



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:07 PM UTC

PDB ID : 6HIX / pdb_00006hix
EMDB ID : EMD-0231
Title : Cryo-EM structure of the Trypanosoma brucei mitochondrial ribosome - This entry contains the large mitoribosomal subunit
Authors : Ramrath, D.J.F.; Niemann, M.; Leibundgut, M.; Bieri, P.; Prange, C.; Horn, K.; Leitner, A.; Boehringer, D.; Schneider, A.; Ban, N.
Deposited on : 2018-08-31
Resolution : 3.39 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:

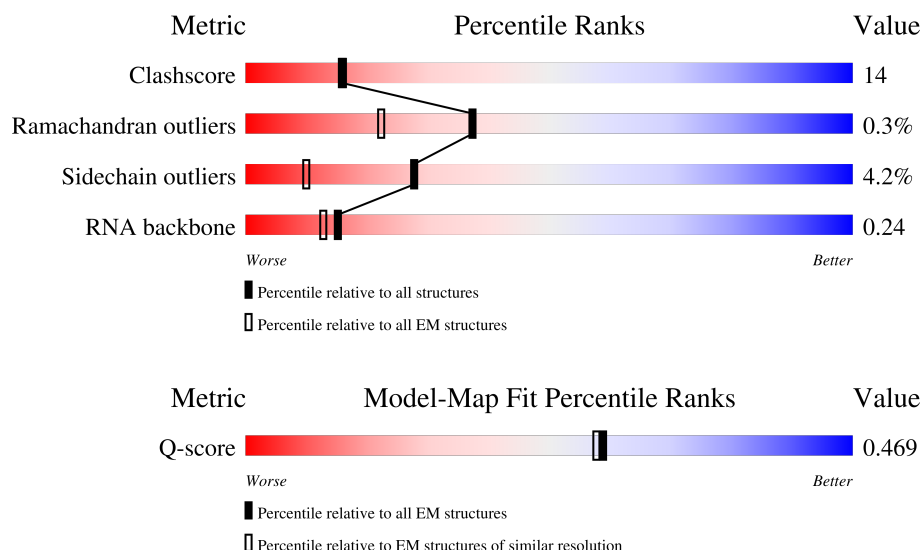
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.39 Å.

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



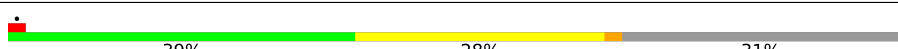
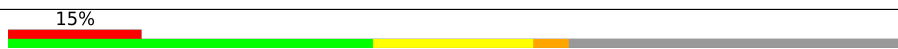
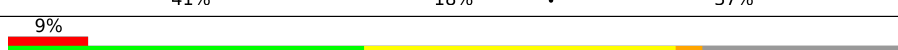
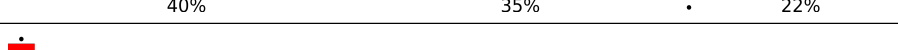
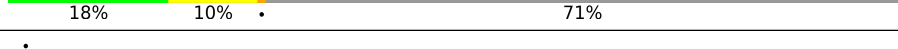
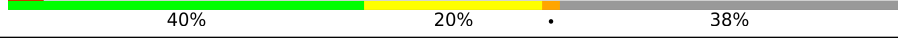
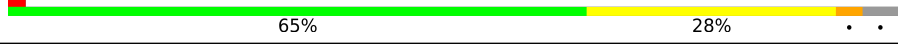
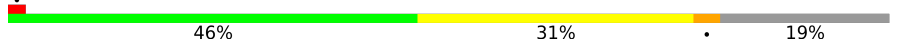
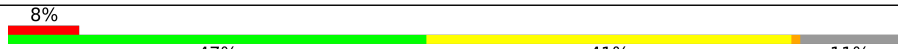
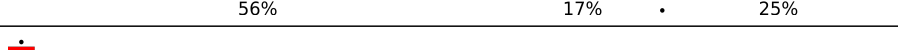
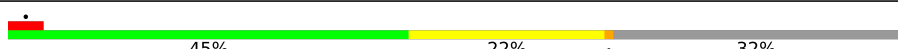
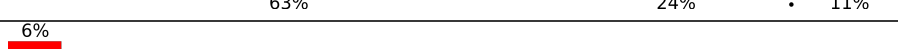
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14220 (2.89 - 3.89)

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

Mol	Chain	Length	Quality of chain
1	A0	185	
2	A1	241	
3	A2	471	

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Mol	Chain	Length	Quality of chain
4	A3	218	
5	A4	183	
6	A5	80	
7	A6	114	
8	A8	181	
9	A9	184	
10	AE	473	
11	AF	459	
12	AI	263	
13	AJ	177	
14	AK	342	
15	AN	202	
16	AP	374	
17	AQ	167	
18	AR	301	
19	AT	144	
20	AU	213	
21	AV	188	
22	AW	278	
23	AX	246	
24	AY	378	
25	Ab	507	
26	Ad	289	
27	Ae	197	
28	Af	189	

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Mol	Chain	Length	Quality of chain
29	Ag	260	
30	Aj	296	
31	Al	218	
32	Ao	259	
33	Ap	309	
34	At	154	
35	Av	242	
36	AB	56	
37	AC	28	
37	AD	28	
38	AG	27	
39	AA	1178	
40	BA	831	
41	BB	541	
42	BC	523	
43	BD	547	
44	BE	449	
45	BF	426	
46	BG	378	
47	BH	349	
48	BI	343	
49	BJ	333	
50	BK	386	
51	BL	312	
52	BM	283	

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Mol	Chain	Length	Quality of chain
53	BN	302	
54	BO	262	
55	BP	266	
56	BQ	231	
57	BR	205	
58	BS	198	
59	BT	191	
60	BU	185	
61	BV	190	
62	BW	188	
63	BX	190	
64	BY	172	
65	BZ	190	
66	Ba	153	
67	Bb	162	
68	Bc	146	
69	Bd	144	
70	Be	113	
71	Bf	113	
72	Bg	105	
73	Bh	92	
74	UA	46	
75	UB	40	
76	UC	12	
76	UH	12	

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Mol	Chain	Length	Quality of chain
77	UD	177	
78	UE	22	
79	UF	24	
79	UG	24	
79	UN	24	
80	UI	17	
81	UK	10	
82	UL	15	
83	UM	6	
84	UU	11	
85	UV	8	
85	UX	8	
86	UW	7	

2 Entry composition [i](#)

There are 89 unique types of molecules in this entry. The entry contains 133849 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 bl27m.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A0	151	Total	C	N	O	S	0	0
			1269	801	236	227	5		

- Molecule 2 is a protein called bl28m.

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

- Molecule 3 is a protein called ul29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A2	449	Total	C	N	O	S	0	0
			3638	2324	631	670	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 ul30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A3	150	Total	C	N	O	S	0	0
			1215	776	234	199	6		

- Molecule 5 is a protein called bl31m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A4	168	Total	C	N	O	S	0	0
			1387	880	262	240	5		

- Molecule 6 is a protein called bl32m.

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

- Molecule 7 is a protein called bl33m.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A6	72	Total	C	N	O	S	0	0
			568	361	102	101	4		

- Molecule 8 is a protein called bl35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A8	142	Total	C	N	O	S	0	0
			1203	753	243	198	9		

- Molecule 9 is a protein called bl36m.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A9	53	Total	C	N	O	S	0	0
			459	288	85	78	8		

- Molecule 10 is a protein called Ribosomal protein L3 mitochondrial, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AE	293	Total	C	N	O	S	0	0
			2390	1543	395	440	12		

- Molecule 11 is a protein called Ribosomal protein L4/L1 family, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AF	442	Total	C	N	O	S	0	0
			3597	2294	624	654	25		

- Molecule 12 is a protein called bl9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AI	212	Total	C	N	O	S	0	0
			1790	1153	316	312	9		

- Molecule 13 is a protein called ul10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AJ	126	Total	C	N	O	S	0	0
			965	606	191	165	3		

- Molecule 14 is a protein called Ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AK	323	Total	C	N	O	S	0	0
			2676	1703	485	469	19		

- Molecule 15 is a protein called 50S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AN	179	Total	C	N	O	S	0	0
			1508	973	275	251	9		

- Molecule 16 is a protein called ul15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	352	Total	C	N	O	S	0	0
			2904	1846	538	507	13		

- Molecule 17 is a protein called 50S ribosomal protein L16, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	125	Total	C	N	O	S	0	0
			1020	658	183	175	4		

- Molecule 18 is a protein called 50S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	227	Total	C	N	O	S	0	0
			1912	1211	356	332	13		

- Molecule 19 is a protein called bl19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AT	35	Total	C	N	O	S	0	0
			287	180	61	45	1		

- Molecule 20 is a protein called bl20m.

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

- Molecule 21 is a protein called bl21m.

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

- Molecule 22 is a protein called ul22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AW	276	Total	C	N	O	S	0	0
			2235	1416	415	391	13		

- Molecule 23 is a protein called ul23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	168	Total	C	N	O	S	0	0
			1416	913	253	245	5		

- Molecule 24 is a protein called ul24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AY	340	Total	C	N	O	S	0	0
			2712	1689	493	517	13		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 25 is a protein called ml38.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Ab	453	Total	C	N	O	S	0	0
			3545	2252	621	657	15		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ab	290	SER	PHE	conflict	UNP Q381T7

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Chain	Residue	Modelled	Actual	Comment	Reference
Ab	299	GLU	LYS	conflict	UNP Q381T7
Ab	471	ASN	ILE	conflict	UNP Q381T7

- Molecule 26 is a protein called ml40.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Ad	257	Total	C	N	O	S	0	0
			2122	1319	386	405	12		

- Molecule 27 is a protein called ml41.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ae	116	Total	C	N	O	S	0	0
			927	594	170	158	5		

- Molecule 28 is a protein called ml42.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Af	126	Total	C	N	O	S	0	0
			1013	630	196	183	4		

- Molecule 29 is a protein called ml43.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ag	259	Total	C	N	O	S	0	0
			2193	1368	422	392	11		

- Molecule 30 is a protein called ml46.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Aj	279	Total	C	N	O	S	0	0
			2246	1408	414	416	8		

- Molecule 31 is a protein called ml49.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Al	209	Total	C	N	O	S	0	0
			1618	1051	281	279	7		

- Molecule 32 is a protein called ml52.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ao	183	Total	C	N	O	S	0	0
			1475	936	272	264	3		

- Molecule 33 is a protein called ml53.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ap	261	Total	C	N	O	S	0	0
			2143	1391	372	368	12		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ap	2	LEU	SER	conflict	UNP Q57YA9

- Molecule 34 is a protein called ml63.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	At	138	Total	C	N	O	S	0	0
			1100	690	210	196	4		

- Molecule 35 is a protein called ml64.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Av	213	Total	C	N	O	S	0	0
			1792	1138	333	308	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Av	164	ARG	GLN	conflict	UNP Q383B7

- Molecule 36 is a protein called bL12m.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	AB	56	Total	C	N	O	0	0
			280	168	56	56		

- Molecule 37 is a protein called bL12m.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	AC	28	Total	C	N	O	0	0
			140	84	28	28		

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Mol	Chain	Residues	Atoms				AltConf	Trace
37	AD	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 38 is a protein called bL12m.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	AG	27	Total	C	N	O	0	0
			135	81	27	27		

- Molecule 39 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	AA	591	Total	C	N	O	P	0	0
			12491	5628	2125	4147	591		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	448	A	U	conflict	GB 343546
AA	622	A	U	conflict	GB 343546
AA	636	A	G	conflict	GB 343546
AA	702	G	A	conflict	GB 343546
AA	706	C	U	conflict	GB 343546
AA	743	C	G	conflict	GB 343546
AA	752	G	A	conflict	GB 343546
AA	757	U	A	conflict	GB 343546
AA	760	U	G	conflict	GB 343546
AA	762	U	G	conflict	GB 343546
AA	789	G	C	conflict	GB 343546
AA	793	G	U	conflict	GB 343546
AA	875	A	G	conflict	GB 343546
AA	876	G	A	conflict	GB 343546
AA	877	A	G	conflict	GB 343546

- Molecule 40 is a protein called ml67.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BA	679	Total	C	N	O	S	0	0
			5384	3422	948	981	33		

- Molecule 41 is a protein called ml68.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BB	389	Total	C	N	O	S	0	0
			2966	1879	535	539	13		

- Molecule 42 is a protein called ml69.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BC	478	Total	C	N	O	S	0	0
			3821	2451	670	680	20		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BC	29	PRO	SER	conflict	UNP Q584V5
BC	42	GLY	SER	conflict	UNP Q584V5

- Molecule 43 is a protein called mL70.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	BD	417	Total	C	N	O	0	0
			2063	1229	417	417		

- Molecule 44 is a protein called ml71.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BE	392	Total	C	N	O	S	0	0
			3105	1970	540	582	13		

- Molecule 45 is a protein called ml72.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BF	345	Total	C	N	O	S	0	0
			2838	1797	517	511	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BF	296	ILE	THR	conflict	UNP C9ZR63

- Molecule 46 is a protein called ml73.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BG	319	Total	C	N	O	S	0	0
			2503	1578	449	459	17		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BG	185	PHE	LEU	conflict	UNP Q57Y49

- Molecule 47 is a protein called ml74.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BH	211	Total	C	N	O	S	0	0
			1729	1110	301	315	3		

- Molecule 48 is a protein called ml75.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BI	319	Total	C	N	O	S	0	0
			2609	1664	473	456	16		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BI	227	ASN	ASP	conflict	UNP Q38CK0
BI	319	ARG	GLN	conflict	UNP Q38CK0
BI	343	ALA	-	expression tag	UNP Q38CK0

- Molecule 49 is a protein called ml76.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BJ	166	Total	C	N	O	S	0	0
			1339	832	262	239	6		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 50 is a protein called Chaperone protein DNAj, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BK	258	Total	C	N	O	S	0	0
			1996	1237	383	368	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BK	348	VAL	LEU	conflict	UNP C9ZQR6

- Molecule 51 is a protein called ml78.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BL	234	Total	C	N	O	S	0	0
			1887	1158	370	349	10		

- Molecule 52 is a protein called ml79.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BM	245	Total	C	N	O	S	0	0
			2015	1280	370	356	9		

- Molecule 53 is a protein called ml80.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BN	214	Total	C	N	O	S	0	0
			1714	1077	320	312	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BN	145	THR	ALA	conflict	UNP Q585A3

- Molecule 54 is a protein called ml81.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BO	147	Total	C	N	O	S	0	0
			1146	719	202	213	12		

- Molecule 55 is a protein called ml82.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BP	202	Total	C	N	O	S	0	0
			1550	973	292	276	9		

- Molecule 56 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BQ	216	Total	C	N	O	S	0	0
			1675	1061	291	315	8		

- Molecule 57 is a protein called ml84.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BR	195	Total	C	N	O	S	0	0
			1650	1059	298	284	9		

- Molecule 58 is a protein called ml85.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BS	97	Total	C	N	O	S	0	0
			784	493	141	144	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 59 is a protein called ml86.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BT	168	Total	C	N	O	S	0	0
			1389	853	270	260	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BT	70	ARG	GLN	conflict	UNP C9ZPU8

- Molecule 60 is a protein called ml87.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BU	82	Total	C	N	O	S	0	0
			694	436	139	115	4		

- Molecule 61 is a protein called ml88.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BV	155	Total	C	N	O	S	0	0
			1307	832	233	236	6		

- Molecule 62 is a protein called ml89.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BW	187	Total	C	N	O	S	0	0
			1557	987	298	264	8		

- Molecule 63 is a protein called ml90.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BX	107	Total	C	N	O	S	0	0
			867	552	160	147	8		

- Molecule 64 is a protein called ml91.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BY	102	Total	C	N	O	S	0	0
			877	549	171	154	3		

- Molecule 65 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BZ	190	Total	C	N	O	S	0	0
			1390	878	242	263	7		

- Molecule 66 is a protein called ml93.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Ba	139	Total	C	N	O	S	0	0
			1224	785	223	209	7		

- Molecule 67 is a protein called ml94.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bb	99	Total	C	N	O	S	0	0
			770	482	144	143	1		

- Molecule 68 is a protein called ml95.

Mol	Chain	Residues	Atoms				AltConf	Trace
68	Bc	90	Total	C	N	O	0	0
			781	495	148	138		

- Molecule 69 is a protein called ml96.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Bd	140	Total	C	N	O	S	0	0
			1113	689	209	204	11		

- Molecule 70 is a protein called ml97.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Be	101	Total	C	N	O	S	0	0
			822	517	152	144	9		

- Molecule 71 is a protein called ml98.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	Bf	50	Total	C	N	O	0	0
			434	279	80	75		

- Molecule 72 is a protein called ml99.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bg	82	Total	C	N	O	S	0	0
			656	412	126	116	2		

- Molecule 73 is a protein called ml100.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bh	91	Total	C	N	O	S	0	0
			730	466	129	125	10		

- Molecule 74 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	UA	46	Total	C	N	O	0	0
			276	184	46	46		

- Molecule 75 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	UB	40	Total	C	N	O	0	0
			240	160	40	40		

- Molecule 76 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	UC	12	Total	C	N	O	0	0
			72	48	12	12		
76	UH	12	Total	C	N	O	0	0
			72	48	12	12		

- Molecule 77 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	UD	177	Total	C	N	O	0	0
			1062	708	177	177		

- Molecule 78 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
78	UE	22	Total	C	N	O	0	0
			132	88	22	22		

- Molecule 79 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
79	UF	24	Total	C	N	O	0	0
			144	96	24	24		
79	UG	24	Total	C	N	O	0	0
			144	96	24	24		
79	UN	24	Total	C	N	O	0	0
			144	96	24	24		

- Molecule 80 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
80	UI	17	Total	C	N	O	0	0
			102	68	17	17		

- Molecule 81 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	UK	10	Total	C	N	O	0	0
			60	40	10	10		

- Molecule 82 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	UL	15	Total	C	N	O	0	0
			90	60	15	15		

- Molecule 83 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
83	UM	6	Total	C	N	O	0	0
			36	24	6	6		

- Molecule 84 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
84	UU	11	Total	C	N	O	0	0
			66	44	11	11		

- Molecule 85 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
85	UV	8	Total	C	N	O	0	0
			48	32	8	8		
85	UX	8	Total	C	N	O	0	0
			48	32	8	8		

- Molecule 86 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
86	UW	7	Total	C	N	O	0	0
			42	28	7	7		

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

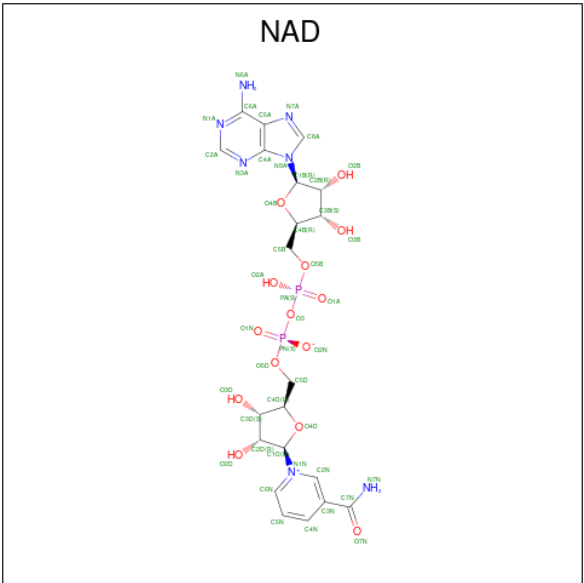
Mol	Chain	Residues	Atoms		AltConf
87	A5	1	Total	Zn	0
			1	1	
87	A9	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
87	BX	2	Total	Zn	0
			2	2	
87	Be	1	Total	Zn	0
			1	1	
87	Bh	1	Total	Zn	0
			1	1	

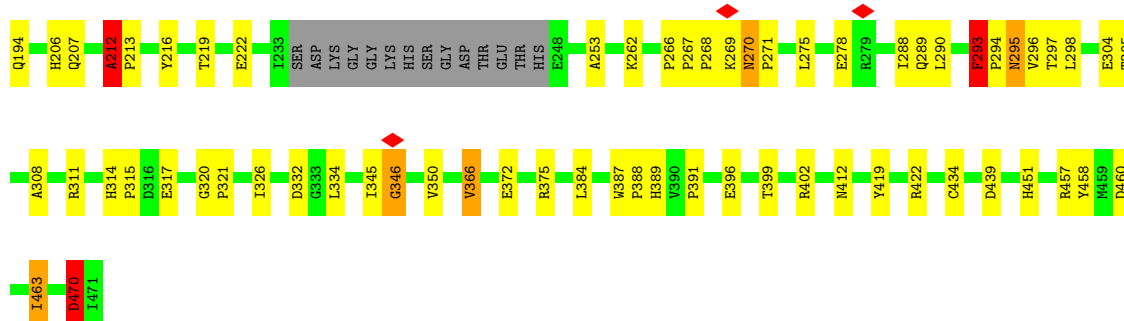
- Molecule 88 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



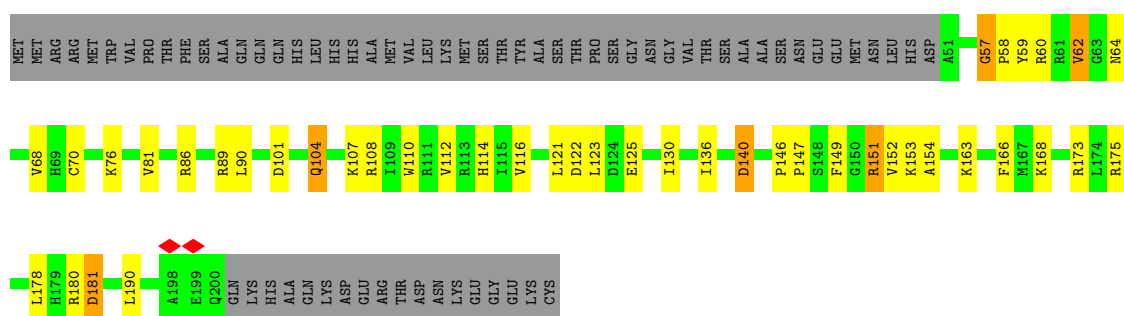
Mol	Chain	Residues	Atoms					AltConf
88	Av	1	Total	C	N	O	P	0
			44	21	7	14	2	

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

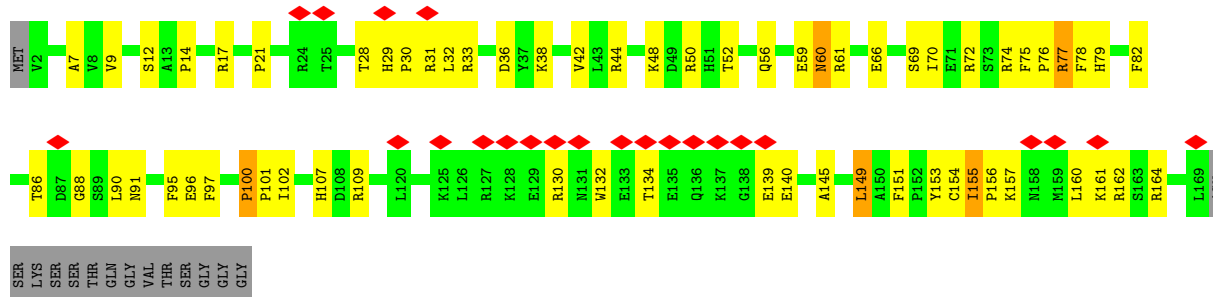
Mol	Chain	Residues	Atoms		AltConf
89	AA	7	Total	Mg	0
			7	7	



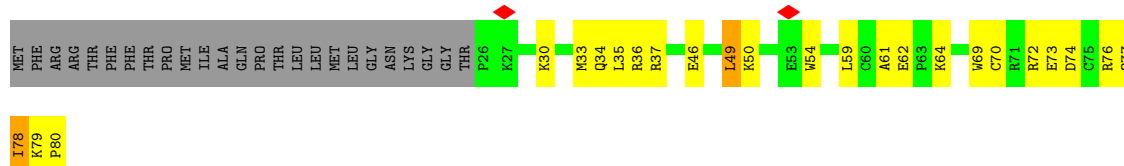
• Molecule 4: ul30m



• Molecule 5: bl31m

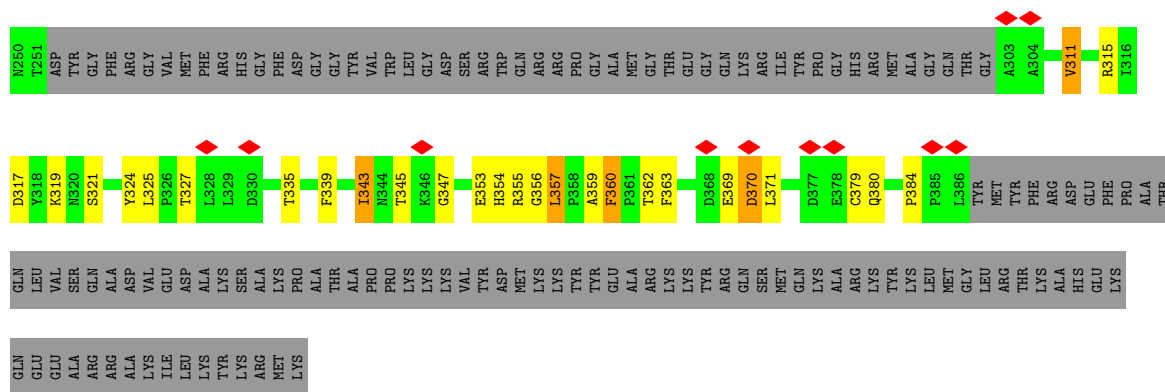


• Molecule 6: bl32m

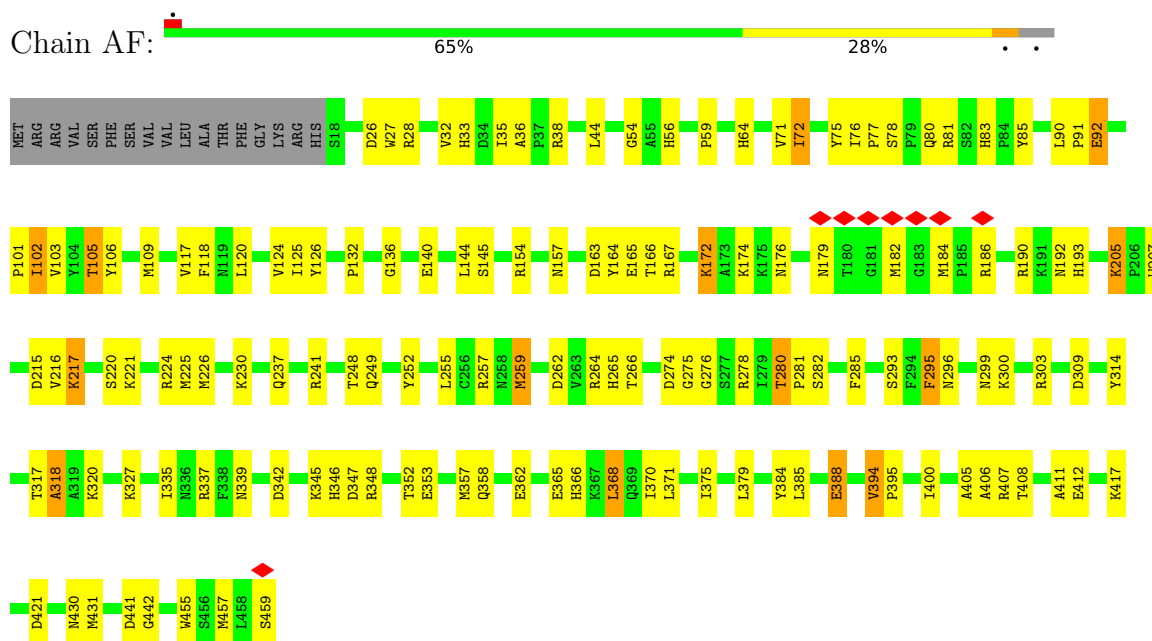


• Molecule 7: bl33m

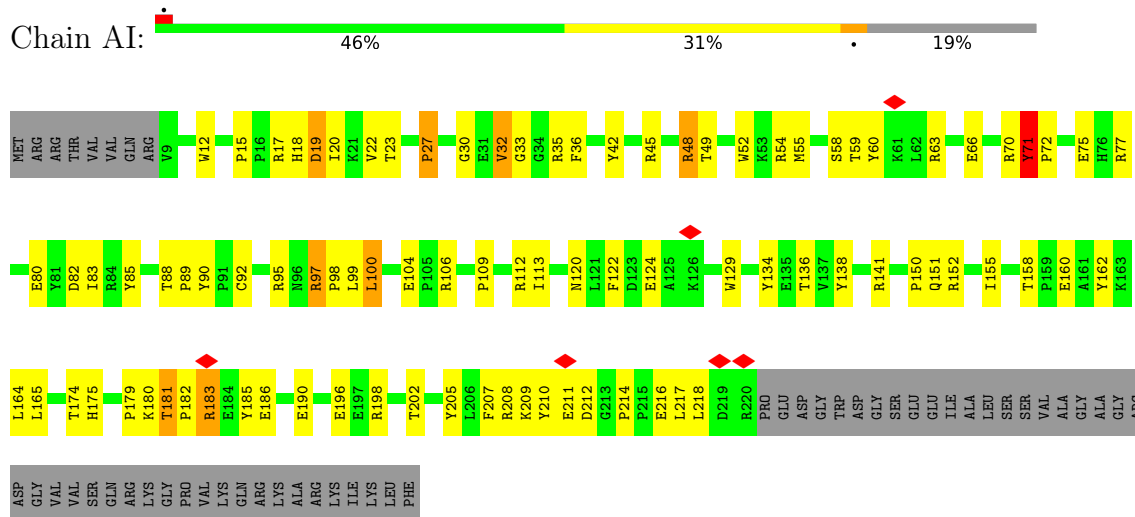


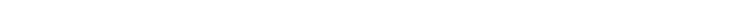


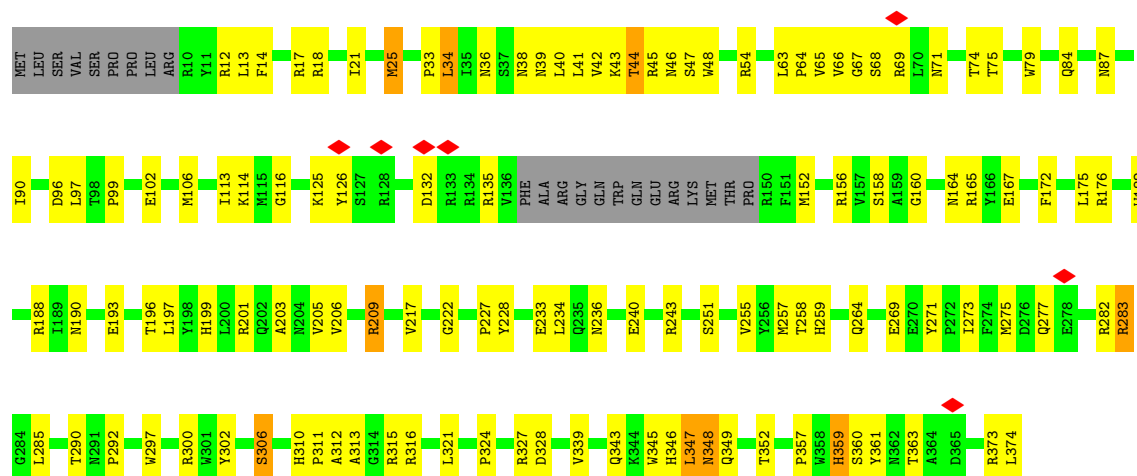
- Molecule 11: Ribosomal protein L4/L1 family, putative



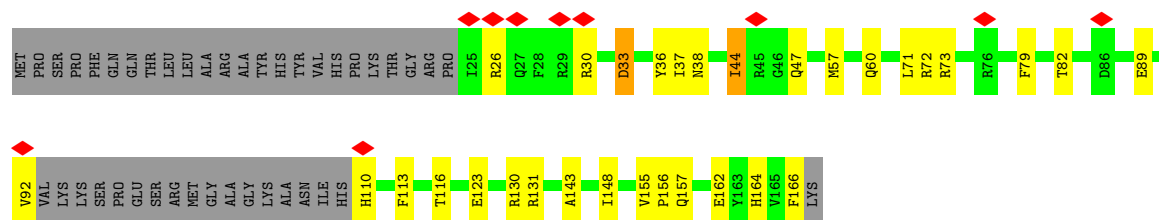
- Molecule 12: bl9m



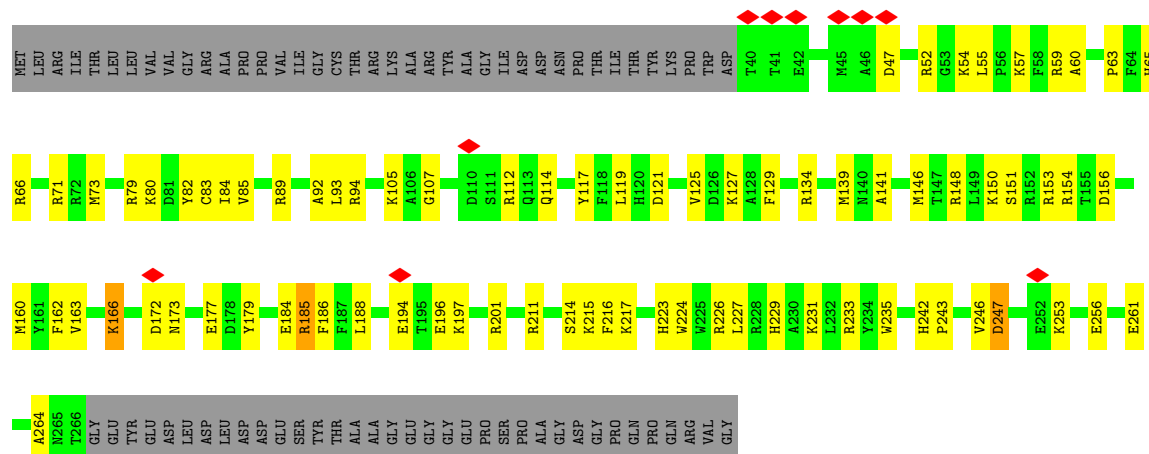
Chain A.J: 



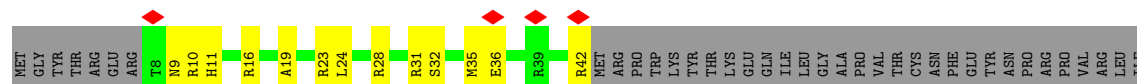
- Molecule 17: 50S ribosomal protein L16, putative



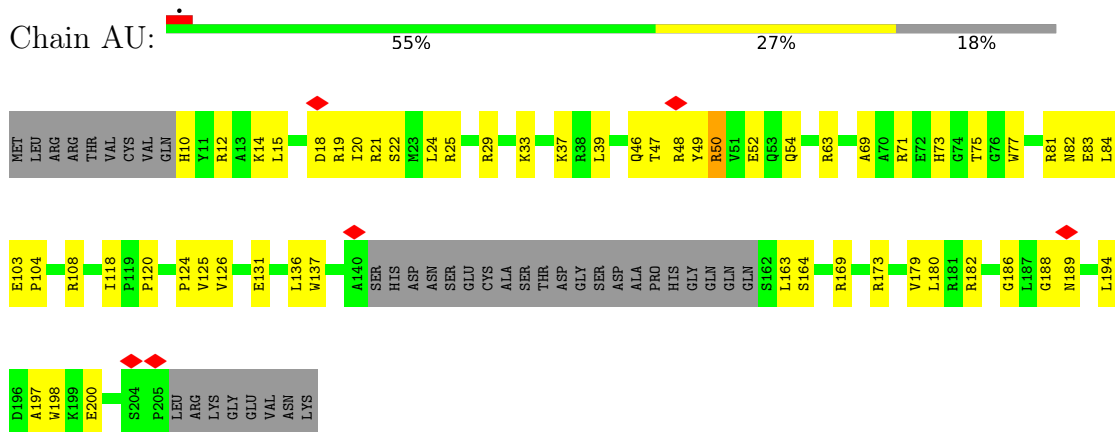
- Molecule 18: 50S ribosomal protein L17, putative



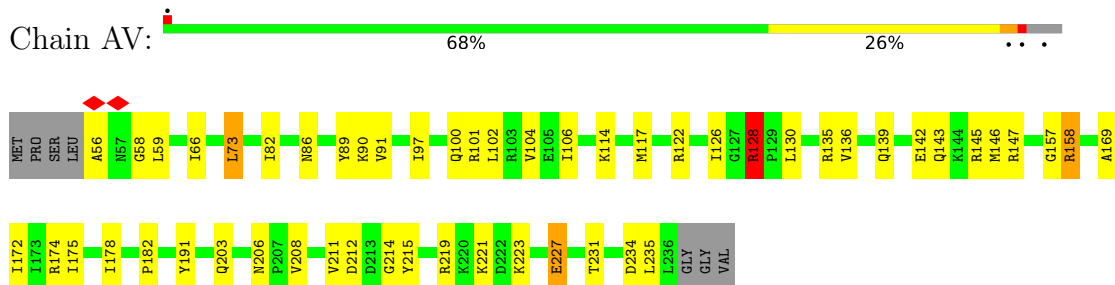
- Molecule 19: bl19m



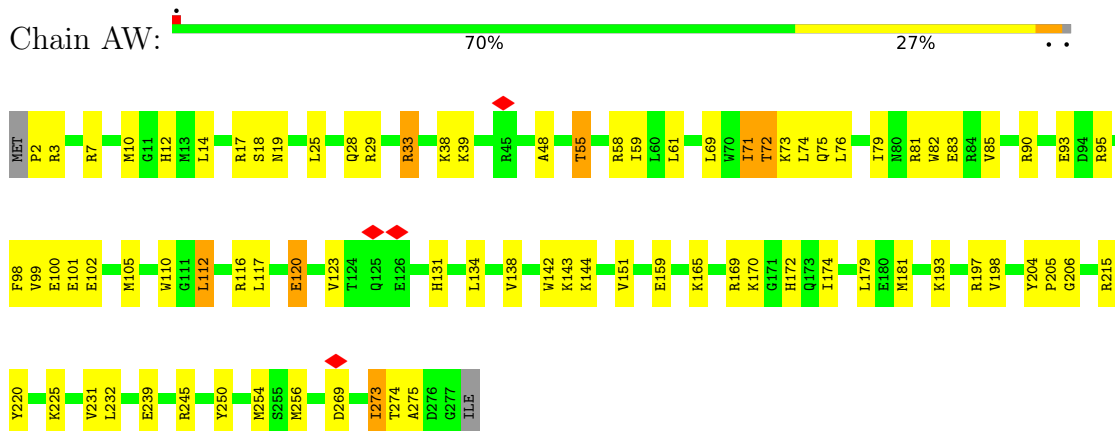
- Molecule 20: bl20m



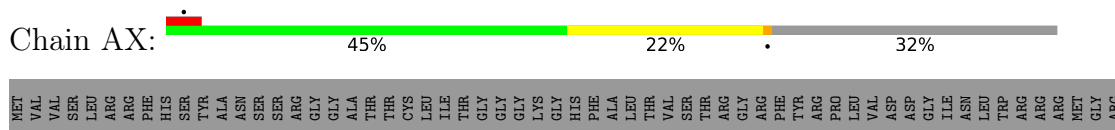
- Molecule 21: bl21m

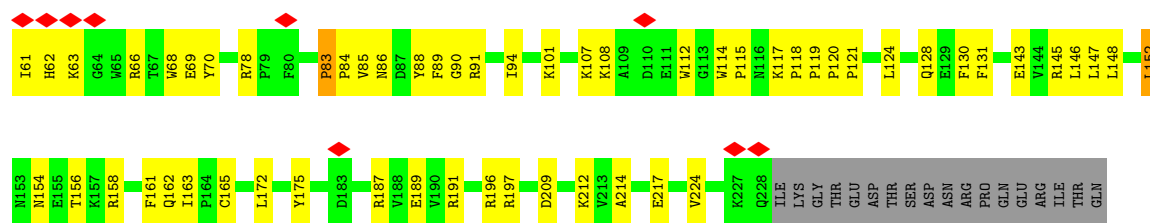


- Molecule 22: ul22m

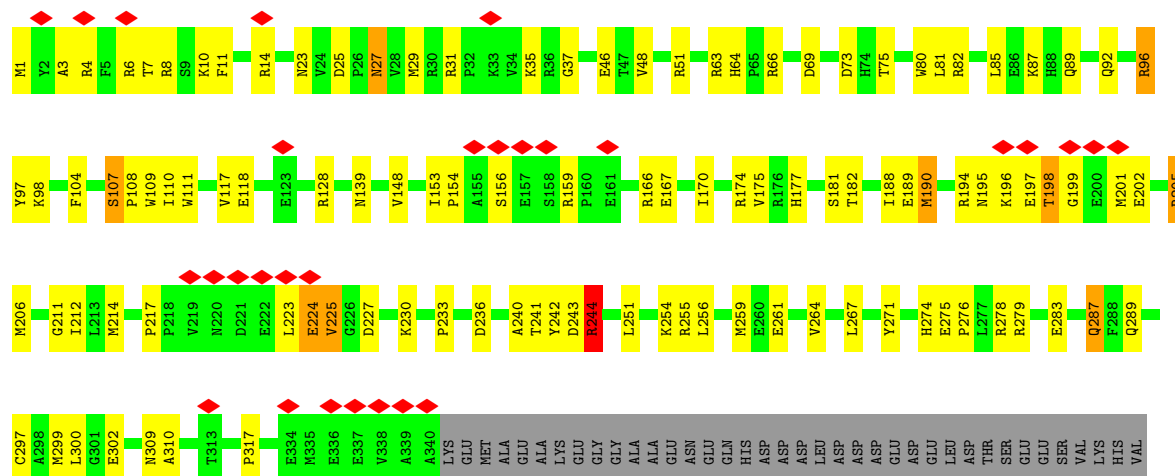


- Molecule 23: ul23m

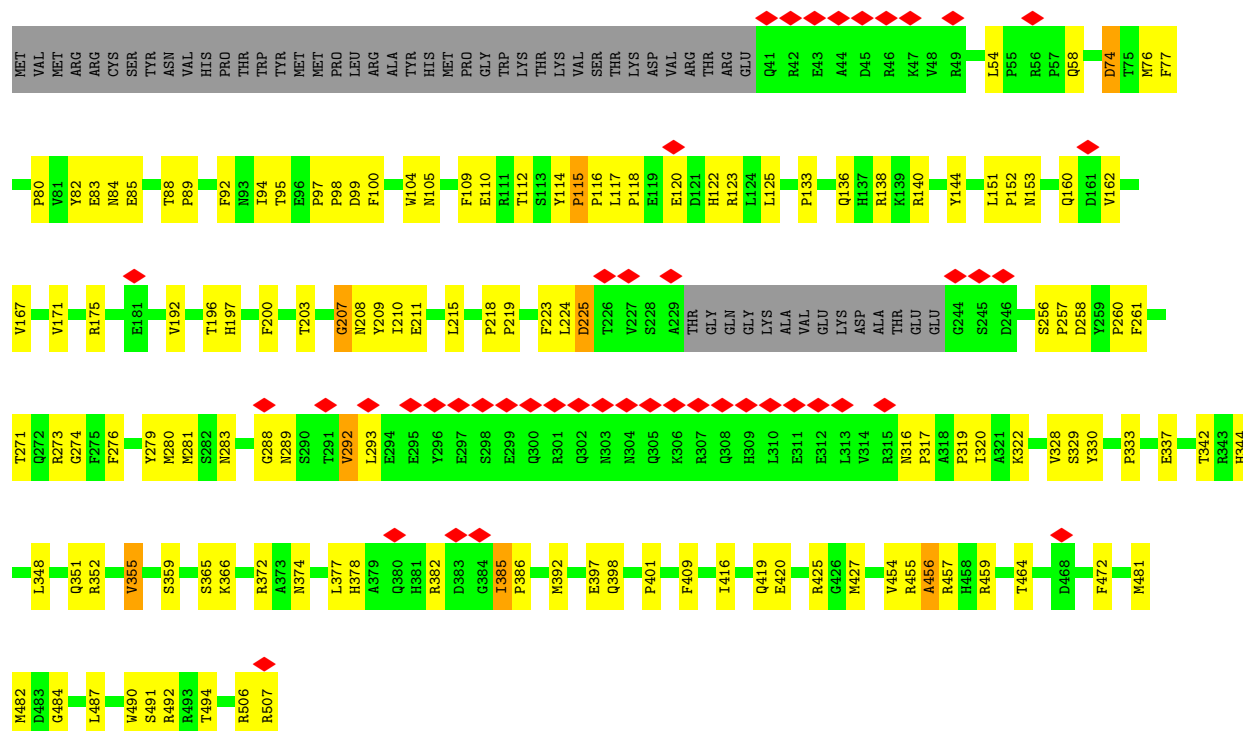


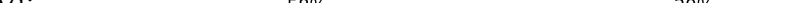


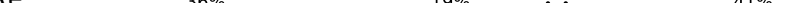
• Molecule 24: ul24m

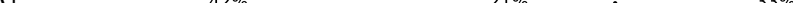


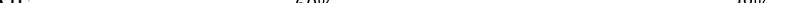
• Molecule 25: ml38

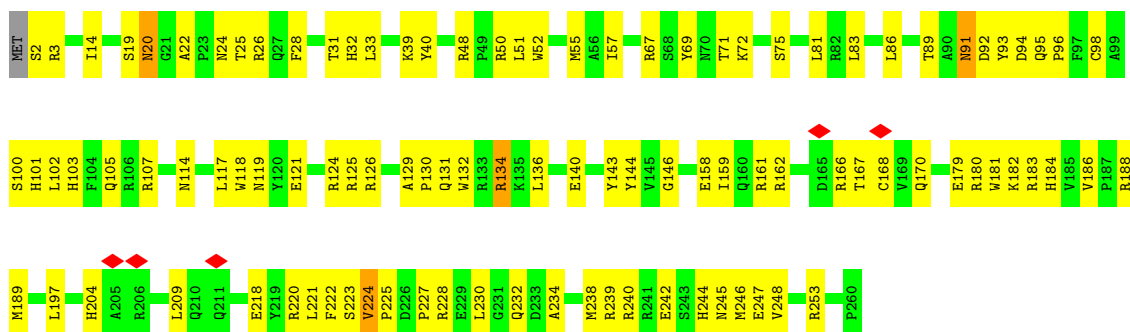


Chain Ad: 

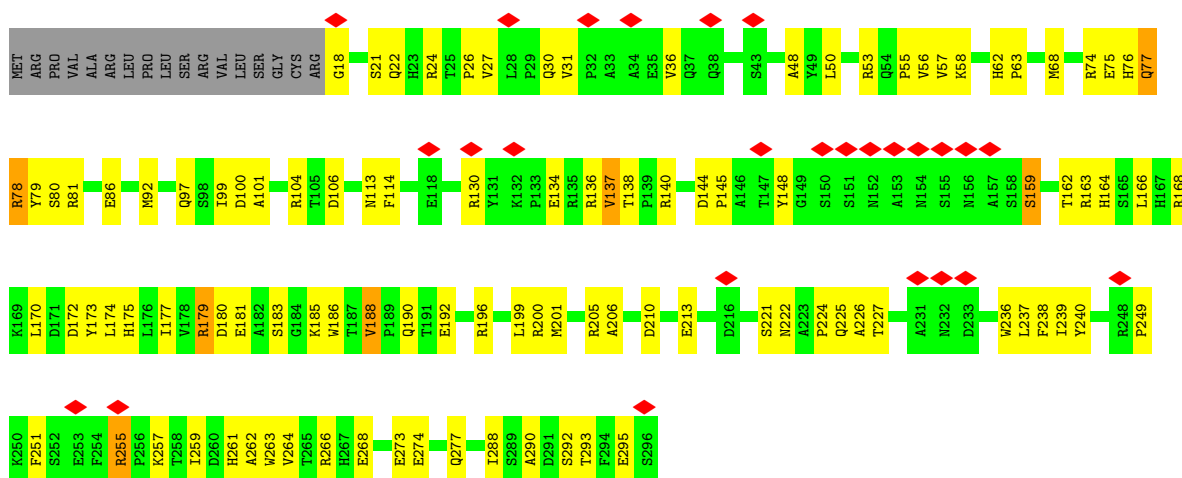
Chain Ae: 

Chain Af: 

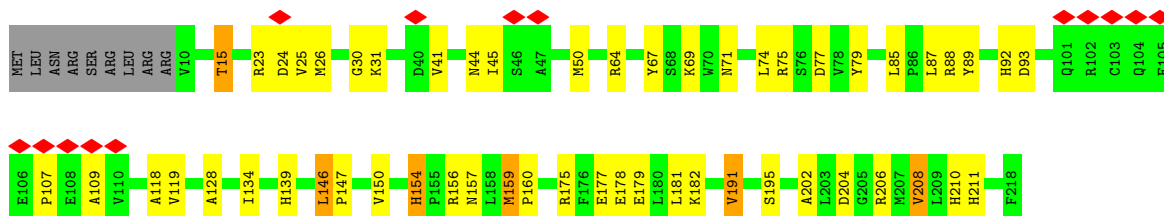
Chain Ag: 



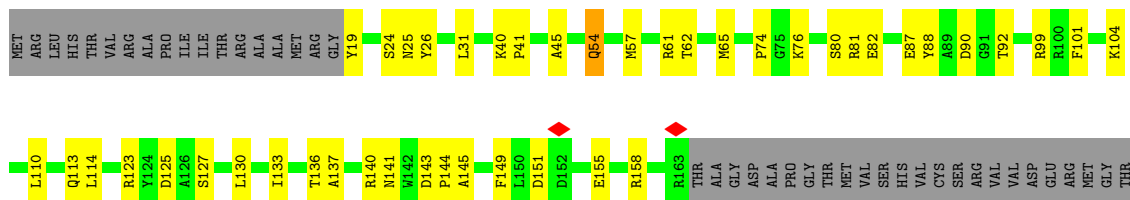
• Molecule 30: ml46

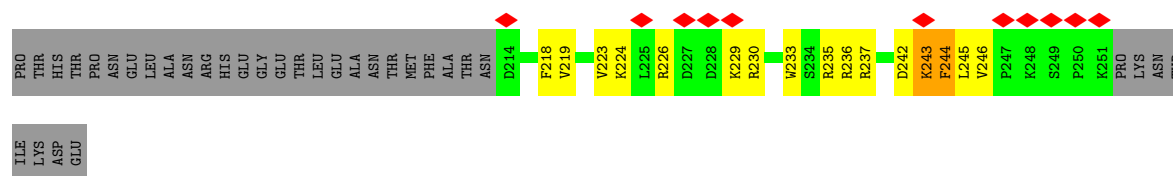


• Molecule 31: ml49

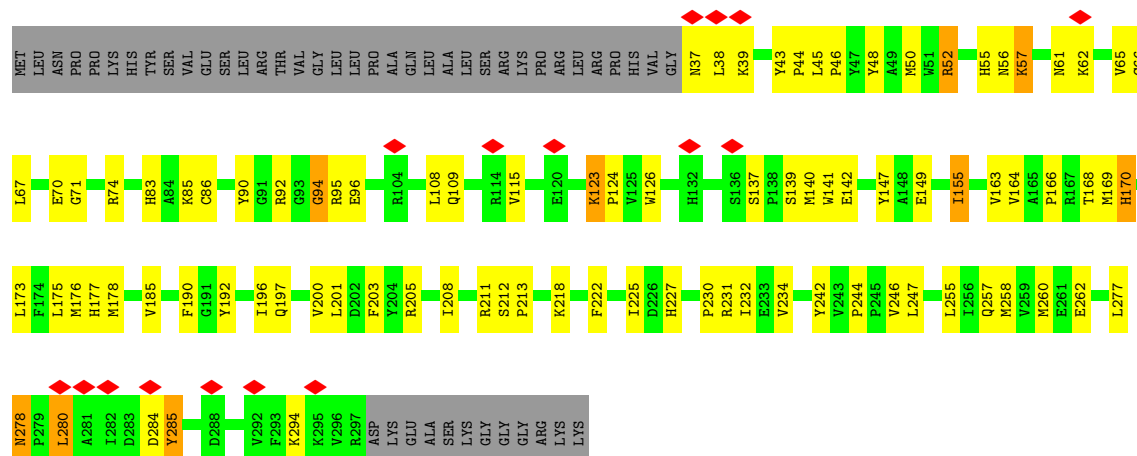


• Molecule 32: ml52

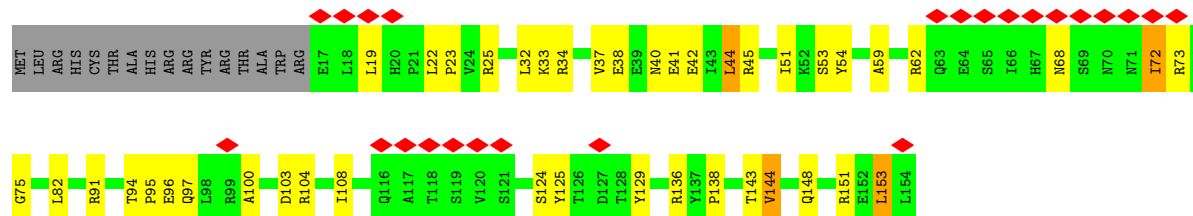




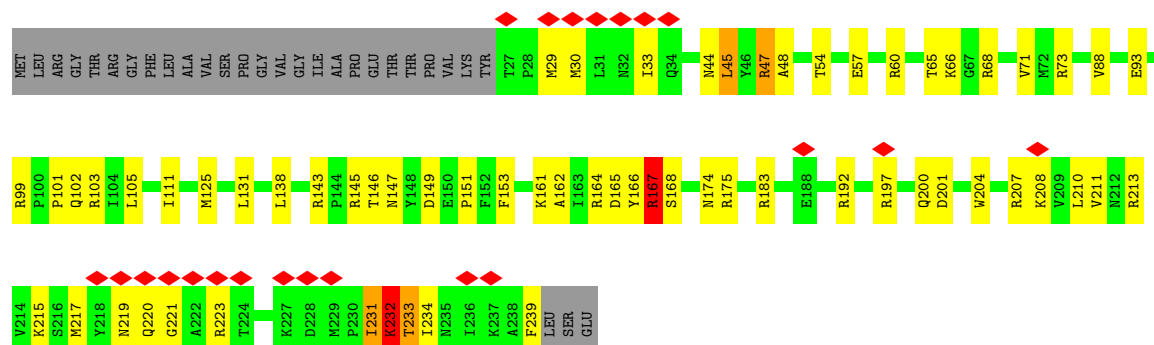
• Molecule 33: ml53



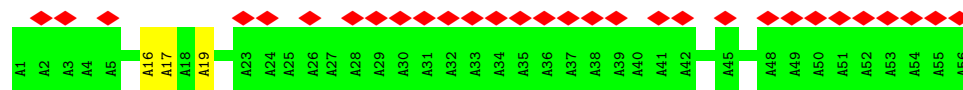
• Molecule 34: ml63



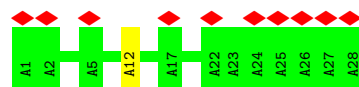
• Molecule 35: ml64



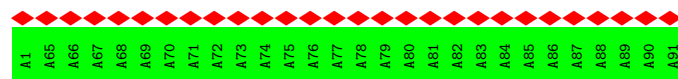
- Molecule 36: bL12m



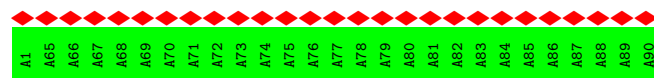
- Molecule 37: bL12m



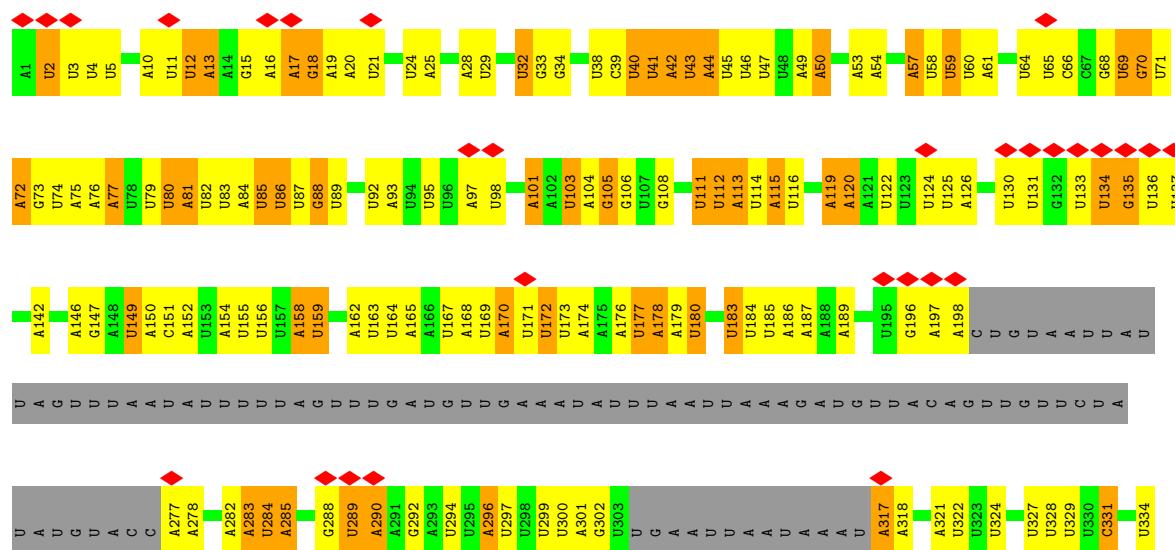
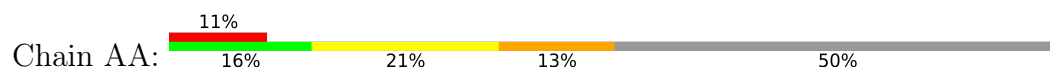
- Molecule 37: bL12m



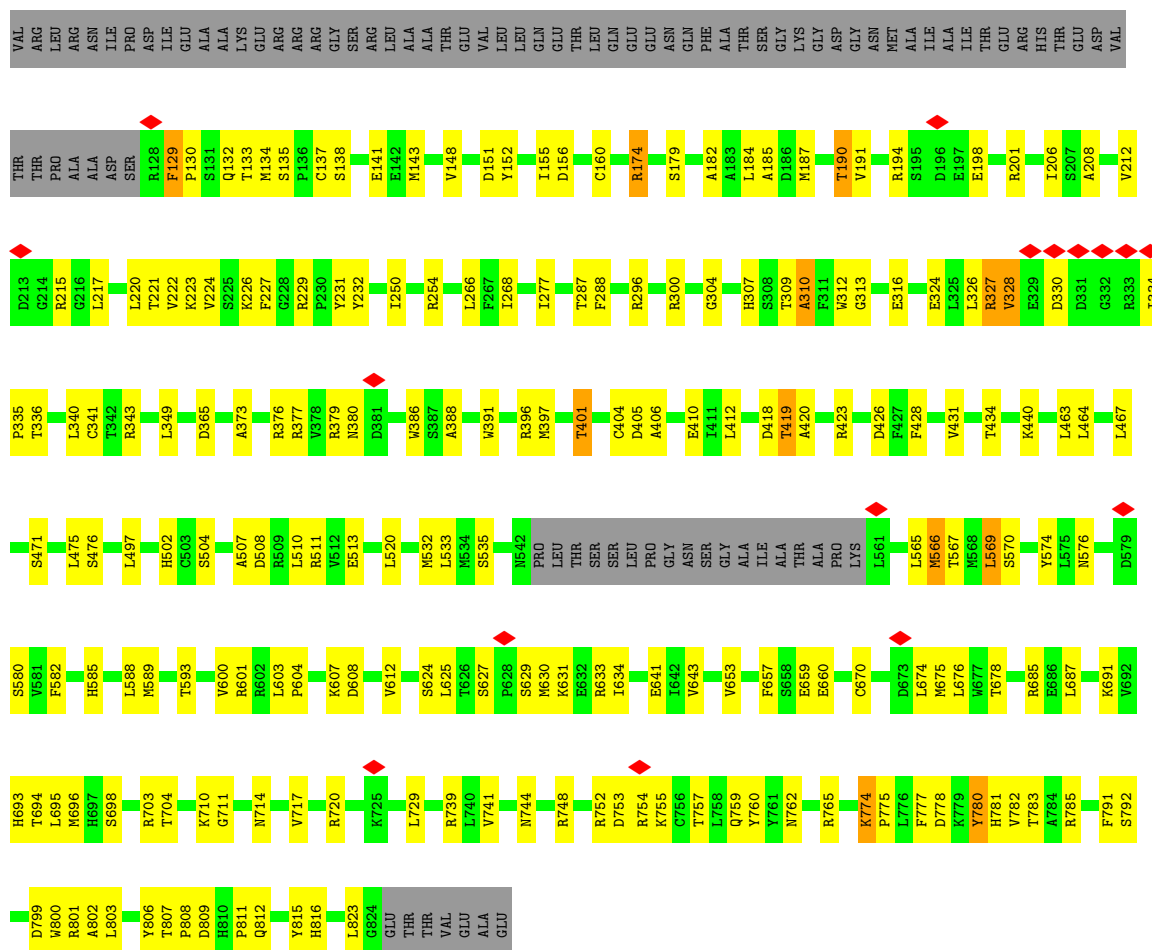
- Molecule 38: bL12m

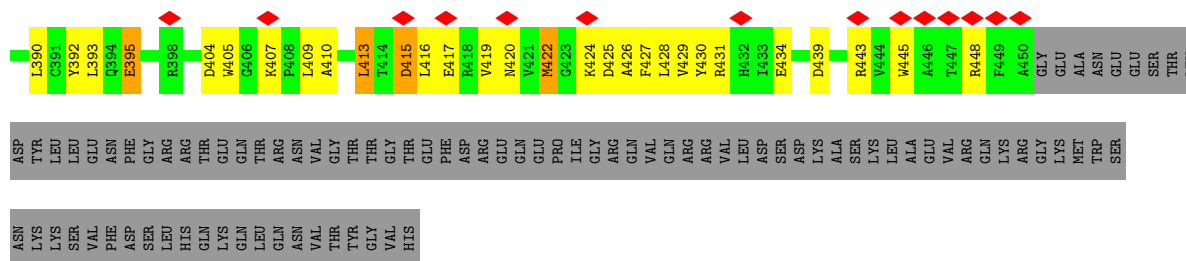


- Molecule 39: 12S rRNA



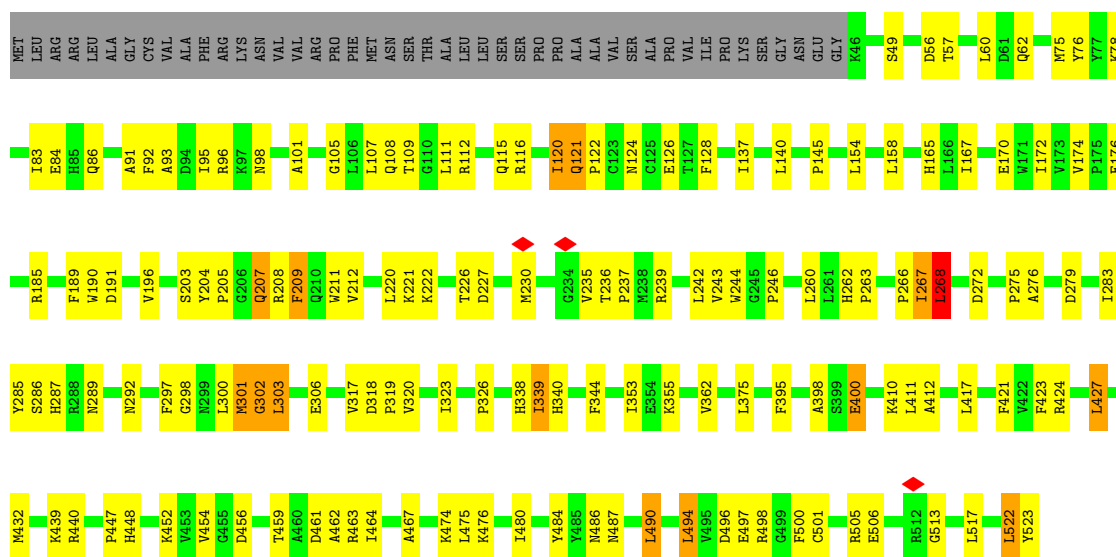






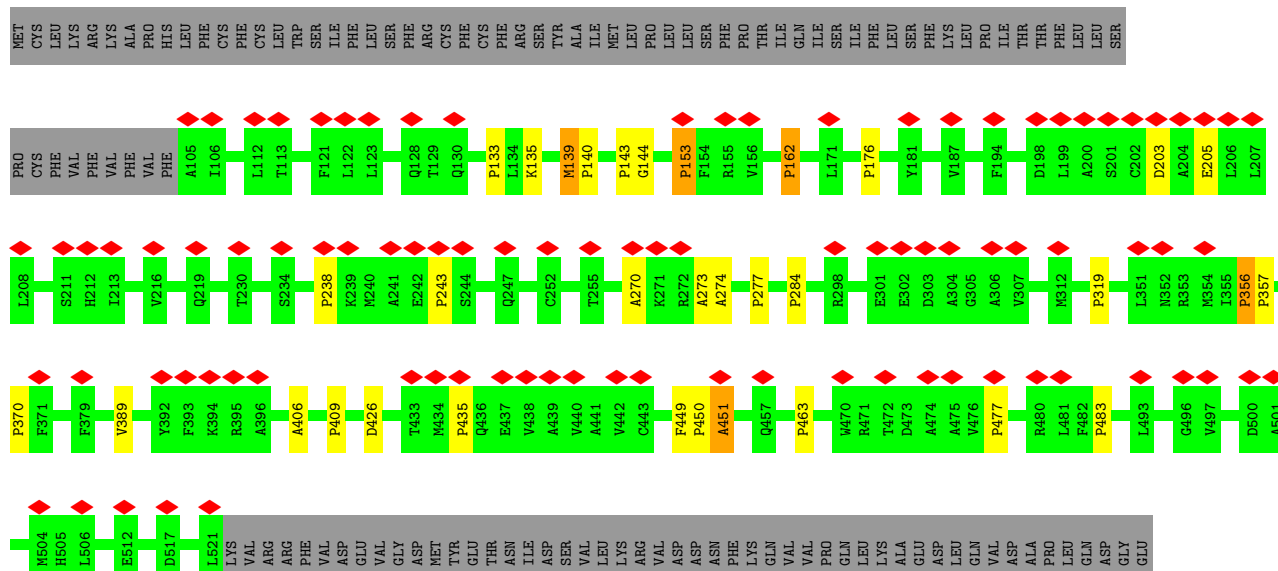
• Molecule 42: ml69

Chain BC: 62% 26% 9%



• Molecule 43: mL70

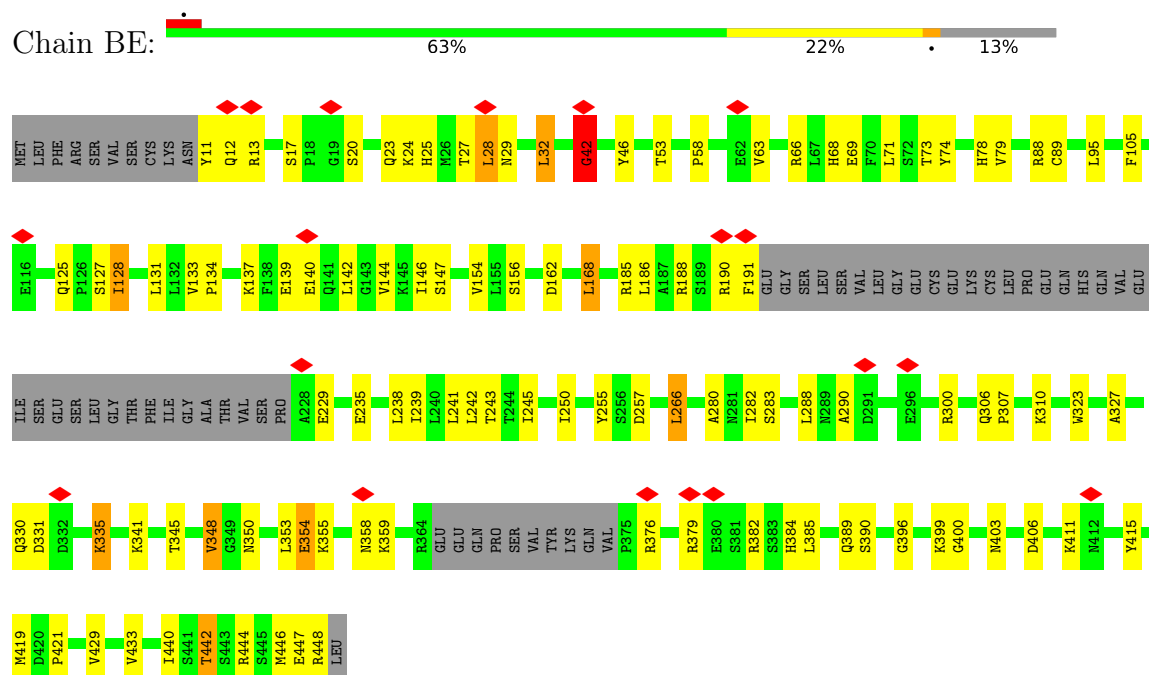
Chain BD: 70% 5% 24%



GLY
GLU
ASP
THR
VAL
ARG
GLU
THR
VAL
ALA
ALA

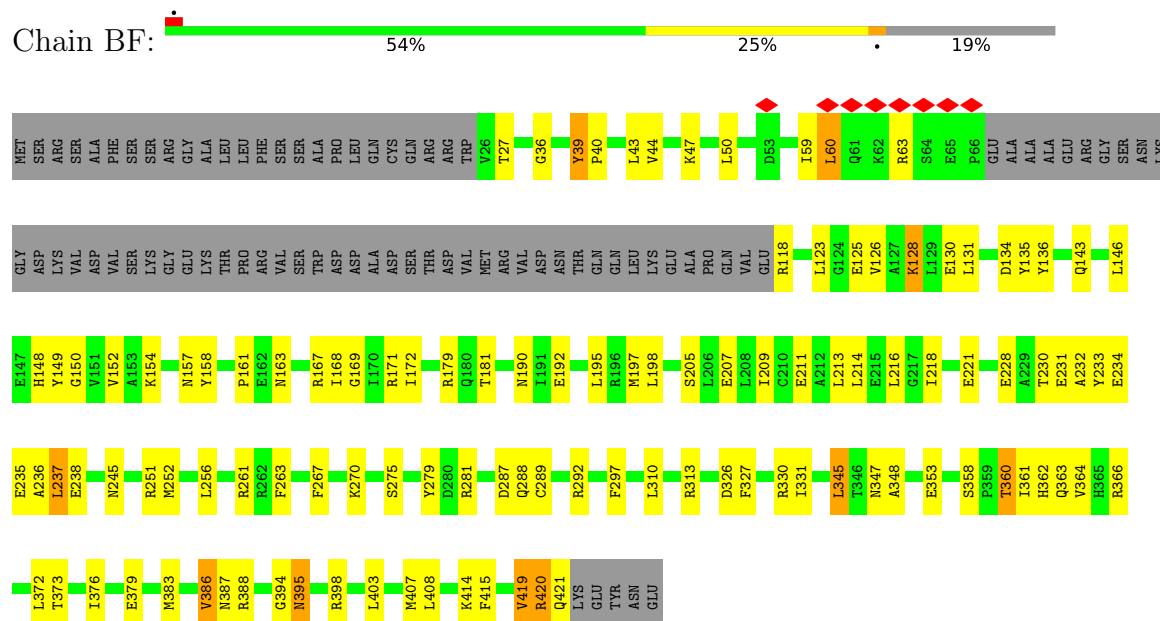
• Molecule 44: ml71

Chain BE:



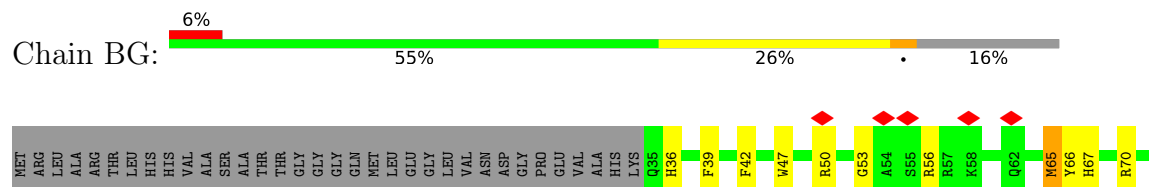
• Molecule 45: ml72

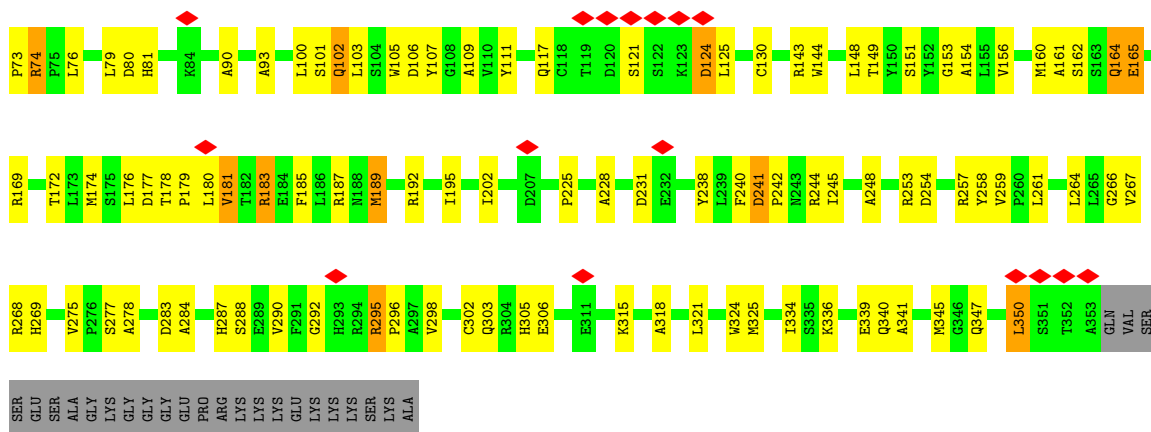
Chain BF:



• Molecule 46: ml73

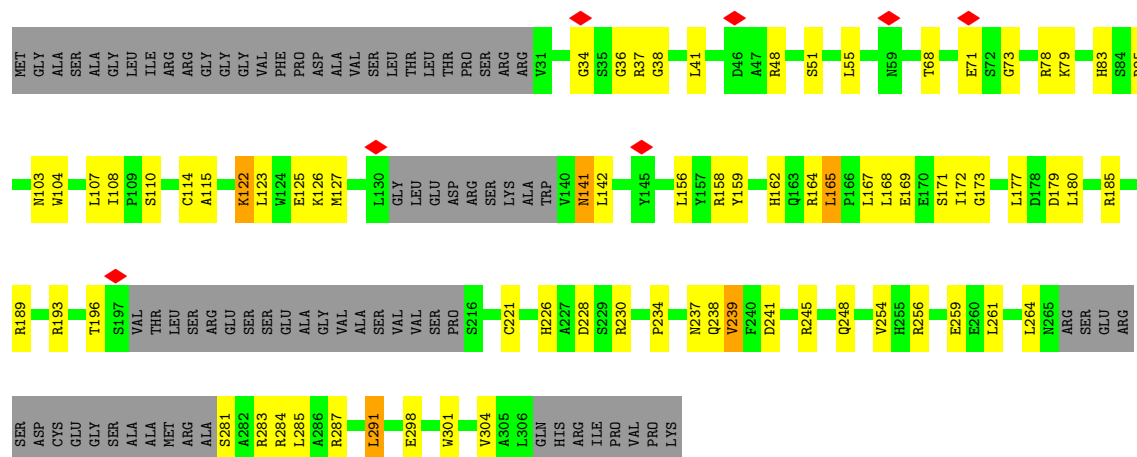
Chain BG:



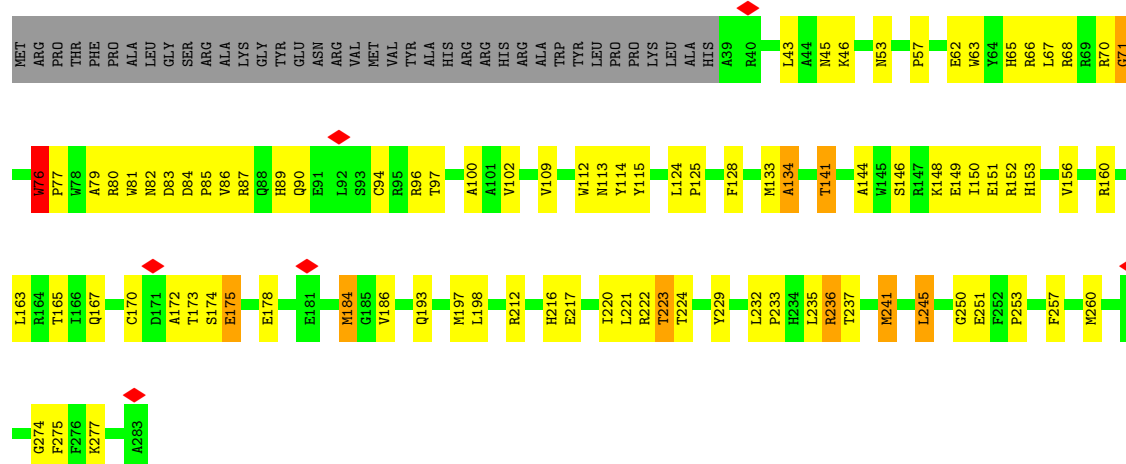


Chain B.J:

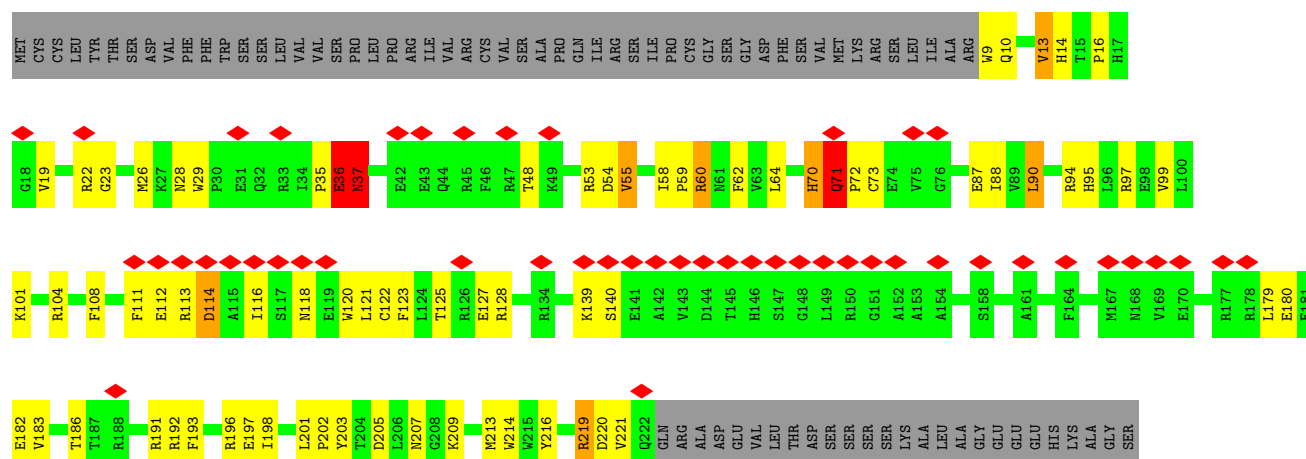




• Molecule 52: ml79



• Molecule 53: ml80



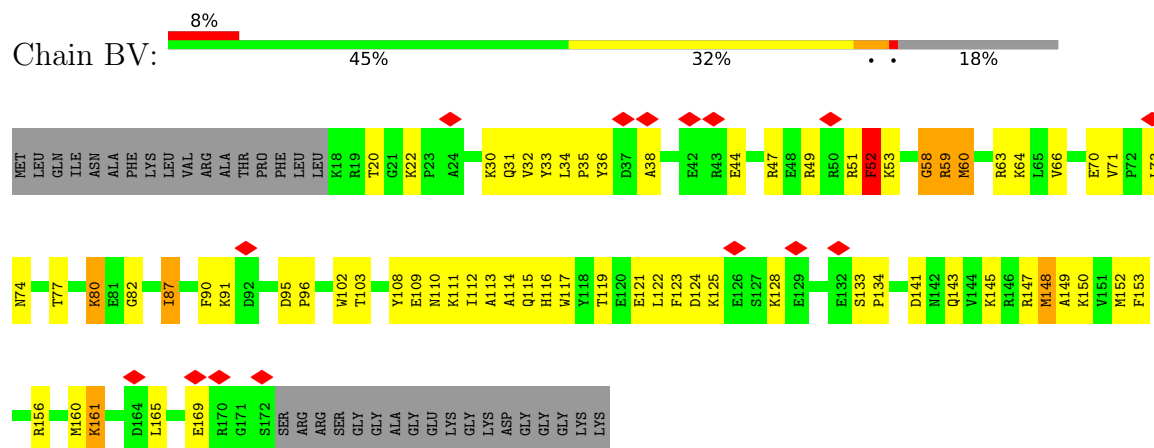
Protein	Residue	Score	Category
Protein 1	E176	0.95	High
	L177	0.92	High
	G178	0.90	High
	I179	0.88	High
	K187	0.85	High
	R188	0.82	High
	V189	0.80	High
	R192	0.78	High
	I193	0.75	High
	K197	0.72	High
Protein 2	E95	0.95	High
	K94	0.92	High
	R95	0.90	High
	Q96	0.88	High
	N105	0.85	High
	T106	0.82	High
	G107	0.80	High
	I108	0.78	High
	L109	0.75	High
	F111	0.72	High
Protein 3	Q118	0.95	High
	G119	0.92	High
	F120	0.90	High
	L121	0.88	High
	N123	0.85	High
	C124	0.82	High
	P125	0.80	High
	L126	0.78	High
	R127	0.75	High
	K128	0.72	High
Protein 4	K134	0.95	High
	L135	0.92	High
	W136	0.90	High
	E137	0.88	High
	Q138	0.85	High
	I139	0.82	High
	K140	0.80	High
	I143	0.78	High
	D144	0.75	High
	R146	0.72	High
Protein 5	K153	0.95	High
	R156	0.92	High
	I159	0.90	High
	Q160	0.88	High
	E161	0.85	High
	L162	0.82	High
	G163	0.80	High
	H164	0.78	High
	N165	0.75	High
	W166	0.72	High
Protein 6	C167	0.95	High
	W168	0.92	High
	L169	0.90	High
	L170	0.88	High
	L171	0.85	High
	P172	0.82	High
	G173	0.80	High
	A174	0.78	High
	D175	0.75	High
	K176	0.72	High
Protein 7	E18	0.95	High
	Y19	0.92	High
	V22	0.90	High
	L23	0.88	High
	R26	0.85	High
	G30	0.82	High
	P31	0.80	High
	Q32	0.78	High
	E38	0.75	High
	E39	0.72	High
Protein 8	R40	0.95	High
	L41	0.92	High
	V42	0.90	High
	K43	0.88	High
	V46	0.85	High
	A47	0.82	High
	R48	0.80	High
	K49	0.78	High
	A56	0.75	High
	E61	0.72	High
Protein 9	R65	0.95	High
	W68	0.92	High
	C69	0.90	High
	Y70	0.88	High
	T74	0.85	High
	D75	0.82	High
	K76	0.80	High
	Y77	0.78	High
	D78	0.75	High
	C79	0.72	High
Protein 10	F80	0.95	High
	I81	0.92	High
	E82	0.90	High
	R83	0.88	High
	L84	0.85	High
	K85	0.82	High
	V86	0.80	High
	L87	0.78	High
	E88	0.75	High
	K89	0.72	High
Protein 11	E90	0.95	High
	L91	0.92	High
	K92	0.90	High
	V93	0.88	High
	L94	0.85	High
	E95	0.82	High
	K96	0.80	High
	V97	0.78	High
	L98	0.75	High
	K99	0.72	High
Protein 12	E100	0.95	High
	L101	0.92	High
	K102	0.90	High
	V103	0.88	High
	L104	0.85	High
	E105	0.82	High
	K106	0.80	High
	V107	0.78	High
	L108	0.75	

Protein	Residue	Score	Rank	Position	Score	Rank	Position
Protein 1	ARG	1.00	1	1	1.00	1	1
	GLU	0.95	2	2	0.95	2	2
	GLU	0.90	3	3	0.90	3	3
	THR	0.85	4	4	0.85	4	4
	LEU	0.80	5	5	0.80	5	5
	LEU	0.75	6	6	0.75	6	6
	LYS	0.70	7	7	0.70	7	7
	LEU	0.65	8	8	0.65	8	8
	ARG	0.60	9	9	0.60	9	9
	GLU	0.55	10	10	0.55	10	10
	ALA	0.50	11	11	0.50	11	11
	ILE	0.45	12	12	0.45	12	12
	ALA	0.40	13	13	0.40	13	13
	LYS	0.35	14	14	0.35	14	14
	ALA	0.30	15	15	0.30	15	15
	ALA	0.25	16	16	0.25	16	16
	ALA	0.20	17	17	0.20	17	17
	MET	0.15	18	18	0.15	18	18
	GLU	0.10	19	19	0.10	19	19
Protein 2	GLN	1.00	1	1	1.00	1	1
	LYS	0.95	2	2	0.95	2	2
	LYS	0.90	3	3	0.90	3	3
	GLN	0.85	4	4	0.85	4	4
	ALA	0.80	5	5	0.80	5	5
	ALA	0.75	6	6	0.75	6	6
	SER	0.70	7	7	0.70	7	7
	GLU	0.65	8	8	0.65	8	8
	ALA	0.60	9	9	0.60	9	9
	TYR	0.55	10	10	0.55	10	10
	LEU	0.50	11	11	0.50	11	11
	GLY	0.45	12	12	0.45	12	12
	GLY	0.40	13	13	0.40	13	13
	SER	0.35	14	14	0.35	14	14
	ASP	0.30	15	15	0.30	15	15
	GLY	0.25	16	16	0.25	16	16
	ALA	0.20	17	17	0.20	17	17
	ARG	0.15	18	18	0.15	18	18
	Protein 3	LYS	1.00	1	1	1.00	1
GLY		0.95	2	2	0.95	2	2
ALA		0.90	3	3	0.90	3	3
ARG		0.85	4	4	0.85	4	4
LYS		0.80	5	5	0.80	5	5
GLY		0.75	6	6	0.75	6	6
GLY		0.70	7	7	0.70	7	7
ALA		0.65	8	8	0.65	8	8
GLU		0.60	9	9	0.60	9	9
GLU		0.55	10	10	0.55	10	10
GLY		0.50	11	11	0.50	11	11
ILE		0.45	12	12	0.45	12	12
LEU		0.40	13	13	0.40	13	13
LYS		0.35	14	14	0.35	14	14
GLU		0.30	15	15	0.30	15	15
GLU		0.25	16	16	0.25	16	16
GLU		0.20	17	17	0.20	17	17
GLU		0.15	18	18	0.15	18	18

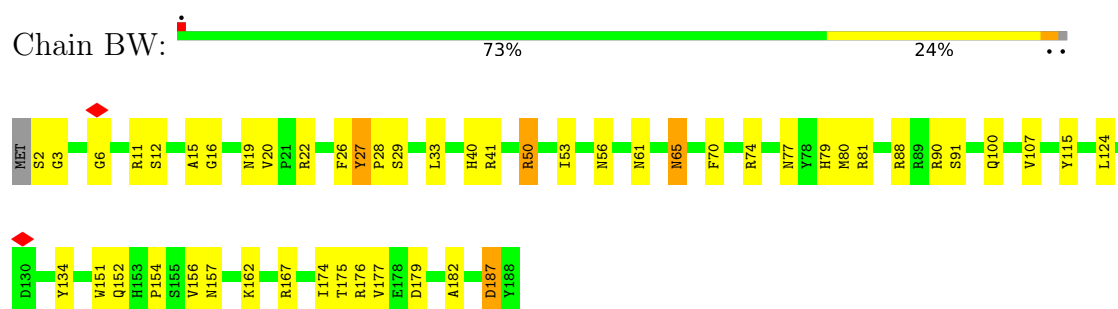
Y105	L108	R112	R113	E117	L131	E140	Y141	D143	E144	S145	K146	G147	P148	L149	N150	H160	I166	L168	P169	D170	L173	I174	R175	G176	G177	ARG	GLU	PHE	PHE	PHE	ILE	GLY	GLU	GLU	ARG	GLY	ASN	GLY	ALA	ALA				
MET	ARG	ARG	CYS	ILE	PRO	ALA	ARG	GLY	G10	F11	T12	M13	K14	Y15	K16	K17	T32	N33	R34	Y35	L36	R39	M42	Q46	R54	L57	R60	R61	N68	L72	G76	A79	R82	R86	E92	R93	Y94	P95	L96	T97	T98	T99	M103	R104

K125	K126	I127	D128	K131	R135	D136	R137	R138	R139	I140	E141	E142	L143	K144	E147	Q156	Q166	R171	Y174	G175	P176	A177	V178	D179	A180	A181	E182	L183	W184	G185																		
ARG	HIS	LEU	TYR	MET	ARG	GLY	THR	ASP	TYR	GLN	GLN	VAL	PRO	PRO	SER	SER	PRO	GLN	GLY	PHE	SER	ASP	VAL	HIS	LYS	LEU	ALA	ASN	HIS	PRO	LYS	PRO	GLN	ARG	E104	S105	R106	V110	L111	T114	P115	R116	I117	V118	H121	A122	M123	F124
MET	ASN	PRO	THR	PHE	SER	LEU	ARG	LYS	THR	LEU	GLN	SER	TYR	VAL	PRO	PRO	LYS	ILE	ARG	HIS	TYR	ASP	ARG	ARG	TRP	TYR	ASN	ASN	GLU	TYR	SER	ARG	PRO	PRO	SER	PHE	TRP	VAL	ASP	PHE								

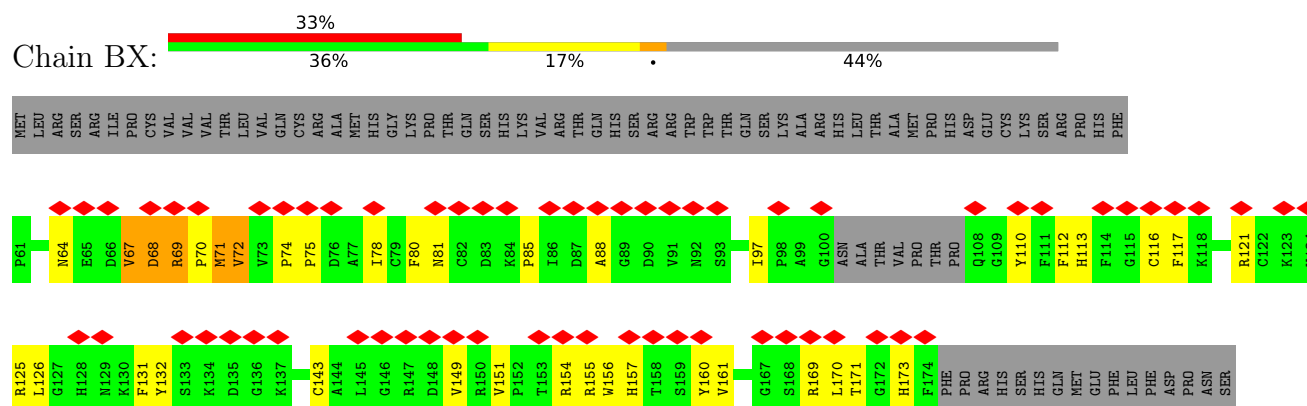
- Molecule 61: ml88



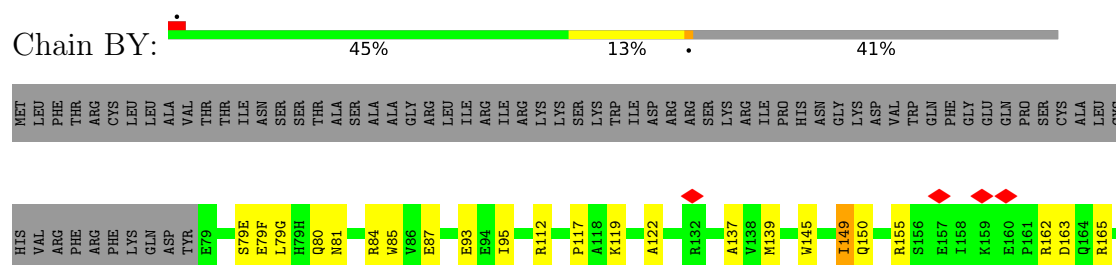
- Molecule 62: ml89



- Molecule 63: ml90



- Molecule 64: ml91



K171
W172

- Molecule 65: Peptidyl-prolyl cis-trans isomerase

Chain BZ:  11% 77% 22%

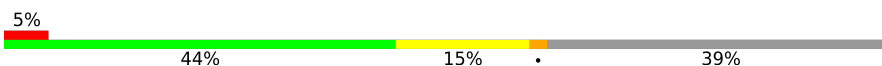


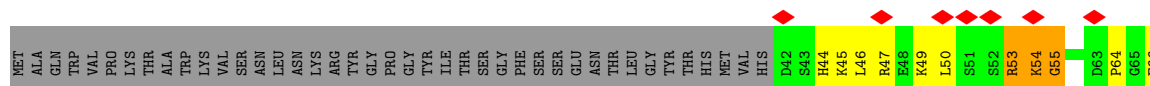
- Molecule 66: ml93

Chain Ba:  63% 27% 9%

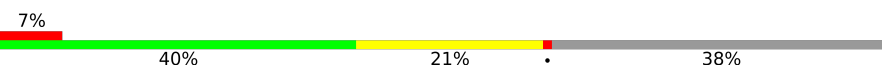


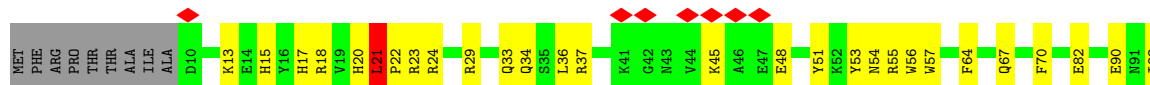
- Molecule 67: ml94

Chain Bb:  5% 44% 15% 39%



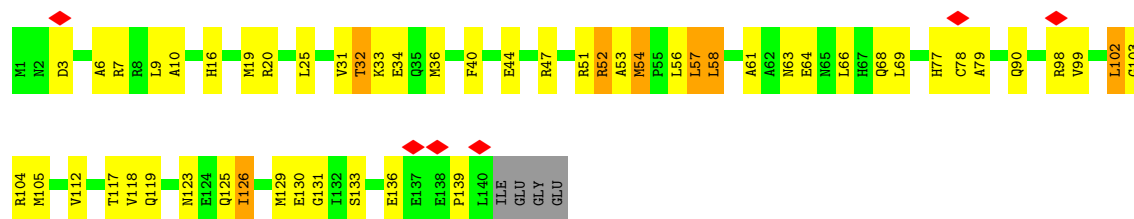
- Molecule 68: ml95

Chain Bc:  7% 40% 21% 38%

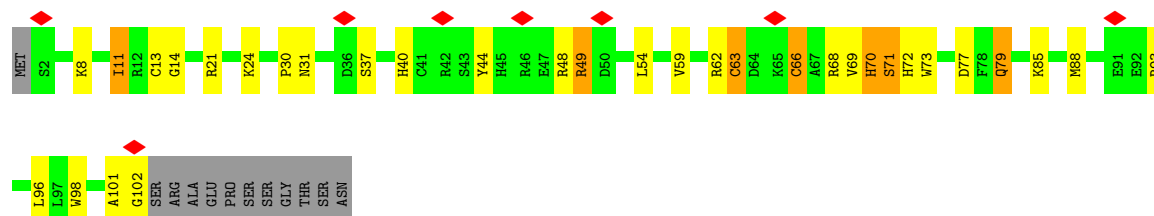


- Molecule 69: ml96

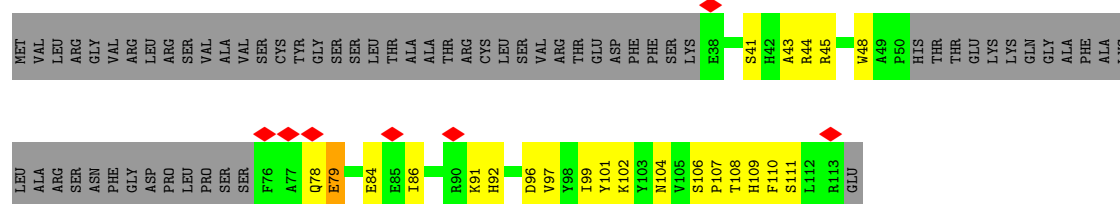
Chain Bd:  60% 32% 5%



• Molecule 70: ml97



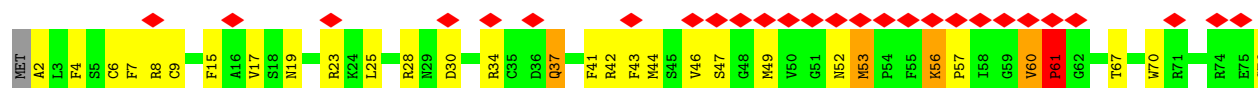
• Molecule 71: ml98

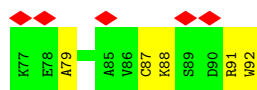


• Molecule 72: ml99



• Molecule 73: ml100

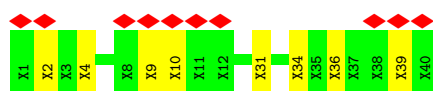
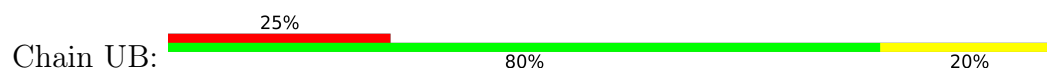




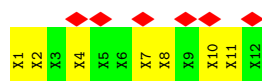
- Molecule 74: UNK



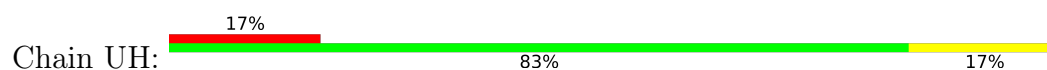
- Molecule 75: UNK



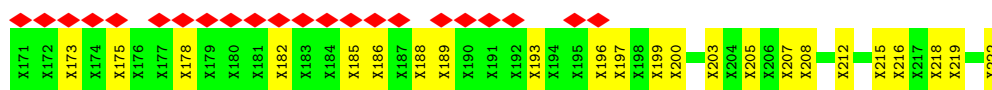
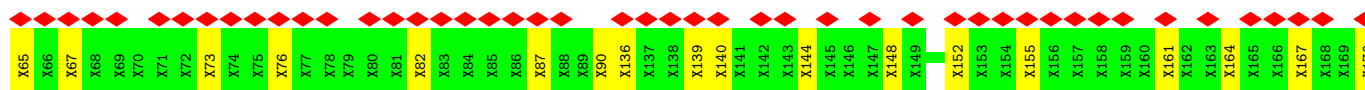
- Molecule 76: UNK



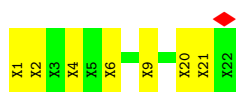
- Molecule 76: UNK



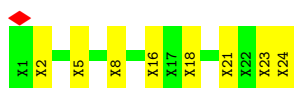
- Molecule 77: UNK



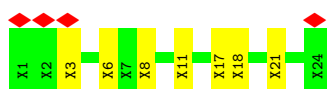
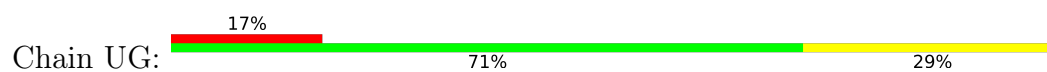
- Molecule 78: UNK



• Molecule 79: UNK



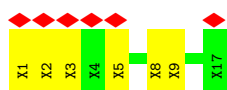
• Molecule 79: UNK



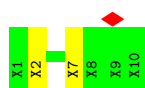
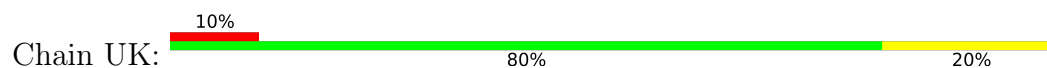
• Molecule 79: UNK



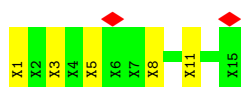
• Molecule 80: UNK



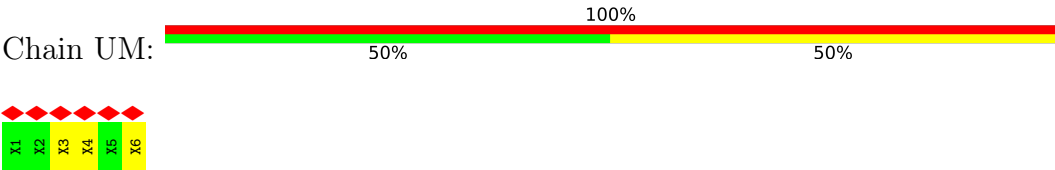
• Molecule 81: UNK



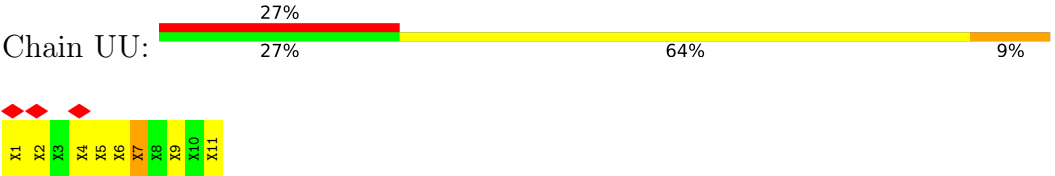
• Molecule 82: UNK



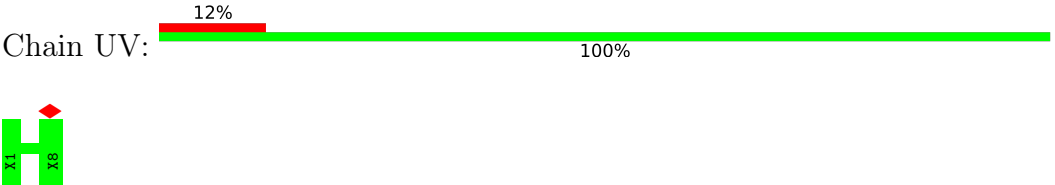
• Molecule 83: UNK



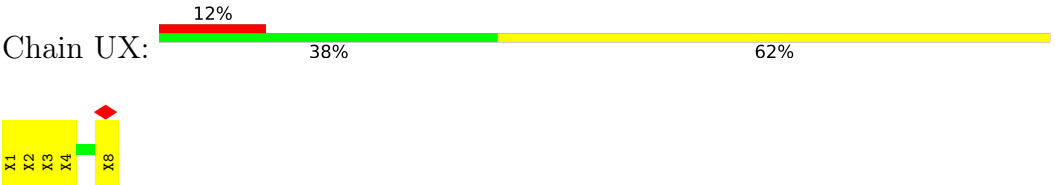
• Molecule 84: UNK



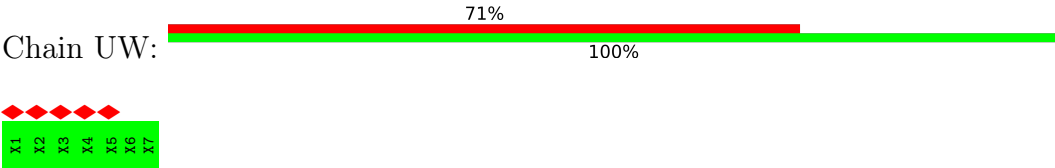
• Molecule 85: UNK



• Molecule 85: UNK



• Molecule 86: UNK



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31619	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.536	Depositor
Minimum map value	-0.224	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality

5.1 Standard geometry

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

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	A0	0.42	0/1297	0.89	4/1750 (0.2%)
2	A1	0.61	3/1828 (0.2%)	1.04	13/2466 (0.5%)
3	A2	0.47	0/3740	0.95	15/5094 (0.3%)
4	A3	0.45	0/1241	0.88	3/1674 (0.2%)
5	A4	0.41	0/1423	0.94	10/1924 (0.5%)
6	A5	0.41	0/498	0.83	0/663
7	A6	0.43	0/578	0.99	4/774 (0.5%)
8	A8	0.50	0/1230	0.96	3/1645 (0.2%)
9	A9	0.47	0/474	0.90	2/639 (0.3%)
10	AE	0.51	0/2469	0.92	6/3364 (0.2%)
11	AF	0.48	0/3706	0.91	10/5029 (0.2%)
12	AI	0.49	0/1850	1.19	14/2515 (0.6%)
13	AJ	0.44	0/986	0.87	2/1339 (0.1%)
14	AK	0.52	2/2745 (0.1%)	1.02	10/3705 (0.3%)
15	AN	0.50	0/1561	0.94	6/2123 (0.3%)
16	AP	0.49	0/2993	0.97	9/4060 (0.2%)
17	AQ	0.43	0/1046	0.95	7/1415 (0.5%)
18	AR	0.47	0/1969	0.93	5/2656 (0.2%)
19	AT	0.42	0/292	0.80	0/390
20	AU	0.45	0/1456	0.92	2/1971 (0.1%)
21	AV	0.48	0/1453	0.99	6/1970 (0.3%)
22	AW	0.46	0/2291	0.86	1/3097 (0.0%)
23	AX	0.49	0/1462	0.97	6/1986 (0.3%)
24	AY	0.44	0/2763	0.92	9/3739 (0.2%)
25	Ab	0.45	0/3651	0.95	13/4988 (0.3%)
26	Ad	0.38	0/2171	0.81	3/2930 (0.1%)
27	Ae	0.49	0/960	1.00	7/1304 (0.5%)
28	Af	0.45	0/1037	0.87	0/1406
29	Ag	0.43	0/2253	0.87	7/3046 (0.2%)
30	Aj	0.44	0/2306	0.94	7/3136 (0.2%)
31	Al	0.50	0/1665	1.01	14/2270 (0.6%)
32	Ao	0.44	0/1523	0.87	0/2070

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ap	0.56	4/2213 (0.2%)	1.04	9/3007 (0.3%)
34	At	0.48	0/1128	0.93	2/1532 (0.1%)
35	Av	0.47	0/1839	0.87	5/2478 (0.2%)
36	AB	0.38	0/279	0.87	0/389
37	AC	0.33	0/139	0.77	0/193
37	AD	0.36	0/139	0.86	0/193
38	AG	0.34	0/134	0.89	0/186
39	AA	0.22	0/13972	0.42	1/21705 (0.0%)
40	BA	0.47	0/5501	0.96	23/7463 (0.3%)
41	BB	0.42	0/3038	0.93	12/4134 (0.3%)
42	BC	0.45	0/3919	0.94	12/5318 (0.2%)
43	BD	0.52	1/2062 (0.0%)	1.14	21/2872 (0.7%)
44	BE	0.46	0/3184	0.93	7/4308 (0.2%)
45	BF	0.43	0/2900	0.89	10/3909 (0.3%)
46	BG	0.43	0/2561	0.92	5/3469 (0.1%)
47	BH	0.52	0/1778	0.96	6/2423 (0.2%)
48	BI	0.42	0/2685	0.93	8/3633 (0.2%)
49	BJ	0.42	0/1366	0.87	1/1846 (0.1%)
50	BK	0.42	0/2038	0.89	5/2753 (0.2%)
51	BL	0.45	0/1924	0.94	5/2596 (0.2%)
52	BM	0.52	1/2082 (0.0%)	0.99	8/2830 (0.3%)
53	BN	0.40	0/1755	0.84	4/2381 (0.2%)
54	BO	0.56	0/1160	0.93	3/1565 (0.2%)
55	BP	0.45	0/1593	1.00	10/2166 (0.5%)
56	BQ	0.53	1/1716 (0.1%)	1.08	8/2324 (0.3%)
57	BR	0.46	0/1693	1.02	8/2284 (0.4%)
58	BS	0.55	0/801	1.01	1/1090 (0.1%)
59	BT	0.46	0/1417	0.88	2/1907 (0.1%)
60	BU	0.44	0/711	0.90	0/955
61	BV	0.65	1/1340 (0.1%)	1.01	6/1802 (0.3%)
62	BW	0.47	0/1604	0.88	5/2167 (0.2%)
63	BX	0.44	0/897	0.98	5/1215 (0.4%)
64	BY	0.44	0/908	0.87	0/1231
65	BZ	0.43	0/1416	0.96	3/1919 (0.2%)
66	Ba	0.49	0/1267	0.98	5/1711 (0.3%)
67	Bb	0.46	0/785	1.09	7/1063 (0.7%)
68	Bc	0.48	0/805	0.92	4/1091 (0.4%)
69	Bd	0.46	0/1133	0.90	0/1528
70	Be	0.46	0/844	0.98	6/1139 (0.5%)
71	Bf	0.43	0/450	0.93	2/609 (0.3%)
72	Bg	0.43	0/671	0.94	2/905 (0.2%)
73	Bh	0.48	0/752	0.99	2/1015 (0.2%)
All	All	0.45	13/135516 (0.0%)	0.90	421/186442 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A1	0	1
3	A2	0	2
4	A3	0	1
8	A8	0	2
11	AF	0	3
18	AR	0	2
21	AV	0	1
22	AW	0	1
23	AX	0	1
24	AY	0	2
25	Ab	0	1
33	Ap	0	1
35	Av	0	1
41	BB	0	1
42	BC	0	2
44	BE	0	1
46	BG	0	1
47	BH	0	1
50	BK	0	2
52	BM	0	2
53	BN	0	3
54	BO	0	3
55	BP	0	2
57	BR	0	3
67	Bb	0	4
71	Bf	0	1
73	Bh	0	3
77	UD	0	1
84	UU	0	1
All	All	0	50

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	Ap	170	HIS	ND1-CE1	-8.14	1.24	1.32
2	A1	223	LYS	N-CA	7.31	1.55	1.46
33	Ap	170	HIS	CG-ND1	7.12	1.46	1.38
43	BD	451	ALA	CA-CB	-6.92	1.44	1.53
52	BM	175	GLU	N-CA	6.46	1.54	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	Ap	170	HIS	CE1-NE2	6.29	1.38	1.32
2	A1	223	LYS	CA-C	6.09	1.60	1.52
61	BV	52	PHE	CD1-CE1	5.71	1.55	1.38
14	AK	198	TYR	CB-CG	5.37	1.63	1.51
2	A1	219	ALA	CA-CB	-5.18	1.44	1.53
56	BQ	99	LEU	CA-C	-5.05	1.48	1.53
14	AK	196	THR	CA-CB	5.04	1.63	1.54
33	Ap	170	HIS	CD2-NE2	-5.03	1.32	1.37

All (421) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	AI	71	TYR	CA-C-N	-20.11	99.33	119.64
12	AI	71	TYR	C-N-CA	-20.11	99.33	119.64
3	A2	212	ALA	CA-C-N	-12.27	107.12	119.76
3	A2	212	ALA	C-N-CA	-12.27	107.12	119.76
56	BQ	179	GLY	N-CA-C	11.07	127.83	110.90
15	AN	164	HIS	CA-C-N	11.03	130.63	119.82
15	AN	164	HIS	C-N-CA	11.03	130.63	119.82
33	Ap	137	SER	CA-C-N	10.71	130.31	119.82
33	Ap	137	SER	C-N-CA	10.71	130.31	119.82
40	BA	174	ARG	CA-C-N	10.16	129.77	119.82
40	BA	174	ARG	C-N-CA	10.16	129.77	119.82
40	BA	208	ALA	CA-C-N	-9.99	111.56	121.65
40	BA	208	ALA	C-N-CA	-9.99	111.56	121.65
10	AE	360	PHE	CA-C-N	-9.38	108.12	119.84
10	AE	360	PHE	C-N-CA	-9.38	108.12	119.84
57	BR	171	LEU	CA-C-N	-9.16	108.39	119.84
57	BR	171	LEU	C-N-CA	-9.16	108.39	119.84
42	BC	121	GLN	CA-C-N	8.99	131.08	119.84
42	BC	121	GLN	C-N-CA	8.99	131.08	119.84
56	BQ	227	LEU	N-CA-C	8.99	124.44	113.38
3	A2	124	TYR	CA-C-N	-8.80	111.32	120.38
3	A2	124	TYR	C-N-CA	-8.80	111.32	120.38
61	BV	52	PHE	N-CA-C	8.72	123.70	112.89
55	BP	209	LYS	CA-C-N	8.47	128.20	119.56
55	BP	209	LYS	C-N-CA	8.47	128.20	119.56
43	BD	356	PRO	N-CA-CB	8.37	111.19	103.08
33	Ap	170	HIS	ND1-CG-CD2	-8.27	97.83	106.10
34	At	72	ILE	N-CA-C	8.21	120.01	112.29
45	BF	395	ASN	CA-C-N	8.19	127.85	119.82
45	BF	395	ASN	C-N-CA	8.19	127.85	119.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	BD	238	PRO	N-CA-CB	8.15	110.12	101.88
29	Ag	167	THR	N-CA-C	8.15	123.40	113.38
30	Aj	159	SER	CA-C-N	8.11	128.74	120.38
30	Aj	159	SER	C-N-CA	8.11	128.74	120.38
27	Ae	71	HIS	CA-C-N	-8.11	109.70	119.84
27	Ae	71	HIS	C-N-CA	-8.11	109.70	119.84
55	BP	159	PRO	N-CA-CB	8.09	110.05	101.88
42	BC	204	TYR	CA-C-N	-8.03	109.81	119.84
42	BC	204	TYR	C-N-CA	-8.03	109.81	119.84
12	AI	97	ARG	N-CA-C	8.00	118.80	109.60
16	AP	39	ASN	N-CA-C	7.98	123.20	113.38
63	BX	69	ARG	NE-CZ-NH2	7.96	126.36	119.20
72	Bg	38	ASN	CA-C-N	7.91	129.73	119.84
72	Bg	38	ASN	C-N-CA	7.91	129.73	119.84
47	BH	230	ASP	CA-C-N	7.86	128.04	119.87
47	BH	230	ASP	C-N-CA	7.86	128.04	119.87
56	BQ	74	CYS	CA-C-N	-7.84	111.36	119.83
56	BQ	74	CYS	C-N-CA	-7.84	111.36	119.83
29	Ag	22	ALA	CA-C-N	7.82	127.46	119.56
29	Ag	22	ALA	C-N-CA	7.82	127.46	119.56
41	BB	304	PRO	N-CA-CB	7.76	110.61	103.08
41	BB	276	PRO	N-CA-CB	7.72	111.36	103.25
44	BE	310	LYS	CA-C-N	7.65	127.37	119.56
44	BE	310	LYS	C-N-CA	7.65	127.37	119.56
46	BG	241	ASP	CA-C-N	7.63	127.34	119.56
46	BG	241	ASP	C-N-CA	7.63	127.34	119.56
2	A1	145	GLY	CA-C-N	7.57	127.20	119.56
2	A1	145	GLY	C-N-CA	7.57	127.20	119.56
41	BB	305	PRO	N-CA-CB	7.54	111.29	103.38
3	A2	293	PHE	CA-C-N	-7.47	111.93	119.93
3	A2	293	PHE	C-N-CA	-7.47	111.93	119.93
2	A1	220	VAL	N-CA-C	-7.46	101.73	111.05
43	BD	143	PRO	N-CA-CB	7.45	111.08	103.25
1	A0	164	ASP	CA-C-N	7.43	127.14	119.56
1	A0	164	ASP	C-N-CA	7.43	127.14	119.56
43	BD	284	PRO	N-CA-CB	7.39	110.31	103.15
52	BM	68	ARG	N-CA-C	-7.35	98.57	109.15
43	BD	435	PRO	N-CA-CB	7.29	110.90	103.25
27	Ae	87	VAL	CA-C-N	-7.27	111.41	118.97
27	Ae	87	VAL	C-N-CA	-7.27	111.41	118.97
56	BQ	178	SER	CA-C-N	-7.25	114.57	121.46
56	BQ	178	SER	C-N-CA	-7.25	114.57	121.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	AR	247	ASP	CA-C-N	7.22	127.22	119.78
18	AR	247	ASP	C-N-CA	7.22	127.22	119.78
61	BV	113	ALA	CA-C-N	-7.21	112.09	122.77
61	BV	113	ALA	C-N-CA	-7.21	112.09	122.77
20	AU	52	GLU	N-CA-C	7.18	122.22	113.38
61	BV	58	GLY	CA-C-N	-7.15	112.65	122.95
61	BV	58	GLY	C-N-CA	-7.15	112.65	122.95
14	AK	192	ILE	CB-CA-C	-7.14	105.64	111.71
24	AY	317	PRO	N-CA-CB	7.13	110.10	103.39
43	BD	409	PRO	N-CA-CB	7.13	110.36	103.51
43	BD	176	PRO	N-CA-CB	7.12	110.72	103.25
41	BB	318	PRO	N-CA-CB	7.12	110.72	103.25
3	A2	434	CYS	CA-C-N	7.11	126.81	119.56
3	A2	434	CYS	C-N-CA	7.11	126.81	119.56
14	AK	167	ARG	CA-C-N	7.07	127.06	119.28
14	AK	167	ARG	C-N-CA	7.07	127.06	119.28
29	Ag	19	SER	N-CA-C	7.07	122.19	113.50
31	Al	146	LEU	CA-C-N	7.01	126.71	119.56
31	Al	146	LEU	C-N-CA	7.01	126.71	119.56
55	BP	144	PHE	CA-C-N	-6.97	111.13	119.84
55	BP	144	PHE	C-N-CA	-6.97	111.13	119.84
44	BE	17	SER	CA-C-N	-6.96	111.15	119.84
44	BE	17	SER	C-N-CA	-6.96	111.15	119.84
29	Ag	20	ASN	N-CA-C	6.95	119.88	111.40
42	BC	522	LEU	N-CA-C	6.95	121.47	112.92
16	AP	38	ASN	N-CA-C	6.94	121.45	112.92
11	AF	295	PHE	N-CA-C	-6.92	98.92	109.85
17	AQ	155	VAL	CA-C-N	6.91	127.08	120.31
17	AQ	155	VAL	C-N-CA	6.91	127.08	120.31
41	BB	265	PRO	N-CA-CB	6.88	110.47	103.25
21	AV	128	ARG	N-CA-C	-6.83	98.81	109.87
56	BQ	67	GLY	N-CA-C	-6.81	105.43	115.72
42	BC	236	THR	CA-C-N	6.81	126.50	119.82
42	BC	236	THR	C-N-CA	6.81	126.50	119.82
29	Ag	31	THR	N-CA-C	6.75	120.73	112.23
43	BD	162	PRO	N-CA-CB	6.74	110.33	103.25
3	A2	470	ASP	N-CA-C	6.74	121.66	113.17
43	BD	153	PRO	N-CA-CB	6.69	110.27	103.25
25	Ab	207	GLY	N-CA-C	6.65	123.86	115.21
33	Ap	86	CYS	CA-C-N	-6.63	111.56	119.84
33	Ap	86	CYS	C-N-CA	-6.63	111.56	119.84
5	A4	155	ILE	CA-C-N	6.62	128.12	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A4	155	ILE	C-N-CA	6.62	128.12	119.84
43	BD	133	PRO	N-CA-CB	6.62	110.20	103.25
12	AI	113	ILE	N-CA-C	6.62	115.10	107.89
33	Ap	170	HIS	CG-CD2-NE2	6.60	113.80	107.20
43	BD	370	PRO	N-CA-CB	6.58	110.82	103.44
56	BQ	129	THR	N-CA-C	6.58	119.62	108.90
21	AV	214	GLY	N-CA-C	-6.56	106.68	115.21
17	AQ	33	ASP	CA-C-N	6.55	126.18	119.56
17	AQ	33	ASP	C-N-CA	6.55	126.18	119.56
43	BD	357	PRO	N-CA-CB	6.55	110.13	103.25
48	BI	48	PHE	CA-C-N	-6.54	111.67	119.84
48	BI	48	PHE	C-N-CA	-6.54	111.67	119.84
44	BE	42	GLY	N-CA-C	6.53	125.67	112.34
40	BA	313	GLY	N-CA-C	-6.53	100.79	110.97
40	BA	774	LYS	CA-C-N	-6.52	112.97	119.56
40	BA	774	LYS	C-N-CA	-6.52	112.97	119.56
31	Al	107	PRO	N-CA-CB	6.52	110.09	103.25
43	BD	319	PRO	N-CA-CB	6.52	110.02	102.33
16	AP	347	LEU	CA-C-N	-6.52	112.83	122.41
16	AP	347	LEU	C-N-CA	-6.52	112.83	122.41
41	BB	294	PRO	N-CA-CB	6.51	110.09	103.25
43	BD	483	PRO	N-CA-CB	6.49	110.23	103.15
23	AX	83	PRO	CA-C-N	6.48	126.17	119.56
23	AX	83	PRO	C-N-CA	6.48	126.17	119.56
66	Ba	59	ASP	CA-C-N	-6.46	115.48	122.59
66	Ba	59	ASP	C-N-CA	-6.46	115.48	122.59
4	A3	146	PRO	CA-C-N	6.46	126.08	119.56
4	A3	146	PRO	C-N-CA	6.46	126.08	119.56
50	BK	268	PRO	N-CA-CB	6.46	110.03	103.25
67	Bb	55	GLY	N-CA-C	6.42	128.38	113.18
67	Bb	72	VAL	CA-C-N	-6.41	111.83	119.84
67	Bb	72	VAL	C-N-CA	-6.41	111.83	119.84
12	AI	22	VAL	N-CA-C	6.40	117.41	111.45
42	BC	302	GLY	N-CA-C	-6.40	98.01	113.18
51	BL	165	LEU	CA-C-N	-6.40	113.04	119.56
51	BL	165	LEU	C-N-CA	-6.40	113.04	119.56
24	AY	27	ASN	N-CA-C	6.37	120.76	112.92
25	Ab	225	ASP	N-CA-C	6.37	121.22	113.38
33	Ap	43	TYR	CA-C-N	6.36	126.05	119.82
33	Ap	43	TYR	C-N-CA	6.36	126.05	119.82
25	Ab	456	ALA	N-CA-C	6.34	116.82	107.88
43	BD	243	PRO	N-CA-CB	6.33	109.90	103.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AP	306	SER	N-CA-C	6.33	118.18	111.28
25	Ab	114	TYR	CA-C-N	6.32	124.28	119.66
25	Ab	114	TYR	C-N-CA	6.32	124.28	119.66
57	BR	76	LYS	CA-C-N	-6.31	112.24	122.34
57	BR	76	LYS	C-N-CA	-6.31	112.24	122.34
52	BM	71	GLY	N-CA-C	6.30	123.12	115.31
43	BD	463	PRO	N-CA-CB	6.29	110.19	103.39
15	AN	94	VAL	N-CA-C	6.29	117.16	109.30
35	Av	234	ILE	N-CA-C	6.28	117.84	109.37
10	AE	360	PHE	N-CA-C	6.27	123.67	109.81
40	BA	780	TYR	N-CA-C	6.27	120.63	112.92
14	AK	66	PRO	N-CA-C	6.27	118.35	110.70
11	AF	205	LYS	CA-C-N	6.27	126.47	119.32
11	AF	205	LYS	C-N-CA	6.27	126.47	119.32
40	BA	687	LEU	CA-C-N	6.27	125.95	119.56
40	BA	687	LEU	C-N-CA	6.27	125.95	119.56
73	Bh	60	VAL	CA-C-N	-6.27	112.00	119.84
73	Bh	60	VAL	C-N-CA	-6.27	112.00	119.84
63	BX	69	ARG	CG-CD-NE	6.23	125.71	112.00
2	A1	40	PRO	CA-C-N	6.21	125.91	119.82
2	A1	40	PRO	C-N-CA	6.21	125.91	119.82
43	BD	477	PRO	N-CA-CB	6.20	110.39	103.44
13	AJ	123	PRO	N-CA-CB	6.20	110.09	103.52
33	Ap	57	LYS	N-CA-C	6.18	120.55	113.19
45	BF	275	SER	CA-C-N	6.17	125.86	119.82
45	BF	275	SER	C-N-CA	6.17	125.86	119.82
45	BF	348	ALA	CA-C-N	-6.16	113.18	119.83
45	BF	348	ALA	C-N-CA	-6.16	113.18	119.83
24	AY	97	TYR	N-CA-C	6.15	119.73	112.72
65	BZ	129	ASN	N-CA-C	6.14	120.91	113.17
8	A8	44	CYS	N-CA-C	6.14	118.62	109.59
14	AK	66	PRO	CA-C-N	-6.13	112.18	119.84
14	AK	66	PRO	C-N-CA	-6.13	112.18	119.84
7	A6	73	ASP	CA-C-N	6.09	125.65	119.19
7	A6	73	ASP	C-N-CA	6.09	125.65	119.19
27	Ae	57	GLY	N-CA-C	6.09	119.03	112.33
41	BB	339	PRO	N-CA-CB	6.07	109.62	103.25
66	Ba	88	VAL	CA-C-N	-6.06	115.24	119.66
66	Ba	88	VAL	C-N-CA	-6.06	115.24	119.66
40	BA	704	THR	CA-C-N	6.05	125.67	119.56
40	BA	704	THR	C-N-CA	6.05	125.67	119.56
40	BA	191	VAL	N-CA-C	6.03	116.69	110.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	BL	171	SER	N-CA-C	6.02	120.75	113.17
42	BC	400	GLU	CA-C-N	6.00	127.34	119.84
42	BC	400	GLU	C-N-CA	6.00	127.34	119.84
46	BG	109	ALA	N-CA-C	6.00	119.26	109.06
27	Ae	118	VAL	N-CA-C	6.00	117.93	112.29
65	BZ	82	LEU	N-CA-C	5.99	116.47	108.38
55	BP	185	ASP	CA-C-N	-5.99	115.00	122.48
55	BP	185	ASP	C-N-CA	-5.99	115.00	122.48
58	BS	32	ARG	NE-CZ-NH2	5.98	124.58	119.20
2	A1	218	ALA	N-CA-C	-5.98	104.34	111.69
23	AX	78	ARG	CA-C-N	-5.98	112.37	119.84
23	AX	78	ARG	C-N-CA	-5.98	112.37	119.84
31	Al	208	VAL	CB-CA-C	-5.97	104.20	112.02
43	BD	277	PRO	N-CA-CB	5.91	110.05	103.44
57	BR	30	GLY	CA-C-N	5.89	125.76	119.28
57	BR	30	GLY	C-N-CA	5.89	125.76	119.28
2	A1	75	VAL	CA-C-N	-5.88	115.13	122.48
2	A1	75	VAL	C-N-CA	-5.88	115.13	122.48
53	BN	37	ASN	N-CA-C	-5.88	105.43	113.30
25	Ab	258	ASP	N-CA-C	5.87	120.14	112.92
11	AF	90	LEU	CA-C-N	5.85	125.53	119.56
11	AF	90	LEU	C-N-CA	5.85	125.53	119.56
45	BF	39	TYR	CA-C-N	5.85	125.52	119.56
45	BF	39	TYR	C-N-CA	5.85	125.52	119.56
2	A1	192	GLU	CB-CA-C	-5.82	109.85	116.54
31	Al	44	ASN	N-CA-C	5.81	121.09	113.30
18	AR	185	ARG	N-CA-C	5.80	120.06	112.92
18	AR	242	HIS	CA-C-N	5.80	125.50	119.82
18	AR	242	HIS	C-N-CA	5.80	125.50	119.82
31	Al	50	MET	CA-C-N	5.80	126.35	120.38
31	Al	50	MET	C-N-CA	5.80	126.35	120.38
31	Al	134	ILE	CA-C-N	5.80	125.42	119.56
31	Al	134	ILE	C-N-CA	5.80	125.42	119.56
52	BM	133	MET	CA-C-N	-5.76	116.40	122.28
52	BM	133	MET	C-N-CA	-5.76	116.40	122.28
41	BB	261	VAL	N-CA-C	-5.76	106.14	113.22
25	Ab	377	LEU	CA-C-N	-5.74	114.27	122.77
25	Ab	377	LEU	C-N-CA	-5.74	114.27	122.77
67	Bb	70	ASN	CA-C-N	5.74	127.02	119.84
67	Bb	70	ASN	C-N-CA	5.74	127.02	119.84
48	BI	234	SER	N-CA-C	5.74	117.30	110.19
47	BH	228	VAL	N-CA-C	5.73	117.01	108.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	AK	301	MET	N-CA-C	5.72	118.05	108.96
15	AN	100	ARG	CA-C-N	-5.71	118.48	122.59
15	AN	100	ARG	C-N-CA	-5.71	118.48	122.59
62	BW	187	ASP	N-CA-C	5.71	118.77	109.06
49	BJ	252	PHE	N-CA-C	5.69	118.42	111.82
68	Bc	53	TYR	CA-C-N	-5.69	114.35	122.77
68	Bc	53	TYR	C-N-CA	-5.69	114.35	122.77
21	AV	227	GLU	CA-C-N	-5.67	114.75	123.14
21	AV	227	GLU	C-N-CA	-5.67	114.75	123.14
52	BM	68	ARG	CA-C-N	-5.66	114.09	122.41
52	BM	68	ARG	C-N-CA	-5.66	114.09	122.41
16	AP	346	HIS	N-CA-C	-5.66	102.52	110.50
11	AF	293	SER	CA-C-N	-5.65	115.00	122.85
11	AF	293	SER	C-N-CA	-5.65	115.00	122.85
61	BV	80	LYS	N-CA-C	5.64	120.16	113.28
5	A4	70	ILE	N-CA-C	-5.63	100.33	108.89
70	Be	31	ASN	CA-C-N	5.63	125.25	119.56
70	Be	31	ASN	C-N-CA	5.63	125.25	119.56
2	A1	189	LEU	CA-C-N	-5.62	114.17	119.85
2	A1	189	LEU	C-N-CA	-5.62	114.17	119.85
26	Ad	179	SER	N-CA-C	5.62	117.08	111.07
8	A8	78	GLY	CA-C-N	5.60	126.15	120.38
8	A8	78	GLY	C-N-CA	5.60	126.15	120.38
12	AI	218	LEU	N-CA-C	5.60	118.54	109.86
52	BM	175	GLU	N-CA-C	-5.60	105.27	111.71
1	A0	104	GLU	CA-C-N	5.60	124.79	118.97
1	A0	104	GLU	C-N-CA	5.60	124.79	118.97
5	A4	77	ARG	CA-C-N	-5.60	114.91	122.86
5	A4	77	ARG	C-N-CA	-5.60	114.91	122.86
65	BZ	88	ILE	N-CA-C	5.59	117.10	111.00
53	BN	71	GLN	CA-C-N	-5.56	114.25	120.14
53	BN	71	GLN	C-N-CA	-5.56	114.25	120.14
42	BC	209	PHE	N-CA-C	5.55	120.16	113.17
31	Al	159	MET	CA-C-N	5.54	125.22	119.56
31	Al	159	MET	C-N-CA	5.54	125.22	119.56
12	AI	30	GLY	N-CA-C	-5.53	108.50	115.08
63	BX	151	VAL	CA-C-N	-5.53	114.88	120.85
63	BX	151	VAL	C-N-CA	-5.53	114.88	120.85
34	At	108	ILE	N-CA-C	5.52	116.18	110.82
12	AI	88	THR	CA-C-N	5.52	125.23	119.82
12	AI	88	THR	C-N-CA	5.52	125.23	119.82
51	BL	108	ILE	CA-C-N	-5.50	114.00	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	BL	108	ILE	C-N-CA	-5.50	114.00	119.56
24	AY	227	ASP	CA-C-N	5.50	124.69	118.97
24	AY	227	ASP	C-N-CA	5.50	124.69	118.97
40	BA	277	ILE	N-CA-C	-5.47	102.52	109.58
70	Be	66	CYS	CA-C-N	-5.47	114.37	122.41
70	Be	66	CYS	C-N-CA	-5.47	114.37	122.41
31	Al	154	HIS	CA-C-N	5.46	125.08	119.56
31	Al	154	HIS	C-N-CA	5.46	125.08	119.56
50	BK	114	HIS	CA-C-N	-5.46	113.01	119.84
50	BK	114	HIS	C-N-CA	-5.46	113.01	119.84
55	BP	144	PHE	N-CA-C	5.46	121.00	108.81
15	AN	100	ARG	N-CA-C	5.46	120.10	113.38
11	AF	172	LYS	CA-C-N	-5.46	115.27	122.85
11	AF	172	LYS	C-N-CA	-5.46	115.27	122.85
57	BR	188	ARG	N-CA-C	5.46	118.12	109.50
35	Av	65	THR	CA-C-N	-5.46	114.70	122.77
35	Av	65	THR	C-N-CA	-5.46	114.70	122.77
9	A9	91	GLN	CA-C-N	5.45	125.16	119.82
9	A9	91	GLN	C-N-CA	5.45	125.16	119.82
40	BA	277	ILE	CA-C-N	-5.45	115.76	122.84
40	BA	277	ILE	C-N-CA	-5.45	115.76	122.84
3	A2	80	ALA	CA-C-N	5.44	125.05	119.56
3	A2	80	ALA	C-N-CA	5.44	125.05	119.56
40	BA	312	TRP	CA-C-N	-5.43	116.09	120.98
40	BA	312	TRP	C-N-CA	-5.43	116.09	120.98
41	BB	190	LEU	N-CA-C	5.42	116.88	109.18
48	BI	340	THR	CA-C-N	-5.40	113.69	122.34
48	BI	340	THR	C-N-CA	-5.40	113.69	122.34
54	BO	133	THR	CB-CA-C	5.40	117.95	109.37
47	BH	262	ARG	N-CA-C	-5.38	105.45	112.23
57	BR	138	GLN	N-CA-C	5.37	120.11	113.50
54	BO	134	PRO	CB-CA-C	-5.36	104.53	113.06
14	AK	191	PHE	CA-C-N	-5.35	117.72	122.97
14	AK	191	PHE	C-N-CA	-5.35	117.72	122.97
39	AA	317	A	O5'-P-OP2	5.35	124.04	108.00
2	A1	78	LEU	CA-C-N	-5.34	115.06	123.13
2	A1	78	LEU	C-N-CA	-5.34	115.06	123.13
17	AQ	148	ILE	CA-C-N	5.34	124.95	119.56
17	AQ	148	ILE	C-N-CA	5.34	124.95	119.56
47	BH	175	GLU	CA-C-N	-5.34	115.43	122.85
47	BH	175	GLU	C-N-CA	-5.34	115.43	122.85
24	AY	217	PRO	CA-C-N	-5.33	115.25	120.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	AY	217	PRO	C-N-CA	-5.33	115.25	120.52
3	A2	346	GLY	N-CA-C	5.32	121.07	114.37
35	Av	232	LYS	N-CA-C	5.31	122.12	110.80
5	A4	100	PRO	CA-C-N	5.30	125.30	120.21
5	A4	100	PRO	C-N-CA	5.30	125.30	120.21
41	BB	114	ALA	CA-C-N	5.30	124.91	119.56
41	BB	114	ALA	C-N-CA	5.30	124.91	119.56
43	BD	140	PRO	N-CA-CB	5.28	109.28	103.26
54	BO	132	GLY	CA-C-O	5.28	126.00	119.25
3	A2	293	PHE	N-CA-C	-5.28	98.15	109.81
14	AK	90	THR	N-CA-C	5.27	119.98	113.50
67	Bb	111	GLY	N-CA-C	-5.26	106.13	112.49
50	BK	287	PRO	CA-C-N	5.25	124.75	119.19
50	BK	287	PRO	C-N-CA	5.25	124.75	119.19
41	BB	415	ASP	N-CA-C	5.24	117.39	111.11
48	BI	293	THR	CA-C-N	-5.24	116.83	122.59
48	BI	293	THR	C-N-CA	-5.24	116.83	122.59
30	Aj	255	ARG	CA-C-N	-5.23	113.30	119.84
30	Aj	255	ARG	C-N-CA	-5.23	113.30	119.84
59	BT	105	VAL	CB-CA-C	-5.23	105.19	111.88
5	A4	60	ASN	N-CA-C	5.22	119.75	113.17
11	AF	430	ASN	N-CA-C	5.22	116.66	111.07
29	Ag	32	HIS	N-CA-C	5.22	119.92	113.50
20	AU	120	PRO	O-C-N	5.22	123.60	121.15
43	BD	450	PRO	N-CA-CB	5.22	108.73	103.25
62	BW	65	ASN	N-CA-C	5.22	119.13	112.87
44	BE	127	SER	CA-C-N	-5.21	116.86	122.59
44	BE	127	SER	C-N-CA	-5.21	116.86	122.59
62	BW	81	ARG	N-CA-C	5.21	116.81	111.03
21	AV	158	ARG	CA-C-N	-5.20	115.07	122.77
21	AV	158	ARG	C-N-CA	-5.20	115.07	122.77
59	BT	76	GLY	N-CA-C	-5.19	107.88	115.72
5	A4	149	LEU	CA-C-N	-5.19	115.46	123.14
5	A4	149	LEU	C-N-CA	-5.19	115.46	123.14
40	BA	674	LEU	N-CA-C	5.19	117.68	111.71
4	A3	58	PRO	N-CA-C	-5.19	101.47	111.69
16	AP	36	ASN	N-CA-C	-5.18	106.46	112.89
24	AY	244	ARG	N-CA-C	5.18	121.84	110.80
40	BA	155	ILE	N-CA-C	5.18	115.31	107.80
26	Ad	126	ARG	CA-C-N	-5.18	114.24	119.83
26	Ad	126	ARG	C-N-CA	-5.18	114.24	119.83
12	AI	211	GLU	N-CA-C	-5.17	106.38	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	Bc	20	HIS	N-CA-C	5.17	119.64	113.23
48	BI	216	MET	N-CA-C	-5.17	99.80	110.80
67	Bb	70	ASN	N-CA-C	5.16	121.20	109.81
12	AI	71	TYR	C-N-CD	5.15	146.13	125.00
43	BD	144	GLY	N-CA-C	-5.15	106.42	113.27
70	Be	70	HIS	CA-C-N	-5.15	115.30	123.12
70	Be	70	HIS	C-N-CA	-5.15	115.30	123.12
24	AY	223	LEU	N-CA-C	-5.13	106.70	113.17
63	BX	69	ARG	N-CA-C	5.13	117.72	109.15
13	AJ	53	TYR	N-CA-C	5.13	117.33	109.07
27	Ae	97	GLY	N-CA-C	-5.12	102.96	112.37
35	Av	167	ARG	NE-CZ-NH1	-5.11	116.39	121.50
40	BA	807	THR	CA-C-N	5.11	124.28	118.97
40	BA	807	THR	C-N-CA	5.11	124.28	118.97
12	AI	97	ARG	CA-C-N	5.10	125.55	120.14
12	AI	97	ARG	C-N-CA	5.10	125.55	120.14
25	Ab	401	PRO	CA-C-N	5.10	124.71	119.56
25	Ab	401	PRO	C-N-CA	5.10	124.71	119.56
68	Bc	21	LEU	CA-CB-CG	5.09	134.13	116.30
17	AQ	79	PHE	N-CA-C	5.08	116.92	109.24
52	BM	134	ALA	N-CA-C	5.08	118.61	110.73
66	Ba	41	ASP	N-CA-C	5.08	115.44	109.60
10	AE	311	VAL	N-CA-C	5.07	119.84	108.88
55	BP	190	THR	CA-C-N	5.07	124.98	119.76
55	BP	190	THR	C-N-CA	5.07	124.98	119.76
25	Ab	292	VAL	N-CA-C	5.06	115.58	108.89
42	BC	207	GLN	N-CA-C	5.06	119.10	113.02
53	BN	116	ILE	N-CA-C	-5.06	98.81	109.34
62	BW	27	TYR	CA-C-N	5.06	124.72	119.56
62	BW	27	TYR	C-N-CA	5.06	124.72	119.56
40	BA	513	GLU	N-CA-C	5.06	119.54	113.17
10	AE	357	LEU	CA-C-N	5.05	125.26	120.31
10	AE	357	LEU	C-N-CA	5.05	125.26	120.31
30	Aj	106	ASP	CA-C-N	5.05	124.54	119.19
30	Aj	106	ASP	C-N-CA	5.05	124.54	119.19
16	AP	44	THR	CA-C-N	-5.05	115.71	122.42
16	AP	44	THR	C-N-CA	-5.05	115.71	122.42
25	Ab	115	PRO	O-C-N	5.05	123.63	121.31
31	Al	195	SER	N-CA-C	5.05	115.97	108.60
45	BF	358	SER	CA-C-N	5.05	124.71	119.56
45	BF	358	SER	C-N-CA	5.05	124.71	119.56
46	BG	124	ASP	N-CA-C	5.04	117.51	111.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	Aj	31	VAL	N-CA-C	5.04	115.67	107.71
3	A2	130	PRO	CA-C-N	5.04	123.34	119.66
3	A2	130	PRO	C-N-CA	5.04	123.34	119.66
25	Ab	200	PHE	N-CA-C	5.03	116.77	111.28
46	BG	240	PHE	N-CA-C	5.03	119.11	112.92
22	AW	72	THR	N-CA-C	5.01	121.48	110.80
23	AX	131	PHE	CA-C-N	-5.01	114.50	119.56
23	AX	131	PHE	C-N-CA	-5.01	114.50	119.56
12	AI	27	PRO	O-C-N	5.01	123.50	121.15
71	Bf	79	GLU	CA-C-N	5.01	124.61	119.05
71	Bf	79	GLU	C-N-CA	5.01	124.61	119.05
7	A6	44	ALA	CA-C-N	-5.00	114.34	122.34
7	A6	44	ALA	C-N-CA	-5.00	114.34	122.34

There are no chirality outliers.

All (50) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A1	78	LEU	Peptide
3	A2	133	GLY	Peptide
3	A2	346	GLY	Peptide
4	A3	57	GLY	Peptide
8	A8	90	GLY	Peptide
8	A8	91	LYS	Peptide
11	AF	314	TYR	Peptide
11	AF	317	THR	Peptide
11	AF	318	ALA	Peptide
18	AR	166	LYS	Peptide
18	AR	235	TRP	Peptide
21	AV	128	ARG	Peptide
22	AW	71	ILE	Peptide
23	AX	152	LEU	Peptide
24	AY	107	SER	Peptide
24	AY	243	ASP	Peptide
25	Ab	288	GLY	Peptide
33	Ap	94	GLY	Peptide
35	Av	231	ILE	Peptide
41	BB	259	GLU	Peptide
42	BC	301	MET	Peptide
42	BC	400	GLU	Peptide
44	BE	42	GLY	Peptide
46	BG	248	ALA	Peptide

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Mol	Chain	Res	Type	Group
47	BH	229	ALA	Peptide
50	BK	311	GLU	Peptide
50	BK	324	LYS	Peptide
52	BM	134	ALA	Peptide
52	BM	76	TRP	Peptide
53	BN	114	ASP	Peptide
53	BN	36	GLU	Peptide
53	BN	37	ASN	Peptide
54	BO	221	GLY	Peptide
54	BO	232	GLU	Peptide
54	BO	75	PHE	Peptide
55	BP	144	PHE	Peptide
55	BP	59	GLN	Peptide
57	BR	119	GLY	Peptide
57	BR	173	GLY	Peptide
57	BR	174	ALA	Peptide
67	Bb	54	LYS	Peptide
67	Bb	55	GLY	Peptide
67	Bb	70	ASN	Peptide
67	Bb	73	PRO	Peptide
71	Bf	92	HIS	Peptide
73	Bh	60	VAL	Peptide
73	Bh	61	PRO	Peptide
73	Bh	88	LYS	Peptide
77	UD	47	UNK	Peptide
84	UU	7	UNK	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A0	1269	0	1285	38	0
2	A1	1788	0	1813	81	0
3	A2	3638	0	3601	130	0
4	A3	1215	0	1272	37	0
5	A4	1387	0	1406	72	0
6	A5	483	0	493	32	0
7	A6	568	0	590	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A8	1203	0	1225	78	0
9	A9	459	0	430	12	0
10	AE	2390	0	2279	100	0
11	AF	3597	0	3509	137	0
12	AI	1790	0	1765	80	0
13	AJ	965	0	906	50	0
14	AK	2676	0	2685	133	0
15	AN	1508	0	1487	76	0
16	AP	2904	0	2847	123	0
17	AQ	1020	0	1011	24	0
18	AR	1912	0	1858	82	0
19	AT	287	0	291	15	0
20	AU	1423	0	1447	49	0
21	AV	1424	0	1456	49	0
22	AW	2235	0	2270	77	0
23	AX	1416	0	1396	54	0
24	AY	2712	0	2605	100	0
25	Ab	3545	0	3343	95	0
26	Ad	2122	0	2031	96	0
27	Ae	927	0	911	41	0
28	Af	1013	0	999	46	0
29	Ag	2193	0	2127	92	0
30	Aj	2246	0	2149	100	0
31	Al	1618	0	1615	44	0
32	Ao	1475	0	1437	66	0
33	Ap	2143	0	2124	90	0
34	At	1100	0	1085	45	0
35	Av	1792	0	1782	61	0
36	AB	280	0	282	3	0
37	AC	140	0	142	2	0
37	AD	140	0	142	0	0
38	AG	135	0	137	0	0
39	AA	12491	0	6245	367	0
40	BA	5384	0	5427	154	0
41	BB	2966	0	2684	116	0
42	BC	3821	0	3778	117	0
43	BD	2063	0	967	7	0
44	BE	3105	0	3030	93	0
45	BF	2838	0	2819	91	0
46	BG	2503	0	2476	101	0
47	BH	1729	0	1691	70	0
48	BI	2609	0	2543	87	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	BJ	1339	0	1307	46	0
50	BK	1996	0	1889	68	0
51	BL	1887	0	1831	66	0
52	BM	2015	0	1937	75	0
53	BN	1714	0	1593	78	0
54	BO	1146	0	1183	48	0
55	BP	1550	0	1519	47	0
56	BQ	1675	0	1619	53	0
57	BR	1650	0	1632	63	0
58	BS	784	0	773	38	0
59	BT	1389	0	1357	47	0
60	BU	694	0	697	39	0
61	BV	1307	0	1295	81	0
62	BW	1557	0	1517	45	0
63	BX	867	0	812	27	0
64	BY	877	0	826	25	0
65	BZ	1390	0	1343	35	0
66	Ba	1224	0	1169	39	0
67	Bb	770	0	773	17	0
68	Bc	781	0	752	26	0
69	Bd	1113	0	1094	66	0
70	Be	822	0	794	33	0
71	Bf	434	0	402	26	0
72	Bg	656	0	649	31	0
73	Bh	730	0	708	44	0
74	UA	276	0	280	20	0
75	UB	240	0	243	5	0
76	UC	72	0	74	13	0
76	UH	72	0	75	2	0
77	UD	1062	0	1074	63	0
78	UE	132	0	134	13	0
79	UF	144	0	146	9	0
79	UG	144	0	146	6	0
79	UN	144	0	147	14	0
80	UI	102	0	105	4	0
81	UK	60	0	62	3	0
82	UL	90	0	94	4	0
83	UM	36	0	38	4	0
84	UU	66	0	69	12	0
85	UV	48	0	50	0	0
85	UX	48	0	50	7	0
86	UW	42	0	44	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	A5	1	0	0	0	0
87	A9	1	0	0	0	0
87	BX	2	0	0	0	0
87	Be	1	0	0	0	0
87	Bh	1	0	0	0	0
88	Av	44	0	26	0	0
89	AA	7	0	0	0	0
All	All	133849	0	124221	3721	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 14.

All (3721) 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)
2:A1:219:ALA:O	2:A1:223:LYS:NZ	1.58	1.32
39:AA:86:U:H5"	50:BK:340:ARG:HH12	1.01	1.17
3:A2:172:ARG:NH1	66:Ba:73:GLU:OE2	1.77	1.17
3:A2:387:TRP:O	23:AX:108:LYS:NZ	1.78	1.16
33:Ap:39:LYS:NZ	39:AA:1111:A:N7	1.95	1.13
2:A1:219:ALA:C	2:A1:223:LYS:HZ1	1.57	1.11
46:BG:74:ARG:HG2	46:BG:74:ARG:HH11	1.18	1.08
1:A0:71:ARG:HH11	31:Al:45:ILE:HD11	1.14	1.07
61:BV:59:ARG:NH1	61:BV:116:HIS:O	1.87	1.07
39:AA:86:U:H5"	50:BK:340:ARG:NH1	1.71	1.04
13:AJ:74:ARG:HH12	14:AK:239:ILE:HD11	1.19	1.04
40:BA:341:CYS:O	40:BA:377:ARG:NH1	1.92	1.02
18:AR:211:ARG:NH1	44:BE:440:ILE:O	1.92	1.01
41:BB:212:HIS:HB3	60:BU:111:LEU:HD22	1.41	1.00
39:AA:404:U:OP1	61:BV:22:LYS:NZ	1.96	0.97
24:AY:214:MET:SD	50:BK:314:LEU:HD21	2.05	0.96
1:A0:160:GLU:O	1:A0:163:LYS:NZ	1.99	0.95
14:AK:185:ARG:HH22	61:BV:115:GLN:HA	1.29	0.95
63:BX:169:ARG:HH12	77:UD:24:UNK:HA	1.31	0.94
54:BO:138:ARG:HH22	58:BS:26:ARG:HH21	1.16	0.93
21:AV:91:VAL:HG13	21:AV:175:ILE:HD13	1.50	0.93
3:A2:95:LYS:NZ	50:BK:361:GLU:OE2	1.99	0.93
6:A5:64:LYS:NZ	6:A5:80:PRO:O	2.02	0.93
32:Ao:61:ARG:NH1	32:Ao:65:MET:SD	2.42	0.93
70:Be:49:ARG:HG2	70:Be:49:ARG:HH11	1.34	0.92
46:BG:183:ARG:HH12	46:BG:187:ARG:HB3	1.34	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:BN:186:THR:HG21	77:UD:215:UNK:HG2	1.50	0.92
8:A8:83:ARG:HH22	8:A8:139:ARG:HH12	1.16	0.91
51:BL:264:LEU:HD21	51:BL:287:ARG:HH12	1.33	0.91
46:BG:238:TYR:O	46:BG:257:ARG:NH1	2.04	0.91
26:Ad:57:ARG:HH12	26:Ad:287:ARG:HD3	1.35	0.91
15:AN:39:ARG:HH11	15:AN:39:ARG:HG3	1.36	0.91
4:A3:168:LYS:NZ	34:At:151:ARG:O	2.04	0.90
3:A2:123:ARG:HH12	65:BZ:76:ARG:NH2	1.69	0.90
41:BB:87:LEU:HD11	41:BB:109:GLU:HG2	1.51	0.90
30:Aj:144:ASP:HB2	46:BG:70:ARG:NH1	1.87	0.89
2:A1:85:ARG:HH12	39:AA:891:G:H5'	1.35	0.89
39:AA:380:G:H1	84:UU:4:UNK:HB2	1.33	0.89
51:BL:172:ILE:O	51:BL:256:ARG:NH1	2.06	0.89
30:Aj:24:ARG:HH12	69:Bd:139:PRO:HG3	1.37	0.89
26:Ad:269:ARG:HH12	55:BP:64:PRO:HG3	1.37	0.88
44:BE:444:ARG:HH11	44:BE:448:ARG:HH21	1.21	0.88
10:AE:176:ARG:NH1	10:AE:179:GLU:OE1	2.05	0.87
1:A0:71:ARG:NH1	31:Al:45:ILE:HD11	1.89	0.87
5:A4:50:ARG:HH22	42:BC:212:VAL:HG11	1.40	0.87
57:BR:61:GLU:OE1	57:BR:65:ARG:NH1	2.08	0.87
10:AE:110:LYS:HG2	79:UN:5:UNK:HG2	1.57	0.86
39:AA:567:G:N3	73:Bh:23:ARG:NH1	2.23	0.86
2:A1:142:LYS:HZ1	2:A1:143:ARG:NH1	1.73	0.85
43:BD:205:GLU:H	43:BD:451:ALA:HB1	1.41	0.85
24:AY:254:LYS:NZ	24:AY:255:ARG:HH12	1.75	0.85
30:Aj:63:PRO:HD3	46:BG:144:TRP:HE1	1.39	0.85
28:Af:58:ARG:NH1	39:AA:381:U:OP1	2.09	0.85
8:A8:173:ARG:NH1	11:AF:442:GLY:O	2.10	0.85
39:AA:86:U:C5'	50:BK:340:ARG:HH12	1.89	0.85
39:AA:876:G:H2'	39:AA:877:A:H8	1.42	0.85
22:AW:100:GLU:OE1	51:BL:238:GLN:NE2	2.10	0.85
23:AX:61:ILE:HG13	35:Av:33:ILE:HA	1.57	0.85
8:A8:83:ARG:NH2	8:A8:139:ARG:HH12	1.72	0.85
30:Aj:104:ARG:NH1	30:Aj:113:ASN:OD1	2.10	0.84
46:BG:74:ARG:HH11	46:BG:74:ARG:CG	1.89	0.84
46:BG:130:CYS:HA	46:BG:160:MET:HE1	1.60	0.84
2:A1:163:ARG:NH1	2:A1:166:GLU:OE2	2.10	0.84
35:Av:167:ARG:NH1	42:BC:484:TYR:OH	2.10	0.84
12:AI:48:ARG:HH11	12:AI:48:ARG:HG2	1.40	0.84
14:AK:185:ARG:NH2	14:AK:195:ASP:OD2	2.11	0.84
41:BB:111:ILE:HD11	49:BJ:194:SER:HB3	1.57	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Ao:230:ARG:HH12	32:Ao:242:ASP:HA	1.43	0.83
15:AN:144:ARG:NH1	39:AA:122:U:OP2	2.12	0.83
48:BI:150:VAL:HG23	48:BI:166:LEU:HD21	1.58	0.83
12:AI:71:TYR:OH	35:Av:105:LEU:O	1.95	0.83
45:BF:60:LEU:HD22	45:BF:63:ARG:NH1	1.94	0.83
29:Ag:55:MET:O	29:Ag:71:THR:OG1	1.96	0.82
25:Ab:329:SER:O	25:Ab:372:ARG:NH2	2.12	0.82
26:Ad:287:ARG:NH2	42:BC:191:ASP:OD1	2.12	0.82
53:BN:186:THR:CG2	77:UD:215:UNK:HG2	2.08	0.82
9:A9:72:CYS:HB2	9:A9:75:CYS:SG	2.20	0.82
15:AN:104:THR:OG1	15:AN:115:ARG:NH1	2.13	0.82
44:BE:444:ARG:NH1	44:BE:448:ARG:HH21	1.78	0.82
49:BJ:222:PRO:O	49:BJ:227:ARG:NH1	2.12	0.82
64:BY:84:ARG:HH21	76:UC:8:UNK:HA	1.45	0.82
11:AF:224:ARG:NH1	39:AA:156:U:O4	2.11	0.82
14:AK:167:ARG:NH1	14:AK:235:GLU:OE1	2.12	0.81
27:Ae:127:CYS:SG	41:BB:146:TYR:OH	2.37	0.81
42:BC:108:GLN:HE22	42:BC:242:LEU:H	1.25	0.81
33:Ap:294:LYS:NZ	39:AA:429:A:N3	2.28	0.81
47:BH:66:GLU:HG3	76:UC:11:UNK:HG1	1.62	0.81
26:Ad:151:GLN:HE22	69:Bd:123:ASN:HB3	1.44	0.81
40:BA:296:ARG:HH21	40:BA:309:THR:HG21	1.44	0.81
15:AN:170:ASN:OD1	21:AV:223:LYS:NZ	2.14	0.80
17:AQ:37:ILE:O	57:BR:192:ARG:NH1	2.15	0.80
2:A1:142:LYS:NZ	2:A1:143:ARG:NH1	2.29	0.80
3:A2:222:GLU:O	11:AF:278:ARG:NH1	2.13	0.80
24:AY:194:ARG:HG2	24:AY:201:MET:HG2	1.62	0.80
39:AA:1166:A:H4'	39:AA:1167:A:H5'	1.64	0.80
11:AF:362:GLU:HA	62:BW:41:ARG:HH12	1.47	0.80
18:AR:264:ALA:O	50:BK:131:ARG:NH2	2.15	0.80
42:BC:84:GLU:OE1	42:BC:355:LYS:NZ	2.14	0.80
29:Ag:89:THR:HG22	29:Ag:91:ASN:H	1.47	0.80
11:AF:103:VAL:HG11	11:AF:371:LEU:HD11	1.64	0.80
3:A2:15:GLU:OE1	3:A2:56:LYS:NZ	2.15	0.79
10:AE:50:ARG:NH2	48:BI:40:GLN:O	2.15	0.79
16:AP:113:ILE:HG22	16:AP:114:LYS:HG3	1.62	0.79
18:AR:153:ARG:NH2	39:AA:515:U:O4	2.16	0.79
41:BB:87:LEU:HA	41:BB:90:LYS:HZ3	1.47	0.79
11:AF:457:MET:HG2	16:AP:275:MET:HE2	1.64	0.79
16:AP:257:MET:HG2	62:BW:11:ARG:HH12	1.46	0.79
16:AP:282:ARG:NH2	42:BC:461:ASP:OD2	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AU:50:ARG:HH11	20:AU:50:ARG:HG3	1.48	0.79
25:Ab:99:ASP:OD2	42:BC:239:ARG:NH1	2.15	0.79
20:AU:131:GLU:HG2	34:At:91:ARG:HH12	1.47	0.79
40:BA:799:ASP:OD1	40:BA:801:ARG:NH1	2.16	0.79
48:BI:80:ASP:OD1	48:BI:254:ARG:NH1	2.15	0.79
6:A5:49:LEU:HB2	24:AY:3:ALA:HB3	1.63	0.78
26:Ad:119:GLN:H	30:Aj:22:GLN:HE21	1.31	0.78
41:BB:422:MET:HB3	41:BB:427:PHE:HE1	1.47	0.78
73:Bh:46:VAL:HG23	77:UD:11:UNK:HG2	1.64	0.78
3:A2:123:ARG:HH12	65:BZ:76:ARG:CZ	1.96	0.78
14:AK:167:ARG:HH12	14:AK:235:GLU:CD	1.91	0.78
47:BH:152:ALA:HA	47:BH:156:LEU:HD22	1.66	0.77
44:BE:88:ARG:NH1	44:BE:89:CYS:SG	2.57	0.77
22:AW:165:LYS:HZ1	44:BE:396:GLY:HA3	1.48	0.77
26:Ad:227:ARG:NH1	69:Bd:34:GLU:OE1	2.17	0.77
56:BQ:22:TYR:HB2	56:BQ:163:GLN:HE21	1.49	0.77
30:Aj:63:PRO:HD3	46:BG:144:TRP:NE1	2.00	0.77
46:BG:244:ARG:HH11	46:BG:257:ARG:NH2	1.81	0.77
17:AQ:131:ARG:NH1	29:Ag:247:GLU:OE1	2.18	0.77
27:Ae:127:CYS:HG	41:BB:146:TYR:HH	1.31	0.77
31:Al:24:ASP:OD2	31:Al:31:LYS:NZ	2.17	0.77
11:AF:38:ARG:CZ	29:Ag:50:ARG:HH12	1.97	0.77
33:Ap:124:PRO:HD2	79:UN:7:UNK:HB1	1.65	0.77
44:BE:69:GLU:HG3	50:BK:380:TYR:HE2	1.50	0.77
44:BE:290:ALA:HB2	44:BE:385:LEU:HD11	1.67	0.77
71:Bf:44:ARG:HD3	78:UE:6:UNK:HG3	1.66	0.76
45:BF:363:GLN:HB2	62:BW:174:ILE:HG23	1.68	0.76
30:Aj:62:HIS:HA	46:BG:144:TRP:HE1	1.50	0.76
46:BG:172:THR:HG21	46:BG:324:TRP:HE1	1.50	0.76
53:BN:97:ARG:HH11	73:Bh:87:CYS:HB3	1.51	0.76
53:BN:179:LEU:HD11	77:UD:212:UNK:HG1	1.67	0.76
53:BN:193:PHE:HE2	77:UD:222:UNK:HG1	1.50	0.76
2:A1:87:ARG:NH1	2:A1:96:TYR:OH	2.18	0.76
23:AX:156:THR:HG22	23:AX:158:ARG:H	1.51	0.76
70:Be:14:GLY:HA3	70:Be:72:HIS:HD2	1.51	0.76
32:Ao:141:ASN:HB2	57:BR:140:LYS:NZ	2.01	0.76
8:A8:166:ALA:HB3	39:AA:72:A:H61	1.49	0.75
23:AX:209:ASP:OD1	50:BK:371:ARG:NH1	2.18	0.75
40:BA:296:ARG:NH2	40:BA:309:THR:HG21	2.01	0.75
40:BA:532:MET:SD	40:BA:576:ASN:ND2	2.59	0.75
40:BA:130:PRO:HB3	54:BO:145:LEU:HD21	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BC:263:PRO:HG2	55:BP:128:ARG:NH1	2.01	0.75
45:BF:60:LEU:HD13	45:BF:63:ARG:HD2	1.67	0.75
58:BS:32:ARG:HH21	58:BS:32:ARG:HG3	1.51	0.75
66:Ba:40:TRP:HE1	66:Ba:99:ARG:NH1	1.84	0.75
27:Ae:75:ARG:HH12	27:Ae:135:THR:HG22	1.50	0.75
26:Ad:116:SER:O	69:Bd:20:ARG:NH2	2.20	0.75
57:BR:70:TYR:HB3	57:BR:77:TYR:HD1	1.51	0.75
12:AI:55:MET:HG3	59:BT:82:ARG:HH12	1.49	0.75
39:AA:440:U:O2	61:BV:156:ARG:NH1	2.20	0.74
51:BL:141:ASN:HD22	51:BL:141:ASN:H	1.34	0.74
14:AK:54:ARG:NH1	39:AA:402:A:OP2	2.20	0.74
23:AX:89:PHE:HE2	24:AY:82:ARG:HH21	1.35	0.74
44:BE:331:ASP:O	44:BE:379:ARG:NH1	2.20	0.74
53:BN:14:HIS:HB3	73:Bh:92:TRP:CD1	2.22	0.74
14:AK:134:ARG:NH1	39:AA:406:U:OP2	2.20	0.74
32:Ao:226:ARG:HG2	32:Ao:226:ARG:HH11	1.52	0.74
39:AA:411:A:N7	39:AA:433:G:O2'	2.19	0.74
40:BA:134:MET:HB2	54:BO:145:LEU:HD13	1.69	0.74
18:AR:173:ASN:O	18:AR:201:ARG:NH1	2.21	0.74
24:AY:214:MET:HE1	50:BK:317:THR:OG1	1.86	0.74
44:BE:66:ARG:HD2	50:BK:381:SER:HA	1.70	0.74
51:BL:281:SER:N	51:BL:284:ARG:HH12	1.86	0.74
26:Ad:287:ARG:HG3	42:BC:190:TRP:HE1	1.53	0.74
15:AN:35:GLN:O	40:BA:710:LYS:NZ	2.21	0.74
33:Ap:123:LYS:HZ2	83:UM:6:UNK:HA	1.52	0.74
61:BV:64:LYS:NZ	61:BV:66:VAL:HG12	2.02	0.74
7:A6:94:LYS:HB2	7:A6:94:LYS:HZ3	1.50	0.74
24:AY:23:ASN:ND2	39:AA:19:A:N7	2.36	0.74
30:Aj:163:ARG:HD3	30:Aj:168:ARG:HH12	1.52	0.74
27:Ae:96:GLN:NE2	39:AA:526:G:O6	2.21	0.74
29:Ag:72:LYS:NZ	39:AA:491:A:OP2	2.18	0.74
6:A5:64:LYS:HZ1	6:A5:69:TRP:CD1	2.06	0.73
3:A2:18:ASP:HB3	3:A2:21:PHE:HB3	1.69	0.73
15:AN:185:LYS:NZ	39:AA:384:U:OP2	2.19	0.73
19:AT:28:ARG:HH11	19:AT:28:ARG:HG3	1.52	0.73
29:Ag:3:ARG:NH1	29:Ag:92:ASP:OD2	2.20	0.73
24:AY:35:LYS:HD3	24:AY:37:GLY:H	1.53	0.73
25:Ab:175:ARG:HH12	42:BC:91:ALA:HB3	1.54	0.73
30:Aj:62:HIS:HA	46:BG:144:TRP:NE1	2.04	0.73
11:AF:394:VAL:HG22	11:AF:395:PRO:HD2	1.71	0.73
18:AR:105:LYS:NZ	18:AR:139:MET:O	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AW:275:ALA:HB2	44:BE:243:THR:HG21	1.71	0.73
47:BH:71:LYS:NZ	76:UC:4:UNK:HG1	2.02	0.73
51:BL:281:SER:OG	51:BL:284:ARG:NH1	2.20	0.73
20:AU:103:GLU:OE2	21:AV:90:LYS:NZ	2.22	0.72
29:Ag:170:GLN:HE22	29:Ag:227:PRO:HG2	1.53	0.72
14:AK:103:ARG:NH1	14:AK:117:GLU:OE1	2.22	0.72
34:At:38:GLU:OE2	57:BR:127:ARG:NH2	2.22	0.72
45:BF:47:LYS:NZ	45:BF:205:SER:OG	2.22	0.72
66:Ba:89:PRO:HG2	66:Ba:92:TYR:HD2	1.53	0.72
18:AR:66:ARG:NH2	39:AA:798:U:OP1	2.23	0.72
46:BG:76:LEU:HD11	46:BG:148:LEU:HG	1.71	0.72
75:UB:2:UNK:HB2	75:UB:4:UNK:HG3	1.70	0.72
3:A2:275:LEU:HD22	50:BK:328:LEU:HD13	1.72	0.72
46:BG:179:PRO:HG3	46:BG:225:PRO:HG2	1.69	0.72
33:Ap:67:LEU:H	33:Ap:70:GLU:HG3	1.55	0.72
40:BA:569:LEU:HD22	40:BA:659:GLU:HB3	1.72	0.72
51:BL:193:ARG:NH1	51:BL:301:TRP:O	2.22	0.72
42:BC:49:SER:HB2	42:BC:467:ALA:HA	1.71	0.72
53:BN:10:GLN:H	53:BN:14:HIS:HD2	1.36	0.72
60:BU:135:ARG:HH22	60:BU:139:ARG:HH21	1.37	0.72
20:AU:81:ARG:NH2	39:AA:377:A:OP1	2.23	0.72
54:BO:78:ARG:HH12	58:BS:104:ARG:NH1	1.88	0.72
40:BA:316:GLU:OE1	68:Bc:29:ARG:NH1	2.23	0.71
41:BB:181:ARG:NH1	41:BB:221:TYR:HD2	1.88	0.71
51:BL:173:GLY:C	51:BL:256:ARG:HH12	1.98	0.71
2:A1:44:ALA:O	55:BP:235:ARG:NH1	2.22	0.71
16:AP:125:LYS:NZ	21:AV:157:GLY:O	2.23	0.71
32:Ao:127:SER:HB3	56:BQ:188:ARG:HH12	1.56	0.71
33:Ap:55:HIS:HD2	33:Ap:57:LYS:H	1.37	0.71
46:BG:336:LYS:HG2	46:BG:340:GLN:HE22	1.55	0.71
34:At:59:ALA:HB1	34:At:62:ARG:HH11	1.54	0.71
44:BE:335:LYS:HG3	50:BK:212:GLN:HE21	1.56	0.71
51:BL:73:GLY:HA2	51:BL:78:ARG:HH21	1.54	0.71
5:A4:61:ARG:HH21	26:Ad:49:ARG:HH11	1.38	0.71
15:AN:124:ARG:O	33:Ap:61:ASN:ND2	2.19	0.71
41:BB:214:PRO:HD3	60:BU:110:VAL:HG13	1.73	0.71
1:A0:108:GLN:HG2	52:BM:84:ASP:HB3	1.72	0.71
16:AP:45:ARG:H	16:AP:45:ARG:HD2	1.54	0.71
23:AX:158:ARG:HG2	23:AX:217:GLU:HG2	1.72	0.71
79:UN:4:UNK:HA	79:UN:13:UNK:HG1	1.73	0.71
1:A0:139:GLU:OE2	52:BM:212:ARG:NH1	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Ad:269:ARG:NH1	55:BP:64:PRO:HG3	2.06	0.71
65:BZ:150:CYS:SG	65:BZ:151:ILE:N	2.63	0.71
70:Be:13:CYS:CB	70:Be:63:CYS:SG	2.78	0.71
10:AE:169:GLN:NE2	40:BA:156:ASP:OD2	2.22	0.70
14:AK:285:ARG:HH11	14:AK:307:ARG:HH21	1.38	0.70
57:BR:122:ILE:HG22	57:BR:124:CYS:H	1.56	0.70
70:Be:14:GLY:HA3	70:Be:72:HIS:CD2	2.26	0.70
13:Aj:14:ARG:HH12	13:Aj:55:ARG:HD2	1.55	0.70
16:AP:359:HIS:O	35:Av:161:LYS:NZ	2.24	0.70
20:AU:108:ARG:HH22	28:Af:81:ARG:HB3	1.54	0.70
39:AA:876:G:H2'	39:AA:877:A:C8	2.25	0.70
47:BH:160:THR:OG1	47:BH:168:THR:OG1	2.02	0.70
8:A8:89:GLY:N	8:A8:111:ARG:HH12	1.89	0.70
14:AK:71:GLU:OE2	39:AA:433:G:N2	2.25	0.70
15:AN:172:ARG:NH1	29:Ag:119:ASN:O	2.19	0.70
29:Ag:228:ARG:HH12	29:Ag:232:GLN:HB2	1.56	0.70
41:BB:111:ILE:HD11	49:BJ:194:SER:CB	2.22	0.70
14:AK:133:ARG:HH12	14:AK:134:ARG:HH21	1.39	0.70
24:AY:96:ARG:CZ	44:BE:71:LEU:HD21	2.21	0.70
33:Ap:71:GLY:HA2	33:Ap:90:TYR:HB3	1.72	0.70
54:BO:78:ARG:HH12	58:BS:104:ARG:HH12	1.39	0.70
71:Bf:44:ARG:NH1	78:UE:6:UNK:HA	2.06	0.70
8:A8:126:ARG:NH1	31:Al:156:ARG:O	2.25	0.70
24:AY:254:LYS:HZ2	24:AY:255:ARG:HH12	1.39	0.70
33:Ap:94:GLY:O	33:Ap:96:GLU:N	2.24	0.70
18:AR:223:HIS:HE1	72:Bg:82:PRO:HD2	1.57	0.70
10:AE:54:ARG:O	33:Ap:85:LYS:NZ	2.21	0.69
45:BF:63:ARG:HE	45:BF:235:GLU:HB2	1.57	0.69
49:BJ:221:ARG:NH2	74:UA:24:UNK:O	2.25	0.69
40:BA:520:LEU:HB2	40:BA:570:SER:HB2	1.74	0.69
2:A1:129:GLU:CD	2:A1:143:ARG:HH12	1.98	0.69
39:AA:407:G:N2	39:AA:410:U:OP2	2.22	0.69
3:A2:102:ASP:OD1	24:AY:255:ARG:NH2	2.25	0.69
10:AE:315:ARG:NH2	19:AT:36:GLU:OE1	2.25	0.69
15:AN:89:LYS:NZ	33:Ap:62:LYS:NZ	2.40	0.69
29:Ag:253:ARG:HH12	52:BM:250:GLY:HA2	1.56	0.69
30:Aj:181:GLU:N	30:Aj:257:LYS:O	2.23	0.69
46:BG:149:THR:HG22	46:BG:151:SER:H	1.58	0.69
3:A2:69:LEU:HD21	50:BK:385:PRO:CG	2.22	0.69
29:Ag:48:ARG:HB3	29:Ag:50:ARG:HH21	1.57	0.69
48:BI:147:TYR:HD2	48:BI:170:MET:HG2	1.55	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A3:86:ARG:NH2	45:BF:27:THR:O	2.25	0.69
13:AJ:53:TYR:OH	13:AJ:55:ARG:NH2	2.25	0.69
16:AP:116:GLY:H	39:AA:321:A:H4'	1.56	0.69
23:AX:121:PRO:HG3	24:AY:259:MET:HE3	1.72	0.69
30:Aj:24:ARG:NH1	69:Bd:139:PRO:HG3	2.08	0.69
32:Ao:158:ARG:HB3	52:BM:217:GLU:HA	1.75	0.69
48:BI:196:ARG:HH12	48:BI:223:GLN:NE2	1.89	0.69
64:BY:79(G):LEU:HD22	76:UC:10:UNK:HG1	1.74	0.69
15:AN:80:GLY:H	15:AN:155:LYS:HZ3	1.40	0.69
11:AF:257:ARG:HH12	45:BF:420:ARG:HD3	1.56	0.69
14:AK:148:LEU:HG	14:AK:192:ILE:HD11	1.73	0.69
44:BE:53:THR:O	72:Bg:69:ARG:NH2	2.26	0.69
44:BE:306:GLN:HG3	44:BE:307:PRO:HD3	1.75	0.69
63:BX:68:ASP:OD1	63:BX:68:ASP:N	2.16	0.68
18:AR:194:GLU:HA	18:AR:197:LYS:HE3	1.75	0.68
14:AK:265:LEU:HD23	29:Ag:230:LEU:HB3	1.76	0.68
16:AP:196:THR:H	16:AP:199:HIS:HD2	1.41	0.68
30:Aj:144:ASP:HB2	46:BG:70:ARG:HH12	1.56	0.68
67:Bb:112:LEU:HD23	67:Bb:128:GLN:HE22	1.58	0.68
11:AF:217:LYS:NZ	39:AA:156:U:OP2	2.27	0.68
25:Ab:84:ASN:HD22	25:Ab:140:ARG:HD2	1.57	0.68
30:Aj:100:ASP:OD1	69:Bd:119:GLN:NE2	2.23	0.68
42:BC:459:THR:O	42:BC:474:LYS:NZ	2.26	0.68
46:BG:244:ARG:HH11	46:BG:257:ARG:HH21	1.42	0.68
53:BN:193:PHE:CE2	77:UD:222:UNK:HG1	2.27	0.68
71:Bf:44:ARG:HH11	78:UE:6:UNK:HA	1.58	0.68
84:UU:6:UNK:HG1	84:UU:9:UNK:HB1	1.74	0.68
12:AI:48:ARG:HH11	12:AI:48:ARG:CG	2.06	0.68
29:Ag:253:ARG:NH1	52:BM:250:GLY:HA2	2.07	0.68
53:BN:10:GLN:H	53:BN:14:HIS:CD2	2.11	0.68
58:BS:48:GLY:HA2	58:BS:72:THR:HG23	1.76	0.68
12:AI:54:ARG:NH2	59:BT:68:ASN:OD1	2.27	0.68
23:AX:66:ARG:HH11	85:UX:8:UNK:HG1	1.59	0.68
30:Aj:221:SER:OG	30:Aj:225:GLN:NE2	2.27	0.68
2:A1:62:GLN:NE2	2:A1:64:SER:OG	2.27	0.68
24:AY:166:ARG:HD3	50:BK:297:PHE:HD1	1.57	0.68
30:Aj:53:ARG:NH1	30:Aj:166:LEU:O	2.23	0.68
33:Ap:163:VAL:HG23	33:Ap:164:VAL:HG23	1.74	0.68
8:A8:56:LEU:HD11	11:AF:327:LYS:NZ	2.08	0.68
14:AK:203:LYS:NZ	61:BV:38:ALA:O	2.27	0.68
14:AK:229:ARG:HA	14:AK:232:GLU:HB3	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AE:43:ARG:NH1	10:AE:44:CYS:SG	2.63	0.68
34:At:100:ALA:O	34:At:104:ARG:NH2	2.27	0.68
44:BE:444:ARG:HH11	44:BE:448:ARG:NH2	1.89	0.68
48:BI:136:HIS:HE2	48:BI:143:ASP:HB2	1.60	0.68
56:BQ:96:ASP:HB2	56:BQ:143:GLN:HE21	1.59	0.68
3:A2:167:HIS:HD2	3:A2:169:GLY:H	1.40	0.67
3:A2:375:ARG:NH1	66:Ba:85:ASN:O	2.26	0.67
15:AN:149:ARG:NH1	39:AA:836:A:H62	1.92	0.67
20:AU:83:GLU:OE2	28:Af:76:LEU:N	2.26	0.67
40:BA:801:ARG:NH2	40:BA:816:HIS:O	2.27	0.67
41:BB:445:TRP:HE3	41:BB:448:ARG:HE	1.40	0.67
67:Bb:47:ARG:HA	67:Bb:50:LEU:HG	1.75	0.67
74:UA:13:UNK:HA	74:UA:16:UNK:HG3	1.74	0.67
3:A2:278:GLU:OE1	50:BK:328:LEU:HD22	1.93	0.67
42:BC:56:ASP:O	55:BP:200:ARG:NH1	2.24	0.67
3:A2:100:GLU:O	3:A2:103:GLU:HG3	1.95	0.67
44:BE:147:SER:HB2	44:BE:257:ASP:OD2	1.93	0.67
2:A1:113:VAL:HG13	2:A1:114:LEU:HD23	1.76	0.67
4:A3:60:ARG:NH1	34:At:53:SER:O	2.25	0.67
15:AN:80:GLY:H	15:AN:155:LYS:NZ	1.92	0.67
26:Ad:66:ARG:HD2	46:BG:266:GLY:HA2	1.75	0.67
39:AA:526:G:N2	66:Ba:15:PHE:O	2.26	0.67
53:BN:14:HIS:O	73:Bh:91:ARG:NH2	2.27	0.67
56:BQ:30:VAL:HB	56:BQ:198:SER:HB2	1.76	0.67
69:Bd:10:ALA:HB2	69:Bd:79:ALA:HB2	1.77	0.67
35:Av:93:GLU:OE1	70:Be:85:LYS:NZ	2.23	0.67
73:Bh:2:ALA:N	73:Bh:47:SER:HG	1.91	0.67
2:A1:85:ARG:NH1	39:AA:891:G:H5'	2.07	0.67
3:A2:185:LYS:NZ	3:A2:315:PRO:O	2.24	0.67
3:A2:457:ARG:NH1	3:A2:460:ASP:OD1	2.28	0.67
19:AT:19:ALA:O	54:BO:130:ARG:NH1	2.27	0.67
3:A2:149:VAL:HG21	3:A2:345:ILE:HD11	1.76	0.67
14:AK:257:GLU:HA	14:AK:260:ARG:HE	1.59	0.67
44:BE:190:ARG:NH1	44:BE:191:PHE:HB3	2.10	0.67
11:AF:71:VAL:O	59:BT:150:ASN:ND2	2.25	0.67
47:BH:257:ASP:OD1	47:BH:257:ASP:N	2.22	0.67
53:BN:113:ARG:NH2	53:BN:118:ASN:OD1	2.28	0.67
56:BQ:56:LYS:HG2	56:BQ:116:GLU:OE2	1.94	0.67
61:BV:87:ILE:HD11	61:BV:96:PRO:HG2	1.77	0.67
3:A2:123:ARG:HH12	65:BZ:76:ARG:HH22	1.41	0.67
26:Ad:45:LEU:HD12	69:Bd:99:VAL:HG13	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:BH:78:LEU:HD22	47:BH:83:GLU:HB3	1.76	0.67
10:AE:110:LYS:HG2	79:UN:5:UNK:CG	2.24	0.67
26:Ad:227:ARG:HH12	69:Bd:40:PHE:HE1	1.42	0.67
57:BR:38:GLU:OE2	57:BR:95:ARG:NH2	2.28	0.67
1:A0:66:PRO:HG3	1:A0:72:MET:HB2	1.77	0.66
20:AU:19:ARG:HH12	51:BL:55:LEU:HD23	1.61	0.66
39:AA:948:A:OP2	64:BY:165:ARG:NH2	2.28	0.66
40:BA:588:LEU:HD11	40:BA:695:LEU:HB3	1.75	0.66
44:BE:69:GLU:HG3	50:BK:380:TYR:CE2	2.29	0.66
63:BX:81:ASN:ND2	63:BX:116:CYS:O	2.25	0.66
8:A8:180:VAL:HG22	35:Av:102:GLN:HG3	1.76	0.66
40:BA:174:ARG:O	40:BA:179:SER:OG	2.11	0.66
41:BB:196:TRP:HZ2	41:BB:213:LEU:HD23	1.60	0.66
57:BR:145:PRO:HG2	79:UF:23:UNK:HG2	1.78	0.66
3:A2:293:PHE:O	3:A2:294:PRO:C	2.39	0.66
35:Av:166:TYR:HE1	55:BP:212:PRO:HB3	1.58	0.66
42:BC:83:ILE:HG12	42:BC:338:HIS:HB2	1.77	0.66
47:BH:71:LYS:HB3	64:BY:149:ILE:HD11	1.76	0.66
10:AE:319:LYS:HA	10:AE:371:LEU:HD11	1.77	0.66
14:AK:275:LEU:HD23	14:AK:285:ARG:HH12	1.60	0.66
46:BG:183:ARG:NH1	46:BG:187:ARG:HB3	2.10	0.66
55:BP:91:GLU:OE1	55:BP:103:ARG:NH1	2.29	0.66
10:AE:191:ASN:HD21	10:AE:213:LYS:NZ	1.93	0.66
13:AJ:103:ARG:HH12	37:AC:12:ALA:HB2	1.59	0.66
40:BA:343:ARG:HH12	40:BA:386:TRP:HZ3	1.44	0.66
12:AI:109:PRO:HG3	12:AI:182:PRO:HA	1.78	0.66
18:AR:73:MET:HE2	18:AR:93:LEU:HG	1.78	0.66
3:A2:314:HIS:CD2	3:A2:315:PRO:HD2	2.31	0.66
11:AF:388:GLU:OE1	62:BW:40:HIS:NE2	2.27	0.66
22:AW:144:LYS:NZ	39:AA:805:U:OP2	2.23	0.66
27:Ae:100:HIS:HB2	27:Ae:106:LEU:HD23	1.76	0.66
14:AK:149:MET:HE2	14:AK:191:PHE:HE1	1.61	0.66
14:AK:163:LEU:HB2	14:AK:171:PRO:HD3	1.77	0.66
25:Ab:481:MET:SD	25:Ab:506:ARG:NH1	2.69	0.66
39:AA:80:U:H4'	39:AA:81:A:H5'	1.77	0.66
60:BU:136:ASP:HB2	72:Bg:37:LEU:HD21	1.78	0.66
4:A3:173:ARG:NH1	31:Al:181:LEU:HD11	2.11	0.66
16:AP:96:ASP:OD1	39:AA:479:A:N6	2.25	0.66
39:AA:317:A:H61	39:AA:344:A:N6	1.94	0.66
44:BE:335:LYS:HG3	50:BK:212:GLN:NE2	2.10	0.66
50:BK:87:LEU:HD23	50:BK:140:LEU:HD13	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Be:13:CYS:HB2	70:Be:63:CYS:SG	2.35	0.66
3:A2:69:LEU:HD22	50:BK:386:TYR:CD2	2.31	0.65
19:AT:31:ARG:HH12	58:BS:20:GLY:N	1.93	0.65
42:BC:60:LEU:H	42:BC:292:ASN:HD21	1.43	0.65
13:AJ:42:PRO:HA	13:AJ:45:GLN:HB2	1.76	0.65
14:AK:304:GLU:OE2	14:AK:307:ARG:NH1	2.30	0.65
15:AN:89:LYS:HZ3	33:Ap:62:LYS:HZ1	1.43	0.65
46:BG:74:ARG:HG2	46:BG:74:ARG:NH1	2.00	0.65
66:Ba:58:MET:HE1	66:Ba:65:GLU:HG2	1.77	0.65
27:Ae:98:VAL:HG23	27:Ae:106:LEU:HB2	1.79	0.65
59:BT:61:ARG:NH1	66:Ba:138:GLU:OE2	2.29	0.65
18:AR:73:MET:HE1	18:AR:89:ARG:HB3	1.79	0.65
50:BK:384:ARG:HG2	50:BK:385:PRO:HD2	1.78	0.65
16:AP:201:ARG:NH1	16:AP:201:ARG:O	2.29	0.65
32:Ao:76:LYS:HD2	39:AA:464:U:H4'	1.77	0.65
40:BA:132:GLN:NE2	54:BO:139:LEU:O	2.29	0.65
3:A2:167:HIS:CD2	3:A2:169:GLY:H	2.14	0.65
3:A2:470:ASP:OD2	45:BF:414:LYS:NZ	2.28	0.65
20:AU:12:ARG:HG3	20:AU:14:LYS:HG3	1.78	0.65
50:BK:322:ASP:OD1	50:BK:323:VAL:N	2.30	0.65
61:BV:108:TYR:HA	61:BV:111:LYS:NZ	2.11	0.65
26:Ad:173:SER:HB2	26:Ad:176:LEU:HB2	1.79	0.65
27:Ae:57:GLY:HA3	27:Ae:62:GLY:HA2	1.77	0.65
31:Al:177:GLU:OE2	31:Al:191:VAL:HG13	1.96	0.65
65:BZ:24:LYS:HD3	65:BZ:155:GLN:HE21	1.62	0.65
15:AN:39:ARG:HG3	15:AN:39:ARG:NH1	2.06	0.65
18:AR:186:PHE:HD1	44:BE:421:PRO:O	1.80	0.65
29:Ag:240:ARG:NH1	61:BV:141:ASP:OD1	2.30	0.65
39:AA:158:A:H4'	39:AA:159:U:H5'	1.79	0.65
8:A8:72:LEU:HD13	16:AP:156:ARG:HE	1.60	0.65
14:AK:285:ARG:NH1	14:AK:307:ARG:HH21	1.94	0.65
20:AU:137:TRP:HZ2	20:AU:163:LEU:HB3	1.61	0.65
65:BZ:68:THR:HG22	65:BZ:70:LYS:H	1.61	0.65
72:Bg:41:TYR:HA	72:Bg:90:LEU:HD21	1.79	0.65
14:AK:225:TYR:OH	14:AK:229:ARG:NH1	2.30	0.65
25:Ab:280:MET:HB3	25:Ab:328:VAL:HB	1.79	0.65
35:Av:166:TYR:CE1	55:BP:212:PRO:HB3	2.32	0.65
47:BH:261:GLU:HA	47:BH:264:SER:HB2	1.79	0.65
83:UM:3:UNK:HG1	79:UN:2:UNK:C	2.28	0.65
10:AE:106:ARG:HH12	33:Ap:124:PRO:HG3	1.62	0.64
10:AE:166:PRO:HG3	10:AE:190:MET:HG2	1.77	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AF:431:MET:HE2	75:UB:10:UNK:HB2	1.78	0.64
14:AK:185:ARG:NH2	61:BV:115:GLN:HA	2.06	0.64
15:AN:164:HIS:HD2	15:AN:166:HIS:HB2	1.62	0.64
48:BI:190:ARG:HH12	48:BI:230:GLU:HB3	1.60	0.64
53:BN:128:ARG:HH21	73:Bh:34:ARG:HH11	1.45	0.64
4:A3:180:ARG:NH2	31:Al:178:GLU:OE1	2.30	0.64
16:AP:251:SER:HB2	55:BP:189:THR:HG21	1.78	0.64
24:AY:14:ARG:NH1	39:AA:12:U:O4	2.30	0.64
32:Ao:104:LYS:HG3	34:At:144:VAL:HG11	1.79	0.64
77:UD:205:UNK:HA	77:UD:208:UNK:HG3	1.79	0.64
11:AF:375:ILE:HG13	62:BW:134:TYR:CD2	2.32	0.64
18:AR:57:LYS:HE2	18:AR:66:ARG:HH12	1.61	0.64
65:BZ:22:VAL:HB	65:BZ:158:ASP:HB3	1.80	0.64
68:Bc:34:GLN:HA	68:Bc:37:ARG:NH1	2.12	0.64
9:A9:106:MET:HE1	15:AN:115:ARG:HB3	1.78	0.64
10:AE:205:TYR:OH	10:AE:216:CYS:SG	2.56	0.64
11:AF:38:ARG:NH2	29:Ag:50:ARG:HH12	1.95	0.64
25:Ab:257:PRO:O	52:BM:96:ARG:NH2	2.31	0.64
26:Ad:245:ASP:OD1	69:Bd:33:LYS:NZ	2.30	0.64
30:Aj:50:LEU:HD11	30:Aj:175:HIS:HB3	1.78	0.64
33:Ap:123:LYS:NZ	83:UM:6:UNK:HA	2.11	0.64
35:Av:48:ALA:HB2	39:AA:50:A:H4'	1.78	0.64
40:BA:792:SER:HG	40:BA:800:TRP:CD1	2.16	0.64
55:BP:54:GLY:H	69:Bd:77:HIS:HE1	1.44	0.64
70:Be:49:ARG:HH11	70:Be:49:ARG:CG	2.07	0.64
13:AJ:72:GLU:OE1	13:AJ:89:ARG:NH2	2.30	0.64
15:AN:89:LYS:HZ3	33:Ap:62:LYS:NZ	1.94	0.64
3:A2:219:THR:HG22	59:BT:112:ARG:HH12	1.61	0.64
11:AF:221:LYS:NZ	39:AA:155:U:O2	2.31	0.64
16:AP:102:GLU:O	45:BF:330:ARG:NH1	2.31	0.64
25:Ab:342:THR:HG1	25:Ab:344:HIS:HE2	1.43	0.64
31:Al:71:ASN:HA	31:Al:119:VAL:HG13	1.80	0.64
41:BB:83:ASN:O	41:BB:87:LEU:HB2	1.97	0.64
52:BM:232:LEU:HD21	57:BR:171:LEU:HD12	1.78	0.64
70:Be:30:PRO:HG2	70:Be:40:HIS:HD2	1.63	0.64
14:AK:185:ARG:HH21	14:AK:195:ASP:CG	2.05	0.64
20:AU:33:LYS:NZ	39:AA:142:A:OP1	2.23	0.64
22:AW:55:THR:HG21	59:BT:35:TYR:H	1.63	0.64
41:BB:72:LYS:NZ	74:UA:44:UNK:HB1	2.13	0.64
2:A1:142:LYS:NZ	2:A1:143:ARG:HH11	1.94	0.64
14:AK:20:GLU:OE2	14:AK:23:SER:HB3	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AK:275:LEU:HD23	14:AK:285:ARG:NH1	2.12	0.64
35:Av:233:THR:HG21	69:Bd:104:ARG:HD3	1.78	0.64
39:AA:76:A:N6	62:BW:77:ASN:OD1	2.31	0.64
39:AA:830:A:H2'	39:AA:831:A:H8	1.62	0.64
45:BF:252:MET:HE1	45:BF:347:ASN:HA	1.80	0.64
46:BG:192:ARG:NH1	46:BG:253:ARG:HD2	2.12	0.64
5:A4:102:ILE:HB	46:BG:345:MET:SD	2.38	0.64
5:A4:107:HIS:HB2	26:Ad:148:ARG:HA	1.79	0.64
12:AI:210:TYR:CE1	47:BH:103:GLU:HG2	2.33	0.64
27:Ae:72:PRO:HB3	39:AA:40:U:H1'	1.79	0.64
40:BA:268:ILE:HG12	40:BA:349:LEU:HB3	1.79	0.64
3:A2:69:LEU:HD21	50:BK:385:PRO:HG2	1.80	0.63
12:AI:80:GLU:HG2	12:AI:95:ARG:HD2	1.81	0.63
18:AR:52:ARG:NH1	39:AA:1169:A:O3'	2.31	0.63
69:Bd:16:HIS:HA	69:Bd:19:MET:HE2	1.80	0.63
14:AK:167:ARG:NH1	14:AK:170:TYR:HE2	1.96	0.63
25:Ab:492:ARG:HG3	56:BQ:215:LEU:HD11	1.81	0.63
29:Ag:228:ARG:NH1	29:Ag:232:GLN:HB2	2.13	0.63
31:Al:67:TYR:O	39:AA:173:U:O2'	2.16	0.63
51:BL:264:LEU:HD21	51:BL:287:ARG:NH1	2.10	0.63
56:BQ:53:ILE:HG23	56:BQ:54:VAL:HG23	1.81	0.63
3:A2:112:ILE:O	3:A2:115:GLU:HG3	1.98	0.63
30:Aj:274:GLU:HG3	46:BG:50:ARG:NH1	2.13	0.63
53:BN:23:GLY:N	53:BN:191:ARG:HH12	1.96	0.63
3:A2:33:SER:OG	3:A2:89:GLU:OE2	2.07	0.63
40:BA:129:PHE:O	54:BO:144:GLN:NE2	2.32	0.63
10:AE:148:CYS:SG	10:AE:149:LYS:N	2.71	0.63
12:AI:92:CYS:SG	35:Av:103:ARG:NH2	2.71	0.63
24:AY:110:ILE:HA	24:AY:190:MET:HE1	1.78	0.63
39:AA:329:U:C4	56:BQ:217:THR:HG22	2.34	0.63
48:BI:196:ARG:HH12	48:BI:223:GLN:HE22	1.46	0.63
61:BV:49:ARG:NH1	61:BV:73:LEU:HD23	2.14	0.63
1:A0:106:ASP:HB3	52:BM:86:VAL:HG21	1.81	0.63
3:A2:181:VAL:HG21	3:A2:320:GLY:HA3	1.81	0.63
12:AI:124:GLU:H	12:AI:124:GLU:CD	2.06	0.63
15:AN:46:LEU:HB2	15:AN:171:PRO:HB2	1.81	0.63
42:BC:276:ALA:HB2	42:BC:505:ARG:HE	1.63	0.63
51:BL:173:GLY:O	51:BL:256:ARG:NH2	2.32	0.63
53:BN:207:ASN:HB3	73:Bh:28:ARG:NH1	2.13	0.63
67:Bb:44:HIS:O	67:Bb:47:ARG:HD2	1.98	0.63
18:AR:148:ARG:HH12	39:AA:1162:G:H1'	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AY:25:ASP:OD2	24:AY:31:ARG:NH2	2.31	0.63
28:Af:141:GLU:HG2	28:Af:142:ASN:N	2.13	0.63
31:Al:15:THR:HG21	31:Al:26:MET:HG2	1.81	0.63
39:AA:387:A:N6	39:AA:448:A:O4'	2.31	0.63
41:BB:392:TYR:HD2	41:BB:393:LEU:HD12	1.64	0.63
12:Al:55:MET:HG3	59:BT:82:ARG:NH1	2.13	0.63
16:AP:300:ARG:HH11	62:BW:16:GLY:HA3	1.64	0.63
39:AA:289:U:H4'	39:AA:290:A:H5'	1.80	0.63
10:AE:198:LYS:NZ	39:AA:1107:U:OP2	2.30	0.62
24:AY:205:ARG:HG2	24:AY:214:MET:HB2	1.79	0.62
29:Ag:105:GLN:HE21	29:Ag:107:ARG:HH22	1.47	0.62
59:BT:99:THR:HG22	59:BT:103:MET:HE2	1.82	0.62
2:A1:113:VAL:HG22	2:A1:163:ARG:HG3	1.81	0.62
47:BH:122:HIS:HD2	47:BH:124:PHE:HB2	1.64	0.62
30:Aj:264:VAL:HG13	30:Aj:268:GLU:HG2	1.81	0.62
8:A8:61:TYR:CE2	8:A8:63:ALA:HB3	2.34	0.62
10:AE:191:ASN:HD21	10:AE:213:LYS:HZ2	1.46	0.62
16:AP:328:ASP:H	47:BH:239:ASN:HD22	1.48	0.62
22:AW:116:ARG:NH2	51:BL:110:SER:O	2.32	0.62
25:Ab:419:GLN:NE2	55:BP:169:SER:OG	2.32	0.62
32:Ao:76:LYS:HA	32:Ao:81:ARG:HD2	1.80	0.62
46:BG:105:TRP:CD1	46:BG:107:TYR:HB2	2.34	0.62
54:BO:141:ASP:HB3	54:BO:153:ARG:H	1.65	0.62
5:A4:76:PRO:HA	30:Aj:81:ARG:HB3	1.80	0.62
11:AF:249:GLN:HE21	11:AF:295:PHE:HD1	1.46	0.62
13:AJ:74:ARG:NH1	14:AK:239:ILE:HD11	2.04	0.62
39:AA:525:A:N1	72:Bg:56:ARG:NH1	2.47	0.62
53:BN:125:THR:HG22	53:BN:127:GLU:H	1.64	0.62
60:BU:174:TYR:HB3	60:BU:178:VAL:HG21	1.81	0.62
5:A4:139:GLU:HG2	5:A4:160:LEU:HD11	1.82	0.62
18:AR:211:ARG:NH2	60:BU:147:GLU:OE2	2.32	0.62
24:AY:196:LYS:HB3	24:AY:197:GLU:OE2	1.98	0.62
34:At:42:GLU:OE1	34:At:45:ARG:NH1	2.33	0.62
46:BG:103:LEU:HB2	46:BG:318:ALA:HB1	1.81	0.62
47:BH:71:LYS:HZ2	76:UC:4:UNK:HG1	1.64	0.62
70:Be:62:ARG:HB3	70:Be:69:VAL:HG22	1.82	0.62
17:AQ:130:ARG:HD3	39:AA:418:G:H5''	1.82	0.62
25:Ab:123:ARG:NH2	25:Ab:196:THR:O	2.33	0.62
26:Ad:230:LEU:HD22	26:Ad:260:MET:HE1	1.80	0.62
31:Al:177:GLU:OE2	31:Al:191:VAL:HG22	1.99	0.62
32:Ao:229:LYS:NZ	39:AA:387:A:H3'	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:BB:359:HIS:CD2	49:BJ:200:ARG:HH12	2.18	0.62
41:BB:419:VAL:HA	41:BB:427:PHE:CZ	2.35	0.62
11:AF:83:HIS:HD2	11:AF:85:TYR:HB2	1.65	0.62
23:AX:84:PRO:HB3	66:Ba:32:LYS:HB3	1.81	0.62
35:Av:73:ARG:NH1	39:AA:77:A:OP1	2.33	0.62
39:AA:1172:A:N6	40:BA:782:VAL:O	2.33	0.62
48:BI:261:GLY:HA3	48:BI:266:GLU:HB3	1.81	0.62
13:AJ:76:PHE:CD2	14:AK:240:GLU:HG2	2.35	0.62
15:AN:149:ARG:HH12	39:AA:836:A:H62	1.45	0.62
24:AY:194:ARG:HA	24:AY:201:MET:HA	1.82	0.62
29:Ag:125:ARG:NH1	29:Ag:129:ALA:HA	2.15	0.62
25:Ab:366:LYS:NZ	25:Ab:425:ARG:O	2.26	0.61
41:BB:347:LYS:HD3	41:BB:422:MET:HG2	1.81	0.61
8:A8:84:VAL:HG12	25:Ab:457:ARG:HD2	1.82	0.61
10:AE:197:HIS:HB3	10:AE:201:VAL:HB	1.82	0.61
13:AJ:14:ARG:NH1	13:AJ:55:ARG:HD2	2.14	0.61
16:AP:315:ARG:HH12	42:BC:506:GLU:CD	2.08	0.61
34:At:129:TYR:OH	45:BF:179:ARG:NH2	2.33	0.61
41:BB:79:ARG:HG3	41:BB:79:ARG:HH11	1.65	0.61
45:BF:207:GLU:OE2	45:BF:281:ARG:HB3	2.00	0.61
9:A9:76:ARG:HH12	9:A9:89:PRO:HG3	1.64	0.61
15:AN:119:THR:HG23	33:Ap:65:VAL:HG21	1.82	0.61
17:AQ:33:ASP:HB3	79:UG:17:UNK:HB2	1.82	0.61
18:AR:226:ARG:HG2	18:AR:246:VAL:HG21	1.83	0.61
24:AY:254:LYS:HZ2	24:AY:255:ARG:NH1	1.97	0.61
32:Ao:219:VAL:HG22	57:BR:170:TYR:HD2	1.64	0.61
39:AA:383:A:H1'	79:UF:8:UNK:HG1	1.82	0.61
51:BL:237:ASN:OD1	51:BL:237:ASN:N	2.33	0.61
2:A1:163:ARG:NH2	49:BJ:289:GLU:OE1	2.33	0.61
5:A4:149:LEU:HD11	30:Aj:26:PRO:HG2	1.81	0.61
12:AI:35:ARG:HD2	66:Ba:130:ASP:HA	1.83	0.61
15:AN:66:THR:HG21	15:AN:68:GLN:HE21	1.64	0.61
22:AW:143:LYS:NZ	39:AA:505:U:OP1	2.28	0.61
26:Ad:153:GLU:HG2	69:Bd:133:SER:HB2	1.81	0.61
29:Ag:162:ARG:HE	48:BI:280:VAL:HG21	1.65	0.61
56:BQ:22:TYR:HB2	56:BQ:163:GLN:NE2	2.14	0.61
21:AV:82:ILE:HD12	21:AV:91:VAL:HG21	1.81	0.61
26:Ad:280:GLU:OE1	42:BC:208:ARG:NH2	2.29	0.61
47:BH:111:TYR:OH	47:BH:265:HIS:ND1	2.29	0.61
55:BP:58:ILE:HD11	69:Bd:7:ARG:HD3	1.82	0.61
5:A4:48:LYS:O	35:Av:192:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AE:94:ASP:HB3	10:AE:97:ARG:HG2	1.82	0.61
11:AF:144:LEU:HD22	11:AF:226:MET:HE2	1.81	0.61
23:AX:158:ARG:NH1	39:AA:536:A:OP1	2.33	0.61
30:Aj:18:GLY:N	69:Bd:78:CYS:O	2.33	0.61
53:BN:71:GLN:OE1	77:UD:197:UNK:HB2	1.99	0.61
53:BN:140:SER:HB3	77:UD:207:UNK:HG2	1.83	0.61
77:UD:56:UNK:HA	77:UD:59:UNK:HG3	1.80	0.61
5:A4:69:SER:O	55:BP:61:LEU:HD22	2.01	0.61
14:AK:93:HIS:N	61:BV:91:LYS:HZ3	1.99	0.61
14:AK:192:ILE:HD12	61:BV:52:PHE:CZ	2.35	0.61
40:BA:224:VAL:HB	40:BA:231:TYR:HB3	1.81	0.61
57:BR:118:GLN:HG3	57:BR:119:GLY:H	1.66	0.61
22:AW:81:ARG:NH1	22:AW:93:GLU:C	2.59	0.61
24:AY:170:ILE:HG23	24:AY:174:ARG:HE	1.66	0.61
39:AA:440:U:O5'	52:BM:277:LYS:NZ	2.34	0.61
53:BN:29:TRP:HH2	60:BU:182:GLU:OE2	1.83	0.61
54:BO:188:ALA:HB2	54:BO:213:ALA:HB1	1.81	0.61
56:BQ:78:TYR:OH	56:BQ:142:SER:O	2.17	0.61
4:A3:151:ARG:NH2	39:AA:334:U:OP2	2.34	0.61
18:AR:79:ARG:NH1	44:BE:448:ARG:HH22	1.99	0.61
32:Ao:230:ARG:HH12	32:Ao:242:ASP:CA	2.12	0.61
34:At:34:ARG:NH1	57:BR:127:ARG:NH1	2.48	0.61
40:BA:215:ARG:NH1	40:BA:287:THR:O	2.34	0.61
45:BF:232:ALA:O	45:BF:235:GLU:HG2	2.00	0.61
56:BQ:115:ASP:HB3	56:BQ:159:VAL:CG2	2.31	0.61
30:Aj:273:GLU:HG2	46:BG:50:ARG:NH1	2.16	0.61
32:Ao:141:ASN:HB2	57:BR:140:LYS:HZ2	1.65	0.61
59:BT:168:LEU:HB3	62:BW:167:ARG:NH1	2.16	0.61
1:A0:45:LYS:HG2	1:A0:80:TYR:HE1	1.66	0.60
5:A4:7:ALA:HB2	8:A8:109:TYR:HE1	1.66	0.60
20:AU:71:ARG:NH2	28:Af:60:GLN:O	2.34	0.60
31:Al:79:TYR:OH	31:Al:92:HIS:O	2.14	0.60
42:BC:319:PRO:HB3	42:BC:323:ILE:HD12	1.83	0.60
46:BG:192:ARG:HH12	46:BG:253:ARG:HD2	1.66	0.60
48:BI:77:ASN:O	48:BI:80:ASP:N	2.33	0.60
11:AF:64:HIS:CD2	45:BF:366:ARG:HH12	2.19	0.60
16:AP:167:GLU:OE2	55:BP:228:HIS:ND1	2.30	0.60
16:AP:233:GLU:OE2	62:BW:12:SER:OG	2.13	0.60
28:Af:83:LEU:HB2	29:Ag:121:GLU:OE2	2.01	0.60
73:Bh:76:GLY:H	73:Bh:79:ALA:HB3	1.65	0.60
75:UB:36:UNK:HA	75:UB:39:UNK:HG3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:AV:117:MET:HG3	21:AV:126:ILE:HA	1.83	0.60
29:Ag:131:GLN:O	29:Ag:134:ARG:NH1	2.28	0.60
54:BO:215:LEU:HA	54:BO:219:ARG:HH11	1.67	0.60
64:BY:93:GLU:OE1	64:BY:93:GLU:N	2.28	0.60
14:AK:247:MET:HG2	29:Ag:234:ALA:HA	1.83	0.60
26:Ad:227:ARG:NH1	69:Bd:40:PHE:HE1	1.98	0.60
53:BN:29:TRP:CH2	60:BU:182:GLU:OE2	2.55	0.60
61:BV:64:LYS:HZ1	61:BV:66:VAL:HG12	1.67	0.60
10:AE:167:ASP:O	10:AE:189:ALA:HA	2.02	0.60
12:AI:190:GLU:HG2	47:BH:253:GLN:HB2	1.84	0.60
46:BG:53:GLY:HA3	46:BG:56:ARG:NH1	2.16	0.60
10:AE:54:ARG:NH1	68:Bc:67:GLN:OE1	2.35	0.60
14:AK:24:ASN:HB2	61:BV:103:THR:HG22	1.84	0.60
26:Ad:196:ARG:HH11	69:Bd:64:GLU:HA	1.66	0.60
28:Af:105:GLU:HB2	28:Af:139:ILE:HG23	1.84	0.60
31:Al:25:VAL:HG12	55:BP:71:ILE:HD13	1.84	0.60
39:AA:292:G:N2	39:AA:498:U:O4	2.33	0.60
51:BL:158:ARG:NH2	51:BL:221:CYS:O	2.34	0.60
6:A5:69:TRP:CD1	6:A5:79:LYS:HB2	2.37	0.60
13:AJ:32:CYS:HB3	71:Bf:96:ASP:OD2	2.00	0.60
14:AK:230:GLN:NE2	14:AK:318:GLY:H	2.00	0.60
30:AJ:226:ALA:HB2	30:AJ:288:ILE:HD12	1.83	0.60
33:Ap:55:HIS:CD2	33:Ap:57:LYS:H	2.20	0.60
40:BA:138:SER:N	40:BA:141:GLU:OE2	2.32	0.60
42:BC:339:ILE:HG22	42:BC:340:HIS:H	1.65	0.60
44:BE:32:LEU:HD23	44:BE:32:LEU:H	1.65	0.60
1:A0:49:GLN:HE21	1:A0:64:TYR:HB2	1.66	0.60
3:A2:253:ALA:CB	11:AF:407:ARG:HH12	2.15	0.60
14:AK:52:ASN:O	39:AA:435:A:H4'	2.01	0.60
18:AR:134:ARG:NH2	60:BU:166:GLN:O	2.31	0.60
21:AV:128:ARG:O	21:AV:130:LEU:N	2.34	0.60
41:BB:404:ASP:HA	41:BB:407:LYS:HZ3	1.67	0.60
49:BJ:198:ALA:HA	49:BJ:201:ARG:NH1	2.17	0.60
73:Bh:9:CYS:HB2	73:Bh:34:ARG:HD2	1.84	0.60
3:A2:123:ARG:HG2	3:A2:125:PRO:HD2	1.83	0.60
5:A4:140:GLU:HB3	5:A4:161:LYS:HB3	1.82	0.60
11:AF:455:TRP:HD1	16:AP:275:MET:HE3	1.66	0.60
19:AT:9:ASN:ND2	39:AA:1104:U:OP1	2.35	0.60
22:AW:33:ARG:HH12	22:AW:39:LYS:HD2	1.67	0.60
25:Ab:273:ARG:O	52:BM:96:ARG:NH1	2.35	0.60
39:AA:380:G:O6	84:UU:5:UNK:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:AA:579:U:O4	39:AA:580:A:N6	2.35	0.60
40:BA:685:ARG:NH1	40:BA:729:LEU:HD23	2.16	0.60
44:BE:327:ALA:HB1	44:BE:335:LYS:HD3	1.83	0.60
69:Bd:57:LEU:HD11	69:Bd:103:GLY:HA3	1.83	0.60
6:A5:72:ARG:O	6:A5:76:ARG:HD3	2.02	0.60
8:A8:56:LEU:HD13	11:AF:207:TRP:HB2	1.84	0.60
11:AF:320:LYS:HG2	39:AA:57:A:H5''	1.83	0.60
16:AP:21:ILE:HG23	32:Ao:110:LEU:HD13	1.84	0.60
21:AV:219:ARG:NH1	21:AV:227:GLU:OE2	2.21	0.60
33:Ap:166:PRO:HB3	78:UE:9:UNK:HG1	1.83	0.60
35:Av:145:ARG:HB2	35:Av:149:ASP:OD2	2.02	0.60
35:Av:207:ARG:NH2	69:Bd:105:MET:SD	2.75	0.60
57:BR:111:PHE:CZ	57:BR:126:LEU:HD21	2.37	0.60
70:Be:30:PRO:HG2	70:Be:40:HIS:CD2	2.37	0.60
3:A2:60:MET:SD	3:A2:61:LEU:HD12	2.41	0.59
5:A4:60:ASN:OD1	26:Ad:49:ARG:NH2	2.34	0.59
14:AK:205:MET:HE3	14:AK:209:GLN:HB3	1.84	0.59
33:Ap:142:GLU:N	33:Ap:142:GLU:OE1	2.34	0.59
44:BE:20:SER:O	44:BE:24:LYS:NZ	2.35	0.59
48:BI:163:CYS:HB3	48:BI:185:MET:HE1	1.84	0.59
54:BO:231:ASP:OD2	58:BS:29:ASN:ND2	2.35	0.59
70:Be:21:ARG:NH1	70:Be:98:TRP:CG	2.70	0.59
5:A4:75:PHE:HB3	5:A4:78:PHE:HE2	1.67	0.59
22:AW:19:ASN:OD1	39:AA:294:U:O2'	2.19	0.59
28:Af:58:ARG:NH1	39:AA:381:U:P	2.74	0.59
39:AA:57:A:O2'	85:UX:2:UNK:HG1	2.00	0.59
48:BI:197:ASP:HA	48:BI:200:GLU:HB3	1.84	0.59
3:A2:70:ARG:HH12	23:AX:147:LEU:HD13	1.67	0.59
20:AU:22:SER:O	20:AU:29:ARG:NH2	2.35	0.59
22:AW:142:TRP:CD1	22:AW:205:PRO:HA	2.37	0.59
25:Ab:97:PRO:O	42:BC:222:LYS:NZ	2.29	0.59
30:Aj:48:ALA:HB2	30:Aj:237:LEU:HD11	1.84	0.59
30:Aj:185:LYS:HD3	30:Aj:277:GLN:HA	1.83	0.59
56:BQ:36:THR:HG1	56:BQ:192:THR:HG1	1.50	0.59
2:A1:110:TYR:CG	12:AI:150:PRO:HA	2.36	0.59
13:AJ:16:ARG:NH1	13:AJ:41:ARG:HA	2.18	0.59
24:AY:51:ARG:NH1	44:BE:42:GLY:O	2.36	0.59
40:BA:675:MET:SD	40:BA:678:THR:OG1	2.61	0.59
44:BE:442:THR:HB	44:BE:444:ARG:HG3	1.85	0.59
53:BN:205:ASP:OD1	53:BN:209:LYS:N	2.26	0.59
8:A8:89:GLY:N	8:A8:111:ARG:NH1	2.49	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AW:215:ARG:NH1	44:BE:23:GLN:HE21	1.99	0.59
39:AA:574:A:H61	39:AA:1167:A:N6	2.00	0.59
41:BB:92:ILE:HD11	41:BB:129:TRP:CE2	2.38	0.59
63:BX:70:PRO:HB2	63:BX:72:VAL:HG13	1.85	0.59
73:Bh:2:ALA:N	73:Bh:47:SER:OG	2.35	0.59
3:A2:167:HIS:O	3:A2:170:ILE:HG22	2.02	0.59
26:Ad:101:LYS:HD3	26:Ad:109:LEU:HD11	1.85	0.59
30:Aj:30:GLN:NE2	30:Aj:222:ASN:OD1	2.36	0.59
33:Ap:37:ASN:HD22	48:BI:27:LEU:HB2	1.67	0.59
33:Ap:45:LEU:HD23	33:Ap:48:TYR:HB3	1.84	0.59
39:AA:86:U:C5'	50:BK:340:ARG:NH1	2.57	0.59
41:BB:179:LEU:HB3	41:BB:247:TYR:CD1	2.37	0.59
48:BI:117:LEU:O	48:BI:125:ASN:ND2	2.35	0.59
54:BO:86:THR:HG22	54:BO:88:ARG:H	1.67	0.59
10:AE:218:GLY:N	39:AA:1110:A:OP1	2.30	0.59
11:AF:44:LEU:HD11	51:BL:228:ASP:HB2	1.85	0.59
14:AK:191:PHE:C	14:AK:192:ILE:HD13	2.27	0.59
15:AN:135:LYS:NZ	39:AA:835:A:OP1	2.24	0.59
25:Ab:283:ASN:H	25:Ab:351:GLN:HE22	1.50	0.59
40:BA:300:ARG:HD2	40:BA:310:ALA:HB1	1.83	0.59
40:BA:774:LYS:O	40:BA:781:HIS:HE1	1.85	0.59
6:A5:46:GLU:OE2	24:AY:1:MET:HG2	2.03	0.59
20:AU:77:TRP:HZ2	20:AU:81:ARG:HH11	1.51	0.59
22:AW:169:ARG:HB2	22:AW:172:HIS:HD2	1.68	0.59
24:AY:92:GLN:OE1	44:BE:68:HIS:NE2	2.33	0.59
33:Ap:177:HIS:CD2	33:Ap:277:LEU:HD12	2.37	0.59
57:BR:126:LEU:HB2	57:BR:159:ILE:HB	1.84	0.59
61:BV:109:GLU:OE2	61:BV:134:PRO:HD2	2.02	0.59
73:Bh:52:ASN:ND2	73:Bh:56:LYS:O	2.33	0.59
1:A0:28:LYS:O	1:A0:50:ARG:NH2	2.35	0.59
11:AF:257:ARG:NH1	45:BF:420:ARG:HD3	2.18	0.59
17:AQ:30:ARG:HH11	17:AQ:30:ARG:HG3	1.67	0.59
41:BB:357:THR:HA	41:BB:364:VAL:HG12	1.84	0.59
42:BC:279:ASP:OD1	42:BC:486:ASN:ND2	2.36	0.59
46:BG:244:ARG:NH1	46:BG:257:ARG:HH21	2.00	0.59
58:BS:46:THR:O	58:BS:49:THR:OG1	2.14	0.59
60:BU:125:LYS:NZ	72:Bg:96:ARG:O	2.34	0.59
3:A2:458:TYR:O	59:BT:54:ARG:NH2	2.35	0.59
12:AI:71:TYR:HB3	12:AI:72:PRO:HD3	1.84	0.59
20:AU:179:VAL:HG22	45:BF:125:GLU:HB3	1.84	0.59
40:BA:327:ARG:HD3	40:BA:365:ASP:OD2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:BH:111:TYR:HD2	47:BH:255:PHE:CE1	2.20	0.59
5:A4:14:PRO:O	55:BP:103:ARG:NH2	2.35	0.58
20:AU:10:HIS:N	39:AA:296:A:O5'	2.36	0.58
40:BA:475:LEU:HD13	40:BA:670:CYS:HB2	1.84	0.58
18:AR:71:ARG:HH12	73:Bh:19:ASN:HB2	1.65	0.58
25:Ab:125:LEU:HD21	25:Ab:133:PRO:HB2	1.85	0.58
28:Af:72:ASP:N	28:Af:72:ASP:OD1	2.35	0.58
58:BS:51:ILE:HD11	58:BS:70:ILE:O	2.03	0.58
1:A0:61:LEU:HD11	1:A0:65:ARG:HD3	1.85	0.58
2:A1:198:GLU:HA	2:A1:201:LEU:HB2	1.85	0.58
8:A8:116:GLN:H	8:A8:116:GLN:CD	2.11	0.58
12:AI:207:PHE:HE2	47:BH:153:ARG:HB3	1.67	0.58
18:AR:127:LYS:HE3	18:AR:173:ASN:HD21	1.67	0.58
22:AW:112:LEU:HD13	51:BL:156:LEU:HD22	1.85	0.58
42:BC:272:ASP:OD2	42:BC:275:PRO:HA	2.02	0.58
43:BD:270:ALA:HB1	43:BD:406:ALA:HB1	1.85	0.58
46:BG:47:TRP:HA	46:BG:50:ARG:HH21	1.68	0.58
48:BI:262:TRP:HE3	48:BI:302:PRO:HG3	1.68	0.58
20:AU:77:TRP:HZ2	20:AU:81:ARG:NH1	2.01	0.58
27:Ae:116:PRO:HA	27:Ae:119:HIS:CD2	2.38	0.58
39:AA:387:A:O2'	39:AA:388:U:O5'	2.18	0.58
41:BB:65:PHE:CD2	49:BJ:212:TYR:HD1	2.22	0.58
44:BE:350:ASN:O	44:BE:353:LEU:N	2.37	0.58
70:Be:21:ARG:HH12	70:Be:98:TRP:CG	2.21	0.58
10:AE:319:LYS:HG3	10:AE:371:LEU:HD21	1.85	0.58
44:BE:188:ARG:NH2	44:BE:229:GLU:OE2	2.33	0.58
47:BH:126:LYS:HB2	47:BH:241:ARG:NH1	2.18	0.58
47:BH:134:GLN:CD	47:BH:135:ARG:HE	2.11	0.58
62:BW:20:VAL:HG21	75:UB:9:UNK:HG2	1.86	0.58
63:BX:169:ARG:NH1	77:UD:24:UNK:HA	2.09	0.58
11:AF:91:PRO:O	59:BT:131:LEU:HD12	2.02	0.58
22:AW:71:ILE:HD13	22:AW:74:LEU:HD22	1.84	0.58
56:BQ:126:LEU:HD23	56:BQ:150:ARG:NH1	2.19	0.58
61:BV:31:GLN:HE22	61:BV:34:LEU:HA	1.68	0.58
73:Bh:56:LYS:HG3	73:Bh:57:PRO:HD2	1.85	0.58
79:UN:5:UNK:HG1	79:UN:11:UNK:O	2.03	0.58
11:AF:407:ARG:HH11	59:BT:108:LEU:CD1	2.17	0.58
14:AK:148:LEU:HD21	61:BV:52:PHE:CE1	2.38	0.58
14:AK:167:ARG:HH11	14:AK:170:TYR:HE2	1.50	0.58
33:Ap:61:ASN:O	33:Ap:92:ARG:NH1	2.37	0.58
66:Ba:38:TYR:O	66:Ba:81:GLN:NE2	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A6:41:ARG:NH2	7:A6:91:PHE:O	2.34	0.58
24:AY:254:LYS:HZ1	24:AY:255:ARG:HH12	1.49	0.58
25:Ab:122:HIS:HA	25:Ab:125:LEU:HD13	1.85	0.58
28:Af:164:HIS:HD2	28:Af:166:LYS:HB2	1.69	0.58
39:AA:518:A:OP2	39:AA:567:G:N2	2.36	0.58
49:BJ:222:PRO:HA	74:UA:43:UNK:HG1	1.86	0.58
55:BP:177:ARG:HB2	55:BP:180:ASP:OD2	2.02	0.58
57:BR:40:ARG:CD	57:BR:95:ARG:HH12	2.17	0.58
59:BT:144:GLU:OE1	62:BW:167:ARG:NH2	2.36	0.58
70:Be:11:ILE:HG21	70:Be:73:TRP:HB3	1.85	0.58
70:Be:77:ASP:OD1	70:Be:77:ASP:N	2.33	0.58
1:A0:92:SER:OG	1:A0:95:ASN:O	2.22	0.58
3:A2:61:LEU:HD23	3:A2:84:LEU:HG	1.85	0.58
3:A2:366:VAL:HG21	66:Ba:67:PRO:HB3	1.84	0.58
6:A5:64:LYS:HZ1	6:A5:69:TRP:HD1	1.52	0.58
13:AJ:55:ARG:HG3	33:Ap:225:ILE:HD12	1.85	0.58
24:AY:75:THR:HG23	44:BE:58:PRO:O	2.02	0.58
25:Ab:385:ILE:HG22	25:Ab:386:PRO:HD2	1.86	0.58
27:Ae:87:VAL:HG12	27:Ae:88:PRO:HD3	1.86	0.58
35:Av:167:ARG:O	35:Av:167:ARG:HD3	2.03	0.58
39:AA:1156:A:H1'	39:AA:1157:A:C8	2.39	0.58
41:BB:359:HIS:CG	49:BJ:200:ARG:NH1	2.72	0.58
9:A9:72:CYS:CB	9:A9:75:CYS:SG	2.90	0.58
15:AN:187:ARG:HH21	39:AA:384:U:H5'	1.68	0.58
35:Av:167:ARG:HD3	35:Av:167:ARG:C	2.28	0.58
40:BA:174:ARG:HD2	40:BA:179:SER:HB3	1.84	0.58
49:BJ:238:LEU:O	49:BJ:242:GLN:HG2	2.04	0.58
52:BM:223:THR:HG22	52:BM:224:THR:H	1.69	0.58
56:BQ:53:ILE:HD13	56:BQ:122:ALA:HB2	1.86	0.58
10:AE:355:ARG:HG2	68:Bc:97:GLN:HE21	1.69	0.57
14:AK:62:ALA:HB2	14:AK:86:PHE:HD2	1.69	0.57
14:AK:134:ARG:NH1	39:AA:406:U:P	2.77	0.57
21:AV:227:GLU:HA	29:Ag:124:ARG:HH12	1.69	0.57
23:AX:187:ARG:NH2	39:AA:535:U:O2'	2.36	0.57
32:Ao:45:ALA:HB2	34:At:75:GLY:HA3	1.85	0.57
40:BA:223:LYS:NZ	40:BA:232:TYR:CD1	2.68	0.57
53:BN:22:ARG:C	53:BN:191:ARG:HH12	2.12	0.57
3:A2:311:ARG:NH2	3:A2:317:GLU:OE2	2.29	0.57
4:A3:108:ARG:NH2	39:AA:331:C:N3	2.52	0.57
4:A3:140:ASP:N	4:A3:140:ASP:OD1	2.32	0.57
16:AP:126:TYR:HE2	21:AV:158:ARG:HH12	1.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:176:ARG:HH12	39:AA:173:U:H5'	1.67	0.57
58:BS:85:ASP:HA	58:BS:88:LYS:HG2	1.85	0.57
59:BT:105:VAL:O	59:BT:108:LEU:HG	2.04	0.57
77:UD:170:UNK:HA	77:UD:173:UNK:HB2	1.86	0.57
5:A4:75:PHE:HB3	5:A4:78:PHE:CE2	2.39	0.57
8:A8:92:MET:HB3	8:A8:107:ARG:NE	2.19	0.57
18:AR:229:HIS:HE1	44:BE:415:TYR:HE1	1.52	0.57
21:AV:212:ASP:OD2	21:AV:221:LYS:NZ	2.36	0.57
24:AY:148:VAL:HG22	24:AY:167:GLU:HG3	1.86	0.57
39:AA:392:A:H2'	48:BI:299:ARG:HH12	1.70	0.57
42:BC:176:GLU:HG2	42:BC:185:ARG:HD2	1.85	0.57
53:BN:201:LEU:HD12	53:BN:202:PRO:HD2	1.86	0.57
63:BX:113:HIS:HB2	63:BX:116:CYS:HB2	1.87	0.57
69:Bd:102:LEU:HB3	69:Bd:112:VAL:HG21	1.85	0.57
1:A0:49:GLN:NE2	1:A0:64:TYR:O	2.36	0.57
4:A3:64:ASN:HB2	4:A3:101:ASP:OD2	2.03	0.57
5:A4:74:ARG:NH2	69:Bd:53:ALA:O	2.37	0.57
5:A4:100:PRO:HG3	30:Aj:114:PHE:HB2	1.85	0.57
26:Ad:39:GLN:OE1	35:Av:204:TRP:NE1	2.31	0.57
34:At:25:ARG:HH22	39:AA:379:U:H4'	1.69	0.57
40:BA:418:ASP:O	40:BA:423:ARG:NH2	2.37	0.57
41:BB:84:PHE:O	41:BB:88:GLU:HB2	2.04	0.57
41:BB:87:LEU:HA	41:BB:90:LYS:NZ	2.18	0.57
47:BH:92:GLY:O	64:BY:155:ARG:NH2	2.37	0.57
57:BR:32:GLN:O	57:BR:40:ARG:NH1	2.38	0.57
22:AW:98:PHE:HB3	22:AW:105:MET:HE2	1.85	0.57
25:Ab:271:THR:HG22	25:Ab:273:ARG:H	1.68	0.57
25:Ab:378:HIS:O	52:BM:100:ALA:HB3	2.04	0.57
47:BH:188:ASP:OD2	47:BH:228:VAL:HG13	2.04	0.57
55:BP:107:VAL:HA	55:BP:114:ARG:NH1	2.18	0.57
56:BQ:120:GLY:O	56:BQ:121:LYS:HB3	2.03	0.57
62:BW:27:TYR:HB3	62:BW:100:GLN:NE2	2.18	0.57
84:UU:4:UNK:HG2	84:UU:6:UNK:HB2	1.87	0.57
4:A3:89:ARG:NH1	32:Ao:113:GLN:HE21	2.01	0.57
5:A4:28:THR:O	5:A4:33:ARG:NH2	2.37	0.57
26:Ad:99:THR:HG21	30:Aj:227:THR:HG21	1.87	0.57
28:Af:148:ALA:N	40:BA:710:LYS:O	2.38	0.57
58:BS:68:ARG:NH2	58:BS:91:GLU:OE2	2.38	0.57
63:BX:97:ILE:HB	63:BX:110:TYR:HB2	1.87	0.57
74:UA:21:UNK:HB2	74:UA:26:UNK:HB1	1.87	0.57
3:A2:86:MET:O	3:A2:89:GLU:HG3	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AF:241:ARG:NH2	59:BT:117:GLU:OE1	2.38	0.57
15:AN:96:ASP:HB3	15:AN:100:ARG:HD3	1.86	0.57
16:AP:315:ARG:HD3	42:BC:456:ASP:OD2	2.05	0.57
16:AP:343:GLN:O	16:AP:348:ASN:ND2	2.38	0.57
77:UD:52:UNK:HB2	77:UD:152:UNK:HG1	1.87	0.57
3:A2:123:ARG:NH1	65:BZ:76:ARG:NH1	2.51	0.57
11:AF:145:SER:OG	16:AP:97:LEU:O	2.13	0.57
15:AN:89:LYS:NZ	33:Ap:62:LYS:HZ1	2.00	0.57
33:Ap:123:LYS:HD2	79:UN:8:UNK:HG3	1.87	0.57
40:BA:221:THR:HG23	40:BA:222:VAL:HG23	1.87	0.57
10:AE:73:LEU:HD23	10:AE:73:LEU:H	1.69	0.57
15:AN:156:ALA:O	68:Bc:23:ARG:NH1	2.33	0.57
18:AR:107:GLY:HA3	60:BU:171:ARG:O	2.05	0.57
18:AR:148:ARG:HH12	39:AA:1162:G:C1'	2.18	0.57
22:AW:142:TRP:HE1	22:AW:206:GLY:H	1.51	0.57
33:Ap:124:PRO:HD2	79:UN:7:UNK:CB	2.35	0.57
35:Av:213:ARG:NH1	35:Av:217:MET:HB2	2.20	0.57
41:BB:85:TYR:O	41:BB:89:THR:OG1	2.15	0.57
47:BH:88:GLU:O	47:BH:91:LYS:HG3	2.04	0.57
77:UD:65:UNK:HB1	77:UD:67:UNK:HG2	1.87	0.57
10:AE:197:HIS:NE2	10:AE:213:LYS:O	2.38	0.57
14:AK:200:SER:HB3	61:BV:80:LYS:HD2	1.86	0.57
20:AU:75:THR:HG21	28:Af:77:VAL:HG13	1.87	0.57
21:AV:100:GLN:NE2	39:AA:466:G:H21	2.03	0.57
40:BA:698:SER:HA	40:BA:703:ARG:NH1	2.19	0.57
43:BD:205:GLU:H	43:BD:451:ALA:CB	2.16	0.57
3:A2:123:ARG:NH1	65:BZ:76:ARG:HH22	2.01	0.56
11:AF:72:ILE:HD13	11:AF:72:ILE:H	1.68	0.56
39:AA:1156:A:O2'	39:AA:1157:A:O5'	2.20	0.56
40:BA:334:ILE:HG13	40:BA:335:PRO:HD2	1.87	0.56
42:BC:145:PRO:HA	42:BC:317:VAL:HG11	1.87	0.56
56:BQ:78:TYR:HA	56:BQ:81:ILE:HD12	1.86	0.56
56:BQ:174:VAL:O	56:BQ:178:SER:OG	2.21	0.56
65:BZ:77:VAL:HG22	65:BZ:83:ILE:HG23	1.87	0.56
2:A1:219:ALA:C	2:A1:223:LYS:NZ	2.39	0.56
3:A2:262:LYS:HG2	3:A2:289:GLN:HB2	1.86	0.56
14:AK:48:ARG:HG2	33:Ap:211:ARG:HA	1.87	0.56
18:AR:214:SER:HA	18:AR:217:LYS:NZ	2.20	0.56
24:AY:271:TYR:CZ	24:AY:275:GLU:HG3	2.40	0.56
26:Ad:171:ASP:OD1	26:Ad:181:ARG:NH1	2.38	0.56
34:At:19:LEU:HD12	84:UU:1:UNK:H2	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:BF:60:LEU:HA	45:BF:63:ARG:HH11	1.69	0.56
50:BK:87:LEU:HD21	50:BK:139:VAL:HB	1.87	0.56
52:BM:165:THR:HG22	52:BM:167:GLN:H	1.70	0.56
54:BO:141:ASP:OD2	54:BO:152:ARG:NH1	2.37	0.56
4:A3:110:TRP:HE3	34:At:44:LEU:HD23	1.70	0.56
8:A8:175:ASP:OD1	8:A8:175:ASP:N	2.39	0.56
10:AE:82:ARG:HH11	48:BI:77:ASN:HD22	1.54	0.56
12:AI:207:PHE:CE2	47:BH:153:ARG:HB3	2.40	0.56
12:AI:214:PRO:HG2	12:AI:217:LEU:HD13	1.86	0.56
14:AK:70:GLN:NE2	39:AA:432:U:O4	2.38	0.56
14:AK:233:LEU:O	14:AK:241:ARG:NH1	2.37	0.56
16:AP:285:LEU:O	16:AP:290:THR:OG1	2.19	0.56
22:AW:59:ILE:HG23	45:BF:394:GLY:HA3	1.87	0.56
24:AY:64:HIS:HD2	24:AY:66:ARG:HB2	1.71	0.56
25:Ab:92:PHE:O	25:Ab:94:ILE:HD12	2.05	0.56
25:Ab:289:ASN:O	25:Ab:316:ASN:ND2	2.38	0.56
26:Ad:126:ARG:HH12	30:Aj:18:GLY:N	2.03	0.56
32:Ao:143:ASP:OD2	32:Ao:145:ALA:HB3	2.05	0.56
33:Ap:176:MET:HA	33:Ap:280:LEU:HD11	1.87	0.56
34:At:94:THR:OG1	34:At:96:GLU:OE1	2.22	0.56
39:AA:196:G:H22	39:AA:277:A:H2	1.49	0.56
40:BA:685:ARG:HH12	40:BA:729:LEU:HD23	1.71	0.56
41:BB:72:LYS:CE	74:UA:44:UNK:HB1	2.35	0.56
41:BB:404:ASP:HA	41:BB:407:LYS:NZ	2.20	0.56
50:BK:382:TYR:CE1	72:Bg:70:PRO:HD2	2.41	0.56
53:BN:209:LYS:HD2	73:Bh:15:PHE:HB2	1.87	0.56
59:BT:145:SER:HB3	59:BT:174:ILE:HG22	1.86	0.56
71:Bf:104:ASN:HB2	71:Bf:111:SER:HB2	1.87	0.56
73:Bh:8:ARG:NH1	73:Bh:37:GLN:HE21	2.02	0.56
77:UD:161:UNK:HA	77:UD:164:UNK:HG3	1.86	0.56
11:AF:140:GLU:H	11:AF:225:MET:CE	2.17	0.56
16:AP:106:MET:HE1	22:AW:25:LEU:HD22	1.86	0.56
18:AR:185:ARG:HH21	44:BE:411:LYS:NZ	2.02	0.56
24:AY:35:LYS:HG2	39:AA:15:G:H5'	1.88	0.56
27:Ae:109:ARG:NH1	39:AA:544:G:C4	2.73	0.56
29:Ag:158:GLU:OE1	29:Ag:161:ARG:NH2	2.36	0.56
32:Ao:218:PHE:CG	52:BM:241:MET:HE3	2.41	0.56
39:AA:551:A:OP1	39:AA:554:A:N6	2.31	0.56
41:BB:134:ARG:HA	41:BB:137:ARG:HH12	1.70	0.56
45:BF:63:ARG:NE	45:BF:235:GLU:HB2	2.20	0.56
63:BX:132:TYR:HA	77:UD:48:UNK:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A8:74:PHE:HD1	8:A8:87:ALA:HB2	1.70	0.56
14:AK:134:ARG:HA	39:AA:405:U:H5''	1.86	0.56
15:AN:63:GLN:NE2	28:Af:60:GLN:OE1	2.38	0.56
39:AA:317:A:H61	39:AA:344:A:H62	1.53	0.56
46:BG:42:PHE:HB2	46:BG:66:TYR:CE1	2.41	0.56
51:BL:165:LEU:HA	51:BL:168:LEU:HB2	1.87	0.56
54:BO:141:ASP:CB	54:BO:153:ARG:H	2.18	0.56
61:BV:115:GLN:O	61:BV:117:TRP:CD1	2.58	0.56
3:A2:288:ILE:HD13	3:A2:295:ASN:OD1	2.06	0.56
14:AK:179:ARG:NH1	39:AA:400:U:C2	2.73	0.56
21:AV:235:LEU:HD21	28:Af:100:THR:HG21	1.86	0.56
41:BB:82:HIS:CE1	41:BB:86:ASN:HD22	2.24	0.56
48:BI:90:TYR:CZ	48:BI:128:LEU:HD22	2.40	0.56
50:BK:290:ASP:O	50:BK:307:ARG:N	2.38	0.56
62:BW:56:ASN:H	62:BW:65:ASN:ND2	2.03	0.56
67:Bb:79:HIS:HD2	67:Bb:81:HIS:HB2	1.70	0.56
1:A0:174:ASN:HB3	55:BP:69:ARG:HH12	1.71	0.56
13:AJ:14:ARG:O	13:AJ:41:ARG:HG3	2.04	0.56
14:AK:34:LYS:O	14:AK:38:ILE:HG12	2.06	0.56
39:AA:535:U:OP1	39:AA:536:A:N6	2.39	0.56
40:BA:739:ARG:HH12	40:BA:744:ASN:ND2	2.04	0.56
41:BB:176:LEU:HB3	41:BB:234:ILE:HG21	1.88	0.56
42:BC:300:LEU:HD11	42:BC:447:PRO:HD2	1.88	0.56
45:BF:60:LEU:HD22	45:BF:63:ARG:HH12	1.71	0.56
47:BH:152:ALA:CA	47:BH:156:LEU:HD22	2.34	0.56
57:BR:19:TYR:HB3	57:BR:43:LYS:HA	1.87	0.56
72:Bg:27:ASN:HB3	72:Bg:30:GLU:HG2	1.88	0.56
17:AQ:60:GLN:NE2	17:AQ:89:GLU:OE2	2.38	0.56
22:AW:95:ARG:NH1	22:AW:110:TRP:CE2	2.73	0.56
23:AX:70:TYR:OH	39:AA:284:U:OP2	2.19	0.56
25:Ab:162:VAL:HG21	25:Ab:348:LEU:HD23	1.87	0.56
39:AA:454:U:O2'	39:AA:455:U:H5''	2.06	0.56
42:BC:109:THR:HG22	42:BC:222:LYS:HG3	1.88	0.56
45:BF:287:ASP:OD1	45:BF:313:ARG:NE	2.38	0.56
2:A1:123:VAL:HG12	2:A1:124:GLU:H	1.71	0.56
11:AF:179:ASN:HD22	11:AF:186:ARG:HB3	1.71	0.56
21:AV:114:LYS:NZ	32:Ao:80:SER:O	2.36	0.56
32:Ao:243:LYS:HB3	32:Ao:245:LEU:HD22	1.88	0.56
40:BA:324:GLU:HA	40:BA:327:ARG:HB2	1.88	0.56
40:BA:676:LEU:HD11	40:BA:694:THR:HG23	1.87	0.56
1:A0:119:ALA:O	1:A0:123:ARG:HG2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:79:TRP:HB2	16:AP:84:GLN:HE21	1.71	0.56
16:AP:360:SER:HB3	35:Av:161:LYS:NZ	2.21	0.56
24:AY:87:LYS:NZ	39:AA:97:A:C2	2.72	0.56
24:AY:194:ARG:HG3	50:BK:325:ASP:OD2	2.05	0.56
30:Aj:172:ASP:OD1	30:Aj:292:SER:OG	2.23	0.56
39:AA:165:A:N7	55:BP:112:ARG:NH2	2.50	0.56
44:BE:280:ALA:O	44:BE:283:SER:OG	2.12	0.56
52:BM:83:ASP:HB3	56:BQ:213:ARG:HA	1.88	0.56
77:UD:82:UNK:HG3	77:UD:136:UNK:N	2.21	0.56
2:A1:55:TYR:HH	2:A1:61:THR:HG1	1.53	0.55
2:A1:163:ARG:NH1	49:BJ:286:ARG:HH11	2.04	0.55
8:A8:59:THR:H	11:AF:318:ALA:HB2	1.71	0.55
29:Ag:224:VAL:HG22	29:Ag:225:PRO:HD2	1.88	0.55
30:Aj:76:HIS:O	30:Aj:80:SER:OG	2.20	0.55
41:BB:134:ARG:HA	41:BB:137:ARG:NH1	2.21	0.55
51:BL:254:VAL:HG21	51:BL:304:VAL:HG11	1.88	0.55
52:BM:76:TRP:O	52:BM:80:ARG:NH2	2.38	0.55
62:BW:2:SER:OG	62:BW:3:GLY:N	2.37	0.55
3:A2:290:LEU:HD21	3:A2:297:THR:HG23	1.88	0.55
11:AF:249:GLN:NE2	11:AF:295:PHE:HD1	2.03	0.55
20:AU:73:HIS:O	28:Af:79:THR:HG23	2.06	0.55
21:AV:91:VAL:HG22	21:AV:97:ILE:HD11	1.86	0.55
25:Ab:416:ILE:HG13	42:BC:76:TYR:CD1	2.42	0.55
33:Ap:67:LEU:N	33:Ap:70:GLU:HG3	2.19	0.55
45:BF:263:PHE:O	45:BF:267:PHE:HB3	2.06	0.55
56:BQ:98:LEU:HG	56:BQ:99:LEU:HG	1.88	0.55
61:BV:64:LYS:HZ2	61:BV:66:VAL:HG12	1.68	0.55
71:Bf:86:ILE:HB	71:Bf:91:LYS:HB3	1.88	0.55
6:A5:50:LYS:HE3	39:AA:1161:A:H5'	1.87	0.55
8:A8:181:VAL:HB	35:Av:103:ARG:HD3	1.89	0.55
13:AJ:73:ARG:HB3	13:AJ:81:ASN:O	2.06	0.55
14:AK:38:ILE:HD11	61:BV:90:PHE:HE1	1.70	0.55
14:AK:303:PRO:HB2	14:AK:307:ARG:HH12	1.71	0.55
15:AN:27:PRO:HG3	39:AA:111:U:O5'	2.07	0.55
18:AR:84:ILE:HG22	18:AR:160:MET:HE3	1.89	0.55
25:Ab:151:LEU:HD21	52:BM:184:MET:HE1	1.87	0.55
25:Ab:352:ARG:NH2	25:Ab:398:GLN:O	2.39	0.55
30:Aj:148:TYR:OH	30:Aj:159:SER:O	2.20	0.55
30:Aj:226:ALA:HB3	30:Aj:239:ILE:HB	1.88	0.55
35:Av:57:GLU:HA	35:Av:60:ARG:HG2	1.89	0.55
42:BC:301:MET:HE1	42:BC:421:PHE:CD1	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:BH:128:ILE:HB	47:BH:168:THR:HG23	1.87	0.55
54:BO:117:LEU:HD12	54:BO:161:MET:HE2	1.87	0.55
66:Ba:73:GLU:OE1	66:Ba:73:GLU:N	2.40	0.55
16:AP:348:ASN:HD22	16:AP:348:ASN:N	2.03	0.55
25:Ab:459:ARG:NH1	25:Ab:472:PHE:HD1	2.04	0.55
46:BG:347:GLN:HA	46:BG:350:LEU:HD23	1.87	0.55
59:BT:170:ASP:HA	62:BW:167:ARG:HB2	1.86	0.55
77:UD:34:UNK:O	77:UD:38:UNK:HG3	2.06	0.55
4:A3:130:ILE:HD11	32:Ao:114:LEU:HD23	1.88	0.55
14:AK:148:LEU:HD21	61:BV:52:PHE:CZ	2.42	0.55
16:AP:132:ASP:OD1	16:AP:135:ARG:NH2	2.39	0.55
27:Ae:51:PRO:HG2	27:Ae:54:MET:HE3	1.86	0.55
32:Ao:125:ASP:HB3	32:Ao:130:LEU:HD12	1.88	0.55
39:AA:1172:A:N6	40:BA:783:THR:O	2.39	0.55
41:BB:356:ASN:HA	41:BB:363:ARG:HH21	1.71	0.55
53:BN:183:VAL:HG22	77:UD:212:UNK:HB1	1.88	0.55
69:Bd:25:LEU:HD21	69:Bd:44:GLU:HG3	1.87	0.55
3:A2:123:ARG:HH12	65:BZ:76:ARG:NH1	2.04	0.55
3:A2:412:ASN:HD21	3:A2:439:ASP:H	1.55	0.55
6:A5:50:LYS:HD2	39:AA:1161:A:OP2	2.06	0.55
11:AF:118:PHE:HE1	11:AF:124:VAL:HG22	1.72	0.55
14:AK:238:LEU:HD23	14:AK:241:ARG:HH21	1.71	0.55
24:AY:309:ASN:OD1	24:AY:310:ALA:N	2.39	0.55
26:Ad:255:TRP:HA	26:Ad:260:MET:HE3	1.88	0.55
39:AA:392:A:H2'	48:BI:299:ARG:NH1	2.21	0.55
51:BL:196:THR:HG21	51:BL:304:VAL:HG22	1.89	0.55
52:BM:63:TRP:HA	52:BM:66:ARG:HG2	1.88	0.55
53:BN:114:ASP:OD2	53:BN:121:LEU:HD22	2.07	0.55
4:A3:68:VAL:HG13	4:A3:116:VAL:HG13	1.88	0.55
16:AP:175:LEU:HD23	16:AP:234:LEU:HD11	1.89	0.55
26:Ad:126:ARG:HH12	69:Bd:78:CYS:HB2	1.71	0.55
27:Ae:71:HIS:CD2	27:Ae:73:LEU:HB2	2.42	0.55
33:Ap:232:ILE:HD12	33:Ap:255:LEU:HD23	1.87	0.55
39:AA:1096:U:H2'	39:AA:1097:A:H8	1.71	0.55
60:BU:131:LYS:HB2	60:BU:131:LYS:NZ	2.22	0.55
3:A2:412:ASN:ND2	3:A2:439:ASP:H	2.05	0.55
8:A8:59:THR:HG23	11:AF:318:ALA:HB2	1.87	0.55
11:AF:83:HIS:CD2	11:AF:85:TYR:HB2	2.41	0.55
14:AK:193:GLY:HA3	61:BV:111:LYS:HG2	1.86	0.55
24:AY:251:LEU:HD23	24:AY:254:LYS:HE3	1.89	0.55
27:Ae:129:LEU:HD11	41:BB:152:ARG:NH2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Aj:138:THR:HG22	30:Aj:140:ARG:H	1.70	0.55
39:AA:441:A:H62	61:BV:148:MET:HE1	1.71	0.55
40:BA:582:PHE:HD1	40:BA:693:HIS:HB2	1.72	0.55
54:BO:75:PHE:O	54:BO:77:ALA:N	2.39	0.55
10:AE:117:ASP:OD1	10:AE:117:ASP:N	2.39	0.55
16:AP:327:ARG:NH1	47:BH:241:ARG:O	2.39	0.55
32:Ao:151:ASP:O	67:Bb:113:ASN:ND2	2.40	0.55
39:AA:561:U:P	63:BX:154:ARG:HH22	2.30	0.55
46:BG:65:MET:SD	46:BG:111:TYR:N	2.80	0.55
53:BN:53:ARG:HB3	53:BN:95:HIS:ND1	2.21	0.55
20:AU:125:VAL:HG22	32:Ao:31:LEU:HD12	1.88	0.55
25:Ab:506:ARG:HH12	31:Al:160:PRO:HB3	1.72	0.55
39:AA:302:G:H22	39:AA:335:G:H2'	1.71	0.55
41:BB:428:LEU:H	41:BB:428:LEU:HD12	1.72	0.55
58:BS:32:ARG:HH21	58:BS:32:ARG:CG	2.18	0.55
69:Bd:54:MET:HB2	69:Bd:61:ALA:HB1	1.88	0.55
7:A6:94:LYS:HB2	7:A6:94:LYS:NZ	2.22	0.54
10:AE:54:ARG:HH11	68:Bc:67:GLN:HE22	1.56	0.54
15:AN:141:HIS:CE1	28:Af:57:PHE:HA	2.42	0.54
22:AW:28:GLN:HG2	22:AW:29:ARG:H	1.73	0.54
29:Ag:95:GLN:OE1	40:BA:720:ARG:NH1	2.40	0.54
30:Aj:163:ARG:NH1	30:Aj:168:ARG:HH22	2.05	0.54
39:AA:134:U:H2'	39:AA:135:G:H5''	1.88	0.54
41:BB:427:PHE:HA	41:BB:430:TYR:CE2	2.41	0.54
50:BK:295:ARG:HB3	50:BK:295:ARG:NH1	2.22	0.54
51:BL:126:LYS:NZ	51:BL:142:LEU:HD23	2.22	0.54
53:BN:111:PHE:HB3	53:BN:120:TRP:HE1	1.71	0.54
55:BP:107:VAL:HA	55:BP:114:ARG:HH11	1.72	0.54
56:BQ:134:HIS:HB2	56:BQ:139:GLN:O	2.07	0.54
3:A2:155:ARG:HG3	3:A2:170:ILE:HG21	1.90	0.54
14:AK:179:ARG:HE	39:AA:422:A:H1'	1.73	0.54
14:AK:185:ARG:HH12	61:BV:115:GLN:CA	2.20	0.54
14:AK:244:ARG:HH12	14:AK:314:ARG:NH1	2.05	0.54
21:AV:73:LEU:HD21	28:Af:100:THR:HG23	1.88	0.54
23:AX:191:ARG:NH1	39:AA:532:U:O3'	2.38	0.54
24:AY:87:LYS:NZ	39:AA:97:A:H2	2.05	0.54
52:BM:97:THR:HG21	52:BM:102:VAL:HG23	1.88	0.54
53:BN:22:ARG:CA	53:BN:191:ARG:HH12	2.20	0.54
3:A2:399:THR:HA	3:A2:402:ARG:HH21	1.73	0.54
5:A4:52:THR:HG22	5:A4:56:GLN:HE22	1.72	0.54
11:AF:140:GLU:H	11:AF:225:MET:HE3	1.71	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AR:215:LYS:HZ1	18:AR:216:PHE:HE1	1.53	0.54
21:AV:211:VAL:HG22	29:Ag:125:ARG:HB2	1.89	0.54
22:AW:179:LEU:HD23	22:AW:232:LEU:HD21	1.88	0.54
39:AA:546:A:OP1	72:Bg:56:ARG:NH1	2.41	0.54
49:BJ:240:VAL:HA	49:BJ:243:LYS:NZ	2.22	0.54
62:BW:40:HIS:ND1	62:BW:90:ARG:NH1	2.55	0.54
3:A2:219:THR:HG22	59:BT:112:ARG:NH1	2.22	0.54
8:A8:61:TYR:OH	39:AA:61:A:OP2	2.16	0.54
11:AF:266:THR:HG21	45:BF:373:THR:OG1	2.07	0.54
12:AI:32:VAL:HG13	12:AI:33:GLY:H	1.72	0.54
12:AI:152:ARG:CB	49:BJ:292:ARG:HE	2.20	0.54
20:AU:164:SER:O	20:AU:169:ARG:NH2	2.41	0.54
24:AY:279:ARG:HH12	65:BZ:174:SER:HB2	1.72	0.54
25:Ab:104:TRP:CH2	42:BC:126:GLU:HB2	2.43	0.54
25:Ab:464:THR:HB	52:BM:71:GLY:O	2.07	0.54
33:Ap:168:THR:HG21	33:Ap:285:TYR:HA	1.87	0.54
39:AA:566:A:C8	60:BU:137:ARG:NH1	2.75	0.54
42:BC:318:ASP:O	42:BC:320:VAL:N	2.39	0.54
53:BN:64:LEU:HD11	53:BN:108:PHE:CD2	2.42	0.54
54:BO:126:MET:HE3	54:BO:130:ARG:H	1.72	0.54
59:BT:61:ARG:HE	66:Ba:141:TYR:HE1	1.54	0.54
3:A2:216:TYR:CZ	11:AF:406:ALA:HB1	2.43	0.54
10:AE:195:GLU:HB3	40:BA:791:PHE:O	2.06	0.54
10:AE:362:THR:HG22	10:AE:363:PHE:O	2.07	0.54
14:AK:42:PRO:HD2	14:AK:115:THR:HG22	1.88	0.54
30:Aj:162:THR:HB	30:Aj:164:HIS:CD2	2.42	0.54
39:AA:830:A:H2'	39:AA:831:A:C8	2.41	0.54
39:AA:1107:U:O2'	39:AA:1109:U:OP2	2.24	0.54
47:BH:130:VAL:HG22	47:BH:182:VAL:HG22	1.89	0.54
53:BN:219:ARG:NH1	53:BN:220:ASP:O	2.40	0.54
69:Bd:64:GLU:OE2	69:Bd:66:LEU:N	2.40	0.54
10:AE:92:THR:OG1	71:Bf:108:THR:O	2.26	0.54
10:AE:356:GLY:O	10:AE:357:LEU:HD23	2.07	0.54
18:AR:148:ARG:HH22	39:AA:1162:G:H1'	1.72	0.54
41:BB:415:ASP:N	41:BB:415:ASP:OD1	2.37	0.54
55:BP:54:GLY:H	69:Bd:77:HIS:CE1	2.25	0.54
61:BV:119:THR:HG21	61:BV:147:ARG:HH12	1.73	0.54
3:A2:123:ARG:NH1	65:BZ:76:ARG:HH12	2.05	0.54
5:A4:162:ARG:NH1	30:Aj:30:GLN:HA	2.22	0.54
11:AF:28:ARG:HD3	39:AA:490:G:C6	2.43	0.54
11:AF:347:ASP:OD1	11:AF:348:ARG:N	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Ab:292:VAL:HG11	25:Ab:320:ILE:HB	1.90	0.54
26:Ad:77:VAL:HG12	26:Ad:80:LYS:NZ	2.22	0.54
32:Ao:230:ARG:NH1	32:Ao:242:ASP:HA	2.18	0.54
34:At:34:ARG:CZ	57:BR:127:ARG:HH12	2.20	0.54
2:A1:80:GLU:HG3	2:A1:123:VAL:HG11	1.89	0.54
3:A2:174:GLU:OE2	3:A2:176:LYS:HD2	2.07	0.54
5:A4:12:SER:OG	55:BP:114:ARG:NH2	2.41	0.54
11:AF:176:ASN:ND2	11:AF:190:ARG:HG2	2.22	0.54
26:Ad:200:ILE:HG22	69:Bd:58:LEU:HD23	1.90	0.54
27:Ae:154:ARG:NH1	27:Ae:154:ARG:HB2	2.23	0.54
29:Ag:179:GLU:HA	29:Ag:182:LYS:HG2	1.90	0.54
33:Ap:175:LEU:HD11	33:Ap:178:MET:O	2.08	0.54
39:AA:455:U:H2'	39:AA:456:U:H4'	1.90	0.54
42:BC:494:LEU:HD21	42:BC:496:ASP:HB3	1.90	0.54
48:BI:103:THR:HG22	48:BI:104:ARG:H	1.73	0.54
50:BK:373:PRO:HG2	50:BK:376:MET:HB2	1.89	0.54
52:BM:174:SER:OG	52:BM:175:GLU:OE1	2.25	0.54
56:BQ:96:ASP:HB2	56:BQ:143:GLN:NE2	2.23	0.54
62:BW:187:ASP:N	62:BW:187:ASP:OD1	2.40	0.54
67:Bb:46:LEU:HB3	67:Bb:47:ARG:NH1	2.23	0.54
77:UD:27:UNK:HA	77:UD:30:UNK:HG3	1.88	0.54
77:UD:216:UNK:HA	77:UD:219:UNK:HG3	1.89	0.54
76:UH:3:UNK:HA	76:UH:7:UNK:HG1	1.89	0.54
1:A0:145:GLU:HG2	1:A0:151:ARG:HH21	1.71	0.54
3:A2:84:LEU:O	3:A2:87:ILE:HG22	2.08	0.54
4:A3:70:CYS:HB2	4:A3:90:LEU:HD13	1.90	0.54
4:A3:81:VAL:HG13	4:A3:112:VAL:HG12	1.89	0.54
16:AP:12:ARG:HE	34:At:33:LYS:HB2	1.72	0.54
16:AP:113:ILE:HG21	39:AA:342:U:H1'	1.90	0.54
16:AP:315:ARG:HG3	16:AP:316:ARG:N	2.21	0.54
18:AR:60:ALA:HB1	18:AR:65:HIS:HD2	1.72	0.54
30:Aj:53:ARG:HH11	30:Aj:174:LEU:HD12	1.73	0.54
33:Ap:168:THR:O	33:Ap:257:GLN:NE2	2.41	0.54
46:BG:121:SER:HB2	46:BG:124:ASP:HB2	1.89	0.54
49:BJ:267:GLU:OE1	49:BJ:270:ARG:NH1	2.41	0.54
57:BR:128:LYS:HE2	79:UF:21:UNK:HA	1.89	0.54
3:A2:54:LEU:HD22	3:A2:87:ILE:HG13	1.90	0.54
5:A4:42:VAL:HG13	5:A4:44:ARG:NH1	2.21	0.54
6:A5:49:LEU:O	24:AY:1:MET:N	2.41	0.54
10:AE:190:MET:O	10:AE:192:VAL:HG23	2.07	0.54
22:AW:204:TYR:CE2	39:AA:101:A:H5'	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Ab:337:GLU:OE2	42:BC:96:ARG:NH2	2.41	0.54
30:Aj:101:ALA:HB2	69:Bd:117:THR:HG21	1.90	0.54
39:AA:379:U:H3	84:UU:7:UNK:HB2	1.72	0.54
39:AA:564:A:N7	77:UD:21:UNK:HB2	2.22	0.54
42:BC:108:GLN:HE22	42:BC:242:LEU:N	1.98	0.54
44:BE:168:LEU:HD12	44:BE:241:LEU:HD22	1.89	0.54
44:BE:185:ARG:NH2	44:BE:235:GLU:OE1	2.41	0.54
45:BF:235:GLU:HA	45:BF:238:GLU:HG2	1.90	0.54
57:BR:94:LYS:HA	57:BR:177:LEU:HD13	1.90	0.54
68:Bc:56:TRP:HD1	68:Bc:64:PHE:HZ	1.56	0.54
69:Bd:56:LEU:O	69:Bd:104:ARG:NH2	2.40	0.54
1:A0:166:ASN:ND2	55:BP:41:TYR:OH	2.40	0.53
3:A2:96:ARG:HB2	50:BK:358:LEU:HD11	1.90	0.53
25:Ab:175:ARG:NH1	42:BC:91:ALA:HB3	2.20	0.53
26:Ad:228:GLN:O	26:Ad:231:ILE:HG13	2.08	0.53
27:Ae:72:PRO:CB	39:AA:40:U:H1'	2.38	0.53
33:Ap:170:HIS:ND1	33:Ap:260:MET:HB3	2.23	0.53
40:BA:791:PHE:HE1	40:BA:801:ARG:HH11	1.54	0.53
41:BB:68:TYR:HE2	49:BJ:194:SER:O	1.90	0.53
11:AF:207:TRP:O	11:AF:327:LYS:HG3	2.08	0.53
13:AJ:104:VAL:HG13	13:AJ:107:GLU:H	1.72	0.53
21:AV:86:ASN:ND2	39:AA:465:A:N3	2.56	0.53
34:At:148:GLN:NE2	45:BF:279:TYR:OH	2.41	0.53
42:BC:267:ILE:O	42:BC:268:LEU:HB2	2.08	0.53
52:BM:128:PHE:HZ	67:Bb:66:GLU:HB3	1.72	0.53
53:BN:14:HIS:NE2	60:BU:181:ALA:O	2.34	0.53
70:Be:70:HIS:HD2	70:Be:72:HIS:H	1.56	0.53
10:AE:135:SER:HB2	10:AE:360:PHE:CE1	2.43	0.53
18:AR:226:ARG:NH1	72:Bg:80:MET:HA	2.24	0.53
22:AW:142:TRP:NE1	22:AW:205:PRO:HA	2.23	0.53
39:AA:877:A:N6	39:AA:893:A:H2	2.06	0.53
41:BB:359:HIS:HD2	41:BB:363:ARG:NH1	2.06	0.53
57:BR:26:ARG:HG2	57:BR:70:TYR:HE1	1.74	0.53
58:BS:20:GLY:N	58:BS:31:ASP:OD2	2.42	0.53
59:BT:173:LEU:HD13	59:BT:176:GLY:HA3	1.90	0.53
69:Bd:53:ALA:HB2	69:Bd:90:GLN:O	2.08	0.53
2:A1:170:ASN:ND2	49:BJ:289:GLU:OE2	2.42	0.53
10:AE:244:VAL:HG11	10:AE:339:PHE:HD2	1.73	0.53
14:AK:219:ARG:NH1	14:AK:220:ILE:HG13	2.24	0.53
26:Ad:160:PRO:HG2	69:Bd:69:LEU:HD11	1.89	0.53
35:Av:165:ASP:OD1	35:Av:166:TYR:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:AA:119:A:H5'	39:AA:120:A:C8	2.44	0.53
39:AA:424:G:OP1	39:AA:424:G:N2	2.38	0.53
40:BA:777:PHE:O	40:BA:781:HIS:NE2	2.41	0.53
42:BC:260:LEU:HB3	55:BP:100:MET:HE1	1.90	0.53
47:BH:194:ARG:NH1	47:BH:196:LEU:HD21	2.22	0.53
49:BJ:210:ILE:HD11	74:UA:20:UNK:HG1	1.91	0.53
2:A1:225:GLN:O	2:A1:226:LEU:HB2	2.08	0.53
11:AF:282:SER:HB2	11:AF:400:ILE:HD12	1.90	0.53
12:AI:18:HIS:HB3	12:AI:27:PRO:HD2	1.90	0.53
14:AK:209:GLN:O	14:AK:212:GLU:HG3	2.08	0.53
14:AK:264:LEU:HD21	14:AK:295:ARG:HE	1.72	0.53
19:AT:28:ARG:NH2	58:BS:23:THR:OG1	2.42	0.53
25:Ab:359:SER:H	25:Ab:392:MET:HE1	1.73	0.53
28:Af:171:TRP:NE1	40:BA:426:ASP:OD1	2.40	0.53
33:Ap:185:VAL:HG13	33:Ap:197:GLN:HE22	1.72	0.53
53:BN:179:LEU:HD23	77:UD:208:UNK:HG2	1.89	0.53
53:BN:197:GLU:OE2	53:BN:219:ARG:HG2	2.08	0.53
66:Ba:53:HIS:ND1	66:Ba:65:GLU:OE2	2.38	0.53
77:UD:39:UNK:O	77:UD:41:UNK:HG2	2.08	0.53
8:A8:150:GLY:HA3	39:AA:59:U:O2	2.09	0.53
14:AK:56:PHE:CD2	61:BV:20:THR:HG22	2.44	0.53
24:AY:69:ASP:OD1	24:AY:69:ASP:N	2.41	0.53
26:Ad:283:TYR:HD1	42:BC:205:PRO:HA	1.74	0.53
28:Af:112:GLN:HB2	28:Af:135:ILE:HG21	1.91	0.53
41:BB:170:GLN:HE21	72:Bg:101:GLY:HA2	1.74	0.53
57:BR:26:ARG:HG2	57:BR:70:TYR:CE1	2.42	0.53
77:UD:219:UNK:O	77:UD:222:UNK:HG3	2.09	0.53
6:A5:76:ARG:NH1	18:AR:162:PHE:CE2	2.77	0.53
16:AP:190:ASN:ND2	16:AP:193:GLU:OE1	2.39	0.53
42:BC:116:ARG:HG3	42:BC:140:LEU:HB3	1.90	0.53
44:BE:134:PRO:HA	44:BE:137:LYS:HZ2	1.72	0.53
45:BF:230:THR:HG21	45:BF:297:PHE:CZ	2.44	0.53
52:BM:83:ASP:HA	52:BM:89:HIS:HE1	1.74	0.53
54:BO:77:ALA:HA	58:BS:32:ARG:NH1	2.24	0.53
3:A2:170:ILE:HD11	3:A2:326:ILE:HG23	1.91	0.53
3:A2:271:PRO:HG3	50:BK:324:LYS:NZ	2.24	0.53
5:A4:155:ILE:HG23	5:A4:157:LYS:HG2	1.91	0.53
15:AN:187:ARG:NH1	39:AA:382:U:H2'	2.24	0.53
42:BC:283:ILE:HD11	42:BC:427:LEU:HD23	1.91	0.53
45:BF:251:ARG:HH12	45:BF:353:GLU:CD	2.17	0.53
61:BV:124:ASP:O	61:BV:128:LYS:HD3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:UD:11:UNK:HA	77:UD:14:UNK:HG3	1.91	0.53
2:A1:115:ASP:O	2:A1:116:HIS:HB2	2.09	0.53
2:A1:143:ARG:HG3	2:A1:147:GLU:HG2	1.90	0.53
4:A3:122:ASP:OD1	4:A3:122:ASP:N	2.40	0.53
9:A9:105:TRP:HB2	9:A9:110:GLN:HB2	1.90	0.53
12:AI:124:GLU:OE2	82:UL:8:UNK:O	2.27	0.53
14:AK:133:ARG:HD3	14:AK:134:ARG:HB3	1.89	0.53
14:AK:171:PRO:HD2	14:AK:176:ARG:HH11	1.74	0.53
31:AI:204:ASP:O	31:AI:208:VAL:HG23	2.09	0.53
39:AA:389:A:C6	39:AA:390:A:C2	2.97	0.53
41:BB:166:LEU:HD11	41:BB:240:HIS:CE1	2.44	0.53
41:BB:422:MET:HB3	41:BB:427:PHE:CE1	2.37	0.53
45:BF:395:ASN:O	45:BF:398:ARG:HD2	2.08	0.53
52:BM:233:PRO:HB3	57:BR:96:GLN:HE21	1.74	0.53
57:BR:74:THR:HB	57:BR:76:LYS:NZ	2.24	0.53
61:BV:153:PHE:O	61:BV:156:ARG:HG2	2.09	0.53
63:BX:125:ARG:NH1	63:BX:154:ARG:HB3	2.24	0.53
77:UD:215:UNK:HA	77:UD:218:UNK:HG3	1.90	0.53
2:A1:179:MET:HE1	49:BJ:243:LYS:HG3	1.91	0.53
3:A2:206:HIS:CE1	3:A2:304:GLU:HA	2.44	0.53
10:AE:54:ARG:NH1	68:Bc:67:GLN:HE22	2.07	0.53
10:AE:134:TYR:O	10:AE:222:THR:HG21	2.08	0.53
14:AK:56:PHE:HD2	61:BV:20:THR:HG22	1.74	0.53
22:AW:33:ARG:NH1	22:AW:39:LYS:HA	2.24	0.53
39:AA:527:U:O2'	39:AA:548:A:N6	2.29	0.53
39:AA:796:A:H2'	39:AA:797:A:H8	1.72	0.53
42:BC:112:ARG:H	42:BC:115:GLN:HE21	1.57	0.53
51:BL:173:GLY:O	51:BL:256:ARG:NH1	2.42	0.53
10:AE:144:LYS:HA	10:AE:163:PHE:HD1	1.74	0.52
11:AF:318:ALA:H	85:UX:1:UNK:HB1	1.74	0.52
12:AI:99:LEU:HD12	12:AI:100:LEU:HD13	1.90	0.52
12:AI:120:ASN:HB3	12:AI:129:TRP:CZ3	2.44	0.52
14:AK:230:GLN:HE21	14:AK:316:PRO:HB2	1.73	0.52
15:AN:28:LEU:HG	68:Bc:18:ARG:NH2	2.24	0.52
32:Ao:226:ARG:HG2	32:Ao:226:ARG:NH1	2.23	0.52
39:AA:1172:A:OP1	54:BO:130:ARG:NH2	2.42	0.52
41:BB:111:ILE:HG13	41:BB:413:LEU:HD21	1.90	0.52
47:BH:186:SER:HB3	47:BH:224:LEU:HG	1.90	0.52
48:BI:77:ASN:HA	48:BI:248:GLY:O	2.09	0.52
54:BO:142:GLU:HB2	54:BO:145:LEU:HD12	1.91	0.52
77:UD:7:UNK:HG2	77:UD:8:UNK:HG3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A0:41:THR:HG23	52:BM:79:ALA:HB2	1.92	0.52
2:A1:181:VAL:HG11	24:AY:299:MET:HB3	1.91	0.52
3:A2:69:LEU:CD2	50:BK:385:PRO:HG2	2.39	0.52
10:AE:370:ASP:OD1	10:AE:370:ASP:N	2.42	0.52
12:AI:15:PRO:O	66:Ba:104:ARG:NH2	2.42	0.52
12:AI:196:GLU:HG2	64:BY:137:ALA:HB3	1.92	0.52
22:AW:93:GLU:HG2	45:BF:388:ARG:HG2	1.91	0.52
22:AW:159:GLU:HG3	40:BA:753:ASP:CG	2.34	0.52
24:AY:4:ARG:HH22	39:AA:105:G:H8	1.54	0.52
26:Ad:196:ARG:NH1	69:Bd:63:ASN:O	2.43	0.52
27:Ae:109:ARG:NH1	39:AA:544:G:N3	2.57	0.52
30:Aj:56:VAL:HB	30:Aj:170:LEU:HB3	1.91	0.52
34:At:54:TYR:HE2	34:At:95:PRO:HG3	1.74	0.52
39:AA:196:G:H2'	39:AA:197:A:H8	1.73	0.52
41:BB:102:ILE:HG21	41:BB:393:LEU:HD11	1.91	0.52
45:BF:143:GLN:O	45:BF:146:LEU:HB3	2.09	0.52
50:BK:382:TYR:HE1	72:Bg:70:PRO:HD2	1.73	0.52
56:BQ:54:VAL:O	56:BQ:54:VAL:HG12	2.09	0.52
7:A6:56:GLU:HA	7:A6:59:ARG:HB2	1.92	0.52
11:AF:303:ARG:HG3	11:AF:337:ARG:NH1	2.24	0.52
13:AJ:82:ILE:HD11	52:BM:275:PHE:CD1	2.45	0.52
14:AK:196:THR:OG1	14:AK:197:PRO:HD2	2.09	0.52
14:AK:206:THR:HG22	14:AK:209:GLN:HB2	1.91	0.52
21:AV:100:GLN:HE22	39:AA:466:G:H21	1.56	0.52
33:Ap:39:LYS:NZ	39:AA:1111:A:C8	2.70	0.52
39:AA:1105:U:N3	39:AA:1161:A:N7	2.58	0.52
46:BG:39:PHE:CZ	46:BG:100:LEU:HD12	2.44	0.52
58:BS:29:ASN:O	58:BS:32:ARG:HB2	2.10	0.52
61:BV:59:ARG:NH2	61:BV:121:GLU:OE2	2.42	0.52
8:A8:83:ARG:HH22	8:A8:139:ARG:NH1	1.96	0.52
8:A8:172:LYS:NZ	16:AP:259:HIS:HD2	2.08	0.52
15:AN:53:GLN:HE22	15:AN:183:GLY:HA2	1.75	0.52
26:Ad:214:TRP:HE3	69:Bd:52:ARG:HB3	1.74	0.52
28:Af:58:ARG:HH11	39:AA:381:U:P	2.31	0.52
28:Af:141:GLU:HG2	28:Af:142:ASN:H	1.74	0.52
39:AA:1115:A:OP2	48:BI:26:ASN:ND2	2.42	0.52
45:BF:60:LEU:HA	45:BF:63:ARG:HD2	1.91	0.52
46:BG:74:ARG:CG	46:BG:74:ARG:NH1	2.60	0.52
68:Bc:45:LYS:NZ	68:Bc:48:GLU:OE1	2.30	0.52
14:AK:244:ARG:NH1	14:AK:314:ARG:NH1	2.58	0.52
16:AP:292:PRO:HD3	42:BC:498:ARG:NH1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AW:10:MET:HE2	22:AW:12:HIS:CD2	2.44	0.52
25:Ab:333:PRO:HB3	25:Ab:344:HIS:NE2	2.25	0.52
27:Ae:65:ILE:HD11	27:Ae:106:LEU:HG	1.92	0.52
39:AA:88:G:H4'	45:BF:403:LEU:HD23	1.89	0.52
42:BC:108:GLN:NE2	42:BC:242:LEU:H	2.01	0.52
45:BF:43:LEU:HD13	45:BF:252:MET:HG3	1.91	0.52
47:BH:99:GLN:NE2	47:BH:171:GLU:OE2	2.43	0.52
48:BI:260:TRP:HD1	48:BI:268:LYS:HA	1.73	0.52
50:BK:114:HIS:CE1	50:BK:194:ARG:HH22	2.28	0.52
50:BK:227:GLN:HA	50:BK:230:GLU:OE2	2.10	0.52
50:BK:321:GLU:OE1	50:BK:321:GLU:N	2.39	0.52
53:BN:121:LEU:HD23	53:BN:123:PHE:CZ	2.44	0.52
57:BR:70:TYR:HB3	57:BR:77:TYR:CD1	2.39	0.52
65:BZ:118:PRO:HG3	65:BZ:141:LYS:HA	1.91	0.52
2:A1:71:GLN:HG2	66:Ba:98:TRP:CE2	2.45	0.52
3:A2:155:ARG:NH1	3:A2:170:ILE:HG23	2.25	0.52
5:A4:52:THR:O	5:A4:56:GLN:NE2	2.43	0.52
31:Al:85:LEU:HB3	31:Al:87:LEU:HD23	1.91	0.52
33:Ap:173:LEU:HD11	33:Ap:203:PHE:CZ	2.45	0.52
39:AA:446:A:H5''	48:BI:273:LYS:HD2	1.91	0.52
41:BB:184:ARG:HA	41:BB:187:GLU:HB2	1.91	0.52
50:BK:97:ALA:O	50:BK:146:ARG:NH2	2.37	0.52
54:BO:171:LEU:O	54:BO:175:VAL:HG23	2.10	0.52
77:UD:73:UNK:HA	77:UD:76:UNK:HG3	1.92	0.52
6:A5:79:LYS:O	40:BA:785:ARG:NH2	2.43	0.52
15:AN:19:HIS:CD2	15:AN:21:HIS:H	2.28	0.52
15:AN:53:GLN:HA	15:AN:92:VAL:O	2.09	0.52
22:AW:71:ILE:HG23	22:AW:74:LEU:HB2	1.92	0.52
30:Aj:200:ARG:NH1	30:Aj:221:SER:O	2.43	0.52
39:AA:524:A:H2'	39:AA:525:A:H5'	1.92	0.52
40:BA:220:LEU:HD23	40:BA:223:LYS:HZ1	1.74	0.52
47:BH:111:TYR:HD2	47:BH:255:PHE:CZ	2.28	0.52
48:BI:147:TYR:CD2	48:BI:170:MET:HG2	2.40	0.52
49:BJ:195:PRO:HG2	49:BJ:200:ARG:HH21	1.75	0.52
51:BL:79:LYS:HG3	51:BL:83:HIS:HD2	1.74	0.52
68:Bc:51:TYR:OH	68:Bc:55:ARG:NH2	2.42	0.52
73:Bh:49:MET:N	73:Bh:61:PRO:HG2	2.24	0.52
77:UD:139:UNK:HG3	77:UD:144:UNK:HB2	1.92	0.52
8:A8:161:ASN:O	8:A8:162:ARG:HG2	2.10	0.52
11:AF:76:ILE:HB	59:BT:148:PRO:HG2	1.90	0.52
11:AF:265:HIS:HD2	22:AW:58:ARG:HH11	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AF:339:ASN:OD1	11:AF:339:ASN:N	2.42	0.52
11:AF:342:ASP:O	11:AF:346:HIS:HD2	1.92	0.52
16:AP:283:ARG:NH2	39:AA:167:U:H5''	2.25	0.52
18:AR:94:ARG:NH1	39:AA:1167:A:H2	2.08	0.52
39:AA:134:U:O2	39:AA:825:A:O2'	2.28	0.52
39:AA:469:G:N2	45:BF:36:GLY:O	2.43	0.52
40:BA:694:THR:HG22	40:BA:696:MET:HG3	1.91	0.52
53:BN:54:ASP:HB2	53:BN:214:TRP:CE2	2.45	0.52
14:AK:234:GLU:HA	14:AK:241:ARG:NH1	2.25	0.52
14:AK:253:GLU:HA	14:AK:256:GLU:HG2	1.91	0.52
16:AP:217:VAL:HG22	16:AP:236:ASN:O	2.10	0.52
39:AA:1166:A:O2'	40:BA:775:PRO:HG2	2.10	0.52
40:BA:160:CYS:SG	40:BA:190:THR:OG1	2.67	0.52
40:BA:710:LYS:HG2	40:BA:711:GLY:H	1.75	0.52
46:BG:39:PHE:CE2	46:BG:65:MET:HE3	2.44	0.52
49:BJ:306:GLN:HA	49:BJ:309:LYS:HG2	1.92	0.52
50:BK:135:GLU:HG3	50:BK:192:PHE:CG	2.45	0.52
58:BS:85:ASP:OD1	58:BS:86:GLU:N	2.43	0.52
69:Bd:25:LEU:HB3	69:Bd:36:MET:HE1	1.90	0.52
10:AE:70:LYS:NZ	10:AE:70:LYS:HB3	2.24	0.52
11:AF:102:ILE:HD11	11:AF:132:PRO:HG2	1.92	0.52
12:AI:70:ARG:HD2	12:AI:75:GLU:HG3	1.92	0.52
14:AK:219:ARG:HH11	14:AK:220:ILE:HG13	1.74	0.52
30:Aj:293:THR:HG22	30:Aj:295:GLU:HG3	1.92	0.52
40:BA:607:LYS:HE3	51:BL:36:GLY:HA3	1.91	0.52
65:BZ:6:ARG:HB2	65:BZ:189:LEU:HB2	1.91	0.52
73:Bh:7:PHE:HE1	73:Bh:42:ARG:HB3	1.75	0.52
2:A1:223:LYS:NZ	2:A1:223:LYS:H	2.07	0.51
3:A2:463:ILE:HD11	59:BT:42:MET:HE2	1.92	0.51
8:A8:166:ALA:CB	39:AA:72:A:H61	2.22	0.51
17:AQ:47:GLN:HE22	17:AQ:131:ARG:HA	1.74	0.51
18:AR:233:ARG:HD3	24:AY:73:ASP:OD2	2.10	0.51
20:AU:200:GLU:OE2	45:BF:154:LYS:HD3	2.10	0.51
26:Ad:173:SER:CB	26:Ad:176:LEU:HB2	2.40	0.51
26:Ad:214:TRP:CE3	69:Bd:52:ARG:HB3	2.45	0.51
35:Av:153:PHE:O	42:BC:463:ARG:NH2	2.43	0.51
40:BA:404:CYS:O	40:BA:405:ASP:HB2	2.10	0.51
42:BC:83:ILE:HG22	42:BC:86:GLN:H	1.75	0.51
48:BI:254:ARG:H	48:BI:254:ARG:HD2	1.75	0.51
54:BO:101:GLN:HG2	54:BO:117:LEU:HD23	1.92	0.51
63:BX:67:VAL:HG11	73:Bh:70:TRP:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A2:207:GLN:NE2	11:AF:411:ALA:HB1	2.25	0.51
4:A3:173:ARG:HH12	31:Al:181:LEU:HD11	1.75	0.51
6:A5:69:TRP:O	18:AR:150:LYS:N	2.43	0.51
13:AJ:67:GLN:HA	33:Ap:208:ILE:HD12	1.91	0.51
23:AX:108:LYS:HB3	23:AX:114:TRP:HB2	1.93	0.51
30:AJ:53:ARG:NH1	30:AJ:174:LEU:HD12	2.25	0.51
39:AA:277:A:H2'	39:AA:278:A:H8	1.75	0.51
39:AA:426:A:O2'	39:AA:427:U:OP1	2.25	0.51
41:BB:87:LEU:HD13	41:BB:90:LYS:NZ	2.26	0.51
42:BC:62:GLN:HE21	55:BP:176:THR:HG21	1.74	0.51
77:UD:193:UNK:HA	77:UD:196:UNK:HG3	1.92	0.51
5:A4:21:PRO:HG3	42:BC:211:TRP:CD1	2.45	0.51
11:AF:154:ARG:NH1	59:BT:32:THR:HG21	2.24	0.51
14:AK:323:GLN:HG2	14:AK:329:MET:HE1	1.90	0.51
18:AR:185:ARG:HH21	44:BE:411:LYS:HZ1	1.58	0.51
23:AX:152:LEU:O	23:AX:154:ASN:N	2.44	0.51
33:Ap:66:CYS:HB3	33:Ap:70:GLU:HB2	1.92	0.51
39:AA:524:A:N6	39:AA:559:A:C4	2.78	0.51
40:BA:141:GLU:OE1	40:BA:141:GLU:N	2.42	0.51
40:BA:376:ARG:O	40:BA:380:ASN:ND2	2.43	0.51
41:BB:355:GLU:O	41:BB:363:ARG:NH2	2.43	0.51
42:BC:286:SER:H	42:BC:289:ASN:HD22	1.59	0.51
61:BV:31:GLN:NE2	61:BV:33:TYR:O	2.43	0.51
77:UD:164:UNK:HA	77:UD:167:UNK:HG3	1.91	0.51
2:A1:75:VAL:HG12	2:A1:121:PRO:HG2	1.93	0.51
5:A4:59:GLU:OE2	26:Ad:206:THR:HA	2.11	0.51
6:A5:49:LEU:HD12	24:AY:1:MET:H2	1.76	0.51
8:A8:56:LEU:HD11	11:AF:327:LYS:HZ3	1.72	0.51
10:AE:222:THR:OG1	10:AE:224:ASP:OD1	2.20	0.51
12:AI:136:THR:HG1	12:AI:162:TYR:HH	1.55	0.51
14:AK:172:LEU:HD23	14:AK:225:TYR:HE1	1.74	0.51
22:AW:239:GLU:OE2	40:BA:601:ARG:NH2	2.42	0.51
22:AW:273:ILE:HG21	44:BE:250:ILE:HD12	1.92	0.51
26:Ad:236:ASN:OD1	26:Ad:237:ASN:N	2.43	0.51
30:AJ:144:ASP:HB2	46:BG:70:ARG:HH11	1.72	0.51
31:Al:64:ARG:HH21	31:Al:75:ARG:HD3	1.74	0.51
40:BA:508:ASP:HA	40:BA:511:ARG:HG2	1.92	0.51
42:BC:111:LEU:HD13	42:BC:165:HIS:HD2	1.75	0.51
74:UA:29:UNK:O	74:UA:33:UNK:HB2	2.11	0.51
12:AI:45:ARG:O	12:AI:49:THR:OG1	2.21	0.51
20:AU:50:ARG:HH11	20:AU:50:ARG:CG	2.21	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AU:63:ARG:NH1	39:AA:460:U:H4'	2.26	0.51
23:AX:145:ARG:HE	23:AX:162:GLN:HB2	1.75	0.51
26:Ad:42:MET:HE1	69:Bd:103:GLY:HA2	1.93	0.51
39:AA:318:A:OP1	52:BM:65:HIS:NE2	2.43	0.51
39:AA:318:A:H61	39:AA:343:U:H3	1.59	0.51
42:BC:266:PRO:HA	42:BC:286:SER:HA	1.93	0.51
42:BC:412:ALA:HA	42:BC:417:LEU:HB2	1.92	0.51
44:BE:350:ASN:O	44:BE:354:GLU:N	2.37	0.51
47:BH:131:TYR:CD1	47:BH:171:GLU:HB2	2.46	0.51
47:BH:228:VAL:HG12	47:BH:229:ALA:O	2.10	0.51
54:BO:97:LYS:HZ2	54:BO:98:ARG:HH21	1.59	0.51
6:A5:64:LYS:HZ3	6:A5:80:PRO:C	2.09	0.51
8:A8:172:LYS:NZ	16:AP:259:HIS:CD2	2.79	0.51
11:AF:365:GLU:HG2	11:AF:366:HIS:N	2.26	0.51
16:AP:182:TRP:HE3	31:Al:119:VAL:HG11	1.76	0.51
18:AR:71:ARG:NH1	73:Bh:19:ASN:HB2	2.25	0.51
18:AR:154:ARG:HD2	44:BE:400:GLY:O	2.10	0.51
26:Ad:196:ARG:NH1	69:Bd:64:GLU:HA	2.25	0.51
29:Ag:98:CYS:HB2	29:Ag:101:HIS:HD2	1.75	0.51
30:Aj:53:ARG:HD2	30:Aj:174:LEU:HB2	1.92	0.51
33:Ap:55:HIS:CE1	48:BI:28:ALA:HA	2.45	0.51
39:AA:440:U:H4'	39:AA:441:A:O5'	2.11	0.51
39:AA:945:U:H3	39:AA:955:G:H22	1.59	0.51
42:BC:170:GLU:HB2	42:BC:227:ASP:OD2	2.10	0.51
46:BG:74:ARG:N	46:BG:74:ARG:HD3	2.26	0.51
48:BI:228:GLN:HG3	71:Bf:106:SER:O	2.11	0.51
57:BR:74:THR:HB	57:BR:76:LYS:HZ3	1.76	0.51
58:BS:29:ASN:N	58:BS:29:ASN:HD22	2.08	0.51
63:BX:160:TYR:O	77:UD:41:UNK:HG1	2.11	0.51
64:BY:119:LYS:HA	64:BY:122:ALA:HB3	1.92	0.51
3:A2:59:ASN:ND2	23:AX:175:TYR:OH	2.41	0.51
9:A9:100:TRP:CG	9:A9:101:LEU:H	2.28	0.51
10:AE:166:PRO:CG	10:AE:190:MET:HG2	2.41	0.51
18:AR:57:LYS:CE	18:AR:66:ARG:HH12	2.24	0.51
28:Af:51:PRO:O	39:AA:832:A:H4'	2.10	0.51
44:BE:341:LYS:O	44:BE:345:THR:OG1	2.22	0.51
52:BM:235:LEU:HD23	57:BR:176:GLU:OE2	2.11	0.51
53:BN:26:MET:HE3	53:BN:53:ARG:NH1	2.25	0.51
3:A2:40:ARG:NH2	3:A2:100:GLU:OE1	2.44	0.51
5:A4:82:PHE:HB2	5:A4:102:ILE:HD13	1.93	0.51
22:AW:33:ARG:H	22:AW:33:ARG:HD3	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Ab:283:ASN:HD21	25:Ab:355:VAL:HG23	1.76	0.51
26:Ad:174:PHE:O	26:Ad:177:VAL:HG23	2.11	0.51
27:Ae:76:LEU:HD23	27:Ae:76:LEU:H	1.76	0.51
28:Af:65:LEU:HG	28:Af:69:SER:HB3	1.92	0.51
39:AA:1166:A:H1'	39:AA:1167:A:C2	2.46	0.51
41:BB:439:ASP:O	41:BB:443:ARG:HG2	2.11	0.51
47:BH:71:LYS:HZ1	76:UC:4:UNK:HG1	1.73	0.51
53:BN:9:TRP:N	60:BU:180:ALA:O	2.44	0.51
61:BV:59:ARG:HH12	61:BV:117:TRP:HA	1.74	0.51
3:A2:189:GLU:HB3	3:A2:315:PRO:HG3	1.93	0.51
3:A2:402:ARG:NH1	39:AA:85:U:N3	2.59	0.51
10:AE:184:LYS:NZ	39:AA:1110:A:H4'	2.26	0.51
15:AN:11:PRO:HB2	39:AA:815:U:C4	2.46	0.51
21:AV:191:TYR:CE1	29:Ag:126:ARG:NH1	2.79	0.51
22:AW:99:VAL:HG11	51:BL:159:TYR:CZ	2.46	0.51
23:AX:61:ILE:HG12	35:Av:33:ILE:HG13	1.92	0.51
30:Aj:24:ARG:HH12	69:Bd:139:PRO:CG	2.16	0.51
34:At:25:ARG:NH1	39:AA:379:U:H5'	2.26	0.51
39:AA:572:U:H2'	39:AA:573:U:H5'	1.93	0.51
40:BA:630:MET:O	40:BA:634:ILE:HD13	2.11	0.51
42:BC:266:PRO:HG3	42:BC:490:LEU:HD11	1.92	0.51
53:BN:90:LEU:HA	53:BN:95:HIS:CD2	2.46	0.51
73:Bh:49:MET:HG3	73:Bh:61:PRO:HG3	1.93	0.51
10:AE:54:ARG:HB2	68:Bc:57:TRP:CZ2	2.46	0.51
10:AE:57:TYR:HB3	78:UE:1:UNK:HG1	1.93	0.51
14:AK:133:ARG:NH1	14:AK:134:ARG:HH21	2.06	0.51
14:AK:192:ILE:HD12	61:BV:52:PHE:CE1	2.46	0.51
25:Ab:144:TYR:HH	55:BP:73:SER:HG	1.50	0.51
46:BG:117:GLN:HA	46:BG:125:LEU:HD21	1.91	0.51
57:BR:95:ARG:O	57:BR:95:ARG:HD3	2.11	0.51
58:BS:108:THR:HB	58:BS:109:PRO:HD3	1.93	0.51
70:Be:63:CYS:HB3	70:Be:66:CYS:O	2.11	0.51
71:Bf:86:ILE:HG23	71:Bf:109:HIS:HE2	1.75	0.51
5:A4:130:ARG:NH1	5:A4:132:TRP:CZ2	2.80	0.50
15:AN:54:LEU:HD11	15:AN:129:LEU:HB3	1.94	0.50
15:AN:144:ARG:HH11	39:AA:122:U:P	2.32	0.50
24:AY:233:PRO:HG2	24:AY:236:ASP:OD2	2.11	0.50
25:Ab:83:GLU:OE1	25:Ab:83:GLU:N	2.44	0.50
25:Ab:167:VAL:HA	25:Ab:203:THR:HA	1.92	0.50
26:Ad:96:ALA:O	26:Ad:99:THR:HB	2.11	0.50
39:AA:410:U:O2'	39:AA:414:A:N6	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:AA:1113:U:O4	40:BA:300:ARG:NH1	2.44	0.50
41:BB:148:LYS:HB2	41:BB:148:LYS:NZ	2.27	0.50
46:BG:336:LYS:HG2	46:BG:340:GLN:NE2	2.23	0.50
47:BH:165:GLN:O	47:BH:241:ARG:NH1	2.43	0.50
48:BI:26:ASN:HD22	48:BI:29:TRP:HD1	1.57	0.50
48:BI:232:LEU:HD23	71:Bf:99:ILE:HG12	1.93	0.50
50:BK:108:GLN:HE21	50:BK:251:ALA:HB2	1.76	0.50
57:BR:170:TYR:HE1	57:BR:188:ARG:HE	1.59	0.50
10:AE:122:ASP:O	33:Ap:109:GLN:NE2	2.36	0.50
14:AK:48:ARG:NH1	33:Ap:213:PRO:HA	2.26	0.50
16:AP:193:GLU:HG3	62:BW:6:GLY:HA2	1.91	0.50
20:AU:124:PRO:HB3	32:Ao:24:SER:HB2	1.93	0.50
21:AV:91:VAL:HG12	21:AV:178:ILE:HD11	1.91	0.50
26:Ad:95:GLU:HA	26:Ad:98:GLU:HG2	1.93	0.50
26:Ad:277:TYR:CE1	42:BC:237:PRO:HG2	2.46	0.50
40:BA:419:THR:HG22	40:BA:420:ALA:H	1.75	0.50
41:BB:77:HIS:HA	41:BB:80:ILE:HG22	1.92	0.50
42:BC:452:LYS:HE3	42:BC:464:ILE:HD11	1.92	0.50
53:BN:108:PHE:HE1	53:BN:128:ARG:HD2	1.75	0.50
54:BO:107:LEU:HD12	54:BO:212:PRO:HB2	1.92	0.50
60:BU:114:THR:O	60:BU:116:ARG:N	2.45	0.50
74:UA:21:UNK:O	74:UA:26:UNK:N	2.45	0.50
1:A0:181:ARG:NH1	1:A0:182:TYR:OH	2.45	0.50
10:AE:317:ASP:OD1	10:AE:380:GLN:NE2	2.42	0.50
12:AI:48:ARG:CG	12:AI:48:ARG:NH1	2.72	0.50
13:AJ:16:ARG:NH1	13:AJ:42:PRO:HD3	2.26	0.50
17:AQ:36:TYR:HB3	79:UG:17:UNK:HG3	1.92	0.50
20:AU:50:ARG:HG3	20:AU:50:ARG:NH1	2.23	0.50
39:AA:387:A:HO2'	39:AA:388:U:P	2.34	0.50
42:BC:285:TYR:OH	42:BC:427:LEU:O	2.29	0.50
42:BC:298:GLY:HA2	42:BC:303:LEU:HD23	1.93	0.50
42:BC:497:GLU:OE2	55:BP:209:LYS:NZ	2.30	0.50
45:BF:60:LEU:CA	45:BF:63:ARG:HH11	2.25	0.50
45:BF:171:ARG:NH2	45:BF:190:ASN:OD1	2.39	0.50
47:BH:88:GLU:HG3	76:UC:2:UNK:HG1	1.92	0.50
55:BP:194:VAL:HG12	55:BP:196:ALA:H	1.77	0.50
2:A1:115:ASP:OD1	12:AI:152:ARG:NH2	2.43	0.50
3:A2:160:ARG:HH22	3:A2:332:ASP:CG	2.19	0.50
3:A2:186:GLU:HB3	12:AI:52:TRP:CZ3	2.46	0.50
10:AE:90:GLN:HB2	71:Bf:110:PHE:HB2	1.92	0.50
22:AW:131:HIS:NE2	24:AY:46:GLU:OE1	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Aj:192:GLU:O	30:Aj:205:ARG:NH2	2.42	0.50
33:Ap:149:GLU:HB3	48:BI:220:THR:HG21	1.93	0.50
40:BA:791:PHE:HE1	40:BA:801:ARG:NH1	2.09	0.50
45:BF:195:LEU:HD11	45:BF:216:LEU:HD22	1.94	0.50
45:BF:198:LEU:HD22	45:BF:209:ILE:HG22	1.93	0.50
50:BK:360:GLU:H	50:BK:360:GLU:CD	2.17	0.50
52:BM:274:GLY:O	52:BM:277:LYS:N	2.40	0.50
56:BQ:18:TYR:OH	56:BQ:164:VAL:O	2.26	0.50
56:BQ:132:MET:HE2	56:BQ:161:CYS:SG	2.51	0.50
2:A1:156:ILE:HG23	49:BJ:279:GLY:HA2	1.93	0.50
6:A5:50:LYS:NZ	6:A5:50:LYS:HB3	2.26	0.50
12:AI:70:ARG:HG3	70:Be:79:GLN:HG2	1.94	0.50
16:AP:69:ARG:NH1	39:AA:470:G:OP1	2.45	0.50
16:AP:321:LEU:HD13	35:Av:151:PRO:HB3	1.93	0.50
19:AT:10:ARG:HG2	39:AA:1107:U:N3	2.26	0.50
27:Ae:151:THR:O	27:Ae:154:ARG:HG2	2.12	0.50
29:Ag:238:MET:HG2	52:BM:257:PHE:CD2	2.46	0.50
31:Al:69:LYS:HB3	31:Al:206:ARG:HH22	1.76	0.50
44:BE:419:MET:HG2	44:BE:429:VAL:HG21	1.93	0.50
53:BN:26:MET:HE3	53:BN:53:ARG:HH11	1.77	0.50
56:BQ:105:ASN:HB3	56:BQ:141:GLY:HA3	1.93	0.50
57:BR:40:ARG:HD2	57:BR:95:ARG:HH12	1.76	0.50
64:BY:85:TRP:CD2	76:UC:11:UNK:HB2	2.47	0.50
77:UD:200:UNK:HA	77:UD:203:UNK:HG3	1.93	0.50
5:A4:88:GLY:HA3	26:Ad:133:VAL:HG22	1.94	0.50
11:AF:262:ASP:OD1	11:AF:264:ARG:HD3	2.12	0.50
18:AR:107:GLY:HA3	60:BU:171:ARG:C	2.37	0.50
24:AY:189:GLU:OE2	50:BK:328:LEU:HD21	2.12	0.50
39:AA:389:A:C6	39:AA:446:A:N6	2.68	0.50
41:BB:359:HIS:HD2	41:BB:363:ARG:HH12	1.59	0.50
50:BK:137:TYR:CZ	50:BK:141:ILE:HG13	2.47	0.50
57:BR:40:ARG:HD2	57:BR:95:ARG:HH22	1.76	0.50
58:BS:74:GLU:HA	58:BS:107:ILE:HD12	1.93	0.50
79:UN:5:UNK:HG1	79:UN:11:UNK:C	2.41	0.50
2:A1:206:ILE:HG23	24:AY:297:CYS:SG	2.51	0.50
5:A4:97:PHE:CE1	69:Bd:118:VAL:HG13	2.46	0.50
10:AE:115:TYR:OH	71:Bf:48:TRP:O	2.29	0.50
10:AE:134:TYR:HB2	68:Bc:70:PHE:CD2	2.47	0.50
21:AV:56:ALA:N	21:AV:58:GLY:H	2.10	0.50
21:AV:122:ARG:NH1	28:Af:102:PRO:HA	2.26	0.50
24:AY:31:ARG:NH1	39:AA:13:A:H1'	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Ap:108:LEU:HG	68:Bc:48:GLU:HG3	1.94	0.50
41:BB:87:LEU:HD13	41:BB:90:LYS:HZ3	1.76	0.50
42:BC:86:GLN:NE2	42:BC:124:ASN:HD22	2.10	0.50
42:BC:476:LYS:HB2	42:BC:500:PHE:HA	1.94	0.50
47:BH:122:HIS:CD2	47:BH:124:PHE:HB2	2.46	0.50
60:BU:139:ARG:HH11	72:Bg:35:LEU:HD21	1.77	0.50
2:A1:13:PHE:HA	16:AP:357:PRO:HB3	1.92	0.50
3:A2:275:LEU:HD11	50:BK:326:VAL:HG11	1.93	0.50
11:AF:264:ARG:HD2	45:BF:376:ILE:HD11	1.94	0.50
13:AJ:73:ARG:HE	13:AJ:81:ASN:HB3	1.76	0.50
14:AK:133:ARG:NH1	14:AK:134:ARG:NH2	2.60	0.50
14:AK:171:PRO:O	14:AK:176:ARG:NH1	2.45	0.50
16:AP:222:GLY:N	39:AA:172:U:OP2	2.23	0.50
18:AR:94:ARG:NH2	18:AR:146:MET:HB3	2.26	0.50
25:Ab:109:PHE:CE1	42:BC:243:VAL:HG11	2.46	0.50
25:Ab:487:LEU:HB3	25:Ab:507:ARG:HH21	1.76	0.50
27:Ae:75:ARG:NH1	27:Ae:135:THR:O	2.45	0.50
33:Ap:227:HIS:CE1	36:AB:17:ALA:HB1	2.47	0.50
34:At:51:ILE:O	67:Bb:90:PRO:HG2	2.12	0.50
40:BA:137:CYS:HB3	40:BA:141:GLU:HG2	1.93	0.50
41:BB:347:LYS:NZ	41:BB:405:TRP:CD2	2.80	0.50
42:BC:230:MET:SD	42:BC:230:MET:N	2.75	0.50
46:BG:149:THR:HG21	46:BG:154:ALA:N	2.27	0.50
48:BI:103:THR:H	48:BI:106:HIS:HD2	1.60	0.50
53:BN:207:ASN:HB3	73:Bh:28:ARG:HH11	1.75	0.50
58:BS:39:LEU:HD11	58:BS:106:ILE:HG12	1.94	0.50
59:BT:32:THR:OG1	59:BT:33:ASN:N	2.45	0.50
62:BW:154:PRO:HA	62:BW:157:ASN:HB2	1.93	0.50
2:A1:76:ILE:O	2:A1:123:VAL:HG23	2.12	0.50
3:A2:164:PHE:HB2	49:BJ:310:PHE:CD2	2.46	0.50
16:AP:188:ARG:NH1	16:AP:203:ALA:O	2.44	0.50
18:AR:227:LEU:HD21	18:AR:231:LYS:HE3	1.93	0.50
27:Ae:109:ARG:NH1	39:AA:544:G:C2	2.80	0.50
42:BC:57:THR:O	42:BC:448:HIS:NE2	2.35	0.50
45:BF:386:VAL:HG12	45:BF:387:ASN:H	1.77	0.50
46:BG:192:ARG:O	46:BG:195:ILE:HG22	2.12	0.50
57:BR:108:TYR:OH	57:BR:164:HIS:HD2	1.95	0.50
2:A1:184:MET:HB3	2:A1:204:TYR:HE2	1.77	0.49
3:A2:64:MET:CE	23:AX:148:LEU:HD11	2.42	0.49
5:A4:38:LYS:NZ	25:Ab:58:GLN:OE1	2.28	0.49
11:AF:215:ASP:N	11:AF:215:ASP:OD1	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AI:58:SER:HB2	12:AI:63:ARG:HE	1.77	0.49
15:AN:39:ARG:NH1	15:AN:39:ARG:CG	2.75	0.49
18:AR:253:LYS:O	18:AR:256:GLU:HG3	2.12	0.49
22:AW:170:LYS:HE3	24:AY:63:ARG:HA	1.95	0.49
39:AA:559:A:H2'	39:AA:560:G:H8	1.76	0.49
40:BA:440:LYS:NZ	40:BA:476:SER:O	2.45	0.49
41:BB:185:ARG:HE	41:BB:193:ASN:H	1.58	0.49
42:BC:260:LEU:HD13	55:BP:92:VAL:HG11	1.94	0.49
49:BJ:259:ASP:OD1	49:BJ:259:ASP:N	2.44	0.49
53:BN:108:PHE:CE1	53:BN:128:ARG:HD2	2.48	0.49
74:UA:33:UNK:HG3	74:UA:38:UNK:HB1	1.94	0.49
2:A1:114:LEU:HB3	2:A1:163:ARG:HG2	1.94	0.49
8:A8:58:PRO:HA	11:AF:318:ALA:CB	2.42	0.49
12:AI:152:ARG:HB2	49:BJ:292:ARG:HE	1.77	0.49
13:AJ:73:ARG:NH1	13:AJ:83:PHE:HE1	2.11	0.49
14:AK:54:ARG:NH1	39:AA:402:A:H5'	2.27	0.49
14:AK:136:THR:O	39:AA:405:U:H5'	2.13	0.49
32:Ao:236:ARG:NH1	52:BM:260:MET:O	2.31	0.49
35:Av:162:ALA:O	35:Av:166:TYR:HB2	2.12	0.49
39:AA:561:U:H5'	39:AA:562:G:OP2	2.12	0.49
43:BD:203:ASP:CB	43:BD:451:ALA:HB2	2.41	0.49
44:BE:235:GLU:O	44:BE:239:ILE:HG22	2.11	0.49
47:BH:252:TYR:HB3	47:BH:255:PHE:O	2.12	0.49
53:BN:97:ARG:HB2	73:Bh:87:CYS:HB2	1.94	0.49
3:A2:470:ASP:OD1	3:A2:470:ASP:N	2.40	0.49
5:A4:12:SER:OG	39:AA:951:C:N3	2.45	0.49
7:A6:67:VAL:HG22	7:A6:84:GLU:HB2	1.94	0.49
13:AJ:27:ARG:HH21	48:BI:278:GLU:HB2	1.77	0.49
25:Ab:175:ARG:HH11	42:BC:93:ALA:HB3	1.76	0.49
30:Aj:74:ARG:O	30:Aj:77:GLN:HB3	2.12	0.49
34:At:125:TYR:CE1	34:At:129:TYR:HD2	2.30	0.49
45:BF:218:ILE:HG23	45:BF:292:ARG:HH12	1.78	0.49
18:AR:60:ALA:HB1	18:AR:65:HIS:CD2	2.47	0.49
30:Aj:293:THR:HG21	46:BG:143:ARG:NH1	2.27	0.49
39:AA:552:U:OP2	39:AA:554:A:N6	2.42	0.49
39:AA:1164:A:O2'	39:AA:1165:G:OP1	2.29	0.49
44:BE:300:ARG:HH11	44:BE:323:TRP:HZ3	1.59	0.49
45:BF:218:ILE:O	45:BF:221:GLU:HG3	2.12	0.49
51:BL:126:LYS:NZ	51:BL:141:ASN:O	2.41	0.49
60:BU:144:LYS:O	60:BU:147:GLU:HG3	2.11	0.49
66:Ba:59:ASP:HB2	66:Ba:66:VAL:HG22	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A3:121:LEU:HD21	16:AP:18:ARG:HE	1.77	0.49
4:A3:163:LYS:HA	4:A3:166:PHE:HB3	1.94	0.49
5:A4:109:ARG:NH1	69:Bd:130:GLU:O	2.41	0.49
8:A8:93:ARG:NH2	55:BP:217:PRO:O	2.45	0.49
12:AI:82:ASP:HB3	12:AI:85:TYR:CD2	2.48	0.49
12:AI:112:ARG:NH1	64:BY:145:TRP:CE3	2.81	0.49
12:AI:181:THR:HG22	12:AI:182:PRO:HD2	1.94	0.49
14:AK:94:PHE:H	61:BV:91:LYS:NZ	2.10	0.49
28:Af:163:THR:O	28:Af:168:GLN:NE2	2.46	0.49
39:AA:454:U:C4	48:BI:319:ARG:NH1	2.80	0.49
41:BB:202:VAL:HG11	41:BB:378:MET:HB3	1.94	0.49
53:BN:94:ARG:HD3	73:Bh:92:TRP:CZ3	2.47	0.49
54:BO:83:VAL:HG12	54:BO:160:MET:HE3	1.95	0.49
70:Be:93:ARG:NH1	70:Be:102:GLY:O	2.46	0.49
75:UB:31:UNK:HA	75:UB:34:UNK:HG3	1.94	0.49
1:A0:165:PRO:HB2	26:Ad:207:THR:HG22	1.95	0.49
4:A3:107:LYS:HB2	32:Ao:136:THR:HG21	1.95	0.49
6:A5:36:ARG:NH1	24:AY:6:ARG:HB3	2.27	0.49
14:AK:186:ARG:NH2	39:AA:420:A:N7	2.59	0.49
40:BA:135:SER:O	54:BO:153:ARG:NH1	2.46	0.49
40:BA:328:VAL:HG12	40:BA:330:ASP:OD1	2.13	0.49
41:BB:201:PRO:HA	60:BU:106:ARG:HG3	1.94	0.49
42:BC:263:PRO:O	42:BC:287:HIS:HB2	2.12	0.49
45:BF:362:HIS:CD2	62:BW:176:ARG:HG3	2.47	0.49
51:BL:115:ALA:HB1	51:BL:189:ARG:HG3	1.94	0.49
66:Ba:47:ASP:O	66:Ba:50:LYS:HG2	2.13	0.49
2:A1:127:MET:O	2:A1:130:VAL:HG12	2.12	0.49
3:A2:271:PRO:HG3	50:BK:324:LYS:CD	2.43	0.49
13:AJ:47:LYS:HE2	13:AJ:53:TYR:HD1	1.78	0.49
18:AR:172:ASP:OD1	18:AR:173:ASN:N	2.44	0.49
22:AW:120:GLU:HA	22:AW:123:VAL:HG12	1.95	0.49
24:AY:85:LEU:HB3	24:AY:89:GLN:HE21	1.78	0.49
24:AY:166:ARG:HD3	50:BK:297:PHE:CD1	2.43	0.49
42:BC:107:LEU:HD22	55:BP:88:LEU:HD11	1.95	0.49
45:BF:161:PRO:O	45:BF:167:ARG:NH1	2.45	0.49
47:BH:243:LEU:HB3	47:BH:246:GLN:HE21	1.77	0.49
53:BN:37:ASN:HB3	58:BS:48:GLY:HA3	1.95	0.49
63:BX:125:ARG:HH11	63:BX:155:ARG:HD2	1.78	0.49
67:Bb:45:LYS:HB3	67:Bb:49:LYS:NZ	2.26	0.49
68:Bc:17:HIS:HD2	68:Bc:24:ARG:HH22	1.61	0.49
74:UA:39:UNK:HG2	74:UA:40:UNK:HG2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A2:69:LEU:HD22	50:BK:386:TYR:HD2	1.78	0.49
3:A2:207:GLN:HE21	11:AF:411:ALA:HB1	1.78	0.49
5:A4:155:ILE:HD13	5:A4:157:LYS:HE3	1.95	0.49
7:A6:86:LYS:HE3	7:A6:88:LYS:O	2.13	0.49
11:AF:106:TYR:HA	31:AI:139:HIS:CE1	2.47	0.49
11:AF:276:GLY:O	11:AF:352:THR:HG21	2.12	0.49
15:AN:146:LEU:HA	15:AN:149:ARG:HE	1.78	0.49
39:AA:492:U:O2'	39:AA:494:U:OP1	2.31	0.49
39:AA:820:A:H2'	39:AA:821:U:C6	2.48	0.49
40:BA:373:ALA:HA	40:BA:376:ARG:NH1	2.28	0.49
40:BA:533:LEU:HD13	51:BL:234:PRO:HD3	1.94	0.49
46:BG:39:PHE:CD2	46:BG:65:MET:HE3	2.48	0.49
65:BZ:24:LYS:HB2	65:BZ:157:ALA:HB2	1.95	0.49
2:A1:55:TYR:OH	2:A1:61:THR:OG1	2.26	0.49
2:A1:125:ALA:HB2	12:AI:99:LEU:HD23	1.95	0.49
2:A1:159:HIS:ND1	49:BJ:281:ALA:HB3	2.28	0.49
11:AF:80:GLN:O	59:BT:146:LYS:NZ	2.46	0.49
15:AN:69:HIS:NE2	15:AN:81:ASP:OD2	2.45	0.49
22:AW:33:ARG:HH12	22:AW:39:LYS:CD	2.25	0.49
23:AX:66:ARG:N	39:AA:284:U:OP1	2.42	0.49
33:Ap:126:TRP:CG	79:UN:4:UNK:HG1	2.48	0.49
39:AA:40:U:C6	39:AA:40:U:H5''	2.48	0.49
39:AA:521:G:O2'	39:AA:561:U:O4	2.28	0.49
40:BA:330:ASP:OD1	40:BA:330:ASP:N	2.46	0.49
46:BG:80:ASP:CG	46:BG:81:HIS:H	2.20	0.49
48:BI:196:ARG:HH22	48:BI:223:GLN:HE21	1.61	0.49
53:BN:13:VAL:HG13	53:BN:14:HIS:H	1.78	0.49
53:BN:111:PHE:HE1	53:BN:122:CYS:HG	1.61	0.49
61:BV:108:TYR:HA	61:BV:111:LYS:HZ1	1.78	0.49
4:A3:181:ASP:OD2	31:AI:182:LYS:NZ	2.46	0.49
12:AI:205:TYR:O	12:AI:208:ARG:NH1	2.46	0.49
15:AN:93:MET:HB3	15:AN:98:TRP:CE2	2.47	0.49
16:AP:240:GLU:HA	16:AP:243:ARG:HG2	1.93	0.49
22:AW:48:ALA:HB3	24:AY:29:MET:HG3	1.94	0.49
24:AY:66:ARG:HD2	39:AA:513:U:O2'	2.13	0.49
39:AA:17:A:H4'	39:AA:18:G:H5'	1.93	0.49
40:BA:532:MET:HA	40:BA:535:SER:HB2	1.95	0.49
47:BH:194:ARG:HH12	47:BH:196:LEU:HD21	1.76	0.49
61:BV:49:ARG:HH12	61:BV:73:LEU:HD23	1.77	0.49
61:BV:58:GLY:O	61:BV:63:ARG:HD3	2.13	0.49
61:BV:110:ASN:O	61:BV:114:ALA:N	2.39	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A1:142:LYS:HZ1	2:A1:143:ARG:HH12	1.53	0.48
4:A3:89:ARG:HH11	32:Ao:113:GLN:HE21	1.61	0.48
5:A4:82:PHE:HB3	5:A4:90:LEU:HD12	1.95	0.48
8:A8:77:MET:HE3	39:AA:163:U:H5'	1.95	0.48
8:A8:141:ARG:NH2	16:AP:164:ASN:HA	2.28	0.48
14:AK:228:LEU:O	14:AK:231:ARG:HD2	2.12	0.48
14:AK:301:MET:HB3	14:AK:306:MET:HG3	1.94	0.48
24:AY:236:ASP:CG	27:Ae:154:ARG:HD3	2.37	0.48
25:Ab:85:GLU:O	25:Ab:88:THR:N	2.39	0.48
30:Aj:75:GLU:HA	30:Aj:78:ARG:HG2	1.94	0.48
30:Aj:163:ARG:HB2	30:Aj:262:ALA:HB1	1.95	0.48
39:AA:379:U:N3	84:UU:7:UNK:HB2	2.28	0.48
39:AA:485:A:O2'	39:AA:486:A:OP1	2.30	0.48
46:BG:283:ASP:OD1	46:BG:283:ASP:N	2.46	0.48
50:BK:311:GLU:H	50:BK:311:GLU:CD	2.19	0.48
53:BN:64:LEU:HD11	53:BN:108:PHE:HD2	1.77	0.48
59:BT:60:ARG:NH1	66:Ba:148:ALA:HB1	2.28	0.48
59:BT:140:GLU:HA	59:BT:175:ARG:NH1	2.28	0.48
10:AE:94:ASP:O	10:AE:98:GLU:HB2	2.13	0.48
12:AI:183:ARG:HA	12:AI:186:GLU:CD	2.37	0.48
14:AK:227:THR:HG22	14:AK:231:ARG:HH21	1.78	0.48
16:AP:257:MET:HG2	62:BW:11:ARG:NH1	2.23	0.48
24:AY:104:PHE:O	24:AY:139:ASN:ND2	2.45	0.48
25:Ab:365:SER:OG	25:Ab:366:LYS:N	2.45	0.48
26:Ad:220:LEU:HB3	69:Bd:47:ARG:HB3	1.95	0.48
33:Ap:200:VAL:O	33:Ap:203:PHE:HB3	2.12	0.48
39:AA:384:U:H2'	39:AA:385:A:H8	1.78	0.48
40:BA:464:LEU:HD23	40:BA:467:LEU:HD12	1.95	0.48
41:BB:83:ASN:HA	41:BB:87:LEU:HD23	1.95	0.48
49:BJ:192:ARG:HH22	74:UA:34:UNK:CB	2.27	0.48
52:BM:81:TRP:O	52:BM:82:ASN:HB2	2.11	0.48
52:BM:87:ARG:O	52:BM:90:GLN:HG2	2.12	0.48
56:BQ:201:LYS:O	56:BQ:205:THR:OG1	2.27	0.48
57:BR:23:LEU:HD21	57:BR:83:ARG:NH1	2.27	0.48
65:BZ:96:GLN:HB3	65:BZ:132:GLY:HA3	1.94	0.48
13:AJ:65:ASP:O	13:AJ:68:LYS:HG2	2.14	0.48
14:AK:28:GLU:OE2	14:AK:30:LEU:HB2	2.13	0.48
16:AP:43:LYS:HG3	45:BF:135:TYR:CE1	2.48	0.48
20:AU:18:ASP:OD1	20:AU:21:ARG:NH2	2.43	0.48
20:AU:24:LEU:HD11	20:AU:39:LEU:HG	1.95	0.48
24:AY:211:GLY:O	50:BK:320:VAL:HG23	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:AA:948:A:H61	55:BP:220:ARG:H	1.60	0.48
40:BA:250:ILE:HG12	40:BA:254:ARG:HH21	1.78	0.48
40:BA:327:ARG:HH11	40:BA:327:ARG:HG3	1.78	0.48
42:BC:98:ASN:HA	42:BC:101:ALA:HB3	1.94	0.48
50:BK:194:ARG:NH1	50:BK:198:ASP:HB2	2.28	0.48
5:A4:72:ARG:NH1	30:Aj:79:TYR:CE1	2.81	0.48
14:AK:179:ARG:HH21	39:AA:422:A:H1'	1.79	0.48
14:AK:243:HIS:NE2	14:AK:272:SER:O	2.47	0.48
15:AN:34:LYS:HB2	15:AN:37:LEU:HD12	1.96	0.48
23:AX:61:ILE:CG1	35:Av:33:ILE:HA	2.37	0.48
24:AY:118:GLU:HG2	24:AY:128:ARG:HG2	1.96	0.48
26:Ad:245:ASP:CG	69:Bd:33:LYS:NZ	2.71	0.48
29:Ag:170:GLN:NE2	29:Ag:227:PRO:HG2	2.27	0.48
32:Ao:158:ARG:CD	52:BM:236:ARG:HH12	2.26	0.48
35:Av:231:ILE:O	35:Av:233:THR:N	2.47	0.48
42:BC:461:ASP:OD1	42:BC:461:ASP:N	2.37	0.48
44:BE:32:LEU:H	44:BE:32:LEU:CD2	2.26	0.48
48:BI:50:ARG:NH1	48:BI:255:ASP:OD1	2.39	0.48
58:BS:84:VAL:HG13	58:BS:96:MET:HG3	1.95	0.48
64:BY:165:ARG:HH11	64:BY:170:PRO:HD2	1.78	0.48
65:BZ:87:ASP:HB3	65:BZ:134:GLN:HE21	1.78	0.48
77:UD:52:UNK:HA	77:UD:55:UNK:HG3	1.95	0.48
2:A1:52:TYR:HE2	2:A1:56:ARG:HH21	1.62	0.48
3:A2:270:ASN:HD22	3:A2:271:PRO:CD	2.27	0.48
4:A3:116:VAL:O	34:At:40:ASN:ND2	2.47	0.48
5:A4:9:VAL:HG12	55:BP:112:ARG:HH11	1.78	0.48
8:A8:66:ARG:HD2	39:AA:61:A:OP1	2.14	0.48
16:AP:349:GLN:NE2	35:Av:168:SER:OG	2.47	0.48
30:Aj:199:LEU:HD13	30:Aj:224:PRO:HG2	1.94	0.48
39:AA:3:U:OP1	40:BA:755:LYS:NZ	2.39	0.48
39:AA:528:A:O2'	39:AA:529:U:OP1	2.29	0.48
39:AA:536:A:N1	72:Bg:89:ARG:HB2	2.29	0.48
48:BI:119:GLU:OE2	48:BI:234:SER:HB2	2.13	0.48
53:BN:16:PRO:O	53:BN:19:VAL:HG12	2.14	0.48
61:BV:60:MET:HE2	61:BV:60:MET:HA	1.96	0.48
68:Bc:56:TRP:HD1	68:Bc:64:PHE:CZ	2.31	0.48
77:UD:193:UNK:O	77:UD:197:UNK:HB1	2.13	0.48
7:A6:94:LYS:NZ	16:AP:345:TRP:CZ3	2.79	0.48
8:A8:92:MET:HE2	8:A8:107:ARG:HE	1.77	0.48
10:AE:347:GLY:HA2	33:Ap:46:PRO:HB3	1.94	0.48
12:AI:71:TYR:O	12:AI:85:TYR:CE2	2.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Ab:224:LEU:HD21	25:Ab:319:PRO:HB3	1.96	0.48
25:Ab:484:GLY:N	31:Al:204:ASP:OD2	2.42	0.48
33:Ap:45:LEU:HD12	33:Ap:46:PRO:HD2	1.96	0.48
39:AA:41:U:H3'	39:AA:42:A:C8	2.49	0.48
42:BC:302:GLY:O	42:BC:303:LEU:HD22	2.13	0.48
65:BZ:144:ASN:O	65:BZ:147:ASN:ND2	2.47	0.48
2:A1:97:ARG:HG2	35:Av:30:MET:HE3	1.96	0.48
2:A1:184:MET:HB3	2:A1:204:TYR:CE2	2.48	0.48
3:A2:253:ALA:HB3	11:AF:407:ARG:HH12	1.78	0.48
8:A8:102:ASP:OD1	8:A8:103:VAL:N	2.47	0.48
14:AK:34:LYS:HE2	61:BV:90:PHE:CG	2.48	0.48
17:AQ:44:ILE:HD11	17:AQ:156:PRO:O	2.12	0.48
24:AY:194:ARG:HD3	24:AY:199:GLY:HA2	1.94	0.48
24:AY:242:TYR:CE2	24:AY:244:ARG:HB3	2.48	0.48
39:AA:441:A:OP2	39:AA:441:A:H8	1.96	0.48
48:BI:38:LEU:HD12	48:BI:41:PHE:HD2	1.78	0.48
50:BK:136:ALA:O	50:BK:140:LEU:HB2	2.13	0.48
53:BN:219:ARG:HH11	53:BN:221:VAL:HG22	1.78	0.48
61:BV:160:MET:HG3	61:BV:161:LYS:N	2.29	0.48
73:Bh:47:SER:HB3	73:Bh:67:THR:HG21	1.95	0.48
74:UA:14:UNK:HA	74:UA:17:UNK:HG3	1.95	0.48
12:AI:77:ARG:HH22	12:AI:83:ILE:HG23	1.79	0.48
16:AP:227:PRO:HD3	31:Al:118:ALA:HB2	1.96	0.48
18:AR:215:LYS:HZ3	44:BE:433:VAL:HG13	1.78	0.48
28:Af:164:HIS:CD2	28:Af:166:LYS:HB2	2.49	0.48
31:Al:41:VAL:O	31:Al:45:ILE:HG23	2.14	0.48
31:Al:93:ASP:N	31:Al:93:ASP:OD1	2.47	0.48
34:At:25:ARG:HH12	39:AA:379:U:H5'	1.78	0.48
34:At:138:PRO:HG3	45:BF:130:GLU:CD	2.39	0.48
41:BB:351:LEU:HD12	41:BB:409:LEU:HD11	1.96	0.48
52:BM:212:ARG:NH1	52:BM:222:ARG:HE	2.12	0.48
56:BQ:52:ASP:OD1	56:BQ:53:ILE:N	2.45	0.48
71:Bf:44:ARG:NE	78:UE:1:UNK:HG2	2.29	0.48
73:Bh:28:ARG:HB2	73:Bh:41:PHE:HB2	1.94	0.48
4:A3:178:LEU:HD23	56:BQ:114:PRO:HD3	1.94	0.48
8:A8:84:VAL:HG13	25:Ab:456:ALA:C	2.38	0.48
11:AF:38:ARG:NH2	29:Ag:50:ARG:NH1	2.62	0.48
14:AK:246:ASN:HD21	14:AK:313:TYR:HB3	1.79	0.48
18:AR:261:GLU:O	18:AR:264:ALA:HB3	2.14	0.48
20:AU:182:ARG:NH2	32:Ao:87:GLU:OE2	2.46	0.48
26:Ad:126:ARG:HG3	26:Ad:127:PRO:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:Al:146:LEU:HD12	31:Al:147:PRO:HD3	1.96	0.48
32:Ao:229:LYS:HZ3	39:AA:387:A:H3'	1.78	0.48
34:At:38:GLU:O	34:At:41:GLU:HG2	2.13	0.48
39:AA:80:U:C6	59:BT:12:THR:HG21	2.49	0.48
40:BA:791:PHE:CE1	40:BA:801:ARG:NH1	2.82	0.48
41:BB:79:ARG:HG3	41:BB:79:ARG:NH1	2.27	0.48
41:BB:443:ARG:HG2	41:BB:443:ARG:HH11	1.79	0.48
44:BE:330:GLN:O	44:BE:331:ASP:HB2	2.14	0.48
45:BF:134:ASP:HB3	45:BF:149:TYR:OH	2.14	0.48
48:BI:76:TYR:CE1	48:BI:82:PHE:HB2	2.49	0.48
53:BN:128:ARG:NH2	73:Bh:34:ARG:HH11	2.10	0.48
56:BQ:82:PRO:HA	56:BQ:190:TRP:HA	1.96	0.48
68:Bc:13:LYS:HB2	68:Bc:13:LYS:HZ2	1.79	0.48
10:AE:319:LYS:HB2	10:AE:379:CYS:SG	2.54	0.48
14:AK:268:LEU:HA	14:AK:292:LEU:HD11	1.95	0.48
15:AN:92:VAL:HG13	48:BI:50:ARG:O	2.14	0.48
16:AP:292:PRO:HD3	42:BC:498:ARG:HH12	1.79	0.48
23:AX:197:ARG:O	39:AA:529:U:N3	2.45	0.48
25:Ab:151:LEU:HB3	25:Ab:152:PRO:HD3	1.96	0.48
29:Ag:52:TRP:O	39:AA:489:G:H5''	2.13	0.48
29:Ag:67:ARG:NH1	51:BL:71:GLU:OE2	2.47	0.48
30:Aj:206:ALA:O	30:Aj:210:ASP:HB2	2.14	0.48
33:Ap:185:VAL:HG22	33:Ap:230:PRO:HB3	1.95	0.48
39:AA:197:A:H2'	39:AA:198:A:H8	1.78	0.48
41:BB:170:GLN:H	72:Bg:103:THR:HG23	1.79	0.48
41:BB:194:TYR:CE2	41:BB:196:TRP:HB2	2.48	0.48
42:BC:398:ALA:HA	42:BC:424:ARG:HE	1.77	0.48
44:BE:446:MET:HG2	44:BE:447:GLU:HG3	1.96	0.48
51:BL:126:LYS:HZ1	51:BL:142:LEU:HD23	1.78	0.48
53:BN:62:PHE:CZ	53:BN:88:ILE:HA	2.49	0.48
54:BO:138:ARG:NH2	58:BS:26:ARG:HH21	1.97	0.48
56:BQ:23:GLU:OE1	56:BQ:23:GLU:N	2.47	0.48
1:A0:91:GLU:HG2	1:A0:99:LYS:HG2	1.96	0.47
10:AE:108:ARG:HA	10:AE:115:TYR:HD2	1.79	0.47
11:AF:385:LEU:HD13	62:BW:33:LEU:HB2	1.96	0.47
19:AT:28:ARG:HG3	19:AT:28:ARG:NH1	2.23	0.47
25:Ab:482:MET:O	31:Al:202:ALA:HB1	2.15	0.47
40:BA:379:ARG:HH21	40:BA:410:GLU:HG3	1.78	0.47
46:BG:277:SER:OG	46:BG:302:CYS:O	2.31	0.47
48:BI:63:LEU:HD23	48:BI:317:PRO:HB2	1.96	0.47
60:BU:114:THR:O	60:BU:117:ILE:HG22	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:BW:177:VAL:HG12	62:BW:179:ASP:H	1.79	0.47
65:BZ:96:GLN:HE22	65:BZ:125:SER:HA	1.79	0.47
70:Be:11:ILE:CG2	70:Be:73:TRP:HB3	2.44	0.47
79:UG:8:UNK:HA	79:UG:11:UNK:HG3	1.95	0.47
3:A2:270:ASN:HD22	3:A2:271:PRO:HD2	1.79	0.47
3:A2:317:GLU:HG3	59:BT:86:ARG:HD2	1.96	0.47
8:A8:168:LEU:HD13	16:AP:165:ARG:NH1	2.28	0.47
8:A8:172:LYS:HZ2	16:AP:259:HIS:CD2	2.32	0.47
11:AF:412:GLU:OE2	59:BT:97:THR:OG1	2.26	0.47
14:AK:302:THR:O	14:AK:305:GLU:HG2	2.14	0.47
20:AU:108:ARG:HG2	28:Af:87:PHE:CZ	2.49	0.47
39:AA:3:U:H5'	40:BA:754:ARG:HH12	1.78	0.47
39:AA:69:U:O2'	39:AA:70:G:OP1	2.30	0.47
40:BA:187:MET:SD	40:BA:206:ILE:HD11	2.54	0.47
40:BA:799:ASP:OD1	40:BA:801:ARG:HG2	2.14	0.47
42:BC:49:SER:O	42:BC:464:ILE:HG23	2.14	0.47
42:BC:86:GLN:HE22	42:BC:124:ASN:HA	1.79	0.47
57:BR:105:ASN:OD1	57:BR:106:THR:N	2.47	0.47
57:BR:146:ARG:HG3	79:UF:23:UNK:HB2	1.96	0.47
62:BW:27:TYR:HB3	62:BW:100:GLN:HE22	1.79	0.47
77:UD:182:UNK:HA	77:UD:185:UNK:HG3	1.95	0.47
2:A1:48:LYS:NZ	39:AA:69:U:O4'	2.46	0.47
2:A1:162:VAL:HG11	49:BJ:256:LEU:HD23	1.94	0.47
3:A2:70:ARG:HH22	23:AX:147:LEU:HD22	1.79	0.47
10:AE:137:ARG:NH1	10:AE:359:ALA:O	2.48	0.47
12:AI:17:ARG:HG2	66:Ba:104:ARG:HH12	1.79	0.47
13:AJ:33:ARG:NH1	48:BI:291:VAL:HG21	2.29	0.47
17:AQ:164:HIS:CD2	52:BM:251:GLU:HG3	2.49	0.47
25:Ab:82:TYR:CE2	25:Ab:89:PRO:HB2	2.50	0.47
29:Ag:204:HIS:HD2	29:Ag:209:LEU:HD11	1.79	0.47
35:Av:29:MET:HB2	35:Av:44:ASN:HD21	1.79	0.47
40:BA:401:THR:HG22	40:BA:406:ALA:O	2.14	0.47
53:BN:192:ARG:HH12	53:BN:193:PHE:HE1	1.62	0.47
11:AF:26:ASP:C	11:AF:26:ASP:OD1	2.56	0.47
15:AN:55:PRO:HG2	15:AN:184:TRP:CD2	2.50	0.47
30:Aj:181:GLU:HB3	30:Aj:257:LYS:HB3	1.95	0.47
30:Aj:181:GLU:HA	30:Aj:259:ILE:HG13	1.95	0.47
32:Ao:127:SER:HB3	56:BQ:188:ARG:NH1	2.28	0.47
39:AA:283:A:O2'	39:AA:285:A:OP2	2.23	0.47
39:AA:564:A:C5	77:UD:21:UNK:HB2	2.50	0.47
41:BB:136:TRP:HB2	41:BB:141:ILE:HD12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:BC:375:LEU:HD21	42:BC:411:LEU:HD23	1.96	0.47
44:BE:154:VAL:HG21	44:BE:245:ILE:HA	1.97	0.47
46:BG:102:GLN:O	46:BG:102:GLN:NE2	2.47	0.47
47:BH:116:GLU:HG2	70:Be:68:ARG:HA	1.96	0.47
47:BH:134:GLN:NE2	47:BH:174:LEU:HB3	2.29	0.47
48:BI:265:THR:CB	48:BI:305:LYS:HZ2	2.27	0.47
53:BN:104:ARG:HH22	73:Bh:79:ALA:HA	1.80	0.47
54:BO:83:VAL:HG23	54:BO:228:PRO:HG3	1.97	0.47
69:Bd:136:GLU:OE1	69:Bd:136:GLU:N	2.48	0.47
12:AI:183:ARG:O	12:AI:186:GLU:HG2	2.15	0.47
14:AK:133:ARG:HH12	14:AK:134:ARG:NH2	2.10	0.47
14:AK:257:GLU:HB3	14:AK:260:ARG:HH21	1.79	0.47
15:AN:44:TRP:CD1	28:Af:127:MET:HE3	2.50	0.47
15:AN:172:ARG:NH1	29:Ag:119:ASN:OD1	2.47	0.47
16:AP:25:MET:CG	32:Ao:82:GLU:HG3	2.45	0.47
16:AP:361:TYR:HB3	16:AP:363:THR:HG23	1.96	0.47
30:Aj:175:HIS:O	30:Aj:263:TRP:HA	2.14	0.47
35:Av:88:VAL:HG11	35:Av:138:LEU:HD11	1.95	0.47
39:AA:454:U:C4	39:AA:455:U:C5	3.02	0.47
39:AA:520:U:H3'	39:AA:521:G:C8	2.50	0.47
39:AA:819:A:H2'	39:AA:820:A:C8	2.50	0.47
41:BB:170:GLN:HG2	72:Bg:101:GLY:O	2.14	0.47
46:BG:153:GLY:O	46:BG:156:VAL:HB	2.15	0.47
47:BH:271:PHE:CE1	70:Be:8:LYS:NZ	2.83	0.47
51:BL:281:SER:O	51:BL:285:LEU:HD13	2.14	0.47
65:BZ:2:ARG:HH11	65:BZ:28:ARG:NE	2.13	0.47
65:BZ:77:VAL:HG13	65:BZ:83:ILE:HG12	1.96	0.47
65:BZ:96:GLN:NE2	65:BZ:124:ALA:O	2.47	0.47
72:Bg:53:PHE:HE1	72:Bg:90:LEU:HB3	1.80	0.47
13:AJ:83:PHE:HD2	33:Ap:205:ARG:HD3	1.79	0.47
16:AP:227:PRO:HG2	16:AP:228:TYR:CD2	2.50	0.47
16:AP:264:GLN:OE1	16:AP:277:GLN:NE2	2.47	0.47
21:AV:146:MET:HE2	29:Ag:95:GLN:O	2.15	0.47
25:Ab:279:TYR:OH	25:Ab:281:MET:HE2	2.14	0.47
26:Ad:42:MET:HE1	69:Bd:103:GLY:CA	2.43	0.47
26:Ad:57:ARG:HH12	26:Ad:287:ARG:CD	2.19	0.47
40:BA:304:GLY:HA2	40:BA:307:HIS:NE2	2.30	0.47
47:BH:134:GLN:HE21	47:BH:174:LEU:HB3	1.79	0.47
52:BM:212:ARG:CZ	52:BM:222:ARG:HG2	2.44	0.47
55:BP:50:GLU:OE2	69:Bd:52:ARG:NH2	2.47	0.47
56:BQ:24:ARG:HH12	56:BQ:30:VAL:CG2	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:BX:126:LEU:HD13	63:BX:131:PHE:HB3	1.96	0.47
70:Be:59:VAL:O	70:Be:71:SER:HB3	2.15	0.47
2:A1:184:MET:SD	24:AY:300:LEU:HD11	2.55	0.47
5:A4:86:THR:HB	26:Ad:138:PRO:HG3	1.97	0.47
6:A5:36:ARG:NH2	24:AY:7:THR:O	2.48	0.47
11:AF:105:THR:HG22	11:AF:106:TYR:H	1.79	0.47
11:AF:176:ASN:HD22	11:AF:190:ARG:HG2	1.79	0.47
12:AI:82:ASP:OD2	12:AI:83:ILE:N	2.48	0.47
14:AK:148:LEU:HD11	61:BV:52:PHE:CE1	2.50	0.47
14:AK:206:THR:HG23	14:AK:209:GLN:H	1.80	0.47
20:AU:83:GLU:OE2	28:Af:76:LEU:HD23	2.15	0.47
22:AW:159:GLU:OE2	22:AW:245:ARG:NE	2.48	0.47
24:AY:153:ILE:HG23	44:BE:79:VAL:HG21	1.95	0.47
26:Ad:126:ARG:NH1	30:Aj:18:GLY:N	2.63	0.47
27:Ae:100:HIS:HB2	27:Ae:106:LEU:CD2	2.43	0.47
27:Ae:153:PHE:HD1	27:Ae:153:PHE:H	1.62	0.47
28:Af:83:LEU:HD13	28:Af:86:ASN:HD22	1.80	0.47
28:Af:154:ARG:HH21	28:Af:157:MET:HE1	1.78	0.47
29:Ag:28:PHE:HZ	29:Ag:83:LEU:HD22	1.80	0.47
33:Ap:126:TRP:CD1	79:UN:4:UNK:HG1	2.49	0.47
34:At:22:LEU:HD12	34:At:23:PRO:HD2	1.97	0.47
39:AA:43:U:H5''	39:AA:44:A:C8	2.48	0.47
39:AA:455:U:H2'	39:AA:456:U:C4'	2.45	0.47
39:AA:1112:U:O2	40:BA:300:ARG:NH1	2.48	0.47
41:BB:213:LEU:O	41:BB:215:ARG:HG2	2.14	0.47
41:BB:431:ARG:O	41:BB:434:GLU:HG2	2.14	0.47
42:BC:75:MET:HB2	42:BC:78:LYS:HB2	1.96	0.47
45:BF:163:ASN:HA	45:BF:197:MET:HE2	1.96	0.47
48:BI:103:THR:H	48:BI:106:HIS:CD2	2.33	0.47
49:BJ:251:GLY:HA3	66:Ba:55:SER:H	1.79	0.47
51:BL:177:LEU:HD21	51:BL:291:LEU:HD11	1.95	0.47
51:BL:226:HIS:O	51:BL:230:ARG:HG3	2.15	0.47
54:BO:78:ARG:NH1	58:BS:104:ARG:HH12	2.08	0.47
56:BQ:127:ARG:NH2	56:BQ:168:TRP:HE1	2.13	0.47
58:BS:63:LYS:HE2	60:BU:184:TRP:HB3	1.97	0.47
60:BU:118:VAL:HG23	72:Bg:102:LEU:HG	1.95	0.47
61:BV:117:TRP:O	61:BV:143:GLN:NE2	2.37	0.47
63:BX:131:PHE:CZ	77:UD:46:UNK:HB1	2.50	0.47
3:A2:212:ALA:O	3:A2:213:PRO:C	2.54	0.47
5:A4:76:PRO:O	30:Aj:80:SER:HB3	2.14	0.47
6:A5:35:LEU:HD11	39:AA:505:U:H5''	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A5:61:ALA:HB1	44:BE:389:GLN:HA	1.97	0.47
8:A8:179:ARG:HH11	8:A8:181:VAL:HG21	1.80	0.47
11:AF:157:ASN:ND2	39:AA:92:U:O2	2.48	0.47
29:Ag:14:ILE:HG12	29:Ag:57:ILE:HD11	1.97	0.47
32:Ao:99:ARG:NH2	39:AA:468:A:N7	2.63	0.47
39:AA:318:A:N6	39:AA:343:U:H3	2.13	0.47
39:AA:582:A:H61	39:AA:794:A:H61	1.62	0.47
39:AA:819:A:H2'	39:AA:820:A:H8	1.80	0.47
40:BA:627:SER:OG	40:BA:633:ARG:NH1	2.48	0.47
41:BB:258:PHE:CZ	41:BB:372:CYS:HB3	2.49	0.47
42:BC:111:LEU:HD23	42:BC:137:ILE:HD11	1.97	0.47
44:BE:69:GLU:O	44:BE:73:THR:HG22	2.15	0.47
45:BF:214:LEU:HD12	45:BF:289:CYS:HB2	1.96	0.47
46:BG:164:GLN:O	46:BG:165:GLU:HG3	2.14	0.47
48:BI:85:THR:HG22	48:BI:86:PRO:O	2.15	0.47
48:BI:85:THR:O	48:BI:88:ALA:HB3	2.15	0.47
52:BM:146:SER:O	52:BM:150:ILE:HG13	2.14	0.47
53:BN:97:ARG:HE	53:BN:101:LYS:HE3	1.80	0.47
61:BV:108:TYR:HA	61:BV:111:LYS:HZ3	1.79	0.47
71:Bf:44:ARG:HH11	78:UE:6:UNK:CA	2.27	0.47
2:A1:216:ALA:O	2:A1:220:VAL:HG23	2.15	0.47
3:A2:18:ASP:HB2	3:A2:64:MET:SD	2.54	0.47
3:A2:387:TRP:CD1	3:A2:388:PRO:HA	2.50	0.47
8:A8:168:LEU:HD23	8:A8:168:LEU:H	1.80	0.47
10:AE:43:ARG:HB2	10:AE:44:CYS:H	1.59	0.47
12:AI:23:THR:HG22	12:AI:66:GLU:OE2	2.15	0.47
18:AR:243:PRO:O	18:AR:246:VAL:HG22	2.14	0.47
20:AU:33:LYS:HD3	20:AU:37:LYS:HE3	1.97	0.47
20:AU:46:GLN:NE2	39:AA:115:A:N7	2.63	0.47
23:AX:124:LEU:O	23:AX:130:PHE:HB2	2.14	0.47
24:AY:64:HIS:CD2	24:AY:66:ARG:HB2	2.50	0.47
25:Ab:100:PHE:HB2	26:Ad:284:HIS:CE1	2.49	0.47
29:Ag:20:ASN:ND2	29:Ag:51:LEU:O	2.48	0.47
29:Ag:224:VAL:HG11	33:Ap:192:TYR:CE1	2.50	0.47
32:Ao:123:ARG:NH2	39:AA:331:C:H5''	2.30	0.47
40:BA:471:SER:HB2	40:BA:657:PHE:CE1	2.49	0.47
46:BG:185:PHE:CD1	46:BG:253:ARG:NH1	2.83	0.47
47:BH:258:THR:HG23	47:BH:261:GLU:OE2	2.15	0.47
61:BV:30:LYS:HZ2	61:BV:32:VAL:HA	1.80	0.47
65:BZ:69:TYR:OH	65:BZ:133:SER:O	2.33	0.47
70:Be:37:SER:HB2	80:UI:9:UNK:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:UI:2:UNK:HA	80:UI:5:UNK:HG3	1.97	0.47
82:UL:1:UNK:O	82:UL:3:UNK:N	2.48	0.47
3:A2:22:LEU:HD12	3:A2:22:LEU:HA	1.71	0.47
3:A2:290:LEU:HD21	3:A2:297:THR:CG2	2.44	0.47
5:A4:96:GLU:HG3	5:A4:97:PHE:HD2	1.80	0.47
8:A8:42:MET:HE1	39:AA:95:U:O2'	2.15	0.47
8:A8:63:ALA:O	8:A8:66:ARG:HG2	2.14	0.47
8:A8:68:GLN:NE2	39:AA:66:C:O2'	2.47	0.47
12:AI:99:LEU:O	12:AI:180:LYS:NZ	2.43	0.47
14:AK:131:LYS:HD3	61:BV:70:GLU:OE1	2.14	0.47
21:AV:59:LEU:HB2	21:AV:182:PRO:HG2	1.96	0.47
22:AW:2:PRO:HD2	39:AA:178:A:P	2.54	0.47
29:Ag:136:LEU:HD21	29:Ag:144:TYR:HD2	1.80	0.47
34:At:104:ARG:HH21	34:At:104:ARG:HB2	1.80	0.47
35:Av:47:ARG:HG2	35:Av:48:ALA:N	2.30	0.47
55:BP:105:PHE:CG	55:BP:106:PRO:HD2	2.50	0.47
67:Bb:53:ARG:HG2	67:Bb:54:LYS:O	2.15	0.47
2:A1:112:ASP:N	2:A1:137:ASP:OD2	2.48	0.46
3:A2:372:GLU:OE1	24:AY:274:HIS:NE2	2.48	0.46
13:AJ:43:GLU:HA	13:AJ:46:LYS:NZ	2.29	0.46
16:AP:66:VAL:HB	21:AV:101:ARG:HH21	1.79	0.46
23:AX:112:TRP:CZ3	23:AX:114:TRP:HA	2.50	0.46
26:Ad:227:ARG:NH1	69:Bd:40:PHE:CE1	2.79	0.46
27:Ae:75:ARG:NH1	27:Ae:135:THR:HG22	2.24	0.46
30:Aj:145:PRO:HG2	46:BG:66:TYR:CG	2.50	0.46
32:Ao:141:ASN:HB2	57:BR:140:LYS:HZ1	1.78	0.46
46:BG:295:ARG:H	46:BG:295:ARG:HD2	1.79	0.46
48:BI:250:SER:OG	48:BI:254:ARG:NH2	2.48	0.46
63:BX:78:ILE:HA	63:BX:85:PRO:HA	1.97	0.46
67:Bb:46:LEU:HD13	67:Bb:137:ALA:HA	1.97	0.46
8:A8:56:LEU:HD11	11:AF:327:LYS:HZ1	1.79	0.46
12:AI:190:GLU:CG	47:BH:253:GLN:HB2	2.44	0.46
14:AK:198:TYR:CD1	61:BV:51:ARG:NH1	2.83	0.46
14:AK:244:ARG:HH12	14:AK:314:ARG:CZ	2.28	0.46
24:AY:289:GLN:HG2	49:BJ:241:MET:HE1	1.98	0.46
27:Ae:123:THR:HG23	27:Ae:132:TRP:HE1	1.80	0.46
34:At:59:ALA:HB1	34:At:62:ARG:NH1	2.25	0.46
44:BE:125:GLN:NE2	44:BE:156:SER:OG	2.48	0.46
45:BF:270:LYS:HE3	45:BF:331:ILE:O	2.15	0.46
47:BH:71:LYS:HB3	64:BY:149:ILE:CD1	2.44	0.46
48:BI:60:GLN:HG3	48:BI:257:TRP:CZ2	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
58:BS:47:PRO:HB2	58:BS:74:GLU:HG3	1.96	0.46
77:UD:60:UNK:O	77:UD:63:UNK:HG3	2.15	0.46
1:A0:118:ARG:NH1	1:A0:118:ARG:HB3	2.30	0.46
2:A1:117:TRP:H	2:A1:117:TRP:CD1	2.32	0.46
8:A8:181:VAL:C	35:Av:103:ARG:HD2	2.40	0.46
10:AE:110:LYS:NZ	79:UN:5:UNK:O	2.45	0.46
11:AF:75:TYR:CG	11:AF:81:ARG:NH1	2.84	0.46
11:AF:309:ASP:OD1	11:AF:309:ASP:N	2.46	0.46
14:AK:19:VAL:HG12	61:BV:102:TRP:HZ2	1.80	0.46
14:AK:172:LEU:HD23	14:AK:225:TYR:CE1	2.49	0.46
14:AK:273:HIS:CG	14:AK:274:PRO:HD2	2.50	0.46
14:AK:281:ASP:HB3	14:AK:284:GLU:HG2	1.97	0.46
14:AK:334:TYR:HD1	29:Ag:218:GLU:HA	1.81	0.46
16:AP:99:PRO:HD3	22:AW:7:ARG:CZ	2.45	0.46
18:AR:177:GLU:OE1	18:AR:179:TYR:OH	2.17	0.46
22:AW:102:GLU:HB3	51:BL:230:ARG:NH2	2.30	0.46
41:BB:141:ILE:HG12	41:BB:172:MET:HE2	1.97	0.46
52:BM:212:ARG:NH1	52:BM:222:ARG:HG2	2.31	0.46
53:BN:28:ASN:O	60:BU:176:PRO:HB2	2.15	0.46
65:BZ:83:ILE:HD12	65:BZ:163:VAL:HG13	1.97	0.46
69:Bd:117:THR:HG22	69:Bd:119:GLN:H	1.81	0.46
8:A8:173:ARG:HH12	11:AF:442:GLY:CA	2.29	0.46
10:AE:171:VAL:HA	10:AE:210:VAL:HG21	1.96	0.46
16:AP:273:ILE:O	16:AP:275:MET:HG3	2.15	0.46
18:AR:114:GLN:HA	18:AR:117:TYR:HD2	1.80	0.46
20:AU:49:TYR:CZ	20:AU:54:GLN:HB3	2.51	0.46
20:AU:180:LEU:HD22	20:AU:188:GLY:O	2.14	0.46
24:AY:117:VAL:HG11	24:AY:175:VAL:HB	1.97	0.46
24:AY:156:SER:OG	24:AY:159:ARG:HG2	2.15	0.46
32:Ao:233:TRP:HE1	32:Ao:237:ARG:HH22	1.63	0.46
33:Ap:170:HIS:CE1	33:Ap:260:MET:HB3	2.49	0.46
41:BB:169:SER:HB3	72:Bg:105:GLU:HG2	1.96	0.46
41:BB:215:ARG:NH1	41:BB:221:TYR:HB2	2.30	0.46
44:BE:128:ILE:HG22	44:BE:131:LEU:HD12	1.98	0.46
45:BF:234:GLU:O	45:BF:237:LEU:HG	2.15	0.46
49:BJ:193:LEU:HD23	49:BJ:193:LEU:HA	1.80	0.46
51:BL:34:GLY:H	51:BL:85:ARG:NH2	2.13	0.46
52:BM:62:GLU:HG3	52:BM:66:ARG:HH21	1.80	0.46
61:BV:119:THR:HG21	61:BV:147:ARG:NH1	2.31	0.46
63:BX:132:TYR:CD1	77:UD:48:UNK:HA	2.51	0.46
70:Be:44:TYR:CZ	70:Be:48:ARG:HD2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
70:Be:49:ARG:HG2	70:Be:49:ARG:NH1	2.14	0.46
73:Bh:46:VAL:HG21	77:UD:12:UNK:HB2	1.96	0.46
77:UD:59:UNK:O	77:UD:63:UNK:HB1	2.14	0.46
10:AE:353:GLU:HG2	10:AE:354:HIS:CD2	2.51	0.46
16:AP:75:THR:O	29:Ag:75:SER:HB3	2.15	0.46
17:AQ:162:GLU:HG3	57:BR:168:TRP:HH2	1.79	0.46
18:AR:184:GLU:HB2	18:AR:188:LEU:HD12	1.97	0.46
22:AW:256:MET:HE1	44:BE:382:ARG:NH1	2.31	0.46
23:AX:163:ILE:HD11	23:AX:172:LEU:HD13	1.98	0.46
30:Aj:163:ARG:NH1	30:Aj:168:ARG:NH2	2.64	0.46
30:Aj:274:GLU:HG3	46:BG:50:ARG:HH12	1.80	0.46
31:Al:89:TYR:CD2	31:Al:179:GLU:OE2	2.68	0.46
35:Av:208:LYS:HA	35:Av:211:VAL:HG22	1.96	0.46
41:BB:165:THR:HG23	41:BB:238:ASN:HB3	1.98	0.46
43:BD:135:LYS:O	43:BD:139:MET:N	2.45	0.46
47:BH:70:TYR:CE2	76:UC:7:UNK:HA	2.51	0.46
48:BI:169:GLU:O	48:BI:173:LEU:HB2	2.15	0.46
50:BK:360:GLU:OE1	50:BK:360:GLU:N	2.39	0.46
65:BZ:25:LEU:O	65:BZ:27:PRO:HD3	2.16	0.46
65:BZ:69:TYR:O	65:BZ:72:SER:OG	2.31	0.46
65:BZ:83:ILE:HD13	65:BZ:166:ILE:HG13	1.96	0.46
71:Bf:78:GLN:HA	78:UE:21:UNK:HB2	1.96	0.46
2:A1:158:ARG:HD3	2:A1:158:ARG:HA	1.74	0.46
8:A8:96:ARG:NE	39:AA:954:U:OP2	2.41	0.46
9:A9:87:ARG:NH1	78:UE:20:UNK:HB1	2.31	0.46
10:AE:106:ARG:NH1	33:Ap:124:PRO:HG3	2.31	0.46
11:AF:278:ARG:HB2	11:AF:353:GLU:OE1	2.16	0.46
14:AK:230:GLN:NE2	14:AK:316:PRO:HB2	2.31	0.46
15:AN:17:ARG:NH1	39:AA:112:U:C2	2.83	0.46
15:AN:44:TRP:CE2	15:AN:169:LYS:HG2	2.51	0.46
20:AU:126:VAL:HG21	34:At:82:LEU:HB2	1.96	0.46
20:AU:198:TRP:HB3	45:BF:150:GLY:HA3	1.97	0.46
26:Ad:37:TRP:HD1	30:Aj:97:GLN:HG3	1.80	0.46
29:Ag:186:VAL:HA	29:Ag:189:MET:HB2	1.98	0.46
32:Ao:137:ALA:HA	32:Ao:140:ARG:HH11	1.80	0.46
40:BA:327:ARG:HD2	40:BA:327:ARG:HA	1.66	0.46
40:BA:741:VAL:HG12	51:BL:79:LYS:NZ	2.30	0.46
49:BJ:303:HIS:O	49:BJ:306:GLN:HG2	2.16	0.46
51:BL:169:GLU:HA	51:BL:172:ILE:HD11	1.97	0.46
53:BN:23:GLY:H	53:BN:191:ARG:HH22	1.62	0.46
62:BW:70:PHE:CE1	62:BW:74:ARG:NH1	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
71:Bf:106:SER:HB3	71:Bf:107:PRO:HD2	1.98	0.46
2:A1:71:GLN:HG2	66:Ba:98:TRP:CD2	2.50	0.46
3:A2:389:HIS:HB3	39:AA:32:U:C4	2.51	0.46
5:A4:30:PRO:HA	5:A4:33:ARG:NH1	2.31	0.46
6:A5:73:GLU:HG2	6:A5:76:ARG:NH2	2.31	0.46
10:AE:110:LYS:CG	79:UN:5:UNK:HG2	2.35	0.46
10:AE:144:LYS:HA	10:AE:163:PHE:CD1	2.51	0.46
11:AF:441:ASP:OD1	11:AF:441:ASP:N	2.48	0.46
16:AP:255:VAL:HB	62:BW:11:ARG:HH11	1.80	0.46
21:AV:82:ILE:HD11	21:AV:136:VAL:HG11	1.97	0.46
25:Ab:97:PRO:HA	25:Ab:98:PRO:HD3	1.84	0.46
39:AA:317:A:N6	39:AA:344:A:H62	2.14	0.46
41:BB:230:THR:HB	41:BB:232:VAL:HG22	1.97	0.46
50:BK:295:ARG:HB3	50:BK:295:ARG:HH11	1.81	0.46
53:BN:97:ARG:HD2	73:Bh:87:CYS:HB3	1.98	0.46
74:UA:17:UNK:O	74:UA:21:UNK:HB1	2.15	0.46
77:UD:212:UNK:HA	77:UD:215:UNK:HG3	1.96	0.46
2:A1:142:LYS:HZ3	2:A1:143:ARG:NH1	2.14	0.46
3:A2:24:ASN:O	81:UK:2:UNK:HB1	2.15	0.46
11:AF:101:PRO:HB2	11:AF:384:TYR:CE2	2.50	0.46
13:AJ:58:ASN:HA	33:Ap:222:PHE:HD1	1.81	0.46
16:AP:74:THR:OG1	29:Ag:75:SER:OG	2.28	0.46
16:AP:324:PRO:O	35:Av:147:ASN:ND2	2.47	0.46
33:Ap:176:MET:HG2	33:Ap:177:HIS:ND1	2.30	0.46
35:Av:197:ARG:O	35:Av:200:GLN:HG3	2.15	0.46
40:BA:217:LEU:HD12	40:BA:217:LEU:HA	1.62	0.46
41:BB:392:TYR:O	41:BB:395:GLU:HG3	2.16	0.46
42:BC:126:GLU:OE2	42:BC:226:THR:HG21	2.16	0.46
60:BU:121:HIS:CG	72:Bg:102:LEU:HD21	2.51	0.46
64:BY:112:ARG:O	64:BY:117:PRO:HD3	2.16	0.46
64:BY:165:ARG:NH1	64:BY:170:PRO:HD2	2.31	0.46
73:Bh:53:MET:SD	73:Bh:53:MET:N	2.85	0.46
1:A0:152:VAL:O	57:BR:11:MET:HG2	2.16	0.46
8:A8:168:LEU:HD13	16:AP:165:ARG:HH12	1.81	0.46
13:AJ:43:GLU:CD	13:AJ:44:GLN:HG3	2.40	0.46
17:AQ:92:VAL:N	17:AQ:110:HIS:O	2.47	0.46
19:AT:32:SER:OG	58:BS:30:GLU:OE1	2.33	0.46
21:AV:215:TYR:HE1	29:Ag:132:TRP:HD1	1.63	0.46
22:AW:225:LYS:HB3	44:BE:46:TYR:CE2	2.51	0.46
26:Ad:166:PHE:HE2	30:Aj:24:ARG:HD3	1.80	0.46
30:Aj:180:ASP:HB2	30:Aj:183:SER:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:AA:321:A:H2'	39:AA:322:U:C6	2.51	0.46
50:BK:325:ASP:OD1	50:BK:325:ASP:N	2.48	0.46
60:BU:140:ILE:HD11	72:Bg:46:TYR:HE2	1.80	0.46
2:A1:181:VAL:HG11	24:AY:299:MET:CB	2.46	0.46
5:A4:61:ARG:HH21	26:Ad:49:ARG:NH1	2.11	0.46
11:AF:118:PHE:CE1	11:AF:124:VAL:HG22	2.50	0.46
12:AI:106:ARG:NH1	39:AA:882:U:O2'	2.49	0.46
14:AK:142:ARG:NH2	39:AA:405:U:H4'	2.30	0.46
16:AP:196:THR:HG22	16:AP:197:LEU:H	1.80	0.46
17:AQ:157:GLN:O	29:Ag:253:ARG:NE	2.48	0.46
22:AW:83:GLU:OE2	22:AW:90:ARG:NE	2.44	0.46
31:Al:159:MET:HE1	39:AA:324:U:H1'	1.98	0.46
34:At:54:TYR:CE2	34:At:95:PRO:HG3	2.50	0.46
39:AA:392:A:H1'	39:AA:393:A:H2'	1.98	0.46
39:AA:877:A:H2'	39:AA:878:A:C8	2.50	0.46
41:BB:75:MET:HE2	41:BB:75:MET:HB3	1.67	0.46
42:BC:92:PHE:HA	42:BC:95:ILE:HG22	1.98	0.46
42:BC:112:ARG:N	42:BC:115:GLN:HE21	2.13	0.46
53:BN:87:GLU:O	53:BN:196:ARG:NH1	2.49	0.46
77:UD:82:UNK:HG3	77:UD:136:UNK:HB1	1.98	0.46
79:UG:3:UNK:HA	79:UG:6:UNK:HG3	1.98	0.46
1:A0:49:GLN:NE2	1:A0:64:TYR:HB2	2.31	0.45
8:A8:83:ARG:O	8:A8:118:GLN:NE2	2.49	0.45
10:AE:78:PRO:HG2	10:AE:84:TRP:CD1	2.51	0.45
10:AE:137:ARG:NH2	10:AE:237:HIS:O	2.49	0.45
11:AF:366:HIS:O	11:AF:370:ILE:HG13	2.17	0.45
13:AJ:66:GLU:HB3	13:AJ:70:TRP:HD1	1.80	0.45
26:Ad:158:GLY:O	69:Bd:68:GLN:NE2	2.49	0.45
28:Af:68:ASN:OD1	28:Af:68:ASN:N	2.49	0.45
39:AA:134:U:OP1	39:AA:825:A:N6	2.49	0.45
40:BA:502:HIS:CD2	40:BA:641:GLU:HB3	2.51	0.45
41:BB:102:ILE:HD11	41:BB:126:ALA:HB1	1.97	0.45
43:BD:426:ASP:O	43:BD:451:ALA:HA	2.16	0.45
62:BW:26:PHE:HB2	62:BW:107:VAL:HG11	1.98	0.45
74:UA:5:UNK:HA	74:UA:8:UNK:HG3	1.98	0.45
2:A1:185:GLU:O	2:A1:189:LEU:N	2.49	0.45
3:A2:269:LYS:O	3:A2:270:ASN:HB2	2.16	0.45
6:A5:69:TRP:NE1	6:A5:79:LYS:HB2	2.31	0.45
8:A8:52:ARG:O	8:A8:53:ARG:NH1	2.47	0.45
8:A8:172:LYS:HZ2	16:AP:259:HIS:HD2	1.64	0.45
11:AF:102:ILE:HD12	11:AF:103:VAL:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AI:122:PHE:HA	12:AI:129:TRP:HA	1.99	0.45
15:AN:49:ALA:HB1	15:AN:91:VAL:HG22	1.98	0.45
18:AR:229:HIS:HE1	44:BE:415:TYR:CE1	2.33	0.45
20:AU:186:GLY:HA3	45:BF:158:TYR:CZ	2.50	0.45
27:Ae:85:SER:HB2	39:AA:44:A:O2'	2.16	0.45
30:Aj:36:VAL:HG22	30:Aj:196:ARG:HE	1.82	0.45
33:Ap:124:PRO:HG3	33:Ap:147:TYR:CE1	2.51	0.45
35:Av:174:ASN:HB2	42:BC:486:ASN:HD21	1.82	0.45
40:BA:698:SER:HA	40:BA:703:ARG:CZ	2.47	0.45
40:BA:741:VAL:HG12	51:BL:79:LYS:HZ3	1.81	0.45
40:BA:811:PRO:HA	54:BO:152:ARG:O	2.17	0.45
48:BI:260:TRP:CD1	48:BI:266:GLU:O	2.69	0.45
51:BL:141:ASN:H	51:BL:141:ASN:ND2	2.08	0.45
51:BL:159:TYR:O	51:BL:162:HIS:HB3	2.16	0.45
53:BN:112:GLU:HB2	53:BN:123:PHE:HE2	1.80	0.45
54:BO:141:ASP:OD2	54:BO:152:ARG:CZ	2.63	0.45
61:BV:124:ASP:OD1	61:BV:125:LYS:N	2.49	0.45
66:Ba:113:VAL:HG12	66:Ba:116:ARG:HG3	1.98	0.45
69:Bd:52:ARG:HD3	69:Bd:52:ARG:HA	1.33	0.45
3:A2:160:ARG:NH2	3:A2:332:ASP:OD1	2.50	0.45
3:A2:396:GLU:HA	3:A2:399:THR:HB	1.97	0.45
8:A8:40:PRO:HB3	8:A8:47:ILE:HG21	1.99	0.45
10:AE:236:ARG:NH2	10:AE:369:GLU:OE2	2.49	0.45
10:AE:239:LYS:HE3	68:Bc:92:ILE:HG23	1.98	0.45
14:AK:218:ARG:HH22	61:BV:112:ILE:HG13	1.81	0.45
18:AR:166:LYS:NZ	39:AA:1175:U:O4	2.48	0.45
22:AW:58:ARG:HD2	39:AA:484:U:H5	1.81	0.45
24:AY:264:VAL:HG21	65:BZ:126:SER:HB3	1.98	0.45
31:Al:146:LEU:HB3	31:Al:210:HIS:CD2	2.51	0.45
39:AA:509:U:H2'	39:AA:510:A:H8	1.82	0.45
42:BC:105:GLY:O	42:BC:109:THR:OG1	2.29	0.45
44:BE:162:ASP:OD1	51:BL:283:ARG:NH2	2.47	0.45
44:BE:266:LEU:HD23	44:BE:282:ILE:HD12	1.98	0.45
46:BG:161:ALA:HB1	46:BG:269:HIS:CD2	2.52	0.45
51:BL:104:TRP:NE1	51:BL:179:ASP:O	2.44	0.45
55:BP:178:PRO:O	55:BP:182:GLN:N	2.45	0.45
57:BR:108:TYR:N	57:BR:139:TYR:OH	2.49	0.45
66:Ba:80:ASP:HB3	66:Ba:99:ARG:NH1	2.31	0.45
66:Ba:104:ARG:O	66:Ba:132:ALA:HB2	2.16	0.45
77:UD:82:UNK:CG	77:UD:87:UNK:HG1	2.46	0.45
3:A2:391:PRO:HB3	39:AA:32:U:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A6:42:SER:HA	7:A6:82:PHE:CD1	2.52	0.45
8:A8:78:GLY:HA2	25:Ab:455:ARG:O	2.17	0.45
16:AP:34:LEU:HD13	45:BF:136:TYR:CD1	2.51	0.45
16:AP:87:ASN:O	16:AP:90:ILE:HG13	2.17	0.45
17:AQ:38:ASN:HB3	17:AQ:116:THR:HG21	1.98	0.45
24:AY:85:LEU:HD23	44:BE:63:VAL:HB	1.99	0.45
29:Ag:57:ILE:HG22	29:Ag:69:TYR:HB2	1.98	0.45
30:Aj:92:MET:HG3	30:Aj:99:ILE:HD11	1.98	0.45
32:Ao:158:ARG:HD2	52:BM:236:ARG:HH22	1.81	0.45
40:BA:627:SER:OG	40:BA:629:SER:O	2.31	0.45
41:BB:124:GLU:O	41:BB:127:VAL:HG12	2.17	0.45
41:BB:128:HIS:CD2	41:BB:132:GLU:OE2	2.70	0.45
41:BB:360:ASP:O	41:BB:364:VAL:HG13	2.17	0.45
42:BC:158:LEU:HD22	42:BC:220:LEU:HD21	1.97	0.45
45:BF:59:ILE:O	45:BF:63:ARG:HG3	2.16	0.45
47:BH:135:ARG:O	47:BH:176:TYR:HA	2.16	0.45
47:BH:198:VAL:HG12	47:BH:200:PRO:HD3	1.98	0.45
51:BL:79:LYS:HG3	51:BL:83:HIS:CD2	2.51	0.45
53:BN:213:MET:HE1	60:BU:156:GLN:HB3	1.98	0.45
57:BR:94:LYS:HE3	57:BR:179:ILE:HD13	1.98	0.45
1:A0:164:ASP:HA	1:A0:165:PRO:HD3	1.66	0.45
2:A1:50:ASN:OD1	2:A1:50:ASN:N	2.50	0.45
2:A1:113:VAL:HG11	2:A1:160:ILE:HG23	1.97	0.45
5:A4:29:HIS:NE2	5:A4:31:ARG:HB2	2.32	0.45
9:A9:76:ARG:NH2	39:AA:392:A:H62	2.15	0.45
14:AK:317:GLU:O	14:AK:320:LYS:HG2	2.16	0.45
15:AN:19:HIS:HD2	15:AN:21:HIS:H	1.64	0.45
15:AN:154:GLU:O	68:Bc:23:ARG:NH2	2.49	0.45
16:AP:47:SER:OG	16:AP:48:TRP:N	2.50	0.45
18:AR:57:LYS:HD3	18:AR:66:ARG:NH2	2.31	0.45
18:AR:154:ARG:HD3	44:BE:406:ASP:CG	2.41	0.45
24:AY:27:ASN:ND2	51:BL:51:SER:O	2.40	0.45
25:Ab:207:GLY:HA2	25:Ab:409:PHE:CE2	2.52	0.45
32:Ao:123:ARG:NH2	39:AA:331:C:OP1	2.40	0.45
39:AA:302:G:N2	39:AA:335:G:H2'	2.32	0.45
39:AA:380:G:H1	84:UU:4:UNK:CB	2.16	0.45
41:BB:169:SER:CB	72:Bg:105:GLU:HG2	2.46	0.45
42:BC:60:LEU:N	42:BC:292:ASN:HD21	2.11	0.45
48:BI:262:TRP:CE3	48:BI:302:PRO:HG3	2.50	0.45
53:BN:72:PRO:CB	53:BN:121:LEU:HD21	2.47	0.45
57:BR:162:LEU:HD21	57:BR:197:LYS:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A2:402:ARG:HD3	39:AA:85:U:O2'	2.17	0.45
4:A3:136:ILE:HD13	16:AP:40:LEU:HD21	1.99	0.45
6:A5:78:ILE:HG23	40:BA:780:TYR:CD2	2.52	0.45
11:AF:220:SER:OG	11:AF:224:ARG:NH2	2.50	0.45
11:AF:281:PRO:HG2	11:AF:357:MET:SD	2.57	0.45
14:AK:185:ARG:HH12	61:BV:115:GLN:C	2.25	0.45
15:AN:20:LYS:HA	15:AN:26:LEU:HD21	1.99	0.45
16:AP:79:TRP:CD2	16:AP:90:ILE:HD13	2.52	0.45
16:AP:315:ARG:NH1	42:BC:506:GLU:OE2	2.44	0.45
17:AQ:72:ARG:HB3	61:BV:169:GLU:HG2	1.99	0.45
18:AR:197:LYS:HB2	50:BK:194:ARG:HB2	1.99	0.45
25:Ab:74:ASP:OD1	25:Ab:74:ASP:N	2.43	0.45
25:Ab:215:LEU:O	25:Ab:330:TYR:OH	2.32	0.45
27:Ae:130:TYR:OH	41:BB:156:TRP:O	2.27	0.45
28:Af:165:GLY:HA2	28:Af:168:GLN:HB2	1.98	0.45
30:Aj:177:ILE:HG22	30:Aj:186:TRP:HE3	1.80	0.45
30:Aj:255:ARG:O	30:Aj:257:LYS:N	2.49	0.45
31:Al:177:GLU:CD	31:Al:191:VAL:HG22	2.42	0.45
33:Ap:242:TYR:CG	33:Ap:262:GLU:HG2	2.51	0.45
34:At:104:ARG:NH2	34:At:104:ARG:HB2	2.31	0.45
39:AA:300:U:OP2	45:BF:261:ARG:NH2	2.41	0.45
40:BA:808:PRO:O	54:BO:152:ARG:NE	2.50	0.45
57:BR:22:VAL:HG13	57:BR:56:ALA:HB1	1.99	0.45
59:BT:94:TYR:HD2	62:BW:80:MET:HE1	1.81	0.45
60:BU:114:THR:O	60:BU:117:ILE:N	2.47	0.45
62:BW:124:LEU:HD23	62:BW:124:LEU:HA	1.76	0.45
78:UE:1:UNK:HA	78:UE:2:UNK:HA	1.76	0.45
3:A2:62:LYS:HE3	23:AX:143:GLU:OE2	2.17	0.45
5:A4:102:ILE:HD11	46:BG:341:ALA:HB3	1.99	0.45
6:A5:59:LEU:HD13	6:A5:74:ASP:HB3	1.98	0.45
10:AE:179:GLU:O	10:AE:182:THR:OG1	2.23	0.45
11:AF:118:PHE:HD2	11:AF:237:GLN:NE2	2.15	0.45
11:AF:362:GLU:HB3	62:BW:41:ARG:HH22	1.82	0.45
11:AF:375:ILE:HG13	62:BW:134:TYR:CE2	2.52	0.45
21:AV:191:TYR:H	21:AV:206:ASN:ND2	2.15	0.45
24:AY:279:ARG:HH12	65:BZ:174:SER:CB	2.30	0.45
31:Al:69:LYS:HB3	31:Al:206:ARG:NH2	2.31	0.45
32:Ao:127:SER:HB3	56:BQ:188:ARG:HH22	1.82	0.45
39:AA:424:G:OP2	61:BV:145:LYS:NZ	2.38	0.45
39:AA:454:U:H1'	39:AA:455:U:O4'	2.17	0.45
39:AA:559:A:O2'	39:AA:560:G:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:BA:428:PHE:HA	40:BA:431:VAL:HG22	1.99	0.45
40:BA:625:LEU:HD13	40:BA:625:LEU:HA	1.81	0.45
42:BC:174:VAL:O	42:BC:185:ARG:HG2	2.17	0.45
45:BF:123:LEU:HA	45:BF:126:VAL:HG22	1.98	0.45
49:BJ:192:ARG:HH22	74:UA:34:UNK:HB2	1.81	0.45
57:BR:43:LYS:HB2	57:BR:46:VAL:HG22	1.98	0.45
79:UF:2:UNK:HB1	79:UF:5:UNK:HG2	1.99	0.45
2:A1:193:ASP:OD1	2:A1:194:GLY:N	2.49	0.45
8:A8:59:THR:H	11:AF:318:ALA:CB	2.29	0.45
10:AE:176:ARG:NH1	39:AA:1112:U:C6	2.85	0.45
10:AE:315:ARG:HB3	10:AE:324:TYR:CD2	2.52	0.45
12:AI:97:ARG:HG2	12:AI:98:PRO:O	2.17	0.45
15:AN:188:ASP:OD1	15:AN:189:PRO:HD2	2.17	0.45
16:AP:13:LEU:HD21	32:Ao:62:THR:HB	1.97	0.45
17:AQ:44:ILE:H	17:AQ:44:ILE:HG13	1.58	0.45
18:AR:55:LEU:HD23	18:AR:55:LEU:H	1.82	0.45
22:AW:134:LEU:HD13	22:AW:231:VAL:HG22	1.97	0.45
22:AW:215:ARG:NH1	44:BE:23:GLN:NE2	2.64	0.45
24:AY:81:LEU:HD11	66:Ba:21:MET:HE1	1.98	0.45
25:Ab:283:ASN:H	25:Ab:351:GLN:NE2	2.14	0.45
29:Ag:239:ARG:O	29:Ag:242:GLU:HG3	2.17	0.45
39:AA:69:U:HO2'	39:AA:70:G:P	2.39	0.45
39:AA:880:C:H2'	39:AA:881:A:H8	1.82	0.45
40:BA:397:MET:O	40:BA:401:THR:OG1	2.32	0.45
40:BA:612:VAL:HG11	40:BA:643:VAL:HG11	1.98	0.45
41:BB:425:ASP:N	41:BB:425:ASP:OD1	2.49	0.45
44:BE:350:ASN:HB3	44:BE:353:LEU:HB2	1.99	0.45
46:BG:288:SER:HA	46:BG:292:GLY:O	2.16	0.45
50:BK:227:GLN:HE21	50:BK:231:LYS:HD2	1.81	0.45
56:BQ:53:ILE:HD13	56:BQ:122:ALA:CB	2.47	0.45
57:BR:145:PRO:HG3	79:UF:24:UNK:HG3	1.98	0.45
2:A1:122:MET:HB3	2:A1:126:ALA:HB3	1.99	0.45
3:A2:451:HIS:HB3	23:AX:115:PRO:HG3	1.98	0.45
7:A6:38:VAL:HG11	7:A6:54:LYS:HE3	1.99	0.45
10:AE:45:TYR:CE1	33:Ap:50:MET:HG3	2.52	0.45
13:AJ:14:ARG:HB3	13:AJ:44:GLN:HE22	1.81	0.45
13:AJ:79:GLN:HB2	39:AA:424:G:H5'	1.99	0.45
16:AP:63:LEU:HD23	45:BF:44:VAL:HG21	1.98	0.45
16:AP:310:HIS:CG	16:AP:311:PRO:HD2	2.52	0.45
17:AQ:33:ASP:HB3	79:UG:17:UNK:CB	2.46	0.45
23:AX:107:LYS:HE2	39:AA:39:C:O2'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Ab:85:GLU:OE1	25:Ab:115:PRO:HB3	2.16	0.45
25:Ab:144:TYR:OH	55:BP:73:SER:OG	2.21	0.45
25:Ab:225:ASP:HB3	25:Ab:289:ASN:HD21	1.81	0.45
30:Aj:145:PRO:HB2	46:BG:66:TYR:CZ	2.52	0.45
30:Aj:175:HIS:CE1	30:Aj:290:ALA:H	2.35	0.45
31:Al:74:LEU:HD22	31:Al:211:HIS:CD2	2.51	0.45
32:Ao:144:PRO:HG3	57:BR:136:TRP:HB3	1.99	0.45
39:AA:438:U:H6	39:AA:438:U:H5'	1.82	0.45
40:BA:762:ASN:HD22	40:BA:765:ARG:NH1	2.14	0.45
44:BE:255:TYR:CD2	44:BE:288:LEU:HB3	2.52	0.45
46:BG:121:SER:HB2	46:BG:124:ASP:CB	2.47	0.45
46:BG:172:THR:CG2	46:BG:324:TRP:HE1	2.27	0.45
47:BH:127:SER:HB2	47:BH:185:HIS:HB2	1.98	0.45
47:BH:194:ARG:HG3	47:BH:224:LEU:HD13	1.98	0.45
53:BN:72:PRO:HB3	53:BN:121:LEU:HD21	1.98	0.45
58:BS:97:ASP:OD1	58:BS:97:ASP:N	2.50	0.45
69:Bd:51:ARG:O	69:Bd:90:GLN:HA	2.17	0.45
5:A4:78:PHE:HA	5:A4:95:PHE:O	2.17	0.45
10:AE:235:VAL:HG21	10:AE:321:SER:HA	1.98	0.45
14:AK:192:ILE:HD13	14:AK:192:ILE:N	2.32	0.45
14:AK:205:MET:CE	14:AK:209:GLN:HB3	2.47	0.45
16:AP:172:PHE:CG	16:AP:217:VAL:HG23	2.52	0.45
24:AY:251:LEU:O	24:AY:255:ARG:HG2	2.17	0.45
28:Af:155:ARG:HD3	28:Af:155:ARG:HA	1.85	0.45
29:Ag:166:ARG:NH1	48:BI:284:VAL:HG11	2.31	0.45
35:Av:54:THR:HG22	35:Av:57:GLU:OE2	2.17	0.45
43:BD:273:ALA:HA	43:BD:274:ALA:HA	1.72	0.45
44:BE:66:ARG:O	44:BE:69:GLU:HG2	2.17	0.45
45:BF:148:HIS:O	45:BF:152:VAL:HG23	2.17	0.45
48:BI:272:ARG:HA	48:BI:275:MET:HG2	1.99	0.45
49:BJ:240:VAL:HA	49:BJ:243:LYS:HZ3	1.79	0.45
50:BK:98:THR:HG22	50:BK:99:SER:H	1.82	0.45
64:BY:79(E):SER:O	64:BY:80:GLN:NE2	2.50	0.45
3:A2:153:ARG:HD2	3:A2:156:GLU:OE2	2.17	0.44
5:A4:164:ARG:NH1	30:Aj:26:PRO:HB3	2.32	0.44
10:AE:77:ILE:HG23	10:AE:90:GLN:HG2	1.99	0.44
14:AK:31:VAL:HG23	61:BV:90:PHE:HE2	1.81	0.44
14:AK:171:PRO:HD2	14:AK:176:ARG:NH1	2.32	0.44
16:AP:310:HIS:HB3	16:AP:313:ALA:HB2	2.00	0.44
18:AR:63:PRO:HD3	39:AA:797:A:H4'	1.99	0.44
23:AX:119:PRO:HA	23:AX:120:PRO:HD3	1.74	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:BI:167:LEU:HG	48:BI:171:ARG:NH1	2.32	0.44
49:BJ:267:GLU:CD	49:BJ:270:ARG:HH12	2.25	0.44
61:BV:32:VAL:N	61:BV:82:GLY:O	2.46	0.44
74:UA:30:UNK:O	74:UA:34:UNK:N	2.50	0.44
84:UU:2:UNK:O	84:UU:2:UNK:HG3	2.17	0.44
5:A4:100:PRO:HA	5:A4:101:PRO:HD3	1.74	0.44
10:AE:111:PHE:CE1	79:UN:15:UNK:HG3	2.52	0.44
10:AE:163:PHE:CD2	10:AE:339:PHE:HZ	2.35	0.44
11:AF:77:PRO:HG2	45:BF:360:THR:HG21	1.99	0.44
12:AI:75:GLU:OE1	12:AI:75:GLU:N	2.40	0.44
12:AI:207:PHE:CD2	47:BH:153:ARG:HD3	2.52	0.44
14:AK:266:ASP:OD1	14:AK:267:THR:N	2.50	0.44
15:AN:117:ARG:HH12	48:BI:42:VAL:CG2	2.31	0.44
16:AP:310:HIS:CD2	16:AP:312:ALA:H	2.35	0.44
18:AR:47:ASP:O	18:AR:55:LEU:HD23	2.17	0.44
23:AX:83:PRO:HA	23:AX:84:PRO:HD3	1.78	0.44
23:AX:128:GLN:NE2	27:Ae:73:LEU:HD23	2.32	0.44
26:Ad:165:GLU:HB3	26:Ad:174:PHE:CD1	2.53	0.44
29:Ag:136:LEU:HD13	48:BI:72:GLU:HG2	1.98	0.44
29:Ag:180:ARG:HB3	29:Ag:221:LEU:HD11	1.99	0.44
32:Ao:158:ARG:CZ	52:BM:236:ARG:HH12	2.30	0.44
35:Av:111:ILE:HD11	35:Av:125:MET:SD	2.57	0.44
41:BB:108:ASP:O	41:BB:111:ILE:HG22	2.17	0.44
41:BB:216:PHE:HZ	63:BX:156:TRP:HZ3	1.65	0.44
45:BF:245:ASN:HD22	62:BW:182:ALA:HB2	1.83	0.44
46:BG:100:LEU:HD23	46:BG:100:LEU:HA	1.80	0.44
46:BG:169:ARG:HA	46:BG:169:ARG:HD3	1.68	0.44
48:BI:86:PRO:HB2	48:BI:117:LEU:HD13	1.98	0.44
55:BP:81:LEU:O	55:BP:85:ARG:HG2	2.17	0.44
61:BV:152:MET:SD	61:BV:156:ARG:NH2	2.89	0.44
62:BW:79:HIS:HD2	62:BW:80:MET:HE2	1.83	0.44
1:A0:52:ARG:NH2	1:A0:63:GLU:OE2	2.51	0.44
2:A1:179:MET:HE2	2:A1:179:MET:HB3	1.82	0.44
3:A2:289:GLN:HB3	3:A2:295:ASN:O	2.17	0.44
10:AE:384:PRO:HD3	68:Bc:96:PRO:HB2	2.00	0.44
11:AF:192:ASN:ND2	39:AA:185:U:O3'	2.50	0.44
12:AI:83:ILE:HB	12:AI:89:PRO:O	2.18	0.44
13:AJ:54:ALA:C	13:AJ:56:VAL:H	2.26	0.44
15:AN:185:LYS:HG3	39:AA:384:U:C5	2.52	0.44
16:AP:67:GLY:O	21:AV:145:ARG:NH2	2.50	0.44
16:AP:269:GLU:O	62:BW:88:ARG:NH1	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:352:THR:HA	35:Av:164:ARG:NH1	2.32	0.44
20:AU:84:LEU:HD23	20:AU:84:LEU:HA	1.79	0.44
22:AW:69:LEU:HD21	39:AA:19:A:C2	2.52	0.44
22:AW:250:TYR:CE2	22:AW:254:MET:HE3	2.52	0.44
24:AY:206:MET:HA	24:AY:212:ILE:O	2.17	0.44
25:Ab:491:SER:HA	56:BQ:69:ARG:HG2	2.00	0.44
29:Ag:94:ASP:OD1	29:Ag:94:ASP:N	2.51	0.44
39:AA:877:A:N6	39:AA:893:A:C2	2.84	0.44
41:BB:101:LEU:HD22	41:BB:104:ILE:HD12	1.99	0.44
42:BC:395:PHE:CD1	42:BC:423:PHE:HB2	2.52	0.44
46:BG:264:LEU:O	46:BG:267:VAL:HG22	2.16	0.44
54:BO:79:VAL:HA	54:BO:80:PRO:HD3	1.86	0.44
57:BR:68:TRP:CZ3	57:BR:80:PHE:HB2	2.51	0.44
73:Bh:49:MET:HG2	77:UD:10:UNK:HA	1.99	0.44
2:A1:11:SER:OG	2:A1:16:ASN:ND2	2.50	0.44
5:A4:29:HIS:HD2	5:A4:32:LEU:HD23	1.82	0.44
9:A9:73:GLU:HG3	61:BV:161:LYS:NZ	2.32	0.44
14:AK:22:GLY:H	61:BV:103:THR:HA	1.83	0.44
16:AP:302:TYR:HA	16:AP:306:SER:HB3	1.99	0.44
22:AW:3:ARG:NH1	39:AA:151:C:C4	2.86	0.44
26:Ad:140:PHE:CG	30:Aj:130:ARG:HD2	2.53	0.44
29:Ag:96:PRO:HG2	29:Ag:101:HIS:CD2	2.52	0.44
32:Ao:54:GLN:HG3	79:UF:16:UNK:CA	2.48	0.44
40:BA:714:ASN:HB3	40:BA:717:VAL:HG22	1.99	0.44
46:BG:275:VAL:HB	46:BG:298:VAL:HG22	2.00	0.44
52:BM:212:ARG:HH22	52:BM:220:ILE:HB	1.83	0.44
52:BM:216:HIS:CD2	52:BM:221:LEU:HD23	2.53	0.44
53:BN:35:PRO:HG3	58:BS:75:GLN:NE2	2.32	0.44
59:BT:79:ALA:O	59:BT:82:ARG:HB3	2.17	0.44
61:BV:148:MET:HE3	61:BV:152:MET:HB2	1.98	0.44
61:BV:148:MET:HG3	61:BV:149:ALA:N	2.31	0.44
77:UD:196:UNK:HA	77:UD:199:UNK:HG3	1.99	0.44
1:A0:104:GLU:HA	1:A0:105:PRO:HD3	1.78	0.44
7:A6:66:LYS:HB3	7:A6:84:GLU:HB3	2.00	0.44
8:A8:175:ASP:OD1	11:AF:459:SER:HA	2.17	0.44
11:AF:72:ILE:HG12	11:AF:72:ILE:O	2.17	0.44
11:AF:280:THR:HB	59:BT:113:ARG:HB3	2.00	0.44
16:AP:135:ARG:HG2	39:AA:183:U:H5'	1.99	0.44
21:AV:147:ARG:HD2	29:Ag:96:PRO:HB3	2.00	0.44
23:AX:88:TYR:OH	39:AA:528:A:OP1	2.32	0.44
24:AY:181:SER:OG	24:AY:182:THR:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:AY:287:GLN:OE1	49:BJ:228:ARG:NH2	2.50	0.44
26:Ad:61:VAL:O	26:Ad:64:GLU:HG2	2.16	0.44
31:Al:109:ALA:HA	62:BW:115:TYR:OH	2.17	0.44
33:Ap:39:LYS:HA	33:Ap:39:LYS:HD2	1.36	0.44
39:AA:2:U:OP1	40:BA:760:TYR:OH	2.35	0.44
39:AA:567:G:C2	73:Bh:23:ARG:NH1	2.84	0.44
40:BA:373:ALA:HA	40:BA:376:ARG:HH11	1.81	0.44
40:BA:660:GLU:OE2	40:BA:675:MET:HG2	2.16	0.44
40:BA:739:ARG:HH22	40:BA:744:ASN:HD21	1.66	0.44
42:BC:439:LYS:HG3	42:BC:440:ARG:HG3	2.00	0.44
47:BH:66:GLU:HG2	47:BH:67:ALA:N	2.32	0.44
48:BI:58:GLU:O	48:BI:61:PHE:HB3	2.18	0.44
53:BN:209:LYS:HD2	73:Bh:15:PHE:CB	2.48	0.44
57:BR:46:VAL:HA	57:BR:49:LYS:HG2	2.00	0.44
60:BU:123:ASN:HA	60:BU:126:ARG:HG2	1.99	0.44
63:BX:125:ARG:NH1	63:BX:160:TYR:OH	2.50	0.44
64:BY:139:MET:HB3	64:BY:145:TRP:CH2	2.52	0.44
77:UD:20:UNK:O	77:UD:25:UNK:HG1	2.18	0.44
8:A8:175:ASP:OD2	35:Av:99:ARG:NH1	2.50	0.44
11:AF:172:LYS:NZ	11:AF:174:LYS:HB3	2.33	0.44
12:AI:202:THR:HG21	64:BY:119:LYS:HE3	1.99	0.44
13:AJ:45:GLN:CD	33:Ap:231:ARG:NH1	2.76	0.44
14:AK:248:SER:N	14:AK:249:PRO:HD2	2.33	0.44
15:AN:82:HIS:CD2	15:AN:157:TRP:HE1	2.35	0.44
21:AV:234:ASP:OD1	21:AV:234:ASP:N	2.47	0.44
21:AV:235:LEU:HD12	28:Af:88:ARG:NH1	2.32	0.44
22:AW:181:MET:CE	24:AY:48:VAL:HG21	2.48	0.44
26:Ad:120:PRO:HA	26:Ad:121:PRO:HD3	1.80	0.44
29:Ag:101:HIS:HA	40:BA:720:ARG:HH12	1.83	0.44
39:AA:1110:A:H2	39:AA:1111:A:C5	2.36	0.44
39:AA:1163:A:C2	39:AA:1166:A:C8	3.05	0.44
40:BA:565:LEU:HD12	40:BA:565:LEU:HA	1.77	0.44
41:BB:443:ARG:HG2	41:BB:443:ARG:NH1	2.33	0.44
48:BI:299:ARG:H	48:BI:299:ARG:HD3	1.82	0.44
52:BM:153:HIS:O	52:BM:156:VAL:HB	2.17	0.44
61:BV:35:PRO:HG2	61:BV:36:TYR:HD1	1.82	0.44
64:BY:150:GLN:OE1	76:UC:1:UNK:N	2.51	0.44
69:Bd:98:ARG:HG2	69:Bd:112:VAL:HG13	1.99	0.44
77:UD:90:UNK:HG2	77:UD:140:UNK:HG2	1.99	0.44
1:A0:32:PHE:CD1	1:A0:47:LYS:HD3	2.53	0.44
2:A1:111:SER:OG	2:A1:114:LEU:HG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A2:212:ALA:HB1	3:A2:213:PRO:HD2	2.00	0.44
3:A2:271:PRO:HG3	50:BK:324:LYS:HD3	2.00	0.44
5:A4:76:PRO:HG2	5:A4:77:ARG:H	1.82	0.44
8:A8:114:GLU:HB2	8:A8:117:TYR:HD2	1.83	0.44
11:AF:252:TYR:OH	11:AF:299:ASN:ND2	2.42	0.44
12:AI:207:PHE:O	12:AI:210:TYR:N	2.50	0.44
13:AJ:78:THR:HG22	13:AJ:80:ARG:H	1.82	0.44
16:AP:45:ARG:HB2	32:Ao:101:PHE:CZ	2.52	0.44
22:AW:269:ASP:OD2	44:BE:355:LYS:HD3	2.18	0.44
25:Ab:54:LEU:HD21	35:Av:213:ARG:HD2	2.00	0.44
25:Ab:77:PHE:HB3	42:BC:209:PHE:CE2	2.52	0.44
25:Ab:167:VAL:HG12	25:Ab:203:THR:HG22	1.99	0.44
32:Ao:90:ASP:OD2	45:BF:118:ARG:NH2	2.50	0.44
32:Ao:158:ARG:HD2	52:BM:236:ARG:HH12	1.82	0.44
32:Ao:224:LYS:O	57:BR:156:ARG:NH2	2.51	0.44
39:AA:483:A:OP2	59:BT:34:ARG:NH2	2.51	0.44
40:BA:231:TYR:HE1	40:BA:296:ARG:HD3	1.83	0.44
41:BB:107:HIS:HB2	41:BB:358:ARG:NH1	2.32	0.44
49:BJ:223:THR:HG22	49:BJ:224:ASP:H	1.82	0.44
49:BJ:320:ARG:NH1	49:BJ:324:MET:HE3	2.33	0.44
54:BO:109:GLU:HG3	54:BO:109:GLU:O	2.17	0.44
58:BS:38:HIS:HA	58:BS:41:CYS:HB2	1.99	0.44
66:Ba:106:VAL:N	66:Ba:131:LEU:O	2.50	0.44
3:A2:419:TYR:HB3	81:UK:7:UNK:HG1	1.99	0.44
10:AE:161:THR:OG1	10:AE:327:THR:O	2.33	0.44
10:AE:353:GLU:H	10:AE:353:GLU:CD	2.26	0.44
14:AK:184:ALA:HB3	14:AK:191:PHE:HZ	1.82	0.44
15:AN:38:CYS:O	15:AN:79:THR:HG23	2.17	0.44
24:AY:195:ASN:HB3	24:AY:198:THR:HB	1.99	0.44
29:Ag:244:HIS:HD2	61:BV:123:PHE:CD1	2.35	0.44
30:Aj:57:VAL:HG11	30:Aj:136:ARG:HD2	2.00	0.44
39:AA:427:U:H3	61:BV:165:LEU:HD21	1.83	0.44
40:BA:589:MET:SD	40:BA:589:MET:N	2.91	0.44
40:BA:624:SER:O	40:BA:633:ARG:HD2	2.17	0.44
44:BE:25:HIS:CD2	44:BE:27:THR:H	2.36	0.44
45:BF:383:MET:O	45:BF:388:ARG:NH2	2.50	0.44
45:BF:408:LEU:HD12	45:BF:408:LEU:O	2.17	0.44
45:BF:415:PHE:O	45:BF:419:VAL:HG23	2.18	0.44
46:BG:42:PHE:HB2	46:BG:66:TYR:CD1	2.53	0.44
49:BJ:222:PRO:HG2	49:BJ:227:ARG:CZ	2.48	0.44
54:BO:135:LEU:HD21	58:BS:25:GLY:HA2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:BR:187:LYS:H	57:BR:187:LYS:HG2	1.63	0.44
63:BX:121:ARG:HD3	63:BX:143:CYS:HB3	1.99	0.44
72:Bg:80:MET:HG3	72:Bg:81:PHE:CD2	2.53	0.44
1:A0:108:GLN:CG	52:BM:84:ASP:HB3	2.46	0.44
2:A1:78:LEU:HD23	2:A1:78:LEU:H	1.83	0.44
5:A4:153:TYR:N	5:A4:153:TYR:CD1	2.86	0.44
11:AF:109:MET:HG2	11:AF:136:GLY:O	2.18	0.44
16:AP:339:VAL:HG11	42:BC:523:TYR:HE1	1.83	0.44
18:AR:52:ARG:HH12	39:AA:1170:U:P	2.41	0.44
21:AV:102:LEU:O	21:AV:143:GLN:NE2	2.51	0.44
23:AX:91:ARG:HD2	39:AA:530:U:OP1	2.18	0.44
26:Ad:85:ARG:HD3	30:Aj:266:ARG:HH12	1.82	0.44
26:Ad:230:LEU:HD23	69:Bd:32:THR:HG23	2.00	0.44
27:Ae:148:ILE:HG23	27:Ae:148:ILE:O	2.17	0.44
28:Af:143:THR:OG1	28:Af:144:VAL:N	2.51	0.44
29:Ag:134:ARG:NH2	29:Ag:140:GLU:OE2	2.47	0.44
45:BF:326:ASP:OD1	45:BF:327:PHE:N	2.49	0.44
46:BG:73:PRO:HB2	46:BG:74:ARG:HD3	1.99	0.44
47:BH:122:HIS:CD2	47:BH:225:GLY:HA3	2.53	0.44
59:BT:142:TYR:HE1	59:BT:165:ILE:HG23	1.82	0.44
63:BX:80:PHE:HB3	63:BX:112:PHE:CE1	2.53	0.44
65:BZ:116:ASP:OD1	65:BZ:144:ASN:ND2	2.51	0.44
67:Bb:64:PRO:HA	67:Bb:67:ARG:HG2	1.99	0.44
72:Bg:37:LEU:HD12	72:Bg:37:LEU:HA	1.69	0.44
72:Bg:69:ARG:H	72:Bg:69:ARG:HG2	1.63	0.44
77:UD:186:UNK:HA	77:UD:189:UNK:HG3	1.98	0.44
4:A3:76:LYS:NZ	84:UU:7:UNK:O	2.39	0.43
5:A4:107:HIS:HD2	26:Ad:148:ARG:O	2.01	0.43
8:A8:99:ARG:O	8:A8:100:GLN:HB2	2.18	0.43
10:AE:134:TYR:O	10:AE:134:TYR:CG	2.71	0.43
13:AJ:89:ARG:HD3	13:AJ:89:ARG:HA	1.69	0.43
15:AN:144:ARG:NE	39:AA:113:A:H62	2.16	0.43
15:AN:168:ASP:OD1	28:Af:125:THR:HG22	2.17	0.43
16:AP:316:ARG:HD2	42:BC:523:TYR:OH	2.16	0.43
18:AR:214:SER:HA	18:AR:217:LYS:HZ3	1.83	0.43
23:AX:91:ARG:HH12	27:Ae:111:GLY:HA3	1.83	0.43
24:AY:201:MET:HB3	24:AY:201:MET:HE2	1.86	0.43
29:Ag:98:CYS:O	29:Ag:102:LEU:HG	2.18	0.43
32:Ao:25:ASN:ND2	32:Ao:26:TYR:H	2.14	0.43
42:BC:221:LYS:HD3	42:BC:221:LYS:HA	1.80	0.43
45:BF:128:LYS:HB2	45:BF:128:LYS:HE2	1.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
56:BQ:59:GLU:OE2	56:BQ:69:ARG:NH2	2.51	0.43
64:BY:163:ASP:OD1	64:BY:163:ASP:N	2.45	0.43
70:Be:37:SER:HB3	80:UI:8:UNK:HG2	1.99	0.43
2:A1:172:VAL:O	2:A1:176:GLN:HG2	2.18	0.43
6:A5:77:GLN:HG3	40:BA:778:ASP:HB3	2.00	0.43
8:A8:153:SER:HB2	8:A8:156:TRP:HD1	1.83	0.43
10:AE:163:PHE:HE2	10:AE:325:LEU:HD22	1.83	0.43
12:AI:138:TYR:CD1	64:BY:139:MET:HG2	2.53	0.43
13:AJ:103:ARG:NH1	37:AC:12:ALA:HB2	2.28	0.43
14:AK:303:PRO:O	14:AK:306:MET:HB2	2.18	0.43
14:AK:336:THR:OG1	29:Ag:188:ARG:O	2.36	0.43
15:AN:56:ARG:NH1	15:AN:182:LYS:O	2.51	0.43
18:AR:156:ASP:OD1	18:AR:156:ASP:N	2.50	0.43
21:AV:106:ILE:H	21:AV:106:ILE:HG13	1.64	0.43
22:AW:204:TYR:HB2	22:AW:205:PRO:HD2	2.00	0.43
25:Ab:203:THR:O	25:Ab:210:ILE:HD11	2.18	0.43
27:Ae:69:ARG:NH1	27:Ae:121:TYR:HE1	2.15	0.43
29:Ag:159:ILE:HD11	48:BI:276:ILE:HA	2.00	0.43
29:Ag:245:ASN:HA	29:Ag:248:VAL:HB	1.99	0.43
30:Aj:226:ALA:O	30:Aj:238:PHE:HA	2.18	0.43
40:BA:215:ARG:HH12	40:BA:288:PHE:HA	1.83	0.43
40:BA:759:GLN:HG3	40:BA:823:LEU:HA	2.00	0.43
41:BB:87:LEU:O	41:BB:91:LEU:HB2	2.17	0.43
42:BC:121:GLN:HE21	42:BC:167:ILE:HG22	1.83	0.43
42:BC:318:ASP:N	42:BC:318:ASP:OD1	2.51	0.43
45:BF:233:TYR:HD1	45:BF:289:CYS:HG	1.64	0.43
46:BG:228:ALA:HB3	46:BG:231:ASP:HB2	2.00	0.43
46:BG:284:ALA:CB	46:BG:296:PRO:HG3	2.47	0.43
47:BH:152:ALA:O	47:BH:156:LEU:HB2	2.18	0.43
47:BH:180:PRO:HG2	47:BH:198:VAL:HB	2.00	0.43
50:BK:106:TYR:CD1	50:BK:133:VAL:HG12	2.53	0.43
52:BM:245:LEU:HA	52:BM:245:LEU:HD13	1.68	0.43
56:BQ:152:ASP:N	56:BQ:152:ASP:OD1	2.44	0.43
68:Bc:33:GLN:O	68:Bc:36:LEU:HB2	2.18	0.43
70:Be:98:TRP:NE1	70:Be:101:ALA:HB2	2.33	0.43
3:A2:463:ILE:HA	3:A2:463:ILE:HD12	1.80	0.43
8:A8:119:ARG:HD3	39:AA:340:U:OP2	2.18	0.43
8:A8:151:SER:OG	8:A8:162:ARG:O	2.25	0.43
8:A8:165:GLY:O	16:AP:259:HIS:CE1	2.72	0.43
9:A9:85:CYS:SG	9:A9:97:ARG:HG2	2.58	0.43
11:AF:407:ARG:HH11	59:BT:108:LEU:HD12	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:AK:334:TYR:CD1	29:Ag:218:GLU:HG2	2.53	0.43
15:AN:108:ALA:O	15:AN:109:TYR:CG	2.71	0.43
15:AN:164:HIS:HA	15:AN:165:PRO:HD3	1.68	0.43
24:AY:177:HIS:CD2	24:AY:188:ILE:HD12	2.53	0.43
25:Ab:120:GLU:O	25:Ab:120:GLU:HG2	2.18	0.43
30:Aj:62:HIS:HA	46:BG:144:TRP:CD1	2.53	0.43
32:Ao:155:GLU:O	52:BM:229:TYR:OH	2.30	0.43
35:Av:73:ARG:HH21	62:BW:77:ASN:HD21	1.65	0.43
41:BB:219:ASN:HB2	63:BX:157:HIS:CD2	2.53	0.43
45:BF:169:GLY:O	45:BF:172:ILE:HB	2.17	0.43
45:BF:420:ARG:O	45:BF:421:GLN:HB2	2.18	0.43
47:BH:65:ARG:O	47:BH:68:ALA:HB3	2.18	0.43
52:BM:149:GLU:HA	52:BM:152:ARG:HG2	2.00	0.43
53:BN:58:ILE:HB	53:BN:59:PRO:HD3	2.00	0.43
60:BU:115:PRO:HA	60:BU:118:VAL:HG12	2.00	0.43
70:Be:88:MET:HE3	70:Be:96:LEU:HD12	2.00	0.43
71:Bf:41:SER:O	71:Bf:45:ARG:HB2	2.18	0.43
2:A1:142:LYS:HZ3	2:A1:143:ARG:HH11	1.66	0.43
2:A1:180:LEU:HD23	2:A1:180:LEU:HA	1.85	0.43
3:A2:87:ILE:O	3:A2:90:SER:HB2	2.19	0.43
4:A3:125:GLU:HG3	34:At:82:LEU:HD21	2.00	0.43
10:AE:55:ASP:OD1	10:AE:55:ASP:N	2.48	0.43
11:AF:163:ASP:OD1	11:AF:164:TYR:N	2.50	0.43
16:AP:126:TYR:HE2	21:AV:158:ARG:NH1	2.17	0.43
18:AR:89:ARG:O	18:AR:92:ALA:HB3	2.18	0.43
21:AV:142:GLU:OE2	29:Ag:3:ARG:NH2	2.51	0.43
23:AX:66:ARG:HH11	85:UX:8:UNK:CG	2.27	0.43
24:AY:261:GLU:O	24:AY:264:VAL:HG12	2.18	0.43
25:Ab:223:PHE:CE1	25:Ab:322:LYS:HG3	2.53	0.43
26:Ad:164:MET:HB3	26:Ad:174:PHE:HE1	1.82	0.43
26:Ad:214:TRP:CD2	69:Bd:54:MET:HE2	2.53	0.43
28:Af:138:ILE:HD13	29:Ag:114:ASN:HD22	1.82	0.43
30:Aj:249:PRO:HB2	30:Aj:251:PHE:CZ	2.54	0.43
34:At:136:ARG:NH1	45:BF:211:GLU:OE2	2.51	0.43
40:BA:148:VAL:HG23	54:BO:148:ASP:HA	2.00	0.43
40:BA:174:ARG:NH1	40:BA:803:LEU:HD21	2.34	0.43
46:BG:102:GLN:OE1	46:BG:318:ALA:HB3	2.18	0.43
46:BG:183:ARG:HH11	46:BG:187:ARG:N	2.16	0.43
49:BJ:178:ILE:HG22	49:BJ:181:ARG:NH2	2.33	0.43
1:A0:31:LEU:HD22	52:BM:57:PRO:HG2	2.00	0.43
2:A1:131:GLU:OE2	12:AI:141:ARG:NE	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A3:104:GLN:HE21	4:A3:104:GLN:HB2	1.58	0.43
6:A5:54:TRP:CH2	22:AW:245:ARG:HG3	2.54	0.43
10:AE:67:HIS:ND1	10:AE:76:LYS:HB2	2.33	0.43
10:AE:198:LYS:NZ	39:AA:1106:U:H2'	2.34	0.43
11:AF:230:LYS:HD3	11:AF:230:LYS:HA	1.81	0.43
11:AF:300:LYS:NZ	11:AF:342:ASP:OD2	2.48	0.43
12:AI:174:THR:HG22	12:AI:175:HIS:CD2	2.53	0.43
13:AJ:57:ILE:HB	29:Ag:197:LEU:HD13	2.01	0.43
18:AR:211:ARG:HG3	72:Bg:25:ARG:NH1	2.33	0.43
22:AW:151:VAL:O	40:BA:752:ARG:NH2	2.51	0.43
24:AY:278:ARG:HD3	24:AY:279:ARG:N	2.34	0.43
26:Ad:242:GLU:O	26:Ad:246:SER:OG	2.33	0.43
29:Ag:181:TRP:NE1	36:AB:19:ALA:O	2.39	0.43
32:Ao:244:PHE:N	32:Ao:244:PHE:CD1	2.86	0.43
40:BA:463:LEU:O	40:BA:467:LEU:HG	2.19	0.43
44:BE:133:VAL:HB	44:BE:134:PRO:HD3	2.00	0.43
48:BI:183:VAL:HG11	71:Bf:97:VAL:HG11	2.00	0.43
48:BI:225:TRP:CZ2	71:Bf:107:PRO:HD3	2.54	0.43
56:BQ:48:GLU:HB2	56:BQ:165:ILE:HD11	2.01	0.43
56:BQ:126:LEU:HD23	56:BQ:150:ARG:HH11	1.82	0.43
3:A2:124:TYR:HB2	24:AY:267:LEU:HB3	1.99	0.43
3:A2:275:LEU:HD21	50:BK:326:VAL:HG12	2.01	0.43
4:A3:114:HIS:HA	34:At:37:VAL:HG22	1.99	0.43
5:A4:29:HIS:CD2	5:A4:32:LEU:HD23	2.54	0.43
6:A5:49:LEU:H	6:A5:49:LEU:HG	1.66	0.43
10:AE:171:VAL:HG22	10:AE:210:VAL:HG11	2.00	0.43
10:AE:172:LYS:HB3	10:AE:186:TYR:CD2	2.53	0.43
10:AE:335:THR:OG1	19:AT:16:ARG:NH1	2.50	0.43
13:AJ:70:TRP:HZ3	13:AJ:86:MET:HE1	1.83	0.43
16:AP:348:ASN:ND2	16:AP:348:ASN:N	2.61	0.43
18:AR:47:ASP:OD2	18:AR:54:LYS:HG2	2.19	0.43
18:AR:211:ARG:HG3	72:Bg:25:ARG:HH12	1.83	0.43
18:AR:247:ASP:OD1	18:AR:247:ASP:N	2.50	0.43
22:AW:17:ARG:HD2	39:AA:149:U:H5'	2.01	0.43
23:AX:68:TRP:CD1	23:AX:69:GLU:HG3	2.53	0.43
25:Ab:175:ARG:HH12	42:BC:91:ALA:CB	2.27	0.43
25:Ab:490:TRP:CZ3	25:Ab:494:THR:HG21	2.53	0.43
26:Ad:256:GLU:OE2	55:BP:36:ARG:NH2	2.50	0.43
29:Ag:125:ARG:HH12	29:Ag:130:PRO:HD2	1.83	0.43
33:Ap:83:HIS:CE1	71:Bf:84:GLU:HB3	2.53	0.43
33:Ap:278:ASN:ND2	33:Ap:278:ASN:H	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:At:94:THR:HG23	34:At:97:GLN:H	1.84	0.43
40:BA:152:TYR:OH	54:BO:143:ARG:NH2	2.45	0.43
40:BA:423:ARG:HA	40:BA:423:ARG:HD3	1.69	0.43
42:BC:454:VAL:HB	42:BC:462:ALA:HB1	2.01	0.43
44:BE:78:HIS:CE1	81:UK:7:UNK:HB1	2.54	0.43
46:BG:189:MET:HE2	46:BG:189:MET:HB2	1.80	0.43
46:BG:283:ASP:O	46:BG:287:HIS:HD2	2.01	0.43
53:BN:128:ARG:NH2	73:Bh:34:ARG:HD3	2.33	0.43
56:BQ:79:LYS:O	56:BQ:230:ARG:NH1	2.45	0.43
57:BR:187:LYS:HZ2	57:BR:188:ARG:CZ	2.31	0.43
61:BV:147:ARG:O	61:BV:150:LYS:HB3	2.18	0.43
64:BY:79(F):GLU:O	64:BY:81:ASN:ND2	2.41	0.43
2:A1:129:GLU:CD	2:A1:143:ARG:NH1	2.73	0.43
5:A4:153:TYR:OH	69:Bd:44:GLU:HG2	2.19	0.43
10:AE:102:ASP:OD1	33:Ap:115:VAL:HG21	2.19	0.43
11:AF:75:TYR:CB	11:AF:81:ARG:NH1	2.82	0.43
15:AN:178:ASP:OD1	15:AN:178:ASP:N	2.51	0.43
16:AP:14:PHE:HE2	34:At:32:LEU:HD22	1.84	0.43
25:Ab:196:THR:HG22	25:Ab:197:HIS:H	1.84	0.43
26:Ad:129:LEU:O	30:Aj:136:ARG:NH1	2.46	0.43
26:Ad:171:ASP:HA	26:Ad:172:PRO:HD3	1.87	0.43
30:Aj:21:SER:HB3	69:Bd:131:GLY:O	2.19	0.43
32:Ao:40:LYS:HA	32:Ao:41:PRO:HD3	1.85	0.43
35:Av:213:ARG:O	35:Av:213:ARG:HD3	2.19	0.43
39:AA:514:G:O2'	39:AA:570:U:O2	2.35	0.43
40:BA:215:ARG:HH12	40:BA:288:PHE:C	2.27	0.43
40:BA:504:SER:O	40:BA:507:ALA:HB3	2.19	0.43
44:BE:131:LEU:HD23	44:BE:131:LEU:HA	1.85	0.43
49:BJ:174:GLU:HA	49:BJ:178:ILE:HD11	2.01	0.43
49:BJ:251:GLY:HA3	66:Ba:55:SER:N	2.33	0.43
52:BM:45:ASN:HB3	52:BM:67:LEU:HD12	2.01	0.43
61:BV:35:PRO:HG2	61:BV:36:TYR:CD1	2.54	0.43
1:A0:108:GLN:O	1:A0:112:ARG:HG2	2.19	0.43
4:A3:175:ARG:NH1	34:At:153:LEU:HG	2.33	0.43
5:A4:91:ASN:CG	26:Ad:128:THR:HG23	2.44	0.43
7:A6:94:LYS:NZ	16:AP:345:TRP:CH2	2.83	0.43
11:AF:27:TRP:HE3	39:AA:490:G:H22	1.66	0.43
11:AF:59:PRO:HG2	16:AP:79:TRP:CZ2	2.54	0.43
18:AR:83:CYS:HB3	18:AR:85:VAL:HG23	2.01	0.43
18:AR:94:ARG:CZ	18:AR:146:MET:HB3	2.48	0.43
18:AR:112:ARG:HH11	18:AR:129:PHE:HB2	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Ad:121:PRO:HD2	26:Ad:124:PHE:HB2	2.01	0.43
27:Ae:82:ARG:HH22	39:AA:39:C:P	2.42	0.43
28:Af:167:LEU:HD23	28:Af:167:LEU:HA	1.70	0.43
29:Ag:162:ARG:HH12	39:AA:444:G:N2	2.16	0.43
30:Aj:293:THR:HG21	46:BG:143:ARG:HH11	1.84	0.43
33:Ap:37:ASN:ND2	48:BI:27:LEU:HB2	2.32	0.43
33:Ap:169:MET:HA	33:Ap:257:GLN:HE22	1.83	0.43
52:BM:46:LYS:NZ	52:BM:53:ASN:O	2.50	0.43
63:BX:74:PRO:HA	63:BX:75:PRO:HD3	1.90	0.43
69:Bd:3:ASP:HA	69:Bd:6:ALA:HB3	2.00	0.43
83:UM:3:UNK:HG2	83:UM:4:UNK:N	2.34	0.43
2:A1:123:VAL:HG12	2:A1:124:GLU:N	2.33	0.43
5:A4:12:SER:HB3	7:A6:77:GLN:HE21	1.83	0.43
8:A8:65:HIS:CD2	8:A8:127:ILE:HD11	2.54	0.43
10:AE:249:GLN:OE1	19:AT:16:ARG:NH2	2.52	0.43
11:AF:125:ILE:HG12	11:AF:126:TYR:H	1.83	0.43
11:AF:385:LEU:HA	11:AF:385:LEU:HD23	1.75	0.43
16:AP:360:SER:HB3	35:Av:161:LYS:HZ1	1.82	0.43
20:AU:48:ARG:HH21	20:AU:48:ARG:HG3	1.83	0.43
22:AW:138:VAL:HG13	22:AW:174:ILE:HD13	1.99	0.43
32:Ao:127:SER:CB	56:BQ:188:ARG:HH12	2.29	0.43
32:Ao:158:ARG:NE	52:BM:236:ARG:HH12	2.16	0.43
39:AA:441:A:N6	61:BV:148:MET:HE1	2.34	0.43
39:AA:486:A:H5'	45:BF:372:LEU:HD12	2.00	0.43
39:AA:834:U:H2'	39:AA:835:A:O4'	2.19	0.43
39:AA:1163:A:H2	39:AA:1166:A:C8	2.37	0.43
45:BF:130:GLU:HB2	45:BF:152:VAL:HG11	2.01	0.43
48:BI:178:ASN:O	48:BI:181:SER:OG	2.22	0.43
51:BL:103:ASN:HD22	51:BL:104:TRP:H	1.67	0.43
52:BM:76:TRP:CE3	52:BM:77:PRO:HD3	2.54	0.43
54:BO:74:LEU:HD21	58:BS:29:ASN:OD1	2.19	0.43
61:BV:148:MET:CE	61:BV:152:MET:HB2	2.49	0.43
71:Bf:99:ILE:O	71:Bf:102:LYS:N	2.52	0.43
3:A2:293:PHE:HD1	3:A2:293:PHE:HA	1.63	0.43
4:A3:180:ARG:NE	31:Al:175:ARG:NH1	2.66	0.43
5:A4:66:GLU:O	26:Ad:65:ARG:HD3	2.18	0.43
5:A4:132:TRP:HA	30:Aj:201:MET:HE3	2.00	0.43
5:A4:151:PHE:HD2	69:Bd:69:LEU:HG	1.83	0.43
12:AI:17:ARG:CZ	66:Ba:104:ARG:NH1	2.82	0.43
14:AK:185:ARG:HH12	61:BV:115:GLN:HA	1.84	0.43
14:AK:216:ARG:O	14:AK:219:ARG:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:AR:82:TYR:HA	18:AR:163:VAL:O	2.19	0.43
22:AW:38:LYS:HA	22:AW:38:LYS:HD2	1.84	0.43
24:AY:279:ARG:NH1	65:BZ:174:SER:HA	2.34	0.43
25:Ab:211:GLU:OE2	42:BC:244:TRP:NE1	2.52	0.43
29:Ag:246:MET:HG2	52:BM:253:PRO:HG2	2.01	0.43
34:At:19:LEU:O	57:BR:118:GLN:HB3	2.18	0.43
34:At:68:ASN:HA	34:At:72:ILE:CB	2.49	0.43
39:AA:566:A:N7	60:BU:137:ARG:NH1	2.67	0.43
40:BA:580:SER:HB2	40:BA:608:ASP:OD1	2.19	0.43
40:BA:603:LEU:N	40:BA:604:PRO:HD2	2.33	0.43
41:BB:151:LEU:H	41:BB:154:GLN:NE2	2.17	0.43
46:BG:183:ARG:HH12	46:BG:187:ARG:CB	2.19	0.43
48:BI:263:HIS:HB2	48:BI:302:PRO:CB	2.49	0.43
51:BL:38:GLY:HA3	51:BL:167:LEU:HD11	2.00	0.43
55:BP:144:PHE:CD2	55:BP:144:PHE:O	2.72	0.43
56:BQ:47:VAL:HG13	56:BQ:163:GLN:O	2.19	0.43
71:Bf:43:ALA:O	71:Bf:44:ARG:HB2	2.18	0.43
5:A4:145:ALA:HA	26:Ad:178:GLU:HA	2.01	0.42
5:A4:155:ILE:HD11	69:Bd:31:VAL:HG21	2.01	0.42
11:AF:75:TYR:HB3	11:AF:81:ARG:HH12	1.84	0.42
11:AF:120:LEU:HD23	11:AF:120:LEU:HA	1.91	0.42
15:AN:103:ILE:HD11	15:AN:118:LEU:HD23	2.01	0.42
16:AP:196:THR:H	16:AP:199:HIS:CD2	2.29	0.42
22:AW:79:ILE:HG13	22:AW:110:TRP:CZ3	2.54	0.42
26:Ad:280:GLU:OE1	42:BC:239:ARG:NH2	2.52	0.42
28:Af:117:GLU:HG2	28:Af:120:LYS:HE3	2.01	0.42
31:Al:88:ARG:HG2	31:Al:89:TYR:H	1.83	0.42
31:Al:92:HIS:CE1	31:Al:128:ALA:HA	2.54	0.42
33:Ap:201:LEU:HA	33:Ap:201:LEU:HD23	1.80	0.42
35:Av:93:GLU:OE2	70:Be:101:ALA:HA	2.19	0.42
39:AA:196:G:H2'	39:AA:197:A:C8	2.53	0.42
40:BA:143:MET:HE1	40:BA:812:GLN:HB2	2.01	0.42
40:BA:386:TRP:HE1	40:BA:391:TRP:NE1	2.17	0.42
42:BC:121:GLN:NE2	42:BC:167:ILE:HG22	2.34	0.42
42:BC:128:PHE:CE1	42:BC:326:PRO:HB2	2.54	0.42
42:BC:375:LEU:HD23	42:BC:375:LEU:HA	1.90	0.42
44:BE:140:GLU:OE1	50:BK:279:SER:CB	2.66	0.42
45:BF:157:ASN:OD1	45:BF:167:ARG:NH2	2.52	0.42
46:BG:74:ARG:HG3	46:BG:144:TRP:HE3	1.85	0.42
46:BG:90:ALA:O	46:BG:93:ALA:HB3	2.19	0.42
46:BG:278:ALA:HB3	46:BG:303:GLN:C	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:BH:122:HIS:HA	47:BH:123:PRO:HD3	1.89	0.42
54:BO:211:GLU:HG2	54:BO:214:GLN:HE22	1.82	0.42
57:BR:111:PHE:CD1	57:BR:134:LYS:HG3	2.54	0.42
60:BU:138:ARG:NE	60:BU:141:GLU:OE2	2.52	0.42
73:Bh:15:PHE:CZ	73:Bh:28:ARG:NH1	2.87	0.42
73:Bh:25:LEU:HD13	77:UD:14:UNK:HG2	2.01	0.42
79:UF:18:UNK:HA	79:UF:21:UNK:HG3	2.01	0.42
3:A2:17:VAL:HG21	23:AX:224:VAL:HG11	2.01	0.42
3:A2:422:ARG:HG2	44:BE:78:HIS:HB3	2.02	0.42
5:A4:90:LEU:HD23	26:Ad:130:THR:OG1	2.18	0.42
5:A4:130:ARG:O	5:A4:134:THR:OG1	2.27	0.42
11:AF:38:ARG:CZ	29:Ag:50:ARG:NH1	2.75	0.42
13:AJ:73:ARG:NH1	13:AJ:83:PHE:CE1	2.87	0.42
20:AU:118:ILE:HG22	21:AV:128:ARG:HH22	1.83	0.42
22:AW:101:GLU:O	51:BL:162:HIS:NE2	2.52	0.42
22:AW:220:TYR:OH	44:BE:29:ASN:O	2.33	0.42
22:AW:273:ILE:HG12	22:AW:274:THR:N	2.31	0.42
25:Ab:76:MET:HB2	31:Al:30:GLY:HA3	2.01	0.42
27:Ae:83:SER:OG	39:AA:45:U:OP1	2.37	0.42
39:AA:438:U:N3	61:BV:160:MET:HE1	2.35	0.42
39:AA:1111:A:O2'	39:AA:1112:U:OP1	2.31	0.42
42:BC:120:ILE:HD12	42:BC:189:PHE:CZ	2.54	0.42
42:BC:267:ILE:O	42:BC:267:ILE:HD12	2.19	0.42
44:BE:376:ARG:HD3	44:BE:379:ARG:HE	1.84	0.42
47:BH:91:LYS:HB3	47:BH:91:LYS:NZ	2.34	0.42
49:BJ:221:ARG:HH21	74:UA:24:UNK:HB2	1.84	0.42
51:BL:141:ASN:HD22	51:BL:141:ASN:N	2.01	0.42
60:BU:122:ALA:N	72:Bg:97:LEU:HD11	2.34	0.42
71:Bf:44:ARG:HH11	78:UE:6:UNK:HG3	1.85	0.42
84:UU:5:UNK:HA	84:UU:11:UNK:HG1	1.99	0.42
1:A0:181:ARG:NH1	1:A0:182:TYR:CZ	2.87	0.42
3:A2:181:VAL:O	3:A2:185:LYS:HG2	2.20	0.42
12:AI:124:GLU:OE1	82:UL:11:UNK:N	2.52	0.42
12:AI:134:TYR:HE1	12:AI:165:LEU:HD12	1.84	0.42
16:AP:68:SER:HA	39:AA:469:G:OP2	2.20	0.42
16:AP:209:ARG:HG3	16:AP:209:ARG:NH1	2.34	0.42
18:AR:80:LYS:HE2	18:AR:82:TYR:CE1	2.53	0.42
24:AY:153:ILE:HA	24:AY:154:PRO:HD3	1.83	0.42
27:Ae:101:LYS:HB2	60:BU:115:PRO:HB2	2.01	0.42
30:Aj:179:ARG:HG2	30:Aj:186:TRP:CE3	2.55	0.42
33:Ap:176:MET:HG3	33:Ap:280:LEU:HG	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Ap:232:ILE:O	33:Ap:244:PRO:HD2	2.19	0.42
39:AA:329:U:N3	56:BQ:217:THR:O	2.52	0.42
39:AA:410:U:HO2'	39:AA:414:A:N6	2.17	0.42
39:AA:565:U:O5'	60:BU:138:ARG:NH1	2.51	0.42
40:BA:574:TYR:HE1	51:BL:37:ARG:HH12	1.67	0.42
44:BE:134:PRO:HA	44:BE:137:LYS:NZ	2.34	0.42
46:BG:106:ASP:OD1	46:BG:106:ASP:N	2.49	0.42
47:BH:159:ILE:O	47:BH:163:ASN:ND2	2.48	0.42
52:BM:84:ASP:HA	52:BM:85:PRO:HD2	1.93	0.42
52:BM:148:LYS:HA	52:BM:151:GLU:HG2	2.00	0.42
57:BR:108:TYR:HD1	57:BR:192:ARG:CZ	2.33	0.42
59:BT:96:LEU:HD22	62:BW:50:ARG:NH2	2.34	0.42
61:BV:44:GLU:HA	61:BV:47:ARG:HG2	2.01	0.42
61:BV:124:ASP:OD1	61:BV:124:ASP:C	2.61	0.42
1:A0:87:MET:HA	1:A0:102:ASP:O	2.19	0.42
1:A0:112:ARG:HD3	52:BM:112:TRP:HH2	1.84	0.42
2:A1:192:GLU:HB3	2:A1:193:ASP:H	1.44	0.42
3:A2:29:VAL:O	24:AY:225:VAL:HG23	2.20	0.42
3:A2:33:SER:HB2	3:A2:90:SER:OG	2.19	0.42
3:A2:131:PRO:HG2	3:A2:134:ALA:HB2	2.01	0.42
5:A4:29:HIS:CE1	5:A4:31:ARG:HE	2.37	0.42
5:A4:154:CYS:HB2	26:Ad:228:GLN:NE2	2.34	0.42
10:AE:89:LEU:HB2	71:Bf:84:GLU:OE2	2.19	0.42
11:AF:27:TRP:HE1	51:BL:68:THR:HA	1.83	0.42
15:AN:145:LYS:HG2	39:AA:113:A:H5''	2.01	0.42
16:AP:205:VAL:HG23	16:AP:206:VAL:HG13	2.02	0.42
22:AW:142:TRP:HB3	24:AY:11:PHE:CE1	2.55	0.42
26:Ad:106:ASP:HA	26:Ad:109:LEU:HD12	2.00	0.42
26:Ad:229:GLN:HG3	26:Ad:258:ARG:HH21	1.84	0.42
27:Ae:75:ARG:HG2	27:Ae:76:LEU:N	2.34	0.42
29:Ag:143:TYR:OH	48:BI:326:VAL:O	2.31	0.42
39:AA:70:G:H5''	85:UX:4:UNK:HG1	2.00	0.42
40:BA:502:HIS:CG	40:BA:641:GLU:HB3	2.54	0.42
41:BB:92:ILE:HD11	41:BB:129:TRP:NE1	2.34	0.42
41:BB:151:LEU:HB2	41:BB:154:GLN:OE1	2.19	0.42
41:BB:176:LEU:HD23	41:BB:176:LEU:HA	1.81	0.42
48:BI:27:LEU:HD23	48:BI:31:PRO:HA	2.02	0.42
48:BI:173:LEU:HD12	48:BI:173:LEU:HA	1.84	0.42
51:BL:127:MET:HE2	51:BL:127:MET:HB3	1.97	0.42
51:BL:245:ARG:HA	51:BL:248:GLN:HG2	2.01	0.42
52:BM:113:ASN:ND2	52:BM:197:MET:SD	2.92	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:BM:141:THR:O	52:BM:144:ALA:HB3	2.19	0.42
53:BN:70:HIS:HB2	53:BN:73:CYS:SG	2.59	0.42
59:BT:17:LYS:HZ3	59:BT:17:LYS:HG3	1.65	0.42
65:BZ:125:SER:HB2	65:BZ:130:ALA:O	2.19	0.42
69:Bd:123:ASN:O	69:Bd:126:ILE:HG13	2.19	0.42
70:Be:24:LYS:HE3	70:Be:24:LYS:HB3	1.92	0.42
73:Bh:30:ASP:HB3	73:Bh:41:PHE:CE2	2.54	0.42
6:A5:69:TRP:CE2	6:A5:79:LYS:HB2	2.54	0.42
11:AF:274:ASP:HB3	11:AF:285:PHE:HD1	1.84	0.42
13:AJ:43:GLU:HA	13:AJ:46:LYS:HZ2	1.83	0.42
13:AJ:73:ARG:HH11	13:AJ:83:PHE:HE1	1.67	0.42
15:AN:144:ARG:NH1	39:AA:122:U:P	2.91	0.42
16:AP:158:SER:O	16:AP:160:GLY:N	2.52	0.42
16:AP:347:LEU:HD13	35:Av:175:ARG:CZ	2.49	0.42
22:AW:18:SER:OG	22:AW:19:ASN:N	2.53	0.42
23:AX:85:VAL:O	66:Ba:28:ARG:NH1	2.53	0.42
24:AY:275:GLU:N	24:AY:276:PRO:HD2	2.33	0.42
25:Ab:427:MET:HE2	25:Ab:427:MET:HB3	1.96	0.42
28:Af:128:ASP:OD1	28:Af:128:ASP:N	2.50	0.42
29:Ag:131:GLN:O	29:Ag:134:ARG:HD2	2.20	0.42
30:Aj:55:PRO:HD3	30:Aj:173:TYR:CE1	2.55	0.42
33:Ap:170:HIS:CD2	33:Ap:257:GLN:HG3	2.54	0.42
34:At:103:ASP:HB2	56:BQ:181:SER:OG	2.19	0.42
39:AA:567:G:C4	73:Bh:23:ARG:NH1	2.86	0.42
40:BA:434:THR:O	40:BA:440:LYS:HE3	2.20	0.42
41:BB:254:ASP:O	41:BB:387:ALA:HB1	2.20	0.42
44:BE:73:THR:HG23	44:BE:74:TYR:N	2.34	0.42
44:BE:105:PHE:CD2	44:BE:168:LEU:HD21	2.54	0.42
48:BI:119:GLU:HG2	48:BI:156:PHE:O	2.20	0.42
52:BM:112:TRP:CD1	52:BM:114:TYR:H	2.37	0.42
54:BO:141:ASP:HB2	54:BO:153:ARG:HG3	2.02	0.42
58:BS:39:LEU:HD21	58:BS:106:ILE:HG23	2.02	0.42
64:BY:85:TRP:HE3	76:UC:8:UNK:CG	2.32	0.42
66:Ba:127:ASP:O	66:Ba:132:ALA:O	2.36	0.42
9:A9:63:MET:HB2	9:A9:67:GLU:OE1	2.19	0.42
10:AE:211:PRO:HA	40:BA:806:TYR:O	2.20	0.42
24:AY:66:ARG:NH1	39:AA:513:U:O2'	2.52	0.42
24:AY:109:TRP:NE1	24:AY:111:TRP:O	2.50	0.42
26:Ad:140:PHE:CD2	30:Aj:130:ARG:HD2	2.54	0.42
26:Ad:212:GLU:OE1	55:BP:44:ARG:HG2	2.19	0.42
30:Aj:58:LYS:HG2	69:Bd:9:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:Aj:224:PRO:HA	30:Aj:240:TYR:HD1	1.84	0.42
31:Al:77:ASP:OD1	31:Al:77:ASP:N	2.53	0.42
33:Ap:139:SER:O	33:Ap:142:GLU:OE2	2.36	0.42
34:At:34:ARG:NH1	57:BR:125:PRO:O	2.39	0.42
39:AA:565:U:H4'	77:UD:22:UNK:HG2	2.00	0.42
40:BA:691:LYS:HB2	51:BL:83:HIS:CE1	2.54	0.42
40:BA:739:ARG:HH12	40:BA:744:ASN:CG	2.27	0.42
44:BE:13:ARG:HD3	44:BE:13:ARG:HA	1.85	0.42
45:BF:213:LEU:HD11	45:BF:236:ALA:HB2	2.01	0.42
46:BG:102:GLN:OE1	46:BG:315:LYS:HA	2.19	0.42
56:BQ:226:ILE:HG23	56:BQ:227:LEU:N	2.35	0.42
2:A1:107:GLY:O	2:A1:119:GLN:HA	2.20	0.42
8:A8:82:SER:OG	25:Ab:481:MET:HE3	2.19	0.42
12:AI:17:ARG:CG	66:Ba:104:ARG:HH12	2.32	0.42
16:AP:282:ARG:NH1	35:Av:153:PHE:CE1	2.87	0.42
20:AU:73:HIS:CE1	20:AU:108:ARG:HD3	2.55	0.42
22:AW:197:ARG:NH1	40:BA:748:ARG:HD3	2.34	0.42
23:AX:66:ARG:NH1	85:UX:8:UNK:HG1	2.32	0.42
23:AX:146:LEU:HD13	23:AX:161:PHE:CE1	2.55	0.42
25:Ab:153:ASN:OD1	52:BM:94:CYS:HB3	2.19	0.42
25:Ab:175:ARG:NH1	42:BC:93:ALA:HB3	2.35	0.42
32:Ao:149:PHE:HD1	67:Bb:81:HIS:HD2	1.68	0.42
35:Av:219:ASN:OD1	35:Av:220:GLN:N	2.53	0.42
40:BA:585:HIS:HB3	40:BA:695:LEU:O	2.20	0.42
41:BB:417:GLU:HA	41:BB:420:ASN:ND2	2.35	0.42
45:BF:345:LEU:H	45:BF:345:LEU:HG	1.64	0.42
46:BG:42:PHE:HB2	46:BG:66:TYR:HE1	1.83	0.42
46:BG:125:LEU:HD23	46:BG:125:LEU:HA	1.77	0.42
46:BG:183:ARG:NH1	46:BG:187:ARG:CB	2.81	0.42
46:BG:258:TYR:CE2	46:BG:259:VAL:HG12	2.54	0.42
46:BG:305:HIS:O	46:BG:306:GLU:HB2	2.19	0.42
48:BI:64:LEU:O	48:BI:272:ARG:HG3	2.20	0.42
51:BL:48:ARG:H	51:BL:48:ARG:HG2	1.66	0.42
51:BL:165:LEU:HD11	51:BL:239:VAL:HG11	2.02	0.42
53:BN:23:GLY:N	53:BN:191:ARG:NH1	2.66	0.42
55:BP:107:VAL:HG13	55:BP:114:ARG:HH12	1.85	0.42
56:BQ:97:ILE:H	56:BQ:97:ILE:HG13	1.40	0.42
57:BR:187:LYS:NZ	57:BR:188:ARG:CZ	2.83	0.42
58:BS:39:LEU:HD23	58:BS:39:LEU:HA	1.71	0.42
60:BU:179:ASP:C	60:BU:179:ASP:OD1	2.62	0.42
61:BV:74:ASN:ND2	61:BV:77:THR:OG1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A3:62:VAL:HG23	4:A3:123:LEU:HB2	2.02	0.42
6:A5:36:ARG:HH12	24:AY:6:ARG:HB3	1.84	0.42
8:A8:167:MET:HB3	39:AA:61:A:C2	2.54	0.42
11:AF:421:ASP:HB3	35:Av:131:LEU:HD22	2.01	0.42
21:AV:128:ARG:HD2	28:Af:95:GLY:O	2.19	0.42
21:AV:208:VAL:HG21	28:Af:85:PRO:HD3	2.02	0.42
22:AW:71:ILE:O	22:AW:73:LYS:N	2.53	0.42
25:Ab:260:PRO:HG2	25:Ab:261:PHE:CD1	2.55	0.42
25:Ab:382:ARG:NH1	25:Ab:397:GLU:OE2	2.50	0.42
34:At:38:GLU:HA	34:At:41:GLU:HG2	2.01	0.42
39:AA:3:U:H5'	40:BA:754:ARG:NH1	2.35	0.42
39:AA:180:U:O2	39:AA:180:U:H2'	2.19	0.42
40:BA:182:ALA:HB2	40:BA:803:LEU:HD13	2.02	0.42
41:BB:252:ASP:O	41:BB:383:LYS:HE3	2.19	0.42
41:BB:354:MET:HE1	41:BB:410:ALA:HA	2.00	0.42
45:BF:168:ILE:HG22	45:BF:197:MET:SD	2.60	0.42
46:BG:65:MET:HE2	46:BG:67:HIS:HB2	2.02	0.42
54:BO:143:ARG:HA	54:BO:152:ARG:HH12	1.85	0.42
59:BT:57:LEU:HD23	59:BT:57:LEU:HA	1.91	0.42
77:UD:185:UNK:HA	77:UD:188:UNK:HG3	2.02	0.42
6:A5:64:LYS:NZ	6:A5:80:PRO:C	2.73	0.42
10:AE:206:LYS:HD3	40:BA:185:ALA:HB3	2.00	0.42
11:AF:80:GLN:NE2	62:BW:162:LYS:HG3	2.35	0.42
11:AF:265:HIS:CD2	22:AW:58:ARG:HB2	2.55	0.42
11:AF:345:LYS:NZ	39:AA:484:U:OP1	2.49	0.42
15:AN:77:MET:HE1	40:BA:710:LYS:NZ	2.35	0.42
18:AR:146:MET:HE1	39:AA:1167:A:N1	2.34	0.42
19:AT:28:ARG:HH11	19:AT:28:ARG:CG	2.27	0.42
25:Ab:88:THR:HG22	25:Ab:208:ASN:HA	2.02	0.42
25:Ab:115:PRO:HA	25:Ab:116:PRO:HD3	1.92	0.42
26:Ad:131:PRO:HB2	30:Aj:134:GLU:HG2	2.01	0.42
30:Aj:18:GLY:N	69:Bd:78:CYS:HB2	2.35	0.42
39:AA:108:G:N2	39:AA:116:U:OP1	2.52	0.42
42:BC:263:PRO:HG2	55:BP:128:ARG:HH12	1.80	0.42
46:BG:79:LEU:O	46:BG:149:THR:HG23	2.19	0.42
46:BG:336:LYS:O	46:BG:340:GLN:NE2	2.52	0.42
47:BH:102:ASN:HD21	47:BH:169:GLU:HG3	1.85	0.42
53:BN:112:GLU:HB2	53:BN:123:PHE:CE2	2.55	0.42
53:BN:179:LEU:HD11	77:UD:212:UNK:CG	2.46	0.42
65:BZ:18:PRO:HG3	65:BZ:184:VAL:HG21	2.01	0.42
66:Ba:80:ASP:OD1	66:Ba:80:ASP:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
77:UD:34:UNK:HB1	77:UD:37:UNK:HG3	2.01	0.42
2:A1:184:MET:O	2:A1:188:ILE:HG12	2.20	0.42
3:A2:61:LEU:HD21	3:A2:83:ARG:HB2	2.00	0.42
7:A6:43:GLU:OE2	35:Av:183:ARG:NE	2.53	0.42
9:A9:72:CYS:N	9:A9:75:CYS:SG	2.92	0.42
10:AE:151:TYR:HB2	19:AT:42:ARG:HE	1.85	0.42
10:AE:191:ASN:ND2	10:AE:213:LYS:HZ2	2.16	0.42
14:AK:33:GLU:O	14:AK:36:ARG:HB2	2.20	0.42
18:AR:119:LEU:HD12	18:AR:125:VAL:HG22	2.02	0.42
18:AR:223:HIS:HE1	72:Bg:82:PRO:CD	2.31	0.42
20:AU:20:ILE:O	20:AU:22:SER:N	2.52	0.42
20:AU:63:ARG:HH11	39:AA:460:U:H4'	1.84	0.42
21:AV:89:TYR:HE1	29:Ag:102:LEU:HD13	1.84	0.42
21:AV:191:TYR:H	21:AV:206:ASN:HD21	1.68	0.42
22:AW:10:MET:HB3	22:AW:12:HIS:CD2	2.55	0.42
23:AX:101:LYS:HE3	39:AA:33:G:N7	2.35	0.42
23:AX:197:ARG:NH1	24:AY:80:TRP:CD1	2.88	0.42
25:Ab:117:LEU:HA	25:Ab:118:PRO:HD3	1.89	0.42
25:Ab:218:PRO:HA	25:Ab:219:PRO:HD3	1.80	0.42
26:Ad:200:ILE:HD11	26:Ad:214:TRP:HE1	1.84	0.42
29:Ag:100:SER:O	40:BA:720:ARG:NH2	2.53	0.42
30:Aj:188:VAL:O	30:Aj:190:GLN:HG3	2.19	0.42
33:Ap:190:PHE:O	36:AB:16:ALA:N	2.52	0.42
35:Av:232:LYS:H	35:Av:232:LYS:HD3	1.85	0.42
39:AA:404:U:H2'	39:AA:405:U:H6	1.84	0.42
44:BE:12:GLN:HG3	44:BE:28:LEU:HD22	2.00	0.42
45:BF:60:LEU:N	45:BF:63:ARG:NH1	2.67	0.42
45:BF:408:LEU:HB3	59:BT:39:ARG:HH22	1.85	0.42
46:BG:245:ILE:O	46:BG:254:ASP:N	2.53	0.42
47:BH:88:GLU:HG3	76:UC:2:UNK:CG	2.50	0.42
61:BV:95:ASP:HA	61:BV:96:PRO:HD3	1.87	0.42
63:BX:69:ARG:HH11	63:BX:71:MET:HE2	1.85	0.42
64:BY:150:GLN:CD	76:UC:1:UNK:H2	2.28	0.42
71:Bf:99:ILE:HD12	71:Bf:99:ILE:HA	1.96	0.42
1:A0:61:LEU:HD22	57:BR:14:GLU:HB3	2.01	0.41
2:A1:163:ARG:O	2:A1:167:ILE:HG12	2.20	0.41
3:A2:145:LEU:O	3:A2:321:PRO:HA	2.20	0.41
4:A3:149:PHE:HE1	16:AP:44:THR:HG21	1.85	0.41
7:A6:72:TRP:O	7:A6:74:PRO:HD3	2.20	0.41
10:AE:138:PHE:HB2	10:AE:219:PHE:CD2	2.55	0.41
11:AF:117:VAL:O	11:AF:125:ILE:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:AI:59:THR:HG22	12:AI:60:TYR:H	1.85	0.41
14:AK:264:LEU:HD23	14:AK:264:LEU:HA	1.78	0.41
14:AK:281:ASP:O	14:AK:285:ARG:HB2	2.20	0.41
15:AN:22:HIS:HA	15:AN:23:PRO:HD3	1.83	0.41
15:AN:71:PRO:HB3	20:AU:69:ALA:HB2	2.01	0.41
16:AP:152:MET:HE2	39:AA:66:C:H41	1.85	0.41
29:Ag:14:ILE:HG12	29:Ag:57:ILE:CD1	2.49	0.41
33:Ap:52:ARG:HD2	33:Ap:55:HIS:O	2.20	0.41
33:Ap:155:ILE:H	33:Ap:155:ILE:HG13	1.63	0.41
39:AA:24:U:H2'	39:AA:25:A:C8	2.55	0.41
41:BB:359:HIS:CD2	49:BJ:200:ARG:NH1	2.84	0.41
42:BC:154:LEU:HD23	42:BC:196:VAL:HG21	2.01	0.41
44:BE:78:HIS:O	44:BE:78:HIS:CG	2.71	0.41
46:BG:241:ASP:HA	46:BG:242:PRO:HD2	1.80	0.41
47:BH:85:ASP:OD1	47:BH:85:ASP:N	2.47	0.41
47:BH:137:SER:HB3	47:BH:176:TYR:HB3	2.01	0.41
48:BI:48:PHE:O	48:BI:50:ARG:N	2.53	0.41
48:BI:270:ILE:H	48:BI:270:ILE:HG13	1.75	0.41
52:BM:170:CYS:O	52:BM:173:THR:OG1	2.28	0.41
56:BQ:99:LEU:O	56:BQ:101:ASP:N	2.53	0.41
63:BX:117:PHE:CE2	63:BX:126:LEU:HD12	2.54	0.41
70:Be:49:ARG:CG	70:Be:49:ARG:NH1	2.71	0.41
77:UD:16:UNK:HA	77:UD:29:UNK:HG1	2.01	0.41
2:A1:129:GLU:OE1	2:A1:143:ARG:NH1	2.53	0.41
2:A1:145:GLY:HA3	2:A1:146:PRO:HD2	1.83	0.41
3:A2:41:ASN:HB3	24:AY:240:ALA:HA	2.02	0.41
3:A2:72:GLN:HA	3:A2:72:GLN:HE21	1.86	0.41
3:A2:186:GLU:O	3:A2:189:GLU:HG3	2.20	0.41
3:A2:266:PRO:HA	3:A2:267:PRO:HD3	1.95	0.41
4:A3:147:PRO:HB3	56:BQ:99:LEU:HD13	2.03	0.41
8:A8:66:ARG:HH12	8:A8:142:ALA:HB2	1.85	0.41
10:AE:343:ILE:H	10:AE:343:ILE:HG13	1.49	0.41
12:AI:19:ASP:OD2	12:AI:45:ARG:NH2	2.53	0.41
13:AJ:43:GLU:O	13:AJ:46:LYS:HD3	2.20	0.41
14:AK:129:LEU:HD11	14:AK:189:VAL:HG22	2.02	0.41
14:AK:179:ARG:NE	39:AA:422:A:H1'	2.34	0.41
15:AN:135:LYS:HE3	15:AN:135:LYS:HB3	1.96	0.41
16:AP:209:ARG:HG3	16:AP:209:ARG:HH11	1.85	0.41
17:AQ:82:THR:HB	17:AQ:123:GLU:HB2	2.03	0.41
18:AR:148:ARG:NH1	39:AA:1162:G:H1'	2.33	0.41
18:AR:223:HIS:CD2	72:Bg:83:LEU:HD12	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AX:165:CYS:HA	23:AX:212:LYS:HE2	2.02	0.41
24:AY:117:VAL:CG1	24:AY:175:VAL:HB	2.50	0.41
25:Ab:138:ARG:HE	25:Ab:160:GLN:HB3	1.85	0.41
27:Ae:120:PRO:HG2	39:AA:542:U:H4'	2.02	0.41
29:Ag:220:ARG:HD3	29:Ag:223:SER:HB2	2.02	0.41
31:Al:157:ASN:O	39:AA:339:A:O2'	2.36	0.41
32:Ao:54:GLN:HG3	79:UF:16:UNK:N	2.35	0.41
32:Ao:235:ARG:HD2	39:AA:391:U:H3	1.84	0.41
39:AA:524:A:N1	39:AA:558:U:O2'	2.48	0.41
39:AA:582:A:H61	39:AA:794:A:N6	2.17	0.41
39:AA:1162:G:O2'	39:AA:1163:A:OP1	2.36	0.41
40:BA:221:THR:HG23	40:BA:222:VAL:N	2.35	0.41
41:BB:348:VAL:HG12	41:BB:426:ALA:HB1	2.01	0.41
42:BC:60:LEU:H	42:BC:292:ASN:ND2	2.13	0.41
46:BG:149:THR:HG21	46:BG:154:ALA:H	1.85	0.41
60:BU:131:LYS:HB2	60:BU:131:LYS:HZ2	1.83	0.41
73:Bh:44:MET:HE2	73:Bh:44:MET:HB3	1.83	0.41
1:A0:114:ARG:O	1:A0:118:ARG:HG3	2.19	0.41
5:A4:155:ILE:HA	5:A4:156:PRO:HD3	1.71	0.41
7:A6:86:LYS:HB2	7:A6:86:LYS:NZ	2.35	0.41
11:AF:193:HIS:HE1	39:AA:184:U:O2'	2.03	0.41
11:AF:205:LYS:HB3	11:AF:205:LYS:HE2	1.79	0.41
15:AN:178:ASP:HA	15:AN:179:PRO:HD3	1.88	0.41
19:AT:11:HIS:CD2	39:AA:1108:A:H4'	2.56	0.41
20:AU:25:ARG:HD2	39:AA:815:U:P	2.60	0.41
24:AY:224:GLU:H	24:AY:224:GLU:HG3	1.62	0.41
31:Al:150:VAL:HG23	31:Al:206:ARG:HD2	2.01	0.41
35:Av:215:LYS:NZ	35:Av:239:PHE:O	2.54	0.41
39:AA:135:G:C2	39:AA:826:A:H5'	2.56	0.41
40:BA:184:LEU:HA	40:BA:187:MET:HG2	2.02	0.41
41:BB:235:ALA:N	41:BB:236:PRO:HD2	2.35	0.41
41:BB:261:VAL:HG11	41:BB:371:LYS:O	2.19	0.41
41:BB:416:LEU:O	41:BB:419:VAL:HB	2.21	0.41
46:BG:334:ILE:HD13	46:BG:334:ILE:HA	1.90	0.41
49:BJ:195:PRO:HB3	49:BJ:199:ASP:OD2	2.20	0.41
53:BN:198:ILE:HG12	53:BN:216:TYR:CD1	2.56	0.41
56:BQ:28:ASN:HB3	56:BQ:49:LEU:O	2.20	0.41
56:BQ:64:LEU:CD2	56:BQ:76:LEU:HB3	2.50	0.41
77:UD:175:UNK:HA	77:UD:178:UNK:HG3	2.02	0.41
3:A2:12:ALA:O	3:A2:15:GLU:HG2	2.20	0.41
4:A3:57:GLY:HA3	4:A3:59:TYR:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A6:75:VAL:HG13	39:AA:950:U:C4	2.55	0.41
11:AF:282:SER:C	11:AF:358:GLN:HE22	2.27	0.41
12:AI:212:ASP:OD1	12:AI:212:ASP:N	2.53	0.41
13:AJ:44:GLN:O	13:AJ:48:VAL:HG23	2.19	0.41
16:AP:71:ASN:HB3	29:Ag:81:LEU:CD1	2.50	0.41
17:AQ:71:LEU:HD23	17:AQ:71:LEU:HA	1.95	0.41
22:AW:117:LEU:HD22	51:BL:41:LEU:HD22	2.03	0.41
23:AX:145:ARG:CG	23:AX:162:GLN:HB2	2.50	0.41
29:Ag:39:LYS:NZ	29:Ag:40:TYR:CE2	2.88	0.41
33:Ap:257:GLN:HG2	48:BI:293:THR:HG21	2.02	0.41
39:AA:41:U:H3'	39:AA:42:A:H8	1.84	0.41
39:AA:446:A:O2'	39:AA:447:U:H5'	2.20	0.41
41:BB:72:LYS:HE2	74:UA:44:UNK:HB1	2.02	0.41
41:BB:365:ARG:HG2	41:BB:377:PHE:CD2	2.55	0.41
44:BE:255:TYR:CZ	44:BE:288:LEU:HD23	2.54	0.41
51:BL:185:ARG:HG2	51:BL:298:GLU:OE2	2.19	0.41
55:BP:216:GLY:HA2	55:BP:217:PRO:HD3	1.77	0.41
57:BR:110:LEU:HA	57:BR:110:LEU:HD13	1.74	0.41
58:BS:28:THR:HG23	58:BS:31:ASP:H	1.85	0.41
60:BU:138:ARG:O	60:BU:141:GLU:HG2	2.20	0.41
61:BV:53:LYS:HA	61:BV:71:VAL:HG21	2.02	0.41
61:BV:115:GLN:O	61:BV:117:TRP:HD1	2.03	0.41
63:BX:69:ARG:NH1	63:BX:71:MET:HE2	2.35	0.41
65:BZ:17:ALA:HA	65:BZ:18:PRO:HD3	1.96	0.41
3:A2:170:ILE:CD1	3:A2:326:ILE:HG23	2.50	0.41
3:A2:305:THR:HB	3:A2:308:ALA:HB2	2.03	0.41
11:AF:32:VAL:HG23	11:AF:33:HIS:CD2	2.55	0.41
11:AF:255:LEU:O	11:AF:259:MET:HG3	2.20	0.41
13:AJ:43:GLU:H	13:AJ:43:GLU:HG3	1.70	0.41
15:AN:24:GLU:OE1	40:BA:229:ARG:NH1	2.53	0.41
17:AQ:30:ARG:HG3	17:AQ:30:ARG:NH1	2.35	0.41
22:AW:116:ARG:CZ	51:BL:114:CYS:HB2	2.51	0.41
26:Ad:126:ARG:HH22	30:Aj:18:GLY:N	2.18	0.41
39:AA:384:U:H2'	39:AA:385:A:C8	2.54	0.41
39:AA:446:A:H8	39:AA:446:A:H3'	1.86	0.41
39:AA:558:U:O2'	39:AA:559:A:O4'	2.38	0.41
41:BB:123:LEU:HD23	41:BB:123:LEU:HA	1.87	0.41
41:BB:352:ARG:O	41:BB:356:ASN:HB2	2.20	0.41
42:BC:95:ILE:HD12	42:BC:95:ILE:HA	1.90	0.41
42:BC:297:PHE:HB2	42:BC:432:MET:HE1	2.02	0.41
44:BE:139:GLU:OE2	44:BE:146:ILE:HB	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:BH:172:MET:HE2	47:BH:172:MET:HB2	1.93	0.41
50:BK:384:ARG:HH21	72:Bg:69:ARG:C	2.28	0.41
51:BL:122:LYS:HZ1	51:BL:126:LYS:HB2	1.84	0.41
57:BR:105:ASN:HB3	57:BR:189:VAL:HG13	2.02	0.41
59:BT:46:GLN:NE2	62:BW:61:ASN:OD1	2.54	0.41
59:BT:92:GLU:OE2	59:BT:95:PRO:HA	2.20	0.41
64:BY:84:ARG:O	64:BY:87:GLU:HB3	2.20	0.41
71:Bf:86:ILE:HG23	71:Bf:109:HIS:NE2	2.35	0.41
5:A4:61:ARG:HE	26:Ad:49:ARG:NH1	2.18	0.41
8:A8:179:ARG:NH1	8:A8:181:VAL:HG21	2.35	0.41
8:A8:179:ARG:NH1	35:Av:101:PRO:HB3	2.36	0.41
10:AE:133:PHE:O	33:Ap:44:PRO:HG2	2.21	0.41
11:AF:335:ILE:H	11:AF:335:ILE:HG13	1.68	0.41
11:AF:368:LEU:HG	11:AF:379:LEU:HD13	2.03	0.41
12:AI:207:PHE:HE1	47:BH:107:VAL:HG21	1.85	0.41
13:AJ:94:LEU:HD11	29:Ag:222:PHE:HZ	1.86	0.41
15:AN:31:ASP:OD1	15:AN:31:ASP:N	2.53	0.41
16:AP:64:PRO:HG3	21:AV:104:VAL:N	2.35	0.41
18:AR:150:LYS:O	44:BE:399:LYS:HG2	2.20	0.41
21:AV:172:ILE:HD13	29:Ag:93:TYR:OH	2.21	0.41
25:Ab:133:PRO:O	25:Ab:136:GLN:HG3	2.19	0.41
25:Ab:274:GLY:HA3	25:Ab:374:ASN:O	2.21	0.41
28:Af:51:PRO:HG3	84:UU:2:UNK:HG1	2.01	0.41
29:Ag:146:GLY:HA2	48:BI:95:GLN:HE22	1.85	0.41
33:Ap:71:GLY:O	33:Ap:74:ARG:HD3	2.21	0.41
33:Ap:242:TYR:CD1	33:Ap:262:GLU:HG2	2.55	0.41
35:Av:143:ARG:HH11	35:Av:145:ARG:NH2	2.18	0.41
35:Av:221:GLY:HA2	35:Av:223:ARG:HH22	1.85	0.41
39:AA:197:A:H2'	39:AA:198:A:C8	2.56	0.41
40:BA:296:ARG:HH11	40:BA:296:ARG:HG3	1.84	0.41
41:BB:424:LYS:HA	41:BB:427:PHE:CE2	2.56	0.41
44:BE:142:LEU:HD21	44:BE:238:LEU:HD21	2.01	0.41
47:BH:156:LEU:HG	47:BH:168:THR:CG2	2.51	0.41
48:BI:204:ARG:HA	48:BI:207:ILE:HG22	2.03	0.41
51:BL:107:LEU:HD22	51:BL:164:ARG:HD2	2.01	0.41
53:BN:60:ARG:HE	53:BN:108:PHE:HE2	1.69	0.41
57:BR:17:LEU:HA	57:BR:17:LEU:HD12	1.75	0.41
63:BX:117:PHE:CZ	63:BX:161:VAL:HG11	2.55	0.41
67:Bb:67:ARG:O	67:Bb:71:PRO:HB3	2.20	0.41
68:Bc:36:LEU:HD23	68:Bc:36:LEU:HA	1.90	0.41
68:Bc:90:GLU:HB3	68:Bc:94:LYS:NZ	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
73:Bh:42:ARG:HB2	77:UD:24:UNK:HG1	2.02	0.41
74:UA:4:UNK:HA	74:UA:7:UNK:HG3	2.02	0.41
79:UG:18:UNK:HA	79:UG:21:UNK:HG3	2.03	0.41
11:AF:417:LYS:HD3	11:AF:417:LYS:HA	1.92	0.41
16:AP:25:MET:HG2	32:Ao:82:GLU:HG3	2.03	0.41
17:AQ:44:ILE:HD12	17:AQ:157:GLN:HA	2.03	0.41
18:AR:59:ARG:HG2	39:AA:573:U:C6	2.55	0.41
24:AY:10:LYS:O	24:AY:14:ARG:HG2	2.20	0.41
25:Ab:256:SER:HB3	25:Ab:276:PHE:HB3	2.01	0.41
26:Ad:245:ASP:CG	69:Bd:33:LYS:HZ1	2.28	0.41
29:Ag:103:HIS:O	40:BA:720:ARG:NH2	2.53	0.41
29:Ag:183:ARG:NH1	29:Ag:184:HIS:NE2	2.69	0.41
32:Ao:74:PRO:O	32:Ao:80:SER:OG	2.32	0.41
39:AA:40:U:O2'	39:AA:41:U:OP1	2.35	0.41
39:AA:384:U:H4'	39:AA:385:A:OP1	2.21	0.41
39:AA:838:A:N1	40:BA:227:PHE:HD1	2.19	0.41
41:BB:82:HIS:HE1	41:BB:86:ASN:HD22	1.68	0.41
41:BB:90:LYS:O	41:BB:94:THR:OG1	2.34	0.41
41:BB:211:ASP:OD1	41:BB:212:HIS:N	2.53	0.41
45:BF:256:LEU:HD23	45:BF:256:LEU:HA	1.75	0.41
46:BG:244:ARG:NH1	46:BG:257:ARG:NH2	2.57	0.41
48:BI:245:ASN:O	48:BI:245:ASN:ND2	2.52	0.41
52:BM:109:VAL:HG13	52:BM:193:GLN:NE2	2.35	0.41
53:BN:36:GLU:H	53:BN:36:GLU:CD	2.29	0.41
53:BN:55:VAL:HG13	53:BN:99:VAL:HA	2.03	0.41
54:BO:212:PRO:HA	54:BO:215:LEU:HD12	2.03	0.41
57:BR:105:ASN:O	57:BR:192:ARG:NH2	2.54	0.41
58:BS:68:ARG:HH21	58:BS:91:GLU:CD	2.27	0.41
59:BT:15:TYR:CE2	59:BT:16:LYS:HG2	2.55	0.41
62:BW:19:ASN:O	62:BW:22:ARG:HG3	2.20	0.41
66:Ba:119:ASN:OD1	66:Ba:119:ASN:N	2.52	0.41
80:UI:1:UNK:HB2	80:UI:3:UNK:HG3	2.03	0.41
85:UX:2:UNK:HG2	85:UX:3:UNK:N	2.35	0.41
5:A4:130:ARG:NH1	30:Aj:213:GLU:OE2	2.54	0.41
10:AE:176:ARG:NH1	39:AA:1112:U:C5	2.89	0.41
13:AJ:58:ASN:HA	33:Ap:222:PHE:CD1	2.55	0.41
14:AK:136:THR:HA	14:AK:142:ARG:HH12	1.85	0.41
16:AP:264:GLN:HG2	16:AP:271:TYR:CE2	2.56	0.41
18:AR:224:TRP:HH2	44:BE:429:VAL:HG12	1.86	0.41
21:AV:101:ARG:HD2	21:AV:169:ALA:HB1	2.03	0.41
22:AW:61:LEU:HD13	22:AW:85:VAL:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:AX:88:TYR:CZ	23:AX:90:GLY:HA3	2.56	0.41
23:AX:94:ILE:HD11	66:Ba:22:PHE:HE1	1.85	0.41
23:AX:212:LYS:NZ	39:AA:543:U:OP1	2.54	0.41
25:Ab:112:THR:HG23	42:BC:244:TRP:CZ2	2.56	0.41
26:Ad:52:ASN:ND2	42:BC:203:SER:O	2.54	0.41
29:Ag:24:ASN:OD1	29:Ag:25:THR:N	2.54	0.41
30:Aj:251:PHE:CD2	30:Aj:261:HIS:ND1	2.89	0.41
33:Ap:141:TRP:CZ3	78:UE:4:UNK:HG3	2.56	0.41
35:Av:66:LYS:HG3	35:Av:71:VAL:HG13	2.03	0.41
41:BB:201:PRO:HB3	60:BU:106:ARG:CZ	2.51	0.41
42:BC:262:HIS:HA	42:BC:263:PRO:HD3	1.82	0.41
44:BE:242:LEU:O	44:BE:245:ILE:HG22	2.20	0.41
45:BF:228:GLU:O	45:BF:231:GLU:HB3	2.20	0.41
46:BG:189:MET:HE3	46:BG:261:LEU:HB2	2.03	0.41
48:BI:115:LEU:HD13	48:BI:156:PHE:CE2	2.56	0.41
49:BJ:292:ARG:HG3	49:BJ:292:ARG:O	2.21	0.41
50:BK:111:LEU:HA	50:BK:111:LEU:HD23	1.78	0.41
50:BK:315:GLY:HA3	50:BK:316:PRO:HD2	1.88	0.41
54:BO:125:GLU:HA	54:BO:158:ARG:NH2	2.35	0.41
61:BV:117:TRP:HB3	61:BV:122:LEU:HG	2.02	0.41
62:BW:28:PRO:O	62:BW:29:SER:OG	2.33	0.41
67:Bb:116:ALA:HA	67:Bb:119:ARG:HG2	2.02	0.41
70:Be:21:ARG:NH1	70:Be:98:TRP:CD2	2.89	0.41
73:Bh:56:LYS:HE2	73:Bh:56:LYS:HA	2.03	0.41
2:A1:73:MET:O	2:A1:150:SER:HA	2.21	0.41
2:A1:142:LYS:NZ	2:A1:142:LYS:HB3	2.36	0.41
2:A1:216:ALA:O	2:A1:219:ALA:HB3	2.21	0.41
3:A2:451:HIS:HB3	23:AX:115:PRO:CG	2.51	0.41
4:A3:190:LEU:HD12	45:BF:310:LEU:HD12	2.03	0.41
5:A4:79:HIS:NE2	30:Aj:86:GLU:O	2.47	0.41
7:A6:105:ILE:HD12	7:A6:106:GLY:N	2.36	0.41
8:A8:69:VAL:O	8:A8:73:ARG:HD3	2.20	0.41
8:A8:83:ARG:CZ	8:A8:139:ARG:HH12	2.30	0.41
8:A8:92:MET:O	8:A8:96:ARG:HD3	2.21	0.41
10:AE:82:ARG:NH1	48:BI:83:GLU:OE1	2.54	0.41
12:AI:100:LEU:HD21	12:AI:106:ARG:HB2	2.02	0.41
12:AI:120:ASN:HB3	12:AI:129:TRP:HZ3	1.84	0.41
12:AI:179:PRO:HG3	12:AI:185:TYR:HD1	1.86	0.41
13:AJ:82:ILE:HD11	52:BM:275:PHE:HD1	1.86	0.41
14:AK:240:GLU:OE1	14:AK:240:GLU:N	2.54	0.41
15:AN:150:ILE:HG23	68:Bc:15:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:33:PRO:HD2	16:AP:41:LEU:O	2.20	0.41
16:AP:106:MET:HE2	16:AP:106:MET:HB3	1.95	0.41
17:AQ:57:MET:HA	17:AQ:113:PHE:O	2.20	0.41
18:AR:151:SER:HB3	44:BE:403:ASN:HD22	1.85	0.41
19:AT:23:ARG:NH1	54:BO:131:HIS:HE1	2.18	0.41
23:AX:86:ASN:HB2	66:Ba:29:LEU:HD21	2.02	0.41
25:Ab:80:PRO:HG2	25:Ab:95:THR:HG21	2.02	0.41
30:Aj:136:ARG:O	30:Aj:137:VAL:HG23	2.21	0.41
31:Al:154:HIS:CD2	31:Al:157:ASN:HB2	2.56	0.41
32:Ao:133:ILE:HG23	32:Ao:149:PHE:CD2	2.56	0.41
33:Ap:246:VAL:HG22	33:Ap:255:LEU:HD21	2.02	0.41
34:At:153:LEU:HD13	34:At:153:LEU:HA	1.88	0.41
35:Av:200:GLN:NE2	35:Av:201:ASP:OD1	2.53	0.41
40:BA:198:GLU:HA	40:BA:201:ARG:NH1	2.36	0.41
40:BA:497:LEU:HD12	40:BA:510:LEU:HD12	2.03	0.41
40:BA:566:MET:HB2	40:BA:653:VAL:HA	2.02	0.41
40:BA:802:ALA:HB3	40:BA:815:TYR:HB2	2.01	0.41
41:BB:154:GLN:O	41:BB:156:TRP:CD1	2.74	0.41
41:BB:230:THR:HG22	41:BB:231:GLU:H	1.85	0.41
41:BB:240:HIS:O	41:BB:243:ILE:HG12	2.21	0.41
44:BE:300:ARG:HB3	44:BE:323:TRP:CE3	2.55	0.41
45:BF:39:TYR:HA	45:BF:40:PRO:HD3	1.84	0.41
45:BF:40:PRO:O	45:BF:43:LEU:HD12	2.20	0.41
45:BF:376:ILE:O	45:BF:379:GLU:HB3	2.21	0.41
46:BG:268:ARG:HD3	46:BG:268:ARG:HA	1.74	0.41
46:BG:321:LEU:O	46:BG:325:MET:HG2	2.20	0.41
47:BH:131:TYR:HD1	47:BH:171:GLU:HB2	1.84	0.41
47:BH:178:GLU:H	47:BH:178:GLU:HG3	1.44	0.41
48:BI:105:LEU:O	48:BI:108:GLU:HG3	2.21	0.41
48:BI:146:ILE:O	48:BI:150:VAL:HG22	2.20	0.41
48:BI:263:HIS:HB2	48:BI:302:PRO:HB2	2.03	0.41
50:BK:110:ALA:O	50:BK:114:HIS:HB2	2.21	0.41
50:BK:227:GLN:HA	50:BK:230:GLU:CD	2.46	0.41
51:BL:162:HIS:HE1	51:BL:239:VAL:H	1.69	0.41
51:BL:284:ARG:HG3	51:BL:285:LEU:HD12	2.03	0.41
52:BM:172:ALA:O	52:BM:173:THR:C	2.64	0.41
55:BP:114:ARG:O	55:BP:118:VAL:HG23	2.21	0.41
56:BQ:145:PHE:HE2	56:BQ:147:ASN:HD21	1.69	0.41
59:BT:15:TYR:HA	62:BW:74:ARG:HH21	1.86	0.41
59:BT:160:HIS:CD2	59:BT:160:HIS:H	2.39	0.41
61:BV:109:GLU:OE2	61:BV:133:SER:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
62:BW:151:TRP:CD1	62:BW:152:GLN:HG3	2.56	0.41
69:Bd:125:GLN:HE21	69:Bd:129:MET:HE3	1.86	0.41
77:UD:152:UNK:HA	77:UD:155:UNK:HG3	2.03	0.41
1:A0:109:LYS:HG3	52:BM:112:TRP:CE2	2.56	0.41
1:A0:161:ARG:HD2	1:A0:181:ARG:HB3	2.03	0.41
3:A2:57:GLU:OE2	24:AY:230:LYS:HE3	2.21	0.41
3:A2:293:PHE:HZ	62:BW:53:ILE:HG12	1.86	0.41
3:A2:470:ASP:HB2	11:AF:249:GLN:OE1	2.21	0.41
4:A3:153:LYS:HG2	4:A3:154:ALA:H	1.85	0.41
5:A4:77:ARG:HG2	30:Aj:86:GLU:O	2.20	0.41
8:A8:126:ARG:NH1	31:Al:157:ASN:HA	2.36	0.41
10:AE:71:MET:HE2	10:AE:71:MET:HB3	1.90	0.41
12:AI:12:TRP:HB2	66:Ba:84:TYR:CZ	2.55	0.41
12:AI:36:PHE:HB3	12:AI:90:TYR:HD1	1.86	0.41
12:AI:151:GLN:NE2	82:UL:5:UNK:O	2.54	0.41
12:AI:160:GLU:O	12:AI:164:LEU:HG	2.21	0.41
12:AI:209:LYS:HE2	12:AI:209:LYS:HB2	1.95	0.41
14:AK:213:GLU:O	14:AK:216:ARG:HG3	2.21	0.41
25:Ab:293:LEU:HD13	25:Ab:317:PRO:HG2	2.03	0.41
26:Ad:276:HIS:H	26:Ad:279:GLN:HG3	1.86	0.41
32:Ao:158:ARG:CB	52:BM:217:GLU:HG3	2.50	0.41
33:Ap:255:LEU:HA	33:Ap:258:MET:HE3	2.02	0.41
39:AA:534:U:O2'	39:AA:535:U:OP1	2.34	0.41
40:BA:190:THR:HB	40:BA:194:ARG:HH21	1.86	0.41
42:BC:505:ARG:HD3	42:BC:517:LEU:HD13	2.03	0.41
66:Ba:105:ARG:NH1	66:Ba:106:VAL:O	2.52	0.41
73:Bh:49:MET:HG3	73:Bh:61:PRO:CG	2.50	0.41
5:A4:17:ARG:HH22	5:A4:21:PRO:HA	1.85	0.40
5:A4:42:VAL:HG13	5:A4:44:ARG:HH12	1.84	0.40
6:A5:33:MET:O	6:A5:37:ARG:HG3	2.21	0.40
8:A8:75:LYS:NZ	8:A8:110:TRP:CE2	2.89	0.40
8:A8:79:PRO:HD2	25:Ab:456:ALA:HB2	2.03	0.40
8:A8:91:LYS:HA	8:A8:91:LYS:HD3	1.67	0.40
8:A8:112:PRO:HD3	25:Ab:454:VAL:HG21	2.03	0.40
11:AF:182:MET:HB3	11:AF:184:MET:HG3	2.03	0.40
11:AF:257:ARG:CZ	45:BF:420:ARG:NH1	2.84	0.40
11:AF:335:ILE:HD13	59:BT:36:LEU:HD11	2.03	0.40
11:AF:405:ALA:O	11:AF:408:THR:HB	2.22	0.40
12:AI:42:TYR:OH	66:Ba:137:PHE:N	2.52	0.40
12:AI:214:PRO:HB2	12:AI:216:GLU:CD	2.47	0.40
14:AK:319:GLU:O	14:AK:323:GLN:HG3	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:AP:97:LEU:HD23	16:AP:97:LEU:HA	1.71	0.40
16:AP:297:TRP:HB2	62:BW:15:ALA:HB2	2.03	0.40
20:AU:82:ASN:C	20:AU:82:ASN:HD22	2.27	0.40
21:AV:139:GLN:N	21:AV:174:ARG:O	2.45	0.40
22:AW:159:GLU:OE2	22:AW:245:ARG:NH2	2.54	0.40
23:AX:117:LYS:HA	23:AX:118:PRO:HD3	1.94	0.40
23:AX:196:ARG:HA	23:AX:196:ARG:HD2	1.87	0.40
24:AY:8:ARG:NH1	39:AA:103:U:OP1	2.54	0.40
25:Ab:209:TYR:CZ	42:BC:246:PRO:HD3	2.56	0.40
27:Ae:50:TRP:CG	27:Ae:79:ASN:HB3	2.56	0.40
27:Ae:67:LEU:HB2	27:Ae:107:TYR:OH	2.21	0.40
29:Ag:83:LEU:O	29:Ag:86:LEU:HB2	2.21	0.40
30:Aj:68:MET:HE1	55:BP:58:ILE:HB	2.03	0.40
33:Ap:212:SER:HA	33:Ap:213:PRO:HD2	1.91	0.40
39:AA:335:G:O2'	39:AA:336:U:P	2.79	0.40
39:AA:410:U:HO2'	39:AA:414:A:H62	1.66	0.40
42:BC:122:PRO:HG3	42:BC:172:ILE:HG13	2.03	0.40
44:BE:11:TYR:O	44:BE:13:ARG:NH1	2.55	0.40
46:BG:174:MET:HE2	46:BG:174:MET:HB3	1.94	0.40
46:BG:181:VAL:HG21	46:BG:290:VAL:HG21	2.02	0.40
51:BL:122:LYS:NZ	51:BL:126:LYS:HB2	2.36	0.40
51:BL:241:ASP:OD1	51:BL:241:ASP:N	2.47	0.40
51:BL:256:ARG:O	51:BL:259:GLU:HB2	2.21	0.40
52:BM:232:LEU:HD13	57:BR:172:PRO:HD2	2.02	0.40
53:BN:62:PHE:HA	53:BN:139:LYS:NZ	2.36	0.40
53:BN:203:TYR:HB3	53:BN:213:MET:HE3	2.02	0.40
61:BV:30:LYS:NZ	61:BV:32:VAL:HA	2.35	0.40
77:UD:51:UNK:HG3	77:UD:148:UNK:HG1	2.02	0.40
2:A1:223:LYS:HE2	2:A1:223:LYS:HB2	1.88	0.40
10:AE:171:VAL:N	10:AE:186:TYR:O	2.50	0.40
11:AF:54:GLY:O	29:Ag:26:ARG:HD2	2.21	0.40
11:AF:56:HIS:HB2	45:BF:364:VAL:HG22	2.04	0.40
11:AF:78:SER:HB2	45:BF:361:ILE:HD11	2.03	0.40
11:AF:265:HIS:CD2	22:AW:58:ARG:HD3	2.56	0.40
12:AI:198:ARG:NH1	70:Be:68:ARG:CZ	2.85	0.40
14:AK:304:GLU:OE2	14:AK:307:ARG:HD2	2.21	0.40
15:AN:185:LYS:HE3	15:AN:185:LYS:HB2	1.75	0.40
16:AP:17:ARG:HD3	16:AP:17:ARG:HA	1.88	0.40
16:AP:54:ARG:HB3	16:AP:63:LEU:HD21	2.03	0.40
20:AU:197:ALA:O	20:AU:200:GLU:HG2	2.21	0.40
21:AV:135:ARG:HD3	32:Ao:19:TYR:CD1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:AW:193:LYS:HZ3	44:BE:390:SER:HG	1.56	0.40
26:Ad:189:CYS:O	26:Ad:193:LEU:HB3	2.21	0.40
32:Ao:88:TYR:HD2	32:Ao:92:THR:HB	1.86	0.40
35:Av:45:LEU:HD11	39:AA:49:A:N6	2.35	0.40
39:AA:518:A:N6	77:UD:18:UNK:HG2	2.36	0.40
39:AA:1164:A:HO2'	39:AA:1165:G:P	2.44	0.40
41:BB:361:ALA:O	41:BB:364:VAL:HG22	2.21	0.40
45:BF:407:MET:O	45:BF:408:LEU:HG	2.20	0.40
47:BH:136:GLN:OE1	47:BH:142:LYS:HG2	2.21	0.40
48:BI:156:PHE:HD1	48:BI:156:PHE:HA	1.79	0.40
48:BI:200:GLU:OE2	48:BI:204:ARG:NE	2.54	0.40
48:BI:259:LEU:HD21	48:BI:262:TRP:O	2.21	0.40
52:BM:43:LEU:HD11	76:UH:7:UNK:HB1	2.03	0.40
53:BN:9:TRP:HA	53:BN:14:HIS:HD2	1.86	0.40
56:BQ:69:ARG:HH11	56:BQ:108:VAL:HB	1.86	0.40
3:A2:108:ARG:O	3:A2:111:GLU:HG2	2.20	0.40
3:A2:190:GLN:O	3:A2:194:GLN:NE2	2.55	0.40
6:A5:30:LYS:HE2	6:A5:34:GLN:HB3	2.03	0.40
7:A6:78:ARG:NH1	42:BC:487:ASN:O	2.53	0.40
8:A8:80:PRO:O	8:A8:81:PHE:HB2	2.21	0.40
11:AF:92:GLU:H	11:AF:92:GLU:HG2	1.66	0.40
13:AJ:78:THR:HG22	13:AJ:80:ARG:N	2.36	0.40
14:AK:95:LYS:HE3	14:AK:95:LYS:HB2	1.93	0.40
17:AQ:166:PHE:HB3	57:BR:166:TRP:CZ2	2.57	0.40
20:AU:50:ARG:CG	20:AU:50:ARG:NH1	2.80	0.40
20:AU:104:PRO:HB3	29:Ag:118:TRP:HE1	1.86	0.40
22:AW:17:ARG:HA	22:AW:17:ARG:HD3	1.79	0.40
33:Ap:140:MET:HG3	78:UE:4:UNK:HG1	2.04	0.40
39:AA:892:U:H3'	39:AA:893:A:C8	2.56	0.40
39:AA:1116:U:H2'	48:BI:25:LYS:HE2	2.02	0.40
39:AA:1157:A:N7	40:BA:226:LYS:NZ	2.70	0.40
40:BA:388:ALA:HA	40:BA:391:TRP:HD1	1.86	0.40
44:BE:440:ILE:HD12	44:BE:440:ILE:H	1.86	0.40
50:BK:280:LEU:O	50:BK:282:ARG:NH1	2.55	0.40
50:BK:297:PHE:HD2	50:BK:300:TRP:NE1	2.18	0.40
52:BM:70:ARG:HB3	52:BM:71:GLY:H	1.77	0.40
52:BM:96:ARG:HG3	52:BM:96:ARG:O	2.22	0.40
52:BM:115:TYR:CE1	52:BM:198:LEU:HD13	2.56	0.40
67:Bb:79:HIS:HB3	67:Bb:82:ASP:HB2	2.03	0.40
5:A4:36:ASP:N	5:A4:36:ASP:OD1	2.54	0.40
18:AR:185:ARG:O	18:AR:186:PHE:CD1	2.73	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:AV:66:ILE:HD11	28:Af:90:PHE:CD1	2.57	0.40
24:AY:96:ARG:NH2	44:BE:71:LEU:HD21	2.35	0.40
26:Ad:103:LEU:HD21	30:Aj:236:TRP:NE1	2.37	0.40
33:Ap:218:LYS:HB3	33:Ap:218:LYS:HE3	1.87	0.40
39:AA:88:G:N2	59:BT:39:ARG:HD2	2.36	0.40
39:AA:177:U:C4	39:AA:178:A:N6	2.89	0.40
46:BG:36:HIS:HA	46:BG:101:SER:OG	2.22	0.40
50:BK:328:LEU:HA	50:BK:328:LEU:HD12	1.85	0.40
51:BL:261:LEU:HD23	51:BL:261:LEU:HA	1.95	0.40
54:BO:138:ARG:HG2	54:BO:224:TYR:OH	2.21	0.40
58:BS:31:ASP:O	58:BS:34:TRP:HB3	2.20	0.40
68:Bc:21:LEU:N	68:Bc:22:PRO:HD2	2.37	0.40
73:Bh:4:PHE:HE1	73:Bh:43:PHE:HB2	1.87	0.40
3:A2:64:MET:HA	3:A2:64:MET:HE2	2.04	0.40
3:A2:267:PRO:HA	3:A2:268:PRO:HD3	1.80	0.40
3:A2:402:ARG:NH1	39:AA:85:U:C4	2.90	0.40
10:AE:55:ASP:N	68:Bc:57:TRP:CZ3	2.90	0.40
11:AF:75:TYR:HB3	11:AF:81:ARG:NH1	2.36	0.40
11:AF:275:GLY:H	11:AF:352:THR:HB	1.87	0.40
12:AI:205:TYR:CE2	12:AI:208:ARG:NH1	2.89	0.40
13:AJ:35:ALA:HB2	33:Ap:247:LEU:HD23	2.04	0.40
13:AJ:78:THR:CG2	13:AJ:80:ARG:H	2.34	0.40
15:AN:139:ASN:HA	15:AN:142:PHE:O	2.22	0.40
16:AP:34:LEU:HD23	16:AP:34:LEU:N	2.37	0.40
17:AQ:73:ARG:HD2	17:AQ:143:ALA:HB2	2.04	0.40
18:AR:57:LYS:HE2	18:AR:66:ARG:NH1	2.31	0.40
21:AV:106:ILE:HG22	29:Ag:2:SER:HB3	2.03	0.40
23:AX:189:GLU:O	23:AX:214:ALA:HA	2.21	0.40
26:Ad:37:TRP:HA	30:Aj:97:GLN:HG2	2.03	0.40
26:Ad:93:MET:HE1	69:Bd:19:MET:O	2.22	0.40
27:Ae:112:LYS:O	39:AA:544:G:H5'	2.21	0.40
28:Af:164:HIS:CD2	28:Af:166:LYS:HE2	2.57	0.40
29:Ag:253:ARG:HA	29:Ag:253:ARG:HD2	1.86	0.40
30:Aj:18:GLY:O	69:Bd:78:CYS:HA	2.22	0.40
33:Ap:38:LEU:O	33:Ap:39:LYS:HD2	2.22	0.40
34:At:124:SER:OG	34:At:125:TYR:N	2.54	0.40
39:AA:169:U:O2'	39:AA:170:A:H5'	2.21	0.40
39:AA:300:U:P	45:BF:261:ARG:HH22	2.44	0.40
39:AA:1107:U:H5	39:AA:1157:A:N3	2.20	0.40
40:BA:600:VAL:HA	40:BA:603:LEU:HG	2.02	0.40
48:BI:70:PRO:HG2	48:BI:73:ILE:HG12	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:BM:124:LEU:HA	52:BM:125:PRO:HD2	1.97	0.40
54:BO:101:GLN:HE21	54:BO:117:LEU:HB2	1.87	0.40
54:BO:104:LEU:HD12	54:BO:117:LEU:HD21	2.03	0.40
64:BY:95:ILE:H	64:BY:95:ILE:HG13	1.66	0.40
67:Bb:112:LEU:HA	67:Bb:128:GLN:HE22	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A0	147/185 (80%)	143 (97%)	4 (3%)	0	100	100
2	A1	215/241 (89%)	209 (97%)	5 (2%)	1 (0%)	24	54
3	A2	445/471 (94%)	432 (97%)	10 (2%)	3 (1%)	18	47
4	A3	148/218 (68%)	143 (97%)	5 (3%)	0	100	100
5	A4	166/183 (91%)	156 (94%)	10 (6%)	0	100	100
6	A5	53/80 (66%)	51 (96%)	2 (4%)	0	100	100
7	A6	70/114 (61%)	70 (100%)	0	0	100	100
8	A8	139/181 (77%)	128 (92%)	11 (8%)	0	100	100
9	A9	51/184 (28%)	49 (96%)	2 (4%)	0	100	100
10	AE	289/473 (61%)	277 (96%)	12 (4%)	0	100	100
11	AF	440/459 (96%)	415 (94%)	24 (6%)	1 (0%)	43	71
12	AI	210/263 (80%)	201 (96%)	7 (3%)	2 (1%)	12	40
13	AJ	124/177 (70%)	116 (94%)	8 (6%)	0	100	100
14	AK	319/342 (93%)	307 (96%)	11 (3%)	1 (0%)	36	65
15	AN	177/202 (88%)	169 (96%)	8 (4%)	0	100	100
16	AP	348/374 (93%)	327 (94%)	20 (6%)	1 (0%)	36	65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	AQ	121/167 (72%)	117 (97%)	4 (3%)	0	100	100
18	AR	225/301 (75%)	211 (94%)	13 (6%)	1 (0%)	30	59
19	AT	33/144 (23%)	33 (100%)	0	0	100	100
20	AU	171/213 (80%)	168 (98%)	3 (2%)	0	100	100
21	AV	178/188 (95%)	174 (98%)	4 (2%)	0	100	100
22	AW	274/278 (99%)	267 (97%)	6 (2%)	1 (0%)	30	59
23	AX	166/246 (68%)	160 (96%)	6 (4%)	0	100	100
24	AY	338/378 (89%)	325 (96%)	9 (3%)	4 (1%)	10	35
25	Ab	449/507 (89%)	425 (95%)	24 (5%)	0	100	100
26	Ad	255/289 (88%)	249 (98%)	6 (2%)	0	100	100
27	Ae	114/197 (58%)	109 (96%)	5 (4%)	0	100	100
28	Af	124/189 (66%)	117 (94%)	7 (6%)	0	100	100
29	Ag	257/260 (99%)	250 (97%)	7 (3%)	0	100	100
30	Aj	277/296 (94%)	259 (94%)	18 (6%)	0	100	100
31	Al	207/218 (95%)	197 (95%)	10 (5%)	0	100	100
32	Ao	179/259 (69%)	169 (94%)	10 (6%)	0	100	100
33	Ap	259/309 (84%)	247 (95%)	11 (4%)	1 (0%)	30	59
34	At	136/154 (88%)	130 (96%)	5 (4%)	1 (1%)	18	47
35	Av	211/242 (87%)	205 (97%)	4 (2%)	2 (1%)	14	42
36	AB	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
37	AC	26/28 (93%)	26 (100%)	0	0	100	100
37	AD	26/28 (93%)	25 (96%)	1 (4%)	0	100	100
38	AG	25/27 (93%)	25 (100%)	0	0	100	100
40	BA	675/831 (81%)	647 (96%)	27 (4%)	1 (0%)	48	78
41	BB	387/541 (72%)	361 (93%)	22 (6%)	4 (1%)	12	40
42	BC	476/523 (91%)	448 (94%)	24 (5%)	4 (1%)	16	44
43	BD	415/547 (76%)	386 (93%)	23 (6%)	6 (1%)	9	31
44	BE	386/449 (86%)	361 (94%)	23 (6%)	2 (0%)	24	54
45	BF	341/426 (80%)	328 (96%)	13 (4%)	0	100	100
46	BG	317/378 (84%)	290 (92%)	27 (8%)	0	100	100
47	BH	209/349 (60%)	202 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	BI	317/343 (92%)	300 (95%)	16 (5%)	1 (0%)	36	65
49	BJ	164/333 (49%)	157 (96%)	7 (4%)	0	100	100
50	BK	252/386 (65%)	241 (96%)	10 (4%)	1 (0%)	30	59
51	BL	226/312 (72%)	220 (97%)	6 (3%)	0	100	100
52	BM	243/283 (86%)	220 (90%)	22 (9%)	1 (0%)	30	59
53	BN	212/302 (70%)	204 (96%)	8 (4%)	0	100	100
54	BO	143/262 (55%)	136 (95%)	6 (4%)	1 (1%)	18	47
55	BP	200/266 (75%)	192 (96%)	6 (3%)	2 (1%)	12	40
56	BQ	214/231 (93%)	201 (94%)	13 (6%)	0	100	100
57	BR	193/205 (94%)	180 (93%)	11 (6%)	2 (1%)	12	40
58	BS	95/198 (48%)	93 (98%)	2 (2%)	0	100	100
59	BT	166/191 (87%)	160 (96%)	6 (4%)	0	100	100
60	BU	80/185 (43%)	79 (99%)	1 (1%)	0	100	100
61	BV	153/190 (80%)	147 (96%)	6 (4%)	0	100	100
62	BW	185/188 (98%)	181 (98%)	4 (2%)	0	100	100
63	BX	103/190 (54%)	94 (91%)	8 (8%)	1 (1%)	12	40
64	BY	100/172 (58%)	90 (90%)	9 (9%)	1 (1%)	12	40
65	BZ	188/190 (99%)	176 (94%)	12 (6%)	0	100	100
66	Ba	137/153 (90%)	130 (95%)	7 (5%)	0	100	100
67	Bb	97/162 (60%)	88 (91%)	9 (9%)	0	100	100
68	Bc	88/146 (60%)	85 (97%)	3 (3%)	0	100	100
69	Bd	138/144 (96%)	132 (96%)	6 (4%)	0	100	100
70	Be	99/113 (88%)	97 (98%)	2 (2%)	0	100	100
71	Bf	46/113 (41%)	41 (89%)	4 (9%)	1 (2%)	5	24
72	Bg	80/105 (76%)	72 (90%)	8 (10%)	0	100	100
73	Bh	89/92 (97%)	84 (94%)	3 (3%)	2 (2%)	5	24
All	All	14660/18620 (79%)	13953 (95%)	658 (4%)	49 (0%)	37	65

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	AW	72	THR
35	Av	232	LYS

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Mol	Chain	Res	Type
41	BB	294	PRO
43	BD	356	PRO
43	BD	389	VAL
3	A2	270	ASN
3	A2	293	PHE
18	AR	141	ALA
24	AY	244	ARG
33	Ap	95	ARG
44	BE	384	HIS
50	BK	268	PRO
54	BO	76	GLY
71	Bf	101	TYR
24	AY	98	LYS
24	AY	108	PRO
34	At	73	ARG
40	BA	310	ALA
42	BC	268	LEU
42	BC	344	PHE
42	BC	513	GLY
48	BI	216	MET
52	BM	76	TRP
57	BR	172	PRO
63	BX	88	ALA
12	AI	19	ASP
12	AI	71	TYR
16	AP	359	HIS
43	BD	162	PRO
44	BE	348	VAL
55	BP	145	PRO
64	BY	162	ARG
73	Bh	61	PRO
2	A1	116	HIS
35	Av	68	ARG
41	BB	318	PRO
41	BB	338	ALA
43	BD	153	PRO
57	BR	120	PHE
3	A2	212	ALA
11	AF	36	ALA
24	AY	107	SER
43	BD	449	PHE
55	BP	146	ALA

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Mol	Chain	Res	Type
73	Bh	37	GLN
43	BD	139	MET
14	AK	17	VAL
41	BB	429	VAL
42	BC	339	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A0	140/167 (84%)	135 (96%)	5 (4%)	31	56
2	A1	195/217 (90%)	181 (93%)	14 (7%)	13	39
3	A2	394/413 (95%)	378 (96%)	16 (4%)	27	52
4	A3	131/193 (68%)	125 (95%)	6 (5%)	24	50
5	A4	153/164 (93%)	153 (100%)	0	100	100
6	A5	52/73 (71%)	48 (92%)	4 (8%)	12	37
7	A6	61/99 (62%)	56 (92%)	5 (8%)	10	35
8	A8	126/161 (78%)	123 (98%)	3 (2%)	43	62
9	A9	51/166 (31%)	45 (88%)	6 (12%)	5	20
10	AE	258/406 (64%)	245 (95%)	13 (5%)	22	49
11	AF	394/409 (96%)	377 (96%)	17 (4%)	26	51
12	AI	192/233 (82%)	183 (95%)	9 (5%)	23	50
13	AJ	90/151 (60%)	87 (97%)	3 (3%)	33	57
14	AK	287/301 (95%)	274 (96%)	13 (4%)	24	51
15	AN	160/182 (88%)	156 (98%)	4 (2%)	42	62
16	AP	310/330 (94%)	299 (96%)	11 (4%)	32	56
17	AQ	106/141 (75%)	104 (98%)	2 (2%)	50	66
18	AR	198/256 (77%)	196 (99%)	2 (1%)	68	75
19	AT	28/124 (23%)	26 (93%)	2 (7%)	13	39
20	AU	151/184 (82%)	143 (95%)	8 (5%)	20	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	AV	153/158 (97%)	150 (98%)	3 (2%)	48	65
22	AW	244/246 (99%)	234 (96%)	10 (4%)	27	52
23	AX	156/221 (71%)	154 (99%)	2 (1%)	61	71
24	AY	283/337 (84%)	271 (96%)	12 (4%)	26	52
25	Ab	373/451 (83%)	365 (98%)	8 (2%)	47	64
26	Ad	225/250 (90%)	219 (97%)	6 (3%)	39	60
27	Ae	100/172 (58%)	94 (94%)	6 (6%)	17	43
28	Af	111/162 (68%)	105 (95%)	6 (5%)	20	47
29	Ag	238/239 (100%)	232 (98%)	6 (2%)	42	62
30	Aj	237/260 (91%)	231 (98%)	6 (2%)	42	62
31	Al	170/186 (91%)	167 (98%)	3 (2%)	51	67
32	Ao	153/216 (71%)	147 (96%)	6 (4%)	28	53
33	Ap	227/267 (85%)	217 (96%)	10 (4%)	25	51
34	At	116/140 (83%)	112 (97%)	4 (3%)	32	57
35	Av	187/210 (89%)	181 (97%)	6 (3%)	34	58
40	BA	598/727 (82%)	576 (96%)	22 (4%)	30	55
41	BB	271/470 (58%)	238 (88%)	33 (12%)	5	19
42	BC	406/443 (92%)	389 (96%)	17 (4%)	26	52
44	BE	334/386 (86%)	320 (96%)	14 (4%)	26	52
45	BF	299/368 (81%)	286 (96%)	13 (4%)	26	51
46	BG	266/310 (86%)	249 (94%)	17 (6%)	16	42
47	BH	182/297 (61%)	163 (90%)	19 (10%)	7	24
48	BI	268/288 (93%)	255 (95%)	13 (5%)	22	49
49	BJ	136/298 (46%)	131 (96%)	5 (4%)	30	55
50	BK	196/331 (59%)	188 (96%)	8 (4%)	27	52
51	BL	201/262 (77%)	194 (96%)	7 (4%)	32	56
52	BM	209/240 (87%)	198 (95%)	11 (5%)	20	47
53	BN	167/265 (63%)	156 (93%)	11 (7%)	15	41
54	BO	129/225 (57%)	125 (97%)	4 (3%)	35	59
55	BP	162/219 (74%)	157 (97%)	5 (3%)	35	59
56	BQ	182/195 (93%)	174 (96%)	8 (4%)	25	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	BR	171/181 (94%)	163 (95%)	8 (5%)	23	50
58	BS	85/164 (52%)	80 (94%)	5 (6%)	18	44
59	BT	147/163 (90%)	141 (96%)	6 (4%)	27	52
60	BU	71/168 (42%)	70 (99%)	1 (1%)	59	70
61	BV	138/163 (85%)	132 (96%)	6 (4%)	26	51
62	BW	163/164 (99%)	159 (98%)	4 (2%)	42	62
63	BX	92/170 (54%)	83 (90%)	9 (10%)	7	27
64	BY	89/151 (59%)	88 (99%)	1 (1%)	65	74
65	BZ	143/160 (89%)	142 (99%)	1 (1%)	76	78
66	Ba	131/144 (91%)	129 (98%)	2 (2%)	57	69
67	Bb	84/135 (62%)	82 (98%)	2 (2%)	43	62
68	Bc	82/134 (61%)	79 (96%)	3 (4%)	30	55
69	Bd	117/120 (98%)	110 (94%)	7 (6%)	17	43
70	Be	89/99 (90%)	83 (93%)	6 (7%)	15	41
71	Bf	45/98 (46%)	44 (98%)	1 (2%)	45	63
72	Bg	65/87 (75%)	63 (97%)	2 (3%)	35	59
73	Bh	79/80 (99%)	75 (95%)	4 (5%)	21	48
All	All	12247/15590 (79%)	11735 (96%)	512 (4%)	28	52

All (512) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A0	43	PHE
1	A0	76	THR
1	A0	116	LEU
1	A0	143	LEU
1	A0	166	ASN
2	A1	49	VAL
2	A1	60	VAL
2	A1	63	ARG
2	A1	75	VAL
2	A1	104	VAL
2	A1	113	VAL
2	A1	114	LEU
2	A1	133	ASP
2	A1	142	LYS

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Mol	Chain	Res	Type
2	A1	156	ILE
2	A1	178	GLN
2	A1	188	ILE
2	A1	192	GLU
2	A1	223	LYS
3	A2	17	VAL
3	A2	22	LEU
3	A2	44	LEU
3	A2	72	GLN
3	A2	94	ILE
3	A2	142	LYS
3	A2	182	LEU
3	A2	295	ASN
3	A2	296	VAL
3	A2	298	LEU
3	A2	334	LEU
3	A2	350	VAL
3	A2	366	VAL
3	A2	384	LEU
3	A2	463	ILE
3	A2	470	ASP
4	A3	62	VAL
4	A3	104	GLN
4	A3	140	ASP
4	A3	151	ARG
4	A3	152	VAL
4	A3	181	ASP
6	A5	49	LEU
6	A5	62	GLU
6	A5	70	CYS
6	A5	78	ILE
7	A6	86	LYS
7	A6	87	ILE
7	A6	88	LYS
7	A6	94	LYS
7	A6	105	ILE
8	A8	83	ARG
8	A8	116	GLN
8	A8	175	ASP
9	A9	60	GLN
9	A9	61	MET
9	A9	63	MET

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Mol	Chain	Res	Type
9	A9	82	ASP
9	A9	109	LYS
9	A9	110	GLN
10	AE	43	ARG
10	AE	70	LYS
10	AE	73	LEU
10	AE	175	THR
10	AE	190	MET
10	AE	195	GLU
10	AE	215	VAL
10	AE	221	ILE
10	AE	236	ARG
10	AE	311	VAL
10	AE	343	ILE
10	AE	345	THR
10	AE	370	ASP
11	AF	35	ILE
11	AF	72	ILE
11	AF	92	GLU
11	AF	102	ILE
11	AF	105	THR
11	AF	165	GLU
11	AF	166	THR
11	AF	167	ARG
11	AF	216	VAL
11	AF	217	LYS
11	AF	248	THR
11	AF	259	MET
11	AF	280	THR
11	AF	296	ASN
11	AF	368	LEU
11	AF	388	GLU
11	AF	394	VAL
12	AI	20	ILE
12	AI	32	VAL
12	AI	48	ARG
12	AI	100	LEU
12	AI	104	GLU
12	AI	155	ILE
12	AI	158	THR
12	AI	181	THR
12	AI	183	ARG

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Mol	Chain	Res	Type
13	AJ	14	ARG
13	AJ	46	LYS
13	AJ	98	THR
14	AK	16	THR
14	AK	19	VAL
14	AK	90	THR
14	AK	150	THR
14	AK	172	LEU
14	AK	174	GLU
14	AK	192	ILE
14	AK	207	GLU
14	AK	208	GLN
14	AK	209	GLN
14	AK	230	GLN
14	AK	239	ILE
14	AK	326	GLU
15	AN	43	ARG
15	AN	54	LEU
15	AN	143	VAL
15	AN	148	THR
16	AP	25	MET
16	AP	34	LEU
16	AP	42	VAL
16	AP	46	ASN
16	AP	65	VAL
16	AP	209	ARG
16	AP	258	THR
16	AP	283	ARG
16	AP	348	ASN
16	AP	373	ARG
16	AP	374	LEU
17	AQ	26	ARG
17	AQ	44	ILE
18	AR	121	ASP
18	AR	196	GLU
19	AT	24	LEU
19	AT	35	MET
20	AU	15	LEU
20	AU	47	THR
20	AU	50	ARG
20	AU	136	LEU
20	AU	173	ARG

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Mol	Chain	Res	Type
20	AU	189	ASN
20	AU	194	LEU
20	AU	195	ILE
21	AV	73	LEU
21	AV	203	GLN
21	AV	231	THR
22	AW	14	LEU
22	AW	33	ARG
22	AW	55	THR
22	AW	75	GLN
22	AW	76	LEU
22	AW	82	TRP
22	AW	112	LEU
22	AW	120	GLU
22	AW	198	VAL
22	AW	273	ILE
23	AX	62	HIS
23	AX	63	LYS
24	AY	96	ARG
24	AY	190	MET
24	AY	198	THR
24	AY	202	GLU
24	AY	205	ARG
24	AY	224	GLU
24	AY	225	VAL
24	AY	241	THR
24	AY	256	LEU
24	AY	283	GLU
24	AY	287	GLN
24	AY	302	GLU
25	Ab	74	ASP
25	Ab	105	ASN
25	Ab	110	GLU
25	Ab	171	VAL
25	Ab	192	VAL
25	Ab	355	VAL
25	Ab	385	ILE
25	Ab	420	GLU
26	Ad	80	LYS
26	Ad	100	ILE
26	Ad	111	GLU
26	Ad	173	SER

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Mol	Chain	Res	Type
26	Ad	192	GLU
26	Ad	193	LEU
27	Ae	75	ARG
27	Ae	80	LEU
27	Ae	87	VAL
27	Ae	98	VAL
27	Ae	148	ILE
27	Ae	154	ARG
28	Af	60	GLN
28	Af	65	LEU
28	Af	72	ASP
28	Af	125	THR
28	Af	127	MET
28	Af	135	ILE
29	Ag	33	LEU
29	Ag	91	ASN
29	Ag	117	LEU
29	Ag	134	ARG
29	Ag	168	CYS
29	Ag	224	VAL
30	Aj	27	VAL
30	Aj	77	GLN
30	Aj	78	ARG
30	Aj	137	VAL
30	Aj	179	ARG
30	Aj	188	VAL
31	Al	15	THR
31	Al	23	ARG
31	Al	191	VAL
32	Ao	54	GLN
32	Ao	57	MET
32	Ao	223	VAL
32	Ao	243	LYS
32	Ao	244	PHE
32	Ao	246	VAL
33	Ap	52	ARG
33	Ap	56	ASN
33	Ap	123	LYS
33	Ap	155	ILE
33	Ap	196	ILE
33	Ap	234	VAL
33	Ap	278	ASN

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Mol	Chain	Res	Type
33	Ap	280	LEU
33	Ap	284	ASP
33	Ap	285	TYR
34	At	44	LEU
34	At	143	THR
34	At	144	VAL
34	At	153	LEU
35	Av	45	LEU
35	Av	47	ARG
35	Av	146	THR
35	Av	167	ARG
35	Av	210	LEU
35	Av	233	THR
40	BA	129	PHE
40	BA	133	THR
40	BA	151	ASP
40	BA	190	THR
40	BA	212	VAL
40	BA	266	LEU
40	BA	326	LEU
40	BA	327	ARG
40	BA	328	VAL
40	BA	336	THR
40	BA	340	LEU
40	BA	396	ARG
40	BA	401	THR
40	BA	412	LEU
40	BA	419	THR
40	BA	566	MET
40	BA	567	THR
40	BA	569	LEU
40	BA	593	THR
40	BA	631	LYS
40	BA	757	THR
40	BA	809	ASP
41	BB	66	GLU
41	BB	75	MET
41	BB	91	LEU
41	BB	94	THR
41	BB	100	GLU
41	BB	105	LEU
41	BB	106	LEU

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Mol	Chain	Res	Type
41	BB	111	ILE
41	BB	132	GLU
41	BB	138	CYS
41	BB	148	LYS
41	BB	169	SER
41	BB	180	GLU
41	BB	188	LEU
41	BB	206	ASP
41	BB	213	LEU
41	BB	230	THR
41	BB	234	ILE
41	BB	240	HIS
41	BB	243	ILE
41	BB	244	LYS
41	BB	251	ILE
41	BB	255	LEU
41	BB	259	GLU
41	BB	261	VAL
41	BB	344	CYS
41	BB	356	ASN
41	BB	357	THR
41	BB	364	VAL
41	BB	390	LEU
41	BB	395	GLU
41	BB	413	LEU
41	BB	422	MET
42	BC	120	ILE
42	BC	207	GLN
42	BC	235	VAL
42	BC	267	ILE
42	BC	268	LEU
42	BC	303	LEU
42	BC	306	GLU
42	BC	353	ILE
42	BC	362	VAL
42	BC	410	LYS
42	BC	427	LEU
42	BC	475	LEU
42	BC	480	ILE
42	BC	490	LEU
42	BC	494	LEU
42	BC	501	CYS

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Mol	Chain	Res	Type
42	BC	522	LEU
44	BE	28	LEU
44	BE	32	LEU
44	BE	95	LEU
44	BE	128	ILE
44	BE	144	VAL
44	BE	168	LEU
44	BE	186	LEU
44	BE	266	LEU
44	BE	335	LYS
44	BE	348	VAL
44	BE	354	GLU
44	BE	358	ASN
44	BE	359	LYS
44	BE	442	THR
45	BF	50	LEU
45	BF	60	LEU
45	BF	128	LYS
45	BF	131	LEU
45	BF	181	THR
45	BF	192	GLU
45	BF	237	LEU
45	BF	288	GLN
45	BF	345	LEU
45	BF	360	THR
45	BF	386	VAL
45	BF	419	VAL
45	BF	420	ARG
46	BG	65	MET
46	BG	74	ARG
46	BG	102	GLN
46	BG	162	SER
46	BG	164	GLN
46	BG	165	GLU
46	BG	176	LEU
46	BG	177	ASP
46	BG	178	THR
46	BG	180	LEU
46	BG	181	VAL
46	BG	183	ARG
46	BG	189	MET
46	BG	202	ILE

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Mol	Chain	Res	Type
46	BG	295	ARG
46	BG	339	GLU
46	BG	350	LEU
47	BH	73	ILE
47	BH	74	ARG
47	BH	113	LEU
47	BH	119	VAL
47	BH	121	VAL
47	BH	135	ARG
47	BH	146	GLU
47	BH	149	ARG
47	BH	156	LEU
47	BH	160	THR
47	BH	168	THR
47	BH	172	MET
47	BH	174	LEU
47	BH	178	GLU
47	BH	253	GLN
47	BH	254	TRP
47	BH	255	PHE
47	BH	257	ASP
47	BH	258	THR
48	BI	60	GLN
48	BI	63	LEU
48	BI	71	LYS
48	BI	73	ILE
48	BI	84	LEU
48	BI	139	ARG
48	BI	140	PHE
48	BI	144	HIS
48	BI	232	LEU
48	BI	270	ILE
48	BI	276	ILE
48	BI	319	ARG
48	BI	338	CYS
49	BJ	223	THR
49	BJ	234	THR
49	BJ	250	LEU
49	BJ	270	ARG
49	BJ	292	ARG
50	BK	98	THR
50	BK	140	LEU

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Mol	Chain	Res	Type
50	BK	193	VAL
50	BK	285	GLN
50	BK	300	TRP
50	BK	302	VAL
50	BK	328	LEU
50	BK	349	VAL
51	BL	122	LYS
51	BL	123	LEU
51	BL	125	GLU
51	BL	141	ASN
51	BL	180	LEU
51	BL	239	VAL
51	BL	291	LEU
52	BM	141	THR
52	BM	160	ARG
52	BM	163	LEU
52	BM	178	GLU
52	BM	184	MET
52	BM	186	VAL
52	BM	223	THR
52	BM	236	ARG
52	BM	237	THR
52	BM	241	MET
52	BM	245	LEU
53	BN	13	VAL
53	BN	36	GLU
53	BN	48	THR
53	BN	55	VAL
53	BN	60	ARG
53	BN	70	HIS
53	BN	71	GLN
53	BN	90	LEU
53	BN	180	GLU
53	BN	182	GLU
53	BN	219	ARG
54	BO	135	LEU
54	BO	139	LEU
54	BO	142	GLU
54	BO	144	GLN
55	BP	39	LEU
55	BP	107	VAL
55	BP	176	THR

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Mol	Chain	Res	Type
55	BP	205	TYR
55	BP	214	ASN
56	BQ	101	ASP
56	BQ	115	ASP
56	BQ	116	GLU
56	BQ	119	GLU
56	BQ	121	LYS
56	BQ	202	LEU
56	BQ	215	LEU
56	BQ	227	LEU
57	BR	19	TYR
57	BR	41	LEU
57	BR	81	ILE
57	BR	110	LEU
57	BR	143	ILE
57	BR	160	GLN
57	BR	176	GLU
57	BR	193	ILE
58	BS	26	ARG
58	BS	29	ASN
58	BS	30	GLU
58	BS	32	ARG
58	BS	99	VAL
59	BT	14	LYS
59	BT	17	LYS
59	BT	33	ASN
59	BT	72	LEU
59	BT	105	VAL
59	BT	174	ILE
60	BU	117	ILE
61	BV	52	PHE
61	BV	59	ARG
61	BV	60	MET
61	BV	87	ILE
61	BV	148	MET
61	BV	161	LYS
62	BW	50	ARG
62	BW	91	SER
62	BW	156	VAL
62	BW	175	THR
63	BX	64	ASN
63	BX	67	VAL

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Mol	Chain	Res	Type
63	BX	68	ASP
63	BX	71	MET
63	BX	72	VAL
63	BX	149	VAL
63	BX	170	LEU
63	BX	171	THR
63	BX	173	HIS
64	BY	149	ILE
65	BZ	151	ILE
66	Ba	25	GLN
66	Ba	113	VAL
67	Bb	53	ARG
67	Bb	78	LEU
68	Bc	21	LEU
68	Bc	54	ASN
68	Bc	82	GLU
69	Bd	32	THR
69	Bd	52	ARG
69	Bd	54	MET
69	Bd	57	LEU
69	Bd	58	LEU
69	Bd	102	LEU
69	Bd	126	ILE
70	Be	11	ILE
70	Be	49	ARG
70	Be	54	LEU
70	Be	63	CYS
70	Be	71	SER
70	Be	79	GLN
71	Bf	79	GLU
72	Bg	35	LEU
72	Bg	104	THR
73	Bh	6	CYS
73	Bh	17	VAL
73	Bh	53	MET
73	Bh	56	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (293) such sidechains are listed below:

Mol	Chain	Res	Type
1	A0	108	GLN
1	A0	166	ASN

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Mol	Chain	Res	Type
2	A1	16	ASN
2	A1	62	GLN
2	A1	116	HIS
2	A1	119	GLN
3	A2	41	ASN
3	A2	59	ASN
3	A2	72	GLN
3	A2	167	HIS
3	A2	207	GLN
3	A2	270	ASN
3	A2	314	HIS
4	A3	104	GLN
4	A3	144	GLN
5	A4	56	GLN
7	A6	77	GLN
7	A6	79	HIS
8	A8	68	GLN
10	AE	88	GLN
10	AE	168	ASN
10	AE	177	ASN
10	AE	191	ASN
10	AE	200	HIS
10	AE	214	HIS
10	AE	354	HIS
11	AF	64	HIS
11	AF	83	HIS
11	AF	192	ASN
11	AF	193	HIS
11	AF	223	ASN
11	AF	265	HIS
11	AF	296	ASN
11	AF	331	ASN
11	AF	377	ASN
13	AJ	44	GLN
13	AJ	81	ASN
14	AK	24	ASN
14	AK	52	ASN
14	AK	93	HIS
14	AK	144	HIS
14	AK	230	GLN
14	AK	246	ASN
15	AN	19	HIS

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Mol	Chain	Res	Type
15	AN	21	HIS
15	AN	22	HIS
15	AN	30	ASN
15	AN	68	GLN
15	AN	97	GLN
15	AN	164	HIS
15	AN	166	HIS
16	AP	15	HIS
16	AP	81	HIS
16	AP	84	GLN
16	AP	111	ASN
16	AP	199	HIS
16	AP	259	HIS
16	AP	310	HIS
16	AP	346	HIS
16	AP	348	ASN
16	AP	349	GLN
16	AP	362	ASN
17	AQ	47	GLN
17	AQ	134	GLN
17	AQ	164	HIS
18	AR	65	HIS
18	AR	223	HIS
18	AR	229	HIS
18	AR	259	HIS
19	AT	11	HIS
20	AU	46	GLN
20	AU	65	ASN
20	AU	73	HIS
20	AU	82	ASN
20	AU	101	GLN
20	AU	165	HIS
21	AV	75	ASN
21	AV	87	HIS
21	AV	100	GLN
21	AV	168	HIS
21	AV	206	ASN
22	AW	12	HIS
22	AW	40	HIS
22	AW	172	HIS
22	AW	183	GLN
22	AW	195	HIS

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Mol	Chain	Res	Type
23	AX	126	HIS
23	AX	128	GLN
24	AY	64	HIS
24	AY	74	HIS
24	AY	89	GLN
24	AY	168	HIS
24	AY	177	HIS
24	AY	248	GLN
25	Ab	90	HIS
25	Ab	105	ASN
25	Ab	122	HIS
25	Ab	205	HIS
25	Ab	351	GLN
25	Ab	419	GLN
25	Ab	471	ASN
26	Ad	52	ASN
26	Ad	151	GLN
26	Ad	188	GLN
26	Ad	284	HIS
27	Ae	48	ASN
28	Af	86	ASN
28	Af	101	HIS
28	Af	104	HIS
28	Af	146	ASN
28	Af	156	HIS
28	Af	159	ASN
28	Af	164	HIS
28	Af	168	GLN
29	Ag	84	ASN
29	Ag	91	ASN
29	Ag	101	HIS
29	Ag	170	GLN
29	Ag	172	GLN
29	Ag	204	HIS
29	Ag	244	HIS
29	Ag	256	GLN
30	Aj	20	HIS
30	Aj	22	GLN
30	Aj	37	GLN
30	Aj	54	GLN
30	Aj	90	HIS
30	Aj	121	GLN

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Mol	Chain	Res	Type
30	Aj	225	GLN
30	Aj	267	HIS
31	Al	66	GLN
31	Al	71	ASN
31	Al	168	GLN
32	Ao	25	ASN
32	Ao	54	GLN
32	Ao	113	GLN
32	Ao	139	GLN
33	Ap	37	ASN
33	Ap	55	HIS
33	Ap	83	HIS
33	Ap	197	GLN
33	Ap	278	ASN
34	At	20	HIS
34	At	80	HIS
34	At	147	HIS
34	At	148	GLN
35	Av	102	GLN
35	Av	107	GLN
35	Av	118	ASN
35	Av	212	ASN
40	BA	301	HIS
40	BA	380	ASN
40	BA	484	HIS
40	BA	490	ASN
40	BA	502	HIS
40	BA	531	GLN
40	BA	539	ASN
40	BA	693	HIS
40	BA	699	ASN
40	BA	714	ASN
40	BA	734	HIS
41	BB	82	HIS
41	BB	128	HIS
41	BB	162	GLN
41	BB	170	GLN
41	BB	218	HIS
41	BB	219	ASN
41	BB	240	HIS
41	BB	242	GLN
41	BB	359	HIS

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Mol	Chain	Res	Type
41	BB	420	ASN
42	BC	62	GLN
42	BC	71	GLN
42	BC	85	HIS
42	BC	86	GLN
42	BC	108	GLN
42	BC	115	GLN
42	BC	148	ASN
42	BC	165	HIS
42	BC	289	ASN
42	BC	292	ASN
42	BC	340	HIS
42	BC	518	HIS
44	BE	23	GLN
44	BE	25	HIS
44	BE	29	ASN
44	BE	78	HIS
44	BE	100	ASN
44	BE	125	GLN
44	BE	141	GLN
44	BE	251	ASN
44	BE	270	HIS
44	BE	279	HIS
44	BE	350	ASN
44	BE	361	GLN
45	BF	132	GLN
45	BF	163	ASN
45	BF	245	ASN
45	BF	250	HIS
45	BF	298	ASN
45	BF	332	HIS
46	BG	35	GLN
46	BG	115	HIS
46	BG	287	HIS
46	BG	305	HIS
46	BG	340	GLN
47	BH	99	GLN
47	BH	102	ASN
47	BH	122	HIS
47	BH	207	HIS
47	BH	239	ASN
47	BH	246	GLN

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Mol	Chain	Res	Type
48	BI	45	HIS
48	BI	52	HIS
48	BI	60	GLN
48	BI	95	GLN
48	BI	106	HIS
48	BI	144	HIS
48	BI	148	ASN
48	BI	152	GLN
48	BI	180	GLN
48	BI	223	GLN
48	BI	263	HIS
48	BI	307	ASN
49	BJ	185	GLN
50	BK	108	GLN
50	BK	200	ASN
50	BK	227	GLN
51	BL	83	HIS
51	BL	88	ASN
51	BL	99	HIS
51	BL	103	ASN
51	BL	141	ASN
51	BL	226	HIS
52	BM	88	GLN
52	BM	89	HIS
52	BM	113	ASN
52	BM	234	HIS
52	BM	247	GLN
53	BN	28	ASN
53	BN	81	HIS
53	BN	95	HIS
54	BO	101	GLN
55	BP	82	GLN
55	BP	98	ASN
55	BP	134	HIS
55	BP	152	ASN
55	BP	166	HIS
55	BP	213	HIS
55	BP	214	ASN
55	BP	233	GLN
56	BQ	17	GLN
56	BQ	147	ASN
57	BR	16	GLN

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Mol	Chain	Res	Type
57	BR	96	GLN
57	BR	133	GLN
57	BR	164	HIS
59	BT	46	GLN
59	BT	51	HIS
59	BT	152	ASN
60	BU	156	GLN
61	BV	31	GLN
61	BV	54	GLN
61	BV	74	ASN
62	BW	46	HIS
62	BW	61	ASN
62	BW	65	ASN
62	BW	100	GLN
63	BX	157	HIS
64	BY	79(B)	HIS
64	BY	79(H)	HIS
64	BY	80	GLN
64	BY	100	HIS
64	BY	102	GLN
64	BY	140	HIS
65	BZ	36	ASN
65	BZ	96	GLN
65	BZ	144	ASN
65	BZ	155	GLN
65	BZ	168	GLN
66	Ba	70	HIS
67	Bb	128	GLN
68	Bc	97	GLN
69	Bd	35	GLN
69	Bd	49	ASN
69	Bd	65	ASN
69	Bd	67	HIS
70	Be	15	ASN
70	Be	72	HIS
71	Bf	92	HIS
72	Bg	27	ASN
72	Bg	58	GLN
73	Bh	37	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
39	AA	581/1178 (49%)	289 (49%)	19 (3%)

All (289) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
39	AA	2	U
39	AA	4	U
39	AA	5	U
39	AA	10	A
39	AA	11	U
39	AA	12	U
39	AA	13	A
39	AA	16	A
39	AA	17	A
39	AA	18	G
39	AA	20	A
39	AA	21	U
39	AA	28	A
39	AA	29	U
39	AA	32	U
39	AA	34	G
39	AA	38	U
39	AA	40	U
39	AA	41	U
39	AA	42	A
39	AA	43	U
39	AA	44	A
39	AA	46	U
39	AA	47	U
39	AA	50	A
39	AA	53	A
39	AA	54	A
39	AA	57	A
39	AA	58	U
39	AA	59	U
39	AA	60	U
39	AA	64	U
39	AA	65	U
39	AA	68	G
39	AA	69	U
39	AA	70	G
39	AA	71	U
39	AA	72	A

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Mol	Chain	Res	Type
39	AA	73	G
39	AA	74	U
39	AA	75	A
39	AA	77	A
39	AA	79	U
39	AA	80	U
39	AA	81	A
39	AA	82	U
39	AA	83	U
39	AA	84	A
39	AA	85	U
39	AA	86	U
39	AA	87	U
39	AA	88	G
39	AA	89	U
39	AA	93	A
39	AA	98	U
39	AA	101	A
39	AA	103	U
39	AA	104	A
39	AA	105	G
39	AA	106	G
39	AA	111	U
39	AA	112	U
39	AA	113	A
39	AA	114	U
39	AA	115	A
39	AA	119	A
39	AA	120	A
39	AA	124	U
39	AA	125	U
39	AA	126	A
39	AA	130	U
39	AA	131	U
39	AA	133	U
39	AA	134	U
39	AA	135	G
39	AA	136	U
39	AA	137	U
39	AA	146	A
39	AA	147	G
39	AA	149	U

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Mol	Chain	Res	Type
39	AA	150	A
39	AA	152	A
39	AA	154	A
39	AA	158	A
39	AA	159	U
39	AA	162	A
39	AA	164	U
39	AA	168	A
39	AA	170	A
39	AA	171	U
39	AA	172	U
39	AA	174	A
39	AA	176	A
39	AA	177	U
39	AA	178	A
39	AA	179	A
39	AA	180	U
39	AA	183	U
39	AA	186	A
39	AA	187	A
39	AA	189	A
39	AA	282	A
39	AA	283	A
39	AA	284	U
39	AA	285	A
39	AA	288	G
39	AA	289	U
39	AA	290	A
39	AA	296	A
39	AA	297	U
39	AA	299	U
39	AA	301	A
39	AA	327	U
39	AA	328	U
39	AA	331	C
39	AA	336	U
39	AA	344	A
39	AA	370	U
39	AA	371	A
39	AA	375	A
39	AA	378	A
39	AA	379	U

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Mol	Chain	Res	Type
39	AA	380	G
39	AA	381	U
39	AA	383	A
39	AA	384	U
39	AA	385	A
39	AA	387	A
39	AA	388	U
39	AA	393	A
39	AA	394	U
39	AA	404	U
39	AA	411	A
39	AA	418	G
39	AA	419	U
39	AA	421	C
39	AA	423	A
39	AA	425	U
39	AA	426	A
39	AA	427	U
39	AA	428	A
39	AA	438	U
39	AA	440	U
39	AA	441	A
39	AA	443	A
39	AA	446	A
39	AA	447	U
39	AA	448	A
39	AA	455	U
39	AA	456	U
39	AA	457	A
39	AA	458	U
39	AA	460	U
39	AA	461	U
39	AA	462	U
39	AA	463	U
39	AA	468	A
39	AA	469	G
39	AA	470	G
39	AA	472	A
39	AA	473	A
39	AA	474	A
39	AA	475	U
39	AA	476	G

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Mol	Chain	Res	Type
39	AA	477	A
39	AA	479	A
39	AA	481	G
39	AA	483	A
39	AA	484	U
39	AA	485	A
39	AA	486	A
39	AA	487	A
39	AA	488	U
39	AA	489	G
39	AA	490	G
39	AA	491	A
39	AA	492	U
39	AA	493	A
39	AA	494	U
39	AA	495	A
39	AA	496	A
39	AA	498	U
39	AA	500	A
39	AA	503	A
39	AA	504	U
39	AA	507	A
39	AA	509	U
39	AA	513	U
39	AA	514	G
39	AA	515	U
39	AA	516	U
39	AA	518	A
39	AA	519	A
39	AA	520	U
39	AA	524	A
39	AA	525	A
39	AA	526	G
39	AA	527	U
39	AA	529	U
39	AA	530	U
39	AA	531	U
39	AA	532	U
39	AA	533	A
39	AA	535	U
39	AA	536	A
39	AA	537	U

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Mol	Chain	Res	Type
39	AA	538	U
39	AA	540	U
39	AA	544	G
39	AA	545	U
39	AA	546	A
39	AA	548	A
39	AA	549	G
39	AA	551	A
39	AA	554	A
39	AA	555	U
39	AA	556	U
39	AA	557	A
39	AA	558	U
39	AA	559	A
39	AA	560	G
39	AA	562	G
39	AA	563	U
39	AA	564	A
39	AA	565	U
39	AA	566	A
39	AA	567	G
39	AA	568	U
39	AA	570	U
39	AA	571	U
39	AA	572	U
39	AA	573	U
39	AA	574	A
39	AA	575	A
39	AA	795	A
39	AA	801	A
39	AA	802	G
39	AA	803	U
39	AA	815	U
39	AA	818	A
39	AA	819	A
39	AA	825	A
39	AA	826	A
39	AA	827	U
39	AA	828	A
39	AA	830	A
39	AA	836	A
39	AA	837	A

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Mol	Chain	Res	Type
39	AA	838	A
39	AA	844	A
39	AA	845	A
39	AA	883	U
39	AA	884	A
39	AA	885	U
39	AA	886	G
39	AA	887	A
39	AA	892	U
39	AA	893	A
39	AA	948	A
39	AA	949	U
39	AA	950	U
39	AA	951	C
39	AA	952	U
39	AA	953	U
39	AA	954	U
39	AA	955	G
39	AA	1100	U
39	AA	1106	U
39	AA	1107	U
39	AA	1110	A
39	AA	1111	A
39	AA	1112	U
39	AA	1113	U
39	AA	1157	A
39	AA	1158	G
39	AA	1159	A
39	AA	1160	A
39	AA	1163	A
39	AA	1164	A
39	AA	1165	G
39	AA	1166	A
39	AA	1168	U
39	AA	1169	A
39	AA	1170	U
39	AA	1171	A
39	AA	1172	A
39	AA	1173	U
39	AA	1174	U
39	AA	1175	U

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
39	AA	40	U
39	AA	69	U
39	AA	86	U
39	AA	125	U
39	AA	171	U
39	AA	335	G
39	AA	379	U
39	AA	384	U
39	AA	387	A
39	AA	392	A
39	AA	418	G
39	AA	422	A
39	AA	425	U
39	AA	440	U
39	AA	485	A
39	AA	528	A
39	AA	534	U
39	AA	951	C
39	AA	1164	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 13 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	NAD	Av	301	-	46,48,48	1.91	10 (21%)	64,73,73	1.96	16 (25%)

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
88	NAD	Av	301	-	-	4/30/62/62	0/5/5/5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
88	Av	301	NAD	C3N-C7N	-7.83	1.38	1.50
88	Av	301	NAD	C2N-N1N	4.27	1.39	1.35
88	Av	301	NAD	C5A-C4A	-3.18	1.33	1.39
88	Av	301	NAD	C5A-N7A	-3.17	1.33	1.39
88	Av	301	NAD	C2A-N1A	3.16	1.39	1.33
88	Av	301	NAD	C2A-N3A	3.06	1.39	1.33
88	Av	301	NAD	C5A-C6A	-2.91	1.32	1.41
88	Av	301	NAD	C8A-N9A	-2.53	1.33	1.37
88	Av	301	NAD	C4A-N9A	-2.50	1.32	1.37
88	Av	301	NAD	C6N-N1N	2.17	1.40	1.35

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	Av	301	NAD	N3A-C2A-N1A	-6.84	118.23	128.58
88	Av	301	NAD	C4D-O4D-C1D	-6.26	104.19	109.92
88	Av	301	NAD	N9A-C8A-N7A	-4.21	107.97	113.94
88	Av	301	NAD	C5A-C4A-N3A	-4.03	121.17	126.72
88	Av	301	NAD	C2B-C3B-C4B	-3.19	96.45	102.61
88	Av	301	NAD	C2A-N3A-C4A	3.11	119.43	111.83
88	Av	301	NAD	C5A-C6A-N6A	-2.92	116.05	123.29
88	Av	301	NAD	C5A-N7A-C8A	2.67	107.65	103.45
88	Av	301	NAD	C4A-N9A-C8A	2.54	108.40	105.74
88	Av	301	NAD	C6A-C5A-C4A	2.53	120.63	117.18
88	Av	301	NAD	N3A-C4A-N9A	2.34	131.14	127.17
88	Av	301	NAD	O3-PN-O1N	-2.15	104.24	110.70
88	Av	301	NAD	O4B-C1B-N9A	2.11	112.14	108.09
88	Av	301	NAD	C3N-C7N-N7N	-2.05	115.21	117.74
88	Av	301	NAD	C2D-C3D-C4D	-2.04	98.67	102.61

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	Av	301	NAD	C4A-C5A-N7A	-2.02	108.28	110.58

There are no chirality outliers.

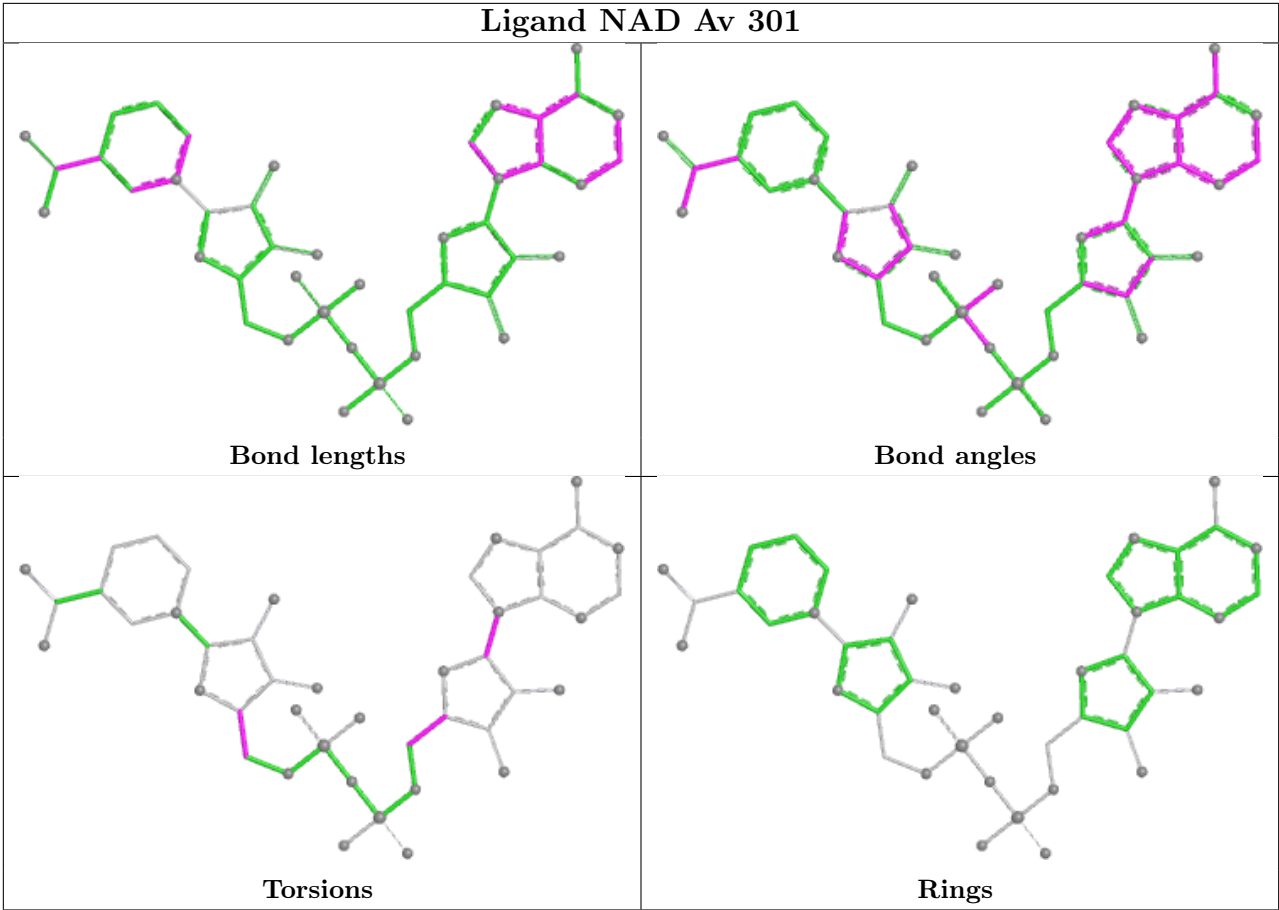
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
88	Av	301	NAD	O4D-C4D-C5D-O5D
88	Av	301	NAD	C3D-C4D-C5D-O5D
88	Av	301	NAD	C2B-C1B-N9A-C8A
88	Av	301	NAD	O4B-C4B-C5B-O5B

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
77	UD	3
39	AA	1
14	AK	1
8	A8	1
21	AV	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	UD	90:UNK	C	136:UNK	N	14.30
1	UD	158:UNK	C	159:UNK	N	11.31

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	UD	68:UNK	C	69:UNK	N	9.93
1	AA	448:A	O3'	454:U	P	9.07
1	AK	250:LEU	C	251:THR	N	5.73
1	A8	40:PRO	C	41:LYS	N	5.37
1	AV	56:ALA	C	57:ASN	N	5.05

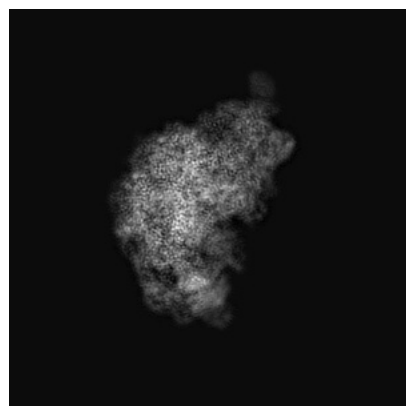
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0231. These allow visual inspection of the internal detail of the map and identification of artifacts.

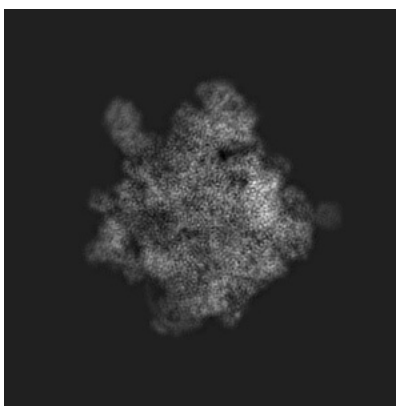
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

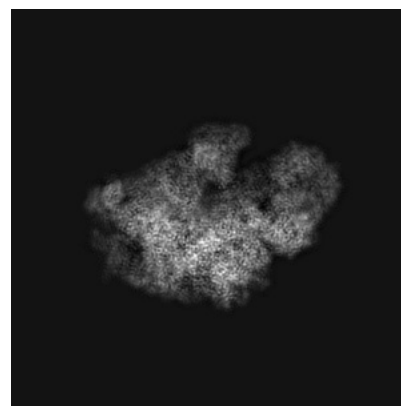
6.1.1 Primary map



X

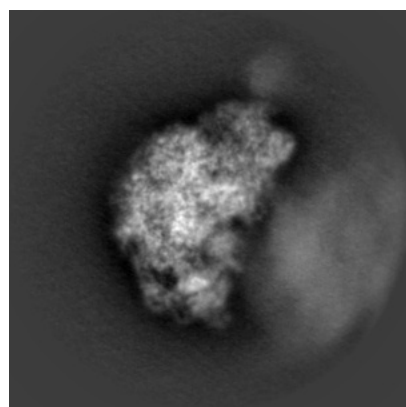


Y

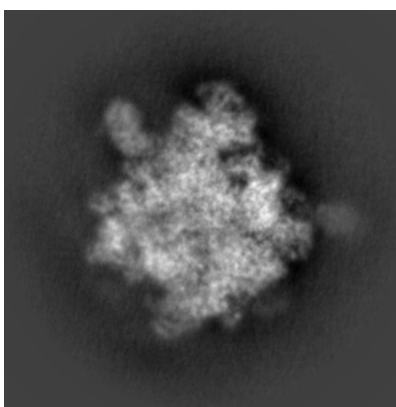


Z

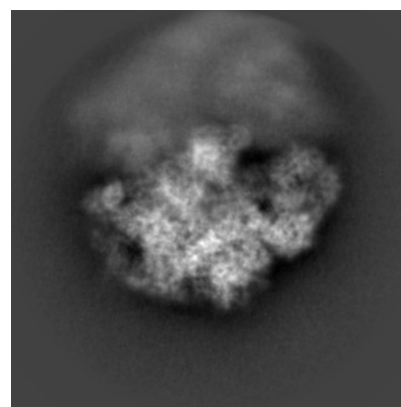
6.1.2 Raw map



X



Y

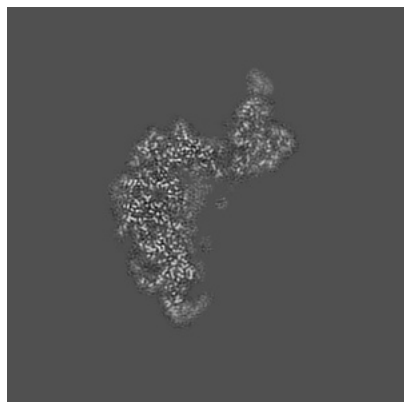


Z

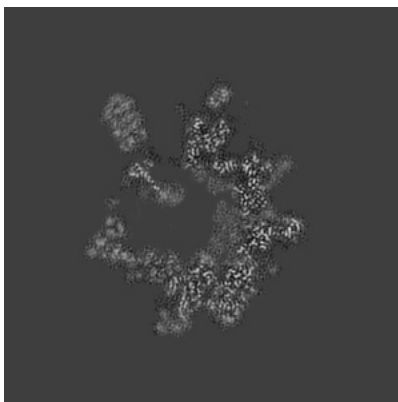
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

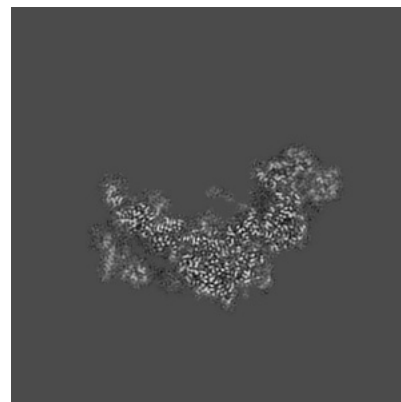
6.2.1 Primary map



X Index: 160

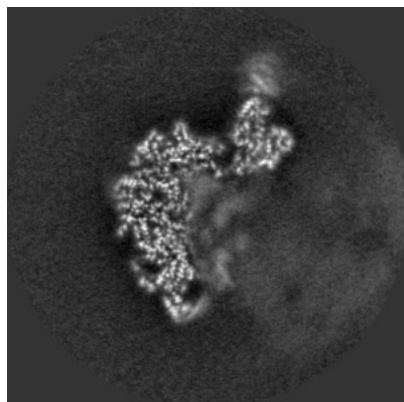


Y Index: 160

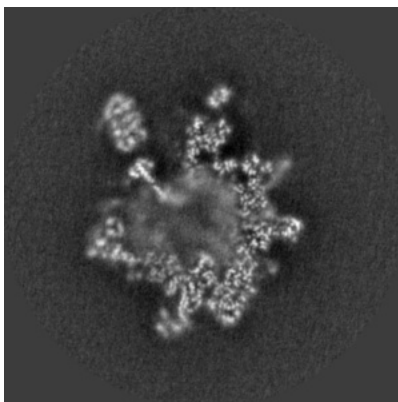


Z Index: 160

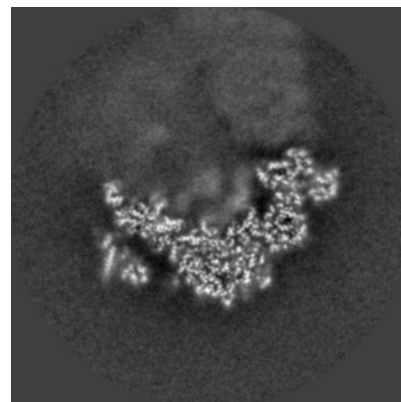
6.2.2 Raw map



X Index: 160



Y Index: 160

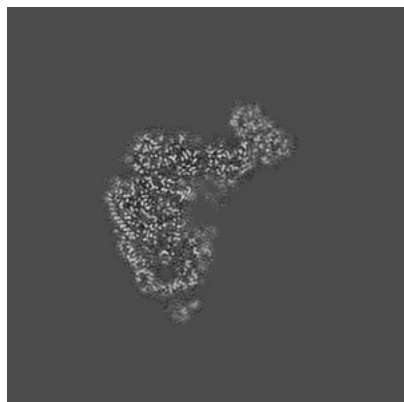


Z Index: 160

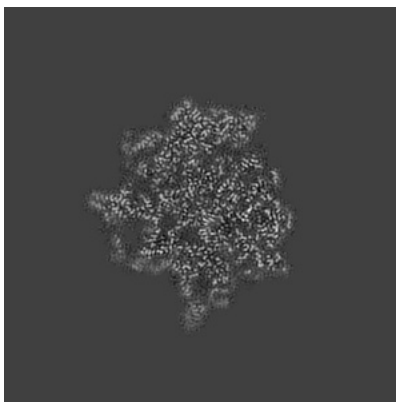
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

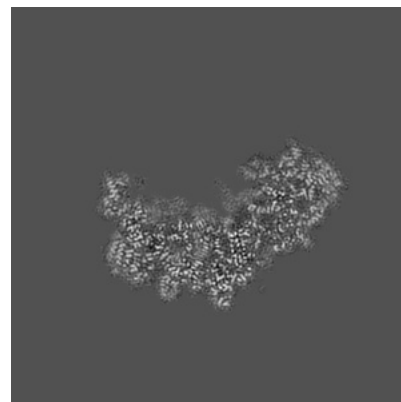
6.3.1 Primary map



X Index: 171

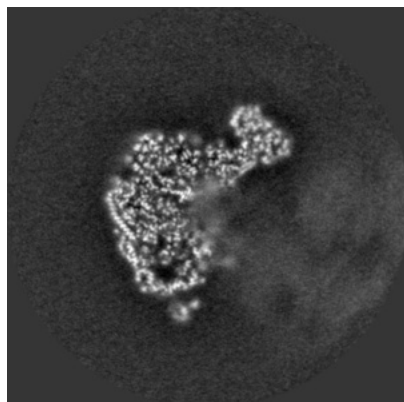


Y Index: 134

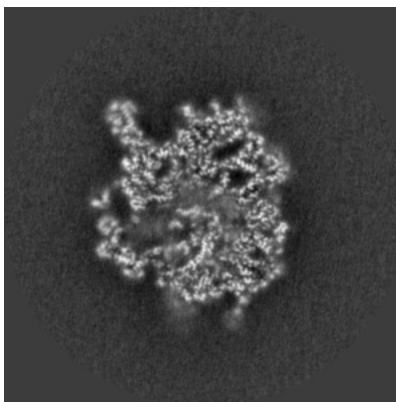


Z Index: 169

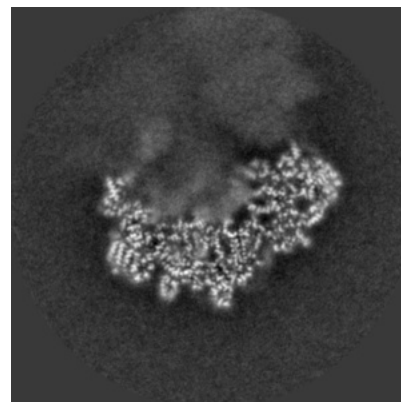
6.3.2 Raw map



X Index: 171



Y Index: 147

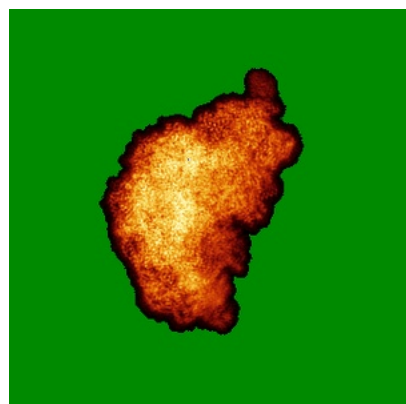


Z Index: 169

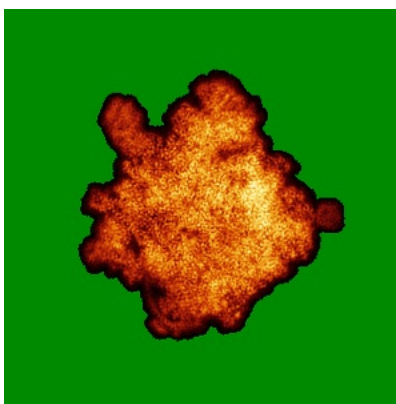
The images above show the largest variance slices of the map in three orthogonal directions.

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

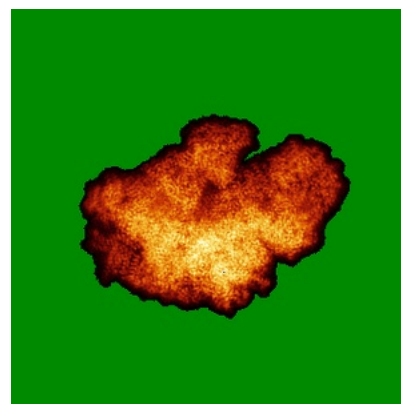
6.4.1 Primary map



X

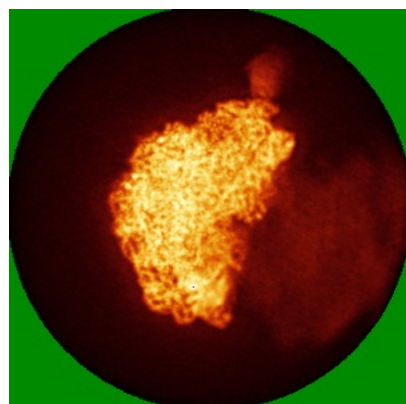


Y

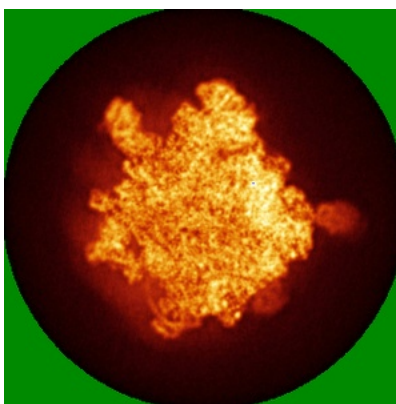


Z

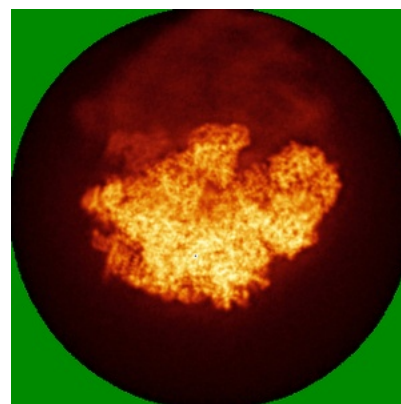
6.4.2 Raw map



X



Y

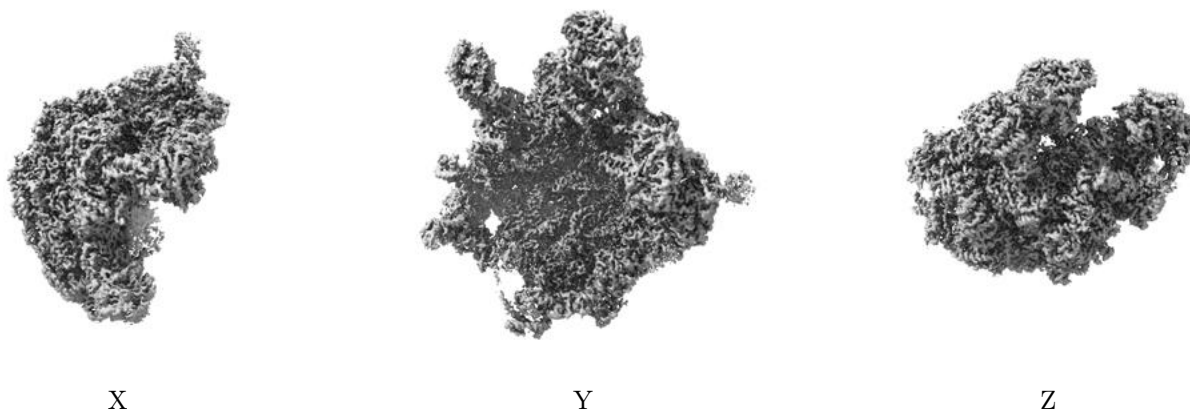


Z

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

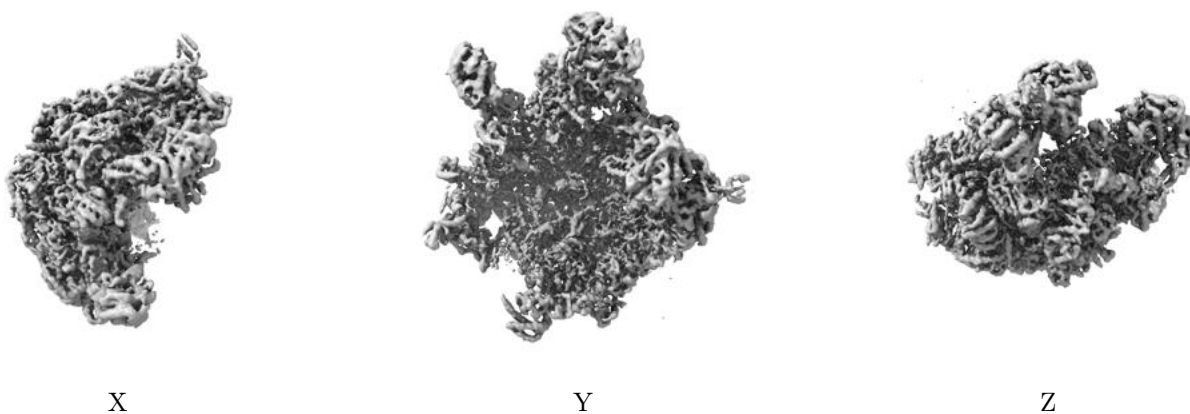
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

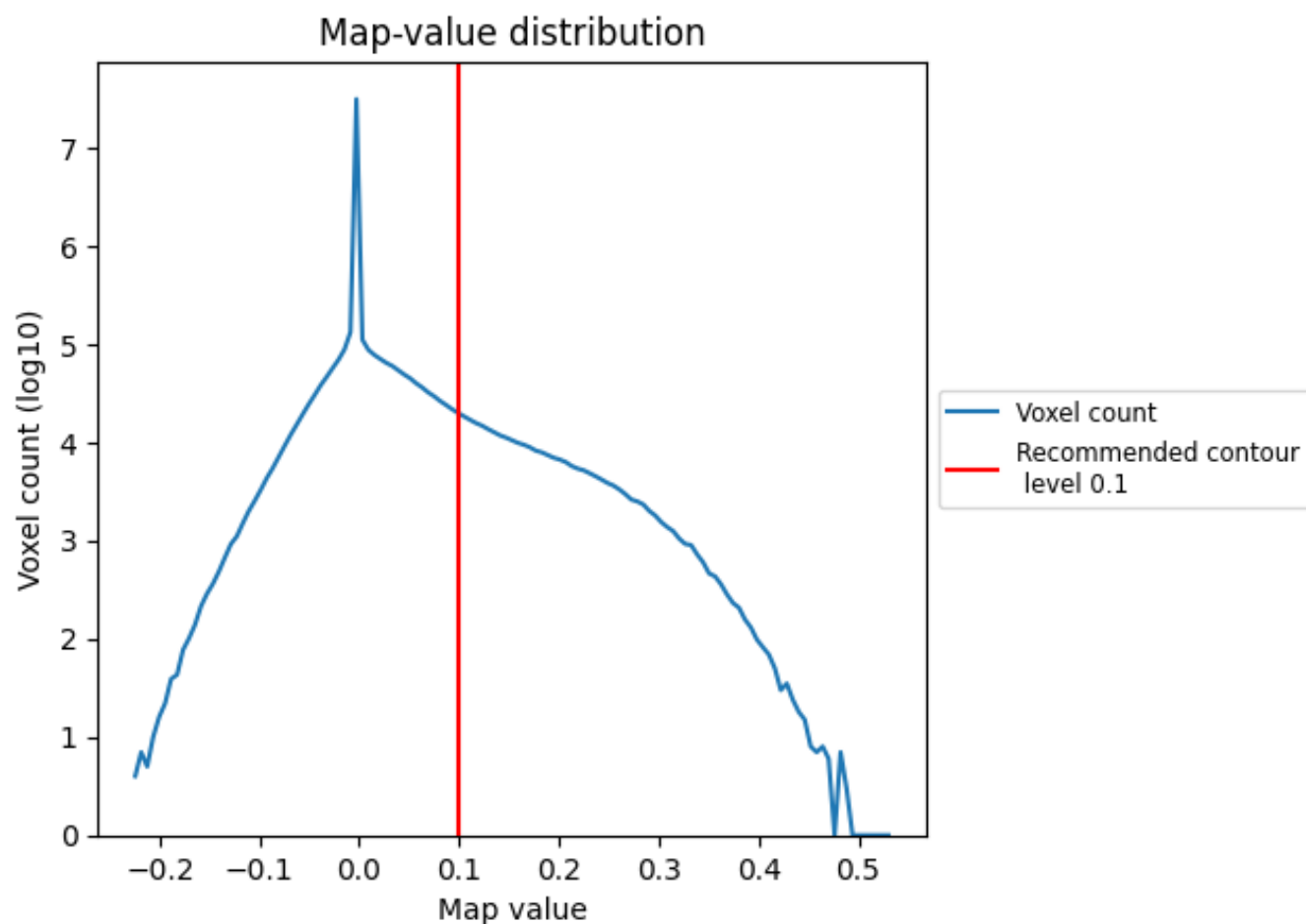
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

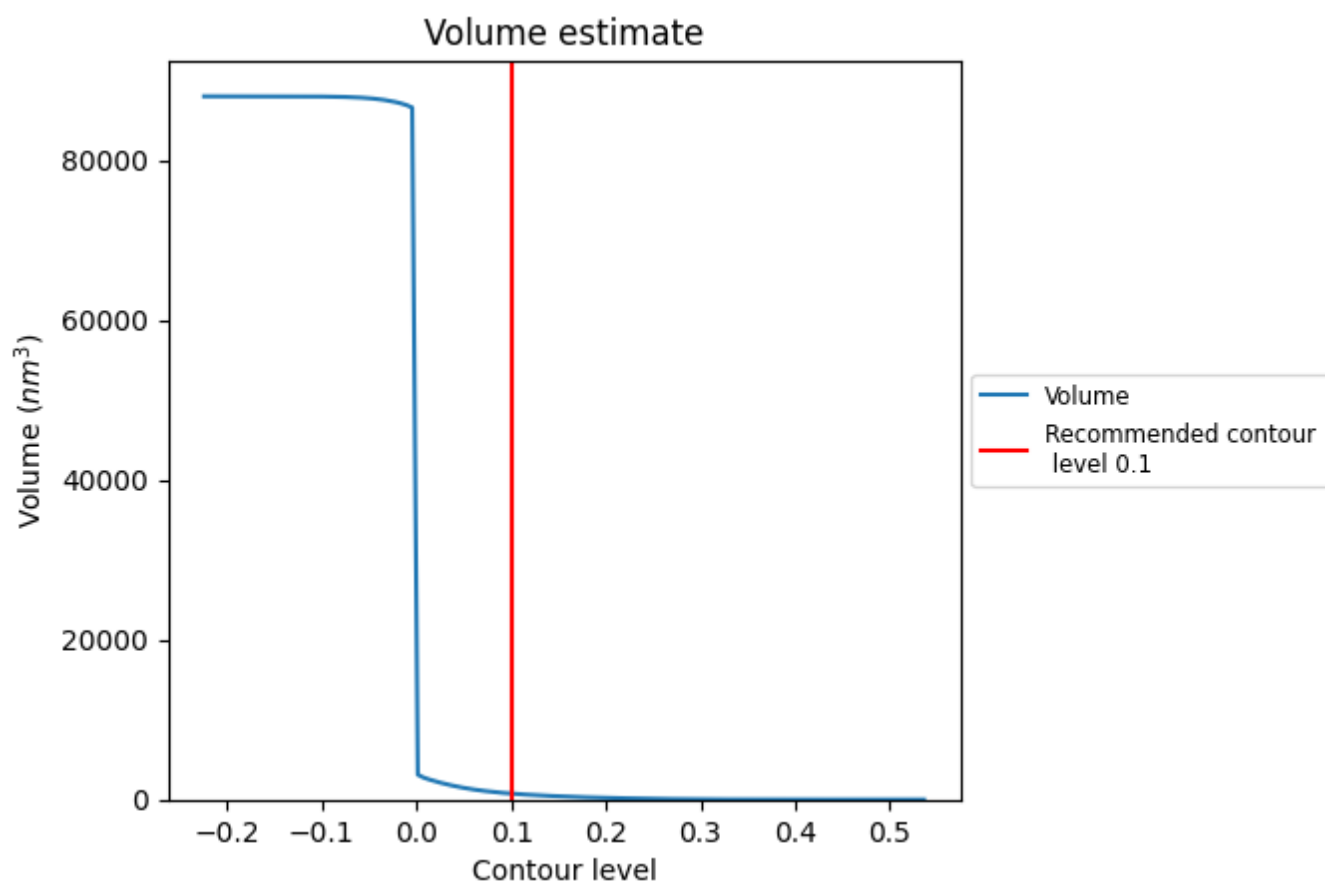
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

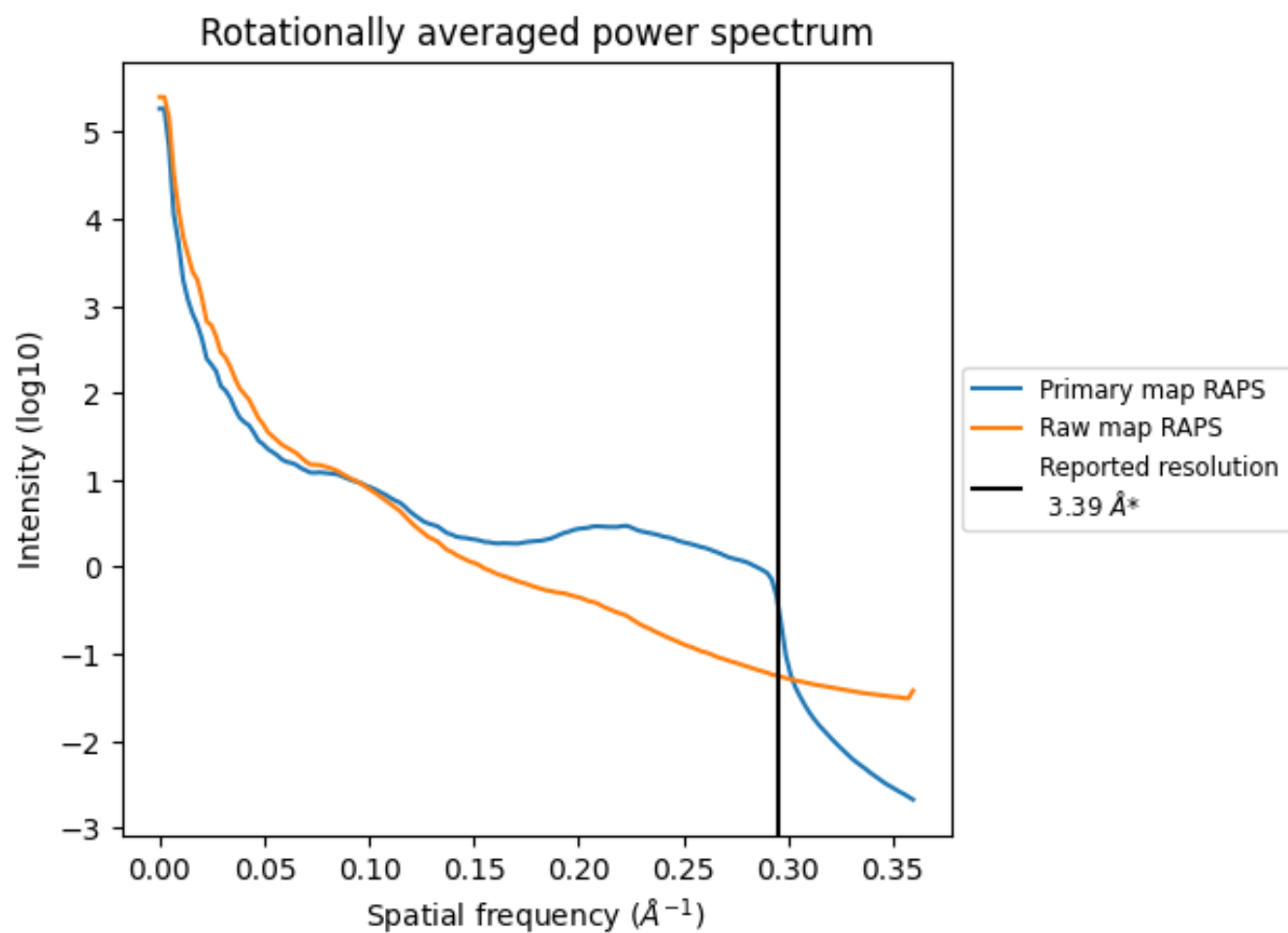
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 751 nm³; this corresponds to an approximate mass of 678 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

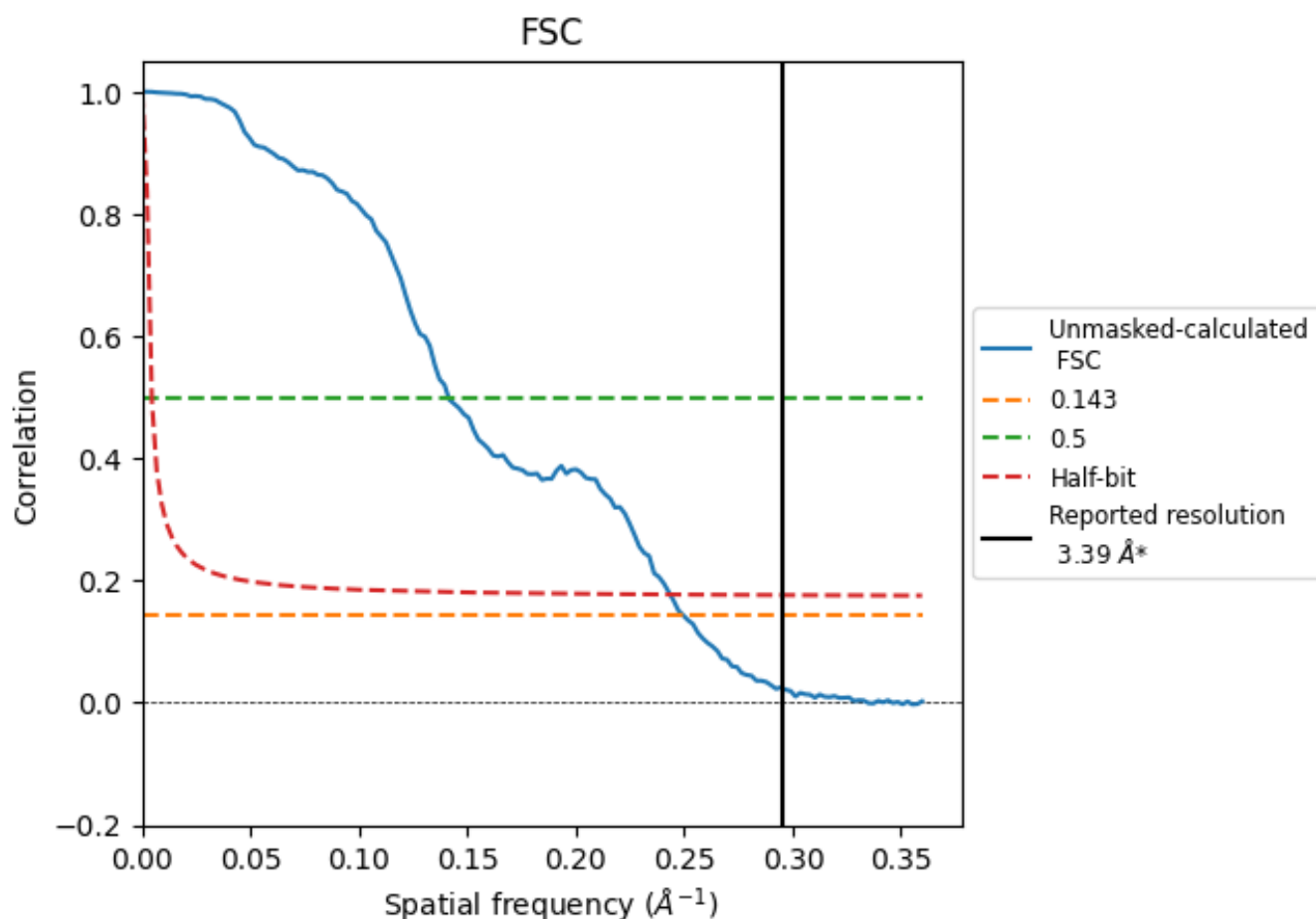


*Reported resolution corresponds to spatial frequency of $0.295 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.295 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

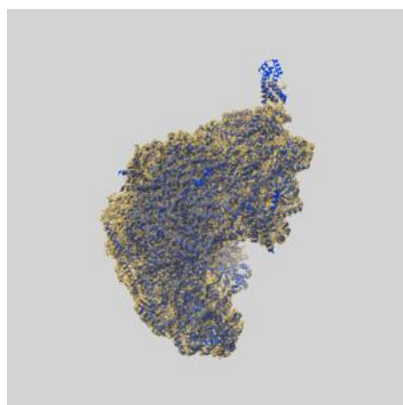
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.39	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.01	7.08	4.11

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.01 differs from the reported value 3.39 by more than 10 %

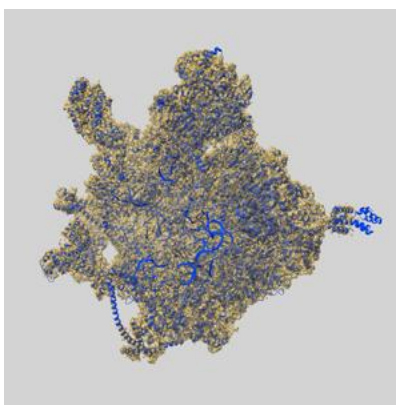
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0231 and PDB model 6HIX. Per-residue inclusion information can be found in section [3](#) on page [23](#).

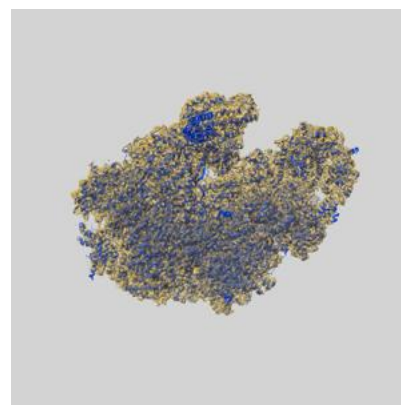
9.1 Map-model overlay [i](#)



X



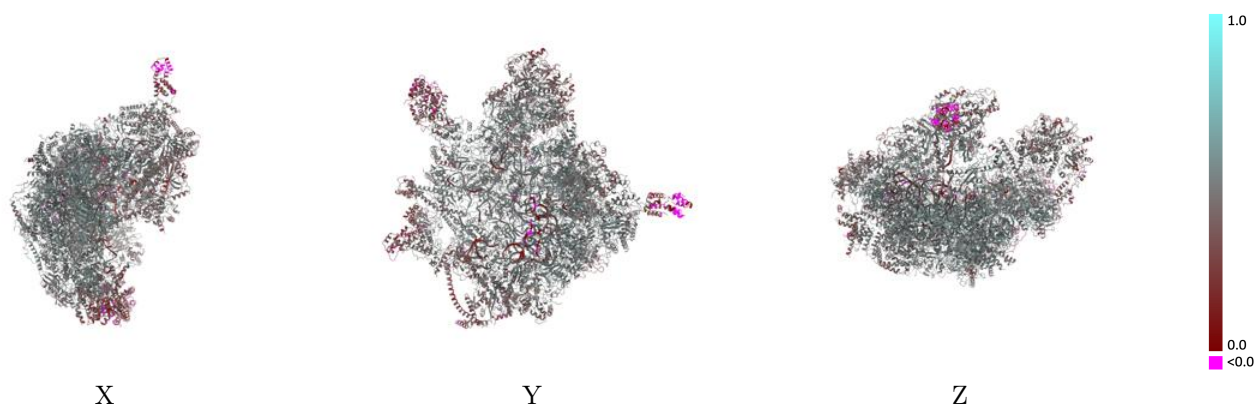
Y



Z

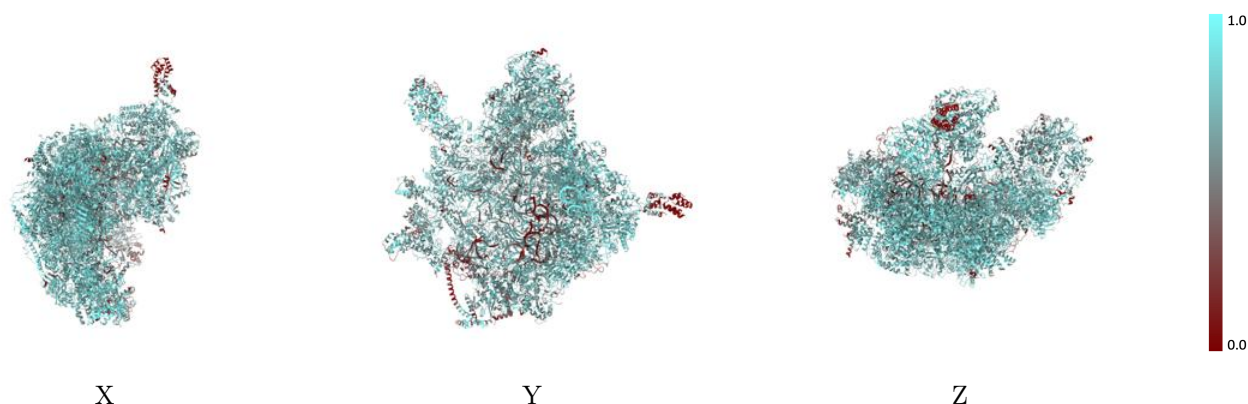
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



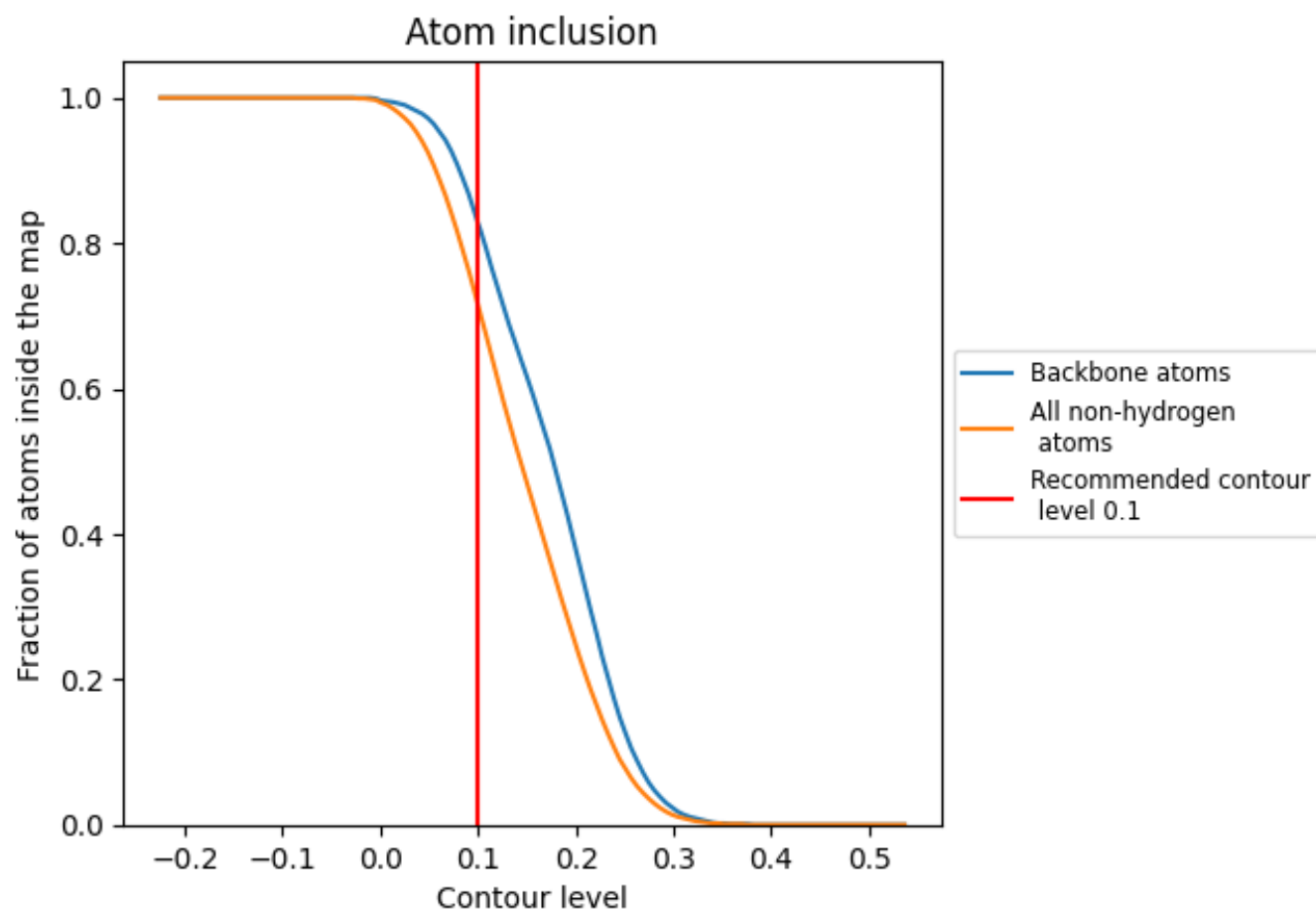
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7160	 0.4690
A0	 0.7170	 0.5000
A1	 0.7090	 0.4740
A2	 0.7980	 0.5020
A3	 0.7970	 0.5290
A4	 0.6250	 0.4470
A5	 0.7530	 0.5120
A6	 0.6130	 0.4720
A8	 0.6890	 0.4970
A9	 0.6540	 0.4950
AA	 0.6660	 0.4290
AB	 0.4570	 0.3200
AC	 0.5140	 0.2850
AD	 0.0000	 -0.0810
AE	 0.7380	 0.5000
AF	 0.7960	 0.5270
AG	 0.0150	 0.0120
AI	 0.7690	 0.5000
AJ	 0.6720	 0.4230
AK	 0.7180	 0.4390
AN	 0.7260	 0.5130
AP	 0.7800	 0.5170
AQ	 0.6800	 0.4990
AR	 0.7580	 0.4910
AT	 0.6780	 0.4690
AU	 0.7590	 0.5150
AV	 0.7700	 0.5100
AW	 0.7480	 0.5180
AX	 0.7410	 0.4970
AY	 0.7080	 0.4620
Ab	 0.7540	 0.4880
Ad	 0.6950	 0.4460
Ae	 0.7780	 0.4990
Af	 0.7370	 0.4950
Ag	 0.7730	 0.4930



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Chain	Atom inclusion	Q-score
Aj	 0.6740	 0.3980
Al	 0.7510	 0.5160
Ao	 0.7590	 0.5150
Ap	 0.7420	 0.5020
At	 0.6940	 0.4710
Av	 0.7350	 0.4970
BA	 0.7640	 0.4990
BB	 0.6440	 0.3940
BC	 0.7870	 0.5060
BD	 0.6970	 0.2880
BE	 0.7350	 0.4730
BF	 0.7840	 0.5120
BG	 0.6850	 0.3960
BH	 0.7380	 0.4660
BI	 0.7880	 0.4930
BJ	 0.6490	 0.4060
BK	 0.4880	 0.3780
BL	 0.7410	 0.4820
BM	 0.7810	 0.5030
BN	 0.6150	 0.3960
BO	 0.6570	 0.4360
BP	 0.6850	 0.4790
BQ	 0.7920	 0.5100
BR	 0.7830	 0.5130
BS	 0.6840	 0.4540
BT	 0.8110	 0.5130
BU	 0.7350	 0.4630
BV	 0.6960	 0.4420
BW	 0.8320	 0.5190
BX	 0.3560	 0.4030
BY	 0.6850	 0.4450
BZ	 0.7240	 0.4600
Ba	 0.8010	 0.5200
Bb	 0.7370	 0.4550
Bc	 0.7090	 0.4810
Bd	 0.6990	 0.4680
Be	 0.7190	 0.5000
Bf	 0.6850	 0.4930
Bg	 0.7200	 0.4870
Bh	 0.4990	 0.4120
UA	 0.6010	 0.3140
UB	 0.6670	 0.4210

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Chain	Atom inclusion	Q-score
UC	 0.3890	 0.3870
UD	 0.4030	 0.3690
UE	 0.6740	 0.4730
UF	 0.7500	 0.4920
UG	 0.5970	 0.4630
UH	 0.7500	 0.5140
UI	 0.4120	 0.4170
UK	 0.7670	 0.4570
UL	 0.6330	 0.4470
UM	 0.1940	 0.3000
UN	 0.1810	 0.3030
UU	 0.4240	 0.3880
UV	 0.6670	 0.4970
UW	 0.2140	 0.2140
UX	 0.6670	 0.4540