



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 05:11 AM UTC

PDB ID : 6YXX / pdb_00006yxx
EMDB ID : EMD-10999
Title : State A of the Trypanosoma brucei mitoribosomal large subunit assembly intermediate
Authors : Jaskolowski, M.; Ramrath, D.J.F.; Bieri, P.; Niemann, M.; Mattei, S.; Calderaro, S.; Leibundgut, M.A.; Horn, E.K.; Boehringer, D.; Schneider, A.; Ban, N.
Deposited on : 2020-05-04
Resolution : 3.90 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

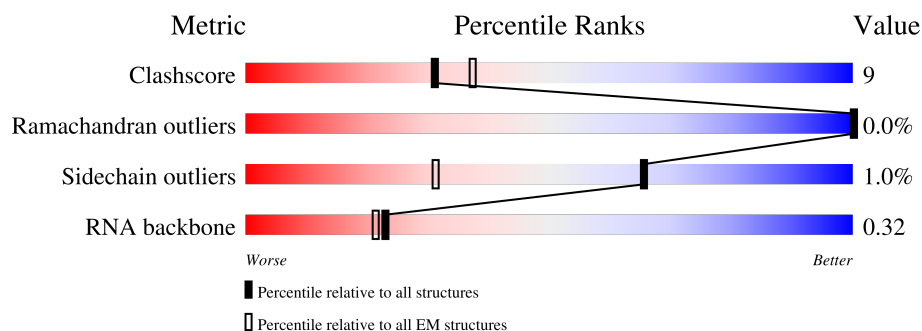
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.



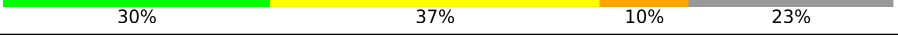
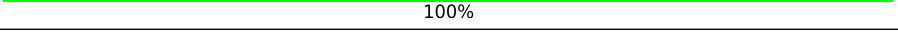
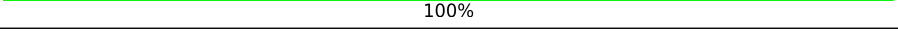
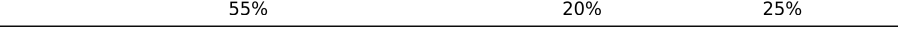
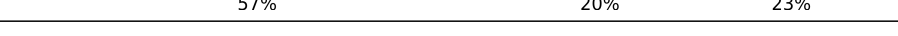
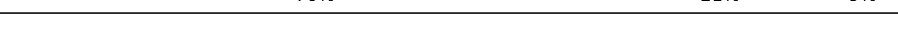
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A1	241	71% 18% 10%
2	E1	482	76% 22% .
3	A2	471	80% 18% .
4	E2	568	50% 15% 35%
5	A3	218	48% 21% 31%
6	E3	557	56% 16% 28%

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Mol	Chain	Length	Quality of chain
7	E4	439	
8	A5	80	
9	E5	376	
10	E6	531	
11	A8	181	
12	AA	1176	
13	BA	831	
14	EA	576	
15	UA	10	
15	Uf	10	
16	BB	541	
17	EB	754	
18	EC	406	
19	BD	547	
20	ED	616	
21	AE	473	
22	BE	449	
23	EE	586	
24	AF	459	
25	BF	426	
26	EF	373	
27	EG	156	
28	BH	349	
29	EH	634	
30	AI	263	

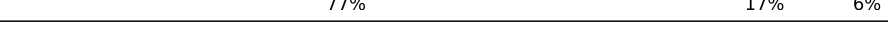
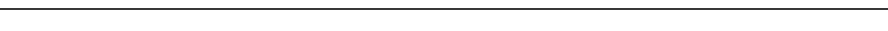
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Mol	Chain	Length	Quality of chain
31	BI	342	
32	UI	21	
32	Ur	21	
33	BJ	333	
34	AK	342	
35	BK	386	
36	UK	25	
37	BL	312	
38	EL	691	
39	EM	451	
40	UM	8	
41	AN	202	
42	BN	302	
43	EN	731	
44	BO	262	
45	EO	319	
45	EP	319	
46	AP	374	
47	BQ	231	
48	AR	301	
49	BR	205	
50	ER	148	
51	BS	198	
52	ES	524	
53	AT	144	

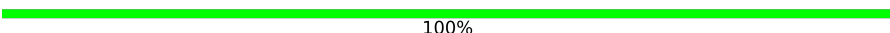
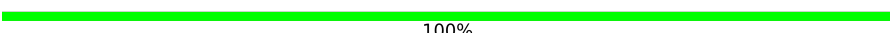
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Mol	Chain	Length	Quality of chain
54	BT	191	
55	ET	102	
56	AU	213	
57	BU	185	
58	AV	188	
59	BV	190	
60	AW	278	
61	BW	188	
62	AX	246	
63	AY	378	
64	BZ	190	
65	Ba	153	
66	Bb	162	
67	Bc	146	
68	Ae	197	
69	Af	189	
70	Bf	113	
71	Ag	260	
72	E7	97	
73	E8	786	
74	E9	343	
75	Al	218	
76	U1	238	
77	Um	27	
78	Un	28	

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Mol	Chain	Length	Quality of chain
79	Ao	1520	 10% 88%
80	Ap	309	 68% 17% 15%
81	Up	87	 100%
82	Us	79	 100%
83	At	154	 75% 14% 10%
84	Av	242	 62% 17% 21%

2 Entry composition [i](#)

There are 92 unique types of molecules in this entry. The entry contains 183043 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 bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	217	Total	C	N	O	S	0	0
			1788	1138	324	317	9		

- Molecule 2 is a protein called mt-LAF21.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E1	473	Total	C	N	O	S	0	0
			3836	2376	745	703	12		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E1	379	SER	ALA	conflict	UNP Q57WG6

- Molecule 3 is a protein called uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A2	463	Total	C	N	O	S	0	0
			3739	2381	651	694	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A2	238	GLY	ALA	conflict	UNP Q38EM7

- Molecule 4 is a protein called DUF4379 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E2	369	Total	C	N	O	S	0	0
			2933	1839	550	517	27		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E2	167	THR	LYS	conflict	UNP C9ZTN9

- Molecule 5 is a protein called uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A3	150	Total	C	N	O	S	0	0
			1226	781	236	203	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A3	198	UNK	ALA	conflict	UNP C9ZY77

- Molecule 6 is a protein called mt-LAF23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E3	403	Total	C	N	O	S	0	0
			3266	2062	590	591	23		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E3	1	MET	-	initiating methionine	UNP D0A795

- Molecule 7 is a protein called mt-LAF24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E4	434	Total	C	N	O	S	0	0
			3418	2159	623	622	14		

- Molecule 8 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A5	55	Total	C	N	O	S	0	0
			483	311	90	76	6		

- Molecule 9 is a protein called mt-LAF25.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E5	327	Total	C	N	O		0	0
			1635	981	327	327			

- Molecule 10 is a protein called KRIPP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E6	434	Total	C	N	O	S	0	0
			3405	2143	608	635	19		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E6	360	SER	ALA	conflict	UNP Q4GZA2

- Molecule 11 is a protein called bL35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A8	133	Total	C	N	O	S	0	0
			1136	712	233	184	7		

- Molecule 12 is a RNA chain called 12S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AA	904	Total	C	N	O	P	0	0
			18187	8161	2902	6220	904		

- Molecule 13 is a protein called mL67.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BA	769	Total	C	N	O	S	0	0
			6059	3847	1074	1104	34		

- Molecule 14 is a protein called mt-EngA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	EA	532	Total	C	N	O	S	0	0
			4263	2672	785	785	21		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EA	12	UNK	ARG	conflict	UNP Q57TZ4

- Molecule 15 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	UA	10	Total	C	N	O	0	0
			50	30	10	10		
15	Uf	10	Total	C	N	O	0	0
			50	30	10	10		

- Molecule 16 is a protein called mL68.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BB	407	Total	C	N	O	S	0	0
			3322	2114	589	599	20		

- Molecule 17 is a protein called DEAD-box helicase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	EB	627	Total	C	N	O	S	0	0
			5039	3181	957	875	26		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EB	301	ALA	THR	conflict	UNP D0A9G9

- Molecule 18 is a protein called Pseudouridylate synthase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	EC	373	Total	C	N	O	S	0	0
			3005	1923	540	524	18		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EC	25	UNK	HIS	conflict	UNP Q38FJ3

- Molecule 19 is a protein called mL70.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BD	419	Total	C	N	O	S	0	0
			3349	2134	586	609	20		

- Molecule 20 is a protein called mt-LAF4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	ED	598	Total	C	N	O	S	0	0
			4764	3026	850	865	23		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ED	252	ARG	LYS	conflict	UNP Q385G9

- Molecule 21 is a protein called Ribosomal protein L3 mitochondrial, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AE	344	Total	C	N	O	S	0	0
			2802	1804	474	509	15		

- Molecule 22 is a protein called mL71.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BE	357	Total	C	N	O	S	0	0
			2822	1801	477	535	9		

- Molecule 23 is a protein called SpoU_methylase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	EE	431	Total	C	N	O	S	0	0
			3423	2132	646	632	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	337	ASP	GLY	conflict	UNP C9ZZ65

- Molecule 24 is a protein called Ribosomal protein L4/L1 family, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AF	419	Total	C	N	O	S	0	0
			3414	2181	584	626	23		

- Molecule 25 is a protein called Tetratricopeptide repeat.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BF	346	Total	C	N	O	S	0	0
			2847	1803	519	512	13		

- Molecule 26 is a protein called SpoU_methylase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	EF	297	Total	C	N	O	S	0	0
			2268	1439	401	420	8		

- Molecule 27 is a protein called mt-LAF7.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	EG	154	Total	C	N	O	S	0	0
			1295	812	256	218	9		

- Molecule 28 is a protein called mL74.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BH	236	Total	C	N	O	S	0	0
			1948	1250	346	349	3		

- Molecule 29 is a protein called mt-LAF8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	EH	443	Total	C	N	O	S	0	0
			3508	2214	635	640	19		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EH	166	UNK	GLY	conflict	UNP A0A1G4IEQ9
EH	495	ARG	LYS	conflict	UNP A0A1G4IEQ9

- Molecule 30 is a protein called RIBOSOMAL_L9 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AI	240	Total	C	N	O	S	0	0
			1967	1260	345	353	9		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	249	UNK	LYS	conflict	UNP Q57UC5
AI	250	UNK	GLY	conflict	UNP Q57UC5
AI	251	UNK	PRO	conflict	UNP Q57UC5
AI	252	UNK	VAL	conflict	UNP Q57UC5

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Chain	Residue	Modelled	Actual	Comment	Reference
AI	253	UNK	LYS	conflict	UNP Q57UC5
AI	254	UNK	GLN	conflict	UNP Q57UC5
AI	255	UNK	ARG	conflict	UNP Q57UC5
AI	256	UNK	LYS	conflict	UNP Q57UC5
AI	257	UNK	ALA	conflict	UNP Q57UC5
AI	258	UNK	ARG	conflict	UNP Q57UC5

- Molecule 31 is a protein called mL75.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BI	303	Total	C	N	O	S	0	0
			2475	1580	447	433	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BI	227	ASN	ASP	conflict	UNP D0A108

- Molecule 32 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	UI	21	Total	C	N	O	0	0
			105	63	21	21		
32	Ur	21	Total	C	N	O	0	0
			105	63	21	21		

- Molecule 33 is a protein called mL76.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BJ	234	Total	C	N	O	S	0	0
			1944	1215	365	356	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BJ	329	GLU	ALA	conflict	UNP Q383M2

- Molecule 34 is a protein called Ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AK	248	Total	C	N	O	S	0	0
			2088	1335	385	356	12		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	327	UNK	ALA	conflict	UNP Q586R9

- Molecule 35 is a protein called Chaperone protein DNAj, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BK	228	Total	C	N	O	S	0	0
			1855	1153	353	341	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BK	33	UNK	HIS	conflict	UNP C9ZQR6
BK	60	UNK	PRO	conflict	UNP C9ZQR6
BK	348	VAL	LEU	conflict	UNP C9ZQR6

- Molecule 36 is a protein called UNK.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	UK	25	Total	C	N	O		0	0
			125	75	25	25			

- Molecule 37 is a protein called mL78.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BL	258	Total	C	N	O	S	0	0
			2014	1236	395	373	10		

- Molecule 38 is a protein called mt-LAF12.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	EL	532	Total	C	N	O	S	0	0
			4259	2732	744	754	29		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EL	104	UNK	ILE	conflict	UNP C9ZVC0
EL	108	GLU	GLY	conflict	UNP C9ZVC0
EL	126	VAL	LEU	conflict	UNP C9ZVC0
EL	188	SER	PHE	conflict	UNP C9ZVC0

- Molecule 39 is a protein called GTP-binding protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	EM	308	Total	C	N	O	S	0	0
			2432	1542	438	437	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EM	407	UNK	PRO	conflict	UNP Q38E75

- Molecule 40 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	UM	8	Total	C	N	O	0	0
			40	24	8	8		

- Molecule 41 is a protein called 50S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AN	193	Total	C	N	O	S	0	0
			1639	1059	301	269	10		

- Molecule 42 is a protein called mL80.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BN	154	Total	C	N	O	S	0	0
			1320	839	239	237	5		

- Molecule 43 is a protein called mt-LAF14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	EN	638	Total	C	N	O	S	0	0
			5025	3152	909	936	28		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EN	18	GLU	GLY	conflict	UNP C9ZPS0
EN	310	LYS	ASN	conflict	UNP C9ZPS0
EN	676	CYS	TYR	conflict	UNP C9ZPS0

- Molecule 44 is a protein called mL81.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BO	192	Total	C	N	O	S	0	0
			1498	936	268	281	13		

- Molecule 45 is a protein called mt-LAF15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	EO	272	Total	C	N	O	S	0	0
			2126	1340	393	383	10		
45	EP	243	Total	C	N	O	S	0	0
			1911	1208	347	347	9		

- Molecule 46 is a protein called Ribosomal_L18e/L15P domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AP	320	Total	C	N	O	S	0	0
			2615	1667	478	457	13		

- Molecule 47 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BQ	218	Total	C	N	O	S	0	0
			1651	1049	288	306	8		

- Molecule 48 is a protein called 50S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AR	267	Total	C	N	O	S	0	0
			2214	1399	403	399	13		

- Molecule 49 is a protein called mL84.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BR	196	Total	C	N	O	S	0	0
			1659	1064	299	287	9		

- Molecule 50 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	ER	84	Total	C	N	O	S	0	0
			669	427	106	135	1		

- Molecule 51 is a protein called mL85.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BS	161	Total	C	N	O	S	0	0
			1120	694	206	214	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BS	45	ILE	VAL	conflict	UNP Q38FG8
BS	173	UNK	LEU	conflict	UNP Q38FG8

- Molecule 52 is a protein called Lipase (Class 3).

Mol	Chain	Residues	Atoms					AltConf	Trace
52	ES	152	Total	C	N	O	S	0	0
			1259	779	246	230	4		

- Molecule 53 is a protein called bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AT	143	Total	C	N	O	S	0	0
			1180	743	224	206	7		

- Molecule 54 is a protein called mL86.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BT	173	Total	C	N	O	S	0	0
			1435	884	278	267	6		

- Molecule 55 is a protein called mt-LAF19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	ET	101	Total	C	N	O	S	0	0
			839	529	166	140	4		

- Molecule 56 is a protein called bL20m.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AU	175	Total	C	N	O	S	0	0
			1423	895	280	243	5		

- Molecule 57 is a protein called mL87.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BU	150	Total	C	N	O	S	0	0
			1275	806	248	215	6		

- Molecule 58 is a protein called bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AV	181	Total	C	N	O	S	0	0
			1424	909	257	252	6		

- Molecule 59 is a protein called mL88.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BV	90	Total	C	N	O	S	0	0
			763	492	133	136	2		

- Molecule 60 is a protein called uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AW	278	Total	C	N	O	S	0	0
			2251	1427	417	393	14		

- Molecule 61 is a protein called mL89.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BW	188	Total	C	N	O	S	0	0
			1565	992	299	265	9		

- Molecule 62 is a protein called uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AX	164	Total	C	N	O	S	0	0
			1387	896	244	242	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AX	126	TYR	HIS	conflict	UNP Q387G3

- Molecule 63 is a protein called uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AY	340	Total	C	N	O	S	0	0
			2790	1741	497	537	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AY	345	GLU	VAL	conflict	UNP C9ZK52

- Molecule 64 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BZ	188	Total	C	N	O	S	0	0
			1396	883	241	266	6		

- Molecule 65 is a protein called mL93.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ba	153	Total	C	N	O	S	0	0
			1287	820	237	223	7		

- Molecule 66 is a protein called mL94.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bb	133	Total	C	N	O	S	0	0
			1048	661	196	188	3		

- Molecule 67 is a protein called mL95.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bc	137	Total	C	N	O	S	0	0
			1194	776	216	201	1		

- Molecule 68 is a protein called mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ae	127	Total	C	N	O	S	0	0
			1031	667	190	169	5		

- Molecule 69 is a protein called mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Af	139	Total	C	N	O	S	0	0
			1107	692	210	200	5		

- Molecule 70 is a protein called mL98.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bf	87	Total	C	N	O	S	0	0
			725	462	131	132			

- Molecule 71 is a protein called L51_S25_CI-B8 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ag	186	Total	C	N	O	S	0	0
			1564	979	295	283	7		

- Molecule 72 is a protein called mt-LAF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	E7	97	Total	C	N	O	S	0	0
			815	501	175	135	4		

- Molecule 73 is a protein called KRIPP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	E8	154	Total	C	N	O	S	0	0
			1181	735	228	218			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E8	208	LYS	GLU	conflict	UNP Q57YZ6
E8	250	GLN	ARG	conflict	UNP Q57YZ6
E8	345	ILE	MET	conflict	UNP Q57YZ6
E8	630	UNK	LEU	conflict	UNP Q57YZ6

- Molecule 74 is a protein called mt-LAF29.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	E9	200	Total	C	N	O	S	0	0
			1642	1022	326	285	9		

- Molecule 75 is a protein called mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Al	181	Total	C	N	O	S	0	0
			1440	936	250	247	7		

- Molecule 76 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	U1	238	Total	C	N	O	0	0
			1190	714	238	238		

- Molecule 77 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	Um	27	Total	C	N	O	0	0
			135	81	27	27		

- Molecule 78 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
78	Un	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 79 is a protein called mL52.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Ao	184	Total	C	N	O	S	0	0
			1443	903	263	270	7		

- Molecule 80 is a protein called mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Ap	263	Total	C	N	O	S	0	0
			2161	1402	374	373	12		

- Molecule 81 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	Up	87	Total	C	N	O	0	0
			435	261	87	87		

- Molecule 82 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	Us	79	Total	C	N	O	0	0
			395	237	79	79		

- Molecule 83 is a protein called mL63.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	At	138	Total	C	N	O	S	0	0
			1149	722	223	200	4		

- Molecule 84 is a protein called mL64.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Av	192	Total	C	N	O	S	0	0
			1633	1038	304	279	12		

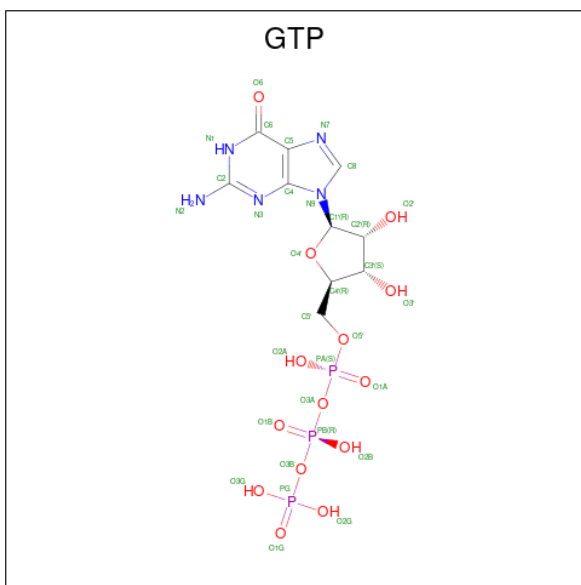
- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	E2	4	Total	Zn	0
			4	4	
85	A5	1	Total	Zn	0
			1	1	
85	EG	1	Total	Zn	0
			1	1	
85	E9	1	Total	Zn	0
			1	1	

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A8	2	Total	Mg	0
			2	2	
86	AA	12	Total	Mg	0
			12	12	
86	EA	2	Total	Mg	0
			2	2	
86	EB	1	Total	Mg	0
			1	1	

- Molecule 87 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

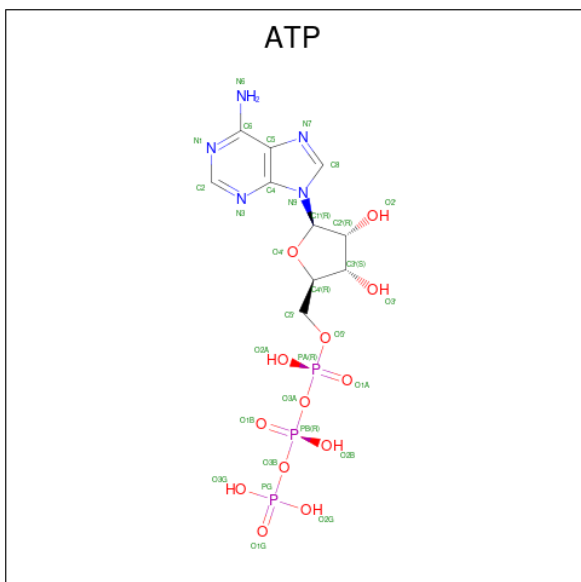


Mol	Chain	Residues	Atoms					AltConf
87	EA	1	Total 32	C 10	N 5	O 14	P 3	0
87	EA	1	Total 32	C 10	N 5	O 14	P 3	0

- Molecule 88 is SODIUM ION (CCD ID: NA) (formula: Na).

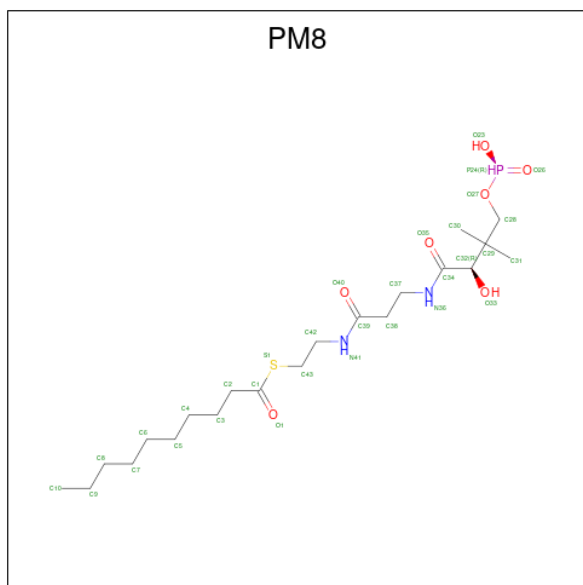
Mol	Chain	Residues	Atoms		AltConf
88	EA	2	Total 2	Na 2	0

- Molecule 89 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



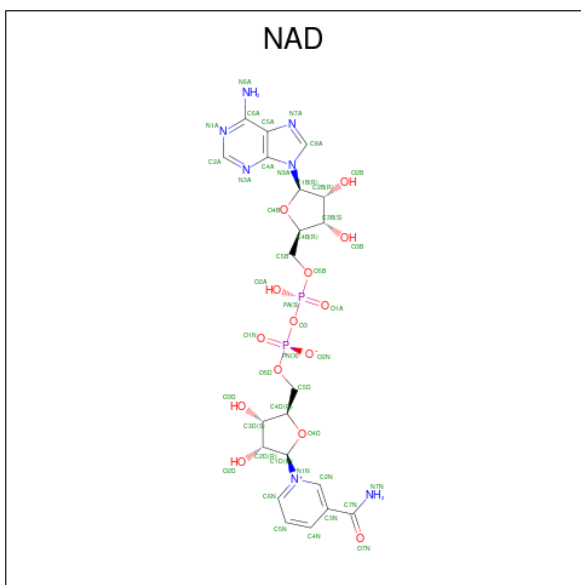
Mol	Chain	Residues	Atoms					AltConf
89	EB	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 90 is S-(2-{[N-(2-HYDROXY-4-{[HYDROXY(OXIDO)PHOSPHINO]OXY}-3,3-DIMETHYLBUTANOYL)-BETA-ALANYL]AMINO}ETHYL) DECANETHIOATE (CCD ID: PM8) (formula: $C_{21}H_{41}N_2O_7PS$).



Mol	Chain	Residues	Atoms						AltConf
90	ER	1	Total	C	N	O	P	S	0
			32	21	2	7	1	1	

- Molecule 91 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					AltConf
91	Av	1	Total	C	N	O	P	0
			44	21	7	14	2	

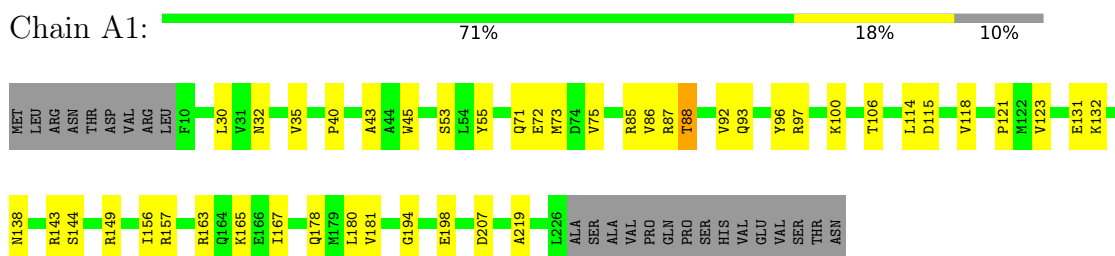
- Molecule 92 is water.

Mol	Chain	Residues	Atoms	AltConf
92	EA	4	Total O 4 4	0
92	EB	4	Total O 4 4	0

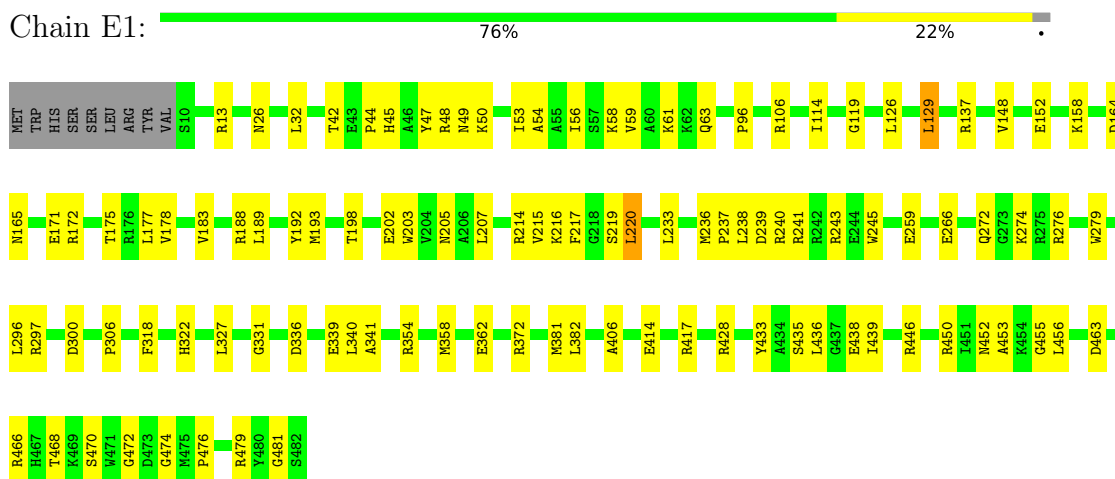
3 Residue-property plots

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

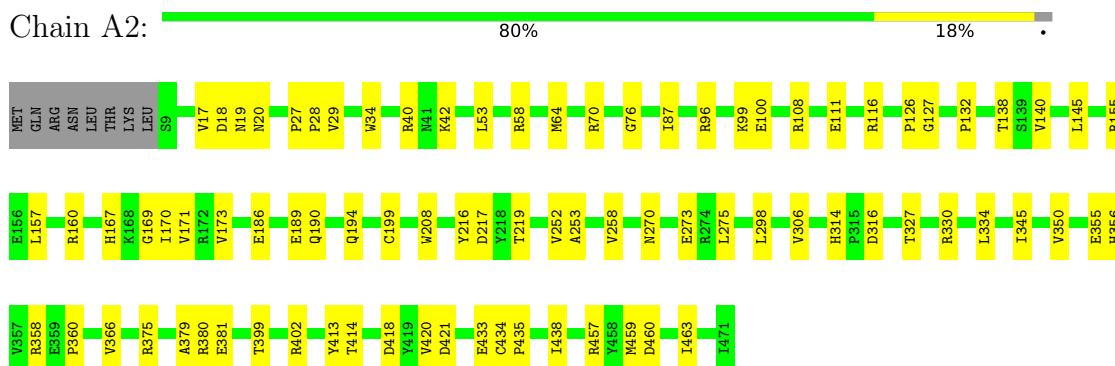
- Molecule 1: bL28m



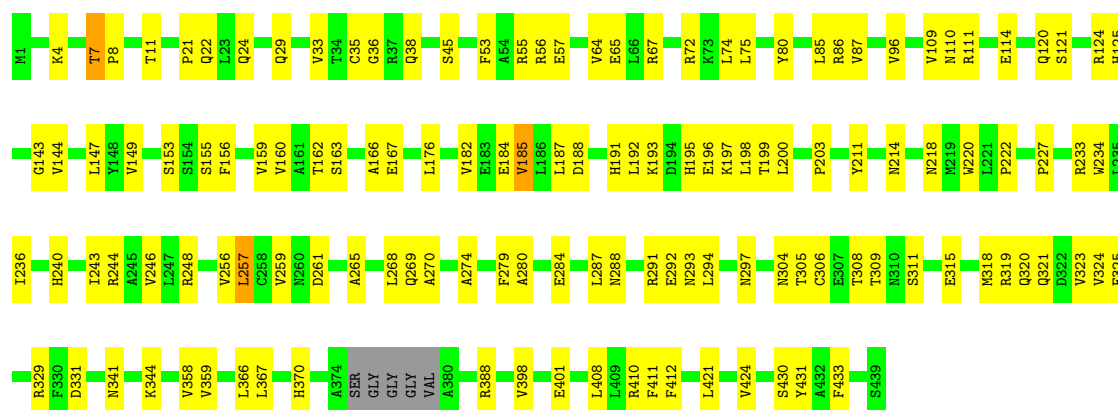
- Molecule 2: mt-LAF21



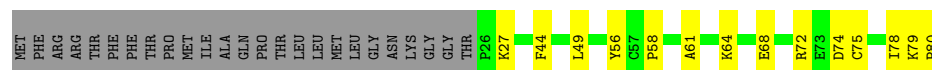
- Molecule 3: uL29m



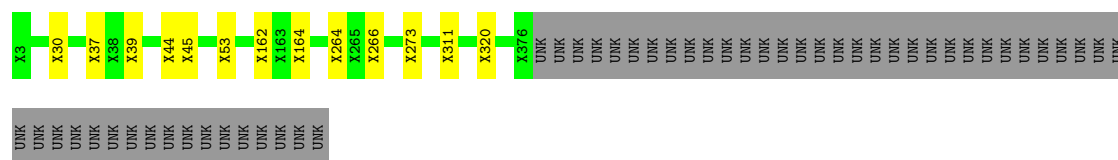
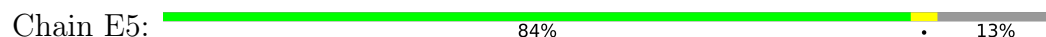
- Molecule 7: mt-LAF24



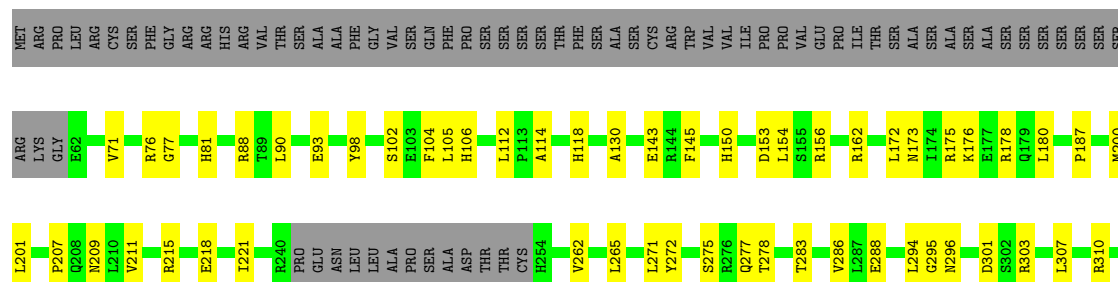
- Molecule 8: bL32m



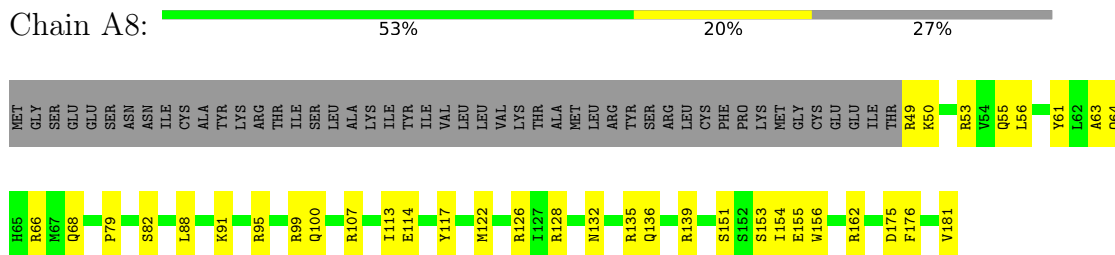
- Molecule 9: mt-LAF25



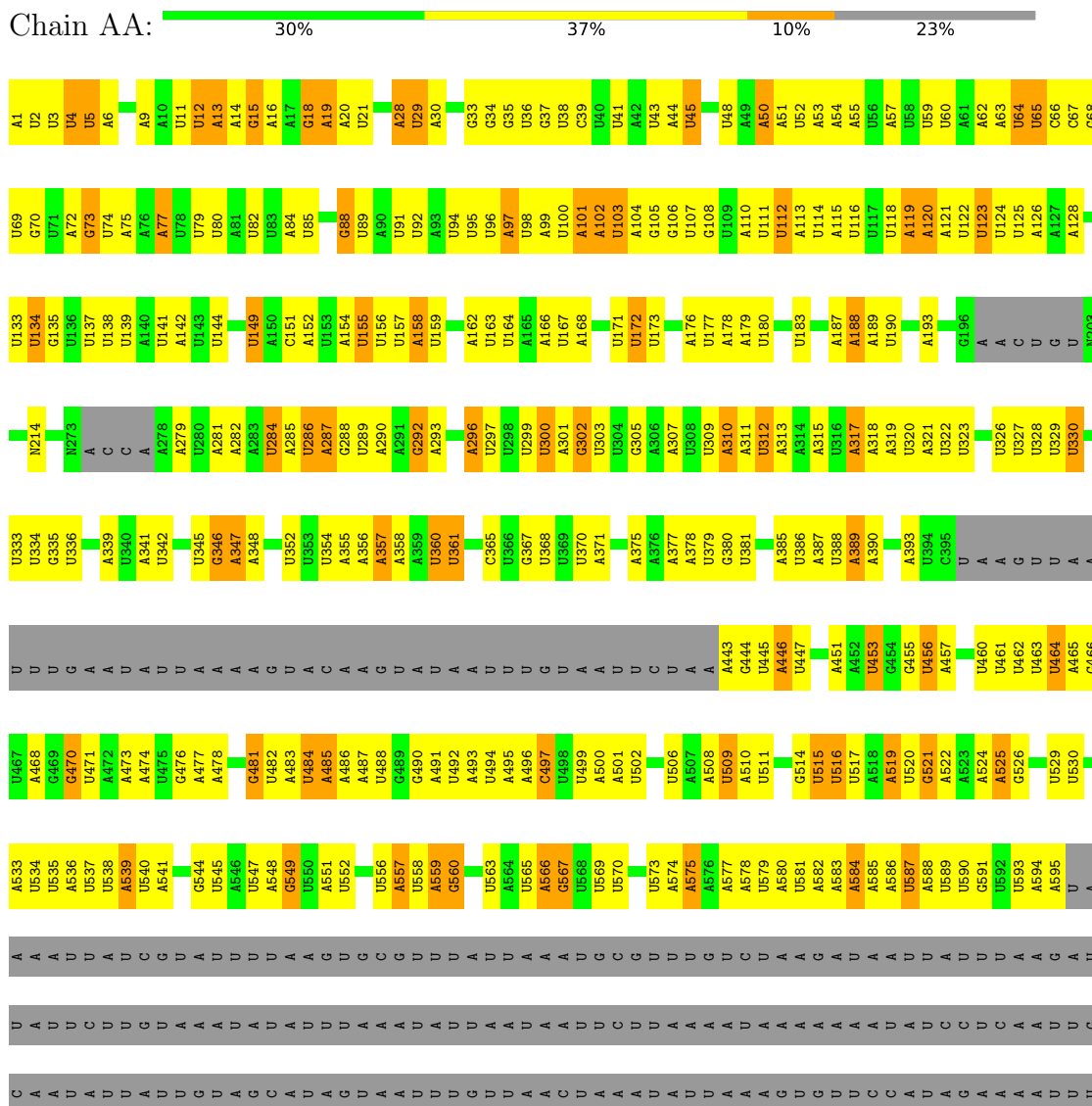
- Molecule 10: KRIPP3



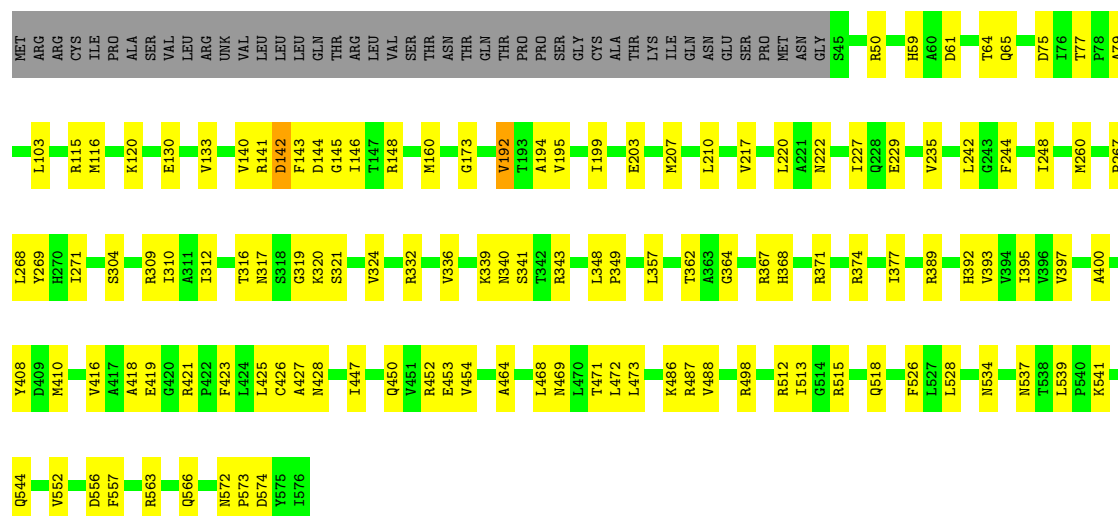
- Molecule 11: bL35m



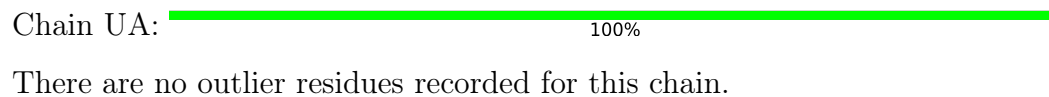
- Molecule 12: 12S ribosomal RNA



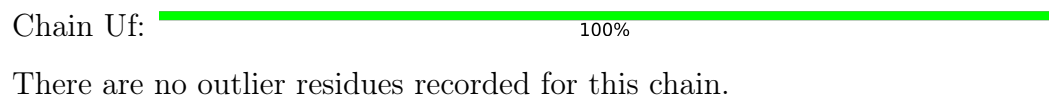




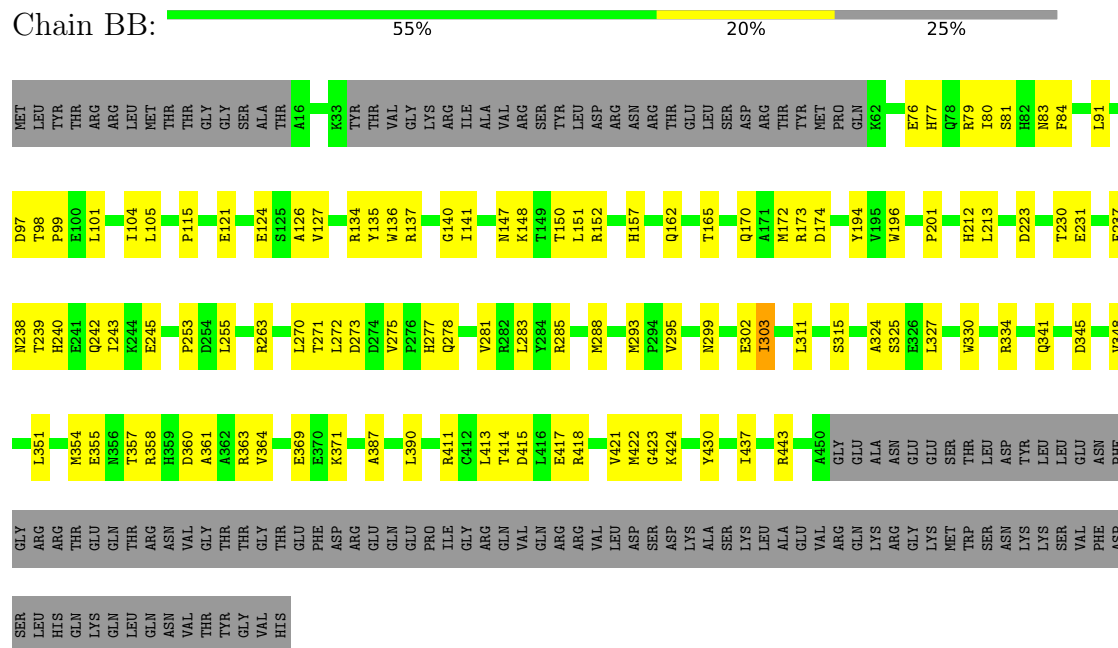
- Molecule 15: UNK



- Molecule 15: UNK



- Molecule 16: mL68



- Molecule 17: DEAD-box helicase, putative

Category	Percentage
Very bad	69%
Bad	14%
Good	17%



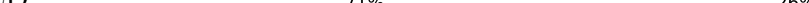
Response	Percentage
Yes, the U.S. is a democracy	73%
No, the U.S. is not a democracy	19%
Don't know	8%

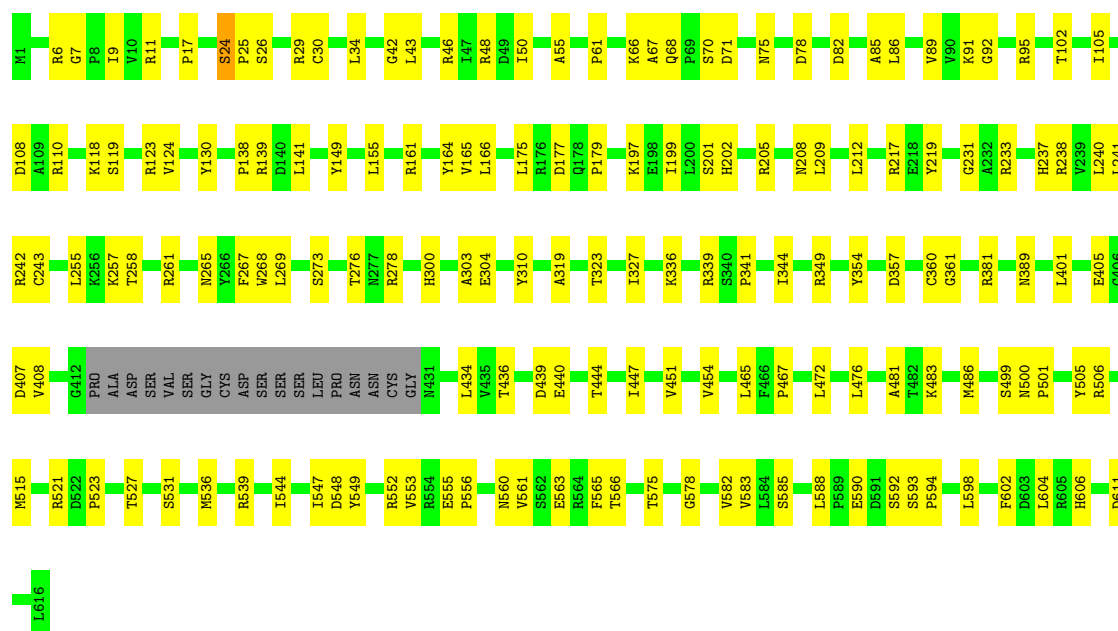


Category	Percentage
Very bad	57%
Bad	20%
Good	23%

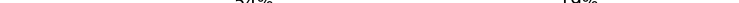


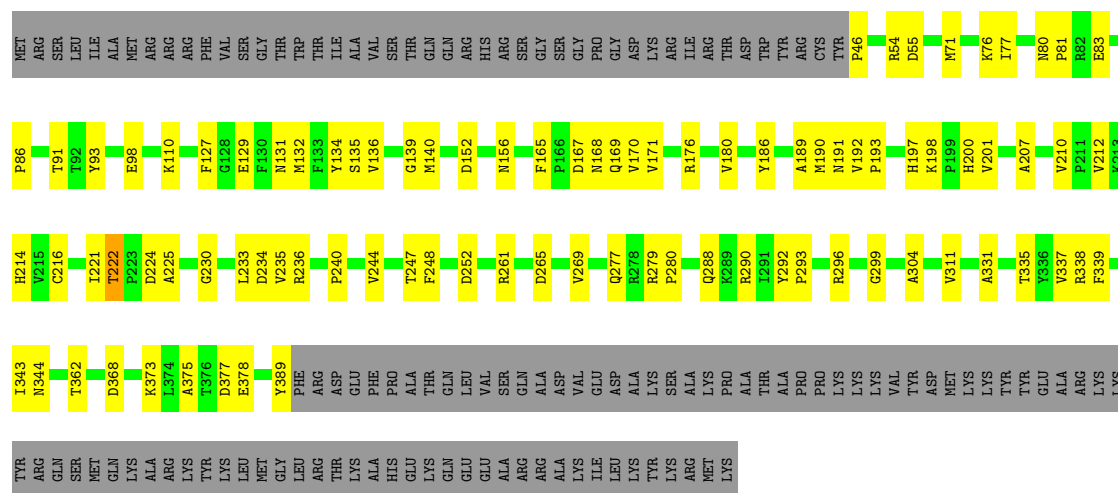
- Molecule 20: mt-LAF4

Chain ED: 

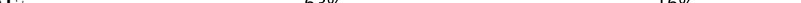


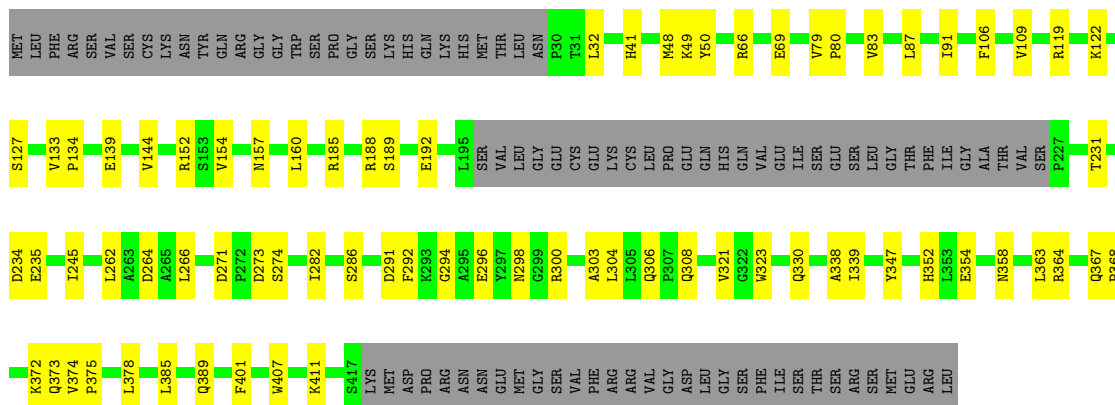
- Molecule 21: Ribosomal protein L3 mitochondrial, putative

Chain AE: 

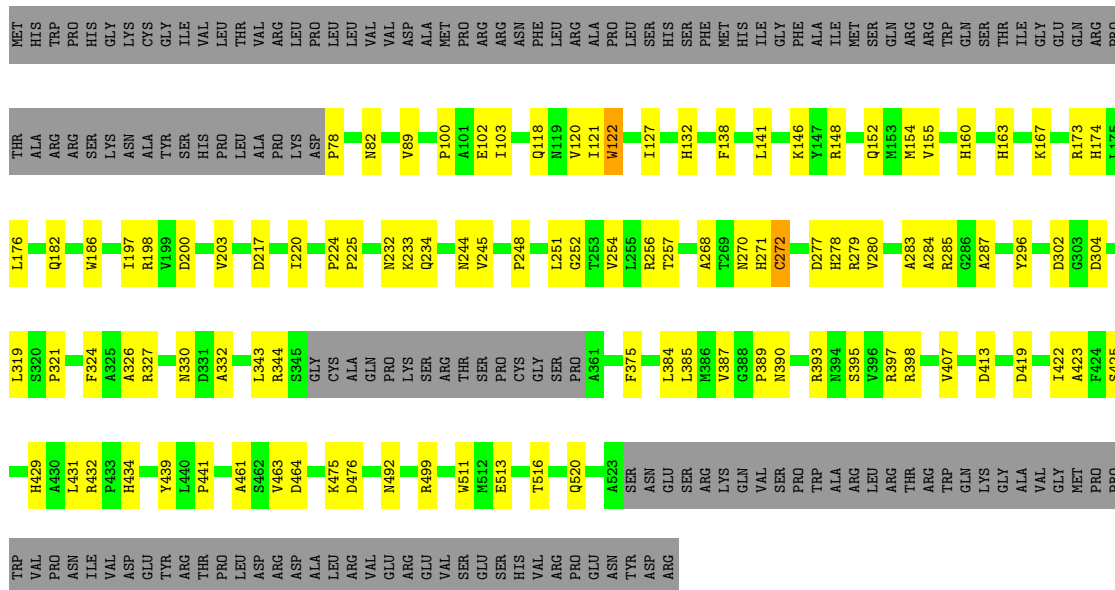


- Molecule 22: mL71

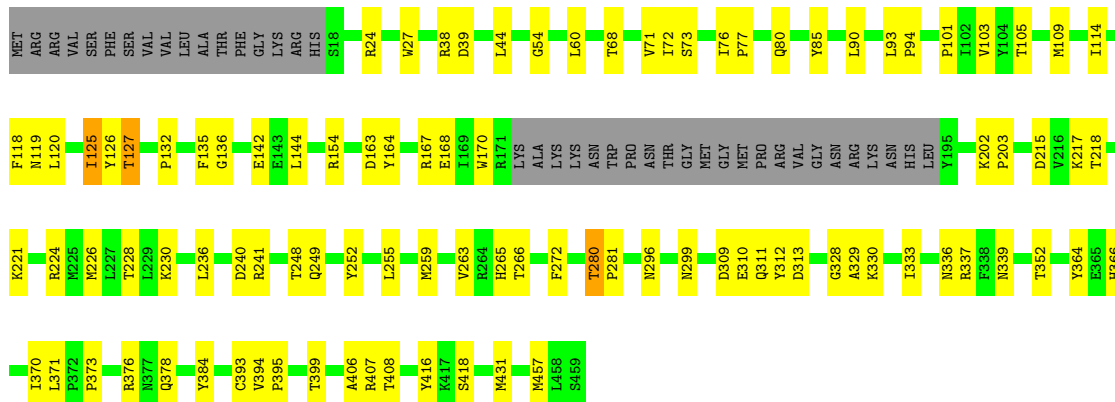
Chain BE: 



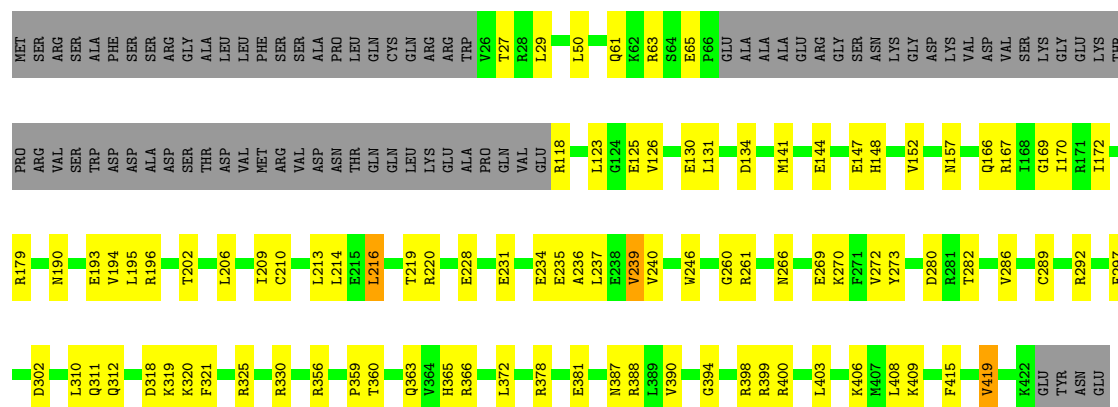
- Molecule 23: SpoU methylase domain-containing protein



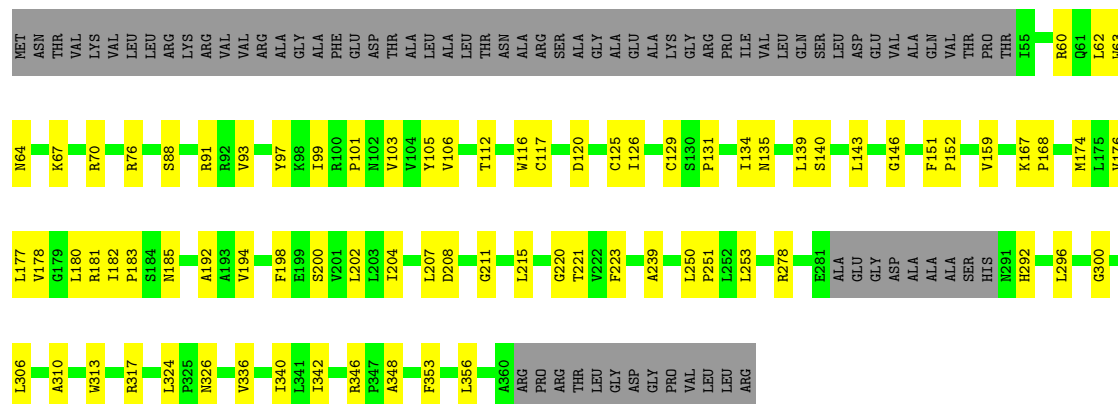
- Molecule 24: Ribosomal protein L4/L1 family, putative



Chain BF: 59% 21% • 19%



Chain EF:

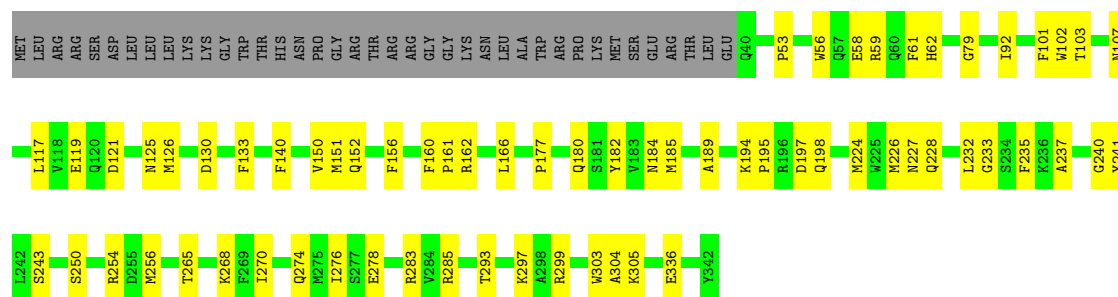


Chain EG: 74% 24%



Chain BH:





- Molecule 32: UNK

Chain UI: 95% 5%



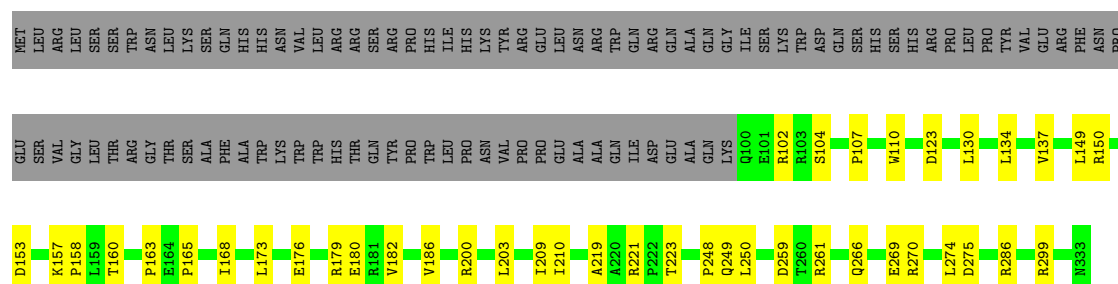
- Molecule 32: UNK

Chain Ur: 95% 5%



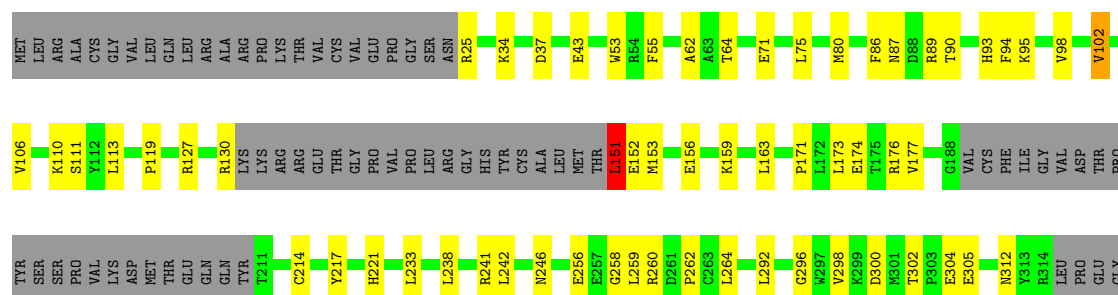
- Molecule 33: mL76

Chain BJ: 58% 13% 30%



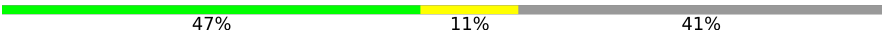
- Molecule 34: Ribosomal protein L11, putative

Chain AK: 55% 17% 27%



GLU
LYS
ARG
LYS
GLN
MET
ASP
GLU
UNK
UNK
MET
ALA
SER
GLY
GLU
VAL
TYR
TRP
THR
ASP
GLY
GLN
LEU

• Molecule 35: Chaperone protein DNAj, putative

Chain BK:  47% 11% 41%

MET TYR PHE ARG PHE HIS ILE SER PHE HIS SER PHE VAL ASN PHE LEU GLN PRO ARG GLY VAL GLY GLU PRO SER ARG LEU UNK HIS LEU THR HIS PRO SER TYR MET ARG ARG VAL THR SER THR ARG VAL SER VAL SER UNK

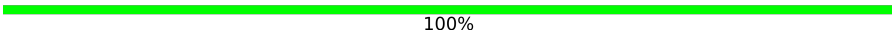
ALA LEU PRO SER PHE ASN GLY THR LEU LEU SER VAL CYS VAL ALA SER CYS SER PRO ARG ALA PRO V84 L87 R90 L91 G92 L93 A97 R109 H14 V17 Y137 D138 Y139 L140 I141 L155 E156 ARG THR VAL HIS ARG PRO THR VAL LYS GLN GLU GLY

GLU GLY VAL CYS ASP SER LYS GLY SER PHE ASN ARG GLY VAL THR PHE THR ARG PRO ARG H188 R189 K190 V193 R194 G195 E203 M208 Q212 V213 R216 K233 GLU ASP ASP GLY SER PRO ALA ARG GLU SER ILE ARG VAL VAL ALA ALA ALA GLU

ARG PHE ALA GLU LYS VAL ARG GLN TYR GLY PRO GLY MET LEU PHE HIS ALA ARG VAL T278 P284 Y291 R295 T301 V302 P303 V306 R307 E311 L328 R340 K344 V348 V349 D353 S356 L357 L358 R359 I363 P373 K376

L379 Y380 S381 R384 P385 Y386

• Molecule 36: UNK

Chain UK:  100%

There are no outlier residues recorded for this chain.

• Molecule 37: mL78

Chain BL:  66% 17% 17%

MET GLY ALA SER GLY LEU ILE ARG ARG GLY GLY VAL PHE PRO ASP VAL SER LEU LEU THR PRO SER ARG ARG V31 G36 L41 Y42 E43 D46 S51 G52 R53 A54 L55 A67 T68 M69 P70 E71 S72 G73 Q74 R78 K79 N103 Y104 S105

E116 I119 V140 T143 Q144 R147 R158 L165 E169 L177 L180 L181 R189 P195 T196 S197 VAL LEU THR SER ARG ALA GLY VAL VAL ALA GLY S216 M219 S220 C221 R226 A227 D228 S229 R230 N237 Q238 Y239

F240 D241 E244 R245 T250 T253 V254 L264 L285 A286 R287 D288 E289 V295 V304 A305 L306 GLN HIS ARG ILE PRO VAL PRO LYS

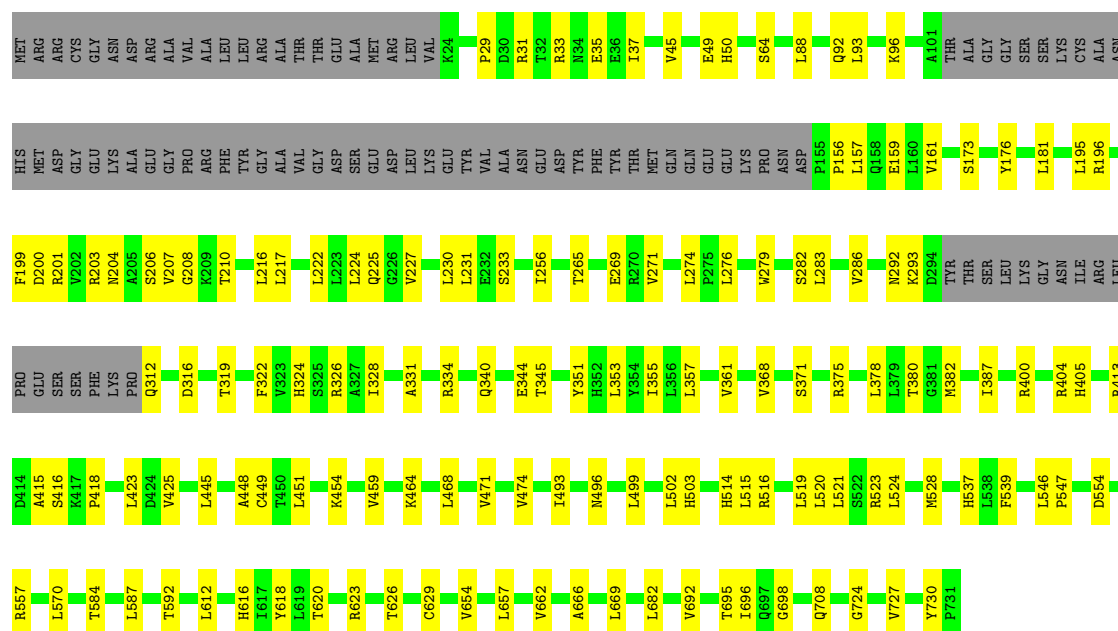
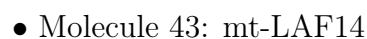
• Molecule 38: mt-LAF12

Chain EL:  58% 19% 23%

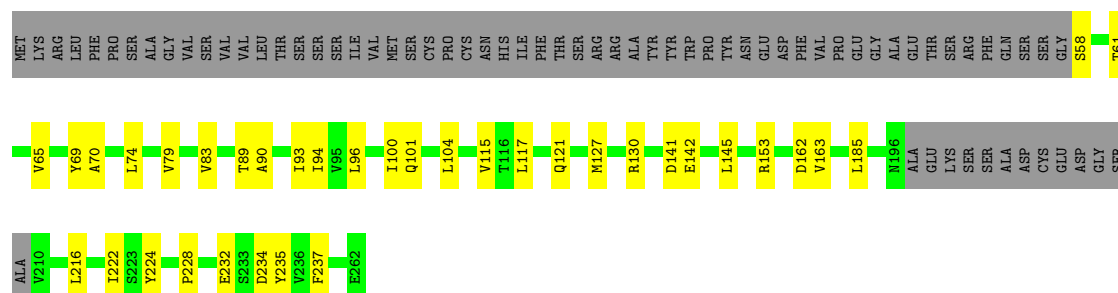
MET ARG ARG LEU PHE ILE THR THR ALA THR THR CYS HIS SER LEU THR CYS HIS SER LEU THR THR THR GLY ALA GLY LYS GLU SER THR PRO THR THR L123 W124 G125 S130 E131 D132 N133 K134 P135 P136 N151 SER GLU ASP ASP ASN MET ASP ASP GLU ALA ALA LEU VAL E61 T62 R70 T71 Y72 S73 T74 W75

V78 R83 E92 PRO SER SER SER SER GLY HIS MET GLU GLN UNK LEU GLU ASN ALU E110 H118 L123 W124 G125 S130 E131 D132 N133 K134 P135 P136 N151 SER GLU ASP ASP ASN MET ASP ASP GLU ALA ALA LEU VAL E61 T62 R70 T71 Y72 S73 T74 W75

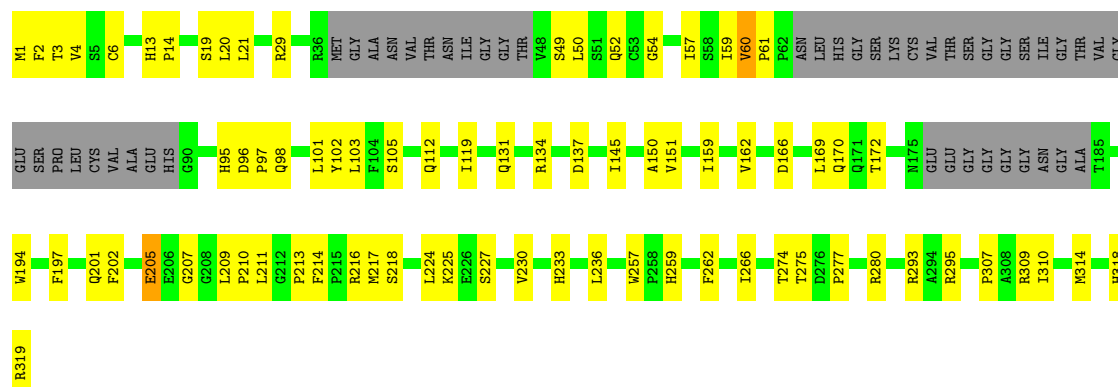
Chain BN:



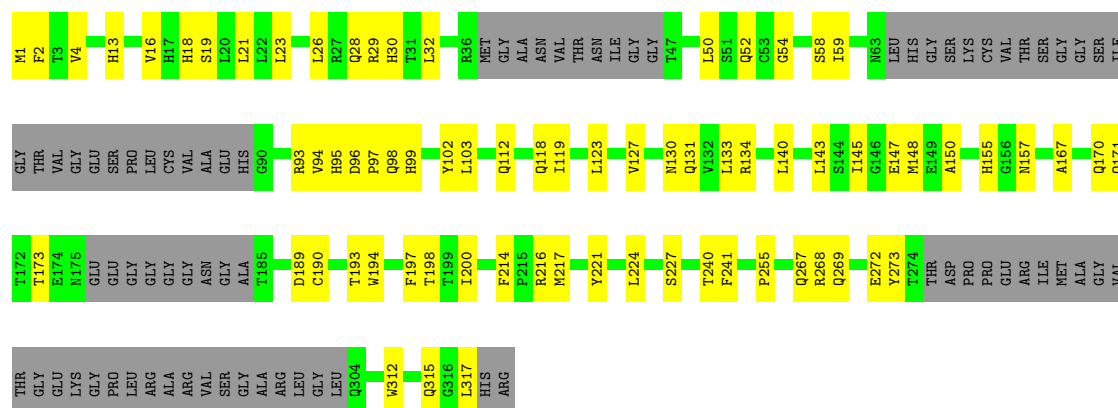
Chain BO: 60% 14% 27%



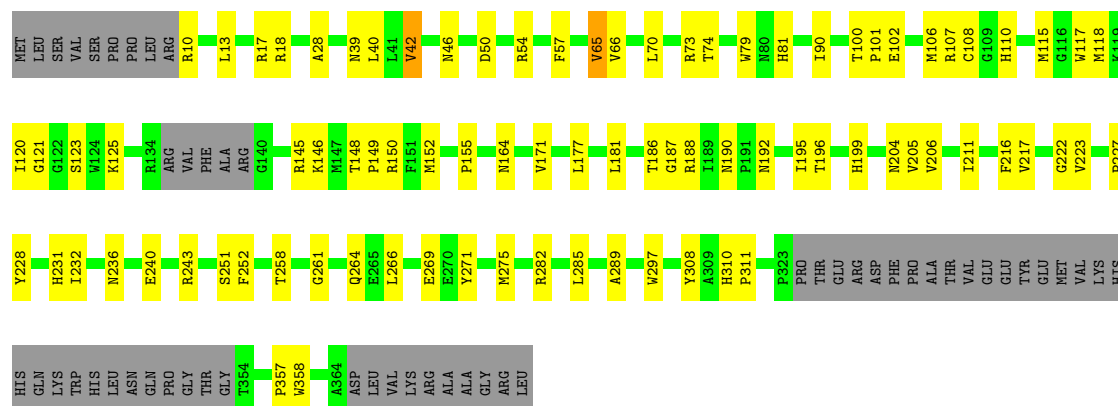
- Molecule 45: mt-LAF15a

Chain EO:  61% 24% 15%

- Molecule 45: mt-LAF15a

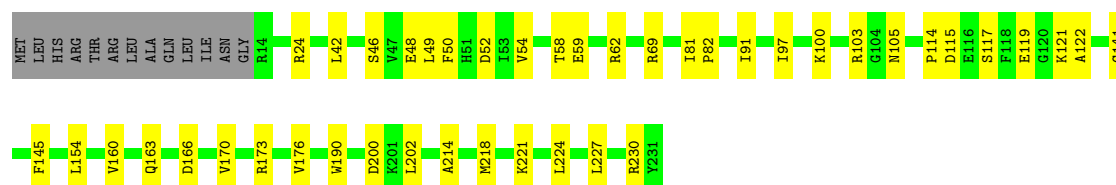
Chain EP:  53% 23% 24%

- Molecule 46: Ribosomal_L18e/L15P domain-containing protein

Chain AP:  63% 22% 14%

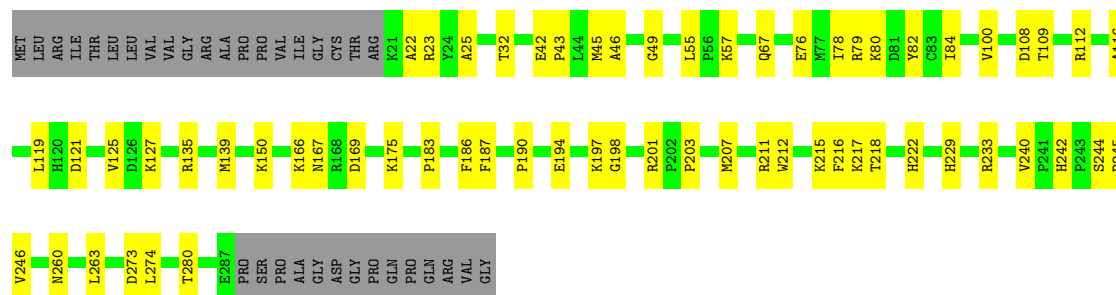
- Molecule 47: Peptidyl-prolyl cis-trans isomerase

Chain BQ: 



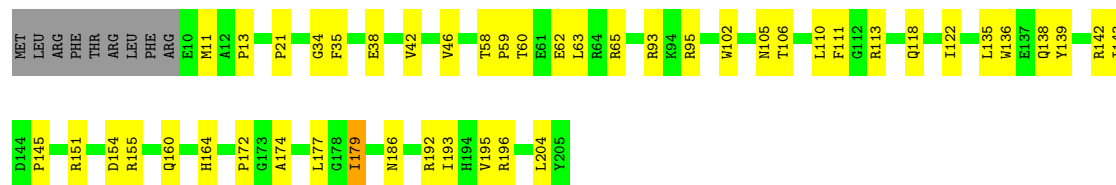
- Molecule 48: 50S ribosomal protein L17, putative

Chain AR: 



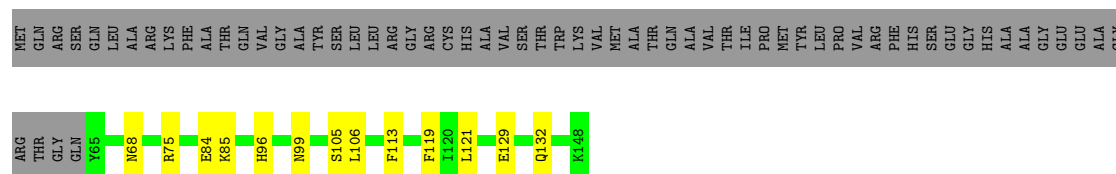
- Molecule 49: mL84

Chain BR: 



- Molecule 50: Acyl carrier protein

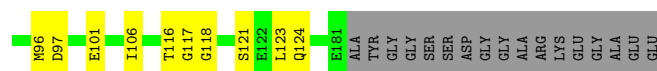
Chain ER: 



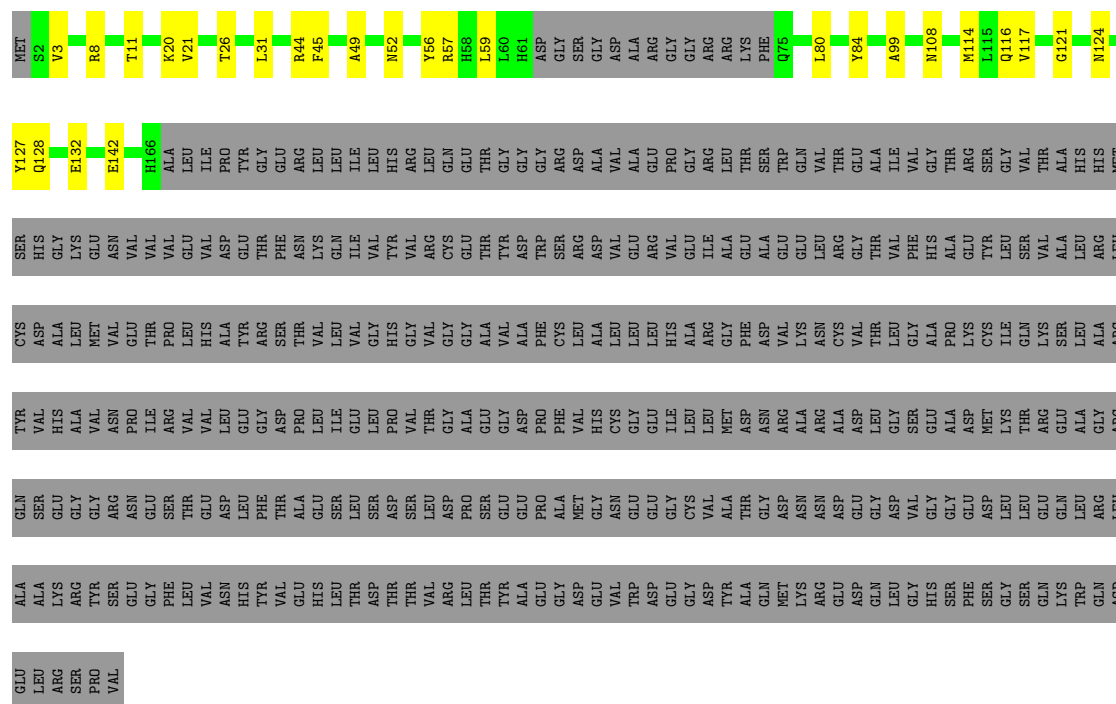
- Molecule 51: mL85

Chain BS: 

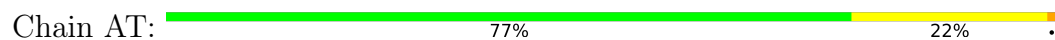




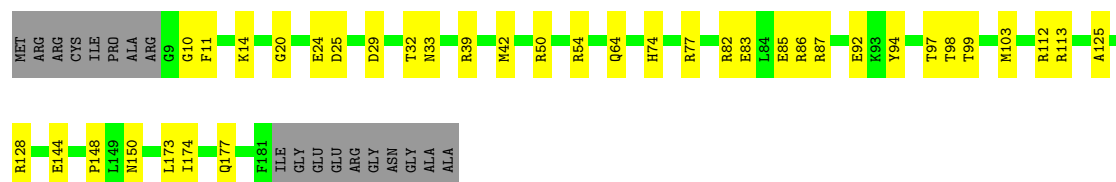
• Molecule 52: Lipase (Class 3)



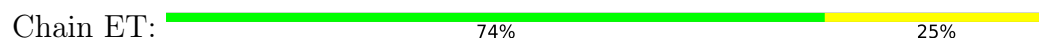
• Molecule 53: bL19m



• Molecule 54: mL86



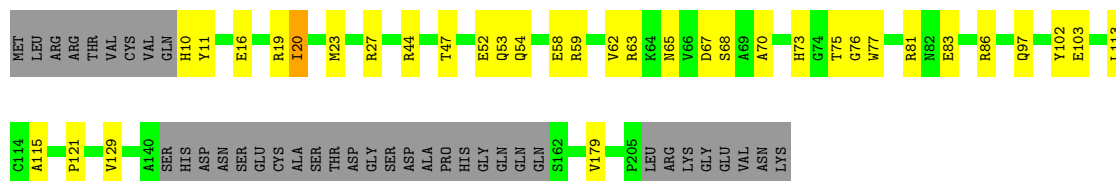
• Molecule 55: mt-LAF19





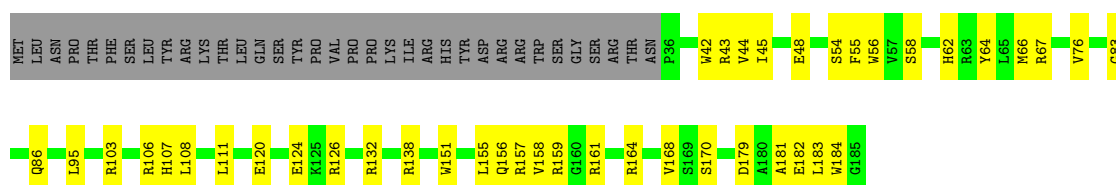
- Molecule 56: bL20m

Chain AU: 66% 16% 18%



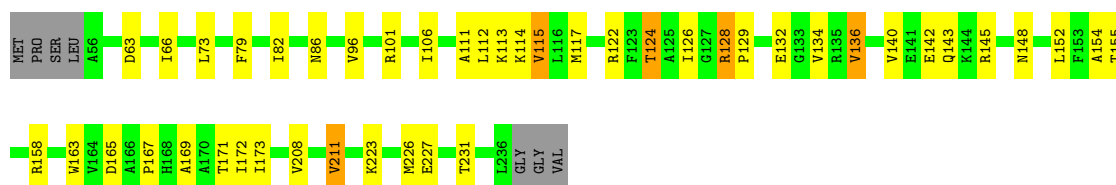
- Molecule 57: mL87

Chain BU: 58% 23% 19%



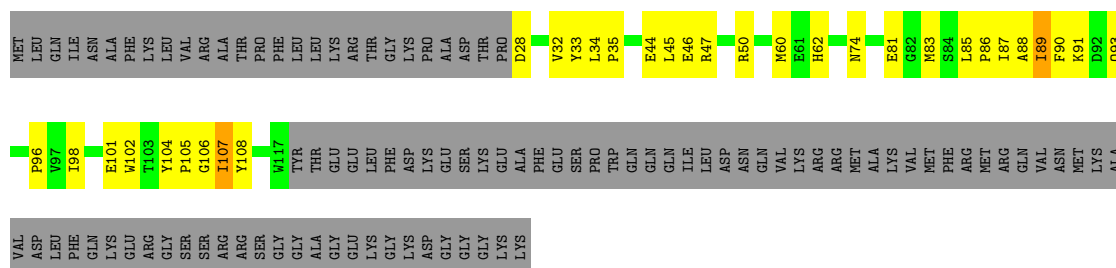
- Molecule 58: bL21m

Chain AV: 72% 21% 7%



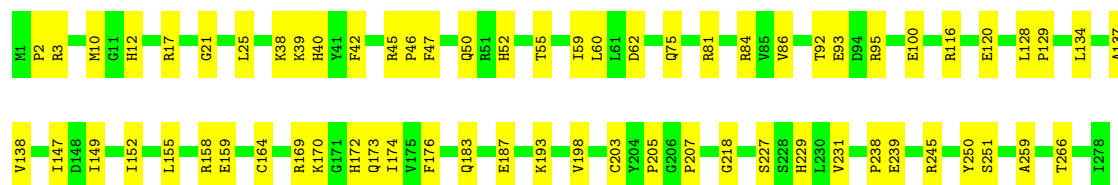
- Molecule 59: mL88

Chain BV: 31% 16% 53%



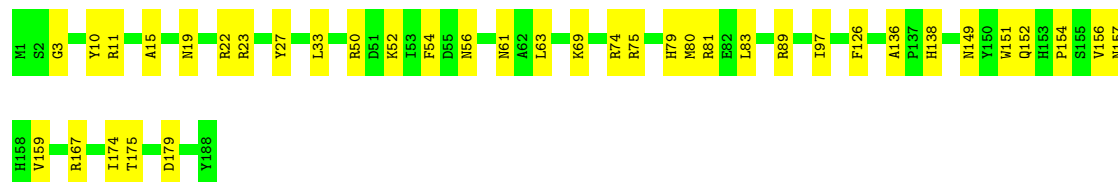
- Molecule 60: uL22m

Chain AW: 76% 24%



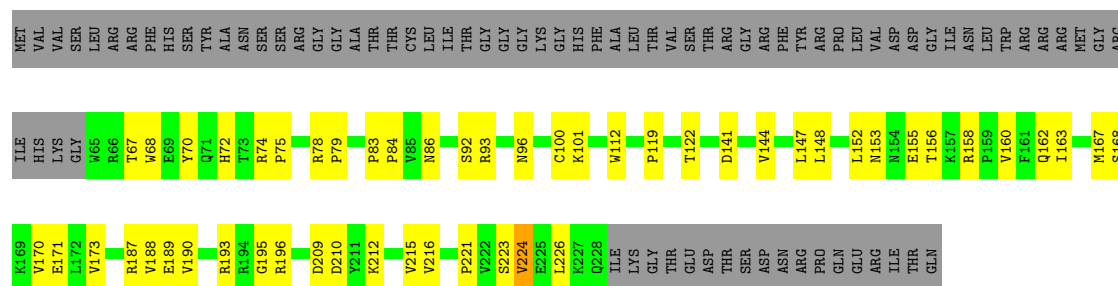
- Molecule 61: mL89

Chain BW: 80% 20%



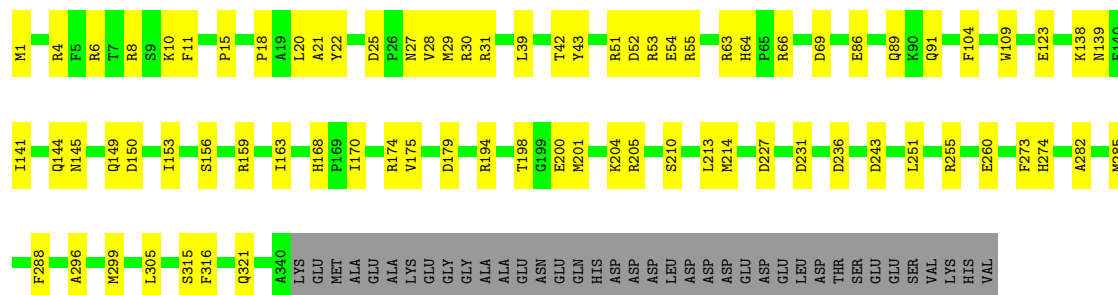
- Molecule 62: uL23m

Chain AX: 46% 21% 33%



- Molecule 63: uL24m

Chain AY: 69% 21% 10%



- Molecule 64: Peptidyl-prolyl cis-trans isomerase

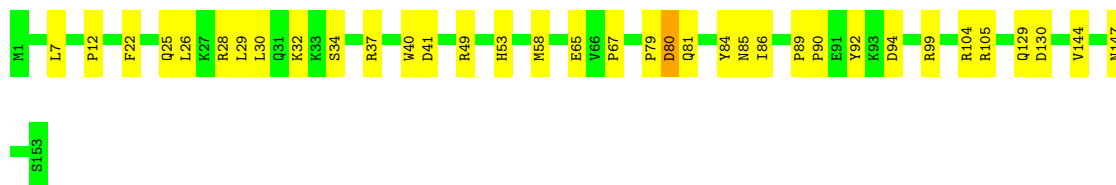
Chain BZ: 78% 21%





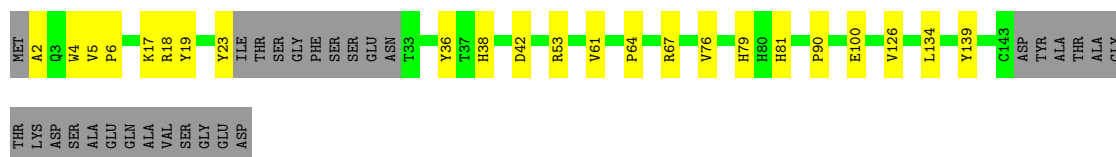
• Molecule 65: mL93

Chain Ba: 77% 22% .



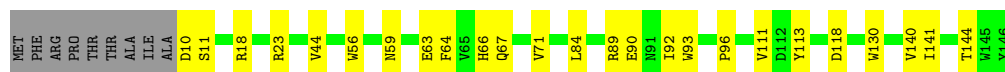
• Molecule 66: mL94

Chain Bb: 68% 14% 18%



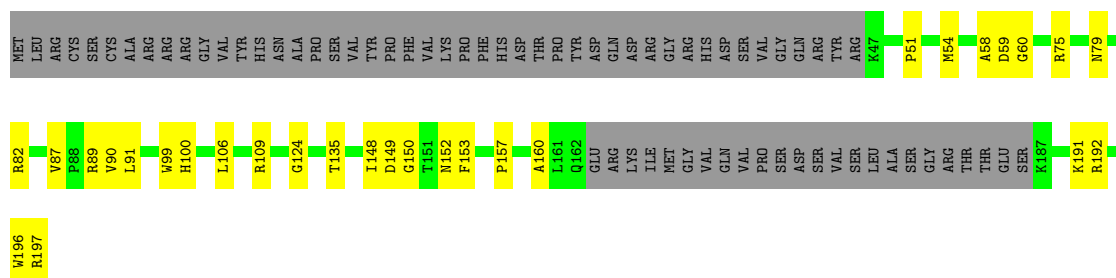
• Molecule 67: mL95

Chain Bc: 77% 17% 6%



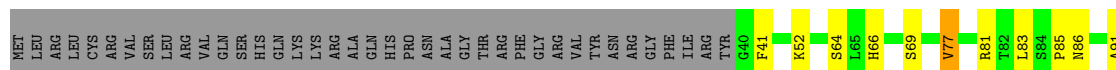
• Molecule 68: mL41

Chain Ae: 50% 15% 36%

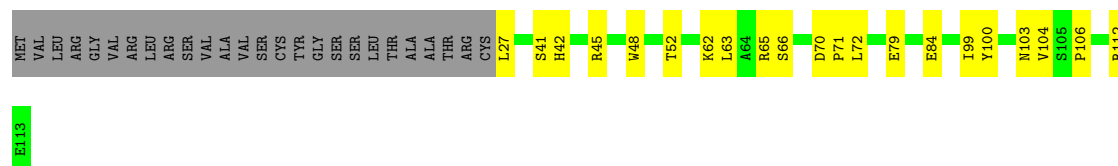


• Molecule 69: mL42

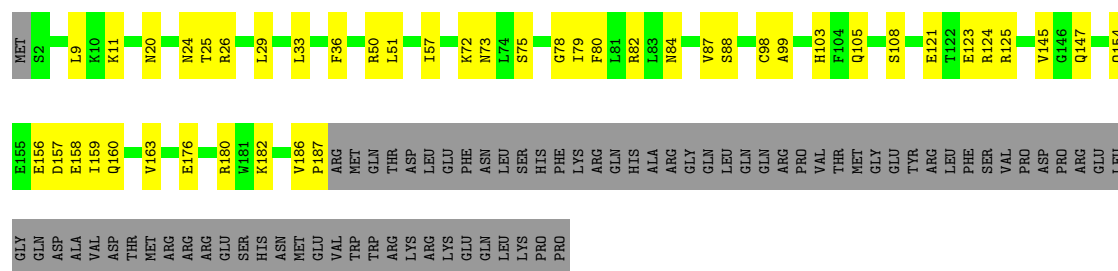
Chain Af: 61% 12% 26%



- Molecule 70: mL98



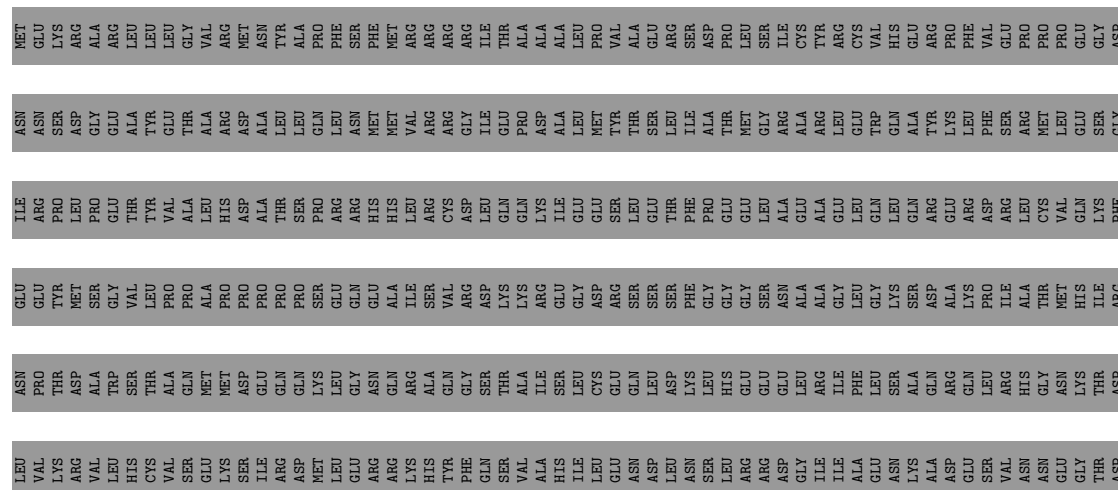
- Molecule 71: L51 S25 CI-B8 domain-containing protein

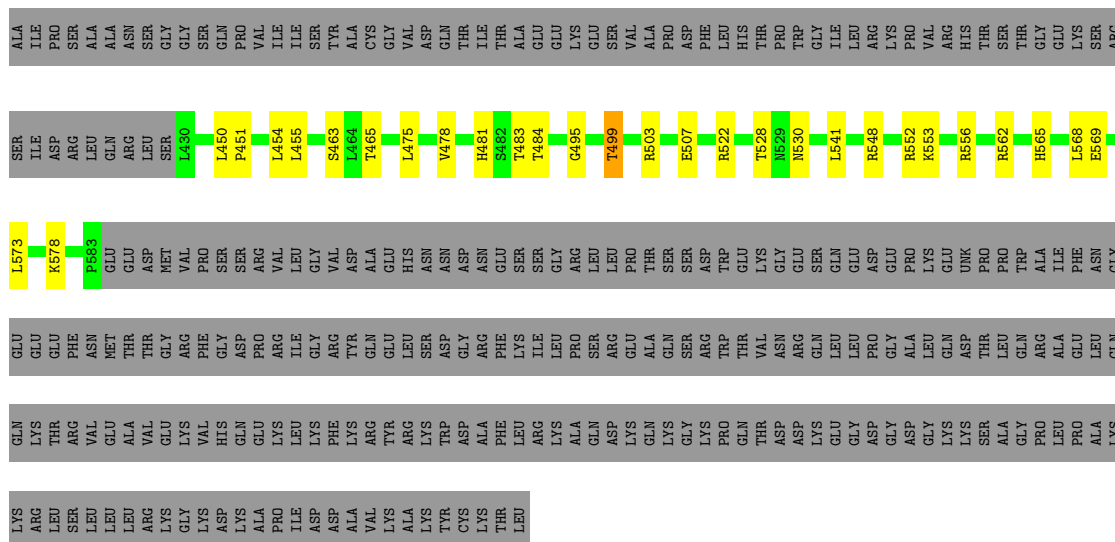


- Molecule 72: mt-LAF27

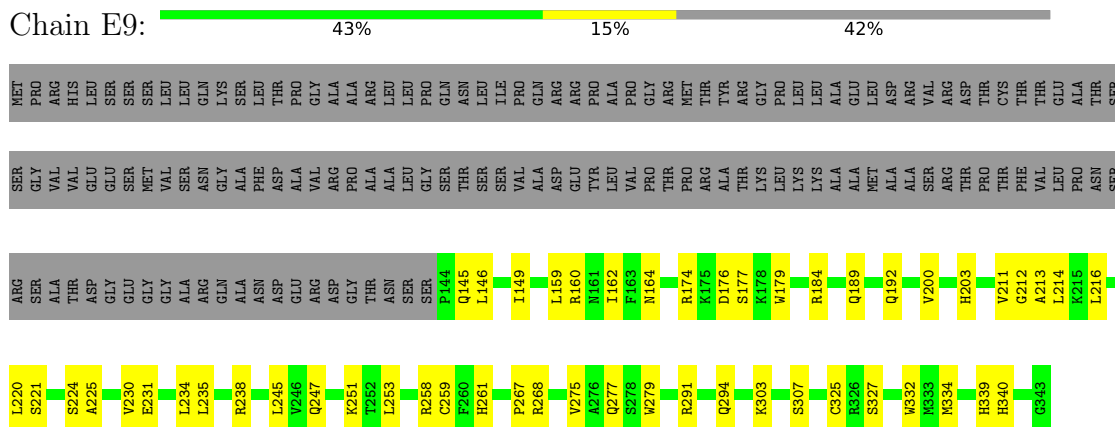


- Molecule 73: KRIPP9

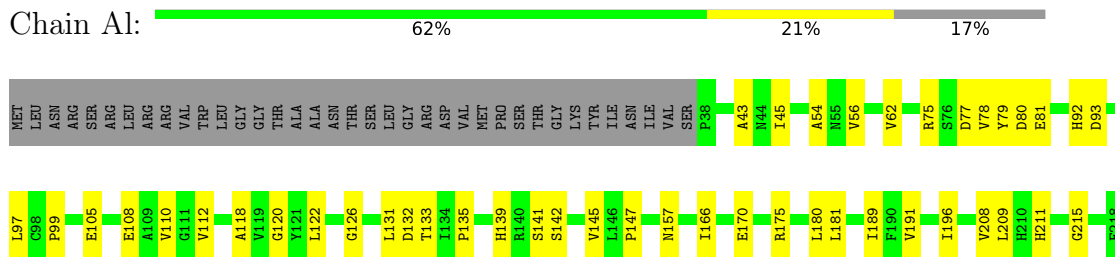




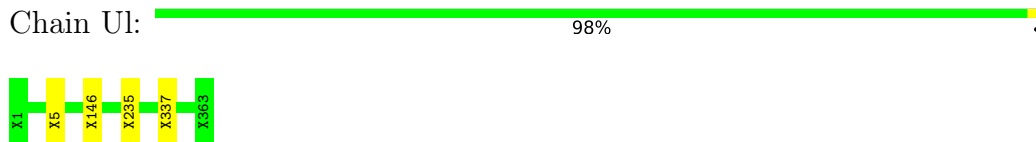
- Molecule 74: mt-LAF29



- Molecule 75: mL49



- Molecule 76: UNK



- Molecule 77: UNK

96%



-

100%

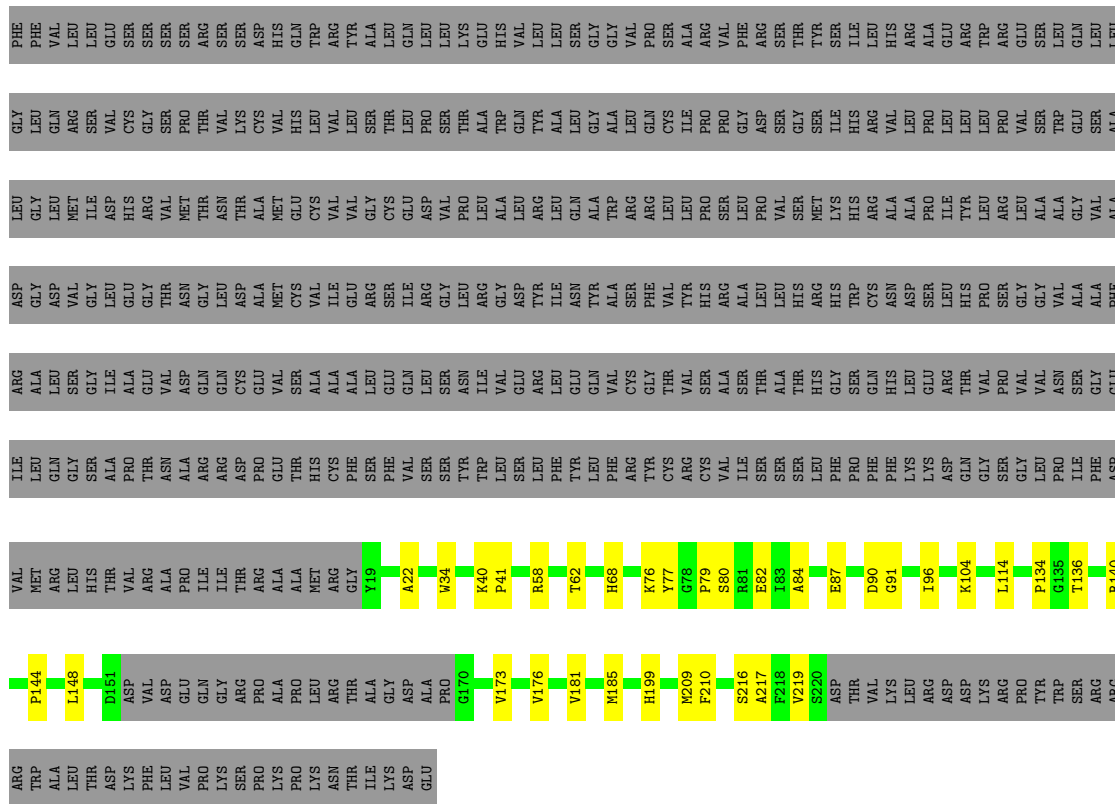
T

-

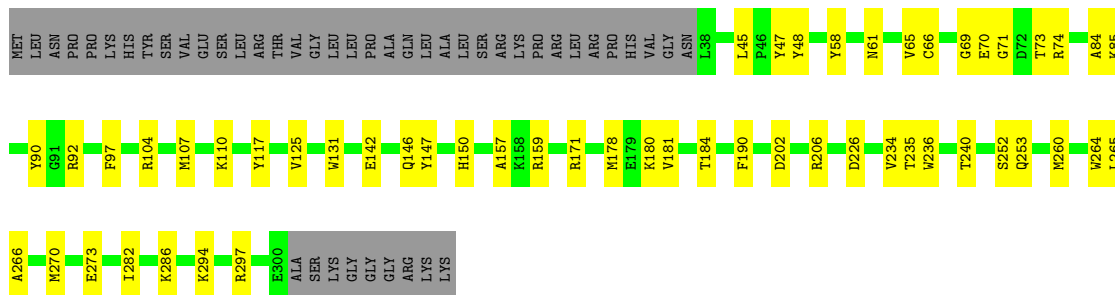
10%

88%

[illegible]



- Molecule 80: mL53



- Molecule 81: UNK



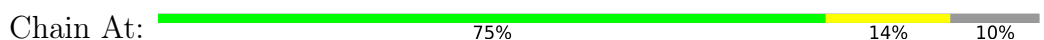
There are no outlier residues recorded for this chain.

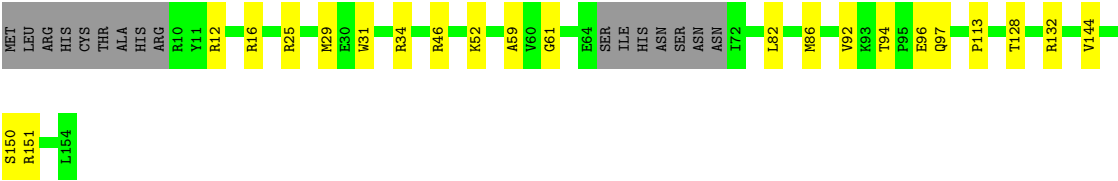
- Molecule 82: UNK



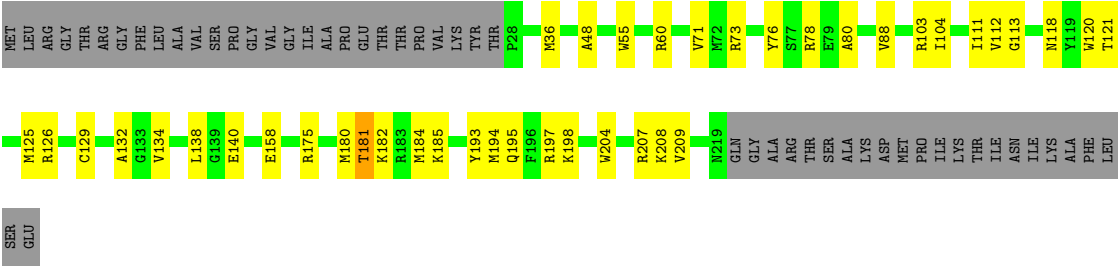
There are no outlier residues recorded for this chain.

- Molecule 83: mL63





• Molecule 84: mL64



SER
GLU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	16215	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 ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PM8, ZN, NA, ATP, MG, NAD, GTP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A1	0.10	0/1828	0.29	0/2466
2	E1	0.11	0/3906	0.32	1/5236 (0.0%)
3	A2	0.11	0/3844	0.27	0/5234
4	E2	0.09	0/3000	0.27	0/4067
5	A3	0.12	0/1246	0.29	0/1678
6	E3	0.09	0/3331	0.26	0/4491
7	E4	0.11	0/3491	0.33	1/4740 (0.0%)
8	A5	0.10	0/498	0.28	0/663
10	E6	0.10	0/3471	0.27	0/4710
11	A8	0.11	0/1163	0.31	0/1558
12	AA	0.09	0/19045	0.22	0/29609
13	BA	0.10	0/6192	0.27	0/8401
14	EA	0.09	0/4337	0.27	0/5856
16	BB	0.10	0/3411	0.28	0/4622
17	EB	0.09	0/5154	0.27	0/6977
18	EC	0.10	0/3090	0.26	0/4190
19	BD	0.11	0/3418	0.29	0/4629
20	ED	0.10	0/4877	0.28	0/6607
21	AE	0.10	0/2897	0.28	0/3938
22	BE	0.10	0/2896	0.26	0/3929
23	EE	0.10	0/3489	0.33	1/4722 (0.0%)
24	AF	0.10	0/3517	0.26	0/4775
25	BF	0.11	0/2909	0.31	0/3920
26	EF	0.10	0/2316	0.29	0/3148
27	EG	0.11	0/1331	0.28	0/1784
28	BH	0.09	0/2005	0.28	0/2734
29	EH	0.10	0/3586	0.28	0/4864
30	AI	0.09	0/1980	0.27	0/2693
31	BI	0.10	0/2548	0.25	0/3449
33	BJ	0.10	0/1985	0.28	0/2681
34	AK	0.23	0/2141	0.38	1/2886 (0.0%)
35	BK	0.10	0/1897	0.27	0/2556

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
37	BL	0.11	0/2055	0.29	0/2782
38	EL	0.09	0/4384	0.26	0/5967
39	EM	0.09	0/2480	0.26	0/3352
41	AN	0.10	0/1698	0.28	0/2308
42	BN	0.10	0/1353	0.29	0/1827
43	EN	0.10	0/5115	0.27	0/6936
44	BO	0.09	0/1518	0.27	0/2051
45	EO	0.11	0/2173	0.30	0/2956
45	EP	0.10	0/1953	0.27	0/2659
46	AP	0.10	0/2695	0.26	0/3657
47	BQ	0.09	0/1691	0.25	0/2293
48	AR	0.11	0/2279	0.30	0/3079
49	BR	0.10	0/1702	0.29	0/2296
50	ER	0.07	0/679	0.23	0/923
51	BS	0.12	0/1131	0.26	0/1547
52	ES	0.10	0/1276	0.27	0/1715
53	AT	0.10	0/1210	0.29	0/1632
54	BT	0.11	0/1465	0.28	0/1970
55	ET	0.10	0/858	0.29	0/1148
56	AU	0.11	0/1456	0.30	0/1971
57	BU	0.11	0/1315	0.30	0/1776
58	AV	0.10	0/1454	0.30	0/1973
59	BV	0.30	0/786	0.49	1/1063 (0.1%)
60	AW	0.11	0/2307	0.28	0/3119
61	BW	0.11	0/1612	0.28	0/2177
62	AX	0.11	0/1432	0.29	0/1947
63	AY	0.10	0/2846	0.27	0/3847
64	BZ	0.09	0/1422	0.25	0/1925
65	Ba	0.11	0/1329	0.37	1/1798 (0.1%)
66	Bb	0.09	0/1073	0.28	0/1454
67	Bc	0.09	0/1238	0.28	0/1685
68	Ae	0.10	0/1068	0.29	0/1447
69	Af	0.09	0/1134	0.25	0/1536
70	Bf	0.10	0/749	0.35	0/1012
71	Ag	0.11	0/1608	0.31	0/2180
72	E7	0.10	0/834	0.31	0/1118
73	E8	0.13	0/1202	0.31	0/1631
74	E9	0.09	0/1678	0.27	0/2257
75	Al	0.10	0/1484	0.26	0/2019
79	Ao	0.10	0/1486	0.26	0/2022
80	Ap	0.09	0/2231	0.25	0/3030
83	At	0.11	0/1179	0.32	0/1596
84	Av	0.10	0/1678	0.27	0/2261

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.10	0/183115	0.28	6/251755 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	BV	89	ILE	N-CA-C	-7.32	106.36	113.53
65	Ba	12	PRO	N-CA-CB	7.19	110.15	103.46
23	EE	441	PRO	N-CA-CB	7.13	110.73	103.25
2	E1	96	PRO	N-CA-CB	6.48	110.56	103.23
7	E4	203	PRO	N-CA-CB	6.26	110.15	103.52
34	AK	151	LEU	CA-CB-CG	-5.22	98.02	116.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	1788	0	1814	39	0
2	E1	3836	0	3800	88	0
3	A2	3739	0	3689	66	0
4	E2	2933	0	2932	53	0
5	A3	1226	0	1282	38	0
6	E3	3266	0	3290	58	0
7	E4	3418	0	3384	84	0
8	A5	483	0	493	12	0
9	E5	1635	0	352	8	0
10	E6	3405	0	3405	76	0
11	A8	1136	0	1158	32	0
12	AA	18187	0	9203	387	0
13	BA	6059	0	6053	136	0
14	EA	4263	0	4306	91	0
15	UA	50	0	14	0	0
15	Uf	50	0	14	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	BB	3322	0	3244	80	0
17	EB	5039	0	5133	77	0
18	EC	3005	0	3010	52	0
19	BD	3349	0	3368	74	0
20	ED	4764	0	4771	98	0
21	AE	2802	0	2661	69	0
22	BE	2822	0	2754	48	0
23	EE	3423	0	3367	81	0
24	AF	3414	0	3316	76	0
25	BF	2847	0	2832	74	0
26	EF	2268	0	2299	50	0
27	EG	1295	0	1250	37	0
28	BH	1948	0	1910	36	0
29	EH	3508	0	3531	71	0
30	AI	1967	0	1887	44	0
31	BI	2475	0	2403	47	0
32	UI	105	0	23	1	0
32	Ur	105	0	23	1	0
33	BJ	1944	0	1922	26	0
34	AK	2088	0	2105	75	0
35	BK	1855	0	1827	29	0
36	UK	125	0	27	0	0
37	BL	2014	0	1903	38	0
38	EL	4259	0	4207	91	0
39	EM	2432	0	2465	55	0
40	UM	40	0	10	1	0
41	AN	1639	0	1612	30	0
42	BN	1320	0	1281	35	0
43	EN	5025	0	5101	92	0
44	BO	1498	0	1512	26	0
45	EO	2126	0	2134	57	0
45	EP	1911	0	1904	50	0
46	AP	2615	0	2546	74	0
47	BQ	1651	0	1571	28	0
48	AR	2214	0	2110	54	0
49	BR	1659	0	1638	33	0
50	ER	669	0	663	10	0
51	BS	1120	0	959	26	0
52	ES	1259	0	1265	22	0
53	AT	1180	0	1170	27	0
54	BT	1435	0	1397	39	0
55	ET	839	0	858	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	AU	1423	0	1447	38	0
57	BU	1275	0	1246	39	0
58	AV	1424	0	1457	40	0
59	BV	763	0	747	55	0
60	AW	2251	0	2292	61	0
61	BW	1565	0	1529	28	0
62	AX	1387	0	1364	44	0
63	AY	2790	0	2726	66	0
64	BZ	1396	0	1369	28	0
65	Ba	1287	0	1193	42	0
66	Bb	1048	0	1045	17	0
67	Bc	1194	0	1169	18	0
68	Ae	1031	0	1024	22	0
69	Af	1107	0	1087	25	0
70	Bf	725	0	687	17	0
71	Ag	1564	0	1507	41	0
72	E7	815	0	821	27	0
73	E8	1181	0	1122	26	0
74	E9	1642	0	1660	41	0
75	Al	1440	0	1448	32	0
76	Ul	1190	0	266	2	0
77	Um	135	0	32	1	0
78	Un	140	0	34	0	0
79	Ao	1443	0	1376	33	0
80	Ap	2161	0	2141	44	0
81	Up	435	0	95	0	0
82	Us	395	0	89	0	0
83	At	1149	0	1164	17	0
84	Av	1633	0	1611	32	0
85	A5	1	0	0	0	0
85	E2	4	0	0	0	0
85	E9	1	0	0	0	0
85	EG	1	0	0	0	0
86	A8	2	0	0	0	0
86	AA	12	0	0	0	0
86	EA	2	0	0	0	0
86	EB	1	0	0	0	0
87	EA	64	0	24	5	0
88	EA	2	0	0	0	0
89	EB	31	0	12	3	0
90	ER	32	0	39	5	0
91	Av	44	0	26	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
92	EA	4	0	0	0	0
92	EB	4	0	0	0	0
All	All	183043	0	169007	3098	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 9.

All (3098) 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)
34:AK:127:ARG:HH21	59:BV:86:PRO:HB2	1.34	0.91
34:AK:217:TYR:CE1	59:BV:102:TRP:HB2	2.06	0.90
34:AK:221:HIS:ND1	59:BV:105:PRO:HA	1.89	0.88
12:AA:586:A:H61	48:AR:22:ALA:H	1.24	0.84
34:AK:174:GLU:OE2	59:BV:105:PRO:HB2	1.77	0.84
23:EE:244:ASN:HD22	23:EE:271:HIS:HB2	1.41	0.83
12:AA:393:A:H2	12:AA:444:G:H1	1.26	0.83
25:BF:213:LEU:HD11	25:BF:236:ALA:HB2	1.58	0.83
27:EG:67:PHE:HB2	27:EG:74:VAL:HG11	1.61	0.83
12:AA:588:A:H5''	74:E9:258:ARG:HG3	1.61	0.82
11:A8:162:ARG:HH21	12:AA:72:A:H2'	1.46	0.80
19:BD:427:SER:HG	19:BD:430:THR:HG1	1.30	0.79
90:ER:200:PM8:H382	52:ES:52:ASN:HB2	1.66	0.78
39:EM:279:VAL:HB	39:EM:282:HIS:HB3	1.66	0.78
12:AA:823:U:H5''	27:EG:51:SER:HB3	1.65	0.77
21:AE:304:ALA:HB1	74:E9:303:LYS:HE3	1.68	0.76
34:AK:152:GLU:HG3	59:BV:98:ILE:HG23	1.68	0.76
59:BV:81:GLU:HA	59:BV:98:ILE:HG22	1.68	0.76
26:EF:178:VAL:HG12	26:EF:204:ILE:HB	1.67	0.75
3:A2:190:GLN:HG2	3:A2:194:GLN:HE22	1.52	0.75
14:EA:227:ILE:HD13	14:EA:235:VAL:HG11	1.68	0.75
41:AN:121:MET:HE2	41:AN:128:MET:HB3	1.66	0.75
33:BJ:269:GLU:HG3	33:BJ:274:LEU:HB2	1.70	0.74
56:AU:83:GLU:HG3	69:Af:77:VAL:HG12	1.68	0.74
13:BA:532:MET:SD	13:BA:576:ASN:ND2	2.60	0.74
68:Ae:124:GLY:HA2	68:Ae:135:THR:HG22	1.70	0.74
34:AK:37:ASP:O	34:AK:89:ARG:NH2	2.21	0.74
2:E1:61:LYS:HD2	2:E1:119:GLY:HA3	1.70	0.74
3:A2:132:PRO:HB2	3:A2:360:PRO:HB2	1.69	0.74
70:Bf:103:ASN:OD1	70:Bf:112:ARG:NH1	2.21	0.74
30:AI:193:ARG:HH12	30:AI:200:LYS:HE3	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:EA:115:ARG:HH11	14:EA:194:ALA:HB3	1.53	0.73
20:ED:257:LYS:HE2	20:ED:261:ARG:HD3	1.71	0.73
52:ES:31:LEU:HA	52:ES:116:GLN:HE22	1.53	0.73
7:E4:268:LEU:HD22	7:E4:297:ASN:HD22	1.53	0.73
35:BK:373:PRO:HG2	35:BK:376:MET:HB2	1.70	0.73
34:AK:156:GLU:OE1	59:BV:85:LEU:HD12	1.88	0.73
4:E2:371:CYS:SG	4:E2:374:CYS:HB2	2.28	0.73
62:AX:93:ARG:HA	65:Ba:25:GLN:HE22	1.54	0.73
6:E3:267:ARG:HD2	6:E3:315:VAL:HG21	1.72	0.72
18:EC:248:CYS:HA	18:EC:328:VAL:HA	1.71	0.72
71:Ag:20:ASN:ND2	71:Ag:51:LEU:O	2.23	0.72
23:EE:385:LEU:HD12	23:EE:431:LEU:HD12	1.72	0.72
14:EA:332:ARG:HG2	14:EA:348:LEU:HD21	1.70	0.72
16:BB:354:MET:O	16:BB:358:ARG:HB2	1.90	0.72
64:BZ:96:GLN:HB3	64:BZ:132:GLY:HA3	1.71	0.72
10:E6:324:ARG:HD3	10:E6:359:ASP:HB2	1.72	0.72
16:BB:341:GLN:O	16:BB:345:ASP:HB2	1.88	0.72
34:AK:152:GLU:HG2	59:BV:104:TYR:CE2	2.25	0.71
12:AA:301:A:N7	25:BF:266:ASN:ND2	2.33	0.71
12:AA:547:U:H4'	72:E7:77:SER:HB3	1.72	0.71
12:AA:377:A:OP2	56:AU:59:ARG:NH2	2.23	0.71
60:AW:39:LYS:HB2	63:AY:21:ALA:HB2	1.73	0.71
14:EA:207:MET:HE1	14:EA:242:LEU:HB3	1.72	0.71
16:BB:124:GLU:OE1	64:BZ:55:ARG:NH2	2.23	0.71
6:E3:257:LEU:HD12	6:E3:300:GLU:HG3	1.72	0.71
26:EF:300:GLY:HA3	26:EF:306:LEU:HD21	1.71	0.71
63:AY:86:GLU:H	63:AY:89:GLN:HE21	1.36	0.71
6:E3:414:ARG:HB3	6:E3:422:TYR:HB2	1.71	0.71
37:BL:51:SER:O	63:AY:27:ASN:ND2	2.24	0.71
13:BA:418:ASP:O	13:BA:423:ARG:NH2	2.24	0.70
34:AK:130:ARG:NH1	59:BV:28:ASP:OD1	2.23	0.70
2:E1:165:ASN:ND2	12:AA:559:A:O2'	2.24	0.70
2:E1:272:GLN:HG2	2:E1:274:LYS:HE3	1.72	0.70
17:EB:342:GLU:HG3	17:EB:343:ARG:HG3	1.72	0.70
28:BH:165:GLN:O	28:BH:241:ARG:NH1	2.25	0.70
80:Ap:181:VAL:HG12	80:Ap:234:VAL:HG12	1.72	0.70
12:AA:1094:U:H5''	72:E7:25:ARG:HH12	1.55	0.70
7:E4:193:LYS:HE3	7:E4:195:HIS:HB2	1.73	0.70
7:E4:287:LEU:HD11	7:E4:306:CYS:HB3	1.73	0.70
16:BB:141:ILE:HG12	16:BB:172:MET:HE2	1.73	0.70
16:BB:239:THR:H	16:BB:242:GLN:HE21	1.38	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:EB:184:PRO:HD2	17:EB:188:LEU:HD23	1.74	0.70
18:EC:168:ILE:HD11	18:EC:222:ARG:HE	1.56	0.70
24:AF:125:ILE:HB	54:BT:128:ARG:HH22	1.57	0.70
62:AX:155:GLU:HG2	62:AX:221:PRO:HB2	1.73	0.70
3:A2:58:ARG:NH2	62:AX:141:ASP:OD1	2.25	0.69
3:A2:126:PRO:O	64:BZ:84:GLN:NE2	2.23	0.69
59:BV:83:MET:HB2	59:BV:98:ILE:HD12	1.73	0.69
12:AA:310:A:OP2	46:AP:146:LYS:NZ	2.25	0.69
23:EE:120:VAL:O	23:EE:122:TRP:N	2.24	0.69
34:AK:221:HIS:HB3	59:BV:106:GLY:H	1.57	0.69
65:Ba:53:HIS:ND1	65:Ba:65:GLU:OE2	2.24	0.69
61:BW:23:ARG:HE	75:Al:108:GLU:HA	1.56	0.69
7:E4:21:PRO:HG2	7:E4:64:VAL:HG12	1.74	0.69
35:BK:384:ARG:HG2	35:BK:385:PRO:HD2	1.75	0.69
12:AA:356:A:O2'	49:BR:196:ARG:NH2	2.26	0.69
13:BA:51:LYS:O	21:AE:110:LYS:NZ	2.26	0.69
12:AA:461:U:OP2	56:AU:59:ARG:NH1	2.26	0.68
3:A2:270:ASN:HB3	3:A2:273:GLU:HG2	1.76	0.68
12:AA:1135:G:N2	12:AA:1138:A:OP2	2.25	0.68
38:EL:251:SER:HG	38:EL:269:SER:HG	1.40	0.68
12:AA:995:A:O2'	17:EB:361:ARG:NH2	2.27	0.68
28:BH:123:PRO:HA	28:BH:165:GLN:HE22	1.57	0.68
56:AU:121:PRO:HD3	58:AV:128:ARG:HE	1.59	0.68
75:Al:181:LEU:HD23	75:Al:189:ILE:HD12	1.75	0.68
12:AA:1106:U:OP2	12:AA:1160:A:N6	2.25	0.68
31:BI:101:PHE:HB2	71:Ag:156:GLU:HG2	1.75	0.68
14:EA:59:HIS:H	14:EA:65:GLN:HE21	1.40	0.68
17:EB:555:VAL:HG23	17:EB:574:THR:HB	1.74	0.68
46:AP:66:VAL:HB	58:AV:101:ARG:HH21	1.59	0.68
3:A2:420:VAL:HG11	3:A2:435:PRO:HG3	1.75	0.68
17:EB:126:GLN:NE2	89:EB:1001:ATP:N7	2.40	0.68
13:BA:335:PRO:HB2	13:BA:338:LEU:HB2	1.75	0.68
33:BJ:165:PRO:HA	33:BJ:168:ILE:HD12	1.76	0.68
12:AA:798:U:OP1	48:AR:57:LYS:NZ	2.27	0.68
25:BF:388:ARG:HG2	60:AW:93:GLU:HG2	1.76	0.68
51:BS:39:LEU:HD13	51:BS:106:ILE:HD11	1.76	0.68
51:BS:116:THR:HG22	51:BS:118:GLY:H	1.59	0.68
12:AA:284:U:OP2	62:AX:70:TYR:OH	2.12	0.67
45:EP:1:MET:HG2	45:EP:29:ARG:HB2	1.77	0.67
45:EP:214:PHE:HB3	45:EP:217:MET:HB3	1.75	0.67
52:ES:3:VAL:O	52:ES:8:ARG:NH1	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A2:216:TYR:O	54:BT:112:ARG:NH1	2.27	0.67
6:E3:258:TYR:O	6:E3:262:ARG:HB2	1.94	0.67
12:AA:925:U:H2'	12:AA:926:A:C8	2.29	0.67
14:EA:374:ARG:HD2	14:EA:377:ILE:HD12	1.76	0.67
46:AP:50:ASP:HB3	83:At:151:ARG:HD3	1.75	0.67
49:BR:113:ARG:HB2	49:BR:122:ILE:HD11	1.76	0.67
13:BA:164:ILE:HB	13:BA:194:ARG:HH12	1.59	0.67
13:BA:784:ALA:HB1	13:BA:787:LEU:HB3	1.77	0.67
28:BH:152:ALA:HA	28:BH:156:LEU:HG	1.75	0.67
50:ER:84:GLU:HG2	50:ER:85:LYS:HD2	1.76	0.67
12:AA:5:U:OP1	63:AY:4:ARG:NH1	2.28	0.67
56:AU:70:ALA:HB1	56:AU:75:THR:HG23	1.75	0.67
19:BD:298:LEU:O	19:BD:489:ARG:NH2	2.27	0.67
34:AK:153:MET:HG2	59:BV:85:LEU:HD11	1.75	0.67
21:AE:248:PHE:HB3	21:AE:337:VAL:HG12	1.75	0.67
12:AA:1175:U:O4	48:AR:166:LYS:NZ	2.28	0.67
62:AX:67:THR:HG21	84:Av:36:MET:HE1	1.74	0.67
56:AU:52:GLU:HG3	56:AU:53:GLN:HG3	1.76	0.67
60:AW:164:CYS:HB3	60:AW:176:PHE:HB2	1.77	0.67
6:E3:435:ARG:HG2	48:AR:280:THR:HB	1.77	0.67
34:AK:130:ARG:NH1	59:BV:28:ASP:HA	2.09	0.67
43:EN:271:VAL:HG22	43:EN:326:ARG:HD2	1.77	0.67
7:E4:246:VAL:HG21	7:E4:410:ARG:HD3	1.77	0.66
17:EB:348:MET:HE1	17:EB:500:VAL:HG23	1.75	0.66
25:BF:179:ARG:HG3	25:BF:219:THR:HG22	1.76	0.66
12:AA:152:A:OP2	46:AP:107:ARG:NH1	2.28	0.66
34:AK:34:LYS:HE2	34:AK:93:HIS:ND1	2.10	0.66
73:E8:541:LEU:O	74:E9:238:ARG:NH2	2.28	0.66
2:E1:468:THR:O	10:E6:76:ARG:NH2	2.28	0.66
31:BI:232:LEU:HD11	70:Bf:104:VAL:HG21	1.76	0.66
39:EM:75:VAL:HB	39:EM:101:ARG:HG2	1.77	0.66
67:Bc:71:VAL:HG21	80:Ap:107:MET:HB2	1.76	0.66
1:A1:71:GLN:NE2	12:AA:48:U:O2	2.29	0.66
64:BZ:19:ARG:NH1	64:BZ:165:GLU:OE1	2.29	0.66
11:A8:181:VAL:HB	84:Av:103:ARG:HD3	1.77	0.66
45:EO:145:ILE:HD13	45:EP:145:ILE:HG21	1.77	0.66
70:Bf:99:ILE:HG22	70:Bf:100:TYR:H	1.60	0.66
13:BA:190:THR:HB	13:BA:194:ARG:HH21	1.61	0.66
45:EP:170:GLN:HB2	45:EP:216:ARG:HD2	1.78	0.66
12:AA:836:A:O2'	12:AA:837:A:N7	2.27	0.66
17:EB:142:ALA:HB3	17:EB:322:ILE:HG22	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:283:LEU:HD23	19:BD:338:VAL:HG21	1.78	0.66
21:AE:81:PRO:HG3	31:BI:241:TYR:HB3	1.76	0.66
23:EE:499:ARG:NH2	31:BI:304:ALA:O	2.29	0.66
64:BZ:76:ARG:HB3	64:BZ:84:GLN:HB3	1.77	0.66
7:E4:72:ARG:NH2	10:E6:209:ASN:OD1	2.29	0.66
12:AA:1105:U:O2'	12:AA:1164:A:N6	2.29	0.66
23:EE:344:ARG:NH1	38:EL:538:GLN:OE1	2.29	0.66
7:E4:33:VAL:HG11	7:E4:75:LEU:HD13	1.78	0.65
14:EA:50:ARG:HH22	84:Av:158:GLU:HB3	1.61	0.65
25:BF:118:ARG:NH2	79:Ao:90:ASP:OD2	2.30	0.65
35:BK:295:ARG:NH1	35:BK:311:GLU:OE1	2.30	0.65
68:Ae:149:ASP:H	68:Ae:152:ASN:HB2	1.61	0.65
7:E4:160:VAL:HG12	7:E4:188:ASP:HB3	1.78	0.65
13:BA:626:THR:HG21	69:Af:169:ARG:HB2	1.77	0.65
26:EF:91:ARG:HE	26:EF:116:TRP:HE1	1.43	0.65
30:AI:12:TRP:HE3	65:Ba:79:PRO:HB3	1.61	0.65
12:AA:77:A:OP1	84:Av:73:ARG:NH1	2.29	0.65
6:E3:429:ASN:HB2	6:E3:432:GLN:HG3	1.78	0.65
10:E6:397:ASN:HB3	10:E6:430:THR:HG22	1.79	0.65
12:AA:485:A:H61	60:AW:50:GLN:HE22	1.44	0.65
29:EH:273:PRO:O	29:EH:300:ARG:NH2	2.30	0.65
38:EL:257:ARG:NH2	38:EL:393:ASP:O	2.29	0.65
12:AA:393:A:C2	12:AA:444:G:N1	2.63	0.65
12:AA:533:A:N7	12:AA:545:U:O4	2.28	0.65
13:BA:754:ARG:HH22	63:AY:1:MET:HA	1.60	0.65
22:BE:338:ALA:HB3	35:BK:212:GLN:HE22	1.62	0.65
26:EF:174:MET:HB3	26:EF:296:LEU:HD23	1.77	0.65
44:BO:101:GLN:HG2	44:BO:117:LEU:HD13	1.79	0.65
1:A1:163:ARG:HH22	33:BJ:286:ARG:HD2	1.60	0.65
34:AK:156:GLU:OE2	59:BV:96:PRO:HB2	1.95	0.65
2:E1:106:ARG:HH12	9:E5:264:UNK:HA	1.62	0.65
38:EL:529:ASP:OD1	38:EL:539:ARG:NH2	2.26	0.65
57:BU:126:ARG:HH21	72:E7:85:PHE:H	1.44	0.65
12:AA:1108:A:OP2	21:AE:200:HIS:NE2	2.29	0.65
29:EH:237:ARG:HH12	71:Ag:158:GLU:HB2	1.60	0.65
2:E1:466:ARG:NH1	12:AA:519:A:N7	2.45	0.65
12:AA:912:G:N3	17:EB:237:LYS:NZ	2.44	0.65
21:AE:233:LEU:HD22	21:AE:362:THR:HG21	1.78	0.65
38:EL:130:SER:HB2	38:EL:136:PRO:HG3	1.79	0.65
38:EL:200:ASP:OD2	38:EL:320:ARG:NH1	2.29	0.65
39:EM:54:TYR:HB2	39:EM:236:LEU:HD23	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AX:148:LEU:O	62:AX:152:LEU:HB2	1.97	0.65
74:E9:159:LEU:HD13	74:E9:162:ILE:HD11	1.79	0.65
10:E6:187:PRO:HB2	57:BU:48:GLU:HB3	1.79	0.64
12:AA:941:G:H2'	12:AA:942:A:C8	2.32	0.64
13:BA:589:MET:HE1	13:BA:596:LEU:HB2	1.79	0.64
34:AK:152:GLU:HG2	59:BV:104:TYR:HE2	1.60	0.64
3:A2:375:ARG:NH1	65:Ba:85:ASN:O	2.31	0.64
7:E4:236:ILE:HD13	7:E4:265:ALA:HB2	1.78	0.64
27:EG:29:PRO:HB3	27:EG:118:ARG:HA	1.79	0.64
43:EN:696:ILE:HG23	43:EN:698:GLY:H	1.62	0.64
12:AA:336:U:H5'	79:Ao:173:VAL:HG11	1.79	0.64
13:BA:174:ARG:HD2	13:BA:179:SER:HB2	1.78	0.64
26:EF:135:ASN:ND2	26:EF:146:GLY:O	2.31	0.64
80:Ap:66:CYS:HB2	80:Ap:70:GLU:HG3	1.80	0.64
6:E3:380:LYS:HE2	48:AR:263:LEU:HD23	1.80	0.64
12:AA:377:A:OP1	56:AU:81:ARG:NH2	2.22	0.64
43:EN:592:THR:OG1	43:EN:618:TYR:OH	2.13	0.64
2:E1:243:ARG:NH2	42:BN:110:THR:OG1	2.30	0.64
2:E1:470:SER:O	48:AR:215:LYS:NZ	2.30	0.64
4:E2:456:ARG:HD3	10:E6:296:ASN:HA	1.78	0.64
13:BA:268:ILE:HG12	13:BA:349:LEU:HB3	1.78	0.64
20:ED:233:ARG:HA	20:ED:590:GLU:HG3	1.80	0.64
31:BI:233:GLY:HA3	31:BI:240:GLY:HA3	1.80	0.64
38:EL:83:ARG:NH2	80:Ap:142:GLU:OE2	2.31	0.64
38:EL:521:MET:HE2	38:EL:530:PHE:HB2	1.78	0.64
45:EO:101:LEU:HD21	45:EO:119:ILE:HD12	1.79	0.64
20:ED:242:ARG:NH1	20:ED:527:THR:O	2.31	0.64
14:EA:77:THR:OG1	14:EA:148:ARG:NH2	2.31	0.64
12:AA:393:A:N1	12:AA:444:G:O6	2.31	0.64
13:BA:135:SER:O	44:BO:153:ARG:NH1	2.31	0.64
57:BU:54:SER:OG	57:BU:86:GLN:NE2	2.30	0.64
61:BW:167:ARG:HG2	61:BW:175:THR:HG22	1.80	0.64
74:E9:213:ALA:HB1	74:E9:234:LEU:HD21	1.80	0.64
12:AA:126:A:OP1	56:AU:44:ARG:NH2	2.31	0.63
12:AA:465:A:N3	58:AV:86:ASN:ND2	2.46	0.63
18:EC:181:THR:HG21	18:EC:212:ARG:HH21	1.63	0.63
45:EP:21:LEU:HB3	45:EP:194:TRP:HE1	1.63	0.63
23:EE:330:ASN:H	23:EE:393:ARG:HB3	1.62	0.63
29:EH:534:ASP:HB3	29:EH:537:ILE:HG22	1.80	0.63
38:EL:61:GLU:HG3	38:EL:73:SER:HB3	1.80	0.63
58:AV:143:GLN:NE2	58:AV:171:THR:OG1	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
64:BZ:77:VAL:HG22	64:BZ:83:ILE:HG23	1.80	0.63
4:E2:273:CYS:SG	4:E2:275:SER:OG	2.56	0.63
13:BA:329:GLU:HG3	13:BA:335:PRO:HA	1.79	0.63
14:EA:320:LYS:HB3	14:EA:397:VAL:HG21	1.80	0.63
24:AF:280:THR:HB	54:BT:113:ARG:HB3	1.80	0.63
37:BL:103:ASN:ND2	37:BL:105:SER:OG	2.31	0.63
69:Af:81:ARG:NH1	71:Ag:123:GLU:OE2	2.31	0.63
12:AA:141:U:O2'	56:AU:27:ARG:NH2	2.31	0.63
42:BN:71:GLN:HG3	42:BN:124:LEU:HD13	1.80	0.63
71:Ag:36:PHE:HB2	71:Ag:80:PHE:HE1	1.63	0.63
2:E1:188:ARG:NH2	2:E1:216:LYS:O	2.31	0.63
12:AA:97:A:H2	63:AY:91:GLN:HE22	1.46	0.63
38:EL:371:PHE:HB2	38:EL:480:VAL:HG12	1.79	0.63
39:EM:36:LYS:O	39:EM:257:ASN:ND2	2.32	0.63
42:BN:54:ASP:OD2	42:BN:216:TYR:OH	2.13	0.63
16:BB:83:ASN:OD1	16:BB:84:PHE:N	2.31	0.63
62:AX:86:ASN:HD21	65:Ba:25:GLN:HE21	1.43	0.63
11:A8:114:GLU:HB2	11:A8:117:TYR:HD2	1.63	0.63
12:AA:29:U:OP1	54:BT:54:ARG:NH2	2.31	0.63
12:AA:826:A:OP2	27:EG:49:ARG:NH2	2.31	0.63
18:EC:269:ASN:ND2	39:EM:62:SER:OG	2.29	0.63
22:BE:364:ARG:HH12	22:BE:373:GLN:HE22	1.47	0.63
25:BF:125:GLU:HB3	56:AU:179:VAL:HG22	1.78	0.63
42:BN:128:ARG:NH2	42:BN:131:GLU:OE1	2.31	0.63
58:AV:128:ARG:NH1	69:Af:95:GLY:O	2.31	0.63
3:A2:140:VAL:HG12	3:A2:327:THR:HG22	1.80	0.63
4:E2:476:LYS:NZ	4:E2:482:SER:OG	2.31	0.63
31:BI:151:MET:HE3	31:BI:185:MET:HE3	1.80	0.63
35:BK:208:MET:SD	35:BK:216:ARG:NH1	2.72	0.63
46:AP:123:SER:OG	46:AP:125:LYS:NZ	2.32	0.63
50:ER:96:HIS:HB3	50:ER:99:ASN:HB2	1.81	0.63
2:E1:137:ARG:NH1	12:AA:521:G:OP1	2.32	0.63
2:E1:331:GLY:HA2	10:E6:414:SER:HB2	1.81	0.63
4:E2:326:GLU:OE1	4:E2:364:ARG:NH2	2.32	0.63
12:AA:836:A:H5''	67:Bc:11:SER:HA	1.81	0.63
13:BA:563:ARG:NH1	13:BA:650:GLY:O	2.32	0.63
14:EA:143:PHE:HB3	14:EA:146:ILE:HD11	1.79	0.63
16:BB:348:VAL:HG23	16:BB:430:TYR:HB2	1.79	0.63
27:EG:118:ARG:HD3	27:EG:143:CYS:HB3	1.79	0.63
30:AI:134:TYR:HB3	30:AI:167:LEU:HD11	1.79	0.63
2:E1:45:HIS:O	2:E1:49:ASN:HB2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A3:72:ASP:HB3	5:A3:115:ILE:HG23	1.80	0.62
13:BA:720:ARG:NH2	71:Ag:103:HIS:O	2.31	0.62
37:BL:226:HIS:HD2	37:BL:228:ASP:H	1.44	0.62
43:EN:539:PHE:HB2	43:EN:570:LEU:HD21	1.81	0.62
12:AA:119:A:H5'	12:AA:120:A:C8	2.34	0.62
13:BA:300:ARG:HH22	21:AE:176:ARG:HH22	1.45	0.62
18:EC:268:GLY:O	39:EM:63:ARG:NH2	2.31	0.62
30:AI:142:GLN:NE2	30:AI:146:GLU:OE2	2.30	0.62
22:BE:66:ARG:HD2	35:BK:381:SER:HA	1.81	0.62
24:AF:44:LEU:HD21	37:BL:229:SER:HB2	1.80	0.62
25:BF:123:LEU:HA	25:BF:126:VAL:HG22	1.82	0.62
4:E2:398:ARG:NH2	4:E2:487:ASP:OD1	2.32	0.62
13:BA:607:LYS:HE3	37:BL:36:GLY:HA3	1.81	0.62
14:EA:173:GLY:HA3	28:BH:84:TRP:HE1	1.64	0.62
20:ED:7:GLY:HA3	20:ED:276:THR:HG21	1.81	0.62
44:BO:74:LEU:HD11	51:BS:32:ARG:HB3	1.80	0.62
73:E8:495:GLY:O	73:E8:499:THR:OG1	2.18	0.62
7:E4:408:LEU:HD21	7:E4:411:PHE:HB2	1.80	0.62
20:ED:407:ASP:HA	20:ED:467:PRO:HB3	1.81	0.62
51:BS:84:VAL:HG23	51:BS:96:MET:HG3	1.81	0.62
4:E2:199:GLN:OE1	4:E2:246:ARG:NH2	2.33	0.62
20:ED:108:ASP:O	20:ED:118:LYS:NZ	2.32	0.62
37:BL:238:GLN:NE2	60:AW:100:GLU:OE2	2.33	0.62
38:EL:257:ARG:NH1	38:EL:398:LEU:O	2.32	0.62
48:AR:135:ARG:NE	48:AR:167:ASN:O	2.30	0.62
55:ET:79:ILE:HD12	84:Av:193:TYR:HB2	1.81	0.62
61:BW:52:LYS:HB3	61:BW:69:LYS:HD3	1.80	0.62
64:BZ:117:LYS:HD2	64:BZ:120:LEU:HD13	1.81	0.62
6:E3:348:VAL:HG22	6:E3:395:ILE:HB	1.81	0.62
29:EH:233:LEU:HG	29:EH:236:ARG:HH22	1.65	0.62
37:BL:73:GLY:HA2	37:BL:78:ARG:HH21	1.63	0.62
43:EN:276:LEU:HD22	43:EN:334:ARG:HD3	1.81	0.62
4:E2:428:ARG:NH1	4:E2:497:LEU:O	2.33	0.62
9:E5:30:UNK:HA	9:E5:45:UNK:HA	1.81	0.62
12:AA:360:U:OP2	27:EG:146:ASN:ND2	2.32	0.62
12:AA:906:A:OP1	17:EB:562:THR:OG1	2.17	0.62
31:BI:117:LEU:O	31:BI:125:ASN:ND2	2.33	0.62
42:BN:53:ARG:NH1	42:BN:91:ASP:OD2	2.33	0.62
43:EN:195:LEU:HB3	43:EN:230:LEU:HD12	1.80	0.62
46:AP:149:PRO:HG2	46:AP:152:MET:HB2	1.80	0.62
48:AR:112:ARG:NH2	57:BU:170:SER:OG	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E1:59:VAL:O	2:E1:63:GLN:HG2	2.00	0.62
12:AA:318:A:H2'	12:AA:319:A:H8	1.64	0.62
13:BA:278:LYS:O	13:BA:285:TRP:NE1	2.33	0.62
21:AE:129:GLU:OE1	38:EL:342:ARG:NH2	2.32	0.62
23:EE:244:ASN:OD1	23:EE:398:ARG:NH1	2.33	0.62
29:EH:237:ARG:NH2	71:Ag:158:GLU:OE1	2.33	0.62
12:AA:537:U:OP2	62:AX:158:ARG:NH2	2.32	0.62
14:EA:410:MET:SD	14:EA:450:GLN:NE2	2.73	0.62
24:AF:265:HIS:NE2	24:AF:296:ASN:O	2.33	0.62
54:BT:77:ARG:NH2	54:BT:92:GLU:OE2	2.33	0.62
58:AV:142:GLU:HG2	58:AV:172:ILE:HB	1.81	0.62
2:E1:188:ARG:HH12	2:E1:219:SER:HB3	1.64	0.61
14:EA:541:LYS:NZ	17:EB:342:GLU:OE1	2.31	0.61
7:E4:257:LEU:HD23	7:E4:324:VAL:HG12	1.82	0.61
29:EH:236:ARG:NH2	71:Ag:158:GLU:OE2	2.31	0.61
29:EH:315:ASN:HD21	41:AN:190:GLN:HE21	1.48	0.61
30:AI:181:THR:HG22	30:AI:183:ARG:H	1.63	0.61
60:AW:116:ARG:NH2	60:AW:120:GLU:OE1	2.33	0.61
29:EH:2:LYS:HG2	29:EH:37:GLN:HE22	1.65	0.61
45:EO:3:THR:HB	45:EO:60:VAL:HG23	1.82	0.61
74:E9:160:ARG:O	74:E9:164:ASN:ND2	2.30	0.61
13:BA:134:MET:HB2	44:BO:145:LEU:HD13	1.82	0.61
14:EA:103:LEU:HD12	14:EA:349:PRO:HB2	1.81	0.61
14:EA:320:LYS:HE2	14:EA:362:THR:O	2.01	0.61
38:EL:372:PRO:HD2	38:EL:482:PRO:HA	1.83	0.61
58:AV:227:GLU:O	71:Ag:124:ARG:NH1	2.24	0.61
59:BV:46:GLU:HG3	59:BV:50:ARG:HE	1.65	0.61
4:E2:70:PRO:HD2	4:E2:73:LEU:HD12	1.83	0.61
12:AA:188:A:O2'	12:AA:189:A:O4'	2.13	0.61
12:AA:360:U:O2'	27:EG:26:GLN:OE1	2.19	0.61
59:BV:83:MET:HE2	59:BV:98:ILE:HD12	1.82	0.61
12:AA:535:U:H2'	12:AA:536:A:C8	2.36	0.61
12:AA:559:A:N3	12:AA:560:G:N2	2.47	0.61
13:BA:563:ARG:NH2	13:BA:566:MET:SD	2.73	0.61
20:ED:86:LEU:HD21	20:ED:149:TYR:HB2	1.81	0.61
23:EE:78:PRO:HA	39:EM:282:HIS:HE1	1.65	0.61
25:BF:321:PHE:HD2	25:BF:325:ARG:HH22	1.49	0.61
38:EL:484:ASN:HB3	38:EL:487:MET:HB3	1.83	0.61
41:AN:104:THR:HB	41:AN:115:ARG:HD2	1.83	0.61
49:BR:143:ILE:HG22	79:Ao:210:PHE:HB2	1.83	0.61
5:A3:148:SER:OG	46:AP:46:ASN:ND2	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AA:360:U:OP1	27:EG:118:ARG:NH2	2.34	0.61
26:EF:76:ARG:NH2	26:EF:208:ASP:OD2	2.34	0.61
29:EH:217:ILE:HG13	29:EH:318:TYR:HB2	1.81	0.61
31:BI:58:GLU:OE2	31:BI:62:HIS:NE2	2.33	0.61
2:E1:237:PRO:HD2	2:E1:240:ARG:HH11	1.66	0.61
12:AA:379:U:OP1	46:AP:10:ARG:N	2.34	0.61
31:BI:278:GLU:HB3	45:EO:310:ILE:HD13	1.82	0.61
8:A5:64:LYS:NZ	8:A5:80:PRO:O	2.34	0.61
12:AA:368:U:OP1	55:ET:21:ARG:NH1	2.28	0.61
13:BA:324:GLU:OE2	13:BA:327:ARG:NH1	2.33	0.61
25:BF:330:ARG:NH1	46:AP:102:GLU:O	2.33	0.61
41:AN:89:LYS:O	41:AN:122:TYR:OH	2.19	0.61
1:A1:178:GLN:HG2	63:AY:299:MET:HE1	1.83	0.60
7:E4:67:ARG:HG2	7:E4:74:LEU:HA	1.81	0.60
29:EH:543:ARG:NH1	29:EH:603:ASP:OD2	2.33	0.60
3:A2:18:ASP:H	3:A2:64:MET:HE3	1.66	0.60
7:E4:329:ARG:HG2	7:E4:331:ASP:H	1.64	0.60
20:ED:323:THR:HG21	75:AI:80:ASP:HB2	1.81	0.60
3:A2:457:ARG:NH1	3:A2:460:ASP:OD1	2.33	0.60
14:EA:267:PRO:HB3	52:ES:114:MET:HG2	1.84	0.60
18:EC:293:VAL:HA	18:EC:304:ILE:HG22	1.83	0.60
20:ED:85:ALA:O	20:ED:217:ARG:NH2	2.34	0.60
20:ED:483:LYS:NZ	47:BQ:224:LEU:O	2.31	0.60
28:BH:260:ASP:OD1	28:BH:261:GLU:N	2.34	0.60
30:AI:80:GLU:HG2	30:AI:95:ARG:HD2	1.81	0.60
5:A3:125:GLU:HG3	83:At:82:LEU:HD21	1.84	0.60
6:E3:181:GLU:OE2	6:E3:402:ARG:NH1	2.35	0.60
10:E6:301:ASP:H	10:E6:337:HIS:HE1	1.48	0.60
11:A8:99:ARG:NH1	12:AA:911:G:OP2	2.34	0.60
12:AA:945:U:O4	46:AP:243:ARG:NH2	2.35	0.60
16:BB:324:ALA:HA	16:BB:327:LEU:HD23	1.81	0.60
19:BD:129:LEU:HB3	19:BD:132:GLU:HB3	1.83	0.60
45:EP:190:CYS:SG	45:EP:193:THR:OG1	2.58	0.60
64:BZ:8:PHE:HB2	64:BZ:20:ARG:HD2	1.83	0.60
4:E2:88:TYR:HB2	16:BB:263:ARG:HB3	1.83	0.60
12:AA:108:G:O6	41:AN:10:ALA:N	2.34	0.60
14:EA:148:ARG:NH1	14:EA:340:ASN:O	2.35	0.60
1:A1:115:ASP:OD1	30:AI:152:ARG:NH2	2.33	0.60
2:E1:266:GLU:OE1	10:E6:310:ARG:NH2	2.35	0.60
12:AA:12:U:OP2	37:BL:53:ARG:NH1	2.35	0.60
45:EP:13:HIS:HE1	45:EP:50:LEU:HA	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A8:154:ILE:HD13	24:AF:310:GLU:HG3	1.84	0.60
12:AA:354:U:H4'	17:EB:92:ASN:HB2	1.83	0.60
12:AA:826:A:O3'	27:EG:45:ARG:NH2	2.35	0.60
14:EA:552:VAL:HA	14:EA:557:PHE:HB2	1.82	0.60
19:BD:224:ARG:NH2	19:BD:519:PRO:O	2.34	0.60
24:AF:71:VAL:O	54:BT:150:ASN:ND2	2.33	0.60
31:BI:119:GLU:HG2	31:BI:235:PHE:HB2	1.83	0.60
45:EP:18:HIS:HB2	45:EP:198:THR:HG21	1.83	0.60
54:BT:94:TYR:HD2	61:BW:80:MET:HE1	1.66	0.60
12:AA:557:A:N7	68:Ae:99:TRP:NE1	2.50	0.60
59:BV:60:MET:HE3	59:BV:62:HIS:HB2	1.83	0.60
64:BZ:84:GLN:NE2	64:BZ:134:GLN:OE1	2.35	0.60
5:A3:178:LEU:HD13	47:BQ:114:PRO:HD3	1.82	0.60
12:AA:877:G:H2'	12:AA:878:A:H8	1.66	0.60
38:EL:449:LYS:NZ	38:EL:565:PRO:O	2.34	0.60
46:AP:258:THR:HG23	46:AP:261:GLY:H	1.66	0.60
75:Al:79:TYR:OH	75:Al:92:HIS:O	2.18	0.60
7:E4:80:TYR:HA	7:E4:87:VAL:HG12	1.84	0.59
27:EG:63:GLU:HB2	27:EG:94:PHE:HE2	1.67	0.59
46:AP:199:HIS:NE2	61:BW:3:GLY:O	2.36	0.59
48:AR:119:LEU:HD12	48:AR:125:VAL:HG22	1.82	0.59
51:BS:48:GLY:HA2	51:BS:72:THR:HG23	1.84	0.59
1:A1:131:GLU:OE2	30:AI:145:ARG:NH2	2.35	0.59
3:A2:379:ALA:HB2	65:Ba:84:TYR:HB2	1.83	0.59
8:A5:56:TYR:HE2	60:AW:158:ARG:HH21	1.49	0.59
22:BE:385:LEU:HD23	22:BE:385:LEU:H	1.67	0.59
23:EE:100:PRO:HD2	23:EE:103:ILE:HD12	1.83	0.59
26:EF:194:VAL:HG11	26:EF:221:THR:HB	1.84	0.59
38:EL:459:LYS:O	38:EL:463:LYS:HB2	2.02	0.59
56:AU:47:THR:HG21	58:AV:152:LEU:H	1.67	0.59
84:Av:126:ARG:NH2	84:Av:140:GLU:OE1	2.35	0.59
12:AA:1045:N:H4'	26:EF:207:LEU:HD12	1.84	0.59
39:EM:82:ARG:NH2	39:EM:332:GLN:O	2.35	0.59
61:BW:56:ASN:ND2	61:BW:61:ASN:O	2.36	0.59
11:A8:79:PRO:HG2	11:A8:82:SER:HB2	1.83	0.59
12:AA:551:A:O2'	72:E7:44:GLN:NE2	2.34	0.59
13:BA:284:LYS:HA	13:BA:287:THR:HG22	1.83	0.59
58:AV:63:ASP:HB3	58:AV:66:ILE:HG22	1.82	0.59
2:E1:202:GLU:O	2:E1:205:ASN:ND2	2.35	0.59
16:BB:369:GLU:OE2	57:BU:67:ARG:NH2	2.32	0.59
42:BN:67:LEU:HB3	42:BN:124:LEU:HD11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AA:14:A:N6	63:AY:18:PRO:O	2.35	0.59
12:AA:189:A:O2'	12:AA:190:U:O4'	2.20	0.59
16:BB:165:THR:HG23	16:BB:238:ASN:HB3	1.84	0.59
12:AA:837:A:OP2	67:Bc:10:ASP:N	2.35	0.59
12:AA:954:U:H5	43:EN:64:SER:H	1.50	0.59
46:AP:285:LEU:HA	46:AP:289:ALA:HB3	1.85	0.59
62:AX:153:ASN:HD21	62:AX:226:LEU:HB3	1.68	0.59
7:E4:109:VAL:HG13	7:E4:176:LEU:HD12	1.85	0.59
7:E4:259:VAL:HG12	7:E4:280:ALA:HB3	1.84	0.59
13:BA:274:MET:HG2	13:BA:279:VAL:HG11	1.85	0.59
16:BB:76:GLU:OE2	16:BB:79:ARG:NH2	2.36	0.59
21:AE:169:GLN:HE21	21:AE:230:GLY:HA2	1.68	0.59
24:AF:103:VAL:HG11	24:AF:371:LEU:HD11	1.85	0.59
24:AF:373:PRO:HA	24:AF:376:ARG:HG2	1.85	0.59
34:AK:221:HIS:CE1	59:BV:105:PRO:HA	2.38	0.59
38:EL:228:TYR:O	38:EL:233:ARG:NH1	2.35	0.59
38:EL:253:ALA:HA	38:EL:268:PRO:HA	1.84	0.59
3:A2:40:ARG:NH2	3:A2:100:GLU:OE1	2.36	0.59
12:AA:993:A:H61	14:EA:515:ARG:HH22	1.49	0.59
16:BB:201:PRO:HA	57:BU:106:ARG:HB3	1.83	0.59
20:ED:205:ARG:HD3	20:ED:208:ASN:HD22	1.68	0.59
24:AF:378:GLN:NE2	61:BW:126:PHE:O	2.35	0.59
29:EH:11:HIS:HD2	29:EH:26:VAL:HG22	1.68	0.59
7:E4:243:ILE:HG12	7:E4:430:SER:HB3	1.85	0.59
10:E6:370:LEU:HD12	10:E6:375:LEU:HB2	1.85	0.59
10:E6:440:ARG:HD2	73:E8:573:LEU:HD12	1.85	0.59
20:ED:547:ILE:HG23	20:ED:585:SER:HB2	1.85	0.59
23:EE:390:ASN:HB3	23:EE:393:ARG:HA	1.85	0.59
75:Al:75:ARG:H	75:Al:211:HIS:CE1	2.21	0.59
1:A1:86:VAL:HG12	1:A1:97:ARG:HG2	1.85	0.58
3:A2:18:ASP:OD1	3:A2:19:ASN:N	2.34	0.58
13:BA:301:HIS:HD2	13:BA:303:ILE:H	1.51	0.58
25:BF:193:GLU:HG3	25:BF:196:ARG:HE	1.67	0.58
46:AP:206:VAL:HG21	46:AP:216:PHE:HZ	1.68	0.58
53:AT:102:LEU:HD23	73:E8:528:THR:HG21	1.85	0.58
84:Av:129:CYS:HB2	84:Av:134:VAL:HB	1.83	0.58
3:A2:155:ARG:HG3	3:A2:170:ILE:HD11	1.85	0.58
4:E2:201:ASP:O	4:E2:205:ASN:ND2	2.30	0.58
12:AA:822:U:H5''	27:EG:126:GLN:HE22	1.68	0.58
23:EE:304:ASP:HB3	38:EL:559:THR:HA	1.83	0.58
42:BN:33:ARG:HB2	51:BS:69:ASN:HD21	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:Al:92:HIS:NE2	75:Al:126:GLY:O	2.33	0.58
14:EA:260:MET:HE3	43:EN:404:ARG:HG3	1.85	0.58
29:EH:52:THR:HG23	29:EH:370:THR:HB	1.85	0.58
31:BI:133:PHE:CD1	45:EO:213:PRO:HG3	2.38	0.58
31:BI:283:ARG:HD2	71:Ag:163:VAL:HG21	1.84	0.58
48:AR:46:ALA:HB1	48:AR:55:LEU:HD13	1.84	0.58
48:AR:233:ARG:NH2	48:AR:240:VAL:O	2.36	0.58
10:E6:393:VAL:O	10:E6:397:ASN:ND2	2.37	0.58
12:AA:13:A:H62	63:AY:39:LEU:HB2	1.68	0.58
12:AA:470:G:H5'	46:AP:70:LEU:HD12	1.86	0.58
14:EA:195:VAL:HG11	14:EA:227:ILE:HD11	1.84	0.58
29:EH:220:VAL:HG21	41:AN:192:ILE:HG12	1.85	0.58
41:AN:126:PRO:HD3	80:Ap:61:ASN:HD21	1.68	0.58
48:AR:183:PRO:HG3	48:AR:190:PRO:HA	1.85	0.58
71:Ag:9:LEU:HD23	71:Ag:87:VAL:HG12	1.86	0.58
4:E2:121:LEU:HD12	4:E2:122:PRO:HD2	1.84	0.58
12:AA:357:A:N1	12:AA:361:U:O2'	2.37	0.58
13:BA:347:VAL:HG11	13:BA:396:ARG:HG3	1.83	0.58
22:BE:157:ASN:HB3	22:BE:160:LEU:HB2	1.85	0.58
33:BJ:203:LEU:HD22	33:BJ:209:ILE:HD13	1.86	0.58
46:AP:188:ARG:NH2	75:Al:142:SER:OG	2.36	0.58
12:AA:1155:A:OP1	74:E9:303:LYS:NZ	2.37	0.58
37:BL:254:VAL:HG21	37:BL:304:VAL:HG11	1.84	0.58
45:EP:118:GLN:NE2	45:EP:189:ASP:O	2.37	0.58
72:E7:2:LYS:HG2	72:E7:6:GLN:HE21	1.69	0.58
83:At:132:ARG:NH2	83:At:150:SER:OG	2.37	0.58
2:E1:297:ARG:NH1	12:AA:552:U:OP1	2.37	0.58
12:AA:563:U:OP1	57:BU:138:ARG:NH1	2.32	0.58
19:BD:245:ARG:HD3	30:AI:222:GLU:HG2	1.85	0.58
34:AK:34:LYS:HZ1	34:AK:94:PHE:HE1	1.50	0.58
34:AK:152:GLU:CG	59:BV:98:ILE:HG23	2.32	0.58
46:AP:106:MET:HE1	60:AW:25:LEU:HD22	1.84	0.58
48:AR:79:ARG:NH2	48:AR:121:ASP:OD2	2.37	0.58
90:ER:200:PM8:H381	52:ES:49:ALA:HA	1.86	0.58
55:ET:17:MET:HA	55:ET:20:MET:HG2	1.86	0.58
2:E1:198:THR:HA	10:E6:162:ARG:HH21	1.69	0.58
3:A2:138:THR:HG23	3:A2:358:ARG:HH12	1.69	0.58
6:E3:401:LEU:HB2	6:E3:424:ASN:HB3	1.85	0.58
11:A8:53:ARG:HA	24:AF:168:GLU:HG2	1.86	0.58
12:AA:307:A:O2'	12:AA:317:A:N3	2.35	0.58
14:EA:141:ARG:NH1	43:EN:29:PRO:O	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:BB:101:LEU:HD22	16:BB:104:ILE:HD12	1.85	0.58
37:BL:55:LEU:HB3	56:AU:19:ARG:HH22	1.69	0.58
38:EL:118:HIS:HD2	38:EL:123:LEU:HD13	1.69	0.58
45:EO:1:MET:N	45:EO:29:ARG:O	2.37	0.58
12:AA:457:A:N1	69:Af:64:SER:OG	2.35	0.58
20:ED:240:LEU:HD13	20:ED:583:VAL:HG22	1.86	0.58
23:EE:304:ASP:OD1	23:EE:304:ASP:N	2.34	0.58
24:AF:328:GLY:O	24:AF:330:LYS:NZ	2.31	0.58
49:BR:154:ASP:OD1	83:At:16:ARG:NH1	2.26	0.58
69:Af:83:LEU:HG	69:Af:86:ASN:HD22	1.67	0.58
13:BA:815:TYR:O	13:BA:816:HIS:ND1	2.37	0.57
30:AI:17:ARG:NH2	65:Ba:130:ASP:OD2	2.36	0.57
62:AX:156:THR:HG22	62:AX:158:ARG:H	1.69	0.57
3:A2:108:ARG:NH1	3:A2:111:GLU:OE1	2.37	0.57
12:AA:305:G:N7	55:ET:2:ALA:N	2.51	0.57
23:EE:422:ILE:HG21	26:EF:192:ALA:HB2	1.85	0.57
12:AA:836:A:N7	41:AN:149:ARG:NH1	2.49	0.57
12:AA:938:U:OP2	84:Av:195:GLN:NE2	2.37	0.57
26:EF:70:ARG:NH2	26:EF:140:SER:OG	2.26	0.57
7:E4:318:MET:SD	7:E4:321:GLN:NE2	2.77	0.57
12:AA:123:U:OP1	69:Af:52:LYS:NZ	2.33	0.57
13:BA:149:SER:OG	13:BA:155:ILE:O	2.21	0.57
14:EA:425:LEU:HD12	14:EA:447:ILE:HD11	1.86	0.57
20:ED:521:ARG:NH2	49:BR:11:MET:O	2.37	0.57
26:EF:174:MET:HE1	26:EF:200:SER:HB2	1.84	0.57
29:EH:375:LEU:HB2	29:EH:380:LYS:HE2	1.85	0.57
90:ER:200:PM8:H312	52:ES:11:THR:HG21	1.87	0.57
6:E3:475:TRP:NE1	6:E3:479:GLU:OE2	2.38	0.57
24:AF:142:GLU:OE2	46:AP:81:HIS:ND1	2.38	0.57
29:EH:245:TYR:HA	29:EH:391:THR:HG21	1.86	0.57
29:EH:548:GLN:HE22	66:Bb:5:VAL:HG11	1.68	0.57
43:EN:626:THR:HG23	43:EN:629:CYS:H	1.69	0.57
65:Ba:80:ASP:OD1	65:Ba:80:ASP:N	2.37	0.57
69:Af:108:MET:HE3	69:Af:135:ILE:HG23	1.85	0.57
72:E7:17:ARG:HG3	72:E7:18:ARG:HE	1.69	0.57
83:At:94:THR:HG23	83:At:97:GLN:H	1.69	0.57
13:BA:304:GLY:HA2	13:BA:307:HIS:CE1	2.40	0.57
21:AE:277:GLN:NE2	27:EG:112:GLU:OE1	2.35	0.57
23:EE:375:PHE:HB2	23:EE:439:TYR:HD2	1.69	0.57
24:AF:313:ASP:OD1	24:AF:330:LYS:NZ	2.37	0.57
26:EF:346:ARG:HG2	26:EF:348:ALA:H	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A3:86:ARG:NH2	25:BF:27:THR:OG1	2.37	0.57
7:E4:65:GLU:OE1	7:E4:67:ARG:NE	2.38	0.57
12:AA:393:A:H2	12:AA:444:G:N1	1.98	0.57
19:BD:468:TRP:HE1	19:BD:474:SER:HB2	1.70	0.57
31:BI:102:TRP:NE1	31:BI:107:ASN:OD1	2.38	0.57
31:BI:274:GLN:O	31:BI:278:GLU:HG2	2.03	0.57
61:BW:19:ASN:O	61:BW:22:ARG:NE	2.38	0.57
51:BS:46:THR:HG23	51:BS:48:GLY:H	1.69	0.57
62:AX:96:ASN:HD22	65:Ba:29:LEU:HB3	1.69	0.57
62:AX:147:LEU:HD21	62:AX:162:GLN:HE21	1.69	0.57
2:E1:446:ARG:NH2	2:E1:463:ASP:OD2	2.38	0.57
3:A2:96:ARG:NH2	35:BK:353:ASP:OD2	2.36	0.57
12:AA:50:A:H4'	84:Av:48:ALA:HB2	1.87	0.57
12:AA:835:A:OP1	41:AN:135:LYS:NZ	2.33	0.57
17:EB:367:THR:HG22	17:EB:369:ILE:H	1.69	0.57
23:EE:302:ASP:O	38:EL:631:ARG:NH1	2.37	0.57
56:AU:86:ARG:O	79:Ao:68:HIS:NE2	2.38	0.57
67:Bc:64:PHE:HB2	67:Bc:141:ILE:HG23	1.85	0.57
12:AA:880:C:H2'	12:AA:881:A:H8	1.70	0.57
30:AI:15:PRO:O	65:Ba:104:ARG:NH2	2.36	0.57
44:BO:69:TYR:HD2	51:BS:40:GLU:HB2	1.70	0.57
59:BV:45:LEU:HD11	59:BV:74:ASN:HA	1.87	0.57
75:Al:131:LEU:HD23	75:Al:131:LEU:H	1.70	0.57
80:Ap:157:ALA:HA	80:Ap:273:GLU:HA	1.87	0.57
4:E2:421:ARG:O	4:E2:478:ARG:NH1	2.38	0.56
12:AA:933:U:OP1	43:EN:50:HIS:ND1	2.38	0.56
12:AA:1133:A:H1'	12:AA:1141:A:C2	2.39	0.56
13:BA:801:ARG:NH2	13:BA:816:HIS:O	2.38	0.56
45:EO:197:PHE:HB2	45:EO:224:LEU:HD13	1.86	0.56
46:AP:187:GLY:O	61:BW:27:TYR:OH	2.23	0.56
12:AA:962:U:O4	14:EA:389:ARG:NH1	2.38	0.56
13:BA:64:ARG:HH22	38:EL:92:GLU:HG3	1.70	0.56
13:BA:156:ASP:OD1	21:AE:169:GLN:NE2	2.38	0.56
14:EA:229:GLU:OE2	43:EN:400:ARG:NH2	2.38	0.56
19:BD:361:ALA:O	19:BD:365:HIS:ND1	2.37	0.56
20:ED:165:VAL:HG13	20:ED:166:LEU:HG	1.87	0.56
3:A2:421:ASP:OD2	63:AY:138:LYS:NZ	2.39	0.56
4:E2:134:THR:OG1	4:E2:160:CYS:SG	2.64	0.56
6:E3:153:GLN:HG2	6:E3:154:GLN:H	1.70	0.56
12:AA:565:U:O3'	12:AA:567:G:N2	2.38	0.56
12:AA:922:A:H2'	12:AA:923:U:C6	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:BA:63:LEU:HB3	13:BA:66:ILE:HD11	1.88	0.56
23:EE:232:ASN:ND2	23:EE:234:GLN:O	2.38	0.56
24:AF:60:LEU:O	71:Ag:26:ARG:NH2	2.38	0.56
24:AF:85:TYR:OH	24:AF:236:LEU:O	2.23	0.56
24:AF:457:MET:HG2	46:AP:275:MET:HE2	1.86	0.56
34:AK:217:TYR:CZ	59:BV:102:TRP:HB2	2.40	0.56
38:EL:498:ASN:HD21	38:EL:505:PHE:H	1.53	0.56
62:AX:74:ARG:HH11	62:AX:75:PRO:HD2	1.69	0.56
63:AY:315:SER:OG	63:AY:321:GLN:NE2	2.39	0.56
64:BZ:121:VAL:HG22	64:BZ:137:ILE:HG22	1.86	0.56
1:A1:88:THR:HG23	28:BH:285:ARG:HG3	1.88	0.56
12:AA:101:A:N6	63:AY:15:PRO:O	2.38	0.56
12:AA:595:A:N1	53:AT:142:ARG:NH2	2.53	0.56
20:ED:92:GLY:O	20:ED:202:HIS:NE2	2.38	0.56
24:AF:154:ARG:NH2	54:BT:29:ASP:O	2.39	0.56
25:BF:157:ASN:OD1	25:BF:167:ARG:NH2	2.38	0.56
5:A3:78:SER:O	5:A3:82:ASN:ND2	2.27	0.56
7:E4:184:GLU:OE2	7:E4:197:LYS:NZ	2.37	0.56
26:EF:131:PRO:HG2	26:EF:134:ILE:HB	1.87	0.56
28:BH:183:VAL:HG12	28:BH:195:ILE:HG12	1.87	0.56
34:AK:95:LYS:NZ	59:BV:88:ALA:HB3	2.20	0.56
63:AY:251:LEU:O	63:AY:255:ARG:HG2	2.05	0.56
3:A2:399:THR:HA	3:A2:402:ARG:HH21	1.71	0.56
13:BA:31:ILE:HD11	38:EL:201:PRO:HG2	1.88	0.56
28:BH:153:ARG:NH2	30:AI:210:TYR:O	2.35	0.56
29:EH:238:LEU:HB3	29:EH:247:ILE:HG21	1.88	0.56
43:EN:199:PHE:HB2	43:EN:230:LEU:HD11	1.86	0.56
51:BS:66:ILE:HG13	57:BU:184:TRP:HH2	1.70	0.56
63:AY:282:ALA:HA	65:Ba:58:MET:HE1	1.86	0.56
5:A3:151:ARG:NH2	12:AA:334:U:OP2	2.39	0.56
11:A8:61:TYR:HB3	11:A8:64:GLN:HB2	1.86	0.56
13:BA:792:SER:HB3	13:BA:800:TRP:HD1	1.70	0.56
17:EB:341:VAL:HG21	17:EB:347:LYS:HG2	1.86	0.56
19:BD:110:LEU:HD13	19:BD:446:LEU:HD22	1.88	0.56
23:EE:254:VAL:HA	23:EE:257:THR:HG22	1.87	0.56
60:AW:81:ARG:NH2	60:AW:92:THR:O	2.39	0.56
74:E9:174:ARG:HG3	74:E9:203:HIS:HD2	1.70	0.56
6:E3:317:MET:O	6:E3:321:TRP:HB2	2.06	0.56
7:E4:193:LYS:HG2	7:E4:195:HIS:HD2	1.69	0.56
14:EA:486:LYS:NZ	14:EA:556:ASP:OD1	2.38	0.56
16:BB:140:GLY:HA2	57:BU:108:LEU:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:EB:65:ARG:NH2	17:EB:625:GLU:OE2	2.38	0.56
18:EC:223:THR:HG22	18:EC:225:ASN:H	1.70	0.56
34:AK:94:PHE:O	59:BV:91:LYS:NZ	2.29	0.56
62:AX:155:GLU:HA	62:AX:223:SER:HB2	1.87	0.56
73:E8:507:GLU:HG2	74:E9:211:VAL:HB	1.88	0.56
6:E3:234:ASP:HB3	6:E3:237:MET:HG3	1.88	0.56
10:E6:478:LEU:HB3	10:E6:481:TYR:HD2	1.70	0.56
19:BD:287:VAL:HG11	19:BD:382:THR:HG22	1.88	0.56
20:ED:48:ARG:NH1	20:ED:55:ALA:O	2.38	0.56
20:ED:439:ASP:O	20:ED:444:THR:N	2.37	0.56
23:EE:245:VAL:HG21	23:EE:251:LEU:HD13	1.87	0.56
34:AK:156:GLU:HG2	59:BV:87:ILE:HD11	1.88	0.56
34:AK:217:TYR:HB3	59:BV:108:TYR:CD2	2.41	0.56
47:BQ:69:ARG:NH2	75:AI:81:GLU:OE2	2.39	0.56
84:Av:118:ASN:ND2	84:Av:121:THR:OG1	2.39	0.56
6:E3:429:ASN:OD1	6:E3:432:GLN:NE2	2.40	0.55
7:E4:220:TRP:CD1	7:E4:222:PRO:HD2	2.41	0.55
7:E4:325:PHE:HD1	7:E4:359:VAL:HB	1.71	0.55
12:AA:292:G:O2'	12:AA:497:C:N4	2.40	0.55
12:AA:850:G:N2	12:AA:1094:U:OP2	2.39	0.55
23:EE:160:HIS:HD2	23:EE:285:ARG:HH21	1.54	0.55
28:BH:127:SER:HB2	28:BH:185:HIS:HB2	1.88	0.55
29:EH:35:GLU:HA	29:EH:106:ARG:HH12	1.70	0.55
34:AK:62:ALA:HB2	34:AK:87:ASN:HD21	1.71	0.55
38:EL:376:GLU:HG3	38:EL:583:LEU:HA	1.88	0.55
47:BQ:82:PRO:HA	47:BQ:190:TRP:HA	1.88	0.55
48:AR:242:HIS:HD2	48:AR:244:SER:H	1.53	0.55
62:AX:168:SER:H	62:AX:171:GLU:HB2	1.70	0.55
4:E2:232:CYS:HB2	4:E2:273:CYS:HB3	1.86	0.55
7:E4:270:ALA:O	7:E4:274:ALA:HB3	2.06	0.55
11:A8:95:ARG:NH2	12:AA:911:G:O6	2.37	0.55
16:BB:135:TYR:OH	16:BB:240:HIS:ND1	2.37	0.55
21:AE:152:ASP:OD1	21:AE:156:ASN:N	2.39	0.55
30:AI:12:TRP:CD1	65:Ba:84:TYR:HH	2.24	0.55
43:EN:612:LEU:O	43:EN:616:HIS:ND1	2.34	0.55
45:EO:21:LEU:HD13	45:EO:194:TRP:HD1	1.70	0.55
48:AR:169:ASP:HA	48:AR:175:LYS:HG3	1.88	0.55
83:At:59:ALA:HB2	83:At:86:MET:HB3	1.88	0.55
2:E1:479:ARG:NH2	12:AA:515:U:OP1	2.38	0.55
3:A2:28:PRO:HG2	63:AY:227:ASP:HB3	1.89	0.55
22:BE:286:SER:OG	22:BE:291:ASP:O	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AF:144:LEU:HD22	24:AF:226:MET:HE2	1.88	0.55
25:BF:387:ASN:OD1	37:BL:144:GLN:NE2	2.35	0.55
26:EF:99:ILE:HD11	26:EF:152:PRO:HG2	1.88	0.55
29:EH:1:MET:N	29:EH:41:ALA:O	2.40	0.55
29:EH:213:ASP:HB2	29:EH:324:ARG:HA	1.88	0.55
34:AK:94:PHE:C	59:BV:91:LYS:HG3	2.32	0.55
39:EM:236:LEU:HD12	39:EM:237:PRO:HD2	1.88	0.55
7:E4:111:ARG:NH1	7:E4:143:GLY:O	2.39	0.55
12:AA:929:U:OP1	17:EB:213:ARG:NH2	2.40	0.55
14:EA:199:ILE:HD13	14:EA:242:LEU:HD11	1.89	0.55
16:BB:355:GLU:OE2	16:BB:430:TYR:OH	2.24	0.55
16:BB:414:THR:HG23	16:BB:417:GLU:H	1.72	0.55
29:EH:459:PRO:HG3	29:EH:490:PRO:HD3	1.88	0.55
45:EO:13:HIS:HE1	45:EO:50:LEU:HA	1.71	0.55
45:EP:26:LEU:HB3	45:EP:28:GLN:HE21	1.70	0.55
2:E1:214:ARG:NH2	2:E1:453:ALA:O	2.38	0.55
12:AA:48:U:OP1	65:Ba:105:ARG:NH2	2.39	0.55
12:AA:474:A:O2'	46:AP:117:TRP:O	2.25	0.55
19:BD:277:MET:HE3	28:BH:175:GLU:HA	1.89	0.55
21:AE:373:LYS:HA	44:BO:232:GLU:HG3	1.88	0.55
21:AE:389:TYR:HB2	74:E9:251:LYS:HE3	1.88	0.55
23:EE:234:GLN:NE2	34:AK:110:LYS:O	2.40	0.55
23:EE:461:ALA:HB2	34:AK:113:LEU:HG	1.89	0.55
54:BT:33:ASN:HD21	60:AW:55:THR:HA	1.70	0.55
58:AV:114:LYS:NZ	79:Ao:80:SER:O	2.38	0.55
58:AV:124:THR:HG23	69:Af:99:PHE:HB2	1.87	0.55
6:E3:435:ARG:NH1	6:E3:439:ASP:OD1	2.39	0.55
12:AA:453:U:OP1	41:AN:185:LYS:NZ	2.38	0.55
18:EC:172:LYS:NZ	18:EC:214:THR:O	2.38	0.55
20:ED:208:ASN:OD1	20:ED:209:LEU:N	2.40	0.55
20:ED:481:ALA:O	20:ED:486:MET:N	2.39	0.55
29:EH:34:THR:O	29:EH:106:ARG:NH1	2.39	0.55
29:EH:234:ARG:HH21	71:Ag:154:GLN:HE22	1.53	0.55
56:AU:65:ASN:HD22	56:AU:97:GLN:HE21	1.53	0.55
75:Al:147:PRO:HB2	75:Al:166:ILE:HG23	1.88	0.55
2:E1:241:ARG:NH1	10:E6:153:ASP:OD2	2.40	0.55
5:A3:114:HIS:HB3	49:BR:204:LEU:HG	1.88	0.55
5:A3:191:LYS:HE2	25:BF:311:GLN:HE21	1.71	0.55
11:A8:91:LYS:HB2	12:AA:312:U:H5'	1.89	0.55
16:BB:147:ASN:OD1	16:BB:148:LYS:N	2.39	0.55
43:EN:371:SER:OG	50:ER:68:ASN:ND2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:ET:56:VAL:H	55:ET:92:GLN:HE22	1.55	0.55
61:BW:10:TYR:OH	61:BW:11:ARG:NH1	2.40	0.55
79:Ao:134:PRO:O	79:Ao:140:ARG:NH1	2.39	0.55
84:Av:194:MET:HG3	84:Av:198:LYS:HE3	1.88	0.55
6:E3:394:GLU:HB2	6:E3:420:ARG:HG2	1.89	0.55
10:E6:143:GLU:HG3	42:BN:207:ASN:HB3	1.88	0.55
12:AA:1107:U:N3	12:AA:1156:A:OP2	2.32	0.55
13:BA:808:PRO:HD2	21:AE:191:ASN:HD21	1.72	0.55
20:ED:48:ARG:HB3	20:ED:261:ARG:HH22	1.71	0.55
21:AE:54:ARG:HD2	80:Ap:97:PHE:HE1	1.72	0.55
24:AF:38:ARG:CZ	71:Ag:50:ARG:HH12	2.19	0.55
10:E6:215:ARG:NH1	10:E6:218:GLU:OE1	2.39	0.55
12:AA:1113:U:OP1	80:Ap:58:TYR:N	2.31	0.55
19:BD:272:VAL:HG13	19:BD:275:ALA:HB2	1.89	0.55
34:AK:93:HIS:HA	59:BV:91:LYS:HD2	1.88	0.55
37:BL:241:ASP:HB2	37:BL:244:GLU:HB2	1.88	0.55
54:BT:20:GLY:O	61:BW:52:LYS:NZ	2.30	0.55
57:BU:54:SER:OG	57:BU:56:TRP:NE1	2.40	0.55
62:AX:86:ASN:HB2	65:Ba:29:LEU:HD21	1.88	0.55
2:E1:474:GLY:HA3	48:AR:212:TRP:HE1	1.71	0.55
12:AA:149:U:OP1	24:AF:202:LYS:NZ	2.40	0.55
12:AA:588:A:OP1	53:AT:140:ARG:NH2	2.40	0.55
12:AA:989:U:OP1	14:EA:512:ARG:NH1	2.40	0.55
13:BA:181:VAL:HG23	13:BA:240:ALA:HB2	1.87	0.55
46:AP:190:ASN:OD1	46:AP:192:ASN:ND2	2.40	0.55
45:EP:312:TRP:HA	45:EP:315:GLN:HG3	1.88	0.55
1:A1:144:SER:HA	1:A1:157:ARG:HH12	1.72	0.54
2:E1:414:GLU:HB3	72:E7:30:LEU:HD13	1.88	0.54
12:AA:158:A:OP2	46:AP:188:ARG:NH2	2.40	0.54
18:EC:112:ARG:NH1	29:EH:480:GLU:OE2	2.35	0.54
38:EL:284:ILE:HD11	38:EL:296:LEU:HD12	1.89	0.54
43:EN:196:ARG:NH1	43:EN:233:SER:O	2.40	0.54
46:AP:177:LEU:HD23	46:AP:223:VAL:HG21	1.89	0.54
54:BT:77:ARG:NH1	54:BT:85:GLU:OE2	2.36	0.54
60:AW:187:GLU:HB2	60:AW:193:LYS:HE3	1.90	0.54
10:E6:348:LYS:HE2	10:E6:352:VAL:HG21	1.89	0.54
12:AA:138:U:H2'	12:AA:139:U:C6	2.42	0.54
13:BA:528:VAL:HG12	13:BA:532:MET:HE3	1.89	0.54
23:EE:461:ALA:HA	34:AK:111:SER:HB2	1.88	0.54
62:AX:78:ARG:HD2	62:AX:79:PRO:HA	1.90	0.54
62:AX:196:ARG:NH2	72:E7:57:TYR:OH	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:E9:259:CYS:HB3	74:E9:325:CYS:HB3	1.90	0.54
75:A1:135:PRO:HG2	75:A1:175:ARG:HE	1.71	0.54
29:EH:218:ALA:HB2	29:EH:316:VAL:HA	1.88	0.54
34:AK:75:LEU:HD21	34:AK:106:VAL:HG11	1.89	0.54
38:EL:236:LEU:HD22	38:EL:291:PRO:HG3	1.89	0.54
60:AW:45:ARG:NH1	60:AW:46:PRO:O	2.39	0.54
75:A1:132:ASP:OD1	75:A1:133:THR:N	2.39	0.54
5:A3:174:LEU:HA	5:A3:177:VAL:HG22	1.89	0.54
6:E3:177:ILE:O	6:E3:273:VAL:HA	2.07	0.54
8:A5:79:LYS:NZ	13:BA:776:LEU:O	2.40	0.54
12:AA:921:U:H2'	12:AA:922:A:C8	2.43	0.54
12:AA:953:U:OP1	20:ED:130:TYR:OH	2.21	0.54
20:ED:588:LEU:HB3	20:ED:592:SER:HB2	1.90	0.54
34:AK:302:THR:OG1	34:AK:304:GLU:OE1	2.26	0.54
56:AU:59:ARG:HA	56:AU:62:VAL:HG12	1.89	0.54
75:A1:99:PRO:HG3	75:A1:120:GLY:HA2	1.89	0.54
1:A1:143:ARG:O	1:A1:157:ARG:NH1	2.41	0.54
3:A2:380:ARG:HH21	62:AX:122:THR:HG21	1.73	0.54
12:AA:137:U:H2'	12:AA:138:U:C6	2.41	0.54
12:AA:787:A:H2'	12:AA:788:A:C8	2.43	0.54
20:ED:381:ARG:HH12	20:ED:500:ASN:HB2	1.71	0.54
24:AF:119:ASN:OD1	24:AF:120:LEU:N	2.39	0.54
12:AA:471:U:O4	25:BF:261:ARG:NH2	2.41	0.54
18:EC:164:ASN:OD1	18:EC:165:GLU:N	2.39	0.54
19:BD:481:GLN:HB2	19:BD:484:LEU:HD13	1.90	0.54
38:EL:72:TYR:HE2	38:EL:75:MET:HB3	1.73	0.54
45:EP:224:LEU:O	45:EP:227:SER:OG	2.24	0.54
60:AW:128:LEU:HD12	60:AW:129:PRO:HD2	1.88	0.54
6:E3:402:ARG:O	6:E3:414:ARG:NH2	2.40	0.54
12:AA:926:A:H2'	12:AA:927:U:O4'	2.07	0.54
17:EB:134:MET:HG3	17:EB:156:PRO:HB3	1.90	0.54
20:ED:139:ARG:NH2	43:EN:176:TYR:O	2.41	0.54
21:AE:46:PRO:HD3	80:Ap:47:TYR:HB3	1.89	0.54
29:EH:56:SER:OG	29:EH:366:ASP:O	2.25	0.54
34:AK:130:ARG:HH12	59:BV:28:ASP:HA	1.71	0.54
39:EM:82:ARG:HH21	39:EM:110:MET:HG2	1.72	0.54
47:BQ:46:SER:OG	47:BQ:166:ASP:OD1	2.21	0.54
49:BR:34:GLY:HA2	49:BR:95:ARG:HE	1.73	0.54
90:ER:200:PM8:H382	52:ES:52:ASN:HD22	1.72	0.54
60:AW:62:ASP:O	60:AW:75:GLN:NE2	2.41	0.54
3:A2:58:ARG:HB2	3:A2:87:ILE:HG21	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A2:414:THR:HG21	35:BK:373:PRO:HG3	1.90	0.54
4:E2:309:GLN:HB2	7:E4:55:ARG:HD3	1.89	0.54
7:E4:29:GLN:HG2	7:E4:45:SER:HB2	1.90	0.54
7:E4:149:VAL:HG22	7:E4:159:VAL:HG12	1.90	0.54
12:AA:103:U:OP2	63:AY:10:LYS:NZ	2.40	0.54
21:AE:135:SER:HA	21:AE:222:THR:HG21	1.89	0.54
23:EE:120:VAL:C	23:EE:122:TRP:H	2.15	0.54
38:EL:125:GLY:HA2	38:EL:132:ASP:HA	1.90	0.54
38:EL:311:GLU:HG2	38:EL:487:MET:HE3	1.89	0.54
48:AR:245:ASP:OD1	72:E7:65:ARG:NH1	2.41	0.54
53:AT:18:ASN:HA	53:AT:21:PHE:HD2	1.70	0.54
7:E4:185:VAL:HG23	7:E4:198:LEU:HB3	1.90	0.54
7:E4:311:SER:O	7:E4:315:GLU:HG2	2.07	0.54
11:A8:68:GLN:NE2	12:AA:65:U:O4	2.41	0.54
13:BA:440:LYS:HD3	13:BA:477:LEU:HD23	1.90	0.54
14:EA:142:ASP:HB3	87:EA:1001:GTP:O3'	2.08	0.54
16:BB:253:PRO:HB2	16:BB:387:ALA:HB2	1.89	0.54
18:EC:363:LYS:NZ	18:EC:400:ASP:OD1	2.38	0.54
24:AF:76:ILE:HB	54:BT:148:PRO:HG2	1.90	0.54
26:EF:310:ALA:HA	26:EF:313:TRP:HD1	1.73	0.54
30:AI:11:PRO:HG3	65:Ba:81:GLN:HA	1.90	0.54
38:EL:251:SER:HB3	38:EL:271:LEU:HD11	1.90	0.54
43:EN:357:LEU:HD12	43:EN:448:ALA:HB1	1.89	0.54
63:AY:316:PHE:O	63:AY:321:GLN:NE2	2.40	0.54
2:E1:203:TRP:HB3	6:E3:197:VAL:HG23	1.89	0.54
3:A2:208:TRP:HH2	24:AF:408:THR:HA	1.71	0.54
12:AA:187:A:H3'	12:AA:287:A:H61	1.73	0.54
12:AA:443:A:H2'	12:AA:444:G:C8	2.43	0.54
13:BA:673:ASP:OD2	69:Af:155:ARG:NH1	2.40	0.54
20:ED:78:ASP:OD1	20:ED:82:ASP:N	2.40	0.54
20:ED:405:GLU:N	20:ED:440:GLU:OE2	2.41	0.54
29:EH:101:PRO:HD3	29:EH:390:TYR:HE2	1.72	0.54
46:AP:100:THR:HG22	46:AP:102:GLU:H	1.72	0.54
8:A5:27:LYS:HZ1	12:AA:506:U:HO2'	1.52	0.53
10:E6:409:PRO:HG3	10:E6:440:ARG:HH11	1.73	0.53
12:AA:533:A:N6	12:AA:545:U:N3	2.56	0.53
12:AA:549:G:N2	72:E7:47:ASP:OD2	2.40	0.53
12:AA:813:U:O2	12:AA:816:C:N4	2.41	0.53
17:EB:741:PRO:HG2	68:Ae:58:ALA:HA	1.89	0.53
19:BD:225:LEU:HD11	19:BD:420:ARG:HD2	1.90	0.53
19:BD:239:ALA:HB1	19:BD:246:GLU:H	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BF:63:ARG:HH22	25:BF:239:VAL:HG23	1.73	0.53
44:BO:121:GLN:NE2	51:BS:97:ASP:OD2	2.40	0.53
48:AR:49:GLY:HA2	48:AR:57:LYS:HE3	1.90	0.53
3:A2:99:LYS:NZ	35:BK:357:LEU:O	2.40	0.53
4:E2:452:SER:OG	4:E2:456:ARG:NH1	2.42	0.53
12:AA:55:A:OP1	62:AX:72:HIS:ND1	2.32	0.53
17:EB:529:ASP:HA	17:EB:534:ARG:HH11	1.73	0.53
24:AF:77:PRO:HG2	25:BF:360:THR:HG21	1.90	0.53
25:BF:406:LYS:HA	25:BF:409:LYS:HG2	1.89	0.53
33:BJ:266:GLN:HE21	33:BJ:270:ARG:HE	1.55	0.53
45:EO:54:GLY:O	45:EO:95:HIS:ND1	2.41	0.53
65:Ba:7:LEU:HA	65:Ba:30:LEU:HD13	1.90	0.53
80:Ap:69:GLY:O	80:Ap:85:LYS:NZ	2.40	0.53
2:E1:417:ARG:NH2	12:AA:581:U:OP1	2.42	0.53
12:AA:317:A:H2'	12:AA:318:A:C8	2.43	0.53
31:BI:276:ILE:HD13	71:Ag:158:GLU:HG2	1.90	0.53
38:EL:464:ASP:OD1	80:Ap:286:LYS:NZ	2.41	0.53
43:EN:423:LEU:HB3	43:EN:516:ARG:HE	1.73	0.53
45:EO:20:LEU:HD21	45:EO:236:LEU:HD11	1.91	0.53
45:EP:21:LEU:HB3	45:EP:194:TRP:NE1	2.23	0.53
71:Ag:57:ILE:HD11	71:Ag:79:ILE:HG23	1.90	0.53
10:E6:265:LEU:HD11	10:E6:294:LEU:HD12	1.89	0.53
12:AA:99:A:O2'	22:BE:41:HIS:O	2.25	0.53
13:BA:175:PRO:HA	13:BA:180:ARG:HE	1.73	0.53
25:BF:280:ASP:OD1	25:BF:280:ASP:N	2.40	0.53
28:BH:165:GLN:HG3	28:BH:166:VAL:HG13	1.91	0.53
34:AK:130:ARG:CZ	59:BV:28:ASP:HA	2.38	0.53
39:EM:41:GLU:HA	39:EM:44:VAL:HG12	1.89	0.53
7:E4:233:ARG:HH22	7:E4:329:ARG:HG3	1.74	0.53
24:AF:272:PHE:HE2	24:AF:299:ASN:HB2	1.73	0.53
26:EF:310:ALA:O	26:EF:317:ARG:NH1	2.41	0.53
33:BJ:104:SER:HB3	33:BJ:223:THR:HG23	1.90	0.53
43:EN:265:THR:HG21	43:EN:319:THR:HA	1.91	0.53
72:E7:89:ALA:HA	72:E7:92:ARG:HG2	1.90	0.53
5:A3:180:ARG:NH1	25:BF:318:ASP:OD1	2.42	0.53
7:E4:421:LEU:HB2	7:E4:424:VAL:HG12	1.89	0.53
11:A8:128:ARG:O	11:A8:135:ARG:NH2	2.42	0.53
12:AA:1172:A:C8	13:BA:774:LYS:HG2	2.43	0.53
14:EA:320:LYS:HG2	87:EA:1004:GTP:O2B	2.07	0.53
20:ED:523:PRO:HD2	49:BR:13:PRO:HD3	1.91	0.53
21:AE:252:ASP:OD2	53:AT:7:ARG:NH2	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AK:156:GLU:HA	34:AK:159:LYS:HD2	1.91	0.53
38:EL:376:GLU:OE1	38:EL:376:GLU:N	2.41	0.53
45:EO:52:GLN:HG3	45:EP:131:GLN:HE22	1.74	0.53
66:Bb:36:TYR:O	66:Bb:38:HIS:ND1	2.41	0.53
10:E6:90:LEU:HD23	48:AR:203:PRO:HG3	1.90	0.53
12:AA:1136:C:H4'	23:EE:146:LYS:HD2	1.91	0.53
22:BE:122:LYS:HD2	60:AW:238:PRO:HB3	1.90	0.53
27:EG:38:GLN:N	27:EG:121:TYR:OH	2.39	0.53
54:BT:14:LYS:O	61:BW:74:ARG:NH2	2.42	0.53
66:Bb:18:ARG:NH2	66:Bb:19:TYR:OH	2.42	0.53
79:Ao:216:SER:HA	79:Ao:219:VAL:HG12	1.91	0.53
7:E4:38:GLN:HB2	7:E4:421:LEU:HD21	1.90	0.53
13:BA:335:PRO:O	13:BA:339:ASP:HB2	2.09	0.53
14:EA:309:ARG:H	14:EA:392:HIS:CD2	2.26	0.53
17:EB:462:TRP:O	29:EH:495:ARG:NH1	2.40	0.53
19:BD:123:LEU:HD13	19:BD:160:ILE:HD11	1.91	0.53
24:AF:125:ILE:HA	54:BT:128:ARG:HH12	1.73	0.53
25:BF:246:TRP:O	25:BF:320:LYS:NZ	2.39	0.53
33:BJ:250:LEU:HD11	63:AY:285:MET:HE2	1.90	0.53
34:AK:233:LEU:HG	34:AK:246:ASN:HD21	1.74	0.53
43:EN:312:GLN:OE1	43:EN:312:GLN:N	2.41	0.53
47:BQ:48:GLU:OE1	47:BQ:163:GLN:NE2	2.39	0.53
49:BR:62:GLU:OE2	49:BR:65:ARG:NH2	2.41	0.53
64:BZ:27:PRO:HA	64:BZ:34:VAL:HG11	1.91	0.53
12:AA:500:A:H2'	12:AA:501:A:H8	1.74	0.53
12:AA:979:U:H5'	12:AA:980:U:H2'	1.91	0.53
12:AA:1106:U:O2'	53:AT:11:HIS:ND1	2.33	0.53
20:ED:141:LEU:HB3	20:ED:219:TYR:HB3	1.90	0.53
29:EH:388:ARG:NH2	34:AK:292:LEU:O	2.42	0.53
41:AN:46:LEU:HB2	41:AN:171:PRO:HB2	1.90	0.53
49:BR:145:PRO:HD2	79:Ao:217:ALA:HB1	1.90	0.53
54:BT:97:THR:O	61:BW:75:ARG:NH2	2.32	0.53
55:ET:79:ILE:HG23	84:Av:197:ARG:HD2	1.91	0.53
3:A2:190:GLN:O	3:A2:194:GLN:NE2	2.41	0.53
13:BA:433:ARG:HH21	69:Af:149:LEU:HD12	1.74	0.53
14:EA:513:ILE:HD13	14:EA:528:LEU:HD23	1.90	0.53
28:BH:75:ARG:O	28:BH:79:GLN:NE2	2.41	0.53
29:EH:9:ARG:HH21	34:AK:298:VAL:HG11	1.74	0.53
29:EH:568:ARG:HH21	66:Bb:36:TYR:HE1	1.57	0.53
31:BI:152:GLN:HE21	31:BI:156:PHE:HE2	1.57	0.53
34:AK:217:TYR:HD1	34:AK:221:HIS:HE2	1.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:BL:229:SER:O	71:Ag:11:LYS:NZ	2.34	0.53
43:EN:554:ASP:N	43:EN:554:ASP:OD1	2.41	0.53
60:AW:170:LYS:HE3	63:AY:63:ARG:HA	1.91	0.53
63:AY:231:ASP:HB3	68:Ae:160:ALA:HB2	1.90	0.53
3:A2:145:LEU:HG	3:A2:350:VAL:HG12	1.90	0.52
6:E3:158:LEU:HD22	6:E3:248:VAL:HG11	1.91	0.52
12:AA:88:G:H4'	25:BF:403:LEU:HD23	1.91	0.52
12:AA:393:A:OP1	31:BI:299:ARG:NH2	2.33	0.52
22:BE:127:SER:HA	22:BE:152:ARG:HH12	1.74	0.52
25:BF:297:PHE:HD1	25:BF:302:ASP:HB3	1.74	0.52
64:BZ:96:GLN:HE22	64:BZ:125:SER:HA	1.73	0.52
12:AA:826:A:OP1	27:EG:45:ARG:N	2.34	0.52
21:AE:331:ALA:HB1	21:AE:335:THR:HG21	1.89	0.52
24:AF:215:ASP:OD1	24:AF:218:THR:OG1	2.22	0.52
29:EH:388:ARG:HH21	34:AK:296:GLY:HA3	1.74	0.52
34:AK:119:PRO:HG2	59:BV:89:ILE:HD12	1.91	0.52
38:EL:484:ASN:ND2	38:EL:487:MET:SD	2.82	0.52
44:BO:58:SER:HB3	44:BO:61:THR:HG22	1.91	0.52
51:BS:72:THR:HG22	51:BS:74:GLU:H	1.74	0.52
53:AT:98:THR:OG1	74:E9:340:HIS:NE2	2.43	0.52
66:Bb:134:LEU:HG	66:Bb:139:TYR:HB3	1.91	0.52
2:E1:336:ASP:HB3	2:E1:339:GLU:HB3	1.92	0.52
3:A2:199:CYS:HB2	3:A2:306:VAL:HG23	1.91	0.52
16:BB:275:VAL:HG12	16:BB:277:HIS:H	1.74	0.52
19:BD:187:ASP:OD2	52:ES:57:ARG:NH2	2.42	0.52
26:EF:88:SER:HA	26:EF:91:ARG:HD2	1.91	0.52
27:EG:146:ASN:O	27:EG:150:ARG:HG2	2.09	0.52
58:AV:96:VAL:HG22	71:Ag:105:GLN:HE22	1.73	0.52
2:E1:164:ASP:HB3	4:E2:495:THR:HG21	1.92	0.52
3:A2:186:GLU:O	3:A2:189:GLU:HG3	2.10	0.52
14:EA:148:ARG:HH11	14:EA:341:SER:HA	1.75	0.52
17:EB:573:ARG:NH1	89:EB:1001:ATP:O3G	2.36	0.52
23:EE:344:ARG:NH2	38:EL:542:ASP:OD1	2.36	0.52
26:EF:253:LEU:HD21	26:EF:313:TRP:HE1	1.74	0.52
28:BH:99:GLN:NE2	28:BH:169:GLU:OE2	2.43	0.52
74:E9:145:GLN:HG3	74:E9:146:LEU:H	1.74	0.52
84:Av:71:VAL:HG21	84:Av:120:TRP:HB3	1.90	0.52
7:E4:86:ARG:NH2	7:E4:163:SER:OG	2.42	0.52
12:AA:379:U:O2'	12:AA:461:U:O2'	2.24	0.52
18:EC:394:GLY:O	74:E9:247:GLN:NE2	2.42	0.52
21:AE:377:ASP:OD2	53:AT:39:ARG:NH1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:EE:319:LEU:HD23	23:EE:384:LEU:HB2	1.92	0.52
24:AF:337:ARG:NH2	54:BT:25:ASP:OD1	2.42	0.52
26:EF:220:GLY:HA2	26:EF:223:PHE:HD1	1.75	0.52
30:AI:28:PRO:HB2	30:AI:83:ILE:HD11	1.92	0.52
34:AK:25:ARG:N	34:AK:159:LYS:HZ1	2.08	0.52
53:AT:62:PHE:HB2	53:AT:69:VAL:HG13	1.91	0.52
54:BT:83:GLU:OE2	54:BT:86:ARG:NH2	2.42	0.52
1:A1:100:LYS:NZ	12:AA:891:G:OP1	2.41	0.52
5:A3:192:ARG:HE	75:AI:131:LEU:HD11	1.73	0.52
7:E4:366:LEU:HG	7:E4:367:LEU:HG	1.91	0.52
20:ED:6:ARG:O	47:BQ:230:ARG:NH2	2.39	0.52
37:BL:55:LEU:O	56:AU:19:ARG:NH2	2.42	0.52
46:AP:206:VAL:HG21	46:AP:216:PHE:CZ	2.44	0.52
59:BV:90:PHE:HB2	59:BV:93:GLN:HB3	1.92	0.52
10:E6:294:LEU:HD21	10:E6:307:LEU:HB3	1.92	0.52
12:AA:500:A:H2'	12:AA:501:A:C8	2.45	0.52
19:BD:222:ALA:HA	19:BD:225:LEU:HD12	1.90	0.52
20:ED:26:SER:HA	20:ED:29:ARG:HD2	1.92	0.52
28:BH:83:GLU:O	28:BH:87:LEU:HG	2.09	0.52
33:BJ:123:ASP:N	33:BJ:221:ARG:HH22	2.08	0.52
38:EL:387:LYS:HG2	38:EL:391:HIS:HE1	1.73	0.52
49:BR:174:ALA:HB1	49:BR:186:ASN:HB2	1.90	0.52
60:AW:138:VAL:HG13	60:AW:174:ILE:HD13	1.91	0.52
62:AX:188:VAL:HG22	62:AX:216:VAL:HG12	1.91	0.52
72:E7:52:MET:HE3	72:E7:56:ILE:HD12	1.91	0.52
75:AI:139:HIS:NE2	75:AI:170:GLU:OE1	2.37	0.52
1:A1:131:GLU:OE1	30:AI:141:ARG:NE	2.43	0.52
1:A1:138:ASN:HD21	33:BJ:299:ARG:HH22	1.55	0.52
4:E2:207:VAL:HG12	4:E2:209:HIS:H	1.75	0.52
6:E3:198:ASP:O	6:E3:319:ARG:NH2	2.40	0.52
12:AA:35:G:N2	12:AA:36:U:O4	2.36	0.52
12:AA:533:A:N6	12:AA:545:U:H3	2.08	0.52
20:ED:555:GLU:O	20:ED:560:ASN:ND2	2.43	0.52
21:AE:71:MET:HE2	80:Ap:110:LYS:HD2	1.92	0.52
24:AF:215:ASP:OD1	24:AF:215:ASP:N	2.43	0.52
26:EF:251:PRO:HA	26:EF:296:LEU:HB2	1.92	0.52
64:BZ:64:LEU:O	64:BZ:66:GLN:NE2	2.38	0.52
80:Ap:260:MET:HA	80:Ap:260:MET:HE2	1.91	0.52
12:AA:157:U:OP2	24:AF:217:LYS:NZ	2.40	0.52
21:AE:170:VAL:HG23	21:AE:233:LEU:HD21	1.91	0.52
24:AF:109:MET:HE1	61:BW:149:ASN:HD21	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:EG:32:TYR:OH	27:EG:136:ASP:O	2.28	0.52
27:EG:123:VAL:HG21	27:EG:140:CYS:HB3	1.92	0.52
43:EN:217:LEU:HD21	43:EN:282:SER:HB3	1.90	0.52
45:EO:19:SER:HB3	45:EO:97:PRO:HB3	1.92	0.52
47:BQ:59:GLU:HG2	47:BQ:62:ARG:HH21	1.75	0.52
64:BZ:58:LEU:HD23	64:BZ:59:ILE:HG23	1.92	0.52
4:E2:313:LEU:HD23	4:E2:315:ARG:HE	1.75	0.52
6:E3:554:LEU:HD12	6:E3:555:PRO:HD2	1.91	0.52
7:E4:187:LEU:HB2	7:E4:196:GLU:HB3	1.91	0.52
12:AA:45:U:O4	65:Ba:37:ARG:NH1	2.40	0.52
13:BA:448:GLN:HB2	13:BA:486:PHE:HE1	1.74	0.52
17:EB:144:PRO:HD2	17:EB:147:GLU:OE1	2.10	0.52
18:EC:311:THR:O	18:EC:312:ARG:NH2	2.35	0.52
63:AY:52:ASP:OD1	63:AY:53:ARG:N	2.43	0.52
64:BZ:4:SER:HB3	64:BZ:190:GLU:HG2	1.91	0.52
66:Bb:53:ARG:HH22	66:Bb:100:GLU:H	1.56	0.52
67:Bc:90:GLU:HA	67:Bc:93:TRP:CD1	2.45	0.52
71:Ag:98:CYS:SG	71:Ag:99:ALA:N	2.82	0.52
4:E2:189:PHE:HA	4:E2:222:LEU:HG	1.92	0.51
4:E2:206:SER:O	57:BU:66:MET:N	2.40	0.51
4:E2:274:PRO:HB3	4:E2:322:LEU:HD12	1.91	0.51
7:E4:22:GLN:HA	7:E4:65:GLU:HG3	1.90	0.51
12:AA:321:A:OP1	55:ET:4:ARG:NH1	2.43	0.51
12:AA:1007:C:H4'	12:AA:1082:C:H1'	1.91	0.51
13:BA:792:SER:HB3	13:BA:800:TRP:CD1	2.45	0.51
14:EA:310:ILE:HD12	14:EA:357:LEU:HD12	1.92	0.51
17:EB:351:LEU:HD21	17:EB:489:ILE:HD13	1.91	0.51
29:EH:15:PRO:HA	34:AK:312:ASN:HB3	1.91	0.51
31:BI:150:VAL:HG13	31:BI:166:LEU:HD13	1.91	0.51
35:BK:349:VAL:HG21	35:BK:363:ILE:HG13	1.91	0.51
43:EN:274:LEU:HB2	43:EN:279:TRP:CE2	2.45	0.51
45:EO:95:HIS:HB2	45:EP:127:VAL:HG21	1.91	0.51
45:EP:155:HIS:NE2	45:EP:267:GLN:OE1	2.37	0.51
58:AV:140:VAL:HA	58:AV:173:ILE:HG22	1.92	0.51
12:AA:94:U:H2'	12:AA:95:U:C6	2.45	0.51
12:AA:318:A:H2'	12:AA:319:A:C8	2.45	0.51
12:AA:456:U:H4'	12:AA:457:A:C8	2.44	0.51
21:AE:180:VAL:HG12	80:Ap:104:ARG:HG3	1.92	0.51
22:BE:79:VAL:O	68:Ae:192:ARG:NH2	2.34	0.51
39:EM:19:VAL:HA	39:EM:22:VAL:HG22	1.92	0.51
44:BO:90:ALA:O	44:BO:94:ILE:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:BQ:173:ARG:HA	47:BQ:176:VAL:HG22	1.92	0.51
48:AR:139:MET:SD	48:AR:167:ASN:ND2	2.83	0.51
63:AY:243:ASP:OD1	63:AY:243:ASP:N	2.42	0.51
3:A2:275:LEU:HD22	35:BK:328:LEU:HG	1.92	0.51
12:AA:952:U:OP1	17:EB:247:ARG:NH2	2.43	0.51
24:AF:132:PRO:O	24:AF:136:GLY:CA	2.59	0.51
30:AI:99:LEU:O	30:AI:180:LYS:NZ	2.43	0.51
41:AN:54:LEU:HD13	41:AN:93:MET:HE2	1.92	0.51
48:AR:80:LYS:NZ	48:AR:82:TYR:O	2.43	0.51
6:E3:435:ARG:HA	48:AR:274:LEU:HD12	1.91	0.51
13:BA:279:VAL:HA	13:BA:285:TRP:HZ2	1.74	0.51
23:EE:163:HIS:HD1	23:EE:186:TRP:CD1	2.28	0.51
37:BL:165:LEU:HD23	37:BL:239:VAL:HG11	1.92	0.51
43:EN:499:LEU:O	43:EN:503:HIS:ND1	2.40	0.51
59:BV:33:TYR:OH	59:BV:98:ILE:O	2.25	0.51
65:Ba:58:MET:HG2	65:Ba:65:GLU:HA	1.92	0.51
2:E1:456:LEU:HB2	12:AA:522:A:N7	2.26	0.51
10:E6:394:GLN:HA	10:E6:397:ASN:HD21	1.74	0.51
12:AA:128:A:H5'	46:AP:125:LYS:HG2	1.91	0.51
17:EB:211:THR:OG1	17:EB:524:ARG:NH2	2.41	0.51
20:ED:161:ARG:HA	20:ED:164:TYR:CE2	2.45	0.51
21:AE:140:MET:SD	21:AE:168:ASN:ND2	2.84	0.51
22:BE:50:TYR:OH	63:AY:69:ASP:HB2	2.09	0.51
24:AF:364:TYR:OH	24:AF:384:TYR:O	2.27	0.51
35:BK:188:ASN:O	35:BK:190:LYS:NZ	2.43	0.51
38:EL:451:PRO:HB3	70:Bf:66:SER:HB3	1.93	0.51
58:AV:82:ILE:HG22	58:AV:115:VAL:HG12	1.91	0.51
60:AW:10:MET:HB3	60:AW:12:HIS:HD2	1.76	0.51
7:E4:155:SER:HA	7:E4:182:VAL:HA	1.91	0.51
8:A5:61:ALA:HB1	22:BE:389:GLN:HA	1.91	0.51
10:E6:351:VAL:HG13	10:E6:352:VAL:HG13	1.91	0.51
12:AA:5:U:H2'	12:AA:6:A:H8	1.75	0.51
12:AA:545:U:H4'	68:Ae:109:ARG:HH21	1.76	0.51
12:AA:1130:A:OP2	67:Bc:130:TRP:NE1	2.44	0.51
12:AA:1156:A:H61	53:AT:3:TYR:HE2	1.59	0.51
13:BA:329:GLU:N	13:BA:329:GLU:OE1	2.44	0.51
20:ED:300:HIS:NE2	20:ED:304:GLU:OE2	2.44	0.51
38:EL:287:SER:HB3	38:EL:433:TYR:CZ	2.46	0.51
39:EM:66:ALA:HA	39:EM:69:VAL:HG22	1.92	0.51
12:AA:347:A:OP1	17:EB:622:ARG:NH1	2.43	0.51
12:AA:1078:A:O2'	18:EC:132:ALA:O	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AA:1107:U:OP2	21:AE:198:LYS:NZ	2.42	0.51
12:AA:1172:A:H61	13:BA:783:THR:HA	1.74	0.51
23:EE:321:PRO:HG2	23:EE:407:VAL:HA	1.92	0.51
35:BK:208:MET:HE3	35:BK:213:VAL:HG22	1.93	0.51
45:EO:49:SER:HB3	45:EO:52:GLN:NE2	2.26	0.51
71:Ag:156:GLU:HA	71:Ag:159:ILE:HG22	1.92	0.51
17:EB:73:VAL:HG13	17:EB:563:ASN:HB3	1.93	0.51
22:BE:300:ARG:O	22:BE:304:LEU:HG	2.11	0.51
24:AF:416:TYR:HH	61:BW:79:HIS:HE2	1.58	0.51
28:BH:129:TYR:CD2	28:BH:169:GLU:HB3	2.46	0.51
37:BL:181:LEU:HD13	37:BL:295:VAL:HG12	1.93	0.51
46:AP:115:MET:HE2	46:AP:118:MET:HG3	1.92	0.51
2:E1:450:ARG:HB3	2:E1:453:ALA:HB3	1.93	0.51
4:E2:369:LYS:HA	10:E6:178:ARG:HH11	1.76	0.51
10:E6:446:ASN:HB3	10:E6:449:ALA:HB3	1.91	0.51
12:AA:18:G:O2'	12:AA:99:A:N6	2.43	0.51
19:BD:122:PHE:HE1	19:BD:157:ASN:HB3	1.75	0.51
20:ED:66:LYS:NZ	20:ED:611:ASP:OD2	2.40	0.51
23:EE:118:GLN:O	23:EE:132:HIS:NE2	2.36	0.51
59:BV:81:GLU:HA	59:BV:98:ILE:CG2	2.39	0.51
60:AW:134:LEU:HD13	60:AW:231:VAL:HG22	1.92	0.51
62:AX:144:VAL:HG22	62:AX:163:ILE:HG22	1.92	0.51
84:Av:181:THR:HG22	84:Av:184:MET:HB2	1.91	0.51
1:A1:30:LEU:HD21	12:AA:62:A:H2	1.76	0.51
10:E6:102:SER:O	10:E6:106:HIS:ND1	2.37	0.51
12:AA:361:U:OP2	27:EG:48:ARG:NH2	2.37	0.51
12:AA:947:U:H4'	55:ET:82:ARG:HG2	1.92	0.51
16:BB:351:LEU:HD11	16:BB:418:ARG:HD3	1.93	0.51
21:AE:293:PRO:HD2	41:AN:110:PRO:HD3	1.93	0.51
24:AF:68:THR:HG21	25:BF:366:ARG:HD3	1.93	0.51
25:BF:141:MET:HE2	46:AP:39:ASN:HB3	1.92	0.51
30:AI:11:PRO:HB2	65:Ba:84:TYR:HD2	1.76	0.51
33:BJ:150:ARG:HB3	33:BJ:160:THR:HG22	1.93	0.51
34:AK:98:VAL:HG11	59:BV:89:ILE:HG23	1.92	0.51
59:BV:90:PHE:HB2	59:BV:93:GLN:CB	2.41	0.51
64:BZ:89:VAL:HG23	64:BZ:90:THR:HG22	1.94	0.51
66:Bb:17:LYS:HG3	79:Ao:209:MET:HE2	1.93	0.51
2:E1:192:TYR:HB2	2:E1:217:PHE:CD1	2.45	0.50
3:A2:96:ARG:NE	3:A2:100:GLU:OE2	2.43	0.50
12:AA:983:C:OP1	17:EB:603:GLN:NE2	2.44	0.50
13:BA:479:ASP:HB3	13:BA:482:VAL:HG12	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:EA:464:ALA:HB3	87:EA:1004:GTP:N7	2.26	0.50
20:ED:68:GLN:HG3	20:ED:70:SER:H	1.76	0.50
23:EE:475:LYS:HG2	80:Ap:206:ARG:HH22	1.76	0.50
29:EH:307:GLU:HA	29:EH:311:ARG:HE	1.77	0.50
31:BI:79:GLY:O	31:BI:268:LYS:NZ	2.43	0.50
44:BO:65:VAL:HG12	51:BS:123:LEU:HD12	1.92	0.50
47:BQ:105:ASN:HB3	47:BQ:141:GLY:HA3	1.93	0.50
51:BS:32:ARG:NH2	51:BS:101:GLU:OE1	2.44	0.50
62:AX:189:GLU:HB3	62:AX:215:VAL:HB	1.93	0.50
75:Al:180:LEU:HB3	75:Al:189:ILE:HD13	1.94	0.50
1:A1:165:LYS:HB3	33:BJ:249:GLN:HE22	1.76	0.50
6:E3:393:GLY:HA2	6:E3:448:GLN:HE22	1.77	0.50
7:E4:147:LEU:HB2	7:E4:166:ALA:HB1	1.94	0.50
12:AA:28:A:OP1	54:BT:50:ARG:NH1	2.34	0.50
14:EA:397:VAL:HG12	14:EA:426:CYS:HB3	1.93	0.50
16:BB:152:ARG:HE	72:E7:97:SER:HB2	1.76	0.50
20:ED:590:GLU:H	20:ED:590:GLU:CD	2.19	0.50
31:BI:180:GLN:NE2	31:BI:184:ASN:OD1	2.44	0.50
34:AK:259:LEU:HA	34:AK:264:LEU:HD22	1.93	0.50
37:BL:227:ALA:HA	37:BL:230:ARG:HD3	1.92	0.50
43:EN:203:ARG:O	43:EN:206:SER:OG	2.29	0.50
45:EO:293:ARG:HH12	45:EO:314:MET:HE1	1.75	0.50
60:AW:207:PRO:HG2	60:AW:227:SER:HB2	1.94	0.50
65:Ba:80:ASP:O	65:Ba:84:TYR:HA	2.11	0.50
1:A1:75:VAL:HG23	1:A1:121:PRO:HB2	1.92	0.50
3:A2:157:LEU:HD13	3:A2:345:ILE:HG21	1.92	0.50
12:AA:119:A:H5'	12:AA:120:A:H8	1.76	0.50
12:AA:590:U:H2'	12:AA:591:G:H8	1.76	0.50
14:EA:77:THR:O	14:EA:343:ARG:NH2	2.32	0.50
16:BB:170:GLN:HE21	16:BB:173:ARG:HH21	1.59	0.50
17:EB:334:LEU:HD11	17:EB:583:VAL:HG23	1.92	0.50
21:AE:244:VAL:HG11	21:AE:339:PHE:CD2	2.46	0.50
34:AK:86:PHE:O	34:AK:90:THR:HG22	2.10	0.50
41:AN:123:GLU:HB3	80:Ap:65:VAL:HG12	1.91	0.50
68:Ae:75:ARG:NH1	68:Ae:135:THR:O	2.42	0.50
84:Av:204:TRP:CH2	84:Av:208:LYS:HD2	2.46	0.50
2:E1:50:LYS:HA	2:E1:56:ILE:HD11	1.91	0.50
5:A3:121:LEU:HD21	46:AP:18:ARG:HE	1.76	0.50
12:AA:594:A:OP2	73:E8:552:ARG:NH2	2.25	0.50
12:AA:861:C:O3'	17:EB:615:LYS:NZ	2.37	0.50
16:BB:355:GLU:CD	16:BB:363:ARG:HH22	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:373:THR:HG21	19:BD:479:LEU:HD11	1.94	0.50
20:ED:401:LEU:HB3	20:ED:447:ILE:HD13	1.92	0.50
25:BF:292:ARG:HH21	83:At:128:THR:HA	1.76	0.50
30:AI:27:PRO:HG3	30:AI:76:HIS:NE2	2.26	0.50
43:EN:206:SER:O	43:EN:256:ILE:HG12	2.12	0.50
43:EN:666:ALA:HA	43:EN:682:LEU:HD23	1.92	0.50
64:BZ:87:ASP:OD1	64:BZ:87:ASP:N	2.44	0.50
70:Bf:71:PRO:HB2	70:Bf:72:LEU:HD23	1.94	0.50
1:A1:71:GLN:HG2	1:A1:72:GLU:HG2	1.94	0.50
10:E6:221:ILE:HD12	10:E6:286:VAL:HG13	1.94	0.50
12:AA:339:A:O2'	75:Al:157:ASN:O	2.28	0.50
12:AA:481:G:O6	60:AW:52:HIS:ND1	2.38	0.50
12:AA:790:A:H2'	12:AA:791:A:C8	2.46	0.50
13:BA:132:GLN:OE1	44:BO:224:TYR:OH	2.23	0.50
14:EA:319:GLY:HA3	14:EA:428:ASN:ND2	2.27	0.50
14:EA:471:THR:HG23	14:EA:472:LEU:HD12	1.94	0.50
16:BB:360:ASP:OD1	16:BB:361:ALA:N	2.45	0.50
22:BE:185:ARG:HG2	22:BE:188:ARG:HH21	1.77	0.50
23:EE:270:ASN:O	23:EE:271:HIS:ND1	2.44	0.50
39:EM:242:LYS:O	39:EM:246:LEU:HG	2.12	0.50
40:UM:1:UNK:O	40:UM:3:UNK:N	2.45	0.50
42:BN:40:PHE:HB3	42:BN:45:ARG:HB3	1.93	0.50
45:EP:54:GLY:HA2	45:EP:95:HIS:HB3	1.93	0.50
71:Ag:24:ASN:OD1	71:Ag:25:THR:N	2.44	0.50
5:A3:157:SER:HB3	5:A3:160:ILE:HG12	1.93	0.50
12:AA:1176:A:N6	13:BA:778:ASP:O	2.45	0.50
13:BA:271:LEU:HB2	13:BA:322:MET:HE1	1.92	0.50
14:EA:423:PHE:HZ	14:EA:454:VAL:HA	1.76	0.50
24:AF:24:ARG:HA	24:AF:27:TRP:HD1	1.77	0.50
28:BH:237:VAL:HA	28:BH:240:GLU:HG2	1.94	0.50
29:EH:208:ILE:HG13	29:EH:273:PRO:HB3	1.94	0.50
43:EN:276:LEU:HD21	43:EN:331:ALA:HA	1.93	0.50
44:BO:216:LEU:HD22	44:BO:222:ILE:HD12	1.94	0.50
45:EO:151:VAL:HG13	45:EO:266:ILE:HD12	1.94	0.50
48:AR:273:ASP:N	48:AR:273:ASP:OD1	2.44	0.50
6:E3:171:ARG:NH1	16:BB:223:ASP:O	2.40	0.50
9:E5:273:UNK:O	9:E5:320:UNK:HA	2.12	0.50
12:AA:110:A:O2'	13:BA:229:ARG:NH1	2.44	0.50
12:AA:1131:G:C8	38:EL:643:ARG:HA	2.47	0.50
13:BA:211:SER:HB2	13:BA:628:PRO:HG3	1.94	0.50
16:BB:255:LEU:HD11	16:BB:390:LEU:HD23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:ED:42:GLY:HA2	47:BQ:227:LEU:HD11	1.94	0.50
20:ED:241:LEU:HD21	20:ED:598:LEU:HD13	1.94	0.50
25:BF:220:ARG:HD3	25:BF:228:GLU:HB3	1.94	0.50
31:BI:92:ILE:HG22	71:Ag:145:VAL:HG13	1.94	0.50
60:AW:183:GLN:HE21	60:AW:193:LYS:HD2	1.77	0.50
65:Ba:80:ASP:HB3	65:Ba:99:ARG:NH1	2.27	0.50
3:A2:216:TYR:CZ	24:AF:406:ALA:HB1	2.47	0.50
4:E2:142:ARG:NH1	16:BB:371:LYS:O	2.39	0.50
6:E3:179:GLU:HG3	6:E3:184:THR:HG22	1.93	0.50
6:E3:379:VAL:HG12	6:E3:384:LEU:HD12	1.94	0.50
12:AA:579:U:H2'	12:AA:580:A:H8	1.76	0.50
18:EC:133:PRO:HB2	18:EC:137:VAL:HG21	1.94	0.50
19:BD:106:ILE:HD11	19:BD:446:LEU:HD11	1.94	0.50
48:AR:187:PHE:HB3	48:AR:216:PHE:HD2	1.77	0.50
75:Al:110:VAL:HG23	75:Al:112:VAL:HG23	1.94	0.50
12:AA:281:A:H5''	62:AX:78:ARG:HG3	1.92	0.50
12:AA:882:U:O2'	30:AI:108:ILE:O	2.27	0.50
14:EA:389:ARG:O	14:EA:421:ARG:NH2	2.45	0.50
14:EA:572:ASN:ND2	14:EA:574:ASP:OD1	2.45	0.50
18:EC:148:LEU:HD22	18:EC:195:ALA:HB2	1.93	0.50
26:EF:159:VAL:HG21	26:EF:239:ALA:HB1	1.94	0.50
28:BH:129:TYR:HD2	28:BH:169:GLU:HB3	1.77	0.50
34:AK:94:PHE:H	59:BV:91:LYS:NZ	2.10	0.50
39:EM:13:PRO:HA	39:EM:16:MET:HE2	1.92	0.50
43:EN:292:ASN:O	43:EN:293:LYS:HG3	2.12	0.50
58:AV:208:VAL:HG21	69:Af:85:PRO:HD3	1.94	0.50
73:E8:481:HIS:HA	73:E8:484:THR:HG22	1.93	0.50
74:E9:146:LEU:HB3	74:E9:149:ILE:HB	1.93	0.50
74:E9:159:LEU:HD21	74:E9:230:VAL:HG12	1.93	0.50
6:E3:183:VAL:HG21	6:E3:231:ARG:HD3	1.94	0.49
8:A5:72:ARG:NH2	8:A5:74:ASP:OD2	2.44	0.49
12:AA:537:U:H5	62:AX:158:ARG:HH22	1.60	0.49
13:BA:187:MET:SD	13:BA:206:ILE:HD11	2.52	0.49
23:EE:163:HIS:NE2	23:EE:167:LYS:HE3	2.27	0.49
41:AN:107:THR:HG22	41:AN:112:GLY:HA3	1.94	0.49
45:EO:61:PRO:HG2	45:EO:103:LEU:HD23	1.92	0.49
50:ER:129:GLU:O	50:ER:132:GLN:NE2	2.45	0.49
62:AX:190:VAL:HG23	62:AX:212:LYS:HD3	1.94	0.49
2:E1:381:MET:HG3	39:EM:11:HIS:CE1	2.47	0.49
2:E1:436:LEU:O	2:E1:439:ILE:HG12	2.12	0.49
6:E3:330:HIS:CE1	6:E3:334:ARG:HH11	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E3:388:LEU:HD23	6:E3:445:GLU:HB2	1.93	0.49
7:E4:284:GLU:OE2	7:E4:288:ASN:ND2	2.46	0.49
16:BB:91:LEU:HD21	16:BB:126:ALA:HA	1.94	0.49
18:EC:72:SER:OG	29:EH:484:ARG:NH2	2.42	0.49
20:ED:303:ALA:HB1	20:ED:310:TYR:HA	1.93	0.49
23:EE:176:LEU:HD23	23:EE:197:ILE:HB	1.94	0.49
31:BI:250:SER:OG	31:BI:254:ARG:NH1	2.44	0.49
39:EM:83:LEU:HD21	39:EM:251:CYS:HB2	1.95	0.49
45:EO:131:GLN:HA	45:EP:52:GLN:HG3	1.94	0.49
48:AR:76:GLU:O	48:AR:80:LYS:HG2	2.12	0.49
52:ES:44:ARG:NE	52:ES:132:GLU:OE2	2.45	0.49
56:AU:75:THR:OG1	56:AU:76:GLY:N	2.45	0.49
61:BW:52:LYS:HD3	61:BW:69:LYS:HD3	1.95	0.49
63:AY:64:HIS:HD2	63:AY:66:ARG:H	1.61	0.49
79:Ao:104:LYS:HG3	83:At:144:VAL:HG21	1.94	0.49
11:A8:88:LEU:HD11	46:AP:155:PRO:HG2	1.94	0.49
12:AA:848:A:H2'	12:AA:849:G:H8	1.76	0.49
18:EC:262:HIS:HB3	18:EC:284:SER:HB2	1.94	0.49
19:BD:194:MET:HE1	19:BD:432:ARG:HA	1.94	0.49
20:ED:138:PRO:HG3	43:EN:528:MET:HE3	1.94	0.49
35:BK:356:SER:HB3	35:BK:359:ARG:HD2	1.95	0.49
38:EL:308:VAL:HG23	38:EL:486:ARG:HB3	1.94	0.49
38:EL:497:PHE:HZ	38:EL:518:LEU:HD22	1.77	0.49
39:EM:82:ARG:NH1	39:EM:331:PHE:O	2.45	0.49
51:BS:23:THR:OG1	51:BS:24:GLY:N	2.45	0.49
74:E9:214:LEU:HD13	74:E9:339:HIS:HA	1.93	0.49
7:E4:153:SER:HB3	7:E4:211:TYR:HB3	1.94	0.49
7:E4:214:ASN:HB3	7:E4:269:GLN:HE22	1.78	0.49
12:AA:138:U:H2'	12:AA:139:U:H6	1.77	0.49
13:BA:138:SER:OG	13:BA:140:GLU:OE1	2.27	0.49
13:BA:647:LEU:HD13	13:BA:654:LEU:HD22	1.94	0.49
13:BA:648:GLU:OE2	22:BE:119:ARG:NH2	2.41	0.49
13:BA:784:ALA:HA	44:BO:127:MET:HE3	1.94	0.49
20:ED:34:LEU:HD23	20:ED:606:HIS:CD2	2.47	0.49
29:EH:497:ASP:OD1	29:EH:497:ASP:N	2.31	0.49
65:Ba:26:LEU:HD22	68:Ae:91:LEU:HD21	1.95	0.49
3:A2:366:VAL:HG21	65:Ba:67:PRO:HB3	1.95	0.49
12:AA:91:U:OP1	25:BF:400:ARG:NH1	2.46	0.49
12:AA:1103:U:OP1	53:AT:7:ARG:N	2.41	0.49
18:EC:239:VAL:HB	21:AE:280:PRO:HG3	1.94	0.49
19:BD:175:TYR:OH	19:BD:334:ARG:NH2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:BE:49:LYS:NZ	63:AY:69:ASP:OD2	2.36	0.49
29:EH:476:MET:HE2	83:At:12:ARG:HH21	1.78	0.49
43:EN:361:VAL:HG21	43:EN:451:LEU:HD22	1.95	0.49
56:AU:11:TYR:OH	56:AU:16:GLU:OE2	2.31	0.49
5:A3:89:ARG:NH1	5:A3:97:THR:OG1	2.45	0.49
5:A3:169:LEU:HD13	25:BF:272:VAL:HA	1.95	0.49
9:E5:44:UNK:HA	9:E5:53:UNK:HA	1.95	0.49
10:E6:340:MET:N	10:E6:341:PRO:HD2	2.27	0.49
12:AA:172:U:OP2	46:AP:222:GLY:N	2.41	0.49
13:BA:357:MET:HE3	13:BA:358:PRO:HD2	1.93	0.49
20:ED:405:GLU:HG3	20:ED:436:THR:HA	1.93	0.49
20:ED:515:MET:HB3	43:EN:730:TYR:HB2	1.94	0.49
21:AE:247:THR:HB	21:AE:338:ARG:HG3	1.95	0.49
37:BL:140:VAL:HA	37:BL:147:ARG:HH22	1.77	0.49
42:BN:58:ILE:HB	42:BN:59:PRO:HD3	1.94	0.49
44:BO:141:ASP:OD1	44:BO:142:GLU:N	2.44	0.49
45:EP:147:GLU:OE1	45:EP:150:ALA:N	2.37	0.49
57:BU:42:TRP:NE1	57:BU:58:SER:HG	2.09	0.49
63:AY:123:GLU:HG2	63:AY:174:ARG:HH12	1.77	0.49
3:A2:116:ARG:NH1	63:AY:260:GLU:OE2	2.46	0.49
4:E2:78:HIS:O	4:E2:82:ASN:ND2	2.36	0.49
5:A3:86:ARG:HD2	25:BF:29:LEU:HD11	1.93	0.49
12:AA:991:A:N6	14:EA:515:ARG:HD2	2.28	0.49
14:EA:419:GLU:OE2	17:EB:345:ARG:NH1	2.45	0.49
17:EB:130:VAL:HG13	17:EB:156:PRO:HG3	1.93	0.49
19:BD:130:ALA:O	19:BD:134:ARG:HG2	2.13	0.49
22:BE:292:PHE:HB2	22:BE:330:GLN:HE21	1.77	0.49
25:BF:399:ARG:HH22	60:AW:75:GLN:HE22	1.60	0.49
29:EH:466:THR:N	29:EH:469:SER:OG	2.46	0.49
33:BJ:259:ASP:OD2	33:BJ:261:ARG:NE	2.45	0.49
43:EN:521:LEU:HD23	43:EN:524:LEU:HD21	1.95	0.49
44:BO:70:ALA:O	51:BS:33:ARG:NH1	2.27	0.49
46:AP:297:TRP:HA	61:BW:15:ALA:HB2	1.94	0.49
55:ET:99:THR:HB	55:ET:102:ARG:HB2	1.95	0.49
58:AV:111:ALA:N	79:Ao:87:GLU:O	2.34	0.49
62:AX:100:CYS:HB3	65:Ba:32:LYS:HE2	1.95	0.49
3:A2:381:GLU:HG3	62:AX:119:PRO:HG2	1.94	0.49
7:E4:24:GLN:NE2	10:E6:207:PRO:O	2.40	0.49
20:ED:472:LEU:HD12	20:ED:476:LEU:HD23	1.94	0.49
23:EE:492:ASN:OD1	31:BI:299:ARG:NH1	2.46	0.49
25:BF:372:LEU:HB3	60:AW:86:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:EF:103:VAL:HA	26:EF:126:ILE:HB	1.95	0.49
26:EF:181:ARG:HA	26:EF:207:LEU:HD22	1.95	0.49
38:EL:296:LEU:HD22	38:EL:489:GLY:HA3	1.95	0.49
43:EN:156:PRO:HG2	43:EN:159:GLU:HB2	1.95	0.49
45:EO:262:PHE:O	45:EO:266:ILE:HG12	2.13	0.49
46:AP:264:GLN:HG2	46:AP:271:TYR:CZ	2.47	0.49
57:BU:44:VAL:HB	57:BU:54:SER:HB3	1.94	0.49
58:AV:231:THR:HG1	69:Af:86:ASN:HD21	1.56	0.49
63:AY:170:ILE:HG23	63:AY:174:ARG:HE	1.78	0.49
3:A2:127:GLY:HA2	64:BZ:124:ALA:HB1	1.95	0.49
4:E2:130:TRP:HZ2	4:E2:143:PRO:HG3	1.78	0.49
8:A5:78:ILE:HG21	60:AW:259:ALA:HB2	1.95	0.49
11:A8:107:ARG:HH21	55:ET:90:ASP:HA	1.77	0.49
12:AA:1155:A:H1'	53:AT:10:ARG:HH11	1.78	0.49
13:BA:215:ARG:HH12	13:BA:699:ASN:HD21	1.58	0.49
19:BD:137:ARG:HH22	30:AI:220:ARG:HH11	1.60	0.49
20:ED:237:HIS:CG	20:ED:594:PRO:HG3	2.47	0.49
23:EE:248:PRO:HB3	23:EE:280:VAL:HG13	1.94	0.49
30:AI:144:MET:HE3	30:AI:149:MET:HE2	1.94	0.49
37:BL:285:LEU:O	37:BL:289:GLU:HG2	2.13	0.49
38:EL:498:ASN:ND2	38:EL:505:PHE:H	2.10	0.49
39:EM:333:LEU:HB2	73:E8:568:LEU:HD11	1.95	0.49
43:EN:669:LEU:HD13	43:EN:692:VAL:HG11	1.95	0.49
45:EO:21:LEU:HB3	45:EO:194:TRP:CD1	2.48	0.49
45:EP:4:VAL:HG13	45:EP:59:ILE:HG13	1.95	0.49
48:AR:112:ARG:NH2	57:BU:170:SER:O	2.46	0.49
10:E6:145:PHE:HD1	10:E6:150:HIS:HB2	1.78	0.49
13:BA:419:THR:OG1	13:BA:420:ALA:N	2.45	0.49
16:BB:424:LYS:NZ	32:Ur:21:UNK:O	2.46	0.49
19:BD:352:VAL:HG11	19:BD:359:LYS:HB3	1.95	0.49
20:ED:598:LEU:HB2	20:ED:604:LEU:HD11	1.95	0.49
27:EG:142:ARG:NH2	49:BR:118:GLN:OE1	2.46	0.49
31:BI:303:TRP:HB3	70:Bf:79:GLU:HB3	1.95	0.49
38:EL:633:GLN:HA	38:EL:636:MET:HG2	1.95	0.49
45:EO:170:GLN:HE21	45:EO:216:ARG:HH11	1.60	0.49
45:EO:201:GLN:O	45:EO:205:GLU:HB2	2.12	0.49
46:AP:231:HIS:ND1	46:AP:251:SER:OG	2.42	0.49
49:BR:102:TRP:O	49:BR:106:THR:OG1	2.24	0.49
59:BV:83:MET:O	59:BV:98:ILE:HG13	2.13	0.49
59:BV:101:GLU:OE2	59:BV:107:ILE:HD11	2.12	0.49
68:Ae:150:GLY:HA2	68:Ae:153:PHE:CE2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:Ap:178:MET:HE2	80:Ap:236:TRP:HZ3	1.78	0.49
5:A3:130:ILE:HG22	46:AP:28:ALA:HB2	1.95	0.48
12:AA:1157:A:O2'	12:AA:1158:G:N2	2.40	0.48
23:EE:173:ARG:HG3	23:EE:174:HIS:HD2	1.78	0.48
23:EE:343:LEU:HD21	38:EL:540:LEU:HB3	1.95	0.48
43:EN:493:ILE:HA	43:EN:496:ASN:HD21	1.78	0.48
55:ET:52:GLY:HA3	55:ET:99:THR:HG23	1.95	0.48
2:E1:450:ARG:NH2	12:AA:521:G:N3	2.61	0.48
4:E2:254:GLN:NE2	4:E2:269:CYS:SG	2.86	0.48
5:A3:130:ILE:HD11	79:Ao:114:LEU:HD13	1.94	0.48
6:E3:419:GLY:HA3	6:E3:448:GLN:HG2	1.94	0.48
12:AA:579:U:H2'	12:AA:580:A:C8	2.48	0.48
16:BB:277:HIS:CD2	16:BB:315:SER:HB2	2.47	0.48
16:BB:360:ASP:HB3	16:BB:363:ARG:HG3	1.94	0.48
17:EB:320:THR:HG22	17:EB:322:ILE:HG23	1.95	0.48
20:ED:269:LEU:HG	20:ED:273:SER:O	2.13	0.48
26:EF:93:VAL:HA	26:EF:97:TYR:CD2	2.47	0.48
30:AI:108:ILE:HG12	30:AI:180:LYS:HA	1.95	0.48
43:EN:616:HIS:O	43:EN:620:THR:OG1	2.27	0.48
51:BS:46:THR:HG22	51:BS:49:THR:HG23	1.94	0.48
60:AW:137:ALA:H	60:AW:229:HIS:CD2	2.31	0.48
74:E9:277:GLN:OE1	74:E9:279:TRP:NE1	2.46	0.48
2:E1:239:ASP:CG	42:BN:104:ARG:HE	2.19	0.48
10:E6:201:LEU:HD21	10:E6:271:LEU:HD13	1.95	0.48
10:E6:301:ASP:OD1	10:E6:303:ARG:NH1	2.47	0.48
11:A8:50:LYS:HD3	11:A8:53:ARG:HH21	1.78	0.48
12:AA:1086:U:P	18:EC:260:ARG:HH22	2.36	0.48
14:EA:140:VAL:HG23	87:EA:1001:GTP:PA	2.54	0.48
14:EA:268:LEU:H	14:EA:268:LEU:HD12	1.78	0.48
19:BD:106:ILE:HA	19:BD:418:LYS:HG2	1.95	0.48
19:BD:409:ASP:O	19:BD:413:GLN:HG2	2.13	0.48
20:ED:273:SER:HB3	20:ED:278:ARG:HG2	1.95	0.48
22:BE:354:GLU:OE1	22:BE:358:ASN:ND2	2.46	0.48
30:AI:111:ILE:HG23	30:AI:185:TYR:HE1	1.78	0.48
39:EM:330:ASP:OD1	39:EM:335:ASN:HB2	2.13	0.48
10:E6:348:LYS:O	10:E6:352:VAL:HG22	2.12	0.48
12:AA:584:A:O2'	12:AA:796:A:N1	2.44	0.48
12:AA:830:A:H2'	12:AA:831:A:H8	1.79	0.48
12:AA:848:A:H2'	12:AA:849:G:C8	2.49	0.48
12:AA:859:U:H2'	12:AA:860:A:C8	2.49	0.48
16:BB:239:THR:HG22	16:BB:242:GLN:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:ED:549:TYR:HA	20:ED:553:VAL:HG12	1.95	0.48
25:BF:269:GLU:HA	25:BF:272:VAL:HG13	1.95	0.48
28:BH:112:ALA:H	28:BH:253:GLN:HE21	1.62	0.48
42:BN:67:LEU:O	42:BN:71:GLN:HB2	2.13	0.48
45:EO:224:LEU:O	45:EO:227:SER:OG	2.27	0.48
47:BQ:42:LEU:HB2	47:BQ:170:VAL:HG13	1.95	0.48
47:BQ:49:LEU:HB3	47:BQ:58:THR:HG23	1.94	0.48
48:AR:79:ARG:O	48:AR:127:LYS:NZ	2.46	0.48
52:ES:21:VAL:HG21	52:ES:99:ALA:HB1	1.96	0.48
57:BU:156:GLN:HA	57:BU:159:ARG:HG2	1.94	0.48
61:BW:151:TRP:CD1	61:BW:152:GLN:HG3	2.47	0.48
4:E2:415:VAL:HA	4:E2:430:PRO:HA	1.95	0.48
12:AA:118:U:H2'	13:BA:719:SER:HB3	1.96	0.48
12:AA:330:U:OP1	47:BQ:100:LYS:NZ	2.38	0.48
12:AA:936:C:O2'	20:ED:95:ARG:NH2	2.47	0.48
12:AA:976:A:H2'	12:AA:977:G:C8	2.48	0.48
13:BA:585:HIS:HD2	13:BA:587:SER:HB3	1.78	0.48
19:BD:282:TYR:O	19:BD:381:SER:OG	2.30	0.48
21:AE:190:MET:HB3	21:AE:214:HIS:HB3	1.94	0.48
23:EE:434:HIS:HD2	34:AK:80:MET:HB2	1.78	0.48
33:BJ:130:LEU:HD21	33:BJ:210:ILE:HG12	1.96	0.48
42:BN:71:GLN:HE21	42:BN:123:PHE:HA	1.77	0.48
45:EP:1:MET:HE3	45:EP:2:PHE:HE1	1.79	0.48
49:BR:110:LEU:H	49:BR:138:GLN:HE22	1.61	0.48
51:BS:117:GLY:O	51:BS:121:SER:OG	2.28	0.48
60:AW:169:ARG:HB2	60:AW:172:HIS:HD2	1.78	0.48
63:AY:198:THR:HG22	63:AY:200:GLU:H	1.77	0.48
3:A2:17:VAL:HG21	62:AX:224:VAL:HG21	1.95	0.48
3:A2:217:ASP:O	54:BT:112:ARG:NH2	2.46	0.48
3:A2:459:MET:HE2	54:BT:54:ARG:HG2	1.96	0.48
7:E4:294:LEU:HD13	7:E4:304:ASN:HD22	1.77	0.48
12:AA:887:A:H3'	12:AA:888:U:H5''	1.95	0.48
13:BA:50:PRO:HB2	21:AE:110:LYS:HE3	1.94	0.48
13:BA:300:ARG:HE	13:BA:307:HIS:HD2	1.61	0.48
16:BB:170:GLN:NE2	72:E7:93:ARG:HH12	2.12	0.48
19:BD:163:ASP:OD1	19:BD:166:SER:N	2.44	0.48
23:EE:141:LEU:HD12	23:EE:148:ARG:HA	1.95	0.48
45:EO:2:PHE:CE2	45:EO:61:PRO:HB3	2.48	0.48
64:BZ:96:GLN:NE2	64:BZ:124:ALA:O	2.46	0.48
70:Bf:70:ASP:OD1	70:Bf:70:ASP:N	2.44	0.48
2:E1:148:VAL:HB	2:E1:152:GLU:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E4:243:ILE:HG13	7:E4:412:PHE:HD2	1.78	0.48
12:AA:286:U:H2'	12:AA:287:A:H5''	1.94	0.48
12:AA:310:A:H2'	12:AA:311:A:C8	2.49	0.48
12:AA:1143:U:H2'	12:AA:1144:G:C4	2.49	0.48
13:BA:275:ALA:HB2	13:BA:356:VAL:HG23	1.96	0.48
18:EC:322:HIS:CE1	39:EM:55:LEU:HD11	2.48	0.48
20:ED:89:VAL:HG13	20:ED:536:MET:HE1	1.95	0.48
23:EE:233:LYS:HB3	23:EE:463:VAL:HG21	1.96	0.48
24:AF:60:LEU:HD11	25:BF:359:PRO:HB3	1.95	0.48
29:EH:45:PHE:HB2	29:EH:379:LEU:HD13	1.96	0.48
2:E1:32:LEU:HD22	53:AT:79:HIS:HD2	1.77	0.48
14:EA:309:ARG:HB2	14:EA:392:HIS:HD2	1.79	0.48
14:EA:400:ALA:HB2	14:EA:427:ALA:HB1	1.96	0.48
16:BB:270:LEU:HD21	16:BB:437:ILE:HG12	1.96	0.48
21:AE:288:GLN:NE2	21:AE:290:ARG:O	2.46	0.48
23:EE:252:GLY:HA3	23:EE:283:ALA:HB3	1.96	0.48
25:BF:63:ARG:NH2	25:BF:239:VAL:HG23	2.29	0.48
34:AK:217:TYR:HD1	34:AK:221:HIS:NE2	2.12	0.48
56:AU:54:GLN:O	56:AU:58:GLU:HG2	2.14	0.48
69:Af:81:ARG:HB3	71:Ag:121:GLU:HG2	1.95	0.48
80:Ap:236:TRP:HD1	80:Ap:240:THR:HB	1.79	0.48
2:E1:114:ILE:HG13	42:BN:120:TRP:CD1	2.49	0.48
2:E1:318:PHE:CE2	2:E1:322:HIS:HE1	2.31	0.48
3:A2:314:HIS:CG	54:BT:86:ARG:HG3	2.49	0.48
12:AA:96:U:OP2	63:AY:22:TYR:OH	2.14	0.48
13:BA:602:ARG:NE	13:BA:608:ASP:OD2	2.43	0.48
16:BB:278:GLN:HA	16:BB:281:VAL:HG22	1.96	0.48
22:BE:48:MET:HG3	63:AY:51:ARG:HB3	1.96	0.48
22:BE:306:GLN:OE1	22:BE:347:TYR:OH	2.30	0.48
24:AF:281:PRO:HG2	24:AF:399:THR:HA	1.96	0.48
27:EG:151:GLY:HA3	29:EH:477:LEU:HD13	1.96	0.48
31:BI:61:PHE:HB2	31:BI:256:MET:HE3	1.95	0.48
45:EP:148:MET:HE2	45:EP:273:TYR:HB2	1.95	0.48
52:ES:26:THR:HG23	52:ES:31:LEU:HB2	1.96	0.48
53:AT:108:ASN:HB3	53:AT:111:LEU:HB3	1.95	0.48
55:ET:22:ARG:HH22	55:ET:28:PRO:C	2.21	0.48
58:AV:231:THR:OG1	69:Af:86:ASN:ND2	2.33	0.48
63:AY:150:ASP:HB3	63:AY:163:ILE:HD11	1.96	0.48
67:Bc:111:VAL:HG12	67:Bc:113:TYR:H	1.77	0.48
83:At:31:TRP:O	83:At:34:ARG:HG2	2.13	0.48
1:A1:181:VAL:HG11	63:AY:299:MET:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A1:194:GLY:O	1:A1:198:GLU:HG2	2.14	0.48
2:E1:175:THR:HA	2:E1:178:VAL:HG22	1.95	0.48
3:A2:34:TRP:NE1	68:Ae:157:PRO:O	2.46	0.48
3:A2:70:ARG:NH1	72:E7:67:ASN:HD21	2.12	0.48
5:A3:70:CYS:HA	5:A3:116:VAL:HG12	1.95	0.48
12:AA:839:A:H2'	12:AA:840:A:H8	1.79	0.48
12:AA:987:C:H2'	12:AA:988:A:C8	2.48	0.48
16:BB:272:LEU:HD21	16:BB:303:ILE:HG13	1.95	0.48
16:BB:285:ARG:HG2	16:BB:295:VAL:HG21	1.96	0.48
16:BB:330:TRP:HE1	16:BB:334:ARG:HE	1.62	0.48
20:ED:265:ASN:OD1	20:ED:506:ARG:NH2	2.47	0.48
21:AE:76:LYS:NZ	21:AE:77:ILE:O	2.44	0.48
22:BE:294:GLY:O	22:BE:298:ASN:ND2	2.38	0.48
34:AK:163:LEU:HB2	34:AK:171:PRO:HD3	1.96	0.48
38:EL:336:ARG:HH22	70:Bf:27:LEU:HD11	1.78	0.48
48:AR:242:HIS:CD2	48:AR:244:SER:H	2.31	0.48
53:AT:25:PRO:HB2	53:AT:28:ARG:HB2	1.94	0.48
74:E9:303:LYS:O	74:E9:307:SER:OG	2.32	0.48
1:A1:180:LEU:HD22	63:AY:296:ALA:HB1	1.96	0.47
10:E6:81:HIS:O	10:E6:88:ARG:NH2	2.47	0.47
12:AA:470:G:OP2	46:AP:70:LEU:HB2	2.13	0.47
18:EC:169:VAL:HG11	18:EC:378:VAL:HG11	1.96	0.47
38:EL:421:GLY:HA3	38:EL:445:SER:HB3	1.96	0.47
42:BN:199:ASP:HB3	42:BN:215:TRP:CD1	2.49	0.47
43:EN:351:TYR:CZ	43:EN:355:ILE:HD11	2.49	0.47
45:EP:59:ILE:HB	45:EP:94:VAL:HG13	1.96	0.47
51:BS:73:ILE:HA	51:BS:76:VAL:HG12	1.96	0.47
56:AU:77:TRP:CZ2	56:AU:81:ARG:HD2	2.49	0.47
57:BU:62:HIS:HB3	57:BU:64:TYR:CE1	2.49	0.47
84:Av:76:TYR:HB3	84:Av:80:ALA:HB3	1.96	0.47
1:A1:132:LYS:HB2	30:AI:175:HIS:HB2	1.95	0.47
2:E1:158:LYS:HG2	12:AA:559:A:H62	1.79	0.47
12:AA:862:U:H5'	17:EB:615:LYS:HZ3	1.79	0.47
13:BA:308:SER:O	13:BA:312:TRP:NE1	2.47	0.47
19:BD:178:ILE:HB	19:BD:181:VAL:HG12	1.94	0.47
21:AE:167:ASP:O	21:AE:189:ALA:HA	2.14	0.47
22:BE:375:PRO:HB2	22:BE:378:LEU:HB2	1.96	0.47
24:AF:132:PRO:O	24:AF:136:GLY:N	2.47	0.47
3:A2:219:THR:HG22	54:BT:112:ARG:HH22	1.79	0.47
6:E3:192:VAL:HG21	6:E3:224:TYR:CZ	2.49	0.47
6:E3:535:SER:OG	6:E3:536:GLY:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AA:14:A:O2'	63:AY:31:ARG:NH2	2.47	0.47
12:AA:509:U:H2'	12:AA:510:A:H8	1.79	0.47
14:EA:468:LEU:HG	14:EA:469:ASN:HD22	1.80	0.47
19:BD:142:VAL:HG22	19:BD:145:TRP:HB3	1.95	0.47
23:EE:429:HIS:O	23:EE:432:ARG:NH1	2.43	0.47
34:AK:34:LYS:NZ	34:AK:94:PHE:HE1	2.09	0.47
39:EM:264:SER:HA	39:EM:324:GLN:HE22	1.79	0.47
51:BS:80:ASP:OD1	51:BS:81:SER:N	2.43	0.47
80:Ap:147:TYR:HB2	80:Ap:150:HIS:HD2	1.79	0.47
1:A1:73:MET:HG3	1:A1:149:ARG:HD3	1.96	0.47
2:E1:207:LEU:HD12	2:E1:215:VAL:HG11	1.97	0.47
3:A2:53:LEU:HG	68:Ae:157:PRO:HG3	1.95	0.47
7:E4:110:ASN:HD21	42:BN:133:GLN:CD	2.22	0.47
12:AA:63:A:OP1	46:AP:164:ASN:ND2	2.43	0.47
14:EA:316:THR:HG22	14:EA:364:GLY:HA3	1.96	0.47
22:BE:234:ASP:OD1	22:BE:235:GLU:N	2.47	0.47
30:AI:177:GLU:OE2	30:AI:191:ARG:NH2	2.48	0.47
34:AK:152:GLU:HA	59:BV:104:TYR:CE2	2.49	0.47
38:EL:124:TRP:CE2	38:EL:135:PRO:HG3	2.49	0.47
38:EL:399:PHE:CE2	38:EL:432:ILE:HA	2.50	0.47
45:EO:6:CYS:HA	45:EO:57:ILE:HG22	1.95	0.47
51:BS:45:ILE:HD12	51:BS:49:THR:HG21	1.96	0.47
60:AW:159:GLU:OE2	60:AW:245:ARG:NE	2.46	0.47
74:E9:174:ARG:HG3	74:E9:203:HIS:CD2	2.49	0.47
83:At:25:ARG:HG3	83:At:29:MET:HE1	1.96	0.47
5:A3:122:ASP:OD1	5:A3:125:GLU:N	2.41	0.47
7:E4:167:GLU:OE2	7:E4:191:HIS:HB3	2.14	0.47
10:E6:130:ALA:HA	42:BN:215:TRP:HB3	1.97	0.47
12:AA:112:U:O2'	12:AA:837:A:N6	2.46	0.47
12:AA:877:G:H2'	12:AA:878:A:C8	2.49	0.47
12:AA:1172:A:N6	13:BA:782:VAL:O	2.47	0.47
13:BA:796:LEU:HD11	60:AW:250:TYR:HB2	1.97	0.47
13:BA:801:ARG:HE	13:BA:815:TYR:HA	1.80	0.47
16:BB:422:MET:HG2	16:BB:423:GLY:H	1.79	0.47
34:AK:217:TYR:HB3	59:BV:108:TYR:CE2	2.50	0.47
38:EL:83:ARG:HH12	80:Ap:159:ARG:HD3	1.79	0.47
38:EL:627:GLU:O	38:EL:633:GLN:NE2	2.46	0.47
39:EM:150:VAL:HG13	39:EM:154:LEU:HD12	1.95	0.47
50:ER:75:ARG:HD2	50:ER:119:PHE:CZ	2.50	0.47
60:AW:169:ARG:O	60:AW:173:GLN:HG2	2.14	0.47
61:BW:50:ARG:HD3	61:BW:83:LEU:HD13	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E1:481:GLY:HA3	48:AR:84:ILE:HB	1.97	0.47
5:A3:106:ARG:NH1	83:At:46:ARG:O	2.38	0.47
11:A8:135:ARG:HD2	11:A8:136:GLN:O	2.14	0.47
12:AA:74:U:H3'	54:BT:11:PHE:HE1	1.79	0.47
12:AA:296:A:C6	46:AP:120:ILE:HD12	2.49	0.47
12:AA:590:U:H2'	12:AA:591:G:C8	2.48	0.47
17:EB:228:LEU:HD21	20:ED:539:ARG:HE	1.79	0.47
21:AE:292:TYR:HB3	41:AN:110:PRO:HG3	1.95	0.47
23:EE:284:ALA:HB1	23:EE:287:ALA:HB3	1.96	0.47
25:BF:394:GLY:HA3	60:AW:59:ILE:HG23	1.96	0.47
43:EN:265:THR:HG22	43:EN:322:PHE:CD2	2.49	0.47
46:AP:13:LEU:HD21	79:Ao:62:THR:HB	1.95	0.47
47:BQ:122:ALA:HA	47:BQ:160:VAL:HB	1.96	0.47
48:AR:23:ARG:NH2	48:AR:45:MET:O	2.48	0.47
48:AR:194:GLU:HA	48:AR:197:LYS:HG3	1.97	0.47
58:AV:113:LYS:HD2	79:Ao:84:ALA:HB3	1.97	0.47
62:AX:96:ASN:HB2	65:Ba:29:LEU:HD22	1.96	0.47
63:AY:144:GLN:HG2	63:AY:145:ASN:HD22	1.80	0.47
75:Al:78:VAL:HG21	75:Al:208:VAL:HG22	1.97	0.47
1:A1:163:ARG:O	1:A1:167:ILE:HG12	2.14	0.47
7:E4:256:VAL:HG11	7:E4:270:ALA:HB1	1.96	0.47
8:A5:58:PRO:HD2	8:A5:80:PRO:HB2	1.96	0.47
11:A8:162:ARG:HG2	12:AA:72:A:C5	2.50	0.47
12:AA:141:U:H2'	12:AA:142:A:C8	2.50	0.47
12:AA:456:U:H5''	69:Af:66:HIS:NE2	2.29	0.47
12:AA:858:C:C2	12:AA:978:G:N2	2.82	0.47
12:AA:922:A:N6	12:AA:932:A:H61	2.13	0.47
14:EA:268:LEU:HD11	52:ES:127:TYR:CE1	2.49	0.47
19:BD:277:MET:HG2	19:BD:280:ARG:HH22	1.80	0.47
20:ED:105:ILE:HD12	20:ED:123:ARG:HD2	1.97	0.47
21:AE:54:ARG:HE	67:Bc:67:GLN:HE22	1.61	0.47
21:AE:197:HIS:HE2	21:AE:214:HIS:HA	1.79	0.47
23:EE:390:ASN:OD1	23:EE:395:SER:OG	2.31	0.47
26:EF:93:VAL:HA	26:EF:97:TYR:HD2	1.80	0.47
28:BH:122:HIS:CD2	28:BH:225:GLY:HA3	2.50	0.47
29:EH:228:PRO:O	29:EH:232:GLU:HG2	2.14	0.47
33:BJ:176:GLU:HA	33:BJ:179:ARG:HG2	1.97	0.47
34:AK:152:GLU:HA	59:BV:104:TYR:HE2	1.80	0.47
34:AK:242:LEU:HD22	80:Ap:190:PHE:HE2	1.79	0.47
43:EN:468:LEU:HA	43:EN:471:VAL:HG22	1.96	0.47
43:EN:546:LEU:HD12	43:EN:547:PRO:HD2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:BO:115:VAL:HG13	44:BO:163:VAL:HG13	1.96	0.47
45:EO:159:ILE:HA	45:EO:162:VAL:HG22	1.95	0.47
46:AP:227:PRO:HG2	46:AP:228:TYR:CD1	2.50	0.47
48:AR:175:LYS:H	48:AR:201:ARG:HH12	1.62	0.47
50:ER:106:LEU:HD21	52:ES:45:PHE:HD1	1.79	0.47
52:ES:121:GLY:HA2	52:ES:128:GLN:HE21	1.79	0.47
53:AT:46:TRP:CZ2	53:AT:83:THR:HA	2.50	0.47
53:AT:143:MET:HE3	53:AT:144:LYS:HB2	1.97	0.47
54:BT:144:GLU:OE1	54:BT:148:PRO:HA	2.15	0.47
68:Ae:87:VAL:HA	68:Ae:90:VAL:HG12	1.95	0.47
80:Ap:61:ASN:O	80:Ap:92:ARG:NH2	2.47	0.47
4:E2:478:ARG:HE	17:EB:721:TRP:HH2	1.61	0.47
5:A3:66:PHE:HB2	5:A3:99:VAL:HG23	1.97	0.47
10:E6:473:LEU:HD22	10:E6:478:LEU:HD12	1.97	0.47
16:BB:418:ARG:HA	16:BB:421:VAL:HG22	1.97	0.47
17:EB:244:ARG:HA	55:ET:94:GLU:HG3	1.97	0.47
26:EF:64:ASN:O	26:EF:67:LYS:HG3	2.15	0.47
30:AI:67:ASN:HB3	84:Av:112:VAL:HB	1.97	0.47
34:AK:130:ARG:NH2	59:BV:28:ASP:HA	2.30	0.47
38:EL:83:ARG:NH2	80:Ap:146:GLN:HE22	2.13	0.47
39:EM:76:LEU:O	39:EM:168:VAL:HA	2.14	0.47
42:BN:114:ASP:OD1	42:BN:115:ALA:N	2.48	0.47
46:AP:232:ILE:HG23	46:AP:252:PHE:HD1	1.79	0.47
45:EP:32:LEU:HD12	45:EP:240:THR:HG21	1.97	0.47
45:EP:167:ALA:O	45:EP:171:GLN:HG2	2.15	0.47
64:BZ:79:LYS:HE3	64:BZ:168:GLN:HE22	1.78	0.47
66:Bb:79:HIS:HD2	66:Bb:81:HIS:HB2	1.80	0.47
75:Al:75:ARG:HB2	75:Al:78:VAL:HG12	1.96	0.47
5:A3:176:ASP:OD2	25:BF:273:TYR:OH	2.31	0.47
8:A5:44:PHE:HB2	12:AA:508:A:N6	2.30	0.47
10:E6:340:MET:HB2	10:E6:373:ASN:HD22	1.80	0.47
13:BA:324:GLU:O	13:BA:328:VAL:HG23	2.15	0.47
14:EA:320:LYS:NZ	87:EA:1004:GTP:O2G	2.47	0.47
17:EB:475:HIS:CD2	17:EB:476:VAL:HG23	2.49	0.47
19:BD:113:GLU:OE1	19:BD:113:GLU:N	2.45	0.47
23:EE:277:ASP:OD1	23:EE:278:HIS:N	2.48	0.47
24:AF:431:MET:N	24:AF:431:MET:SD	2.88	0.47
25:BF:297:PHE:CD1	25:BF:302:ASP:HB3	2.50	0.47
25:BF:398:ARG:NH2	60:AW:60:LEU:O	2.48	0.47
39:EM:218:VAL:HG13	39:EM:228:LEU:HB2	1.97	0.47
39:EM:300:ILE:HG21	74:E9:225:ALA:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:AN:198:ASN:OD1	41:AN:199:GLU:N	2.47	0.47
60:AW:205:PRO:HD3	63:AY:11:PHE:HE1	1.80	0.47
63:AY:86:GLU:H	63:AY:89:GLN:NE2	2.08	0.47
3:A2:379:ALA:HB1	65:Ba:81:GLN:O	2.14	0.47
4:E2:371:CYS:O	4:E2:375:THR:HG22	2.15	0.47
7:E4:120:GLN:O	7:E4:124:ARG:HB2	2.15	0.47
11:A8:63:ALA:HB1	11:A8:66:ARG:HD2	1.97	0.47
12:AA:281:A:H2'	12:AA:282:A:C8	2.50	0.47
12:AA:347:A:H2'	12:AA:348:A:H8	1.80	0.47
13:BA:569:LEU:HD23	13:BA:659:GLU:HB3	1.96	0.47
13:BA:675:MET:HA	13:BA:678:THR:HG22	1.96	0.47
13:BA:754:ARG:O	60:AW:245:ARG:NH2	2.48	0.47
14:EA:267:PRO:HG2	52:ES:117:VAL:HG11	1.97	0.47
14:EA:452:ARG:O	14:EA:453:GLU:HG2	2.15	0.47
19:BD:344:PHE:HA	19:BD:347:GLU:HG2	1.97	0.47
22:BE:363:LEU:O	22:BE:367:GLN:HG2	2.15	0.47
33:BJ:134:LEU:HA	33:BJ:137:VAL:HG22	1.96	0.47
35:BK:90:ARG:O	35:BK:109:ARG:NH1	2.46	0.47
37:BL:169:GLU:OE1	37:BL:245:ARG:NH2	2.43	0.47
38:EL:78:VAL:HA	38:EL:470:LYS:HE3	1.97	0.47
38:EL:237:CYS:HA	38:EL:292:PRO:HG2	1.97	0.47
41:AN:82:HIS:CD2	41:AN:157:TRP:HE1	2.32	0.47
48:AR:78:ILE:HD11	48:AR:100:VAL:HG11	1.97	0.47
68:Ae:59:ASP:OD1	68:Ae:60:GLY:N	2.48	0.47
4:E2:402:ARG:NH2	17:EB:723:ASP:OD2	2.48	0.46
7:E4:244:ARG:HB3	7:E4:269:GLN:HG3	1.97	0.46
13:BA:298:ASP:OD1	67:Bc:18:ARG:NH2	2.44	0.46
14:EA:488:VAL:H	14:EA:518:GLN:NE2	2.13	0.46
16:BB:273:ASP:O	16:BB:443:ARG:NH1	2.45	0.46
17:EB:182:LEU:HD12	17:EB:258:VAL:HG22	1.96	0.46
20:ED:155:LEU:HD11	20:ED:177:ASP:HA	1.97	0.46
20:ED:267:PHE:HB2	20:ED:389:ASN:HD21	1.79	0.46
25:BF:240:VAL:HG21	25:BF:286:VAL:HG11	1.97	0.46
25:BF:415:PHE:O	25:BF:419:VAL:HG23	2.15	0.46
33:BJ:107:PRO:HD2	33:BJ:110:TRP:CZ2	2.50	0.46
38:EL:411:HIS:NE2	80:Ap:131:TRP:HB2	2.29	0.46
41:AN:30:ASN:O	41:AN:39:ARG:NH2	2.48	0.46
49:BR:21:PRO:HB2	49:BR:59:PRO:HG3	1.96	0.46
49:BR:151:ARG:O	49:BR:155:ARG:HG3	2.15	0.46
79:Ao:40:LYS:HD3	79:Ao:41:PRO:HD2	1.97	0.46
8:A5:44:PHE:HZ	60:AW:147:ILE:HD12	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E6:98:TYR:CE2	57:BU:157:ARG:HB3	2.50	0.46
11:A8:175:ASP:OD1	11:A8:176:PHE:N	2.46	0.46
12:AA:465:A:H2'	12:AA:466:G:C8	2.50	0.46
12:AA:920:A:H2'	12:AA:921:U:C6	2.50	0.46
17:EB:548:LEU:H	17:EB:573:ARG:NH1	2.13	0.46
17:EB:656:LEU:HD23	27:EG:45:ARG:HH11	1.81	0.46
21:AE:80:ASN:HB3	21:AE:83:GLU:HG3	1.97	0.46
31:BI:265:THR:HG21	31:BI:305:LYS:HE2	1.97	0.46
45:EO:307:PRO:HG2	45:EO:309:ARG:NH2	2.31	0.46
47:BQ:81:ILE:HG13	47:BQ:97:ILE:HG22	1.97	0.46
55:ET:14:ASN:OD1	55:ET:15:ASN:N	2.48	0.46
84:Av:181:THR:HB	84:Av:185:LYS:HE3	1.97	0.46
3:A2:463:ILE:HD11	54:BT:42:MET:HE2	1.97	0.46
4:E2:204:ARG:HD3	57:BU:83:GLY:HA3	1.97	0.46
6:E3:489:ARG:HA	6:E3:492:ARG:HE	1.80	0.46
13:BA:215:ARG:HE	13:BA:287:THR:HG23	1.81	0.46
14:EA:418:ALA:O	14:EA:563:ARG:NH2	2.31	0.46
16:BB:136:TRP:HB3	16:BB:141:ILE:HD12	1.98	0.46
16:BB:157:HIS:CE1	16:BB:162:GLN:HG3	2.51	0.46
17:EB:252:ASP:HA	17:EB:290:TRP:HZ2	1.80	0.46
20:ED:357:ASP:HB2	20:ED:360:CYS:HB3	1.97	0.46
20:ED:408:VAL:HG23	20:ED:467:PRO:HG3	1.97	0.46
23:EE:324:PHE:HB3	23:EE:387:VAL:HG12	1.97	0.46
28:BH:272:GLU:HB2	28:BH:275:GLN:HB3	1.97	0.46
38:EL:461:MET:HE3	80:Ap:282:ILE:HD13	1.97	0.46
38:EL:479:VAL:HG11	38:EL:509:ILE:HD11	1.98	0.46
39:EM:267:ALA:HB3	39:EM:324:GLN:HE21	1.80	0.46
74:E9:176:ASP:OD1	74:E9:177:SER:N	2.49	0.46
80:Ap:264:TRP:HE3	80:Ap:265:LEU:HD12	1.80	0.46
3:A2:190:GLN:HG2	3:A2:194:GLN:NE2	2.27	0.46
10:E6:359:ASP:OD1	10:E6:360:SER:N	2.47	0.46
12:AA:863:C:H2'	12:AA:864:U:H6	1.81	0.46
12:AA:1127:A:H5''	12:AA:1128:U:H5	1.80	0.46
13:BA:665:ASP:OD1	13:BA:665:ASP:N	2.46	0.46
23:EE:141:LEU:HD23	23:EE:155:VAL:HG23	1.98	0.46
25:BF:231:GLU:O	25:BF:234:GLU:HG3	2.15	0.46
25:BF:408:LEU:HB3	54:BT:39:ARG:HH21	1.81	0.46
26:EF:167:LYS:HB3	26:EF:168:PRO:HD3	1.98	0.46
30:AI:251:UNK:N	43:EN:344:GLU:O	2.48	0.46
31:BI:59:ARG:NH2	41:AN:180:GLU:OE1	2.49	0.46
39:EM:171:MET:HB2	39:EM:174:VAL:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BN:201:LEU:HD12	42:BN:202:PRO:HD2	1.98	0.46
43:EN:88:LEU:O	43:EN:92:GLN:HG2	2.15	0.46
43:EN:181:LEU:HB2	84:Av:209:VAL:HG11	1.96	0.46
49:BR:93:ARG:NH1	66:Bb:18:ARG:O	2.48	0.46
50:ER:119:PHE:O	50:ER:121:LEU:HG	2.16	0.46
76:Ul:146:UNK:N	76:Ul:337:UNK:O	2.47	0.46
3:A2:189:GLU:HG2	30:AI:52:TRP:HB2	1.97	0.46
5:A3:144:GLN:HG3	46:AP:40:LEU:HD22	1.97	0.46
6:E3:351:ASP:HB2	6:E3:396:CYS:SG	2.56	0.46
14:EA:160:MET:HE3	14:EA:269:TYR:HB2	1.98	0.46
16:BB:354:MET:HB3	16:BB:358:ARG:HH21	1.81	0.46
18:EC:253:THR:HG1	39:EM:36:LYS:HZ1	1.58	0.46
19:BD:154:GLU:HG2	19:BD:155:GLN:H	1.80	0.46
19:BD:232:LEU:HD22	19:BD:261:MET:HB3	1.97	0.46
28:BH:123:PRO:HA	28:BH:165:GLN:NE2	2.29	0.46
39:EM:223:ASP:HB3	39:EM:224:PRO:HD3	1.98	0.46
43:EN:93:LEU:HA	43:EN:96:LYS:HG2	1.98	0.46
57:BU:156:GLN:NE2	57:BU:159:ARG:HD3	2.31	0.46
60:AW:81:ARG:HE	60:AW:92:THR:HG22	1.78	0.46
71:Ag:72:LYS:HG2	71:Ag:73:ASN:HD22	1.81	0.46
74:E9:275:VAL:HG22	74:E9:277:GLN:HG3	1.97	0.46
75:Al:45:ILE:HD11	75:Al:54:ALA:HB3	1.97	0.46
80:Ap:45:LEU:HD22	80:Ap:48:TYR:HB3	1.96	0.46
7:E4:214:ASN:ND2	7:E4:248:ARG:HH12	2.13	0.46
13:BA:521:ILE:HD11	13:BA:659:GLU:HG2	1.98	0.46
13:BA:715:LEU:HD21	41:AN:72:ASP:HB3	1.97	0.46
16:BB:135:TYR:HH	16:BB:240:HIS:CE1	2.31	0.46
17:EB:317:ASP:OD1	17:EB:317:ASP:N	2.41	0.46
21:AE:86:PRO:HB2	45:EO:307:PRO:HB3	1.98	0.46
21:AE:127:PHE:CZ	21:AE:224:ASP:HB3	2.51	0.46
27:EG:129:ALA:HB3	27:EG:139:MET:HB2	1.96	0.46
28:BH:180:PRO:HG2	28:BH:198:VAL:HB	1.98	0.46
34:AK:300:ASP:OD1	34:AK:300:ASP:N	2.49	0.46
45:EO:96:ASP:O	45:EO:98:GLN:N	2.49	0.46
45:EO:275:THR:HB	45:EO:280:ARG:HH21	1.80	0.46
53:AT:63:GLU:HA	53:AT:68:PRO:HB3	1.97	0.46
63:AY:194:ARG:HG2	63:AY:201:MET:HB3	1.98	0.46
10:E6:105:LEU:HD11	42:BN:58:ILE:HG12	1.97	0.46
10:E6:262:VAL:HB	10:E6:265:LEU:HB2	1.97	0.46
11:A8:66:ARG:NH2	11:A8:139:ARG:O	2.49	0.46
13:BA:66:ILE:HG22	13:BA:69:ILE:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:EA:487:ARG:HD3	14:EA:518:GLN:NE2	2.31	0.46
20:ED:255:LEU:HA	20:ED:258:THR:HG22	1.98	0.46
23:EE:513:GLU:HG2	29:EH:471:ARG:HH22	1.81	0.46
26:EF:70:ARG:NH2	26:EF:139:LEU:O	2.49	0.46
31:BI:224:MET:HE2	70:Bf:106:PRO:HB2	1.98	0.46
38:EL:443:HIS:HB2	38:EL:474:PRO:HG2	1.98	0.46
39:EM:183:LEU:HD22	39:EM:220:VAL:HG12	1.97	0.46
43:EN:33:ARG:O	43:EN:37:ILE:HG12	2.15	0.46
58:AV:211:VAL:HA	71:Ag:125:ARG:HH12	1.81	0.46
63:AY:69:ASP:OD1	63:AY:69:ASP:N	2.46	0.46
63:AY:205:ARG:HB2	63:AY:214:MET:HB2	1.98	0.46
73:E8:565:HIS:O	73:E8:569:GLU:HG2	2.15	0.46
74:E9:332:TRP:CE2	74:E9:334:MET:HB3	2.51	0.46
80:Ap:69:GLY:H	80:Ap:73:THR:HG21	1.81	0.46
5:A3:81:VAL:HG22	79:Ao:185:MET:HE1	1.98	0.46
6:E3:394:GLU:OE1	6:E3:420:ARG:NE	2.49	0.46
10:E6:387:GLN:O	72:E7:12:ASN:ND2	2.49	0.46
12:AA:530:U:O2'	72:E7:49:ASN:N	2.48	0.46
12:AA:535:U:H2'	12:AA:536:A:H8	1.77	0.46
12:AA:1040:N:H1'2	23:EE:285:ARG:CZ	2.46	0.46
16:BB:80:ILE:HA	16:BB:83:ASN:ND2	2.31	0.46
20:ED:548:ASP:O	20:ED:552:ARG:N	2.35	0.46
25:BF:319:LYS:HA	61:BW:159:VAL:HG13	1.98	0.46
30:AI:12:TRP:HD1	65:Ba:84:TYR:HH	1.61	0.46
38:EL:237:CYS:SG	38:EL:241:THR:HA	2.55	0.46
49:BR:142:ARG:NH1	79:Ao:144:PRO:O	2.49	0.46
55:ET:12:ILE:HD13	55:ET:18:LEU:HD21	1.97	0.46
73:E8:483:THR:HG23	73:E8:503:ARG:HG3	1.98	0.46
2:E1:406:ALA:HB2	12:AA:511:U:H4'	1.97	0.46
5:A3:81:VAL:HG13	5:A3:112:VAL:HG12	1.98	0.46
6:E3:167:GLU:HA	6:E3:170:ARG:HG2	1.98	0.46
10:E6:173:ASN:HD21	10:E6:211:VAL:H	1.63	0.46
12:AA:303:U:O2'	55:ET:33:ARG:NH2	2.30	0.46
21:AE:265:ASP:HB3	21:AE:296:ARG:NH1	2.31	0.46
25:BF:130:GLU:HB2	25:BF:152:VAL:HG11	1.98	0.46
26:EF:182:ILE:HB	26:EF:185:ASN:HB2	1.98	0.46
27:EG:63:GLU:HB2	27:EG:94:PHE:CE2	2.50	0.46
29:EH:528:PRO:HD2	66:Bb:18:ARG:HH11	1.81	0.46
31:BI:195:PRO:HB2	31:BI:197:ASP:OD1	2.15	0.46
31:BI:224:MET:O	31:BI:228:GLN:HG2	2.16	0.46
39:EM:17:ARG:NH1	72:E7:23:LEU:O	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:AN:22:HIS:ND1	41:AN:23:PRO:HD2	2.30	0.46
45:EO:14:PRO:HG3	45:EO:202:PHE:CG	2.51	0.46
45:EO:105:SER:HB3	45:EO:112:GLN:HG3	1.98	0.46
45:EP:4:VAL:HG22	45:EP:59:ILE:HG23	1.97	0.46
45:EP:23:LEU:HD13	45:EP:30:HIS:HB3	1.98	0.46
63:AY:149:GLN:HB2	63:AY:168:HIS:CD2	2.51	0.46
69:Af:69:SER:O	79:Ao:58:ARG:NH1	2.42	0.46
71:Ag:160:GLN:HA	71:Ag:163:VAL:HG12	1.98	0.46
74:E9:291:ARG:NH1	74:E9:294:GLN:OE1	2.49	0.46
1:A1:219:ALA:HB2	63:AY:305:LEU:HD11	1.99	0.46
2:E1:238:LEU:O	2:E1:241:ARG:HB2	2.16	0.46
6:E3:424:ASN:O	6:E3:428:MET:HB2	2.16	0.46
6:E3:468:ASP:OD1	6:E3:469:PHE:N	2.45	0.46
13:BA:37:PRO:HD3	38:EL:264:VAL:HB	1.97	0.46
13:BA:277:ILE:O	13:BA:277:ILE:HG13	2.15	0.46
14:EA:310:ILE:HG12	14:EA:393:VAL:HB	1.97	0.46
16:BB:201:PRO:HB3	57:BU:106:ARG:HH11	1.81	0.46
17:EB:98:VAL:H	17:EB:127:GLN:HB3	1.81	0.46
19:BD:253:LEU:HD21	19:BD:258:TYR:HE1	1.81	0.46
21:AE:127:PHE:HE1	21:AE:134:TYR:HE2	1.64	0.46
24:AF:94:PRO:O	24:AF:126:TYR:HB2	2.16	0.46
31:BI:177:PRO:HB2	31:BI:182:TYR:CZ	2.51	0.46
38:EL:359:ARG:HA	38:EL:405:ARG:HB3	1.98	0.46
52:ES:59:LEU:HD21	52:ES:80:LEU:HB3	1.97	0.46
53:AT:143:MET:HE1	74:E9:258:ARG:HD3	1.97	0.46
58:AV:117:MET:HG3	58:AV:126:ILE:HA	1.97	0.46
60:AW:45:ARG:HG2	60:AW:46:PRO:HD2	1.98	0.46
62:AX:195:GLY:N	62:AX:210:ASP:OD1	2.45	0.46
68:Ae:148:ILE:HD11	68:Ae:153:PHE:HB3	1.97	0.46
2:E1:279:TRP:NE1	2:E1:452:ASN:HB2	2.31	0.45
2:E1:341:ALA:HB1	2:E1:382:LEU:HD12	1.98	0.45
4:E2:430:PRO:HG2	4:E2:433:LEU:HB2	1.98	0.45
6:E3:436:ALA:O	6:E3:440:ASN:ND2	2.36	0.45
11:A8:154:ILE:HD11	24:AF:312:TYR:HA	1.98	0.45
12:AA:144:U:H4'	60:AW:40:HIS:HD2	1.81	0.45
12:AA:587:U:O2'	74:E9:325:CYS:O	2.34	0.45
12:AA:1111:A:OP1	21:AE:176:ARG:NH1	2.49	0.45
23:EE:326:ALA:HB3	23:EE:389:PRO:HA	1.97	0.45
26:EF:177:LEU:HD11	26:EF:180:LEU:HD22	1.98	0.45
34:AK:173:LEU:O	34:AK:176:ARG:HG2	2.16	0.45
34:AK:256:GLU:O	34:AK:260:ARG:HG2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:EN:378:LEU:O	43:EN:382:MET:HG2	2.16	0.45
45:EO:150:ALA:HB2	45:EP:145:ILE:HD13	1.98	0.45
2:E1:322:HIS:CD2	2:E1:327:LEU:HD23	2.52	0.45
3:A2:42:LYS:NZ	63:AY:236:ASP:O	2.50	0.45
6:E3:437:LEU:O	6:E3:441:LEU:HB2	2.16	0.45
10:E6:272:TYR:OH	10:E6:314:ASP:OD2	2.31	0.45
10:E6:409:PRO:HB2	10:E6:441:SER:HB3	1.98	0.45
10:E6:439:GLU:OE2	10:E6:471:LYS:NZ	2.45	0.45
12:AA:529:U:O4	12:AA:549:G:O6	2.35	0.45
12:AA:589:U:OP2	74:E9:258:ARG:NE	2.47	0.45
12:AA:839:A:H2'	12:AA:840:A:C8	2.52	0.45
16:BB:137:ARG:HG3	57:BU:107:HIS:HA	1.99	0.45
16:BB:173:ARG:NH2	72:E7:93:ARG:O	2.48	0.45
16:BB:238:ASN:H	16:BB:242:GLN:NE2	2.15	0.45
17:EB:161:MET:HE2	17:EB:205:LEU:HD13	1.99	0.45
19:BD:218:ASN:HD22	19:BD:420:ARG:NH1	2.14	0.45
23:EE:513:GLU:HG2	29:EH:471:ARG:NH2	2.31	0.45
31:BI:285:ARG:NH2	45:EO:318:HIS:HB2	2.31	0.45
41:AN:156:ALA:O	67:Bc:23:ARG:NH1	2.48	0.45
44:BO:96:LEU:O	44:BO:100:ILE:HG12	2.16	0.45
46:AP:106:MET:HE2	60:AW:21:GLY:HA2	1.96	0.45
45:EP:112:GLN:HG3	45:EP:119:ILE:HD11	1.97	0.45
56:AU:103:GLU:HG2	58:AV:79:PHE:CZ	2.51	0.45
62:AX:170:VAL:HA	62:AX:173:VAL:HG12	1.97	0.45
1:A1:40:PRO:HG2	1:A1:43:ALA:HB2	1.97	0.45
2:E1:13:ARG:HG3	12:AA:575:A:N3	2.32	0.45
7:E4:35:CYS:SG	7:E4:36:GLY:N	2.89	0.45
12:AA:320:U:H2'	12:AA:321:A:C8	2.51	0.45
12:AA:446:A:H2'	12:AA:447:U:C6	2.51	0.45
12:AA:1091:U:H2'	12:AA:1092:U:C5	2.50	0.45
13:BA:60:PRO:HD3	21:AE:110:LYS:HE2	1.98	0.45
13:BA:155:ILE:HD11	67:Bc:84:LEU:HB3	1.98	0.45
13:BA:493:ASP:OD1	13:BA:493:ASP:N	2.49	0.45
24:AF:119:ASN:HB2	24:AF:125:ILE:HG23	1.98	0.45
26:EF:112:THR:OG1	26:EF:117:CYS:SG	2.69	0.45
34:AK:152:GLU:CD	59:BV:98:ILE:HG23	2.41	0.45
46:AP:240:GLU:HA	46:AP:243:ARG:HG2	1.99	0.45
57:BU:42:TRP:NE1	57:BU:58:SER:OG	2.44	0.45
58:AV:132:GLU:HB2	79:Ao:22:ALA:HB2	1.97	0.45
10:E6:301:ASP:H	10:E6:337:HIS:CE1	2.32	0.45
13:BA:437:THR:HG22	13:BA:441:LYS:HE3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:EA:317:ASN:HB2	14:EA:339:LYS:HG2	1.99	0.45
16:BB:170:GLN:NE2	16:BB:173:ARG:HH21	2.14	0.45
22:BE:339:ILE:HG13	35:BK:212:GLN:HE21	1.80	0.45
25:BF:231:GLU:O	25:BF:235:GLU:HG3	2.16	0.45
29:EH:99:VAL:HG21	29:EH:386:LYS:HB3	1.98	0.45
29:EH:276:ASP:OD1	29:EH:277:CYS:N	2.49	0.45
35:BK:93:LEU:HD12	35:BK:97:ALA:HB3	1.99	0.45
38:EL:471:MET:HE1	70:Bf:62:LYS:HD2	1.98	0.45
47:BQ:117:SER:HB2	47:BQ:119:GLU:HG2	1.98	0.45
55:ET:57:PRO:HG3	75:Al:56:VAL:HG23	1.97	0.45
59:BV:35:PRO:HB3	59:BV:81:GLU:HB3	1.98	0.45
80:Ap:226:ASP:OD1	80:Ap:226:ASP:N	2.47	0.45
1:A1:32:ASN:HA	1:A1:35:VAL:HG12	1.98	0.45
2:E1:171:GLU:OE1	10:E6:215:ARG:NH2	2.45	0.45
7:E4:408:LEU:HD13	7:E4:433:PHE:CE2	2.51	0.45
10:E6:476:GLU:O	10:E6:477:ARG:HG3	2.17	0.45
12:AA:460:U:H4'	56:AU:63:ARG:CZ	2.47	0.45
12:AA:813:U:OP1	56:AU:27:ARG:NH1	2.44	0.45
14:EA:304:SER:HB2	17:EB:367:THR:HG23	1.99	0.45
16:BB:360:ASP:O	16:BB:364:VAL:HG23	2.17	0.45
19:BD:449:LEU:HD22	19:BD:453:ARG:HG2	1.99	0.45
20:ED:119:SER:HB2	43:EN:33:ARG:HH21	1.82	0.45
24:AF:114:ILE:HG22	24:AF:127:THR:HG22	1.99	0.45
25:BF:166:GLN:NE2	46:AP:57:PHE:O	2.49	0.45
34:AK:151:LEU:HD13	59:BV:107:ILE:HG13	1.99	0.45
41:AN:125:ASP:HB3	41:AN:128:MET:HG3	1.99	0.45
43:EN:31:ARG:NE	43:EN:35:GLU:HB3	2.32	0.45
43:EN:340:GLN:NE2	43:EN:345:THR:OG1	2.49	0.45
45:EO:166:ASP:HB2	45:EO:217:MET:HE3	1.99	0.45
63:AY:20:LEU:HD22	63:AY:25:ASP:HA	1.98	0.45
74:E9:189:GLN:O	74:E9:192:GLN:NE2	2.49	0.45
80:Ap:294:LYS:HD3	80:Ap:297:ARG:HD3	1.98	0.45
83:At:94:THR:OG1	83:At:96:GLU:OE1	2.34	0.45
2:E1:193:MET:HG3	2:E1:245:TRP:CZ3	2.51	0.45
11:A8:55:GLN:HG2	11:A8:56:LEU:H	1.81	0.45
12:AA:15:G:H2'	12:AA:16:A:C8	2.52	0.45
12:AA:886:G:H2'	12:AA:886:G:N3	2.32	0.45
13:BA:728:PRO:O	13:BA:731:SER:OG	2.30	0.45
17:EB:351:LEU:HD13	17:EB:556:VAL:HG11	1.98	0.45
20:ED:243:CYS:HB3	20:ED:578:GLY:HA3	1.99	0.45
22:BE:373:GLN:HE21	22:BE:374:VAL:HG22	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BF:131:LEU:HA	25:BF:134:ASP:OD2	2.16	0.45
25:BF:209:ILE:HG13	25:BF:210:CYS:N	2.32	0.45
38:EL:591:THR:HG22	38:EL:595:LEU:HD23	1.99	0.45
42:BN:57:THR:HA	42:BN:60:ARG:HG2	1.98	0.45
43:EN:387:ILE:HG13	43:EN:445:LEU:HD11	1.99	0.45
49:BR:160:GLN:NE2	83:At:16:ARG:HD3	2.31	0.45
72:E7:12:ASN:OD1	72:E7:13:LEU:N	2.48	0.45
73:E8:463:SER:O	74:E9:224:SER:OG	2.34	0.45
2:E1:322:HIS:CE1	2:E1:340:LEU:HD22	2.51	0.45
3:A2:253:ALA:HB3	24:AF:407:ARG:HH12	1.82	0.45
4:E2:165:ALA:HB2	4:E2:188:ARG:CZ	2.47	0.45
6:E3:418:ASP:OD1	6:E3:418:ASP:N	2.50	0.45
12:AA:4:U:H1'	13:BA:698:SER:HB3	1.99	0.45
12:AA:33:G:N1	65:Ba:34:SER:O	2.39	0.45
12:AA:159:U:O2'	46:AP:205:VAL:O	2.33	0.45
12:AA:354:U:H2'	79:Ao:199:HIS:CE1	2.51	0.45
12:AA:566:A:OP1	72:E7:78:ARG:NH1	2.37	0.45
14:EA:469:ASN:HB2	14:EA:472:LEU:HD13	1.97	0.45
18:EC:193:LEU:HB2	18:EC:203:LYS:HD2	1.99	0.45
20:ED:451:VAL:HG11	20:ED:505:TYR:HB3	1.98	0.45
24:AF:230:LYS:HD3	24:AF:230:LYS:HA	1.81	0.45
25:BF:214:LEU:HD12	25:BF:289:CYS:HB2	1.97	0.45
26:EF:120:ASP:HB3	26:EF:125:CYS:SG	2.56	0.45
31:BI:189:ALA:HB1	31:BI:194:LYS:HB2	1.98	0.45
43:EN:157:LEU:HD13	43:EN:201:ARG:HD2	1.99	0.45
44:BO:185:LEU:HA	44:BO:185:LEU:HD23	1.81	0.45
56:AU:113:LEU:HB2	69:Af:99:PHE:CE2	2.51	0.45
58:AV:128:ARG:HA	58:AV:129:PRO:HA	1.82	0.45
2:E1:42:THR:HG21	53:AT:77:ASP:HB2	1.99	0.45
4:E2:477:LYS:HE3	12:AA:214:N:H1'2	1.99	0.45
5:A3:62:VAL:HG21	83:At:52:LYS:HD2	1.99	0.45
5:A3:146:PRO:HD3	46:AP:42:VAL:HG21	1.98	0.45
5:A3:163:LYS:NZ	12:AA:326:U:OP2	2.47	0.45
10:E6:93:GLU:HG3	57:BU:161:ARG:HH12	1.82	0.45
12:AA:969:U:H4'	12:AA:970:U:H5	1.82	0.45
12:AA:1003:G:H22	18:EC:39:ARG:HG2	1.81	0.45
12:AA:1104:U:H5''	12:AA:1105:U:H5'	1.99	0.45
14:EA:116:MET:HE3	14:EA:144:ASP:HB3	1.99	0.45
16:BB:97:ASP:OD1	57:BU:103:ARG:NE	2.40	0.45
19:BD:450:MET:HG3	19:BD:451:GLY:H	1.81	0.45
20:ED:24:SER:OG	20:ED:25:PRO:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:ED:179:PRO:HB2	20:ED:593:SER:HB3	1.99	0.45
25:BF:193:GLU:O	25:BF:196:ARG:HG3	2.17	0.45
38:EL:70:ARG:NH2	38:EL:553:THR:OG1	2.49	0.45
38:EL:294:MET:HE3	38:EL:511:VAL:HB	1.99	0.45
43:EN:454:LYS:HD3	43:EN:454:LYS:HA	1.85	0.45
45:EO:214:PHE:HB3	45:EO:217:MET:HB3	1.99	0.45
63:AY:64:HIS:CD2	63:AY:66:ARG:H	2.35	0.45
4:E2:376:GLY:HA2	4:E2:383:ASN:ND2	2.32	0.45
6:E3:543:ASP:OD1	6:E3:543:ASP:N	2.45	0.45
11:A8:113:ILE:HG22	46:AP:150:ARG:HH21	1.81	0.45
12:AA:302:G:N2	12:AA:335:G:H1'	2.32	0.45
12:AA:591:G:P	73:E8:548:ARG:HD3	2.57	0.45
12:AA:874:A:H2'	12:AA:875:G:O4'	2.16	0.45
12:AA:962:U:H1'	17:EB:344:GLU:HB3	1.98	0.45
13:BA:484:HIS:CD2	13:BA:658:SER:HB2	2.52	0.45
13:BA:542:ASN:OD1	13:BA:542:ASN:N	2.50	0.45
14:EA:192:VAL:HG23	14:EA:222:ASN:HB2	1.99	0.45
17:EB:134:MET:SD	17:EB:159:GLN:NE2	2.90	0.45
17:EB:254:ARG:HG2	17:EB:292:VAL:HG23	1.99	0.45
18:EC:322:HIS:HD2	39:EM:53:TRP:HD1	1.65	0.45
21:AE:93:TYR:CE1	21:AE:98:GLU:HG3	2.51	0.45
37:BL:158:ARG:NH2	37:BL:221:CYS:O	2.44	0.45
43:EN:227:VAL:O	43:EN:231:LEU:N	2.41	0.45
60:AW:203:CYS:O	63:AY:8:ARG:NH2	2.50	0.45
62:AX:160:VAL:HG12	62:AX:215:VAL:HG22	1.98	0.45
63:AY:25:ASP:HB3	63:AY:28:VAL:HG23	1.98	0.45
75:AI:97:LEU:HD11	75:AI:215:GLY:HA2	1.99	0.45
4:E2:386:SER:HB2	57:BU:95:LEU:HD23	1.99	0.45
6:E3:540:ILE:HD11	6:E3:544:VAL:HG11	1.99	0.45
12:AA:499:U:H2'	12:AA:500:A:C8	2.52	0.45
12:AA:559:A:H1'	12:AA:560:G:C2	2.52	0.45
12:AA:915:A:N6	43:EN:49:GLU:OE1	2.50	0.45
14:EA:75:ASP:OD1	14:EA:75:ASP:N	2.50	0.45
14:EA:321:SER:O	14:EA:324:VAL:HG12	2.17	0.45
18:EC:211:ASP:OD1	18:EC:212:ARG:N	2.50	0.45
19:BD:164:LEU:HA	19:BD:169:ALA:HB2	1.99	0.45
19:BD:224:ARG:HH22	19:BD:519:PRO:HG2	1.81	0.45
23:EE:332:ALA:O	23:EE:397:ARG:NH1	2.47	0.45
26:EF:353:PHE:HA	26:EF:356:LEU:HD12	1.99	0.45
33:BJ:180:GLU:OE2	33:BJ:200:ARG:NH1	2.50	0.45
34:AK:174:GLU:CD	59:BV:105:PRO:HB2	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BN:200:TYR:OH	57:BU:179:ASP:OD2	2.34	0.45
46:AP:65:VAL:HG11	71:Ag:80:PHE:CE2	2.52	0.45
45:EP:268:ARG:NH2	45:EP:269:GLN:OE1	2.49	0.45
49:BR:135:LEU:O	49:BR:139:TYR:HB2	2.17	0.45
58:AV:115:VAL:HG21	58:AV:134:VAL:HB	1.98	0.45
60:AW:47:PHE:HD1	63:AY:30:ARG:HH21	1.65	0.45
66:Bb:42:ASP:OD1	66:Bb:42:ASP:N	2.49	0.45
7:E4:200:LEU:HD23	7:E4:200:LEU:HA	1.87	0.44
10:E6:77:GLY:HA3	48:AR:211:ARG:HG3	1.98	0.44
12:AA:9:A:N7	63:AY:6:ARG:NH2	2.65	0.44
12:AA:831:A:H2'	12:AA:832:A:H8	1.82	0.44
13:BA:785:ARG:HG2	60:AW:251:SER:HB2	2.00	0.44
16:BB:121:GLU:O	16:BB:124:GLU:HG3	2.17	0.44
18:EC:69:ARG:HH12	29:EH:477:LEU:HD11	1.82	0.44
23:EE:476:ASP:OD1	80:Ap:206:ARG:NH1	2.50	0.44
33:BJ:182:VAL:O	33:BJ:186:VAL:HG22	2.17	0.44
34:AK:163:LEU:HD23	34:AK:171:PRO:HG3	1.98	0.44
38:EL:311:GLU:OE2	38:EL:487:MET:N	2.49	0.44
42:BN:94:ARG:O	42:BN:98:GLU:HG2	2.16	0.44
47:BQ:163:GLN:OE1	47:BQ:163:GLN:N	2.49	0.44
75:Al:180:LEU:HD21	75:Al:209:LEU:HD13	1.99	0.44
80:Ap:294:LYS:HA	80:Ap:297:ARG:HG2	1.99	0.44
2:E1:300:ASP:OD1	2:E1:300:ASP:N	2.51	0.44
5:A3:160:ILE:HA	5:A3:163:LYS:HG2	1.99	0.44
7:E4:121:SER:O	7:E4:125:HIS:ND1	2.40	0.44
7:E4:162:THR:OG1	7:E4:370:HIS:O	2.30	0.44
7:E4:398:VAL:O	7:E4:401:GLU:HG3	2.16	0.44
12:AA:74:U:O2	61:BW:81:ARG:NH2	2.49	0.44
12:AA:166:A:H2'	12:AA:167:U:C6	2.52	0.44
12:AA:499:U:H2'	12:AA:500:A:H8	1.80	0.44
13:BA:283:ASN:O	13:BA:294:SER:OG	2.35	0.44
13:BA:685:ARG:HH21	13:BA:722:LEU:HA	1.82	0.44
14:EA:244:PHE:CD1	52:ES:124:ASN:HB3	2.52	0.44
17:EB:149:LYS:N	89:EB:1001:ATP:O1A	2.49	0.44
18:EC:127:TRP:CE3	18:EC:133:PRO:HB3	2.53	0.44
19:BD:493:ASP:OD1	19:BD:494:GLU:N	2.50	0.44
22:BE:368:PRO:HA	22:BE:372:LYS:HA	1.99	0.44
23:EE:82:ASN:OD1	23:EE:82:ASN:N	2.50	0.44
34:AK:151:LEU:HD12	34:AK:152:GLU:N	2.31	0.44
43:EN:161:VAL:HG22	43:EN:222:LEU:HD12	1.99	0.44
44:BO:104:LEU:HD12	44:BO:117:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:AR:207:MET:HE3	57:BU:155:LEU:HD12	1.99	0.44
49:BR:177:LEU:HB2	49:BR:179:ILE:HD11	1.99	0.44
56:AU:63:ARG:HG3	56:AU:77:TRP:CE2	2.52	0.44
56:AU:67:ASP:HB2	56:AU:77:TRP:HB2	1.99	0.44
60:AW:149:ILE:HD13	60:AW:149:ILE:HA	1.85	0.44
71:Ag:84:ASN:HA	71:Ag:87:VAL:HG22	1.99	0.44
1:A1:165:LYS:NZ	65:Ba:92:TYR:OH	2.50	0.44
2:E1:53:ILE:HG23	2:E1:129:LEU:HD13	1.99	0.44
6:E3:412:GLY:O	6:E3:424:ASN:ND2	2.50	0.44
7:E4:243:ILE:HG13	7:E4:412:PHE:CD2	2.52	0.44
10:E6:156:ARG:HA	42:BN:128:ARG:NH1	2.32	0.44
10:E6:288:GLU:HA	10:E6:326:THR:HG22	2.00	0.44
12:AA:930:A:OP2	17:EB:219:ARG:NH1	2.50	0.44
12:AA:991:A:OP2	14:EA:498:ARG:NH2	2.47	0.44
12:AA:1129:A:H5''	12:AA:1130:A:H2'	1.99	0.44
13:BA:38:LYS:HD3	38:EL:351:LEU:HD21	2.00	0.44
14:EA:539:LEU:HB2	14:EA:566:GLN:HE22	1.81	0.44
17:EB:385:LEU:H	17:EB:385:LEU:HD12	1.82	0.44
18:EC:42:SER:O	18:EC:46:ARG:HG3	2.17	0.44
23:EE:160:HIS:CD2	23:EE:285:ARG:HH21	2.36	0.44
24:AF:339:ASN:OD1	24:AF:339:ASN:N	2.50	0.44
27:EG:112:GLU:OE2	27:EG:138:ARG:NH1	2.50	0.44
29:EH:107:GLY:HA3	66:Bb:2:ALA:HB2	2.00	0.44
43:EN:316:ASP:HB3	43:EN:319:THR:HB	2.00	0.44
63:AY:104:PHE:O	63:AY:139:ASN:ND2	2.48	0.44
2:E1:433:TYR:HB2	48:AR:67:GLN:HE22	1.82	0.44
3:A2:334:LEU:HD22	3:A2:355:GLU:HB2	1.99	0.44
3:A2:433:GLU:OE1	3:A2:433:GLU:N	2.50	0.44
7:E4:321:GLN:OE1	7:E4:321:GLN:N	2.50	0.44
10:E6:172:LEU:O	10:E6:176:LYS:HG2	2.17	0.44
12:AA:73:G:O2'	84:Av:60:ARG:NH2	2.50	0.44
12:AA:968:G:OP1	27:EG:3:ASN:ND2	2.47	0.44
12:AA:1003:G:N7	18:EC:37:ARG:NH1	2.66	0.44
19:BD:369:ARG:HH21	19:BD:468:TRP:NE1	2.15	0.44
20:ED:102:THR:HG22	20:ED:124:VAL:HG12	2.00	0.44
20:ED:319:ALA:HB2	20:ED:327:ILE:HD12	1.99	0.44
30:AI:11:PRO:HB2	65:Ba:84:TYR:CD2	2.53	0.44
31:BI:130:ASP:OD1	31:BI:162:ARG:NH2	2.42	0.44
39:EM:27:LYS:HA	39:EM:30:MET:HE2	1.98	0.44
39:EM:246:LEU:HA	39:EM:266:VAL:HG12	1.99	0.44
41:AN:53:GLN:HA	41:AN:92:VAL:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BN:215:TRP:CE2	57:BU:164:ARG:HD3	2.52	0.44
43:EN:724:GLY:HA2	43:EN:727:VAL:HG12	1.99	0.44
45:EP:200:ILE:HD12	45:EP:221:TYR:HB2	1.98	0.44
57:BU:43:ARG:CZ	57:BU:45:ILE:HD11	2.47	0.44
70:Bf:41:SER:O	70:Bf:45:ARG:HG3	2.17	0.44
72:E7:86:ASP:HB3	72:E7:89:ALA:HB3	1.99	0.44
80:Ap:202:ASP:HB3	80:Ap:252:SER:OG	2.17	0.44
7:E4:111:ARG:HA	7:E4:114:GLU:HG2	1.98	0.44
10:E6:104:PHE:CE1	10:E6:112:LEU:HD13	2.52	0.44
12:AA:305:G:N1	12:AA:346:G:OP1	2.50	0.44
13:BA:597:VAL:O	13:BA:601:ARG:HG2	2.17	0.44
14:EA:544:GLN:HE21	14:EA:566:GLN:NE2	2.16	0.44
16:BB:357:THR:HA	16:BB:364:VAL:HG22	1.99	0.44
18:EC:63:GLN:O	49:BR:192:ARG:NH2	2.51	0.44
21:AE:139:GLY:HA3	21:AE:339:PHE:O	2.16	0.44
24:AF:309:ASP:OD1	24:AF:309:ASP:N	2.48	0.44
37:BL:69:MET:SD	58:AV:148:ASN:HB2	2.58	0.44
39:EM:287:LEU:HD13	39:EM:303:ILE:HD11	1.99	0.44
45:EO:277:PRO:HA	45:EO:280:ARG:HG2	1.99	0.44
46:AP:181:LEU:HD13	75:Al:118:ALA:HB3	1.99	0.44
45:EP:241:PHE:CE1	45:EP:255:PRO:HD3	2.53	0.44
57:BU:42:TRP:CD1	57:BU:58:SER:HG	2.35	0.44
64:BZ:107:PRO:HA	64:BZ:110:VAL:HG12	1.99	0.44
66:Bb:90:PRO:HD3	83:At:61:GLY:HA3	2.00	0.44
7:E4:270:ALA:O	7:E4:274:ALA:CB	2.66	0.44
12:AA:948:A:C2	20:ED:339:ARG:HD3	2.53	0.44
12:AA:1041:N:OP2	23:EE:256:ARG:NH1	2.43	0.44
13:BA:357:MET:HG3	13:BA:362:ALA:HA	1.99	0.44
13:BA:378:VAL:O	13:BA:382:ILE:HB	2.17	0.44
13:BA:600:VAL:HA	13:BA:603:LEU:HG	1.98	0.44
16:BB:330:TRP:NE1	16:BB:334:ARG:HE	2.15	0.44
17:EB:294:THR:O	17:EB:294:THR:OG1	2.30	0.44
18:EC:192:MET:HG2	23:EE:122:TRP:CZ3	2.53	0.44
19:BD:334:ARG:O	19:BD:338:VAL:HG23	2.17	0.44
25:BF:260:GLY:O	25:BF:270:LYS:NZ	2.48	0.44
26:EF:62:LEU:HD12	26:EF:62:LEU:H	1.82	0.44
30:AI:71:TYR:HA	30:AI:72:PRO:HA	1.79	0.44
34:AK:55:PHE:HB2	34:AK:102:VAL:HG23	1.99	0.44
37:BL:55:LEU:HG	56:AU:19:ARG:HH12	1.83	0.44
38:EL:468:LEU:HD13	70:Bf:63:LEU:HD11	2.00	0.44
45:EO:50:LEU:N	45:EO:137:ASP:OD1	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:AP:110:HIS:CD2	46:AP:120:ILE:HG12	2.52	0.44
46:AP:217:VAL:HG23	46:AP:236:ASN:O	2.17	0.44
45:EP:94:VAL:HB	45:EP:103:LEU:HD22	1.99	0.44
66:Bb:64:PRO:HA	66:Bb:67:ARG:HG2	2.00	0.44
73:E8:450:LEU:HD21	73:E8:454:LEU:HD23	1.99	0.44
84:Av:182:LYS:HA	84:Av:185:LYS:HD2	1.99	0.44
2:E1:322:HIS:HD2	2:E1:327:LEU:HD23	1.82	0.44
6:E3:198:ASP:OD1	6:E3:199:ASP:N	2.51	0.44
12:AA:962:U:H4'	12:AA:964:A:H62	1.81	0.44
19:BD:132:GLU:O	19:BD:136:LEU:HG	2.17	0.44
21:AE:186:TYR:HB3	21:AE:216:CYS:SG	2.57	0.44
21:AE:269:VAL:HG21	21:AE:296:ARG:HB2	1.99	0.44
21:AE:343:ILE:HG13	21:AE:344:ASN:H	1.83	0.44
27:EG:147:THR:HG23	27:EG:152:MET:HB2	1.99	0.44
34:AK:94:PHE:H	59:BV:91:LYS:HZ3	1.64	0.44
39:EM:328:ILE:O	39:EM:332:GLN:HG2	2.18	0.44
45:EO:134:ARG:NH2	45:EP:130:ASN:OD1	2.49	0.44
45:EP:269:GLN:O	45:EP:272:GLU:HG3	2.17	0.44
71:Ag:157:ASP:O	71:Ag:160:GLN:HG3	2.17	0.44
84:Av:111:ILE:HD11	84:Av:125:MET:SD	2.58	0.44
3:A2:219:THR:OG1	24:AF:395:PRO:O	2.25	0.44
10:E6:275:SER:HA	10:E6:278:THR:HG22	1.99	0.44
12:AA:154:A:C2	60:AW:2:PRO:HA	2.52	0.44
12:AA:793:U:H2'	12:AA:794:A:C8	2.53	0.44
12:AA:907:U:OP1	17:EB:562:THR:HG21	2.17	0.44
13:BA:474:LEU:HD23	13:BA:477:LEU:HD12	2.00	0.44
16:BB:124:GLU:HA	16:BB:127:VAL:HG12	2.00	0.44
16:BB:283:LEU:HD21	16:BB:325:SER:HA	1.99	0.44
19:BD:236:LYS:NZ	19:BD:251:ALA:O	2.49	0.44
21:AE:190:MET:O	21:AE:192:VAL:HG13	2.18	0.44
23:EE:327:ARG:O	23:EE:390:ASN:ND2	2.51	0.44
24:AF:163:ASP:HB3	24:AF:203:PRO:HB2	2.00	0.44
25:BF:169:GLY:HA2	25:BF:172:ILE:HD12	2.00	0.44
29:EH:100:LEU:HD13	29:EH:102:TRP:CZ2	2.52	0.44
29:EH:368:GLU:OE1	41:AN:194:ARG:NH1	2.50	0.44
37:BL:71:GLU:OE1	37:BL:74:GLN:NE2	2.50	0.44
43:EN:224:LEU:HA	43:EN:227:VAL:HG23	2.00	0.44
45:EO:318:HIS:CD2	45:EO:319:ARG:H	2.35	0.44
46:AP:54:ARG:HG2	79:Ao:96:ILE:O	2.17	0.44
46:AP:227:PRO:HG2	46:AP:228:TYR:HD1	1.81	0.44
45:EP:21:LEU:C	45:EP:194:TRP:HE1	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:BR:93:ARG:HE	66:Bb:23:TYR:HB2	1.82	0.44
56:AU:102:TYR:O	71:Ag:108:SER:OG	2.26	0.44
64:BZ:116:ASP:OD1	64:BZ:116:ASP:N	2.49	0.44
4:E2:154:PHE:CE1	16:BB:299:ASN:HB3	2.53	0.44
12:AA:137:U:O2'	17:EB:681:GLN:HB2	2.17	0.44
12:AA:360:U:P	27:EG:118:ARG:HH12	2.41	0.44
12:AA:393:A:N1	12:AA:444:G:C6	2.85	0.44
12:AA:1078:A:O3'	18:EC:46:ARG:NH1	2.51	0.44
13:BA:176:GLN:O	13:BA:180:ARG:HG2	2.18	0.44
13:BA:677:TRP:NE1	13:BA:702:ALA:O	2.43	0.44
13:BA:799:ASP:OD1	13:BA:801:ARG:HG2	2.17	0.44
16:BB:174:ASP:HB3	16:BB:213:LEU:HD11	2.00	0.44
22:BE:133:VAL:HB	22:BE:134:PRO:HD3	2.00	0.44
25:BF:378:ARG:NE	25:BF:381:GLU:OE1	2.45	0.44
26:EF:198:PHE:CE1	26:EF:342:ILE:HG23	2.53	0.44
39:EM:24:ALA:O	39:EM:28:GLU:HG2	2.18	0.44
58:AV:226:MET:HE2	69:Af:118:GLU:HG3	2.00	0.44
1:A1:156:ILE:HD12	1:A1:156:ILE:HA	1.93	0.43
4:E2:66:LEU:HD22	4:E2:69:LEU:HD21	1.99	0.43
12:AA:66:C:O2	20:ED:110:ARG:NH1	2.50	0.43
12:AA:137:U:H2'	12:AA:138:U:H6	1.83	0.43
14:EA:518:GLN:HA	14:EA:526:PHE:HA	2.00	0.43
18:EC:236:LYS:HG3	18:EC:310:THR:HG22	1.99	0.43
19:BD:309:ASP:OD1	19:BD:310:LYS:N	2.51	0.43
23:EE:324:PHE:CZ	23:EE:423:ALA:HB1	2.53	0.43
25:BF:190:ASN:O	25:BF:194:VAL:HG23	2.18	0.43
25:BF:206:LEU:HD12	25:BF:209:ILE:HD11	1.99	0.43
25:BF:282:THR:O	25:BF:286:VAL:HG22	2.18	0.43
26:EF:324:LEU:HD23	26:EF:326:ASN:H	1.83	0.43
31:BI:270:ILE:HD12	31:BI:274:GLN:HG3	2.01	0.43
37:BL:237:ASN:OD1	37:BL:237:ASN:N	2.50	0.43
43:EN:31:ARG:HB3	43:EN:35:GLU:HB2	2.00	0.43
43:EN:173:SER:HB3	43:EN:176:TYR:HD2	1.83	0.43
44:BO:162:ASP:OD1	44:BO:162:ASP:N	2.44	0.43
47:BQ:91:ILE:HG23	47:BQ:145:PHE:HB2	1.99	0.43
49:BR:136:TRP:HB3	79:Ao:144:PRO:HG3	2.00	0.43
90:ER:200:PM8:O33	52:ES:3:VAL:HG21	2.17	0.43
54:BT:64:GLN:CD	65:Ba:144:VAL:HG23	2.43	0.43
73:E8:530:ASN:HB2	74:E9:261:HIS:CE1	2.53	0.43
3:A2:20:ASN:HD22	3:A2:27:PRO:HA	1.83	0.43
12:AA:187:A:H3'	12:AA:287:A:N6	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AA:577:A:C4	12:AA:578:A:C8	3.06	0.43
12:AA:593:U:H5''	73:E8:556:ARG:NH2	2.33	0.43
12:AA:857:C:H2'	12:AA:858:C:C6	2.53	0.43
12:AA:974:G:H2'	12:AA:975:C:C6	2.53	0.43
13:BA:207:SER:HB2	13:BA:276:LEU:HD23	1.99	0.43
14:EA:61:ASP:HB3	14:EA:64:THR:HG22	1.99	0.43
16:BB:237:PHE:HB3	16:BB:243:ILE:HG22	1.99	0.43
18:EC:165:GLU:HG3	18:EC:166:HIS:CD2	2.53	0.43
22:BE:231:THR:HG22	22:BE:271:ASP:HB2	2.00	0.43
23:EE:425:SER:HB2	26:EF:336:VAL:HG13	1.99	0.43
24:AF:73:SER:H	54:BT:150:ASN:HD22	1.66	0.43
25:BF:144:GLU:HA	25:BF:147:GLU:HG2	1.99	0.43
38:EL:130:SER:OG	38:EL:134:LYS:O	2.36	0.43
38:EL:387:LYS:O	38:EL:391:HIS:ND1	2.35	0.43
42:BN:200:TYR:HB3	42:BN:214:TRP:CE3	2.53	0.43
43:EN:269:GLU:O	43:EN:326:ARG:NH2	2.50	0.43
44:BO:83:VAL:HG23	44:BO:228:PRO:HD3	1.99	0.43
45:EP:58:SER:OG	45:EP:93:ARG:NE	2.51	0.43
49:BR:42:VAL:HG12	49:BR:46:VAL:HG13	1.99	0.43
58:AV:106:ILE:HD13	71:Ag:88:SER:HA	2.00	0.43
71:Ag:78:GLY:O	71:Ag:82:ARG:HG2	2.18	0.43
72:E7:26:LEU:HD12	72:E7:26:LEU:H	1.83	0.43
73:E8:465:THR:OG1	74:E9:221:SER:OG	2.31	0.43
73:E8:475:LEU:HA	73:E8:478:VAL:HG12	2.00	0.43
2:E1:44:PRO:HB2	2:E1:48:ARG:HH11	1.83	0.43
2:E1:306:PRO:HD3	4:E2:488:ASN:HD22	1.83	0.43
12:AA:37:G:H5''	12:AA:38:U:C5	2.54	0.43
12:AA:57:A:H5''	54:BT:10:GLY:HA2	2.00	0.43
12:AA:116:U:H1'	56:AU:23:MET:HE1	2.00	0.43
12:AA:155:U:O2	24:AF:221:LYS:NZ	2.40	0.43
12:AA:296:A:H2	46:AP:108:CYS:HB3	1.83	0.43
17:EB:102:GLU:HA	17:EB:111:ARG:HH12	1.83	0.43
23:EE:278:HIS:CD2	23:EE:279:ARG:HG3	2.53	0.43
25:BF:213:LEU:O	25:BF:216:LEU:HG	2.18	0.43
35:BK:137:TYR:CE1	35:BK:141:ILE:HG13	2.53	0.43
37:BL:264:LEU:HD11	37:BL:287:ARG:HH22	1.83	0.43
79:Ao:79:PRO:HA	79:Ao:82:GLU:HG2	1.99	0.43
4:E2:250:LEU:HD13	4:E2:271:PRO:HB3	2.00	0.43
5:A3:108:ARG:O	5:A3:112:VAL:HG22	2.18	0.43
6:E3:228:ARG:HH21	6:E3:322:ARG:HA	1.83	0.43
7:E4:110:ASN:ND2	42:BN:133:GLN:OE1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E4:156:PHE:CD1	7:E4:184:GLU:HB3	2.53	0.43
7:E4:291:ARG:HE	7:E4:306:CYS:HB2	1.82	0.43
12:AA:474:A:H62	58:AV:158:ARG:HD3	1.84	0.43
12:AA:803:U:O2	63:AY:66:ARG:NH1	2.52	0.43
12:AA:1171:A:H3'	44:BO:130:ARG:HH12	1.83	0.43
13:BA:326:LEU:HD23	13:BA:326:LEU:HA	1.83	0.43
20:ED:9:ILE:HG12	20:ED:300:HIS:CE1	2.53	0.43
21:AE:171:VAL:HG13	21:AE:210:VAL:HG11	1.99	0.43
23:EE:419:ASP:HB3	23:EE:422:ILE:HG12	1.99	0.43
28:BH:117:ARG:HE	30:AI:203:ILE:HD11	1.83	0.43
31:BI:140:PHE:HD1	45:EO:274:THR:HG21	1.83	0.43
34:AK:95:LYS:HZ1	59:BV:88:ALA:HB3	1.82	0.43
45:EO:209:LEU:HD12	45:EO:210:PRO:HD2	2.01	0.43
51:BS:31:ASP:OD1	53:AT:31:ARG:NH2	2.52	0.43
67:Bc:89:ARG:HB2	67:Bc:92:ILE:HB	2.01	0.43
1:A1:207:ASP:OD1	1:A1:207:ASP:N	2.52	0.43
2:E1:233:LEU:HA	2:E1:236:MET:HG2	1.99	0.43
3:A2:160:ARG:HH12	3:A2:330:ARG:HD2	1.83	0.43
12:AA:322:U:H2'	12:AA:323:U:C6	2.53	0.43
12:AA:978:G:H2'	12:AA:979:U:O4'	2.18	0.43
16:BB:242:GLN:O	16:BB:245:GLU:HG3	2.18	0.43
19:BD:450:MET:O	19:BD:454:THR:HG22	2.18	0.43
22:BE:122:LYS:N	60:AW:239:GLU:OE2	2.44	0.43
24:AF:393:CYS:SG	24:AF:394:VAL:N	2.91	0.43
26:EF:336:VAL:O	26:EF:340:ILE:HG12	2.18	0.43
29:EH:112:VAL:HB	29:EH:210:GLN:HE22	1.84	0.43
29:EH:217:ILE:HG13	29:EH:318:TYR:CB	2.48	0.43
37:BL:241:ASP:OD1	37:BL:241:ASP:N	2.49	0.43
41:AN:146:LEU:HA	41:AN:149:ARG:HG2	2.00	0.43
42:BN:131:GLU:HG2	42:BN:134:ARG:NH2	2.34	0.43
42:BN:202:PRO:HB3	42:BN:212:PHE:CE2	2.54	0.43
43:EN:519:LEU:O	43:EN:523:ARG:HG3	2.19	0.43
46:AP:195:ILE:HB	46:AP:232:ILE:HA	2.00	0.43
45:EP:190:CYS:HG	45:EP:193:THR:HG1	1.54	0.43
48:AR:218:THR:O	48:AR:222:HIS:ND1	2.51	0.43
58:AV:145:ARG:HD3	58:AV:169:ALA:HB2	2.01	0.43
60:AW:10:MET:HE2	60:AW:12:HIS:CD2	2.54	0.43
60:AW:218:GLY:HA3	72:E7:38:ALA:HB3	2.00	0.43
65:Ba:41:ASP:N	65:Ba:41:ASP:OD1	2.52	0.43
65:Ba:49:ARG:HB3	65:Ba:86:ILE:HD13	2.00	0.43
65:Ba:89:PRO:HA	65:Ba:90:PRO:HD3	1.94	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
69:Af:91:ALA:HB1	79:Ao:34:TRP:CE2	2.53	0.43
80:Ap:180:LYS:HG2	80:Ap:235:THR:OG1	2.18	0.43
2:E1:259:GLU:OE2	10:E6:310:ARG:NH1	2.51	0.43
5:A3:117:LYS:HD3	46:AP:17:ARG:CZ	2.48	0.43
17:EB:464:HIS:ND1	17:EB:464:HIS:O	2.52	0.43
22:BE:66:ARG:NH1	22:BE:69:GLU:OE2	2.51	0.43
26:EF:250:LEU:HD12	26:EF:251:PRO:HD2	1.98	0.43
29:EH:101:PRO:HD3	29:EH:390:TYR:CE2	2.52	0.43
29:EH:389:LEU:O	29:EH:393:TYR:HB3	2.19	0.43
30:AI:144:MET:HA	30:AI:148:LEU:HB2	2.01	0.43
31:BI:194:LYS:HB3	31:BI:198:GLN:HG2	2.00	0.43
35:BK:340:ARG:NH1	35:BK:344:LYS:HB3	2.33	0.43
45:EO:207:GLY:HA2	45:EO:262:PHE:CE2	2.53	0.43
45:EP:170:GLN:HG2	45:EP:216:ARG:HH11	1.84	0.43
54:BT:83:GLU:OE2	54:BT:87:ARG:NE	2.52	0.43
58:AV:223:LYS:HB2	58:AV:226:MET:HG2	2.00	0.43
67:Bc:10:ASP:N	67:Bc:10:ASP:OD1	2.48	0.43
75:Al:105:GLU:OE1	75:Al:105:GLU:N	2.46	0.43
12:AA:593:U:H5''	73:E8:556:ARG:HH21	1.84	0.43
12:AA:954:U:H4'	12:AA:955:G:O4'	2.18	0.43
12:AA:989:U:H2'	12:AA:990:U:C6	2.53	0.43
13:BA:532:MET:HE2	13:BA:532:MET:HB3	1.86	0.43
13:BA:761:TYR:HE1	13:BA:793:ARG:HG2	1.83	0.43
20:ED:61:PRO:HG2	20:ED:602:PHE:HD1	1.83	0.43
20:ED:561:VAL:HB	20:ED:565:PHE:HD2	1.84	0.43
21:AE:91:THR:OG1	70:Bf:84:GLU:OE2	2.30	0.43
24:AF:255:LEU:O	24:AF:259:MET:HG2	2.18	0.43
26:EF:278:ARG:HB2	26:EF:292:HIS:HE1	1.83	0.43
31:BI:160:PHE:N	31:BI:161:PRO:HD2	2.33	0.43
35:BK:91:LEU:HB2	35:BK:93:LEU:HD22	2.01	0.43
38:EL:133:ASN:OD1	38:EL:134:LYS:N	2.50	0.43
38:EL:292:PRO:HA	38:EL:295:TRP:CG	2.53	0.43
43:EN:423:LEU:HD11	43:EN:515:LEU:HD23	1.99	0.43
45:EO:295:ARG:NH1	70:Bf:112:ARG:HH21	2.17	0.43
47:BQ:50:PHE:CE1	47:BQ:121:LYS:HE2	2.53	0.43
62:AX:112:TRP:CH2	62:AX:119:PRO:HB3	2.52	0.43
80:Ap:74:ARG:HB3	80:Ap:90:TYR:CD1	2.53	0.43
1:A1:118:VAL:HG11	1:A1:156:ILE:HD11	2.01	0.43
7:E4:243:ILE:HG12	7:E4:430:SER:CB	2.48	0.43
10:E6:497:TRP:CZ3	73:E8:578:LYS:HE2	2.54	0.43
12:AA:328:U:H2'	12:AA:329:U:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AA:352:U:H5''	18:EC:99:ARG:NH2	2.33	0.43
12:AA:954:U:H5	43:EN:64:SER:N	2.15	0.43
14:EA:534:ASN:HB2	14:EA:537:ASN:ND2	2.33	0.43
18:EC:332:ALA:O	23:EE:102:GLU:HG2	2.19	0.43
19:BD:386:ARG:NE	19:BD:392:ALA:HA	2.34	0.43
20:ED:17:PRO:HD2	75:AI:43:ALA:HB1	2.00	0.43
20:ED:476:LEU:HD13	47:BQ:221:LYS:HD3	2.01	0.43
21:AE:261:ARG:HD2	21:AE:299:GLY:H	1.84	0.43
23:EE:173:ARG:HG3	23:EE:174:HIS:CD2	2.54	0.43
24:AF:373:PRO:HB3	46:AP:186:THR:HG23	2.00	0.43
28:BH:239:ASN:OD1	84:AV:175:ARG:HG2	2.19	0.43
31:BI:126:MET:HE2	31:BI:126:MET:HA	2.01	0.43
34:AK:238:LEU:HB3	34:AK:258:GLY:HA3	2.00	0.43
38:EL:387:LYS:HG2	38:EL:391:HIS:CE1	2.52	0.43
43:EN:207:VAL:O	43:EN:210:THR:OG1	2.36	0.43
46:AP:357:PRO:HD2	46:AP:358:TRP:CZ3	2.53	0.43
50:ER:84:GLU:H	50:ER:84:GLU:CD	2.27	0.43
61:BW:136:ALA:HB1	61:BW:138:HIS:CE1	2.54	0.43
2:E1:362:GLU:OE1	2:E1:362:GLU:N	2.46	0.43
2:E1:435:SER:O	2:E1:439:ILE:HG23	2.19	0.43
4:E2:280:GLY:HA3	7:E4:56:ARG:CZ	2.48	0.43
7:E4:218:ASN:HD22	7:E4:293:ASN:HD21	1.67	0.43
7:E4:233:ARG:NH2	7:E4:329:ARG:HG3	2.34	0.43
10:E6:295:GLY:HA2	10:E6:333:ILE:HD11	2.00	0.43
11:A8:135:ARG:HE	11:A8:135:ARG:HB3	1.67	0.43
12:AA:99:A:H2'	12:AA:100:U:O4'	2.19	0.43
12:AA:102:A:N6	63:AY:43:TYR:O	2.51	0.43
12:AA:134:U:H2'	12:AA:135:G:H2'	2.01	0.43
12:AA:158:A:OP1	46:AP:204:ASN:ND2	2.51	0.43
12:AA:1071:U:H2'	12:AA:1072:C:C6	2.54	0.43
13:BA:770:TYR:HE1	13:BA:787:LEU:HD22	1.82	0.43
17:EB:515:HIS:HD2	17:EB:517:ALA:H	1.67	0.43
19:BD:236:LYS:HE2	19:BD:236:LYS:HB3	1.91	0.43
20:ED:197:LYS:HE3	20:ED:219:TYR:CE2	2.54	0.43
21:AE:368:ASP:OD1	21:AE:368:ASP:N	2.49	0.43
21:AE:375:ALA:HB3	21:AE:378:GLU:HG2	2.01	0.43
22:BE:83:VAL:O	22:BE:87:LEU:HG	2.18	0.43
25:BF:61:GLN:O	25:BF:65:GLU:HG3	2.18	0.43
30:AI:12:TRP:HB2	65:BA:84:TYR:CZ	2.53	0.43
37:BL:177:LEU:HA	37:BL:180:LEU:HD12	2.01	0.43
39:EM:148:ARG:HA	39:EM:151:THR:HG22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:EN:283:LEU:HA	43:EN:286:VAL:HG22	2.00	0.43
45:EO:205:GLU:OE2	45:EO:225:LYS:NZ	2.48	0.43
54:BT:32:THR:OG1	54:BT:33:ASN:N	2.51	0.43
54:BT:144:GLU:HG3	54:BT:173:LEU:HD23	2.01	0.43
54:BT:174:ILE:HB	54:BT:177:GLN:HG2	2.01	0.43
71:Ag:186:VAL:HB	71:Ag:187:PRO:HD3	2.01	0.43
13:BA:301:HIS:CD2	13:BA:303:ILE:H	2.33	0.43
13:BA:509:ARG:NH1	13:BA:648:GLU:O	2.49	0.43
13:BA:655:LEU:HD23	13:BA:655:LEU:HA	1.88	0.43
16:BB:115:PRO:O	16:BB:411:ARG:NH2	2.51	0.43
16:BB:141:ILE:HG23	16:BB:152:ARG:HD2	2.00	0.43
22:BE:303:ALA:O	22:BE:306:GLN:HB3	2.18	0.43
26:EF:183:PRO:HG3	26:EF:207:LEU:HD11	2.00	0.43
37:BL:195:PRO:HD3	37:BL:219:MET:HB2	2.01	0.43
39:EM:289:LEU:HB3	39:EM:302:MET:SD	2.59	0.43
42:BN:108:PHE:CZ	42:BN:128:ARG:HD2	2.54	0.43
43:EN:413:ARG:H	43:EN:413:ARG:HG2	1.70	0.43
54:BT:98:THR:OG1	54:BT:99:THR:N	2.51	0.43
55:ET:40:ALA:HB2	79:Ao:176:VAL:HG11	2.00	0.43
68:Ae:149:ASP:OD1	68:Ae:150:GLY:N	2.48	0.43
71:Ag:182:LYS:HE2	71:Ag:186:VAL:HG21	2.01	0.43
84:Av:204:TRP:HA	84:Av:207:ARG:HD2	2.01	0.43
6:E3:508:LEU:HA	6:E3:511:LYS:HG2	2.00	0.42
13:BA:521:ILE:HG12	13:BA:569:LEU:HB3	2.01	0.42
16:BB:134:ARG:HA	16:BB:137:ARG:NH1	2.34	0.42
17:EB:266:SER:HA	17:EB:306:LYS:HG2	2.01	0.42
19:BD:119:PHE:HB2	19:BD:164:LEU:HD11	2.00	0.42
24:AF:248:THR:OG1	24:AF:249:GLN:N	2.52	0.42
32:UI:21:UNK:HA	39:EM:113:GLU:HG3	2.00	0.42
33:BJ:270:ARG:HG2	33:BJ:275:ASP:OD2	2.19	0.42
35:BK:379:LEU:O	35:BK:384:ARG:NH1	2.51	0.42
43:EN:496:ASN:HB2	43:EN:537:HIS:HD2	1.84	0.42
43:EN:502:LEU:HD13	43:EN:514:HIS:CD2	2.53	0.42
43:EN:587:LEU:H	43:EN:587:LEU:HD23	1.84	0.42
44:BO:69:TYR:CD2	51:BS:40:GLU:HB2	2.51	0.42
45:EO:102:TYR:OH	45:EP:98:GLN:O	2.24	0.42
45:EO:197:PHE:CZ	45:EO:230:VAL:HG11	2.54	0.42
48:AR:76:GLU:OE1	48:AR:79:ARG:NH1	2.50	0.42
51:BS:38:HIS:HE2	53:AT:83:THR:HG22	1.83	0.42
61:BW:33:LEU:HD23	61:BW:97:ILE:HD13	2.00	0.42
62:AX:84:PRO:HA	65:Ba:28:ARG:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:E8:450:LEU:HD12	73:E8:451:PRO:HD2	2.01	0.42
2:E1:243:ARG:NH2	42:BN:111:PHE:O	2.52	0.42
3:A2:140:VAL:HG23	3:A2:356:HIS:HB3	2.00	0.42
6:E3:256:ARG:O	6:E3:260:VAL:HG22	2.19	0.42
13:BA:220:LEU:HD21	13:BA:286:PHE:HA	2.01	0.42
14:EA:115:ARG:O	14:EA:120:LYS:NZ	2.42	0.42
14:EA:268:LEU:HD11	52:ES:127:TYR:HE1	1.84	0.42
14:EA:312:ILE:HG22	14:EA:320:LYS:HB2	2.01	0.42
17:EB:67:ASN:OD1	46:AP:145:ARG:NH1	2.52	0.42
20:ED:91:LYS:O	20:ED:201:SER:OG	2.33	0.42
23:EE:268:ALA:HB1	23:EE:272:CYS:SG	2.59	0.42
23:EE:413:ASP:OD1	23:EE:413:ASP:N	2.43	0.42
23:EE:516:THR:O	23:EE:520:GLN:HG2	2.19	0.42
29:EH:503:ARG:O	29:EH:506:GLN:HG3	2.19	0.42
31:BI:227:ASN:HD22	80:Ap:117:TYR:HE1	1.67	0.42
31:BI:237:ALA:O	31:BI:243:SER:HB3	2.18	0.42
38:EL:312:PHE:CZ	38:EL:487:MET:HG3	2.54	0.42
38:EL:392:VAL:HG22	38:EL:520:VAL:HG11	2.00	0.42
38:EL:447:GLU:OE1	70:Bf:65:ARG:HD2	2.19	0.42
43:EN:324:HIS:CE1	43:EN:328:ILE:HD11	2.55	0.42
43:EN:416:SER:HA	43:EN:557:ARG:HH22	1.84	0.42
46:AP:74:THR:HG1	71:Ag:75:SER:HG	1.61	0.42
56:AU:73:HIS:O	69:Af:81:ARG:NH1	2.49	0.42
58:AV:145:ARG:HD2	58:AV:167:PRO:HB2	2.01	0.42
58:AV:148:ASN:HD21	58:AV:165:ASP:HB3	1.84	0.42
65:Ba:94:ASP:N	65:Ba:94:ASP:OD1	2.52	0.42
1:A1:53:SER:HB3	28:BH:293:TYR:OH	2.19	0.42
12:AA:445:U:H2'	12:AA:446:A:C8	2.54	0.42
12:AA:539:A:O2'	62:AX:187:ARG:HD3	2.19	0.42
12:AA:541:A:O3'	62:AX:168:SER:OG	2.37	0.42
14:EA:367:ARG:HE	14:EA:408:TYR:HB2	1.84	0.42
14:EA:368:HIS:HA	14:EA:371:ARG:HG2	2.01	0.42
16:BB:77:HIS:HA	16:BB:80:ILE:HG22	2.02	0.42
17:EB:389:VAL:HG11	17:EB:450:VAL:HB	2.00	0.42
19:BD:514:PHE:HA	19:BD:517:VAL:HG22	2.00	0.42
21:AE:234:ASP:OD2	21:AE:236:ARG:NH2	2.38	0.42
22:BE:296:GLU:HG3	22:BE:323:TRP:CD1	2.55	0.42
23:EE:224:PRO:HA	23:EE:225:PRO:HD3	1.95	0.42
24:AF:54:GLY:N	25:BF:365:HIS:O	2.50	0.42
26:EF:176:VAL:HG22	26:EF:202:LEU:HB2	2.00	0.42
26:EF:177:LEU:HD21	26:EF:180:LEU:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AK:302:THR:HG23	34:AK:305:GLU:H	1.84	0.42
37:BL:143:THR:O	37:BL:147:ARG:HG3	2.20	0.42
38:EL:296:LEU:HD21	38:EL:511:VAL:HG11	2.00	0.42
39:EM:111:SER:HB3	39:EM:116:ASN:HD21	1.84	0.42
46:AP:65:VAL:HG11	71:Ag:80:PHE:HE2	1.85	0.42
46:AP:73:ARG:HH22	71:Ag:82:ARG:HH11	1.67	0.42
49:BR:164:HIS:HE1	49:BR:192:ARG:HB3	1.85	0.42
67:Bc:59:ASN:OD1	67:Bc:63:GLU:HG2	2.19	0.42
68:Ae:51:PRO:HD2	68:Ae:54:MET:SD	2.59	0.42
4:E2:356:GLU:OE1	4:E2:356:GLU:N	2.39	0.42
7:E4:261:ASP:HB3	7:E4:279:PHE:CE2	2.55	0.42
10:E6:378:GLU:OE2	10:E6:378:GLU:N	2.44	0.42
12:AA:464:U:H4'	79:Ao:76:LYS:HD2	2.01	0.42
12:AA:525:A:H2'	12:AA:526:G:H8	1.84	0.42
12:AA:985:A:C8	18:EC:49:LEU:HD21	2.55	0.42
13:BA:300:ARG:HG3	13:BA:306:ASN:O	2.19	0.42
13:BA:350:LEU:HB2	13:BA:370:ILE:HG21	2.01	0.42
16:BB:150:THR:HA	64:BZ:58:LEU:HD13	1.99	0.42
19:BD:110:LEU:HD23	19:BD:449:LEU:HD12	2.00	0.42
21:AE:240:PRO:HG2	67:Bc:96:PRO:HB3	2.01	0.42
24:AF:163:ASP:OD1	24:AF:164:TYR:N	2.49	0.42
24:AF:240:ASP:OD1	24:AF:241:ARG:N	2.52	0.42
24:AF:336:ASN:HD21	54:BT:24:GLU:CD	2.26	0.42
27:EG:69:HIS:HA	69:Af:41:PHE:HB3	2.02	0.42
35:BK:137:TYR:OH	35:BK:203:GLU:OE1	2.24	0.42
39:EM:101:ARG:NH2	39:EM:128:ASN:HD21	2.16	0.42
43:EN:216:LEU:HD23	43:EN:216:LEU:HA	1.89	0.42
44:BO:89:THR:O	44:BO:93:ILE:HG12	2.19	0.42
58:AV:163:TRP:NE1	58:AV:165:ASP:OD1	2.51	0.42
79:Ao:173:VAL:HA	79:Ao:176:VAL:HG12	2.01	0.42
80:Ap:125:VAL:HB	80:Ap:146:GLN:HE21	1.85	0.42
1:A1:85:ARG:NH1	1:A1:87:ARG:HH21	2.18	0.42
7:E4:287:LEU:HD22	7:E4:308:THR:HB	2.02	0.42
8:A5:75:CYS:SG	8:A5:80:PRO:HG3	2.60	0.42
11:A8:122:MET:O	11:A8:126:ARG:HG3	2.19	0.42
12:AA:45:U:C4	65:Ba:37:ARG:HD3	2.55	0.42
12:AA:537:U:H2'	12:AA:538:U:C6	2.55	0.42
12:AA:1015:A:H2'	12:AA:1016:C:H6	1.85	0.42
16:BB:212:HIS:HB2	57:BU:111:LEU:HD21	2.02	0.42
17:EB:218:HIS:NE2	17:EB:222:ARG:HD2	2.33	0.42
18:EC:243:VAL:HG23	18:EC:404:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:AE:140:MET:HE1	21:AE:235:VAL:HA	2.02	0.42
22:BE:80:PRO:HG2	22:BE:83:VAL:HB	2.01	0.42
29:EH:235:GLN:O	29:EH:239:GLN:HG2	2.20	0.42
29:EH:268:HIS:ND1	29:EH:327:LEU:HD12	2.34	0.42
29:EH:328:ARG:HH21	29:EH:332:ARG:NH2	2.16	0.42
34:AK:241:ARG:HD3	34:AK:246:ASN:HB3	2.01	0.42
37:BL:53:ARG:HG3	60:AW:42:PHE:CD1	2.54	0.42
38:EL:585:ASP:HB3	38:EL:588:ILE:HB	2.02	0.42
39:EM:82:ARG:NH2	39:EM:110:MET:HG2	2.35	0.42
41:AN:178:ASP:OD1	41:AN:178:ASP:N	2.53	0.42
43:EN:199:PHE:CE2	43:EN:203:ARG:HD3	2.53	0.42
45:EO:54:GLY:HA2	45:EO:95:HIS:HB3	1.99	0.42
45:EP:19:SER:HB3	45:EP:97:PRO:HB3	2.01	0.42
48:AR:42:GLU:N	48:AR:43:PRO:HA	2.34	0.42
56:AU:65:ASN:ND2	56:AU:97:GLN:HE21	2.17	0.42
62:AX:68:TRP:CD1	62:AX:68:TRP:H	2.36	0.42
66:Bb:4:TRP:CZ3	66:Bb:6:PRO:HA	2.54	0.42
69:Af:163:THR:HG22	69:Af:165:GLY:H	1.84	0.42
79:Ao:148:LEU:HD23	79:Ao:148:LEU:HA	1.87	0.42
1:A1:45:TRP:HA	12:AA:64:U:O2'	2.19	0.42
7:E4:341:ASN:HA	7:E4:344:LYS:HG2	2.02	0.42
8:A5:68:GLU:HB2	48:AR:150:LYS:HA	2.00	0.42
10:E6:156:ARG:HA	42:BN:128:ARG:HH11	1.85	0.42
12:AA:19:A:OP2	12:AA:97:A:N6	2.52	0.42
12:AA:320:U:H2'	12:AA:321:A:H8	1.84	0.42
12:AA:587:U:N3	12:AA:794:A:N1	2.67	0.42
12:AA:1015:A:OP1	23:EE:103:ILE:HD13	2.20	0.42
12:AA:1080:A:OP2	27:EG:23:GLN:NE2	2.52	0.42
20:ED:149:TYR:OH	20:ED:531:SER:OG	2.36	0.42
22:BE:308:GLN:OE1	22:BE:308:GLN:N	2.53	0.42
24:AF:80:GLN:OE1	24:AF:80:GLN:N	2.51	0.42
24:AF:101:PRO:HB2	24:AF:384:TYR:CE2	2.55	0.42
24:AF:418:SER:O	84:Av:78:ARG:NH2	2.51	0.42
25:BF:50:LEU:HD11	25:BF:209:ILE:HD13	2.00	0.42
29:EH:255:GLU:HA	29:EH:261:VAL:HG11	2.01	0.42
30:AI:179:PRO:HG3	30:AI:185:TYR:HD1	1.84	0.42
31:BI:53:PRO:HD2	31:BI:56:TRP:CD2	2.55	0.42
33:BJ:153:ASP:H	33:BJ:158:PRO:HD2	1.84	0.42
38:EL:556:TYR:O	38:EL:564:ASN:ND2	2.52	0.42
39:EM:289:LEU:HD22	39:EM:302:MET:HG2	2.02	0.42
43:EN:322:PHE:HZ	43:EN:326:ARG:HH21	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:EN:449:CYS:SG	43:EN:474:VAL:HG11	2.59	0.42
46:AP:121:GLY:O	56:AU:10:HIS:N	2.53	0.42
46:AP:282:ARG:HE	84:Av:180:MET:HG2	1.84	0.42
48:AR:175:LYS:HE3	48:AR:175:LYS:HB2	1.88	0.42
49:BR:111:PHE:HB2	49:BR:195:VAL:HG12	2.02	0.42
60:AW:152:ILE:HA	60:AW:155:LEU:HD12	2.01	0.42
2:E1:274:LYS:HD3	2:E1:276:ARG:HH12	1.85	0.42
6:E3:531:ASP:HB2	6:E3:539:TYR:HB3	2.02	0.42
9:E5:37:UNK:O	9:E5:39:UNK:N	2.53	0.42
12:AA:1091:U:H2'	12:AA:1092:U:H5	1.85	0.42
16:BB:302:GLU:HG3	16:BB:303:ILE:H	1.85	0.42
19:BD:247:LEU:HB3	30:AI:225:TRP:CZ2	2.54	0.42
20:ED:238:ARG:HH12	20:ED:552:ARG:HG3	1.84	0.42
22:BE:273:ASP:OD1	22:BE:274:SER:N	2.51	0.42
45:EP:134:ARG:HH12	45:EP:157:ASN:ND2	2.18	0.42
57:BU:55:PHE:HB2	57:BU:76:VAL:HG11	2.01	0.42
58:AV:155:THR:HB	58:AV:158:ARG:HG2	2.00	0.42
60:AW:155:LEU:O	60:AW:198:VAL:HG22	2.19	0.42
2:E1:58:LYS:HZ2	48:AR:25:ALA:HA	1.85	0.42
6:E3:346:PHE:CB	6:E3:393:GLY:H	2.33	0.42
9:E5:266:UNK:HA	9:E5:311:UNK:HA	2.02	0.42
10:E6:385:ARG:HB3	72:E7:11:TRP:HD1	1.84	0.42
11:A8:49:ARG:N	24:AF:170:TRP:HE1	2.17	0.42
12:AA:389:A:H5'	23:EE:511:TRP:HZ2	1.85	0.42
12:AA:486:A:H5'	25:BF:372:LEU:HD12	2.02	0.42
12:AA:487:A:OP1	60:AW:84:ARG:NE	2.48	0.42
12:AA:980:U:C4	17:EB:636:ARG:HG3	2.55	0.42
13:BA:42:ASP:OD1	13:BA:76:ARG:HA	2.19	0.42
14:EA:145:GLY:O	14:EA:343:ARG:NH1	2.52	0.42
18:EC:285:LYS:HB3	18:EC:312:ARG:HE	1.83	0.42
19:BD:239:ALA:HB3	19:BD:249:PRO:HB3	2.02	0.42
19:BD:420:ARG:O	19:BD:424:VAL:HG23	2.20	0.42
20:ED:75:ASN:ND2	20:ED:544:ILE:HD12	2.34	0.42
20:ED:563:GLU:HA	20:ED:566:THR:HG22	2.00	0.42
21:AE:165:PHE:HB3	21:AE:168:ASN:HD21	1.84	0.42
23:EE:200:ASP:HB2	23:EE:203:VAL:HG22	2.02	0.42
29:EH:4:VAL:HG11	29:EH:100:LEU:HD11	2.02	0.42
30:AI:29:GLY:H	65:Ba:129:GLN:HE22	1.67	0.42
34:AK:130:ARG:HE	34:AK:130:ARG:HB2	1.25	0.42
38:EL:412:ALA:O	38:EL:416:ILE:HG13	2.18	0.42
38:EL:578:GLN:HE21	38:EL:606:GLY:HA2	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:EN:654:VAL:HG11	43:EN:708:GLN:HG3	2.02	0.42
46:AP:81:HIS:CE1	46:AP:101:PRO:HD3	2.54	0.42
50:ER:119:PHE:O	50:ER:121:LEU:N	2.53	0.42
60:AW:38:LYS:HA	60:AW:38:LYS:HD3	1.71	0.42
75:AI:99:PRO:HA	75:AI:122:LEU:HD11	2.01	0.42
84:AV:78:ARG:NH2	84:AV:132:ALA:O	2.44	0.42
12:AA:525:A:H2'	12:AA:526:G:C8	2.55	0.42
12:AA:952:U:H4'	55:ET:87:ARG:HH12	1.85	0.42
12:AA:1113:U:H3	13:BA:301:HIS:HA	1.84	0.42
14:EA:115:ARG:HD3	14:EA:203:GLU:OE2	2.19	0.42
17:EB:189:ILE:HD11	17:EB:235:ASP:OD1	2.19	0.42
20:ED:231:GLY:N	20:ED:501:PRO:HG2	2.35	0.42
23:EE:277:ASP:HB3	23:EE:280:VAL:HG22	2.01	0.42
24:AF:135:PHE:C	24:AF:228:THR:HG22	2.44	0.42
24:AF:311:GLN:HE21	24:AF:333:ILE:HD11	1.83	0.42
31:BI:293:THR:O	31:BI:297:LYS:HG3	2.20	0.42
31:BI:336:GLU:OE1	31:BI:336:GLU:N	2.51	0.42
34:AK:173:LEU:O	34:AK:177:VAL:HG13	2.19	0.42
35:BK:193:VAL:HA	48:AR:198:GLY:HA3	2.00	0.42
37:BL:67:ALA:HB2	56:AU:20:ILE:HG12	2.02	0.42
47:BQ:24:ARG:HG2	47:BQ:202:LEU:HD13	2.01	0.42
49:BR:105:ASN:OD1	49:BR:192:ARG:NH1	2.51	0.42
53:AT:143:MET:HE2	53:AT:143:MET:HB3	1.90	0.42
58:AV:73:LEU:HD22	58:AV:122:ARG:HG2	2.02	0.42
63:AY:282:ALA:HB1	64:BZ:173:PRO:HB3	2.01	0.42
71:Ag:29:LEU:HD22	71:Ag:33:LEU:HD22	2.02	0.42
5:A3:154:ALA:HB2	12:AA:333:U:H5''	2.01	0.42
7:E4:24:GLN:HE21	7:E4:72:ARG:HH12	1.67	0.42
7:E4:227:PRO:HG3	7:E4:234:TRP:CD1	2.55	0.42
11:A8:132:ASN:ND2	11:A8:135:ARG:HB2	2.34	0.42
17:EB:174:GLU:HA	17:EB:228:LEU:HD22	2.02	0.42
17:EB:232:MET:HE1	17:EB:248:VAL:HG11	2.01	0.42
18:EC:109:LEU:HD12	27:EG:152:MET:HE1	2.02	0.42
19:BD:193:GLN:NE2	19:BD:425:TYR:OH	2.52	0.42
20:ED:30:CYS:SG	20:ED:575:THR:OG1	2.70	0.42
20:ED:46:ARG:O	20:ED:50:ILE:HG13	2.19	0.42
21:AE:279:ARG:NH2	27:EG:136:ASP:OD1	2.53	0.42
22:BE:106:PHE:HA	22:BE:109:VAL:HG22	2.02	0.42
23:EE:127:ILE:HG12	23:EE:198:ARG:O	2.20	0.42
23:EE:152:GLN:HA	23:EE:220:ILE:HD12	2.02	0.42
28:BH:254:TRP:HA	30:AI:187:LYS:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:EL:75:MET:HE2	38:EL:75:MET:HB2	1.87	0.42
38:EL:554:LYS:HB3	38:EL:566:GLU:OE1	2.20	0.42
43:EN:353:LEU:HD21	43:EN:380:THR:HG22	2.02	0.42
43:EN:418:PRO:HB3	43:EN:557:ARG:CZ	2.50	0.42
44:BO:234:ASP:OD1	44:BO:235:TYR:N	2.52	0.42
45:EO:233:HIS:O	45:EO:236:LEU:HG	2.20	0.42
45:EO:257:TRP:HE1	45:EO:259:HIS:HD2	1.68	0.42
46:AP:310:HIS:ND1	46:AP:311:PRO:HD2	2.35	0.42
45:EP:140:LEU:O	45:EP:143:LEU:HG	2.19	0.42
73:E8:455:LEU:HD13	73:E8:478:VAL:HG11	2.01	0.42
84:Av:88:VAL:HG11	84:Av:138:LEU:HD21	2.02	0.42
2:E1:26:ASN:OD1	2:E1:26:ASN:N	2.52	0.41
2:E1:433:TYR:CG	2:E1:439:ILE:HG22	2.55	0.41
2:E1:450:ARG:HG3	2:E1:455:GLY:HA2	2.01	0.41
3:A2:413:TYR:OH	3:A2:418:ASP:OD2	2.38	0.41
4:E2:394:ARG:HD3	4:E2:421:ARG:NH1	2.35	0.41
4:E2:404:LYS:O	4:E2:408:MET:HG2	2.20	0.41
7:E4:110:ASN:HD21	42:BN:133:GLN:NE2	2.17	0.41
11:A8:100:GLN:OE1	12:AA:912:G:N2	2.45	0.41
12:AA:162:A:H2'	12:AA:163:U:O4'	2.20	0.41
12:AA:823:U:H2'	12:AA:824:U:C6	2.55	0.41
12:AA:971:C:H2'	12:AA:972:G:O4'	2.20	0.41
13:BA:313:GLY:HA2	13:BA:316:GLU:OE1	2.20	0.41
14:EA:75:ASP:HB3	14:EA:374:ARG:HG2	2.01	0.41
16:BB:415:ASP:HA	16:BB:418:ARG:HG2	2.02	0.41
17:EB:129:ALA:O	17:EB:133:ILE:HG12	2.20	0.41
17:EB:593:VAL:HG21	17:EB:615:LYS:HB2	2.02	0.41
22:BE:91:ILE:O	35:BK:284:PRO:HG3	2.20	0.41
25:BF:195:LEU:HD11	25:BF:216:LEU:HD22	2.02	0.41
26:EF:60:ARG:HG3	26:EF:63:TRP:CZ3	2.55	0.41
28:BH:204:THR:HB	28:BH:208:THR:HG23	2.01	0.41
31:BI:226:MET:HE2	31:BI:226:MET:HA	2.02	0.41
34:AK:43:GLU:CD	34:AK:262:PRO:HG3	2.45	0.41
45:EP:170:GLN:HA	45:EP:173:THR:HG22	2.02	0.41
74:E9:176:ASP:HB3	74:E9:179:TRP:HB3	2.01	0.41
76:U1:5:UNK:O	76:U1:235:UNK:HA	2.19	0.41
7:E4:57:GLU:CD	10:E6:175:ARG:HH21	2.28	0.41
7:E4:388:ARG:HB2	7:E4:431:TYR:OH	2.20	0.41
10:E6:180:LEU:HD13	10:E6:200:MET:HE1	2.01	0.41
12:AA:33:G:N7	62:AX:101:LYS:NZ	2.61	0.41
12:AA:102:A:C8	63:AY:42:THR:HG23	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AA:300:U:OP2	25:BF:261:ARG:NH1	2.46	0.41
17:EB:300:THR:HG21	17:EB:307:LEU:HD22	2.02	0.41
29:EH:390:TYR:O	29:EH:394:VAL:HG22	2.19	0.41
37:BL:46:ASP:OD2	37:BL:78:ARG:NH2	2.53	0.41
38:EL:72:TYR:CE2	38:EL:75:MET:HB3	2.54	0.41
41:AN:54:LEU:HD13	41:AN:93:MET:HB2	2.02	0.41
44:BO:70:ALA:HB1	44:BO:237:PHE:CD1	2.54	0.41
45:EO:211:LEU:HG	45:EO:218:SER:HB3	2.02	0.41
48:AR:108:ASP:OD1	48:AR:109:THR:N	2.52	0.41
52:ES:56:TYR:HB2	52:ES:84:TYR:CZ	2.55	0.41
53:AT:44:ARG:HH22	53:AT:114:GLU:HG3	1.84	0.41
55:ET:94:GLU:OE1	55:ET:102:ARG:NH2	2.53	0.41
56:AU:103:GLU:HG2	58:AV:79:PHE:CE1	2.55	0.41
61:BW:54:PHE:CE2	61:BW:69:LYS:HA	2.55	0.41
62:AX:209:ASP:N	62:AX:209:ASP:OD1	2.51	0.41
63:AY:86:GLU:HB2	63:AY:89:GLN:HG2	2.02	0.41
66:Bb:79:HIS:CD2	66:Bb:81:HIS:HB2	2.56	0.41
73:E8:522:ARG:HA	74:E9:253:LEU:HD11	2.02	0.41
2:E1:58:LYS:NZ	48:AR:25:ALA:HA	2.35	0.41
3:A2:76:GLY:H	68:Ae:191:LYS:HG3	1.84	0.41
4:E2:426:ILE:HD11	4:E2:486:VAL:HG13	2.02	0.41
6:E3:218:ASP:OD1	57:BU:132:ARG:NE	2.53	0.41
7:E4:240:HIS:HA	7:E4:243:ILE:HD13	2.02	0.41
13:BA:338:LEU:HA	13:BA:341:CYS:SG	2.60	0.41
14:EA:210:LEU:HD13	14:EA:217:VAL:HG21	2.02	0.41
16:BB:99:PRO:HD2	57:BU:106:ARG:HE	1.85	0.41
16:BB:288:MET:HB3	16:BB:293:MET:O	2.20	0.41
17:EB:590:ARG:HD3	17:EB:590:ARG:HA	1.83	0.41
19:BD:222:ALA:O	19:BD:225:LEU:HB2	2.20	0.41
20:ED:303:ALA:O	20:ED:310:TYR:HB2	2.20	0.41
22:BE:321:VAL:HG21	22:BE:352:HIS:HB3	2.02	0.41
23:EE:224:PRO:HB2	23:EE:296:TYR:CE2	2.55	0.41
23:EE:279:ARG:HH22	26:EF:143:LEU:HD21	1.84	0.41
29:EH:322:THR:OG1	29:EH:323:ARG:N	2.51	0.41
35:BK:114:HIS:HB3	35:BK:117:VAL:HG22	2.02	0.41
38:EL:636:MET:HA	38:EL:639:LEU:HG	2.02	0.41
43:EN:459:VAL:HG12	43:EN:464:LYS:HD3	2.01	0.41
45:EP:50:LEU:C	45:EP:133:LEU:HD21	2.45	0.41
45:EP:96:ASP:HB3	45:EP:99:HIS:HD2	1.86	0.41
55:ET:36:ILE:HG23	79:Ao:176:VAL:HG13	2.02	0.41
59:BV:107:ILE:HG23	59:BV:108:TYR:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AX:167:MET:O	62:AX:212:LYS:NZ	2.49	0.41
63:AY:54:GLU:HG3	63:AY:55:ARG:HG2	2.01	0.41
2:E1:106:ARG:NH1	9:E5:264:UNK:HA	2.31	0.41
2:E1:417:ARG:H	2:E1:417:ARG:HG2	1.70	0.41
10:E6:381:LEU:O	10:E6:385:ARG:HG2	2.21	0.41
12:AA:310:A:OP1	17:EB:71:SER:OG	2.28	0.41
12:AA:930:A:H2'	12:AA:931:U:C6	2.56	0.41
12:AA:1084:G:OP1	18:EC:286:VAL:N	2.48	0.41
14:EA:573:PRO:HG3	17:EB:335:ARG:CZ	2.50	0.41
16:BB:275:VAL:HG11	16:BB:311:LEU:HD21	2.02	0.41
16:BB:413:LEU:HD23	16:BB:413:LEU:H	1.85	0.41
19:BD:162:ILE:HD11	19:BD:169:ALA:HA	2.02	0.41
19:BD:281:ALA:HB2	28:BH:176:TYR:HB2	2.02	0.41
19:BD:402:GLU:H	19:BD:402:GLU:CD	2.28	0.41
20:ED:166:LEU:HD22	20:ED:199:ILE:HG12	2.01	0.41
22:BE:144:VAL:HG23	22:BE:264:ASP:HB3	2.03	0.41
22:BE:401:PHE:CE1	60:AW:173:GLN:HB3	2.56	0.41
29:EH:102:TRP:CD1	29:EH:103:GLU:HG3	2.55	0.41
38:EL:323:HIS:CE1	38:EL:367:PRO:HG3	2.55	0.41
38:EL:339:GLU:O	38:EL:342:ARG:NH1	2.53	0.41
39:EM:65:LEU:HB2	39:EM:234:LEU:HD22	2.01	0.41
39:EM:69:VAL:HG12	39:EM:167:LEU:HD23	2.03	0.41
42:BN:74:GLU:O	42:BN:78:LEU:HG	2.19	0.41
47:BQ:24:ARG:HH21	47:BQ:200:ASP:H	1.68	0.41
48:AR:211:ARG:HD2	57:BU:151:TRP:CE2	2.55	0.41
59:BV:34:LEU:HD12	59:BV:35:PRO:HD2	2.01	0.41
60:AW:116:ARG:HA	60:AW:116:ARG:HD2	1.82	0.41
63:AY:109:TRP:HH2	63:AY:139:ASN:HA	1.86	0.41
63:AY:156:SER:HB3	63:AY:159:ARG:HG2	2.02	0.41
65:Ba:40:TRP:HZ3	65:Ba:80:ASP:HA	1.84	0.41
2:E1:177:LEU:HD21	2:E1:183:VAL:HB	2.01	0.41
2:E1:476:PRO:HD3	48:AR:186:PHE:CG	2.56	0.41
4:E2:71:PRO:HA	4:E2:74:GLN:HG3	2.02	0.41
11:A8:132:ASN:HB2	60:AW:3:ARG:NH2	2.35	0.41
12:AA:149:U:OP2	60:AW:17:ARG:NH1	2.53	0.41
12:AA:878:A:H2'	12:AA:879:A:H8	1.85	0.41
13:BA:436:ASP:HB3	13:BA:439:THR:HB	2.01	0.41
13:BA:806:TYR:CE2	13:BA:808:PRO:HG3	2.55	0.41
17:EB:452:HIS:HA	17:EB:457:VAL:HG12	2.02	0.41
17:EB:557:ASN:HB2	17:EB:585:SER:HA	2.02	0.41
18:EC:357:LEU:HD22	18:EC:359:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:BD:206:ALA:HB2	19:BD:452:SER:HA	2.03	0.41
20:ED:175:LEU:O	20:ED:499:SER:OG	2.38	0.41
26:EF:62:LEU:HB3	26:EF:105:TYR:OH	2.20	0.41
26:EF:211:GLY:O	26:EF:215:LEU:HG	2.19	0.41
28:BH:118:VAL:HG22	28:BH:162:HIS:CE1	2.55	0.41
33:BJ:102:ARG:HH21	33:BJ:219:ALA:HA	1.85	0.41
33:BJ:157:LYS:N	33:BJ:158:PRO:HD3	2.36	0.41
35:BK:291:TYR:HA	35:BK:307:ARG:HB3	2.02	0.41
43:EN:224:LEU:HA	43:EN:224:LEU:HD13	1.95	0.41
43:EN:415:ALA:O	43:EN:557:ARG:NH2	2.54	0.41
46:AP:269:GLU:HG3	61:BW:89:ARG:HE	1.85	0.41
51:BS:51:ILE:HD12	51:BS:65:LEU:HD12	2.02	0.41
56:AU:121:PRO:HD3	58:AV:128:ARG:NE	2.29	0.41
64:BZ:79:LYS:HA	64:BZ:167:GLU:HG2	2.03	0.41
68:Ae:196:TRP:CG	68:Ae:197:ARG:HD3	2.56	0.41
1:A1:30:LEU:HD21	12:AA:62:A:C2	2.56	0.41
2:E1:32:LEU:HD13	53:AT:79:HIS:CD2	2.55	0.41
3:A2:434:CYS:SG	3:A2:438:ILE:HD11	2.61	0.41
4:E2:375:THR:HG23	4:E2:377:GLU:OE1	2.20	0.41
6:E3:554:LEU:HA	6:E3:555:PRO:HD2	1.88	0.41
7:E4:192:LEU:HD23	7:E4:196:GLU:HG2	2.03	0.41
12:AA:389:A:H2'	12:AA:390:A:C8	2.55	0.41
16:BB:81:SER:OG	64:BZ:63:ALA:O	2.39	0.41
16:BB:151:LEU:HG	64:BZ:58:LEU:HD12	2.03	0.41
18:EC:215:SER:O	18:EC:360:HIS:ND1	2.53	0.41
22:BE:407:TRP:CZ3	22:BE:411:LYS:HD3	2.56	0.41
23:EE:464:ASP:HA	45:EP:317:LEU:HD21	2.02	0.41
25:BF:356:ARG:NH1	61:BW:179:ASP:OD2	2.53	0.41
27:EG:50:ILE:HB	27:EG:125:SER:HB3	2.01	0.41
27:EG:128:VAL:HG23	27:EG:138:ARG:HB3	2.03	0.41
30:AI:85:TYR:HB3	84:Av:104:ILE:HG23	2.02	0.41
30:AI:202:THR:HG23	30:AI:205:TYR:H	1.86	0.41
33:BJ:248:PRO:HG3	63:AY:288:PHE:CE2	2.55	0.41
34:AK:53:TRP:CZ2	34:AK:71:GLU:HB3	2.56	0.41
37:BL:250:THR:HA	37:BL:253:THR:HG22	2.02	0.41
38:EL:203:VAL:HG12	77:Um:18:UNK:HA	2.02	0.41
38:EL:385:PRO:O	38:EL:389:MET:HG2	2.20	0.41
43:EN:222:LEU:O	43:EN:225:GLN:HG2	2.20	0.41
48:AR:229:HIS:HD1	48:AR:246:VAL:HG11	1.85	0.41
49:BR:110:LEU:H	49:BR:138:GLN:NE2	2.19	0.41
54:BT:74:HIS:CD2	65:Ba:147:ASN:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:Al:77:ASP:OD1	75:Al:77:ASP:N	2.53	0.41
75:Al:141:SER:HB2	75:Al:145:VAL:HG12	2.02	0.41
1:A1:92:VAL:O	1:A1:93:GLN:HG3	2.20	0.41
2:E1:56:ILE:HB	2:E1:126:LEU:HD21	2.02	0.41
2:E1:472:GLY:HA3	12:AA:516:U:C6	2.56	0.41
5:A3:147:PRO:HB3	47:BQ:103:ARG:NH1	2.36	0.41
10:E6:403:LEU:HB2	10:E6:412:CYS:HB3	2.02	0.41
12:AA:501:A:H2'	12:AA:502:U:C6	2.56	0.41
12:AA:533:A:OP2	62:AX:193:ARG:NH2	2.54	0.41
18:EC:281:THR:HB	18:EC:284:SER:HB3	2.01	0.41
22:BE:79:VAL:HG21	63:AY:153:ILE:HG23	2.03	0.41
23:EE:138:PHE:CZ	23:EE:217:ASP:HB2	2.56	0.41
23:EE:154:MET:HE3	23:EE:220:ILE:HA	2.01	0.41
23:EE:182:GLN:OE1	23:EE:182:GLN:N	2.39	0.41
24:AF:39:ASP:OD1	24:AF:39:ASP:N	2.53	0.41
24:AF:224:ARG:O	24:AF:228:THR:HG23	2.20	0.41
25:BF:237:LEU:HD21	25:BF:312:GLN:HG3	2.02	0.41
28:BH:163:ASN:HB3	28:BH:165:GLN:HG2	2.03	0.41
29:EH:472:PRO:HG3	29:EH:478:ALA:HA	2.02	0.41
43:EN:208:GLY:HA2	43:EN:216:LEU:HD12	2.03	0.41
43:EN:328:ILE:HG22	43:EN:375:ARG:NH1	2.36	0.41
45:EO:169:LEU:HA	45:EO:172:THR:HG22	2.03	0.41
58:AV:112:LEU:HB2	58:AV:136:VAL:HG13	2.02	0.41
73:E8:455:LEU:HD22	73:E8:478:VAL:HG21	2.01	0.41
2:E1:354:ARG:O	2:E1:358:MET:HG3	2.21	0.41
5:A3:80:GLU:HB3	79:Ao:181:VAL:HG23	2.03	0.41
7:E4:53:PHE:CE2	10:E6:172:LEU:HD21	2.55	0.41
10:E6:505:LYS:HD2	10:E6:505:LYS:HA	1.96	0.41
11:A8:155:GLU:HG2	11:A8:156:TRP:CD1	2.56	0.41
12:AA:92:U:OP2	25:BF:400:ARG:NH2	2.35	0.41
12:AA:141:U:H2'	12:AA:142:A:H8	1.85	0.41
12:AA:859:U:H2'	12:AA:860:A:H8	1.86	0.41
12:AA:999:A:H2'	12:AA:1000:U:C6	2.56	0.41
14:EA:220:LEU:HD12	14:EA:248:ILE:HB	2.03	0.41
16:BB:230:THR:OG1	16:BB:231:GLU:N	2.54	0.41
18:EC:335:GLY:HA3	39:EM:38:MET:HE1	2.03	0.41
19:BD:108:PRO:O	19:BD:343:ARG:HD3	2.21	0.41
21:AE:55:ASP:OD1	21:AE:55:ASP:N	2.51	0.41
22:BE:189:SER:O	22:BE:192:GLU:HG3	2.21	0.41
24:AF:72:ILE:HD11	24:AF:118:PHE:CZ	2.56	0.41
24:AF:252:TYR:OH	24:AF:299:ASN:ND2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BF:152:VAL:HB	25:BF:170:ILE:HD11	2.02	0.41
28:BH:91:LYS:HE3	28:BH:91:LYS:HB3	1.97	0.41
29:EH:190:PHE:HB2	29:EH:319:VAL:HB	2.02	0.41
31:BI:276:ILE:HG23	71:Ag:159:ILE:HD13	2.02	0.41
35:BK:193:VAL:HG23	35:BK:195:GLY:H	1.86	0.41
43:EN:200:ASP:O	43:EN:204:ASN:ND2	2.52	0.41
45:EO:4:VAL:HG22	45:EO:59:ILE:HD13	2.02	0.41
46:AP:264:GLN:HG2	46:AP:271:TYR:CE1	2.56	0.41
51:BS:121:SER:HA	51:BS:124:GLN:NE2	2.36	0.41
56:AU:44:ARG:HD3	58:AV:154:ALA:HB3	2.03	0.41
60:AW:39:LYS:HD2	60:AW:39:LYS:HA	1.87	0.41
62:AX:92:SER:HB3	65:Ba:22:PHE:CE1	2.56	0.41
74:E9:184:ARG:CZ	74:E9:200:VAL:HG21	2.51	0.41
74:E9:220:LEU:HD23	74:E9:220:LEU:HA	1.93	0.41
74:E9:245:LEU:HG	74:E9:267:PRO:HB3	2.01	0.41
75:Al:93:ASP:OD1	75:Al:93:ASP:N	2.40	0.41
80:Ap:66:CYS:SG	80:Ap:71:GLY:HA3	2.60	0.41
1:A1:144:SER:HA	1:A1:157:ARG:NH1	2.34	0.41
2:E1:47:TYR:CD1	2:E1:48:ARG:HG3	2.56	0.41
2:E1:54:ALA:HA	2:E1:438:GLU:OE2	2.21	0.41
3:A2:27:PRO:HA	3:A2:28:PRO:HD3	1.91	0.41
3:A2:167:HIS:HD2	3:A2:169:GLY:H	1.69	0.41
3:A2:316:ASP:OD2	54:BT:82:ARG:NH1	2.54	0.41
4:E2:124:TRP:CD1	4:E2:126:HIS:HB2	2.56	0.41
6:E3:553:LEU:HD23	6:E3:553:LEU:HA	1.97	0.41
9:E5:162:UNK:O	9:E5:164:UNK:N	2.54	0.41
10:E6:446:ASN:O	10:E6:450:ILE:HG12	2.21	0.41
10:E6:470:LEU:HD11	10:E6:489:MET:HG3	2.01	0.41
12:AA:1:A:H62	13:BA:209:PRO:HB2	1.86	0.41
12:AA:39:C:OP1	68:Ae:82:ARG:NH1	2.50	0.41
12:AA:179:A:H3'	12:AA:180:U:O2	2.21	0.41
12:AA:484:U:O2'	24:AF:266:THR:HA	2.21	0.41
12:AA:519:A:O2'	12:AA:520:U:O4'	2.36	0.41
12:AA:976:A:H2'	12:AA:977:G:H8	1.85	0.41
12:AA:988:A:H2'	12:AA:989:U:C6	2.56	0.41
12:AA:1012:U:H2'	12:AA:1013:C:C6	2.56	0.41
13:BA:316:GLU:OE2	13:BA:316:GLU:N	2.54	0.41
13:BA:368:LYS:NZ	69:Af:123:GLY:HA2	2.35	0.41
13:BA:588:LEU:HD22	13:BA:695:LEU:HB3	2.02	0.41
13:BA:810:HIS:CE1	21:AE:193:PRO:HD3	2.55	0.41
14:EA:79:ALA:HB2	14:EA:145:GLY:HA3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:EA:130:GLU:HG2	14:EA:133:VAL:H	1.86	0.41
16:BB:194:TYR:CZ	16:BB:196:TRP:HB2	2.56	0.41
17:EB:199:LEU:O	17:EB:203:THR:HG22	2.21	0.41
17:EB:386:GLU:H	17:EB:386:GLU:CD	2.29	0.41
19:BD:145:TRP:NE1	19:BD:149:ARG:HH11	2.19	0.41
19:BD:282:TYR:O	19:BD:284:PRO:HD3	2.21	0.41
19:BD:343:ARG:HH21	19:BD:365:HIS:CE1	2.39	0.41
20:ED:336:LYS:HD2	20:ED:349:ARG:HH21	1.86	0.41
20:ED:556:PRO:HB2	49:BR:13:PRO:HB2	2.02	0.41
21:AE:131:ASN:OD1	21:AE:132:MET:N	2.54	0.41
22:BE:154:VAL:HG11	22:BE:245:ILE:HA	2.01	0.41
24:AF:311:GLN:HB3	24:AF:329:ALA:HB1	2.02	0.41
25:BF:123:LEU:HB2	79:Ao:91:GLY:O	2.20	0.41
25:BF:148:HIS:O	25:BF:152:VAL:HG23	2.21	0.41
26:EF:101:PRO:HB3	26:EF:151:PHE:CE1	2.55	0.41
27:EG:52:GLY:HA2	27:EG:69:HIS:HE1	1.86	0.41
28:BH:82:ASP:O	28:BH:86:GLN:HG2	2.21	0.41
28:BH:126:LYS:HB3	28:BH:187:LEU:HD23	2.03	0.41
29:EH:208:ILE:HD12	29:EH:212:ILE:HG13	2.02	0.41
30:AI:14:PRO:HA	30:AI:15:PRO:HD3	1.93	0.41
31:BI:121:ASP:O	31:BI:125:ASN:ND2	2.54	0.41
34:AK:214:CYS:HA	59:BV:108:TYR:CD1	2.56	0.41
35:BK:87:LEU:HD21	35:BK:139:VAL:HB	2.01	0.41
35:BK:303:PRO:HD2	35:BK:306:VAL:HG11	2.02	0.41
37:BL:42:TYR:CE1	60:AW:100:GLU:HB2	2.56	0.41
38:EL:641:ARG:HB3	67:Bc:118:ASP:HB3	2.02	0.41
39:EM:112:ASN:HA	39:EM:338:ARG:HA	2.02	0.41
39:EM:239:CYS:SG	39:EM:240:PHE:N	2.94	0.41
39:EM:264:SER:HA	39:EM:324:GLN:NE2	2.35	0.41
39:EM:345:PRO:O	39:EM:348:VAL:HG12	2.20	0.41
41:AN:68:GLN:O	56:AU:68:SER:OG	2.29	0.41
42:BN:79:TRP:HE3	42:BN:96:LEU:HD13	1.86	0.41
43:EN:405:HIS:NE2	43:EN:425:VAL:HG21	2.36	0.41
47:BQ:115:ASP:OD1	47:BQ:115:ASP:N	2.53	0.41
48:AR:207:MET:HE1	57:BU:158:VAL:HG21	2.03	0.41
49:BR:172:PRO:HD2	79:Ao:210:PHE:CE2	2.56	0.41
52:ES:108:ASN:ND2	52:ES:142:GLU:OE2	2.54	0.41
54:BT:125:ALA:HA	54:BT:128:ARG:HD2	2.02	0.41
55:ET:90:ASP:OD1	55:ET:90:ASP:N	2.54	0.41
60:AW:95:ARG:NH2	63:AY:29:MET:O	2.54	0.41
61:BW:154:PRO:HA	61:BW:157:ASN:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:AX:83:PRO:HA	62:AX:84:PRO:HD3	1.92	0.41
63:AY:273:PHE:HD2	63:AY:274:HIS:HD2	1.69	0.41
67:Bc:56:TRP:HD1	67:Bc:64:PHE:HZ	1.69	0.41
72:E7:8:ARG:HG3	72:E7:9:ARG:O	2.21	0.41
74:E9:212:GLY:O	74:E9:216:LEU:HB2	2.21	0.41
74:E9:231:GLU:O	74:E9:235:LEU:HG	2.21	0.41
80:Ap:171:ARG:HH11	80:Ap:253:GLN:HG3	1.85	0.41
80:Ap:266:ALA:O	80:Ap:270:MET:HG2	2.20	0.41
1:A1:55:TYR:CE2	84:Av:55:TRP:HB2	2.55	0.41
1:A1:96:TYR:HB2	28:BH:300:HIS:CE1	2.56	0.41
2:E1:372:ARG:HB3	12:AA:972:G:H4'	2.03	0.41
4:E2:227:ILE:HG12	4:E2:242:SER:HB2	2.03	0.41
12:AA:357:A:H2'	12:AA:358:A:O4'	2.20	0.41
13:BA:582:PHE:HD1	13:BA:693:HIS:HB2	1.86	0.41
18:EC:58:TYR:CD2	18:EC:120:VAL:HG22	2.56	0.41
18:EC:251:LYS:HD3	18:EC:299:GLU:HG3	2.03	0.41
19:BD:145:TRP:NE1	19:BD:168:ASP:OD1	2.51	0.41
20:ED:341:PRO:HD2	20:ED:344:ILE:HD12	2.03	0.41
30:AI:68:ALA:HA	84:Av:113:GLY:O	2.21	0.41
37:BL:41:LEU:HB3	37:BL:43:GLU:OE1	2.21	0.41
45:EO:112:GLN:HE21	45:EP:102:TYR:HH	1.58	0.41
47:BQ:52:ASP:OD1	47:BQ:52:ASP:N	2.53	0.41
50:ER:113:PHE:CE1	52:ES:20:LYS:HG2	2.55	0.41
53:AT:142:ARG:HH11	73:E8:541:LEU:HD11	1.86	0.41
63:AY:179:ASP:OD2	63:AY:210:SER:OG	2.38	0.41
74:E9:325:CYS:SG	74:E9:327:SER:OG	2.69	0.41
75:Al:191:VAL:HG23	75:Al:196:ILE:HG12	2.03	0.41
80:Ap:74:ARG:HD3	80:Ap:90:TYR:HB2	2.02	0.41
2:E1:53:ILE:HG23	2:E1:129:LEU:HD22	2.02	0.40
6:E3:380:LYS:NZ	48:AR:260:ASN:OD1	2.53	0.40
12:AA:178:A:O2'	60:AW:3:ARG:NH2	2.53	0.40
12:AA:516:U:C4	12:AA:567:G:C6	3.09	0.40
12:AA:987:C:H2'	12:AA:988:A:H8	1.85	0.40
12:AA:998:A:H2'	12:AA:999:A:C8	2.56	0.40
14:EA:572:ASN:HA	14:EA:573:PRO:HD3	1.98	0.40
19:BD:123:LEU:O	19:BD:131:VAL:HB	2.20	0.40
19:BD:221:ILE:HD13	19:BD:420:ARG:HG3	2.03	0.40
19:BD:292:LEU:HD13	19:BD:342:PHE:CE2	2.56	0.40
21:AE:197:HIS:HB3	21:AE:201:VAL:HG13	2.02	0.40
25:BF:363:GLN:HB2	61:BW:174:ILE:HG23	2.02	0.40
25:BF:409:LYS:HD3	25:BF:409:LYS:HA	1.71	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:BH:188:ASP:OD2	28:BH:191:GLN:N	2.54	0.40
33:BJ:149:LEU:HD11	33:BJ:163:PRO:HG3	2.03	0.40
38:EL:605:MET:HE3	38:EL:609:LYS:HE3	2.03	0.40
39:EM:55:LEU:HD13	39:EM:55:LEU:HA	1.91	0.40
45:EO:216:ARG:H	45:EO:216:ARG:HG2	1.74	0.40
45:EP:197:PHE:HB2	45:EP:224:LEU:HD23	2.02	0.40
49:BR:35:PHE:CE1	49:BR:38:GLU:HB2	2.57	0.40
49:BR:58:THR:O	49:BR:63:LEU:HD12	2.21	0.40
64:BZ:40:LEU:O	64:BZ:68:THR:HA	2.21	0.40
6:E3:260:VAL:HG23	6:E3:261:HIS:H	1.85	0.40
13:BA:378:VAL:HG23	13:BA:386:TRP:HH2	1.85	0.40
14:EA:395:ILE:HD13	14:EA:473:LEU:HD21	2.03	0.40
14:EA:416:VAL:HG11	14:EA:423:PHE:HB3	2.03	0.40
14:EA:541:LYS:HE2	27:EG:3:ASN:HD21	1.86	0.40
18:EC:58:TYR:HB3	18:EC:118:LEU:HD22	2.02	0.40
18:EC:87:LYS:HD3	27:EG:155:ASP:OD2	2.21	0.40
19:BD:120:ARG:HG3	30:AI:237:ALA:HB2	2.03	0.40
21:AE:55:ASP:HB2	80:Ap:84:ALA:HB1	2.03	0.40
21:AE:221:ILE:HD12	21:AE:225:ALA:HB3	2.04	0.40
22:BE:32:LEU:HD23	22:BE:32:LEU:H	1.87	0.40
22:BE:262:LEU:HB3	22:BE:282:ILE:HG12	2.03	0.40
24:AF:366:HIS:O	24:AF:370:ILE:HG13	2.20	0.40
26:EF:180:LEU:HD23	26:EF:182:ILE:H	1.86	0.40
28:BH:231:PRO:HB2	46:AP:308:TYR:HB2	2.03	0.40
45:EO:20:LEU:HD23	45:EO:233:HIS:ND1	2.36	0.40
47:BQ:154:LEU:HD21	83:At:113:PRO:HB3	2.03	0.40
48:AR:116:ALA:HA	48:AR:125:VAL:HG21	2.02	0.40
48:AR:211:ARG:HD2	57:BU:151:TRP:CZ2	2.56	0.40
57:BU:181:ALA:C	57:BU:182:GLU:HG3	2.46	0.40
59:BV:44:GLU:HA	59:BV:47:ARG:HG2	2.04	0.40
59:BV:104:TYR:O	59:BV:107:ILE:HG22	2.21	0.40
68:Ae:79:ASN:O	68:Ae:89:ARG:NH2	2.38	0.40
70:Bf:42:HIS:CE1	70:Bf:48:TRP:HE1	2.39	0.40
70:Bf:52:THR:HA	80:Ap:131:TRP:NE1	2.35	0.40
74:E9:179:TRP:HB2	74:E9:268:ARG:NH2	2.35	0.40
1:A1:114:LEU:HB3	1:A1:163:ARG:HG2	2.03	0.40
1:A1:138:ASN:HD21	33:BJ:299:ARG:NH2	2.18	0.40
3:A2:171:VAL:HB	3:A2:327:THR:OG1	2.21	0.40
3:A2:298:LEU:HD11	54:BT:103:MET:HB2	2.04	0.40
4:E2:273:CYS:O	4:E2:277:GLU:HG2	2.21	0.40
4:E2:497:LEU:HD21	10:E6:324:ARG:HE	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A3:190:LEU:HD12	25:BF:310:LEU:HD12	2.04	0.40
6:E3:249:SER:O	6:E3:253:ARG:HG2	2.22	0.40
7:E4:8:PRO:O	7:E4:11:THR:OG1	2.39	0.40
7:E4:288:ASN:O	7:E4:292:GLU:HG2	2.22	0.40
10:E6:71:VAL:HG22	48:AR:217:LYS:HB2	2.03	0.40
10:E6:114:ALA:O	10:E6:118:HIS:HB2	2.21	0.40
10:E6:323:THR:OG1	10:E6:326:THR:HG23	2.21	0.40
12:AA:94:U:H2'	12:AA:95:U:H6	1.85	0.40
12:AA:284:U:H5'	24:AF:167:ARG:HD3	2.03	0.40
12:AA:880:C:H2'	12:AA:881:A:C8	2.53	0.40
12:AA:940:A:C5	84:Av:198:LYS:HE2	2.56	0.40
13:BA:185:ALA:HB1	21:AE:207:ALA:HA	2.03	0.40
13:BA:758:LEU:O	13:BA:765:ARG:NH2	2.54	0.40
19:BD:468:TRP:NE1	19:BD:474:SER:HB2	2.36	0.40
20:ED:67:ALA:N	20:ED:71:ASP:OD2	2.53	0.40
20:ED:268:TRP:CG	20:ED:269:LEU:H	2.40	0.40
26:EF:106:VAL:HG12	26:EF:129:CYS:HA	2.04	0.40
43:EN:201:ARG:HA	43:EN:204:ASN:HD21	1.86	0.40
43:EN:405:HIS:CE1	43:EN:425:VAL:HG21	2.57	0.40
46:AP:79:TRP:CD2	46:AP:90:ILE:HD12	2.56	0.40
45:EP:119:ILE:O	45:EP:123:LEU:HG	2.21	0.40
48:AR:76:GLU:HB3	48:AR:80:LYS:HE3	2.03	0.40
53:AT:60:CYS:SG	53:AT:71:LEU:HB3	2.62	0.40
57:BU:120:GLU:O	57:BU:124:GLU:HG2	2.21	0.40
67:Bc:66:HIS:CD2	67:Bc:144:THR:HG21	2.57	0.40
68:Ae:100:HIS:HB2	68:Ae:106:LEU:HD23	2.02	0.40
79:Ao:76:LYS:HG2	79:Ao:77:TYR:CD2	2.57	0.40
2:E1:172:ARG:HA	2:E1:175:THR:HG22	2.04	0.40
2:E1:189:LEU:HB2	2:E1:220:LEU:HD22	2.03	0.40
2:E1:243:ARG:HG2	7:E4:96:VAL:HG21	2.04	0.40
2:E1:428:ARG:NH2	12:AA:519:A:O2'	2.52	0.40
7:E4:319:ARG:HG2	7:E4:320:GLN:H	1.85	0.40
10:E6:347:PHE:CD1	10:E6:362:MET:HE2	2.57	0.40
11:A8:151:SER:HB2	12:AA:59:U:O4	2.21	0.40
11:A8:153:SER:HB2	11:A8:156:TRP:HD1	1.86	0.40
12:AA:813:U:H2'	12:AA:816:C:H41	1.86	0.40
12:AA:1133:A:H1'	12:AA:1141:A:N1	2.36	0.40
13:BA:528:VAL:O	13:BA:532:MET:HG2	2.22	0.40
18:EC:161:LEU:HD11	18:EC:171:ASN:HB2	2.02	0.40
20:ED:11:ARG:HD2	20:ED:310:TYR:CD2	2.56	0.40
20:ED:110:ARG:NH1	20:ED:110:ARG:HA	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:ED:205:ARG:N	20:ED:212:LEU:O	2.45	0.40
20:ED:354:TYR:CD1	20:ED:361:GLY:HA2	2.57	0.40
20:ED:434:LEU:HG	20:ED:465:LEU:HD21	2.04	0.40
21:AE:136:VAL:H	21:AE:222:THR:CG2	2.35	0.40
24:AF:90:LEU:HD12	24:AF:93:LEU:HD12	2.03	0.40
29:EH:327:LEU:O	29:EH:331:ILE:HG12	2.21	0.40
37:BL:119:ILE:O	37:BL:189:ARG:NH2	2.53	0.40
39:EM:322:ARG:HH11	73:E8:553:LYS:HB2	1.86	0.40
46:AP:211:ILE:HG21	46:AP:266:LEU:HD11	2.02	0.40
47:BQ:214:ALA:O	47:BQ:218:MET:HG2	2.22	0.40
60:AW:158:ARG:NH2	60:AW:245:ARG:HB2	2.37	0.40
63:AY:204:LYS:HD3	63:AY:213:LEU:HB3	2.03	0.40
72:E7:2:LYS:HD2	73:E8:562:ARG:NH1	2.37	0.40
5:A3:197:ASN:HA	5:A3:200:GLN:HG2	2.04	0.40
7:E4:4:LYS:O	7:E4:7:THR:OG1	2.39	0.40
12:AA:5:U:H2'	12:AA:6:A:C8	2.56	0.40
12:AA:370:U:O2'	55:ET:9:ARG:HD2	2.21	0.40
12:AA:1158:G:H1'	13:BA:222:VAL:HG21	2.02	0.40
13:BA:741:VAL:HG23	37:BL:79:LYS:HD2	2.02	0.40
14:EA:271:ILE:HD13	14:EA:271:ILE:HA	1.93	0.40
23:EE:82:ASN:HA	39:EM:338:ARG:HD3	2.04	0.40
27:EG:45:ARG:HG3	27:EG:47:HIS:CD2	2.56	0.40
29:EH:31:LEU:HD13	29:EH:540:LEU:HD23	2.03	0.40
29:EH:94:LEU:HG	29:EH:184:ILE:HG21	2.02	0.40
29:EH:224:ALA:HB2	71:Ag:147:GLN:HB3	2.04	0.40
33:BJ:173:LEU:HB3	33:BJ:179:ARG:HB3	2.03	0.40
34:AK:151:LEU:HD13	59:BV:107:ILE:CD1	2.51	0.40
43:EN:584:THR:HG21	43:EN:623:ARG:HH22	1.87	0.40
51:BS:70:ILE:HD13	51:BS:79:LEU:HD21	2.03	0.40
56:AU:115:ALA:HA	69:Af:77:VAL:HG13	2.02	0.40
63:AY:141:ILE:HD12	63:AY:175:VAL:HG21	2.03	0.40
71:Ag:176:GLU:OE2	71:Ag:180:ARG:NH2	2.55	0.40
80:Ap:236:TRP:CD1	80:Ap:240:THR:HB	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	215/241 (89%)	207 (96%)	8 (4%)	0	100	100
2	E1	471/482 (98%)	459 (98%)	12 (2%)	0	100	100
3	A2	461/471 (98%)	449 (97%)	12 (3%)	0	100	100
4	E2	359/568 (63%)	341 (95%)	18 (5%)	0	100	100
5	A3	147/218 (67%)	142 (97%)	5 (3%)	0	100	100
6	E3	401/557 (72%)	393 (98%)	8 (2%)	0	100	100
7	E4	430/439 (98%)	417 (97%)	13 (3%)	0	100	100
8	A5	53/80 (66%)	53 (100%)	0	0	100	100
10	E6	430/531 (81%)	417 (97%)	13 (3%)	0	100	100
11	A8	131/181 (72%)	129 (98%)	2 (2%)	0	100	100
13	BA	763/831 (92%)	741 (97%)	22 (3%)	0	100	100
14	EA	530/576 (92%)	520 (98%)	10 (2%)	0	100	100
16	BB	403/541 (74%)	385 (96%)	18 (4%)	0	100	100
17	EB	619/754 (82%)	603 (97%)	16 (3%)	0	100	100
18	EC	371/406 (91%)	359 (97%)	12 (3%)	0	100	100
19	BD	417/547 (76%)	402 (96%)	15 (4%)	0	100	100
20	ED	594/616 (96%)	577 (97%)	17 (3%)	0	100	100
21	AE	342/473 (72%)	328 (96%)	14 (4%)	0	100	100
22	BE	353/449 (79%)	345 (98%)	8 (2%)	0	100	100
23	EE	427/586 (73%)	413 (97%)	13 (3%)	1 (0%)	43	74
24	AF	415/459 (90%)	405 (98%)	10 (2%)	0	100	100
25	BF	342/426 (80%)	328 (96%)	14 (4%)	0	100	100
26	EF	293/373 (79%)	283 (97%)	10 (3%)	0	100	100
27	EG	152/156 (97%)	150 (99%)	2 (1%)	0	100	100
28	BH	234/349 (67%)	228 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	EH	429/634 (68%)	425 (99%)	4 (1%)	0	100	100
30	AI	228/263 (87%)	224 (98%)	4 (2%)	0	100	100
31	BI	301/342 (88%)	295 (98%)	6 (2%)	0	100	100
33	BJ	232/333 (70%)	227 (98%)	5 (2%)	0	100	100
34	AK	242/342 (71%)	237 (98%)	5 (2%)	0	100	100
35	BK	222/386 (58%)	220 (99%)	2 (1%)	0	100	100
37	BL	254/312 (81%)	245 (96%)	9 (4%)	0	100	100
38	EL	526/691 (76%)	513 (98%)	13 (2%)	0	100	100
39	EM	302/451 (67%)	296 (98%)	6 (2%)	0	100	100
41	AN	191/202 (95%)	185 (97%)	6 (3%)	0	100	100
42	BN	150/302 (50%)	145 (97%)	5 (3%)	0	100	100
43	EN	632/731 (86%)	612 (97%)	20 (3%)	0	100	100
44	BO	188/262 (72%)	185 (98%)	3 (2%)	0	100	100
45	EO	264/319 (83%)	256 (97%)	8 (3%)	0	100	100
45	EP	233/319 (73%)	226 (97%)	7 (3%)	0	100	100
46	AP	314/374 (84%)	308 (98%)	6 (2%)	0	100	100
47	BQ	216/231 (94%)	206 (95%)	10 (5%)	0	100	100
48	AR	265/301 (88%)	252 (95%)	13 (5%)	0	100	100
49	BR	194/205 (95%)	190 (98%)	4 (2%)	0	100	100
50	ER	82/148 (55%)	79 (96%)	3 (4%)	0	100	100
51	BS	158/198 (80%)	152 (96%)	6 (4%)	0	100	100
52	ES	148/524 (28%)	146 (99%)	2 (1%)	0	100	100
53	AT	141/144 (98%)	137 (97%)	4 (3%)	0	100	100
54	BT	171/191 (90%)	165 (96%)	6 (4%)	0	100	100
55	ET	99/102 (97%)	96 (97%)	3 (3%)	0	100	100
56	AU	171/213 (80%)	167 (98%)	4 (2%)	0	100	100
57	BU	148/185 (80%)	141 (95%)	7 (5%)	0	100	100
58	AV	179/188 (95%)	172 (96%)	7 (4%)	0	100	100
59	BV	88/190 (46%)	86 (98%)	2 (2%)	0	100	100
60	AW	276/278 (99%)	270 (98%)	6 (2%)	0	100	100
61	BW	186/188 (99%)	178 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	AX	162/246 (66%)	161 (99%)	1 (1%)	0	100	100
63	AY	338/378 (89%)	336 (99%)	2 (1%)	0	100	100
64	BZ	186/190 (98%)	178 (96%)	8 (4%)	0	100	100
65	Ba	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
66	Bb	129/162 (80%)	123 (95%)	6 (5%)	0	100	100
67	Bc	135/146 (92%)	131 (97%)	4 (3%)	0	100	100
68	Ae	123/197 (62%)	118 (96%)	5 (4%)	0	100	100
69	Af	137/189 (72%)	137 (100%)	0	0	100	100
70	Bf	85/113 (75%)	80 (94%)	5 (6%)	0	100	100
71	Ag	184/260 (71%)	175 (95%)	9 (5%)	0	100	100
72	E7	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
73	E8	152/786 (19%)	146 (96%)	6 (4%)	0	100	100
74	E9	198/343 (58%)	193 (98%)	5 (2%)	0	100	100
75	Al	179/218 (82%)	177 (99%)	2 (1%)	0	100	100
79	Ao	180/1520 (12%)	175 (97%)	5 (3%)	0	100	100
80	Ap	261/309 (84%)	258 (99%)	3 (1%)	0	100	100
83	At	134/154 (87%)	128 (96%)	6 (4%)	0	100	100
84	Av	190/242 (78%)	185 (97%)	5 (3%)	0	100	100
All	All	19602/26562 (74%)	19044 (97%)	557 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	EE	121	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A1	195/217 (90%)	192 (98%)	3 (2%)	57	70
2	E1	393/419 (94%)	390 (99%)	3 (1%)	73	77
3	A2	405/413 (98%)	401 (99%)	4 (1%)	68	75
4	E2	328/505 (65%)	323 (98%)	5 (2%)	57	70
5	A3	134/193 (69%)	132 (98%)	2 (2%)	57	70
6	E3	361/493 (73%)	361 (100%)	0	100	100
7	E4	367/378 (97%)	357 (97%)	10 (3%)	39	60
8	A5	52/73 (71%)	51 (98%)	1 (2%)	50	66
10	E6	372/454 (82%)	368 (99%)	4 (1%)	65	74
11	A8	118/161 (73%)	118 (100%)	0	100	100
13	BA	662/727 (91%)	657 (99%)	5 (1%)	73	77
14	EA	463/502 (92%)	460 (99%)	3 (1%)	78	80
16	BB	351/470 (75%)	347 (99%)	4 (1%)	65	74
17	EB	548/649 (84%)	543 (99%)	5 (1%)	70	75
18	EC	327/354 (92%)	322 (98%)	5 (2%)	57	70
19	BD	356/472 (75%)	355 (100%)	1 (0%)	86	85
20	ED	529/544 (97%)	525 (99%)	4 (1%)	73	77
21	AE	295/406 (73%)	292 (99%)	3 (1%)	68	75
22	BE	304/386 (79%)	302 (99%)	2 (1%)	76	78
23	EE	364/514 (71%)	361 (99%)	3 (1%)	73	77
24	AF	375/409 (92%)	369 (98%)	6 (2%)	55	69
25	BF	300/368 (82%)	295 (98%)	5 (2%)	53	68
26	EF	250/307 (81%)	250 (100%)	0	100	100
27	EG	134/136 (98%)	134 (100%)	0	100	100
28	BH	206/297 (69%)	202 (98%)	4 (2%)	50	66
29	EH	389/527 (74%)	387 (100%)	2 (0%)	81	82
30	AI	205/225 (91%)	203 (99%)	2 (1%)	68	75
31	BI	254/288 (88%)	253 (100%)	1 (0%)	84	83
33	BJ	208/298 (70%)	208 (100%)	0	100	100
34	AK	221/301 (73%)	218 (99%)	3 (1%)	59	71
35	BK	200/329 (61%)	196 (98%)	4 (2%)	48	65
37	BL	202/262 (77%)	201 (100%)	1 (0%)	81	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	EL	461/598 (77%)	455 (99%)	6 (1%)	61	71
39	EM	266/386 (69%)	262 (98%)	4 (2%)	57	70
41	AN	173/182 (95%)	173 (100%)	0	100	100
42	BN	142/265 (54%)	139 (98%)	3 (2%)	47	65
43	EN	564/640 (88%)	558 (99%)	6 (1%)	65	74
44	BO	162/225 (72%)	161 (99%)	1 (1%)	78	80
45	EO	232/263 (88%)	230 (99%)	2 (1%)	70	75
45	EP	211/263 (80%)	210 (100%)	1 (0%)	81	82
46	AP	277/330 (84%)	272 (98%)	5 (2%)	51	67
47	BQ	172/195 (88%)	171 (99%)	1 (1%)	78	80
48	AR	225/256 (88%)	224 (100%)	1 (0%)	84	83
49	BR	172/181 (95%)	169 (98%)	3 (2%)	53	68
50	ER	78/127 (61%)	77 (99%)	1 (1%)	61	71
51	BS	91/164 (56%)	89 (98%)	2 (2%)	45	64
52	ES	134/437 (31%)	134 (100%)	0	100	100
53	AT	123/124 (99%)	120 (98%)	3 (2%)	43	63
54	BT	151/163 (93%)	151 (100%)	0	100	100
55	ET	87/88 (99%)	87 (100%)	0	100	100
56	AU	151/184 (82%)	149 (99%)	2 (1%)	61	71
57	BU	134/168 (80%)	132 (98%)	2 (2%)	57	70
58	AV	153/158 (97%)	148 (97%)	5 (3%)	33	56
59	BV	79/163 (48%)	77 (98%)	2 (2%)	42	62
60	AW	246/246 (100%)	245 (100%)	1 (0%)	84	83
61	BW	164/164 (100%)	162 (99%)	2 (1%)	63	72
62	AX	153/221 (69%)	152 (99%)	1 (1%)	76	78
63	AY	305/337 (90%)	305 (100%)	0	100	100
64	BZ	148/160 (92%)	147 (99%)	1 (1%)	76	78
65	Ba	130/144 (90%)	129 (99%)	1 (1%)	73	77
66	Bb	113/135 (84%)	110 (97%)	3 (3%)	39	60
67	Bc	127/134 (95%)	125 (98%)	2 (2%)	55	69
68	Ae	110/172 (64%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Af	120/162 (74%)	118 (98%)	2 (2%)	53	68
70	Bf	77/98 (79%)	77 (100%)	0	100	100
71	Ag	170/239 (71%)	170 (100%)	0	100	100
72	E7	87/87 (100%)	87 (100%)	0	100	100
73	E8	112/678 (16%)	111 (99%)	1 (1%)	70	75
74	E9	177/292 (61%)	177 (100%)	0	100	100
75	Al	155/186 (83%)	154 (99%)	1 (1%)	78	80
79	Ao	151/1258 (12%)	150 (99%)	1 (1%)	76	78
80	Ap	229/267 (86%)	228 (100%)	1 (0%)	84	83
83	At	125/140 (89%)	124 (99%)	1 (1%)	73	77
84	Av	170/210 (81%)	169 (99%)	1 (1%)	78	80
All	All	17175/22967 (75%)	17011 (99%)	164 (1%)	65	75

All (164) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A1	88	THR
1	A1	106	THR
1	A1	123	VAL
2	E1	129	LEU
2	E1	220	LEU
2	E1	296	LEU
3	A2	29	VAL
3	A2	173	VAL
3	A2	252	VAL
3	A2	258	VAL
4	E2	69	LEU
4	E2	123	THR
4	E2	151	VAL
4	E2	220	VAL
4	E2	337	THR
5	A3	132	VAL
5	A3	152	VAL
7	E4	7	THR
7	E4	85	LEU
7	E4	144	VAL
7	E4	185	VAL
7	E4	199	THR

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Mol	Chain	Res	Type
7	E4	257	LEU
7	E4	305	THR
7	E4	309	THR
7	E4	323	VAL
7	E4	358	VAL
8	A5	49	LEU
10	E6	154	LEU
10	E6	277	GLN
10	E6	283	THR
10	E6	386	LEU
13	BA	190	THR
13	BA	342	THR
13	BA	366	VAL
13	BA	692	VAL
13	BA	757	THR
14	EA	142	ASP
14	EA	192	VAL
14	EA	336	VAL
16	BB	98	THR
16	BB	105	LEU
16	BB	271	THR
16	BB	303	ILE
17	EB	114	LEU
17	EB	149	LYS
17	EB	292	VAL
17	EB	510	THR
17	EB	573	ARG
18	EC	62	THR
18	EC	199	THR
18	EC	219	VAL
18	EC	235	VAL
18	EC	283	THR
19	BD	373	THR
20	ED	24	SER
20	ED	43	LEU
20	ED	454	VAL
20	ED	582	VAL
21	AE	212	VAL
21	AE	222	THR
21	AE	311	VAL
22	BE	139	GLU
22	BE	266	LEU

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Mol	Chain	Res	Type
23	EE	89	VAL
23	EE	122	TRP
23	EE	272	CYS
24	AF	105	THR
24	AF	125	ILE
24	AF	127	THR
24	AF	263	VAL
24	AF	280	THR
24	AF	352	THR
25	BF	202	THR
25	BF	216	LEU
25	BF	239	VAL
25	BF	390	VAL
25	BF	419	VAL
28	BH	87	LEU
28	BH	88	GLU
28	BH	119	VAL
28	BH	284	THR
29	EH	52	THR
29	EH	497	ASP
30	AI	13	VAL
30	AI	59	THR
31	BI	103	THR
34	AK	64	THR
34	AK	102	VAL
34	AK	151	LEU
35	BK	155	LEU
35	BK	301	THR
35	BK	348	VAL
35	BK	349	VAL
37	BL	116	GLU
38	EL	62	THR
38	EL	227	THR
38	EL	229	THR
38	EL	408	VAL
38	EL	531	LEU
38	EL	568	THR
39	EM	83	LEU
39	EM	218	VAL
39	EM	254	ILE
39	EM	324	GLN
42	BN	88	ILE

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Mol	Chain	Res	Type
42	BN	204	THR
42	BN	221	VAL
43	EN	45	VAL
43	EN	368	VAL
43	EN	520	LEU
43	EN	657	LEU
43	EN	662	VAL
43	EN	695	THR
44	BO	79	VAL
45	EO	60	VAL
45	EO	205	GLU
46	AP	42	VAL
46	AP	65	VAL
46	AP	148	THR
46	AP	171	VAL
46	AP	196	THR
45	EP	16	VAL
47	BQ	54	VAL
48	AR	32	THR
49	BR	60	THR
49	BR	179	ILE
49	BR	193	ILE
50	ER	105	SER
51	BS	28	THR
51	BS	79	LEU
53	AT	8	THR
53	AT	59	THR
53	AT	69	VAL
56	AU	20	ILE
56	AU	129	VAL
57	BU	168	VAL
57	BU	183	LEU
58	AV	115	VAL
58	AV	124	THR
58	AV	128	ARG
58	AV	136	VAL
58	AV	211	VAL
59	BV	32	VAL
59	BV	107	ILE
60	AW	266	THR
61	BW	63	LEU
61	BW	156	VAL

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Mol	Chain	Res	Type
62	AX	224	VAL
64	BZ	151	ILE
65	Ba	80	ASP
66	Bb	61	VAL
66	Bb	76	VAL
66	Bb	126	VAL
67	Bc	44	VAL
67	Bc	140	VAL
69	Af	77	VAL
69	Af	119	THR
73	E8	499	THR
75	Al	62	VAL
79	Ao	136	THR
80	Ap	184	THR
83	At	92	VAL
84	Av	181	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (333) such sidechains are listed below:

Mol	Chain	Res	Type
1	A1	62	GLN
1	A1	138	ASN
2	E1	49	ASN
2	E1	146	GLN
2	E1	162	HIS
2	E1	165	ASN
2	E1	205	ASN
2	E1	278	HIS
2	E1	322	HIS
2	E1	366	HIS
3	A2	71	HIS
3	A2	167	HIS
3	A2	194	GLN
3	A2	389	HIS
4	E2	85	ASN
4	E2	234	HIS
4	E2	254	GLN
4	E2	343	ASN
5	A3	144	GLN
6	E3	295	GLN
6	E3	316	GLN
6	E3	330	HIS

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Mol	Chain	Res	Type
6	E3	332	GLN
6	E3	361	GLN
6	E3	383	ASN
6	E3	432	GLN
6	E3	448	GLN
6	E3	500	GLN
7	E4	29	GLN
7	E4	110	ASN
7	E4	180	HIS
7	E4	191	HIS
7	E4	195	HIS
7	E4	214	ASN
7	E4	293	ASN
7	E4	297	ASN
7	E4	338	GLN
7	E4	362	GLN
7	E4	370	HIS
8	A5	34	GLN
10	E6	147	HIS
10	E6	150	HIS
10	E6	157	GLN
10	E6	171	HIS
10	E6	173	ASN
10	E6	274	HIS
10	E6	337	HIS
10	E6	372	GLN
10	E6	373	ASN
10	E6	397	ASN
10	E6	421	HIS
11	A8	55	GLN
11	A8	136	GLN
11	A8	174	GLN
13	BA	43	ASN
13	BA	139	HIS
13	BA	301	HIS
13	BA	307	HIS
13	BA	389	HIS
13	BA	529	GLN
13	BA	693	HIS
13	BA	810	HIS
14	EA	59	HIS
14	EA	65	GLN

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Mol	Chain	Res	Type
14	EA	89	GLN
14	EA	246	ASN
14	EA	317	ASN
14	EA	392	HIS
14	EA	469	ASN
14	EA	476	GLN
14	EA	518	GLN
14	EA	544	GLN
14	EA	572	ASN
16	BB	82	HIS
16	BB	170	GLN
16	BB	242	GLN
16	BB	313	HIS
17	EB	159	GLN
17	EB	193	HIS
17	EB	271	HIS
17	EB	275	HIS
17	EB	336	HIS
17	EB	515	HIS
17	EB	577	GLN
17	EB	603	GLN
17	EB	644	GLN
17	EB	650	HIS
17	EB	683	GLN
18	EC	166	HIS
18	EC	208	HIS
18	EC	294	ASN
18	EC	315	GLN
18	EC	322	HIS
19	BD	155	GLN
19	BD	193	GLN
19	BD	297	GLN
19	BD	317	ASN
19	BD	513	ASN
20	ED	75	ASN
20	ED	178	GLN
20	ED	352	HIS
20	ED	402	ASN
20	ED	543	GLN
20	ED	576	HIS
20	ED	606	HIS
21	AE	380	GLN

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Mol	Chain	Res	Type
22	BE	78	HIS
22	BE	183	HIS
22	BE	251	ASN
22	BE	279	HIS
22	BE	330	GLN
22	BE	373	GLN
23	EE	90	HIS
23	EE	109	GLN
23	EE	160	HIS
23	EE	166	HIS
23	EE	174	HIS
23	EE	202	HIS
23	EE	211	ASN
23	EE	234	GLN
23	EE	317	ASN
23	EE	429	HIS
23	EE	434	HIS
23	EE	468	ASN
24	AF	46	GLN
24	AF	65	ASN
24	AF	249	GLN
25	BF	132	GLN
25	BF	143	GLN
25	BF	163	ASN
25	BF	288	GLN
25	BF	298	ASN
25	BF	311	GLN
25	BF	344	HIS
25	BF	365	HIS
25	BF	413	HIS
25	BF	417	ASN
26	EF	64	ASN
26	EF	292	HIS
27	EG	69	HIS
27	EG	126	GLN
28	BH	79	GLN
28	BH	122	HIS
28	BH	253	GLN
29	EH	392	ASN
29	EH	502	GLN
29	EH	548	GLN
30	AI	40	GLN

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Mol	Chain	Res	Type
30	AI	76	HIS
31	BI	125	ASN
31	BI	144	HIS
31	BI	152	GLN
31	BI	198	GLN
31	BI	263	HIS
31	BI	279	GLN
31	BI	301	GLN
33	BJ	105	HIS
33	BJ	249	GLN
33	BJ	266	GLN
33	BJ	272	HIS
33	BJ	273	HIS
33	BJ	303	HIS
34	AK	87	ASN
34	AK	105	GLN
34	AK	254	GLN
34	AK	293	ASN
35	BK	114	HIS
35	BK	149	HIS
35	BK	200	ASN
35	BK	212	GLN
35	BK	339	GLN
37	BL	74	GLN
37	BL	83	HIS
37	BL	95	GLN
37	BL	103	ASN
37	BL	226	HIS
37	BL	262	GLN
38	EL	118	HIS
38	EL	277	GLN
38	EL	278	GLN
38	EL	331	HIS
38	EL	484	ASN
38	EL	498	ASN
38	EL	548	GLN
38	EL	582	GLN
38	EL	593	GLN
39	EM	57	HIS
39	EM	128	ASN
39	EM	173	ASN
39	EM	192	HIS

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Mol	Chain	Res	Type
39	EM	282	HIS
39	EM	324	GLN
41	AN	19	HIS
41	AN	63	GLN
41	AN	82	HIS
41	AN	190	GLN
42	BN	81	HIS
42	BN	102	GLN
42	BN	118	ASN
42	BN	133	GLN
43	EN	34	ASN
43	EN	55	HIS
43	EN	71	GLN
43	EN	168	HIS
43	EN	255	ASN
43	EN	312	GLN
43	EN	340	GLN
43	EN	374	HIS
43	EN	514	HIS
43	EN	537	HIS
43	EN	694	GLN
45	EO	13	HIS
45	EO	124	ASN
45	EO	130	ASN
45	EO	170	GLN
45	EO	201	GLN
45	EO	235	GLN
45	EO	259	HIS
45	EO	315	GLN
45	EO	318	HIS
46	AP	46	ASN
46	AP	89	GLN
45	EP	13	HIS
45	EP	28	GLN
45	EP	95	HIS
45	EP	131	GLN
45	EP	157	ASN
45	EP	201	GLN
45	EP	233	HIS
45	EP	235	GLN
47	BQ	105	ASN
47	BQ	143	GLN

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Mol	Chain	Res	Type
47	BQ	147	ASN
48	AR	67	GLN
48	AR	113	GLN
48	AR	120	HIS
48	AR	140	ASN
48	AR	174	HIS
48	AR	242	HIS
49	BR	138	GLN
49	BR	160	GLN
49	BR	164	HIS
51	BS	69	ASN
52	ES	52	ASN
52	ES	128	GLN
53	AT	61	ASN
53	AT	65	ASN
54	BT	52	GLN
55	ET	15	ASN
55	ET	71	ASN
55	ET	92	GLN
56	AU	46	GLN
56	AU	65	ASN
56	AU	82	ASN
56	AU	165	HIS
57	BU	49	ASN
57	BU	81	GLN
57	BU	121	HIS
57	BU	156	GLN
58	AV	109	HIS
58	AV	143	GLN
58	AV	168	HIS
58	AV	183	ASN
60	AW	12	HIS
60	AW	26	HIS
60	AW	50	GLN
60	AW	75	GLN
60	AW	106	HIS
60	AW	172	HIS
60	AW	183	GLN
61	BW	61	ASN
61	BW	99	GLN
61	BW	138	HIS
62	AX	178	ASN

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Mol	Chain	Res	Type
63	AY	64	HIS
63	AY	89	GLN
63	AY	91	GLN
63	AY	145	ASN
63	AY	162	GLN
63	AY	168	HIS
63	AY	183	ASN
63	AY	248	GLN
63	AY	265	GLN
63	AY	289	GLN
63	AY	321	GLN
64	BZ	96	GLN
64	BZ	147	ASN
65	Ba	24	HIS
65	Ba	25	GLN
65	Ba	31	GLN
65	Ba	129	GLN
65	Ba	147	ASN
66	Bb	44	HIS
66	Bb	70	ASN
66	Bb	79	HIS
67	Bc	15	HIS
67	Bc	62	HIS
67	Bc	66	HIS
67	Bc	67	GLN
68	Ae	96	GLN
68	Ae	115	ASN
68	Ae	162	GLN
69	Af	60	GLN
69	Af	86	ASN
69	Af	164	HIS
69	Af	168	GLN
70	Bf	108	HIS
71	Ag	73	ASN
71	Ag	101	HIS
71	Ag	105	GLN
72	E7	6	GLN
72	E7	44	GLN
72	E7	67	ASN
73	E8	517	ASN
73	E8	532	GLN
74	E9	156	GLN

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Mol	Chain	Res	Type
74	E9	161	ASN
74	E9	192	GLN
74	E9	203	HIS
74	E9	247	GLN
75	Al	157	ASN
75	Al	167	GLN
75	Al	211	HIS
79	Ao	106	HIS
79	Ao	139	GLN
80	Ap	78	HIS
80	Ap	132	HIS
80	Ap	146	GLN
80	Ap	150	HIS
83	At	147	HIS
84	Av	44	ASN
84	Av	118	ASN
84	Av	128	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	AA	810/1176 (68%)	310 (38%)	3 (0%)

All (310) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	AA	2	U
12	AA	3	U
12	AA	4	U
12	AA	5	U
12	AA	11	U
12	AA	12	U
12	AA	13	A
12	AA	15	G
12	AA	18	G
12	AA	19	A
12	AA	20	A
12	AA	21	U
12	AA	28	A
12	AA	29	U
12	AA	30	A

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Mol	Chain	Res	Type
12	AA	34	G
12	AA	41	U
12	AA	43	U
12	AA	44	A
12	AA	45	U
12	AA	50	A
12	AA	51	A
12	AA	52	U
12	AA	53	A
12	AA	54	A
12	AA	60	U
12	AA	64	U
12	AA	65	U
12	AA	67	C
12	AA	68	G
12	AA	69	U
12	AA	70	G
12	AA	73	G
12	AA	75	A
12	AA	77	A
12	AA	79	U
12	AA	80	U
12	AA	82	U
12	AA	84	A
12	AA	85	U
12	AA	88	G
12	AA	89	U
12	AA	97	A
12	AA	98	U
12	AA	101	A
12	AA	102	A
12	AA	103	U
12	AA	104	A
12	AA	105	G
12	AA	106	G
12	AA	107	U
12	AA	111	U
12	AA	112	U
12	AA	113	A
12	AA	114	U
12	AA	115	A
12	AA	119	A

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Mol	Chain	Res	Type
12	AA	120	A
12	AA	121	A
12	AA	122	U
12	AA	123	U
12	AA	124	U
12	AA	125	U
12	AA	133	U
12	AA	134	U
12	AA	149	U
12	AA	151	C
12	AA	155	U
12	AA	156	U
12	AA	158	A
12	AA	164	U
12	AA	168	A
12	AA	171	U
12	AA	172	U
12	AA	173	U
12	AA	176	A
12	AA	177	U
12	AA	183	U
12	AA	188	A
12	AA	193	A
12	AA	279	A
12	AA	284	U
12	AA	285	A
12	AA	286	U
12	AA	287	A
12	AA	288	G
12	AA	289	U
12	AA	290	A
12	AA	292	G
12	AA	293	A
12	AA	296	A
12	AA	297	U
12	AA	299	U
12	AA	300	U
12	AA	302	G
12	AA	309	U
12	AA	310	A
12	AA	312	U
12	AA	313	A

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Mol	Chain	Res	Type
12	AA	315	A
12	AA	317	A
12	AA	327	U
12	AA	330	U
12	AA	341	A
12	AA	342	U
12	AA	345	U
12	AA	346	G
12	AA	347	A
12	AA	355	A
12	AA	357	A
12	AA	360	U
12	AA	361	U
12	AA	365	C
12	AA	367	G
12	AA	371	A
12	AA	375	A
12	AA	378	A
12	AA	380	G
12	AA	381	U
12	AA	385	A
12	AA	386	U
12	AA	387	A
12	AA	388	U
12	AA	389	A
12	AA	446	A
12	AA	451	A
12	AA	453	U
12	AA	455	G
12	AA	456	U
12	AA	462	U
12	AA	463	U
12	AA	464	U
12	AA	468	A
12	AA	470	G
12	AA	473	A
12	AA	476	G
12	AA	477	A
12	AA	478	A
12	AA	481	G
12	AA	482	U
12	AA	483	A

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Mol	Chain	Res	Type
12	AA	485	A
12	AA	488	U
12	AA	490	G
12	AA	491	A
12	AA	492	U
12	AA	493	A
12	AA	494	U
12	AA	495	A
12	AA	496	A
12	AA	497	C
12	AA	509	U
12	AA	514	G
12	AA	515	U
12	AA	516	U
12	AA	517	U
12	AA	519	A
12	AA	521	G
12	AA	524	A
12	AA	525	A
12	AA	534	U
12	AA	539	A
12	AA	540	U
12	AA	544	G
12	AA	548	A
12	AA	549	G
12	AA	556	U
12	AA	557	A
12	AA	558	U
12	AA	559	A
12	AA	560	G
12	AA	566	A
12	AA	567	G
12	AA	569	U
12	AA	570	U
12	AA	573	U
12	AA	574	A
12	AA	575	A
12	AA	582	A
12	AA	583	A
12	AA	584	A
12	AA	585	A
12	AA	587	U

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Mol	Chain	Res	Type
12	AA	793	U
12	AA	799	A
12	AA	800	A
12	AA	801	A
12	AA	803	U
12	AA	804	A
12	AA	807	A
12	AA	814	A
12	AA	816	C
12	AA	817	A
12	AA	818	A
12	AA	825	A
12	AA	826	A
12	AA	827	U
12	AA	828	A
12	AA	829	A
12	AA	838	A
12	AA	844	A
12	AA	845	A
12	AA	846	A
12	AA	848	A
12	AA	851	G
12	AA	853	A
12	AA	854	A
12	AA	868	U
12	AA	870	A
12	AA	871	C
12	AA	873	A
12	AA	874	A
12	AA	883	U
12	AA	885	U
12	AA	886	G
12	AA	887	A
12	AA	888	U
12	AA	892	U
12	AA	895	U
12	AA	896	U
12	AA	897	G
12	AA	902	U
12	AA	905	G
12	AA	906	A
12	AA	924	U

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Mol	Chain	Res	Type
12	AA	928	U
12	AA	931	U
12	AA	932	A
12	AA	933	U
12	AA	934	A
12	AA	936	C
12	AA	941	G
12	AA	942	A
12	AA	945	U
12	AA	946	A
12	AA	947	U
12	AA	948	A
12	AA	956	A
12	AA	961	A
12	AA	963	A
12	AA	970	U
12	AA	980	U
12	AA	984	A
12	AA	985	A
12	AA	986	G
12	AA	990	U
12	AA	991	A
12	AA	992	A
12	AA	993	A
12	AA	994	A
12	AA	995	A
12	AA	996	U
12	AA	998	A
12	AA	1003	G
12	AA	1004	U
12	AA	1006	U
12	AA	1008	A
12	AA	1010	C
12	AA	1014	U
12	AA	1015	A
12	AA	1018	U
12	AA	1019	A
12	AA	1021	U
12	AA	1079	A
12	AA	1089	G
12	AA	1091	U
12	AA	1092	U

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Mol	Chain	Res	Type
12	AA	1094	U
12	AA	1096	U
12	AA	1097	A
12	AA	1102	A
12	AA	1107	U
12	AA	1112	U
12	AA	1113	U
12	AA	1114	A
12	AA	1116	U
12	AA	1117	A
12	AA	1119	U
12	AA	1122	U
12	AA	1123	U
12	AA	1125	A
12	AA	1127	A
12	AA	1128	U
12	AA	1131	G
12	AA	1133	A
12	AA	1139	G
12	AA	1140	G
12	AA	1141	A
12	AA	1148	A
12	AA	1152	A
12	AA	1153	A
12	AA	1154	A
12	AA	1155	A
12	AA	1156	A
12	AA	1157	A
12	AA	1158	G
12	AA	1159	A
12	AA	1160	A
12	AA	1161	A
12	AA	1162	G
12	AA	1163	A
12	AA	1164	A
12	AA	1165	G
12	AA	1166	A
12	AA	1168	U
12	AA	1169	A
12	AA	1171	A
12	AA	1173	U
12	AA	1175	U

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Mol	Chain	Res	Type
12	AA	1176	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	AA	102	A
12	AA	484	U
12	AA	895	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 26 are monoatomic - leaving 5 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	$\# Z > 2$
87	GTP	EA	1001	88,86	33,34,34	0.98	1 (3%)	50,54,54	1.56	9 (18%)
87	GTP	EA	1004	88,86	33,34,34	0.94	1 (3%)	50,54,54	1.57	8 (16%)
90	PM8	ER	200	50	26,31,31	0.52	0	30,38,38	1.35	2 (6%)
89	ATP	EB	1001	86	32,33,33	1.42	5 (15%)	48,52,52	1.75	9 (18%)
91	NAD	Av	301	-	46,48,48	0.57	1 (2%)	64,73,73	0.59	1 (1%)

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
87	GTP	EA	1001	88,86	-	0/22/38/38	0/3/3/3
87	GTP	EA	1004	88,86	-	1/22/38/38	0/3/3/3
90	PM8	ER	200	50	-	10/36/38/38	-
89	ATP	EB	1001	86	-	1/22/38/38	0/3/3/3
91	NAD	Av	301	-	-	4/30/62/62	0/5/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	EB	1001	ATP	C5-C4	4.65	1.47	1.39
89	EB	1001	ATP	C5-C6	2.73	1.48	1.41
89	EB	1001	ATP	C8-N7	2.35	1.36	1.31
91	Av	301	NAD	C2N-N1N	2.35	1.37	1.35
89	EB	1001	ATP	C5-N7	-2.31	1.34	1.39
87	EA	1004	GTP	C2-N3	2.15	1.38	1.33
87	EA	1001	GTP	C2-N3	2.08	1.38	1.33
89	EB	1001	ATP	PB-O3B	2.06	1.61	1.59

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	EB	1001	ATP	C5-C4-N3	-5.91	118.58	126.72
87	EA	1004	GTP	C5-C4-N3	-5.01	120.42	128.39
87	EA	1004	GTP	C2-N3-C4	4.67	120.34	112.30
89	EB	1001	ATP	N3-C4-N9	4.62	135.02	127.17
87	EA	1001	GTP	C2-N3-C4	4.51	120.06	112.30
87	EA	1001	GTP	C5-C4-N3	-4.51	121.22	128.39
89	EB	1001	ATP	C2-N3-C4	3.75	121.00	111.83
89	EB	1001	ATP	C4-C5-N7	-3.56	106.52	110.58
89	EB	1001	ATP	N3-C2-N1	-3.26	123.64	128.58
90	ER	200	PM8	O1-C1-C2	-3.22	120.27	123.98
87	EA	1004	GTP	N9-C4-N3	3.04	132.03	125.95
87	EA	1001	GTP	N9-C8-N7	-3.00	107.84	113.40
87	EA	1004	GTP	C2-N1-C6	-2.91	119.84	125.11
87	EA	1004	GTP	N9-C8-N7	-2.84	108.14	113.40
87	EA	1001	GTP	N9-C4-N3	2.83	131.62	125.95
87	EA	1001	GTP	C2-N1-C6	-2.76	120.11	125.11
87	EA	1004	GTP	C8-N7-C5	2.74	109.14	104.26
90	ER	200	PM8	C3-C2-C1	-2.71	106.28	112.27
87	EA	1001	GTP	C8-N7-C5	2.60	108.89	104.26
89	EB	1001	ATP	C5-N7-C8	2.59	107.53	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	EB	1001	ATP	C4-N9-C8	2.57	108.43	105.74
87	EA	1001	GTP	C5-C6-N1	2.54	119.72	113.25
87	EA	1004	GTP	C5-C6-N1	2.49	119.60	113.25
87	EA	1001	GTP	O3'-C3'-C2'	-2.46	103.92	111.82
87	EA	1004	GTP	O6-C6-C5	-2.35	120.33	126.53
87	EA	1001	GTP	O6-C6-C5	-2.35	120.34	126.53
91	Av	301	NAD	C6N-N1N-C2N	-2.34	119.89	121.88
89	EB	1001	ATP	C6-C5-N7	2.15	136.23	132.09
89	EB	1001	ATP	C3'-C2'-C1'	2.04	105.33	101.46

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
90	ER	200	PM8	O27-C28-C29-C30
90	ER	200	PM8	O27-C28-C29-C31
90	ER	200	PM8	O27-C28-C29-C32
90	ER	200	PM8	O33-C32-C34-N36
90	ER	200	PM8	N41-C42-C43-S1
90	ER	200	PM8	O1-C1-S1-C43
90	ER	200	PM8	C2-C1-S1-C43
90	ER	200	PM8	C1-C2-C3-C4
90	ER	200	PM8	C38-C37-N36-C34
90	ER	200	PM8	O33-C32-C34-O35
91	Av	301	NAD	O4D-C4D-C5D-O5D
89	EB	1001	ATP	PA-O3A-PB-O1B
87	EA	1004	GTP	C5'-O5'-PA-O3A
91	Av	301	NAD	C2B-C1B-N9A-C8A
91	Av	301	NAD	O4B-C4B-C5B-O5B
91	Av	301	NAD	C3D-C4D-C5D-O5D

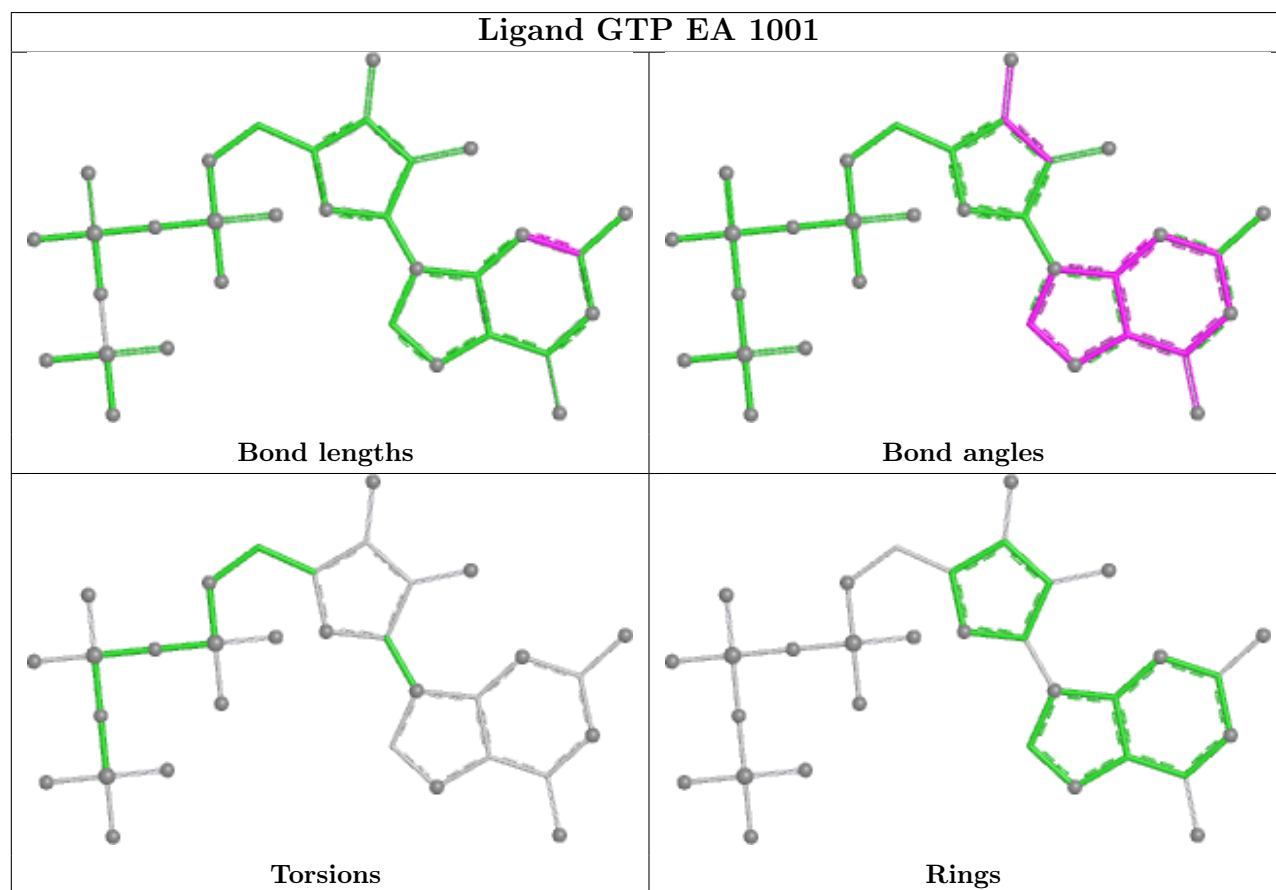
There are no ring outliers.

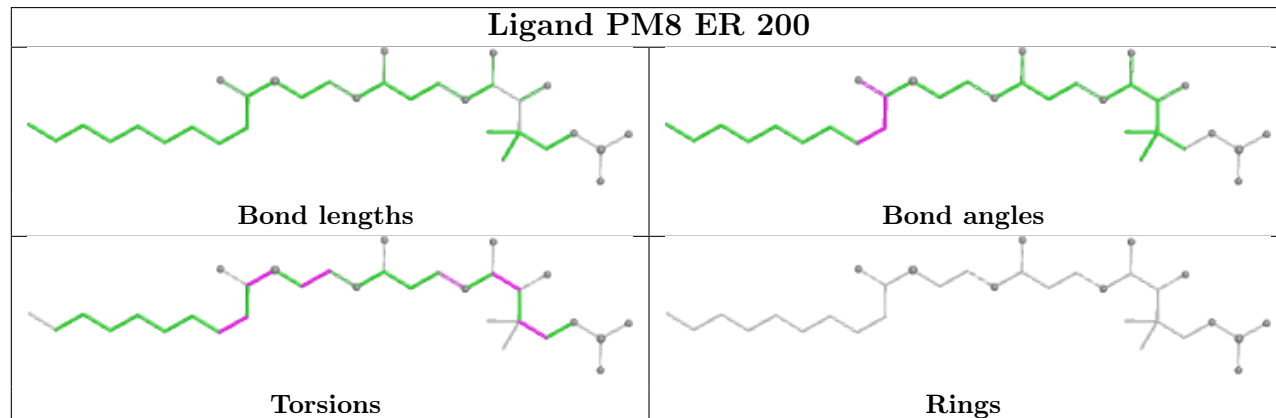
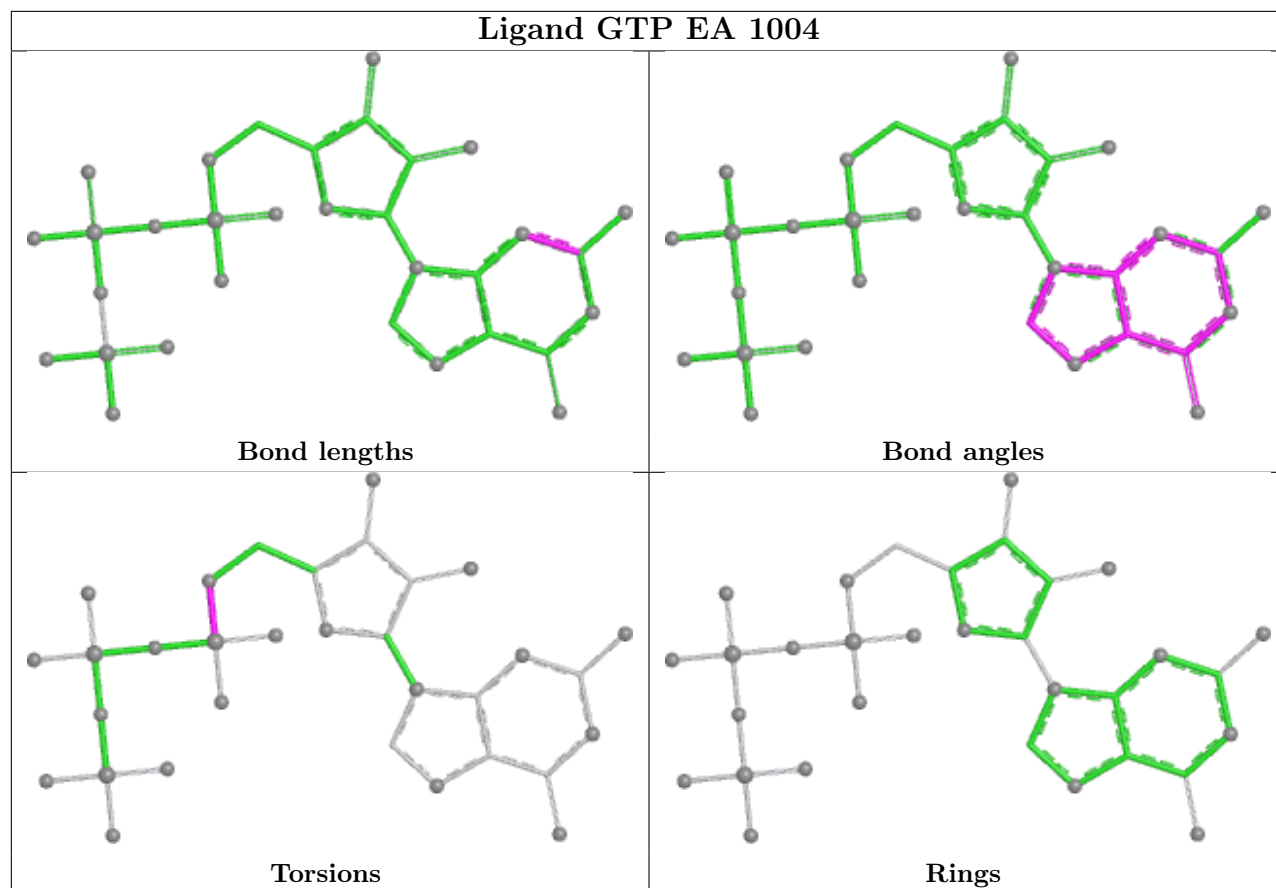
4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	EA	1001	GTP	2	0
87	EA	1004	GTP	3	0
90	ER	200	PM8	5	0
89	EB	1001	ATP	3	0

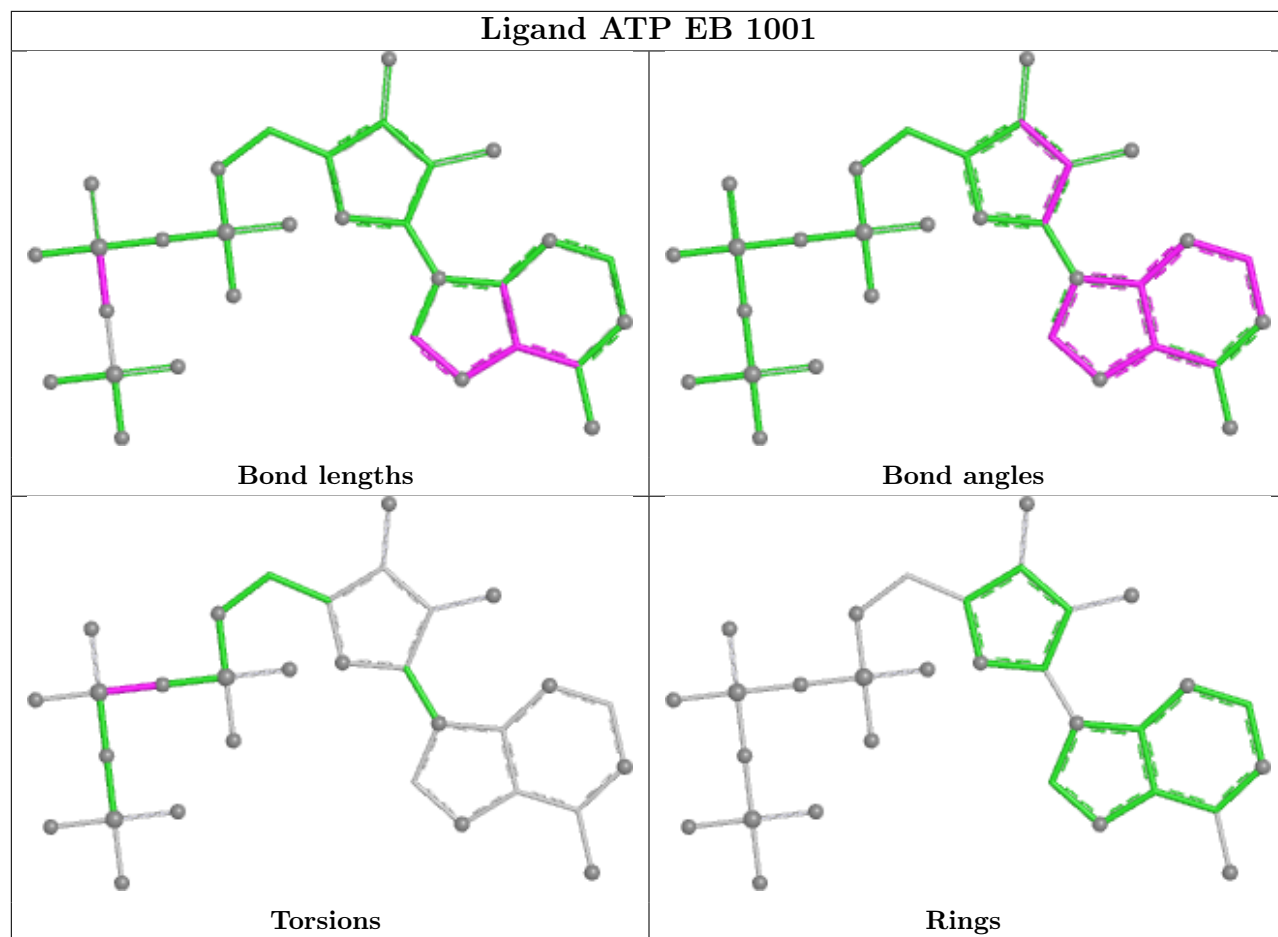
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

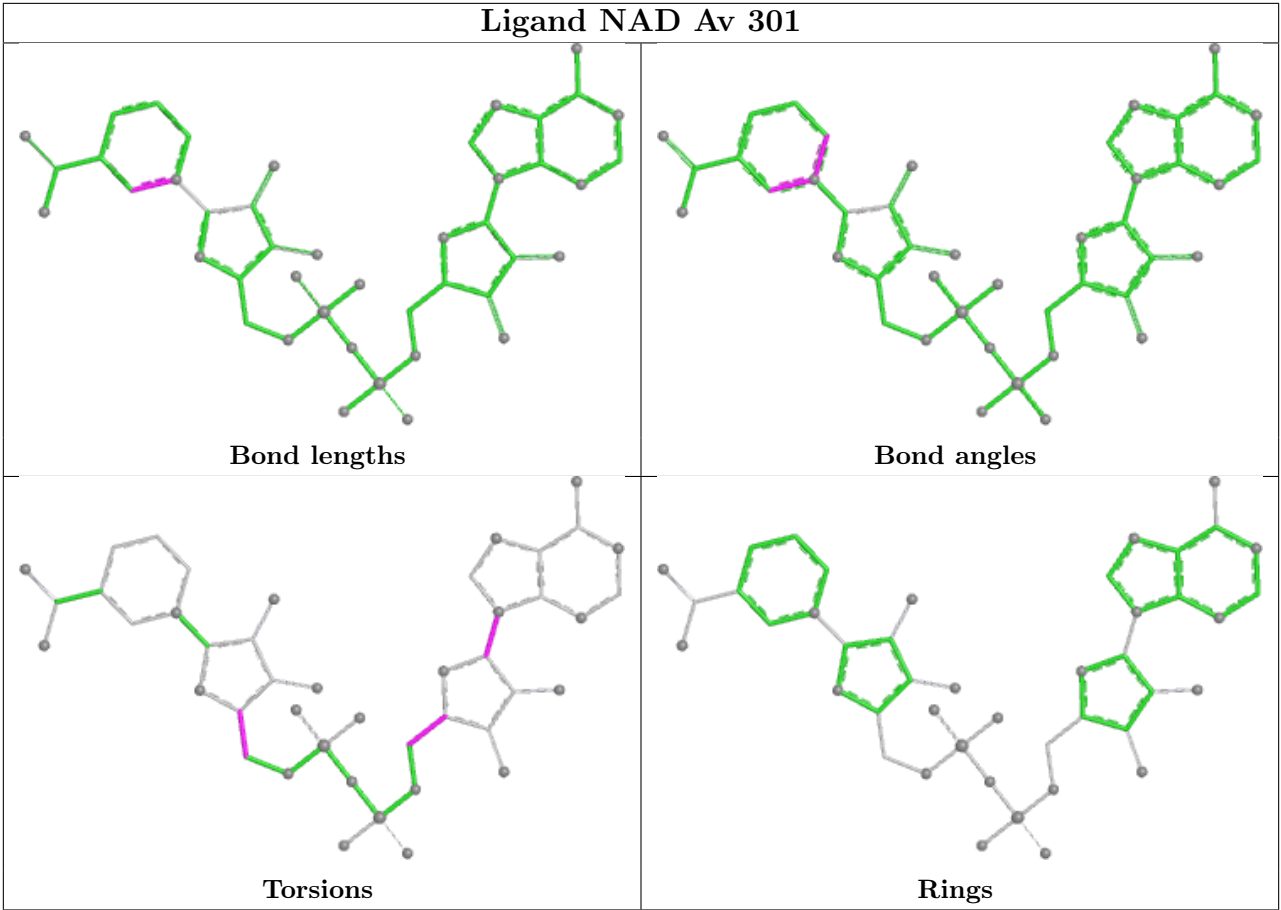
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





Ligand ATP EB 1001





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
76	U1	7
9	E5	5
82	Us	4
81	Up	3
77	Um	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U1	249:UNK	C	280:UNK	N	50.91
1	U1	115:UNK	C	146:UNK	N	43.56

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U1	158:UNK	C	179:UNK	N	35.52
1	Us	63:UNK	C	82:UNK	N	32.92
1	U1	295:UNK	C	311:UNK	N	29.90
1	Us	38:UNK	C	52:UNK	N	20.32
1	Us	96:UNK	C	110:UNK	N	17.98
1	U1	337:UNK	C	348:UNK	N	15.67
1	E5	103:UNK	C	124:UNK	N	15.44
1	E5	133:UNK	C	144:UNK	N	15.38
1	Us	14:UNK	C	19:UNK	N	15.06
1	E5	88:UNK	C	94:UNK	N	13.57
1	E5	279:UNK	C	290:UNK	N	12.66
1	Up	83:UNK	C	89:UNK	N	11.90
1	Up	53:UNK	C	64:UNK	N	6.74
1	U1	221:UNK	C	232:UNK	N	6.33
1	Um	21:UNK	C	100:UNK	N	5.55
1	Up	33:UNK	C	44:UNK	N	4.72
1	U1	45:UNK	C	56:UNK	N	3.64
1	E5	311:UNK	C	314:UNK	N	3.12

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10999. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.