-CA-C	-6.03	109.04	117.23
35	Cr	29	PRO	N-CA-CB	6.02	109.57	103.25
31	Cm	34	THR	N-CA-C	5.95	117.63	111.03
30	Cj	38	MET	CA-C-N	5.89	125.43	119.19
30	Cj	38	MET	C-N-CA	5.89	125.43	119.19
27	Ca	168	TYR	CA-C-N	5.88	125.58	119.05
27	Ca	168	TYR	C-N-CA	5.88	125.58	119.05
27	Ca	31	GLU	CA-C-N	5.87	126.43	120.38
27	Ca	31	GLU	C-N-CA	5.87	126.43	120.38
2	DD	469	GLY	N-CA-C	-5.84	102.47	111.64
32	Cn	157	TYR	CA-C-N	-5.79	112.61	119.84
32	Cn	157	TYR	C-N-CA	-5.79	112.61	119.84
10	DR	92	LEU	CA-C-N	5.78	125.79	119.90
10	DR	92	LEU	C-N-CA	5.78	125.79	119.90
35	Cr	115	PRO	CA-C-N	5.77	125.14	118.85
35	Cr	115	PRO	C-N-CA	5.77	125.14	118.85
5	DM	2	GLU	N-CA-C	5.75	117.41	111.03
6	DN	130	ASN	CA-C-N	5.72	125.70	120.03
6	DN	130	ASN	C-N-CA	5.72	125.70	120.03
17	CH	125	LYS	CA-C-N	5.72	126.17	119.99
17	CH	125	LYS	C-N-CA	5.72	126.17	119.99
1	DA	949	ARG	CA-C-N	5.65	125.35	119.82
1	DA	949	ARG	C-N-CA	5.65	125.35	119.82
27	Ca	524	VAL	CA-C-N	5.64	125.66	119.90
27	Ca	524	VAL	C-N-CA	5.64	125.66	119.90
1	DA	732	ALA	CB-CA-C	-5.61	110.12	116.63
22	CP	65	GLY	N-CA-C	5.59	119.16	110.88
1	DA	883	ASN	CA-C-N	5.58	125.20	119.56
1	DA	883	ASN	C-N-CA	5.58	125.20	119.56
34	Cq	146	PRO	CA-C-N	5.54	126.08	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	Cq	146	PRO	C-N-CA	5.54	126.08	120.38
5	DM	284	ARG	CA-C-N	-5.53	113.56	119.98
5	DM	284	ARG	C-N-CA	-5.53	113.56	119.98
24	CR	80	LEU	N-CA-C	5.53	117.74	111.11
2	DD	255	VAL	N-CA-C	5.51	120.77	108.88
36	Cv	1084	GLU	CA-C-N	5.49	124.95	119.24
36	Cv	1084	GLU	C-N-CA	5.49	124.95	119.24
12	DU	205	ALA	CA-C-N	-5.48	112.99	119.84
12	DU	205	ALA	C-N-CA	-5.48	112.99	119.84
24	CR	71	PHE	CA-C-N	5.48	125.30	119.28
24	CR	71	PHE	C-N-CA	5.48	125.30	119.28
36	Cv	1021	SER	N-CA-C	-5.47	105.23	111.14
5	DM	208	HIS	N-CA-C	5.47	120.06	113.17
2	DD	752	PHE	CA-C-N	5.46	126.67	119.84
2	DD	752	PHE	C-N-CA	5.46	126.67	119.84
31	Cm	65	GLY	N-CA-C	-5.46	107.71	115.30
1	DA	952	ASN	N-CA-C	5.45	118.40	111.69
1	DA	1526	GLY	CA-C-N	5.45	125.06	119.56
1	DA	1526	GLY	C-N-CA	5.45	125.06	119.56
2	DD	713	GLY	CA-C-N	5.41	125.02	119.56
2	DD	713	GLY	C-N-CA	5.41	125.02	119.56
23	CQ	156	TYR	N-CA-C	5.39	119.96	113.17
33	Cp	53	VAL	CA-C-N	5.38	124.71	118.85
33	Cp	53	VAL	C-N-CA	5.38	124.71	118.85
1	DA	108	TYR	N-CA-C	5.37	116.99	111.03
1	DA	254	PHE	CA-C-N	-5.37	115.02	123.13
1	DA	254	PHE	C-N-CA	-5.37	115.02	123.13
4	DL	209	ARG	CA-C-N	5.37	125.44	119.32
4	DL	209	ARG	C-N-CA	5.37	125.44	119.32
3	DI	64	GLU	N-CA-C	5.36	116.98	111.03
27	Ca	438	SER	N-CA-C	5.35	115.35	108.34
2	DD	683	ASP	N-CA-C	5.34	118.26	111.69
10	DR	188	LYS	N-CA-C	-5.29	105.03	112.12
33	Cp	48	PRO	O-C-N	5.28	123.63	121.15
5	DM	164	ILE	N-CA-C	5.26	113.63	107.89
22	CP	185	ALA	N-CA-C	5.26	120.71	113.77
6	DN	276	GLN	N-CA-C	5.25	115.99	108.74
12	DU	124	SER	CA-C-N	5.25	125.33	119.87
12	DU	124	SER	C-N-CA	5.25	125.33	119.87
1	DA	1004	GLY	N-CA-C	-5.24	106.48	115.08
1	DA	323	HIS	ND1-CG-CD2	-5.24	100.86	106.10
22	CP	169	ASN	N-CA-C	5.24	117.94	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	Cr	83	VAL	CB-CA-C	-5.22	108.74	113.70
35	Cr	170	ALA	CB-CA-C	-5.22	110.53	116.54
1	DA	1088	ALA	N-CA-C	-5.21	103.73	110.19
32	Cn	234	GLY	N-CA-C	5.21	118.94	112.64
34	Cq	227	ILE	N-CA-C	5.21	115.42	110.42
15	CE	255	ASN	N-CA-C	5.20	118.89	111.92
3	DI	331	VAL	N-CA-C	5.19	115.30	110.42
36	Cv	1116	GLU	N-CA-C	5.18	119.76	113.38
27	Ca	254	ARG	N-CA-C	5.17	117.66	111.71
27	Ca	599	ILE	N-CA-C	5.17	120.04	108.88
1	DA	947	GLY	CA-C-N	5.15	124.91	119.76
1	DA	947	GLY	C-N-CA	5.15	124.91	119.76
13	DZ	40	ILE	CA-C-N	5.15	124.76	119.56
13	DZ	40	ILE	C-N-CA	5.15	124.76	119.56
6	DN	40	ASP	CA-C-N	-5.13	113.43	119.84
6	DN	40	ASP	C-N-CA	-5.13	113.43	119.84
8	DP	85	GLY	N-CA-C	5.11	122.77	112.34
1	DA	149	GLY	N-CA-C	5.10	120.76	114.69
1	DA	890	VAL	CA-C-N	5.09	125.25	119.90
1	DA	890	VAL	C-N-CA	5.09	125.25	119.90
36	Cv	995	VAL	N-CA-C	5.09	119.92	109.34
15	CE	210	GLY	CA-C-N	5.08	124.84	119.76
15	CE	210	GLY	C-N-CA	5.08	124.84	119.76
7	DO	116	ALA	N-CA-C	-5.05	106.62	112.89
6	DN	269	LEU	N-CA-C	-5.04	106.91	113.16
1	DA	1181	THR	N-CA-C	5.02	117.14	111.11
1	DA	774	GLY	N-CA-C	5.02	121.74	114.67

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	CH	92	PRO	Peptide
27	Ca	599	ILE	Peptide
30	Cj	53	ASN	Peptide
36	Cv	545	THR	Peptide
36	Cv	943	LEU	Peptide
1	DA	166	TYR	Peptide
2	DD	248	ASP	Peptide
2	DD	255	VAL	Peptide
6	DN	142	ARG	Peptide
6	DN	292	TYR	Peptide

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Mol	Chain	Res	Type	Group
7	DO	124	CYS	Peptide
7	DO	251	ASN	Peptide
10	DR	23	VAL	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DA	11489	0	11135	280	0
2	DD	6523	0	6307	215	0
3	DI	3182	0	3153	71	0
4	DL	1134	0	1128	31	0
5	DM	2430	0	2427	86	0
6	DN	2091	0	2076	120	0
7	DO	1804	0	1752	51	0
8	DP	1760	0	1723	77	0
9	DQ	2061	0	2041	85	0
10	DR	2025	0	2029	107	0
11	DS	1904	0	1855	61	0
12	DU	1754	0	1687	82	0
13	DZ	697	0	644	26	0
14	Da	501	0	473	26	0
15	CE	3399	0	3376	145	0
16	CF	1292	0	1261	30	0
17	CH	2228	0	2204	65	0
18	CI	1632	0	1568	54	0
19	CK	1980	0	1922	85	0
20	CL	733	0	738	35	0
21	CO	3003	0	2995	111	0
22	CP	1489	0	1510	58	0
23	CQ	1584	0	1601	52	0
24	CR	2567	0	2508	87	0
25	CU	1538	0	1539	54	0
26	CZ	1212	0	1178	27	0
27	Ca	5004	0	4776	184	0
28	Cb	2056	0	2031	79	0
29	Cd	2389	0	2232	67	0
30	Cj	1792	0	1744	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	Cm	1577	0	1505	66	0
32	Cn	912	0	969	33	0
33	Cp	1483	0	1438	58	0
34	Cq	2005	0	1916	52	0
35	Cr	1999	0	2007	62	0
36	Cv	8557	0	8252	265	0
37	CA	10092	0	5051	221	0
38	UQ	192	0	194	2	0
39	UR	48	0	50	6	0
40	US	324	0	326	8	0
41	UT	264	0	267	10	0
42	Cr	1	0	0	0	0
42	DA	1	0	0	0	0
42	DS	2	0	0	0	0
43	CA	32	0	0	0	0
43	CO	1	0	0	0	0
43	CQ	1	0	0	0	0
43	Ca	1	0	0	0	0
43	Cv	1	0	0	0	0
44	CA	20	0	38	1	0
45	CA	14	0	26	1	0
All	All	100780	0	93652	2556	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (2556) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:DR:128:PRO:CD	10:DR:133:LEU:O	1.77	1.31
10:DR:261:ARG:HH21	37:CA:81:U:P	1.53	1.29
22:CP:23:ALA:HB2	22:CP:51:HIS:CG	1.68	1.28
2:DD:339:ARG:NH2	37:CA:85:U:O2	1.65	1.25
10:DR:128:PRO:HD2	10:DR:133:LEU:O	1.34	1.22
24:CR:320:VAL:C	25:CU:185:ARG:NH2	1.98	1.21
10:DR:261:ARG:NH2	37:CA:81:U:OP2	1.76	1.19
6:DN:75:VAL:HG11	6:DN:110:ALA:CB	1.73	1.18
5:DM:64:THR:HG23	5:DM:69:PHE:O	1.43	1.15
2:DD:339:ARG:CZ	37:CA:85:U:O2	1.96	1.13
12:DU:191:SER:HB3	12:DU:192:PRO:HD2	1.31	1.12
22:CP:23:ALA:CB	22:CP:51:HIS:CG	2.32	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:DN:113:ALA:HB3	6:DN:133:PHE:CE1	1.85	1.10
15:CE:231:ARG:NH1	37:CA:16:U:O4	1.83	1.10
2:DD:339:ARG:NH1	37:CA:85:U:O2	1.85	1.09
21:CO:151:LYS:NZ	21:CO:179:ASP:OD2	1.89	1.06
22:CP:23:ALA:HB2	22:CP:51:HIS:CD2	1.92	1.05
9:DQ:250:ARG:CD	9:DQ:252:LYS:HE3	1.87	1.05
10:DR:261:ARG:NH2	37:CA:81:U:P	2.29	1.05
10:DR:18:LYS:NZ	37:CA:165:A:OP1	1.91	1.04
19:CK:104:MET:HE1	28:Cb:100:ARG:NH1	1.74	1.02
1:DA:1058:ARG:NH1	34:Cq:253:ARG:HH12	1.57	1.01
5:DM:65:THR:HG22	5:DM:69:PHE:HB3	1.43	1.01
9:DQ:250:ARG:HD3	9:DQ:252:LYS:HE3	1.39	1.00
6:DN:73:VAL:HG11	6:DN:112:ILE:CD1	1.92	0.99
26:CZ:254:ILE:HG21	26:CZ:318:LEU:HD21	1.44	0.99
6:DN:75:VAL:HG11	6:DN:110:ALA:HB3	1.42	0.98
9:DQ:250:ARG:NE	9:DQ:252:LYS:HE3	1.78	0.98
23:CQ:56:ARG:HG2	23:CQ:56:ARG:HH11	1.29	0.98
15:CE:345:ASP:O	15:CE:348:TYR:O	1.82	0.98
1:DA:90:MET:O	2:DD:123:ARG:NH1	1.98	0.97
2:DD:339:ARG:NH2	37:CA:85:U:H1'	1.80	0.96
6:DN:75:VAL:CG1	6:DN:110:ALA:HB3	1.95	0.96
37:CA:564:U:H3	37:CA:570:A:H61	1.04	0.96
2:DD:647:ARG:NH2	10:DR:230:ARG:HH11	1.64	0.95
22:CP:23:ALA:HB1	22:CP:51:HIS:HB2	1.49	0.94
3:DI:340:ARG:HH12	3:DI:342:ARG:NH1	1.66	0.94
36:Cv:590:THR:O	36:Cv:787:LYS:NZ	1.99	0.94
6:DN:75:VAL:HG11	6:DN:110:ALA:HB2	1.49	0.93
2:DD:339:ARG:HH22	37:CA:85:U:H1'	1.31	0.93
33:Cp:52:TYR:O	33:Cp:62:ARG:NH1	2.02	0.92
1:DA:1505:ASP:HB2	5:DM:163:THR:HG23	1.50	0.92
31:Cm:117:ARG:HH12	31:Cm:121:ALA:HB2	1.31	0.92
10:DR:128:PRO:HD3	10:DR:133:LEU:O	1.65	0.92
1:DA:225:GLY:HA3	1:DA:233:ARG:HH11	1.35	0.92
21:CO:411:ARG:HH11	21:CO:424:LYS:HD2	1.35	0.92
15:CE:308:ARG:HA	15:CE:311:LYS:NZ	1.84	0.91
6:DN:73:VAL:HG11	6:DN:112:ILE:HD11	1.50	0.91
1:DA:1058:ARG:HH11	34:Cq:253:ARG:HH12	0.93	0.91
6:DN:74:HIS:O	6:DN:109:ASN:ND2	2.03	0.91
24:CR:320:VAL:C	25:CU:185:ARG:HH21	1.77	0.91
6:DN:75:VAL:CG1	6:DN:110:ALA:CB	2.47	0.91
6:DN:113:ALA:HB3	6:DN:133:PHE:HE1	1.34	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Cm:196:GLY:O	31:Cm:200:VAL:HG22	1.71	0.90
32:Cn:236:LYS:H	32:Cn:245:LYS:HZ3	1.16	0.90
10:DR:128:PRO:HG3	10:DR:133:LEU:CB	2.03	0.89
18:Cl:106:LEU:HD21	19:CK:107:GLN:HG3	1.52	0.88
27:Ca:299:ARG:HH11	27:Ca:299:ARG:HG3	1.37	0.87
37:CA:81:U:O2	37:CA:82:U:C5	2.28	0.87
21:CO:87:THR:HG23	21:CO:88:PRO:HD3	1.55	0.87
2:DD:607:GLN:O	10:DR:227:ARG:NH2	2.07	0.86
22:CP:23:ALA:HB1	22:CP:51:HIS:CB	2.04	0.86
16:CF:129:ASN:HB3	24:CR:125:ASN:HD22	1.39	0.86
8:DP:195:THR:O	8:DP:211:GLU:HG2	1.76	0.86
24:CR:320:VAL:C	25:CU:185:ARG:HH22	1.81	0.86
6:DN:293:PRO:C	15:CE:118:ARG:HH21	1.83	0.85
27:Ca:536:ARG:NH1	27:Ca:539:GLN:OE1	2.09	0.85
17:CH:68:GLN:NE2	37:CA:4:A:N1	2.25	0.85
1:DA:1058:ARG:HH11	34:Cq:253:ARG:NH1	1.75	0.84
3:DI:88:GLN:NE2	3:DI:92:GLU:OE2	2.11	0.83
10:DR:79:LEU:O	12:DU:139:LYS:NZ	2.10	0.83
17:CH:16:VAL:HB	17:CH:17:PRO:HD2	1.60	0.83
8:DP:139:ARG:NH1	8:DP:176:PRO:O	2.12	0.83
12:DU:189:LYS:NZ	12:DU:190:ARG:HB2	1.94	0.83
12:DU:113:GLN:O	12:DU:117:LEU:HG	1.77	0.83
1:DA:74:LYS:NZ	37:CA:71:U:OP1	2.12	0.82
4:DL:181:ARG:HH11	4:DL:181:ARG:HG3	1.44	0.82
11:DS:201:HIS:HD2	11:DS:203:ASP:H	1.25	0.82
35:Cr:125:GLN:HE21	35:Cr:162:PRO:HD2	1.44	0.82
32:Cn:171:MET:HE2	37:CA:555:A:H4'	1.62	0.82
5:DM:65:THR:CG2	5:DM:69:PHE:HB3	2.09	0.82
10:DR:255:PRO:O	10:DR:268:HIS:ND1	2.11	0.81
2:DD:129:ARG:HA	23:CQ:88:PRO:HB3	1.63	0.81
16:CF:136:ALA:HB3	19:CK:171:GLN:HB3	1.63	0.81
22:CP:130:GLN:O	27:Ca:432:ARG:NH1	2.14	0.81
1:DA:695:MET:HE2	1:DA:713:PHE:HB3	1.61	0.81
11:DS:168:LYS:NZ	33:Cp:34:GLU:OE2	2.12	0.81
35:Cr:172:ARG:HH21	35:Cr:176:LEU:HD23	1.44	0.81
1:DA:90:MET:HE1	2:DD:122:GLN:HE22	1.45	0.81
19:CK:104:MET:HE1	28:Cb:100:ARG:HH11	1.46	0.80
11:DS:54:ASN:HB3	11:DS:87:ARG:HG2	1.63	0.80
6:DN:235:ASN:ND2	15:CE:18:LYS:O	2.13	0.80
9:DQ:23:ARG:HD3	21:CO:397:MET:HE1	1.62	0.80
1:DA:1058:ARG:NH1	34:Cq:253:ARG:NH1	2.30	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CP:23:ALA:HB2	22:CP:51:HIS:ND1	1.96	0.80
36:Cv:283:ASP:HB3	36:Cv:398:ARG:HD2	1.64	0.80
10:DR:128:PRO:CG	10:DR:133:LEU:H	1.94	0.80
15:CE:71:ILE:HG23	15:CE:320:GLY:HA2	1.64	0.79
27:Ca:367:ASN:HA	36:Cv:954:ARG:HH22	1.47	0.79
1:DA:1465:ASP:HA	1:DA:1605:ARG:HH12	1.46	0.79
8:DP:195:THR:HG23	8:DP:211:GLU:HB3	1.63	0.79
2:DD:537:ARG:HA	10:DR:218:TRP:HZ3	1.48	0.79
2:DD:746:PRO:HD3	17:CH:77:VAL:HG12	1.65	0.79
12:DU:171:ASP:HA	12:DU:174:ARG:HH12	1.47	0.79
21:CO:313:THR:OG1	23:CQ:166:GLU:OE1	2.00	0.79
6:DN:235:ASN:HD21	15:CE:18:LYS:H	1.28	0.79
2:DD:605:ARG:NH1	2:DD:642:ASP:OD2	2.16	0.79
31:Cm:210:ARG:NH2	37:CA:358:U:OP2	2.16	0.79
15:CE:220:ASP:HB2	36:Cv:44:ARG:HH12	1.46	0.79
37:CA:39:U:C5'	37:CA:39:U:H6	1.96	0.78
1:DA:212:ARG:HA	11:DS:134:GLN:HE22	1.48	0.78
22:CP:22:GLY:HA3	37:CA:164:G:O6	1.82	0.78
25:CU:52:GLU:HB2	29:Cd:250:LEU:HD11	1.64	0.78
2:DD:647:ARG:NH2	10:DR:230:ARG:NH1	2.30	0.78
6:DN:142:ARG:HH12	17:CH:18:PRO:HB2	1.49	0.78
18:CI:106:LEU:HD11	19:CK:107:GLN:HE21	1.46	0.78
5:DM:168:LYS:NZ	15:CE:342:GLY:O	2.16	0.78
12:DU:189:LYS:HZ3	12:DU:190:ARG:HB2	1.49	0.78
36:Cv:67:THR:HG22	36:Cv:69:GLN:H	1.46	0.78
36:Cv:702:ILE:HG21	36:Cv:761:MET:HB2	1.64	0.78
5:DM:26:ARG:HH22	27:Ca:266:GLU:HG3	1.47	0.78
19:CK:158:ARG:NH2	36:Cv:617:ASP:OD2	2.18	0.77
12:DU:191:SER:HB3	12:DU:192:PRO:CD	2.12	0.77
10:DR:128:PRO:HG3	10:DR:133:LEU:HB3	1.67	0.77
15:CE:149:MET:HE2	15:CE:161:GLN:HB3	1.65	0.77
21:CO:127:THR:HG22	21:CO:131:LYS:NZ	2.00	0.77
5:DM:27:GLN:HE22	36:Cv:1013:ARG:H	1.29	0.77
11:DS:114:LYS:NZ	37:CA:206:A:OP1	2.16	0.77
24:CR:313:PRO:O	24:CR:318:LYS:HB2	1.85	0.77
15:CE:42:ARG:HH11	15:CE:105:GLN:NE2	1.83	0.77
15:CE:400:LEU:HD13	15:CE:406:THR:O	1.84	0.77
24:CR:24:ASN:HD22	36:Cv:144:PHE:HA	1.50	0.77
10:DR:100:ARG:HH12	10:DR:122:ALA:HB1	1.50	0.77
1:DA:286:VAL:HG11	1:DA:370:GLN:HB3	1.65	0.76
15:CE:308:ARG:O	15:CE:311:LYS:NZ	2.17	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:DS:37:VAL:CG1	37:CA:199:U:OP1	2.34	0.76
18:CI:115:LEU:HD21	19:CK:82:MET:HE1	1.65	0.76
1:DA:615:ALA:HB1	1:DA:628:LEU:HD12	1.66	0.76
3:DI:88:GLN:CD	3:DI:92:GLU:OE2	2.29	0.76
16:CF:71:MET:HG3	16:CF:76:MET:HE3	1.66	0.76
31:Cm:117:ARG:NH1	31:Cm:121:ALA:HB2	2.00	0.76
1:DA:1440:ILE:HD11	1:DA:1562:GLN:HB3	1.66	0.76
9:DQ:215:PRO:HA	9:DQ:218:ARG:NH1	2.01	0.76
2:DD:272:LYS:NZ	23:CQ:84:ILE:O	2.16	0.76
3:DI:340:ARG:HH12	3:DI:342:ARG:HH11	1.33	0.76
8:DP:203:ASP:HB3	8:DP:205:LEU:HG	1.67	0.75
20:CL:78:MET:HE3	20:CL:105:ARG:HH21	1.52	0.75
25:CU:185:ARG:NH1	25:CU:189:ARG:O	2.19	0.75
1:DA:74:LYS:O	22:CP:59:ARG:NH2	2.19	0.75
1:DA:446:ARG:NH1	1:DA:503:SER:OG	2.18	0.75
15:CE:102:GLU:HG3	28:Cb:56:ARG:NH2	2.00	0.75
1:DA:1181:THR:OG1	1:DA:1182:ARG:NH1	2.20	0.75
18:CI:175:ARG:NH1	18:CI:179:CYS:SG	2.59	0.75
21:CO:411:ARG:NH1	21:CO:424:LYS:HD2	2.01	0.75
2:DD:736:TYR:HB3	17:CH:84:PRO:HG3	1.67	0.75
16:CF:50:ARG:HD3	25:CU:35:ILE:HD11	1.68	0.75
4:DL:242:ARG:NH2	31:Cm:38:ASP:OD2	2.19	0.75
36:Cv:304:THR:HG22	36:Cv:306:TYR:H	1.51	0.75
1:DA:59:HIS:HD2	1:DA:86:TYR:H	1.32	0.74
11:DS:37:VAL:HG13	37:CA:199:U:OP1	1.87	0.74
19:CK:215:ARG:NH2	37:CA:298:U:O2'	2.20	0.74
36:Cv:293:LEU:HD11	36:Cv:407:MET:HB2	1.69	0.74
5:DM:45:ARG:HH11	5:DM:45:ARG:HG3	1.51	0.74
21:CO:128:ARG:NH2	21:CO:209:GLU:OE1	2.20	0.74
26:CZ:305:HIS:HD2	26:CZ:307:LYS:HB2	1.50	0.74
1:DA:1486:ALA:O	1:DA:1488:GLN:NE2	2.20	0.74
8:DP:208:PRO:HD2	8:DP:211:GLU:HB2	1.70	0.74
32:Cn:236:LYS:N	32:Cn:245:LYS:HZ3	1.85	0.74
1:DA:916:ASP:HB2	6:DN:11:ARG:HA	1.68	0.74
19:CK:262:ARG:NH1	19:CK:269:MET:SD	2.61	0.74
21:CO:70:HIS:HB3	21:CO:71:PRO:HD2	1.67	0.74
22:CP:96:ILE:HD11	27:Ca:470:ARG:CZ	2.18	0.74
12:DU:46:THR:HG22	12:DU:48:PHE:H	1.53	0.73
1:DA:235:THR:HG23	1:DA:281:MET:HE2	1.70	0.73
19:CK:201:ARG:NH1	25:CU:79:TYR:OH	2.21	0.73
35:Cr:275:TYR:HD1	35:Cr:280:ARG:NH1	1.85	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:DP:128:LEU:HD22	8:DP:161:VAL:HG21	1.69	0.73
24:CR:134:ARG:HH21	24:CR:185:PHE:HB3	1.53	0.73
35:Cr:282:GLU:HG3	35:Cr:285:ARG:HH21	1.54	0.73
15:CE:60:TYR:HB3	15:CE:85:ASN:HD21	1.54	0.73
6:DN:74:HIS:O	6:DN:109:ASN:CG	2.31	0.73
15:CE:156:PRO:HG2	24:CR:307:ARG:HE	1.53	0.73
23:CQ:16:THR:HG21	33:Cp:18:SER:HA	1.70	0.73
36:Cv:255:PHE:HB3	36:Cv:292:LYS:HG3	1.71	0.73
37:CA:84:U:H3'	37:CA:84:U:P	2.29	0.73
31:Cm:164:HIS:HB3	37:CA:611:U:H5''	1.70	0.73
3:DI:340:ARG:NH1	3:DI:342:ARG:HD2	2.04	0.72
5:DM:64:THR:CG2	5:DM:69:PHE:O	2.32	0.72
2:DD:213:CYS:HB3	2:DD:297:ARG:HH12	1.52	0.72
3:DI:233:ARG:NH2	3:DI:272:CYS:O	2.22	0.72
36:Cv:1006:GLU:OE2	36:Cv:1008:ARG:NH1	2.22	0.72
3:DI:27:THR:H	3:DI:30:GLN:HE21	1.34	0.72
9:DQ:122:ILE:HG23	9:DQ:130:LEU:HD12	1.71	0.72
37:CA:39:U:H6	37:CA:39:U:H5'	1.54	0.72
34:Cq:177:THR:OG1	35:Cr:64:ARG:NH1	2.22	0.72
9:DQ:103:CYS:HA	9:DQ:106:MET:HE3	1.72	0.72
12:DU:86:ILE:HD11	12:DU:99:GLN:HB2	1.70	0.72
14:Da:35:ALA:HB2	14:Da:42:ARG:HD2	1.70	0.72
19:CK:214:LYS:HB3	19:CK:214:LYS:NZ	2.05	0.72
1:DA:502:LYS:NZ	1:DA:502:LYS:HB3	2.04	0.72
6:DN:16:ASP:HB3	6:DN:175:LYS:HE2	1.70	0.72
15:CE:311:LYS:H	15:CE:311:LYS:HD2	1.53	0.72
16:CF:149:PHE:HA	36:Cv:627:LEU:HD11	1.72	0.72
28:Cb:221:VAL:HG21	35:Cr:303:LEU:HD11	1.70	0.72
1:DA:1090:GLY:O	1:DA:1384:ARG:NH2	2.22	0.71
3:DI:367:SER:H	3:DI:370:GLN:HE21	1.38	0.71
36:Cv:626:VAL:HB	36:Cv:628:LYS:NZ	2.05	0.71
2:DD:340:ARG:NH1	12:DU:58:HIS:HB3	2.05	0.71
2:DD:340:ARG:HH11	12:DU:58:HIS:HB3	1.56	0.71
6:DN:288:PHE:O	15:CE:118:ARG:NH1	2.23	0.71
10:DR:128:PRO:HG3	10:DR:133:LEU:CA	2.20	0.71
2:DD:637:ARG:NH1	22:CP:153:ARG:HD2	2.04	0.71
12:DU:171:ASP:HA	12:DU:174:ARG:NH1	2.06	0.71
2:DD:637:ARG:HH11	22:CP:153:ARG:NH1	1.87	0.71
15:CE:308:ARG:CA	15:CE:311:LYS:NZ	2.54	0.71
1:DA:985:LYS:NZ	1:DA:985:LYS:HB3	2.06	0.71
1:DA:1052:ALA:HB1	18:CI:202:LEU:HD21	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CR:112:GLY:H	24:CR:149:PRO:HB2	1.56	0.71
1:DA:577:ASP:OD1	1:DA:578:LYS:N	2.23	0.70
26:CZ:234:ILE:HG12	26:CZ:240:VAL:HG21	1.71	0.70
28:Cb:19:PRO:HD2	31:Cm:156:THR:HG21	1.71	0.70
33:Cp:53:VAL:HG11	33:Cp:59:PHE:HD1	1.56	0.70
37:CA:85:U:C5'	37:CA:85:U:H6	2.04	0.70
36:Cv:594:LEU:HD23	36:Cv:600:GLY:HA2	1.73	0.70
2:DD:734:ARG:NH2	3:DI:164:GLU:OE2	2.24	0.70
7:DO:178:ARG:NH2	29:Cd:136:GLU:OE2	2.24	0.70
10:DR:266:TRP:CG	30:Cj:210:PRO:HA	2.26	0.70
12:DU:170:ARG:O	12:DU:174:ARG:NH1	2.24	0.70
2:DD:414:ARG:NH1	2:DD:568:GLU:OE1	2.25	0.70
9:DQ:250:ARG:HD3	9:DQ:252:LYS:CE	2.19	0.70
24:CR:184:LYS:HZ2	24:CR:184:LYS:HB2	1.56	0.70
9:DQ:215:PRO:HA	9:DQ:218:ARG:HH12	1.57	0.70
9:DQ:254:SER:N	9:DQ:255:PRO:HD2	2.06	0.70
10:DR:126:LEU:HD12	10:DR:137:CYS:SG	2.31	0.70
8:DP:10:ALA:N	37:CA:55:U:O4	2.25	0.70
31:Cm:27:ASN:HD22	31:Cm:32:LYS:HG3	1.57	0.70
17:CH:154:ASP:O	17:CH:158:ARG:HG2	1.92	0.70
18:CI:90:GLU:H	19:CK:114:MET:HE3	1.57	0.70
2:DD:527:THR:HB	10:DR:223:GLN:HG3	1.74	0.70
2:DD:52:LYS:NZ	37:CA:138:U:O4	2.25	0.69
10:DR:126:LEU:CD1	10:DR:137:CYS:SG	2.80	0.69
24:CR:320:VAL:HG22	25:CU:185:ARG:CZ	2.21	0.69
2:DD:647:ARG:HH22	10:DR:230:ARG:HH11	1.36	0.69
22:CP:26:ALA:HB2	37:CA:77:A:O4'	1.92	0.69
6:DN:12:MET:HE3	6:DN:171:LEU:HD13	1.72	0.69
6:DN:29:ARG:HH11	6:DN:29:ARG:HG3	1.56	0.69
16:CF:44:ILE:HD11	16:CF:63:ARG:HH12	1.58	0.69
19:CK:156:LYS:HB2	19:CK:156:LYS:NZ	2.07	0.69
1:DA:463:VAL:HG11	1:DA:840:TYR:HB3	1.75	0.69
2:DD:149:SER:O	2:DD:153:THR:OG1	2.10	0.69
11:DS:225:GLU:HB3	11:DS:229:ARG:HH12	1.56	0.69
13:DZ:44:PHE:CZ	15:CE:24:GLY:HA3	2.27	0.69
36:Cv:292:LYS:NZ	36:Cv:511:HIS:O	2.24	0.69
37:CA:309:A:H4'	37:CA:350:U:O2'	1.92	0.69
11:DS:182:TYR:OH	11:DS:189:ARG:NH2	2.25	0.69
21:CO:90:MET:HB3	21:CO:91:PRO:HD2	1.73	0.69
1:DA:1416:VAL:HG11	1:DA:1442:VAL:HG13	1.75	0.69
35:Cr:125:GLN:HE22	35:Cr:161:ARG:HG3	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:420:ASN:ND2	1:DA:491:VAL:O	2.26	0.68
2:DD:247:VAL:HG12	2:DD:250:LYS:HZ2	1.58	0.68
21:CO:411:ARG:HH21	37:CA:68:A:H5'	1.57	0.68
37:CA:351:A:H3'	37:CA:351:A:P	2.32	0.68
5:DM:51:VAL:HA	36:Cv:987:SER:HB3	1.75	0.68
37:CA:73:U:H4'	37:CA:74:G:H5'	1.76	0.68
37:CA:79:A:H2'	37:CA:79:A:N3	2.09	0.68
1:DA:1558:ASN:HA	1:DA:1596:VAL:HG21	1.76	0.68
6:DN:293:PRO:HB3	15:CE:109:LYS:NZ	2.08	0.68
31:Cm:210:ARG:O	37:CA:357:A:N6	2.26	0.68
8:DP:183:ASP:HB3	8:DP:186:HIS:HD2	1.57	0.68
27:Ca:522:GLU:HG2	27:Ca:588:LYS:HE3	1.75	0.68
8:DP:183:ASP:HB3	8:DP:186:HIS:CD2	2.29	0.68
10:DR:128:PRO:HG2	10:DR:133:LEU:H	1.57	0.68
10:DR:249:GLU:HG3	10:DR:265:MET:HG2	1.75	0.68
23:CQ:193:ARG:HH12	32:Cn:194:PRO:HD3	1.59	0.68
1:DA:1134:ILE:HG12	34:Cq:70:ALA:HA	1.76	0.68
9:DQ:254:SER:N	9:DQ:255:PRO:CD	2.57	0.68
13:DZ:20:ARG:HH11	13:DZ:20:ARG:HG3	1.59	0.68
21:CO:127:THR:HG22	21:CO:131:LYS:HZ2	1.59	0.68
27:Ca:76:GLN:HA	27:Ca:79:MET:HE2	1.75	0.68
4:DL:164:ARG:HH22	28:Cb:64:ASN:HD21	1.40	0.68
7:DO:94:ILE:HG23	7:DO:99:LEU:HB2	1.75	0.68
19:CK:78:ASP:HB2	28:Cb:178:ARG:NH1	2.08	0.68
9:DQ:46:ARG:NH1	12:DU:121:GLU:OE2	2.24	0.67
10:DR:51:LEU:HD22	10:DR:84:LEU:HD21	1.76	0.67
3:DI:349:THR:HG23	3:DI:350:TYR:HD1	1.60	0.67
15:CE:81:LYS:NZ	36:Cv:512:MET:O	2.26	0.67
2:DD:449:LEU:HD23	2:DD:452:LEU:HD11	1.75	0.67
2:DD:777:GLY:O	27:Ca:332:ARG:NH2	2.27	0.67
17:CH:132:ASP:N	17:CH:132:ASP:OD1	2.25	0.67
25:CU:16:HIS:HD2	25:CU:18:LYS:H	1.40	0.67
8:DP:20:MET:HE1	8:DP:29:TRP:HB2	1.77	0.67
17:CH:172:VAL:HG22	17:CH:173:PRO:HD2	1.77	0.67
2:DD:173:GLN:OE1	12:DU:65:TRP:NE1	2.28	0.67
2:DD:264:LEU:HD12	2:DD:272:LYS:HE3	1.77	0.67
10:DR:96:PHE:HE1	10:DR:128:PRO:HD3	1.58	0.67
27:Ca:461:LEU:HD22	27:Ca:488:MET:HE2	1.76	0.67
37:CA:85:U:H2'	37:CA:86:G:C8	2.30	0.67
21:CO:93:ARG:HH21	37:CA:358:U:H3	1.41	0.66
31:Cm:118:GLU:N	31:Cm:118:GLU:OE1	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:DM:76:ASN:ND2	36:Cv:971:LEU:H	1.93	0.66
15:CE:22:ARG:HH21	15:CE:240:ASP:HB3	1.60	0.66
27:Ca:521:GLN:HG2	27:Ca:564:ARG:HH22	1.61	0.66
28:Cb:289:LYS:NZ	35:Cr:177:LEU:O	2.19	0.66
31:Cm:210:ARG:HG2	37:CA:288:U:H5"	1.76	0.66
3:DI:88:GLN:O	3:DI:92:GLU:HG3	1.95	0.66
9:DQ:14:ARG:HH11	9:DQ:14:ARG:HB2	1.59	0.66
15:CE:15:TRP:HA	15:CE:18:LYS:HE2	1.77	0.66
20:CL:72:PHE:HB2	20:CL:119:PHE:HE1	1.60	0.66
27:Ca:474:ARG:NH1	27:Ca:478:GLY:O	2.28	0.66
6:DN:222:LEU:HD11	27:Ca:301:ILE:HD11	1.78	0.66
1:DA:502:LYS:HB3	1:DA:502:LYS:HZ3	1.60	0.66
8:DP:199:LEU:HD12	8:DP:206:TYR:CZ	2.30	0.66
11:DS:49:VAL:HB	27:Ca:600:PRO:HG3	1.78	0.66
6:DN:57:ARG:HG3	6:DN:66:GLY:HA3	1.78	0.66
6:DN:73:VAL:HG21	6:DN:132:TYR:CE1	2.31	0.66
7:DO:122:LEU:O	7:DO:163:ARG:NH1	2.28	0.66
8:DP:64:MET:HE1	8:DP:68:PRO:HG3	1.77	0.66
17:CH:229:GLU:HG2	17:CH:276:ARG:HD3	1.78	0.66
24:CR:184:LYS:HB2	24:CR:184:LYS:NZ	2.11	0.66
37:CA:564:U:H3	37:CA:570:A:N6	1.87	0.66
6:DN:114:GLY:HA3	6:DN:130:ASN:OD1	1.95	0.66
8:DP:199:LEU:HD12	8:DP:206:TYR:CE2	2.30	0.66
1:DA:225:GLY:HA3	1:DA:233:ARG:NH1	2.10	0.66
1:DA:1113:LEU:HB3	1:DA:1145:THR:HG21	1.78	0.66
15:CE:42:ARG:HH11	15:CE:42:ARG:HG3	1.59	0.66
33:Cp:135:THR:HG21	33:Cp:139:SER:H	1.59	0.66
36:Cv:286:THR:HG21	36:Cv:402:ALA:HB1	1.78	0.66
37:CA:232:G:N1	37:CA:248:A:OP1	2.26	0.66
1:DA:1179:GLN:HE22	34:Cq:147:PRO:HA	1.61	0.66
3:DI:45:LEU:HD13	3:DI:158:ARG:HB2	1.77	0.66
29:Cd:137:ARG:HG2	29:Cd:137:ARG:HH11	1.59	0.66
29:Cd:194:VAL:HG12	29:Cd:195:GLU:HG3	1.78	0.66
8:DP:189:TYR:CG	8:DP:197:TYR:HB3	2.31	0.65
10:DR:67:LYS:HA	10:DR:67:LYS:NZ	2.11	0.65
23:CQ:56:ARG:HG2	23:CQ:56:ARG:NH1	2.01	0.65
36:Cv:969:ASP:OD1	36:Cv:969:ASP:N	2.28	0.65
11:DS:57:LEU:HD11	11:DS:83:LEU:HD23	1.77	0.65
20:CL:137:ARG:NH2	37:CA:265:U:O2	2.28	0.65
28:Cb:56:ARG:HH11	28:Cb:57:MET:CE	2.09	0.65
6:DN:237:ARG:NH2	27:Ca:350:GLU:OE2	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:DU:107:LYS:NZ	12:DU:107:LYS:HB3	2.10	0.65
31:Cm:171:ALA:HB1	36:Cv:54:ASN:HB3	1.78	0.65
34:Cq:195:VAL:HG23	34:Cq:196:HIS:HD2	1.61	0.65
1:DA:70:ARG:NH2	37:CA:73:U:OP2	2.29	0.65
32:Cn:178:LYS:HE3	32:Cn:182:PHE:HE2	1.62	0.65
8:DP:206:TYR:HE1	8:DP:215:LEU:HD13	1.61	0.65
19:CK:283:GLY:H	19:CK:311:THR:HG23	1.60	0.65
25:CU:77:ARG:HH11	36:Cv:175:ARG:HH22	1.45	0.65
1:DA:568:SER:OG	6:DN:144:ARG:NH1	2.29	0.65
8:DP:13:ARG:NH1	37:CA:55:U:OP1	2.28	0.65
23:CQ:198:LEU:O	23:CQ:199:ASN:ND2	2.30	0.65
1:DA:1662:ARG:HH22	15:CE:402:ARG:HH12	1.45	0.65
10:DR:128:PRO:HG3	10:DR:133:LEU:N	2.11	0.65
1:DA:385:ARG:HH11	6:DN:195:TYR:HD1	1.45	0.65
6:DN:57:ARG:NH2	6:DN:70:GLU:OE2	2.30	0.65
26:CZ:282:ALA:HB1	26:CZ:321:MET:HG3	1.79	0.65
9:DQ:171:GLU:OE2	23:CQ:172:ARG:NH1	2.31	0.64
19:CK:188:TYR:HA	19:CK:192:MET:HE3	1.80	0.64
22:CP:23:ALA:HB2	22:CP:51:HIS:CE1	2.32	0.64
2:DD:339:ARG:HH22	37:CA:85:U:C1'	2.08	0.64
12:DU:147:LEU:CD2	12:DU:152:ILE:HD12	2.26	0.64
1:DA:195:MET:HE3	1:DA:198:ARG:HH11	1.62	0.64
8:DP:90:LEU:HD13	8:DP:127:ASP:HB3	1.78	0.64
8:DP:199:LEU:HD21	8:DP:204:ASN:HA	1.79	0.64
9:DQ:217:GLN:HB3	9:DQ:221:LEU:HD12	1.78	0.64
15:CE:42:ARG:HG3	15:CE:105:GLN:HE22	1.62	0.64
28:Cb:303:GLU:C	35:Cr:105:ARG:HH12	2.06	0.64
36:Cv:531:MET:HE3	36:Cv:531:MET:H	1.63	0.64
2:DD:357:TRP:O	2:DD:626:ARG:NH2	2.31	0.64
2:DD:637:ARG:NH1	22:CP:153:ARG:HH11	1.94	0.64
18:CI:89:ARG:NH1	19:CK:117:GLU:OE2	2.30	0.64
6:DN:224:ARG:HB3	6:DN:224:ARG:HH11	1.61	0.64
7:DO:186:MET:HE1	29:Cd:132:PHE:HD2	1.62	0.64
16:CF:129:ASN:HB3	24:CR:125:ASN:ND2	2.12	0.64
3:DI:313:ARG:HH11	3:DI:407:LEU:C	2.06	0.64
24:CR:167:ARG:NH1	37:CA:317:U:O4	2.31	0.64
19:CK:315:LEU:O	36:Cv:175:ARG:NH1	2.31	0.64
29:Cd:139:SER:O	29:Cd:143:GLN:HG2	1.97	0.64
36:Cv:1042:ARG:HH21	36:Cv:1046:ASN:HB2	1.63	0.64
1:DA:151:PRO:HG3	2:DD:280:LEU:HD21	1.80	0.64
8:DP:195:THR:OG1	8:DP:211:GLU:HG3	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Cb:12:PRO:HG2	28:Cb:15:MET:CG	2.28	0.64
36:Cv:1042:ARG:NH2	36:Cv:1046:ASN:HB2	2.13	0.64
9:DQ:120:MET:HB2	9:DQ:196:LEU:HD23	1.81	0.63
10:DR:100:ARG:HH12	10:DR:122:ALA:CB	2.11	0.63
23:CQ:57:HIS:O	37:CA:97:U:O2'	2.16	0.63
11:DS:225:GLU:HB3	11:DS:229:ARG:NH1	2.13	0.63
23:CQ:105:LYS:H	23:CQ:137:LEU:HD21	1.62	0.63
2:DD:312:GLN:HE22	2:DD:440:ARG:NH1	1.96	0.63
8:DP:200:SER:HB3	8:DP:203:ASP:HB2	1.80	0.63
12:DU:142:ASP:HB2	12:DU:145:LYS:HG2	1.79	0.63
1:DA:150:ILE:HG12	1:DA:151:PRO:HD2	1.80	0.63
1:DA:319:ARG:HG2	1:DA:319:ARG:HH11	1.61	0.63
5:DM:293:ARG:HE	34:Cq:59:ARG:HB2	1.64	0.63
7:DO:86:ARG:NH2	7:DO:126:PRO:HG2	2.13	0.63
33:Cp:163:PRO:HG2	33:Cp:165:TYR:HE1	1.62	0.63
2:DD:247:VAL:HG12	2:DD:250:LYS:NZ	2.13	0.63
6:DN:10:PHE:HE1	6:DN:12:MET:HE2	1.61	0.63
27:Ca:570:THR:O	37:CA:30:U:O2'	2.17	0.63
36:Cv:692:LYS:HD3	36:Cv:732:LEU:HD22	1.80	0.63
4:DL:176:ARG:HE	28:Cb:79:PRO:HA	1.63	0.63
10:DR:93:PRO:HB2	10:DR:96:PHE:HD2	1.63	0.63
12:DU:207:ARG:HD3	37:CA:161:G:O6	1.98	0.63
34:Cq:64:VAL:HG11	34:Cq:77:PHE:CD2	2.33	0.63
6:DN:77:LEU:N	6:DN:78:PRO:HD2	2.14	0.63
9:DQ:142:PHE:HE2	9:DQ:246:VAL:HG11	1.64	0.63
17:CH:106:THR:HG23	36:Cv:107:LEU:HD11	1.79	0.63
33:Cp:162:LEU:HD12	33:Cp:163:PRO:HD2	1.79	0.63
6:DN:118:LEU:HD22	6:DN:129:LEU:HD11	1.79	0.63
31:Cm:202:THR:HG23	37:CA:338:U:H3	1.64	0.63
2:DD:626:ARG:HD3	2:DD:627:TYR:CZ	2.33	0.63
12:DU:147:LEU:HD22	12:DU:152:ILE:HD12	1.80	0.63
15:CE:156:PRO:HG3	24:CR:308:MET:HE2	1.80	0.63
15:CE:308:ARG:C	15:CE:311:LYS:NZ	2.57	0.63
9:DQ:41:GLN:HE21	12:DU:123:GLN:H	1.47	0.62
9:DQ:105:PRO:HG2	9:DQ:221:LEU:HD21	1.81	0.62
10:DR:128:PRO:CD	10:DR:133:LEU:C	2.68	0.62
20:CL:122:GLU:HG3	37:CA:266:A:H4'	1.81	0.62
28:Cb:101:LYS:NZ	28:Cb:101:LYS:HB3	2.14	0.62
36:Cv:408:THR:HG21	36:Cv:422:SER:HA	1.80	0.62
11:DS:33:LEU:HG	11:DS:35:TYR:HB2	1.81	0.62
11:DS:166:THR:HG21	11:DS:194:GLU:HG3	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CK:314:PRO:HB3	25:CU:15:TYR:CZ	2.35	0.62
12:DU:147:LEU:HD22	12:DU:152:ILE:CD1	2.30	0.62
18:CI:89:ARG:HD2	19:CK:114:MET:HE2	1.80	0.62
34:Cq:99:THR:HG23	34:Cq:101:LEU:H	1.64	0.62
37:CA:35:U:H3'	37:CA:36:U:H5''	1.80	0.62
5:DM:10:ARG:HH12	15:CE:325:LEU:HB2	1.62	0.62
9:DQ:79:LEU:HB3	9:DQ:83:ASN:ND2	2.15	0.62
17:CH:107:ARG:HH12	17:CH:133:ARG:CZ	2.13	0.62
1:DA:112:GLN:HG2	1:DA:131:ASP:CG	2.24	0.62
6:DN:29:ARG:HG3	6:DN:29:ARG:NH1	2.12	0.62
2:DD:28:MET:HE1	17:CH:236:MET:HB3	1.82	0.62
2:DD:417:THR:HG22	2:DD:419:ALA:H	1.65	0.62
35:Cr:22:LEU:HD22	35:Cr:90:ILE:HD13	1.80	0.62
7:DO:114:GLY:O	7:DO:116:ALA:N	2.33	0.62
10:DR:269:TRP:H	30:Cj:126:TYR:HB2	1.64	0.62
36:Cv:292:LYS:O	36:Cv:405:PRO:HG2	1.99	0.62
15:CE:308:ARG:C	15:CE:311:LYS:HZ3	2.05	0.62
19:CK:71:SER:O	19:CK:73:GLN:NE2	2.33	0.62
2:DD:637:ARG:NH1	22:CP:153:ARG:NH1	2.48	0.62
13:DZ:39:ASN:ND2	37:CA:225:A:OP1	2.26	0.62
37:CA:394:A:H8	37:CA:394:A:H5'	1.64	0.62
1:DA:653:LYS:HB2	1:DA:726:GLU:HB2	1.81	0.61
3:DI:296:ASN:HA	3:DI:334:ILE:HD11	1.81	0.61
6:DN:62:ARG:NH2	27:Ca:390:GLN:OE1	2.33	0.61
9:DQ:134:ILE:HG21	9:DQ:248:LEU:HD22	1.82	0.61
17:CH:253:TYR:CE2	17:CH:280:MET:HE3	2.35	0.61
19:CK:180:ASP:HA	29:Cd:182:GLN:HE21	1.65	0.61
34:Cq:195:VAL:HG23	34:Cq:196:HIS:CD2	2.35	0.61
28:Cb:175:ILE:HG23	28:Cb:179:GLU:HB2	1.82	0.61
5:DM:45:ARG:HG3	5:DM:45:ARG:NH1	2.11	0.61
8:DP:111:THR:HG22	8:DP:113:ASP:H	1.65	0.61
24:CR:137:THR:HG23	24:CR:139:THR:H	1.65	0.61
1:DA:466:VAL:HG11	36:Cv:1067:LEU:HD22	1.81	0.61
6:DN:209:ARG:HD3	6:DN:211:TRP:CZ2	2.36	0.61
32:Cn:236:LYS:H	32:Cn:245:LYS:NZ	1.97	0.61
2:DD:431:LEU:HD11	2:DD:469:GLY:HA3	1.81	0.61
8:DP:70:TRP:CD2	12:DU:182:GLU:HG2	2.35	0.61
15:CE:227:TYR:OH	37:CA:15:U:H2'	2.00	0.61
24:CR:261:ILE:HG13	24:CR:262:SER:H	1.65	0.61
34:Cq:181:HIS:ND1	34:Cq:201:GLU:OE2	2.33	0.61
36:Cv:681:HIS:NE2	36:Cv:695:SER:OG	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:649:LEU:HD12	1:DA:729:ARG:HH11	1.65	0.61
4:DL:139:ARG:HH22	4:DL:203:ARG:HH12	1.48	0.61
10:DR:127:VAL:HG22	10:DR:134:LEU:CD2	2.29	0.61
16:CF:2:VAL:HG13	16:CF:37:ARG:HD2	1.82	0.61
2:DD:11:ARG:NH2	32:Cn:157:TYR:O	2.34	0.61
15:CE:308:ARG:HA	15:CE:311:LYS:HZ2	1.61	0.61
23:CQ:174:ARG:HH21	23:CQ:183:PRO:HD3	1.65	0.61
32:Cn:179:ARG:HD2	32:Cn:183:ARG:NH1	2.16	0.61
37:CA:39:U:H5'	37:CA:39:U:C6	2.35	0.61
6:DN:75:VAL:CG1	6:DN:110:ALA:HB2	2.20	0.61
14:Da:53:ARG:NH1	37:CA:333:U:OP2	2.33	0.61
36:Cv:813:ARG:HG2	36:Cv:926:ILE:HD13	1.81	0.61
6:DN:73:VAL:CG1	6:DN:112:ILE:CD1	2.74	0.61
8:DP:132:LEU:HD21	8:DP:154:PHE:HE1	1.65	0.61
10:DR:252:ALA:HA	10:DR:262:ARG:HG3	1.82	0.61
27:Ca:43:VAL:HG21	36:Cv:1129:ASN:HB3	1.83	0.61
28:Cb:301:THR:HG22	35:Cr:180:TRP:HH2	1.65	0.61
36:Cv:204:ILE:HD12	36:Cv:209:VAL:HG11	1.82	0.61
9:DQ:142:PHE:HE1	9:DQ:180:ALA:HB1	1.66	0.61
19:CK:205:TYR:HD2	19:CK:221:THR:HG23	1.65	0.61
26:CZ:236:ARG:O	26:CZ:237:ARG:HB3	2.01	0.61
1:DA:617:PRO:HG2	1:DA:746:GLN:NE2	2.16	0.60
4:DL:181:ARG:NH2	36:Cv:494:THR:O	2.33	0.60
6:DN:142:ARG:CZ	17:CH:19:LEU:HD12	2.31	0.60
23:CQ:21:ARG:NH1	37:CA:197:A:OP2	2.29	0.60
27:Ca:507:MET:HE3	27:Ca:557:PHE:HB3	1.82	0.60
2:DD:541:ARG:HD2	10:DR:215:ARG:NH1	2.16	0.60
6:DN:75:VAL:O	6:DN:75:VAL:HG13	2.01	0.60
8:DP:195:THR:C	8:DP:211:GLU:HG2	2.26	0.60
1:DA:80:PRO:HD3	37:CA:154:G:N2	2.16	0.60
4:DL:139:ARG:NH2	4:DL:203:ARG:HH12	1.98	0.60
5:DM:227:LEU:HB2	36:Cv:1008:ARG:HD3	1.83	0.60
13:DZ:11:LYS:H	27:Ca:91:ASP:HA	1.66	0.60
14:Da:14:TYR:OH	23:CQ:40:ARG:NH2	2.34	0.60
22:CP:23:ALA:CB	22:CP:51:HIS:CD2	2.73	0.60
3:DI:340:ARG:NH1	3:DI:342:ARG:NH1	2.43	0.60
6:DN:223:GLN:HB2	27:Ca:256:GLU:CD	2.26	0.60
15:CE:83:MET:HE1	15:CE:307:ILE:HD11	1.83	0.60
15:CE:209:GLU:OE2	27:Ca:347:ARG:NH1	2.34	0.60
2:DD:647:ARG:HG3	2:DD:647:ARG:HH11	1.66	0.60
17:CH:146:GLU:OE2	17:CH:149:TYR:OH	2.12	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Ca:61:LEU:HB2	27:Ca:76:GLN:NE2	2.17	0.60
1:DA:1583:LEU:O	1:DA:1587:LEU:HG	2.01	0.60
9:DQ:41:GLN:NE2	12:DU:123:GLN:H	2.00	0.60
10:DR:63:ILE:HG22	10:DR:64:ILE:HG13	1.82	0.60
36:Cv:440:GLY:HA2	36:Cv:443:VAL:HG22	1.82	0.60
41:UT:19:UNK:HA	41:UT:24:UNK:HB1	1.82	0.60
1:DA:1399:ASN:HD21	1:DA:1502:PHE:H	1.50	0.60
12:DU:73:ARG:NH1	12:DU:73:ARG:O	2.34	0.60
30:Cj:132:LEU:HD21	30:Cj:135:ILE:HG13	1.83	0.60
36:Cv:95:ARG:HH11	36:Cv:95:ARG:HG3	1.66	0.60
2:DD:149:SER:HB2	2:DD:152:ALA:HB3	1.83	0.60
4:DL:241:GLU:OE1	4:DL:242:ARG:N	2.35	0.60
1:DA:195:MET:HE3	1:DA:198:ARG:NH1	2.16	0.60
9:DQ:171:GLU:HG2	21:CO:319:MET:HE2	1.84	0.60
9:DQ:250:ARG:CZ	9:DQ:252:LYS:HE3	2.31	0.60
10:DR:261:ARG:NH2	37:CA:81:U:OP1	2.29	0.60
37:CA:360:C:H2'	37:CA:361:A:H5'	1.84	0.60
2:DD:352:VAL:HG12	2:DD:359:LEU:HD22	1.84	0.59
24:CR:25:GLU:HB3	36:Cv:143:THR:HG21	1.83	0.59
24:CR:109:ASP:HB3	24:CR:112:GLY:HA2	1.84	0.59
37:CA:85:U:H6	37:CA:85:U:H5'	1.66	0.59
1:DA:630:ASP:OD2	1:DA:694:ARG:NH1	2.36	0.59
2:DD:700:ASP:HB2	2:DD:709:ARG:HD3	1.85	0.59
6:DN:73:VAL:HG11	6:DN:112:ILE:HD12	1.83	0.59
21:CO:75:LEU:HD11	32:Cn:230:VAL:HG22	1.84	0.59
28:Cb:307:TYR:OH	35:Cr:97:ASP:OD2	2.18	0.59
36:Cv:470:PHE:HD1	36:Cv:556:PHE:HE2	1.51	0.59
6:DN:217:MET:HE3	27:Ca:267:LEU:HD23	1.83	0.59
11:DS:52:ASP:O	11:DS:58:ASN:ND2	2.35	0.59
36:Cv:84:GLY:HA2	36:Cv:87:GLN:HG3	1.84	0.59
2:DD:242:LEU:HG	2:DD:246:GLU:HG2	1.84	0.59
15:CE:188:GLU:OE2	31:Cm:29:TYR:OH	2.20	0.59
21:CO:70:HIS:HB3	21:CO:71:PRO:CD	2.33	0.59
24:CR:317:ILE:HG23	37:CA:588:U:C6	2.37	0.59
25:CU:13:MET:HE3	37:CA:314:A:H5''	1.83	0.59
2:DD:283:MET:HE1	3:DI:69:PRO:HB3	1.84	0.59
8:DP:88:THR:HG22	8:DP:90:LEU:H	1.67	0.59
20:CL:59:MET:HG3	20:CL:62:LEU:HD12	1.83	0.59
28:Cb:287:ARG:HH12	35:Cr:52:ARG:HH12	1.50	0.59
17:CH:107:ARG:NH1	17:CH:133:ARG:CZ	2.65	0.59
1:DA:1181:THR:OG1	1:DA:1182:ARG:CZ	2.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:DP:189:TYR:CD1	8:DP:197:TYR:N	2.71	0.59
12:DU:94:TRP:CH2	12:DU:196:MET:HE1	2.38	0.59
15:CE:115:ASN:HD22	15:CE:134:GLY:HA2	1.68	0.59
20:CL:129:LEU:HD12	20:CL:130:PRO:HD2	1.82	0.59
21:CO:124:ILE:HG13	21:CO:168:GLU:HG3	1.85	0.59
11:DS:128:SER:HB3	11:DS:197:GLN:NE2	2.18	0.59
17:CH:251:VAL:HG11	17:CH:280:MET:HE2	1.85	0.59
36:Cv:367:ASP:OD1	36:Cv:367:ASP:N	2.35	0.59
1:DA:1016:MET:HG2	15:CE:110:LEU:HD11	1.85	0.59
6:DN:160:CYS:HB2	6:DN:162:LEU:HB2	1.85	0.59
7:DO:136:ASP:HA	7:DO:139:GLU:HG3	1.84	0.59
7:DO:244:ARG:O	29:Ca:129:ARG:NH2	2.36	0.59
23:CQ:48:ARG:NH2	37:CA:375:A:O2'	2.36	0.59
25:CU:108:PHE:HZ	31:Ca:85:ILE:HG23	1.68	0.59
1:DA:1179:GLN:O	1:DA:1182:ARG:NH1	2.36	0.59
1:DA:212:ARG:HD2	11:DS:134:GLN:NE2	2.18	0.58
19:CK:320:MET:H	25:CU:81:GLU:HG2	1.68	0.58
37:CA:394:A:H5'	37:CA:394:A:C8	2.39	0.58
10:DR:100:ARG:NH1	10:DR:122:ALA:HB1	2.16	0.58
24:CR:295:LYS:HE3	24:CR:298:ASN:HB3	1.83	0.58
11:DS:108:ASN:OD1	11:DS:108:ASN:N	2.30	0.58
17:CH:259:ASP:HB3	17:CH:261:ARG:HD3	1.85	0.58
24:CR:276:ARG:HH21	31:Ca:114:THR:HG23	1.68	0.58
30:Cj:28:LYS:NZ	30:Cj:28:LYS:HB3	2.19	0.58
2:DD:735:GLY:HA3	3:DI:96:CYS:SG	2.43	0.58
12:DU:207:ARG:H	12:DU:207:ARG:HD2	1.67	0.58
13:DZ:13:ALA:H	27:Ca:177:GLN:HE22	1.51	0.58
31:Ca:193:PHE:HD2	31:Ca:197:ALA:HB1	1.68	0.58
36:Cv:718:THR:N	36:Cv:757:ASP:HB2	2.19	0.58
3:DI:291:LEU:HD13	3:DI:300:LEU:HD23	1.86	0.58
27:Ca:579:VAL:O	37:CA:260:U:O2'	2.20	0.58
36:Cv:147:HIS:HD2	36:Cv:149:ASP:H	1.50	0.58
1:DA:512:GLU:OE1	1:DA:512:GLU:N	2.33	0.58
6:DN:123:GLN:HG2	6:DN:160:CYS:HB3	1.86	0.58
11:DS:150:GLN:HE22	11:DS:176:ARG:HH21	1.50	0.58
35:Cr:18:LEU:HD23	35:Cr:90:ILE:HG13	1.84	0.58
24:CR:89:VAL:HG21	34:Cq:112:LYS:HG3	1.85	0.58
2:DD:156:GLN:HE22	29:Ca:67:GLU:HG3	1.68	0.58
2:DD:181:MET:HE1	2:DD:215:TYR:HD1	1.68	0.58
5:DM:271:ARG:NH2	34:Cq:21:MET:SD	2.76	0.58
6:DN:26:ARG:HD2	27:Ca:406:MET:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:DN:183:ARG:NE	6:DN:194:ARG:HH12	2.00	0.58
15:CE:209:GLU:CD	27:Ca:347:ARG:HH12	2.10	0.58
21:CO:207:TYR:HB3	21:CO:226:VAL:HG11	1.85	0.58
1:DA:112:GLN:HG2	1:DA:131:ASP:OD1	2.03	0.58
1:DA:910:HIS:CD2	27:Ca:318:ASP:HB2	2.39	0.58
5:DM:3:VAL:HG21	15:CE:318:PRO:HD2	1.86	0.58
15:CE:280:ARG:HD2	17:CH:217:ASN:HD21	1.69	0.58
27:Ca:299:ARG:HG3	27:Ca:299:ARG:NH1	2.10	0.58
30:Cj:138:ASP:OD1	30:Cj:138:ASP:N	2.31	0.58
1:DA:776:GLY:O	1:DA:925:SER:HA	2.03	0.58
13:DZ:62:ASP:OD1	13:DZ:62:ASP:N	2.29	0.58
16:CF:133:GLN:NE2	29:Cd:178:ASN:O	2.37	0.58
18:CI:132:GLY:HA3	24:CR:225:LEU:HD13	1.83	0.58
27:Ca:225:PRO:HG2	27:Ca:228:LYS:HB2	1.86	0.58
37:CA:39:U:C5'	37:CA:39:U:C6	2.85	0.58
6:DN:113:ALA:HB3	6:DN:133:PHE:CD1	2.37	0.57
9:DQ:73:HIS:CE1	9:DQ:250:ARG:HB2	2.38	0.57
12:DU:83:ARG:CZ	12:DU:157:GLN:HG3	2.33	0.57
15:CE:12:LEU:HB2	37:CA:12:C:C6	2.39	0.57
17:CH:97:ARG:HG2	36:Cv:246:ARG:HD2	1.85	0.57
21:CO:112:LYS:HB2	21:CO:112:LYS:NZ	2.17	0.57
24:CR:153:GLU:HG2	36:Cv:183:LEU:HD23	1.85	0.57
1:DA:602:LEU:HB3	1:DA:803:LEU:HB2	1.84	0.57
3:DI:349:THR:HG23	3:DI:350:TYR:CD1	2.39	0.57
7:DO:151:GLU:HB2	36:Cv:608:ARG:HD3	1.86	0.57
19:CK:258:LEU:HD13	19:CK:275:VAL:HG21	1.86	0.57
30:Cj:50:VAL:HG22	37:CA:51:U:H2'	1.86	0.57
35:Cr:10:ARG:HH12	35:Cr:13:ARG:CB	2.17	0.57
36:Cv:311:LEU:HD21	36:Cv:389:LEU:HD23	1.85	0.57
37:CA:110:U:H5'	37:CA:111:A:OP2	2.04	0.57
2:DD:108:THR:HB	2:DD:707:GLN:HE21	1.69	0.57
6:DN:288:PHE:HD1	6:DN:288:PHE:H	1.52	0.57
11:DS:32:PHE:O	37:CA:206:A:O2'	2.22	0.57
11:DS:37:VAL:HG12	37:CA:199:U:OP1	2.04	0.57
17:CH:133:ARG:NH2	36:Cv:108:HIS:HB2	2.19	0.57
19:CK:215:ARG:NH1	19:CK:218:ASN:HA	2.19	0.57
28:Cb:168:ALA:HB1	28:Cb:174:PHE:HD2	1.67	0.57
2:DD:156:GLN:NE2	29:Cd:70:ARG:HH11	2.02	0.57
15:CE:400:LEU:O	15:CE:404:GLY:N	2.32	0.57
19:CK:113:ARG:NH2	24:CR:192:GLU:OE1	2.36	0.57
19:CK:320:MET:N	25:CU:81:GLU:HG2	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:CU:185:ARG:HD2	25:CU:187:ASN:O	2.05	0.57
36:Cv:27:LYS:HD2	36:Cv:29:LEU:H	1.68	0.57
36:Cv:305:ASP:OD1	36:Cv:305:ASP:N	2.27	0.57
1:DA:912:LEU:HD12	27:Ca:276:SER:HB3	1.86	0.57
1:DA:1060:LEU:HD13	1:DA:1163:MET:HE1	1.86	0.57
2:DD:799:ASP:OD1	2:DD:799:ASP:N	2.34	0.57
4:DL:190:ARG:NH1	24:CR:71:PHE:CE1	2.73	0.57
12:DU:207:ARG:HB2	37:CA:160:U:C5	2.39	0.57
17:CH:176:ILE:HD13	17:CH:179:ARG:HH12	1.69	0.57
9:DQ:34:THR:O	10:DR:27:LYS:NZ	2.38	0.57
9:DQ:92:MET:HE1	9:DQ:210:VAL:HG11	1.85	0.57
10:DR:149:ALA:HB3	10:DR:152:ALA:HB2	1.85	0.57
35:Cr:19:LEU:HD21	35:Cr:41:LEU:HD11	1.86	0.57
36:Cv:77:TYR:HB2	36:Cv:165:GLU:HG3	1.86	0.57
36:Cv:318:PHE:HE1	36:Cv:887:ARG:HB2	1.68	0.57
2:DD:576:MET:HE1	2:DD:606:ARG:HB2	1.87	0.57
7:DO:198:ARG:NH1	7:DO:256:ARG:NH1	2.53	0.57
1:DA:904:TRP:CE2	27:Ca:399:ASN:HA	2.40	0.57
1:DA:1414:LEU:HD21	1:DA:1421:GLU:HG3	1.87	0.57
2:DD:654:ARG:HB2	29:Cd:48:ASN:HD22	1.70	0.57
5:DM:76:ASN:HD21	36:Cv:971:LEU:H	1.51	0.57
6:DN:47:VAL:HG22	6:DN:132:TYR:HB2	1.86	0.57
7:DO:114:GLY:C	7:DO:116:ALA:H	2.12	0.57
27:Ca:597:LYS:HB2	27:Ca:597:LYS:NZ	2.20	0.57
33:Cp:171:MET:HE2	33:Cp:175:ALA:HB1	1.85	0.57
1:DA:90:MET:HE1	2:DD:122:GLN:NE2	2.17	0.57
1:DA:251:SER:OG	1:DA:253:ASP:OD1	2.15	0.57
1:DA:1507:VAL:HB	5:DM:175:GLU:HG3	1.87	0.57
10:DR:101:VAL:HG21	10:DR:123:VAL:HG12	1.86	0.57
10:DR:128:PRO:CG	10:DR:133:LEU:N	2.65	0.57
15:CE:32:TRP:CD1	15:CE:33:MET:HG3	2.39	0.57
28:Cb:56:ARG:HH11	28:Cb:57:MET:HE1	1.69	0.57
1:DA:1029:LYS:HZ1	5:DM:254:HIS:CE1	2.21	0.56
10:DR:93:PRO:HB2	10:DR:96:PHE:CD2	2.40	0.56
2:DD:626:ARG:NH1	30:Cj:156:THR:O	2.39	0.56
6:DN:227:LYS:HE2	6:DN:287:ARG:HH22	1.70	0.56
6:DN:251:PHE:CD2	6:DN:273:SER:HB3	2.40	0.56
10:DR:112:ARG:HH11	30:Cj:158:THR:HG23	1.71	0.56
15:CE:308:ARG:CA	15:CE:311:LYS:HZ2	2.17	0.56
19:CK:200:ARG:NE	19:CK:205:TYR:OH	2.39	0.56
19:CK:322:ARG:HH11	19:CK:326:LYS:HE2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Cr:42:ILE:HD11	35:Cr:95:SER:HA	1.86	0.56
1:DA:333:VAL:HG13	13:DZ:62:ASP:HB2	1.87	0.56
2:DD:704:ASP:OD1	2:DD:704:ASP:N	2.31	0.56
25:CU:65:VAL:HG12	25:CU:71:ARG:HB3	1.88	0.56
30:Cj:107:ALA:HB2	30:Cj:173:MET:HE1	1.87	0.56
35:Cr:152:VAL:HG12	35:Cr:181:PRO:HA	1.88	0.56
36:Cv:62:LEU:O	36:Cv:99:VAL:HG22	2.05	0.56
36:Cv:626:VAL:HB	36:Cv:628:LYS:HZ1	1.70	0.56
1:DA:193:GLU:N	1:DA:193:GLU:OE1	2.37	0.56
2:DD:575:THR:HG22	2:DD:577:LYS:HB2	1.86	0.56
10:DR:128:PRO:HD3	10:DR:133:LEU:C	2.30	0.56
21:CO:332:ARG:NH1	21:CO:340:ASP:OD2	2.39	0.56
25:CU:69:ARG:NE	25:CU:94:GLU:OE2	2.39	0.56
27:Ca:62:TRP:CD1	27:Ca:79:MET:HE1	2.40	0.56
27:Ca:569:ARG:NH1	37:CA:143:U:H5''	2.21	0.56
35:Cr:143:ARG:HD3	35:Cr:187:VAL:HG21	1.87	0.56
36:Cv:559:GLN:HG3	39:UR:3:UNK:HB1	1.87	0.56
1:DA:562:LYS:HA	1:DA:567:ALA:HB3	1.86	0.56
5:DM:21:ARG:HB3	5:DM:236:MET:HE2	1.87	0.56
17:CH:16:VAL:HB	17:CH:17:PRO:CD	2.34	0.56
18:CI:183:PRO:HD2	24:CR:87:GLU:HG2	1.87	0.56
19:CK:322:ARG:NH1	19:CK:326:LYS:HE2	2.19	0.56
35:Cr:46:GLY:HA3	35:Cr:176:LEU:HD11	1.86	0.56
36:Cv:79:ASP:O	36:Cv:83:TRP:HB2	2.05	0.56
37:CA:233:C:H4'	37:CA:234:C:H5''	1.88	0.56
3:DI:66:ARG:HG3	3:DI:178:PHE:CE2	2.41	0.56
8:DP:20:MET:O	8:DP:23:LEU:HB2	2.06	0.56
9:DQ:79:LEU:HB3	9:DQ:83:ASN:HD21	1.69	0.56
19:CK:214:LYS:HB3	19:CK:214:LYS:HZ2	1.71	0.56
21:CO:371:LYS:NZ	21:CO:382:GLU:OE2	2.32	0.56
33:Cp:85:PHE:CD2	33:Cp:109:VAL:HG13	2.40	0.56
37:CA:85:U:C5'	37:CA:85:U:C6	2.88	0.56
37:CA:310:A:N3	37:CA:310:A:H2'	2.19	0.56
1:DA:518:GLU:OE2	1:DA:837:ARG:NH2	2.39	0.56
2:DD:94:LYS:HE3	2:DD:99:THR:O	2.06	0.56
15:CE:192:GLU:OE2	15:CE:195:ARG:NH1	2.38	0.56
21:CO:80:ARG:NH1	21:CO:84:GLU:OE2	2.39	0.56
22:CP:173:LYS:NZ	22:CP:181:GLU:OE1	2.38	0.56
27:Ca:88:ARG:NH2	36:Cv:1110:GLU:OE1	2.38	0.56
34:Cq:150:LEU:HB2	34:Cq:252:GLU:HG3	1.87	0.56
36:Cv:200:ASP:HB2	36:Cv:612:THR:HG23	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Cv:405:PRO:HB3	36:Cv:427:TYR:HE2	1.69	0.56
37:CA:80:U:O2	37:CA:80:U:H2'	2.06	0.56
1:DA:1506:ASN:HB2	1:DA:1507:VAL:HG13	1.87	0.56
15:CE:42:ARG:NH1	15:CE:105:GLN:NE2	2.52	0.56
18:CI:250:ASN:ND2	18:CI:276:ASP:OD2	2.36	0.56
19:CK:326:LYS:HD2	25:CU:83:SER:H	1.71	0.56
36:Cv:1012:TRP:CD1	36:Cv:1014:ARG:HG3	2.40	0.56
34:Cq:55:PHE:H	34:Cq:93:ASN:HD21	1.53	0.56
37:CA:63:G:N2	37:CA:156:U:HO2'	2.04	0.56
1:DA:649:LEU:CD1	1:DA:729:ARG:HH11	2.19	0.56
6:DN:142:ARG:HG3	17:CH:19:LEU:HD11	1.87	0.56
15:CE:110:LEU:HB2	15:CE:113:GLU:HG3	1.87	0.56
19:CK:113:ARG:HG2	19:CK:113:ARG:HH11	1.70	0.56
28:Cb:276:LYS:NZ	35:Cr:292:GLU:HB3	2.21	0.56
33:Cp:163:PRO:HG2	33:Cp:165:TYR:CE1	2.40	0.56
5:DM:217:ALA:O	5:DM:221:LYS:NZ	2.39	0.55
6:DN:183:ARG:CZ	6:DN:194:ARG:NH1	2.69	0.55
6:DN:291:PRO:O	15:CE:114:TYR:OH	2.10	0.55
9:DQ:14:ARG:HB2	9:DQ:14:ARG:NH1	2.20	0.55
17:CH:253:TYR:CZ	17:CH:280:MET:HE3	2.41	0.55
19:CK:156:LYS:HB2	19:CK:156:LYS:HZ3	1.70	0.55
19:CK:203:ASN:OD1	19:CK:204:THR:N	2.38	0.55
19:CK:280:ARG:HA	19:CK:308:GLU:O	2.06	0.55
21:CO:82:ASN:ND2	32:Cn:142:TRP:H	2.04	0.55
21:CO:399:ILE:HD12	21:CO:400:ARG:H	1.70	0.55
37:CA:217:U:H3'	37:CA:218:A:H8	1.71	0.55
1:DA:584:PHE:HB3	1:DA:759:GLY:HA3	1.89	0.55
10:DR:128:PRO:HG3	10:DR:133:LEU:H	1.66	0.55
20:CL:59:MET:HE2	20:CL:123:GLY:HA3	1.87	0.55
27:Ca:570:THR:HG21	33:Cp:16:HIS:CD2	2.42	0.55
36:Cv:626:VAL:HB	36:Cv:628:LYS:HZ2	1.70	0.55
6:DN:165:GLU:HG3	6:DN:171:LEU:H	1.70	0.55
19:CK:207:VAL:HG22	19:CK:219:THR:HG23	1.88	0.55
21:CO:245:ASN:OD1	21:CO:245:ASN:N	2.38	0.55
23:CQ:140:VAL:HG21	23:CQ:172:ARG:HG3	1.88	0.55
24:CR:198:THR:HB	24:CR:200:SER:H	1.72	0.55
28:Cb:298:ASP:HB3	35:Cr:40:HIS:CG	2.41	0.55
32:Cn:141:ARG:HD2	37:CA:280:A:N1	2.21	0.55
36:Cv:559:GLN:NE2	39:UR:3:UNK:HG1	2.21	0.55
36:Cv:945:VAL:HG13	36:Cv:946:PRO:HD3	1.88	0.55
2:DD:356:PRO:HB2	30:Cj:157:THR:CG2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:605:ARG:HH12	2:DD:642:ASP:CG	2.14	0.55
5:DM:41:GLU:OE2	27:Ca:286:ARG:NH2	2.36	0.55
13:DZ:20:ARG:HG3	13:DZ:20:ARG:NH1	2.19	0.55
17:CH:133:ARG:CZ	36:Cv:108:HIS:HB2	2.36	0.55
19:CK:317:GLY:HA2	31:Cm:195:PHE:CD1	2.41	0.55
3:DI:113:VAL:HG22	3:DI:114:PRO:HD2	1.88	0.55
12:DU:27:ARG:HB3	12:DU:27:ARG:HH11	1.70	0.55
15:CE:397:GLU:OE2	15:CE:401:LYS:NZ	2.39	0.55
21:CO:217:ASP:OD1	21:CO:220:SER:HB3	2.07	0.55
29:Cd:178:ASN:HB2	29:Cd:182:GLN:H	1.72	0.55
32:Cn:179:ARG:HG3	32:Cn:183:ARG:HD3	1.89	0.55
34:Cq:191:VAL:HG12	34:Cq:215:PRO:HA	1.89	0.55
6:DN:71:GLU:O	6:DN:111:ILE:HG23	2.06	0.55
18:CI:191:LEU:HD11	34:Cq:257:MET:HE3	1.87	0.55
30:Cj:147:TYR:CE1	30:Cj:162:GLN:HG2	2.41	0.55
36:Cv:678:HIS:HD2	36:Cv:680:ARG:HD2	1.72	0.55
36:Cv:955:LEU:HG	36:Cv:959:LEU:HD23	1.89	0.55
1:DA:949:ARG:HD2	5:DM:18:HIS:HA	1.89	0.55
10:DR:108:GLN:HE22	30:Cj:147:TYR:CB	2.20	0.55
15:CE:13:ASN:OD1	15:CE:13:ASN:N	2.39	0.55
26:CZ:265:GLN:HB3	26:CZ:308:TYR:CE1	2.42	0.55
30:Cj:94:ILE:HG23	30:Cj:98:LYS:HG3	1.89	0.55
34:Cq:92:LEU:O	34:Cq:96:THR:OG1	2.23	0.55
1:DA:1065:ALA:H	1:DA:1161:GLY:HA3	1.71	0.55
2:DD:21:ARG:NH2	37:CA:274:A:N7	2.53	0.55
2:DD:347:GLU:OE1	2:DD:347:GLU:N	2.39	0.55
3:DI:256:ARG:NH1	3:DI:271:TYR:O	2.40	0.55
11:DS:238:ARG:HG3	11:DS:239:SER:N	2.21	0.55
21:CO:71:PRO:HB3	32:Cn:192:ASN:HD21	1.71	0.55
21:CO:399:ILE:HD12	21:CO:400:ARG:N	2.22	0.55
41:UT:30:UNK:O	41:UT:32:UNK:N	2.40	0.55
1:DA:216:LEU:HB3	1:DA:238:VAL:HG22	1.89	0.55
1:DA:945:ILE:HB	5:DM:128:ILE:HD11	1.89	0.55
1:DA:1662:ARG:NH2	15:CE:402:ARG:HH12	2.04	0.55
6:DN:141:MET:HB2	6:DN:149:ASP:HB3	1.89	0.55
10:DR:67:LYS:HA	10:DR:67:LYS:HZ3	1.70	0.55
15:CE:83:MET:CE	15:CE:83:MET:H	2.20	0.55
19:CK:231:ASP:HB3	19:CK:232:ARG:HD2	1.87	0.55
27:Ca:332:ARG:NH1	27:Ca:333:ASP:OD1	2.40	0.55
1:DA:319:ARG:HG2	1:DA:319:ARG:NH1	2.22	0.55
8:DP:189:TYR:OH	8:DP:208:PRO:HD3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:DQ:218:ARG:HD2	9:DQ:223:ASP:OD1	2.07	0.55
10:DR:131:LEU:HD11	12:DU:170:ARG:HH21	1.71	0.55
17:CH:249:ARG:HD3	17:CH:266:ILE:HD13	1.88	0.55
19:CK:321:PRO:HD3	25:CU:16:HIS:CE1	2.42	0.55
24:CR:75:GLN:HB3	24:CR:94:MET:HE3	1.89	0.55
29:Cd:13:ARG:CZ	29:Cd:26:ARG:HH21	2.20	0.55
31:Cm:146:TRP:CD1	31:Cm:150:ASN:HD22	2.25	0.55
35:Cr:168:MET:HE1	35:Cr:177:LEU:HD12	1.88	0.55
1:DA:247:ASP:OD1	27:Ca:553:ARG:NH1	2.36	0.54
12:DU:207:ARG:HB2	37:CA:160:U:C6	2.42	0.54
19:CK:307:PHE:HE1	25:CU:61:ILE:HD12	1.72	0.54
23:CQ:103:MET:HB2	23:CQ:106:THR:HB	1.90	0.54
28:Cb:52:TYR:O	28:Cb:56:ARG:HB2	2.08	0.54
31:Cm:85:ILE:HD13	31:Cm:87:LEU:HD12	1.88	0.54
4:DL:246:GLU:CD	31:Cm:61:ARG:HH12	2.15	0.54
5:DM:43:GLN:NE2	15:CE:313:MET:H	2.05	0.54
11:DS:56:LEU:HG	11:DS:88:TRP:HA	1.90	0.54
11:DS:76:GLU:OE1	11:DS:76:GLU:N	2.40	0.54
21:CO:138:LEU:HD23	21:CO:138:LEU:H	1.72	0.54
21:CO:285:ASP:OD1	21:CO:285:ASP:N	2.30	0.54
27:Ca:323:LYS:HG3	27:Ca:330:TRP:CD2	2.42	0.54
36:Cv:827:ALA:HB3	36:Cv:830:ASN:HD22	1.73	0.54
13:DZ:34:LYS:HG3	13:DZ:35:LYS:H	1.72	0.54
24:CR:122:MET:HE1	36:Cv:192:LEU:HA	1.90	0.54
28:Cb:19:PRO:HD2	31:Cm:156:THR:CG2	2.37	0.54
28:Cb:168:ALA:HB2	35:Cr:144:ARG:HD3	1.89	0.54
34:Cq:181:HIS:HB2	34:Cq:201:GLU:HG3	1.88	0.54
1:DA:230:PHE:O	11:DS:62:ARG:NH2	2.39	0.54
2:DD:421:PHE:HB3	2:DD:531:LYS:HG3	1.89	0.54
5:DM:90:LEU:HD12	36:Cv:941:ALA:HB2	1.88	0.54
7:DO:254:ASP:OD1	7:DO:254:ASP:N	2.38	0.54
9:DQ:31:PRO:HG2	37:CA:85:U:H4'	1.90	0.54
11:DS:150:GLN:HE22	11:DS:176:ARG:NH2	2.05	0.54
16:CF:112:GLN:HA	36:Cv:204:ILE:HG12	1.88	0.54
1:DA:131:ASP:O	1:DA:133:SER:N	2.41	0.54
1:DA:938:ILE:HD13	5:DM:126:MET:HE3	1.89	0.54
2:DD:387:GLN:HE22	2:DD:453:ASN:H	1.53	0.54
2:DD:787:ARG:NH1	27:Ca:206:LEU:HD13	2.22	0.54
3:DI:161:MET:O	3:DI:165:ARG:HG3	2.08	0.54
5:DM:23:MET:HE3	5:DM:28:PHE:HB2	1.89	0.54
21:CO:261:HIS:O	21:CO:265:ARG:HG3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CR:276:ARG:NH2	31:Cm:114:THR:HG23	2.22	0.54
28:Cb:298:ASP:OD1	28:Cb:298:ASP:N	2.40	0.54
30:Cj:112:ARG:NH1	30:Cj:183:PHE:HA	2.23	0.54
1:DA:1384:ARG:HH12	1:DA:1628:ARG:HE	1.55	0.54
3:DI:25:PRO:HB3	3:DI:79:ILE:HD11	1.90	0.54
4:DL:119:MET:HE3	4:DL:153:ALA:HB2	1.90	0.54
2:DD:741:ARG:CB	2:DD:741:ARG:HH11	2.20	0.54
3:DI:88:GLN:OE1	3:DI:92:GLU:OE2	2.25	0.54
7:DO:60:MET:HE1	7:DO:111:ARG:HB3	1.89	0.54
11:DS:216:TRP:CZ2	11:DS:220:MET:HE3	2.43	0.54
21:CO:301:TRP:HZ2	23:CQ:182:VAL:HG21	1.72	0.54
24:CR:142:MET:HE1	24:CR:155:VAL:HG13	1.89	0.54
26:CZ:250:PRO:HB3	26:CZ:321:MET:HE2	1.90	0.54
30:Cj:124:GLY:O	30:Cj:207:LYS:NZ	2.24	0.54
31:Cm:211:LEU:HD23	31:Cm:212:PRO:HD2	1.90	0.54
37:CA:134:U:H2'	37:CA:135:U:H5''	1.89	0.54
7:DO:139:GLU:HB3	7:DO:176:THR:HG23	1.90	0.54
19:CK:176:TYR:CZ	19:CK:180:ASP:HB3	2.43	0.54
28:Cb:303:GLU:HB2	35:Cr:105:ARG:NH1	2.21	0.54
29:Cd:137:ARG:HG2	29:Cd:137:ARG:NH1	2.22	0.54
1:DA:65:ILE:HD11	2:DD:164:ARG:HG3	1.89	0.54
8:DP:143:ASN:ND2	30:Cj:142:ASN:OD1	2.41	0.54
12:DU:205:ALA:HB1	12:DU:206:PRO:HD2	1.88	0.54
15:CE:88:ASP:OD2	15:CE:302:PRO:HB2	2.08	0.54
16:CF:123:ARG:HG3	16:CF:127:GLU:CD	2.33	0.54
17:CH:107:ARG:HH11	17:CH:107:ARG:HG3	1.72	0.54
18:CI:202:LEU:HA	18:CI:211:ASN:HD21	1.73	0.54
21:CO:259:LEU:HD22	21:CO:286:ILE:HD11	1.90	0.54
36:Cv:27:LYS:HE3	36:Cv:29:LEU:HB2	1.89	0.54
36:Cv:470:PHE:HD1	36:Cv:556:PHE:CE2	2.26	0.54
3:DI:307:ASN:HB2	3:DI:310:LEU:HB2	1.90	0.54
5:DM:56:TRP:O	5:DM:59:ARG:HG2	2.08	0.54
11:DS:34:SER:O	11:DS:34:SER:OG	2.21	0.54
14:Da:10:ILE:HG23	14:Da:22:ARG:HH11	1.71	0.54
15:CE:10:LYS:N	37:CA:11:U:O4'	2.41	0.54
16:CF:15:ARG:NH1	29:Cd:165:ASP:OD1	2.39	0.54
17:CH:150:THR:HG22	17:CH:151:PRO:HD2	1.89	0.54
20:CL:97:LEU:HD11	40:US:40:UNK:HG3	1.89	0.54
24:CR:320:VAL:HG22	25:CU:185:ARG:NH2	2.23	0.54
30:Cj:46:TYR:HA	30:Cj:165:PHE:HE2	1.72	0.54
36:Cv:738:ARG:HH21	36:Cv:788:ARG:HD2	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:CA:81:U:O2	37:CA:81:U:H2'	2.06	0.54
37:CA:88:A:H3'	37:CA:88:A:OP2	2.08	0.54
2:DD:527:THR:HG21	10:DR:224:ALA:H	1.73	0.53
2:DD:610:VAL:HG21	10:DR:229:ARG:O	2.08	0.53
5:DM:266:ALA:HB2	15:CE:61:PHE:CE2	2.42	0.53
9:DQ:146:GLN:CG	9:DQ:176:ARG:HH12	2.21	0.53
9:DQ:181:VAL:O	9:DQ:184:ILE:HG13	2.08	0.53
36:Cv:561:SER:HG	36:Cv:564:ASP:H	1.56	0.53
1:DA:80:PRO:HB3	37:CA:153:A:N1	2.22	0.53
1:DA:834:PRO:HA	1:DA:837:ARG:HD2	1.90	0.53
1:DA:1414:LEU:HD23	1:DA:1424:VAL:HG21	1.90	0.53
2:DD:631:ALA:HB1	2:DD:635:LEU:HD23	1.90	0.53
2:DD:665:GLU:HG3	27:Ca:427:TRP:HA	1.89	0.53
5:DM:52:VAL:HG22	5:DM:63:VAL:HG22	1.90	0.53
5:DM:130:ASP:O	5:DM:164:ILE:HD11	2.08	0.53
6:DN:113:ALA:O	6:DN:131:PRO:HD2	2.08	0.53
8:DP:48:GLN:OE1	8:DP:75:ARG:NH2	2.34	0.53
19:CK:73:GLN:HG3	28:Cb:178:ARG:NH2	2.24	0.53
21:CO:353:GLU:HB3	23:CQ:104:LEU:HD21	1.90	0.53
27:Ca:191:MET:SD	27:Ca:195:ARG:NH2	2.80	0.53
36:Cv:78:ILE:HD11	36:Cv:80:TYR:CZ	2.43	0.53
6:DN:23:VAL:HG12	6:DN:116:VAL:CG1	2.38	0.53
26:CZ:341:LYS:HD2	37:CA:578:C:P	2.48	0.53
31:Cm:56:ASN:HD21	31:Cm:62:ALA:HB2	1.74	0.53
31:Cm:83:LYS:HZ1	37:CA:393:U:H5'	1.72	0.53
31:Cm:95:MET:SD	31:Cm:95:MET:N	2.81	0.53
1:DA:1524:ARG:HH21	1:DA:1601:ARG:HH21	1.57	0.53
2:DD:83:THR:O	2:DD:87:MET:N	2.31	0.53
2:DD:106:ALA:HB2	27:Ca:457:LYS:HD3	1.90	0.53
4:DL:181:ARG:HG3	4:DL:181:ARG:NH1	2.17	0.53
16:CF:35:LEU:HD21	21:CO:187:LYS:HD3	1.91	0.53
22:CP:88:LEU:HD21	33:Cp:33:ILE:HD13	1.90	0.53
26:CZ:305:HIS:CD2	26:CZ:307:LYS:HB2	2.39	0.53
27:Ca:507:MET:O	27:Ca:513:ASN:ND2	2.41	0.53
31:Cm:53:THR:H	31:Cm:56:ASN:HB3	1.72	0.53
36:Cv:847:ARG:NE	36:Cv:938:ASP:OD2	2.38	0.53
37:CA:153:A:C4	37:CA:154:G:C8	2.96	0.53
1:DA:651:ARG:HG2	1:DA:727:SER:HB3	1.90	0.53
5:DM:77:PRO:HD3	36:Cv:968:LEU:O	2.07	0.53
8:DP:132:LEU:HD21	8:DP:154:PHE:CE1	2.43	0.53
9:DQ:77:LEU:HB2	9:DQ:115:ILE:HB	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:DU:206:PRO:HB3	21:CO:387:VAL:HG13	1.91	0.53
24:CR:199:TYR:CZ	25:CU:106:LYS:NZ	2.76	0.53
24:CR:295:LYS:HE2	24:CR:299:LEU:HA	1.90	0.53
28:Cb:168:ALA:HB1	28:Cb:174:PHE:CD2	2.43	0.53
36:Cv:690:GLU:HB2	36:Cv:798:TYR:CE1	2.44	0.53
1:DA:650:LEU:HB3	1:DA:728:VAL:HG12	1.91	0.53
17:CH:138:LYS:NZ	17:CH:138:LYS:HB2	2.23	0.53
2:DD:17:ALA:O	15:CE:223:ARG:NH1	2.41	0.53
2:DD:763:TYR:CD1	27:Ca:387:GLN:HG2	2.44	0.53
6:DN:129:LEU:HD21	6:DN:156:ALA:HB2	1.91	0.53
10:DR:87:LEU:HB2	10:DR:178:TYR:HE2	1.74	0.53
11:DS:142:GLN:O	11:DS:145:PRO:HD3	2.09	0.53
17:CH:113:LYS:O	17:CH:120:TYR:OH	2.21	0.53
27:Ca:225:PRO:HD2	27:Ca:228:LYS:HD2	1.91	0.53
36:Cv:604:LEU:HD23	36:Cv:766:THR:HG22	1.91	0.53
1:DA:135:ASP:OD2	29:Cd:109:MET:HE2	2.09	0.53
9:DQ:72:THR:O	9:DQ:251:MET:HG3	2.09	0.53
11:DS:111:VAL:HG12	11:DS:117:ALA:HB3	1.90	0.53
11:DS:238:ARG:HG3	11:DS:239:SER:H	1.73	0.53
22:CP:69:PRO:HA	22:CP:90:MET:HE1	1.91	0.53
36:Cv:559:GLN:OE1	36:Cv:565:ILE:HG12	2.08	0.53
8:DP:171:LEU:HD11	8:DP:187:ARG:HA	1.91	0.53
21:CO:264:ARG:NH1	21:CO:303:TYR:HB3	2.24	0.53
32:Cn:163:ARG:NH1	37:CA:591:A:O2'	2.41	0.53
33:Cp:93:ARG:HH12	37:CA:187:A:H2	1.55	0.53
35:Cr:103:VAL:HG23	35:Cr:184:VAL:HG13	1.91	0.53
37:CA:360:C:C2'	37:CA:361:A:H5'	2.39	0.53
1:DA:1606:THR:HG22	1:DA:1607:MET:HG3	1.91	0.53
8:DP:206:TYR:O	8:DP:212:ASN:HB2	2.09	0.53
9:DQ:142:PHE:HB3	9:DQ:267:LEU:HD21	1.91	0.53
24:CR:23:TRP:CD2	36:Cv:494:THR:HG21	2.43	0.53
27:Ca:89:ARG:HD2	27:Ca:177:GLN:HE21	1.74	0.53
27:Ca:569:ARG:NH1	37:CA:143:U:OP1	2.37	0.53
36:Cv:392:HIS:HB3	36:Cv:417:THR:HG21	1.90	0.53
36:Cv:454:LEU:HA	36:Cv:457:ARG:HD2	1.91	0.53
37:CA:43:A:H62	37:CA:173:A:H62	1.57	0.53
1:DA:410:ASP:OD1	1:DA:494:ARG:NH1	2.41	0.52
1:DA:565:ASN:HA	6:DN:144:ARG:NH1	2.23	0.52
1:DA:1650:MET:HE1	15:CE:425:PRO:HD2	1.91	0.52
2:DD:296:LEU:HD13	2:DD:392:SER:HB2	1.90	0.52
2:DD:576:MET:HE3	10:DR:221:ARG:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:DZ:11:LYS:O	27:Ca:89:ARG:NH1	2.42	0.52
23:CQ:197:LYS:NZ	23:CQ:199:ASN:O	2.41	0.52
25:CU:62:MET:HB3	25:CU:171:VAL:HG11	1.90	0.52
28:Cb:222:SER:OG	28:Cb:273:VAL:O	2.22	0.52
31:Cm:77:PRO:HB3	31:Cm:155:HIS:HE1	1.73	0.52
34:Cq:78:ASP:O	34:Cq:82:SER:OG	2.27	0.52
1:DA:1060:LEU:O	34:Cq:140:ARG:NE	2.36	0.52
2:DD:283:MET:HG3	3:DI:65:MET:HE3	1.90	0.52
4:DL:139:ARG:HH22	4:DL:203:ARG:NH1	2.06	0.52
6:DN:214:MET:HE2	6:DN:217:MET:HE2	1.91	0.52
11:DS:17:SER:OG	11:DS:18:ARG:N	2.43	0.52
15:CE:240:ASP:HA	15:CE:243:CYS:HB2	1.91	0.52
17:CH:107:ARG:HH12	17:CH:133:ARG:NE	2.08	0.52
18:CI:139:ASP:OD1	18:CI:139:ASP:N	2.41	0.52
19:CK:77:MET:HG2	28:Cb:286:LEU:HD13	1.92	0.52
35:Cr:247:ILE:HG13	35:Cr:248:ARG:N	2.24	0.52
1:DA:130:ALA:N	17:CH:260:ASN:HD21	2.07	0.52
10:DR:60:VAL:HG22	10:DR:63:ILE:HG12	1.90	0.52
12:DU:115:LYS:O	12:DU:119:ILE:HG13	2.09	0.52
14:Da:25:ARG:C	14:Da:25:ARG:HD3	2.34	0.52
16:CF:34:GLY:HA2	21:CO:193:MET:HE1	1.91	0.52
24:CR:60:PHE:CE2	24:CR:62:GLN:HB3	2.44	0.52
36:Cv:592:TYR:HE1	36:Cv:785:ILE:HD11	1.74	0.52
36:Cv:1108:GLN:HA	36:Cv:1108:GLN:HE21	1.74	0.52
37:CA:261:U:OP2	44:CA:733:SPD:H42	2.10	0.52
2:DD:347:GLU:OE2	10:DR:188:LYS:NZ	2.40	0.52
3:DI:307:ASN:OD1	29:Cd:107:GLN:HG2	2.10	0.52
9:DQ:63:PRO:HB3	12:DU:34:TYR:HD2	1.74	0.52
25:CU:16:HIS:CD2	25:CU:18:LYS:H	2.25	0.52
25:CU:52:GLU:HG3	29:Cd:250:LEU:HD21	1.91	0.52
27:Ca:272:PHE:CE1	27:Ca:309:ALA:HB1	2.45	0.52
35:Cr:10:ARG:HH12	35:Cr:13:ARG:HB3	1.75	0.52
36:Cv:77:TYR:N	36:Cv:165:GLU:OE2	2.37	0.52
2:DD:27:MET:HE1	17:CH:239:ARG:HD2	1.90	0.52
3:DI:66:ARG:HA	3:DI:177:THR:HG21	1.91	0.52
5:DM:55:GLU:HB2	5:DM:94:ALA:HB2	1.92	0.52
9:DQ:135:GLN:HA	9:DQ:138:MET:HE2	1.89	0.52
10:DR:127:VAL:HG22	10:DR:134:LEU:HD23	1.92	0.52
1:DA:1510:GLU:OE1	1:DA:1510:GLU:N	2.42	0.52
2:DD:133:GLU:OE2	12:DU:50:SER:OG	2.25	0.52
13:DZ:74:MET:HE3	27:Ca:194:LEU:HD13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:Da:11:ALA:HB2	37:CA:149:U:H5''	1.92	0.52
15:CE:173:LYS:HB3	28:Cb:45:PHE:CE2	2.45	0.52
27:Ca:38:TRP:CH2	41:UT:25:UNK:HA	2.44	0.52
27:Ca:233:ARG:NH1	27:Ca:233:ARG:HB3	2.24	0.52
30:Cj:47:VAL:HG22	30:Cj:48:PRO:HD2	1.90	0.52
34:Cq:146:PRO:HG3	34:Cq:167:MET:HE2	1.91	0.52
1:DA:617:PRO:HG2	1:DA:746:GLN:HE22	1.74	0.52
7:DO:59:ALA:HA	7:DO:62:LEU:HD23	1.92	0.52
10:DR:30:TRP:CE3	12:DU:98:MET:HB2	2.44	0.52
12:DU:62:ARG:HG2	12:DU:64:TYR:CZ	2.45	0.52
20:CL:128:ASP:OD2	37:CA:237:C:N4	2.43	0.52
21:CO:127:THR:HG22	21:CO:131:LYS:HZ1	1.72	0.52
21:CO:211:TYR:CD2	21:CO:226:VAL:HG21	2.45	0.52
21:CO:214:HIS:CD2	21:CO:216:PHE:H	2.28	0.52
22:CP:32:ARG:NH1	22:CP:52:LYS:HD3	2.25	0.52
2:DD:797:PHE:HB2	2:DD:803:GLN:HE21	1.75	0.52
6:DN:74:HIS:O	6:DN:109:ASN:OD1	2.27	0.52
8:DP:101:PHE:O	30:Cj:139:ARG:HD2	2.10	0.52
10:DR:117:ILE:HG22	10:DR:118:VAL:H	1.75	0.52
17:CH:107:ARG:NH1	17:CH:133:ARG:NE	2.57	0.52
26:CZ:306:ILE:HG12	26:CZ:308:TYR:HE1	1.75	0.52
36:Cv:1003:HIS:HB3	36:Cv:1006:GLU:O	2.10	0.52
1:DA:1038:HIS:CG	1:DA:1045:ILE:HD11	2.45	0.52
1:DA:1045:ILE:HD12	5:DM:291:ILE:HG23	1.92	0.52
6:DN:293:PRO:HB3	15:CE:109:LYS:HZ3	1.75	0.52
8:DP:196:TRP:CD1	8:DP:196:TRP:H	2.26	0.52
17:CH:167:LYS:HD3	36:Cv:102:ASP:OD1	2.10	0.52
24:CR:89:VAL:O	28:Cb:112:TYR:OH	2.22	0.52
27:Ca:577:PRO:HG2	27:Ca:579:VAL:HG12	1.91	0.52
31:Cm:47:ASN:ND2	37:CA:387:U:H4'	2.25	0.52
37:CA:84:U:H2'	37:CA:84:U:OP2	2.09	0.52
1:DA:971:GLU:HG2	1:DA:972:PRO:HD3	1.92	0.52
3:DI:48:LEU:HD23	3:DI:165:ARG:HH21	1.74	0.52
24:CR:36:THR:HG23	24:CR:99:ASN:HD22	1.75	0.52
28:Cb:294:THR:HG23	35:Cr:283:LYS:HB3	1.92	0.52
34:Cq:104:HIS:HB3	34:Cq:108:THR:OG1	2.09	0.52
37:CA:351:A:H3'	37:CA:351:A:OP2	2.10	0.52
1:DA:501:GLU:HG2	1:DA:889:VAL:HB	1.92	0.51
3:DI:27:THR:N	3:DI:30:GLN:HE21	2.07	0.51
6:DN:118:LEU:HB3	6:DN:127:VAL:HG23	1.90	0.51
11:DS:215:SER:O	11:DS:218:PRO:HD2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CR:136:LEU:HD13	24:CR:140:GLY:O	2.10	0.51
24:CR:308:MET:HE3	37:CA:388:U:H5'	1.92	0.51
25:CU:142:PRO:HD3	25:CU:154:LYS:HE2	1.91	0.51
36:Cv:441:PRO:HD3	36:Cv:447:PRO:HD3	1.91	0.51
1:DA:164:TRP:HZ3	2:DD:201:GLU:HG2	1.75	0.51
1:DA:303:TYR:HB2	1:DA:306:GLU:HG3	1.93	0.51
3:DI:351:LEU:O	3:DI:381:TYR:OH	2.23	0.51
5:DM:289:GLU:OE1	5:DM:289:GLU:N	2.39	0.51
15:CE:311:LYS:HD2	15:CE:311:LYS:N	2.24	0.51
24:CR:37:PRO:HD3	28:Cb:110:MET:HG3	1.91	0.51
26:CZ:276:HIS:HB3	26:CZ:305:HIS:NE2	2.25	0.51
36:Cv:584:SER:HB2	36:Cv:790:THR:CG2	2.41	0.51
9:DQ:33:VAL:HA	9:DQ:37:GLU:HG3	1.92	0.51
17:CH:173:PRO:O	17:CH:178:THR:HG21	2.10	0.51
27:Ca:335:ARG:NH2	27:Ca:391:ASP:OD1	2.42	0.51
1:DA:182:ARG:HH12	27:Ca:414:THR:CG2	2.23	0.51
8:DP:120:ASP:O	8:DP:160:ARG:NH1	2.40	0.51
10:DR:113:LEU:HD21	10:DR:140:PHE:HE1	1.76	0.51
36:Cv:938:ASP:OD1	36:Cv:938:ASP:N	2.42	0.51
1:DA:212:ARG:HA	11:DS:134:GLN:NE2	2.22	0.51
1:DA:907:GLN:NE2	27:Ca:399:ASN:HD22	2.08	0.51
2:DD:91:TYR:CE1	23:CQ:25:MET:HG3	2.45	0.51
2:DD:115:GLU:O	17:CH:53:ARG:NH2	2.44	0.51
3:DI:405:LEU:HD13	17:CH:116:HIS:CD2	2.45	0.51
8:DP:189:TYR:CE1	8:DP:208:PRO:HD3	2.46	0.51
9:DQ:29:ILE:HD13	9:DQ:40:VAL:HG21	1.93	0.51
15:CE:22:ARG:NH2	15:CE:240:ASP:HB3	2.25	0.51
15:CE:286:ALA:HB2	27:Ca:355:PHE:CE1	2.46	0.51
1:DA:222:GLU:CD	1:DA:222:GLU:H	2.18	0.51
5:DM:174:ASP:OD1	5:DM:177:ARG:NH2	2.43	0.51
10:DR:112:ARG:HD2	30:Cj:158:THR:HG23	1.91	0.51
18:CI:194:THR:HG23	18:CI:218:ARG:NH1	2.26	0.51
27:Ca:205:LEU:HA	27:Ca:208:VAL:HG22	1.93	0.51
27:Ca:365:LEU:HD13	36:Cv:287:ASN:HB3	1.92	0.51
35:Cr:243:LYS:O	35:Cr:247:ILE:HG23	2.10	0.51
35:Cr:281:GLY:O	35:Cr:285:ARG:HG3	2.11	0.51
37:CA:309:A:H2'	37:CA:309:A:N3	2.24	0.51
1:DA:774:GLY:H	5:DM:206:ALA:HA	1.76	0.51
2:DD:140:SER:HB2	37:CA:86:G:H22	1.74	0.51
9:DQ:227:GLN:HG3	9:DQ:230:TRP:CZ2	2.46	0.51
20:CL:122:GLU:OE2	20:CL:137:ARG:NE	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:CQ:58:HIS:CD2	37:CA:132:G:H21	2.29	0.51
24:CR:190:TYR:HB3	24:CR:192:GLU:HG2	1.93	0.51
27:Ca:11:TYR:O	27:Ca:14:ASN:ND2	2.44	0.51
31:Cm:153:ASP:OD1	31:Cm:153:ASP:N	2.42	0.51
1:DA:192:ASP:OD1	1:DA:192:ASP:N	2.44	0.51
2:DD:465:PHE:CG	2:DD:479:ARG:NH1	2.79	0.51
5:DM:10:ARG:NH1	15:CE:325:LEU:HB2	2.26	0.51
8:DP:101:PHE:CD2	8:DP:110:PRO:HG3	2.45	0.51
14:Da:10:ILE:N	37:CA:270:U:OP1	2.44	0.51
15:CE:340:LYS:HA	15:CE:343:TYR:HB2	1.93	0.51
30:Cj:53:ASN:O	30:Cj:55:ARG:HG3	2.11	0.51
34:Cq:227:ILE:HG22	34:Cq:228:LEU:HD12	1.93	0.51
1:DA:59:HIS:CD2	1:DA:86:TYR:H	2.19	0.51
1:DA:1077:ARG:NH2	1:DA:1085:GLU:OE1	2.43	0.51
1:DA:1645:GLU:HG2	15:CE:425:PRO:HB2	1.93	0.51
3:DI:27:THR:H	3:DI:30:GLN:NE2	2.07	0.51
5:DM:198:THR:HG22	5:DM:199:LEU:H	1.75	0.51
10:DR:189:GLU:HA	10:DR:191:GLN:HE21	1.76	0.51
10:DR:250:ARG:NH2	30:Cj:23:GLY:O	2.44	0.51
12:DU:107:LYS:HB3	12:DU:107:LYS:HZ2	1.73	0.51
18:CI:203:ASP:OD1	18:CI:211:ASN:ND2	2.44	0.51
21:CO:264:ARG:HH12	21:CO:303:TYR:HB3	1.75	0.51
27:Ca:568:ARG:NH2	37:CA:144:A:OP2	2.41	0.51
31:Cm:191:LYS:NZ	37:CA:337:U:OP2	2.43	0.51
33:Cp:10:ASP:N	37:CA:29:A:OP2	2.44	0.51
33:Cp:65:ILE:O	33:Cp:124:LYS:HG3	2.11	0.51
35:Cr:10:ARG:O	35:Cr:10:ARG:HD3	2.10	0.51
7:DO:209:ARG:O	7:DO:213:GLU:HG2	2.10	0.51
15:CE:21:MET:HG2	15:CE:23:GLY:H	1.76	0.51
25:CU:10:GLY:HA3	37:CA:344:C:OP1	2.11	0.51
29:Cd:188:ASP:HB3	29:Cd:194:VAL:HG21	1.92	0.51
9:DQ:65:TRP:HA	9:DQ:68:ARG:NH1	2.26	0.50
11:DS:89:ASN:O	11:DS:110:SER:HB3	2.11	0.50
12:DU:73:ARG:HD3	12:DU:73:ARG:H	1.76	0.50
17:CH:218:VAL:HG22	17:CH:282:HIS:CE1	2.46	0.50
19:CK:78:ASP:HB2	28:Cb:178:ARG:HH11	1.76	0.50
23:CQ:152:LYS:HD2	23:CQ:154:SER:O	2.12	0.50
27:Ca:124:ILE:HD11	36:Cv:1033:GLU:HA	1.93	0.50
29:Cd:102:ARG:HG3	29:Cd:103:ILE:N	2.26	0.50
36:Cv:681:HIS:O	36:Cv:781:PRO:HA	2.11	0.50
1:DA:557:SER:CB	1:DA:562:LYS:HZ2	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:DN:45:ARG:HB3	6:DN:132:TYR:CE2	2.46	0.50
7:DO:63:ALA:O	7:DO:67:ARG:HG2	2.11	0.50
15:CE:253:ARG:NH1	15:CE:256:LEU:O	2.43	0.50
20:CL:78:MET:HG2	20:CL:129:LEU:HD11	1.93	0.50
21:CO:82:ASN:HD21	32:Cn:142:TRP:H	1.57	0.50
21:CO:334:ARG:HD2	23:CQ:164:ILE:HG12	1.92	0.50
27:Ca:46:ARG:NH2	36:Cv:1113:TYR:O	2.44	0.50
28:Cb:12:PRO:HG2	28:Cb:15:MET:HG2	1.91	0.50
1:DA:349:PRO:HG2	1:DA:350:TYR:CD2	2.47	0.50
3:DI:74:ASP:OD1	3:DI:75:GLN:N	2.42	0.50
14:Da:32:SER:O	17:CH:144:ARG:NH1	2.45	0.50
15:CE:376:LEU:O	15:CE:380:GLN:HG2	2.11	0.50
21:CO:131:LYS:HA	21:CO:134:GLU:HG2	1.93	0.50
24:CR:12:ALA:HB1	36:Cv:803:GLN:HB2	1.92	0.50
29:Cd:10:ARG:HE	37:CA:47:U:H4'	1.75	0.50
29:Cd:58:ARG:HH11	29:Cd:58:ARG:HG3	1.76	0.50
35:Cr:246:GLU:O	35:Cr:249:GLU:HG3	2.10	0.50
1:DA:1566:ARG:O	1:DA:1570:ASN:ND2	2.44	0.50
1:DA:1647:SER:OG	1:DA:1648:ALA:N	2.44	0.50
2:DD:26:ARG:NH1	37:CA:145:A:H2	2.08	0.50
2:DD:774:VAL:HG23	15:CE:294:HIS:CE1	2.46	0.50
3:DI:104:ILE:HG12	3:DI:152:LEU:HD21	1.93	0.50
17:CH:16:VAL:CB	17:CH:17:PRO:HD2	2.38	0.50
27:Ca:295:PHE:CD2	27:Ca:299:ARG:NH1	2.80	0.50
36:Cv:719:THR:O	36:Cv:723:ARG:HG3	2.11	0.50
1:DA:1066:LEU:HD22	1:DA:1143:LEU:HD21	1.93	0.50
8:DP:103:SER:O	30:Cj:139:ARG:NH2	2.35	0.50
8:DP:188:ARG:HH11	8:DP:194:GLN:NE2	2.09	0.50
12:DU:83:ARG:HD3	12:DU:159:ASP:OD1	2.11	0.50
15:CE:83:MET:H	15:CE:83:MET:HE2	1.77	0.50
19:CK:71:SER:HB3	28:Cb:280:ASN:HD22	1.76	0.50
21:CO:327:CYS:HB3	21:CO:330:THR:HB	1.94	0.50
23:CQ:10:PRO:HD2	37:CA:196:U:O4	2.12	0.50
24:CR:237:ARG:HD2	24:CR:237:ARG:O	2.11	0.50
26:CZ:314:TRP:O	26:CZ:318:LEU:HD23	2.12	0.50
26:CZ:315:THR:O	26:CZ:318:LEU:HB2	2.12	0.50
35:Cr:67:PRO:HG2	35:Cr:70:GLU:HB2	1.92	0.50
1:DA:155:ILE:HG21	29:Cd:84:LYS:HE2	1.93	0.50
1:DA:853:LYS:HE3	36:Cv:1005:TRP:CE2	2.46	0.50
1:DA:1029:LYS:NZ	5:DM:254:HIS:ND1	2.46	0.50
2:DD:608:ASP:O	10:DR:227:ARG:NH1	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:778:PRO:HB3	15:CE:32:TRP:CD2	2.46	0.50
12:DU:207:ARG:NH2	37:CA:159:G:H4'	2.26	0.50
21:CO:71:PRO:HB3	32:Cn:192:ASN:ND2	2.26	0.50
23:CQ:79:ASP:O	23:CQ:83:LEU:HB2	2.12	0.50
26:CZ:278:THR:HG22	26:CZ:279:SER:OG	2.12	0.50
36:Cv:902:ILE:HG22	36:Cv:903:ASP:OD1	2.12	0.50
1:DA:1658:GLU:HB3	15:CE:394:ARG:HG3	1.93	0.50
2:DD:21:ARG:HB2	2:DD:26:ARG:HH21	1.77	0.50
8:DP:36:GLN:HG2	12:DU:204:LEU:HG	1.94	0.50
11:DS:34:SER:HA	11:DS:39:ARG:HB3	1.93	0.50
13:DZ:13:ALA:H	27:Ca:177:GLN:NE2	2.09	0.50
21:CO:251:VAL:HG22	37:CA:285:A:C5	2.47	0.50
36:Cv:636:ALA:HB3	36:Cv:650:HIS:CE1	2.46	0.50
1:DA:751:GLU:HG3	5:DM:197:LEU:HD22	1.93	0.50
2:DD:13:GLY:O	32:Cn:155:ARG:NH2	2.42	0.50
2:DD:537:ARG:HA	10:DR:218:TRP:CZ3	2.36	0.50
2:DD:593:ASP:OD2	2:DD:595:ARG:NE	2.35	0.50
5:DM:176:VAL:HG21	5:DM:226:PRO:HD3	1.93	0.50
6:DN:144:ARG:HA	6:DN:144:ARG:HE	1.76	0.50
8:DP:200:SER:O	8:DP:204:ASN:N	2.44	0.50
19:CK:284:PHE:O	25:CU:71:ARG:NH2	2.34	0.50
27:Ca:14:ASN:HD22	27:Ca:14:ASN:N	2.09	0.50
29:Cd:24:HIS:HE2	37:CA:51:U:HO2'	1.58	0.50
30:Cj:209:TYR:CE1	30:Cj:212:TYR:HB2	2.47	0.50
37:CA:370:A:O2'	37:CA:371:U:H5'	2.12	0.50
1:DA:591:LEU:HD13	1:DA:598:ALA:HA	1.94	0.50
6:DN:267:GLU:CD	6:DN:267:GLU:H	2.20	0.50
8:DP:62:LYS:NZ	12:DU:206:PRO:O	2.45	0.50
10:DR:100:ARG:HG3	10:DR:102:LEU:HG	1.94	0.50
15:CE:222:VAL:HG21	15:CE:267:HIS:HB3	1.94	0.50
18:CI:203:ASP:OD1	18:CI:203:ASP:N	2.44	0.50
28:Cb:161:ALA:HA	34:Cq:121:VAL:HG21	1.94	0.50
28:Cb:303:GLU:OE2	35:Cr:267:GLN:NE2	2.44	0.50
35:Cr:172:ARG:HH21	35:Cr:176:LEU:CD2	2.19	0.50
36:Cv:112:ILE:HD11	36:Cv:150:LEU:HB3	1.94	0.50
1:DA:715:GLY:HA3	1:DA:721:ILE:HG12	1.94	0.49
8:DP:143:ASN:HB2	30:Cj:141:GLY:HA3	1.93	0.49
9:DQ:31:PRO:HB3	37:CA:86:G:OP1	2.12	0.49
9:DQ:254:SER:H	9:DQ:255:PRO:CD	2.25	0.49
11:DS:207:TRP:CZ2	22:CP:134:ILE:HG23	2.47	0.49
16:CF:63:ARG:NH2	29:Cd:187:GLU:OE2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:CL:111:PHE:HB2	27:Ca:15:LYS:HB2	1.94	0.49
27:Ca:444:PHE:HB2	27:Ca:472:VAL:HG12	1.93	0.49
29:Cd:284:THR:HG22	29:Cd:285:ASP:H	1.77	0.49
31:Cm:178:GLU:HG3	31:Cm:183:GLY:HA2	1.95	0.49
35:Cr:65:LYS:NZ	35:Cr:65:LYS:HB2	2.26	0.49
1:DA:779:LEU:O	1:DA:812:PRO:HD3	2.12	0.49
1:DA:825:GLU:OE1	1:DA:825:GLU:N	2.45	0.49
1:DA:1107:ARG:O	1:DA:1109:ARG:HG2	2.13	0.49
5:DM:104:LYS:HB2	5:DM:104:LYS:NZ	2.27	0.49
20:CL:111:PHE:HB3	27:Ca:15:LYS:HA	1.94	0.49
23:CQ:56:ARG:NH1	37:CA:97:U:H2'	2.27	0.49
23:CQ:191:VAL:HG21	23:CQ:195:ILE:HD11	1.93	0.49
28:Cb:298:ASP:HB3	35:Cr:40:HIS:ND1	2.27	0.49
29:Cd:13:ARG:NH2	29:Cd:28:MET:O	2.45	0.49
35:Cr:9:LEU:HG	35:Cr:100:TYR:CG	2.46	0.49
1:DA:618:TYR:CE2	1:DA:711:ILE:HD11	2.47	0.49
6:DN:68:PHE:CD2	6:DN:69:VAL:HG23	2.47	0.49
8:DP:30:LYS:HG3	33:Cp:144:PRO:HG2	1.94	0.49
10:DR:26:ASN:ND2	30:Cj:37:ARG:NH1	2.60	0.49
10:DR:228:THR:HG22	10:DR:228:THR:O	2.11	0.49
15:CE:109:LYS:HB3	15:CE:113:GLU:HB2	1.94	0.49
15:CE:408:ARG:HH11	15:CE:408:ARG:HG3	1.77	0.49
36:Cv:813:ARG:HG2	36:Cv:813:ARG:NH1	2.27	0.49
36:Cv:893:GLU:OE2	36:Cv:898:ARG:NH1	2.45	0.49
36:Cv:1123:GLN:CD	36:Cv:1124:PRO:HD2	2.38	0.49
6:DN:26:ARG:NH1	27:Ca:407:PHE:CE2	2.80	0.49
6:DN:224:ARG:HB3	6:DN:287:ARG:HD2	1.93	0.49
8:DP:67:GLN:HE22	8:DP:75:ARG:NH1	2.11	0.49
10:DR:60:VAL:HG23	10:DR:61:PRO:HD2	1.95	0.49
27:Ca:228:LYS:O	27:Ca:232:GLN:HG2	2.12	0.49
36:Cv:975:ASP:OD1	36:Cv:976:ASP:N	2.34	0.49
37:CA:196:U:H5'	37:CA:197:A:OP2	2.13	0.49
12:DU:211:ARG:HB2	12:DU:211:ARG:HH11	1.77	0.49
15:CE:42:ARG:HG3	15:CE:105:GLN:NE2	2.26	0.49
15:CE:328:ASP:OD1	15:CE:328:ASP:N	2.44	0.49
21:CO:73:ILE:HD13	32:Cn:226:LEU:HD23	1.93	0.49
21:CO:376:GLU:OE2	21:CO:379:ARG:NH2	2.45	0.49
21:CO:429:ASN:ND2	37:CA:92:A:OP1	2.46	0.49
27:Ca:14:ASN:HD22	27:Ca:14:ASN:H	1.59	0.49
33:Cp:93:ARG:HG3	33:Cp:102:ARG:NH1	2.27	0.49
36:Cv:744:TRP:HZ2	36:Cv:767:ASP:HB2	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Cv:977:LYS:NZ	36:Cv:979:GLU:CD	2.71	0.49
1:DA:651:ARG:HG3	1:DA:726:GLU:HB3	1.94	0.49
1:DA:914:THR:HG21	1:DA:917:ARG:HH21	1.77	0.49
7:DO:236:PRO:HG2	7:DO:239:LYS:HG3	1.94	0.49
10:DR:246:GLY:HA2	29:Ca:32:LEU:HD12	1.93	0.49
20:CL:111:PHE:CB	27:Ca:15:LYS:HA	2.43	0.49
21:CO:214:HIS:HD2	21:CO:216:PHE:H	1.60	0.49
25:CU:85:SER:HB3	37:CA:609:A:H5''	1.94	0.49
27:Ca:102:TRP:CE2	27:Ca:159:LEU:HD13	2.48	0.49
34:Cq:175:TRP:HZ3	34:Cq:235:LEU:HD23	1.76	0.49
1:DA:222:GLU:O	1:DA:233:ARG:HD3	2.12	0.49
1:DA:828:LYS:NZ	6:DN:200:ASP:OD2	2.42	0.49
1:DA:1131:ASN:HA	1:DA:1134:ILE:HD12	1.94	0.49
2:DD:368:LEU:O	2:DD:589:GLN:O	2.31	0.49
2:DD:687:HIS:HE1	2:DD:691:PHE:O	1.95	0.49
11:DS:200:LEU:HD22	33:Cp:40:GLU:HB3	1.94	0.49
20:CL:135:TYR:CG	27:Ca:10:ARG:NH1	2.81	0.49
27:Ca:272:PHE:O	27:Ca:276:SER:OG	2.30	0.49
27:Ca:521:GLN:HG3	27:Ca:586:ILE:O	2.13	0.49
1:DA:387:SER:OG	1:DA:389:GLU:OE1	2.28	0.49
1:DA:985:LYS:HB3	1:DA:985:LYS:HZ3	1.75	0.49
1:DA:1589:ALA:HB3	1:DA:1591:ARG:O	2.12	0.49
3:DI:280:SER:OG	3:DI:281:GLY:N	2.44	0.49
5:DM:21:ARG:NH2	5:DM:232:PRO:O	2.44	0.49
7:DO:138:LEU:HD23	7:DO:176:THR:HG21	1.94	0.49
29:Ca:20:SER:HB3	29:Ca:29:THR:HG23	1.94	0.49
36:Cv:531:MET:HG2	36:Cv:535:HIS:CD2	2.48	0.49
1:DA:364:LEU:HD23	1:DA:380:PHE:CE1	2.48	0.49
1:DA:751:GLU:HG2	5:DM:197:LEU:HB3	1.95	0.49
1:DA:1417:PHE:C	1:DA:1419:GLY:H	2.20	0.49
5:DM:169:ALA:HB2	15:CE:343:TYR:CE2	2.47	0.49
27:Ca:189:GLU:OE1	27:Ca:189:GLU:N	2.31	0.49
36:Cv:172:THR:HG21	36:Cv:178:GLU:HB3	1.95	0.49
1:DA:551:LYS:HA	1:DA:554:GLU:HG2	1.95	0.49
17:CH:225:ASP:HB3	17:CH:227:ARG:H	1.78	0.49
22:CP:102:TRP:HB3	22:CP:108:CYS:SG	2.53	0.49
24:CR:18:VAL:HG21	36:Cv:543:ALA:HA	1.94	0.49
36:Cv:458:PRO:HG3	36:Cv:828:ALA:HA	1.95	0.49
5:DM:104:LYS:O	5:DM:107:GLU:HG2	2.13	0.48
6:DN:212:THR:C	27:Ca:193:ARG:HH12	2.20	0.48
9:DQ:142:PHE:CE1	9:DQ:180:ALA:HB1	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CR:49:ARG:HB2	24:CR:53:GLN:HB2	1.95	0.48
24:CR:168:ILE:HG23	24:CR:170:LEU:HG	1.94	0.48
24:CR:202:LYS:NZ	24:CR:202:LYS:HB3	2.27	0.48
29:CD:177:LEU:HD11	36:Cv:648:VAL:HG22	1.95	0.48
29:CD:217:GLU:H	29:CD:217:GLU:CD	2.21	0.48
31:Cm:184:HIS:HE1	37:CA:282:A:N3	2.11	0.48
33:Cp:23:TYR:CE2	33:Cp:25:PRO:HD3	2.48	0.48
34:Cq:76:GLN:OE1	34:Cq:228:LEU:HB2	2.13	0.48
36:Cv:686:LEU:HD21	36:Cv:788:ARG:HE	1.78	0.48
36:Cv:930:ARG:HB3	36:Cv:930:ARG:HH11	1.78	0.48
37:CA:194:A:O2'	37:CA:195:A:H2'	2.13	0.48
1:DA:385:ARG:HD3	6:DN:195:TYR:CD1	2.48	0.48
1:DA:492:ASN:HB2	1:DA:495:GLU:HB2	1.95	0.48
7:DO:74:TRP:CE2	7:DO:259:THR:HG23	2.48	0.48
10:DR:103:ASP:OD1	10:DR:104:PRO:HD2	2.13	0.48
11:DS:131:ARG:HB2	11:DS:134:GLN:HB2	1.95	0.48
17:CH:105:ILE:HD12	36:Cv:226:PHE:CE1	2.47	0.48
18:CI:256:LYS:H	18:CI:256:LYS:HD2	1.77	0.48
19:CK:70:ILE:HD12	28:Cb:189:LYS:HD3	1.94	0.48
20:CL:71:LEU:HD23	20:CL:118:LEU:HB3	1.95	0.48
26:CZ:216:ASP:HB2	26:CZ:247:PHE:HA	1.93	0.48
27:Ca:443:MET:HG2	27:Ca:473:ILE:HG12	1.95	0.48
32:Cn:152:PHE:O	32:Cn:152:PHE:CG	2.66	0.48
4:DL:228:MET:HG3	4:DL:229:THR:HG22	1.95	0.48
6:DN:67:TYR:HB3	6:DN:114:GLY:O	2.13	0.48
6:DN:73:VAL:HG21	6:DN:132:TYR:CD1	2.48	0.48
9:DQ:68:ARG:NH2	12:DU:29:GLU:O	2.37	0.48
10:DR:244:LEU:HD22	10:DR:269:TRP:CE2	2.48	0.48
14:Da:36:SER:OG	14:Da:38:ASP:OD1	2.26	0.48
28:Cb:291:GLU:HB3	28:Cb:296:PHE:O	2.14	0.48
33:Cp:53:VAL:HG11	33:Cp:59:PHE:CD1	2.44	0.48
36:Cv:975:ASP:HB3	36:Cv:979:GLU:HG3	1.94	0.48
1:DA:79:LEU:HD21	22:CP:53:ARG:NH1	2.28	0.48
1:DA:985:LYS:HB3	1:DA:985:LYS:HZ2	1.78	0.48
2:DD:181:MET:HE1	2:DD:215:TYR:HA	1.95	0.48
2:DD:323:LEU:HD22	2:DD:448:ARG:HH21	1.78	0.48
6:DN:44:LYS:HD3	6:DN:44:LYS:HA	1.62	0.48
7:DO:114:GLY:H	36:Cv:780:PRO:HG3	1.77	0.48
12:DU:46:THR:HG23	21:CO:332:ARG:HA	1.95	0.48
15:CE:257:LYS:HB3	15:CE:260:ASN:ND2	2.27	0.48
21:CO:359:HIS:CE1	21:CO:366:ARG:HH12	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CP:173:LYS:NZ	22:CP:181:GLU:CD	2.71	0.48
24:CR:297:HIS:CG	29:Cd:279:ARG:HG2	2.48	0.48
31:Cm:56:ASN:HD21	31:Cm:62:ALA:CB	2.26	0.48
2:DD:353:HIS:HE1	10:DR:196:TYR:OH	1.96	0.48
3:DI:251:VAL:HG13	3:DI:258:VAL:HG13	1.95	0.48
8:DP:19:TRP:CZ3	8:DP:20:MET:HG2	2.49	0.48
10:DR:39:GLN:O	10:DR:42:MET:HB3	2.14	0.48
15:CE:137:LEU:HD11	28:Cb:47:ILE:HG13	1.95	0.48
16:CF:16:ARG:HB2	16:CF:16:ARG:NH1	2.27	0.48
2:DD:177:TYR:CE2	2:DD:200:MET:HG3	2.49	0.48
6:DN:128:VAL:HB	27:Ca:405:ARG:HB3	1.94	0.48
9:DQ:127:ARG:HH12	9:DQ:262:GLU:CD	2.21	0.48
11:DS:107:LYS:NZ	37:CA:208:U:OP1	2.43	0.48
11:DS:110:SER:OG	37:CA:206:A:OP2	2.27	0.48
11:DS:127:PRO:O	11:DS:168:LYS:HE2	2.13	0.48
12:DU:189:LYS:HZ2	12:DU:190:ARG:HB2	1.77	0.48
13:DZ:73:HIS:HA	13:DZ:76:TYR:CE2	2.48	0.48
18:CI:106:LEU:HD11	19:CK:107:GLN:NE2	2.23	0.48
21:CO:208:MET:HG2	21:CO:223:VAL:HG13	1.96	0.48
26:CZ:216:ASP:O	26:CZ:256:LYS:HG3	2.12	0.48
26:CZ:277:PHE:CG	26:CZ:309:PRO:HD3	2.48	0.48
35:Cr:176:LEU:HD12	35:Cr:176:LEU:HA	1.72	0.48
36:Cv:509:THR:HG23	36:Cv:520:GLN:NE2	2.28	0.48
37:CA:617:U:H5'	37:CA:618:U:OP2	2.13	0.48
2:DD:17:ALA:HB2	37:CA:273:A:H5''	1.95	0.48
2:DD:274:PHE:CE1	21:CO:329:GLU:HB2	2.49	0.48
2:DD:361:ASN:OD1	2:DD:366:LEU:HA	2.14	0.48
6:DN:258:ASP:OD2	6:DN:277:LYS:HG3	2.14	0.48
37:CA:293:A:H1'	37:CA:315:A:H5''	1.96	0.48
40:US:15:UNK:HB2	40:US:18:UNK:HG2	1.96	0.48
2:DD:171:ASN:HA	2:DD:172:PRO:HD3	1.72	0.48
2:DD:395:GLU:OE2	2:DD:398:ARG:NH2	2.29	0.48
2:DD:647:ARG:HH22	10:DR:230:ARG:NH1	2.03	0.48
5:DM:106:MET:HE3	15:CE:313:MET:HG2	1.95	0.48
9:DQ:154:GLY:HA2	9:DQ:234:GLN:O	2.13	0.48
10:DR:128:PRO:HB2	10:DR:130:ASP:OD1	2.13	0.48
13:DZ:13:ALA:HB2	27:Ca:89:ARG:HA	1.96	0.48
15:CE:48:ASN:N	15:CE:48:ASN:OD1	2.45	0.48
15:CE:396:LEU:HD22	15:CE:415:ILE:HD13	1.96	0.48
17:CH:24:GLY:HA3	17:CH:29:HIS:ND1	2.29	0.48
27:Ca:515:PRO:HG2	27:Ca:518:GLU:OE1	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Cd:170:GLY:O	29:Cd:171:LYS:HG2	2.14	0.48
36:Cv:233:LYS:HG3	36:Cv:500:TYR:CD2	2.49	0.48
36:Cv:566:MET:SD	36:Cv:918:LEU:HD13	2.54	0.48
37:CA:349:U:OP2	37:CA:349:U:H6	1.96	0.48
1:DA:344:ARG:NH1	27:Ca:546:PHE:O	2.47	0.48
1:DA:1042:HIS:HD2	1:DA:1045:ILE:H	1.62	0.48
3:DI:234:SER:O	3:DI:237:ARG:HG3	2.13	0.48
6:DN:183:ARG:CD	6:DN:194:ARG:HH12	2.26	0.48
21:CO:151:LYS:HD2	21:CO:156:TRP:HZ3	1.78	0.48
29:Cd:103:ILE:O	29:Cd:107:GLN:HG3	2.13	0.48
32:Cn:169:PHE:CZ	36:Cv:26:LEU:HD11	2.48	0.48
36:Cv:922:ASP:OD2	36:Cv:924:SER:OG	2.32	0.48
5:DM:292:ASN:O	18:CI:208:HIS:NE2	2.46	0.48
10:DR:108:GLN:HE22	30:Cj:147:TYR:HB2	1.78	0.48
10:DR:189:GLU:HA	10:DR:191:GLN:NE2	2.28	0.48
13:DZ:90:VAL:HG22	27:Ca:149:ARG:HH12	1.78	0.48
15:CE:171:SER:C	15:CE:173:LYS:H	2.21	0.48
16:CF:42:GLU:OE1	29:Cd:179:PHE:HD1	1.97	0.48
23:CQ:66:VAL:O	23:CQ:67:LEU:HB2	2.14	0.48
30:Cj:195:THR:OG1	30:Cj:196:ASP:N	2.47	0.48
32:Cn:151:THR:O	32:Cn:151:THR:OG1	2.32	0.48
34:Cq:25:PHE:O	34:Cq:27:PRO:HD3	2.14	0.48
1:DA:987:LEU:HD11	1:DA:1173:ALA:HB1	1.96	0.47
1:DA:1662:ARG:HH22	15:CE:402:ARG:NH1	2.10	0.47
2:DD:543:LEU:O	2:DD:547:VAL:HG23	2.13	0.47
5:DM:254:HIS:CG	15:CE:47:ARG:HH11	2.32	0.47
10:DR:41:HIS:HA	10:DR:44:VAL:HG12	1.96	0.47
12:DU:83:ARG:HG2	12:DU:98:MET:HE3	1.96	0.47
15:CE:253:ARG:HE	37:CA:15:U:H1'	1.79	0.47
31:Cm:181:GLN:OE1	31:Cm:212:PRO:HG2	2.14	0.47
1:DA:575:PHE:CG	1:DA:576:PRO:HD2	2.49	0.47
1:DA:907:GLN:HE22	27:Ca:399:ASN:HD22	1.59	0.47
7:DO:67:ARG:NH1	36:Cv:780:PRO:HG3	2.29	0.47
10:DR:39:GLN:HG2	10:DR:42:MET:HE2	1.96	0.47
12:DU:103:ILE:H	12:DU:103:ILE:HG13	1.43	0.47
24:CR:12:ALA:HA	36:Cv:689:CYS:SG	2.54	0.47
25:CU:115:LYS:NZ	31:Cm:142:GLU:OE1	2.32	0.47
27:Ca:62:TRP:HB3	27:Ca:79:MET:HE1	1.96	0.47
31:Cm:77:PRO:HB3	31:Cm:155:HIS:CE1	2.48	0.47
32:Cn:226:LEU:O	32:Cn:230:VAL:HG23	2.14	0.47
36:Cv:292:LYS:HE2	36:Cv:512:MET:HE3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Cv:897:GLU:HB2	36:Cv:912:ARG:HE	1.80	0.47
36:Cv:930:ARG:HB3	36:Cv:930:ARG:NH1	2.29	0.47
1:DA:717:ASP:O	1:DA:721:ILE:HG13	2.15	0.47
5:DM:272:GLN:HB2	34:Cq:9:TYR:HB3	1.95	0.47
7:DO:131:ASP:OD1	7:DO:132:ALA:N	2.44	0.47
9:DQ:120:MET:HE3	9:DQ:120:MET:HB3	1.60	0.47
18:CI:89:ARG:HA	19:CK:111:ASN:HD21	1.79	0.47
27:Ca:294:ASP:OD1	27:Ca:297:LEU:HB2	2.14	0.47
28:Cb:91:ARG:O	28:Cb:95:ARG:HG2	2.14	0.47
29:Cd:10:ARG:HA	37:CA:177:A:OP2	2.14	0.47
36:Cv:871:ILE:HD13	36:Cv:890:PRO:HG2	1.95	0.47
36:Cv:977:LYS:HZ1	36:Cv:979:GLU:CD	2.22	0.47
1:DA:48:GLN:O	2:DD:63:GLN:NE2	2.37	0.47
1:DA:48:GLN:OE1	23:CQ:29:ALA:HB1	2.14	0.47
1:DA:224:VAL:HG11	1:DA:287:HIS:HB3	1.97	0.47
1:DA:1060:LEU:HD22	1:DA:1163:MET:HE1	1.95	0.47
1:DA:1134:ILE:HG22	1:DA:1135:PRO:O	2.15	0.47
1:DA:1163:MET:HE3	34:Cq:62:TYR:HB3	1.96	0.47
2:DD:345:PRO:HB3	12:DU:98:MET:HE1	1.96	0.47
4:DL:214:TYR:CD2	18:CI:219:LEU:HD11	2.49	0.47
9:DQ:232:ASP:OD1	9:DQ:232:ASP:N	2.48	0.47
9:DQ:250:ARG:CZ	9:DQ:252:LYS:CE	2.92	0.47
9:DQ:255:PRO:HG3	9:DQ:260:HIS:HB2	1.96	0.47
18:CI:265:ASP:HB3	18:CI:267:TYR:CE1	2.50	0.47
27:Ca:457:LYS:HD2	27:Ca:492:TYR:CG	2.49	0.47
31:Cm:85:ILE:HG12	31:Cm:140:CYS:HB2	1.96	0.47
36:Cv:1136:ASN:OD1	36:Cv:1136:ASN:N	2.47	0.47
15:CE:34:ARG:HD3	15:CE:205:ASP:OD1	2.14	0.47
21:CO:248:ILE:HD11	37:CA:287:A:N3	2.29	0.47
27:Ca:367:ASN:OD1	36:Cv:954:ARG:NH2	2.47	0.47
30:Cj:50:VAL:O	30:Cj:54:ALA:HB2	2.13	0.47
37:CA:106:U:H5'	37:CA:107:U:OP1	2.15	0.47
41:UT:5:UNK:O	41:UT:7:UNK:HG3	2.14	0.47
1:DA:794:ARG:NH1	1:DA:794:ARG:HB2	2.29	0.47
22:CP:113:LYS:HB2	22:CP:114:PRO:HD3	1.96	0.47
27:Ca:61:LEU:HB2	27:Ca:76:GLN:HE22	1.79	0.47
27:Ca:400:TYR:O	27:Ca:404:ARG:HB3	2.14	0.47
31:Cm:168:HIS:CD2	31:Cm:168:HIS:H	2.33	0.47
34:Cq:79:MET:O	34:Cq:83:LEU:HB3	2.15	0.47
35:Cr:25:LEU:HD13	35:Cr:83:VAL:HG22	1.96	0.47
1:DA:791:THR:HA	1:DA:794:ARG:NH2	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:683:ASP:O	29:Cd:64:GLN:NE2	2.47	0.47
3:DI:404:TRP:HB3	36:Cv:212:ARG:NH1	2.29	0.47
4:DL:189:THR:HB	24:CR:73:ASP:OD2	2.15	0.47
5:DM:30:ARG:HD2	36:Cv:1011:SER:O	2.14	0.47
6:DN:114:GLY:CA	6:DN:130:ASN:OD1	2.63	0.47
7:DO:114:GLY:HA3	36:Cv:780:PRO:HB3	1.95	0.47
9:DQ:35:VAL:HG12	9:DQ:36:GLU:HG3	1.97	0.47
10:DR:210:SER:HA	10:DR:215:ARG:NH1	2.29	0.47
18:CI:89:ARG:HE	24:CR:193:ASN:HD21	1.61	0.47
19:CK:304:VAL:HG12	25:CU:48:VAL:HG21	1.97	0.47
21:CO:122:VAL:HG22	21:CO:123:ASN:H	1.80	0.47
27:Ca:359:ARG:NH2	36:Cv:257:LYS:HD3	2.29	0.47
27:Ca:588:LYS:O	37:CA:261:U:H5	1.98	0.47
28:Cb:97:GLU:O	28:Cb:101:LYS:HG3	2.15	0.47
30:Cj:90:ARG:NE	30:Cj:94:ILE:HD11	2.29	0.47
30:Cj:217:PRO:HG2	30:Cj:220:PHE:CD2	2.50	0.47
31:Cm:125:CYS:O	31:Cm:129:VAL:HG23	2.15	0.47
32:Cn:243:ARG:HG3	32:Cn:244:PRO:HD2	1.96	0.47
33:Cp:93:ARG:HG3	33:Cp:102:ARG:HH12	1.79	0.47
33:Cp:93:ARG:NH1	37:CA:187:A:H2	2.12	0.47
34:Cq:223:GLU:HG2	34:Cq:227:ILE:HG13	1.96	0.47
36:Cv:395:LEU:HD21	36:Cv:421:LEU:HD12	1.97	0.47
36:Cv:585:ASP:OD1	36:Cv:586:GLU:N	2.48	0.47
36:Cv:617:ASP:HB3	36:Cv:663:ARG:HD2	1.97	0.47
1:DA:43:TYR:HB3	2:DD:95:ARG:HA	1.97	0.47
1:DA:1580:ASN:O	1:DA:1584:GLN:HG3	2.14	0.47
2:DD:37:LEU:HD22	2:DD:42:MET:HG3	1.97	0.47
15:CE:40:ARG:HD2	15:CE:94:ARG:HD3	1.96	0.47
15:CE:373:ARG:HD3	15:CE:407:THR:HG22	1.97	0.47
18:CI:104:ASN:HD22	18:CI:105:THR:N	2.12	0.47
21:CO:409:THR:HG22	37:CA:69:U:OP1	2.15	0.47
28:Cb:168:ALA:O	28:Cb:171:THR:HG22	2.15	0.47
31:Cm:117:ARG:NH1	31:Cm:117:ARG:O	2.44	0.47
2:DD:118:ARG:NH1	27:Ca:467:LYS:HE2	2.29	0.47
2:DD:347:GLU:OE1	12:DU:83:ARG:NH2	2.48	0.47
3:DI:50:LEU:HD12	3:DI:50:LEU:HA	1.75	0.47
19:CK:307:PHE:CE1	25:CU:61:ILE:HD12	2.50	0.47
24:CR:225:LEU:HD23	24:CR:225:LEU:HA	1.79	0.47
27:Ca:75:LEU:O	27:Ca:79:MET:HG3	2.15	0.47
27:Ca:548:GLU:OE1	27:Ca:548:GLU:N	2.47	0.47
27:Ca:559:GLY:O	37:CA:12:C:N4	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Cp:178:GLU:HA	33:Cp:181:ARG:HG3	1.97	0.47
37:CA:232:G:H22	37:CA:248:A:P	2.38	0.47
1:DA:897:SER:OG	1:DA:898:VAL:N	2.46	0.47
1:DA:1029:LYS:NZ	5:DM:254:HIS:CE1	2.82	0.47
2:DD:612:MET:O	2:DD:616:LEU:HB2	2.14	0.47
7:DO:67:ARG:HH11	36:Cv:780:PRO:HG3	1.80	0.47
12:DU:80:LEU:HB2	12:DU:103:ILE:HD12	1.97	0.47
13:DZ:20:ARG:HD2	27:Ca:172:PHE:CE2	2.49	0.47
13:DZ:63:LEU:HD11	27:Ca:540:SER:H	1.80	0.47
14:Da:46:ARG:HD2	37:CA:362:A:N6	2.30	0.47
18:CI:99:VAL:O	28:Cb:103:ARG:NH1	2.44	0.47
21:CO:194:MET:HE2	21:CO:198:GLU:HB3	1.97	0.47
27:Ca:98:PRO:HB2	27:Ca:174:ASP:OD2	2.15	0.47
27:Ca:194:LEU:HA	27:Ca:194:LEU:HD23	1.71	0.47
33:Cp:11:GLN:HG2	37:CA:32:A:H62	1.80	0.47
37:CA:253:U:H2'	37:CA:254:A:C8	2.49	0.47
1:DA:324:GLN:HE21	27:Ca:68:SER:HB3	1.80	0.46
1:DA:647:ARG:HG2	1:DA:731:ALA:HB3	1.97	0.46
2:DD:26:ARG:HH11	37:CA:145:A:H2	1.61	0.46
2:DD:296:LEU:HG	2:DD:300:GLN:HE21	1.80	0.46
6:DN:73:VAL:HG21	6:DN:132:TYR:HE1	1.79	0.46
7:DO:136:ASP:OD1	7:DO:137:ASN:N	2.48	0.46
14:Da:10:ILE:HG23	14:Da:22:ARG:NH1	2.29	0.46
15:CE:213:TYR:HB3	17:CH:250:LEU:HD23	1.96	0.46
18:CI:271:TYR:CE2	18:CI:275:LYS:HD3	2.51	0.46
21:CO:111:GLN:HE22	21:CO:236:ARG:NH1	2.12	0.46
22:CP:177:GLU:OE1	22:CP:177:GLU:N	2.46	0.46
28:Cb:288:GLU:HA	28:Cb:291:GLU:OE1	2.15	0.46
29:Cd:12:ILE:HG23	33:Cp:120:ARG:HE	1.80	0.46
30:Cj:141:GLY:C	30:Cj:143:LYS:H	2.23	0.46
36:Cv:321:HIS:CD2	36:Cv:888:PRO:HG3	2.50	0.46
36:Cv:808:SER:HB3	36:Cv:913:TRP:CE3	2.50	0.46
1:DA:565:ASN:HA	6:DN:144:ARG:HH12	1.80	0.46
9:DQ:202:ASP:OD2	12:DU:39:ARG:HG2	2.16	0.46
10:DR:55:ALA:HB1	10:DR:154:LEU:HG	1.97	0.46
12:DU:27:ARG:HB3	12:DU:27:ARG:NH1	2.29	0.46
12:DU:227:SER:HA	30:Cj:161:VAL:HG13	1.97	0.46
21:CO:182:ASN:HB2	29:Cd:146:ASN:OD1	2.15	0.46
21:CO:296:ARG:NH2	37:CA:124:U:OP2	2.47	0.46
29:Cd:185:PHE:CD2	29:Cd:193:ILE:HD12	2.51	0.46
29:Cd:264:ILE:HG22	31:Cm:104:ARG:CZ	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:CA:36:U:OP1	37:CA:36:U:H6	1.99	0.46
2:DD:685:VAL:HG22	22:CP:100:LYS:HD2	1.97	0.46
9:DQ:16:LEU:HD21	21:CO:404:PRO:O	2.14	0.46
14:Da:25:ARG:O	14:Da:28:ARG:HB3	2.16	0.46
22:CP:53:ARG:HD2	22:CP:58:ILE:HG21	1.98	0.46
24:CR:153:GLU:HA	36:Cv:183:LEU:HD23	1.97	0.46
31:Cm:89:GLY:O	31:Cm:92:GLN:HB3	2.15	0.46
37:CA:4:A:OP2	37:CA:4:A:H8	1.99	0.46
1:DA:151:PRO:CG	2:DD:280:LEU:HD21	2.44	0.46
2:DD:371:PRO:O	2:DD:560:ALA:HB3	2.16	0.46
27:Ca:76:GLN:HG3	36:Cv:1120:TRP:HZ2	1.80	0.46
36:Cv:89:GLN:OE1	36:Cv:91:ARG:HD3	2.15	0.46
36:Cv:260:MET:HB3	36:Cv:299:ALA:HB2	1.96	0.46
1:DA:1386:ASP:HB3	15:CE:339:LEU:HD21	1.97	0.46
5:DM:55:GLU:CD	5:DM:56:TRP:H	2.23	0.46
6:DN:291:PRO:O	15:CE:114:TYR:CE1	2.68	0.46
7:DO:85:LYS:HE3	7:DO:85:LYS:HB3	1.76	0.46
8:DP:206:TYR:CE1	8:DP:215:LEU:HD13	2.46	0.46
10:DR:269:TRP:O	30:Cj:125:THR:OG1	2.33	0.46
12:DU:211:ARG:HA	12:DU:212:PRO:HD3	1.76	0.46
13:DZ:48:ARG:H	27:Ca:586:ILE:HD11	1.80	0.46
14:Da:16:GLY:HA3	14:Da:21:HIS:ND1	2.31	0.46
14:Da:46:ARG:HD2	37:CA:362:A:C6	2.50	0.46
15:CE:409:ASP:HA	36:Cv:1051:ARG:HD2	1.96	0.46
19:CK:315:LEU:HD21	37:CA:316:A:C6	2.51	0.46
25:CU:14:MET:SD	25:CU:20:MET:HE3	2.55	0.46
26:CZ:243:THR:HG21	26:CZ:245:LYS:HE3	1.97	0.46
29:Cd:129:ARG:HD3	36:Cv:209:VAL:O	2.15	0.46
33:Cp:61:GLU:OE2	33:Cp:75:LYS:NZ	2.48	0.46
36:Cv:718:THR:OG1	36:Cv:719:THR:N	2.48	0.46
1:DA:205:HIS:ND1	22:CP:82:VAL:HG21	2.31	0.46
7:DO:69:GLU:HA	7:DO:72:GLU:HB3	1.97	0.46
7:DO:123:LEU:HD12	7:DO:123:LEU:HA	1.78	0.46
7:DO:206:GLN:O	7:DO:210:ASN:HB2	2.16	0.46
9:DQ:148:LEU:HD23	9:DQ:176:ARG:NH2	2.30	0.46
14:Da:45:LYS:NZ	14:Da:46:ARG:HH22	2.14	0.46
24:CR:47:ALA:HA	28:Cb:67:GLN:HE22	1.80	0.46
27:Ca:579:VAL:HG23	37:CA:259:U:O2'	2.15	0.46
31:Cm:83:LYS:NZ	37:CA:393:U:H5'	2.29	0.46
32:Cn:193:LEU:HD23	32:Cn:193:LEU:HA	1.76	0.46
33:Cp:150:TYR:H	33:Cp:154:GLN:NE2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:Cr:143:ARG:HE	35:Cr:143:ARG:HB3	1.53	0.46
36:Cv:842:PHE:HB2	36:Cv:943:LEU:HD22	1.98	0.46
37:CA:128:A:OP1	45:CA:735:SPM:H111	2.16	0.46
1:DA:47:LEU:HD11	2:DD:38:ARG:HB3	1.97	0.46
9:DQ:86:THR:HG22	9:DQ:90:LYS:HE3	1.97	0.46
9:DQ:152:PHE:CE1	9:DQ:168:VAL:HG22	2.51	0.46
15:CE:30:TYR:CE2	15:CE:206:LEU:HB2	2.51	0.46
20:CL:81:ARG:NH2	20:CL:130:PRO:HB3	2.30	0.46
25:CU:169:ASN:OD1	25:CU:169:ASN:N	2.46	0.46
33:Cp:133:PHE:CE2	33:Cp:142:VAL:HG13	2.50	0.46
37:CA:282:A:C6	37:CA:283:U:O4	2.69	0.46
41:UT:37:UNK:HA	41:UT:40:UNK:HB2	1.98	0.46
1:DA:237:HIS:HE1	1:DA:310:ASP:HB2	1.81	0.46
2:DD:575:THR:HG23	10:DR:208:PHE:CZ	2.50	0.46
2:DD:693:ASP:OD1	2:DD:694:ARG:N	2.49	0.46
9:DQ:186:ARG:HB3	9:DQ:186:ARG:HH11	1.79	0.46
22:CP:90:MET:HB3	22:CP:90:MET:HE2	1.67	0.46
26:CZ:315:THR:HG22	26:CZ:319:ARG:HE	1.80	0.46
29:Cd:55:GLU:O	29:Cd:58:ARG:HB2	2.15	0.46
31:Cm:146:TRP:NE1	31:Cm:150:ASN:HD22	2.13	0.46
36:Cv:490:ASP:HB3	36:Cv:491:LEU:HD12	1.96	0.46
36:Cv:813:ARG:HH11	36:Cv:813:ARG:CG	2.29	0.46
37:CA:198:A:N6	37:CA:263:A:H5'	2.30	0.46
41:UT:6:UNK:O	41:UT:38:UNK:HG1	2.14	0.46
41:UT:24:UNK:HG2	41:UT:29:UNK:HG3	1.97	0.46
1:DA:1163:MET:HE2	5:DM:149:LEU:HD21	1.96	0.46
2:DD:20:PHE:HZ	15:CE:256:LEU:H	1.64	0.46
8:DP:188:ARG:HD3	8:DP:194:GLN:HG3	1.98	0.46
10:DR:26:ASN:CG	30:Cj:37:ARG:NH1	2.74	0.46
11:DS:57:LEU:HD21	11:DS:83:LEU:HD21	1.98	0.46
17:CH:201:ARG:HG2	17:CH:201:ARG:HH11	1.81	0.46
19:CK:316:ASN:OD1	19:CK:317:GLY:N	2.48	0.46
22:CP:9:ALA:HB3	37:CA:58:A:N7	2.31	0.46
27:Ca:397:GLY:HA3	27:Ca:502:PHE:CZ	2.50	0.46
30:Cj:53:ASN:O	30:Cj:55:ARG:N	2.49	0.46
37:CA:80:U:O2'	37:CA:81:U:C4	2.62	0.46
1:DA:1638:LEU:O	1:DA:1642:LEU:HB2	2.16	0.46
2:DD:654:ARG:NH1	30:Cj:15:ASN:HB2	2.31	0.46
7:DO:161:PHE:O	7:DO:198:ARG:NH2	2.49	0.46
15:CE:356:SER:HB2	27:Ca:134:LEU:HD13	1.97	0.46
16:CF:71:MET:HE3	16:CF:71:MET:HB3	1.74	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CP:173:LYS:HZ1	22:CP:181:GLU:CD	2.24	0.46
24:CR:209:ALA:O	24:CR:213:VAL:HG23	2.16	0.46
27:Ca:418:VAL:HG21	27:Ca:484:LYS:HG2	1.98	0.46
31:Cm:177:ARG:HA	31:Cm:177:ARG:HD2	1.64	0.46
36:Cv:922:ASP:HB3	36:Cv:925:ASP:OD2	2.16	0.46
37:CA:340:U:O2'	37:CA:355:A:N6	2.49	0.46
1:DA:164:TRP:CZ3	2:DD:201:GLU:HG2	2.51	0.45
1:DA:236:ARG:HH12	27:Ca:542:PRO:C	2.24	0.45
2:DD:247:VAL:HG22	12:DU:35:PRO:HD3	1.98	0.45
3:DI:328:VAL:HG22	7:DO:226:ILE:HD13	1.98	0.45
6:DN:144:ARG:HA	6:DN:144:ARG:NE	2.31	0.45
8:DP:87:GLU:O	8:DP:92:LYS:NZ	2.48	0.45
10:DR:96:PHE:HE1	10:DR:128:PRO:CD	2.27	0.45
16:CF:12:PRO:HG3	16:CF:62:ALA:HA	1.98	0.45
16:CF:47:PRO:HD2	16:CF:60:THR:O	2.16	0.45
19:CK:104:MET:CE	28:Cb:100:ARG:HH11	2.22	0.45
20:CL:112:ILE:HG22	38:UQ:19:UNK:HB2	1.97	0.45
22:CP:86:ARG:HH22	33:Cp:31:ALA:HB1	1.81	0.45
25:CU:80:GLN:NE2	25:CU:180:GLN:O	2.49	0.45
27:Ca:46:ARG:HH11	27:Ca:46:ARG:HG3	1.80	0.45
27:Ca:229:GLU:O	27:Ca:232:GLN:HB2	2.15	0.45
34:Cq:189:TYR:HB3	34:Cq:191:VAL:HG13	1.97	0.45
1:DA:225:GLY:H	1:DA:233:ARG:HD2	1.81	0.45
2:DD:88:TYR:HD1	2:DD:92:MET:HE2	1.82	0.45
2:DD:408:HIS:CE1	2:DD:424:THR:HG21	2.51	0.45
2:DD:700:ASP:HB3	2:DD:704:ASP:OD1	2.16	0.45
7:DO:70:ILE:O	7:DO:73:LEU:HD23	2.17	0.45
9:DQ:73:HIS:ND1	9:DQ:250:ARG:HB2	2.31	0.45
12:DU:64:TYR:CE1	21:CO:330:THR:HG23	2.51	0.45
15:CE:328:ASP:HA	34:Cq:21:MET:HE2	1.99	0.45
20:CL:98:TYR:CZ	40:US:40:UNK:HG2	2.52	0.45
24:CR:8:ILE:HG21	36:Cv:909:LEU:CD2	2.45	0.45
24:CR:48:TYR:CE1	28:Cb:68:GLU:HG3	2.52	0.45
29:Cd:13:ARG:NH2	29:Cd:26:ARG:HE	2.15	0.45
2:DD:448:ARG:HH11	2:DD:448:ARG:HG3	1.80	0.45
2:DD:647:ARG:HH21	10:DR:230:ARG:NH1	2.10	0.45
3:DI:186:ILE:HG23	3:DI:195:ILE:HG23	1.98	0.45
6:DN:75:VAL:HG12	6:DN:110:ALA:HB3	1.89	0.45
9:DQ:115:ILE:HD11	9:DQ:152:PHE:HZ	1.81	0.45
10:DR:105:THR:HG23	30:Cj:147:TYR:HE2	1.81	0.45
17:CH:196:ASP:HA	17:CH:203:PHE:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CK:280:ARG:HD3	19:CK:308:GLU:OE2	2.15	0.45
22:CP:23:ALA:CB	22:CP:51:HIS:CB	2.71	0.45
22:CP:184:VAL:C	22:CP:188:LEU:HB3	2.41	0.45
24:CR:138:ARG:HG3	24:CR:179:TRP:CG	2.51	0.45
27:Ca:496:GLU:OE1	27:Ca:496:GLU:N	2.48	0.45
34:Cq:158:TYR:OH	34:Cq:198:ASP:HA	2.17	0.45
41:UT:39:UNK:HA	41:UT:42:UNK:HB2	1.97	0.45
2:DD:368:LEU:HD13	2:DD:591:SER:HB3	1.98	0.45
4:DL:202:ARG:NH1	4:DL:203:ARG:HG3	2.31	0.45
6:DN:127:VAL:HG11	6:DN:160:CYS:SG	2.57	0.45
10:DR:128:PRO:CG	10:DR:133:LEU:O	2.56	0.45
12:DU:207:ARG:HD2	12:DU:207:ARG:N	2.31	0.45
15:CE:124:THR:O	15:CE:124:THR:OG1	2.19	0.45
17:CH:107:ARG:HH22	17:CH:132:ASP:CG	2.24	0.45
18:CI:105:THR:HG22	19:CK:108:ARG:O	2.16	0.45
18:CI:202:LEU:HA	18:CI:211:ASN:ND2	2.32	0.45
18:CI:240:ASN:N	18:CI:240:ASN:OD1	2.50	0.45
19:CK:315:LEU:HD12	19:CK:315:LEU:H	1.81	0.45
21:CO:267:ARG:HB3	21:CO:274:TYR:CD2	2.51	0.45
25:CU:77:ARG:NH1	36:Cv:175:ARG:HH22	2.11	0.45
31:Cm:93:LEU:HD22	31:Cm:136:MET:HE1	1.99	0.45
35:Cr:143:ARG:HH12	35:Cr:148:TRP:N	2.15	0.45
36:Cv:238:MET:HE2	36:Cv:238:MET:HB3	1.82	0.45
1:DA:523:LEU:HD13	1:DA:719:ILE:HD12	1.97	0.45
1:DA:639:PHE:CD2	1:DA:696:LEU:HB2	2.51	0.45
2:DD:22:ASP:OD1	2:DD:24:SER:OG	2.34	0.45
2:DD:248:ASP:O	2:DD:249:PRO:C	2.59	0.45
2:DD:534:PHE:CE2	2:DD:536:PRO:HG3	2.51	0.45
5:DM:274:LEU:O	5:DM:278:THR:HG22	2.17	0.45
7:DO:67:ARG:NH2	36:Cv:771:GLU:OE1	2.49	0.45
10:DR:14:ARG:NH1	37:CA:87:U:OP2	2.50	0.45
12:DU:106:PRO:HG2	12:DU:109:SER:HB3	1.99	0.45
15:CE:257:LYS:HB3	15:CE:260:ASN:HD22	1.82	0.45
17:CH:134:VAL:HG21	36:Cv:97:GLN:HA	1.97	0.45
20:CL:63:TYR:O	40:US:41:UNK:HB1	2.17	0.45
20:CL:120:ILE:HD11	40:US:46:UNK:HG1	1.98	0.45
22:CP:23:ALA:HB2	22:CP:51:HIS:NE2	2.29	0.45
27:Ca:467:LYS:NZ	29:Cd:72:ASN:ND2	2.65	0.45
31:Cm:88:SER:HB3	37:CA:394:A:H5''	1.99	0.45
33:Cp:99:ARG:NH1	37:CA:187:A:H4'	2.31	0.45
35:Cr:155:ALA:HA	35:Cr:158:ALA:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Cv:573:GLU:OE2	36:Cv:798:TYR:HA	2.16	0.45
36:Cv:1037:TYR:O	36:Cv:1046:ASN:HB3	2.17	0.45
1:DA:653:LYS:HE3	1:DA:653:LYS:HB3	1.54	0.45
1:DA:946:SER:HB3	5:DM:10:ARG:HD2	1.98	0.45
1:DA:1000:ASN:OD1	1:DA:1000:ASN:N	2.50	0.45
2:DD:226:THR:HG23	22:CP:188:LEU:HD13	1.97	0.45
12:DU:196:MET:HG2	12:DU:208:TYR:CZ	2.52	0.45
16:CF:106:SER:O	36:Cv:187:PRO:HA	2.16	0.45
18:CI:100:PRO:HD3	24:CR:96:GLN:HG3	1.98	0.45
18:CI:265:ASP:HB3	18:CI:267:TYR:CD1	2.52	0.45
19:CK:198:VAL:HB	19:CK:205:TYR:CE1	2.51	0.45
19:CK:320:MET:HE1	25:CU:16:HIS:HA	1.97	0.45
21:CO:424:LYS:NZ	37:CA:66:U:OP1	2.29	0.45
22:CP:32:ARG:CZ	22:CP:52:LYS:HD3	2.46	0.45
25:CU:182:HIS:HE1	25:CU:193:ASN:HA	1.82	0.45
27:Ca:243:THR:HG22	27:Ca:245:GLU:H	1.81	0.45
28:Cb:57:MET:H	28:Cb:57:MET:HG2	1.56	0.45
28:Cb:78:GLU:HG3	28:Cb:79:PRO:HD2	1.99	0.45
31:Cm:47:ASN:HD21	37:CA:387:U:H4'	1.82	0.45
33:Cp:69:ARG:HG2	33:Cp:104:ALA:HB2	1.98	0.45
36:Cv:298:ALA:H	36:Cv:411:ASN:HD21	1.64	0.45
36:Cv:566:MET:HE2	36:Cv:566:MET:HB3	1.65	0.45
39:UR:1:UNK:O	39:UR:2:UNK:HG3	2.16	0.45
1:DA:1038:HIS:CD2	1:DA:1045:ILE:HD11	2.51	0.45
2:DD:297:ARG:HH11	2:DD:297:ARG:HG3	1.81	0.45
4:DL:177:GLU:OE1	36:Cv:501:HIS:NE2	2.48	0.45
5:DM:75:VAL:HG13	5:DM:79:VAL:HB	1.98	0.45
6:DN:73:VAL:CG1	6:DN:112:ILE:HD12	2.43	0.45
9:DQ:39:ASP:HB2	10:DR:27:LYS:HE3	1.99	0.45
9:DQ:40:VAL:HG22	12:DU:100:VAL:HB	1.99	0.45
9:DQ:146:GLN:HG3	9:DQ:176:ARG:HH12	1.81	0.45
15:CE:173:LYS:HD2	28:Cb:45:PHE:CZ	2.52	0.45
21:CO:293:VAL:HG22	23:CQ:189:TYR:CE2	2.52	0.45
27:Ca:538:ILE:HG12	27:Ca:539:GLN:N	2.31	0.45
30:Cj:143:LYS:NZ	30:Cj:143:LYS:HB3	2.31	0.45
31:Cm:96:CYS:HB3	31:Cm:125:CYS:SG	2.57	0.45
36:Cv:1010:SER:OG	36:Cv:1011:SER:N	2.50	0.45
1:DA:150:ILE:HG23	1:DA:151:PRO:O	2.16	0.45
1:DA:237:HIS:CE1	1:DA:310:ASP:HB2	2.52	0.45
1:DA:1651:GLU:HA	1:DA:1654:ARG:NH2	2.32	0.45
2:DD:518:PHE:CE2	2:DD:602:VAL:HG11	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DL:194:ILE:HD12	24:CR:77:ILE:HD13	1.99	0.45
5:DM:1:MET:HE1	15:CE:317:HIS:HA	1.99	0.45
6:DN:224:ARG:HH11	6:DN:224:ARG:CB	2.26	0.45
6:DN:224:ARG:HH11	6:DN:224:ARG:CG	2.30	0.45
7:DO:111:ARG:HD3	36:Cv:673:LEU:HD11	1.98	0.45
8:DP:153:VAL:O	8:DP:156:GLU:HG3	2.16	0.45
15:CE:17:THR:HG21	27:Ca:560:PHE:CG	2.52	0.45
18:CI:97:GLU:OE2	19:CK:108:ARG:NH1	2.47	0.45
18:CI:126:TRP:NE1	18:CI:133:VAL:O	2.39	0.45
19:CK:232:ARG:HD2	19:CK:232:ARG:N	2.32	0.45
20:CL:81:ARG:NH1	36:Cv:29:LEU:HD11	2.32	0.45
21:CO:259:LEU:HD13	21:CO:286:ILE:HD13	1.99	0.45
27:Ca:10:ARG:NH1	27:Ca:10:ARG:HB3	2.32	0.45
31:Cm:153:ASP:HB3	31:Cm:157:LYS:HE3	1.98	0.45
33:Cp:74:PHE:HE2	33:Cp:101:THR:HG21	1.82	0.45
34:Cq:26:MET:HG2	34:Cq:30:ILE:HD11	1.99	0.45
34:Cq:155:GLN:HA	34:Cq:166:ALA:HB2	1.98	0.45
1:DA:234:HIS:HB2	1:DA:237:HIS:CD2	2.52	0.45
1:DA:562:LYS:HA	1:DA:567:ALA:CB	2.47	0.45
2:DD:442:PHE:HD2	2:DD:486:ARG:CZ	2.30	0.45
5:DM:62:VAL:HG13	5:DM:70:LEU:HD13	1.99	0.45
5:DM:68:GLY:O	5:DM:95:TYR:OH	2.29	0.45
15:CE:118:ARG:HD2	15:CE:137:LEU:HD23	1.98	0.45
20:CL:106:CYS:HB2	20:CL:134:TYR:O	2.17	0.45
23:CQ:72:ARG:O	23:CQ:118:PRO:HD2	2.17	0.45
34:Cq:169:GLU:CD	34:Cq:172:ARG:HH21	2.25	0.45
36:Cv:491:LEU:HB3	36:Cv:529:PHE:HB3	1.98	0.45
3:DI:67:ILE:CD1	3:DI:80:ARG:HG2	2.47	0.45
9:DQ:250:ARG:NE	9:DQ:252:LYS:CE	2.65	0.45
11:DS:211:CYS:HB2	11:DS:214:CYS:H	1.82	0.45
15:CE:358:GLU:CD	15:CE:358:GLU:H	2.25	0.45
16:CF:44:ILE:HD11	16:CF:63:ARG:NH1	2.28	0.45
21:CO:82:ASN:HD22	21:CO:82:ASN:HA	1.58	0.45
27:Ca:380:ASP:OD1	27:Ca:380:ASP:N	2.50	0.45
27:Ca:427:TRP:CE3	29:Cd:53:GLN:HB2	2.52	0.45
36:Cv:33:GLU:CD	36:Cv:33:GLU:H	2.25	0.45
36:Cv:136:TRP:HB3	36:Cv:225:PRO:HA	1.98	0.45
1:DA:174:HIS:NE2	2:DD:685:VAL:O	2.49	0.44
1:DA:619:ASP:OD1	1:DA:626:GLN:NE2	2.50	0.44
1:DA:935:MET:HG3	5:DM:118:LEU:HD12	1.99	0.44
2:DD:656:LEU:HD12	22:CP:142:LYS:HE2	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:803:GLN:OE1	6:DN:249:LYS:HG3	2.17	0.44
7:DO:131:ASP:HB3	7:DO:133:LYS:HG2	1.98	0.44
7:DO:132:ALA:O	7:DO:135:THR:HG22	2.17	0.44
8:DP:130:TYR:OH	30:Cj:71:ILE:O	2.21	0.44
8:DP:189:TYR:CD1	8:DP:196:TRP:C	2.95	0.44
9:DQ:146:GLN:HG2	9:DQ:176:ARG:HH12	1.82	0.44
14:Da:13:TRP:CZ3	23:CQ:39:HIS:HA	2.53	0.44
15:CE:95:ILE:HD13	36:Cv:289:VAL:HG11	1.99	0.44
19:CK:70:ILE:HD11	28:Cb:186:VAL:HA	1.98	0.44
20:CL:59:MET:HA	20:CL:59:MET:HE3	1.99	0.44
21:CO:114:ARG:NH1	21:CO:207:TYR:OH	2.50	0.44
21:CO:206:MET:HE2	21:CO:210:ARG:HH21	1.82	0.44
21:CO:250:THR:HG21	31:Cm:182:ASN:ND2	2.32	0.44
23:CQ:180:LYS:HB3	23:CQ:180:LYS:HE2	1.79	0.44
24:CR:137:THR:HG23	24:CR:139:THR:N	2.31	0.44
27:Ca:38:TRP:CZ2	41:UT:25:UNK:HA	2.52	0.44
27:Ca:538:ILE:HG12	27:Ca:539:GLN:H	1.82	0.44
32:Cn:214:ARG:H	32:Cn:214:ARG:HD3	1.81	0.44
34:Cq:47:LYS:O	34:Cq:50:GLU:HG2	2.17	0.44
34:Cq:85:HIS:NE2	34:Cq:129:HIS:HD2	2.14	0.44
36:Cv:366:ALA:O	36:Cv:369:ARG:HB3	2.16	0.44
36:Cv:1012:TRP:HD1	36:Cv:1014:ARG:HG3	1.83	0.44
37:CA:299:U:O2'	37:CA:300:G:O5'	2.32	0.44
1:DA:108:TYR:OH	1:DA:123:HIS:HD2	2.00	0.44
4:DL:190:ARG:NH1	24:CR:71:PHE:CD1	2.86	0.44
11:DS:49:VAL:HG23	27:Ca:598:ALA:HB1	1.98	0.44
24:CR:23:TRP:CE2	36:Cv:494:THR:HG21	2.52	0.44
36:Cv:227:PHE:O	36:Cv:302:GLY:HA2	2.17	0.44
39:UR:6:UNK:CG	39:UR:8:UNK:HG2	2.46	0.44
1:DA:84:PRO:HG3	2:DD:46:VAL:HG23	1.99	0.44
1:DA:872:LYS:HD3	1:DA:872:LYS:HA	1.61	0.44
2:DD:87:MET:HE1	23:CQ:26:TYR:CE1	2.53	0.44
2:DD:307:GLU:OE2	3:DI:195:ILE:HB	2.17	0.44
2:DD:390:VAL:HG13	2:DD:457:LEU:HD22	2.00	0.44
2:DD:702:TYR:HB3	17:CH:233:SER:HB2	2.00	0.44
5:DM:277:GLU:OE2	15:CE:67:SER:OG	2.31	0.44
6:DN:23:VAL:HG13	6:DN:118:LEU:HD12	1.99	0.44
6:DN:43:PHE:CZ	6:DN:151:ARG:HD2	2.52	0.44
6:DN:109:ASN:OD1	6:DN:109:ASN:N	2.50	0.44
13:DZ:48:ARG:H	27:Ca:586:ILE:CD1	2.30	0.44
15:CE:308:ARG:HD3	27:Ca:368:ARG:NH1	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CP:23:ALA:CB	22:CP:51:HIS:ND1	2.69	0.44
24:CR:94:MET:O	24:CR:98:ARG:HB2	2.16	0.44
27:Ca:570:THR:HG21	33:Cp:16:HIS:CE1	2.53	0.44
36:Cv:627:LEU:HD23	36:Cv:627:LEU:HA	1.85	0.44
1:DA:650:LEU:HD13	1:DA:725:TRP:CZ3	2.53	0.44
2:DD:535:ASP:OD2	2:DD:538:THR:OG1	2.23	0.44
6:DN:227:LYS:HE2	6:DN:287:ARG:NH2	2.32	0.44
7:DO:197:GLN:NE2	7:DO:233:ALA:HB1	2.33	0.44
8:DP:84:ASP:C	8:DP:86:PRO:HD3	2.43	0.44
18:CI:110:ARG:HD2	25:CU:143:TRP:HA	2.00	0.44
18:CI:195:ILE:HG12	34:Cq:254:TYR:CE1	2.53	0.44
18:CI:218:ARG:O	18:CI:221:GLU:HG2	2.18	0.44
24:CR:125:ASN:OD1	24:CR:125:ASN:N	2.49	0.44
36:Cv:162:SER:H	36:Cv:166:HIS:CD2	2.35	0.44
4:DL:147:ILE:HG23	28:Cb:50:GLU:OE1	2.18	0.44
5:DM:7:ILE:O	5:DM:10:ARG:HB3	2.18	0.44
6:DN:124:SER:O	27:Ca:383:TYR:OH	2.24	0.44
14:Da:33:LEU:HA	17:CH:144:ARG:NH1	2.32	0.44
17:CH:186:HIS:HD2	36:Cv:240:ARG:HH21	1.64	0.44
20:CL:81:ARG:NH2	37:CA:379:A:OP1	2.51	0.44
29:Cd:195:GLU:HG2	29:Cd:214:LYS:HB2	2.00	0.44
31:Cm:23:ASP:OD1	31:Cm:24:SER:N	2.50	0.44
36:Cv:577:PHE:HD2	36:Cv:792:TYR:CE2	2.35	0.44
36:Cv:836:GLU:OE1	36:Cv:836:GLU:N	2.51	0.44
1:DA:1494:LEU:HD22	1:DA:1605:ARG:HB3	1.99	0.44
3:DI:310:LEU:HD12	3:DI:310:LEU:HA	1.70	0.44
6:DN:183:ARG:NE	6:DN:194:ARG:NH1	2.66	0.44
8:DP:64:MET:SD	12:DU:179:THR:HA	2.58	0.44
11:DS:43:MET:HE1	37:CA:204:U:H5'	2.00	0.44
17:CH:229:GLU:HG2	17:CH:276:ARG:CD	2.45	0.44
21:CO:106:ASP:OD1	21:CO:107:LEU:N	2.50	0.44
24:CR:65:GLN:HE21	24:CR:70:ARG:HH22	1.65	0.44
24:CR:258:ASN:C	24:CR:259:GLN:HG2	2.42	0.44
25:CU:59:ARG:HH21	25:CU:170:VAL:HA	1.83	0.44
27:Ca:66:PRO:HG3	27:Ca:529:ASP:HB3	2.00	0.44
28:Cb:193:GLU:H	28:Cb:193:GLU:HG3	1.59	0.44
30:Cj:46:TYR:HA	30:Cj:165:PHE:CE2	2.52	0.44
36:Cv:292:LYS:NZ	36:Cv:509:THR:CG2	2.80	0.44
37:CA:82:U:O5'	37:CA:82:U:H6	2.00	0.44
37:CA:588:U:H5''	37:CA:588:U:O2	2.17	0.44
1:DA:95:THR:OG1	1:DA:96:ASP:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:776:GLY:O	1:DA:777:SER:HB2	2.18	0.44
1:DA:1089:ASP:HB3	1:DA:1632:LYS:HG2	2.00	0.44
1:DA:1658:GLU:OE1	1:DA:1658:GLU:N	2.40	0.44
2:DD:70:SER:O	11:DS:28:TYR:OH	2.23	0.44
3:DI:320:GLN:NE2	7:DO:238:ASN:HA	2.33	0.44
5:DM:83:THR:HG22	5:DM:85:TYR:H	1.83	0.44
8:DP:148:LYS:HE2	8:DP:148:LYS:HB2	1.84	0.44
10:DR:185:ARG:NE	10:DR:189:GLU:OE2	2.46	0.44
11:DS:201:HIS:CD2	11:DS:203:ASP:H	2.17	0.44
15:CE:326:MET:HE3	15:CE:326:MET:HB2	1.88	0.44
19:CK:153:ASP:N	19:CK:153:ASP:OD1	2.44	0.44
19:CK:195:LEU:HD12	19:CK:207:VAL:O	2.18	0.44
20:CL:76:TYR:HE2	20:CL:78:MET:HE2	1.83	0.44
21:CO:164:ARG:HH22	21:CO:201:PHE:HD1	1.64	0.44
21:CO:216:PHE:CZ	29:Cd:124:ARG:HA	2.53	0.44
22:CP:184:VAL:O	22:CP:188:LEU:HB3	2.17	0.44
27:Ca:10:ARG:HB3	27:Ca:10:ARG:CZ	2.47	0.44
27:Ca:347:ARG:O	27:Ca:350:GLU:HG3	2.17	0.44
27:Ca:509:TRP:HA	27:Ca:514:THR:OG1	2.18	0.44
36:Cv:166:HIS:CD2	36:Cv:185:VAL:HG21	2.52	0.44
1:DA:1094:VAL:O	1:DA:1098:LEU:HB2	2.17	0.44
8:DP:139:ARG:HA	8:DP:139:ARG:HD2	1.84	0.44
16:CF:22:LEU:HD21	16:CF:65:ILE:HD13	1.97	0.44
19:CK:180:ASP:HA	29:Cd:182:GLN:NE2	2.32	0.44
21:CO:140:ALA:O	21:CO:144:ARG:HB2	2.18	0.44
26:CZ:240:VAL:HG23	26:CZ:291:PHE:O	2.17	0.44
27:Ca:130:TYR:HB3	27:Ca:131:MET:HE2	2.00	0.44
31:Cm:185:ALA:HB1	31:Cm:188:ARG:HB2	2.00	0.44
33:Cp:54:PRO:HD2	33:Cp:58:THR:HG21	2.00	0.44
34:Cq:253:ARG:O	34:Cq:257:MET:HG3	2.17	0.44
36:Cv:207:PHE:C	36:Cv:208:LYS:HG2	2.42	0.44
36:Cv:959:LEU:HA	36:Cv:959:LEU:HD13	1.83	0.44
1:DA:172:GLY:C	1:DA:174:HIS:N	2.75	0.44
1:DA:961:LYS:NZ	1:DA:983:GLU:OE1	2.49	0.44
1:DA:1656:ASN:HD21	1:DA:1659:ARG:HD2	1.82	0.44
3:DI:276:GLU:HG2	3:DI:277:SER:N	2.33	0.44
3:DI:290:PHE:HB2	3:DI:301:ILE:HB	1.99	0.44
4:DL:160:ARG:HD2	28:Cb:28:TYR:CG	2.53	0.44
7:DO:162:ALA:HA	7:DO:198:ARG:HH21	1.83	0.44
15:CE:152:VAL:HG22	31:Cm:42:PRO:HG2	2.00	0.44
33:Cp:135:THR:HG22	33:Cp:138:TYR:H	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Cv:262:ASN:OD1	36:Cv:264:PRO:HD3	2.18	0.44
36:Cv:559:GLN:HE21	39:UR:3:UNK:HG1	1.83	0.44
37:CA:30:U:H2'	37:CA:31:U:C6	2.53	0.44
1:DA:287:HIS:HD2	1:DA:290:TYR:CD1	2.35	0.43
1:DA:414:HIS:CD2	1:DA:416:HIS:H	2.36	0.43
1:DA:587:ASP:OD1	1:DA:588:GLU:N	2.51	0.43
1:DA:924:TRP:CD1	36:Cv:1000:MET:HE2	2.53	0.43
2:DD:782:ILE:HG21	27:Ca:303:VAL:HG11	2.00	0.43
3:DI:190:PRO:O	3:DI:193:ASN:N	2.39	0.43
4:DL:156:GLU:OE2	15:CE:135:ARG:NH2	2.51	0.43
5:DM:164:ILE:HG23	15:CE:343:TYR:OH	2.18	0.43
9:DQ:65:TRP:HA	9:DQ:68:ARG:HH11	1.82	0.43
9:DQ:129:GLU:O	9:DQ:133:ASN:HB2	2.18	0.43
10:DR:27:LYS:O	12:DU:97:ARG:NH2	2.50	0.43
10:DR:186:PRO:C	10:DR:188:LYS:H	2.25	0.43
14:Da:61:ARG:HB3	14:Da:61:ARG:NH1	2.33	0.43
15:CE:144:ILE:HD11	15:CE:190:LYS:HD2	1.99	0.43
21:CO:74:TRP:CE2	21:CO:86:PRO:HG3	2.53	0.43
24:CR:53:GLN:HB3	24:CR:56:GLU:OE1	2.18	0.43
27:Ca:506:GLN:O	27:Ca:556:SER:HA	2.17	0.43
27:Ca:507:MET:HE2	27:Ca:507:MET:HB3	1.77	0.43
33:Cp:52:TYR:CD1	33:Cp:62:ARG:NH1	2.85	0.43
35:Cr:192:LEU:O	35:Cr:196:VAL:HG23	2.18	0.43
36:Cv:169:LYS:HB3	36:Cv:174:ARG:HG2	2.00	0.43
36:Cv:295:VAL:HG22	36:Cv:407:MET:HE3	2.00	0.43
37:CA:152:U:H2'	37:CA:153:A:O4'	2.17	0.43
2:DD:237:THR:HG23	3:DI:184:ASN:HB3	2.00	0.43
5:DM:213:ARG:NH1	5:DM:219:GLY:HA3	2.34	0.43
5:DM:284:ARG:NH1	34:Cq:46:ASP:OD2	2.51	0.43
8:DP:115:LEU:HD21	8:DP:135:LEU:HD13	2.00	0.43
16:CF:149:PHE:HZ	29:Cd:143:GLN:HB2	1.82	0.43
25:CU:69:ARG:HA	25:CU:72:HIS:HD2	1.83	0.43
27:Ca:359:ARG:HD2	37:CA:3:A:N6	2.33	0.43
33:Cp:67:ARG:NH2	37:CA:45:G:N7	2.66	0.43
36:Cv:407:MET:HE3	36:Cv:407:MET:HB3	1.74	0.43
1:DA:93:TRP:O	1:DA:97:THR:OG1	2.30	0.43
1:DA:744:GLU:O	1:DA:747:ARG:HG2	2.19	0.43
8:DP:212:ASN:OD1	8:DP:215:LEU:HB3	2.18	0.43
9:DQ:106:MET:HE2	9:DQ:221:LEU:HD22	2.00	0.43
11:DS:36:SER:O	11:DS:40:LYS:HG3	2.18	0.43
18:CI:82:HIS:O	31:Cm:128:ARG:NH2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CO:76:TRP:HZ2	32:Cn:143:ALA:HB2	1.82	0.43
25:CU:115:LYS:HD3	25:CU:115:LYS:HA	1.70	0.43
26:CZ:249:SER:HB3	26:CZ:252:CYS:SG	2.58	0.43
27:Ca:293:LEU:HD13	27:Ca:297:LEU:HD13	2.01	0.43
30:Cj:28:LYS:HB3	30:Cj:28:LYS:HZ3	1.82	0.43
32:Cn:206:GLU:OE1	32:Cn:206:GLU:N	2.50	0.43
36:Cv:833:PRO:HG2	36:Cv:836:GLU:OE1	2.18	0.43
1:DA:324:GLN:HG2	1:DA:330:TRP:HE1	1.83	0.43
2:DD:119:TYR:CD1	29:Cd:76:TYR:HD1	2.37	0.43
2:DD:298:MET:HG2	2:DD:314:PHE:CZ	2.54	0.43
2:DD:323:LEU:HD11	2:DD:444:SER:OG	2.19	0.43
2:DD:745:ASN:OD1	2:DD:746:PRO:HD2	2.19	0.43
7:DO:106:GLU:H	7:DO:106:GLU:CD	2.26	0.43
9:DQ:52:PHE:CE1	9:DQ:235:HIS:HE1	2.36	0.43
10:DR:250:ARG:HB3	10:DR:250:ARG:NH1	2.33	0.43
15:CE:42:ARG:HH11	15:CE:42:ARG:CG	2.28	0.43
15:CE:62:ARG:HA	15:CE:62:ARG:HD2	1.81	0.43
21:CO:245:ASN:ND2	21:CO:248:ILE:HD12	2.32	0.43
21:CO:311:ILE:O	21:CO:311:ILE:HG22	2.18	0.43
21:CO:317:ASP:OD1	21:CO:318:VAL:N	2.52	0.43
27:Ca:217:LEU:HD12	27:Ca:217:LEU:HA	1.90	0.43
27:Ca:506:GLN:HE21	27:Ca:506:GLN:HB3	1.57	0.43
29:Cd:198:GLU:OE1	29:Cd:198:GLU:N	2.50	0.43
36:Cv:739:ASN:HB3	36:Cv:789:CYS:HB2	2.00	0.43
39:UR:6:UNK:HG2	39:UR:8:UNK:HG2	2.00	0.43
1:DA:125:LEU:HD13	17:CH:150:THR:HG23	2.01	0.43
1:DA:441:SER:HA	1:DA:442:PRO:HD2	1.75	0.43
1:DA:973:LEU:H	1:DA:973:LEU:HG	1.70	0.43
1:DA:1179:GLN:HG3	1:DA:1181:THR:HG23	2.00	0.43
1:DA:1517:ARG:NH1	5:DM:179:ARG:HH11	2.16	0.43
3:DI:52:GLU:OE2	3:DI:93:TRP:NE1	2.33	0.43
4:DL:136:MET:HE2	4:DL:136:MET:HB3	1.86	0.43
14:Da:53:ARG:HB2	14:Da:54:TRP:CE3	2.53	0.43
15:CE:16:TYR:HB2	27:Ca:341:LEU:O	2.18	0.43
23:CQ:140:VAL:N	23:CQ:143:ASP:OD2	2.47	0.43
24:CR:101:GLN:HB3	24:CR:102:PRO:HD2	2.01	0.43
24:CR:312:ASN:HA	24:CR:313:PRO:HD3	1.87	0.43
27:Ca:32:PRO:O	41:UT:18:UNK:HG1	2.19	0.43
27:Ca:569:ARG:HD2	27:Ca:569:ARG:HA	1.74	0.43
28:Cb:161:ALA:HA	34:Cq:121:VAL:CG2	2.47	0.43
35:Cr:102:PHE:HD2	35:Cr:184:VAL:HG12	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Cv:948:HIS:O	36:Cv:952:ALA:HB2	2.18	0.43
1:DA:905:GLU:O	1:DA:908:ARG:HG2	2.18	0.43
1:DA:1557:THR:HG22	1:DA:1558:ASN:H	1.83	0.43
2:DD:42:MET:HE3	2:DD:42:MET:HB3	1.83	0.43
2:DD:189:GLU:CD	2:DD:192:MET:HE3	2.43	0.43
2:DD:280:LEU:HA	2:DD:280:LEU:HD23	1.71	0.43
2:DD:621:LEU:O	30:Cj:210:PRO:HG2	2.19	0.43
2:DD:765:ARG:HH21	36:Cv:960:GLN:HE21	1.67	0.43
8:DP:207:TYR:HA	8:DP:208:PRO:C	2.41	0.43
11:DS:232:GLN:CD	11:DS:234:LEU:HD11	2.44	0.43
15:CE:174:GLY:HA2	15:CE:245:PHE:O	2.18	0.43
28:Cb:56:ARG:NH1	28:Cb:57:MET:HE1	2.31	0.43
28:Cb:90:GLU:OE1	28:Cb:90:GLU:N	2.47	0.43
31:Cm:175:LEU:HD11	36:Cv:54:ASN:HB2	1.99	0.43
34:Cq:79:MET:HE3	34:Cq:79:MET:HB2	1.85	0.43
36:Cv:738:ARG:HH21	36:Cv:788:ARG:CD	2.31	0.43
36:Cv:740:ILE:HD13	36:Cv:740:ILE:HA	1.86	0.43
40:US:25:UNK:O	40:US:29:UNK:HB1	2.19	0.43
1:DA:74:LYS:NZ	37:CA:71:U:P	2.90	0.43
1:DA:324:GLN:HG2	1:DA:330:TRP:NE1	2.34	0.43
1:DA:695:MET:HG3	1:DA:713:PHE:HD2	1.83	0.43
2:DD:84:LYS:O	2:DD:87:MET:HB3	2.18	0.43
2:DD:156:GLN:HE22	29:Cd:67:GLU:CG	2.31	0.43
2:DD:624:THR:HG23	2:DD:629:ALA:O	2.18	0.43
6:DN:142:ARG:HG2	6:DN:142:ARG:HH11	1.83	0.43
6:DN:173:TYR:CZ	6:DN:182:VAL:HG13	2.54	0.43
9:DQ:147:PRO:O	9:DQ:176:ARG:NH2	2.47	0.43
11:DS:201:HIS:HB2	33:Cp:41:ILE:O	2.17	0.43
15:CE:220:ASP:HB2	36:Cv:44:ARG:NH1	2.24	0.43
15:CE:311:LYS:NZ	27:Ca:368:ARG:O	2.32	0.43
15:CE:362:GLU:OE2	15:CE:364:ARG:HG3	2.18	0.43
16:CF:67:LEU:HD22	16:CF:69:LEU:HD21	2.01	0.43
18:CI:93:MET:HE2	18:CI:93:MET:HB3	1.88	0.43
18:CI:270:PHE:O	18:CI:274:LEU:HB2	2.19	0.43
19:CK:73:GLN:HB3	28:Cb:179:GLU:HG3	2.01	0.43
23:CQ:69:GLN:HE21	23:CQ:69:GLN:HB3	1.51	0.43
26:CZ:277:PHE:CE1	26:CZ:280:ILE:HG13	2.53	0.43
28:Cb:125:MET:HE3	28:Cb:146:VAL:HG12	2.00	0.43
31:Cm:215:LYS:HE3	37:CA:336:U:OP2	2.19	0.43
36:Cv:413:LYS:HA	36:Cv:435:GLU:HB3	2.00	0.43
37:CA:44:U:H2'	37:CA:45:G:H3'	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:CA:233:C:H4'	37:CA:234:C:C5'	2.48	0.43
2:DD:785:MET:HE2	2:DD:785:MET:HB2	1.97	0.43
5:DM:74:ARG:HB3	36:Cv:971:LEU:HD11	2.00	0.43
6:DN:212:THR:OG1	27:Ca:193:ARG:NH1	2.50	0.43
6:DN:229:THR:HB	15:CE:29:TYR:CE1	2.53	0.43
7:DO:116:ALA:HA	7:DO:119:ARG:HG2	2.01	0.43
12:DU:147:LEU:HD23	12:DU:152:ILE:HD12	1.98	0.43
17:CH:142:ARG:HH22	36:Cv:74:ASN:ND2	2.17	0.43
19:CK:310:ILE:HD12	25:CU:38:PHE:CE1	2.54	0.43
22:CP:55:ASN:OD1	22:CP:58:ILE:HG13	2.19	0.43
26:CZ:247:PHE:CE2	26:CZ:332:GLY:HA2	2.53	0.43
27:Ca:475:GLN:HE21	27:Ca:481:ARG:HE	1.67	0.43
30:Cj:227:ASP:OD1	33:Cp:117:PRO:HD3	2.19	0.43
36:Cv:797:ALA:HA	36:Cv:800:VAL:HG12	2.01	0.43
1:DA:225:GLY:O	1:DA:232:SER:HB2	2.19	0.43
1:DA:529:ILE:O	1:DA:532:ARG:N	2.51	0.43
2:DD:527:THR:CB	10:DR:223:GLN:HG3	2.46	0.43
2:DD:668:ARG:HG3	2:DD:668:ARG:HH11	1.83	0.43
8:DP:200:SER:HB2	8:DP:207:TYR:HE2	1.84	0.43
17:CH:263:ILE:HG22	17:CH:264:ASP:O	2.18	0.43
21:CO:78:PRO:HG2	32:Cn:185:TYR:HB3	2.01	0.43
21:CO:107:LEU:HB2	21:CO:112:LYS:NZ	2.34	0.43
23:CQ:48:ARG:HG2	37:CA:565:A:C6	2.53	0.43
23:CQ:104:LEU:HD23	23:CQ:104:LEU:HA	1.63	0.43
23:CQ:192:SER:OG	37:CA:101:A:OP2	2.23	0.43
24:CR:25:GLU:CB	36:Cv:143:THR:HG21	2.48	0.43
25:CU:104:LEU:O	25:CU:107:SER:OG	2.24	0.43
27:Ca:359:ARG:HH21	36:Cv:257:LYS:HD3	1.84	0.43
28:Cb:296:PHE:HA	28:Cb:297:PRO:HD3	1.89	0.43
35:Cr:10:ARG:HH22	35:Cr:13:ARG:HB2	1.84	0.43
36:Cv:320:LEU:HA	36:Cv:320:LEU:HD23	1.76	0.43
1:DA:112:GLN:CD	1:DA:131:ASP:OD2	2.62	0.43
1:DA:1020:MET:HE3	1:DA:1020:MET:HB3	1.73	0.43
2:DD:656:LEU:HD23	2:DD:656:LEU:HA	1.90	0.43
5:DM:45:ARG:O	5:DM:49:MET:HE3	2.19	0.43
6:DN:73:VAL:HG23	6:DN:75:VAL:HB	2.01	0.43
15:CE:89:LEU:HD23	15:CE:89:LEU:HA	1.94	0.43
20:CL:66:CYS:C	20:CL:67:LEU:HD12	2.44	0.43
21:CO:88:PRO:O	21:CO:89:HIS:HB2	2.18	0.43
21:CO:320:ASP:OD2	21:CO:322:ARG:NH1	2.52	0.43
21:CO:416:THR:OG1	21:CO:417:LYS:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:CR:116:PRO:HB3	24:CR:135:PHE:HZ	1.84	0.43
24:CR:134:ARG:NH2	24:CR:185:PHE:HB3	2.29	0.43
28:Cb:169:LYS:NZ	28:Cb:176:THR:OG1	2.42	0.43
30:Cj:73:ARG:HB2	33:Cp:169:ASN:HA	2.01	0.43
30:Cj:99:ASN:OD1	30:Cj:100:ILE:N	2.52	0.43
36:Cv:247:THR:HG23	36:Cv:263:GLU:HG3	2.00	0.43
37:CA:263:A:O2'	37:CA:264:A:H8	2.02	0.43
1:DA:60:GLU:O	1:DA:64:GLY:N	2.49	0.42
1:DA:126:GLU:OE2	17:CH:150:THR:HG22	2.19	0.42
1:DA:493:TRP:NE1	1:DA:494:ARG:HG3	2.34	0.42
2:DD:208:CYS:O	2:DD:212:ILE:HG13	2.19	0.42
2:DD:620:ALA:O	2:DD:623:TRP:HB2	2.19	0.42
3:DI:227:ASN:HB3	3:DI:231:GLY:HA2	2.01	0.42
4:DL:246:GLU:CD	31:Cm:61:ARG:NH1	2.77	0.42
6:DN:27:ASP:CG	6:DN:29:ARG:HG2	2.44	0.42
6:DN:235:ASN:OD1	6:DN:238:ASN:ND2	2.52	0.42
10:DR:86:LEU:HD11	10:DR:177:LEU:HD12	2.01	0.42
13:DZ:57:GLY:O	13:DZ:58:ASP:HB3	2.18	0.42
16:CF:11:LYS:HA	16:CF:12:PRO:HD3	1.75	0.42
19:CK:269:MET:HG3	19:CK:273:GLU:OE1	2.18	0.42
20:CL:123:GLY:O	37:CA:266:A:O3'	2.37	0.42
21:CO:111:GLN:HE22	21:CO:236:ARG:HH11	1.67	0.42
24:CR:9:TYR:CE1	36:Cv:896:PHE:CE1	3.07	0.42
36:Cv:444:GLY:HA2	36:Cv:808:SER:OG	2.19	0.42
36:Cv:678:HIS:CD2	36:Cv:680:ARG:HD2	2.51	0.42
36:Cv:917:THR:HG22	36:Cv:919:GLN:H	1.84	0.42
37:CA:565:A:H4'	37:CA:566:U:OP1	2.19	0.42
1:DA:341:LEU:HD23	1:DA:341:LEU:HA	1.81	0.42
2:DD:393:VAL:HG21	2:DD:441:LEU:HD13	2.00	0.42
2:DD:504:ASN:OD1	2:DD:504:ASN:N	2.51	0.42
3:DI:306:ASP:OD1	3:DI:306:ASP:N	2.45	0.42
6:DN:77:LEU:N	6:DN:78:PRO:CD	2.82	0.42
10:DR:83:MET:HE2	10:DR:83:MET:HB3	1.96	0.42
15:CE:102:GLU:HG3	28:Cb:56:ARG:CZ	2.49	0.42
18:CI:110:ARG:HG2	18:CI:110:ARG:HH11	1.84	0.42
27:Ca:154:GLU:HA	27:Ca:157:LYS:HB2	2.00	0.42
28:Cb:10:LYS:HB2	37:CA:542:G:H5'	2.01	0.42
29:Cd:57:LEU:HD23	29:Cd:57:LEU:HA	1.80	0.42
31:Cm:32:LYS:HA	31:Cm:33:PRO:HD3	1.91	0.42
35:Cr:14:GLU:OE1	35:Cr:14:GLU:N	2.49	0.42
2:DD:742:ASP:N	2:DD:742:ASP:OD1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DI:18:HIS:CD2	3:DI:65:MET:HB2	2.54	0.42
3:DI:284:CYS:SG	7:DO:238:ASN:ND2	2.93	0.42
4:DL:120:PHE:HE1	4:DL:213:SER:HA	1.83	0.42
4:DL:164:ARG:HH11	4:DL:164:ARG:HG2	1.85	0.42
8:DP:27:ASP:OD1	8:DP:27:ASP:N	2.41	0.42
8:DP:132:LEU:HD23	8:DP:132:LEU:HA	1.85	0.42
8:DP:199:LEU:HD23	8:DP:200:SER:C	2.45	0.42
12:DU:115:LYS:HG2	12:DU:132:PHE:CE2	2.54	0.42
18:CI:198:GLU:O	34:Cq:137:LYS:HE3	2.20	0.42
22:CP:30:ARG:HD2	22:CP:48:GLU:OE2	2.19	0.42
23:CQ:108:VAL:HG11	23:CQ:129:ARG:NH2	2.34	0.42
27:Ca:14:ASN:O	27:Ca:15:LYS:HG2	2.20	0.42
27:Ca:46:ARG:HG3	27:Ca:46:ARG:NH1	2.34	0.42
28:Cb:300:TYR:CZ	28:Cb:302:GLY:HA3	2.54	0.42
35:Cr:12:ALA:O	35:Cr:16:HIS:HB2	2.19	0.42
36:Cv:681:HIS:HE2	36:Cv:695:SER:HG	1.64	0.42
37:CA:81:U:O2	37:CA:82:U:C4	2.71	0.42
1:DA:162:PRO:HA	1:DA:165:ARG:HE	1.83	0.42
1:DA:1043:ASP:OD1	4:DL:140:LEU:HB2	2.20	0.42
2:DD:471:GLU:HB3	2:DD:475:ALA:HB3	2.01	0.42
14:Da:45:LYS:HZ3	14:Da:46:ARG:HH22	1.67	0.42
17:CH:195:ARG:HD3	37:CA:1:U:O4	2.19	0.42
17:CH:211:GLN:HG2	28:Cb:31:TRP:CZ3	2.54	0.42
18:CI:90:GLU:HG3	19:CK:107:GLN:O	2.20	0.42
19:CK:325:PHE:HE1	37:CA:590:A:H5'	1.84	0.42
20:CL:69:PHE:HZ	40:US:46:UNK:CG	2.33	0.42
20:CL:78:MET:HE3	20:CL:105:ARG:NH2	2.28	0.42
21:CO:287:LEU:HD23	21:CO:287:LEU:HA	1.84	0.42
25:CU:86:THR:O	25:CU:90:LEU:HG	2.20	0.42
37:CA:84:U:P	37:CA:84:U:C3'	3.04	0.42
37:CA:153:A:H2'	37:CA:154:G:H8	1.83	0.42
1:DA:421:GLY:HA2	1:DA:489:ARG:HD2	2.01	0.42
2:DD:344:ALA:HB2	9:DQ:30:ALA:HB3	2.00	0.42
3:DI:404:TRP:CE3	36:Cv:212:ARG:NH1	2.87	0.42
6:DN:45:ARG:HA	6:DN:155:ASP:HB2	2.01	0.42
6:DN:74:HIS:CE1	6:DN:76:SER:HB2	2.54	0.42
7:DO:74:TRP:CZ2	7:DO:259:THR:HG23	2.55	0.42
8:DP:17:PRO:HG2	8:DP:20:MET:HG3	2.00	0.42
15:CE:336:PRO:HD2	15:CE:339:LEU:HD12	2.02	0.42
20:CL:114:LEU:O	20:CL:116:MET:HE2	2.20	0.42
21:CO:206:MET:CE	21:CO:210:ARG:HH21	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:CP:92:THR:HB	27:Ca:444:PHE:CD1	2.54	0.42
23:CQ:173:GLU:O	23:CQ:177:LEU:HD13	2.20	0.42
28:Cb:14:ASN:ND2	31:Cm:154:ASN:O	2.47	0.42
32:Cn:190:VAL:HB	32:Cn:193:LEU:HD12	2.02	0.42
36:Cv:1005:TRP:CD1	36:Cv:1006:GLU:H	2.37	0.42
37:CA:88:A:C4	37:CA:89:U:C5	3.07	0.42
37:CA:352:G:H8	37:CA:352:G:OP2	2.03	0.42
37:CA:580:U:H5'	37:CA:581:G:OP2	2.18	0.42
1:DA:41:PHE:HD1	1:DA:42:LYS:H	1.66	0.42
1:DA:733:SER:O	1:DA:736:VAL:HG22	2.18	0.42
1:DA:1466:TYR:O	1:DA:1492:LEU:HD12	2.19	0.42
1:DA:1530:ALA:HA	1:DA:1531:PRO:HD3	1.90	0.42
2:DD:10:HIS:N	32:Cn:154:PRO:HA	2.35	0.42
5:DM:36:TYR:CZ	15:CE:314:MET:HE2	2.54	0.42
7:DO:125:LEU:HD22	7:DO:125:LEU:HA	1.74	0.42
12:DU:154:GLU:H	12:DU:154:GLU:HG3	1.59	0.42
14:Da:36:SER:O	14:Da:40:ARG:HG2	2.20	0.42
15:CE:288:SER:OG	17:CH:215:THR:HG23	2.18	0.42
19:CK:102:ASP:OD2	28:Cb:104:LEU:HB2	2.19	0.42
20:CL:80:PRO:HG2	20:CL:84:SER:O	2.20	0.42
21:CO:270:ASP:OD2	21:CO:273:LYS:HG3	2.20	0.42
22:CP:135:MET:HE2	22:CP:135:MET:HB3	1.79	0.42
25:CU:27:LYS:HG2	37:CA:297:G:H1	1.83	0.42
27:Ca:406:MET:C	27:Ca:408:PRO:HD3	2.45	0.42
31:Cm:61:ARG:CZ	31:Cm:61:ARG:HB3	2.45	0.42
33:Cp:88:ASP:O	33:Cp:92:LEU:HB2	2.19	0.42
36:Cv:312:ASN:HD22	36:Cv:314:GLU:H	1.67	0.42
36:Cv:682:VAL:O	36:Cv:695:SER:HA	2.19	0.42
1:DA:623:HIS:HB3	1:DA:625:LYS:HE3	2.00	0.42
1:DA:1440:ILE:HD11	1:DA:1562:GLN:CB	2.44	0.42
2:DD:124:TYR:CD1	29:Cd:84:LYS:HB2	2.54	0.42
2:DD:162:LEU:HD12	2:DD:165:MET:HE3	2.02	0.42
13:DZ:20:ARG:HD2	27:Ca:172:PHE:CD2	2.54	0.42
15:CE:34:ARG:HA	15:CE:35:PRO:HD3	1.88	0.42
15:CE:69:GLU:O	15:CE:72:ALA:N	2.52	0.42
20:CL:112:ILE:CG2	38:UQ:19:UNK:HB2	2.50	0.42
22:CP:52:LYS:HE3	22:CP:52:LYS:HB3	1.81	0.42
25:CU:41:ARG:O	25:CU:43:PRO:HD3	2.20	0.42
26:CZ:318:LEU:HD22	26:CZ:318:LEU:HA	1.77	0.42
33:Cp:90:ARG:NH1	37:CA:185:A:OP2	2.52	0.42
33:Cp:151:ARG:O	33:Cp:154:GLN:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Cq:131:ASN:HB3	34:Cq:187:TRP:CE2	2.54	0.42
36:Cv:696:PHE:HB2	36:Cv:727:ARG:HH12	1.84	0.42
1:DA:904:TRP:CD1	27:Ca:399:ASN:HB3	2.54	0.42
1:DA:1029:LYS:HE3	5:DM:257:GLU:OE1	2.19	0.42
3:DI:304:ALA:HB2	3:DI:345:LEU:CD1	2.50	0.42
4:DL:181:ARG:NH1	4:DL:181:ARG:CG	2.79	0.42
5:DM:282:TRP:CH2	34:Cq:39:GLU:HG3	2.55	0.42
7:DO:70:ILE:HD13	7:DO:120:LEU:HB2	2.01	0.42
9:DQ:16:LEU:HA	9:DQ:16:LEU:HD23	1.76	0.42
9:DQ:58:ARG:HH12	12:DU:42:THR:HB	1.85	0.42
9:DQ:182:CYS:SG	9:DQ:203:SER:HB3	2.60	0.42
12:DU:207:ARG:O	12:DU:207:ARG:HG2	2.20	0.42
20:CL:127:VAL:HG13	20:CL:129:LEU:H	1.83	0.42
24:CR:309:GLY:HA3	37:CA:388:U:O2	2.20	0.42
29:Cd:177:LEU:HD11	36:Cv:648:VAL:CG2	2.49	0.42
36:Cv:943:LEU:O	36:Cv:944:HIS:C	2.62	0.42
37:CA:84:U:H3'	37:CA:84:U:OP2	2.19	0.42
2:DD:368:LEU:HD23	2:DD:368:LEU:HA	1.87	0.42
2:DD:748:ARG:HH12	3:DI:147:ASP:CG	2.28	0.42
5:DM:76:ASN:HD21	36:Cv:970:GLY:N	2.18	0.42
7:DO:249:ASP:OD1	7:DO:249:ASP:N	2.53	0.42
10:DR:51:LEU:HD11	10:DR:63:ILE:HD11	2.02	0.42
14:Da:33:LEU:O	14:Da:42:ARG:NH2	2.53	0.42
15:CE:66:ASP:OD2	15:CE:69:GLU:HB2	2.20	0.42
18:CI:100:PRO:O	28:Cb:103:ARG:NH1	2.53	0.42
23:CQ:17:GLU:OE2	33:Cp:21:TYR:OH	2.35	0.42
27:Ca:367:ASN:HA	36:Cv:954:ARG:NH2	2.25	0.42
27:Ca:403:TYR:OH	27:Ca:410:MET:HG2	2.20	0.42
28:Cb:132:LEU:HD11	28:Cb:145:LYS:HD3	2.01	0.42
32:Cn:239:GLY:HA2	37:CA:338:U:O2'	2.20	0.42
36:Cv:86:GLU:H	36:Cv:86:GLU:HG3	1.68	0.42
36:Cv:1106:ALA:HB3	36:Cv:1111:LYS:HE3	2.01	0.42
37:CA:85:U:C6	37:CA:85:U:C4'	3.03	0.42
3:DI:286:GLY:O	3:DI:288:ILE:HG23	2.19	0.42
5:DM:56:TRP:CD1	5:DM:56:TRP:C	2.98	0.42
6:DN:75:VAL:HG12	6:DN:110:ALA:CB	2.45	0.42
6:DN:152:LEU:HA	6:DN:152:LEU:HD12	1.78	0.42
8:DP:35:ILE:HD13	8:DP:44:GLU:OE1	2.19	0.42
8:DP:139:ARG:HH12	8:DP:176:PRO:C	2.28	0.42
9:DQ:26:ASP:OD1	9:DQ:28:ARG:HG2	2.20	0.42
10:DR:126:LEU:HD11	10:DR:137:CYS:SG	2.59	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:DS:128:SER:OG	11:DS:131:ARG:HG3	2.20	0.42
12:DU:94:TRP:HH2	12:DU:196:MET:HE1	1.82	0.42
12:DU:97:ARG:NH2	12:DU:211:ARG:HH21	2.17	0.42
12:DU:111:ILE:HD12	12:DU:142:ASP:O	2.19	0.42
36:Cv:493:THR:HB	36:Cv:529:PHE:HD1	1.85	0.42
36:Cv:559:GLN:NE2	36:Cv:568:THR:OG1	2.53	0.42
1:DA:1036:HIS:HB3	5:DM:294:TRP:CD1	2.55	0.41
1:DA:1535:PHE:O	1:DA:1553:VAL:HA	2.20	0.41
2:DD:92:MET:HA	2:DD:93:PRO:HD3	1.95	0.41
2:DD:741:ARG:HH11	2:DD:741:ARG:HB3	1.85	0.41
3:DI:243:LEU:HD12	3:DI:243:LEU:HA	1.79	0.41
4:DL:174:ALA:HB2	36:Cv:501:HIS:CG	2.55	0.41
7:DO:114:GLY:C	7:DO:116:ALA:N	2.78	0.41
8:DP:120:ASP:C	8:DP:160:ARG:HH12	2.25	0.41
8:DP:148:LYS:HG3	8:DP:181:PHE:CD2	2.55	0.41
9:DQ:151:ARG:HG2	9:DQ:240:ASP:OD1	2.20	0.41
14:Da:30:HIS:HA	14:Da:31:PRO:HD3	1.93	0.41
15:CE:257:LYS:HE2	15:CE:257:LYS:HB2	1.89	0.41
18:CI:142:TYR:HA	18:CI:145:VAL:HG22	2.01	0.41
22:CP:163:LYS:HG2	22:CP:167:TYR:CE2	2.54	0.41
24:CR:144:PRO:HG2	24:CR:147:ILE:HG12	2.01	0.41
27:Ca:393:GLU:HG3	27:Ca:403:TYR:HE1	1.85	0.41
27:Ca:524:VAL:HA	27:Ca:525:PRO:HD2	1.77	0.41
28:Cb:128:GLU:HG3	28:Cb:146:VAL:HG22	2.02	0.41
33:Cp:66:HIS:HD2	33:Cp:68:LEU:H	1.68	0.41
35:Cr:86:LEU:HG	35:Cr:90:ILE:HD12	2.01	0.41
35:Cr:177:LEU:HD23	35:Cr:177:LEU:HA	1.85	0.41
36:Cv:914:ASN:CG	36:Cv:915:PRO:HD3	2.45	0.41
2:DD:343:TRP:CZ3	2:DD:345:PRO:HD3	2.55	0.41
2:DD:694:ARG:NH1	27:Ca:459:LEU:HD13	2.36	0.41
5:DM:242:LEU:HD23	5:DM:242:LEU:HA	1.81	0.41
6:DN:123:GLN:N	6:DN:123:GLN:OE1	2.53	0.41
8:DP:189:TYR:HD1	8:DP:196:TRP:C	2.28	0.41
12:DU:225:LYS:O	30:Cj:159:ARG:NH2	2.42	0.41
13:DZ:10:MET:N	27:Ca:181:GLU:OE1	2.53	0.41
15:CE:116:GLN:HA	15:CE:122:TRP:CG	2.54	0.41
15:CE:136:PHE:HZ	15:CE:201:ILE:HD12	1.85	0.41
17:CH:60:LEU:HD23	17:CH:60:LEU:HA	1.84	0.41
18:CI:265:ASP:O	18:CI:266:SER:OG	2.30	0.41
21:CO:222:ALA:O	21:CO:226:VAL:HG23	2.20	0.41
22:CP:80:THR:HG22	22:CP:82:VAL:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:Cd:210:ASP:OD1	29:Cd:210:ASP:N	2.53	0.41
35:Cr:261:TRP:CE3	35:Cr:264:ILE:HD12	2.55	0.41
35:Cr:282:GLU:O	35:Cr:286:VAL:HG23	2.20	0.41
36:Cv:98:ARG:H	36:Cv:98:ARG:HG2	1.67	0.41
36:Cv:971:LEU:HD23	36:Cv:971:LEU:HA	1.90	0.41
1:DA:702:ASP:OD2	1:DA:705:LYS:HG3	2.20	0.41
1:DA:959:LYS:HD2	1:DA:959:LYS:N	2.35	0.41
2:DD:271:LYS:HD2	2:DD:271:LYS:HA	1.87	0.41
5:DM:273:ARG:HA	5:DM:273:ARG:HD2	1.80	0.41
8:DP:48:GLN:NE2	8:DP:67:GLN:OE1	2.50	0.41
8:DP:78:LEU:HA	8:DP:78:LEU:HD23	1.79	0.41
9:DQ:27:HIS:HB2	12:DU:57:LEU:HD23	2.02	0.41
15:CE:32:TRP:O	27:Ca:348:PHE:HB2	2.21	0.41
15:CE:417:ASN:C	15:CE:417:ASN:HD22	2.28	0.41
21:CO:82:ASN:HD21	32:Cn:141:ARG:HA	1.85	0.41
21:CO:230:LEU:HD23	21:CO:233:ARG:HH12	1.84	0.41
22:CP:96:ILE:HD11	27:Ca:470:ARG:NH2	2.34	0.41
24:CR:30:LEU:HD12	24:CR:30:LEU:HA	1.89	0.41
24:CR:147:ILE:HD13	24:CR:147:ILE:HA	1.81	0.41
24:CR:168:ILE:HA	24:CR:168:ILE:HD12	1.81	0.41
29:Cd:18:LEU:HD12	29:Cd:19:PRO:HD2	2.02	0.41
29:Cd:108:MET:HE3	29:Cd:108:MET:HB2	1.85	0.41
33:Cp:151:ARG:H	33:Cp:154:GLN:HE21	1.67	0.41
36:Cv:39:MET:HB3	36:Cv:44:ARG:HD2	2.01	0.41
2:DD:744:ARG:NH2	3:DI:144:LEU:HD13	2.36	0.41
3:DI:51:VAL:HG13	3:DI:182:PHE:CE2	2.55	0.41
3:DI:147:ASP:O	3:DI:151:ARG:HG2	2.21	0.41
15:CE:310:ARG:O	15:CE:315:ALA:HB2	2.21	0.41
15:CE:367:LEU:HD23	15:CE:367:LEU:HA	1.77	0.41
16:CF:81:LYS:HB2	16:CF:81:LYS:HE3	1.82	0.41
17:CH:261:ARG:NH2	17:CH:271:GLU:OE2	2.46	0.41
18:CI:122:LEU:HD23	18:CI:122:LEU:HA	1.85	0.41
21:CO:353:GLU:H	21:CO:353:GLU:HG2	1.28	0.41
23:CQ:144:LEU:HB3	23:CQ:166:GLU:HB3	2.02	0.41
33:Cp:66:HIS:HB3	33:Cp:69:ARG:HB2	2.01	0.41
33:Cp:128:LEU:HD23	33:Cp:128:LEU:HA	1.70	0.41
35:Cr:143:ARG:HH12	35:Cr:147:GLY:C	2.28	0.41
36:Cv:899:ASP:OD1	36:Cv:906:ARG:NH1	2.54	0.41
36:Cv:954:ARG:HD3	36:Cv:954:ARG:HA	1.79	0.41
1:DA:1591:ARG:C	1:DA:1593:ALA:H	2.27	0.41
2:DD:626:ARG:HD2	30:Cj:155:GLU:OE1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DI:302:ILE:O	3:DI:345:LEU:HA	2.20	0.41
8:DP:12:LEU:HA	8:DP:12:LEU:HD23	1.75	0.41
11:DS:79:LEU:HB3	11:DS:81:VAL:HG23	2.03	0.41
11:DS:79:LEU:HD21	11:DS:93:ARG:O	2.20	0.41
14:Da:51:THR:HG23	23:CQ:193:ARG:O	2.21	0.41
18:CI:219:LEU:HD12	18:CI:219:LEU:O	2.20	0.41
19:CK:318:PRO:HB2	37:CA:344:C:HI'	2.02	0.41
21:CO:224:LEU:HD12	21:CO:224:LEU:HA	1.77	0.41
24:CR:13:LEU:HD12	24:CR:13:LEU:H	1.85	0.41
27:Ca:89:ARG:HD2	27:Ca:177:GLN:NE2	2.34	0.41
27:Ca:290:MET:HE2	27:Ca:290:MET:HB2	1.94	0.41
27:Ca:423:GLN:HE21	27:Ca:479:THR:HA	1.86	0.41
36:Cv:278:LEU:HD22	36:Cv:282:ILE:HG13	2.02	0.41
37:CA:38:U:O2	37:CA:190:U:O4	2.38	0.41
1:DA:147:TYR:HB3	3:DI:80:ARG:HD3	2.02	0.41
2:DD:244:PRO:HD3	2:DD:326:PRO:HD3	2.02	0.41
2:DD:616:LEU:HD12	2:DD:616:LEU:HA	1.89	0.41
2:DD:679:ASN:C	2:DD:679:ASN:HD22	2.27	0.41
18:CI:238:LYS:HD3	18:CI:238:LYS:HA	1.87	0.41
19:CK:109:VAL:HG11	25:CU:123:GLN:NE2	2.36	0.41
21:CO:160:TYR:CD2	21:CO:166:ALA:HB2	2.56	0.41
27:Ca:82:PRO:HB3	36:Cv:1114:ASP:OD2	2.21	0.41
27:Ca:443:MET:CE	27:Ca:491:TRP:HE1	2.34	0.41
35:Cr:265:LEU:HD23	35:Cr:265:LEU:HA	1.77	0.41
36:Cv:283:ASP:CB	36:Cv:398:ARG:HD2	2.44	0.41
36:Cv:292:LYS:HZ1	36:Cv:509:THR:HG22	1.84	0.41
1:DA:201:LYS:HD3	27:Ca:481:ARG:HD3	2.03	0.41
1:DA:677:GLU:N	1:DA:677:GLU:OE1	2.54	0.41
3:DI:24:VAL:HG12	3:DI:25:PRO:O	2.20	0.41
17:CH:107:ARG:HH12	17:CH:133:ARG:CD	2.34	0.41
18:CI:104:ASN:HD22	18:CI:104:ASN:C	2.28	0.41
29:Cd:169:ALA:HA	29:Cd:186:LEU:HB3	2.03	0.41
33:Cp:70:PRO:HB2	33:Cp:73:ASP:OD2	2.21	0.41
36:Cv:155:ASP:HB3	36:Cv:158:TYR:HB2	2.01	0.41
36:Cv:740:ILE:HG23	36:Cv:786:VAL:HG13	2.01	0.41
36:Cv:812:LEU:HD23	36:Cv:812:LEU:HA	1.85	0.41
37:CA:69:U:H4'	37:CA:70:U:O5'	2.20	0.41
1:DA:115:LEU:HD13	23:CQ:80:LEU:CD1	2.51	0.41
1:DA:209:TRP:HA	22:CP:81:PRO:HG3	2.01	0.41
1:DA:418:LEU:HD23	1:DA:418:LEU:HA	1.94	0.41
1:DA:681:ILE:HG13	1:DA:701:VAL:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:683:MET:HG2	1:DA:698:ALA:HA	2.01	0.41
1:DA:1556:VAL:HG21	1:DA:1599:PHE:CE2	2.55	0.41
1:DA:1656:ASN:HB2	1:DA:1658:GLU:OE2	2.20	0.41
2:DD:194:ARG:HD2	2:DD:227:TRP:CD2	2.56	0.41
2:DD:198:LYS:HE3	2:DD:198:LYS:HB3	1.95	0.41
2:DD:448:ARG:HG3	2:DD:448:ARG:NH1	2.35	0.41
3:DI:286:GLY:H	3:DI:320:GLN:HE22	1.69	0.41
5:DM:164:ILE:HG21	5:DM:164:ILE:HD13	1.85	0.41
6:DN:23:VAL:HG12	6:DN:116:VAL:HG11	2.03	0.41
10:DR:182:ARG:NH1	12:DU:161:ILE:HG21	2.36	0.41
11:DS:31:MET:HG3	37:CA:206:A:O3'	2.21	0.41
12:DU:207:ARG:HG2	37:CA:161:G:N1	2.35	0.41
15:CE:292:VAL:HA	15:CE:293:PRO:HD3	1.96	0.41
19:CK:221:THR:H	19:CK:224:ASN:HB3	1.86	0.41
21:CO:414:LEU:HD23	21:CO:414:LEU:HA	1.82	0.41
27:Ca:121:ALA:HB2	36:Cv:1054:VAL:HG13	2.02	0.41
31:Cm:33:PRO:HB3	31:Cm:45:LEU:HD11	2.03	0.41
35:Cr:19:LEU:N	35:Cr:20:PRO:HD2	2.35	0.41
35:Cr:125:GLN:NE2	35:Cr:161:ARG:HA	2.36	0.41
36:Cv:738:ARG:NH2	36:Cv:788:ARG:HD2	2.35	0.41
36:Cv:834:LEU:HA	36:Cv:834:LEU:HD12	1.81	0.41
37:CA:154:G:N3	37:CA:154:G:H2'	2.35	0.41
37:CA:293:A:H2'	37:CA:294:A:C8	2.56	0.41
1:DA:1542:SER:OG	1:DA:1552:GLU:OE1	2.28	0.41
2:DD:15:ALA:HB2	37:CA:277:A:N1	2.35	0.41
2:DD:242:LEU:HD11	2:DD:248:ASP:HA	2.03	0.41
3:DI:111:THR:HG21	3:DI:125:TRP:HZ2	1.86	0.41
6:DN:27:ASP:OD1	6:DN:27:ASP:N	2.42	0.41
6:DN:29:ARG:HH11	6:DN:29:ARG:CG	2.28	0.41
8:DP:207:TYR:HA	8:DP:208:PRO:HA	1.77	0.41
9:DQ:48:LEU:HB3	12:DU:47:ARG:HH21	1.85	0.41
10:DR:126:LEU:HB2	10:DR:135:CYS:HB3	2.03	0.41
11:DS:185:THR:HB	11:DS:188:SER:HB3	2.03	0.41
11:DS:196:GLY:O	22:CP:84:GLN:HG3	2.21	0.41
12:DU:184:THR:OG1	12:DU:186:GLU:HB3	2.20	0.41
13:DZ:14:ASP:CG	27:Ca:164:ARG:HH22	2.29	0.41
13:DZ:36:LEU:HD12	13:DZ:36:LEU:HA	1.94	0.41
14:Da:30:HIS:CG	14:Da:31:PRO:HD2	2.56	0.41
15:CE:306:GLU:O	15:CE:310:ARG:HB2	2.20	0.41
18:CI:196:THR:HG21	34:Cq:106:LEU:HB3	2.02	0.41
18:CI:233:GLU:OE1	18:CI:238:LYS:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CK:200:ARG:NH2	25:CU:20:MET:H	2.19	0.41
19:CK:311:THR:HA	19:CK:312:PRO:HD2	1.85	0.41
20:CL:69:PHE:HZ	40:US:46:UNK:HG2	1.86	0.41
21:CO:253:ALA:O	21:CO:257:ARG:HG3	2.20	0.41
21:CO:266:LEU:HD13	21:CO:274:TYR:HA	2.02	0.41
21:CO:381:MET:HE2	21:CO:385:ARG:NH2	2.36	0.41
22:CP:92:THR:HB	27:Ca:444:PHE:CE1	2.55	0.41
22:CP:108:CYS:O	29:Cd:58:ARG:NH2	2.54	0.41
24:CR:317:ILE:HG22	24:CR:317:ILE:O	2.21	0.41
26:CZ:276:HIS:NE2	26:CZ:292:ALA:HB3	2.35	0.41
26:CZ:359:MET:HA	26:CZ:359:MET:HE2	2.02	0.41
27:Ca:153:LYS:HG3	27:Ca:154:GLU:N	2.36	0.41
28:Cb:101:LYS:HB3	28:Cb:101:LYS:HZ2	1.82	0.41
28:Cb:132:LEU:HD23	28:Cb:132:LEU:HA	1.90	0.41
29:Cd:58:ARG:HG3	29:Cd:58:ARG:NH1	2.35	0.41
30:Cj:66:LEU:HD23	30:Cj:66:LEU:HA	1.83	0.41
31:Cm:115:CYS:HB2	31:Cm:118:GLU:OE1	2.21	0.41
33:Cp:93:ARG:NH1	37:CA:187:A:C2	2.88	0.41
33:Cp:164:ASP:O	33:Cp:168:ILE:HG13	2.21	0.41
35:Cr:164:LEU:HD13	35:Cr:166:VAL:HG23	2.01	0.41
36:Cv:397:TRP:CE2	36:Cv:946:PRO:HB3	2.56	0.41
36:Cv:544:ILE:O	36:Cv:544:ILE:HG22	2.19	0.41
36:Cv:813:ARG:NH1	36:Cv:813:ARG:CG	2.83	0.41
36:Cv:911:PRO:HG2	36:Cv:913:TRP:CZ2	2.55	0.41
1:DA:79:LEU:HD21	22:CP:53:ARG:HH11	1.86	0.41
1:DA:105:PHE:CD1	23:CQ:83:LEU:HD13	2.56	0.41
1:DA:311:THR:HA	1:DA:312:PRO:HD3	1.74	0.41
1:DA:1081:GLN:HA	1:DA:1642:LEU:HD21	2.02	0.41
2:DD:181:MET:HE1	2:DD:215:TYR:CD1	2.54	0.41
2:DD:465:PHE:CD2	2:DD:479:ARG:HD3	2.56	0.41
2:DD:637:ARG:HH12	22:CP:153:ARG:HD2	1.83	0.41
2:DD:669:HIS:HE1	27:Ca:423:GLN:O	2.04	0.41
5:DM:145:ILE:HG13	5:DM:146:GLY:N	2.36	0.41
5:DM:228:ASP:CG	5:DM:230:PRO:HD3	2.45	0.41
9:DQ:185:ARG:HH21	9:DQ:204:TYR:HB2	1.86	0.41
10:DR:60:VAL:CG2	10:DR:63:ILE:HG12	2.51	0.41
11:DS:213:SER:HA	33:Cp:46:ILE:HB	2.02	0.41
13:DZ:90:VAL:HG22	27:Ca:149:ARG:NH1	2.36	0.41
18:CI:99:VAL:O	28:Cb:103:ARG:HD2	2.21	0.41
19:CK:214:LYS:HB3	19:CK:214:LYS:HZ3	1.83	0.41
19:CK:262:ARG:HB3	19:CK:267:ARG:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:CK:319:LYS:HB3	25:CU:81:GLU:HG3	2.03	0.41
19:CK:322:ARG:NH1	19:CK:326:LYS:HA	2.36	0.41
21:CO:93:ARG:NH2	37:CA:358:U:H3	2.14	0.41
23:CQ:56:ARG:HH11	23:CQ:56:ARG:CG	2.12	0.41
24:CR:8:ILE:HG21	36:Cv:909:LEU:HD22	2.02	0.41
24:CR:317:ILE:HG23	37:CA:588:U:C5	2.56	0.41
27:Ca:370:GLU:O	36:Cv:951:LYS:NZ	2.54	0.41
29:Cd:88:LEU:HD23	29:Cd:88:LEU:HA	1.89	0.41
29:Cd:195:GLU:HB3	29:Cd:216:HIS:HB2	2.02	0.41
31:Cm:46:ILE:H	31:Cm:46:ILE:HG13	1.77	0.41
35:Cr:114:LEU:HA	35:Cr:115:PRO:HD2	1.92	0.41
1:DA:71:ASN:HA	1:DA:74:LYS:HD2	2.03	0.40
1:DA:74:LYS:HZ3	37:CA:71:U:P	2.43	0.40
1:DA:148:LYS:HB2	1:DA:148:LYS:NZ	2.35	0.40
1:DA:955:LYS:HA	1:DA:956:PRO:HD3	1.94	0.40
2:DD:131:PRO:HG3	21:CO:331:GLY:HA3	2.03	0.40
2:DD:190:LEU:HD21	2:DD:221:GLU:OE1	2.21	0.40
6:DN:226:PRO:HD2	6:DN:289:LEU:HB2	2.03	0.40
6:DN:284:PRO:O	6:DN:285:GLU:HG2	2.21	0.40
10:DR:13:PHE:CG	10:DR:14:ARG:N	2.89	0.40
12:DU:95:GLU:OE2	12:DU:211:ARG:NE	2.42	0.40
13:DZ:68:LYS:HD2	27:Ca:71:MET:HG2	2.03	0.40
15:CE:42:ARG:HG3	15:CE:42:ARG:NH1	2.33	0.40
21:CO:112:LYS:HB2	21:CO:112:LYS:HZ2	1.83	0.40
22:CP:87:HIS:HE1	33:Cp:36:THR:OG1	2.03	0.40
30:Cj:168:VAL:HA	30:Cj:169:PRO:HD3	1.80	0.40
33:Cp:99:ARG:O	33:Cp:102:ARG:HG2	2.21	0.40
35:Cr:96:GLU:O	35:Cr:99:CYS:HB2	2.21	0.40
36:Cv:86:GLU:OE1	36:Cv:95:ARG:HG2	2.21	0.40
36:Cv:407:MET:HA	36:Cv:427:TYR:O	2.21	0.40
36:Cv:592:TYR:CE2	36:Cv:753:PRO:HB3	2.56	0.40
36:Cv:827:ALA:HB3	36:Cv:830:ASN:ND2	2.36	0.40
37:CA:79:A:N3	37:CA:79:A:C2'	2.83	0.40
1:DA:602:LEU:HD23	1:DA:755:GLY:O	2.21	0.40
1:DA:1399:ASN:HD21	1:DA:1502:PHE:N	2.18	0.40
2:DD:668:ARG:HG3	2:DD:668:ARG:NH1	2.36	0.40
6:DN:17:MET:HB3	6:DN:17:MET:HE3	1.69	0.40
8:DP:109:ARG:HA	8:DP:110:PRO:HD3	1.90	0.40
8:DP:175:GLU:CD	8:DP:176:PRO:HD3	2.45	0.40
19:CK:205:TYR:CD2	19:CK:221:THR:HG23	2.50	0.40
19:CK:324:VAL:HG11	25:CU:181:ILE:HG13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:CO:257:ARG:NH1	37:CA:328:U:OP1	2.55	0.40
23:CQ:56:ARG:HG2	37:CA:99:G:OP1	2.21	0.40
29:CD:174:PRO:HD3	29:CD:219:HIS:CE1	2.56	0.40
30:Cj:147:TYR:CD1	30:Cj:162:GLN:HG2	2.56	0.40
33:Cp:146:LEU:HD12	33:Cp:146:LEU:HA	1.93	0.40
36:Cv:235:MET:HE1	36:Cv:258:THR:HG21	2.04	0.40
36:Cv:454:LEU:HD23	36:Cv:457:ARG:HD2	2.04	0.40
36:Cv:702:ILE:HD11	36:Cv:764:LEU:HD12	2.03	0.40
1:DA:259:LEU:HD12	1:DA:259:LEU:HA	1.91	0.40
1:DA:886:ALA:HA	6:DN:207:VAL:HG21	2.03	0.40
2:DD:94:LYS:HG3	23:CQ:12:TRP:HB2	2.03	0.40
2:DD:350:LYS:HB2	2:DD:350:LYS:NZ	2.37	0.40
2:DD:621:LEU:C	30:Cj:210:PRO:HG2	2.47	0.40
4:DL:240:GLU:H	4:DL:240:GLU:HG2	1.61	0.40
9:DQ:36:GLU:HB3	10:DR:28:LEU:CD1	2.52	0.40
9:DQ:74:PHE:CE1	9:DQ:76:SER:HB3	2.56	0.40
10:DR:87:LEU:HA	10:DR:87:LEU:HD23	1.85	0.40
10:DR:105:THR:HG23	30:Cj:147:TYR:CE2	2.57	0.40
11:DS:150:GLN:HE22	11:DS:176:ARG:HE	1.68	0.40
14:Da:64:PRO:HG2	21:CO:279:ARG:HG2	2.03	0.40
16:CF:143:GLU:HA	16:CF:146:TRP:HB2	2.04	0.40
25:CU:69:ARG:HA	25:CU:72:HIS:CD2	2.56	0.40
26:CZ:291:PHE:CZ	26:CZ:308:TYR:CE2	3.09	0.40
28:Cb:59:PRO:HG3	36:Cv:510:GLU:HB2	2.03	0.40
30:Cj:26:GLY:O	37:CA:177:A:O2'	2.28	0.40
35:Cr:27:ASP:HA	35:Cr:30:VAL:O	2.20	0.40
36:Cv:296:LEU:HD21	36:Cv:421:LEU:HD21	2.02	0.40
36:Cv:858:GLY:O	36:Cv:861:THR:HB	2.22	0.40
37:CA:174:A:H4'	37:CA:175:A:OP1	2.21	0.40
1:DA:414:HIS:HD2	1:DA:416:HIS:H	1.68	0.40
1:DA:904:TRP:HB2	27:Ca:401:ASP:OD2	2.22	0.40
2:DD:610:VAL:O	2:DD:613:TRP:HB3	2.20	0.40
3:DI:404:TRP:CZ2	29:CD:122:LEU:HB3	2.56	0.40
6:DN:59:PRO:O	17:CH:59:LEU:HD11	2.22	0.40
7:DO:118:ASP:O	7:DO:122:LEU:HG	2.22	0.40
7:DO:198:ARG:HH11	7:DO:256:ARG:HH12	1.70	0.40
8:DP:20:MET:HE2	8:DP:20:MET:HB3	1.95	0.40
11:DS:227:VAL:HG21	22:CP:139:LEU:HD12	2.03	0.40
11:DS:234:LEU:N	11:DS:234:LEU:HD12	2.36	0.40
12:DU:80:LEU:HD11	12:DU:147:LEU:HD11	2.03	0.40
15:CE:221:GLY:H	36:Cv:45:PHE:HE1	1.70	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:CF:76:MET:HG2	16:CF:76:MET:O	2.22	0.40
21:CO:169:TYR:HE1	21:CO:175:VAL:HG13	1.87	0.40
23:CQ:51:PHE:HB3	23:CQ:57:HIS:ND1	2.36	0.40
24:CR:184:LYS:NZ	24:CR:185:PHE:CE2	2.85	0.40
25:CU:57:VAL:HA	25:CU:60:ARG:HH21	1.86	0.40
28:Cb:22:ASP:OD1	28:Cb:22:ASP:N	2.46	0.40
32:Cn:236:LYS:N	32:Cn:245:LYS:NZ	2.64	0.40
33:Cp:10:ASP:HB2	37:CA:28:U:OP1	2.21	0.40
33:Cp:92:LEU:HD23	33:Cp:102:ARG:HB2	2.03	0.40
36:Cv:53:PRO:O	36:Cv:54:ASN:CG	2.64	0.40
36:Cv:806:LEU:HD13	36:Cv:907:PHE:CD1	2.57	0.40
37:CA:196:U:O2	37:CA:196:U:C2'	2.70	0.40
37:CA:259:U:H5'	37:CA:260:U:P	2.61	0.40
37:CA:593:A:H2'	37:CA:594:U:C6	2.57	0.40
1:DA:172:GLY:C	1:DA:174:HIS:H	2.29	0.40
1:DA:410:ASP:HB3	1:DA:420:ASN:HB3	2.03	0.40
1:DA:854:LYS:HE3	1:DA:854:LYS:HB3	1.98	0.40
2:DD:229:MET:HG3	2:DD:302:MET:HE1	2.04	0.40
2:DD:497:ARG:NH1	2:DD:497:ARG:HB3	2.36	0.40
3:DI:344:LEU:HD13	3:DI:346:LEU:HD21	2.03	0.40
5:DM:140:ASN:ND2	34:Cq:20:GLN:HE22	2.20	0.40
5:DM:186:TRP:O	5:DM:192:GLY:HA3	2.21	0.40
6:DN:213:ARG:NH2	27:Ca:192:GLN:OE1	2.54	0.40
7:DO:141:LEU:HA	7:DO:141:LEU:HD23	1.89	0.40
9:DQ:101:GLN:OE1	9:DQ:101:GLN:N	2.52	0.40
9:DQ:141:THR:HG21	9:DQ:184:ILE:HG23	2.03	0.40
15:CE:69:GLU:HG3	36:Cv:400:TYR:OH	2.22	0.40
15:CE:153:LYS:NZ	37:CA:547:U:OP2	2.54	0.40
16:CF:51:PHE:HB2	16:CF:90:LEU:HD13	2.03	0.40
18:CI:83:GLY:HA3	18:CI:87:TYR:OH	2.22	0.40
19:CK:196:TYR:O	19:CK:206:ALA:HA	2.21	0.40
21:CO:94:ARG:NH1	37:CA:333:U:OP1	2.54	0.40
21:CO:105:ASN:O	21:CO:240:LEU:HD11	2.21	0.40
21:CO:173:ILE:HA	21:CO:174:PRO:HD2	1.95	0.40
23:CQ:109:VAL:HG21	23:CQ:147:ILE:HD11	2.02	0.40
27:Ca:341:LEU:HB3	27:Ca:500:PHE:CE1	2.56	0.40
27:Ca:549:SER:O	27:Ca:552:THR:HB	2.20	0.40
27:Ca:576:TRP:HA	27:Ca:577:PRO:C	2.46	0.40
30:Cj:90:ARG:CZ	30:Cj:94:ILE:HD11	2.51	0.40
33:Cp:60:LEU:HB3	33:Cp:71:THR:HG22	2.03	0.40
35:Cr:292:GLU:O	35:Cr:296:VAL:HG23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:CA:43:A:H62	37:CA:173:A:N6	2.19	0.40
37:CA:293:A:H2'	37:CA:294:A:H8	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DA	1420/1788 (79%)	1370 (96%)	48 (3%)	2 (0%)	48	76
2	DD	787/812 (97%)	747 (95%)	38 (5%)	2 (0%)	36	66
3	DI	388/407 (95%)	366 (94%)	21 (5%)	1 (0%)	36	66
4	DL	138/307 (45%)	130 (94%)	8 (6%)	0	100	100
5	DM	292/294 (99%)	283 (97%)	9 (3%)	0	100	100
6	DN	253/293 (86%)	242 (96%)	11 (4%)	0	100	100
7	DO	220/282 (78%)	213 (97%)	6 (3%)	1 (0%)	24	55
8	DP	205/274 (75%)	195 (95%)	9 (4%)	1 (0%)	24	55
9	DQ	254/268 (95%)	246 (97%)	6 (2%)	2 (1%)	16	44
10	DR	247/270 (92%)	239 (97%)	8 (3%)	0	100	100
11	DS	234/261 (90%)	227 (97%)	7 (3%)	0	100	100
12	DU	211/228 (92%)	202 (96%)	7 (3%)	2 (1%)	14	43
13	DZ	80/94 (85%)	75 (94%)	5 (6%)	0	100	100
14	Da	53/64 (83%)	52 (98%)	1 (2%)	0	100	100
15	CE	413/435 (95%)	395 (96%)	18 (4%)	0	100	100
16	CF	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
17	CH	271/282 (96%)	265 (98%)	5 (2%)	1 (0%)	30	60
18	CI	200/443 (45%)	196 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	CK	237/326 (73%)	225 (95%)	12 (5%)	0	100	100
20	CL	85/87 (98%)	80 (94%)	5 (6%)	0	100	100
21	CO	359/429 (84%)	343 (96%)	14 (4%)	2 (1%)	21	51
22	CP	178/188 (95%)	171 (96%)	7 (4%)	0	100	100
23	CQ	188/307 (61%)	182 (97%)	6 (3%)	0	100	100
24	CR	312/320 (98%)	297 (95%)	14 (4%)	1 (0%)	36	66
25	CU	182/193 (94%)	177 (97%)	4 (2%)	1 (0%)	24	55
26	CZ	149/360 (41%)	142 (95%)	6 (4%)	1 (1%)	18	48
27	Ca	590/602 (98%)	556 (94%)	29 (5%)	5 (1%)	16	44
28	Cb	248/324 (76%)	242 (98%)	6 (2%)	0	100	100
29	Cd	289/440 (66%)	281 (97%)	6 (2%)	2 (1%)	18	48
30	Cj	224/257 (87%)	216 (96%)	7 (3%)	1 (0%)	30	60
31	Cm	194/215 (90%)	184 (95%)	10 (5%)	0	100	100
32	Cn	108/250 (43%)	103 (95%)	5 (5%)	0	100	100
33	Cp	173/187 (92%)	169 (98%)	4 (2%)	0	100	100
34	Cq	250/263 (95%)	243 (97%)	7 (3%)	0	100	100
35	Cr	253/439 (58%)	243 (96%)	9 (4%)	1 (0%)	30	60
36	Cv	1051/1211 (87%)	1011 (96%)	40 (4%)	0	100	100
All	All	10893/13360 (82%)	10460 (96%)	407 (4%)	26 (0%)	44	71

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	CZ	296	PRO
27	Ca	32	PRO
27	Ca	33	PRO
27	Ca	35	PRO
24	CR	10	ALA
27	Ca	34	LYS
2	DD	256	PRO
12	DU	191	SER
17	CH	16	VAL
30	Cj	54	ALA
1	DA	132	GLY
3	DI	190	PRO
8	DP	62	LYS

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Mol	Chain	Res	Type
25	CU	19	ALA
29	Cd	224	ILE
29	Cd	247	LYS
2	DD	248	ASP
7	DO	115	ASP
9	DQ	173	ASP
12	DU	205	ALA
21	CO	70	HIS
1	DA	229	GLU
27	Ca	31	GLU
9	DQ	254	SER
21	CO	90	MET
35	Cr	29	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DA	1211/1514 (80%)	1130 (93%)	81 (7%)	15	42
2	DD	694/711 (98%)	651 (94%)	43 (6%)	16	44
3	DI	350/365 (96%)	323 (92%)	27 (8%)	12	37
4	DL	118/263 (45%)	109 (92%)	9 (8%)	12	38
5	DM	252/252 (100%)	232 (92%)	20 (8%)	11	37
6	DN	229/256 (90%)	209 (91%)	20 (9%)	9	32
7	DO	186/229 (81%)	176 (95%)	10 (5%)	20	48
8	DP	187/239 (78%)	179 (96%)	8 (4%)	26	54
9	DQ	228/239 (95%)	218 (96%)	10 (4%)	25	54
10	DR	220/235 (94%)	196 (89%)	24 (11%)	6	23
11	DS	209/228 (92%)	196 (94%)	13 (6%)	16	44
12	DU	190/201 (94%)	171 (90%)	19 (10%)	7	27
13	DZ	72/84 (86%)	68 (94%)	4 (6%)	19	47
14	Da	50/59 (85%)	46 (92%)	4 (8%)	11	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	CE	358/372 (96%)	321 (90%)	37 (10%)	7	26
16	CF	136/144 (94%)	126 (93%)	10 (7%)	13	39
17	CH	237/246 (96%)	217 (92%)	20 (8%)	10	34
18	CI	171/371 (46%)	167 (98%)	4 (2%)	44	66
19	CK	210/283 (74%)	191 (91%)	19 (9%)	9	31
20	CL	79/79 (100%)	73 (92%)	6 (8%)	12	38
21	CO	318/377 (84%)	290 (91%)	28 (9%)	9	32
22	CP	160/168 (95%)	143 (89%)	17 (11%)	6	24
23	CQ	171/270 (63%)	151 (88%)	20 (12%)	5	21
24	CR	275/279 (99%)	256 (93%)	19 (7%)	14	42
25	CU	160/169 (95%)	149 (93%)	11 (7%)	14	42
26	CZ	121/313 (39%)	110 (91%)	11 (9%)	9	31
27	Ca	516/543 (95%)	477 (92%)	39 (8%)	12	38
28	Cb	219/277 (79%)	207 (94%)	12 (6%)	19	47
29	Cd	240/381 (63%)	218 (91%)	22 (9%)	8	30
30	Cj	193/219 (88%)	180 (93%)	13 (7%)	15	42
31	Cm	165/184 (90%)	141 (86%)	24 (14%)	3	15
32	Cn	95/210 (45%)	90 (95%)	5 (5%)	20	49
33	Cp	163/175 (93%)	152 (93%)	11 (7%)	15	42
34	Cq	210/221 (95%)	193 (92%)	17 (8%)	11	36
35	Cr	211/369 (57%)	189 (90%)	22 (10%)	7	25
36	Cv	912/1034 (88%)	830 (91%)	82 (9%)	9	31
All	All	9516/11559 (82%)	8775 (92%)	741 (8%)	14	37

All (741) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	DA	41	PHE
1	DA	60	GLU
1	DA	74	LYS
1	DA	77	ARG
1	DA	79	LEU
1	DA	85	LEU
1	DA	87	THR

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Mol	Chain	Res	Type
1	DA	112	GLN
1	DA	117	GLN
1	DA	131	ASP
1	DA	148	LYS
1	DA	150	ILE
1	DA	158	LEU
1	DA	167	THR
1	DA	174	HIS
1	DA	194	LEU
1	DA	200	ILE
1	DA	201	LYS
1	DA	230	PHE
1	DA	254	PHE
1	DA	255	ARG
1	DA	259	LEU
1	DA	274	LEU
1	DA	300	THR
1	DA	309	VAL
1	DA	408	LEU
1	DA	419	THR
1	DA	436	ASN
1	DA	456	ARG
1	DA	486	LYS
1	DA	493	TRP
1	DA	509	LEU
1	DA	539	LEU
1	DA	540	GLU
1	DA	579	ASP
1	DA	583	VAL
1	DA	602	LEU
1	DA	630	ASP
1	DA	632	THR
1	DA	650	LEU
1	DA	653	LYS
1	DA	680	VAL
1	DA	708	GLU
1	DA	711	ILE
1	DA	712	VAL
1	DA	729	ARG
1	DA	781	ARG
1	DA	783	VAL
1	DA	849	THR

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Mol	Chain	Res	Type
1	DA	859	GLN
1	DA	870	GLU
1	DA	914	THR
1	DA	920	LEU
1	DA	934	GLU
1	DA	958	SER
1	DA	963	LEU
1	DA	973	LEU
1	DA	988	CYS
1	DA	1000	ASN
1	DA	1045	ILE
1	DA	1057	VAL
1	DA	1062	TYR
1	DA	1077	ARG
1	DA	1097	LEU
1	DA	1098	LEU
1	DA	1145	THR
1	DA	1152	HIS
1	DA	1381	LEU
1	DA	1404	ARG
1	DA	1433	ASP
1	DA	1440	ILE
1	DA	1488	GLN
1	DA	1498	LEU
1	DA	1517	ARG
1	DA	1544	ASN
1	DA	1591	ARG
1	DA	1597	GLU
1	DA	1605	ARG
1	DA	1624	ILE
1	DA	1662	ARG
1	DA	1664	ILE
2	DD	12	SER
2	DD	27	MET
2	DD	48	MET
2	DD	79	GLN
2	DD	84	LYS
2	DD	94	LYS
2	DD	108	THR
2	DD	122	GLN
2	DD	129	ARG
2	DD	146	ARG

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Mol	Chain	Res	Type
2	DD	149	SER
2	DD	151	SER
2	DD	173	GLN
2	DD	226	THR
2	DD	233	ASN
2	DD	237	THR
2	DD	275	ASP
2	DD	298	MET
2	DD	350	LYS
2	DD	377	GLU
2	DD	379	GLN
2	DD	439	GLU
2	DD	452	LEU
2	DD	454	THR
2	DD	504	ASN
2	DD	521	ASN
2	DD	541	ARG
2	DD	546	VAL
2	DD	577	LYS
2	DD	592	TRP
2	DD	616	LEU
2	DD	624	THR
2	DD	646	ILE
2	DD	651	ARG
2	DD	654	ARG
2	DD	704	ASP
2	DD	741	ARG
2	DD	761	ARG
2	DD	770	SER
2	DD	787	ARG
2	DD	794	ARG
2	DD	799	ASP
2	DD	812	TYR
3	DI	79	ILE
3	DI	90	LEU
3	DI	107	ILE
3	DI	113	VAL
3	DI	134	ARG
3	DI	144	LEU
3	DI	161	MET
3	DI	164	GLU
3	DI	172	LEU

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Mol	Chain	Res	Type
3	DI	175	GLN
3	DI	178	PHE
3	DI	180	GLU
3	DI	192	THR
3	DI	205	GLU
3	DI	232	TYR
3	DI	233	ARG
3	DI	243	LEU
3	DI	258	VAL
3	DI	282	ASP
3	DI	310	LEU
3	DI	313	ARG
3	DI	344	LEU
3	DI	345	LEU
3	DI	353	LYS
3	DI	362	ILE
3	DI	373	LEU
3	DI	399	THR
4	DL	136	MET
4	DL	145	LEU
4	DL	158	THR
4	DL	165	PHE
4	DL	183	LEU
4	DL	200	VAL
4	DL	204	MET
4	DL	240	GLU
4	DL	243	LEU
5	DM	1	MET
5	DM	15	LEU
5	DM	30	ARG
5	DM	46	PHE
5	DM	56	TRP
5	DM	59	ARG
5	DM	72	ARG
5	DM	75	VAL
5	DM	76	ASN
5	DM	84	LEU
5	DM	90	LEU
5	DM	104	LYS
5	DM	128	ILE
5	DM	129	ARG
5	DM	131	ASN

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Mol	Chain	Res	Type
5	DM	157	LEU
5	DM	179	ARG
5	DM	198	THR
5	DM	199	LEU
5	DM	275	LEU
6	DN	17	MET
6	DN	23	VAL
6	DN	24	LEU
6	DN	42	THR
6	DN	109	ASN
6	DN	116	VAL
6	DN	118	LEU
6	DN	125	VAL
6	DN	141	MET
6	DN	152	LEU
6	DN	162	LEU
6	DN	171	LEU
6	DN	223	GLN
6	DN	224	ARG
6	DN	237	ARG
6	DN	246	GLN
6	DN	261	ARG
6	DN	267	GLU
6	DN	276	GLN
6	DN	288	PHE
7	DO	62	LEU
7	DO	73	LEU
7	DO	115	ASP
7	DO	118	ASP
7	DO	122	LEU
7	DO	125	LEU
7	DO	136	ASP
7	DO	192	MET
7	DO	234	LEU
7	DO	255	ARG
8	DP	21	MET
8	DP	23	LEU
8	DP	28	ASN
8	DP	34	VAL
8	DP	69	LEU
8	DP	172	GLU
8	DP	195	THR

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Mol	Chain	Res	Type
8	DP	208	PRO
9	DQ	37	GLU
9	DQ	41	GLN
9	DQ	61	ILE
9	DQ	119	VAL
9	DQ	120	MET
9	DQ	149	GLN
9	DQ	177	LEU
9	DQ	192	LEU
9	DQ	216	ASN
9	DQ	250	ARG
10	DR	23	VAL
10	DR	32	VAL
10	DR	39	GLN
10	DR	44	VAL
10	DR	54	LEU
10	DR	60	VAL
10	DR	63	ILE
10	DR	67	LYS
10	DR	68	HIS
10	DR	78	ARG
10	DR	91	THR
10	DR	108	GLN
10	DR	117	ILE
10	DR	118	VAL
10	DR	131	LEU
10	DR	133	LEU
10	DR	148	VAL
10	DR	174	CYS
10	DR	188	LYS
10	DR	190	LEU
10	DR	201	CYS
10	DR	245	MET
10	DR	261	ARG
10	DR	265	MET
11	DS	34	SER
11	DS	44	LYS
11	DS	56	LEU
11	DS	61	ASN
11	DS	92	ARG
11	DS	106	ARG
11	DS	108	ASN

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Mol	Chain	Res	Type
11	DS	109	VAL
11	DS	115	TYR
11	DS	119	CYS
11	DS	170	TYR
11	DS	175	CYS
11	DS	205	VAL
12	DU	33	THR
12	DU	46	THR
12	DU	47	ARG
12	DU	73	ARG
12	DU	83	ARG
12	DU	86	ILE
12	DU	90	VAL
12	DU	103	ILE
12	DU	107	LYS
12	DU	124	SER
12	DU	140	GLU
12	DU	146	THR
12	DU	153	THR
12	DU	157	GLN
12	DU	165	ASP
12	DU	180	VAL
12	DU	189	LYS
12	DU	207	ARG
12	DU	211	ARG
13	DZ	17	LEU
13	DZ	20	ARG
13	DZ	62	ASP
13	DZ	63	LEU
14	Da	15	CYS
14	Da	25	ARG
14	Da	38	ASP
14	Da	42	ARG
15	CE	13	ASN
15	CE	17	THR
15	CE	27	ARG
15	CE	41	ARG
15	CE	48	ASN
15	CE	58	SER
15	CE	64	THR
15	CE	65	ARG
15	CE	80	ILE

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Mol	Chain	Res	Type
15	CE	83	MET
15	CE	87	ILE
15	CE	112	THR
15	CE	121	THR
15	CE	124	THR
15	CE	137	LEU
15	CE	163	ILE
15	CE	165	CYS
15	CE	188	GLU
15	CE	201	ILE
15	CE	217	VAL
15	CE	232	ILE
15	CE	233	VAL
15	CE	279	LEU
15	CE	285	ILE
15	CE	313	MET
15	CE	314	MET
15	CE	332	ASP
15	CE	364	ARG
15	CE	365	MET
15	CE	370	ASP
15	CE	391	THR
15	CE	395	THR
15	CE	396	LEU
15	CE	405	LYS
15	CE	410	LEU
15	CE	420	VAL
15	CE	422	VAL
16	CF	2	VAL
16	CF	39	ILE
16	CF	42	GLU
16	CF	71	MET
16	CF	93	LEU
16	CF	124	LEU
16	CF	133	GLN
16	CF	138	ILE
16	CF	141	GLN
16	CF	152	THR
17	CH	26	ARG
17	CH	29	HIS
17	CH	88	LEU
17	CH	89	VAL

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Mol	Chain	Res	Type
17	CH	108	LEU
17	CH	118	LEU
17	CH	128	VAL
17	CH	131	ASP
17	CH	132	ASP
17	CH	138	LYS
17	CH	150	THR
17	CH	152	ILE
17	CH	163	THR
17	CH	170	VAL
17	CH	172	VAL
17	CH	229	GLU
17	CH	248	ASN
17	CH	276	ARG
17	CH	279	MET
17	CH	280	MET
18	CI	139	ASP
18	CI	179	CYS
18	CI	218	ARG
18	CI	219	LEU
19	CK	70	ILE
19	CK	73	GLN
19	CK	98	LEU
19	CK	107	GLN
19	CK	109	VAL
19	CK	112	GLU
19	CK	113	ARG
19	CK	149	VAL
19	CK	156	LYS
19	CK	174	VAL
19	CK	192	MET
19	CK	205	TYR
19	CK	207	VAL
19	CK	232	ARG
19	CK	264	SER
19	CK	311	THR
19	CK	315	LEU
19	CK	324	VAL
19	CK	326	LYS
20	CL	59	MET
20	CL	91	LEU
20	CL	97	LEU

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Mol	Chain	Res	Type
20	CL	118	LEU
20	CL	121	ILE
20	CL	122	GLU
21	CO	69	GLU
21	CO	75	LEU
21	CO	82	ASN
21	CO	87	THR
21	CO	108	THR
21	CO	112	LYS
21	CO	190	SER
21	CO	209	GLU
21	CO	210	ARG
21	CO	220	SER
21	CO	224	LEU
21	CO	237	ASN
21	CO	240	LEU
21	CO	242	ASN
21	CO	245	ASN
21	CO	247	ILE
21	CO	266	LEU
21	CO	285	ASP
21	CO	304	ASP
21	CO	329	GLU
21	CO	336	GLU
21	CO	353	GLU
21	CO	362	VAL
21	CO	395	VAL
21	CO	399	ILE
21	CO	400	ARG
21	CO	412	ARG
21	CO	419	VAL
22	CP	13	ILE
22	CP	14	LYS
22	CP	15	ARG
22	CP	28	ILE
22	CP	36	VAL
22	CP	37	VAL
22	CP	40	PHE
22	CP	59	ARG
22	CP	68	CYS
22	CP	90	MET
22	CP	93	THR

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Mol	Chain	Res	Type
22	CP	123	LEU
22	CP	129	THR
22	CP	152	ASN
22	CP	163	LYS
22	CP	170	SER
22	CP	188	LEU
23	CQ	16	THR
23	CQ	21	ARG
23	CQ	31	THR
23	CQ	34	THR
23	CQ	56	ARG
23	CQ	66	VAL
23	CQ	67	LEU
23	CQ	69	GLN
23	CQ	73	ARG
23	CQ	83	LEU
23	CQ	103	MET
23	CQ	108	VAL
23	CQ	114	MET
23	CQ	136	ASP
23	CQ	147	ILE
23	CQ	158	HIS
23	CQ	169	VAL
23	CQ	173	GLU
23	CQ	182	VAL
23	CQ	199	ASN
24	CR	15	GLN
24	CR	30	LEU
24	CR	44	GLU
24	CR	59	LEU
24	CR	80	LEU
24	CR	92	ILE
24	CR	96	GLN
24	CR	167	ARG
24	CR	184	LYS
24	CR	198	THR
24	CR	202	LYS
24	CR	228	VAL
24	CR	233	SER
24	CR	235	SER
24	CR	239	SER
24	CR	259	GLN

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Mol	Chain	Res	Type
24	CR	278	VAL
24	CR	305	THR
24	CR	315	LEU
25	CU	13	MET
25	CU	32	HIS
25	CU	35	ILE
25	CU	44	MET
25	CU	74	GLN
25	CU	148	ASN
25	CU	161	GLN
25	CU	168	VAL
25	CU	169	ASN
25	CU	170	VAL
25	CU	171	VAL
26	CZ	218	VAL
26	CZ	236	ARG
26	CZ	240	VAL
26	CZ	244	ILE
26	CZ	260	MET
26	CZ	265	GLN
26	CZ	273	ILE
26	CZ	277	PHE
26	CZ	318	LEU
26	CZ	321	MET
26	CZ	360	ASP
27	Ca	14	ASN
27	Ca	15	LYS
27	Ca	39	ARG
27	Ca	67	ARG
27	Ca	71	MET
27	Ca	160	GLU
27	Ca	168	TYR
27	Ca	179	LEU
27	Ca	181	GLU
27	Ca	194	LEU
27	Ca	201	ARG
27	Ca	221	THR
27	Ca	227	ASN
27	Ca	240	SER
27	Ca	297	LEU
27	Ca	299	ARG
27	Ca	314	CYS

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Mol	Chain	Res	Type
27	Ca	338	LYS
27	Ca	350	GLU
27	Ca	365	LEU
27	Ca	376	VAL
27	Ca	380	ASP
27	Ca	384	ARG
27	Ca	398	ASP
27	Ca	399	ASN
27	Ca	410	MET
27	Ca	433	GLN
27	Ca	447	ILE
27	Ca	451	VAL
27	Ca	479	THR
27	Ca	480	LEU
27	Ca	506	GLN
27	Ca	520	TYR
27	Ca	538	ILE
27	Ca	541	ARG
27	Ca	552	THR
27	Ca	569	ARG
27	Ca	585	GLN
27	Ca	599	ILE
28	Cb	40	LEU
28	Cb	57	MET
28	Cb	71	LEU
28	Cb	108	GLU
28	Cb	110	MET
28	Cb	144	ARG
28	Cb	171	THR
28	Cb	193	GLU
28	Cb	195	LEU
28	Cb	288	GLU
28	Cb	291	GLU
28	Cb	306	THR
29	Cd	44	GLU
29	Cd	74	ASP
29	Cd	102	ARG
29	Cd	106	ARG
29	Cd	108	MET
29	Cd	112	ARG
29	Cd	120	LEU
29	Cd	122	LEU

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Mol	Chain	Res	Type
29	Cd	125	GLU
29	Cd	164	LEU
29	Cd	168	VAL
29	Cd	180	VAL
29	Cd	182	GLN
29	Cd	193	ILE
29	Cd	208	HIS
29	Cd	210	ASP
29	Cd	216	HIS
29	Cd	217	GLU
29	Cd	219	HIS
29	Cd	259	GLU
29	Cd	267	GLU
29	Cd	284	THR
30	Cj	10	ARG
30	Cj	66	LEU
30	Cj	71	ILE
30	Cj	77	LEU
30	Cj	80	LEU
30	Cj	135	ILE
30	Cj	138	ASP
30	Cj	145	THR
30	Cj	155	GLU
30	Cj	161	VAL
30	Cj	173	MET
30	Cj	206	LEU
30	Cj	210	PRO
31	Cm	21	GLN
31	Cm	35	ASN
31	Cm	50	ARG
31	Cm	60	ARG
31	Cm	61	ARG
31	Cm	80	THR
31	Cm	85	ILE
31	Cm	92	GLN
31	Cm	93	LEU
31	Cm	94	THR
31	Cm	95	MET
31	Cm	98	SER
31	Cm	106	CYS
31	Cm	124	SER
31	Cm	125	CYS

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Mol	Chain	Res	Type
31	Cm	126	LEU
31	Cm	128	ARG
31	Cm	153	ASP
31	Cm	160	GLN
31	Cm	162	ARG
31	Cm	168	HIS
31	Cm	173	GLU
31	Cm	178	GLU
31	Cm	202	THR
32	Cn	165	LEU
32	Cn	172	LYS
32	Cn	195	PHE
32	Cn	203	MET
32	Cn	214	ARG
33	Cp	30	LEU
33	Cp	50	THR
33	Cp	67	ARG
33	Cp	84	LEU
33	Cp	87	CYS
33	Cp	105	ILE
33	Cp	107	THR
33	Cp	123	THR
33	Cp	137	ASP
33	Cp	166	ARG
33	Cp	168	ILE
34	Cq	19	VAL
34	Cq	24	THR
34	Cq	30	ILE
34	Cq	52	THR
34	Cq	64	VAL
34	Cq	65	SER
34	Cq	78	ASP
34	Cq	79	MET
34	Cq	96	THR
34	Cq	106	LEU
34	Cq	107	GLU
34	Cq	144	THR
34	Cq	185	CYS
34	Cq	207	CYS
34	Cq	227	ILE
34	Cq	235	LEU
34	Cq	250	LEU

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Mol	Chain	Res	Type
35	Cr	18	LEU
35	Cr	25	LEU
35	Cr	26	LEU
35	Cr	36	VAL
35	Cr	37	CYS
35	Cr	45	THR
35	Cr	58	ASN
35	Cr	61	VAL
35	Cr	65	LYS
35	Cr	74	ASP
35	Cr	96	GLU
35	Cr	103	VAL
35	Cr	122	VAL
35	Cr	161	ARG
35	Cr	163	LEU
35	Cr	171	GLN
35	Cr	176	LEU
35	Cr	247	ILE
35	Cr	248	ARG
35	Cr	250	LYS
35	Cr	265	LEU
35	Cr	282	GLU
36	Cv	27	LYS
36	Cv	28	THR
36	Cv	32	ARG
36	Cv	35	ARG
36	Cv	60	GLN
36	Cv	87	GLN
36	Cv	98	ARG
36	Cv	151	SER
36	Cv	162	SER
36	Cv	172	THR
36	Cv	192	LEU
36	Cv	195	LEU
36	Cv	201	THR
36	Cv	204	ILE
36	Cv	209	VAL
36	Cv	235	MET
36	Cv	261	ILE
36	Cv	266	CYS
36	Cv	278	LEU
36	Cv	283	ASP

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Mol	Chain	Res	Type
36	Cv	284	LYS
36	Cv	301	SER
36	Cv	305	ASP
36	Cv	312	ASN
36	Cv	367	ASP
36	Cv	382	GLU
36	Cv	399	VAL
36	Cv	401	THR
36	Cv	407	MET
36	Cv	411	ASN
36	Cv	417	THR
36	Cv	437	ILE
36	Cv	446	THR
36	Cv	462	LEU
36	Cv	512	MET
36	Cv	531	MET
36	Cv	562	VAL
36	Cv	566	MET
36	Cv	569	LEU
36	Cv	594	LEU
36	Cv	612	THR
36	Cv	613	LEU
36	Cv	617	ASP
36	Cv	618	ILE
36	Cv	638	VAL
36	Cv	647	VAL
36	Cv	649	THR
36	Cv	673	LEU
36	Cv	678	HIS
36	Cv	689	CYS
36	Cv	739	ASN
36	Cv	754	ILE
36	Cv	782	ILE
36	Cv	795	GLU
36	Cv	813	ARG
36	Cv	818	LEU
36	Cv	838	LEU
36	Cv	861	THR
36	Cv	916	ARG
36	Cv	918	LEU
36	Cv	921	VAL
36	Cv	927	LEU

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Mol	Chain	Res	Type
36	Cv	938	ASP
36	Cv	945	VAL
36	Cv	959	LEU
36	Cv	967	VAL
36	Cv	969	ASP
36	Cv	987	SER
36	Cv	993	THR
36	Cv	995	VAL
36	Cv	996	SER
36	Cv	1002	ARG
36	Cv	1018	THR
36	Cv	1030	ARG
36	Cv	1034	ARG
36	Cv	1039	GLU
36	Cv	1040	GLU
36	Cv	1069	GLN
36	Cv	1070	GLU
36	Cv	1077	GLU
36	Cv	1108	GLN
36	Cv	1136	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (245) such sidechains are listed below:

Mol	Chain	Res	Type
1	DA	49	HIS
1	DA	59	HIS
1	DA	91	ASN
1	DA	112	GLN
1	DA	123	HIS
1	DA	134	ASN
1	DA	196	GLN
1	DA	237	HIS
1	DA	287	HIS
1	DA	316	HIS
1	DA	402	GLN
1	DA	414	HIS
1	DA	436	ASN
1	DA	457	GLN
1	DA	565	ASN
1	DA	623	HIS
1	DA	626	GLN
1	DA	644	HIS

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Mol	Chain	Res	Type
1	DA	746	GLN
1	DA	860	HIS
1	DA	907	GLN
1	DA	910	HIS
1	DA	940	GLN
1	DA	979	GLN
1	DA	984	GLN
1	DA	993	GLN
1	DA	1038	HIS
1	DA	1048	ASN
1	DA	1117	ASN
1	DA	1175	HIS
1	DA	1179	GLN
1	DA	1376	HIS
1	DA	1399	ASN
1	DA	1452	HIS
1	DA	1488	GLN
1	DA	1506	ASN
1	DA	1513	GLN
1	DA	1550	GLN
1	DA	1570	ASN
1	DA	1614	GLN
1	DA	1619	HIS
1	DA	1629	GLN
2	DD	76	ASN
2	DD	82	ASN
2	DD	137	HIS
2	DD	156	GLN
2	DD	176	HIS
2	DD	300	GLN
2	DD	312	GLN
2	DD	313	HIS
2	DD	348	HIS
2	DD	353	HIS
2	DD	379	GLN
2	DD	387	GLN
2	DD	404	HIS
2	DD	408	HIS
2	DD	453	ASN
2	DD	499	ASN
2	DD	507	GLN
2	DD	521	ASN

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Mol	Chain	Res	Type
2	DD	542	HIS
2	DD	649	GLN
2	DD	679	ASN
2	DD	687	HIS
3	DI	30	GLN
3	DI	61	ASN
3	DI	140	ASN
3	DI	320	GLN
3	DI	370	GLN
4	DL	125	HIS
5	DM	27	GLN
5	DM	43	GLN
5	DM	76	ASN
5	DM	89	GLN
5	DM	159	HIS
5	DM	188	ASN
5	DM	193	GLN
5	DM	211	GLN
5	DM	287	ASN
6	DN	28	HIS
6	DN	74	HIS
6	DN	79	ASN
6	DN	179	ASN
6	DN	223	GLN
6	DN	234	HIS
6	DN	235	ASN
6	DN	238	ASN
6	DN	246	GLN
6	DN	266	ASN
6	DN	272	HIS
7	DO	181	HIS
8	DP	66	ASN
8	DP	98	HIS
8	DP	116	HIS
8	DP	186	HIS
8	DP	194	GLN
8	DP	204	ASN
9	DQ	27	HIS
9	DQ	41	GLN
9	DQ	73	HIS
9	DQ	95	HIS
9	DQ	227	GLN

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Mol	Chain	Res	Type
9	DQ	235	HIS
10	DR	26	ASN
10	DR	75	HIS
10	DR	99	ASN
10	DR	108	GLN
10	DR	145	HIS
10	DR	191	GLN
11	DS	47	ASN
11	DS	134	GLN
11	DS	150	GLN
11	DS	197	GLN
11	DS	201	HIS
12	DU	63	HIS
12	DU	96	GLN
12	DU	133	HIS
12	DU	199	GLN
14	Da	41	ASN
14	Da	48	HIS
15	CE	85	ASN
15	CE	105	GLN
15	CE	108	HIS
15	CE	132	HIS
15	CE	187	GLN
15	CE	235	ASN
15	CE	260	ASN
15	CE	317	HIS
15	CE	417	ASN
16	CF	41	ASN
17	CH	80	HIS
17	CH	116	HIS
17	CH	247	HIS
17	CH	260	ASN
17	CH	267	HIS
17	CH	272	ASN
17	CH	282	HIS
18	CI	84	ASN
18	CI	104	ASN
18	CI	165	ASN
18	CI	211	ASN
19	CK	73	GLN
19	CK	105	GLN
19	CK	107	GLN

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Mol	Chain	Res	Type
19	CK	111	ASN
19	CK	244	HIS
19	CK	300	ASN
21	CO	82	ASN
21	CO	92	GLN
21	CO	111	GLN
21	CO	117	GLN
21	CO	129	GLN
21	CO	214	HIS
21	CO	281	HIS
21	CO	359	HIS
21	CO	426	HIS
22	CP	70	HIS
22	CP	87	HIS
22	CP	152	ASN
23	CQ	13	ASN
23	CQ	18	HIS
24	CR	24	ASN
24	CR	63	GLN
24	CR	96	GLN
24	CR	214	GLN
25	CU	16	HIS
25	CU	32	HIS
25	CU	72	HIS
25	CU	123	GLN
25	CU	148	ASN
25	CU	174	HIS
26	CZ	283	ASN
26	CZ	305	HIS
27	Ca	14	ASN
27	Ca	105	GLN
27	Ca	150	ASN
27	Ca	177	GLN
27	Ca	227	ASN
27	Ca	423	GLN
27	Ca	440	HIS
27	Ca	506	GLN
27	Ca	519	GLN
28	Cb	64	ASN
28	Cb	67	GLN
28	Cb	75	ASN
28	Cb	81	GLN

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Mol	Chain	Res	Type
28	Cb	191	HIS
28	Cb	198	HIS
28	Cb	207	GLN
28	Cb	280	ASN
29	Cd	48	ASN
29	Cd	72	ASN
29	Cd	155	GLN
29	Cd	159	HIS
29	Cd	182	GLN
30	Cj	34	HIS
30	Cj	153	HIS
31	Cm	56	ASN
31	Cm	73	HIS
31	Cm	155	HIS
31	Cm	168	HIS
31	Cm	182	ASN
31	Cm	184	HIS
32	Cn	149	GLN
32	Cn	170	GLN
32	Cn	192	ASN
32	Cn	232	ASN
32	Cn	240	GLN
33	Cp	91	GLN
33	Cp	154	GLN
33	Cp	182	GLN
34	Cq	20	GLN
34	Cq	29	ASN
34	Cq	61	ASN
34	Cq	93	ASN
34	Cq	104	HIS
34	Cq	129	HIS
34	Cq	196	HIS
34	Cq	237	GLN
35	Cr	80	HIS
35	Cr	125	GLN
35	Cr	142	ASN
35	Cr	287	HIS
36	Cv	147	HIS
36	Cv	166	HIS
36	Cv	245	ASN
36	Cv	312	ASN
36	Cv	321	HIS

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Mol	Chain	Res	Type
36	Cv	392	HIS
36	Cv	411	ASN
36	Cv	511	HIS
36	Cv	523	HIS
36	Cv	535	HIS
36	Cv	559	GLN
36	Cv	581	HIS
36	Cv	678	HIS
36	Cv	739	ASN
36	Cv	755	HIS
36	Cv	830	ASN
36	Cv	878	ASN
36	Cv	948	HIS
36	Cv	960	GLN
36	Cv	1066	GLN
36	Cv	1108	GLN
36	Cv	1129	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
37	CA	476/621 (76%)	213 (44%)	2 (0%)

All (213) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
37	CA	2	A
37	CA	3	A
37	CA	4	A
37	CA	5	U
37	CA	6	U
37	CA	8	U
37	CA	10	G
37	CA	11	U
37	CA	14	A
37	CA	16	U
37	CA	19	U
37	CA	20	A
37	CA	25	U
37	CA	26	C
37	CA	27	A

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Mol	Chain	Res	Type
37	CA	33	A
37	CA	36	U
37	CA	37	U
37	CA	38	U
37	CA	39	U
37	CA	40	U
37	CA	42	A
37	CA	44	U
37	CA	45	G
37	CA	46	U
37	CA	50	A
37	CA	52	C
37	CA	53	A
37	CA	56	U
37	CA	57	U
37	CA	58	A
37	CA	59	U
37	CA	60	A
37	CA	61	A
37	CA	64	G
37	CA	67	U
37	CA	68	A
37	CA	70	U
37	CA	74	G
37	CA	78	G
37	CA	79	A
37	CA	80	U
37	CA	84	U
37	CA	85	U
37	CA	86	G
37	CA	87	U
37	CA	88	A
37	CA	89	U
37	CA	91	A
37	CA	94	U
37	CA	95	U
37	CA	97	U
37	CA	100	G
37	CA	102	A
37	CA	103	U
37	CA	104	A
37	CA	105	G

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Mol	Chain	Res	Type
37	CA	107	U
37	CA	108	A
37	CA	109	A
37	CA	110	U
37	CA	111	A
37	CA	112	A
37	CA	113	U
37	CA	114	A
37	CA	115	A
37	CA	116	U
37	CA	117	U
37	CA	124	U
37	CA	127	G
37	CA	132	G
37	CA	135	U
37	CA	136	G
37	CA	138	U
37	CA	139	U
37	CA	146	U
37	CA	152	U
37	CA	156	U
37	CA	159	G
37	CA	160	U
37	CA	167	A
37	CA	170	U
37	CA	171	A
37	CA	172	A
37	CA	173	A
37	CA	174	A
37	CA	175	A
37	CA	178	A
37	CA	179	U
37	CA	183	U
37	CA	188	U
37	CA	189	A
37	CA	191	A
37	CA	193	C
37	CA	194	A
37	CA	197	A
37	CA	199	U
37	CA	200	A
37	CA	202	A

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Mol	Chain	Res	Type
37	CA	203	U
37	CA	204	U
37	CA	205	A
37	CA	206	A
37	CA	208	U
37	CA	209	U
37	CA	210	A
37	CA	211	A
37	CA	214	U
37	CA	216	U
37	CA	217	U
37	CA	218	A
37	CA	219	G
37	CA	221	C
37	CA	223	G
37	CA	230	A
37	CA	236	G
37	CA	242	G
37	CA	246	U
37	CA	247	A
37	CA	250	U
37	CA	256	G
37	CA	258	U
37	CA	259	U
37	CA	261	U
37	CA	262	A
37	CA	263	A
37	CA	272	C
37	CA	275	U
37	CA	276	U
37	CA	279	C
37	CA	280	A
37	CA	281	U
37	CA	282	A
37	CA	283	U
37	CA	286	A
37	CA	296	U
37	CA	297	G
37	CA	299	U
37	CA	300	G
37	CA	301	A
37	CA	305	A

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Mol	Chain	Res	Type
37	CA	311	U
37	CA	315	A
37	CA	316	A
37	CA	321	A
37	CA	323	U
37	CA	325	A
37	CA	326	U
37	CA	327	U
37	CA	328	U
37	CA	330	U
37	CA	334	U
37	CA	335	G
37	CA	337	U
37	CA	338	U
37	CA	340	U
37	CA	341	A
37	CA	342	A
37	CA	343	A
37	CA	350	U
37	CA	351	A
37	CA	352	G
37	CA	356	U
37	CA	357	A
37	CA	358	U
37	CA	359	G
37	CA	360	C
37	CA	361	A
37	CA	364	U
37	CA	367	A
37	CA	368	A
37	CA	369	A
37	CA	371	U
37	CA	374	U
37	CA	378	A
37	CA	380	U
37	CA	384	A
37	CA	385	A
37	CA	386	A
37	CA	389	A
37	CA	394	A
37	CA	539	A
37	CA	540	A

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Mol	Chain	Res	Type
37	CA	544	U
37	CA	546	U
37	CA	547	U
37	CA	548	G
37	CA	555	A
37	CA	556	C
37	CA	558	A
37	CA	560	U
37	CA	564	U
37	CA	565	A
37	CA	566	U
37	CA	567	A
37	CA	570	A
37	CA	576	A
37	CA	581	G
37	CA	586	A
37	CA	587	A
37	CA	588	U
37	CA	590	A
37	CA	602	A
37	CA	603	A
37	CA	611	U
37	CA	613	U
37	CA	614	U
37	CA	615	U
37	CA	616	U
37	CA	617	U
37	CA	618	U
37	CA	619	U
37	CA	620	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
37	CA	38	U
37	CA	39	U

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 43 ligands modelled in this entry, 40 are monoatomic - leaving 3 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	$\# Z > 2$
45	SPM	CA	735	-	13,13,13	0.33	0	12,12,12	0.84	0
44	SPD	CA	734	-	9,9,9	0.34	0	8,8,8	0.67	0
44	SPD	CA	733	-	9,9,9	0.48	0	8,8,8	0.48	0

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
45	SPM	CA	735	-	-	8/11/11/11	-
44	SPD	CA	734	-	-	3/7/7/7	-
44	SPD	CA	733	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
45	CA	735	SPM	C2-C3-C4-N5
45	CA	735	SPM	N10-C11-C12-C13
44	CA	733	SPD	C3-C4-C5-N6
45	CA	735	SPM	C6-C7-C8-C9

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Mol	Chain	Res	Type	Atoms
45	CA	735	SPM	C7-C8-C9-N10
44	CA	733	SPD	N1-C2-C3-C4
44	CA	733	SPD	C7-C8-C9-N10
44	CA	734	SPD	C7-C8-C9-N10
45	CA	735	SPM	C11-C12-C13-N14
45	CA	735	SPM	C12-C11-N10-C9
44	CA	734	SPD	C3-C4-C5-N6
45	CA	735	SPM	C7-C6-N5-C4
44	CA	733	SPD	C4-C5-N6-C7
44	CA	733	SPD	C8-C7-N6-C5
44	CA	734	SPD	C2-C3-C4-C5
45	CA	735	SPM	N1-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	CA	735	SPM	1	0
44	CA	733	SPD	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

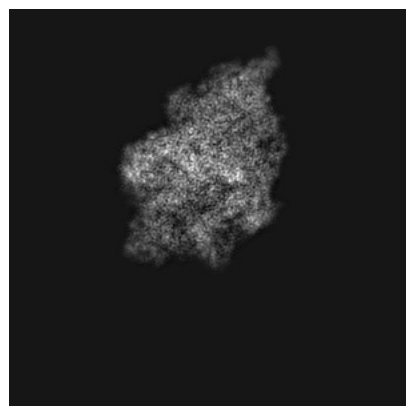
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0232. These allow visual inspection of the internal detail of the map and identification of artifacts.

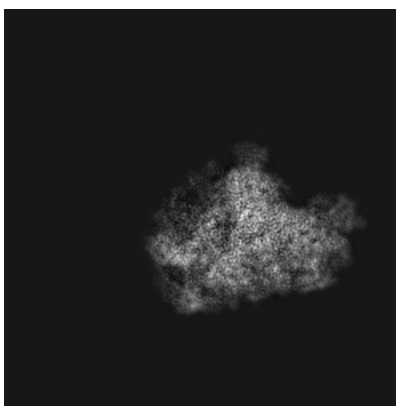
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

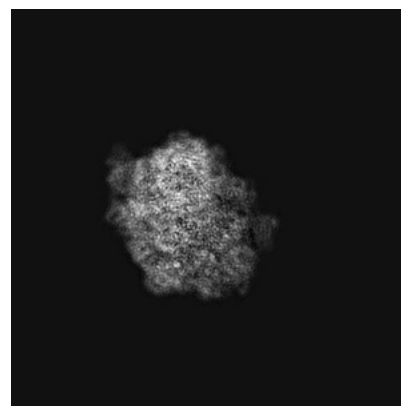
6.1.1 Primary map



X

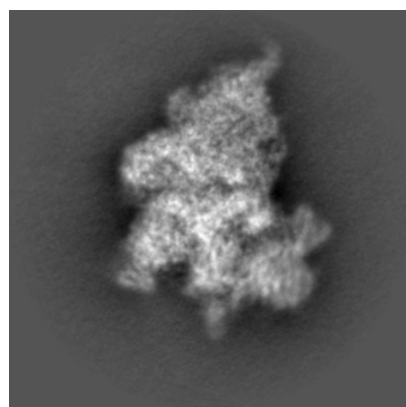


Y

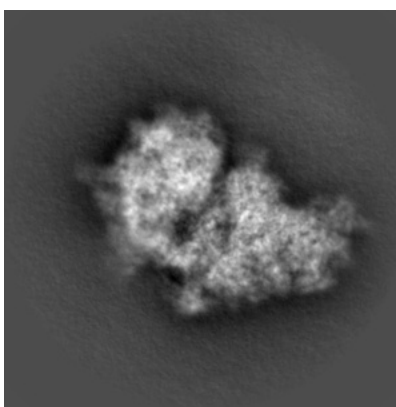


Z

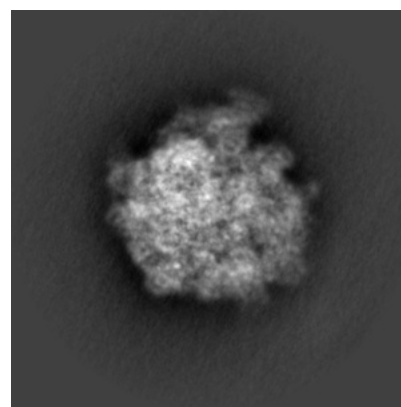
6.1.2 Raw map



X



Y

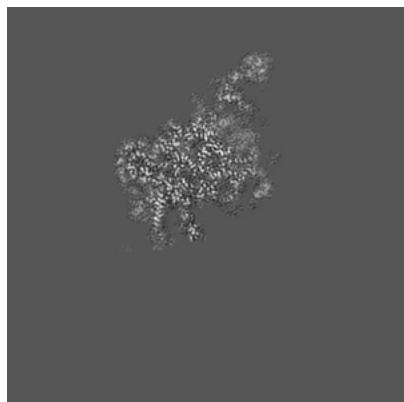


Z

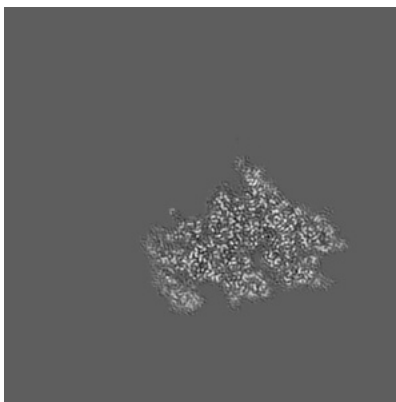
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

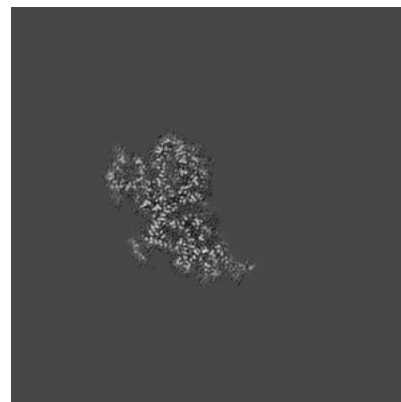
6.2.1 Primary map



X Index: 160

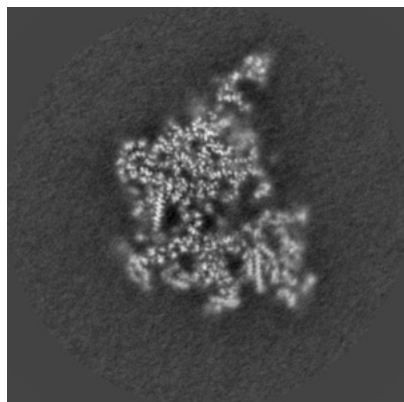


Y Index: 160

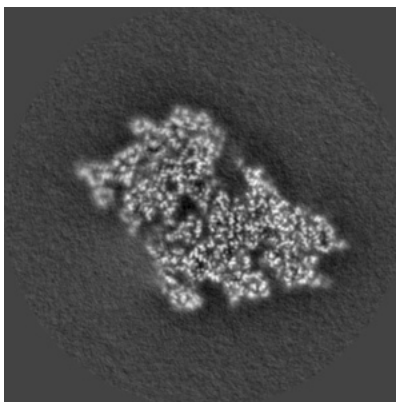


Z Index: 160

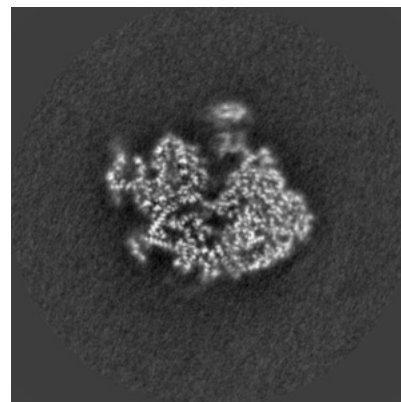
6.2.2 Raw map



X Index: 160



Y Index: 160

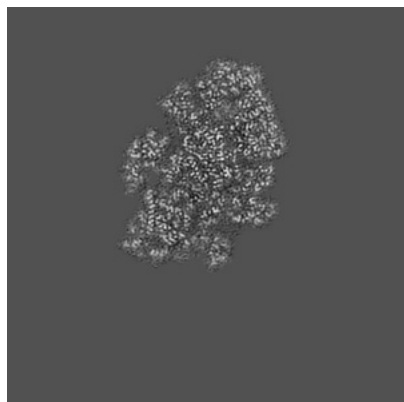


Z Index: 160

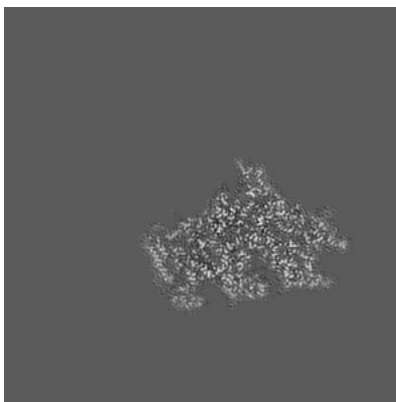
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

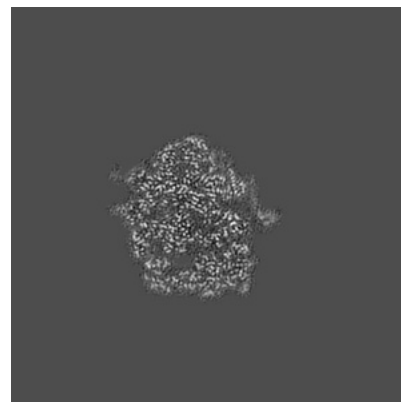
6.3.1 Primary map



X Index: 133

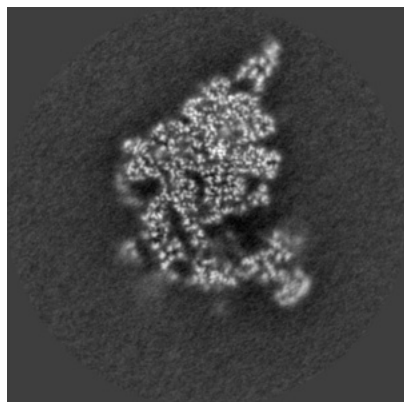


Y Index: 162

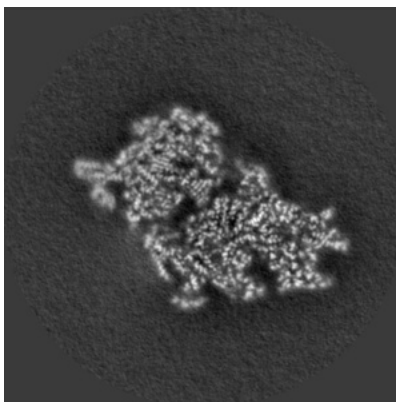


Z Index: 187

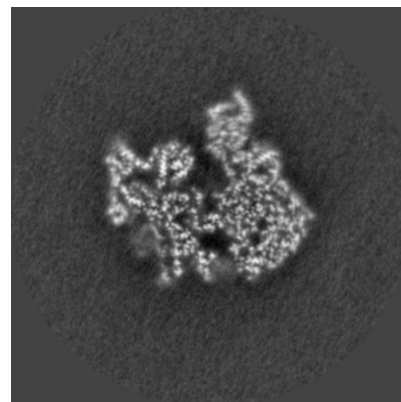
6.3.2 Raw map



X Index: 151



Y Index: 164

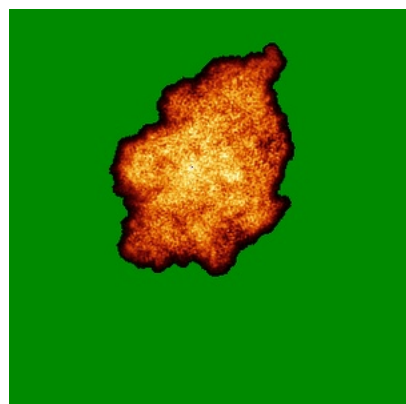


Z Index: 152

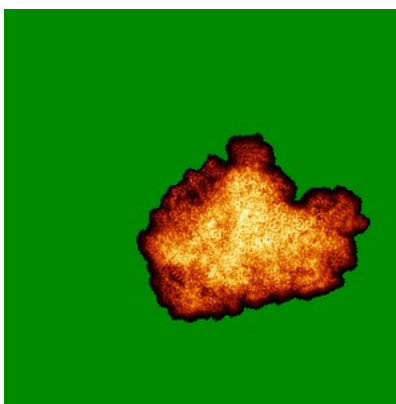
The images above show the largest variance slices of the map in three orthogonal directions.

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

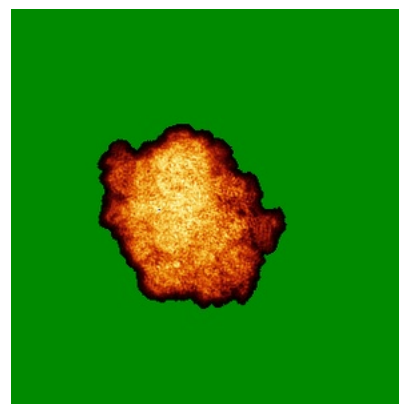
6.4.1 Primary map



X

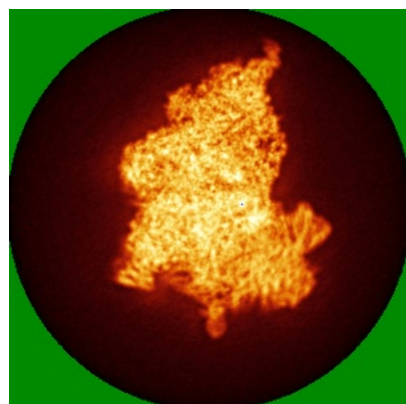


Y

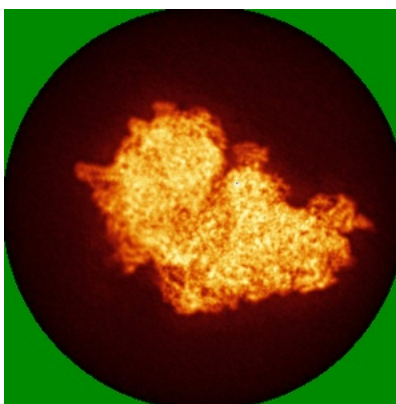


Z

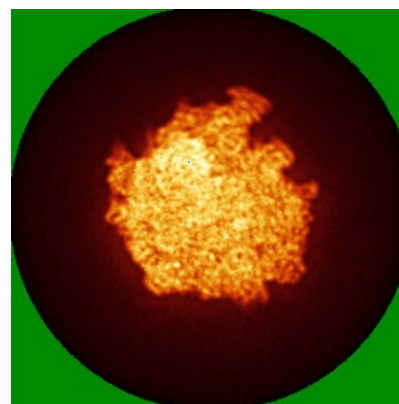
6.4.2 Raw map



X



Y

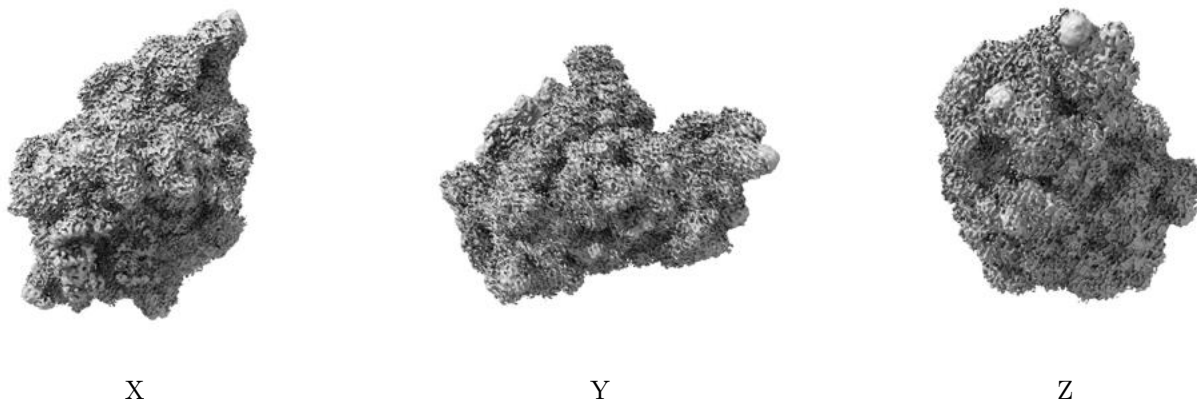


Z

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

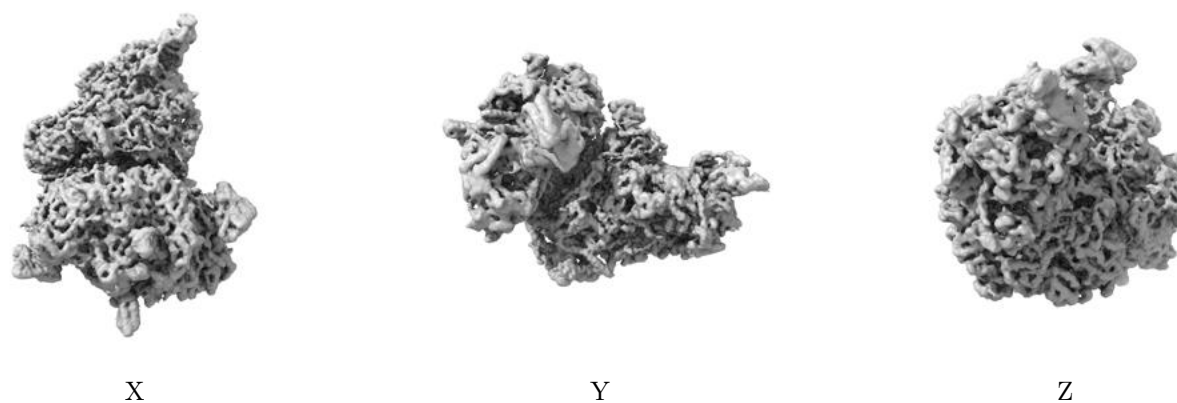
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0115. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

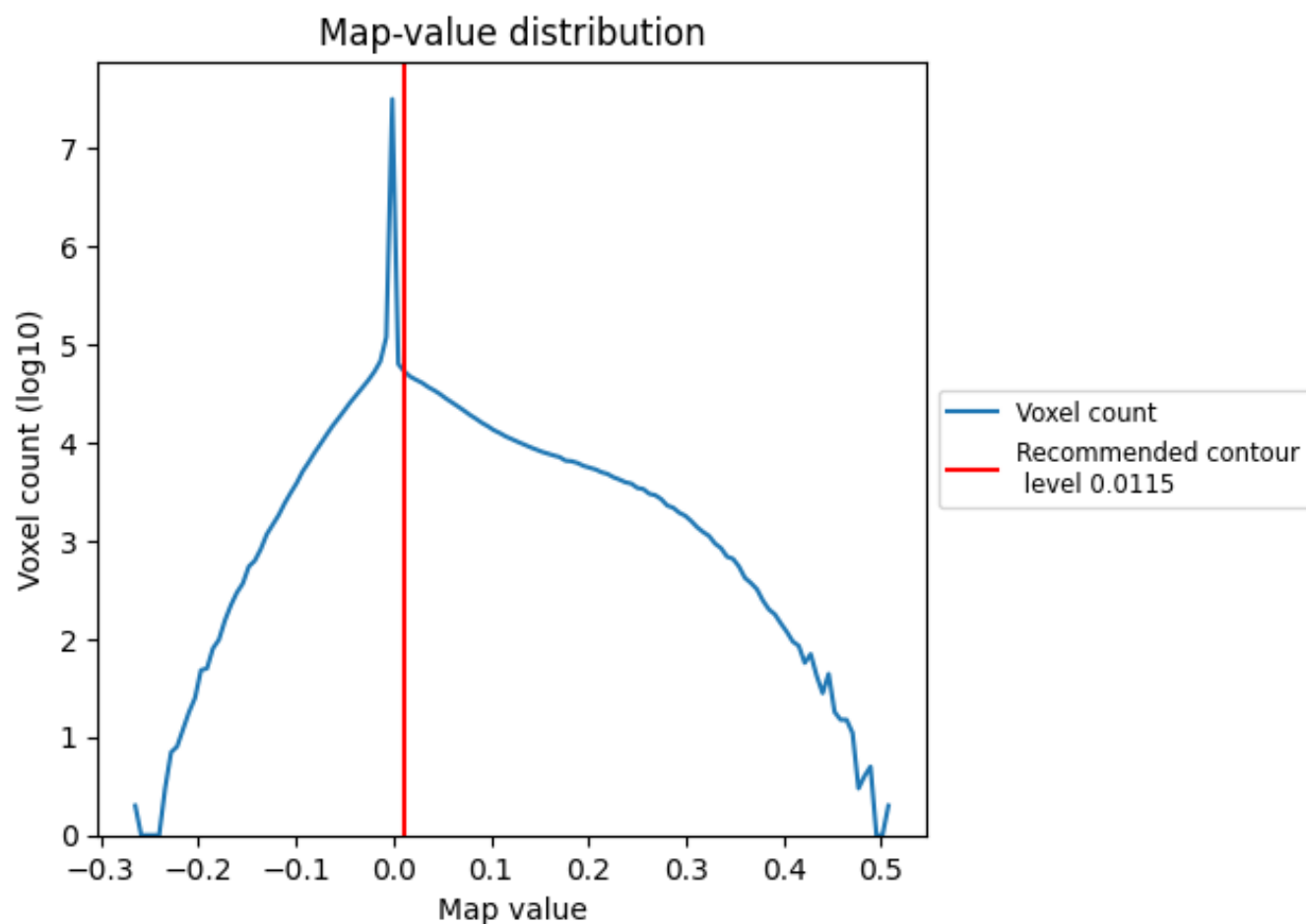
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

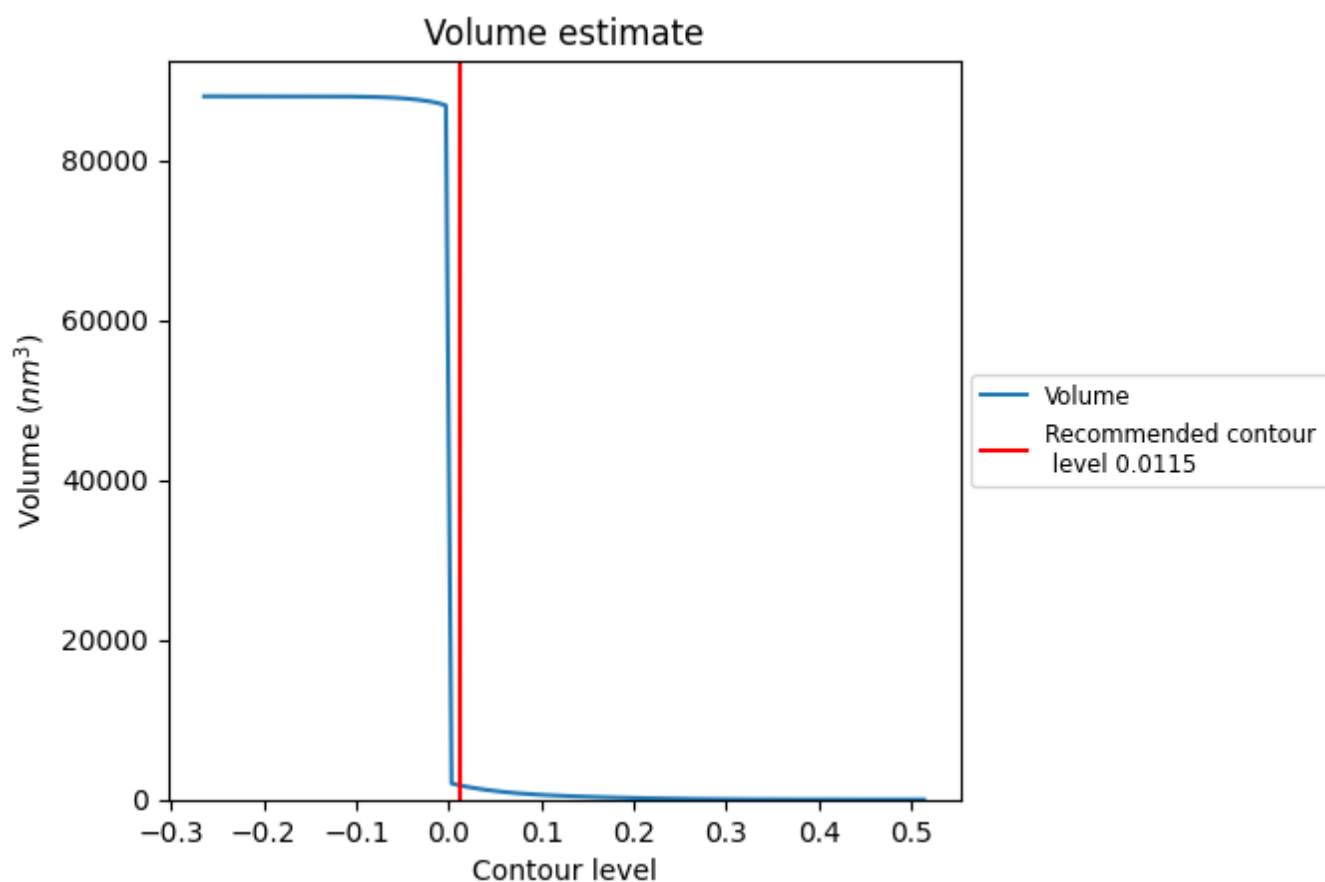
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

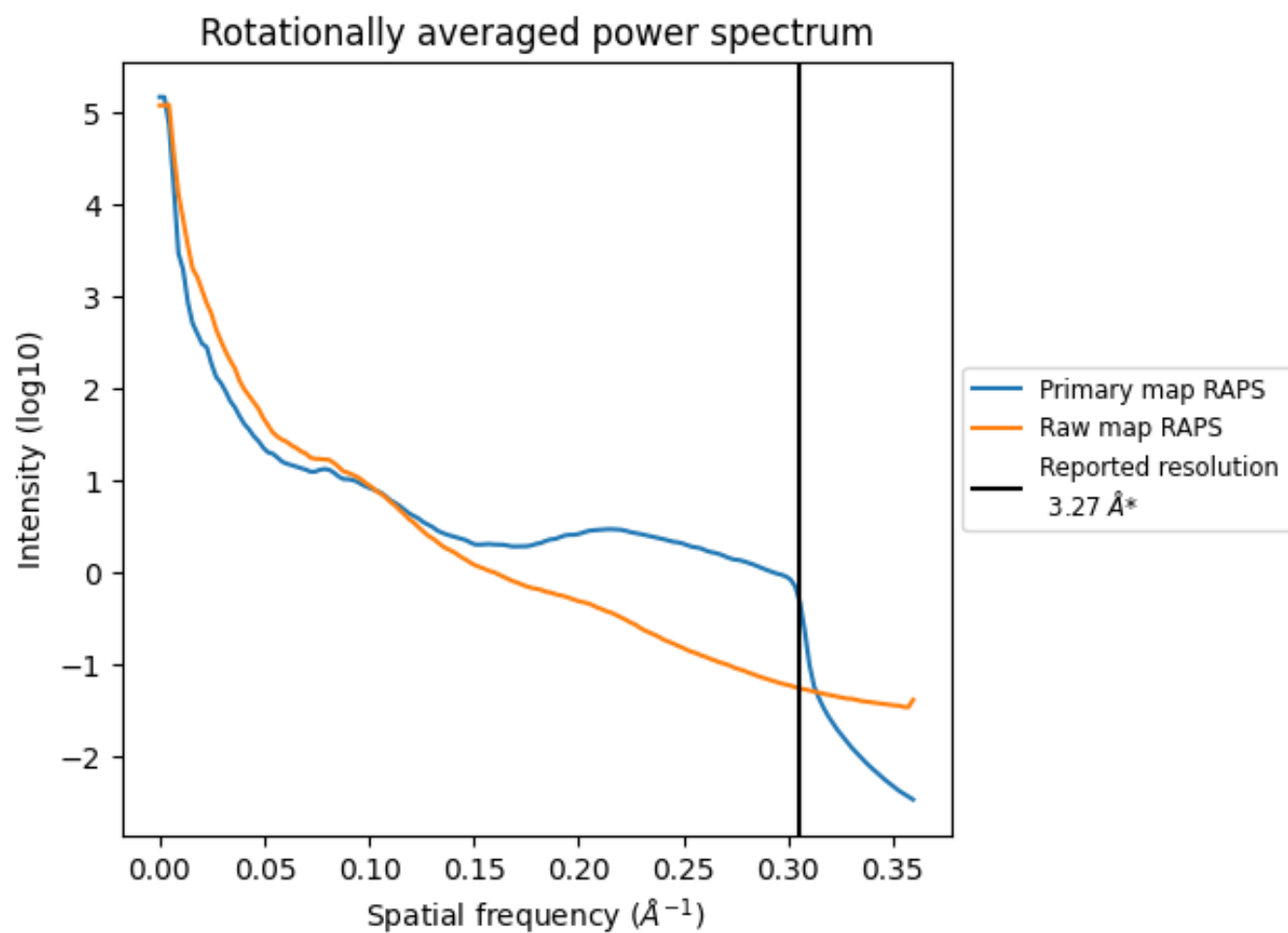
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1779 nm^3 ; this corresponds to an approximate mass of 1607 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

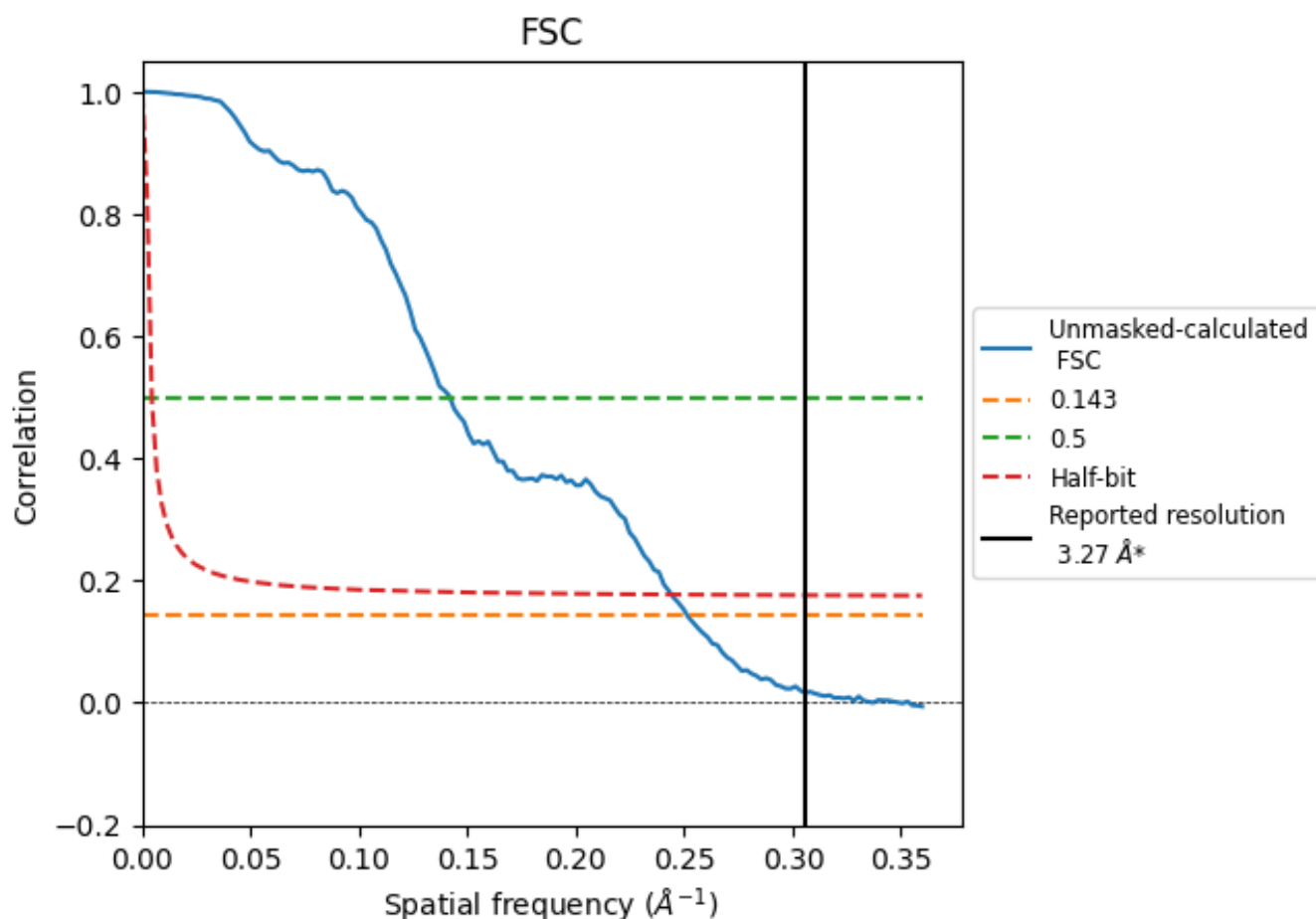


*Reported resolution corresponds to spatial frequency of $0.306 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.306 Å⁻¹

8.2 Resolution estimates [i](#)

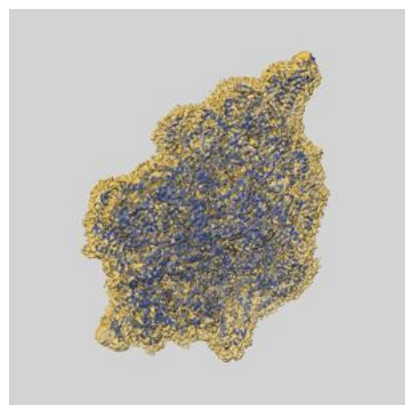
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.27	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.98	7.05	4.10

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.98 differs from the reported value 3.27 by more than 10 %

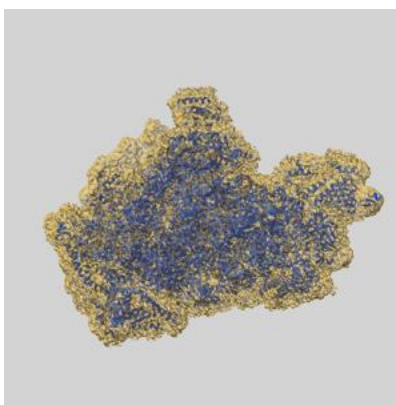
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0232 and PDB model 6HIY. Per-residue inclusion information can be found in section [3](#) on page [16](#).

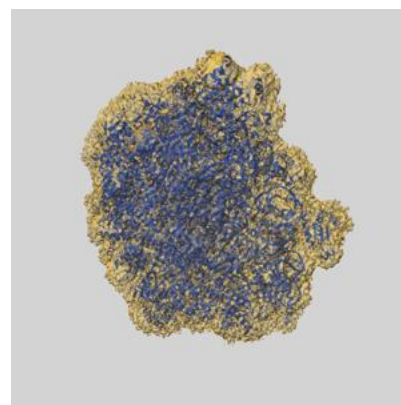
9.1 Map-model overlay [i](#)



X



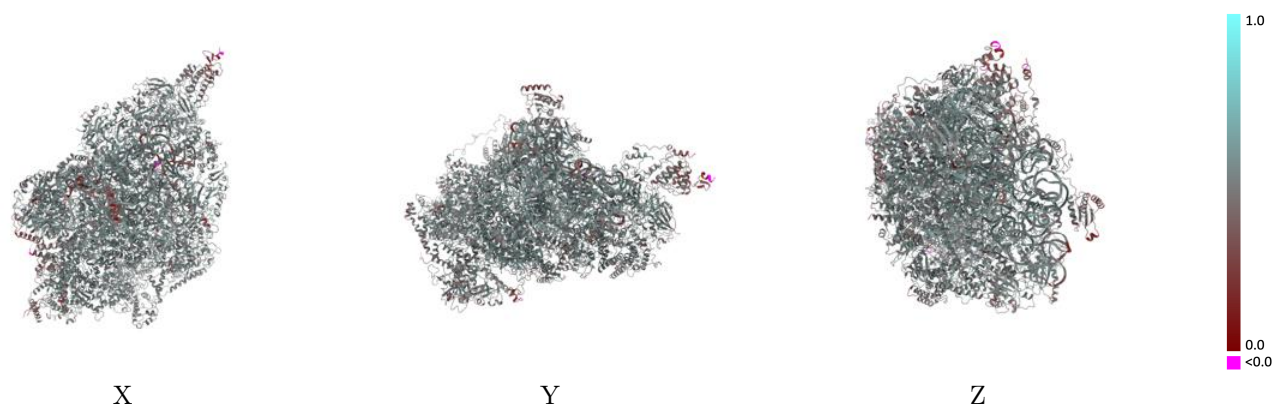
Y



Z

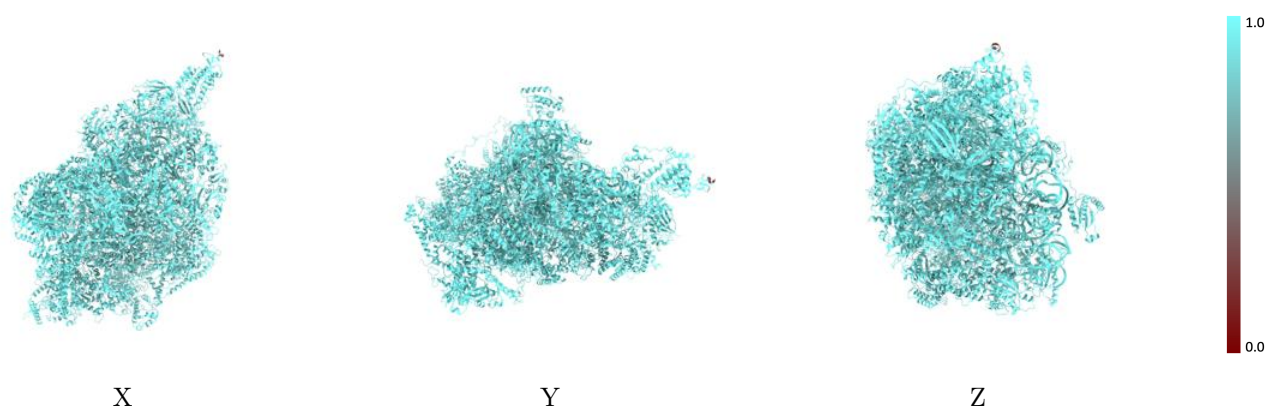
The images above show the 3D surface view of the map at the recommended contour level 0.0115 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



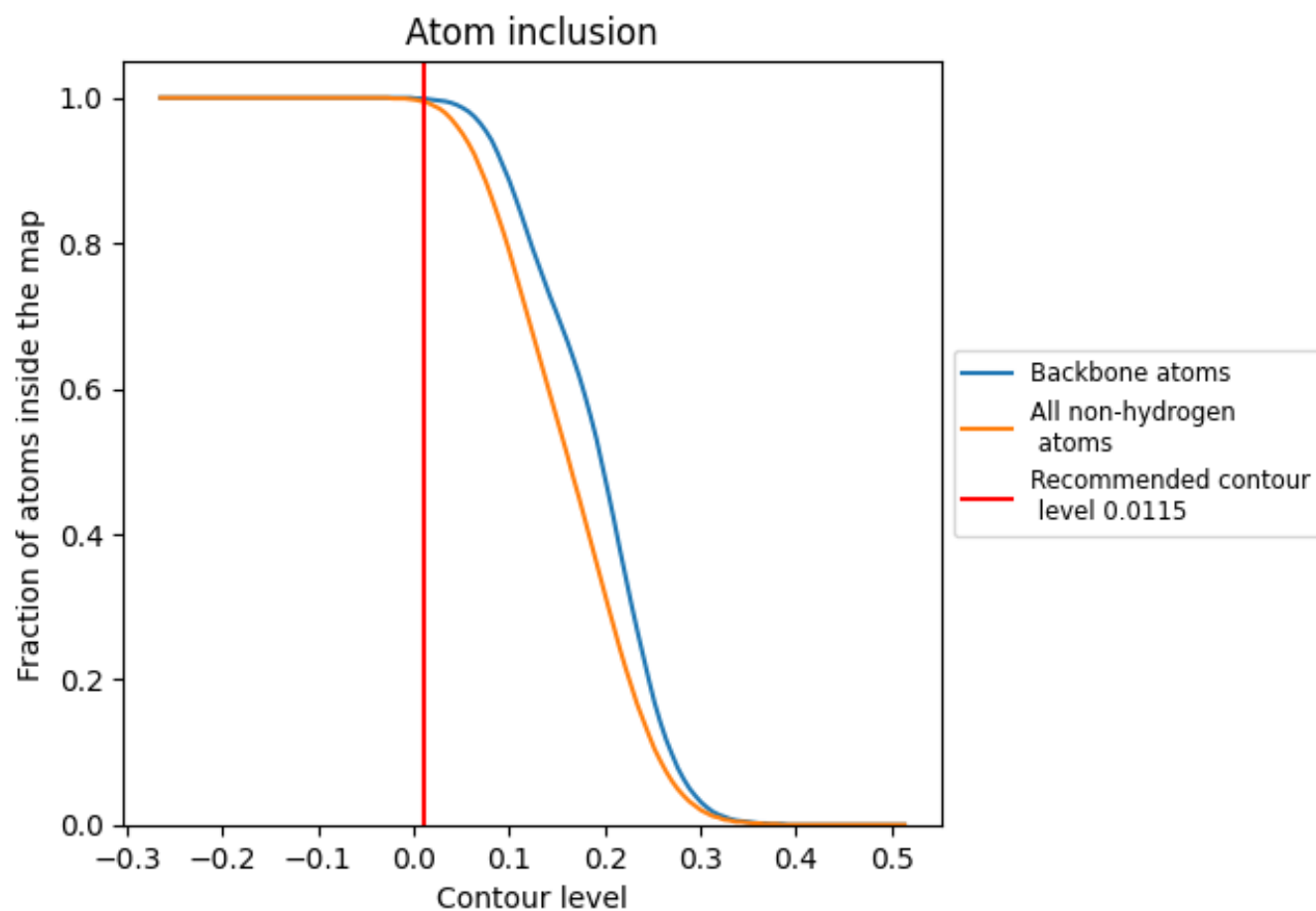
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0115).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0115) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9940	 0.5160
CA	 0.9960	 0.5150
CE	 0.9910	 0.5410
CF	 0.9820	 0.5040
CH	 0.9910	 0.5270
CI	 0.9910	 0.5300
CK	 0.9950	 0.5020
CL	 0.9970	 0.5380
CO	 0.9990	 0.5330
CP	 0.9980	 0.5360
CQ	 0.9980	 0.5640
CR	 0.9880	 0.5220
CU	 0.9970	 0.5270
CZ	 0.9800	 0.4120
Ca	 0.9930	 0.5320
Cb	 0.9930	 0.5060
Cd	 0.9930	 0.5030
Cj	 0.9990	 0.5140
Cm	 0.9840	 0.5160
Cn	 0.9980	 0.5310
Cp	 0.9990	 0.4980
Cq	 0.9910	 0.5240
Cr	 0.9970	 0.4760
Cv	 0.9950	 0.5290
DA	 0.9950	 0.5030
DD	 0.9930	 0.5250
DI	 0.9970	 0.5100
DL	 0.9880	 0.5430
DM	 0.9960	 0.5400
DN	 0.9910	 0.5360
DO	 0.9970	 0.4930
DP	 0.9840	 0.4450
DQ	 0.9970	 0.5010
DR	 1.0000	 0.5020
DS	 0.9970	 0.5160



Continued on next page...

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Chain	Atom inclusion	Q-score
DU	 0.9960	 0.5150
DZ	 0.9930	 0.5400
Da	 0.9980	 0.5600
UQ	 1.0000	 0.4100
UR	 1.0000	 0.4000
US	 0.9880	 0.4230
UT	 0.9660	 0.3910