



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:37 PM UTC

PDB ID : 9YA0 / pdb_00009ya0
EMDB ID : EMD-72716
Title : Cryo-EM structure of pre-conoid ring 2 (PCR P2 ring)from Toxoplasma gondii
Authors : Zeng, J.; Zhang, R.
Deposited on : 2025-09-15
Resolution : 3.54 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:

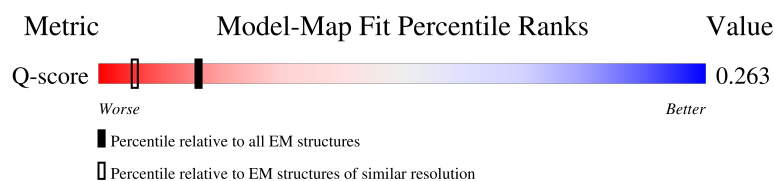
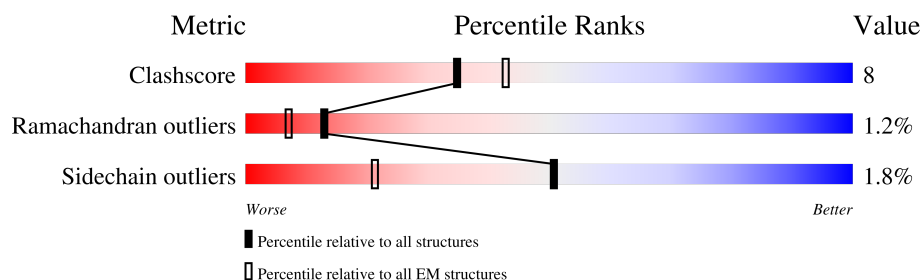
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.54 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.



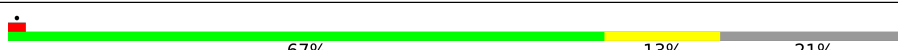
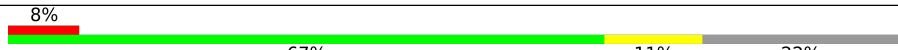
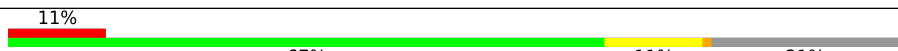
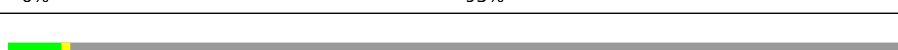
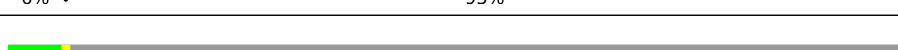
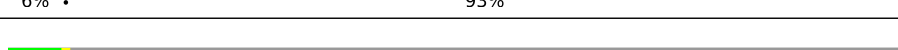
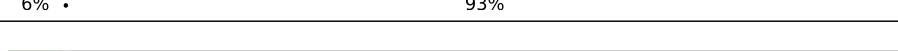
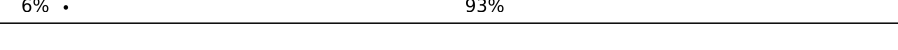
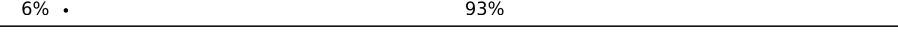
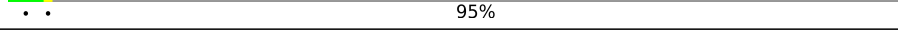
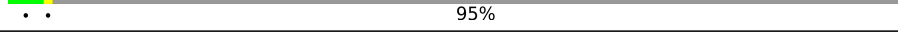
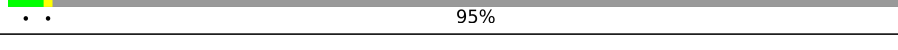
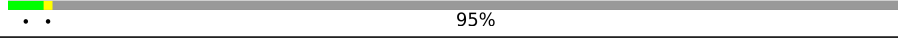
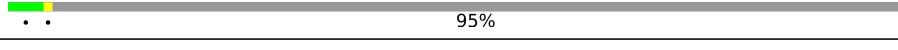
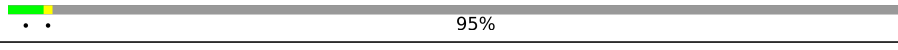
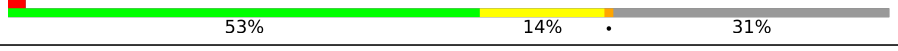
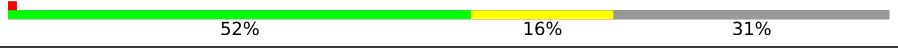
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12891 (3.04 - 4.04)

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	AA	1073	
1	AD	1073	
1	AE	1073	
1	AH	1073	

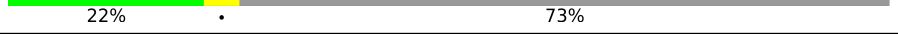
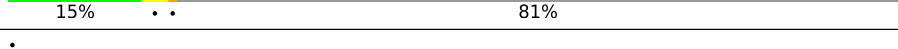
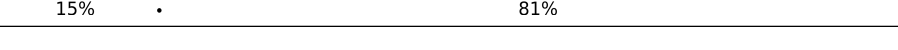
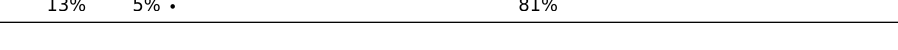
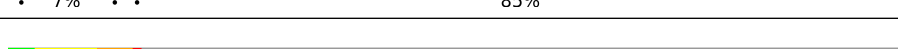
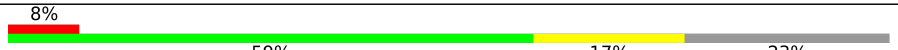
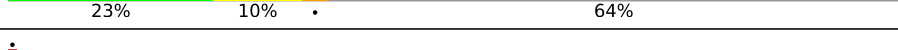
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	AI	1073	
1	AL	1073	
2	AB	603	
2	AC	603	
2	AF	603	
2	AG	603	
2	AJ	603	
2	AK	603	
3	BA	5051	
3	BB	5051	
3	BC	5051	
3	CA	5051	
3	CB	5051	
3	CC	5051	
3	CE	5051	
3	CF	5051	
3	CG	5051	
3	CI	5051	
3	CJ	5051	
3	CL	5051	
4	DA	505	
4	DB	505	
4	DC	505	
4	DD	505	
4	DE	505	

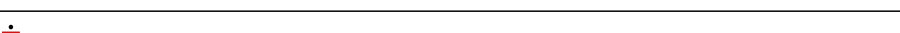
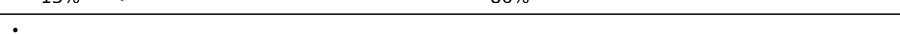
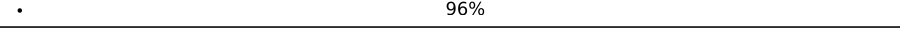
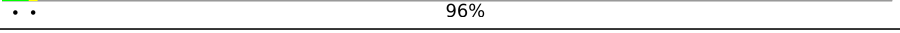
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	DF	505	
5	EA	4956	
5	EB	4956	
5	EC	4956	
6	FA	2777	
6	FB	2777	
6	FC	2777	
6	FD	2777	
6	FE	2777	
6	FF	2777	
7	GA	1019	
7	GC	1019	
7	GE	1019	
7	GG	1019	
7	GI	1019	
7	GK	1019	
8	GB	791	
8	GD	791	
8	GF	791	
8	GH	791	
8	GJ	791	
8	GL	791	
9	HA	1192	
9	HB	1192	
9	HC	1192	

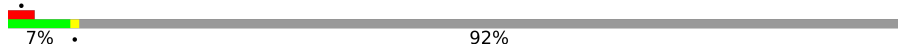
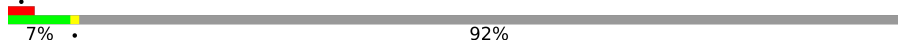
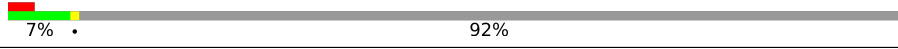
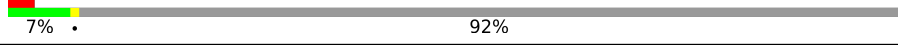
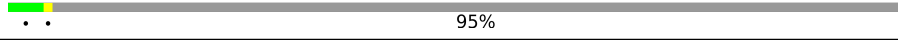
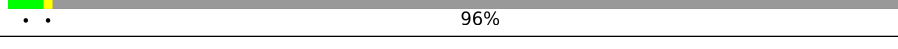
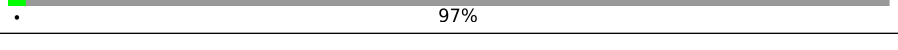
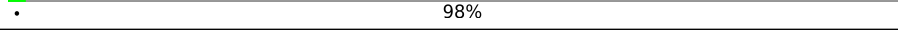
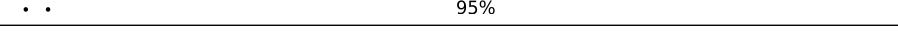
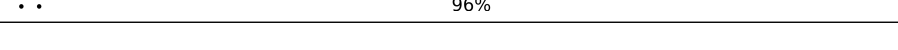
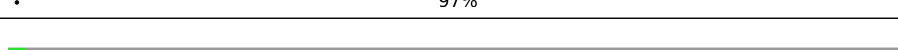
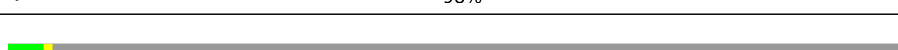
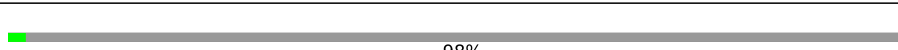
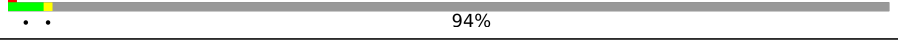
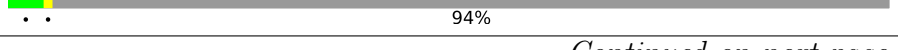
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	HD	1192	 5% 5% 89%
10	IA	1599	 61% 11% 28%
10	IB	1599	 59% 13% 28%
10	IC	1599	 60% 12% 28%
11	JA	2316	 55% 14% 31%
11	JB	2316	 6% 56% 12% 31%
11	JC	2316	 54% 14% 31%
12	KA	728	 45% 18% 36%
12	KB	728	 49% 14% 36%
12	KC	728	 8% 44% 17% 36%
12	KE	728	 19% 48% 13% 39%
12	KF	728	 15% 49% 13% 39%
12	KG	728	 16% 51% 11% 39%
13	LA	1322	 12% 86%
13	LB	1322	 13% 86%
13	LC	1322	 12% 88%
13	LD	1322	 11% 88%
13	LE	1322	 9% 89%
13	LF	1322	 10% 89%
13	LG	1322	 96%
13	LH	1322	 96%
13	LI	1322	 11% 86%
13	LJ	1322	 11% 86%
13	LK	1322	 11% 88%
13	LL	1322	 11% 88%

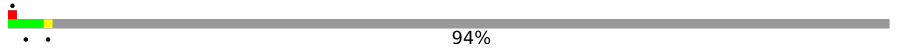
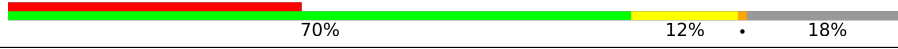
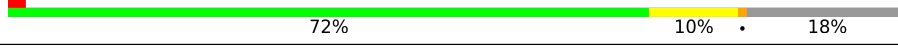
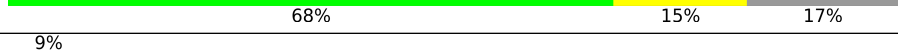
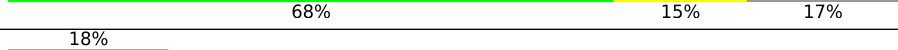
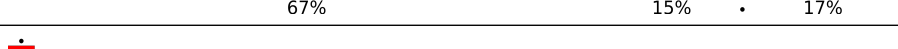
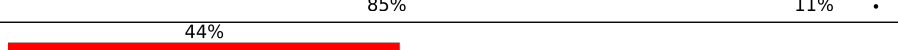
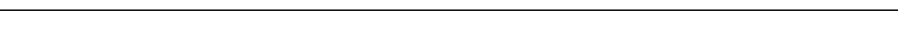
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
13	LM	1322	 7% 92%
13	LN	1322	 7% 92%
13	LO	1322	 7% 92%
13	LP	1322	 7% 92%
14	MA	2736	 95%
14	MB	2736	 96%
14	MC	2736	 97%
14	MD	2736	 98%
14	ME	2736	 95%
14	MF	2736	 96%
14	MG	2736	 97%
14	MH	2736	 98%
14	MI	2736	 95%
14	MJ	2736	 96%
14	MK	2736	 97%
14	ML	2736	 98%
15	NA	2484	 26% 10% 64%
15	NB	2484	 24% 27% 9% 64%
15	NC	2484	 25% 10% 64%
15	ND	2484	 20% 28% 8% 64%
16	OA	2333	 16% 81%
16	OB	2333	 16% 81%
16	OC	2333	 16% 81%
17	PA	1822	 94%
17	PB	1822	 94%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
17	PC	1822	 94%
18	QA	172	 72% 10% 18%
18	QB	172	 33% 70% 12% 18%
18	QC	172	 72% 10% 18%
18	QD	172	 69% 13% 18%
19	RA	179	 8% 59% 23% 17%
19	RB	179	 22% 68% 15% 17%
19	RC	179	 9% 68% 15% 17%
19	RD	179	 18% 67% 15% 17%
20	SA	149	 85% 11%
20	SB	149	 44% 83% 12%
20	SC	149	 6% 83% 13%
20	SD	149	 5% 85% 11%

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 415078 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 PCR5, TGME49_242320.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	829	Total	C	N	O	S	0	0
			6540	4168	1127	1203	42		
1	AD	865	Total	C	N	O	S	0	0
			6810	4327	1180	1262	41		
1	AE	829	Total	C	N	O	S	0	0
			6540	4168	1127	1203	42		
1	AH	865	Total	C	N	O	S	0	0
			6810	4327	1180	1262	41		
1	AI	829	Total	C	N	O	S	0	0
			6540	4168	1127	1203	42		
1	AL	865	Total	C	N	O	S	0	0
			6810	4327	1180	1262	41		

- Molecule 2 is a protein called PCR4, TGME49_201220.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	473	Total	C	N	O	S	0	0
			3821	2396	699	696	30		
2	AC	479	Total	C	N	O	S	0	0
			3847	2418	699	700	30		
2	AF	473	Total	C	N	O	S	0	0
			3821	2396	699	696	30		
2	AG	479	Total	C	N	O	S	0	0
			3847	2418	699	700	30		
2	AJ	473	Total	C	N	O	S	0	0
			3815	2393	696	696	30		
2	AK	479	Total	C	N	O	S	0	0
			3847	2418	699	700	30		

- Molecule 3 is a protein called Formin 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BA	346	Total	C	N	O	S	0	0
			2727	1731	482	500	14		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BB	346	Total	C	N	O	S	0	0
			2727	1731	482	500	14		
3	BC	346	Total	C	N	O	S	0	0
			2727	1731	482	500	14		
3	CA	344	Total	C	N	O	S	0	0
			2712	1720	480	498	14		
3	CB	344	Total	C	N	O	S	0	0
			2712	1720	480	498	14		
3	CC	344	Total	C	N	O	S	0	0
			2712	1720	480	498	14		
3	CE	242	Total	C	N	O	S	0	0
			1874	1207	318	342	7		
3	CF	242	Total	C	N	O	S	0	0
			1874	1207	318	342	7		
3	CG	242	Total	C	N	O	S	0	0
			1874	1207	318	342	7		
3	CI	259	Total	C	N	O	S	0	0
			2012	1293	346	365	8		
3	CJ	259	Total	C	N	O	S	0	0
			2012	1293	346	365	8		
3	CL	259	Total	C	N	O	S	0	0
			2012	1293	346	365	8		

- Molecule 4 is a protein called PCR11, TGME49_209490.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DA	347	Total	C	N	O	S	0	0
			2753	1754	487	496	16		
4	DB	347	Total	C	N	O	S	0	0
			2753	1754	487	496	16		
4	DC	347	Total	C	N	O	S	0	0
			2753	1754	487	496	16		
4	DD	332	Total	C	N	O	S	0	0
			2631	1674	474	468	15		
4	DE	332	Total	C	N	O	S	0	0
			2631	1674	474	468	15		
4	DF	332	Total	C	N	O	S	0	0
			2631	1674	474	468	15		

- Molecule 5 is a protein called CGP, TGME49_240380.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	EA	1349	Total	C	N	O	S	0	0
			10670	6808	1899	1905	58		
5	EB	1349	Total	C	N	O	S	0	0
			10670	6808	1899	1905	58		
5	EC	1349	Total	C	N	O	S	0	0
			10666	6805	1898	1905	58		

- Molecule 6 is a protein called FLM1, TGME49_271780.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	FA	531	Total	C	N	O	S	0	0
			4210	2640	742	802	26		
6	FB	531	Total	C	N	O	S	0	0
			4210	2640	742	802	26		
6	FC	531	Total	C	N	O	S	0	0
			4210	2640	742	802	26		
6	FD	423	Total	C	N	O	S	0	0
			3255	2086	573	580	16		
6	FE	423	Total	C	N	O	S	0	0
			3261	2089	576	580	16		
6	FF	413	Total	C	N	O	S	0	0
			3182	2038	561	567	16		

- Molecule 7 is a protein called Transport protein Sec24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	GA	837	Total	C	N	O	S	0	0
			6320	3979	1124	1183	34		
7	GC	781	Total	C	N	O	S	0	0
			5960	3767	1055	1105	33		
7	GE	781	Total	C	N	O	S	0	0
			5960	3767	1055	1105	33		
7	GG	837	Total	C	N	O	S	0	0
			6320	3979	1124	1183	34		
7	GI	781	Total	C	N	O	S	0	0
			5960	3767	1055	1105	33		
7	GK	837	Total	C	N	O	S	0	0
			6320	3979	1124	1183	34		

- Molecule 8 is a protein called Protein transport protein SEC23.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	GB	758	Total	C	N	O	S	0	0
			5949	3791	1016	1101	41		
8	GD	758	Total	C	N	O	S	0	0
			5949	3791	1016	1101	41		
8	GF	791	Total	C	N	O	S	0	0
			6155	3916	1054	1142	43		
8	GH	738	Total	C	N	O	S	0	0
			5781	3687	984	1070	40		
8	GJ	791	Total	C	N	O	S	0	0
			6155	3916	1054	1142	43		
8	GL	791	Total	C	N	O	S	0	0
			6155	3916	1054	1142	43		

- Molecule 9 is a protein called FLM2, TGME49_285990.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	HA	432	Total	C	N	O	S	0	0
			3361	2105	589	657	10		
9	HB	432	Total	C	N	O	S	0	0
			3361	2105	589	657	10		
9	HC	296	Total	C	N	O	S	0	0
			2288	1435	403	444	6		
9	HD	136	Total	C	N	O	S	0	0
			1073	670	186	213	4		

- Molecule 10 is a protein called PCR12, TGME49_292170.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	IA	1156	Total	C	N	O	S	0	0
			9113	5757	1663	1633	60		
10	IB	1156	Total	C	N	O	S	0	0
			9113	5757	1663	1633	60		
10	IC	1156	Total	C	N	O	S	0	0
			9113	5757	1663	1633	60		

- Molecule 11 is a protein called PCR10, TGME49_298010.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	JA	1593	Total	C	N	O	S	0	0
			12718	8089	2293	2271	65		
11	JB	1593	Total	C	N	O	S	0	0
			12718	8089	2293	2271	65		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
11	JC	1593	Total	C	N	O	S	0	0
			12718	8089	2293	2271	65		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JA	2314	VAL	-	expression tag	UNP S8FEI7
JA	2315	SER	-	expression tag	UNP S8FEI7
JA	2316	SER	-	expression tag	UNP S8FEI7
JB	2314	VAL	-	expression tag	UNP S8FEI7
JB	2315	SER	-	expression tag	UNP S8FEI7
JB	2316	SER	-	expression tag	UNP S8FEI7
JC	2314	VAL	-	expression tag	UNP S8FEI7
JC	2315	SER	-	expression tag	UNP S8FEI7
JC	2316	SER	-	expression tag	UNP S8FEI7

- Molecule 12 is a protein called PCR14, TGME49_311880.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	KA	464	Total	C	N	O	S	0	0
			3674	2356	645	653	20		
12	KB	464	Total	C	N	O	S	0	0
			3674	2356	645	653	20		
12	KC	464	Total	C	N	O	S	0	0
			3668	2353	642	653	20		
12	KE	447	Total	C	N	O	S	0	0
			3544	2270	626	629	19		
12	KF	447	Total	C	N	O	S	0	0
			3544	2270	626	629	19		
12	KG	447	Total	C	N	O	S	0	0
			3544	2270	626	629	19		

- Molecule 13 is a protein called ICAP16, TGME49_202120.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LA	190	Total	C	N	O	S	0	0
			1516	925	286	299	6		
13	LB	191	Total	C	N	O	S	0	0
			1529	934	289	300	6		
13	LC	162	Total	C	N	O	S	0	0
			1312	802	245	259	6		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LD	161	Total	C	N	O	S	0	0
			1304	801	240	257	6		
13	LE	149	Total	C	N	O	S	0	0
			1190	727	227	231	5		
13	LF	150	Total	C	N	O	S	0	0
			1198	732	227	233	6		
13	LG	57	Total	C	N	O	S	0	0
			461	287	83	88	3		
13	LH	55	Total	C	N	O	S	0	0
			448	280	80	85	3		
13	LI	190	Total	C	N	O	S	0	0
			1516	925	286	299	6		
13	LJ	191	Total	C	N	O	S	0	0
			1529	934	289	300	6		
13	LK	163	Total	C	N	O	S	0	0
			1320	808	246	260	6		
13	LL	161	Total	C	N	O	S	0	0
			1304	801	240	257	6		
13	LM	106	Total	C	N	O	S	0	0
			859	521	163	172	3		
13	LN	106	Total	C	N	O	S	0	0
			856	521	160	172	3		
13	LO	105	Total	C	N	O	S	0	0
			841	508	159	171	3		
13	LP	110	Total	C	N	O	S	0	0
			882	535	167	177	3		

- Molecule 14 is a protein called PCR12, TGME49_219070.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	MA	142	Total	C	N	O	S	0	0
			1132	694	210	222	6		
14	MB	120	Total	C	N	O	S	0	0
			976	594	185	192	5		
14	MC	75	Total	C	N	O		0	0
			594	365	114	115			
14	MD	65	Total	C	N	O		0	0
			521	319	103	99			
14	ME	142	Total	C	N	O	S	0	0
			1132	694	210	222	6		
14	MF	120	Total	C	N	O	S	0	0
			976	594	185	192	5		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
14	MG	75	Total	C	N	O		0	0
			594	365	114	115			
14	MH	65	Total	C	N	O		0	0
			521	319	103	99			
14	MI	142	Total	C	N	O	S	0	0
			1132	694	210	222	6		
14	MJ	120	Total	C	N	O	S	0	0
			976	594	185	192	5		
14	MK	75	Total	C	N	O		0	0
			594	365	114	115			
14	ML	65	Total	C	N	O		0	0
			521	319	103	99			

There are 204 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
MA	999	GLU	-	insertion	UNP S8EN17
MA	1000	LYS	-	insertion	UNP S8EN17
MA	1001	SER	-	insertion	UNP S8EN17
MA	1002	GLY	-	insertion	UNP S8EN17
MA	1003	THR	-	insertion	UNP S8EN17
MA	1004	ALA	-	insertion	UNP S8EN17
MA	1005	ALA	-	insertion	UNP S8EN17
MA	1006	SER	-	insertion	UNP S8EN17
MA	1007	HIS	-	insertion	UNP S8EN17
MA	1008	ILE	-	insertion	UNP S8EN17
MA	1009	ASP	-	insertion	UNP S8EN17
MA	1010	GLU	-	insertion	UNP S8EN17
MA	1011	GLU	-	insertion	UNP S8EN17
MA	1012	ASP	-	insertion	UNP S8EN17
MA	1013	SER	-	insertion	UNP S8EN17
MA	1014	ARG	-	insertion	UNP S8EN17
MA	1015	SER	ALA	conflict	UNP S8EN17
MB	999	GLU	-	insertion	UNP S8EN17
MB	1000	LYS	-	insertion	UNP S8EN17
MB	1001	SER	-	insertion	UNP S8EN17
MB	1002	GLY	-	insertion	UNP S8EN17
MB	1003	THR	-	insertion	UNP S8EN17
MB	1004	ALA	-	insertion	UNP S8EN17
MB	1005	ALA	-	insertion	UNP S8EN17
MB	1006	SER	-	insertion	UNP S8EN17
MB	1007	HIS	-	insertion	UNP S8EN17
MB	1008	ILE	-	insertion	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
MB	1009	ASP	-	insertion	UNP S8EN17
MB	1010	GLU	-	insertion	UNP S8EN17
MB	1011	GLU	-	insertion	UNP S8EN17
MB	1012	ASP	-	insertion	UNP S8EN17
MB	1013	SER	-	insertion	UNP S8EN17
MB	1014	ARG	-	insertion	UNP S8EN17
MB	1015	SER	ALA	conflict	UNP S8EN17
MC	999	GLU	-	insertion	UNP S8EN17
MC	1000	LYS	-	insertion	UNP S8EN17
MC	1001	SER	-	insertion	UNP S8EN17
MC	1002	GLY	-	insertion	UNP S8EN17
MC	1003	THR	-	insertion	UNP S8EN17
MC	1004	ALA	-	insertion	UNP S8EN17
MC	1005	ALA	-	insertion	UNP S8EN17
MC	1006	SER	-	insertion	UNP S8EN17
MC	1007	HIS	-	insertion	UNP S8EN17
MC	1008	ILE	-	insertion	UNP S8EN17
MC	1009	ASP	-	insertion	UNP S8EN17
MC	1010	GLU	-	insertion	UNP S8EN17
MC	1011	GLU	-	insertion	UNP S8EN17
MC	1012	ASP	-	insertion	UNP S8EN17
MC	1013	SER	-	insertion	UNP S8EN17
MC	1014	ARG	-	insertion	UNP S8EN17
MC	1015	SER	ALA	conflict	UNP S8EN17
MD	999	GLU	-	insertion	UNP S8EN17
MD	1000	LYS	-	insertion	UNP S8EN17
MD	1001	SER	-	insertion	UNP S8EN17
MD	1002	GLY	-	insertion	UNP S8EN17
MD	1003	THR	-	insertion	UNP S8EN17
MD	1004	ALA	-	insertion	UNP S8EN17
MD	1005	ALA	-	insertion	UNP S8EN17
MD	1006	SER	-	insertion	UNP S8EN17
MD	1007	HIS	-	insertion	UNP S8EN17
MD	1008	ILE	-	insertion	UNP S8EN17
MD	1009	ASP	-	insertion	UNP S8EN17
MD	1010	GLU	-	insertion	UNP S8EN17
MD	1011	GLU	-	insertion	UNP S8EN17
MD	1012	ASP	-	insertion	UNP S8EN17
MD	1013	SER	-	insertion	UNP S8EN17
MD	1014	ARG	-	insertion	UNP S8EN17
MD	1015	SER	ALA	conflict	UNP S8EN17
ME	999	GLU	-	insertion	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
ME	1000	LYS	-	insertion	UNP S8EN17
ME	1001	SER	-	insertion	UNP S8EN17
ME	1002	GLY	-	insertion	UNP S8EN17
ME	1003	THR	-	insertion	UNP S8EN17
ME	1004	ALA	-	insertion	UNP S8EN17
ME	1005	ALA	-	insertion	UNP S8EN17
ME	1006	SER	-	insertion	UNP S8EN17
ME	1007	HIS	-	insertion	UNP S8EN17
ME	1008	ILE	-	insertion	UNP S8EN17
ME	1009	ASP	-	insertion	UNP S8EN17
ME	1010	GLU	-	insertion	UNP S8EN17
ME	1011	GLU	-	insertion	UNP S8EN17
ME	1012	ASP	-	insertion	UNP S8EN17
ME	1013	SER	-	insertion	UNP S8EN17
ME	1014	ARG	-	insertion	UNP S8EN17
ME	1015	SER	ALA	conflict	UNP S8EN17
MF	999	GLU	-	insertion	UNP S8EN17
MF	1000	LYS	-	insertion	UNP S8EN17
MF	1001	SER	-	insertion	UNP S8EN17
MF	1002	GLY	-	insertion	UNP S8EN17
MF	1003	THR	-	insertion	UNP S8EN17
MF	1004	ALA	-	insertion	UNP S8EN17
MF	1005	ALA	-	insertion	UNP S8EN17
MF	1006	SER	-	insertion	UNP S8EN17
MF	1007	HIS	-	insertion	UNP S8EN17
MF	1008	ILE	-	insertion	UNP S8EN17
MF	1009	ASP	-	insertion	UNP S8EN17
MF	1010	GLU	-	insertion	UNP S8EN17
MF	1011	GLU	-	insertion	UNP S8EN17
MF	1012	ASP	-	insertion	UNP S8EN17
MF	1013	SER	-	insertion	UNP S8EN17
MF	1014	ARG	-	insertion	UNP S8EN17
MF	1015	SER	ALA	conflict	UNP S8EN17
MG	999	GLU	-	insertion	UNP S8EN17
MG	1000	LYS	-	insertion	UNP S8EN17
MG	1001	SER	-	insertion	UNP S8EN17
MG	1002	GLY	-	insertion	UNP S8EN17
MG	1003	THR	-	insertion	UNP S8EN17
MG	1004	ALA	-	insertion	UNP S8EN17
MG	1005	ALA	-	insertion	UNP S8EN17
MG	1006	SER	-	insertion	UNP S8EN17
MG	1007	HIS	-	insertion	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
MG	1008	ILE	-	insertion	UNP S8EN17
MG	1009	ASP	-	insertion	UNP S8EN17
MG	1010	GLU	-	insertion	UNP S8EN17
MG	1011	GLU	-	insertion	UNP S8EN17
MG	1012	ASP	-	insertion	UNP S8EN17
MG	1013	SER	-	insertion	UNP S8EN17
MG	1014	ARG	-	insertion	UNP S8EN17
MG	1015	SER	ALA	conflict	UNP S8EN17
MH	999	GLU	-	insertion	UNP S8EN17
MH	1000	LYS	-	insertion	UNP S8EN17
MH	1001	SER	-	insertion	UNP S8EN17
MH	1002	GLY	-	insertion	UNP S8EN17
MH	1003	THR	-	insertion	UNP S8EN17
MH	1004	ALA	-	insertion	UNP S8EN17
MH	1005	ALA	-	insertion	UNP S8EN17
MH	1006	SER	-	insertion	UNP S8EN17
MH	1007	HIS	-	insertion	UNP S8EN17
MH	1008	ILE	-	insertion	UNP S8EN17
MH	1009	ASP	-	insertion	UNP S8EN17
MH	1010	GLU	-	insertion	UNP S8EN17
MH	1011	GLU	-	insertion	UNP S8EN17
MH	1012	ASP	-	insertion	UNP S8EN17
MH	1013	SER	-	insertion	UNP S8EN17
MH	1014	ARG	-	insertion	UNP S8EN17
MH	1015	SER	ALA	conflict	UNP S8EN17
MI	999	GLU	-	insertion	UNP S8EN17
MI	1000	LYS	-	insertion	UNP S8EN17
MI	1001	SER	-	insertion	UNP S8EN17
MI	1002	GLY	-	insertion	UNP S8EN17
MI	1003	THR	-	insertion	UNP S8EN17
MI	1004	ALA	-	insertion	UNP S8EN17
MI	1005	ALA	-	insertion	UNP S8EN17
MI	1006	SER	-	insertion	UNP S8EN17
MI	1007	HIS	-	insertion	UNP S8EN17
MI	1008	ILE	-	insertion	UNP S8EN17
MI	1009	ASP	-	insertion	UNP S8EN17
MI	1010	GLU	-	insertion	UNP S8EN17
MI	1011	GLU	-	insertion	UNP S8EN17
MI	1012	ASP	-	insertion	UNP S8EN17
MI	1013	SER	-	insertion	UNP S8EN17
MI	1014	ARG	-	insertion	UNP S8EN17
MI	1015	SER	ALA	conflict	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
MJ	999	GLU	-	insertion	UNP S8EN17
MJ	1000	LYS	-	insertion	UNP S8EN17
MJ	1001	SER	-	insertion	UNP S8EN17
MJ	1002	GLY	-	insertion	UNP S8EN17
MJ	1003	THR	-	insertion	UNP S8EN17
MJ	1004	ALA	-	insertion	UNP S8EN17
MJ	1005	ALA	-	insertion	UNP S8EN17
MJ	1006	SER	-	insertion	UNP S8EN17
MJ	1007	HIS	-	insertion	UNP S8EN17
MJ	1008	ILE	-	insertion	UNP S8EN17
MJ	1009	ASP	-	insertion	UNP S8EN17
MJ	1010	GLU	-	insertion	UNP S8EN17
MJ	1011	GLU	-	insertion	UNP S8EN17
MJ	1012	ASP	-	insertion	UNP S8EN17
MJ	1013	SER	-	insertion	UNP S8EN17
MJ	1014	ARG	-	insertion	UNP S8EN17
MJ	1015	SER	ALA	conflict	UNP S8EN17
MK	999	GLU	-	insertion	UNP S8EN17
MK	1000	LYS	-	insertion	UNP S8EN17
MK	1001	SER	-	insertion	UNP S8EN17
MK	1002	GLY	-	insertion	UNP S8EN17
MK	1003	THR	-	insertion	UNP S8EN17
MK	1004	ALA	-	insertion	UNP S8EN17
MK	1005	ALA	-	insertion	UNP S8EN17
MK	1006	SER	-	insertion	UNP S8EN17
MK	1007	HIS	-	insertion	UNP S8EN17
MK	1008	ILE	-	insertion	UNP S8EN17
MK	1009	ASP	-	insertion	UNP S8EN17
MK	1010	GLU	-	insertion	UNP S8EN17
MK	1011	GLU	-	insertion	UNP S8EN17
MK	1012	ASP	-	insertion	UNP S8EN17
MK	1013	SER	-	insertion	UNP S8EN17
MK	1014	ARG	-	insertion	UNP S8EN17
MK	1015	SER	ALA	conflict	UNP S8EN17
ML	999	GLU	-	insertion	UNP S8EN17
ML	1000	LYS	-	insertion	UNP S8EN17
ML	1001	SER	-	insertion	UNP S8EN17
ML	1002	GLY	-	insertion	UNP S8EN17
ML	1003	THR	-	insertion	UNP S8EN17
ML	1004	ALA	-	insertion	UNP S8EN17
ML	1005	ALA	-	insertion	UNP S8EN17
ML	1006	SER	-	insertion	UNP S8EN17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
ML	1007	HIS	-	insertion	UNP S8EN17
ML	1008	ILE	-	insertion	UNP S8EN17
ML	1009	ASP	-	insertion	UNP S8EN17
ML	1010	GLU	-	insertion	UNP S8EN17
ML	1011	GLU	-	insertion	UNP S8EN17
ML	1012	ASP	-	insertion	UNP S8EN17
ML	1013	SER	-	insertion	UNP S8EN17
ML	1014	ARG	-	insertion	UNP S8EN17
ML	1015	SER	ALA	conflict	UNP S8EN17

- Molecule 15 is a protein called myosin L, TGME49_291020.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	NA	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		
15	NB	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		
15	NC	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		
15	ND	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		

- Molecule 16 is a protein called PCR13, TGME49_284620.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	OA	448	Total	C	N	O	S	0	0
			3510	2191	650	661	8		
16	OB	448	Total	C	N	O	S	0	0
			3510	2191	650	661	8		
16	OC	448	Total	C	N	O	S	0	0
			3510	2191	650	661	8		

- Molecule 17 is a protein called PCR15, TGME49_232560.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	PA	101	Total	C	N	O	S	0	0
			807	507	142	156	2		
17	PB	101	Total	C	N	O	S	0	0
			807	507	142	156	2		
17	PC	101	Total	C	N	O	S	0	0
			807	507	142	156	2		

- Molecule 18 is a protein called MLC4, TGME49_294390.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	QA	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		
18	QB	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		
18	QC	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		
18	QD	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		

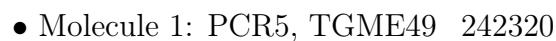
- Molecule 19 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	RA	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		
19	RB	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		
19	RC	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		
19	RD	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		

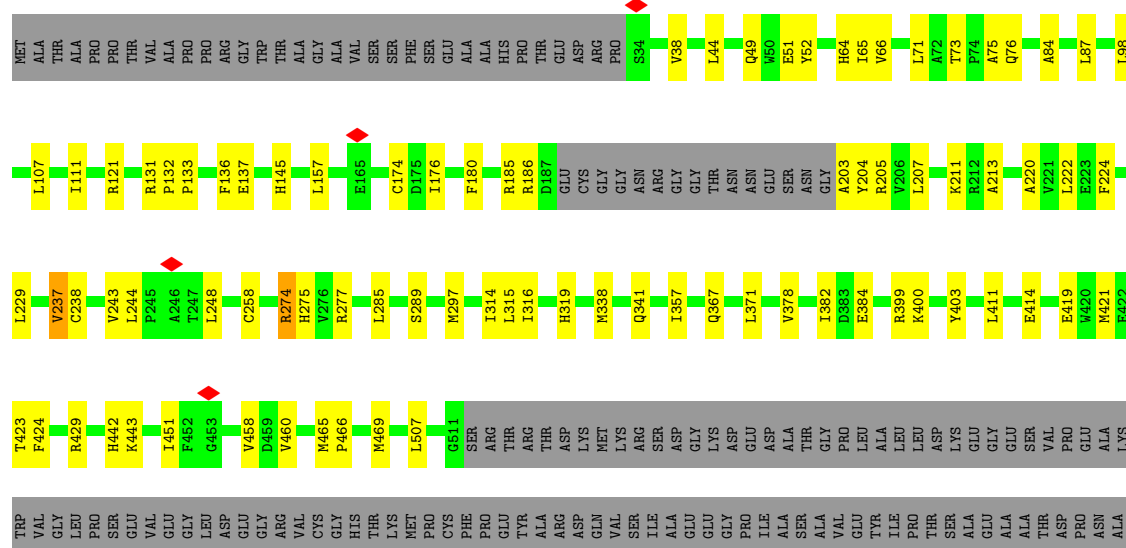
- Molecule 20 is a protein called Calmodulin.

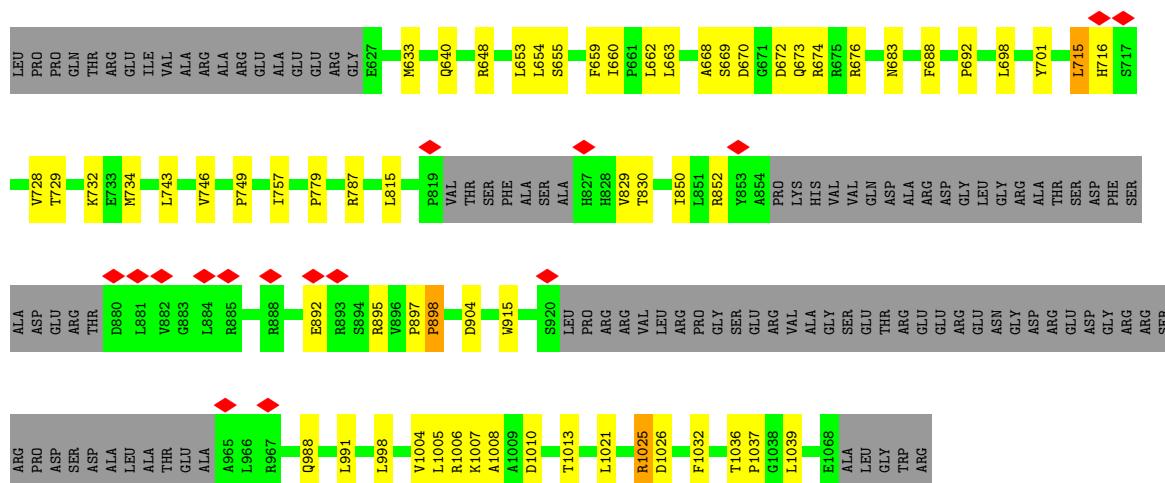
Mol	Chain	Residues	Atoms					AltConf	Trace
20	SA	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		
20	SB	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		
20	SC	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		
20	SD	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		

App Type	Percentage
Shopping app	70%
Social media app	10%
Productivity app	19%



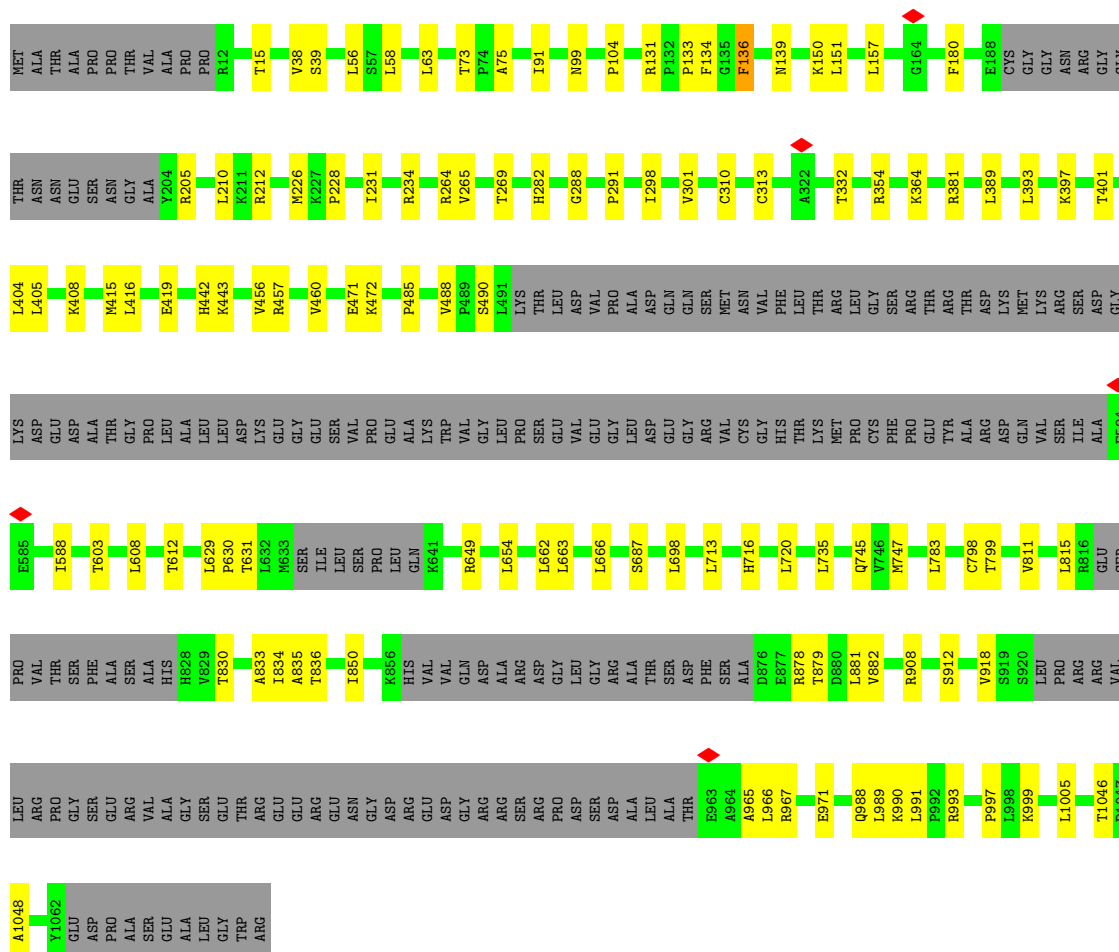
Frequency	Percentage
Daily	64%
Weekly	13%
Monthly	23%





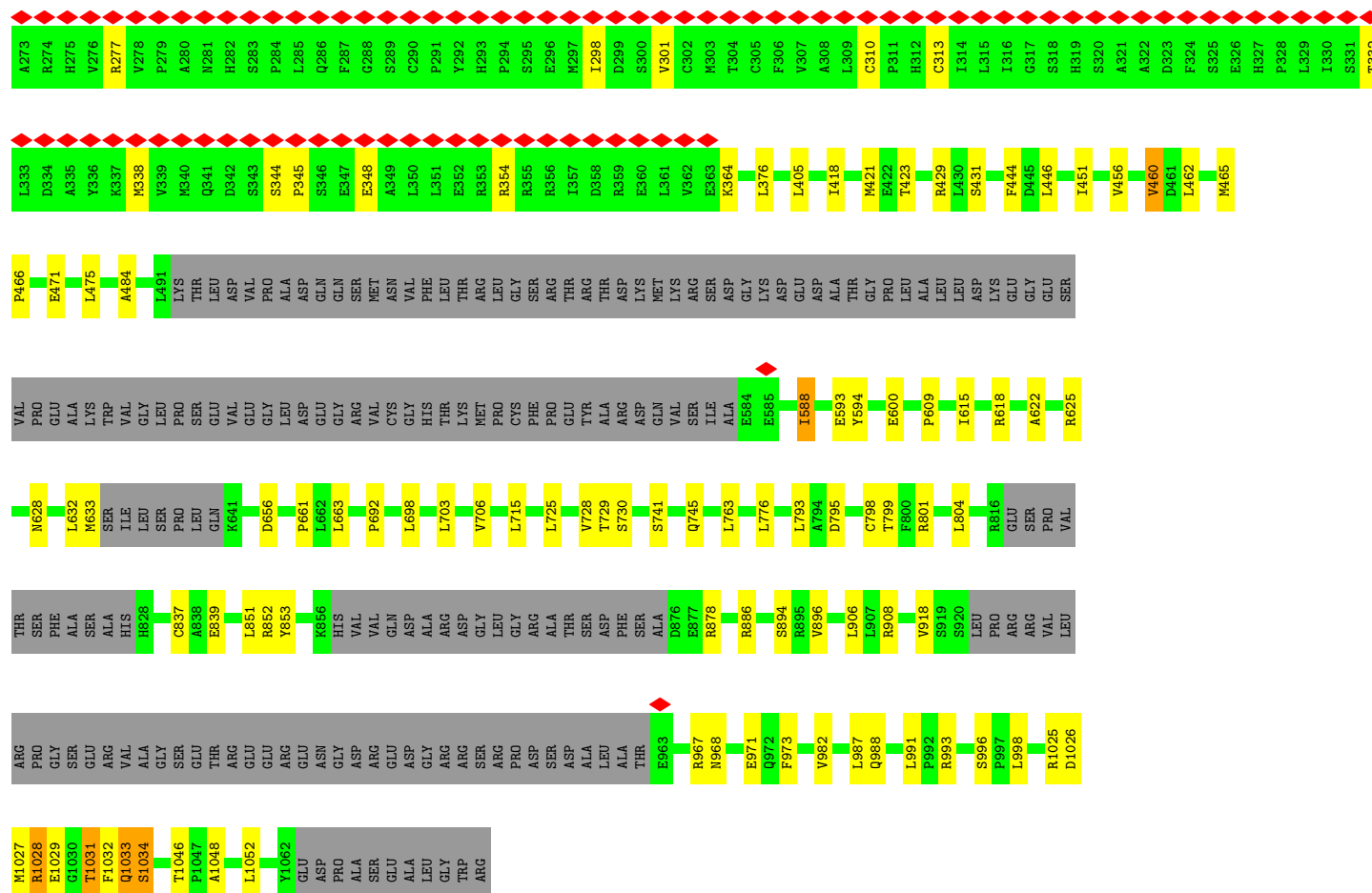
• Molecule 1: PCR5, TGME49_242320

Chain AH: 70% 10% 19%



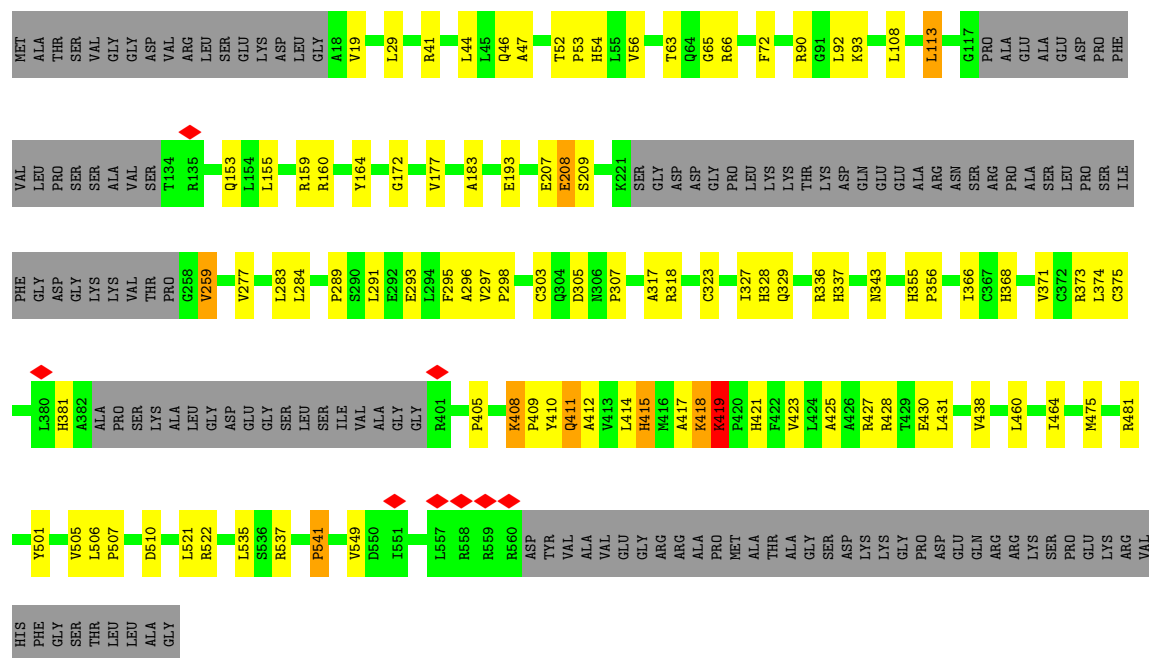
• Molecule 1: PCR5, TGME49_242320

Chain AI: 65% 12% 23%

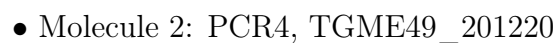
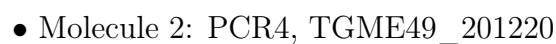


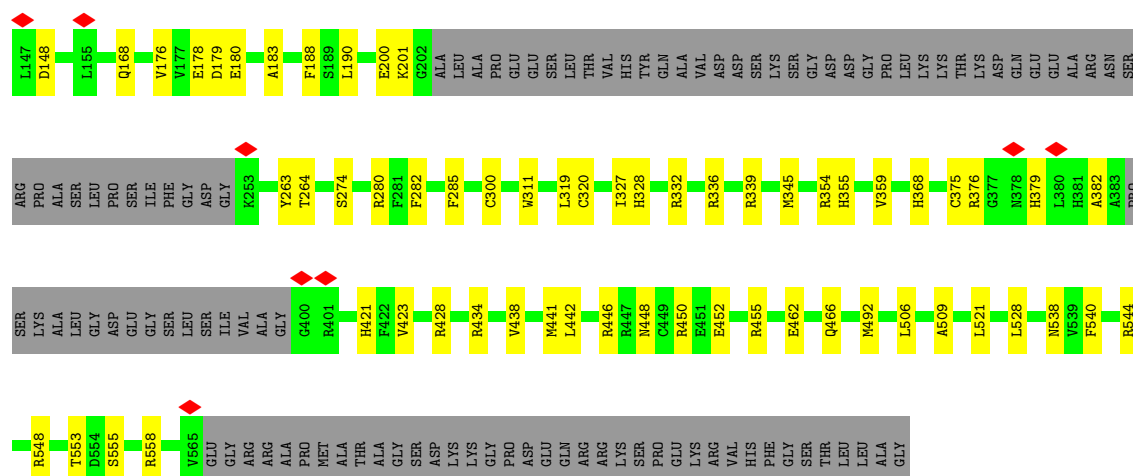
• Molecule 2: PCR4, TGME49_201220

Chain AB: 62% 15% 22%

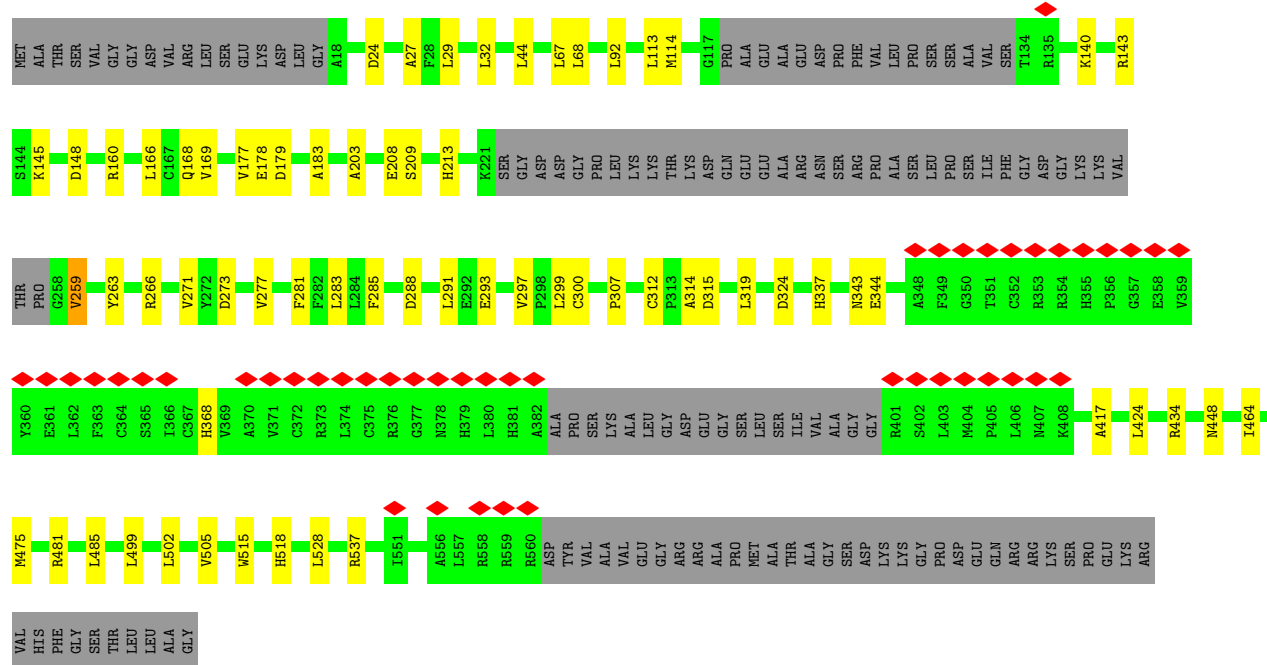


Chain AC:

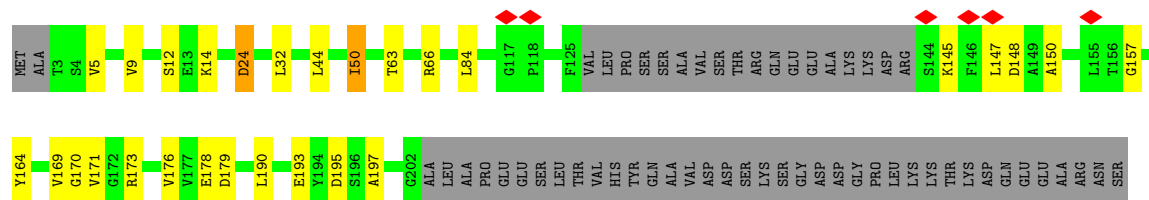


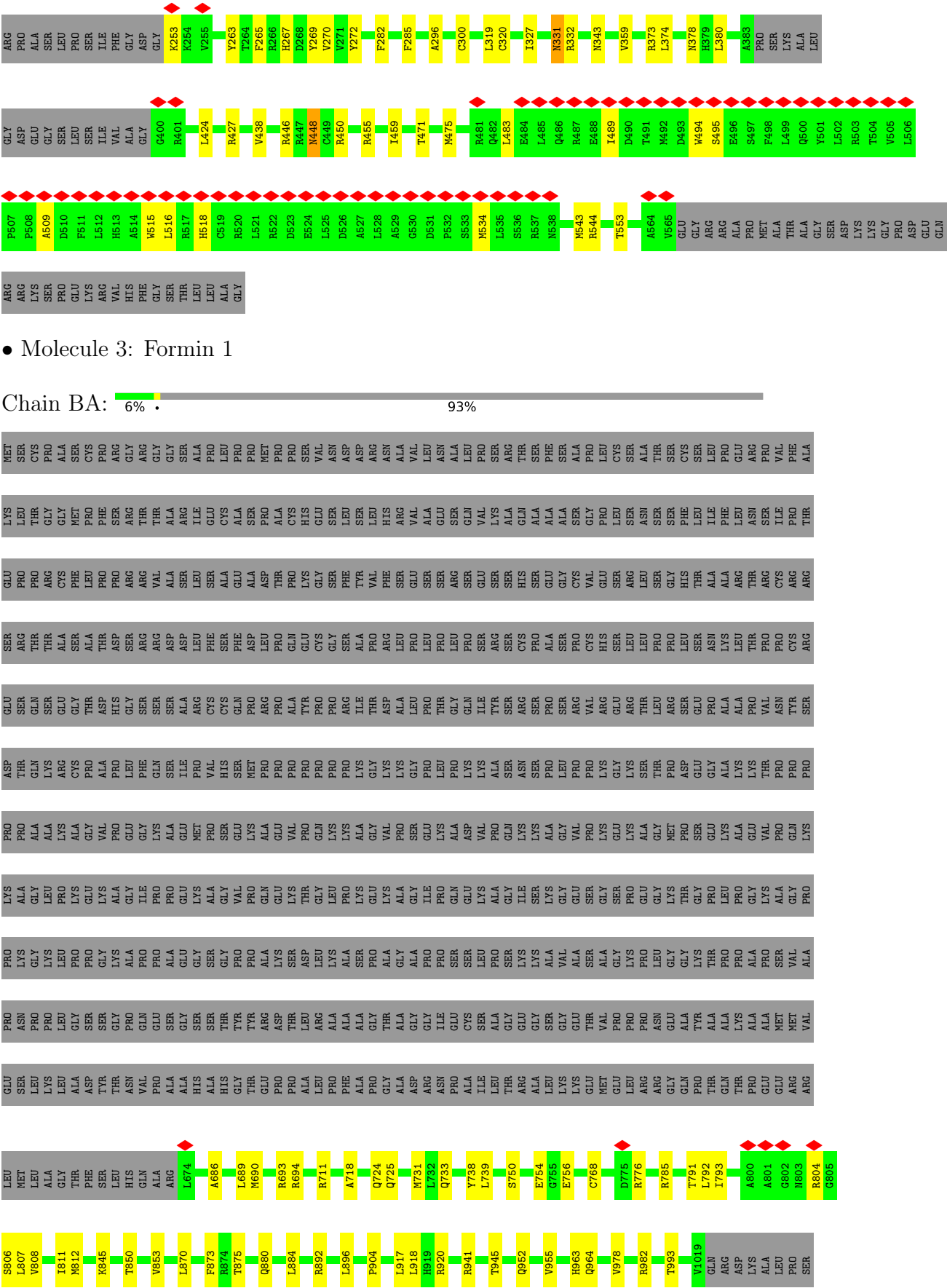


• Molecule 2: PCR4, TGME49_201220



• Molecule 2: PCR4, TGME49_201220





• Molecule 3: Formin 1

Chain BA: 6% 93%



































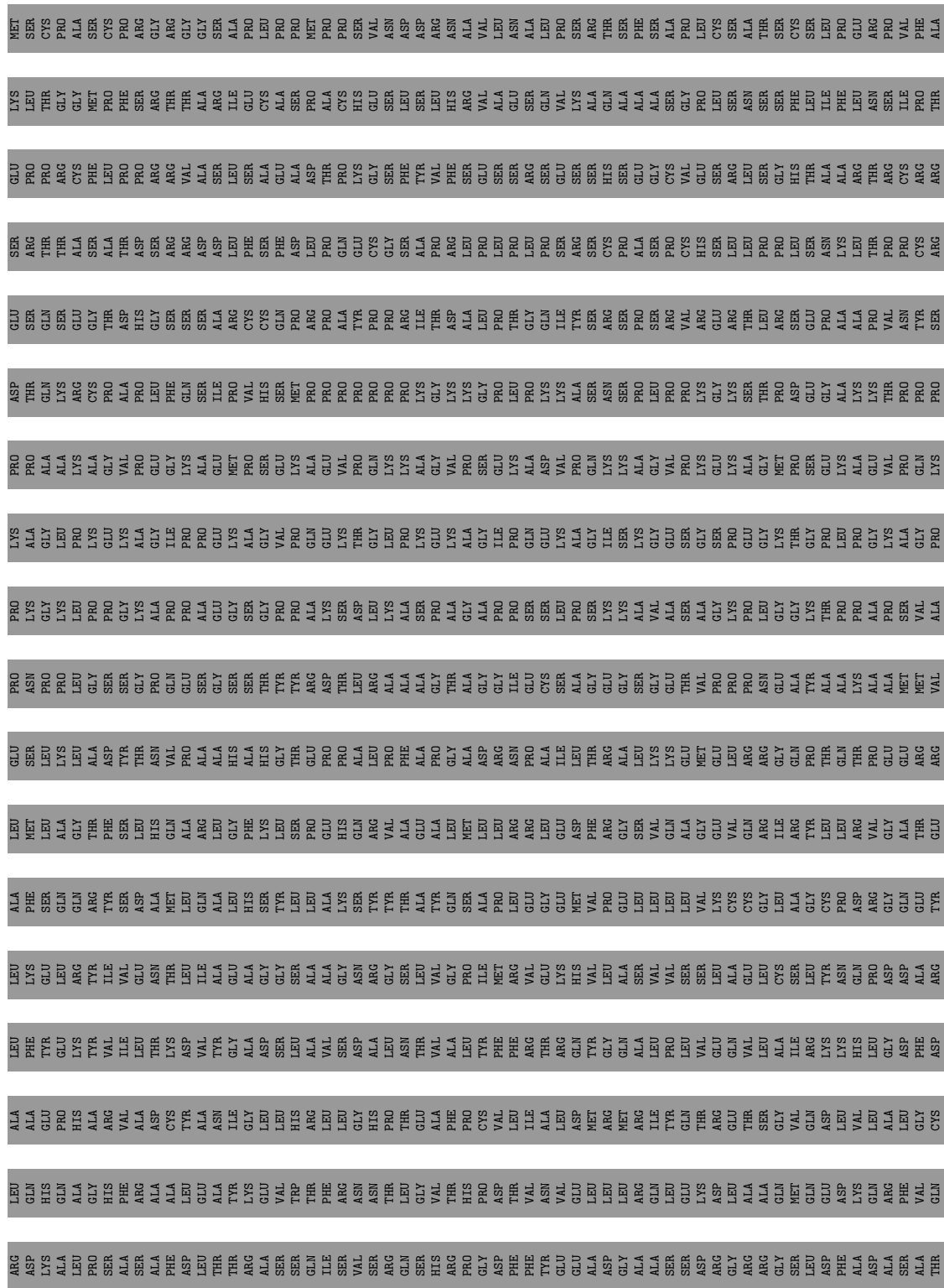
















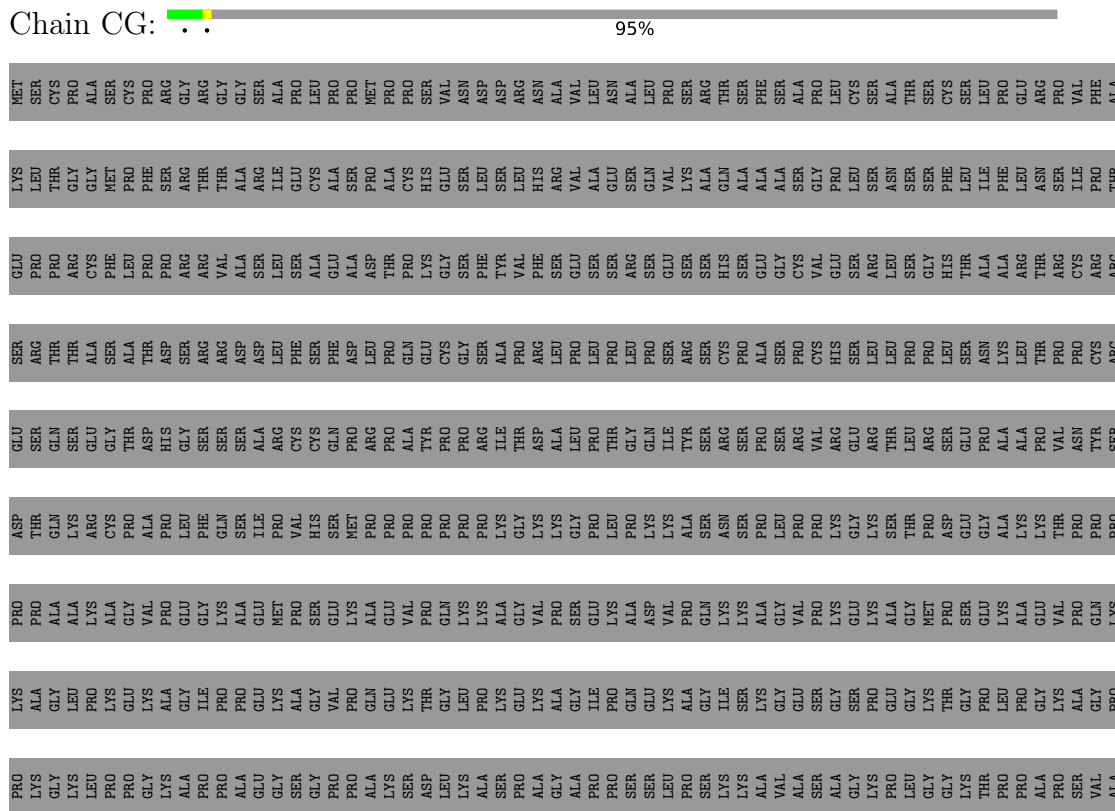








- Molecule 3: Formin 1













- Molecule 3: Formin 1

95%









[illegible]

- Molecule 3: Formin 1

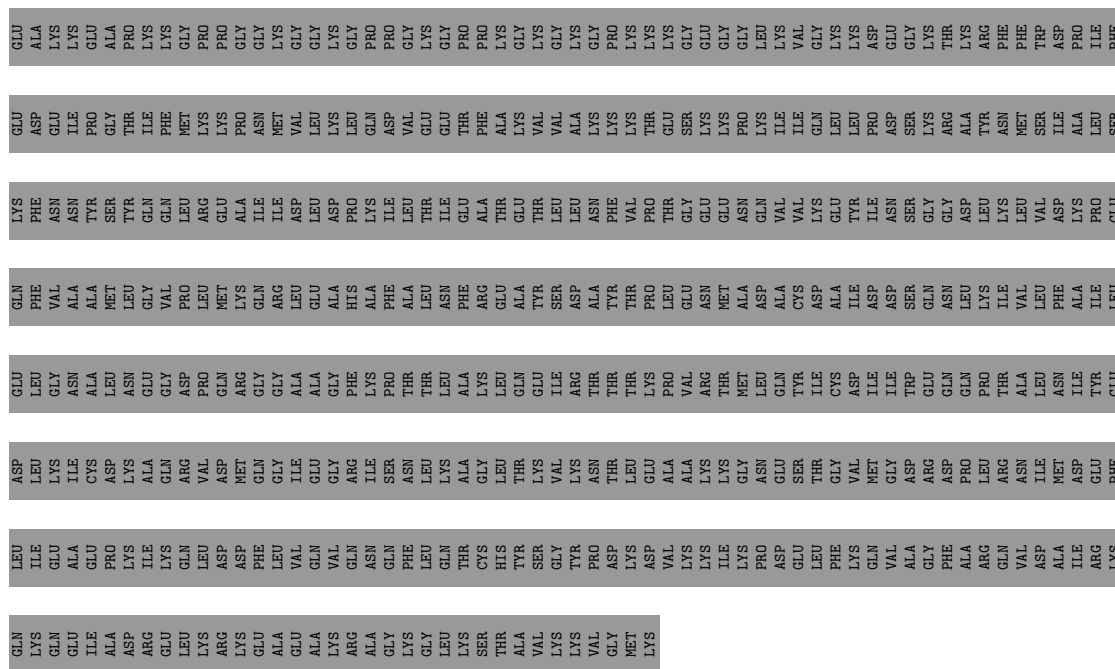
Chain CL: 95%

[illegible]

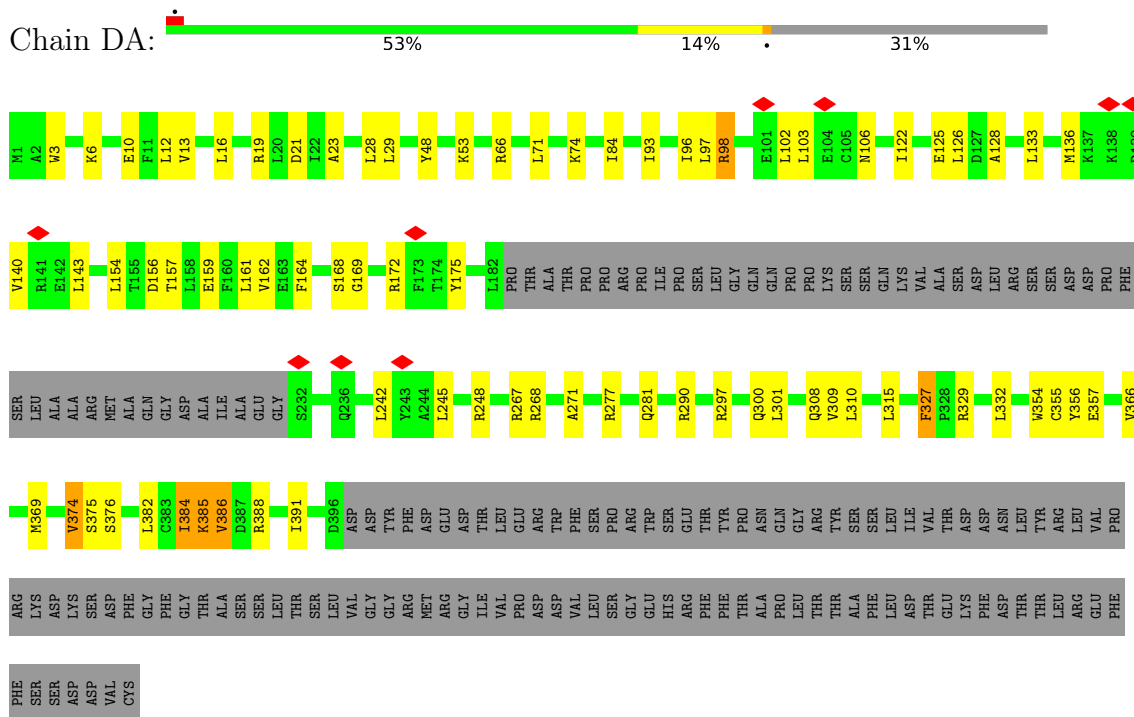




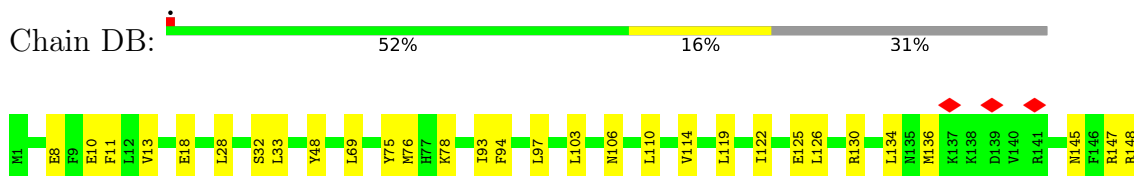


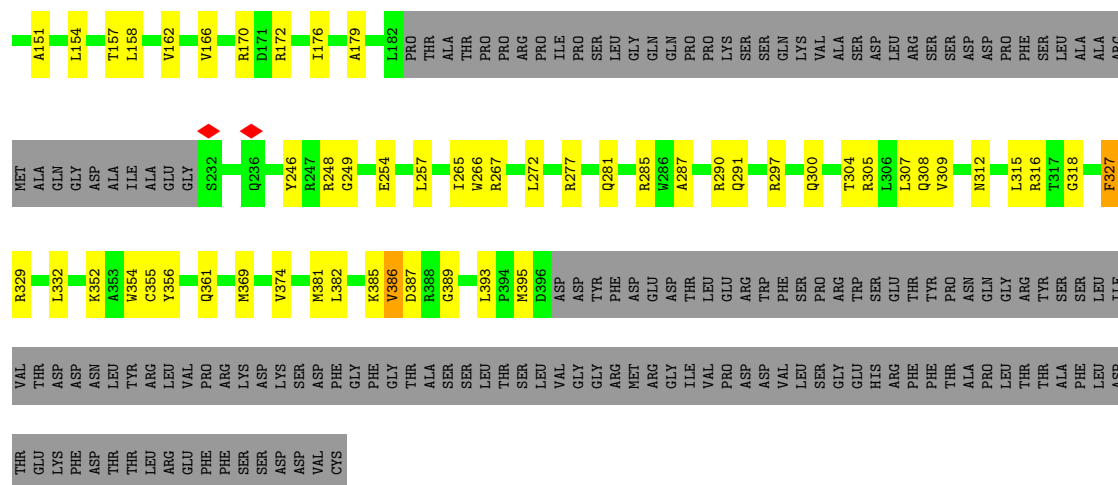


- Molecule 4: PCR11, TGME49 209490

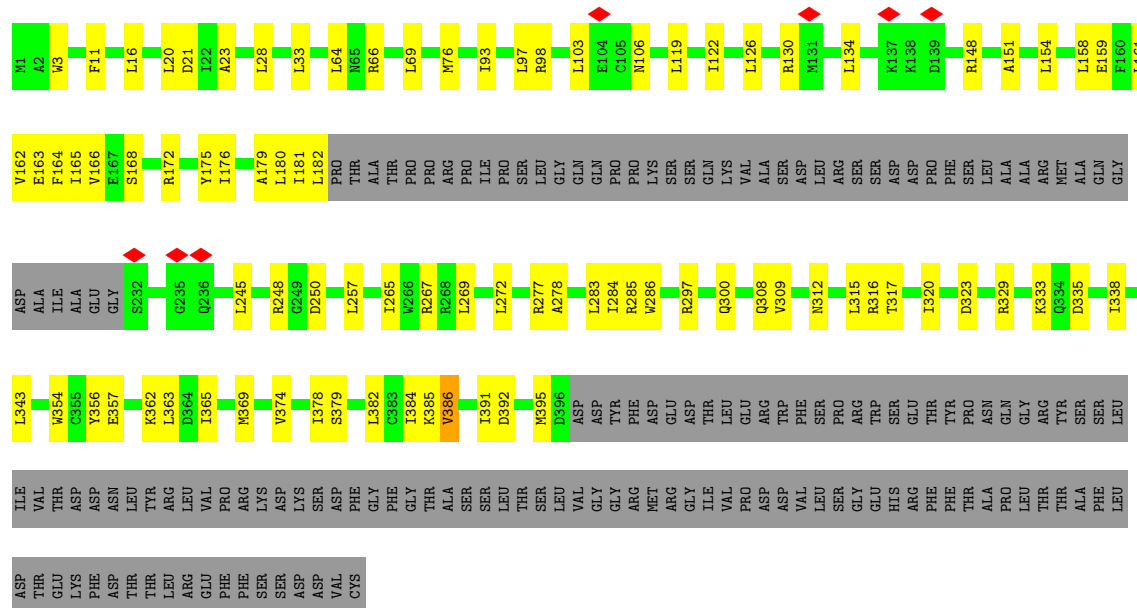


- Molecule 4: PCR11, TGME49_209490

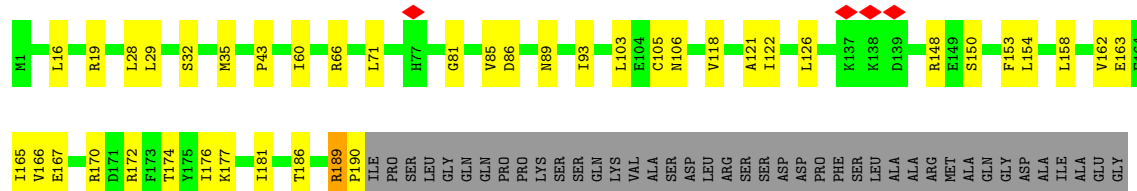


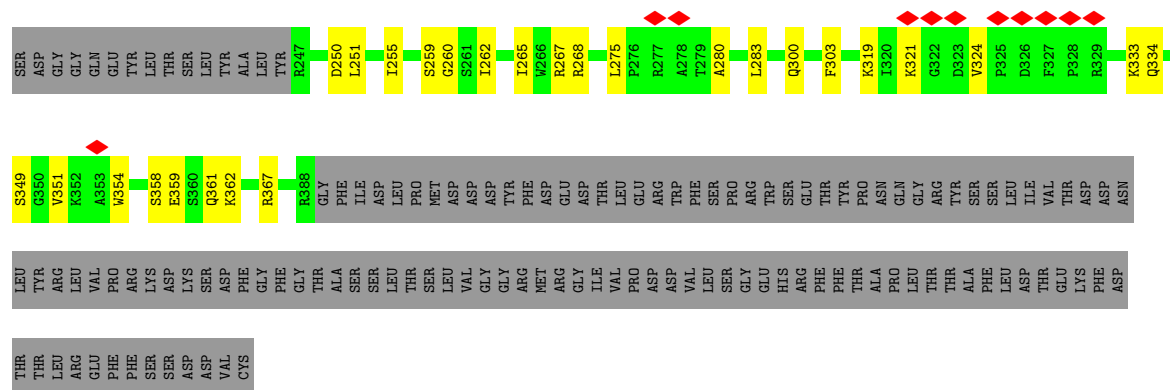


● Molecule 4: PCR11, TGME49_209490

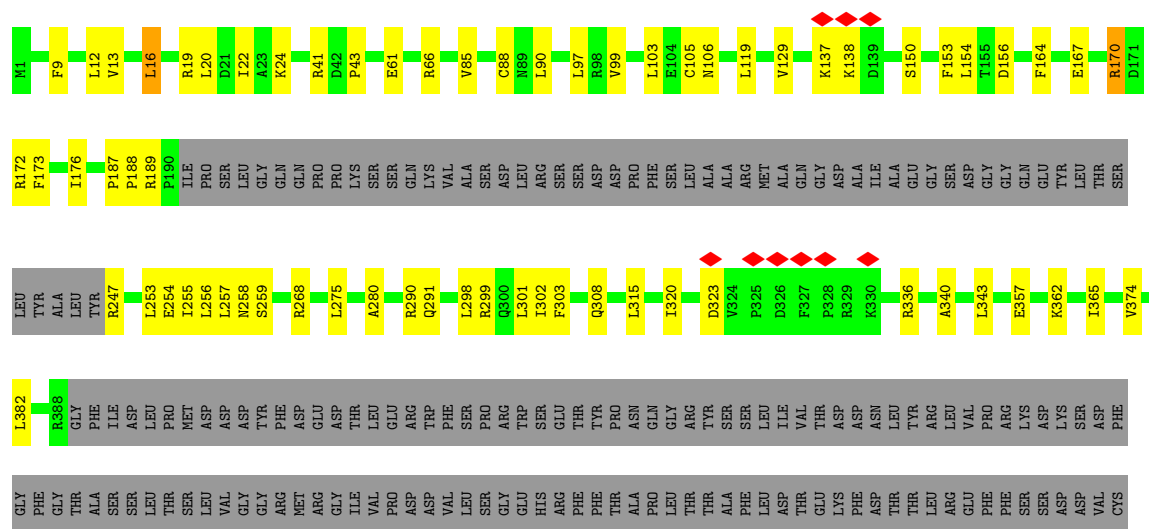


● Molecule 4: PCR11, TGME49_209490

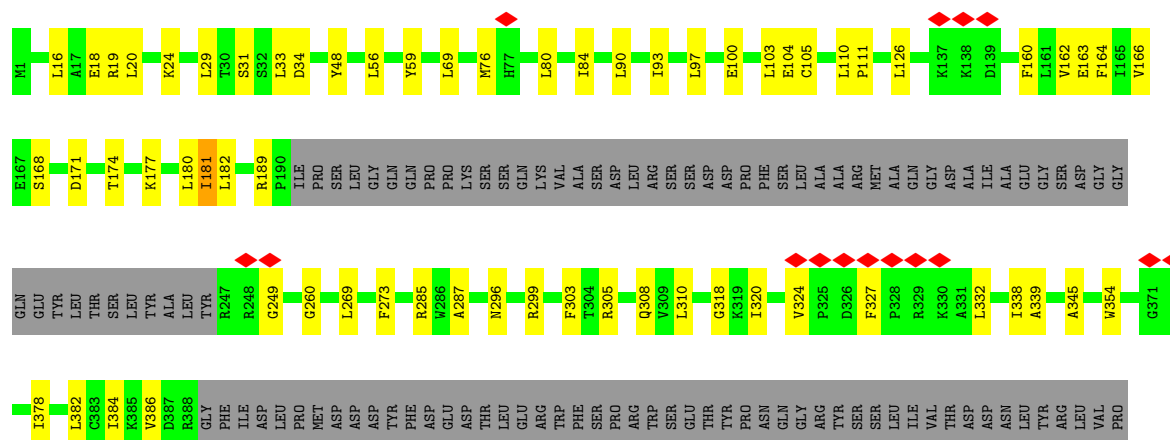




• Molecule 4: PCR11, TGME49_209490

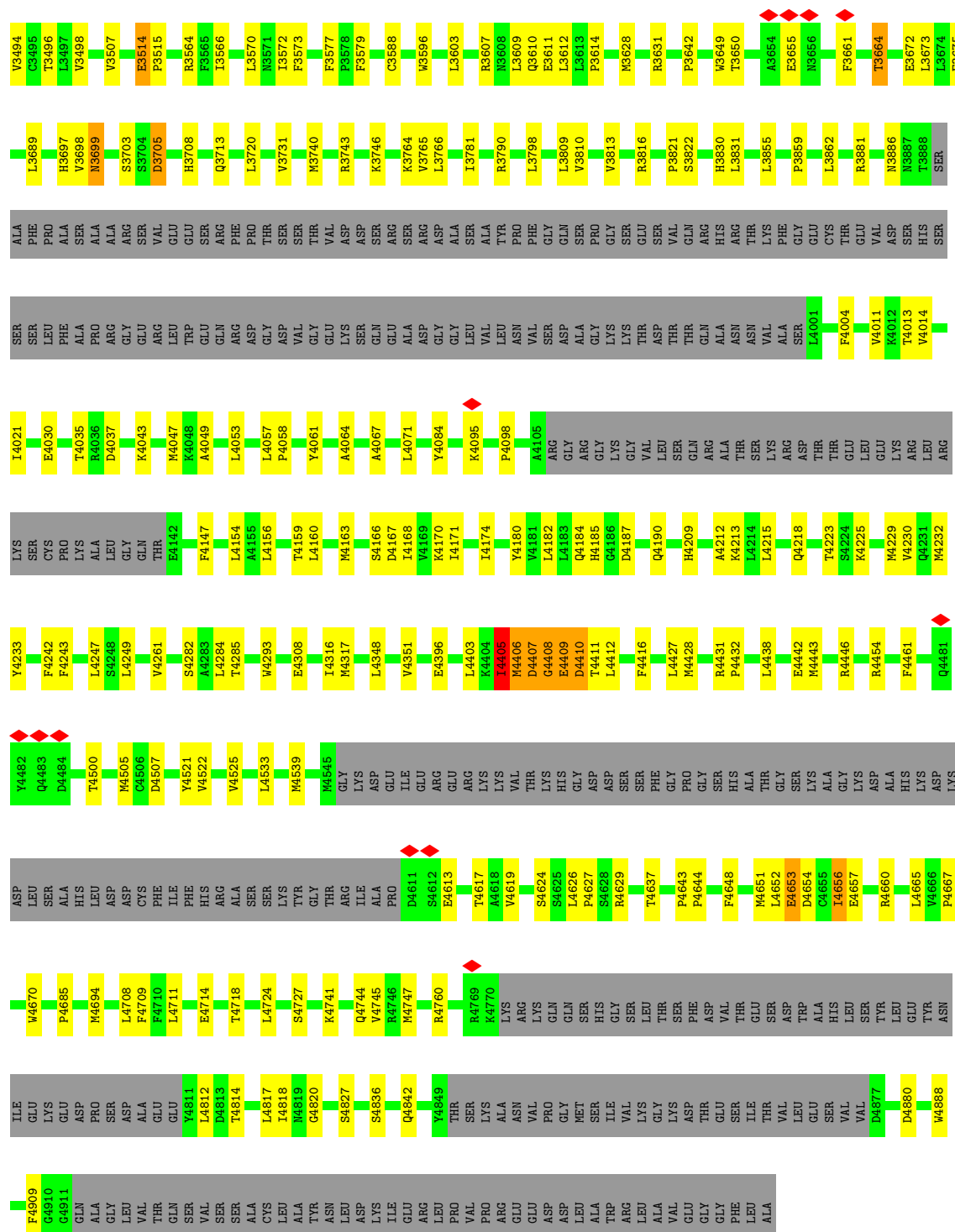


• Molecule 4: PCR11, TGME49_209490











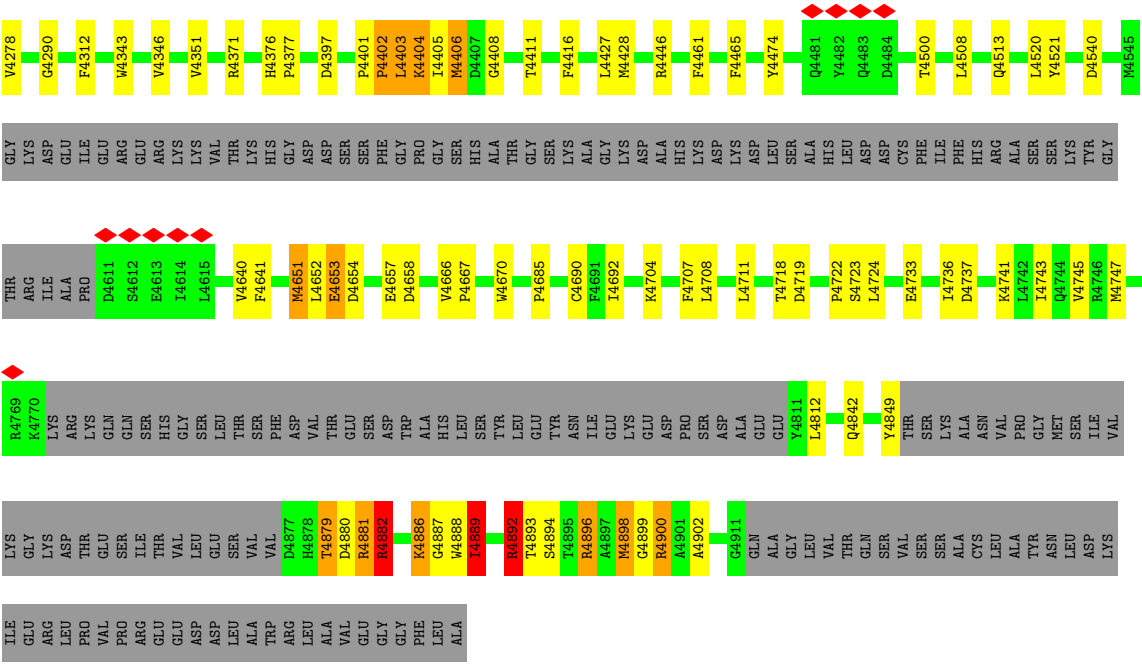




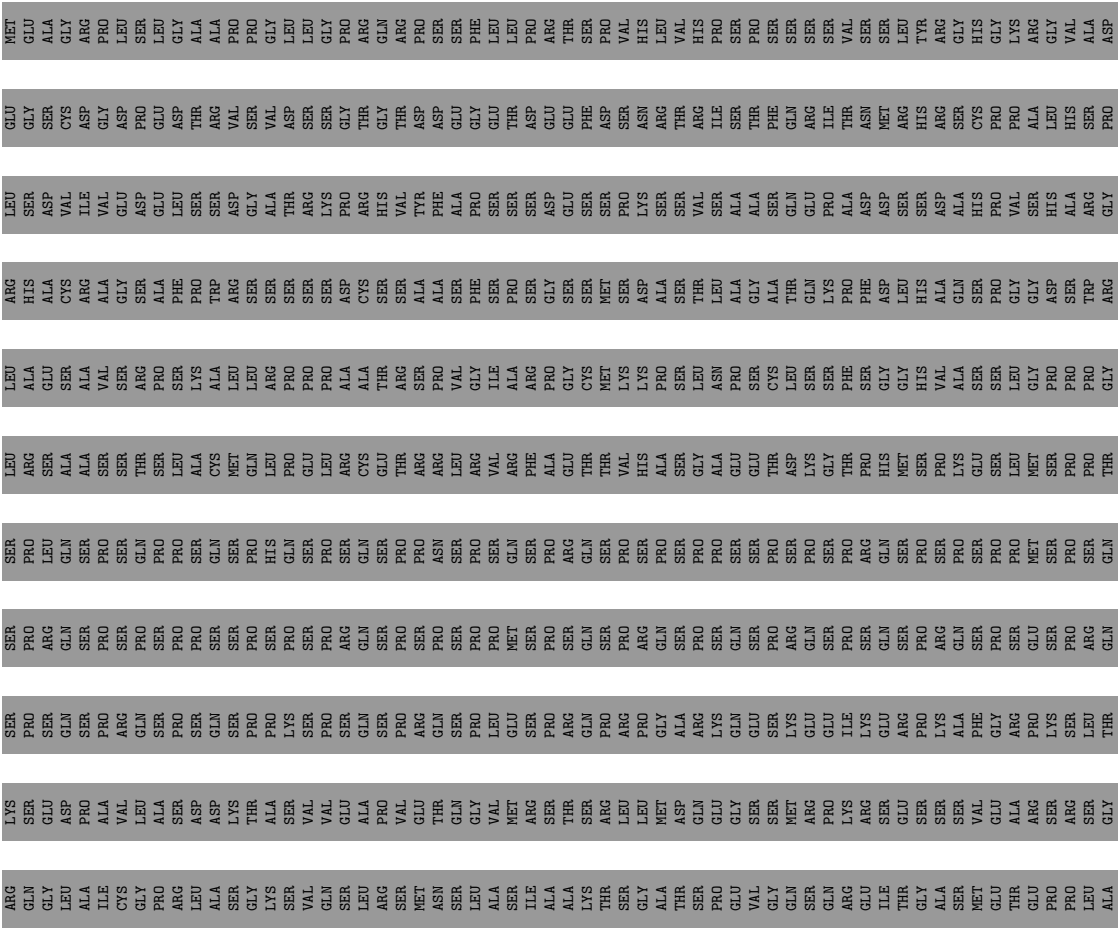




THR	L4001	GLU	I3877	PHE	LYS	F3277	PRO	SER	SER
GLU	R4002	CYS	I3877	ALA	GLY	F3277	LEU	ALA	ALA
THR	F4003	THR	L3673	ARG	LYS	F3281	HIS	GLU	GLU
GLU	F4004	GLU	L3673	LYS	MET	V3281	THR	ILE	ILE
VAL	P4009	VAL	V3698	THR	SER	E3282	GLN	ALA	ALA
ASP	Q4010	ASP	N3699	GLN	GLN	E3283	LYS	PRO	PRO
SER	V4011	SER	F3700	ASP	ASP	R3286	ASP	ASP	ASP
HIS		HIS	S3703	LEU	GLY	R3292	GLY	TYR	TYR
SER		SER	S3703	ASP	GLY	R3292	GLY	GLN	GLN
ALA	V4014	ALA	S3705	F3485	A3377	R3299	GLY	GLY	GLY
SER		SER	D3706	Y3490	Q3378	K3294	LEU	LEU	LEU
PRO	T4024	PRO	V3706	A3491	R3393	D3297	THR	ALA	ALA
PHE	E4030	PHE	S3707	V3499	V3394	L3301	GLY	ARG	ARG
ALA		ALA	H3708	V3499	Y3395	K3304	ASP	GLY	GLY
PRO	T4035	PRO	K3746	C3495	F3399	E3305	GLY	GLY	GLY
GLY	R4036	GLY		V3495	S3409	I3306	LEU	ASP	ASP
GLN	D4037	GLN				T3310	LYS	GLY	GLY
THR	E4142	THR	R3768	V3498	S3409	R3314	ALA	ALA	ALA
			R3768	R3504	S3409	T3323	GLY	GLY	GLY
F4150		TRP	K3769	R3505	S3409	D3330	TRP	GLY	GLY
	I4044	GLU	R3763	M3506	S3409	A3331	LEU	ASP	ASP
T4159		GLN	K3764	V3507	S3409	T3310	ALA	ALA	ALA
	M4047	ARG	V3765		S3409	R3314	VAL	VAL	VAL
M4163	K4048	ASP		L3510	S3409	SER	THR	THR	THR
		GLY	V3768		S3409	GLY	GLY	GLY	GLY
S4166	P4058	ASP		E3516	S3409	T3323	THR	THR	THR
D4167	M4059	VAL	E3787	P3517	S3409	D3330	PRO	PRO	PRO
T4168		GLY			S3409	A3331	GLY	GLY	GLY
V4169	L4071	GLU	R3790	L3570	S3409	T3310	THR	THR	THR
K4170		LYS			S3409	R3314	VAL	VAL	VAL
T4171	H4089	SER	L3798	H3581	S3409	T3323	LYS	LYS	LYS
G4172	C4090	GLN	I3804	C3588	S3409	D3330	THR	THR	THR
T4174	S4093	ALA			S3409	A3331	GLY	GLY	GLY
	L4094	ASP	V3813	L3603	S3409	E3336	LEU	LEU	LEU
V4181	K4095	GLY	P3821	R3607	S3409	T3323	THR	THR	THR
	R4096	GLY			S3409	E3336	ALA	ALA	ALA
T4205		LEU	F3829	E3611	S3409	D3330	GLY	GLY	GLY
L4208	T4099	VAL	H3830		S3409	A3331	THR	THR	THR
H4209		ASN	L3831	R3627	S3409	T3310	VAL	VAL	VAL
		VAL			S3409	R3314	GLY	GLY	GLY
L4217	A4105	ASP	E3836	P3642	S3409	K3246	VAL	VAL	VAL
	ARG	GLY			S3409	R3246	GLY	GLY	GLY
ARG	ARG	ASP	Q3841	A3645	S3409	K3246	LEU	LEU	LEU
GLY	GLY	ALA			S3409	R3246	THR	THR	THR
LYS	LYS	GLY	K3842	A3646	S3409	A3249	GLY	GLY	GLY
GLY	GLY	LYS	T3843	P3648	S3409	K3249	ASN	ASN	ASN
VAL	VAL	LYS		V3649	S3409	E3255	ARG	ARG	ARG
THR	THR	THR	F3852	T3650	S3409	L3264	GLY	GLY	GLY
ASP	SER	ASP		P3651	S3409	L3264	LYS	LYS	LYS
	GLN	THR	L3855	P3652	S3409	L3264	THR	THR	THR
GLN	GLN	THR			S3409	L3264	GLY	GLY	GLY
ALA	ALA	GLN	A3860		S3409	L3264	ALA	ALA	ALA
THR	THR	ALA		E3655	S3409	L3264	VAL	VAL	VAL
ASN	ASN	ASN	S3863	N3656	S3409	L3264	GLY	GLY	GLY
LYS	LYS	LYS		T3657	S3409	L3264	ALA	ALA	ALA
ARG	ARG	VAL	R3869	I3658	S3409	L3264	THR	THR	THR
ASP	ASP	ALA			S3409	L3264	GLN	GLN	GLN
THR	THR	SER	F3874	S3659	S3409	L3264	LYS	LYS	LYS
				R3660	S3409	L3264	ILE	ILE	ILE

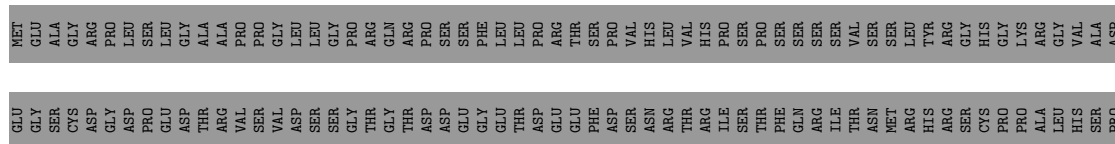


● Molecule 6: FLM1, TGME49_271780













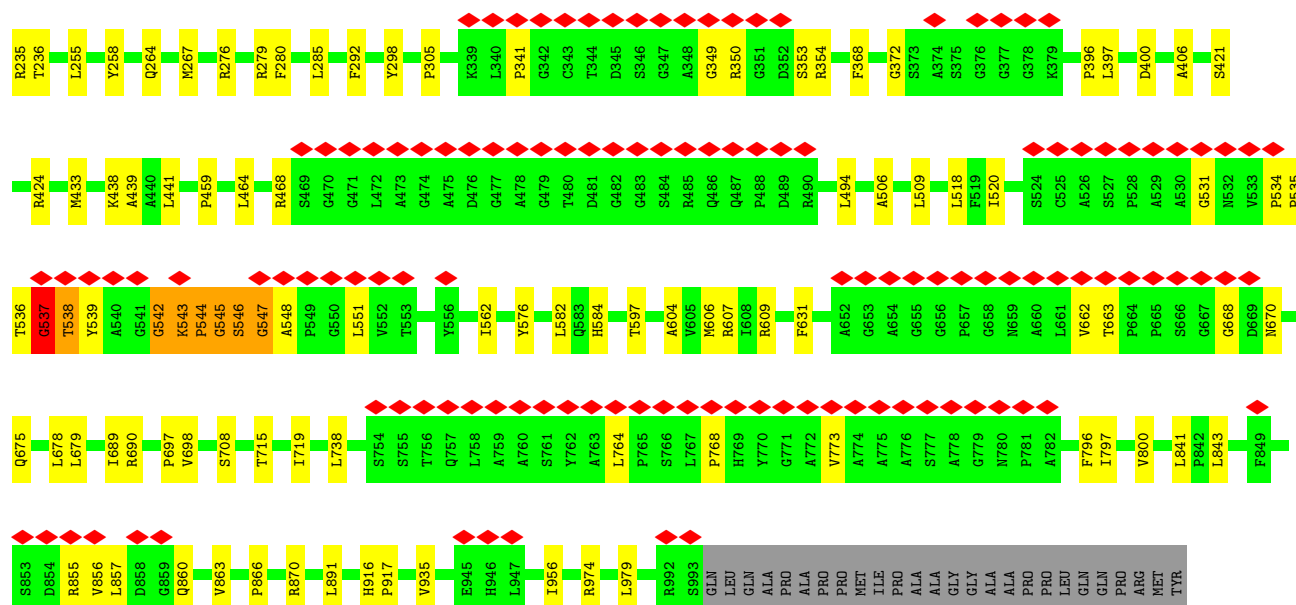




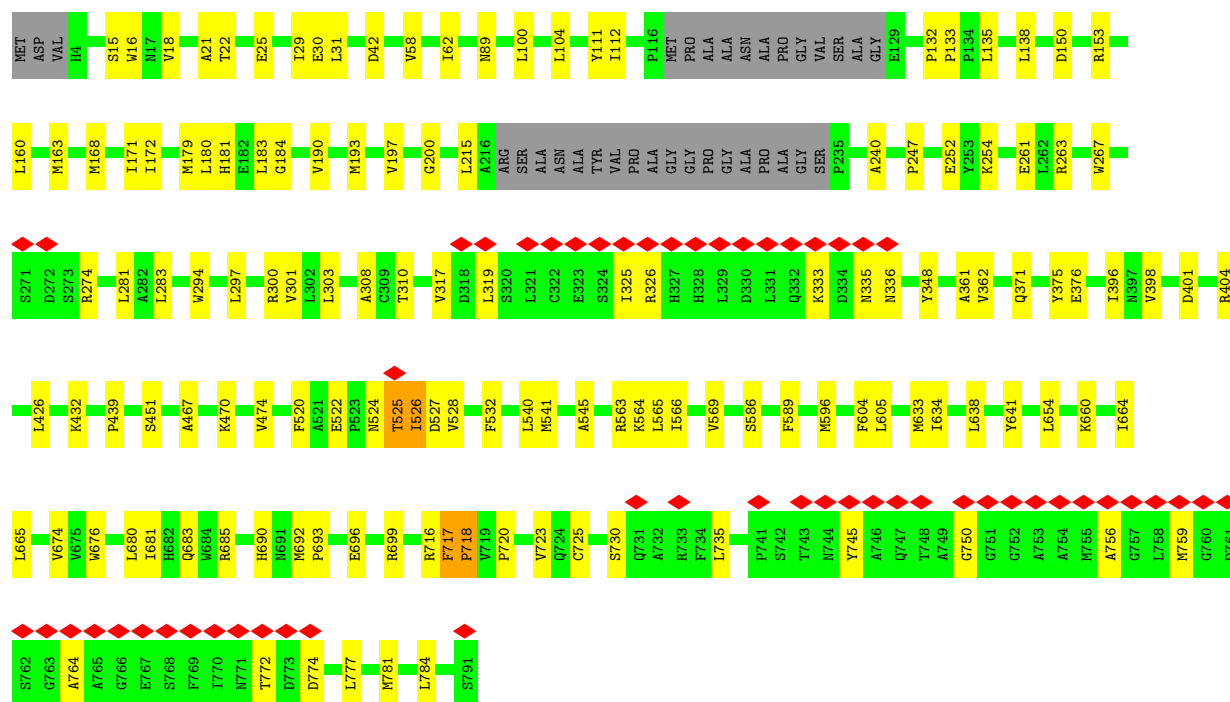
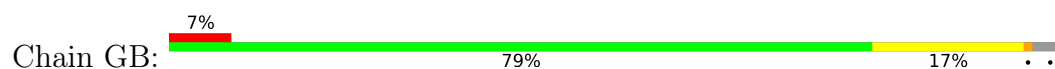




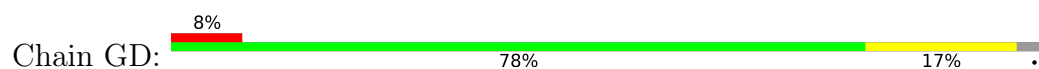




• Molecule 8: Protein transport protein SEC23

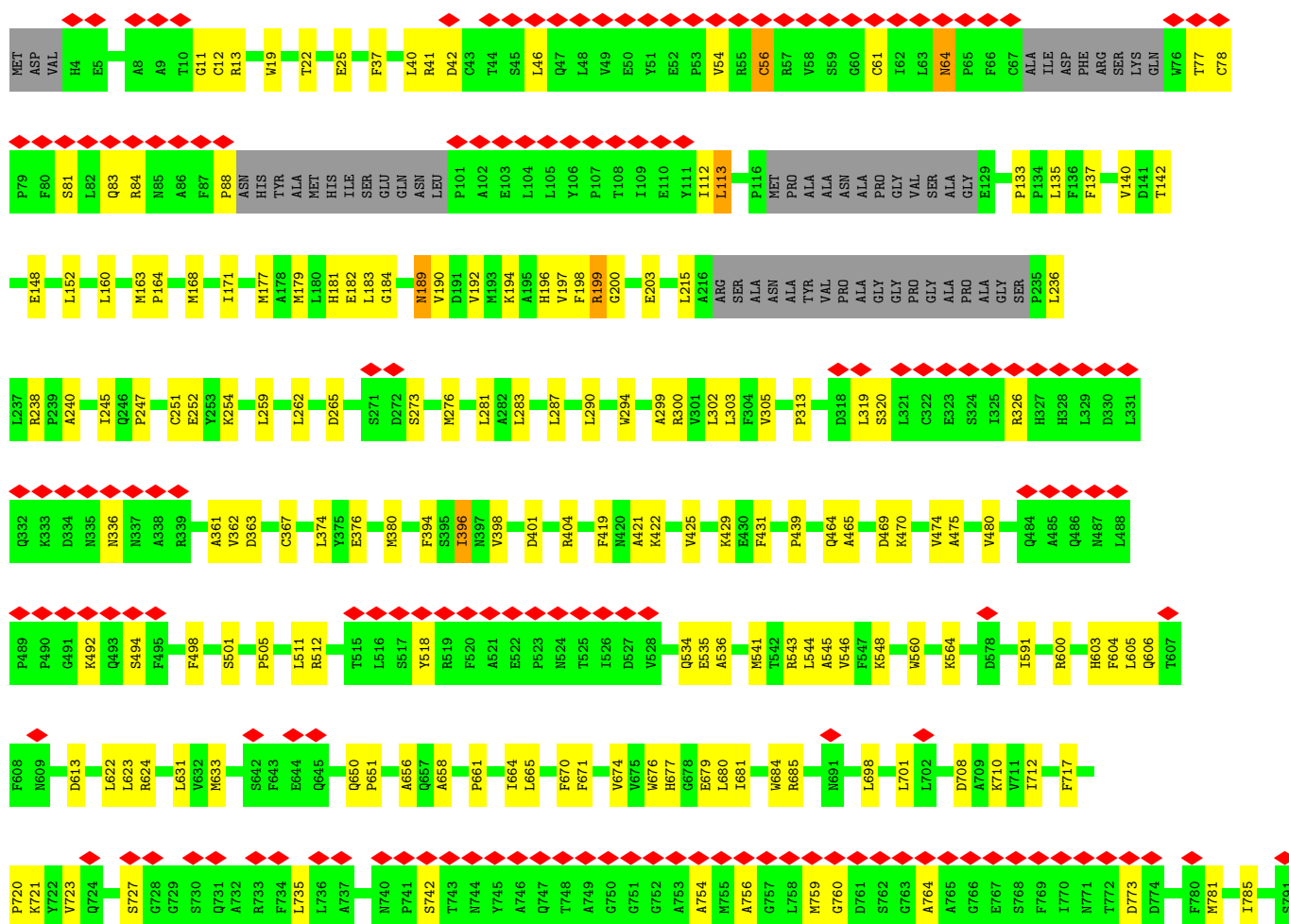
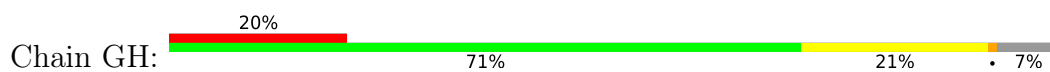


• Molecule 8: Protein transport protein SEC23

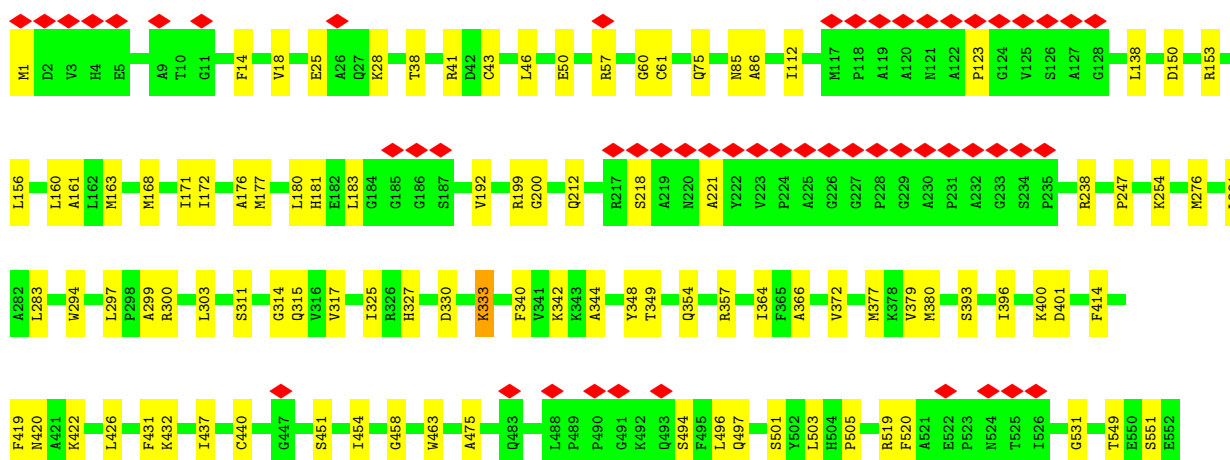
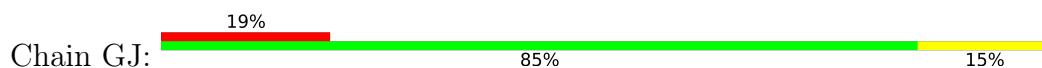


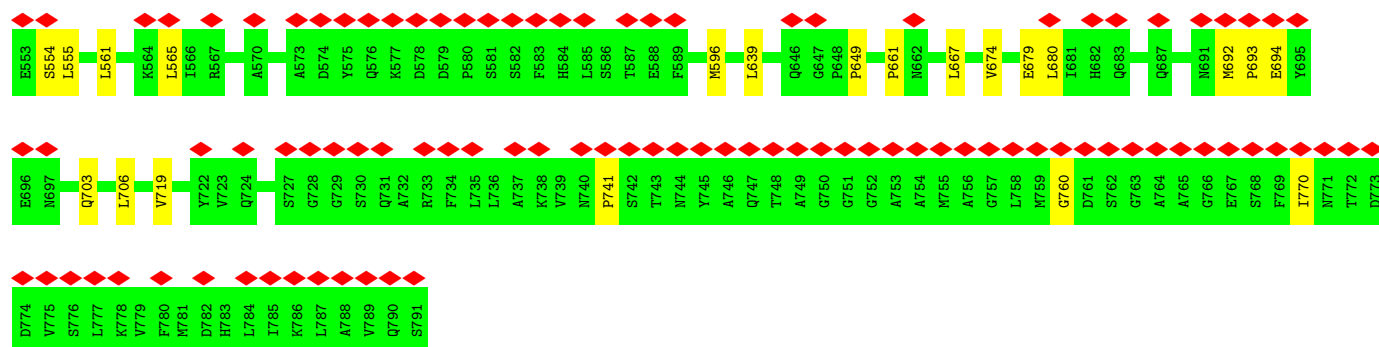


• Molecule 8: Protein transport protein SEC23

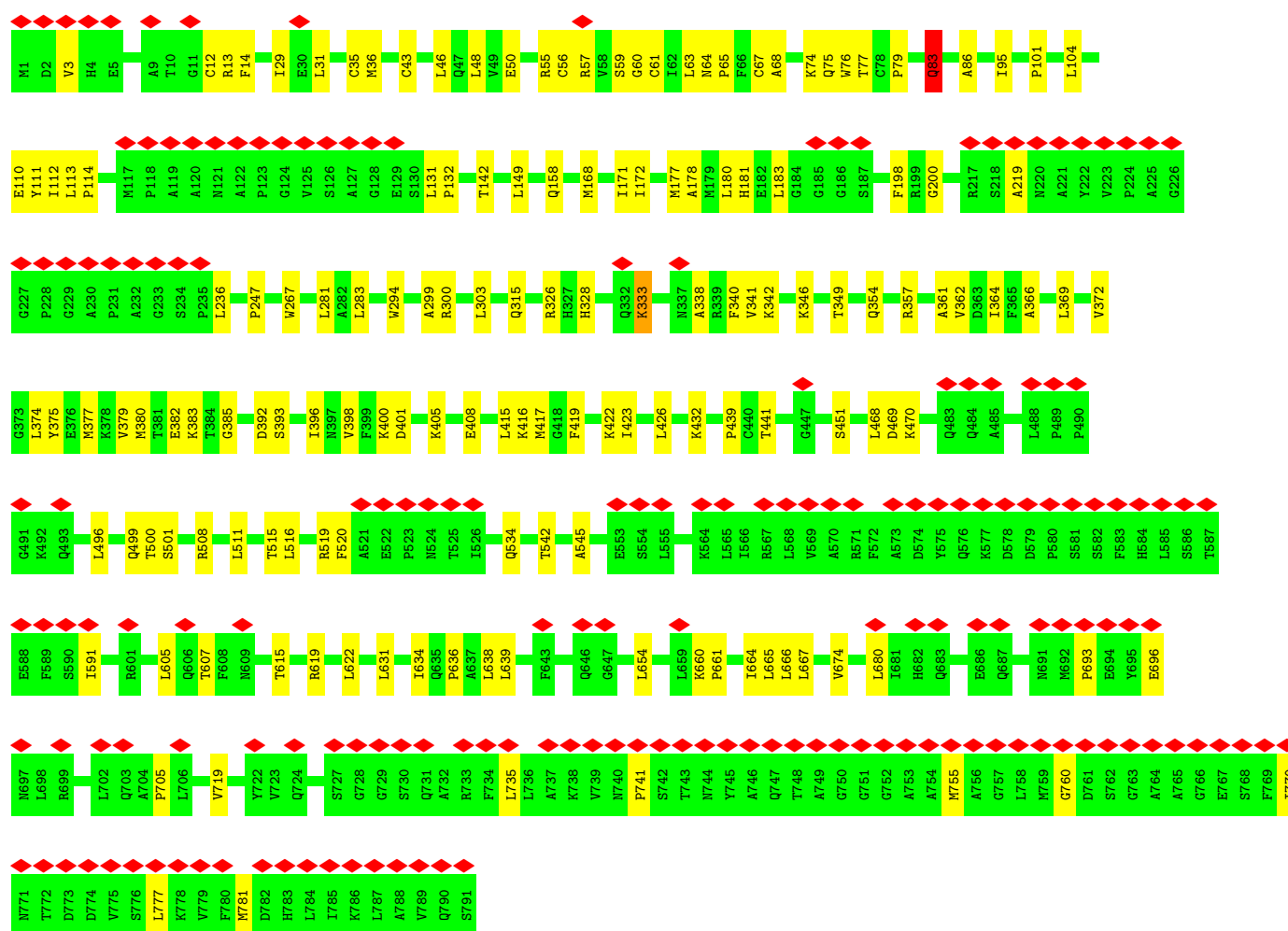
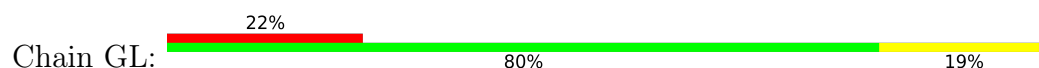


• Molecule 8: Protein transport protein SEC23





• Molecule 8: Protein transport protein SEC23



• Molecule 9: FLM2, TGME49_285990











Frequency	Percentage
Daily	61%
Weekly	11%
Monthly	28%

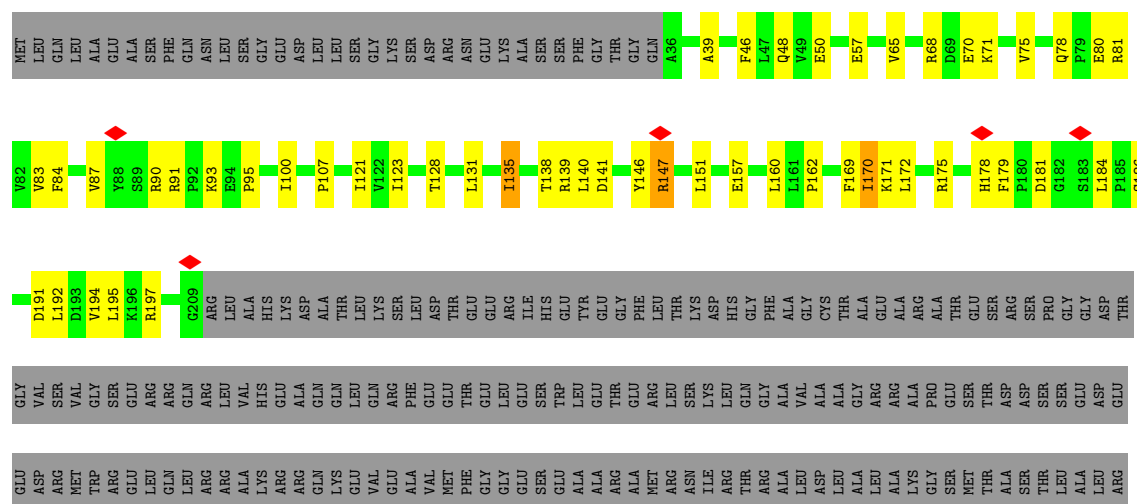


Chain IB: 59% 13% 28%

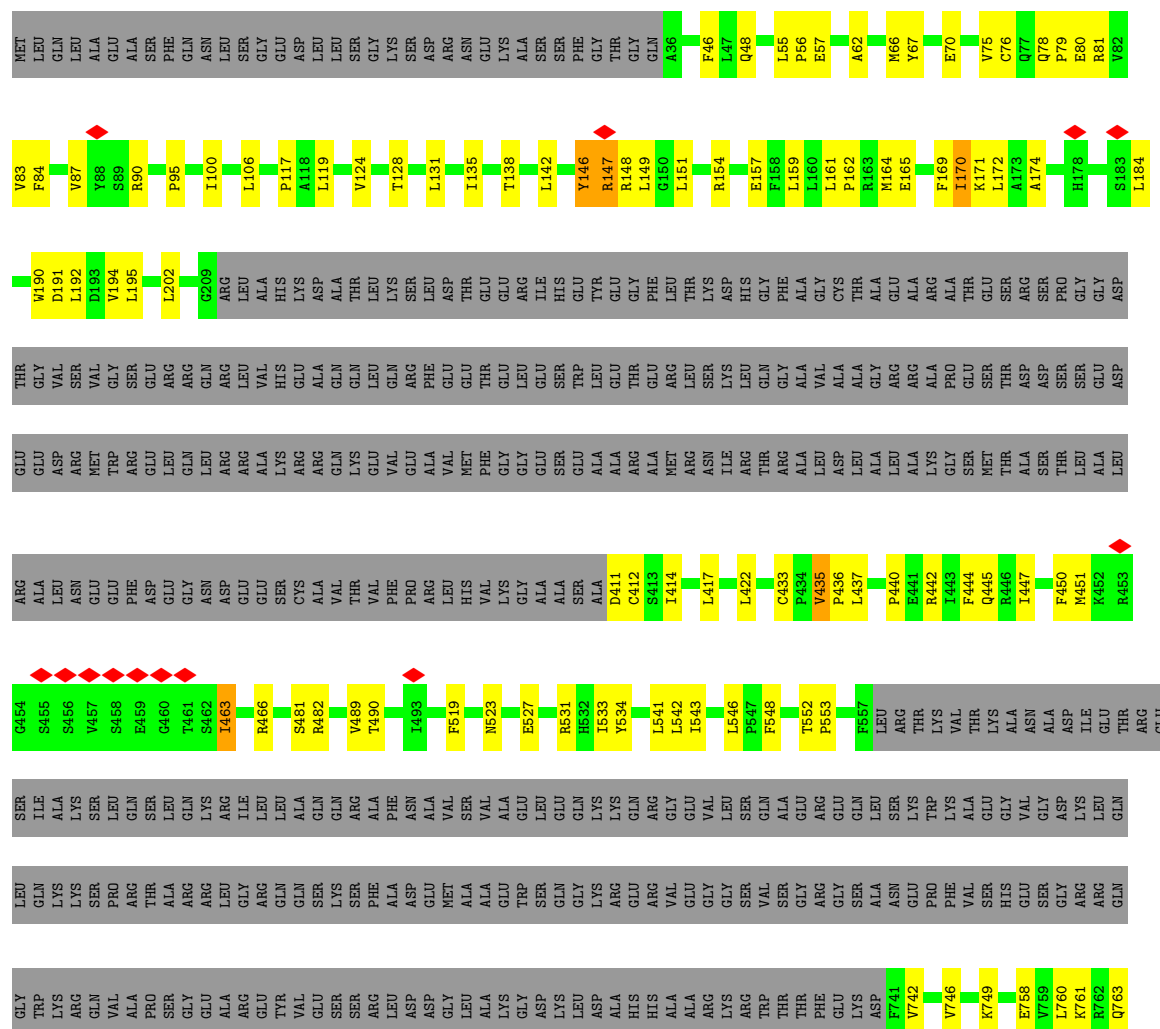


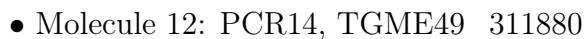




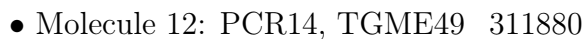






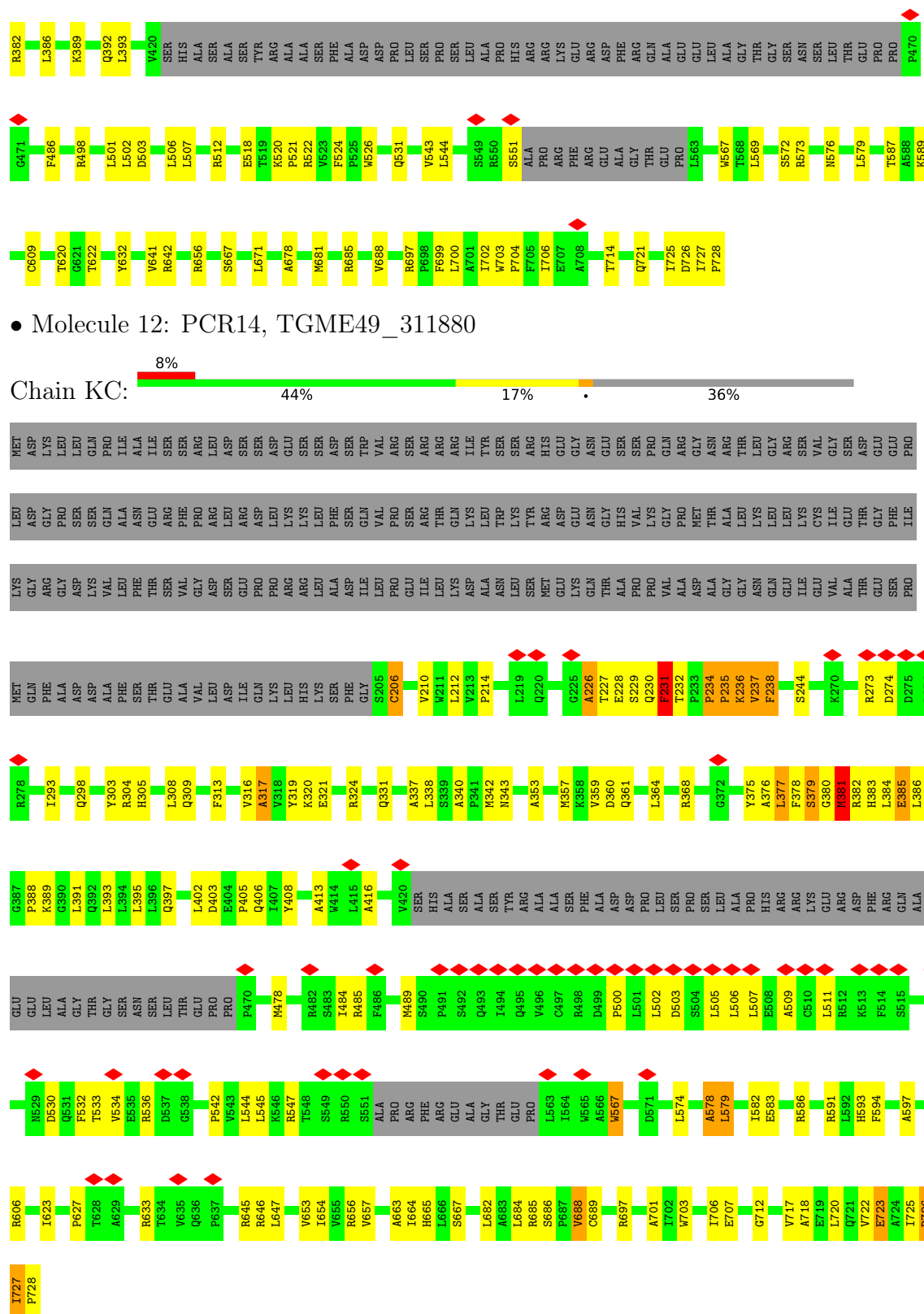


Frequency	Percentage
Daily	45%
Weekly	18%
Monthly	36%
Other	1%



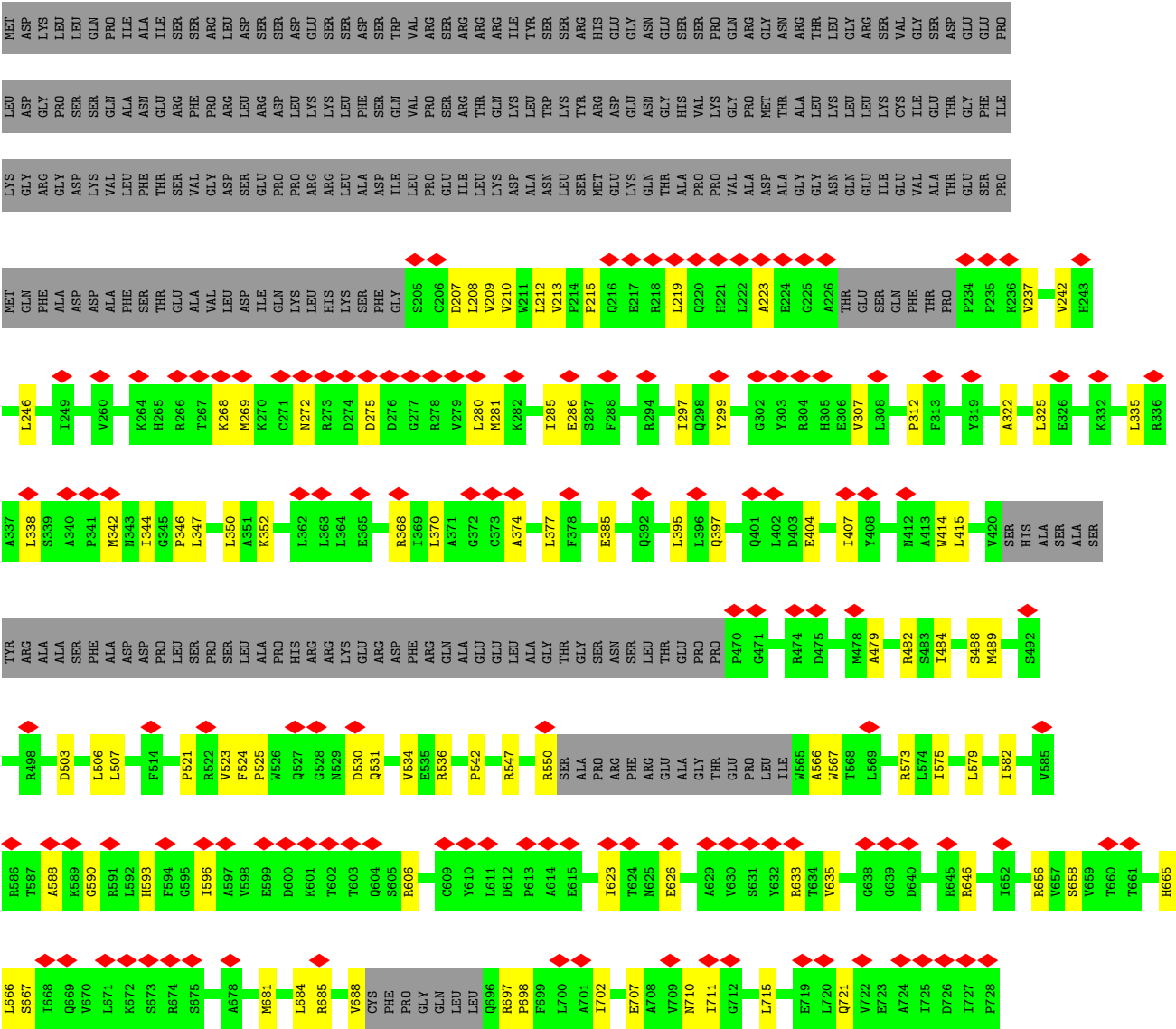
Frequency	Percentage
Often	49%
Sometimes	14%
Never	36%



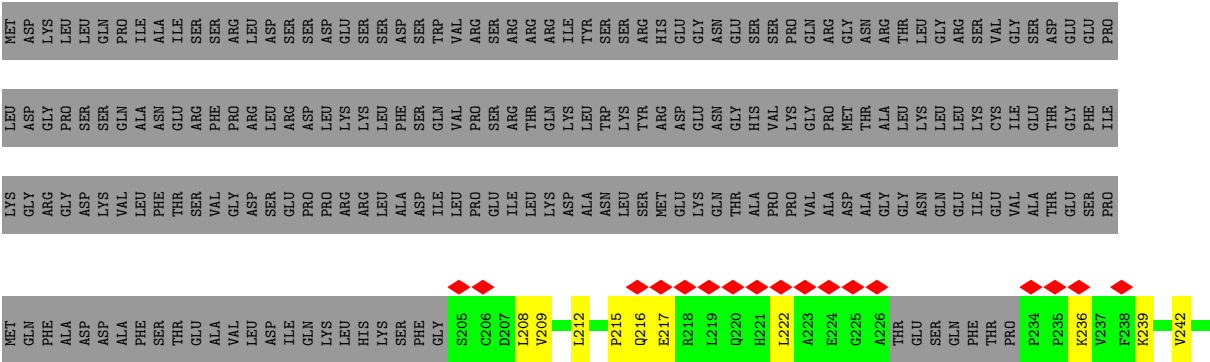


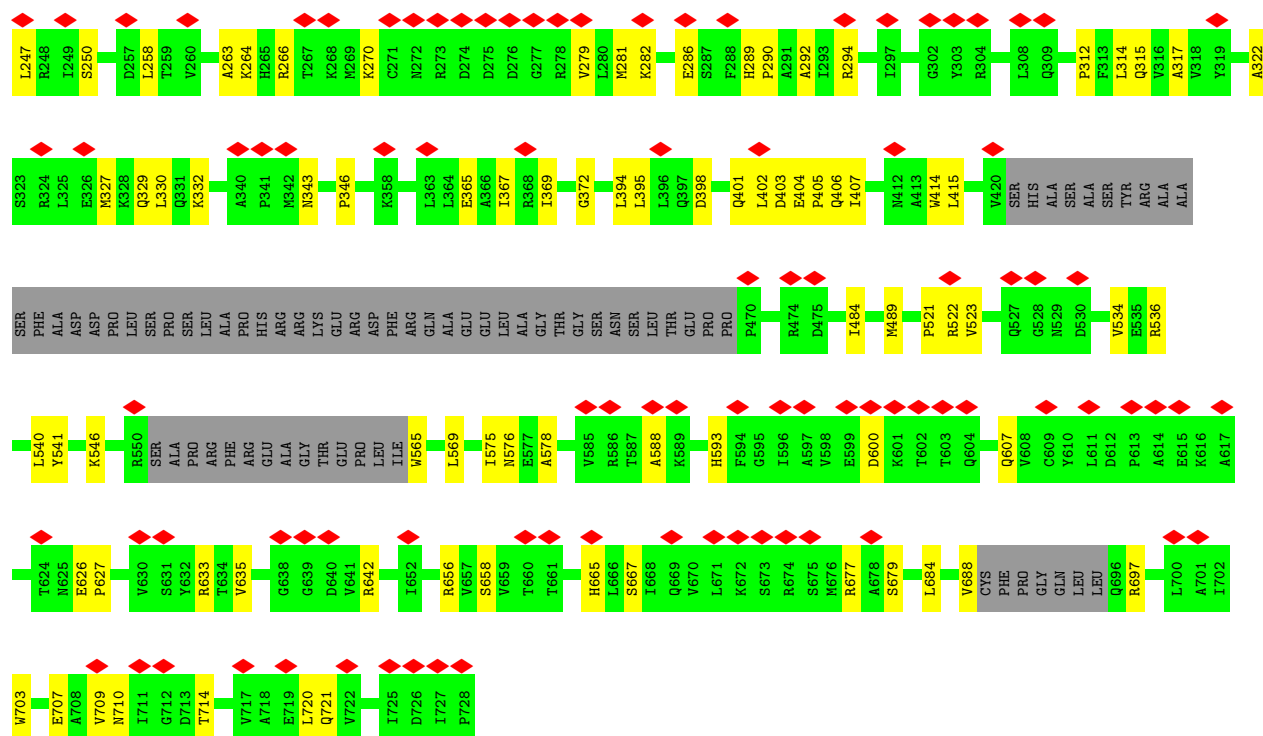
• Molecule 12: PCR14, TGME49_311880



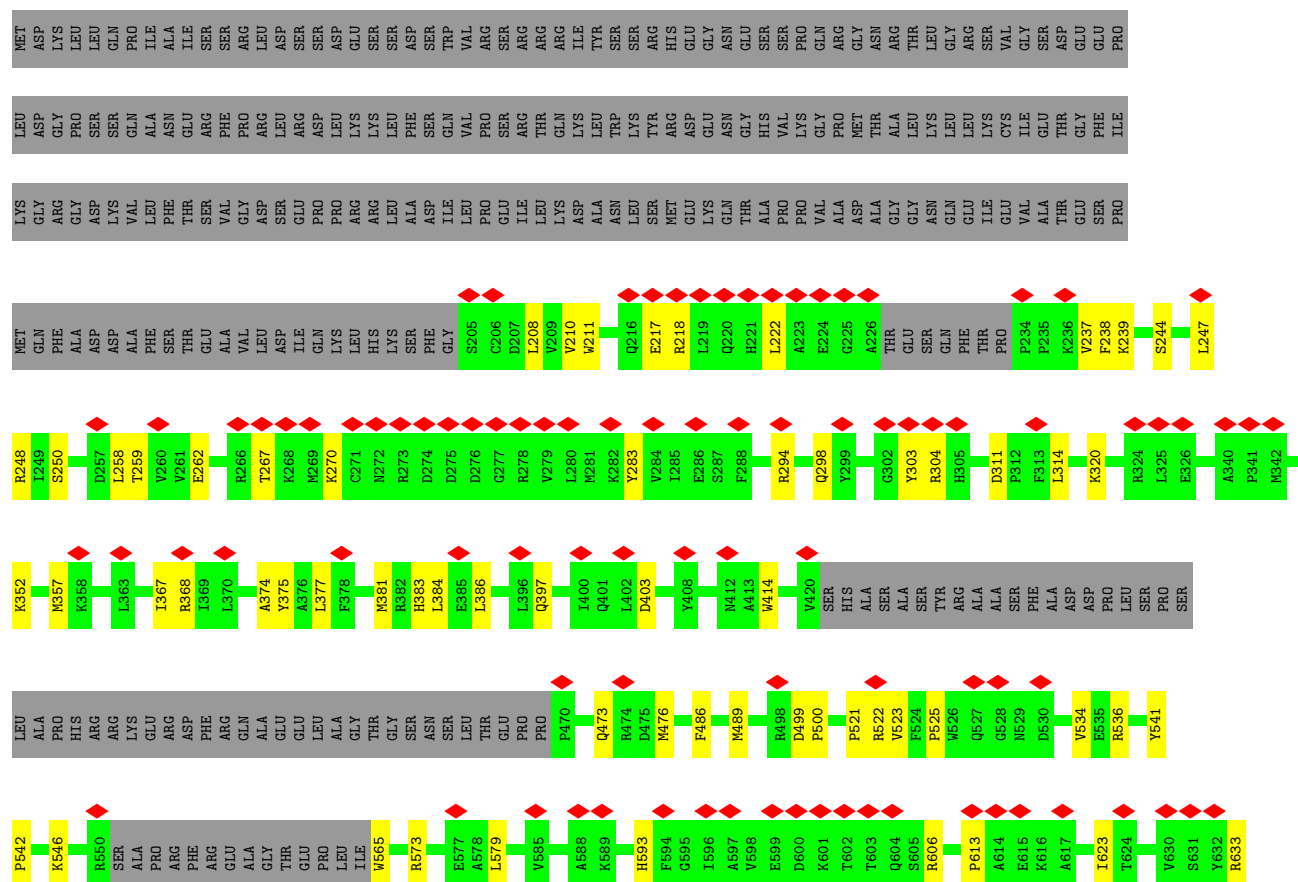


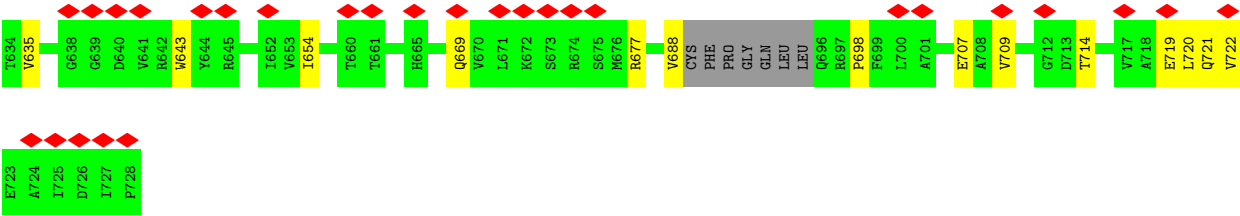
● Molecule 12: PCR14, TGME49_311880



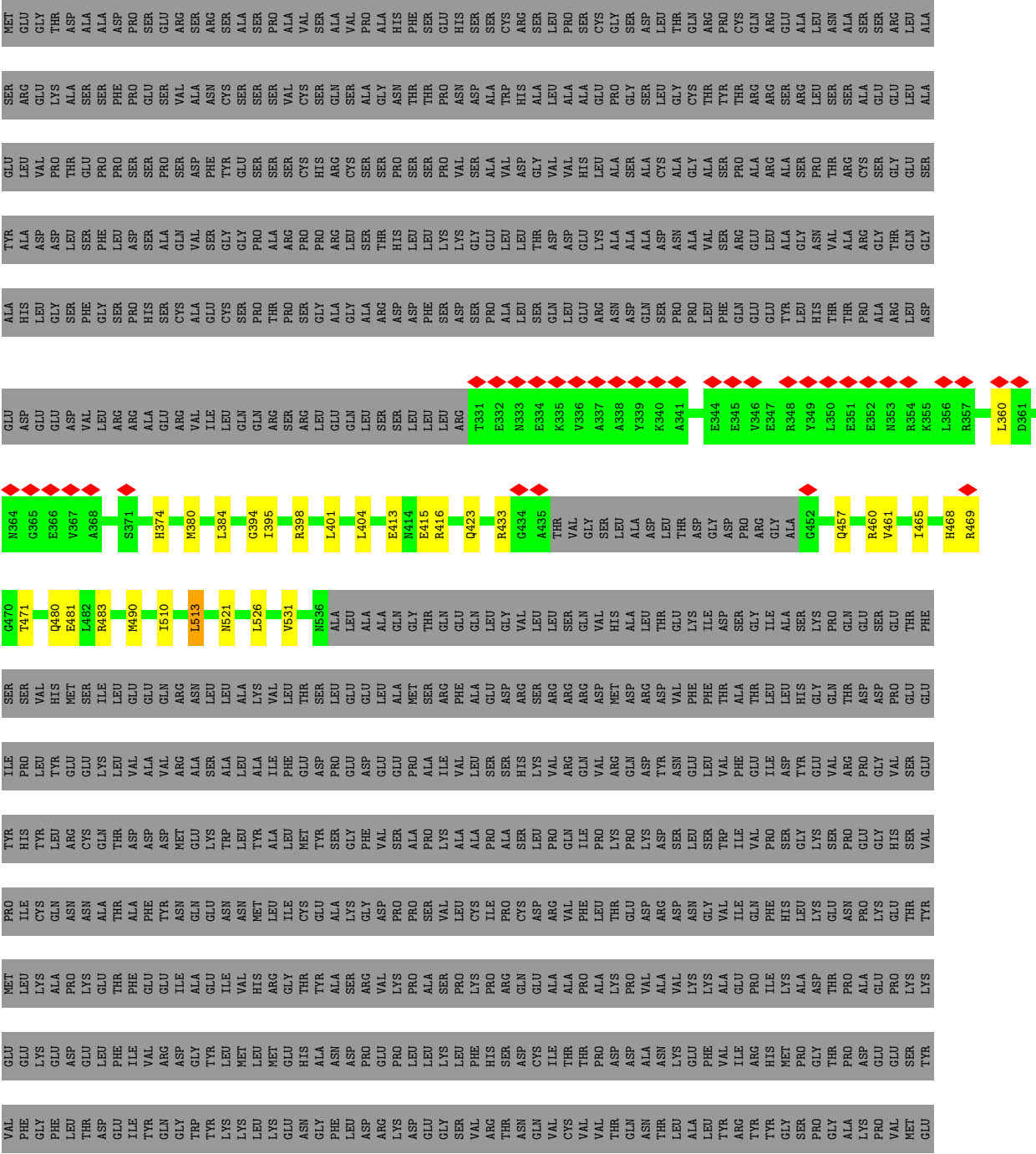


• Molecule 12: PCR14, TGME49_311880





• Molecule 13: ICAP16, TGME49_202120

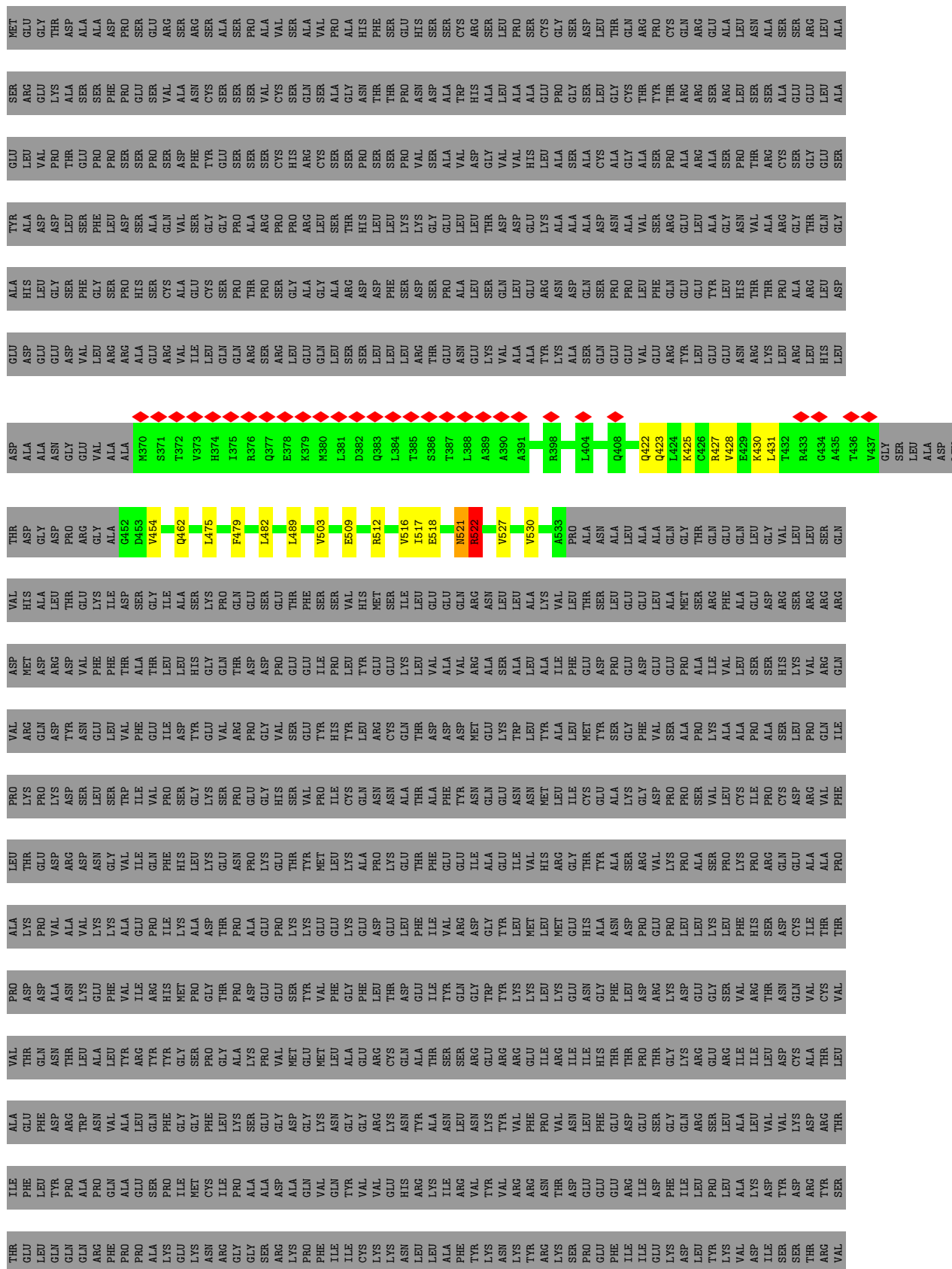


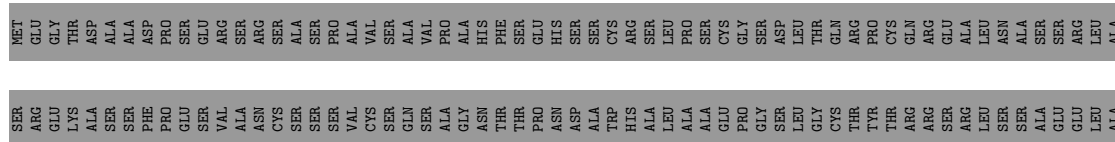
SER	PHE	PHE	GLU	GLU	THR	THR	PHE	ASN	ALA
	ALA	ILE	ARG	ASP	THR	THR	LEU	ASP	SER
	GLU	ILE	ILE	GLU	PRO	PRO	ASP	PRO	ARG
	SER	GLY	ASP	GLY	THR	GLY	ARG	GLU	VAL
	THR	LYS	PHE	GLY	GLY	THR	LYS	PRO	SER
	PRO	ASP	ILE	GLN	LYS	ARG	ASP	LEU	PRO
	ARG	LEU	LEU	ARG	ARG	GLY	GLY	LEU	ALA
	PRO	TYR	PRO	SER	GLU	GLU	GLY	LYS	SER
	PHE	LYS	LEU	LEU	ARG	VAL	VAL	PRO	PRO
	PHE	VAL	ALA	ALA	ILE	ILE	VAL	LEU	LYS
SER	PRO	ASP	LYS	LEU	ILE	ILE	ARG	HIS	PRO
	GLN	ILE	ASP	VAL	ASP	THR	THR	SER	ARG
	ILE	SER	TYR	VAL	ASP	ASP	ASN	ASP	GLN
	ILE	SER	ARG	ASP	LYS	GLN	GLY	CYS	GLU
	TYR	THR	ARG	ASP	ALA	VAL	VAL	ILE	ALA
	GLY	ARG	TYR	ARG	THR	CYS	THR	THR	ALA
	PHE	VAL	SER	THR	LEU	VAL	VAL	THR	PRO
	VAL	ILE	THR	ILE	ALA	VAL	VAL	PRO	LYS
	SER	THR	GLU	PHE	GLU	THR	THR	ASP	LYS
	ALA	PHE	LEU	LEU	PHE	GLN	GLN	ASP	PRO
SER	PRO	LYS	GLN	TYR	ARG	ASN	ASN	ASN	VAL
	ALA	PRO	GLN	PRO	ARG	THR	LEU	LYS	VAL
	ALA	LEU	GLN	ALA	TRP	GLN	VAL	GLY	LYS
	ASP	GLN	ARG	PRO	ASN	ALA	ALA	GLU	LYS
	LEU	PRO	PHE	GLN	VAL	LEU	LEU	PHE	LYS
	ARG	THR	PRO	ALA	ALA	TYR	TYR	VAL	ALA
	GLY	SER	PRO	GLU	LEU	ARG	ILE	GLU	ALA
	PRO	GLU	ALA	SER	GLN	THR	ARG	PRO	THR
	GLY	LYS	LYS	PRO	PHE	TYR	TYR	HIS	ILE
	ARG	GLY	GLU	ILE	GLY	GLY	GLY	MET	LYS
SER	MET	GLU	ASN	CYS	PHE	SER	SER	PRO	ALA
	PHE	SER	ASN	GLY	THR	GLY	GLY	GLY	ASP
	GLY	LEU	ARG	ILE	LEU	ALA	ALA	THR	PRO
	ARG	ILE	GLY	PRO	LYS	LYS	ASP	PRO	GLU
	LEU	GLN	GLY	ALA	SER	LYS	PRO	GLU	GLY
	GLY	ARG	SER	ASP	GLY	VAL	GLU	GLU	PRO
	LEU	SER	ARG	ASP	GLY	VAL	PHE	GLY	LYS
	GLY	LEU	LEU	CYS	GLY	ARG	GLY	PHE	ASP
	VAL	LEU	LYS	VAL	GLY	ARG	GLY	GLY	ASP
	VAL	ASP	ILE	ILE	THR	THR	ALA	GLY	LYS
SER	ARG	ASP	CYS	VAL	GLY	GLY	PHE	GLY	ASP
	VAL	LEU	LYS	VAL	ARG	ARG	ARG	LEU	ASP
	GLN	GLN	LYS	HIS	ASN	GLN	ASP	LEU	GLY
	ALA	ASN	ARG	ALA	TYR	ALA	GLU	PHE	LEU
	VAL	LYS	LEU	LYS	THR	THR	ILE	ILE	THR
	PRO	TRP	ALA	ILE	ASN	SER	THR	TYR	VAL
	GLU	PHE	GLN	VAL	ASN	SER	GLN	GLY	ARG
	ASP	PHE	TYR	VAL	ASN	ARG	THR	TRP	ASP
	ASP	CYS	LYS	TYR	LYS	GLY	GLY	TYR	GLY
	ALA	LEU	ASN	VAL	ARG	ARG	ARG	LYS	TYR
SER	GLN	LYS	LYS	ARG	VAL	ARG	ARG	LYS	LEU
	ASP	LEU	ARG	ARG	PHE	GLU	GLY	LYS	MET
	LEU	ILE	THR	ASN	PRO	ILE	ILE	LEU	LEU
	SER	ILE	ARG	THR	VAL	GLY	ILE	LYS	MET
	SER	PHE	LYS	SER	ASN	ARG	ILE	GLU	GLY
	SER	THR	GLY	SER	ASN	THR	THR	GLY	ASN
	GLY	PHE	SER	GLY	THR	THR	THR	THR	HIS
	VAL	SER	THR	THR	GLU	THR	THR	THR	ALA
	VAL	THR	GLU	PHE	GLU	THR	THR	THR	ALA
	SER	THR	THR	THR	THR	THR	THR	THR	ALA

- Molecule 13: ICAP16, TGME49_202120

[illegible]

• Molecule 13: ICAP16, TGME49 202120





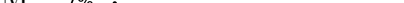


Chain LL: 11% . 88%



VAL	SER	ALA	PRO	ALA	ALA	ASP	LEU	ARG	GLY	PRO	GLY	ARG	MET	PHE	GLY	ARG	LEU	GLY	LEU	ASP	THR	PRO	LYS	ASP	ARG	VAL	SER	PHE	ALA	VAL	PRO	GLU	ASP	ASP	ASP	ALA	GLN	ASP	LEU	SER	SER	ARG	SER	SER	THR	SER	GLY	SER	GLY
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

● Molecule 13: ICAP16, TGME49 202120

Chain LM:  7% 92%

SER ARG GLU LYS ALA SER SER PHE PRO PRO GLU SER SER VAL ALA ALA ASN CYS SER SER SER CYS SER SER GLY ASN THR THR PRO PRO ASN ASP ALA ALA ALA THR TRP HIS ALA LEU LEU ALA ALA GLU GLU PRO PRO GLY SER SER LEU GLY CYS THR THR TYR THR ARG ARG SER SER LEU ARG SER SER ALA ALA GLU GLU LEU LEU

Tyr	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Ser	Ala	Gln	Val	Ser	Gly	Gly	Pro	Pro	Ala	Arg	Pro	Pro	Arg	Leu	Lys	Lys	Gly	Glu	Leu	Leu	Thr	Asp	Asp	Glu	Lys	Ala	Ala	Ala	Ala	Asp	Asn	Ala	Arg	Glu	Leu	Leu	Gly	Gly	Asn	Val	Ala	Ala	Arg	Gly	Thr	Gln	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ALA	HIS	LEU	GLY	SER	PHE	GLY	SER	HIS	SER	CYS	ALA	ALA	GLU	CYS	SER	PRO	THR	PRO	SER	GLY	GLY	ALA	ALA	ARG	ASP	ASP	PHE	SER	ASP	SER	PRO	ALA	ALA	LEU	SER	GLN	LEU	GLU	GLU	ARG	ASN	ASP	GLN	SER	PRO	PRO	LEU	LEU	PHE	GLY	GLN	GLU	TYR	GLU	LEU	HIS	THR	THR	PRO	ALA	ARG	ALA	LEU	SER
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Amino Acid	Count
GLU	1
ASP	1
GLU	1
GLU	1
ASP	1
VAL	1
LEU	1
ARG	1
ARG	1
ALA	1
GLU	1
VAL	1
LEU	1
LEU	1
LEU	1
SER	1
SER	1
LEU	1
LEU	1
SER	1
SER	1
LEU	1
L328	1
L329	1
R330	1
T331	1
E332	1
K335	1
V336	1
A337	1
A338	1
Y339	1
K340	1
N353	1
R354	1
K355	1
H359	1
Q377	1
E378	1
L388	1
A389	1
E392	1
R398	1
D399	1
R400	1
L404	1
L405	1

Q406	R407	Q408	D409	K410	S411	E412	E413	N414	E415	R416	L417	K418	S419	E420	V421	Q422	Q423	L424	K425	C426	R427	V428	E429	K430	L431	T432	R433	GLY	ALA	THR	VAL	GLY	SER	LEU	ALA	ASP	LEU	THR	ASP	GLY	ASP	PRO	ARG	GLY	ALA	GLY	ASP	VAL	ALA	ALA	GLN	LEU	ALA	ARG	VAL	GLN	ARG	ASP	TLE
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ASP GLN HIS ARG GLY THR LYS GLN LEU LEU THR PHE GLN GLY LEU LEU VAL SER SER MET ARG MET SER SER ASP LEU LEU LEU VAL GLY GLN ALA ALA GLN LYS MET MET VAL GLY GLU GLU GLU GLN ARG LEU LEU LEU ILE LYS VAL VAL LYS VAL ILE ILE LYS SER LEU TYR ASN ASN ARG ARG LYS

LEU	VAL	PRO	PRO	VAL	VAL	LEU	ALA	ALA	PRO	ALA	ASN	ALA	ALA	LEU	ALA	ALA	GLN	GLY	THR	GLN	GLU	GLN	LEU	GLY	GLY	VAL	LEU	LEU	SER	SER	GLN	VAL	HIS	ALA	LEU	LEU	THR	GLU	THR	LYS	ILE	ASP	LE	SER	GLY	GLY	ILE	ALA	ALA	SER	LYS	PRO	GLN	GLN	GLU	GLU	SER	GLU	THR	PHE	SER	SER	SER	HIS	VAL	MET	SER	ILE	ILE	LEU	LEU	GLU	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLN ARG ASN LEU LEU ALA LYS VAL VAL LEU LEU THR SER SER LEU LEU GLU GLU LEU LEU ALA ALA MET MET SER SER ARG ARG ARG ARG ASP ASP MET ASP ASP ASP PHE PHE THR THR THR THR LEU LEU LEU HIS GLY GLN THR THR ASP ASP ASP PRO PRO GLU GLU LEU LEU LYS LYS VAL VAL

VAL	ARG	ALA	ARG	ALA	ALA	LEU	ALA	ALA	ILE	PHE	GLU	ASP	PRO	GLU	ASP	GLU	GLU	PRO	ALA	ILE	VAL	VAL	LEU	SER	SER	HIS	LYS	VAL	ARG	GLN	GLN	VAL	ARG	GLN	ASP	TYR	LEU	LEU	VAL	PHE	GLU	ILE	ASP	TYR	GLU	VAL	ARG	PRO	GLY	VAL	SER	GLU	TYR	HIS	TYR	LEU	ARG	CYS	GLN	THR	ASP	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ASP	MET	GLU	LYS	TRP	LEU	TYR	ALA	LEU	MET	MET	SER	GLY	PHE	VAL	ALA	ALA	PRO	LYS	ALA	ALA	PRO	SER	LEU	PRO	GLN	ILE	PRO	LYS	LYS	ASP	SER	SER	LEU	SER	TRP	ILE	VAL	PRO	SER	SER	GLY	LYS	SER	PRO	GLU	GLY	GLY	HIS	SER	VAL	PRO	PRO	ILE	CYS	GLN	ASN	ASN	ALA	ALA	ALA	ALA	ALA	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

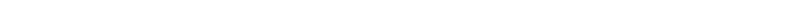
TYR	ASN	GLN	GLU	ASN	MET	LEU	ILE	CYS	GLU	ALA	LYS	GLY	ASP	PRO	SER	VAL	LEU	ILE	CYS	PRO	CYS	ASP	ARG	VAL	PHE	THR	GLU	ASP	ASP	ASN	GLY	VAL	ILE	GLN	PHE	HIS	LEU	LYS	GLU	THR	TYR	MET	LEU	LYS	ALA	PRO	LYS	GLU	THR	PHE	ILE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU	ILE	ALA	ALA	ILE	VAL	HIS	ARG	HIS	GLY	THR	TYR	ALA	ALA	SER	ARG	VAL	LYS	PRO	PRO	PRO	ARG	GLN	GLU	ALA	ALA	ALA	ALA	LYS	PRO	VAL	VAL	VAL	LYS	LYS	ALA	ASP	THR	PRO	ALA	ALA	GLU	PRO	PRO	ILE	LYS	LYS	ALA	GLU	LYS	GLU	GLY	GLU	ASP	GLU	LEU	PHE	ILE	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ARG	ASP	GLY	TYR	LEU	MET	LEU	MET	MET	HIS	ALA	ASN	ASP	PRO	GLU	PRO	PRO	LEU	LEU	LYS	PHE	HIS	SER	ASP	CYS	ILE	THR	THR	PRO	PRO	ASP	ASP	ALA	ASN	LYS	GLU	PHE	VAL	ILE	ILE	ARG	HIS	MET	PRO	PRO	GLY	THR	PRO	ASP	GLU	GLU	SER	TYR	VAL	PHE	PHE	PHE	LEU	THR	ASP	GLU	ILE	THR
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

[illegible]

- Molecule 13: ICAP16, TGME49 202120

Chain LN:  7% 92%

[illegible][illegible]















- Molecule 14: PCR12, TGME49_219070

98%







[illegible]

- Molecule 14: PCR12, TGME49_219070

Chain MF: 96%

ALA	GLY	K287	PRO	GLN	ARG	MET
VAL	VAL	R290	ALA	ALA	LEU	GLU
PRO	GLY	L291	VAL	ASN	THR	ARG
CYS	GLY	A292	LEU	ALA	SER	ARG
GLU	GLY	L293	ASP	ARG	LEU	MET
ARG	ASN	A294	ASN	SER	VAL	GLY
GLU	GLY	E295	LYS	ASP	ASN	ALA
SER	SER	S296	HIS	GLU	CYS	PRO
LEU	LEU	V297	LEU	GLY	PRO	THR
ARG	ARG		ARG	LYS	SER	SER
LEU	LEU	L301	LEU	ARG	ALA	ALA
LEU	LEU	E308	ARG	TYR	ALA	GLU
GLN	GLN	R309	ASP	PHE	THR	GLY
ALA	ALA	S310	ALA	GLY	GLY	GLY
ALA	ALA	T311	ASN	LEU	GLU	ASP
ASP	ASP	S312	GLU	ALA	LEU	GLY
ARG	ARG	R313	HIS	ARG	ALA	GLY
ILE	ILE	S314	CYS	ASP	ARG	GLY
ASP	ASP	W315	LEU	ALA	ARG	ASP
SER	SER	Q316	C203	ALA	TYR	PRO
ASP	ASP			ARG	GLY	PRO
ALA	ALA	R320	L210	GLY	PRO	ARG
LYS	LYS	Q323		SER	LEU	ARG
ARG	ARG	R324	L218	ILE	GLU	TYR
LEU	LEU	R325		SER	ALA	ARG
GLU	GLU	E326	Q227	LYS	HIS	ARG
VAL	VAL	L326		VAL	ALA	SER
TYR	TYR	L330	V230	VAL	PHE	LEU
SER	SER	L333	K243	MET	SER	ARG
ARG	ARG			LEU	SER	GLU
ILE	ILE		L264	GLU	LEU	ASP
ALA	ALA	R339		ALA	SER	LEU
GLU	GLU	SER	K257	GLY	ASP	GLU
LEU	LEU	GLY	L258	ALA	GLU	GLU
GLU	GLU	MET	M259	CYS	ASN	ALA
ARG	ARG	SER	N260	GLY	LYS	ARG
GLY	GLY	CYS	ASP	SER	LEU	LYS
VAL	VAL	ASP	PRO	SER	LYS	LEU
LYS	LYS	LEU	PHE	ALA	VAL	LEU
ASP	ASP	PHE	LEU	ARG	LYS	LYS
LEU	LEU	ARG	SER	GLY	LEU	LYS
ARG	ARG	GLY	ALA	ASP	GLN	LYS
PHE	PHE	GLY	LYS	VAL	SER	LYS
SER	SER	ILE	TYR	GLY	SER	MET
ASN	ASN	LEU	ALA	ASP	GLN	ASN
THR	THR	GLN	ALA	SER	ARG	GLU
ARG	ARG	ALA	ALA	PRO	ALA	LEU
LEU	LEU	ALA	GLY	PHE	GLU	GLY
ALA	ALA	GLU	THR	VAL	VAL	GLU
GLU	GLU	ALA	PRO	ARG	ARG	GLY
SER	SER	ALA	GLY	GLY	ALA	GLU
THR	THR	ALA	ALA	ASP	ILE	ASN
ARG	ARG	ARG	ARG	VAL	ARG	GLN
VAL	VAL	LEU	P278	VAL	ARG	ASN
LYS	LYS	THR	C382	GLY	ALA	ARG









[illegible]

- Molecule 14: PCR12, TGME49_219070

Chain MH: 98%

[illegible]











[illegible]

- Molecule 14: PCR12, TGME49 219070

Chain MK: 97%

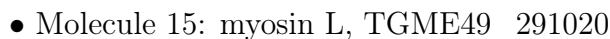
[illegible]

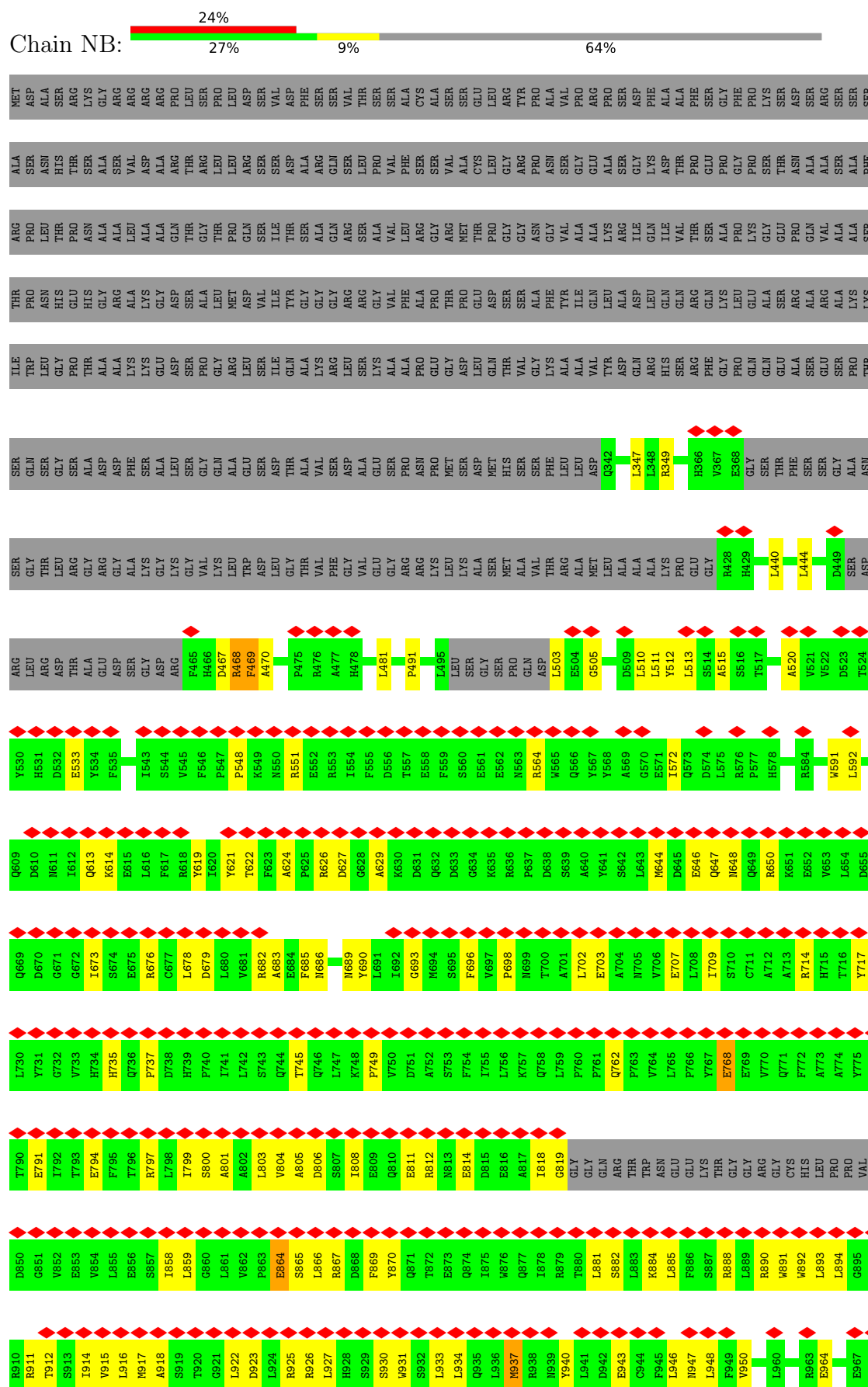










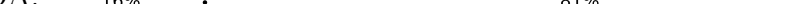




ALA	ALA	THR	LEU	K1472	R1473	ARG	ALA	THR	SER	ALA	P1157	ASN	L986	I897	THR	THR	F617
THR	THR	THR	THR	R1473	R1473	ALA	ALA	THR	THR	LYS	H1158	ARG	L987	N898	THR	THR	R618
ARG	ARG	ARG	ARG	L1478	L1478	GLN	GLN	GLU	VAL	LYS	T1159	ASN	Q988	D899	ASN	ASN	Y619
ILE	ILE	ILE	ILE	E1479	E1479	GLN	GLN	GLU	THR	ARG	L1160	VAL	Q989	A900	GLU	GLU	I620
ARG	ARG	ARG	ARG	R1482	R1482	LYS	LYS	LYS	THR	ASP	T1163	VAL	V999	R902	LYS	LYS	Y621
LYS	LYS	LYS	LYS	R1482	R1482	ASP	ASP	ASP	THR	THR	V1166	VAL	V1005	D905	THR	THR	T622
MET	MET	MET	MET	R1487	R1487	PRO	PRO	PRO	THR	PHE	V1169	VAL	S1008	R910	GLY	GLY	G628
THR	THR	THR	THR	R1488	R1488	ASP	ASP	ASP	THR	ALA	F1169	ALA	S1008	R911	GLY	GLY	A629
LEU	LEU	LEU	LEU	F1392	F1392	ASP	ASP	ASP	THR	ALA	M1173	GLN	N1014	R912	GLY	GLY	K630
SER	SER	SER	SER	H1386	H1386	VAL	VAL	VAL	THR	ILE	L1177	GLN	A1015	T912	CYS	CYS	D631
ARG	ARG	ARG	ARG	V1387	V1387	GLY	GLY	GLY	THR	GLY	L1177	GLN	D1022	S913	HIS	HIS	Q632
ASP	ASP	ASP	ASP	L1391	L1391	ASP	ASP	ASP	THR	ASN	D1180	GLY	S1027	I914	LEU	LEU	D633
LYS	LYS	LYS	LYS	L1397	L1397	GLY	GLY	GLY	THR	ASN	P1185	GLY	A1041	V915	PRO	PRO	G634
VAL	VAL	VAL	VAL	G1400	G1400	LYS	LYS	LYS	THR	ASN	P1185	GLY	A1042	L916	VAL	VAL	K635
ALA	ALA	ALA	ALA	H1404	H1404	ALA	ALA	ALA	THR	ALA	A1191	GLY	R1043	M917	ASN	ASN	R636
ALA	ALA	ALA	ALA	M1407	M1407	LYS	LYS	LYS	THR	ALA	S1192	GLY	R1043	S919	THR	THR	P637
THR	THR	THR	THR	T1442	T1442	THR	THR	THR	THR	THR	V1193	GLY	R1043	T920	THR	THR	D638
THR	THR	THR	THR	E1415	E1415	ASP	ASP	ASP	THR	THR	N1194	GLY	R1043	N943	THR	THR	S639
LEU	LEU	LEU	LEU	Y1420	Y1420	ASP	ASP	ASP	THR	THR	S1195	GLY	R1043	P944	THR	THR	A640
ALA	ALA	ALA	ALA	A1421	A1421	ASP	ASP	ASP	THR	THR	T1196	GLY	R1043	L845	THR	THR	Y641
TRP	TRP	TRP	TRP	V1422	V1422	ASP	ASP	ASP	THR	THR	R1197	GLY	R1043	G948	THR	THR	R650
TRP	TRP	TRP	TRP	P1426	P1426	ASP	ASP	ASP	THR	THR	I1198	GLY	R1043	V854	THR	THR	K651
GLY	GLY	GLY	GLY	ILE	ILE	ASP	ASP	ASP	THR	THR	GLU	GLY	R1043	L855	THR	THR	E652
ILE	ILE	ILE	ILE	VAL	VAL	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	L859	THR	THR	V653
LEU	LEU	LEU	LEU	TRP	TRP	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	T858	THR	THR	L660
ALA	ALA	ALA	ALA	S1521	S1521	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	V862	THR	THR	R661
ALA	ALA	ALA	ALA	R1524	R1524	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	P863	THR	THR	I666
ILE	ILE	ILE	ILE	R1525	R1525	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	E864	THR	THR	T667
GLN	GLN	GLN	GLN	I1526	I1526	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	S865	THR	THR	I792
ALA	ALA	ALA	ALA	V1527	V1527	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	L866	THR	THR	T793
ALA	ALA	ALA	ALA	S1528	S1528	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	R867	THR	THR	E794
ALA	ALA	ALA	ALA	Q1531	Q1531	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	D868	THR	THR	I673
GLY	GLY	GLY	GLY	Q1536	Q1536	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	F869	THR	THR	C677
MET	MET	MET	MET	K1537	K1537	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	Y870	THR	THR	L680
GLN	GLN	GLN	GLN	V1538	V1538	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	I878	THR	THR	V681
ALA	ALA	ALA	ALA	I1539	I1539	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	R879	THR	THR	R682
ALA	ALA	ALA	ALA	V1545	V1545	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	T880	THR	THR	F685
VAL	VAL	VAL	VAL	V1546	V1546	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	L881	THR	THR	N686
VAL	VAL	VAL	VAL	M1550	M1550	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	S882	THR	THR	Y690
THR	THR	THR	THR	H1551	H1551	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	L883	THR	THR	L691
THR	THR	THR	THR	I1552	I1552	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	K884	THR	THR	I692
ALA	ALA	ALA	ALA	Q1553	Q1553	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	L885	THR	THR	I696
ALA	ALA	ALA	ALA	K1554	K1554	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	R888	THR	THR	V697
ILE	ILE	ILE	ILE	Y1555	Y1555	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	L889	THR	THR	P698
ILE	ILE	ILE	ILE	ARG	ARG	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	R890	THR	THR	N699
ASN	ASN	ASN	ASN	ASP	ASP	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	W891	THR	THR	T700
ASN	ASN	ASN	ASN	SER	SER	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	W892	THR	THR	E707
ASN	ASN	ASN	ASN	SER	SER	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	L893	THR	THR	L708
ASN	ASN	ASN	ASN	SER	SER	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	W892	THR	THR	I709
ASN	ASN	ASN	ASN	SER	SER	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	L894	THR	THR	L708
ASN	ASN	ASN	ASN	SER	SER	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	W892	THR	THR	I709
ASN	ASN	ASN	ASN	SER	SER	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	L895	THR	THR	S710
ASN	ASN	ASN	ASN	SER	SER	ASP	ASP	ASP	THR	THR	LEU	GLY	R1043	R896	THR	THR	C711





Chain OA:  16% . 81%





Chain OB:





Chain OC: 16% . 81%

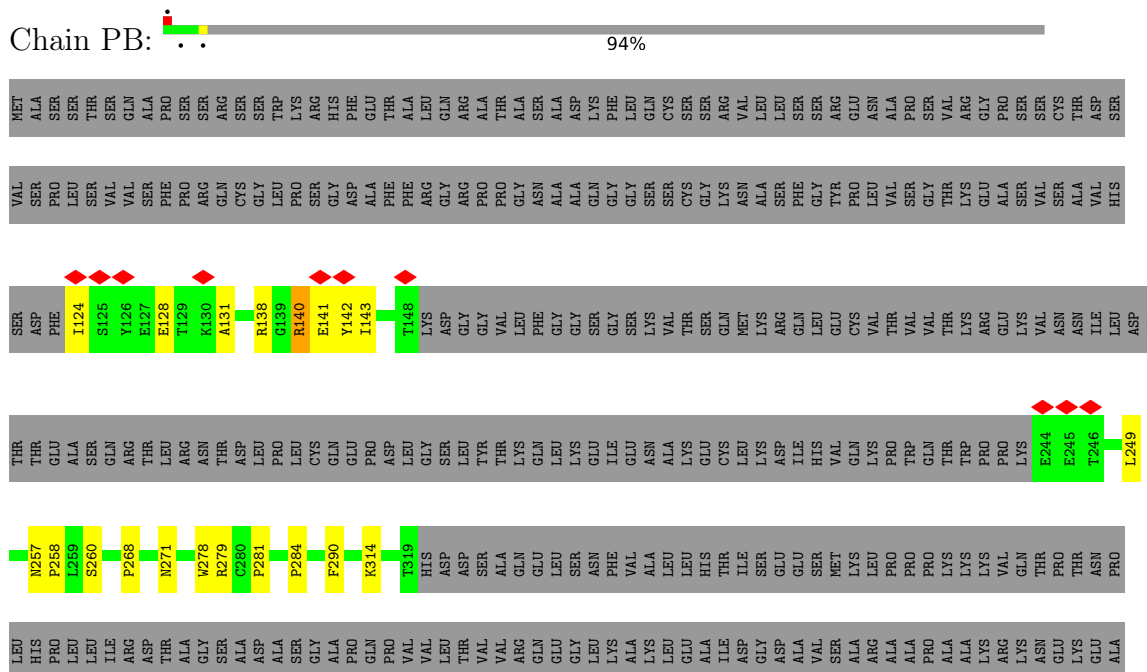


- Molecule 17: PCR15, TGME49 232560



[illegible]

- Molecule 17: PCR15, TGME49_232560



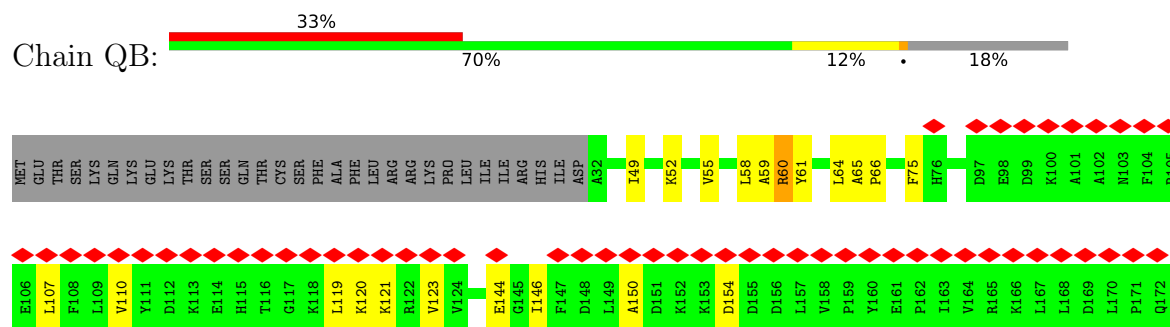


[illegible]

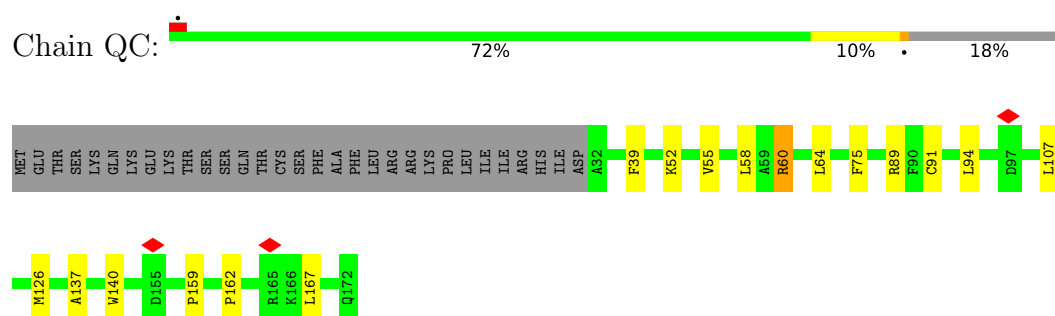
- Molecule 17: PCR15, TGME49 232560

[illegible]

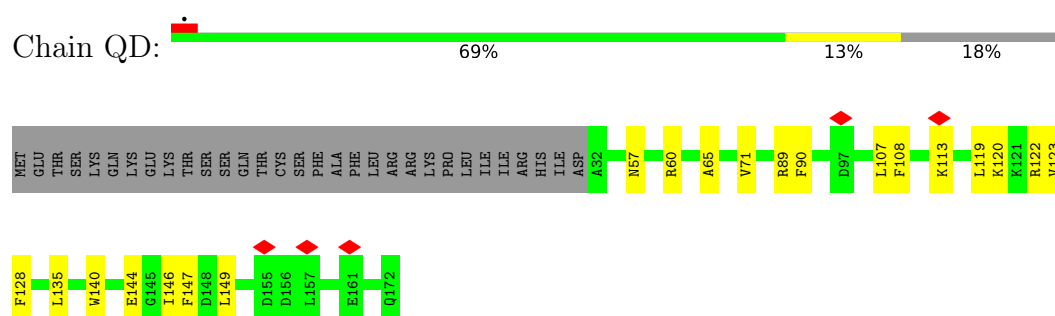
- Molecule 18: MLC4, TGME49_294390



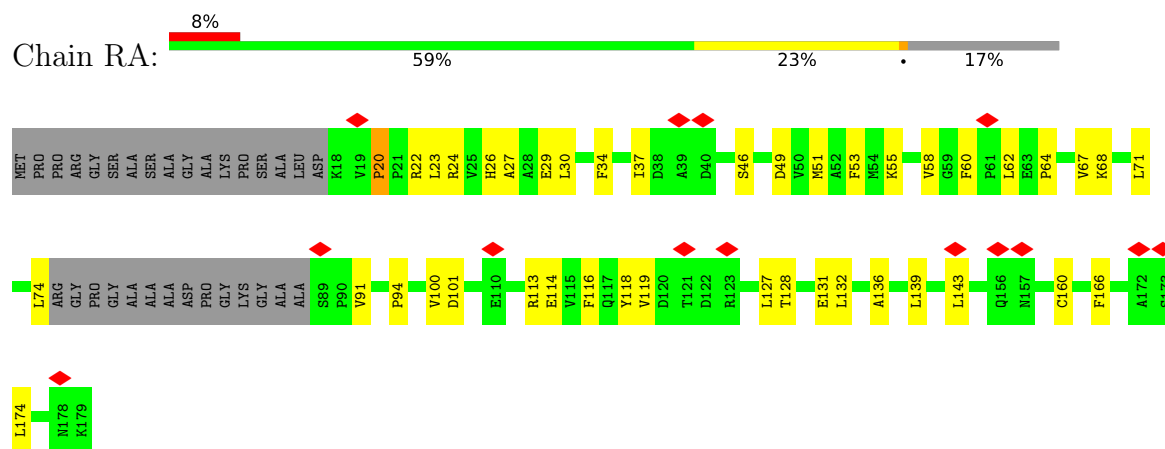
- Molecule 18: MLC4, TGME49_294390



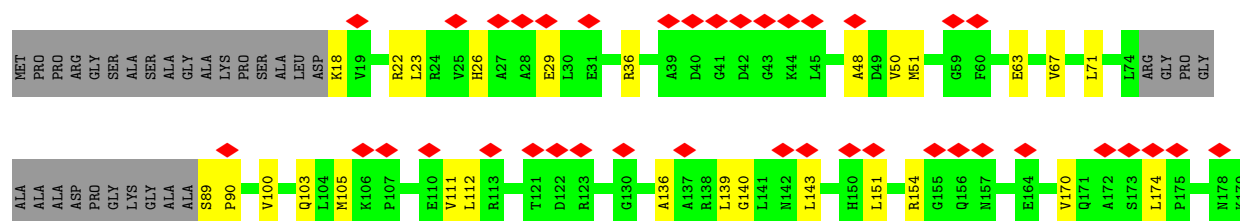
- Molecule 18: MLC4, TGME49_294390



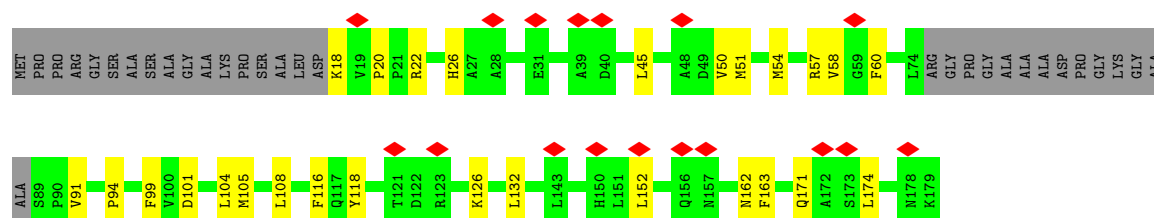
- Molecule 19: Calmodulin



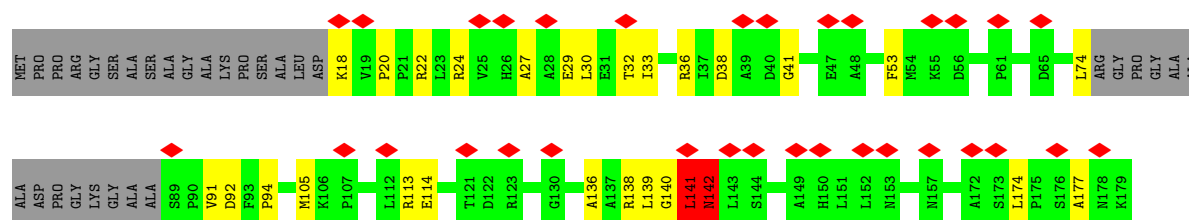
- Molecule 19: Calmodulin



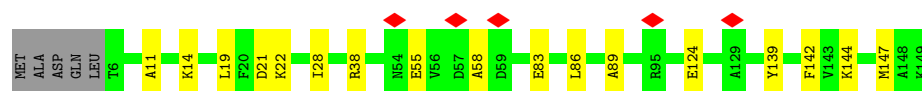
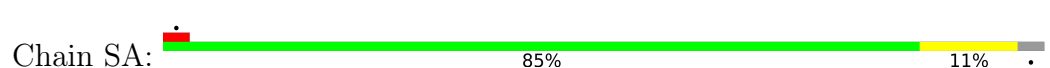
• Molecule 19: Calmodulin



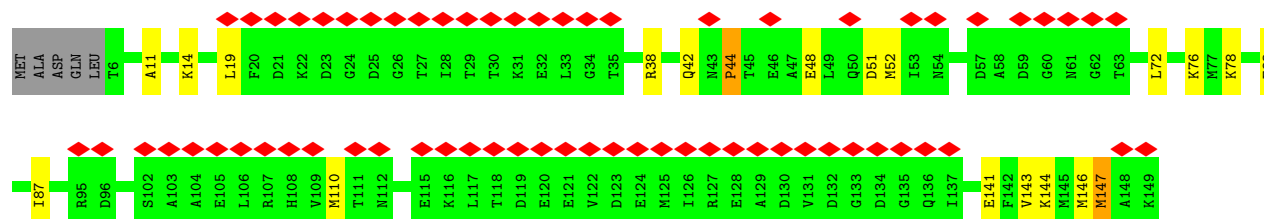
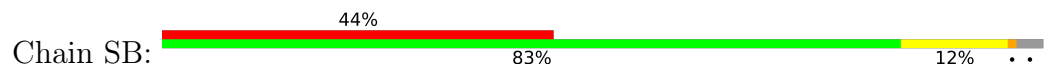
• Molecule 19: Calmodulin



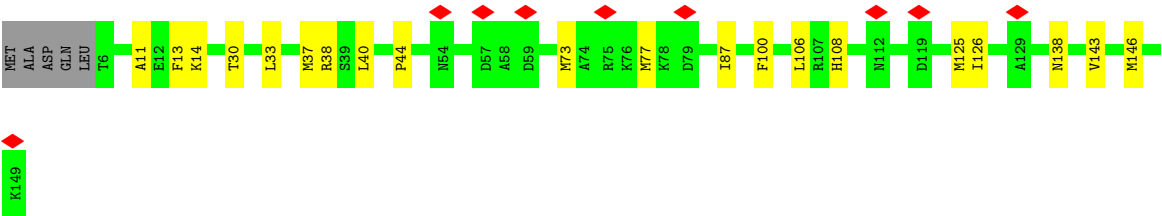
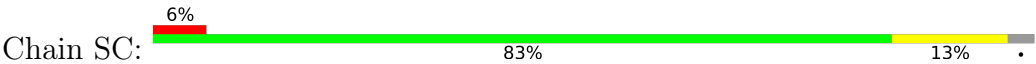
• Molecule 20: Calmodulin



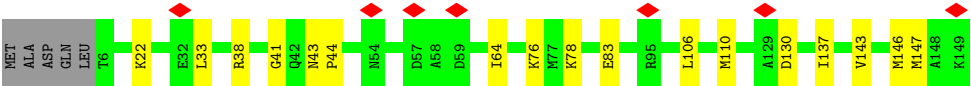
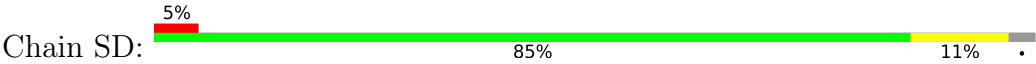
• Molecule 20: Calmodulin



• Molecule 20: Calmodulin



• Molecule 20: Calmodulin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	131707	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.073	Depositor
Minimum map value	0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	686.08, 686.08, 686.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AA	0.24	1/6682 (0.0%)	0.65	5/9057 (0.1%)
1	AD	0.22	0/6958	0.58	0/9433
1	AE	0.24	0/6682	0.67	4/9057 (0.0%)
1	AH	0.22	0/6958	0.59	3/9433 (0.0%)
1	AI	0.24	0/6682	0.64	3/9057 (0.0%)
1	AL	0.23	0/6958	0.57	0/9433
2	AB	0.34	1/3898 (0.0%)	0.66	4/5265 (0.1%)
2	AC	0.20	0/3926	0.51	0/5305
2	AF	0.25	0/3898	0.65	3/5265 (0.1%)
2	AG	0.21	0/3926	0.54	0/5305
2	AJ	0.23	0/3892	0.60	2/5258 (0.0%)
2	AK	0.22	0/3926	0.57	1/5305 (0.0%)
3	BA	0.22	0/2777	0.60	0/3759
3	BB	0.23	0/2777	0.62	0/3759
3	BC	0.22	0/2777	0.64	0/3759
3	CA	0.23	0/2762	0.60	1/3738 (0.0%)
3	CB	0.23	0/2762	0.62	0/3738
3	CC	0.22	0/2762	0.61	1/3738 (0.0%)
3	CE	0.24	0/1921	0.66	0/2628
3	CF	0.28	0/1921	0.74	0/2628
3	CG	0.32	0/1921	0.74	0/2628
3	CI	0.23	0/2062	0.68	0/2816
3	CJ	0.25	0/2062	0.67	1/2816 (0.0%)
3	CL	0.24	0/2062	0.69	0/2816
4	DA	0.27	0/2795	0.74	6/3763 (0.2%)
4	DB	0.25	0/2795	0.70	2/3763 (0.1%)
4	DC	0.26	0/2795	0.73	2/3763 (0.1%)
4	DD	0.23	0/2672	0.63	3/3600 (0.1%)
4	DE	0.24	0/2672	0.69	3/3600 (0.1%)
4	DF	0.25	0/2672	0.68	0/3600
5	EA	0.24	0/10890	0.64	2/14730 (0.0%)
5	EB	0.28	0/10890	0.66	4/14730 (0.0%)
5	EC	0.28	0/10886	0.67	7/14726 (0.0%)
6	FA	0.39	0/4286	0.77	2/5798 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	FB	0.34	0/4286	0.70	0/5798
6	FC	0.57	0/4286	0.89	1/5798 (0.0%)
6	FD	0.98	0/3323	1.16	4/4521 (0.1%)
6	FE	0.98	0/3329	1.12	3/4528 (0.1%)
6	FF	0.98	0/3245	1.11	2/4410 (0.0%)
7	GA	0.25	0/6456	0.59	10/8779 (0.1%)
7	GC	0.25	1/6087 (0.0%)	0.61	0/8272
7	GE	0.24	0/6087	0.62	0/8272
7	GG	0.24	0/6456	0.61	11/8779 (0.1%)
7	GI	0.24	0/6087	0.64	0/8272
7	GK	0.23	0/6456	0.58	9/8779 (0.1%)
8	GB	0.23	0/6087	0.61	3/8257 (0.0%)
8	GD	0.23	0/6087	0.61	1/8257 (0.0%)
8	GF	0.19	0/6301	0.52	2/8556 (0.0%)
8	GH	0.24	0/5913	0.66	5/8019 (0.1%)
8	GJ	0.21	0/6301	0.55	0/8556
8	GL	0.21	0/6301	0.59	3/8556 (0.0%)
9	HA	0.67	3/3439 (0.1%)	0.95	7/4668 (0.1%)
9	HB	0.66	1/3439 (0.0%)	0.93	9/4668 (0.2%)
9	HC	0.27	0/2345	0.73	7/3182 (0.2%)
9	HD	1.11	1/1094 (0.1%)	1.24	0/1486
10	IA	0.22	0/9289	0.59	6/12571 (0.0%)
10	IB	0.22	0/9289	0.61	6/12571 (0.0%)
10	IC	0.22	1/9289 (0.0%)	0.60	4/12571 (0.0%)
11	JA	0.25	0/12997	0.67	16/17611 (0.1%)
11	JB	0.23	0/12997	0.66	18/17611 (0.1%)
11	JC	0.24	0/12997	0.68	9/17611 (0.1%)
12	KA	0.29	0/3752	0.83	5/5093 (0.1%)
12	KB	0.29	0/3752	0.79	2/5093 (0.0%)
12	KC	0.39	0/3746	0.90	7/5086 (0.1%)
12	KE	0.18	0/3616	0.52	0/4901
12	KF	0.18	0/3616	0.49	0/4901
12	KG	0.20	0/3616	0.55	0/4901
13	LA	0.18	0/1524	0.51	1/2040 (0.0%)
13	LB	0.17	0/1536	0.51	0/2055
13	LC	0.18	0/1318	0.47	0/1763
13	LD	0.16	0/1310	0.51	0/1753
13	LE	0.24	0/1195	0.70	5/1598 (0.3%)
13	LF	0.22	0/1202	0.66	3/1606 (0.2%)
13	LG	0.21	0/464	0.53	0/623
13	LH	0.22	0/451	0.70	0/605
13	LI	0.38	0/1524	0.77	2/2040 (0.1%)
13	LJ	0.26	0/1536	0.74	3/2055 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
13	LK	0.15	0/1326	0.50	0/1774
13	LL	0.21	0/1310	0.58	1/1753 (0.1%)
13	LM	0.16	0/862	0.50	0/1151
13	LN	0.17	0/859	0.55	0/1148
13	LO	0.16	0/844	0.55	0/1127
13	LP	0.18	0/885	0.56	0/1183
14	MA	0.27	0/1144	0.80	2/1541 (0.1%)
14	MB	0.24	0/981	0.72	1/1315 (0.1%)
14	MC	0.17	0/601	0.51	0/807
14	MD	0.16	0/527	0.40	0/703
14	ME	0.30	0/1144	0.85	2/1541 (0.1%)
14	MF	0.27	0/981	0.83	1/1315 (0.1%)
14	MG	0.21	0/601	0.59	0/807
14	MH	0.17	0/527	0.52	0/703
14	MI	0.26	0/1144	0.78	0/1541
14	MJ	0.32	0/981	0.88	3/1315 (0.2%)
14	MK	0.18	0/601	0.51	0/807
14	ML	0.30	0/527	0.61	0/703
15	NA	0.27	0/7422	0.71	9/10053 (0.1%)
15	NB	0.24	0/7422	0.64	4/10053 (0.0%)
15	NC	0.28	0/7422	0.74	6/10053 (0.1%)
15	ND	0.27	0/7422	0.72	17/10053 (0.2%)
16	OA	0.24	0/3570	0.69	4/4821 (0.1%)
16	OB	0.24	0/3570	0.70	3/4821 (0.1%)
16	OC	0.25	0/3570	0.72	4/4821 (0.1%)
17	PA	0.26	0/831	0.74	2/1127 (0.2%)
17	PB	0.28	0/831	0.77	2/1127 (0.2%)
17	PC	0.25	0/831	0.69	0/1127
18	QA	0.22	0/1151	0.59	0/1548
18	QB	0.20	0/1151	0.52	0/1548
18	QC	0.21	0/1151	0.58	0/1548
18	QD	0.25	0/1151	0.59	0/1548
19	RA	0.28	0/1163	0.71	0/1573
19	RB	0.22	0/1163	0.63	0/1573
19	RC	0.24	0/1163	0.65	0/1573
19	RD	0.27	0/1163	0.86	7/1573 (0.4%)
20	SA	0.25	0/1146	0.65	0/1536
20	SB	0.19	0/1146	0.56	1/1536 (0.1%)
20	SC	0.23	0/1146	0.65	0/1536
20	SD	0.23	0/1146	0.64	0/1536
All	All	0.31	9/423302 (0.0%)	0.67	292/573059 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	3
1	AE	0	5
1	AI	0	3
1	AL	0	2
2	AB	0	3
2	AC	0	1
2	AK	0	1
3	BC	0	1
3	CB	0	1
3	CC	0	1
3	CF	0	2
3	CG	0	1
3	CL	0	1
4	DC	0	1
4	DD	0	1
5	EA	0	5
5	EB	0	6
5	EC	0	7
6	FA	0	8
6	FB	0	3
6	FC	0	13
6	FD	0	26
6	FE	0	22
6	FF	0	26
7	GA	0	6
7	GC	0	1
7	GE	0	1
7	GG	0	8
7	GI	0	1
7	GK	0	7
8	GB	0	4
8	GD	0	4
8	GF	0	1
8	GH	0	6
8	GJ	0	4
8	GL	0	4
9	HA	0	8
9	HB	0	7
9	HC	0	2
9	HD	0	5

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
10	IA	0	2
10	IB	0	1
10	IC	0	1
11	JA	0	10
11	JB	0	7
11	JC	0	10
12	KA	0	5
12	KB	0	4
12	KC	0	5
12	KE	0	1
12	KF	0	1
12	KG	0	2
13	LE	0	4
13	LF	0	1
13	LI	0	3
13	LJ	0	2
13	LO	0	1
14	MC	0	1
14	ME	0	3
14	MG	0	1
14	MI	0	2
14	MJ	0	2
14	MK	0	1
15	NA	0	5
15	NB	0	5
15	NC	0	10
15	ND	0	7
16	OA	0	3
16	OB	0	2
16	OC	0	1
17	PB	0	1
18	QB	0	1
18	QC	0	1
19	RA	0	1
19	RB	0	1
19	RD	0	4
20	SB	0	1
All	All	0	325

All (9) bond length outliers are listed below:

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
-----	-------	-----	------	-------	---	-------------	----------

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	415	HIS	C-O	8.28	1.33	1.24
9	HA	749	ASN	C-O	6.18	1.31	1.24
9	HB	749	ASN	C-O	6.12	1.31	1.24
9	HD	749	ASN	C-O	5.95	1.31	1.24
1	AA	714	PHE	CA-C	5.84	1.60	1.52
9	HA	763	GLN	C-O	5.43	1.30	1.24
9	HA	760	LYS	C-O	5.31	1.30	1.24
7	GC	875	GLU	CA-CB	5.19	1.61	1.52
10	IC	593	PRO	CA-C	-5.02	1.49	1.51

All (292) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	RD	141	LEU	CA-CB-CG	10.66	153.62	116.30
19	RD	141	LEU	CB-CA-C	9.90	130.13	110.42
7	GK	546	SER	N-CA-C	9.12	121.58	110.91
7	GA	543	LYS	N-CA-C	8.84	129.34	109.81
7	GG	543	LYS	N-CA-C	8.81	129.28	109.81
11	JB	767	GLY	CA-C-N	8.56	137.89	121.54
11	JB	767	GLY	C-N-CA	8.56	137.89	121.54
11	JC	767	GLY	CA-C-N	8.53	137.83	121.54
11	JC	767	GLY	C-N-CA	8.53	137.83	121.54
15	ND	1550	MET	CB-CG-SD	8.36	137.79	112.70
7	GK	547	GLY	N-CA-C	8.20	120.54	111.85
1	AH	735	LEU	CA-C-N	7.97	131.81	120.49
1	AH	735	LEU	C-N-CA	7.97	131.81	120.49
7	GA	542	GLY	CA-C-N	7.90	141.09	121.80
7	GA	542	GLY	C-N-CA	7.90	141.09	121.80
5	EC	3704	SER	CA-C-N	7.88	136.59	121.54
5	EC	3704	SER	C-N-CA	7.88	136.59	121.54
9	HB	553	TYR	CA-CB-CG	7.74	127.83	113.90
1	AE	640	GLN	CA-CB-CG	7.56	129.22	114.10
11	JA	1012	ARG	CG-CD-NE	-7.36	95.80	112.00
15	ND	1153	ALA	N-CA-C	7.35	123.75	108.53
9	HB	649	ASP	CA-C-N	7.34	135.57	121.54
9	HB	649	ASP	C-N-CA	7.34	135.57	121.54
11	JA	1305	ASP	CA-C-N	7.28	124.83	120.24
11	JA	1305	ASP	C-N-CA	7.28	124.83	120.24
4	DE	170	ARG	CA-CB-CG	7.24	128.59	114.10
8	GH	671	PHE	N-CA-C	-7.24	105.36	114.56

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	MJ	286	GLU	CA-C-N	7.24	135.36	121.54
14	MJ	286	GLU	C-N-CA	7.24	135.36	121.54
7	GK	543	LYS	N-CA-C	7.19	125.69	109.81
4	DA	308	GLN	CA-C-N	7.01	134.58	121.97
4	DA	308	GLN	C-N-CA	7.01	134.58	121.97
13	LI	513	LEU	CB-CG-CD2	-6.98	89.75	110.70
5	EC	4651	MET	CB-CG-SD	-6.97	91.79	112.70
7	GA	855	ARG	CA-C-N	6.94	134.47	121.97
7	GA	855	ARG	C-N-CA	6.94	134.47	121.97
9	HC	649	ASP	CA-C-N	6.94	134.80	121.54
9	HC	649	ASP	C-N-CA	6.94	134.80	121.54
19	RD	141	LEU	CB-CG-CD1	6.94	131.51	110.70
12	KC	377	LEU	N-CA-C	-6.92	104.71	113.01
5	EB	3262	VAL	N-CA-C	-6.87	107.18	113.71
7	GG	542	GLY	CA-C-N	6.87	138.56	121.80
7	GG	542	GLY	C-N-CA	6.87	138.56	121.80
14	MB	278	PRO	N-CA-CB	6.87	110.55	103.00
14	MJ	278	PRO	N-CA-CB	6.83	110.51	103.00
11	JC	969	ALA	CA-C-N	6.83	133.91	120.94
11	JC	969	ALA	C-N-CA	6.83	133.91	120.94
19	RD	142	ASN	N-CA-CB	6.80	121.98	110.49
6	FD	862	GLU	N-CA-C	-6.79	106.89	114.62
14	MF	278	PRO	N-CA-CB	6.76	110.44	103.00
9	HC	551	GLU	CA-C-N	6.72	134.38	121.54
9	HC	551	GLU	C-N-CA	6.72	134.38	121.54
20	SB	147	MET	CA-CB-CG	6.67	127.44	114.10
11	JB	1875	ILE	N-CA-C	-6.64	106.52	111.90
2	AB	419	LYS	O-C-N	-6.63	113.69	121.32
6	FA	2010	LYS	N-CA-C	-6.54	104.07	111.07
10	IA	1068	ARG	CB-CG-CD	6.53	126.33	111.30
10	IC	779	ASP	CA-C-N	6.48	134.11	122.13
10	IC	779	ASP	C-N-CA	6.48	134.11	122.13
15	NA	468	ARG	CA-C-N	6.44	133.84	121.54
15	NA	468	ARG	C-N-CA	6.44	133.84	121.54
4	DA	98	ARG	CA-CB-CG	6.44	126.98	114.10
9	HA	553	TYR	CA-CB-CG	6.35	125.33	113.90
15	NC	1153	ALA	N-CA-C	6.35	120.67	112.41
8	GL	77	THR	CA-C-N	6.35	137.29	121.80
8	GL	77	THR	C-N-CA	6.35	137.29	121.80
12	KB	671	LEU	CA-C-N	6.33	133.62	121.54
12	KB	671	LEU	C-N-CA	6.33	133.62	121.54
19	RD	141	LEU	CA-C-O	-6.32	111.48	120.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	ND	1549	GLY	N-CA-C	6.30	128.12	113.18
6	FC	1709	GLU	CA-CB-CG	6.29	126.69	114.10
10	IB	779	ASP	CA-C-N	6.28	133.75	122.13
10	IB	779	ASP	C-N-CA	6.28	133.75	122.13
11	JB	135	ILE	N-CA-C	-6.27	107.39	113.53
16	OA	1089	LEU	CA-C-N	6.23	133.44	121.54
16	OA	1089	LEU	C-N-CA	6.23	133.44	121.54
10	IA	779	ASP	CA-C-N	6.23	133.65	122.13
10	IA	779	ASP	C-N-CA	6.23	133.65	122.13
7	GA	537	GLY	N-CA-C	6.22	127.93	113.18
11	JB	451	MET	CA-CB-CG	6.19	126.48	114.10
8	GF	56	CYS	CA-C-N	6.19	133.36	121.54
8	GF	56	CYS	C-N-CA	6.19	133.36	121.54
4	DA	385	LYS	N-CA-C	6.18	118.68	108.48
7	GG	539	TYR	N-CA-C	6.18	116.02	107.73
9	HA	551	GLU	CA-C-N	6.18	133.35	121.54
9	HA	551	GLU	C-N-CA	6.18	133.35	121.54
11	JA	1588	GLU	CA-C-N	6.17	133.31	121.54
11	JA	1588	GLU	C-N-CA	6.17	133.31	121.54
15	ND	1155	GLU	CA-C-N	6.17	136.84	121.80
15	ND	1155	GLU	C-N-CA	6.17	136.84	121.80
10	IB	397	VAL	N-CA-C	-6.16	107.86	113.71
8	GH	199	ARG	CB-CG-CD	-6.15	97.16	111.30
7	GA	538	THR	N-CA-C	6.13	123.86	110.80
15	NB	468	ARG	CA-C-N	6.12	133.23	121.54
15	NB	468	ARG	C-N-CA	6.12	133.23	121.54
10	IA	711	VAL	N-CA-C	-6.08	107.57	113.53
1	AA	670	ASP	N-CA-C	-6.08	97.85	110.80
6	FF	913	LEU	N-CA-C	-6.06	104.75	111.36
15	NA	1153	ALA	N-CA-C	6.04	120.26	112.41
12	KA	685	ARG	CA-C-N	6.04	136.53	121.80
12	KA	685	ARG	C-N-CA	6.04	136.53	121.80
7	GK	542	GLY	CA-C-N	6.03	136.51	121.80
7	GK	542	GLY	C-N-CA	6.03	136.51	121.80
4	DB	308	GLN	CA-C-N	6.03	132.82	121.97
4	DB	308	GLN	C-N-CA	6.03	132.82	121.97
7	GG	546	SER	N-CA-C	6.03	123.64	110.80
7	GA	541	GLY	N-CA-C	6.01	127.42	113.18
7	GK	545	GLY	N-CA-C	6.01	127.42	113.18
11	JA	741	PHE	CA-C-N	6.00	132.78	121.97
11	JA	741	PHE	C-N-CA	6.00	132.78	121.97
16	OC	1089	LEU	CA-C-N	6.00	133.01	121.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	OC	1089	LEU	C-N-CA	6.00	133.01	121.54
11	JC	147	ARG	N-CA-C	-5.98	103.91	111.92
4	DA	384	ILE	CA-C-N	-5.97	114.47	121.64
4	DA	384	ILE	C-N-CA	-5.97	114.47	121.64
9	HB	750	PRO	N-CA-C	-5.97	105.15	113.81
9	HC	552	ASP	N-CA-C	5.97	123.51	110.80
7	GG	545	GLY	CA-C-N	5.96	132.93	121.54
7	GG	545	GLY	C-N-CA	5.96	132.93	121.54
7	GK	537	GLY	N-CA-C	5.95	127.28	113.18
15	ND	1408	THR	N-CA-C	5.95	119.36	111.75
16	OB	1089	LEU	CA-C-N	5.93	132.87	121.54
16	OB	1089	LEU	C-N-CA	5.93	132.87	121.54
4	DE	16	LEU	CA-CB-CG	5.92	137.02	116.30
11	JC	135	ILE	N-CA-C	-5.92	107.73	113.53
8	GH	189	ASN	CA-C-N	5.89	132.58	121.97
8	GH	189	ASN	C-N-CA	5.89	132.58	121.97
7	GK	538	THR	N-CA-C	5.89	123.35	110.80
11	JB	450	PHE	CA-C-N	5.89	132.79	121.54
11	JB	450	PHE	C-N-CA	5.89	132.79	121.54
14	MA	283	GLN	N-CA-C	-5.88	107.34	114.75
12	KC	382	ARG	N-CA-C	-5.86	106.09	113.18
11	JA	1092	HIS	CA-C-N	5.84	136.05	121.80
11	JA	1092	HIS	C-N-CA	5.84	136.05	121.80
15	ND	468	ARG	CA-CB-CG	5.83	125.77	114.10
11	JB	147	ARG	N-CA-C	-5.83	104.11	111.92
4	DD	85	VAL	N-CA-C	-5.82	106.73	111.91
5	EC	4652	LEU	CA-C-N	5.81	132.63	121.54
5	EC	4652	LEU	C-N-CA	5.81	132.63	121.54
11	JC	1092	HIS	CA-C-N	5.81	135.97	121.80
11	JC	1092	HIS	C-N-CA	5.81	135.97	121.80
16	OB	882	ARG	CA-CB-CG	5.81	125.72	114.10
15	ND	1153	ALA	CA-C-N	5.79	132.68	121.63
15	ND	1153	ALA	C-N-CA	5.79	132.68	121.63
3	CJ	1131	LEU	CA-CB-CG	5.76	136.46	116.30
15	ND	1550	MET	N-CA-C	5.76	120.84	113.18
9	HA	552	ASP	N-CA-C	5.75	123.06	110.80
4	DD	189	ARG	CG-CD-NE	-5.75	99.35	112.00
14	MA	259	MET	CA-CB-CG	5.75	125.59	114.10
13	LF	521	ASN	CA-C-N	5.75	132.51	121.54
13	LF	521	ASN	C-N-CA	5.75	132.51	121.54
13	LF	522	ARG	N-CA-C	5.74	123.02	110.80
11	JB	178	HIS	CA-C-N	5.73	135.79	121.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	JB	178	HIS	C-N-CA	5.73	135.79	121.80
7	GG	538	THR	N-CA-C	5.73	123.01	110.80
8	GL	83	GLN	CB-CG-CD	5.73	122.34	112.60
7	GG	537	GLY	N-CA-C	5.72	126.75	113.18
4	DC	308	GLN	CA-C-N	5.70	132.23	121.97
4	DC	308	GLN	C-N-CA	5.70	132.23	121.97
9	HC	553	TYR	CA-CB-CG	5.70	124.16	113.90
11	JB	1092	HIS	CA-C-N	5.70	135.70	121.80
11	JB	1092	HIS	C-N-CA	5.70	135.70	121.80
11	JA	450	PHE	CA-C-N	5.69	132.40	121.54
11	JA	450	PHE	C-N-CA	5.69	132.40	121.54
11	JB	415	LYS	CA-CB-CG	5.68	125.47	114.10
2	AJ	344	GLU	CA-C-N	5.67	128.73	120.51
2	AJ	344	GLU	C-N-CA	5.67	128.73	120.51
15	NA	891	TRP	N-CA-C	5.67	117.70	110.61
11	JB	462	SER	CA-C-N	5.66	132.15	121.97
11	JB	462	SER	C-N-CA	5.66	132.15	121.97
7	GK	542	GLY	N-CA-C	5.65	126.58	113.18
17	PB	140	ARG	CA-C-N	5.64	132.31	121.54
17	PB	140	ARG	C-N-CA	5.64	132.31	121.54
11	JA	767	GLY	CA-C-N	5.62	132.28	121.54
11	JA	767	GLY	C-N-CA	5.62	132.28	121.54
6	FF	1005	PRO	CB-CA-C	5.62	117.78	110.92
13	LJ	416	ARG	CA-CB-CG	5.62	125.33	114.10
9	HB	553	TYR	CB-CA-C	-5.61	99.26	110.42
13	LE	464	ASP	CA-C-N	5.60	132.06	121.97
13	LE	464	ASP	C-N-CA	5.60	132.06	121.97
6	FE	1011	TYR	CB-CA-C	5.60	116.47	110.65
11	JA	451	MET	CA-CB-CG	5.59	125.28	114.10
10	IC	172	GLN	CB-CA-C	-5.59	110.12	116.54
15	NA	1423	LEU	CB-CA-C	-5.59	109.14	115.79
13	LA	513	LEU	CB-CG-CD2	-5.58	93.94	110.70
17	PA	140	ARG	CA-C-N	5.58	132.20	121.54
17	PA	140	ARG	C-N-CA	5.58	132.20	121.54
15	NC	691	LEU	N-CA-C	5.54	117.39	110.91
7	GG	542	GLY	N-CA-C	5.54	126.30	113.18
11	JA	2004	GLY	CA-C-N	5.54	131.93	121.97
11	JA	2004	GLY	C-N-CA	5.54	131.93	121.97
12	KC	359	VAL	CA-C-N	5.51	132.06	121.54
12	KC	359	VAL	C-N-CA	5.51	132.06	121.54
1	AA	43	ASP	CA-C-N	5.49	128.40	120.38
1	AA	43	ASP	C-N-CA	5.49	128.40	120.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	ND	468	ARG	CA-C-N	5.48	132.01	121.54
15	ND	468	ARG	C-N-CA	5.48	132.01	121.54
15	ND	1423	LEU	CB-CA-C	-5.48	109.27	115.79
13	LJ	413	GLU	CA-CB-CG	5.46	125.02	114.10
12	KC	633	ARG	CB-CA-C	-5.46	109.29	115.79
7	GA	544	PRO	N-CA-C	5.44	120.85	111.77
15	NA	1408	THR	N-CA-C	5.44	118.71	111.75
6	FA	1964	MET	CB-CG-SD	-5.43	96.40	112.70
9	HB	481	ALA	CA-C-N	5.43	131.91	121.54
9	HB	481	ALA	C-N-CA	5.43	131.91	121.54
1	AA	898	PRO	N-CA-C	5.41	123.62	112.47
13	LE	467	GLN	N-CA-C	-5.38	107.37	114.31
4	DD	16	LEU	CA-CB-CG	5.38	135.12	116.30
3	CA	1011	MET	CB-CG-SD	5.37	128.81	112.70
15	NA	1471	ARG	CA-C-N	5.37	131.79	121.54
15	NA	1471	ARG	C-N-CA	5.37	131.79	121.54
2	AK	50	ILE	N-CA-C	-5.37	107.89	113.10
9	HC	551	GLU	N-CA-C	5.36	116.88	109.54
19	RD	141	LEU	N-CA-CB	-5.34	101.46	110.49
13	LE	472	GLY	N-CA-C	-5.33	105.36	110.21
6	FD	829	ARG	N-CA-C	-5.32	107.81	114.56
15	NC	468	ARG	CA-C-N	5.32	131.69	121.54
15	NC	468	ARG	C-N-CA	5.32	131.69	121.54
13	LL	522	ARG	CA-CB-CG	5.31	124.73	114.10
2	AF	541	PRO	CA-C-N	5.31	131.69	121.54
2	AF	541	PRO	C-N-CA	5.31	131.69	121.54
7	GG	541	GLY	N-CA-C	5.31	125.77	113.18
5	EB	4653	GLU	CB-CA-C	-5.30	109.49	115.79
10	IB	357	PHE	CA-C-N	5.29	132.70	123.91
10	IB	357	PHE	C-N-CA	5.29	132.70	123.91
13	LJ	531	VAL	N-CA-C	-5.29	108.68	113.71
10	IA	916	LYS	CA-C-N	5.25	126.90	122.28
10	IA	916	LYS	C-N-CA	5.25	126.90	122.28
15	ND	1524	ARG	CA-CB-CG	5.24	124.58	114.10
6	FE	913	LEU	N-CA-C	-5.24	106.84	114.12
12	KC	388	PRO	CA-C-N	5.22	131.51	121.54
12	KC	388	PRO	C-N-CA	5.22	131.51	121.54
16	OA	1103	GLU	CA-C-N	-5.21	112.90	121.92
16	OA	1103	GLU	C-N-CA	-5.21	112.90	121.92
5	EB	3809	LEU	CA-CB-CG	5.21	134.54	116.30
8	GB	30	GLU	N-CA-CB	-5.21	108.23	114.17
15	ND	1550	MET	CA-CB-CG	5.20	124.51	114.10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AB	113	LEU	CA-CB-CG	5.20	134.51	116.30
1	AE	237	VAL	CA-C-N	5.20	131.76	122.09
1	AE	237	VAL	C-N-CA	5.20	131.76	122.09
15	NC	891	TRP	CA-C-N	5.20	131.46	121.54
15	NC	891	TRP	C-N-CA	5.20	131.46	121.54
1	AH	264	ARG	N-CA-C	-5.19	107.97	114.56
15	ND	1550	MET	CB-CA-C	-5.19	101.09	110.23
6	FD	913	LEU	N-CA-C	-5.19	106.35	113.30
9	HA	760	LYS	N-CA-C	-5.17	105.08	111.33
12	KA	282	LYS	CA-CB-CG	5.15	124.41	114.10
2	AB	541	PRO	CA-C-N	5.14	131.35	121.54
2	AB	541	PRO	C-N-CA	5.14	131.35	121.54
11	JB	931	LYS	CB-CG-CD	5.13	123.10	111.30
5	EB	4892	ARG	N-CA-C	-5.12	107.19	112.93
10	IC	778	GLN	CA-CB-CG	5.11	124.32	114.10
5	EC	4718	THR	CA-C-N	5.10	129.37	122.07
5	EC	4718	THR	C-N-CA	5.10	129.37	122.07
6	FD	1005	PRO	CB-CA-C	5.10	117.14	110.92
3	CC	724	GLN	CB-CG-CD	5.10	121.27	112.60
2	AF	376	ARG	CB-CG-CD	-5.10	99.58	111.30
15	NA	469	PHE	N-CA-C	5.10	121.66	110.80
1	AI	816	ARG	CA-CB-CG	5.09	124.29	114.10
10	IB	321	ASP	CB-CA-C	-5.09	110.68	116.54
15	NB	1421	ALA	CA-C-N	5.09	131.13	121.97
15	NB	1421	ALA	C-N-CA	5.09	131.13	121.97
1	AI	343	SER	CA-C-N	5.07	134.18	121.80
1	AI	343	SER	C-N-CA	5.07	134.18	121.80
4	DE	85	VAL	N-CA-C	-5.07	107.40	111.91
6	FE	1118	GLN	N-CA-C	-5.06	107.78	114.31
1	AA	259	ASP	CB-CA-C	-5.06	110.72	116.54
5	EA	4718	THR	CA-C-N	5.06	131.20	121.54
5	EA	4718	THR	C-N-CA	5.06	131.20	121.54
8	GH	56	CYS	CA-CB-SG	5.06	126.04	114.40
14	ME	259	MET	CB-CG-SD	5.05	127.84	112.70
13	LI	423	GLN	CA-CB-CG	5.05	124.19	114.10
12	KA	304	ARG	CA-C-N	5.04	131.17	121.54
12	KA	304	ARG	C-N-CA	5.04	131.17	121.54
19	RD	142	ASN	CB-CA-C	-5.04	100.39	110.42
1	AE	898	PRO	N-CA-C	5.04	122.84	112.47
13	LE	471	THR	CA-C-O	5.04	125.52	119.43
16	OC	1075	TYR	CA-C-N	5.04	131.03	121.97
16	OC	1075	TYR	C-N-CA	5.04	131.03	121.97

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	JB	741	PHE	CA-C-N	5.03	131.02	121.97
11	JB	741	PHE	C-N-CA	5.03	131.02	121.97
15	ND	903	CYS	N-CA-C	5.03	114.67	108.19
7	GA	542	GLY	N-CA-C	5.02	125.08	113.18
8	GD	372	VAL	N-CA-C	-5.02	107.94	112.96
9	HA	551	GLU	N-CA-C	5.02	116.47	110.44
8	GB	525	THR	CA-C-N	5.02	131.00	121.97
8	GB	525	THR	C-N-CA	5.02	131.00	121.97
9	HA	653	ILE	CG1-CB-CG2	-5.00	95.69	110.70
9	HB	551	GLU	CA-C-N	5.00	130.48	122.93
9	HB	551	GLU	C-N-CA	5.00	130.48	122.93
11	JC	1850	THR	N-CA-C	5.00	116.54	111.14
14	ME	284	LEU	CA-CB-CG	5.00	133.80	116.30

There are no chirality outliers.

All (325) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	136	PHE	Peptide
1	AA	715	LEU	Peptide
1	AA	897	PRO	Peptide
2	AB	207	GLU	Peptide
2	AB	295	PHE	Peptide
2	AB	419	LYS	Mainchain
2	AC	517	ARG	Sidechain
1	AE	1025	ARG	Sidechain
1	AE	136	PHE	Peptide
1	AE	274	ARG	Peptide
1	AE	715	LEU	Peptide
1	AE	897	PRO	Peptide
1	AI	136	PHE	Peptide
1	AI	245	PRO	Peptide
1	AI	897	PRO	Peptide
2	AK	24	ASP	Peptide
1	AL	1028	ARG	Sidechain
1	AL	886	ARG	Sidechain
3	BC	691	LEU	Peptide
3	CB	772	GLY	Peptide
3	CC	772	GLY	Peptide
3	CF	4450	PRO	Peptide
3	CF	4487	LEU	Peptide
3	CG	4450	PRO	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
3	CL	4476	ASP	Peptide
4	DC	175	TYR	Peptide
4	DD	19	ARG	Sidechain
5	EA	3419	ARG	Sidechain
5	EA	3514	GLU	Peptide
5	EA	3705	ASP	Peptide
5	EA	3855	LEU	Peptide
5	EA	4013	THR	Peptide
5	EB	3514	GLU	Peptide
5	EB	3855	LEU	Peptide
5	EB	4881	ARG	Sidechain
5	EB	4882	ARG	Sidechain
5	EB	4892	ARG	Sidechain
5	EB	4896	ARG	Sidechain
5	EC	3855	LEU	Peptide
5	EC	4096	ARG	Sidechain
5	EC	4881	ARG	Sidechain
5	EC	4882	ARG	Sidechain
5	EC	4892	ARG	Sidechain
5	EC	4896	ARG	Sidechain
5	EC	4900	ARG	Sidechain
6	FA	1716	SER	Peptide
6	FA	2012	ARG	Sidechain
6	FA	2016	ARG	Sidechain
6	FA	2017	ARG	Sidechain
6	FA	2018	ARG	Sidechain
6	FA	2024	ARG	Sidechain
6	FA	2034	ARG	Sidechain
6	FA	2061	ARG	Sidechain
6	FB	1716	SER	Peptide
6	FB	2034	ARG	Sidechain
6	FB	2047	ARG	Sidechain
6	FC	1716	SER	Peptide
6	FC	1983	ARG	Sidechain
6	FC	1988	ARG	Sidechain
6	FC	1994	ARG	Sidechain
6	FC	2012	ARG	Sidechain
6	FC	2016	ARG	Sidechain
6	FC	2018	ARG	Sidechain
6	FC	2024	ARG	Sidechain
6	FC	2034	ARG	Sidechain
6	FC	2039	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
6	FC	2047	ARG	Sidechain
6	FC	2071	ARG	Sidechain
6	FC	2081	ARG	Sidechain
6	FD	1008	ARG	Sidechain
6	FD	1069	ARG	Sidechain
6	FD	1072	ARG	Sidechain
6	FD	1077	ARG	Sidechain
6	FD	1084	ARG	Sidechain
6	FD	1089	ARG	Sidechain
6	FD	1190	ARG	Sidechain
6	FD	1203	ARG	Sidechain
6	FD	1220	ARG	Sidechain
6	FD	1227	ARG	Sidechain
6	FD	1228	ARG	Sidechain
6	FD	1231	ARG	Sidechain
6	FD	1238	ARG	Sidechain
6	FD	1251	ARG	Sidechain
6	FD	1265	ARG	Sidechain
6	FD	1389	ARG	Sidechain
6	FD	1420	ARG	Sidechain
6	FD	1444	ARG	Sidechain
6	FD	803	ARG	Sidechain
6	FD	821	ARG	Sidechain
6	FD	829	ARG	Sidechain
6	FD	831	ARG	Sidechain
6	FD	879	ARG	Sidechain
6	FD	887	ARG	Sidechain
6	FD	891	ARG	Sidechain
6	FD	920	ARG	Sidechain
6	FE	1008	ARG	Sidechain
6	FE	1010	ARG	Sidechain
6	FE	1069	ARG	Sidechain
6	FE	1072	ARG	Sidechain
6	FE	1077	ARG	Sidechain
6	FE	1089	ARG	Sidechain
6	FE	1105	ARG	Sidechain
6	FE	1220	ARG	Sidechain
6	FE	1227	ARG	Sidechain
6	FE	1231	ARG	Sidechain
6	FE	1238	ARG	Sidechain
6	FE	1251	ARG	Sidechain
6	FE	1265	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
6	FE	1389	ARG	Sidechain
6	FE	1444	ARG	Sidechain
6	FE	803	ARG	Sidechain
6	FE	821	ARG	Sidechain
6	FE	829	ARG	Sidechain
6	FE	879	ARG	Sidechain
6	FE	887	ARG	Sidechain
6	FE	920	ARG	Sidechain
6	FE	991	ARG	Sidechain
6	FF	1008	ARG	Sidechain
6	FF	1010	ARG	Sidechain
6	FF	1072	ARG	Sidechain
6	FF	1077	ARG	Sidechain
6	FF	1084	ARG	Sidechain
6	FF	1089	ARG	Sidechain
6	FF	1105	ARG	Sidechain
6	FF	1190	ARG	Sidechain
6	FF	1203	ARG	Sidechain
6	FF	1220	ARG	Sidechain
6	FF	1227	ARG	Sidechain
6	FF	1228	ARG	Sidechain
6	FF	1231	ARG	Sidechain
6	FF	1238	ARG	Sidechain
6	FF	1251	ARG	Sidechain
6	FF	1265	ARG	Sidechain
6	FF	1389	ARG	Sidechain
6	FF	1394	ARG	Sidechain
6	FF	803	ARG	Sidechain
6	FF	821	ARG	Sidechain
6	FF	829	ARG	Sidechain
6	FF	831	ARG	Sidechain
6	FF	879	ARG	Sidechain
6	FF	887	ARG	Sidechain
6	FF	891	ARG	Sidechain
6	FF	920	ARG	Sidechain
7	GA	350	ARG	Peptide
7	GA	537	GLY	Peptide
7	GA	538	THR	Peptide
7	GA	541	GLY	Peptide
7	GA	544	PRO	Peptide
7	GA	856	VAL	Peptide
8	GB	112	ILE	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
8	GB	525	THR	Peptide
8	GB	717	PHE	Peptide
8	GB	764	ALA	Peptide
7	GC	381	ARG	Peptide
8	GD	112	ILE	Peptide
8	GD	525	THR	Peptide
8	GD	526	ILE	Peptide
8	GD	717	PHE	Peptide
7	GE	276	ARG	Sidechain
8	GF	760	GLY	Peptide
7	GG	350	ARG	Peptide
7	GG	537	GLY	Peptide
7	GG	538	THR	Peptide
7	GG	541	GLY	Peptide
7	GG	542	GLY	Peptide
7	GG	544	PRO	Peptide
7	GG	855	ARG	Peptide
7	GG	856	VAL	Peptide
8	GH	112	ILE	Peptide
8	GH	396	ILE	Peptide
8	GH	717	PHE	Peptide
8	GH	759	MET	Peptide
8	GH	760	GLY	Peptide
8	GH	764	ALA	Peptide
7	GI	397	LEU	Peptide
8	GJ	333	LYS	Peptide
8	GJ	60	GLY	Peptide
8	GJ	61	CYS	Peptide
8	GJ	760	GLY	Peptide
7	GK	350	ARG	Peptide
7	GK	396	PRO	Peptide
7	GK	537	GLY	Peptide
7	GK	538	THR	Peptide
7	GK	542	GLY	Peptide
7	GK	544	PRO	Peptide
7	GK	856	VAL	Peptide
8	GL	333	LYS	Peptide
8	GL	660	LYS	Peptide
8	GL	760	GLY	Peptide
8	GL	83	GLN	Peptide
9	HA	552	ASP	Peptide
9	HA	564	ARG	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
9	HA	565	PRO	Peptide
9	HA	792	ARG	Sidechain
9	HA	810	ARG	Sidechain
9	HA	826	ARG	Sidechain
9	HA	855	ARG	Sidechain
9	HA	857	ARG	Sidechain
9	HB	552	ASP	Peptide
9	HB	565	PRO	Peptide
9	HB	792	ARG	Sidechain
9	HB	810	ARG	Sidechain
9	HB	826	ARG	Sidechain
9	HB	855	ARG	Sidechain
9	HB	857	ARG	Sidechain
9	HC	552	ASP	Peptide
9	HC	564	ARG	Peptide
9	HD	792	ARG	Sidechain
9	HD	810	ARG	Sidechain
9	HD	826	ARG	Sidechain
9	HD	855	ARG	Sidechain
9	HD	857	ARG	Sidechain
10	IA	312	ARG	Peptide
10	IA	776	PRO	Peptide
10	IB	381	HIS	Peptide
10	IC	776	PRO	Peptide
11	JA	1012	ARG	Sidechain
11	JA	1450	SER	Peptide
11	JA	146	TYR	Peptide
11	JA	170	ILE	Peptide
11	JA	172	LEU	Peptide
11	JA	184	LEU	Peptide
11	JA	2248	ILE	Peptide
11	JA	2251	PRO	Peptide
11	JA	435	VAL	Peptide
11	JA	481	SER	Peptide
11	JB	146	TYR	Peptide
11	JB	170	ILE	Peptide
11	JB	184	LEU	Peptide
11	JB	2251	PRO	Peptide
11	JB	435	VAL	Peptide
11	JB	481	SER	Peptide
11	JB	482	ARG	Peptide
11	JC	1450	SER	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
11	JC	146	TYR	Peptide
11	JC	1680	ARG	Sidechain
11	JC	170	ILE	Peptide
11	JC	184	LEU	Peptide
11	JC	2251	PRO	Peptide
11	JC	433	CYS	Peptide
11	JC	435	VAL	Peptide
11	JC	481	SER	Peptide
11	JC	482	ARG	Peptide
12	KA	344	ILE	Peptide
12	KA	524	PHE	Peptide
12	KA	606	ARG	Sidechain
12	KA	626	GLU	Peptide
12	KA	727	ILE	Peptide
12	KB	234	PRO	Peptide
12	KB	321	GLU	Peptide
12	KB	374	ALA	Peptide
12	KB	642	ARG	Peptide
12	KC	317	ALA	Peptide
12	KC	342	MET	Peptide
12	KC	500	PRO	Peptide
12	KC	509	ALA	Peptide
12	KC	578	ALA	Peptide
12	KE	721	GLN	Peptide
12	KF	721	GLN	Peptide
12	KG	304	ARG	Peptide
12	KG	721	GLN	Peptide
13	LE	460	ARG	Sidechain
13	LE	464	ASP	Peptide
13	LE	475	LEU	Peptide
13	LE	476	GLY	Peptide
13	LF	521	ASN	Peptide
13	LI	475	LEU	Peptide
13	LI	476	GLY	Peptide
13	LI	522	ARG	Sidechain
13	LJ	514	TYR	Peptide
13	LJ	521	ASN	Peptide
13	LO	413	GLU	Peptide
14	MC	173	PHE	Peptide
14	ME	223	ARG	Sidechain
14	ME	282	THR	Peptide
14	ME	283	GLN	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
14	MG	173	PHE	Peptide
14	MI	223	ARG	Sidechain
14	MI	268	TYR	Peptide
14	MJ	283	GLN	Peptide
14	MJ	290	ARG	Peptide
14	MK	173	PHE	Peptide
15	NA	468	ARG	Peptide
15	NA	470	ALA	Peptide
15	NA	708	LEU	Peptide
15	NA	901	LEU	Peptide
15	NA	902	ARG	Peptide
15	NB	468	ARG	Peptide
15	NB	470	ALA	Peptide
15	NB	901	LEU	Peptide
15	NB	902	ARG	Peptide
15	NB	937	MET	Peptide
15	NC	1156	LEU	Peptide
15	NC	1407	MET	Peptide
15	NC	1550	MET	Peptide
15	NC	468	ARG	Peptide
15	NC	470	ALA	Peptide
15	NC	537	LYS	Peptide
15	NC	885	LEU	Peptide
15	NC	890	ARG	Sidechain
15	NC	901	LEU	Peptide
15	NC	902	ARG	Peptide
15	ND	1153	ALA	Peptide
15	ND	1407	MET	Peptide
15	ND	1551	HIS	Peptide
15	ND	468	ARG	Peptide
15	ND	470	ALA	Peptide
15	ND	565	TRP	Peptide
15	ND	902	ARG	Peptide
16	OA	1089	LEU	Peptide
16	OA	1095	ARG	Peptide
16	OA	939	MET	Peptide
16	OB	1089	LEU	Peptide
16	OB	883	PRO	Peptide
16	OC	1089	LEU	Peptide
17	PB	140	ARG	Peptide
18	QB	60	ARG	Sidechain
18	QC	60	ARG	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
19	RA	20	PRO	Peptide
19	RB	63	GLU	Peptide
19	RD	140	GLY	Peptide
19	RD	141	LEU	Peptide,Mainchain
19	RD	142	ASN	Peptide
20	SB	44	PRO	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	AA	6540	0	6548	95	0
1	AD	6810	0	6785	85	0
1	AE	6540	0	6548	107	0
1	AH	6810	0	6785	81	0
1	AI	6540	0	6548	91	0
1	AL	6810	0	6785	84	0
2	AB	3821	0	3771	71	0
2	AC	3847	0	3808	65	0
2	AF	3821	0	3771	61	0
2	AG	3847	0	3808	61	0
2	AJ	3815	0	3760	43	0
2	AK	3847	0	3808	56	0
3	BA	2727	0	2744	42	0
3	BB	2727	0	2744	37	0
3	BC	2727	0	2744	33	0
3	CA	2712	0	2724	24	0
3	CB	2712	0	2724	29	0
3	CC	2712	0	2724	30	0
3	CE	1874	0	1903	32	0
3	CF	1874	0	1903	29	0
3	CG	1874	0	1903	33	0
3	CI	2012	0	2046	31	0
3	CJ	2012	0	2046	40	0
3	CL	2012	0	2046	32	0
4	DA	2753	0	2847	60	0
4	DB	2753	0	2847	57	0
4	DC	2753	0	2847	58	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	DD	2631	0	2743	40	0
4	DE	2631	0	2743	45	0
4	DF	2631	0	2743	39	0
5	EA	10670	0	10838	157	0
5	EB	10670	0	10838	169	0
5	EC	10666	0	10827	146	0
6	FA	4210	0	4162	97	0
6	FB	4210	0	4162	72	0
6	FC	4210	0	4162	136	0
6	FD	3255	0	3343	295	0
6	FE	3261	0	3354	271	0
6	FF	3182	0	3272	236	0
7	GA	6320	0	6301	101	0
7	GC	5960	0	5962	130	0
7	GE	5960	0	5962	113	0
7	GG	6320	0	6301	102	0
7	GI	5960	0	5962	123	0
7	GK	6320	0	6301	78	0
8	GB	5949	0	5884	85	0
8	GD	5949	0	5884	84	0
8	GF	6155	0	6082	83	0
8	GH	5781	0	5723	114	0
8	GJ	6155	0	6081	68	0
8	GL	6155	0	6082	97	0
9	HA	3361	0	3225	143	0
9	HB	3361	0	3225	153	0
9	HC	2288	0	2172	45	0
9	HD	1073	0	1053	59	0
10	IA	9113	0	9248	120	0
10	IB	9113	0	9248	139	0
10	IC	9113	0	9248	134	0
11	JA	12718	0	12853	190	0
11	JB	12718	0	12853	168	0
11	JC	12718	0	12853	201	0
12	KA	3674	0	3771	97	0
12	KB	3674	0	3771	73	0
12	KC	3668	0	3760	101	0
12	KE	3544	0	3640	55	0
12	KF	3544	0	3640	53	0
12	KG	3544	0	3640	41	0
13	LA	1516	0	1551	30	0
13	LB	1529	0	1573	18	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	LC	1312	0	1352	6	0
13	LD	1304	0	1350	9	0
13	LE	1190	0	1235	34	0
13	LF	1198	0	1247	19	0
13	LG	461	0	486	2	0
13	LH	448	0	475	8	0
13	LI	1516	0	1551	35	0
13	LJ	1529	0	1573	43	0
13	LK	1320	0	1363	16	0
13	LL	1304	0	1350	18	0
13	LM	859	0	877	10	0
13	LN	856	0	875	10	0
13	LO	841	0	850	11	0
13	LP	882	0	901	10	0
14	MA	1132	0	1134	24	0
14	MB	976	0	982	15	0
14	MC	594	0	593	6	0
14	MD	521	0	517	7	0
14	ME	1132	0	1134	27	0
14	MF	976	0	982	23	0
14	MG	594	0	593	7	0
14	MH	521	0	517	4	0
14	MI	1132	0	1135	22	0
14	MJ	976	0	983	28	0
14	MK	594	0	593	5	0
14	ML	521	0	517	7	0
15	NA	7263	0	7230	177	0
15	NB	7263	0	7230	161	0
15	NC	7263	0	7230	190	0
15	ND	7263	0	7230	155	0
16	OA	3510	0	3532	55	0
16	OB	3510	0	3532	59	0
16	OC	3510	0	3532	50	0
17	PA	807	0	769	23	0
17	PB	807	0	769	18	0
17	PC	807	0	769	21	0
18	QA	1129	0	1127	12	0
18	QB	1129	0	1127	18	0
18	QC	1129	0	1127	16	0
18	QD	1129	0	1127	19	0
19	RA	1143	0	1133	33	0
19	RB	1143	0	1133	16	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	RC	1143	0	1133	19	0
19	RD	1143	0	1133	27	0
20	SA	1134	0	1074	12	0
20	SB	1134	0	1074	14	0
20	SC	1134	0	1074	12	0
20	SD	1134	0	1074	11	0
All	All	415078	0	416877	6651	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 8.

All (6651) 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)
6:FD:1002:ALA:HB3	6:FD:1010:ARG:NH1	1.37	1.36
6:FD:803:ARG:CG	6:FD:1118:GLN:HG3	1.76	1.14
6:FD:1002:ALA:CB	6:FD:1010:ARG:HH11	1.60	1.14
9:HB:776:PRO:HA	13:LE:521:ASN:HD21	1.09	1.13
6:FD:803:ARG:HG2	6:FD:1118:GLN:HE21	1.10	1.11
6:FD:803:ARG:HG3	6:FD:1118:GLN:CG	1.79	1.11
6:FF:1425:PRO:HD2	6:FF:1429:LEU:HD12	1.18	1.11
6:FD:861:LEU:H	6:FD:861:LEU:CD2	1.67	1.05
6:FF:1425:PRO:CD	6:FF:1429:LEU:HD12	1.86	1.05
6:FD:861:LEU:H	6:FD:861:LEU:HD23	0.90	1.04
6:FC:2030:ILE:HD11	9:HB:813:THR:HG22	1.42	1.01
6:FD:861:LEU:HD23	6:FD:861:LEU:N	1.74	1.00
15:ND:892:TRP:H	15:ND:1154:ASP:H	1.02	1.00
6:FE:1424:CYS:HB2	6:FE:1425:PRO:HD3	1.44	1.00
6:FD:1424:CYS:HB2	6:FD:1425:PRO:HD3	1.43	1.00
6:FE:993:ALA:HB3	12:KB:229:SER:HB3	1.45	0.98
9:HB:808:HIS:O	9:HB:812:THR:HG23	1.65	0.97
6:FE:992:PRO:HB3	12:KB:231:PHE:CE1	2.02	0.95
15:NC:892:TRP:H	15:NC:1154:ASP:H	0.99	0.94
6:FD:895:ILE:HG21	7:GC:967:PHE:HZ	1.32	0.93
6:FF:1098:VAL:HA	6:FF:1101:ALA:HB3	1.50	0.93
6:FD:803:ARG:HG2	6:FD:1118:GLN:NE2	1.83	0.92
6:FD:1098:VAL:HA	6:FD:1101:ALA:HB3	1.52	0.92
6:FE:983:LEU:HB3	12:KB:725:ILE:HD11	1.50	0.92
6:FF:983:LEU:HD21	12:KC:656:ARG:HD2	1.52	0.92
6:FC:2083:GLN:HA	6:FC:2087:LEU:HB2	1.52	0.91
6:FF:1425:PRO:HD2	6:FF:1429:LEU:CD1	2.01	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1187:ILE:HG23	6:FE:1419:LEU:HD13	1.54	0.90
8:GF:61:CYS:HG	8:GF:80:PHE:HD2	1.11	0.90
6:FD:981:HIS:HA	12:KA:656:ARG:HH22	1.36	0.90
15:NA:892:TRP:H	15:NA:1154:ASP:H	0.92	0.90
9:HB:776:PRO:HA	13:LE:521:ASN:ND2	1.87	0.90
16:OC:882:ARG:HE	16:OC:885:GLN:HE21	1.18	0.89
9:HB:776:PRO:CA	13:LE:521:ASN:HD21	1.84	0.89
6:FE:884:VAL:HG21	6:FE:902:VAL:HA	1.51	0.89
9:HA:795:LEU:HD13	9:HA:797:TYR:CE2	2.07	0.88
9:HB:795:LEU:HD13	9:HB:797:TYR:CE2	2.07	0.88
6:FC:2024:ARG:HA	9:HB:778:PRO:HG2	1.54	0.88
6:FD:803:ARG:HG3	6:FD:1118:GLN:HG3	0.90	0.87
6:FA:2095:GLN:HE22	9:HA:875:THR:HG21	1.39	0.87
6:FF:1103:SER:HB2	9:HC:393:VAL:HG21	1.56	0.87
6:FE:1182:ALA:HB2	6:FE:1429:LEU:HB2	1.53	0.87
6:FD:1182:ALA:HB2	6:FD:1429:LEU:HB2	1.56	0.87
15:NA:892:TRP:H	15:NA:1154:ASP:N	1.73	0.86
6:FA:2024:ARG:HA	9:HA:778:PRO:HG2	1.57	0.86
12:KF:365:GLU:HB3	12:KF:697:ARG:HH22	1.40	0.86
6:FD:884:VAL:HG21	6:FD:902:VAL:HA	1.57	0.85
6:FD:888:PRO:HG2	7:GC:897:SER:HB3	1.58	0.85
6:FF:884:VAL:HG21	6:FF:902:VAL:HA	1.59	0.85
15:ND:881:LEU:HA	15:ND:884:LYS:HB2	1.58	0.85
6:FF:1182:ALA:HB2	6:FF:1429:LEU:HB2	1.57	0.85
8:GF:61:CYS:SG	8:GF:80:PHE:CD2	2.70	0.85
15:NB:892:TRP:H	15:NB:1154:ASP:N	1.73	0.85
15:NB:892:TRP:N	15:NB:1154:ASP:H	1.73	0.84
6:FF:803:ARG:HG3	6:FF:1118:GLN:HG3	1.59	0.84
8:GF:61:CYS:SG	8:GF:80:PHE:HD2	2.00	0.84
15:NB:892:TRP:H	15:NB:1154:ASP:H	0.87	0.84
6:FE:992:PRO:HA	12:KB:230:GLN:O	1.76	0.84
12:KC:234:PRO:HD2	12:KC:235:PRO:HD2	1.59	0.84
15:NA:892:TRP:N	15:NA:1154:ASP:H	1.76	0.83
1:AL:968:ASN:HB2	1:AL:971:GLU:HG2	1.61	0.82
15:NC:892:TRP:H	15:NC:1154:ASP:N	1.74	0.82
6:FD:1211:SER:HA	6:FD:1234:THR:HA	1.61	0.82
6:FA:2075:GLU:HB3	9:HA:858:LEU:HD11	1.62	0.81
6:FE:1098:VAL:HA	6:FE:1101:ALA:HB3	1.61	0.80
6:FE:893:GLY:HA2	7:GE:873:ALA:O	1.80	0.80
6:FE:1388:PHE:HB2	6:FE:1418:GLU:HB3	1.63	0.80
2:AB:415:HIS:HB2	6:FC:2077:HIS:HB2	1.61	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:SA:83:GLU:HG2	20:SA:147:MET:HG3	1.63	0.80
6:FE:846:CYS:HB3	12:KB:305:HIS:CE1	2.16	0.80
11:JA:1581:ARG:HH22	15:NC:354:PHE:HB3	1.47	0.79
8:GL:519:ARG:HH21	8:GL:520:PHE:HB2	1.48	0.79
2:AB:412:ALA:HB2	6:FC:2074:ALA:HB2	1.64	0.79
6:FF:822:GLY:HA2	7:GI:976:PRO:HB3	1.63	0.79
5:EB:4405:ILE:HG13	5:EB:4428:MET:HE1	1.63	0.79
6:FD:981:HIS:HA	12:KA:656:ARG:NH2	1.98	0.79
6:FA:2079:MET:CE	9:HA:865:ILE:HG12	2.13	0.79
14:MI:285:ARG:HH12	14:MJ:257:LYS:HA	1.44	0.79
2:AG:558:ARG:HD3	11:JC:1116:ARG:HH12	1.48	0.78
3:CF:1132:MET:HG2	10:IB:1237:GLN:HE21	1.48	0.78
7:GC:584:HIS:HA	7:GC:952:ARG:HH22	1.48	0.78
10:IA:943:ASN:HD22	16:OA:1034:PRO:HG3	1.48	0.78
7:GG:546:SER:HB3	9:HA:496:GLU:HA	1.64	0.78
2:AB:113:LEU:HD12	2:AB:208:GLU:HG2	1.63	0.77
8:GD:526:ILE:HG13	14:MA:324:ARG:HH22	1.48	0.77
5:EA:4880:ASP:OD1	5:EA:4888:TRP:CD2	2.37	0.77
5:EA:4760:ARG:HH12	11:JA:743:PHE:HA	1.48	0.77
7:GK:546:SER:HB3	9:HC:496:GLU:HA	1.65	0.77
15:NC:892:TRP:N	15:NC:1154:ASP:H	1.78	0.77
6:FF:1190:ARG:HB2	6:FF:1418:GLU:HB2	1.67	0.77
7:GE:240:PRO:HA	7:GE:285:LEU:HD13	1.67	0.77
15:ND:894:LEU:HD23	15:ND:1153:ALA:HB3	1.65	0.77
5:EA:4167:ASP:HB3	5:EA:4170:LYS:HB2	1.66	0.76
6:FD:1187:ILE:HG23	6:FD:1419:LEU:HD13	1.65	0.76
6:FD:895:ILE:HG21	7:GC:967:PHE:CZ	2.17	0.76
10:IA:580:LEU:HB3	10:IA:603:ARG:HH12	1.51	0.76
6:FC:1978:LEU:HD11	9:HB:817:VAL:HG22	1.65	0.76
6:FA:2095:GLN:NE2	9:HA:875:THR:HG21	2.00	0.76
15:NC:1328:VAL:HG13	15:NC:1332:MET:HE2	1.68	0.76
12:KB:573:ARG:HH22	12:KB:704:PRO:HG3	1.51	0.76
3:BC:689:LEU:HG	17:PC:258:PRO:HG2	1.66	0.76
6:FD:1002:ALA:CB	6:FD:1010:ARG:NH1	2.32	0.76
11:JC:1852:HIS:HD2	11:JC:1985:LEU:HG	1.50	0.75
15:ND:892:TRP:H	15:ND:1154:ASP:N	1.82	0.75
6:FE:888:PRO:HG2	7:GE:897:SER:HB3	1.69	0.75
7:GA:864:ILE:HG22	7:GA:866:PRO:HD3	1.68	0.75
15:NC:686:ASN:HD22	15:NC:905:ASP:HB3	1.50	0.75
6:FF:988:SER:HB3	12:KC:313:PHE:CZ	2.21	0.75
12:KG:368:ARG:HD2	12:KG:397:GLN:HE22	1.51	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NC:892:TRP:HB3	15:NC:1154:ASP:HB2	1.68	0.75
7:GC:878:GLN:HE21	7:GC:896:ARG:HG2	1.52	0.74
7:GA:211:ARG:HE	7:GA:212:PRO:HD2	1.52	0.74
7:GG:541:GLY:H	9:HA:579:LEU:HD21	1.52	0.74
15:NB:881:LEU:HA	15:NB:884:LYS:HB2	1.68	0.74
15:ND:1550:MET:H	19:RD:142:ASN:HB3	1.52	0.74
1:AD:233:VAL:HB	10:IB:1271:TYR:HB2	1.69	0.74
6:FF:918:GLN:HB3	6:FF:922:LEU:HG	1.70	0.74
7:GK:678:LEU:HB3	7:GK:690:ARG:HB3	1.69	0.74
15:ND:892:TRP:N	15:ND:1154:ASP:H	1.83	0.74
5:EA:4880:ASP:OD1	5:EA:4888:TRP:CE3	2.40	0.74
1:AD:310:CYS:H	1:AD:313:CYS:HB2	1.53	0.74
6:FF:925:GLU:HG2	6:FF:1092:PRO:HB2	1.70	0.74
6:FE:1391:TYR:HB2	6:FE:1417:ILE:HG23	1.69	0.73
4:DB:329:ARG:HH12	8:GL:48:LEU:HD22	1.53	0.73
6:FF:1441:ILE:HB	6:FF:1444:ARG:HB2	1.69	0.73
8:GD:294:TRP:HB3	8:GD:297:LEU:HB2	1.70	0.73
12:KE:404:GLU:HB2	12:KE:489:MET:HE1	1.70	0.73
7:GG:275:LYS:HE3	7:GG:279:ARG:HH22	1.53	0.73
9:HA:781:PRO:HG3	13:LA:531:VAL:HG12	1.68	0.73
4:DC:267:ARG:HH22	14:MI:294:ALA:HA	1.54	0.73
3:CG:4488:MET:HE3	3:CG:4492:ASN:H	1.51	0.73
6:FD:1198:TYR:HA	6:FD:1257:ASP:HA	1.70	0.73
6:FF:1005:PRO:HB2	6:FF:1006:PRO:HD3	1.70	0.73
8:GD:746:ALA:HA	8:GJ:342:LYS:HE2	1.69	0.73
11:JA:1480:VAL:HG13	15:NC:440:LEU:HD12	1.71	0.73
1:AI:315:LEU:HD23	1:AI:316:ILE:HG12	1.70	0.73
3:CJ:4467:THR:HG23	3:CJ:4468:LYS:HG3	1.70	0.73
6:FD:980:SER:HA	12:KA:343:ASN:HB2	1.70	0.73
6:FD:999:PRO:CA	12:KA:229:SER:HA	2.18	0.73
10:IB:740:ARG:HH12	10:IB:777:GLY:HA3	1.54	0.73
20:SA:21:ASP:HA	20:SA:28:ILE:HD13	1.71	0.73
6:FD:803:ARG:CG	6:FD:1118:GLN:CG	2.52	0.73
7:GA:546:SER:HB3	9:HB:496:GLU:HA	1.68	0.73
15:NC:1407:MET:HG3	15:NC:1471:ARG:HG3	1.71	0.73
6:FF:1280:VAL:HG13	6:FF:1300:LEU:HD11	1.70	0.73
12:KC:383:HIS:HA	12:KC:386:LEU:HD23	1.70	0.73
1:AL:310:CYS:H	1:AL:313:CYS:HB2	1.54	0.72
6:FE:1283:TYR:HB3	6:FE:1290:ILE:HG23	1.70	0.72
15:NC:1102:VAL:HG22	15:NC:1111:ARG:HG2	1.71	0.72
1:AL:987:LEU:HD13	7:GK:424:ARG:HH22	1.53	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AK:427:ARG:HH21	1:AL:456:VAL:HG22	1.54	0.72
8:GH:665:LEU:HB2	8:GH:676:TRP:HB3	1.71	0.72
15:NB:696:PHE:HB2	15:NB:894:LEU:HD11	1.72	0.72
1:AE:442:HIS:HB2	2:AF:368:HIS:HB2	1.70	0.72
8:GJ:519:ARG:HH21	8:GJ:520:PHE:HB2	1.52	0.72
3:BB:982:ARG:HB3	3:BB:993:THR:HG22	1.71	0.72
3:BC:964:GLN:HE21	16:OC:127:ILE:HG21	1.52	0.72
4:DC:297:ARG:HE	4:DC:391:ILE:HD13	1.54	0.72
15:NA:881:LEU:HA	15:NA:884:LYS:HB2	1.71	0.72
11:JC:772:CYS:HB2	11:JC:793:MET:HB2	1.72	0.72
12:KA:415:LEU:HD11	12:KA:480:VAL:HG21	1.70	0.72
12:KC:231:PHE:CZ	12:KC:313:PHE:CG	2.78	0.72
2:AG:448:ASN:HD21	1:AH:472:LYS:HA	1.55	0.71
6:FE:962:PHE:CE2	6:FE:965:TRP:HB2	2.25	0.71
7:GI:570:GLY:HA2	7:GI:622:ARG:HB3	1.72	0.71
12:KC:304:ARG:HE	12:KC:305:HIS:H	1.38	0.71
5:EC:4405:ILE:HG23	5:EC:4411:THR:HG21	1.72	0.71
6:FE:1424:CYS:HB2	6:FE:1425:PRO:CD	2.20	0.71
6:FE:870:ALA:HB3	12:KB:235:PRO:HD2	1.73	0.71
6:FF:1112:ILE:HG13	6:FF:1114:VAL:HG22	1.71	0.71
12:KC:579:LEU:HD12	12:KC:654:ILE:HG21	1.72	0.71
3:BC:982:ARG:HB3	3:BC:993:THR:HG22	1.71	0.71
6:FD:888:PRO:HD3	12:KA:305:HIS:ND1	2.05	0.71
7:GC:988:LYS:HD2	9:HB:402:ARG:HE	1.54	0.71
15:ND:1512:MET:HA	15:ND:1515:LEU:HB2	1.71	0.71
4:DC:33:LEU:HB3	4:DC:103:LEU:HA	1.73	0.71
8:GJ:422:LYS:HB3	8:GJ:501:SER:HB3	1.73	0.71
10:IC:616:GLY:H	10:IC:758:ASN:HD21	1.36	0.71
6:FF:818:VAL:HG12	6:FF:819:PRO:HD2	1.73	0.71
17:PB:257:ASN:HB3	17:PB:260:SER:HB3	1.71	0.71
1:AL:376:LEU:HD11	11:JB:1639:GLU:HG3	1.72	0.70
6:FE:879:ARG:HE	6:FE:908:ILE:HG23	1.56	0.70
7:GA:185:ARG:HB2	7:GA:705:ILE:HG22	1.73	0.70
4:DB:277:ARG:HD3	4:DB:281:GLN:HE22	1.55	0.70
6:FA:2079:MET:HE1	9:HA:865:ILE:HG12	1.73	0.70
6:FF:852:VAL:HG12	6:FF:880:VAL:HG22	1.73	0.70
11:JA:791:MET:HG2	11:JA:809:ILE:HG12	1.73	0.70
5:EB:3873:LEU:HD21	5:EB:4205:ILE:HD11	1.72	0.70
6:FC:1677:PRO:HG3	6:FC:1696:HIS:HD2	1.55	0.70
8:GH:13:ARG:HE	8:GH:536:ALA:HB2	1.56	0.70
19:RD:138:ARG:HG3	19:RD:139:LEU:HD12	1.72	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FD:831:ARG:HG3	6:FD:979:LEU:HD21	1.73	0.70
6:FF:1424:CYS:HB2	6:FF:1425:PRO:HD3	1.73	0.70
12:KC:533:THR:HG22	12:KC:534:VAL:HG13	1.71	0.70
11:JA:1379:GLN:HE22	11:JA:1386:PHE:HB2	1.56	0.70
11:JC:523:ASN:HD21	11:JC:766:GLY:H	1.38	0.70
11:JA:882:ALA:HB3	11:JA:1416:ARG:HB3	1.74	0.70
15:ND:1548:PHE:H	19:RD:141:LEU:HD12	1.56	0.70
3:CF:1236:LEU:HD21	3:CF:1255:VAL:HG13	1.74	0.70
4:DC:250:ASP:HB2	4:DC:283:LEU:HD23	1.74	0.70
6:FC:2055:THR:HG22	9:HB:837:LEU:HD11	1.74	0.70
11:JC:489:VAL:HG13	11:JC:490:THR:HG23	1.74	0.70
6:FC:2085:GLU:O	6:FC:2089:PRO:HD2	1.91	0.70
6:FF:988:SER:HB3	12:KC:313:PHE:HZ	1.55	0.70
15:ND:1488:ARG:HH12	15:ND:1491:PRO:HD2	1.56	0.70
4:DA:248:ARG:HE	4:DA:290:ARG:HH12	1.40	0.69
10:IA:616:GLY:H	10:IA:758:ASN:HD21	1.39	0.69
3:CC:684:ARG:HD2	3:CC:713:LEU:HB3	1.74	0.69
4:DE:61:GLU:HA	4:DE:66:ARG:HH22	1.56	0.69
6:FE:1425:PRO:HD2	6:FE:1429:LEU:HD12	1.75	0.69
10:IC:609:GLU:HG2	10:IC:614:LEU:HG	1.74	0.69
4:DF:110:LEU:HD12	4:DF:111:PRO:HD2	1.75	0.69
9:HB:848:ASP:C	9:HB:848:ASP:OD1	2.36	0.69
4:DE:129:VAL:HG13	4:DE:154:LEU:HD21	1.75	0.69
9:HA:766:SER:O	9:HA:768:THR:N	2.26	0.69
10:IB:174:PHE:HB3	10:IB:205:GLN:HE21	1.58	0.69
10:IB:1064:GLN:HB3	10:IB:1068:ARG:HH12	1.57	0.69
15:NC:505:GLY:H	15:NC:512:TYR:HB2	1.57	0.69
7:GA:828:PRO:HG2	7:GA:831:ARG:HG2	1.74	0.69
8:GB:526:ILE:HB	14:ME:321:ALA:HB2	1.74	0.69
7:GG:539:TYR:HB2	9:HA:576:LYS:HG2	1.74	0.69
7:GG:670:ASN:HB3	7:GG:698:VAL:HB	1.75	0.69
7:GI:510:THR:HG23	7:GI:632:VAL:HG11	1.75	0.69
14:MI:244:VAL:HG13	14:MI:243:LYS:HZ1	1.57	0.69
7:GG:808:PRO:HD2	7:GG:977:SER:HB2	1.75	0.69
10:IA:883:SER:HB3	16:OA:1045:LEU:HD11	1.74	0.69
6:FF:836:GLY:HA3	6:FF:840:ALA:HB3	1.73	0.69
11:JC:1489:LEU:HD11	15:NA:483:VAL:HG23	1.76	0.69
15:NA:614:LYS:HB3	15:NA:678:LEU:HD22	1.74	0.69
15:ND:1498:ARG:HE	20:SB:38:ARG:HD2	1.58	0.69
20:SB:42:GLN:HB2	20:SB:78:LYS:HB2	1.75	0.69
1:AL:988:GLN:HA	1:AL:991:LEU:HD23	1.75	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GB:326:ARG:HH12	8:GB:375:TYR:HB3	1.58	0.68
10:IA:165:ILE:HD11	10:IA:180:LEU:HD22	1.74	0.68
10:IB:616:GLY:H	10:IB:758:ASN:HD21	1.41	0.68
11:JB:192:LEU:HB3	11:JB:1063:ILE:HD13	1.74	0.68
5:EB:4307:MET:HE1	5:EB:4346:VAL:HG12	1.74	0.68
15:ND:679:ASP:HB2	15:ND:696:PHE:HB3	1.75	0.68
6:FF:923:ALA:HB1	6:FF:928:SER:HA	1.74	0.68
14:MJ:290:ARG:HA	14:MJ:293:LEU:HD23	1.74	0.68
6:FD:995:VAL:N	12:KA:385:GLU:OE2	2.24	0.68
9:HB:778:PRO:HB2	9:HB:779:PRO:HD3	1.75	0.68
1:AI:248:LEU:HB2	1:AI:258:CYS:HA	1.75	0.68
7:GG:353:SER:HB3	7:GG:406:ALA:HB2	1.74	0.68
8:GL:131:LEU:HD12	8:GL:132:PRO:HD2	1.74	0.68
11:JC:770:ASP:HB2	11:JC:795:ARG:HB2	1.75	0.68
15:NA:892:TRP:HB2	15:NA:1155:GLU:HB2	1.75	0.68
3:CA:867:THR:HA	3:CA:870:LEU:HD23	1.76	0.68
4:DE:254:GLU:HG2	4:DE:291:GLN:HE22	1.58	0.68
6:FE:971:SER:HB3	6:FE:1022:THR:HG23	1.76	0.68
6:FF:808:SER:HB3	6:FF:1113:PHE:HB2	1.73	0.68
8:GB:294:TRP:HB3	8:GB:297:LEU:HB2	1.76	0.68
7:GG:538:THR:HG23	9:HA:555:SER:HB3	1.75	0.68
12:KB:367:ILE:HD13	12:KB:393:LEU:HB2	1.76	0.68
6:FE:1005:PRO:HB2	6:FE:1006:PRO:HD3	1.76	0.68
6:FF:1188:GLU:HG3	6:FF:1267:GLN:HB3	1.73	0.68
9:HA:676:ALA:HB2	9:HA:682:ILE:HG12	1.74	0.68
11:JB:162:PRO:HD2	11:JB:169:PHE:HA	1.76	0.68
3:CE:1260:VAL:HG21	3:CE:4466:ILE:HD13	1.74	0.68
11:JA:1078:MET:HB2	11:JA:1509:HIS:HD2	1.58	0.68
12:KC:380:GLY:HA3	12:KC:723:GLU:O	1.94	0.68
1:AH:228:PRO:HG2	10:IA:1254:GLY:HA2	1.74	0.68
12:KC:273:ARG:HD2	12:KC:274:ASP:HB2	1.76	0.68
5:EA:4095:LYS:HB3	9:HB:796:ASP:OD1	1.94	0.67
8:GB:171:ILE:HG22	8:GB:183:LEU:HD21	1.76	0.67
7:GE:764:LEU:HD13	7:GE:870:ARG:HD2	1.75	0.67
12:KE:209:VAL:HG23	12:KE:280:LEU:HB2	1.75	0.67
1:AE:460:VAL:HG13	1:AE:465:MET:HE1	1.75	0.67
1:AH:990:LYS:HB3	7:GG:424:ARG:HH12	1.59	0.67
5:EC:3491:ALA:HB2	5:EC:3603:LEU:HD13	1.74	0.67
6:FD:1182:ALA:HB2	6:FD:1430:PHE:H	1.58	0.67
6:FD:1187:ILE:HG21	6:FD:1282:LEU:HD21	1.76	0.67
6:FE:1030:ILE:HG23	6:FE:1116:LEU:HD13	1.76	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:91:ILE:HB	2:AJ:528:LEU:HG	1.76	0.67
6:FC:1653:ARG:HD3	6:FC:1658:LEU:HD13	1.76	0.67
7:GG:543:LYS:H	9:HA:596:TYR:HB3	1.59	0.67
15:ND:895:GLY:HA2	15:ND:898:ASN:HB2	1.75	0.67
5:EC:3698:VAL:HG13	5:EC:4059:MET:HE1	1.75	0.67
6:FD:825:PRO:O	6:FD:826:LEU:C	2.36	0.67
8:GB:750:GLY:H	8:GF:334:ASP:HB2	1.60	0.67
7:GG:397:LEU:HD21	8:GJ:176:ALA:HB3	1.76	0.67
4:DF:104:GLU:HA	4:DF:260:GLY:HA3	1.77	0.67
6:FA:2098:TYR:CE2	9:HA:875:THR:HG22	2.29	0.67
3:CC:784:LEU:HD22	3:CC:826:LEU:HD13	1.76	0.67
6:FA:2009:SER:HA	6:FA:2012:ARG:HG2	1.76	0.67
6:FF:799:GLN:HB3	6:FF:911:SER:HA	1.77	0.67
11:JC:1572:LEU:HD13	11:JC:1604:HIS:HE1	1.60	0.67
16:OB:876:GLU:HB2	16:OB:939:MET:HG3	1.76	0.67
4:DB:18:GLU:HG2	14:ME:283:GLN:HE21	1.57	0.67
7:GC:614:TRP:HE1	7:GC:661:LEU:HD21	1.59	0.67
13:LN:350:LEU:HB3	13:LN:354:ARG:HH12	1.60	0.67
15:NC:680:LEU:HB3	15:NC:682:ARG:HH12	1.59	0.67
16:OC:191:PRO:HD3	16:OC:245:LEU:HD12	1.75	0.67
2:AC:514:ALA:HA	2:AC:517:ARG:HD2	1.77	0.67
4:DC:11:PHE:HE1	14:MJ:288:SER:HB3	1.59	0.67
6:FD:999:PRO:HA	12:KA:229:SER:HA	1.76	0.67
8:GF:61:CYS:HB2	8:GF:78:CYS:SG	2.35	0.67
12:KA:524:PHE:H	12:KA:525:PRO:HD3	1.58	0.67
6:FC:2048:GLU:HG2	9:HB:765:TRP:CD1	2.30	0.67
6:FF:834:VAL:HG12	6:FF:981:HIS:HB2	1.77	0.67
11:JB:774:LEU:HD21	11:JB:793:MET:HG3	1.77	0.67
11:JC:963:PHE:HB3	11:JC:966:LEU:HD21	1.77	0.67
12:KA:523:VAL:HG11	12:KA:573:ARG:HE	1.60	0.67
1:AE:248:LEU:HB2	1:AE:258:CYS:HA	1.76	0.66
3:BA:711:ARG:HH12	3:BA:756:GLU:HG2	1.60	0.66
3:BB:695:LEU:HD21	17:PB:290:PHE:HB3	1.77	0.66
6:FD:808:SER:O	6:FD:809:ILE:C	2.37	0.66
6:FF:1251:ARG:HE	11:JB:774:LEU:H	1.42	0.66
7:GA:353:SER:HB3	7:GA:406:ALA:HB2	1.76	0.66
8:GB:150:ASP:HA	8:GB:153:ARG:HD3	1.77	0.66
8:GJ:414:PHE:HB3	8:GJ:505:PRO:HB2	1.77	0.66
15:NC:787:LEU:HD22	15:NC:791:GLU:HG3	1.77	0.66
9:HA:758:ALA:HA	9:HA:761:CYS:SG	2.35	0.66
14:MI:302:GLU:HA	14:MI:305:LEU:HD23	1.77	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:301:VAL:HG23	1:AH:332:THR:HG22	1.77	0.66
4:DC:317:THR:H	14:MJ:246:ASN:HD21	1.43	0.66
6:FC:2009:SER:HA	6:FC:2012:ARG:HE	1.60	0.66
6:FF:819:PRO:HG3	6:FF:895:ILE:HD13	1.77	0.66
8:GL:422:LYS:HB3	8:GL:501:SER:HB3	1.76	0.66
10:IA:1094:ASN:HA	10:IA:1123:ASN:HD22	1.60	0.66
11:JA:124:VAL:HB	11:JA:132:ARG:HG3	1.77	0.66
1:AA:769:LEU:HD12	13:LL:375:ILE:HG12	1.78	0.66
5:EA:3491:ALA:HB2	5:EA:3603:LEU:HB3	1.77	0.66
6:FC:2059:VAL:HG22	9:HB:754:LEU:HB3	1.78	0.66
6:FD:842:GLY:HA2	7:GC:959:GLY:HA3	1.77	0.66
5:EC:3269:TRP:HD1	5:EC:3409:SER:HB3	1.60	0.66
9:HD:778:PRO:HB2	9:HD:779:PRO:HD3	1.76	0.66
11:JA:1220:LEU:HD23	11:JA:1283:ARG:HH21	1.59	0.66
11:JB:160:LEU:HB2	11:JB:171:LYS:HG2	1.78	0.66
4:DB:386:VAL:HG13	4:DB:387:ASP:H	1.60	0.66
5:EB:4728:HIS:HB2	5:EB:4817:LEU:HD13	1.78	0.66
8:GD:148:GLU:HB2	8:GD:394:PHE:HB2	1.77	0.66
9:HB:757:LEU:HD11	9:HB:833:VAL:HG13	1.78	0.66
15:NC:895:GLY:HA2	15:NC:898:ASN:HB2	1.77	0.66
1:AD:991:LEU:HD13	7:GA:424:ARG:HH12	1.60	0.66
3:CC:758:VAL:HG21	3:CC:812:MET:HE1	1.77	0.66
5:EC:4461:PHE:HB3	5:EC:4500:THR:HG22	1.76	0.66
6:FD:844:ALA:C	7:GC:896:ARG:HH12	2.04	0.66
6:FD:850:CYS:HB3	6:FD:973:ILE:HG12	1.77	0.66
6:FD:992:PRO:HD3	12:KA:313:PHE:CE1	2.31	0.66
8:GF:489:PRO:HD2	8:GF:492:LYS:HD2	1.78	0.66
1:AD:736:LEU:HD23	1:AD:738:GLY:H	1.59	0.66
1:AH:151:LEU:HD13	1:AH:210:LEU:HD21	1.78	0.66
5:EC:4446:ARG:HH12	17:PC:143:ILE:HD11	1.61	0.66
6:FD:1210:LEU:HD23	6:FD:1286:LEU:HD23	1.78	0.66
11:JB:1560:LEU:HD21	11:JB:1607:VAL:HG11	1.76	0.66
12:KB:685:ARG:HH11	12:KB:700:LEU:HD12	1.60	0.66
16:OC:731:ALA:HB2	20:SA:144:LYS:HE3	1.77	0.66
5:EA:4827:SER:HB3	11:JA:1343:GLU:HG2	1.78	0.66
5:EC:4405:ILE:CG2	5:EC:4427:LEU:HB3	2.25	0.66
6:FD:860:PRO:HG2	6:FD:861:LEU:CD2	2.26	0.66
6:FE:894:ALA:HB1	6:FE:897:LEU:HB2	1.78	0.66
10:IB:342:LEU:HD12	10:IB:343:PRO:HD2	1.78	0.66
15:NB:943:GLU:HA	15:NB:946:LEU:HG	1.76	0.66
1:AA:411:LEU:HB3	1:AA:458:VAL:HG11	1.78	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:52:TYR:HB2	2:AF:517:ARG:HE	1.59	0.66
9:HA:778:PRO:HB2	9:HA:779:PRO:HD3	1.78	0.66
15:NC:812:ARG:HE	15:NC:870:TYR:HB2	1.59	0.66
3:BA:791:THR:HG22	3:BA:811:ILE:HG13	1.78	0.65
5:EA:4071:LEU:HD13	5:EA:4218:GLN:HB3	1.77	0.65
6:FE:1203:ARG:HB2	11:JC:901:ARG:NH1	2.10	0.65
8:GD:132:PRO:HG3	8:GD:236:LEU:HG	1.77	0.65
7:GG:802:LYS:HB2	7:GG:971:MET:HE1	1.78	0.65
11:JA:57:GLU:HA	11:JA:90:ARG:HH21	1.61	0.65
11:JC:437:LEU:HB2	11:JC:1465:THR:HG21	1.78	0.65
15:NB:1102:VAL:HG22	15:NB:1111:ARG:HG2	1.77	0.65
3:BB:754:GLU:HA	17:PB:278:TRP:HH2	1.60	0.65
4:DC:180:LEU:HD12	4:DC:181:ILE:HG13	1.77	0.65
5:EB:3841:GLN:HG3	5:EB:3854:GLN:HE22	1.60	0.65
5:EB:4167:ASP:HB2	5:EB:4171:ILE:HG12	1.78	0.65
5:EC:3652:PRO:HG3	9:HA:500:LEU:HB2	1.77	0.65
6:FF:1300:LEU:O	6:FF:1301:ALA:C	2.38	0.65
7:GE:374:ALA:HB2	7:GE:380:ARG:HE	1.60	0.65
11:JB:1324:ASP:HA	11:JB:1327:LEU:HD12	1.78	0.65
15:NB:964:GLU:HG3	15:NB:1467:LEU:HG	1.79	0.65
6:FA:1612:ASN:HD21	6:FA:1616:GLU:HB2	1.61	0.65
7:GE:518:LEU:HD23	7:GE:566:ALA:HB2	1.78	0.65
11:JB:71:LYS:HE2	11:JB:191:ASP:HA	1.77	0.65
11:JC:66:MET:HE1	11:JC:75:VAL:HG11	1.78	0.65
11:JC:791:MET:HG2	11:JC:809:ILE:HG12	1.79	0.65
15:ND:726:CYS:HB3	15:ND:803:LEU:HD12	1.77	0.65
3:BC:694:ARG:HD2	17:PC:290:PHE:HE1	1.61	0.65
6:FE:1244:LEU:HB3	6:FE:1249:ILE:HG12	1.79	0.65
10:IC:725:LYS:HB3	10:IC:729:ARG:HH12	1.61	0.65
15:NA:894:LEU:H	15:NA:1153:ALA:H	1.42	0.65
1:AD:396:MET:HE3	5:EA:4617:THR:HG22	1.79	0.65
11:JB:2110:LEU:HD12	11:JB:2113:PHE:HB3	1.77	0.65
12:KB:382:ARG:HG2	12:KB:727:ILE:HG21	1.79	0.65
12:KB:503:ASP:HA	12:KB:506:LEU:HB3	1.78	0.65
12:KE:368:ARG:HD3	12:KE:397:GLN:HE22	1.61	0.65
13:LL:350:LEU:HG	13:LL:354:ARG:HE	1.62	0.65
14:MI:233:LEU:HD23	14:MI:236:GLU:HG3	1.77	0.65
1:AE:382:ILE:HG21	2:AF:464:ILE:HD11	1.78	0.65
5:EC:3283:GLU:HA	5:EC:3286:ARG:HE	1.61	0.65
6:FD:1210:LEU:HD22	6:FD:1284:LEU:HD21	1.79	0.65
14:MJ:292:ALA:HA	14:MJ:295:GLU:HB2	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:442:HIS:HB2	2:AB:368:HIS:HB2	1.77	0.65
4:DC:23:ALA:HA	4:DC:28:LEU:HD12	1.79	0.65
5:EC:3331:ALA:HA	5:EC:3763:ARG:HA	1.78	0.65
5:EC:3419:ARG:HH22	5:EC:3758:ARG:HA	1.61	0.65
6:FD:971:SER:HA	6:FD:1022:THR:HA	1.78	0.65
6:FD:1231:ARG:HB3	6:FD:1270:LEU:HD21	1.79	0.65
9:HA:675:ALA:HB3	9:HA:711:SER:HB2	1.77	0.65
9:HB:795:LEU:HD13	9:HB:797:TYR:HE2	1.61	0.65
14:MI:285:ARG:HH22	14:MJ:257:LYS:HG2	1.60	0.65
2:AB:66:ARG:HG2	2:AB:172:GLY:HA3	1.77	0.65
6:FB:1901:LEU:HB3	6:FB:1904:GLU:HA	1.78	0.65
6:FE:1253:SER:HB3	11:JC:778:HIS:CD2	2.32	0.65
8:GD:132:PRO:HG2	8:GD:297:LEU:HD12	1.78	0.65
7:GE:738:LEU:HD12	7:GE:797:ILE:HG23	1.79	0.65
8:GF:199:ARG:HE	8:GF:202:LYS:HD3	1.62	0.65
11:JB:426:PRO:HB3	11:JB:1524:PHE:HB3	1.77	0.65
11:JC:2065:MET:HE1	11:JC:2276:ARG:HE	1.62	0.65
12:KA:721:GLN:HE22	12:KA:725:ILE:HG23	1.61	0.65
14:MI:247:LEU:HD11	14:MJ:251:LEU:HD21	1.79	0.65
15:NA:1526:ILE:HG21	18:QA:146:ILE:HG13	1.79	0.65
15:NC:1138:THR:HG23	15:NC:1140:LEU:H	1.61	0.65
2:AF:63:THR:HA	2:AF:66:ARG:HD2	1.79	0.65
6:FF:890:ALA:O	6:FF:891:ARG:C	2.40	0.65
7:GC:767:LEU:HB3	7:GC:839:ARG:HH12	1.61	0.65
8:GH:148:GLU:HB2	8:GH:394:PHE:HB2	1.77	0.65
18:QD:122:ARG:HA	18:QD:125:LYS:HE2	1.78	0.65
6:FE:1217:GLU:O	6:FE:1218:ALA:C	2.40	0.65
11:JA:746:VAL:HA	11:JA:749:LYS:HG2	1.78	0.65
15:ND:751:ASP:HB3	15:ND:849:ARG:HD3	1.79	0.65
1:AL:405:LEU:HD11	16:OB:24:LEU:HD22	1.76	0.64
6:FE:826:LEU:HB2	6:FE:841:TYR:HE2	1.62	0.64
8:GJ:349:THR:HG22	8:GJ:379:VAL:HG21	1.79	0.64
9:HB:777:TYR:H	13:LE:521:ASN:ND2	1.95	0.64
10:IB:740:ARG:HD2	10:IB:772:LEU:HG	1.78	0.64
11:JA:1975:THR:HG23	11:JA:1977:GLN:H	1.61	0.64
15:NA:1550:MET:HE3	19:RC:174:LEU:HD21	1.79	0.64
2:AB:408:LYS:HB3	2:AB:409:PRO:HD3	1.78	0.64
6:FD:826:LEU:HD21	6:FD:843:LEU:HD23	1.78	0.64
6:FE:823:GLY:C	6:FE:825:PRO:HD3	2.22	0.64
8:GJ:661:PRO:HB2	8:GJ:680:LEU:HB2	1.79	0.64
10:IC:813:ALA:HB2	10:IC:840:PRO:HB2	1.79	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:882:ALA:HB3	11:JC:1416:ARG:HB3	1.77	0.64
12:KG:238:PHE:HB3	12:KG:294:ARG:HH22	1.62	0.64
19:RA:23:LEU:HA	19:RA:26:HIS:HB2	1.77	0.64
3:CB:945:THR:HG22	3:CB:947:GLU:H	1.61	0.64
3:CG:1187:GLU:HB2	3:CG:1192:HIS:HB3	1.80	0.64
5:EC:3649:TRP:HE1	5:EC:3673:LEU:HD22	1.61	0.64
6:FF:1187:ILE:HG23	6:FF:1419:LEU:HD13	1.78	0.64
7:GE:184:ALA:HB3	7:GE:708:SER:HB2	1.80	0.64
7:GI:284:GLU:HA	7:GI:290:VAL:HG11	1.79	0.64
15:NA:570:GLY:HA3	15:NA:575:LEU:HD21	1.79	0.64
15:NB:1511:GLU:HB3	18:QC:107:LEU:HD11	1.80	0.64
4:DC:257:LEU:HD23	4:DC:265:ILE:HD13	1.79	0.64
8:GJ:426:LEU:HB2	8:GJ:497:GLN:HB3	1.77	0.64
15:ND:947:ASN:HA	15:ND:950:VAL:HB	1.78	0.64
2:AG:544:ARG:HH21	1:AH:485:PRO:HD3	1.63	0.64
8:GJ:393:SER:HB3	8:GJ:396:ILE:HG12	1.80	0.64
9:HC:574:ARG:HB3	9:HC:578:THR:HG21	1.80	0.64
11:JC:758:GLU:HA	11:JC:761:LYS:HB3	1.79	0.64
15:NB:1472:LYS:HA	15:NB:1475:PHE:HB3	1.80	0.64
6:FC:2051:VAL:O	6:FC:2055:THR:HG23	1.98	0.64
8:GH:396:ILE:HG22	8:GH:721:LYS:HZ1	1.63	0.64
10:IB:634:ALA:HB2	10:IB:692:GLU:HB3	1.78	0.64
12:KC:308:LEU:HD13	12:KC:337:ALA:HB2	1.78	0.64
1:AL:801:ARG:HE	1:AL:996:SER:HB3	1.63	0.64
4:DD:35:MET:HG2	4:DD:106:ASN:HB2	1.79	0.64
5:EA:3273:LEU:HD13	5:EA:3494:VAL:HG11	1.80	0.64
7:GA:538:THR:HG23	9:HB:555:SER:HB3	1.78	0.64
7:GE:606:MET:HB3	7:GE:631:PHE:HB2	1.79	0.64
8:GH:283:LEU:HD21	8:GH:303:LEU:HD22	1.79	0.64
10:IA:551:ASN:HD21	10:IA:803:ARG:HH21	1.43	0.64
19:RC:58:VAL:HG13	19:RC:60:PHE:H	1.62	0.64
5:EB:3258:GLY:HA3	5:EB:3263:SER:HB3	1.80	0.64
5:EC:3705:ASP:HA	5:EC:3708:HIS:HB3	1.79	0.64
6:FD:832:GLY:HA3	6:FD:844:ALA:HB2	1.79	0.64
12:KG:218:ARG:HB3	12:KG:222:LEU:H	1.61	0.64
2:AG:115:ARG:HH11	16:OC:148:ARG:H	1.46	0.64
6:FF:818:VAL:HG23	6:FF:821:ARG:HG2	1.80	0.64
7:GG:987:GLN:HB3	7:GG:991:MET:HE1	1.79	0.64
11:JA:422:LEU:HD23	11:JA:1441:CYS:HB3	1.79	0.64
11:JB:1717:TRP:HB3	16:OB:931:PRO:HG3	1.80	0.64
15:NB:1017:GLN:HG3	15:NB:1094:LYS:HG3	1.80	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:QC:123:VAL:HA	18:QC:126:MET:HE3	1.80	0.64
3:CB:757:MET:HB3	3:CB:761:LEU:HD23	1.81	0.63
5:EC:4653:GLU:HG3	5:EC:4654:ASP:H	1.62	0.63
6:FF:894:ALA:HB1	6:FF:897:LEU:HB2	1.80	0.63
12:KF:395:LEU:HD13	12:KF:484:ILE:HD11	1.80	0.63
14:MC:126:LEU:HD22	14:MD:126:LEU:HD12	1.78	0.63
2:AG:548:ARG:HD2	5:EB:4620:LYS:HZ1	1.62	0.63
6:FE:839:GLY:HA3	12:KB:681:MET:HE3	1.80	0.63
8:GJ:43:CYS:HB2	8:GJ:46:LEU:HB2	1.80	0.63
9:HB:554:ASP:HB2	9:HB:557:ALA:HB3	1.80	0.63
11:JA:1852:HIS:HB2	11:JA:1985:LEU:HD22	1.78	0.63
13:LE:502:MET:HG3	13:LF:503:VAL:HG21	1.79	0.63
14:MI:243:LYS:HE2	14:MI:247:LEU:HD22	1.79	0.63
15:NA:812:ARG:HH21	15:NA:878:ILE:HD12	1.63	0.63
15:NA:1524:ARG:HE	18:QA:57:ASN:HD22	1.47	0.63
15:NC:1528:SER:HA	15:NC:1531:GLN:HG3	1.80	0.63
15:ND:892:TRP:HB2	15:ND:1155:GLU:HB2	1.78	0.63
2:AC:175:VAL:HG21	16:OA:29:PRO:HG3	1.81	0.63
1:AI:239:GLU:HB2	1:AI:257:LEU:HD12	1.80	0.63
6:FC:2052:HIS:HE1	9:HB:762:HIS:HB2	1.63	0.63
7:GE:370:ALA:HB3	7:GE:383:GLN:HB2	1.79	0.63
10:IC:936:LEU:HD21	10:IC:969:LYS:HB3	1.79	0.63
16:OA:742:PHE:HA	18:QD:89:ARG:HH12	1.62	0.63
17:PC:257:ASN:HB2	17:PC:260:SER:HB3	1.80	0.63
2:AC:554:ASP:HB3	1:AD:471:GLU:HG2	1.80	0.63
6:FC:2001:CYS:O	6:FC:2002:THR:C	2.42	0.63
11:JC:422:LEU:HD23	11:JC:1441:CYS:HB3	1.79	0.63
12:KF:367:ILE:HD11	12:KF:394:LEU:HB2	1.81	0.63
2:AK:32:LEU:HD21	1:AL:451:ILE:HD11	1.80	0.63
1:AL:376:LEU:HB3	11:JB:1643:LEU:HD22	1.81	0.63
6:FA:2059:VAL:CG2	9:HA:754:LEU:HB2	2.28	0.63
6:FF:1222:CYS:HB3	6:FF:1225:ILE:HG13	1.80	0.63
8:GB:300:ARG:HG2	8:GB:361:ALA:HB3	1.81	0.63
8:GF:349:THR:HG22	8:GF:379:VAL:HG21	1.81	0.63
7:GG:506:ALA:HA	7:GG:509:LEU:HD12	1.81	0.63
11:JB:1744:ILE:HD11	11:JB:1759:LEU:HB3	1.79	0.63
15:NB:982:ILE:HD11	15:NB:1029:SER:H	1.63	0.63
20:SB:83:GLU:HA	20:SB:147:MET:HE1	1.79	0.63
1:AH:405:LEU:HD11	16:OC:24:LEU:HB3	1.79	0.63
6:FD:1429:LEU:HD23	6:FD:1430:PHE:CD2	2.33	0.63
8:GD:372:VAL:HG12	8:GD:377:MET:HE1	1.81	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GE:433:MET:HE2	7:GE:459:PRO:HD3	1.80	0.63
7:GG:311:LEU:HD13	7:GG:451:ILE:HG23	1.80	0.63
10:IA:864:GLN:HB3	10:IA:1241:LEU:HD22	1.80	0.63
16:OA:1101:PHE:HA	16:OA:1104:LYS:HZ1	1.64	0.63
3:BC:956:LEU:HD13	3:BC:978:VAL:HG21	1.79	0.63
6:FB:2055:THR:HG22	9:HD:837:LEU:HD11	1.81	0.63
7:GI:406:ALA:HA	7:GI:409:ARG:HB2	1.79	0.63
9:HA:554:ASP:HB2	9:HA:557:ALA:HB3	1.81	0.63
11:JA:1746:LEU:HD21	11:JA:1854:HIS:HE1	1.63	0.63
5:EA:3798:LEU:HD23	5:EA:3810:VAL:HA	1.80	0.63
6:FE:1190:ARG:HB2	6:FE:1418:GLU:HB2	1.81	0.63
8:GB:756:ALA:HB3	8:GF:333:LYS:HD2	1.81	0.63
8:GD:665:LEU:HB2	8:GD:676:TRP:HB3	1.80	0.63
8:GH:203:GLU:HB2	8:GH:313:PRO:HG3	1.81	0.63
8:GL:112:ILE:HD11	8:GL:508:ARG:HB2	1.80	0.63
10:IA:888:THR:HG21	15:NA:565:TRP:HD1	1.64	0.63
12:KE:524:PHE:HD1	12:KE:573:ARG:HH22	1.46	0.63
12:KE:606:ARG:HE	12:KE:623:ILE:HG13	1.62	0.63
13:LA:521:ASN:HB3	13:LB:520:LEU:HD13	1.80	0.63
15:ND:894:LEU:H	15:ND:1153:ALA:H	1.44	0.63
5:EA:3514:GLU:HG2	5:EA:3515:PRO:HD3	1.80	0.63
6:FC:2048:GLU:HG2	9:HB:765:TRP:NE1	2.14	0.63
6:FD:1432:THR:HB	6:FD:1435:GLU:HB2	1.80	0.63
8:GD:338:ALA:HA	8:GD:341:VAL:HG12	1.80	0.63
7:GG:169:ILE:HG23	7:GG:173:ASN:HD22	1.64	0.63
8:GH:773:ASP:H	8:GL:346:LYS:HD2	1.63	0.63
10:IA:968:ARG:HE	10:IA:1061:LEU:HD21	1.64	0.63
11:JB:48:GLN:HA	11:JB:95:PRO:HB3	1.80	0.63
19:RC:57:ARG:HH12	19:RC:118:TYR:HB3	1.64	0.63
1:AL:429:ARG:HH22	16:OB:5:VAL:HG21	1.62	0.62
3:CC:972:LEU:HD11	3:CF:1149:PRO:HG3	1.79	0.62
5:EA:3798:LEU:HB3	5:EA:3810:VAL:HG22	1.81	0.62
5:EB:4398:ILE:HG22	5:EB:4703:GLN:HE21	1.63	0.62
6:FC:1724:ARG:HE	6:FC:1808:VAL:HG13	1.64	0.62
6:FD:1233:ILE:HD11	6:FD:1268:VAL:HG22	1.80	0.62
6:FE:918:GLN:HB3	6:FE:922:LEU:HG	1.81	0.62
7:GA:284:GLU:HB3	7:GA:290:VAL:HG21	1.81	0.62
7:GG:844:HIS:HD2	7:GG:881:ALA:H	1.47	0.62
9:HB:643:PHE:HB2	9:HB:729:GLY:HA2	1.81	0.62
9:HC:675:ALA:HB3	9:HC:711:SER:HB2	1.80	0.62
10:IC:921:LEU:HD21	10:IC:938:ILE:HD13	1.81	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JA:2076:ASN:HD21	11:JA:2255:ARG:HH12	1.47	0.62
11:JC:541:LEU:HD11	11:JC:548:PHE:HA	1.79	0.62
1:AA:303:MET:HE2	1:AA:345:PRO:HD2	1.81	0.62
6:FD:813:GLN:O	6:FD:814:THR:C	2.41	0.62
6:FE:1244:LEU:O	6:FE:1246:ILE:N	2.33	0.62
7:GE:309:LEU:HD22	7:GE:444:MET:HE3	1.80	0.62
7:GI:371:LEU:HD12	7:GI:412:VAL:HG22	1.80	0.62
5:EA:4064:ALA:HB1	5:EA:4180:TYR:HD2	1.65	0.62
6:FD:1238:ARG:HH21	6:FD:1238:ARG:HA	1.64	0.62
15:NC:350:ARG:HE	15:NC:486:ARG:HD3	1.62	0.62
4:DA:356:TYR:HB3	4:DA:382:LEU:HD22	1.82	0.62
6:FD:997:THR:CG2	12:KA:230:GLN:HE22	2.11	0.62
6:FE:917:TRP:HD1	6:FE:918:GLN:HE21	1.46	0.62
8:GD:326:ARG:HH12	8:GD:375:TYR:HB3	1.63	0.62
7:GE:185:ARG:HH21	7:GE:704:ASP:HB2	1.64	0.62
7:GG:397:LEU:HD11	8:GJ:177:MET:H	1.64	0.62
8:GH:171:ILE:HG23	8:GH:181:HIS:HB2	1.80	0.62
10:IC:643:GLY:HA3	16:OC:1075:TYR:H	1.65	0.62
11:JA:1873:ARG:HH21	11:JA:1877:ALA:HB2	1.63	0.62
15:NB:1512:MET:HG2	18:QC:107:LEU:HD22	1.81	0.62
1:AH:310:CYS:H	1:AH:313:CYS:HB2	1.63	0.62
1:AL:462:LEU:HA	1:AL:465:MET:HG2	1.82	0.62
3:CB:711:ARG:HH12	3:CB:757:MET:HE1	1.64	0.62
4:DD:105:CYS:H	4:DD:260:GLY:HA2	1.64	0.62
6:FC:1755:VAL:HB	6:FC:1759:GLU:HG3	1.81	0.62
6:FD:888:PRO:HG2	7:GC:897:SER:CB	2.28	0.62
6:FD:1283:TYR:HB3	6:FD:1290:ILE:HG23	1.82	0.62
6:FE:1222:CYS:HB3	6:FE:1225:ILE:HB	1.81	0.62
6:FF:1433:ALA:O	6:FF:1434:ALA:C	2.42	0.62
8:GF:218:SER:HB3	8:GF:221:ALA:HB2	1.81	0.62
7:GG:535:PRO:HG2	9:HA:553:TYR:CD1	2.35	0.62
7:GK:353:SER:HB3	7:GK:406:ALA:HB2	1.80	0.62
11:JC:57:GLU:HA	11:JC:90:ARG:HH21	1.63	0.62
12:KE:207:ASP:HA	12:KE:280:LEU:HB3	1.81	0.62
1:AE:1025:ARG:HD2	14:ML:85:PRO:HD2	1.80	0.62
2:AK:378:ASN:HB3	5:EA:4396:GLU:HG3	1.82	0.62
11:JB:1982:SER:HA	11:JB:1985:LEU:HD23	1.81	0.62
15:NB:1536:GLN:HB2	19:RB:111:VAL:HG23	1.81	0.62
15:NC:1498:ARG:HH12	15:NC:1501:PRO:HG2	1.64	0.62
1:AA:64:HIS:HB2	1:AA:229:LEU:HD21	1.82	0.62
1:AE:728:VAL:HG13	1:AE:729:THR:HG23	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EC:3498:VAL:HG12	5:EC:4011:VAL:HG22	1.81	0.62
9:HA:777:TYR:CD1	9:HA:778:PRO:HD2	2.35	0.62
9:HB:810:ARG:HA	9:HB:813:THR:HG23	1.81	0.62
10:IC:784:LEU:HD23	11:JC:2057:LEU:HD21	1.81	0.62
11:JB:1749:LYS:HE2	11:JB:1858:ILE:HD11	1.81	0.62
11:JB:1818:ILE:HA	11:JB:1821:LEU:HD23	1.81	0.62
13:LI:526:LEU:HG	13:LJ:525:SER:HB3	1.81	0.62
15:NB:707:GLU:HB2	15:NB:934:LEU:HD21	1.81	0.62
15:NC:1526:ILE:HG21	18:QD:146:ILE:HG21	1.82	0.62
15:ND:1160:LEU:HD12	15:ND:1165:VAL:HG11	1.81	0.62
1:AD:228:PRO:HD2	10:IB:1251:VAL:HA	1.81	0.62
4:DA:126:LEU:HD21	4:DA:157:THR:HG22	1.82	0.62
4:DB:130:ARG:HH21	4:DB:154:LEU:HD12	1.63	0.62
5:EC:4879:THR:HG22	5:EC:4892:ARG:HB3	1.81	0.62
5:EC:4882:ARG:HG3	5:EC:4887:GLY:HA2	1.81	0.62
6:FE:808:SER:O	6:FE:809:ILE:C	2.42	0.62
6:FF:828:GLN:HA	6:FF:831:ARG:HG2	1.81	0.62
8:GF:422:LYS:HB2	8:GF:501:SER:HB2	1.80	0.62
7:GG:536:THR:HA	9:HA:553:TYR:HB2	1.80	0.62
8:GH:674:VAL:HG12	8:GH:723:VAL:HB	1.81	0.62
11:JB:1852:HIS:HB2	11:JB:1985:LEU:HD12	1.82	0.62
12:KF:588:ALA:HB3	12:KF:710:ASN:HD21	1.65	0.62
15:NC:1126:THR:H	15:NC:1159:THR:HA	1.65	0.62
15:ND:922:LEU:HD21	15:ND:1106:SER:HB3	1.81	0.62
2:AB:177:VAL:HG11	2:AB:183:ALA:HB2	1.82	0.62
2:AG:27:ALA:HB1	1:AH:443:LYS:HG2	1.81	0.62
1:AL:1046:THR:HG22	1:AL:1048:ALA:H	1.65	0.62
3:CJ:1154:LEU:HG	3:CJ:1158:PHE:HE2	1.65	0.62
6:FD:993:ALA:HB2	12:KA:230:GLN:HB2	1.80	0.62
6:FF:1217:GLU:O	6:FF:1218:ALA:C	2.42	0.62
9:HB:552:ASP:HB2	9:HB:576:LYS:HD3	1.82	0.62
11:JC:46:PHE:H	11:JC:170:ILE:HG21	1.63	0.62
12:KA:296:ILE:HD11	12:KA:318:VAL:HG13	1.81	0.62
12:KA:660:THR:HG22	12:KA:662:SER:H	1.65	0.62
14:MK:105:LEU:HD21	14:ML:104:LYS:HD2	1.80	0.62
15:ND:468:ARG:HD3	15:ND:469:PHE:HD1	1.65	0.62
1:AE:44:LEU:HD11	17:PC:268:PRO:HB2	1.81	0.62
1:AI:64:HIS:HB2	1:AI:229:LEU:HD21	1.82	0.62
3:BA:808:VAL:HG22	17:PA:279:ARG:HH21	1.64	0.62
3:BB:694:ARG:HD2	17:PB:290:PHE:HE2	1.65	0.62
4:DB:154:LEU:HA	4:DB:157:THR:HG22	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DE:336:ARG:HH12	4:DE:340:ALA:HB2	1.65	0.62
5:EB:4405:ILE:HG23	5:EB:4431:ARG:HD3	1.82	0.62
7:GC:606:MET:HE2	7:GC:678:LEU:HD13	1.82	0.62
8:GF:544:LEU:HG	8:GF:560:TRP:HH2	1.65	0.62
7:GI:746:LEU:HA	7:GI:749:LEU:HD12	1.82	0.62
9:HA:761:CYS:O	9:HA:762:HIS:C	2.43	0.62
12:KE:374:ALA:HA	12:KE:377:LEU:HB3	1.82	0.62
12:KF:642:ARG:HE	12:KF:677:ARG:HB3	1.65	0.62
15:NB:685:PHE:HE2	15:NB:689:ASN:HA	1.65	0.62
1:AD:22:PHE:HB3	1:AD:25:ALA:HB3	1.82	0.61
2:AG:168:GLN:HG3	2:AG:280:ARG:HD2	1.80	0.61
2:AK:489:ILE:HG23	1:AL:354:ARG:HH12	1.65	0.61
5:EC:4167:ASP:HB2	5:EC:4171:ILE:HG12	1.82	0.61
6:FE:807:ALA:O	6:FE:808:SER:HB2	1.98	0.61
11:JA:1168:THR:HG21	11:JA:1173:LEU:HB3	1.80	0.61
11:JC:805:CYS:HB2	11:JC:895:LEU:HB3	1.82	0.61
15:NC:925:ARG:HE	15:NC:926:ARG:H	1.47	0.61
1:AL:38:VAL:HG12	1:AL:111:ILE:HD12	1.82	0.61
5:EB:3445:VAL:HG21	5:EB:3570:LEU:HD23	1.80	0.61
6:FE:1218:ALA:O	6:FE:1219:GLU:C	2.41	0.61
14:ML:140:ARG:HB2	14:ML:144:ARG:HH12	1.63	0.61
16:OB:1042:PRO:HB3	16:OB:1044:ARG:HH21	1.65	0.61
3:BB:948:THR:HG22	3:BB:950:GLY:H	1.65	0.61
6:FC:1892:ILE:HG22	6:FC:1894:THR:H	1.65	0.61
6:FD:803:ARG:HB3	6:FD:907:ASN:HD22	1.65	0.61
6:FD:918:GLN:O	6:FD:919:GLN:C	2.43	0.61
6:FD:1217:GLU:O	6:FD:1218:ALA:C	2.43	0.61
6:FE:918:GLN:O	6:FE:919:GLN:C	2.43	0.61
7:GC:185:ARG:HH21	7:GC:704:ASP:HB2	1.65	0.61
10:IC:791:VAL:HG21	10:IC:812:LEU:HD22	1.82	0.61
15:NA:708:LEU:HB3	15:NA:714:ARG:HH11	1.65	0.61
15:NA:1197:ARG:HD2	15:NA:1386:HIS:HB2	1.82	0.61
6:FF:833:GLY:H	6:FF:979:LEU:HD23	1.66	0.61
7:GA:543:LYS:H	9:HB:596:TYR:HB3	1.64	0.61
7:GA:823:ARG:HE	7:GA:827:LEU:HD11	1.65	0.61
15:NA:558:GLU:HB2	15:NA:578:HIS:HE2	1.64	0.61
15:NA:922:LEU:HD11	15:NA:1105:HIS:HE1	1.65	0.61
1:AA:460:VAL:HG23	1:AA:465:MET:HE3	1.81	0.61
2:AB:41:ARG:HG2	2:AB:291:LEU:HB2	1.81	0.61
6:FD:971:SER:HB3	6:FD:1022:THR:HG23	1.82	0.61
6:FE:1292:ALA:HB1	6:FE:1393:LEU:HG	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GB:745:TYR:HB3	8:GF:342:LYS:HG3	1.82	0.61
7:GI:606:MET:HB3	7:GI:631:PHE:HB2	1.81	0.61
12:KE:503:ASP:HA	12:KE:506:LEU:HD13	1.82	0.61
15:NC:983:ILE:HG23	15:NC:989:ILE:HB	1.82	0.61
15:ND:505:GLY:H	15:ND:512:TYR:HB2	1.65	0.61
1:AL:632:LEU:HD23	1:AL:633:MET:HG3	1.83	0.61
4:DB:93:ILE:HG23	4:DB:97:LEU:HD12	1.83	0.61
5:EC:4041:ASP:HB3	5:EC:4371:ARG:HH21	1.65	0.61
6:FF:1193:VAL:HB	6:FF:1416:GLN:HB3	1.82	0.61
8:GF:327:HIS:H	8:GF:330:ASP:HB2	1.65	0.61
8:GL:415:LEU:HB3	8:GL:417:MET:HE2	1.82	0.61
9:HB:848:ASP:OD1	9:HB:849:ALA:N	2.34	0.61
12:KF:656:ARG:HB3	12:KF:667:SER:HB3	1.83	0.61
13:LP:410:LYS:HG3	13:LP:413:GLU:HB3	1.81	0.61
14:ME:326:LEU:HD13	14:MF:326:LEU:HD11	1.82	0.61
19:RC:18:LYS:HB3	19:RC:105:MET:HA	1.81	0.61
5:EA:4745:VAL:HG13	5:EA:4842:GLN:HE22	1.66	0.61
5:EC:4640:VAL:HG21	5:EC:4708:LEU:HD21	1.83	0.61
6:FD:962:PHE:CE2	6:FD:965:TRP:HB2	2.35	0.61
6:FD:1218:ALA:O	6:FD:1219:GLU:C	2.44	0.61
6:FD:1222:CYS:O	6:FD:1223:ALA:C	2.43	0.61
6:FE:1185:VAL:O	6:FE:1186:TRP:C	2.44	0.61
6:FE:1188:GLU:HG3	6:FE:1267:GLN:HB3	1.82	0.61
7:GI:350:ARG:HH12	7:GI:352:ASP:HB2	1.65	0.61
11:JC:1581:ARG:HH22	15:NA:354:PHE:HB3	1.64	0.61
12:KA:534:VAL:HG13	12:KA:542:PRO:HB3	1.83	0.61
12:KC:727:ILE:HB	12:KC:728:PRO:HD3	1.82	0.61
6:FD:1424:CYS:HB2	6:FD:1425:PRO:CD	2.24	0.61
8:GJ:440:CYS:HB2	8:GJ:463:TRP:HB3	1.83	0.61
11:JA:1591:HIS:HD2	11:JA:1593:VAL:HG22	1.65	0.61
11:JC:1818:ILE:HA	11:JC:1821:LEU:HD23	1.82	0.61
12:KC:377:LEU:HD23	12:KC:377:LEU:H	1.65	0.61
1:AA:366:ARG:HH12	1:AA:370:GLN:HG2	1.65	0.61
2:AK:50:ILE:HD11	2:AK:282:PHE:HB2	1.81	0.61
5:EC:3445:VAL:HG21	5:EC:3570:LEU:HG	1.83	0.61
6:FB:1962:GLN:HG2	6:FB:2047:ARG:HD2	1.82	0.61
6:FD:1388:PHE:HD1	6:FD:1418:GLU:HA	1.66	0.61
6:FE:1222:CYS:O	6:FE:1223:ALA:C	2.44	0.61
6:FE:1393:LEU:HD13	6:FE:1417:ILE:HG21	1.82	0.61
7:GA:239:ASN:HD22	7:GA:693:THR:HG21	1.65	0.61
7:GA:301:ARG:HH12	7:GA:304:GLN:HB3	1.64	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GG:433:MET:HE2	7:GG:459:PRO:HD3	1.82	0.61
8:GL:385:GLY:HA2	8:GL:439:PRO:HB2	1.82	0.61
10:IA:940:SER:HA	10:IA:975:PHE:HZ	1.65	0.61
15:NC:515:ALA:HB3	15:NC:520:ALA:HB2	1.81	0.61
15:NC:787:LEU:HD21	15:NC:896:ARG:HD3	1.83	0.61
3:BB:791:THR:HG21	3:BB:812:MET:HG2	1.82	0.61
3:CC:842:PHE:HA	3:CC:845:LYS:HE2	1.83	0.61
5:EA:3650:THR:HG23	9:HC:499:ARG:HA	1.81	0.61
5:EA:3705:ASP:HA	5:EA:3708:HIS:HB3	1.83	0.61
6:FD:1002:ALA:HB3	6:FD:1010:ARG:HH11	0.67	0.61
7:GI:605:VAL:HB	7:GI:630:LEU:HD11	1.82	0.61
10:IA:174:PHE:HB3	10:IA:205:GLN:HE21	1.65	0.61
11:JA:1327:LEU:HD21	11:JA:1384:ILE:HG12	1.83	0.61
12:KC:402:LEU:HD11	12:KC:720:LEU:HD21	1.82	0.61
13:LA:374:HIS:HE1	13:LB:370:MET:HB2	1.65	0.61
15:NA:741:ILE:HG23	15:NA:793:THR:HG22	1.83	0.61
2:AC:192:TRP:HE1	5:EA:4613:GLU:HG2	1.66	0.60
3:BA:982:ARG:HB3	3:BA:993:THR:HG22	1.82	0.60
3:CJ:1182:GLY:H	3:CJ:4512:SER:HB2	1.66	0.60
5:EA:4880:ASP:OD1	5:EA:4888:TRP:CE2	2.53	0.60
5:EC:3760:LYS:HG3	5:EC:3763:ARG:HG3	1.81	0.60
6:FB:2072:ILE:HG21	9:HD:854:ASN:HB3	1.83	0.60
7:GA:807:ARG:HG3	7:GA:977:SER:HB3	1.83	0.60
7:GC:916:HIS:HB3	7:GC:919:VAL:HG12	1.83	0.60
9:HB:646:LEU:HD13	9:HB:730:GLY:H	1.66	0.60
10:IB:644:VAL:H	16:OB:1074:TYR:HB2	1.66	0.60
10:IB:813:ALA:HB2	10:IB:840:PRO:HB2	1.82	0.60
11:JB:1583:ILE:HG21	11:JB:1594:ARG:HB2	1.83	0.60
15:NA:515:ALA:HB3	15:NA:520:ALA:HB2	1.83	0.60
15:NB:925:ARG:HE	15:NB:926:ARG:H	1.47	0.60
15:NC:725:ILE:HG13	15:NC:799:ILE:HG21	1.83	0.60
2:AJ:209:SER:HB3	2:AJ:259:VAL:HA	1.83	0.60
4:DC:300:GLN:HE21	4:DC:354:TRP:HA	1.65	0.60
5:EB:3242:LEU:HD23	5:EB:3249:ALA:HA	1.83	0.60
5:EC:4641:PHE:HE1	5:EC:4704:LYS:HB3	1.66	0.60
5:EC:4651:MET:HE3	5:EC:4657:GLU:HB3	1.83	0.60
7:GA:535:PRO:HG2	9:HB:553:TYR:CD1	2.36	0.60
7:GI:196:LEU:HB3	7:GI:198:LEU:HD23	1.81	0.60
7:GK:171:GLN:HG3	7:GK:172:PHE:HD2	1.67	0.60
8:GL:300:ARG:HG2	8:GL:361:ALA:HB3	1.83	0.60
9:HB:681:LYS:HE2	13:LD:483:ARG:NH1	2.17	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:1003:VAL:HB	10:IC:1043:PHE:HB2	1.84	0.60
11:JA:1032:VAL:HG21	11:JA:1063:ILE:HG12	1.82	0.60
11:JA:1676:ARG:HD3	11:JA:1736:THR:HG22	1.83	0.60
11:JC:147:ARG:HA	11:JC:151:LEU:HD22	1.84	0.60
13:LJ:459:ALA:HA	13:LJ:462:GLN:HB2	1.82	0.60
2:AG:44:LEU:HD21	2:AG:47:ALA:HB2	1.83	0.60
1:AH:58:LEU:HB3	3:CE:1117:VAL:HG11	1.82	0.60
3:CA:996:VAL:HA	3:CA:999:LEU:HD12	1.83	0.60
4:DC:16:LEU:HD22	4:DC:97:LEU:HD12	1.83	0.60
6:FD:842:GLY:N	7:GC:957:ARG:HH21	1.98	0.60
7:GA:890:MET:HE3	7:GA:953:LEU:HB2	1.82	0.60
8:GH:160:LEU:HA	8:GH:163:MET:HG2	1.83	0.60
10:IC:838:LEU:HD11	10:IC:875:VAL:HG11	1.83	0.60
10:IC:1232:ARG:HG2	10:IC:1302:ARG:HH22	1.65	0.60
11:JA:84:PHE:HB3	11:JA:2092:PHE:HZ	1.66	0.60
11:JC:1078:MET:HG2	11:JC:1509:HIS:HD2	1.65	0.60
15:NB:564:ARG:HH21	15:NB:619:TYR:HA	1.67	0.60
19:RD:24:ARG:HA	19:RD:27:ALA:HB2	1.83	0.60
4:DD:126:LEU:HD23	4:DD:158:LEU:HA	1.83	0.60
6:FD:978:LYS:HZ1	6:FD:984:THR:H	1.49	0.60
6:FE:1003:ILE:HG13	6:FE:1009:VAL:HG13	1.84	0.60
7:GI:715:THR:HG21	7:GI:796:PHE:HB3	1.83	0.60
12:KC:298:GLN:HB3	12:KC:303:TYR:HB2	1.83	0.60
13:LE:427:ARG:HE	13:LE:430:LYS:HZ1	1.49	0.60
15:NB:735:HIS:HD2	15:NB:768:GLU:HG2	1.65	0.60
3:CI:4467:THR:HG23	3:CI:4468:LYS:HG3	1.82	0.60
4:DB:327:PHE:HE1	14:ME:259:MET:HG2	1.67	0.60
6:FC:1991:ALA:HA	6:FC:1994:ARG:HE	1.64	0.60
6:FE:803:ARG:HB3	6:FE:1118:GLN:HG3	1.82	0.60
6:FF:1189:ILE:HD11	6:FF:1282:LEU:HD13	1.83	0.60
7:GG:319:VAL:HG13	7:GG:424:ARG:HG2	1.83	0.60
8:GJ:315:GLN:HG2	8:GJ:340:PHE:HB3	1.82	0.60
12:KA:206:CYS:HA	12:KA:243:HIS:HA	1.84	0.60
12:KG:534:VAL:HG13	12:KG:536:ARG:HH12	1.65	0.60
14:ME:285:ARG:HH12	14:MF:257:LYS:HA	1.66	0.60
3:CL:1263:SER:HA	3:CL:4457:PRO:HG3	1.83	0.60
5:EB:3765:VAL:HG12	11:JA:932:PRO:HG2	1.84	0.60
6:FC:2009:SER:HA	6:FC:2012:ARG:NE	2.17	0.60
6:FD:1102:TYR:O	6:FD:1103:SER:C	2.44	0.60
6:FE:837:ALA:O	6:FE:838:ASN:C	2.44	0.60
6:FE:993:ALA:HB3	12:KB:229:SER:CB	2.27	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GG:464:LEU:HB3	7:GG:502:TYR:HE1	1.67	0.60
8:GJ:50:GLU:H	14:MI:259:MET:HE1	1.67	0.60
12:KC:231:PHE:HZ	12:KC:313:PHE:CG	2.18	0.60
15:NB:947:ASN:HA	15:NB:950:VAL:HG22	1.83	0.60
1:AE:64:HIS:HE1	17:PC:268:PRO:HD2	1.65	0.60
4:DB:329:ARG:HA	4:DB:332:LEU:HB2	1.84	0.60
5:EB:4438:LEU:HD11	5:EB:4709:PHE:HE2	1.66	0.60
5:EC:3765:VAL:HG12	11:JC:932:PRO:HG2	1.82	0.60
6:FC:1955:THR:HG21	9:HB:838:LYS:HA	1.82	0.60
6:FD:1190:ARG:HB2	6:FD:1418:GLU:HB2	1.83	0.60
6:FD:1209:GLU:O	6:FD:1210:LEU:C	2.44	0.60
8:GF:43:CYS:HB2	8:GF:46:LEU:HB2	1.82	0.60
7:GI:314:VAL:HG23	7:GI:363:ASP:HB3	1.84	0.60
9:HB:675:ALA:HB3	9:HB:711:SER:HB2	1.83	0.60
10:IA:634:ALA:HB2	10:IA:692:GLU:HB3	1.83	0.60
12:KA:335:LEU:HD23	12:KA:338:LEU:HD22	1.83	0.60
12:KF:593:HIS:HB2	12:KF:707:GLU:HB3	1.83	0.60
15:NA:508:GLY:HA3	15:NA:577:PRO:HG3	1.83	0.60
15:NC:696:PHE:HB2	15:NC:894:LEU:HD22	1.83	0.60
15:ND:686:ASN:HB2	15:ND:692:ILE:HG22	1.83	0.60
2:AB:159:ARG:HG3	5:EA:4626:LEU:HD22	1.82	0.60
2:AB:507:PRO:HG3	3:BA:750:SER:HB2	1.83	0.60
4:DB:8:GLU:HA	4:DB:11:PHE:HD1	1.67	0.60
6:FA:1661:GLY:HA2	6:FA:1809:SER:HB2	1.83	0.60
6:FD:844:ALA:O	7:GC:896:ARG:NH2	2.33	0.60
6:FF:1108:PRO:HD3	9:HC:394:LEU:HG	1.84	0.60
8:GD:716:ARG:HH11	8:GD:720:PRO:HG3	1.67	0.60
7:GE:423:TRP:HB3	7:GE:426:ASN:HD22	1.65	0.60
9:HA:761:CYS:HA	9:HA:765:TRP:CD2	2.36	0.60
11:JB:46:PHE:H	11:JB:170:ILE:HG21	1.66	0.60
15:NC:1518:ARG:HH21	18:QD:65:ALA:HB2	1.67	0.60
15:ND:1526:ILE:HD13	18:QB:146:ILE:HG13	1.84	0.60
1:AA:666:LEU:HB3	1:AA:720:LEU:HD11	1.83	0.60
1:AE:633:MET:HE3	7:GG:930:PRO:HG3	1.84	0.60
1:AH:835:ALA:HB2	1:AH:918:VAL:HG21	1.84	0.60
6:FB:1750:LEU:HD13	6:FB:1752:LEU:HD23	1.84	0.60
8:GL:315:GLN:HG2	8:GL:340:PHE:HB3	1.83	0.60
9:HB:680:ALA:HB2	9:HB:708:VAL:HG13	1.83	0.60
10:IC:995:PRO:HA	10:IC:1103:ARG:HD2	1.84	0.60
11:JA:147:ARG:HA	11:JA:151:LEU:HD22	1.83	0.60
13:LN:336:VAL:HG12	13:LN:340:LYS:HE2	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:ND:1548:PHE:N	19:RD:141:LEU:HD12	2.16	0.60
2:AF:177:VAL:HG11	2:AF:183:ALA:HB2	1.83	0.60
1:AH:912:SER:HB2	13:LI:486:ARG:HG2	1.83	0.60
1:AI:382:ILE:HG21	2:AJ:464:ILE:HD11	1.84	0.60
2:AJ:299:LEU:HA	2:AJ:307:PRO:HA	1.84	0.60
7:GA:807:ARG:HD2	7:GA:812:VAL:HG23	1.82	0.60
7:GC:890:MET:HE2	7:GC:951:MET:HB2	1.84	0.60
11:JC:2001:ILE:HG22	11:JC:2270:MET:HG3	1.84	0.60
12:KF:292:ALA:HB2	12:KF:314:LEU:HD22	1.83	0.60
15:NA:729:VAL:HG11	15:NA:800:SER:HB3	1.83	0.60
15:NA:895:GLY:HA2	15:NA:898:ASN:HB2	1.83	0.60
2:AG:376:ARG:HH22	5:EC:4405:ILE:HD13	1.67	0.59
3:CG:1133:VAL:HG11	10:IC:1094:ASN:HD21	1.67	0.59
4:DC:335:ASP:HA	4:DC:338:ILE:HG12	1.84	0.59
5:EC:3581:HIS:HD2	5:EC:3647:ALA:HA	1.67	0.59
6:FB:2083:GLN:HG3	9:HD:865:ILE:HD11	1.83	0.59
6:FC:1704:MET:HE3	6:FC:1720:VAL:HG21	1.83	0.59
6:FD:844:ALA:O	6:FD:845:PRO:C	2.44	0.59
6:FF:1009:VAL:HG21	6:FF:1219:GLU:HA	1.84	0.59
9:HD:875:THR:O	9:HD:879:ILE:HG13	2.02	0.59
11:JA:1220:LEU:HD21	11:JA:1286:LEU:HD12	1.83	0.59
14:MI:211:MET:HE1	14:MJ:210:LEU:HD13	1.83	0.59
15:NB:614:LYS:HB3	15:NB:678:LEU:HD22	1.84	0.59
18:QA:125:LYS:HG2	18:QA:140:TRP:HZ2	1.66	0.59
1:AD:632:LEU:HD23	1:AD:633:MET:HG3	1.84	0.59
1:AE:73:THR:HG22	1:AE:75:ALA:H	1.67	0.59
4:DA:66:ARG:HD3	4:DA:71:LEU:HA	1.83	0.59
6:FC:2080:GLN:HB3	9:HB:861:TYR:HE2	1.66	0.59
6:FE:1211:SER:HA	6:FE:1234:THR:HA	1.84	0.59
8:GD:725:CYS:HB3	8:GD:732:ALA:HB2	1.84	0.59
8:GH:670:PHE:HA	8:GH:720:PRO:HG3	1.84	0.59
10:IA:342:LEU:HD12	10:IA:343:PRO:HD2	1.84	0.59
10:IC:614:LEU:HD21	10:IC:797:VAL:HG21	1.84	0.59
11:JA:435:VAL:HA	11:JA:437:LEU:HD12	1.83	0.59
11:JB:1474:TRP:HA	11:JB:1477:TRP:HB2	1.83	0.59
11:JB:1666:VAL:HG22	16:OB:917:ILE:HD11	1.85	0.59
14:MA:258:ILE:HG13	14:MA:264:LEU:HG	1.83	0.59
15:NC:1511:GLU:HB2	18:QD:107:LEU:HD21	1.84	0.59
2:AB:317:ALA:HB2	1:AI:274:ARG:HH22	1.66	0.59
1:AE:131:ARG:HD3	1:AE:132:PRO:HD2	1.83	0.59
1:AE:1005:LEU:HD13	1:AE:1007:LYS:HZ3	1.67	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CE:4468:LYS:HB2	3:CE:4488:MET:HB2	1.85	0.59
3:CF:4477:PRO:HG2	3:CF:4479:LEU:HG	1.84	0.59
3:CG:1146:VAL:HG23	3:CL:1137:ALA:HB2	1.84	0.59
4:DE:150:SER:HA	4:DE:153:PHE:HB3	1.84	0.59
5:EC:4030:GLU:HB3	5:EC:4058:PRO:HB3	1.84	0.59
6:FD:833:GLY:H	6:FD:979:LEU:HD23	1.67	0.59
6:FF:808:SER:CB	6:FF:1113:PHE:HB2	2.31	0.59
6:FF:1184:ALA:N	6:FF:1424:CYS:HB3	2.17	0.59
8:GD:115:GLN:HE22	8:GD:508:ARG:HD2	1.67	0.59
7:GE:605:VAL:HB	7:GE:630:LEU:HD11	1.84	0.59
11:JA:46:PHE:H	11:JA:170:ILE:HG21	1.67	0.59
11:JA:1138:PRO:HG3	11:JA:1837:GLN:HB3	1.83	0.59
12:KB:234:PRO:HG2	12:KB:236:LYS:HE2	1.84	0.59
12:KG:606:ARG:HG3	12:KG:623:ILE:HG13	1.85	0.59
13:LA:395:ILE:HD13	13:LA:398:ARG:HH12	1.67	0.59
16:OA:171:PHE:HA	16:OA:182:ALA:HA	1.84	0.59
1:AE:654:LEU:HD13	1:AE:662:LEU:HD13	1.84	0.59
3:CI:1171:LEU:HD22	3:CI:4502:VAL:HG12	1.84	0.59
3:CJ:1244:PRO:HB2	3:CJ:1252:PRO:HB3	1.84	0.59
4:DA:28:LEU:HD13	4:DA:154:LEU:HD11	1.84	0.59
7:GE:276:ARG:NH2	7:GE:285:LEU:HG	2.16	0.59
7:GI:458:PRO:HB3	7:GI:562:ILE:HD11	1.83	0.59
11:JB:57:GLU:HA	11:JB:90:ARG:HH21	1.67	0.59
12:KF:677:ARG:HH12	12:KF:679:SER:HB3	1.66	0.59
12:KG:217:GLU:HG3	12:KG:218:ARG:H	1.66	0.59
13:LI:523:GLU:C	13:LI:525:SER:H	2.09	0.59
15:NC:579:PRO:HB2	15:NC:616:LEU:HD21	1.84	0.59
18:QB:121:LYS:HD3	18:QB:154:ASP:HA	1.85	0.59
1:AA:301:VAL:HG23	1:AA:332:THR:HG22	1.85	0.59
5:EB:4641:PHE:HB3	5:EB:4812:LEU:HD23	1.84	0.59
5:EC:3268:ASN:HA	5:EC:3271:ASP:HB2	1.84	0.59
6:FB:1656:THR:HB	6:FB:1659:ILE:HD13	1.84	0.59
6:FF:834:VAL:O	6:FF:835:SER:C	2.45	0.59
6:FF:895:ILE:HG12	7:GI:967:PHE:HE2	1.66	0.59
9:HB:762:HIS:HD2	9:HB:763:GLN:HE22	1.49	0.59
12:KG:320:LYS:HE3	12:KG:357:MET:HB2	1.84	0.59
15:NA:1138:THR:HG23	15:NA:1140:LEU:H	1.67	0.59
15:NC:361:VAL:HG11	15:NC:445:ILE:HD11	1.84	0.59
2:AB:46:GLN:HB2	5:EA:4522:VAL:HG21	1.83	0.59
4:DA:21:ASP:HB3	14:MA:277:VAL:HG13	1.84	0.59
6:FD:844:ALA:C	7:GC:896:ARG:HH22	2.10	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1209:GLU:O	6:FE:1210:LEU:C	2.45	0.59
7:GE:988:LYS:HD2	9:HA:402:ARG:HE	1.67	0.59
15:NC:604:GLU:HG3	15:NC:1198:ILE:HG21	1.84	0.59
15:NC:866:LEU:HD23	15:NC:869:PHE:HD2	1.68	0.59
1:AE:121:ARG:HB3	1:AE:213:ALA:HB2	1.84	0.59
1:AE:988:GLN:HA	1:AE:991:LEU:HG	1.84	0.59
4:DE:105:CYS:HA	4:DE:259:SER:HB2	1.83	0.59
5:EC:3255:GLU:HG3	7:GE:732:ALA:HB2	1.85	0.59
6:FA:2062:LEU:HA	6:FA:2065:THR:HG22	1.83	0.59
8:GD:13:ARG:HG3	8:GD:627:VAL:HG11	1.84	0.59
8:GH:287:LEU:HA	8:GH:290:LEU:HD23	1.85	0.59
8:GH:362:VAL:HG21	8:GH:380:MET:HE3	1.84	0.59
8:GH:469:ASP:HB2	8:GH:624:ARG:HH22	1.67	0.59
11:JA:1410:LEU:HD22	11:JA:1502:ILE:HD11	1.84	0.59
11:JC:1515:LEU:HD22	11:JC:1554:LEU:HD12	1.84	0.59
11:JC:1980:VAL:HG12	11:JC:1982:SER:H	1.67	0.59
2:AG:555:SER:HA	2:AG:558:ARG:HG2	1.84	0.59
3:BA:694:ARG:HD2	17:PA:290:PHE:HE1	1.67	0.59
3:CJ:1263:SER:HA	3:CJ:4457:PRO:HG3	1.85	0.59
6:FD:1182:ALA:CB	6:FD:1429:LEU:HB2	2.31	0.59
6:FE:1301:ALA:HA	6:FE:1430:PHE:HB3	1.85	0.59
6:FE:1436:PHE:O	6:FE:1437:ALA:C	2.45	0.59
6:FF:888:PRO:HG2	7:GI:897:SER:HB3	1.84	0.59
7:GG:747:SER:HB3	7:GG:993:SER:HB2	1.83	0.59
8:GH:656:ALA:HB3	8:GH:742:SER:H	1.68	0.59
8:GL:639:LEU:HD12	8:GL:666:LEU:HD23	1.83	0.59
16:OA:289:ALA:HB1	16:OA:297:LEU:HD21	1.85	0.59
18:QA:39:PHE:HA	18:QA:58:LEU:HD21	1.85	0.59
1:AD:71:LEU:HD11	1:AD:218:PRO:HB2	1.83	0.59
2:AG:178:GLU:HG3	2:AG:179:ASP:H	1.67	0.59
1:AI:243:VAL:HG21	19:RA:94:PRO:HG3	1.85	0.59
2:AJ:114:MET:HE1	2:AJ:143:ARG:HG3	1.84	0.59
4:DE:299:ARG:HD3	4:DE:302:ILE:HD13	1.84	0.59
5:EA:3650:THR:HG22	9:HC:500:LEU:HD22	1.83	0.59
5:EB:3255:GLU:HG2	7:GC:732:ALA:HB2	1.85	0.59
6:FB:1599:HIS:H	6:FB:1604:ASN:HD21	1.50	0.59
8:GD:526:ILE:HG12	8:GD:530:PRO:HD3	1.84	0.59
7:GE:980:LEU:HD12	7:GE:984:GLU:HG3	1.83	0.59
9:HA:795:LEU:HD13	9:HA:797:TYR:HE2	1.62	0.59
11:JA:900:PRO:HB2	11:JA:951:LEU:HD12	1.85	0.59
11:JB:68:ARG:HG3	11:JB:140:LEU:HD11	1.83	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:1555:VAL:HG11	15:NA:349:ARG:HH21	1.67	0.59
15:NA:564:ARG:HH22	15:NA:619:TYR:HA	1.67	0.59
15:ND:887:SER:HB2	15:ND:1156:LEU:HD12	1.85	0.59
1:AA:382:ILE:HG21	2:AB:464:ILE:HD11	1.84	0.59
3:CJ:1154:LEU:HD13	3:CJ:4516:ILE:HA	1.84	0.59
4:DD:43:PRO:HG3	8:GD:680:LEU:HD21	1.85	0.59
4:DF:56:LEU:HD23	4:DF:162:VAL:HG23	1.85	0.59
6:FC:1771:GLU:HG2	6:FC:1776:GLY:HA3	1.83	0.59
6:FD:1223:ALA:O	6:FD:1224:ALA:C	2.46	0.59
8:GD:762:SER:HA	8:GJ:555:LEU:HB3	1.85	0.59
11:JB:78:GLN:HE22	11:JB:80:GLU:HB3	1.67	0.59
11:JC:1032:VAL:HG21	11:JC:1063:ILE:HG23	1.85	0.59
11:JC:1412:LEU:HB3	11:JC:1504:ARG:HB2	1.85	0.59
12:KG:383:HIS:HA	12:KG:386:LEU:HD23	1.84	0.59
15:NA:983:ILE:HG23	15:NA:989:ILE:HB	1.85	0.59
15:NB:794:GLU:HG3	15:NB:797:ARG:HH11	1.67	0.59
15:NC:607:ALA:HB3	15:NC:609:GLN:HE22	1.67	0.59
3:BC:939:ARG:HH11	3:BC:954:LEU:HD11	1.68	0.58
3:CG:1236:LEU:HD21	3:CG:1255:VAL:HG13	1.85	0.58
5:EC:3611:GLU:HA	5:EC:3627:ARG:HH21	1.67	0.58
6:FB:1701:PHE:HZ	13:LL:484:VAL:HG11	1.68	0.58
6:FD:1184:ALA:N	6:FD:1424:CYS:HB3	2.18	0.58
6:FD:1233:ILE:HD11	6:FD:1268:VAL:CG2	2.33	0.58
6:FF:1388:PHE:HD1	6:FF:1418:GLU:HA	1.68	0.58
7:GG:548:ALA:HB1	9:HA:666:LYS:HG2	1.85	0.58
9:HB:798:ASP:OD2	13:LE:536:ASN:ND2	2.36	0.58
10:IA:466:GLN:HA	10:IA:638:ARG:HH21	1.68	0.58
15:NB:898:ASN:HA	15:NB:901:LEU:HB3	1.84	0.58
15:NB:1138:THR:HG23	15:NB:1140:LEU:H	1.68	0.58
15:NC:893:LEU:H	15:NC:1154:ASP:N	1.99	0.58
15:NC:910:ARG:HH12	15:NC:912:THR:HB	1.67	0.58
15:NC:931:TRP:HB2	15:NC:934:LEU:HB2	1.85	0.58
16:OB:289:ALA:HB1	16:OB:297:LEU:HD21	1.84	0.58
2:AB:336:ARG:HH12	1:AI:254:ARG:HG3	1.68	0.58
1:AE:411:LEU:HB3	1:AE:458:VAL:HG11	1.85	0.58
3:CI:1237:VAL:HA	3:CI:1244:PRO:HA	1.83	0.58
4:DE:255:ILE:HD11	8:GB:759:MET:HG3	1.85	0.58
4:DE:308:GLN:HA	4:DE:365:ILE:HD11	1.85	0.58
5:EB:4049:ALA:HA	6:FA:1905:GLN:HG2	1.86	0.58
6:FD:1184:ALA:HB3	6:FD:1424:CYS:HA	1.85	0.58
6:FF:1441:ILE:O	6:FF:1442:GLU:C	2.46	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GH:600:ARG:HH22	8:GH:605:LEU:HD22	1.68	0.58
12:KB:369:ILE:HG23	12:KB:576:ASN:HB3	1.85	0.58
3:BC:791:THR:HG21	3:BC:812:MET:HG2	1.85	0.58
4:DB:126:LEU:HD22	4:DB:158:LEU:HB3	1.84	0.58
5:EC:4405:ILE:HG21	5:EC:4427:LEU:HB3	1.85	0.58
6:FB:2051:VAL:O	6:FB:2055:THR:HG23	2.04	0.58
6:FC:2024:ARG:HA	9:HB:778:PRO:CG	2.29	0.58
6:FF:1073:HIS:O	6:FF:1074:ASP:C	2.46	0.58
8:GL:43:CYS:HB2	8:GL:46:LEU:HB2	1.85	0.58
15:NA:579:PRO:HB3	15:NA:616:LEU:HD12	1.83	0.58
15:NA:667:THR:HA	15:NA:673:ILE:HG23	1.85	0.58
3:CF:1175:ASN:HD21	3:CF:1253:VAL:HA	1.68	0.58
6:FC:2034:ARG:HG2	6:FC:2034:ARG:NH1	2.19	0.58
6:FD:1301:ALA:HA	6:FD:1430:PHE:HB3	1.85	0.58
7:GE:840:MET:HE1	7:GE:869:LEU:HD23	1.84	0.58
8:GF:377:MET:HB2	8:GF:380:MET:HE1	1.85	0.58
9:HB:808:HIS:O	9:HB:812:THR:CG2	2.44	0.58
10:IA:886:LEU:HD23	10:IA:888:THR:H	1.68	0.58
10:IA:910:LEU:HA	10:IA:913:LEU:HD13	1.86	0.58
10:IC:1236:VAL:HG22	10:IC:1285:VAL:HG12	1.83	0.58
11:JB:1873:ARG:HG3	11:JB:1874:ARG:HE	1.69	0.58
15:NA:613:GLN:HG2	15:NA:918:ALA:HB2	1.84	0.58
1:AI:157:LEU:HD12	1:AI:180:PHE:HD2	1.68	0.58
1:AI:429:ARG:HH21	2:AJ:417:ALA:HB1	1.67	0.58
1:AL:918:VAL:HB	1:AL:982:VAL:HG21	1.85	0.58
4:DA:133:LEU:HA	4:DA:136:MET:HE3	1.86	0.58
6:FE:968:LEU:HB2	6:FE:1027:LEU:HD11	1.85	0.58
6:FE:1108:PRO:HD3	9:HA:394:LEU:HG	1.85	0.58
7:GE:675:GLN:HE22	7:GE:691:VAL:HG13	1.67	0.58
8:GL:64:ASN:HD22	8:GL:515:THR:HG21	1.68	0.58
8:GL:111:TYR:HB2	8:GL:511:LEU:HB3	1.84	0.58
8:GL:374:LEU:HA	8:GL:377:MET:HB2	1.86	0.58
9:HA:758:ALA:O	9:HA:761:CYS:HB2	2.04	0.58
10:IC:1140:GLN:HA	10:IC:1143:MET:HG2	1.84	0.58
12:KC:593:HIS:HB2	12:KC:707:GLU:HB3	1.85	0.58
15:NB:1138:THR:HG21	15:NB:1143:LEU:HB3	1.85	0.58
15:ND:1138:THR:HG23	15:ND:1140:LEU:H	1.68	0.58
15:ND:1546:VAL:HG11	19:RD:174:LEU:HD21	1.85	0.58
2:AB:415:HIS:O	2:AB:418:LYS:HB3	2.03	0.58
2:AG:180:GLU:HA	2:AG:183:ALA:HB3	1.85	0.58
3:BA:964:GLN:HE21	16:OA:127:ILE:HG21	1.68	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:920:ARG:HH12	16:OB:266:GLN:HG3	1.69	0.58
4:DB:356:TYR:HB3	4:DB:382:LEU:HD22	1.86	0.58
4:DF:69:LEU:HB3	4:DF:76:MET:HG3	1.86	0.58
6:FA:2059:VAL:HG22	9:HA:754:LEU:HB2	1.85	0.58
7:GA:747:SER:HB3	7:GA:993:SER:HB2	1.86	0.58
7:GC:278:ASP:HB2	7:GC:281:GLU:HB3	1.84	0.58
7:GG:180:ARG:HD3	7:GG:829:VAL:HG21	1.84	0.58
8:GJ:327:HIS:H	8:GJ:330:ASP:HB2	1.68	0.58
9:HA:760:LYS:O	9:HA:763:GLN:HG2	2.04	0.58
11:JB:1319:HIS:HA	15:NB:1326:VAL:HG21	1.86	0.58
11:JC:1571:ARG:HH22	15:NA:346:SER:HB2	1.69	0.58
14:ME:217:ASN:HB3	14:ME:322:MET:HE1	1.85	0.58
15:NA:937:MET:HA	15:NA:940:TYR:HB3	1.84	0.58
2:AC:521:LEU:HD21	1:AD:56:LEU:HD22	1.86	0.58
1:AL:301:VAL:HG23	1:AL:332:THR:HG22	1.83	0.58
3:CG:1259:ALA:HB2	3:CG:4487:LEU:HD13	1.86	0.58
4:DE:275:LEU:HB2	4:DE:280:ALA:HB2	1.86	0.58
6:FD:806:ILE:HG23	6:FD:1112:ILE:HD11	1.85	0.58
7:GE:572:GLU:HA	7:GE:622:ARG:HH21	1.68	0.58
8:GF:13:ARG:HH22	8:GF:535:GLU:HB2	1.67	0.58
9:HB:553:TYR:HE1	9:HB:575:ARG:HH21	1.50	0.58
16:OC:289:ALA:HB1	16:OC:297:LEU:HD21	1.85	0.58
1:AL:345:PRO:HA	1:AL:348:GLU:HB3	1.85	0.58
3:CB:812:MET:HG3	3:CB:819:LEU:HD13	1.86	0.58
6:FA:2024:ARG:HA	9:HA:778:PRO:CG	2.30	0.58
6:FA:2030:ILE:HD11	9:HA:813:THR:HG22	1.85	0.58
7:GA:920:ALA:HB3	7:GA:955:VAL:HG11	1.86	0.58
7:GC:185:ARG:HG2	7:GC:697:PRO:HG2	1.84	0.58
7:GC:236:THR:HG21	7:GC:255:LEU:HD13	1.86	0.58
11:JA:805:CYS:HB3	11:JA:895:LEU:HB3	1.85	0.58
13:LK:353:ASN:HA	13:LK:356:LEU:HG	1.85	0.58
1:AL:793:LEU:HG	1:AL:988:GLN:HG3	1.86	0.58
3:BC:693:ARG:HA	3:BC:696:GLU:HG3	1.86	0.58
3:CB:761:LEU:HB3	3:CB:784:LEU:HD12	1.86	0.58
3:CI:1229:HIS:HB2	3:CI:4463:LEU:HB3	1.86	0.58
5:EB:3373:LYS:HG3	5:EB:3378:GLY:HA2	1.86	0.58
5:EC:4474:TYR:HB3	13:LK:532:LEU:HD12	1.86	0.58
6:FC:1684:THR:HG22	6:FC:1685:GLU:H	1.69	0.58
6:FD:1103:SER:O	6:FD:1104:GLY:C	2.47	0.58
8:GH:398:VAL:HG23	8:GH:721:LYS:HZ2	1.69	0.58
8:GJ:703:GLN:HA	8:GJ:706:LEU:HD23	1.85	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JA:489:VAL:HG11	11:JA:1439:LEU:HD23	1.85	0.58
11:JB:523:ASN:HD21	11:JB:766:GLY:H	1.52	0.58
15:NB:512:TYR:HA	15:NB:1473:ARG:HH22	1.69	0.58
15:NC:1118:VAL:HA	15:NC:1121:ASN:HB2	1.85	0.58
16:OA:184:ASN:HA	16:OA:295:LEU:HD11	1.86	0.58
5:EB:4405:ILE:HG13	5:EB:4428:MET:CE	2.33	0.58
6:FE:962:PHE:HE2	6:FE:965:TRP:HB2	1.68	0.58
6:FF:1103:SER:O	6:FF:1104:GLY:C	2.46	0.58
6:FF:1284:LEU:HB3	6:FF:1292:ALA:HB3	1.84	0.58
6:FF:1432:THR:O	6:FF:1433:ALA:C	2.47	0.58
7:GG:284:GLU:HA	7:GG:290:VAL:HG11	1.84	0.58
8:GH:78:CYS:HB3	8:GH:83:GLN:H	1.67	0.58
11:JA:81:ARG:HG3	11:JA:106:LEU:HD11	1.84	0.58
15:NA:733:VAL:HB	15:NA:742:LEU:HD13	1.84	0.58
15:ND:347:LEU:HB3	15:ND:491:PRO:HD2	1.85	0.58
2:AK:448:ASN:C	2:AK:448:ASN:HD22	2.12	0.57
3:CG:1195:LEU:HD22	3:CG:1210:LEU:HD11	1.86	0.57
5:EA:3283:GLU:HG2	5:EA:3286:ARG:HH21	1.68	0.57
6:FD:1200:LEU:HB3	6:FD:1205:ILE:HG12	1.85	0.57
6:FF:1213:VAL:HA	6:FF:1231:ARG:O	2.04	0.57
7:GA:166:LEU:HA	7:GA:169:ILE:HD12	1.86	0.57
7:GG:967:PHE:HA	7:GG:970:LEU:HD23	1.86	0.57
8:GH:64:ASN:C	8:GH:64:ASN:HD22	2.10	0.57
8:GH:179:MET:HG2	8:GH:197:VAL:HG12	1.86	0.57
7:GI:940:GLN:HA	7:GI:943:GLN:HB2	1.86	0.57
9:HD:766:SER:O	9:HD:768:THR:N	2.37	0.57
12:KB:512:ARG:HB3	12:KB:518:GLU:HG3	1.86	0.57
5:EB:4881:ARG:HB2	5:EB:4886:LYS:HB2	1.86	0.57
6:FE:1216:TRP:O	6:FE:1217:GLU:C	2.46	0.57
10:IA:414:ALA:HB2	10:IA:424:VAL:HG11	1.86	0.57
10:IC:627:CYS:HA	10:IC:699:CYS:HA	1.87	0.57
11:JA:192:LEU:HB3	11:JA:1063:ILE:HD13	1.85	0.57
12:KA:319:TYR:HB2	12:KA:334:VAL:HG11	1.84	0.57
14:ME:249:GLU:HA	14:ME:252:THR:HG22	1.85	0.57
15:NA:885:LEU:HA	15:NA:888:ARG:HB2	1.86	0.57
15:NB:647:GLN:HA	15:NB:650:ARG:HD2	1.85	0.57
16:OB:284:GLU:HA	16:OB:287:LEU:HD23	1.85	0.57
1:AI:240:MET:HA	19:RA:24:ARG:HD2	1.86	0.57
5:EA:4648:PHE:HA	5:EA:4651:MET:HE3	1.86	0.57
5:EC:3273:LEU:HD23	5:EC:3494:VAL:HG21	1.87	0.57
6:FE:1097:SER:O	6:FE:1101:ALA:N	2.37	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GF:172:ILE:HG12	8:GF:180:LEU:HA	1.86	0.57
10:IB:1053:ARG:HG2	10:IB:1107:GLU:HG2	1.85	0.57
1:AD:107:LEU:HD13	1:AD:221:VAL:HG11	1.86	0.57
1:AI:247:THR:HG23	1:AI:248:LEU:HD12	1.86	0.57
3:CG:4468:LYS:HB2	3:CG:4488:MET:HB3	1.86	0.57
5:EB:3238:SER:H	5:EB:3241:GLU:HG3	1.70	0.57
5:EB:4207:PHE:HB3	5:EB:4250:ARG:HH22	1.68	0.57
5:EC:3227:ALA:HB2	5:EC:4159:THR:HG22	1.85	0.57
6:FC:1844:LEU:HD12	6:FC:1922:VAL:HG21	1.86	0.57
6:FE:822:GLY:O	6:FE:823:GLY:C	2.47	0.57
6:FE:1187:ILE:HG21	6:FE:1282:LEU:HD21	1.87	0.57
6:FF:1218:ALA:HA	6:FF:1220:ARG:HH21	1.69	0.57
7:GC:738:LEU:HD12	7:GC:797:ILE:HG13	1.85	0.57
7:GG:294:ALA:HB3	7:GG:687:ARG:HB3	1.85	0.57
7:GG:502:TYR:HE2	7:GG:562:ILE:HG22	1.69	0.57
10:IB:169:LEU:HD11	10:IB:201:LEU:HA	1.86	0.57
11:JB:1726:LEU:HB3	11:JB:1730:THR:HG21	1.87	0.57
12:KC:378:PHE:O	12:KC:379:SER:C	2.47	0.57
15:NA:679:ASP:HB2	15:NA:696:PHE:HB3	1.85	0.57
15:NB:737:PRO:HG3	15:NB:749:PRO:HD3	1.86	0.57
15:NC:343:VAL:HG21	15:NC:490:VAL:HG11	1.87	0.57
1:AL:25:ALA:HB1	15:NB:1336:THR:HG22	1.87	0.57
4:DC:297:ARG:HA	4:DC:300:GLN:HB3	1.85	0.57
5:EC:4044:ILE:HG22	5:EC:4048:LYS:HE3	1.86	0.57
6:FD:994:PRO:HD2	12:KA:230:GLN:NE2	2.19	0.57
6:FE:1104:GLY:N	9:HA:393:VAL:HG11	2.19	0.57
7:GC:319:VAL:HG21	7:GC:426:ASN:HD21	1.70	0.57
11:JB:147:ARG:HA	11:JB:151:LEU:HD22	1.87	0.57
11:JC:1130:LEU:HD21	11:JC:1164:MET:HG2	1.86	0.57
11:JC:2276:ARG:HB3	11:JC:2280:ARG:HH12	1.68	0.57
12:KC:526:TRP:HZ2	12:KC:582:ILE:HG23	1.70	0.57
12:KE:525:PRO:HA	12:KE:542:PRO:HG3	1.86	0.57
15:NC:622:THR:HG23	15:NC:650:ARG:HH12	1.70	0.57
2:AK:5:VAL:HA	2:AK:84:LEU:HB3	1.86	0.57
4:DC:69:LEU:HB3	4:DC:76:MET:HG3	1.86	0.57
5:EA:4095:LYS:HB3	9:HB:796:ASP:CG	2.30	0.57
5:EA:4629:ARG:HH21	5:EA:4714:GLU:HB3	1.70	0.57
8:GF:143:CYS:HB2	8:GF:277:ARG:HD3	1.86	0.57
12:KB:370:LEU:HD13	12:KB:377:LEU:HD11	1.87	0.57
15:NC:883:LEU:HD23	15:NC:1123:ALA:HB1	1.84	0.57
15:ND:597:GLN:HB2	15:ND:914:ILE:HG22	1.86	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:ND:869:PHE:HE2	15:ND:1131:LEU:HD13	1.70	0.57
1:AL:728:VAL:HG13	1:AL:729:THR:HG23	1.85	0.57
4:DF:269:LEU:HD13	4:DF:338:ILE:HG21	1.86	0.57
5:EC:3399:PHE:HB3	5:EC:3418:SER:HB2	1.86	0.57
6:FF:922:LEU:O	6:FF:925:GLU:HB2	2.05	0.57
7:GA:670:ASN:HB3	7:GA:698:VAL:HB	1.87	0.57
8:GB:100:LEU:HD12	8:GB:104:LEU:HD12	1.86	0.57
8:GD:150:ASP:HA	8:GD:153:ARG:HD3	1.87	0.57
9:HD:852:LYS:HD3	9:HD:855:ARG:HH11	1.70	0.57
13:LC:489:LEU:HD22	13:LD:489:LEU:HD13	1.87	0.57
15:NC:1493:VAL:HG12	15:NC:1496:LEU:HD12	1.86	0.57
19:RD:32:THR:HG22	19:RD:36:ARG:HH12	1.70	0.57
1:AA:437:PHE:HB3	2:AB:410:TYR:HE1	1.69	0.57
1:AD:212:ARG:HH12	11:JA:1339:SER:N	2.02	0.57
2:AG:200:GLU:HG3	2:AG:201:LYS:H	1.70	0.57
3:BB:753:LEU:HD22	3:BB:787:ILE:HD11	1.87	0.57
4:DE:13:VAL:HA	4:DE:16:LEU:HD23	1.85	0.57
5:EC:4312:PHE:HB3	5:EC:4351:VAL:HG22	1.87	0.57
6:FF:1071:PHE:HB2	6:FF:1076:ILE:HD11	1.87	0.57
7:GA:305:PRO:HB3	7:GA:354:ARG:HG2	1.86	0.57
7:GC:350:ARG:HH12	7:GC:352:ASP:HB2	1.69	0.57
7:GG:236:THR:HG21	7:GG:255:LEU:HD13	1.87	0.57
10:IB:882:VAL:HG12	16:OB:1044:ARG:HH22	1.70	0.57
11:JA:541:LEU:HD11	11:JA:548:PHE:HA	1.86	0.57
12:KB:215:PRO:HG2	12:KB:288:PHE:HB3	1.87	0.57
15:NA:618:ARG:HH21	15:NA:661:ARG:HH22	1.53	0.57
15:NA:725:ILE:HG13	15:NA:799:ILE:HG21	1.85	0.57
15:NB:791:GLU:HG2	15:NB:1142:LEU:HD21	1.87	0.57
16:OC:70:THR:HG23	16:OC:72:SER:H	1.70	0.57
1:AD:227:LYS:HB2	10:IB:1251:VAL:HG13	1.87	0.57
4:DC:356:TYR:HB3	4:DC:382:LEU:HD22	1.87	0.57
6:FB:1729:ALA:HA	6:FB:1902:LEU:HD23	1.86	0.57
6:FD:1222:CYS:HB3	6:FD:1225:ILE:HD12	1.87	0.57
6:FD:1425:PRO:HD2	6:FD:1429:LEU:HD12	1.86	0.57
6:FE:1282:LEU:HD11	6:FE:1419:LEU:HD22	1.86	0.57
8:GD:7:GLU:HB2	8:GD:13:ARG:HD3	1.86	0.57
7:GE:311:LEU:HD11	7:GE:436:ALA:HB1	1.86	0.57
7:GI:293:VAL:HA	7:GI:688:ARG:HG3	1.87	0.57
7:GK:536:THR:HA	9:HC:553:TYR:HB2	1.86	0.57
11:JA:157:GLU:HB3	11:JA:172:LEU:HD11	1.87	0.57
12:KE:212:LEU:HD22	12:KE:285:ILE:HG12	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:ME:313:ARG:HD3	14:ME:316:GLN:HE22	1.69	0.57
15:NB:866:LEU:HD23	15:NB:869:PHE:HD2	1.70	0.57
15:ND:613:GLN:HG2	15:ND:918:ALA:HB2	1.87	0.57
2:AB:371:VAL:HG13	2:AB:375:CYS:HB3	1.87	0.57
1:AH:1046:THR:HG22	1:AH:1048:ALA:H	1.70	0.57
5:EC:3412:LEU:HG	5:EC:3507:VAL:HG22	1.86	0.57
6:FC:1942:PHE:HZ	6:FC:2050:LEU:HD11	1.70	0.57
6:FC:2104:GLN:HA	6:FC:2107:GLN:HE21	1.70	0.57
6:FD:837:ALA:O	6:FD:838:ASN:C	2.48	0.57
7:GI:516:VAL:HG11	7:GI:565:LEU:HG	1.85	0.57
8:GJ:218:SER:HB3	8:GJ:221:ALA:HB2	1.86	0.57
10:IC:725:LYS:HB3	10:IC:729:ARG:NH1	2.19	0.57
11:JB:1687:LEU:HA	11:JB:1690:ASP:HB2	1.86	0.57
4:DA:277:ARG:HG2	4:DA:281:GLN:HE22	1.69	0.56
6:FD:809:ILE:HD13	6:FD:972:VAL:HG21	1.87	0.56
6:FD:1185:VAL:O	6:FD:1186:TRP:C	2.48	0.56
6:FE:1182:ALA:HA	6:FE:1425:PRO:HD3	1.87	0.56
6:FF:1004:GLY:O	6:FF:1005:PRO:C	2.48	0.56
6:FF:1182:ALA:HB2	6:FF:1430:PHE:H	1.68	0.56
7:GA:464:LEU:HB3	7:GA:502:TYR:HE2	1.69	0.56
11:JC:1813:ILE:HG23	11:JC:1992:LEU:HD22	1.87	0.56
11:JC:1852:HIS:CD2	11:JC:1985:LEU:HG	2.37	0.56
12:KC:606:ARG:HB2	12:KC:623:ILE:HB	1.87	0.56
14:MD:82:ARG:HG2	14:MD:87:LEU:HD22	1.87	0.56
15:NA:541:MET:HE1	15:NA:1189:PHE:HD2	1.69	0.56
1:AA:248:LEU:HB2	1:AA:258:CYS:HA	1.86	0.56
1:AE:316:ILE:CD1	9:HD:872:MET:HG2	2.35	0.56
1:AE:815:LEU:HD13	13:LM:354:ARG:HG3	1.87	0.56
1:AH:63:LEU:HD12	1:AH:226:MET:HE2	1.85	0.56
6:FD:807:ALA:O	6:FD:808:SER:HB2	2.03	0.56
6:FE:1095:LEU:O	6:FE:1096:LEU:C	2.48	0.56
6:FE:1249:ILE:HG13	6:FE:1250:GLU:N	2.19	0.56
7:GA:764:LEU:HD12	7:GA:870:ARG:HE	1.69	0.56
7:GC:885:GLU:HA	7:GC:890:MET:HG2	1.86	0.56
8:GH:133:PRO:HD2	8:GH:294:TRP:HH2	1.70	0.56
10:IB:233:ARG:HH11	10:IB:785:LEU:HD11	1.71	0.56
11:JC:148:ARG:HG3	11:JC:149:LEU:H	1.70	0.56
15:NC:924:LEU:HB3	15:NC:1107:THR:HG23	1.85	0.56
2:AC:29:LEU:HD13	2:AC:283:LEU:HD21	1.87	0.56
1:AH:408:LYS:HE3	16:OC:24:LEU:HD13	1.88	0.56
3:CB:790:ASN:HD22	3:CB:807:LEU:HB3	1.71	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CE:4484:VAL:HA	3:CE:4499:PRO:HA	1.87	0.56
4:DB:179:ALA:HB3	4:DE:189:ARG:HH12	1.70	0.56
4:DC:316:ARG:HB2	14:MJ:246:ASN:ND2	2.20	0.56
5:EA:4167:ASP:HB2	5:EA:4171:ILE:HG12	1.87	0.56
5:EB:3642:PRO:HD3	5:EB:3673:LEU:HD23	1.85	0.56
5:EC:4898:MET:HG3	5:EC:4902:ALA:HB3	1.88	0.56
6:FD:861:LEU:CD2	6:FD:861:LEU:N	2.46	0.56
6:FD:973:ILE:HG22	6:FD:1019:VAL:HG22	1.88	0.56
6:FE:825:PRO:O	6:FE:826:LEU:C	2.48	0.56
6:FE:842:GLY:N	7:GE:957:ARG:HH21	2.04	0.56
6:FF:803:ARG:HB3	6:FF:907:ASN:HA	1.86	0.56
7:GC:605:VAL:HB	7:GC:679:LEU:HB3	1.86	0.56
8:GD:112:ILE:HG22	8:GD:510:ARG:HG2	1.86	0.56
7:GE:828:PRO:HG2	7:GE:831:ARG:HG2	1.88	0.56
8:GH:77:THR:HB	8:GH:84:ARG:HH11	1.70	0.56
7:GK:518:LEU:HD23	7:GK:520:ILE:HD11	1.86	0.56
7:GK:543:LYS:H	9:HC:596:TYR:HB3	1.70	0.56
9:HC:674:VAL:HG13	9:HC:712:ILE:HG12	1.87	0.56
10:IA:341:GLU:HG3	10:IA:536:ARG:HD3	1.86	0.56
11:JA:75:VAL:HG23	11:JA:81:ARG:HD2	1.86	0.56
11:JC:1425:LEU:HB3	11:JC:1428:LEU:HD23	1.87	0.56
14:ME:301:LEU:HB3	14:MF:301:LEU:HD22	1.87	0.56
15:NA:893:LEU:H	15:NA:1154:ASP:N	2.03	0.56
15:NB:812:ARG:HD2	15:NB:870:TYR:HB2	1.87	0.56
15:NB:894:LEU:HB2	15:NB:1152:GLU:HB3	1.86	0.56
15:NC:578:HIS:CE1	15:NC:580:PHE:HB2	2.41	0.56
15:ND:666:ILE:HG21	15:ND:720:LEU:HD13	1.86	0.56
15:ND:818:ILE:HB	15:ND:842:THR:HA	1.86	0.56
19:RD:139:LEU:HB2	19:RD:141:LEU:HD23	1.88	0.56
3:CC:791:THR:HG22	3:CC:811:ILE:HA	1.88	0.56
3:CE:1231:ARG:H	3:CE:4466:ILE:HD11	1.70	0.56
6:FD:1190:ARG:HE	6:FD:1420:ARG:HD3	1.69	0.56
7:GA:207:LEU:HD13	7:GA:690:ARG:HH21	1.71	0.56
8:GB:665:LEU:HB2	8:GB:676:TRP:HB3	1.88	0.56
7:GE:276:ARG:HH21	7:GE:285:LEU:HG	1.69	0.56
8:GJ:160:LEU:HA	8:GJ:163:MET:HE3	1.87	0.56
2:AB:29:LEU:HD13	2:AB:283:LEU:HD21	1.87	0.56
3:BA:917:LEU:HD21	16:OA:174:VAL:HG21	1.88	0.56
4:DF:327:PHE:HB3	4:DF:332:LEU:HD22	1.88	0.56
5:EA:3609:LEU:HD23	5:EA:3612:LEU:HD22	1.86	0.56
6:FD:822:GLY:O	6:FD:823:GLY:C	2.48	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:918:GLN:O	6:FF:919:GLN:C	2.48	0.56
7:GA:371:LEU:HD13	7:GA:412:VAL:HG22	1.88	0.56
15:NA:1546:VAL:HG12	15:NA:1550:MET:HE1	1.88	0.56
15:NC:880:THR:HB	15:NC:884:LYS:HE3	1.88	0.56
15:ND:537:LYS:HA	15:ND:542:LEU:HD12	1.87	0.56
19:RB:50:VAL:HG21	19:RB:71:LEU:HD11	1.86	0.56
1:AA:994:LEU:HA	7:GA:215:PRO:HA	1.88	0.56
5:EC:4376:HIS:HD2	5:EC:4377:PRO:HD2	1.71	0.56
6:FC:1901:LEU:HB3	6:FC:1904:GLU:HA	1.87	0.56
6:FC:2087:LEU:HD13	9:HB:872:MET:HE1	1.87	0.56
6:FD:854:TRP:CD1	6:FD:854:TRP:H	2.24	0.56
6:FD:1223:ALA:HA	6:FD:1226:LEU:HD12	1.87	0.56
6:FE:992:PRO:HB3	12:KB:231:PHE:CZ	2.39	0.56
6:FE:1103:SER:O	6:FE:1104:GLY:C	2.48	0.56
6:FE:1223:ALA:O	6:FE:1226:LEU:N	2.35	0.56
6:FF:866:PHE:HB3	6:FF:1274:PRO:HD2	1.88	0.56
6:FF:990:PHE:HB2	12:KC:313:PHE:HE2	1.70	0.56
9:HB:761:CYS:O	9:HB:762:HIS:C	2.49	0.56
11:JA:837:ASN:HA	11:JA:840:ILE:HG22	1.87	0.56
11:JC:542:LEU:HD11	11:JC:1320:PHE:HB2	1.87	0.56
11:JC:1873:ARG:HH21	11:JC:1877:ALA:HB2	1.69	0.56
12:KE:215:PRO:HB3	12:KE:286:GLU:HB3	1.86	0.56
12:KF:521:PRO:HB2	12:KF:523:VAL:HG12	1.88	0.56
19:RC:126:LYS:HE3	19:RC:162:ASN:HB3	1.88	0.56
1:AI:159:LYS:HE2	1:AI:183:LEU:HD12	1.88	0.56
4:DA:385:LYS:HZ3	13:LB:461:VAL:HG23	1.70	0.56
4:DD:32:SER:HB2	4:DD:121:ALA:HB1	1.87	0.56
5:EB:3418:SER:HB3	5:EB:3423:VAL:HB	1.88	0.56
5:EC:3304:LYS:HD3	5:EC:4163:MET:HE3	1.88	0.56
6:FD:806:ILE:HD13	6:FD:1114:VAL:HG13	1.86	0.56
6:FD:1233:ILE:CD1	6:FD:1268:VAL:HG22	2.36	0.56
8:GB:310:THR:HB	8:GB:319:LEU:HA	1.86	0.56
8:GH:396:ILE:HG22	8:GH:721:LYS:NZ	2.20	0.56
8:GL:200:GLY:HA2	8:GL:281:LEU:HD22	1.88	0.56
9:HA:765:TRP:N	9:HA:765:TRP:HE3	2.04	0.56
10:IC:634:ALA:HB2	10:IC:692:GLU:HB3	1.87	0.56
11:JA:758:GLU:HA	11:JA:761:LYS:HB3	1.88	0.56
11:JA:1090:LEU:HB2	11:JA:1128:LYS:HZ3	1.69	0.56
12:KC:574:LEU:HA	12:KC:701:ALA:HA	1.88	0.56
12:KE:588:ALA:HB3	12:KE:710:ASN:HD21	1.71	0.56
1:AH:397:LYS:HE2	1:AH:401:THR:HG21	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CA:784:LEU:HD22	3:CA:826:LEU:HD13	1.87	0.56
4:DB:136:MET:HB3	4:DB:147:ARG:HH12	1.69	0.56
5:EC:3281:VAL:HG21	5:EC:3450:ASN:HB3	1.88	0.56
5:EC:4667:PRO:HA	5:EC:4670:TRP:HB3	1.86	0.56
6:FD:824:TYR:CE2	7:GC:963:GLU:HG2	2.41	0.56
6:FF:1424:CYS:SG	6:FF:1429:LEU:HG	2.46	0.56
11:JC:87:VAL:HG22	11:JC:90:ARG:HH12	1.70	0.56
13:LI:524:LYS:O	13:LJ:525:SER:HA	2.06	0.56
14:MF:254:ILE:HA	14:MF:257:LYS:HG2	1.87	0.56
15:ND:893:LEU:H	15:ND:1153:ALA:C	2.14	0.56
15:ND:1547:ILE:HB	19:RD:141:LEU:HD13	1.88	0.56
1:AI:266:HIS:HB3	1:AI:277:ARG:HH21	1.71	0.56
6:FD:887:ARG:HA	12:KA:305:HIS:ND1	2.21	0.56
6:FD:1022:THR:HG22	6:FD:1023:ALA:H	1.71	0.56
6:FD:1242:GLN:HB2	6:FD:1259:LEU:HD12	1.88	0.56
6:FD:1280:VAL:HG23	6:FD:1300:LEU:HD11	1.88	0.56
6:FF:1434:ALA:O	6:FF:1435:GLU:C	2.49	0.56
8:GB:545:ALA:HB1	8:GB:605:LEU:HD11	1.87	0.56
7:GC:516:VAL:HG11	7:GC:565:LEU:HB3	1.87	0.56
7:GG:518:LEU:HD12	7:GG:573:VAL:HG22	1.88	0.56
7:GG:537:GLY:H	9:HA:554:ASP:N	2.04	0.56
7:GK:607:ARG:HH12	7:GK:609:ARG:HE	1.53	0.56
9:HC:683:VAL:HG12	9:HC:684:GLU:HG2	1.88	0.56
9:HD:773:ALA:HB3	13:LJ:527:VAL:HG13	1.88	0.56
10:IB:1326:THR:HG23	10:IB:1328:LYS:H	1.71	0.56
10:IC:239:LEU:HD23	10:IC:792:ILE:HD11	1.87	0.56
12:KE:272:ASN:HD21	12:KE:275:ASP:HB2	1.71	0.56
12:KE:582:ILE:HD12	12:KE:715:LEU:HB3	1.88	0.56
14:MK:93:SER:HA	14:MK:96:ASP:HB2	1.87	0.56
2:AC:173:ARG:HH11	1:AD:407:VAL:HG22	1.71	0.56
1:AE:672:ASP:HB3	1:AE:676:ARG:HH21	1.71	0.56
2:AG:462:GLU:HG3	2:AG:466:GLN:HE21	1.71	0.56
6:FD:808:SER:HB3	6:FD:1113:PHE:HD2	1.70	0.56
6:FD:1203:ARG:HH21	6:FD:1207:GLU:HG3	1.71	0.56
7:GA:437:VAL:HG13	7:GA:505:PHE:HE2	1.71	0.56
8:GH:419:PHE:HE2	8:GH:505:PRO:HG3	1.71	0.56
8:GJ:432:LYS:HB2	8:GJ:451:SER:HB3	1.87	0.56
7:GK:184:ALA:HB3	7:GK:708:SER:HB2	1.88	0.56
10:IC:806:ILE:HG21	10:IC:858:LEU:HD21	1.88	0.56
11:JA:1726:LEU:HB3	11:JA:1730:THR:HG21	1.88	0.56
11:JB:2013:LEU:HD21	11:JB:2262:LEU:HD22	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:444:PHE:HA	11:JC:447:ILE:HG22	1.87	0.56
12:KF:404:GLU:HB2	12:KF:489:MET:HE1	1.88	0.56
12:KG:546:LYS:HG3	12:KG:714:THR:HG22	1.88	0.56
15:NA:892:TRP:HB3	15:NA:1154:ASP:HB2	1.88	0.56
19:RA:64:PRO:HA	19:RA:67:VAL:HG22	1.88	0.56
3:CC:689:LEU:HA	3:CC:692:LEU:HD12	1.88	0.55
3:CJ:4522:LEU:HB3	3:CJ:4524:LEU:HD23	1.88	0.55
5:EB:4198:ILE:HA	5:EB:4202:LEU:HD23	1.87	0.55
6:FD:1189:ILE:HG23	6:FD:1417:ILE:HD11	1.88	0.55
6:FE:983:LEU:HA	12:KB:726:ASP:OD1	2.06	0.55
6:FF:1425:PRO:HD3	6:FF:1429:LEU:HD12	1.85	0.55
7:GA:502:TYR:HE1	7:GA:562:ILE:HG22	1.71	0.55
8:GH:302:LEU:HA	8:GH:363:ASP:HB2	1.88	0.55
7:GI:598:ARG:HH22	7:GI:637:ASN:HD22	1.52	0.55
9:HB:640:GLY:HA3	9:HB:653:ILE:HG12	1.88	0.55
11:JA:446:ARG:HH12	11:JA:505:LEU:HD11	1.72	0.55
11:JA:542:LEU:HD11	11:JA:1320:PHE:HB2	1.89	0.55
11:JB:2023:LEU:HD13	11:JB:2129:ARG:HD2	1.88	0.55
11:JC:1084:VAL:HG11	11:JC:1153:LEU:HD23	1.88	0.55
11:JC:2271:ASP:HB3	11:JC:2274:ILE:HG22	1.88	0.55
12:KB:543:VAL:HG13	12:KB:544:LEU:HG	1.88	0.55
14:ME:288:SER:HA	14:ME:291:LEU:HB3	1.88	0.55
15:NC:667:THR:HA	15:NC:673:ILE:HG23	1.89	0.55
15:NC:812:ARG:HH21	15:NC:870:TYR:HD2	1.54	0.55
15:ND:892:TRP:N	15:ND:1155:GLU:H	2.03	0.55
15:ND:982:ILE:HD11	15:ND:1029:SER:H	1.71	0.55
19:RD:92:ASP:HB3	19:RD:94:PRO:HD2	1.88	0.55
20:SD:143:VAL:HA	20:SD:146:MET:HB2	1.87	0.55
2:AF:209:SER:HB3	2:AF:259:VAL:HA	1.87	0.55
1:AH:131:ARG:HG2	1:AH:205:ARG:HH12	1.71	0.55
3:CB:676:PHE:HA	17:PC:251:HIS:HB2	1.87	0.55
3:CE:1129:ARG:HD3	10:IA:1264:ILE:HD11	1.86	0.55
4:DA:6:LYS:HZ3	4:DD:181:ILE:HA	1.71	0.55
4:DA:300:GLN:HG3	4:DA:355:CYS:HB2	1.88	0.55
5:EA:4095:LYS:HD3	9:HB:796:ASP:OD2	2.07	0.55
5:EC:3267:SER:HB2	5:EC:3409:SER:HB2	1.87	0.55
6:FD:839:GLY:HA3	12:KA:681:MET:CE	2.36	0.55
6:FD:997:THR:HG23	12:KA:230:GLN:HE22	1.70	0.55
6:FE:1003:ILE:HG12	6:FE:1009:VAL:HG22	1.87	0.55
7:GA:515:SER:HB3	7:GA:634:PRO:HB2	1.88	0.55
8:GH:421:ALA:HB3	8:GH:465:ALA:HB3	1.87	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GL:534:GLN:HE22	8:GL:591:ILE:HD13	1.71	0.55
10:IC:1098:HIS:HE1	10:IC:1121:LYS:HG3	1.70	0.55
11:JA:440:PRO:HG2	11:JA:1477:TRP:HB3	1.88	0.55
12:KC:664:ILE:HB	12:KC:682:LEU:HB3	1.89	0.55
12:KG:298:GLN:HG3	12:KG:303:TYR:HB2	1.87	0.55
2:AC:464:ILE:HD11	1:AD:382:ILE:HG21	1.89	0.55
1:AE:38:VAL:HG11	1:AE:111:ILE:HG23	1.87	0.55
3:CC:695:LEU:HD22	3:CC:743:SER:HB2	1.88	0.55
5:EA:3445:VAL:HG21	5:EA:3570:LEU:HD23	1.88	0.55
5:EB:3650:THR:HG22	9:HB:500:LEU:HD22	1.87	0.55
6:FD:1005:PRO:HB2	6:FD:1006:PRO:HD3	1.88	0.55
6:FD:1186:TRP:CE3	6:FD:1267:GLN:HB2	2.41	0.55
6:FF:1124:ILE:O	6:FF:1125:ASN:C	2.50	0.55
8:GD:422:LYS:HB3	8:GD:501:SER:HB3	1.88	0.55
8:GJ:317:VAL:HG11	8:GJ:325:ILE:HG22	1.88	0.55
9:HA:782:ALA:O	9:HA:783:SER:C	2.49	0.55
11:JB:191:ASP:HB3	11:JB:194:VAL:HG12	1.88	0.55
14:MJ:288:SER:HA	14:MJ:291:LEU:HB3	1.88	0.55
2:AG:553:THR:HB	1:AH:471:GLU:HG2	1.89	0.55
2:AK:319:LEU:HD22	2:AK:327:ILE:HD11	1.89	0.55
1:AL:793:LEU:HD13	1:AL:801:ARG:HG3	1.88	0.55
3:CF:1173:VAL:HA	3:CF:1255:VAL:HG12	1.87	0.55
5:EA:3765:VAL:HG12	11:JB:932:PRO:HG2	1.89	0.55
6:FE:1193:VAL:HG21	6:FE:1416:GLN:HB3	1.89	0.55
8:GH:142:THR:HG23	8:GH:265:ASP:HB2	1.87	0.55
8:GH:215:LEU:HA	8:GH:238:ARG:HH22	1.70	0.55
7:GI:186:VAL:HG23	7:GI:696:MET:HG2	1.87	0.55
7:GK:236:THR:HG21	7:GK:255:LEU:HD13	1.88	0.55
9:HA:765:TRP:HE3	9:HA:765:TRP:H	1.52	0.55
10:IB:1294:ILE:HD12	10:IB:1358:LEU:HD11	1.88	0.55
11:JB:1869:ALA:HB2	11:JB:2072:GLN:HE22	1.72	0.55
15:NB:1160:LEU:HD12	15:NB:1165:VAL:HG11	1.89	0.55
19:RD:113:ARG:NH1	19:RD:114:GLU:HB3	2.22	0.55
1:AE:357:ILE:HG23	2:AF:485:LEU:HD12	1.88	0.55
2:AJ:92:LEU:HD23	2:AJ:277:VAL:HG11	1.89	0.55
3:CJ:4479:LEU:HB3	3:CJ:4482:LEU:HD23	1.88	0.55
5:EA:3436:TYR:HE1	5:EA:4014:VAL:HG22	1.72	0.55
6:FC:1968:LYS:HA	6:FC:1971:LYS:HD2	1.87	0.55
6:FD:1003:ILE:HG12	6:FD:1009:VAL:HG13	1.89	0.55
6:FE:817:VAL:O	6:FE:818:VAL:C	2.49	0.55
6:FE:1186:TRP:HE3	6:FE:1267:GLN:HB2	1.70	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:1026:PRO:HB2	6:FF:1029:GLN:HG2	1.88	0.55
7:GA:544:PRO:HD3	9:HB:596:TYR:HA	1.88	0.55
8:GB:168:MET:HG2	8:GB:247:PRO:HA	1.89	0.55
7:GE:292:PHE:HD2	7:GE:689:ILE:HD11	1.72	0.55
7:GG:169:ILE:HD11	7:GG:697:PRO:HD3	1.88	0.55
8:GH:374:LEU:HD23	8:GH:613:ASP:HB2	1.87	0.55
7:GI:176:ARG:HD3	7:GI:180:ARG:HH22	1.71	0.55
8:GJ:171:ILE:HG23	8:GJ:181:HIS:HB2	1.88	0.55
8:GJ:561:LEU:HD11	8:GJ:596:MET:HG3	1.89	0.55
9:HA:642:THR:HG22	9:HA:643:PHE:H	1.70	0.55
12:KB:240:ILE:HD11	12:KB:294:ARG:HH11	1.69	0.55
13:LK:483:ARG:HG2	13:LK:487:MET:HE1	1.87	0.55
1:AE:378:VAL:HG11	2:AF:543:MET:HE3	1.89	0.55
2:AF:213:HIS:HE1	2:AF:258:GLY:HA3	1.70	0.55
1:AH:91:ILE:HG21	1:AH:150:LYS:HZ2	1.72	0.55
1:AH:988:GLN:HA	1:AH:991:LEU:HD23	1.88	0.55
3:CE:1229:HIS:HB3	3:CE:4463:LEU:HD13	1.88	0.55
4:DF:378:ILE:HG23	4:DF:382:LEU:HD13	1.89	0.55
5:EC:4719:ASP:HA	5:EC:4722:PRO:HD2	1.89	0.55
7:GA:604:ALA:HB1	7:GA:678:LEU:HD11	1.88	0.55
8:GD:726:ASN:HB2	8:GD:729:GLY:HA3	1.89	0.55
8:GL:354:GLN:HA	8:GL:357:ARG:HG2	1.88	0.55
9:HA:496:GLU:HG3	9:HA:499:ARG:HH11	1.71	0.55
9:HB:722:SER:HA	9:HB:724:PHE:H	1.71	0.55
9:HB:778:PRO:HB2	9:HB:779:PRO:CD	2.37	0.55
10:IA:451:VAL:HG13	10:IA:455:LEU:HD12	1.89	0.55
10:IB:1139:VAL:HG13	10:IB:1203:LEU:HD22	1.88	0.55
11:JC:1499:HIS:HB3	11:JC:1502:ILE:HG22	1.89	0.55
12:KA:319:TYR:HE2	12:KA:357:MET:HE1	1.71	0.55
12:KC:383:HIS:O	12:KC:386:LEU:HD23	2.07	0.55
12:KC:502:LEU:HA	12:KC:505:LEU:HB2	1.87	0.55
12:KF:343:ASN:HB2	12:KF:346:PRO:HD2	1.89	0.55
12:KG:374:ALA:HA	12:KG:377:LEU:HB3	1.88	0.55
13:LJ:394:GLY:HA3	13:LJ:398:ARG:HH21	1.70	0.55
15:NA:892:TRP:N	15:NA:1155:GLU:H	2.05	0.55
1:AD:301:VAL:HG23	1:AD:332:THR:HG22	1.88	0.55
1:AH:488:VAL:HG12	1:AH:490:SER:H	1.71	0.55
1:AI:472:LYS:HD2	2:AJ:448:ASN:HD22	1.72	0.55
2:AK:145:LYS:HA	2:AK:148:ASP:HB2	1.89	0.55
3:CB:730:ALA:HB1	3:CB:763:LEU:HD21	1.87	0.55
5:EA:4880:ASP:OD1	5:EA:4888:TRP:CZ3	2.59	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:4523:LEU:HA	5:EB:4537:ALA:HB1	1.89	0.55
6:FC:2023:ILE:HG22	9:HB:778:PRO:HB3	1.87	0.55
6:FD:1442:GLU:C	6:FD:1444:ARG:H	2.14	0.55
6:FE:826:LEU:HB2	6:FE:841:TYR:CE2	2.42	0.55
6:FE:1022:THR:HG22	6:FE:1023:ALA:H	1.72	0.55
6:FE:1208:ALA:HB3	6:FE:1286:LEU:HD22	1.88	0.55
7:GC:680:TYR:HE2	7:GC:690:ARG:HB2	1.72	0.55
8:GD:661:PRO:HB2	8:GD:680:LEU:HB2	1.89	0.55
7:GG:883:LEU:HD11	7:GG:890:MET:HE2	1.88	0.55
8:GH:681:ILE:HA	8:GH:684:TRP:HD1	1.72	0.55
10:IB:1236:VAL:HG22	10:IB:1285:VAL:HG12	1.89	0.55
11:JC:1867:LEU:HB3	11:JC:2273:ARG:HH12	1.70	0.55
13:LC:364:ASN:HA	13:LC:367:VAL:HG12	1.89	0.55
15:NC:363:LEU:HD11	15:NC:430:ARG:HD3	1.87	0.55
1:AL:763:LEU:HD13	1:AL:776:LEU:HD13	1.89	0.55
3:CL:4475:LYS:HE3	3:CL:4484:VAL:HG21	1.88	0.55
5:EC:3650:THR:HG23	9:HA:499:ARG:HA	1.88	0.55
7:GK:298:TYR:HB3	7:GK:679:LEU:HD11	1.89	0.55
10:IA:1128:VAL:HG12	10:IA:1131:HIS:CD2	2.41	0.55
11:JB:157:GLU:HB3	11:JB:172:LEU:HD11	1.89	0.55
11:JB:880:MET:HE2	11:JB:1418:THR:HG21	1.89	0.55
13:LI:520:LEU:O	13:LI:521:ASN:C	2.49	0.55
14:MI:280:ALA:HA	14:MI:283:GLN:HE22	1.71	0.55
14:MJ:253:GLU:O	14:MJ:257:LYS:HG3	2.07	0.55
1:AE:915:TRP:HB3	13:LM:355:LYS:HZ3	1.71	0.55
2:AG:538:ASN:HB3	5:EB:4818:ILE:HD12	1.89	0.55
1:AI:443:LYS:HD3	2:AJ:27:ALA:HB1	1.89	0.55
1:AI:995:GLU:HB3	7:GK:216:THR:HG22	1.89	0.55
3:CG:1178:GLN:HE22	3:CG:1180:GLU:HG2	1.71	0.55
3:CJ:1164:LEU:HD12	3:CJ:1168:ARG:HG2	1.89	0.55
5:EA:4814:THR:HA	5:EA:4817:LEU:HD21	1.88	0.55
5:EB:4738:THR:HG21	5:EB:4828:LEU:HD12	1.88	0.55
6:FE:1073:HIS:O	6:FE:1074:ASP:C	2.49	0.55
8:GF:317:VAL:HG11	8:GF:325:ILE:HG22	1.89	0.55
8:GF:440:CYS:HG	8:GF:463:TRP:CD1	2.25	0.55
7:GI:713:VAL:HG22	7:GI:829:VAL:HG11	1.87	0.55
8:GJ:18:VAL:HG12	8:GJ:531:GLY:HA3	1.89	0.55
8:GJ:401:ASP:HB2	8:GJ:719:VAL:HG11	1.89	0.55
8:GL:113:LEU:HD12	8:GL:114:PRO:HD2	1.89	0.55
10:IB:165:ILE:HD11	10:IB:180:LEU:HD22	1.88	0.55
10:IB:451:VAL:HG13	10:IB:455:LEU:HD12	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IB:698:GLN:HE21	16:OB:1081:ILE:HD11	1.72	0.55
12:KF:546:LYS:HG3	12:KF:714:THR:HG22	1.89	0.55
15:NB:794:GLU:HA	15:NB:797:ARG:HD2	1.89	0.55
15:NB:894:LEU:HB3	15:NB:898:ASN:HB3	1.87	0.55
15:NC:343:VAL:HG22	15:NC:364:ARG:HH21	1.71	0.55
15:NC:613:GLN:HG2	15:NC:918:ALA:HB2	1.88	0.55
1:AA:147:MET:HE1	1:AA:218:PRO:HB3	1.89	0.55
2:AC:327:ILE:HG22	1:AH:269:THR:HG21	1.89	0.55
2:AF:161:ILE:HG22	5:EB:4624:SER:HA	1.87	0.55
1:AH:288:GLY:HA3	1:AH:298:ILE:HD12	1.88	0.55
3:BC:781:LEU:HD22	3:BC:833:TYR:HD2	1.72	0.55
5:EB:3706:VAL:HG11	5:EB:3739:GLU:HG3	1.88	0.55
5:EB:4403:LEU:HB3	5:EB:4405:ILE:HD11	1.88	0.55
6:FA:1729:ALA:HA	6:FA:1902:LEU:HD23	1.89	0.55
6:FB:1612:ASN:HD21	6:FB:1616:GLU:HB3	1.71	0.55
6:FD:845:PRO:N	7:GC:896:ARG:HH12	2.04	0.55
6:FF:1184:ALA:HB3	6:FF:1424:CYS:HA	1.88	0.55
7:GG:268:ARG:HB2	7:GG:276:ARG:HH12	1.72	0.55
7:GK:539:TYR:HB2	9:HC:576:LYS:HG2	1.88	0.55
9:HD:809:LEU:O	9:HD:813:THR:HG23	2.07	0.55
10:IB:258:SER:HA	10:IB:979:ARG:HH12	1.72	0.55
11:JA:795:ARG:HE	11:JA:796:SER:H	1.55	0.55
11:JB:440:PRO:HG3	11:JB:1477:TRP:HB3	1.89	0.55
12:KA:403:ASP:HA	12:KA:541:TYR:HE1	1.72	0.55
12:KC:214:PRO:HG3	12:KC:236:LYS:HB3	1.89	0.55
12:KC:234:PRO:CD	12:KC:235:PRO:HD2	2.33	0.55
14:MI:225:VAL:HG21	14:MI:315:TRP:HE1	1.72	0.55
14:MJ:218:LEU:HD21	14:MJ:323:GLN:HB3	1.89	0.55
15:NA:577:PRO:HA	15:NA:581:LEU:HD12	1.87	0.55
15:NA:687:SER:HB2	15:NA:910:ARG:HD3	1.88	0.55
15:NA:735:HIS:HD2	15:NA:768:GLU:HG2	1.71	0.55
15:NA:1193:VAL:HG11	15:NA:1391:LEU:HD21	1.89	0.55
15:NB:983:ILE:HG23	15:NB:989:ILE:HB	1.89	0.55
15:NC:599:ILE:HB	15:NC:916:LEU:HA	1.89	0.55
15:ND:737:PRO:HG3	15:ND:749:PRO:HD3	1.89	0.55
1:AA:815:LEU:HD13	13:LK:354:ARG:HG3	1.88	0.54
1:AI:309:LEU:HD13	1:AI:314:ILE:HD13	1.87	0.54
1:AL:715:LEU:HD21	1:AL:839:GLU:HG2	1.88	0.54
5:EA:3373:LYS:HG3	5:EA:3378:GLY:HA2	1.89	0.54
6:FA:1656:THR:HB	6:FA:1659:ILE:HD13	1.88	0.54
6:FE:1012:PRO:HB2	6:FE:1016:PRO:HD3	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GE:189:SER:HB3	7:GE:192:LEU:HB2	1.89	0.54
7:GG:678:LEU:HB3	7:GG:690:ARG:HB3	1.89	0.54
7:GI:515:SER:HB3	7:GI:634:PRO:HB2	1.89	0.54
7:GI:873:ALA:HA	7:GI:876:MET:HE1	1.87	0.54
8:GJ:75:GLN:HG3	8:GJ:86:ALA:HA	1.89	0.54
12:KA:240:ILE:HD11	12:KA:294:ARG:HD2	1.89	0.54
12:KC:231:PHE:HZ	12:KC:313:PHE:CD1	2.25	0.54
12:KF:575:ILE:HD12	12:KF:578:ALA:HB2	1.88	0.54
15:NA:1409:VAL:HB	15:NA:1470:PHE:HB2	1.88	0.54
15:NC:618:ARG:HG2	15:NC:654:LEU:HD21	1.88	0.54
15:ND:548:PRO:HA	15:ND:551:ARG:HE	1.72	0.54
19:RA:27:ALA:HA	19:RA:30:LEU:HB3	1.89	0.54
1:AI:1001:SER:HA	7:GK:860:GLN:HG2	1.89	0.54
2:AK:157:GLY:HA3	2:AK:253:LYS:HE3	1.89	0.54
3:CJ:4469:LEU:HD11	3:CJ:4485:VAL:HB	1.89	0.54
3:CL:4519:ALA:HB1	3:CL:4525:LEU:HB2	1.88	0.54
4:DA:354:TRP:HB3	4:DA:382:LEU:HD23	1.90	0.54
5:EA:3227:ALA:HB2	5:EA:4159:THR:HG22	1.88	0.54
5:EB:3412:LEU:HG	5:EB:3507:VAL:HG22	1.89	0.54
5:EB:4893:THR:O	5:EB:4894:SER:C	2.49	0.54
6:FD:843:LEU:O	7:GC:896:ARG:NH1	2.40	0.54
6:FE:1196:PRO:O	6:FE:1197:ILE:C	2.50	0.54
6:FF:1431:MET:O	6:FF:1435:GLU:HB3	2.08	0.54
8:GH:721:LYS:HA	8:GH:721:LYS:HE3	1.89	0.54
13:LO:371:SER:HA	13:LO:374:HIS:CE1	2.42	0.54
15:ND:1546:VAL:HA	19:RD:142:ASN:H	1.72	0.54
16:OA:213:LEU:HB3	16:OA:246:LEU:HD21	1.89	0.54
19:RB:48:ALA:HA	19:RB:51:MET:HE3	1.88	0.54
1:AA:428:LEU:HD12	1:AA:432:LEU:HD11	1.87	0.54
4:DC:163:GLU:HA	4:DC:166:VAL:HG12	1.89	0.54
5:EA:3642:PRO:HD3	5:EA:3673:LEU:HD23	1.88	0.54
5:EB:4454:ARG:HD2	5:EB:4507:ASP:HB2	1.89	0.54
6:FB:1844:LEU:HD12	6:FB:1922:VAL:HG21	1.88	0.54
6:FD:1030:ILE:HG23	6:FD:1116:LEU:HD22	1.89	0.54
6:FD:1188:GLU:HG3	6:FD:1267:GLN:HB3	1.89	0.54
6:FF:1222:CYS:O	6:FF:1223:ALA:C	2.51	0.54
7:GE:719:ILE:HD11	7:GE:800:VAL:HG21	1.88	0.54
8:GH:300:ARG:HG2	8:GH:361:ALA:HB3	1.89	0.54
9:HA:643:PHE:HB3	9:HA:729:GLY:HA2	1.89	0.54
9:HA:809:LEU:O	9:HA:813:THR:HG23	2.07	0.54
10:IC:615:ARG:HG2	10:IC:759:PHE:HE1	1.71	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:1326:THR:HG23	10:IC:1328:LYS:H	1.73	0.54
11:JB:2256:SER:HB3	11:JB:2259:LEU:HB2	1.89	0.54
11:JC:1136:MET:HE3	11:JC:1668:ASN:HD21	1.72	0.54
12:KC:578:ALA:HB3	12:KC:657:VAL:H	1.72	0.54
15:NA:755:ILE:HG21	15:NA:803:LEU:HD21	1.89	0.54
15:NB:794:GLU:HG2	15:NB:1140:LEU:HD13	1.88	0.54
15:NB:1005:VAL:H	15:NB:1008:SER:HB2	1.72	0.54
16:OB:1075:TYR:HE2	16:OB:1077:LYS:HB2	1.72	0.54
20:SC:87:ILE:HG13	20:SC:143:VAL:HG21	1.90	0.54
3:BA:718:ALA:HB2	3:BA:733:GLN:HB2	1.88	0.54
4:DE:362:LYS:HE2	4:DE:382:LEU:HD13	1.90	0.54
5:EA:3496:THR:HB	5:EA:3507:VAL:HB	1.89	0.54
5:EA:4095:LYS:HD3	9:HB:796:ASP:HA	1.89	0.54
6:FD:1223:ALA:O	6:FD:1226:LEU:N	2.39	0.54
7:GA:236:THR:HG21	7:GA:255:LEU:HD13	1.89	0.54
7:GA:967:PHE:HA	7:GA:970:LEU:HD23	1.90	0.54
8:GB:772:THR:HG23	8:GB:774:ASP:H	1.73	0.54
8:GD:278:CYS:HB3	8:GD:281:LEU:HB3	1.90	0.54
9:HB:776:PRO:HB3	13:LE:521:ASN:OD1	2.07	0.54
12:KA:291:ALA:HB3	12:KA:314:LEU:HD11	1.89	0.54
15:NC:741:ILE:HG23	15:NC:793:THR:HG22	1.88	0.54
3:BA:690:MET:HE1	17:PA:257:ASN:HA	1.89	0.54
3:BA:873:PHE:HZ	16:OA:174:VAL:HG22	1.71	0.54
4:DE:167:GLU:HA	4:DE:170:ARG:HB3	1.89	0.54
5:EC:4405:ILE:HG23	5:EC:4411:THR:CG2	2.37	0.54
6:FE:1223:ALA:HA	6:FE:1226:LEU:HD12	1.90	0.54
6:FF:1105:ARG:O	6:FF:1106:LEU:C	2.49	0.54
7:GC:232:LYS:HB3	7:GC:258:TYR:HE2	1.72	0.54
8:GD:574:ASP:HA	14:MA:320:ARG:HH21	1.72	0.54
8:GF:29:ILE:HG22	8:GF:31:LEU:H	1.72	0.54
8:GF:625:ALA:HB1	8:GF:629:ASN:HB2	1.89	0.54
8:GL:55:ARG:HD3	8:GL:60:GLY:HA2	1.90	0.54
8:GL:405:LYS:HA	8:GL:408:GLU:HB2	1.88	0.54
10:IC:466:GLN:HA	10:IC:638:ARG:HH21	1.72	0.54
10:IC:1221:THR:H	10:IC:1224:HIS:HB2	1.72	0.54
11:JA:1285:SER:HA	11:JA:1288:ARG:HD3	1.89	0.54
11:JB:138:THR:HA	11:JB:162:PRO:HA	1.88	0.54
11:JB:1480:VAL:HG13	15:NB:440:LEU:HD12	1.89	0.54
15:NA:748:LYS:HE2	15:NA:849:ARG:HH12	1.72	0.54
15:ND:1518:ARG:HH22	18:QB:65:ALA:HB2	1.73	0.54
18:QA:104:PHE:HD2	18:QA:168:LEU:HD11	1.73	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CC:762:LEU:HD23	3:CC:784:LEU:HD11	1.88	0.54
4:DD:93:ILE:HD13	4:DD:165:ILE:HG12	1.90	0.54
5:EA:3439:ARG:HH22	5:EA:3607:ARG:HH11	1.55	0.54
6:FA:2055:THR:HA	9:HA:837:LEU:HD21	1.89	0.54
6:FD:879:ARG:HE	6:FD:908:ILE:HG23	1.72	0.54
6:FD:1445:SER:O	6:FD:1446:ASN:C	2.51	0.54
8:GB:676:TRP:HB2	8:GB:735:LEU:HD13	1.89	0.54
7:GK:368:PHE:HZ	7:GK:439:ALA:HB1	1.72	0.54
10:IA:890:GLY:H	15:NA:566:GLN:HE22	1.53	0.54
14:MA:259:MET:HA	14:MA:265:SER:HB2	1.89	0.54
17:PA:257:ASN:HB2	17:PA:260:SER:HB2	1.89	0.54
1:AE:274:ARG:HG3	1:AE:275:HIS:H	1.72	0.54
3:BC:783:GLU:HA	3:BC:786:TYR:HD2	1.73	0.54
3:CF:1209:ALA:HB3	3:CF:1223:GLU:HA	1.90	0.54
4:DC:179:ALA:HB3	4:DF:189:ARG:HE	1.73	0.54
6:FD:799:GLN:HB3	6:FD:911:SER:HA	1.90	0.54
7:GC:371:LEU:HD12	7:GC:412:VAL:HG22	1.88	0.54
8:GD:18:VAL:HG13	8:GD:520:PHE:HA	1.89	0.54
8:GD:300:ARG:HG2	8:GD:361:ALA:HB3	1.88	0.54
8:GF:314:GLY:HA2	8:GF:344:ALA:HA	1.88	0.54
8:GL:283:LEU:HD22	8:GL:380:MET:HE1	1.89	0.54
9:HB:579:LEU:HD23	9:HB:595:TYR:HB2	1.90	0.54
10:IB:864:GLN:HB3	10:IB:1241:LEU:HD22	1.90	0.54
11:JA:1451:PRO:HB2	11:JA:1456:ILE:HD11	1.89	0.54
11:JA:1560:LEU:HD23	11:JA:1561:HIS:CD2	2.43	0.54
11:JC:896:PRO:HB3	11:JC:953:LEU:HD12	1.89	0.54
12:KF:534:VAL:HG13	12:KF:536:ARG:HH12	1.72	0.54
13:LB:500:GLN:HE21	14:MC:178:VAL:HG23	1.72	0.54
15:NC:1005:VAL:H	15:NC:1008:SER:HB3	1.73	0.54
15:ND:794:GLU:HA	15:ND:797:ARG:HB2	1.89	0.54
16:OC:190:LEU:HD23	16:OC:241:ALA:HB3	1.89	0.54
1:AA:632:LEU:HD22	7:GA:856:VAL:HG22	1.90	0.54
1:AD:229:LEU:HD11	10:IB:824:LYS:HB3	1.89	0.54
1:AH:713:LEU:HD12	13:LJ:484:VAL:HG13	1.90	0.54
1:AH:834:ILE:HD13	1:AH:989:LEU:HD23	1.89	0.54
4:DA:156:ASP:HA	4:DA:159:GLU:HG3	1.90	0.54
4:DC:126:LEU:HD22	4:DC:158:LEU:HD13	1.88	0.54
5:EC:4743:ILE:HG22	5:EC:4747:MET:HE2	1.89	0.54
6:FA:2084:GLN:HA	6:FA:2088:MET:HE1	1.90	0.54
6:FD:860:PRO:HD2	6:FD:861:LEU:HD23	1.90	0.54
6:FE:890:ALA:O	6:FE:891:ARG:C	2.50	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:967:PHE:CD2	6:FF:1095:LEU:HD23	2.43	0.54
9:HB:681:LYS:HB3	13:LD:483:ARG:HD2	1.88	0.54
12:KA:335:LEU:HD21	12:KA:362:LEU:HD11	1.90	0.54
14:MB:246:ASN:HA	14:MB:249:GLU:HG3	1.90	0.54
15:NA:1120:VAL:HA	15:NA:1123:ALA:HB2	1.89	0.54
15:NA:1442:LYS:HD3	15:NA:1444:LYS:H	1.73	0.54
15:NC:686:ASN:HB2	15:NC:692:ILE:HG22	1.89	0.54
15:NC:996:LEU:HD22	15:NC:1015:ALA:HB1	1.88	0.54
15:ND:515:ALA:HB3	15:ND:520:ALA:HB2	1.89	0.54
19:RB:151:LEU:HD23	19:RB:154:ARG:HH12	1.72	0.54
2:AK:331:ASN:HD22	2:AK:331:ASN:C	2.13	0.54
3:BB:908:VAL:HB	3:BB:938:MET:HE1	1.89	0.54
5:EB:3730:ALA:HB3	5:EB:4285:THR:HA	1.89	0.54
6:FE:1124:ILE:O	6:FE:1125:ASN:C	2.51	0.54
8:GB:586:SER:HB3	14:ME:320:ARG:HH22	1.73	0.54
11:JB:1414:ALA:HB2	11:JB:1504:ARG:HE	1.73	0.54
14:MH:99:LYS:HA	14:MH:102:LYS:HG2	1.90	0.54
15:NB:505:GLY:H	15:NB:512:TYR:HB2	1.73	0.54
15:ND:996:LEU:HD22	15:ND:1015:ALA:HB1	1.89	0.54
2:AC:368:HIS:HB2	1:AD:442:HIS:HB2	1.88	0.54
3:CI:1164:LEU:HB3	3:CI:1168:ARG:HB2	1.90	0.54
4:DC:285:ARG:HG3	4:DC:286:TRP:CD1	2.43	0.54
4:DC:385:LYS:HZ3	13:LJ:461:VAL:HG22	1.73	0.54
5:EB:3660:LYS:HZ1	5:EB:4055:ARG:HH22	1.54	0.54
6:FA:1958:LEU:HD22	6:FA:2054:PHE:CD2	2.43	0.54
6:FA:2079:MET:HE2	9:HA:865:ILE:HG12	1.87	0.54
6:FD:993:ALA:HA	12:KA:230:GLN:CG	2.38	0.54
6:FE:1026:PRO:HB2	6:FE:1029:GLN:HG2	1.90	0.54
6:FE:1231:ARG:HH21	6:FE:1271:PRO:HD2	1.73	0.54
7:GA:646:MET:HE1	7:GA:696:MET:HE1	1.90	0.54
8:GD:325:ILE:HD13	8:GD:371:GLN:HB2	1.90	0.54
7:GE:607:ARG:HB2	7:GE:609:ARG:HH22	1.72	0.54
8:GH:475:ALA:HB2	8:GH:543:ARG:HD2	1.90	0.54
9:HA:559:ARG:HA	9:HA:562:GLN:HG3	1.90	0.54
9:HA:804:THR:O	9:HA:805:THR:C	2.51	0.54
11:JC:1328:LEU:HD21	11:JC:1408:LEU:HD11	1.90	0.54
12:KB:609:CYS:HA	12:KB:620:THR:HG22	1.90	0.54
12:KB:656:ARG:HB3	12:KB:667:SER:HB2	1.90	0.54
15:NA:1121:ASN:HA	15:NA:1162:ARG:HE	1.73	0.54
2:AC:481:ARG:HH21	2:AC:533:SER:H	1.56	0.53
1:AL:1033:GLN:O	1:AL:1034:SER:C	2.51	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BB:754:GLU:HG2	17:PB:284:PRO:HB2	1.89	0.53
3:BB:1014:ASP:HA	3:BB:1017:ARG:HE	1.73	0.53
3:CL:1257:ASN:HB3	3:CL:1260:VAL:HG12	1.90	0.53
4:DF:31:SER:HB2	4:DF:48:TYR:HE2	1.72	0.53
6:FA:2098:TYR:HE1	9:HA:878:SER:HB2	1.73	0.53
6:FD:999:PRO:N	12:KA:229:SER:HA	2.24	0.53
6:FD:1186:TRP:HE3	6:FD:1267:GLN:HB2	1.72	0.53
6:FE:1085:GLU:HA	6:FE:1088:LYS:HB2	1.90	0.53
6:FE:1212:VAL:HG23	6:FE:1264:ILE:HD12	1.90	0.53
7:GA:268:ARG:HB2	7:GA:276:ARG:HH12	1.73	0.53
7:GA:279:ARG:HG3	7:GA:285:LEU:HB3	1.90	0.53
8:GF:62:ILE:HG21	8:GF:513:VAL:HG11	1.90	0.53
7:GK:576:TYR:HB3	7:GK:584:HIS:HD1	1.73	0.53
9:HB:766:SER:O	9:HB:768:THR:N	2.41	0.53
9:HB:777:TYR:CD1	9:HB:778:PRO:HD2	2.44	0.53
12:KC:525:PRO:HD2	12:KC:542:PRO:HD2	1.90	0.53
14:MA:240:LEU:HD22	14:MA:243:LYS:HZ3	1.73	0.53
15:NC:508:GLY:HA3	15:NC:577:PRO:HG3	1.89	0.53
19:RB:23:LEU:HA	19:RB:26:HIS:HB3	1.89	0.53
2:AC:456:CYS:SG	1:AD:389:LEU:HD22	2.49	0.53
1:AL:1026:ASP:OD2	1:AL:1032:PHE:N	2.41	0.53
6:FF:1102:TYR:O	6:FF:1103:SER:C	2.51	0.53
7:GC:519:PHE:HZ	7:GC:595:ILE:HG13	1.72	0.53
7:GC:633:LEU:HD23	7:GC:636:VAL:HG12	1.90	0.53
8:GF:432:LYS:HB2	8:GF:451:SER:HB2	1.91	0.53
8:GF:596:MET:HA	8:GF:599:LEU:HB3	1.91	0.53
11:JC:84:PHE:HB3	11:JC:2092:PHE:HZ	1.73	0.53
14:ME:284:LEU:HD13	14:MF:283:GLN:NE2	2.23	0.53
15:NB:667:THR:HA	15:NB:673:ILE:HG23	1.89	0.53
15:NB:892:TRP:N	15:NB:1155:GLU:H	2.06	0.53
15:NB:931:TRP:CD1	15:NB:934:LEU:HB2	2.43	0.53
15:NC:682:ARG:HE	15:NC:917:MET:HE1	1.73	0.53
15:NC:818:ILE:HB	15:NC:842:THR:HA	1.88	0.53
2:AG:438:VAL:HG11	1:AH:408:LYS:HB2	1.90	0.53
1:AI:97:ASP:HB3	1:AI:100:GLU:HB2	1.90	0.53
4:DA:356:TYR:CZ	4:DA:385:LYS:HG3	2.44	0.53
6:FD:806:ILE:HG21	6:FD:851:THR:HG21	1.89	0.53
6:FD:1073:HIS:O	6:FD:1074:ASP:C	2.50	0.53
6:FE:1011:TYR:O	6:FE:1012:PRO:C	2.52	0.53
6:FF:1218:ALA:O	6:FF:1219:GLU:C	2.51	0.53
7:GC:246:ALA:HB2	7:GC:250:ARG:HE	1.74	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:HA:754:LEU:HG	9:HA:840:HIS:CD2	2.43	0.53
9:HD:777:TYR:CD1	9:HD:778:PRO:HD2	2.44	0.53
10:IB:1094:ASN:HA	10:IB:1123:ASN:HD22	1.72	0.53
11:JA:414:ILE:HD11	11:JA:437:LEU:HB3	1.89	0.53
11:JC:1975:THR:HG23	11:JC:1977:GLN:H	1.73	0.53
12:KB:298:GLN:HB3	12:KB:303:TYR:HB2	1.90	0.53
12:KG:259:THR:HA	12:KG:262:GLU:HG2	1.90	0.53
15:NB:1407:MET:HA	15:NB:1471:ARG:HD3	1.90	0.53
15:NC:895:GLY:H	15:NC:1152:GLU:HB3	1.72	0.53
16:OB:213:LEU:HD13	16:OB:246:LEU:HD13	1.89	0.53
5:EB:3227:ALA:HB2	5:EB:4159:THR:HG22	1.91	0.53
6:FD:1436:PHE:O	6:FD:1437:ALA:C	2.50	0.53
6:FE:1182:ALA:CB	6:FE:1429:LEU:HB2	2.34	0.53
6:FF:908:ILE:HD13	6:FF:968:LEU:HD21	1.90	0.53
7:GE:441:LEU:HD13	7:GE:509:LEU:HD23	1.90	0.53
9:HA:644:PHE:HD2	9:HA:726:PRO:HB2	1.73	0.53
9:HB:762:HIS:HD2	9:HB:763:GLN:NE2	2.06	0.53
10:IB:891:VAL:HG13	10:IB:892:ILE:HG23	1.90	0.53
11:JA:1078:MET:HB2	11:JA:1509:HIS:CD2	2.42	0.53
11:JB:1369:ILE:HG21	11:JB:1374:LEU:HD22	1.90	0.53
12:KA:234:PRO:HG2	12:KA:236:LYS:HE2	1.89	0.53
12:KB:382:ARG:HH12	12:KB:728:PRO:HD3	1.72	0.53
13:LO:377:GLN:HA	13:LO:380:MET:HB3	1.90	0.53
13:LP:350:LEU:HB3	13:LP:354:ARG:HH21	1.73	0.53
15:NB:948:LEU:HD21	15:NB:1173:MET:HE1	1.91	0.53
15:NB:1165:VAL:HA	15:NB:1168:GLN:HG2	1.89	0.53
15:NC:614:LYS:HD2	15:NC:661:ARG:HH12	1.73	0.53
1:AD:25:ALA:HB2	11:JA:1306:ILE:HG23	1.90	0.53
2:AG:115:ARG:HD2	16:OC:148:ARG:HG3	1.89	0.53
2:AG:442:LEU:HD23	2:AG:446:ARG:HH12	1.74	0.53
3:BC:904:PRO:HG3	3:BC:941:ARG:HH11	1.72	0.53
3:CG:1132:MET:HE1	10:IC:1243:PRO:HG3	1.90	0.53
3:CL:4520:ARG:HH22	3:CL:4525:LEU:HD22	1.73	0.53
4:DA:297:ARG:HD2	13:LA:460:ARG:HH22	1.72	0.53
6:FE:1182:ALA:HB2	6:FE:1430:PHE:H	1.73	0.53
6:FE:1202:PHE:CE1	6:FE:1243:PRO:HA	2.43	0.53
7:GC:311:LEU:HD11	7:GC:436:ALA:HB1	1.88	0.53
8:GH:22:THR:HG23	8:GH:25:GLU:H	1.72	0.53
8:GH:603:HIS:HA	8:GH:606:GLN:HG2	1.90	0.53
9:HA:761:CYS:HA	9:HA:765:TRP:CE3	2.43	0.53
10:IA:400:HIS:HA	10:IA:403:GLU:HB3	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:1094:ASN:HA	10:IC:1123:ASN:HD22	1.72	0.53
11:JB:91:ARG:HE	11:JB:93:LYS:HE2	1.74	0.53
13:LF:422:GLN:HA	13:LF:425:LYS:HZ3	1.73	0.53
15:NA:890:ARG:HD2	15:NA:1156:LEU:HD21	1.89	0.53
15:NC:892:TRP:HB2	15:NC:1155:GLU:OE1	2.09	0.53
15:ND:564:ARG:HH12	15:ND:618:ARG:HB2	1.73	0.53
2:AG:368:HIS:HB2	1:AH:442:HIS:HB2	1.90	0.53
3:BC:719:THR:HG22	16:OC:287:LEU:HD13	1.91	0.53
4:DC:159:GLU:HA	4:DC:162:VAL:HG12	1.90	0.53
5:EC:4265:HIS:HB2	5:EC:4267:GLN:HE22	1.73	0.53
6:FB:2098:TYR:CD1	9:HD:879:ILE:HG12	2.44	0.53
6:FD:1105:ARG:O	6:FD:1106:LEU:C	2.52	0.53
6:FF:855:PHE:O	6:FF:857:GLU:N	2.42	0.53
7:GE:284:GLU:HA	7:GE:290:VAL:HG21	1.91	0.53
7:GG:184:ALA:HB3	7:GG:708:SER:HB2	1.89	0.53
8:GJ:38:THR:HB	8:GJ:41:ARG:HG2	1.90	0.53
7:GK:670:ASN:HB3	7:GK:698:VAL:HB	1.89	0.53
9:HD:778:PRO:HB2	9:HD:779:PRO:CD	2.38	0.53
10:IA:1245:GLN:HA	10:IA:1272:LEU:HD22	1.89	0.53
11:JA:1518:VAL:HG21	11:JA:1534:ALA:HB2	1.89	0.53
11:JA:2018:LEU:HD13	11:JA:2067:ALA:HB2	1.91	0.53
11:JB:2280:ARG:HG2	11:JB:2284:LYS:HE3	1.90	0.53
12:KA:299:TYR:HA	12:KA:304:ARG:HG3	1.91	0.53
12:KB:359:VAL:HG11	12:KB:362:LEU:HD23	1.91	0.53
15:NA:676:ARG:HH22	15:NA:706:VAL:HG23	1.74	0.53
15:NA:894:LEU:H	15:NA:1153:ALA:N	2.06	0.53
15:NC:885:LEU:HA	15:NC:888:ARG:HB2	1.91	0.53
1:AA:229:LEU:HG	17:PA:272:ARG:HD3	1.89	0.53
2:AK:455:ARG:HB2	1:AL:475:LEU:HD23	1.90	0.53
3:CI:1108:LEU:HD22	3:CI:1128:TRP:HE1	1.74	0.53
4:DD:167:GLU:HA	4:DD:170:ARG:HB3	1.89	0.53
5:EA:4521:TYR:HB2	5:EA:4711:LEU:HD21	1.91	0.53
5:EB:4442:GLU:HB3	5:EB:4446:ARG:HH11	1.73	0.53
6:FE:813:GLN:O	6:FE:814:THR:C	2.50	0.53
7:GA:540:ALA:HA	9:HB:577:ASP:HA	1.91	0.53
8:GB:215:LEU:HA	8:GB:240:ALA:HB1	1.90	0.53
7:GG:434:GLY:HA3	7:GG:464:LEU:HB2	1.89	0.53
8:GL:83:GLN:O	8:GL:83:GLN:NE2	2.41	0.53
10:IB:368:PRO:HD2	10:IB:388:CYS:HB2	1.90	0.53
11:JC:1687:LEU:HA	11:JC:1690:ASP:HB2	1.91	0.53
12:KG:384:LEU:HA	12:KG:414:TRP:HD1	1.72	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NC:958:GLU:HA	15:NC:961:TYR:HB2	1.90	0.53
1:AE:732:LYS:HE3	1:AE:852:ARG:HB2	1.91	0.53
2:AF:299:LEU:HA	2:AF:307:PRO:HA	1.91	0.53
3:CI:4479:LEU:HB3	3:CI:4482:LEU:HD23	1.90	0.53
4:DD:250:ASP:HB2	4:DD:283:LEU:HB3	1.91	0.53
5:EB:3399:PHE:HB3	5:EB:3418:SER:HB2	1.90	0.53
6:FA:1684:THR:HG22	6:FA:1685:GLU:H	1.73	0.53
6:FC:2077:HIS:O	6:FC:2080:GLN:HG3	2.09	0.53
6:FE:1238:ARG:CZ	6:FE:1238:ARG:HA	2.37	0.53
6:FF:819:PRO:HA	6:FF:824:TYR:OH	2.09	0.53
8:GB:638:LEU:HD22	8:GB:654:LEU:HA	1.91	0.53
8:GB:696:GLU:HA	8:GB:699:ARG:HG2	1.91	0.53
7:GC:292:PHE:HB2	7:GC:689:ILE:HB	1.91	0.53
7:GI:614:TRP:HE3	7:GI:646:MET:HG2	1.74	0.53
10:IB:349:LEU:HA	10:IB:422:THR:HG21	1.91	0.53
10:IB:883:SER:HB3	16:OB:1045:LEU:HD11	1.90	0.53
10:IC:442:ARG:HD3	10:IC:443:PRO:HD2	1.89	0.53
11:JA:908:PRO:HG2	11:JA:911:SER:HB3	1.90	0.53
11:JB:128:THR:HG21	11:JB:2086:PRO:HB2	1.91	0.53
11:JC:1717:TRP:HZ3	16:OC:940:LEU:HD12	1.74	0.53
12:KA:322:ALA:HA	12:KA:327:MET:HB2	1.89	0.53
12:KC:236:LYS:C	12:KC:238:PHE:H	2.17	0.53
14:MI:298:ASN:HD21	14:MJ:294:ALA:HA	1.73	0.53
15:NC:1514:TRP:HA	15:NC:1517:VAL:HG22	1.91	0.53
15:ND:1521:SER:HB3	18:QB:60:ARG:HH21	1.73	0.53
15:ND:1550:MET:HG3	19:RD:29:GLU:HG2	1.89	0.53
2:AC:427:ARG:HE	1:AD:452:PHE:HB3	1.74	0.53
3:CL:1274:ARG:HH11	3:CL:4449:ILE:HB	1.74	0.53
4:DA:242:LEU:HD12	4:DA:245:LEU:HD11	1.91	0.53
4:DB:305:ARG:HE	4:DB:361:GLN:HE22	1.56	0.53
6:FD:1087:LEU:HD23	6:FD:1092:PRO:HB3	1.90	0.53
6:FE:833:GLY:O	6:FE:979:LEU:HB3	2.09	0.53
6:FE:1184:ALA:N	6:FE:1424:CYS:HB3	2.24	0.53
8:GD:410:ASP:HB3	8:GD:416:LYS:HD3	1.91	0.53
7:GE:798:LEU:HG	7:GE:802:LYS:NZ	2.23	0.53
9:HB:778:PRO:O	9:HB:779:PRO:C	2.52	0.53
11:JB:1004:ARG:HH22	11:JB:1152:HIS:HB3	1.74	0.53
12:KC:526:TRP:HE1	12:KC:706:ILE:HG21	1.74	0.53
13:LO:378:GLU:HG3	13:LP:377:GLN:HE22	1.73	0.53
15:ND:755:ILE:HD12	15:ND:846:PHE:HE2	1.74	0.53
15:ND:881:LEU:HD22	15:ND:884:LYS:HD2	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:16:LEU:HD22	2:AC:50:ILE:HA	1.91	0.53
1:AE:275:HIS:HB3	1:AE:277:ARG:HH21	1.73	0.53
1:AH:630:PRO:HA	13:LL:512:ARG:HH22	1.74	0.53
1:AH:687:SER:HA	1:AH:1005:LEU:HD11	1.90	0.53
3:BC:675:GLY:HA3	17:PC:264:GLU:HA	1.91	0.53
3:CF:1223:GLU:CD	3:CF:1224:ALA:H	2.17	0.53
4:DA:267:ARG:HE	14:MA:297:VAL:HG21	1.73	0.53
4:DB:248:ARG:HE	4:DB:290:ARG:HH12	1.56	0.53
6:FA:1942:PHE:HA	6:FA:1945:VAL:HG12	1.91	0.53
6:FF:888:PRO:HG3	7:GI:896:ARG:HD2	1.91	0.53
7:GA:171:GLN:HG3	7:GA:172:PHE:HD2	1.74	0.53
8:GB:42:ASP:H	8:GB:470:LYS:HD2	1.74	0.53
7:GC:604:ALA:HB1	7:GC:678:LEU:HD11	1.91	0.53
8:GL:393:SER:HB3	8:GL:396:ILE:HG13	1.90	0.53
9:HB:777:TYR:O	9:HB:778:PRO:C	2.52	0.53
9:HB:804:THR:O	9:HB:805:THR:C	2.50	0.53
10:IC:698:GLN:HE21	10:IC:703:GLY:HA2	1.74	0.53
10:IC:1266:ASN:HD21	10:IC:1289:ALA:HA	1.74	0.53
11:JB:1220:LEU:HD21	11:JB:1286:LEU:HD12	1.89	0.53
11:JC:81:ARG:HG3	11:JC:106:LEU:HD11	1.90	0.53
12:KB:335:LEU:HD23	12:KB:338:LEU:HD21	1.91	0.53
13:LP:427:ARG:HH11	13:LP:431:LEU:HD12	1.73	0.53
14:MJ:254:ILE:HD12	14:MJ:257:LYS:HD3	1.90	0.53
15:NA:898:ASN:HA	15:NA:901:LEU:HB3	1.91	0.53
2:AB:41:ARG:HD2	2:AB:289:PRO:HA	1.91	0.52
3:CI:1263:SER:HA	3:CI:4457:PRO:HG3	1.91	0.52
3:CJ:1108:LEU:HD22	3:CJ:1128:TRP:HE1	1.74	0.52
5:EA:4229:MET:HE3	5:EA:4261:VAL:HG11	1.90	0.52
6:FB:2069:ASN:HA	6:FB:2072:ILE:HD12	1.92	0.52
6:FD:827:PRO:C	6:FD:829:ARG:H	2.18	0.52
6:FE:1223:ALA:O	6:FE:1224:ALA:C	2.52	0.52
8:GD:212:GLN:HB3	7:GE:388:PRO:HB2	1.92	0.52
8:GL:56:CYS:HB3	8:GL:60:GLY:H	1.74	0.52
8:GL:423:ILE:HD11	8:GL:468:LEU:HD11	1.91	0.52
10:IA:462:VAL:HG12	10:IA:470:ARG:HG3	1.92	0.52
10:IA:1326:THR:HG22	10:IA:1330:TYR:H	1.74	0.52
11:JC:489:VAL:HG11	11:JC:1439:LEU:HD23	1.90	0.52
13:LJ:376:ARG:HA	13:LJ:379:LYS:HD2	1.90	0.52
13:LO:404:LEU:HD23	13:LO:407:ARG:HD2	1.91	0.52
15:NA:931:TRP:NE1	15:NA:934:LEU:HB2	2.24	0.52
2:AF:115:ARG:HH22	11:JC:1651:LEU:HD13	1.74	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AK:438:VAL:HG22	1:AL:460:VAL:HG21	1.90	0.52
3:CA:761:LEU:HB3	3:CA:784:LEU:HD12	1.90	0.52
3:CF:1237:VAL:HA	3:CF:1244:PRO:HA	1.91	0.52
3:CL:1108:LEU:HD22	3:CL:1128:TRP:HE1	1.74	0.52
4:DA:175:TYR:HB3	4:DD:189:ARG:CZ	2.39	0.52
5:EB:3521:GLU:HB3	5:EB:3546:TYR:HE1	1.74	0.52
6:FD:860:PRO:C	6:FD:862:GLU:H	2.17	0.52
7:GA:975:VAL:HG23	7:GA:977:SER:H	1.74	0.52
8:GB:604:PHE:HZ	8:GB:633:MET:HG2	1.73	0.52
7:GC:731:ILE:HD13	7:GC:821:TRP:HZ2	1.74	0.52
8:GD:672:HIS:HB3	8:GD:674:VAL:HG13	1.91	0.52
9:HB:773:ALA:HB3	13:LF:527:VAL:CG1	2.39	0.52
10:IB:549:THR:HG23	10:IB:563:LEU:HD11	1.91	0.52
10:IB:888:THR:HA	15:NC:566:GLN:HE22	1.73	0.52
13:LI:395:ILE:HG23	13:LJ:398:ARG:HH12	1.74	0.52
13:LJ:413:GLU:HA	13:LJ:416:ARG:HD3	1.91	0.52
15:NA:511:LEU:HB2	15:NA:539:GLY:HA2	1.92	0.52
15:NA:1407:MET:HG3	15:NA:1471:ARG:HB2	1.91	0.52
15:NB:811:GLU:HA	15:NB:814:GLU:HB2	1.91	0.52
15:NB:933:LEU:HD11	15:NB:1117:PHE:HD1	1.74	0.52
15:ND:667:THR:HA	15:ND:673:ILE:HG23	1.91	0.52
1:AE:98:LEU:HD23	1:AE:145:HIS:HB3	1.92	0.52
3:BC:689:LEU:HD13	3:CB:731:MET:HG2	1.90	0.52
4:DB:119:LEU:HD12	4:DB:122:ILE:HD12	1.92	0.52
5:EA:3395:TYR:HA	5:EA:3607:ARG:HH21	1.73	0.52
5:EC:3323:THR:HB	5:EC:3377:ALA:HB2	1.91	0.52
5:EC:4540:ASP:HA	5:EC:4685:PRO:HD3	1.91	0.52
6:FB:1653:ARG:HH21	6:FB:1657:MET:HG3	1.73	0.52
6:FB:2030:ILE:HD11	9:HD:813:THR:HG22	1.90	0.52
6:FD:891:ARG:HH11	6:FD:891:ARG:HB2	1.73	0.52
6:FE:1212:VAL:O	6:FE:1233:ILE:HD12	2.09	0.52
6:FE:1242:GLN:HB2	6:FE:1259:LEU:HD12	1.90	0.52
7:GE:798:LEU:HG	7:GE:802:LYS:HZ1	1.73	0.52
7:GG:799:GLY:HA2	7:GG:971:MET:HE2	1.91	0.52
10:IA:834:GLY:HA2	10:IA:873:LEU:HD13	1.91	0.52
10:IC:1198:ARG:HG2	10:IC:1305:GLU:HB2	1.90	0.52
11:JA:489:VAL:HG13	11:JA:490:THR:HG23	1.91	0.52
11:JA:824:LYS:HE2	11:JA:1159:ARG:HH21	1.73	0.52
11:JA:1196:SER:HA	11:JA:1207:THR:HG21	1.91	0.52
11:JB:1142:MET:HG2	11:JB:1593:VAL:HG21	1.91	0.52
11:JB:1738:TYR:HB2	11:JB:1774:ARG:HH12	1.74	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JB:2072:GLN:HA	11:JB:2267:TYR:HE1	1.73	0.52
13:LI:418:LYS:HG3	13:LJ:417:LEU:HD21	1.91	0.52
14:ME:211:MET:HE1	14:MF:210:LEU:HD13	1.91	0.52
14:MI:305:LEU:HD21	14:MJ:301:LEU:HD22	1.91	0.52
15:NC:512:TYR:HA	15:NC:1473:ARG:HH12	1.73	0.52
15:NC:598:PHE:HB2	15:NC:1185:PRO:HB2	1.91	0.52
16:OA:190:LEU:HD11	16:OA:234:ALA:HB1	1.91	0.52
18:QC:64:LEU:HB3	18:QC:94:LEU:HD22	1.90	0.52
2:AB:259:VAL:HB	2:AB:297:VAL:HB	1.91	0.52
1:AI:751:LEU:HD13	1:AI:903:MET:HG3	1.92	0.52
2:AK:544:ARG:HE	1:AL:484:ALA:HB2	1.75	0.52
4:DC:97:LEU:HD11	4:DC:164:PHE:HE1	1.75	0.52
4:DC:312:ASN:ND2	4:DC:315:LEU:HB2	2.24	0.52
5:EA:4047:MET:HG3	13:LG:516:VAL:HG21	1.90	0.52
6:FA:1640:VAL:HG12	6:FA:1651:ALA:HB3	1.91	0.52
6:FC:2087:LEU:HD21	9:HB:869:GLN:NE2	2.25	0.52
6:FE:1244:LEU:HA	6:FE:1259:LEU:HD11	1.92	0.52
6:FF:1185:VAL:HG23	6:FF:1270:LEU:H	1.73	0.52
8:GB:172:ILE:HD12	8:GB:180:LEU:HD13	1.92	0.52
7:GC:169:ILE:HG13	7:GC:697:PRO:HD3	1.91	0.52
8:GD:273:SER:HA	8:GD:320:SER:HA	1.92	0.52
7:GE:812:VAL:HG11	7:GE:817:ARG:HE	1.73	0.52
7:GI:975:VAL:HG23	7:GI:978:LEU:H	1.75	0.52
10:IB:889:VAL:HG21	10:IB:914:VAL:HG21	1.92	0.52
10:IB:1003:VAL:HB	10:IB:1043:PHE:HB2	1.91	0.52
10:IB:1190:MET:HG2	10:IB:1222:VAL:HA	1.91	0.52
11:JB:194:VAL:HA	11:JB:197:ARG:HG2	1.91	0.52
12:KE:575:ILE:HD11	12:KE:702:ILE:HD12	1.92	0.52
12:KG:211:TRP:HE1	12:KG:239:LYS:HE3	1.74	0.52
14:MF:320:ARG:HH22	14:MF:324:ARG:HH22	1.56	0.52
15:NB:1391:LEU:HD23	15:NB:1397:LEU:HG	1.91	0.52
15:ND:891:TRP:HA	15:ND:1152:GLU:O	2.10	0.52
2:AC:522:ARG:HD3	1:AD:350:LEU:HD13	1.92	0.52
1:AD:137:GLU:HB2	10:IB:928:LEU:HD21	1.90	0.52
1:AH:879:THR:HB	13:LJ:515:LYS:HG3	1.92	0.52
3:CI:1156:GLU:HA	10:IA:398:ARG:HH22	1.74	0.52
5:EC:3494:VAL:HA	5:EC:4014:VAL:HG11	1.92	0.52
6:FB:1798:VAL:HG21	6:FB:1900:VAL:HG11	1.90	0.52
6:FB:1946:LEU:HD21	6:FB:2054:PHE:CE2	2.44	0.52
6:FC:1958:LEU:HD22	6:FC:2054:PHE:CD2	2.45	0.52
6:FC:2059:VAL:O	6:FC:2063:GLN:HG2	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1103:SER:HB2	9:HA:393:VAL:HG21	1.92	0.52
7:GC:506:ALA:HA	7:GC:509:LEU:HD12	1.92	0.52
7:GC:974:ARG:HH21	7:GC:981:THR:HG23	1.73	0.52
7:GE:590:ASN:HD22	7:GE:950:ALA:HB3	1.74	0.52
8:GF:420:ASN:HB2	8:GF:503:LEU:HD23	1.92	0.52
8:GH:398:VAL:HG23	8:GH:721:LYS:NZ	2.25	0.52
8:GL:283:LEU:HD11	8:GL:303:LEU:HD22	1.90	0.52
9:HA:778:PRO:HB2	9:HA:779:PRO:CD	2.39	0.52
9:HB:869:GLN:HA	9:HB:872:MET:HE2	1.90	0.52
11:JB:556:LEU:HD21	11:JB:810:LEU:HD23	1.90	0.52
11:JB:1538:LEU:HD12	15:NB:349:ARG:HH22	1.74	0.52
11:JC:786:PHE:HB3	11:JC:814:ASP:HB2	1.91	0.52
12:KA:547:ARG:HG2	12:KA:711:ILE:HA	1.92	0.52
12:KB:685:ARG:HH22	12:KB:688:VAL:HG23	1.73	0.52
15:NB:528:ARG:HH21	15:NB:533:GLU:HB3	1.73	0.52
16:OB:230:LEU:HD21	16:OB:245:LEU:HB3	1.90	0.52
1:AD:686:ASN:HB2	1:AD:734:MET:HE1	1.90	0.52
2:AF:412:ALA:HB2	6:FA:2074:ALA:HB2	1.92	0.52
2:AG:421:HIS:CE1	2:AG:423:VAL:HG12	2.44	0.52
1:AI:486:TYR:HE1	6:FC:1645:SER:HA	1.74	0.52
5:EB:3398:LYS:HA	5:EB:3591:PRO:HD2	1.91	0.52
6:FE:1293:THR:HG23	6:FE:1394:ARG:HG2	1.90	0.52
6:FF:980:SER:C	6:FF:982:SER:H	2.16	0.52
8:GB:21:ALA:HB3	8:GB:25:GLU:HG3	1.90	0.52
7:GC:354:ARG:HH12	7:GC:685:GLY:HA3	1.74	0.52
7:GE:892:LEU:HD23	7:GE:955:VAL:HG12	1.92	0.52
10:IC:1077:LYS:HG3	10:IC:1080:ASP:H	1.74	0.52
11:JA:1631:ASN:HB2	16:OA:934:VAL:HG21	1.91	0.52
11:JA:2018:LEU:HD11	11:JA:2063:SER:HB2	1.91	0.52
11:JB:2069:GLU:HA	11:JB:2072:GLN:HB2	1.90	0.52
12:KA:215:PRO:HG3	12:KA:288:PHE:HB3	1.91	0.52
12:KC:383:HIS:CA	12:KC:386:LEU:HD23	2.39	0.52
12:KE:404:GLU:HA	12:KE:407:ILE:HB	1.90	0.52
12:KF:216:GLN:HA	12:KF:222:LEU:HD23	1.91	0.52
15:NA:1539:ILE:HG21	19:RC:99:PHE:HE1	1.75	0.52
15:NC:347:LEU:HD22	15:NC:491:PRO:HG2	1.92	0.52
16:OB:215:ALA:HA	16:OB:218:LYS:HE3	1.90	0.52
2:AB:417:ALA:O	2:AB:418:LYS:C	2.52	0.52
3:BB:917:LEU:HD21	16:OB:174:VAL:HG21	1.91	0.52
5:EA:3790:ARG:HH12	5:EA:3816:ARG:HH22	1.56	0.52
5:EC:3581:HIS:CD2	5:EC:3647:ALA:HA	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FA:1955:THR:HG21	9:HA:838:LYS:HA	1.90	0.52
6:FB:2055:THR:O	6:FB:2059:VAL:HG23	2.10	0.52
6:FE:1102:TYR:O	6:FE:1103:SER:C	2.52	0.52
8:GB:58:VAL:HG13	14:MH:139:ALA:HB2	1.92	0.52
8:GD:36:MET:HE2	8:GD:540:LEU:HG	1.92	0.52
8:GH:140:VAL:HG13	8:GH:152:LEU:HD21	1.92	0.52
12:KC:403:ASP:H	12:KC:717:VAL:HG11	1.73	0.52
15:NA:696:PHE:H	15:NA:894:LEU:HD21	1.74	0.52
15:NA:996:LEU:HD22	15:NA:1015:ALA:HB1	1.91	0.52
15:NB:891:TRP:H	15:NB:1155:GLU:N	2.06	0.52
15:NC:881:LEU:HA	15:NC:884:LYS:HB2	1.92	0.52
2:AJ:263:TYR:HE2	16:OB:73:ALA:HA	1.75	0.52
4:DC:316:ARG:HB2	14:MJ:246:ASN:HD22	1.73	0.52
4:DD:105:CYS:HA	4:DD:259:SER:HB2	1.92	0.52
5:EC:4343:TRP:HA	5:EC:4346:VAL:HG12	1.91	0.52
6:FE:1439:LEU:HB3	6:FE:1441:ILE:HG12	1.92	0.52
6:FF:1424:CYS:HB2	6:FF:1425:PRO:CD	2.40	0.52
7:GG:537:GLY:H	9:HA:554:ASP:H	1.57	0.52
8:GH:12:CYS:HA	8:GH:37:PHE:HA	1.90	0.52
7:GI:268:ARG:HB2	7:GI:276:ARG:HH11	1.75	0.52
7:GI:680:TYR:HE2	7:GI:690:ARG:HB2	1.74	0.52
8:GL:366:ALA:HB1	8:GL:372:VAL:HG21	1.91	0.52
10:IA:784:LEU:HD23	11:JA:2057:LEU:HD21	1.91	0.52
10:IB:982:GLU:HG2	10:IB:983:LEU:HD12	1.91	0.52
11:JA:206:ILE:HG23	11:JA:1051:LEU:HD12	1.92	0.52
11:JB:414:ILE:HG12	11:JB:437:LEU:HD22	1.91	0.52
12:KB:572:SER:HB2	12:KB:703:TRP:HE1	1.74	0.52
15:NC:711:CYS:HB2	15:NC:806:ASP:HB2	1.92	0.52
2:AC:551:ILE:HG13	1:AD:475:LEU:HD13	1.92	0.52
1:AD:99:ASN:HD22	10:IB:902:ARG:HA	1.75	0.52
3:BA:693:ARG:HH11	17:PA:256:ARG:HG2	1.75	0.52
3:BB:991:PRO:HG2	16:OB:173:ARG:HH12	1.75	0.52
3:CE:4460:PRO:HA	3:CE:4463:LEU:HD23	1.92	0.52
4:DA:122:ILE:HA	4:DA:125:GLU:HG2	1.92	0.52
4:DE:41:ARG:HH21	8:GB:660:LYS:HE2	1.75	0.52
6:FD:1218:ALA:O	6:FD:1220:ARG:HB2	2.10	0.52
7:GC:450:LYS:HG2	7:GC:515:SER:HB3	1.91	0.52
7:GG:450:LYS:HG2	7:GG:635:THR:HG21	1.92	0.52
9:HD:778:PRO:O	9:HD:779:PRO:C	2.53	0.52
10:IA:259:ARG:HH22	10:IA:854:PRO:HB2	1.74	0.52
10:IA:1181:LYS:HD2	10:IA:1185:GLY:HA2	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JA:548:PHE:HB3	11:JA:1288:ARG:HG3	1.92	0.52
11:JA:2013:LEU:HD21	11:JA:2266:LEU:HD21	1.91	0.52
12:KA:270:LYS:HD2	12:KE:269:MET:HE1	1.92	0.52
12:KF:600:ASP:HB2	12:KF:607:GLN:HG2	1.92	0.52
15:NB:1540:ASN:HD21	19:RB:112:LEU:HD13	1.75	0.52
15:ND:702:LEU:HB3	15:ND:937:MET:HB3	1.92	0.52
18:QD:146:ILE:HG13	18:QD:147:PHE:HD1	1.74	0.52
20:SD:83:GLU:HA	20:SD:147:MET:HE3	1.92	0.52
3:CB:766:LYS:HG2	3:CB:829:LEU:HD21	1.90	0.52
3:CB:826:LEU:HA	3:CB:829:LEU:HB2	1.92	0.52
3:CC:907:ARG:HH12	17:PB:314:LYS:HE2	1.74	0.52
3:CF:1260:VAL:HG21	3:CF:4466:ILE:HD13	1.92	0.52
4:DF:18:GLU:HB3	4:DF:320:ILE:HD11	1.90	0.52
5:EA:4405:ILE:HD13	5:EA:4431:ARG:HD3	1.91	0.52
5:EA:4656:ILE:HD11	5:EA:4660:ARG:HE	1.74	0.52
6:FE:1202:PHE:HE1	6:FE:1243:PRO:HA	1.74	0.52
7:GA:433:MET:HE3	7:GA:459:PRO:HD3	1.92	0.52
7:GE:679:LEU:HA	7:GE:689:ILE:HG22	1.91	0.52
8:GJ:177:MET:HE2	8:GJ:199:ARG:HA	1.92	0.52
9:HA:680:ALA:HB2	9:HA:708:VAL:HG13	1.92	0.52
9:HB:506:GLN:HG2	9:HB:514:PHE:CE2	2.44	0.52
10:IB:468:GLU:HA	10:IB:471:ARG:HG2	1.91	0.52
11:JA:1560:LEU:HD21	11:JA:1607:VAL:HG11	1.91	0.52
12:KA:645:ARG:H	12:KA:676:MET:HE3	1.75	0.52
12:KB:544:LEU:HB3	12:KB:714:THR:HG22	1.91	0.52
12:KF:633:ARG:HH22	12:KF:635:VAL:HG23	1.74	0.52
19:RC:20:PRO:HG3	19:RC:104:LEU:HD13	1.90	0.52
4:DA:16:LEU:HD22	4:DA:97:LEU:HD12	1.92	0.51
4:DD:255:ILE:HD11	8:GD:759:MET:HG3	1.92	0.51
6:FA:1704:MET:HE3	6:FA:1720:VAL:HG21	1.91	0.51
6:FB:2023:ILE:HG22	9:HD:778:PRO:HB3	1.90	0.51
6:FE:812:LEU:HG	6:FE:813:GLN:H	1.74	0.51
6:FE:818:VAL:O	6:FE:819:PRO:C	2.53	0.51
6:FE:1186:TRP:CE3	6:FE:1267:GLN:HB2	2.45	0.51
7:GA:663:THR:HG23	7:GA:668:GLY:HA2	1.90	0.51
7:GE:166:LEU:HA	7:GE:169:ILE:HG12	1.92	0.51
7:GG:205:ARG:HG2	7:GG:641:THR:HG22	1.91	0.51
7:GG:676:ALA:HB3	7:GG:692:HIS:HB2	1.92	0.51
7:GI:579:PHE:HZ	7:GI:588:LEU:HD22	1.75	0.51
7:GK:537:GLY:H	9:HC:554:ASP:N	2.08	0.51
9:HB:506:GLN:HG2	9:HB:514:PHE:HE2	1.74	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:HC:524:VAL:HG22	9:HC:607:VAL:HG22	1.92	0.51
10:IA:208:PHE:HB2	10:IA:239:LEU:HD13	1.92	0.51
10:IA:888:THR:HG21	15:NA:565:TRP:CD1	2.45	0.51
11:JC:78:GLN:HE22	11:JC:80:GLU:HG3	1.74	0.51
11:JC:119:LEU:HB2	11:JC:142:LEU:HD21	1.92	0.51
14:MA:214:LEU:HD11	14:MB:214:LEU:HD21	1.91	0.51
15:NA:735:HIS:CD2	15:NA:768:GLU:HG2	2.46	0.51
15:ND:1442:LYS:HD3	15:ND:1444:LYS:H	1.74	0.51
2:AG:509:ALA:HB1	1:AH:231:ILE:HD11	1.91	0.51
1:AI:157:LEU:HB3	1:AI:183:LEU:HD13	1.93	0.51
5:EB:3292:ARG:HH12	9:HB:436:ASN:HA	1.75	0.51
6:FA:2018:ARG:HH22	6:FA:2022:GLU:HB2	1.74	0.51
6:FD:1012:PRO:HB2	6:FD:1016:PRO:HD3	1.91	0.51
7:GA:169:ILE:HD11	7:GA:697:PRO:HD3	1.93	0.51
8:GB:132:PRO:HG3	8:GB:297:LEU:HD22	1.92	0.51
8:GF:499:GLN:HG3	8:GF:513:VAL:HG22	1.91	0.51
7:GK:547:GLY:H	9:HC:625:THR:HG23	1.75	0.51
11:JB:443:ILE:HD12	11:JB:1474:TRP:HH2	1.75	0.51
11:JB:543:ILE:HD11	15:NB:1328:VAL:HG22	1.92	0.51
12:KE:352:LYS:HE2	12:KE:385:GLU:HB3	1.92	0.51
13:LI:415:GLU:HA	13:LI:418:LYS:HB2	1.91	0.51
15:NA:818:ILE:HB	15:NA:842:THR:HA	1.91	0.51
15:NB:881:LEU:HD22	15:NB:884:LYS:HD2	1.92	0.51
15:NC:597:GLN:HB2	15:NC:914:ILE:HG22	1.92	0.51
18:QD:123:VAL:HA	18:QD:126:MET:HE3	1.91	0.51
19:RB:136:ALA:HA	19:RB:139:LEU:HB2	1.91	0.51
1:AE:237:VAL:HG23	1:AE:238:CYS:H	1.76	0.51
2:AG:108:LEU:HD21	2:AG:285:PHE:HE2	1.75	0.51
1:AH:799:THR:HG22	1:AH:999:LYS:H	1.75	0.51
1:AH:815:LEU:HD12	1:AH:830:THR:HG21	1.92	0.51
2:AJ:178:GLU:HG3	2:AJ:179:ASP:H	1.75	0.51
2:AK:332:ARG:NH2	11:JB:2284:LYS:HG3	2.26	0.51
1:AL:257:LEU:HD23	1:AL:261:CYS:HB3	1.91	0.51
4:DF:181:ILE:HG22	4:DF:182:LEU:HG	1.93	0.51
5:EC:3495:CYS:H	5:EC:4014:VAL:HG11	1.74	0.51
6:FE:1203:ARG:HD2	11:JC:901:ARG:HH12	1.75	0.51
8:GB:16:TRP:HZ2	8:GB:31:LEU:HB2	1.74	0.51
7:GG:846:LEU:HD13	7:GG:934:ARG:HG2	1.91	0.51
7:GG:975:VAL:HG23	7:GG:977:SER:H	1.76	0.51
10:IC:896:PHE:HE1	10:IC:921:LEU:HD22	1.74	0.51
11:JA:60:PRO:HB3	11:JA:86:SER:HA	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:553:PRO:HG2	11:JC:1199:PHE:HE1	1.75	0.51
15:NB:893:LEU:H	15:NB:1154:ASP:N	2.09	0.51
15:NC:733:VAL:HG21	15:NC:747:LEU:HD13	1.92	0.51
15:NC:888:ARG:HD2	15:NC:1156:LEU:HD12	1.91	0.51
15:ND:367:VAL:HG23	15:ND:428:ARG:HE	1.74	0.51
15:ND:665:SER:HB2	15:ND:675:GLU:HA	1.92	0.51
16:OA:200:VAL:HG22	17:PA:282:ALA:HB2	1.91	0.51
1:AA:243:VAL:HG21	19:RC:94:PRO:HG3	1.92	0.51
1:AE:84:ALA:HA	1:AE:87:LEU:HB2	1.91	0.51
2:AF:416:MET:HE3	6:FA:2073:LEU:HD21	1.92	0.51
3:BA:870:LEU:HD11	16:OA:167:LEU:HD11	1.91	0.51
3:CC:956:LEU:HB2	3:CC:978:VAL:HG11	1.92	0.51
6:FA:2016:ARG:O	6:FA:2019:GLU:HG3	2.10	0.51
6:FE:841:TYR:H	7:GE:957:ARG:NH2	2.08	0.51
6:FE:994:PRO:HB3	12:KB:382:ARG:CD	2.41	0.51
6:FE:1184:ALA:HB3	6:FE:1424:CYS:HA	1.93	0.51
6:FF:1209:GLU:O	6:FF:1210:LEU:C	2.54	0.51
6:FF:1282:LEU:HD11	6:FF:1419:LEU:HD22	1.91	0.51
7:GE:230:ARG:HE	7:GE:235:ARG:HD2	1.74	0.51
7:GE:636:VAL:HG21	7:GE:678:LEU:HD21	1.92	0.51
8:GH:19:TRP:HE1	8:GH:518:TYR:HB2	1.75	0.51
8:GH:546:VAL:HG11	8:GH:623:LEU:HD21	1.92	0.51
10:IA:644:VAL:H	16:OA:1074:TYR:HB2	1.75	0.51
11:JA:1222:ARG:HH12	11:JA:1279:PRO:HG3	1.76	0.51
12:KA:593:HIS:HB2	12:KA:707:GLU:HB3	1.90	0.51
12:KC:380:GLY:O	12:KC:381:MET:C	2.53	0.51
15:NA:685:PHE:HB2	15:NA:914:ILE:HG12	1.92	0.51
15:NC:1442:LYS:HD3	15:NC:1444:LYS:H	1.76	0.51
1:AA:60:THR:HG22	3:BA:806:SER:HB2	1.93	0.51
1:AA:274:ARG:HG3	1:AA:275:HIS:H	1.76	0.51
2:AG:434:ARG:HE	1:AH:456:VAL:HG21	1.76	0.51
1:AI:743:LEU:HA	1:AI:746:VAL:HG12	1.93	0.51
2:AK:197:ALA:HB3	2:AK:270:VAL:HB	1.92	0.51
3:CI:1177:PRO:HD2	3:CI:4509:LEU:HG	1.93	0.51
3:CI:4459:ALA:HB3	3:CI:4462:VAL:HG22	1.92	0.51
4:DB:94:PHE:HZ	4:DB:103:LEU:HD21	1.74	0.51
4:DC:362:LYS:HZ1	4:DC:379:SER:HA	1.74	0.51
5:EA:3572:ILE:HD11	5:EA:3614:PRO:HD3	1.93	0.51
5:EB:4096:ARG:HD3	5:EB:4478:THR:HA	1.93	0.51
6:FD:817:VAL:O	6:FD:818:VAL:C	2.52	0.51
6:FD:1426:ALA:O	6:FD:1427:ASN:OD1	2.28	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:1104:GLY:O	6:FF:1105:ARG:C	2.54	0.51
7:GA:292:PHE:HB2	7:GA:689:ILE:HB	1.93	0.51
7:GA:451:ILE:HD13	7:GA:516:VAL:HG22	1.93	0.51
8:GH:492:LYS:HG2	8:GH:494:SER:H	1.75	0.51
7:GI:230:ARG:HH21	7:GI:235:ARG:HB3	1.75	0.51
8:GL:326:ARG:HH21	8:GL:375:TYR:HB3	1.74	0.51
9:HB:765:TRP:N	9:HB:765:TRP:HE3	2.08	0.51
10:IA:575:SER:HB3	10:IA:580:LEU:HD21	1.91	0.51
12:KC:338:LEU:HD23	12:KC:697:ARG:HH12	1.75	0.51
13:LA:513:LEU:HD22	13:LB:513:LEU:HB3	1.91	0.51
13:LB:404:LEU:HD23	13:LB:407:ARG:HE	1.75	0.51
14:MF:310:SER:HA	14:MF:313:ARG:HB3	1.93	0.51
15:NA:801:ALA:HB2	15:NA:859:LEU:HD21	1.93	0.51
15:NA:992:GLN:HE22	15:NA:1022:ASP:HB2	1.75	0.51
15:NC:575:LEU:HD12	15:NC:581:LEU:HD21	1.93	0.51
15:ND:983:ILE:HG23	15:ND:989:ILE:HB	1.92	0.51
16:OB:742:PHE:HA	18:QC:89:ARG:HH22	1.75	0.51
3:BC:874:ARG:HD2	16:OC:163:TYR:HB3	1.92	0.51
3:CJ:1168:ARG:HH21	3:CJ:4499:PRO:HB3	1.76	0.51
4:DA:366:VAL:HG12	4:DA:375:SER:HB2	1.93	0.51
5:EA:3256:LEU:HD12	5:EA:3268:ASN:HA	1.91	0.51
5:EA:4067:ALA:HB1	5:EA:4293:TRP:HZ2	1.75	0.51
5:EB:4497:VAL:HG23	5:EB:4667:PRO:HG3	1.92	0.51
8:GD:28:LYS:HB3	8:GD:571:ARG:HH12	1.74	0.51
8:GJ:366:ALA:HB1	8:GJ:372:VAL:HG21	1.92	0.51
7:GK:292:PHE:HB2	7:GK:689:ILE:HB	1.92	0.51
10:IB:1375:VAL:HG11	16:OA:755:ILE:HG23	1.92	0.51
11:JA:87:VAL:HG22	11:JA:90:ARG:HH12	1.76	0.51
11:JA:450:PHE:HE2	11:JA:474:LYS:HE2	1.76	0.51
11:JC:835:VAL:HG11	11:JC:1009:VAL:HG21	1.93	0.51
12:KA:526:TRP:HB3	12:KA:545:LEU:HD11	1.91	0.51
12:KG:208:LEU:HD13	12:KG:244:SER:HA	1.91	0.51
12:KG:267:THR:HA	12:KG:270:LYS:HG2	1.91	0.51
15:NA:503:LEU:HB3	15:NA:512:TYR:HB3	1.92	0.51
15:NA:1546:VAL:HG22	19:RC:26:HIS:CE1	2.46	0.51
15:NB:1407:MET:HG3	15:NB:1471:ARG:HB2	1.92	0.51
15:ND:853:GLU:HB2	15:ND:867:ARG:HH12	1.76	0.51
1:AE:414:GLU:HB3	2:AF:67:LEU:HD11	1.93	0.51
1:AI:247:THR:H	1:AI:258:CYS:HB3	1.75	0.51
2:AK:459:ILE:HG12	11:JB:1166:ARG:HG3	1.92	0.51
3:CE:1126:GLU:HB3	10:IA:995:PRO:HG2	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:CG:1229:HIS:HB3	3:CG:4463:LEU:HD22	1.92	0.51
5:EC:3787:GLU:HG2	5:EC:3790:ARG:HH12	1.75	0.51
5:EC:4888:TRP:O	5:EC:4889:ILE:C	2.53	0.51
6:FD:1082:THR:O	6:FD:1085:GLU:HG3	2.11	0.51
6:FE:910:ILE:HG12	6:FE:962:PHE:CE2	2.45	0.51
6:FF:807:ALA:O	6:FF:808:SER:HB2	2.10	0.51
7:GC:742:CYS:HB2	7:GC:797:ILE:HD13	1.92	0.51
7:GI:368:PHE:HB3	7:GI:401:LEU:HD11	1.92	0.51
7:GI:731:ILE:HD13	7:GI:817:ARG:HH12	1.76	0.51
8:GL:349:THR:HG22	8:GL:379:VAL:HG21	1.93	0.51
8:GL:369:LEU:HD23	8:GL:392:ASP:HB3	1.93	0.51
10:IB:480:LEU:HD23	10:IB:497:LEU:HD21	1.92	0.51
10:IB:1179:ASN:HD22	10:IB:1179:ASN:C	2.18	0.51
10:IC:1087:THR:HG21	10:IC:1091:LEU:HD12	1.92	0.51
11:JA:529:ILE:HD13	11:JA:885:TYR:HD2	1.76	0.51
14:MA:301:LEU:HB3	14:MB:301:LEU:HD22	1.93	0.51
15:ND:593:LYS:HG2	15:ND:595:ARG:HG2	1.92	0.51
15:ND:725:ILE:HG23	15:ND:799:ILE:HD11	1.91	0.51
16:OB:889:VAL:HG21	16:OB:913:VAL:HG21	1.93	0.51
2:AC:373:ARG:HH11	5:EB:4404:LYS:HG3	1.76	0.51
2:AC:535:LEU:HD22	5:EA:4820:GLY:HA3	1.91	0.51
1:AE:1025:ARG:NH1	14:ML:84:GLY:HA3	2.26	0.51
2:AF:94:ILE:HG13	2:AF:99:MET:HE2	1.92	0.51
1:AI:805:TYR:HE2	1:AI:994:LEU:HB2	1.75	0.51
3:CC:724:GLN:O	3:CC:724:GLN:NE2	2.44	0.51
3:CF:1172:PRO:HD2	3:CF:1202:LEU:HD22	1.92	0.51
3:CL:1221:ASN:HD21	3:CL:1226:LEU:HD12	1.75	0.51
5:EA:4405:ILE:HG22	5:EA:4427:LEU:HD12	1.93	0.51
5:EB:3491:ALA:HB2	5:EB:3603:LEU:HB3	1.92	0.51
6:FC:1817:VAL:HG11	6:FC:1838:VAL:HG11	1.92	0.51
6:FD:1216:TRP:O	6:FD:1217:GLU:C	2.54	0.51
6:FE:833:GLY:H	6:FE:979:LEU:HD23	1.76	0.51
6:FE:917:TRP:CD1	6:FE:918:GLN:HE21	2.26	0.51
8:GL:178:ALA:HB3	8:GL:198:PHE:HB2	1.91	0.51
10:IB:1095:GLY:H	10:IB:1098:HIS:HD2	1.59	0.51
10:IB:1419:HIS:HA	10:IB:1426:LYS:HZ1	1.76	0.51
11:JB:503:HIS:HE1	11:JB:1426:PRO:HB2	1.75	0.51
11:JB:512:SER:HB3	11:JB:1474:TRP:HZ3	1.76	0.51
11:JC:1553:LEU:HD21	11:JC:1597:LEU:HD13	1.92	0.51
11:JC:1765:ARG:HH12	16:OC:893:PRO:CD	2.23	0.51
12:KG:579:LEU:HD11	12:KG:654:ILE:HG22	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LD:481:GLU:HB3	13:LD:486:ARG:HD3	1.92	0.51
18:QB:49:ILE:HG21	18:QB:55:VAL:HB	1.91	0.51
1:AD:309:LEU:HD12	1:AD:329:LEU:HD21	1.93	0.51
2:AK:424:LEU:HD12	1:AL:418:ILE:HB	1.93	0.51
3:BC:750:SER:H	17:PC:254:ALA:HB1	1.76	0.51
3:CE:4474:GLU:CD	3:CE:4475:LYS:H	2.19	0.51
4:DA:140:VAL:HB	4:DA:143:LEU:HB2	1.92	0.51
5:EA:4461:PHE:HB3	5:EA:4500:THR:HG22	1.92	0.51
5:EB:3383:VAL:HG12	5:EB:3392:TRP:HE3	1.75	0.51
5:EC:4169:VAL:HB	5:EC:4205:ILE:HD11	1.93	0.51
6:FB:1727:ALA:HA	6:FB:1802:ASP:HA	1.92	0.51
6:FE:803:ARG:CB	6:FE:1118:GLN:HG3	2.41	0.51
6:FE:844:ALA:O	7:GE:896:ARG:NH2	2.43	0.51
6:FE:852:VAL:HG11	6:FE:864:LEU:HG	1.92	0.51
6:FF:1239:CYS:HB3	6:FF:1260:LEU:HD11	1.93	0.51
8:GH:273:SER:HA	8:GH:320:SER:HA	1.93	0.51
7:GI:184:ALA:HB3	7:GI:708:SER:HB2	1.91	0.51
8:GL:326:ARG:HB3	8:GL:338:ALA:HB2	1.93	0.51
11:JA:1666:VAL:HG13	16:OA:917:ILE:HD11	1.92	0.51
11:JC:1794:LEU:HD21	11:JC:1859:GLN:HG2	1.93	0.51
12:KE:246:LEU:HD13	12:KE:297:ILE:HG23	1.92	0.51
12:KE:596:ILE:HG12	12:KE:666:LEU:HD11	1.92	0.51
13:LD:370:MET:HA	13:LD:373:VAL:HG22	1.93	0.51
15:NA:805:ALA:HB2	15:NA:885:LEU:HD12	1.92	0.51
19:RA:22:ARG:HG2	19:RA:174:LEU:HD12	1.93	0.51
1:AA:38:VAL:HG21	1:AA:111:ILE:HG23	1.92	0.51
2:AG:300:CYS:HB2	2:AG:320:CYS:HB3	1.93	0.51
1:AI:148:VAL:HG23	1:AI:219:THR:HB	1.91	0.51
3:BB:788:VAL:HG21	3:BB:826:LEU:HD22	1.92	0.51
3:CG:1236:LEU:HD23	3:CG:1253:VAL:HG23	1.93	0.51
5:EA:4412:LEU:HD13	5:EA:4416:PHE:HE2	1.75	0.51
5:EB:4814:THR:HG22	5:EB:4817:LEU:HD21	1.93	0.51
5:EC:4172:GLY:HA3	5:EC:4208:LEU:HD21	1.93	0.51
5:EC:4893:THR:O	5:EC:4894:SER:C	2.54	0.51
6:FC:2080:GLN:O	6:FC:2083:GLN:HG3	2.11	0.51
6:FF:1429:LEU:HD23	6:FF:1430:PHE:CD2	2.46	0.51
8:GB:401:ASP:HA	8:GB:404:ARG:HG2	1.93	0.51
7:GI:709:MET:HE2	7:GI:714:VAL:HG21	1.92	0.51
9:HA:674:VAL:HG22	9:HA:712:ILE:HG23	1.92	0.51
9:HA:778:PRO:O	9:HA:779:PRO:C	2.54	0.51
10:IC:1097:LEU:HA	10:IC:1112:LEU:HD13	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:KA:375:TYR:HD1	12:KA:402:LEU:HD11	1.76	0.51
15:NB:1442:LYS:HG3	15:NB:1444:LYS:H	1.75	0.51
15:ND:1518:ARG:HH21	18:QB:60:ARG:NH2	2.08	0.51
20:SC:30:THR:HA	20:SC:33:LEU:HD23	1.93	0.51
20:SD:130:ASP:HB2	20:SD:137:ILE:HD11	1.91	0.51
2:AC:517:ARG:HH12	1:AD:48:ALA:HB1	1.76	0.50
1:AE:65:ILE:HG12	1:AE:222:LEU:HB3	1.94	0.50
2:AG:319:LEU:HD21	2:AG:327:ILE:HD12	1.93	0.50
3:BA:791:THR:HG21	3:BA:812:MET:SD	2.51	0.50
3:CF:4484:VAL:HG12	3:CF:4499:PRO:HA	1.91	0.50
3:CI:1239:PRO:HG3	3:CI:4471:PRO:HD2	1.92	0.50
3:CJ:1152:LEU:HD23	10:IB:397:VAL:HG13	1.93	0.50
4:DA:376:SER:HA	13:LA:433:ARG:HH22	1.75	0.50
4:DB:10:GLU:HA	4:DB:13:VAL:HB	1.93	0.50
4:DB:385:LYS:HZ1	13:LF:462:GLN:HA	1.76	0.50
4:DD:162:VAL:HA	4:DD:165:ILE:HD12	1.92	0.50
5:EA:4741:LYS:HD2	5:EA:4836:SER:HA	1.94	0.50
5:EC:3292:ARG:HH22	9:HA:436:ASN:N	2.09	0.50
6:FD:993:ALA:HA	12:KA:230:GLN:HG2	1.93	0.50
7:GA:768:PRO:HG2	7:GA:773:VAL:HG22	1.92	0.50
8:GD:7:GLU:HB2	8:GD:13:ARG:HH11	1.76	0.50
7:GE:396:PRO:HD2	7:GE:401:LEU:HD11	1.93	0.50
8:GF:101:PRO:HD2	8:GF:104:LEU:HD12	1.93	0.50
8:GH:199:ARG:NH2	7:GI:394:PHE:HB2	2.26	0.50
8:GL:416:LYS:HB3	8:GL:470:LYS:HG2	1.93	0.50
9:HB:574:ARG:HG3	9:HB:578:THR:HB	1.93	0.50
10:IC:615:ARG:HB2	10:IC:629:PRO:HG3	1.92	0.50
11:JA:874:VAL:HG12	11:JA:961:VAL:HG22	1.93	0.50
11:JA:1720:ASP:HB3	16:OA:930:ALA:HA	1.93	0.50
11:JC:1734:VAL:HG11	11:JC:1774:ARG:HG3	1.92	0.50
12:KA:370:LEU:HD22	12:KA:377:LEU:HD11	1.93	0.50
12:KC:591:ARG:H	12:KC:646:ARG:HH22	1.59	0.50
12:KE:344:ILE:HA	12:KE:347:LEU:HD12	1.93	0.50
14:MF:287:ALA:HA	14:MF:290:ARG:HB2	1.92	0.50
15:NC:355:LEU:HD22	15:NC:434:VAL:HG21	1.92	0.50
16:OA:177:THR:HG23	16:OA:179:GLU:HG3	1.92	0.50
16:OC:1097:SER:H	16:OC:1100:GLU:HB3	1.76	0.50
2:AK:193:GLU:HG3	1:AL:466:PRO:HG3	1.92	0.50
3:BB:951:VAL:HG13	3:BB:952:GLN:HE21	1.75	0.50
5:EC:4745:VAL:HG13	5:EC:4842:GLN:HE22	1.76	0.50
6:FB:1640:VAL:HG13	6:FB:1643:PRO:HB3	1.91	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FC:1970:LEU:HD12	6:FC:2040:LEU:HD22	1.93	0.50
7:GA:386:VAL:HB	8:GF:196:HIS:HA	1.91	0.50
8:GH:544:LEU:HD23	8:GH:548:LYS:HZ3	1.77	0.50
8:GJ:57:ARG:HH21	8:GJ:85:ASN:HA	1.76	0.50
7:GK:551:LEU:HB2	9:HC:666:LYS:HD2	1.93	0.50
9:HC:575:ARG:H	9:HC:578:THR:HB	1.76	0.50
10:IA:1294:ILE:HD12	10:IA:1358:LEU:HD11	1.92	0.50
10:IB:1245:GLN:HA	10:IB:1272:LEU:HD12	1.94	0.50
11:JB:1856:ARG:HH21	11:JB:1860:PRO:HD3	1.77	0.50
12:KA:582:ILE:HG23	12:KA:653:VAL:HG13	1.93	0.50
12:KA:598:VAL:HG12	12:KA:702:ILE:HG22	1.93	0.50
13:LA:398:ARG:HA	13:LA:401:LEU:HB2	1.93	0.50
13:LJ:489:LEU:HG	14:ML:113:VAL:HG21	1.92	0.50
15:NA:343:VAL:HG21	15:NA:490:VAL:HG11	1.91	0.50
15:NA:617:PHE:HD1	15:NA:916:LEU:HD22	1.77	0.50
15:NA:891:TRP:H	15:NA:1154:ASP:C	2.20	0.50
15:NB:598:PHE:HZ	15:NB:948:LEU:HD13	1.76	0.50
15:NB:621:TYR:HB2	15:NB:626:ARG:HH22	1.76	0.50
16:OC:1059:LEU:HD12	16:OC:1060:GLN:HG2	1.93	0.50
1:AL:588:ILE:HD11	1:AL:594:TYR:HE1	1.77	0.50
1:AL:852:ARG:HG2	1:AL:853:TYR:H	1.75	0.50
3:BB:817:HIS:CE1	16:OB:241:ALA:HB2	2.46	0.50
3:CE:1236:LEU:HD21	3:CE:1255:VAL:HG13	1.93	0.50
3:CG:4486:ILE:HD12	3:CG:4494:GLU:HG3	1.92	0.50
4:DC:93:ILE:HD12	4:DC:164:PHE:HB3	1.94	0.50
5:EA:4652:LEU:H	5:EA:4657:GLU:HB2	1.75	0.50
5:EB:4167:ASP:HB3	5:EB:4170:LYS:HB3	1.92	0.50
5:EB:4394:GLY:HA2	5:EB:4450:ARG:HB3	1.92	0.50
6:FB:1724:ARG:HE	6:FB:1808:VAL:HG13	1.77	0.50
6:FD:826:LEU:HB3	6:FD:841:TYR:HE2	1.77	0.50
6:FD:1026:PRO:HB2	6:FD:1029:GLN:HG2	1.93	0.50
6:FD:1200:LEU:H	6:FD:1256:GLU:HG3	1.74	0.50
6:FE:878:LEU:HB3	6:FE:907:ASN:H	1.76	0.50
6:FE:917:TRP:O	6:FE:918:GLN:C	2.54	0.50
8:GH:192:VAL:HG11	7:GI:422:LEU:HD11	1.93	0.50
7:GI:762:TYR:HA	7:GI:986:LEU:HD11	1.92	0.50
7:GI:764:LEU:HD13	7:GI:870:ARG:HD2	1.93	0.50
8:GJ:25:GLU:HA	8:GJ:28:LYS:HG2	1.93	0.50
7:GK:606:MET:HB2	7:GK:631:PHE:HB2	1.92	0.50
9:HA:759:GLU:O	9:HA:760:LYS:C	2.54	0.50
9:HD:777:TYR:O	9:HD:778:PRO:C	2.55	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IB:791:VAL:HG21	10:IB:812:LEU:HD22	1.92	0.50
11:JA:2125:ILE:HD11	11:JA:2259:LEU:HD11	1.93	0.50
12:KC:231:PHE:CE1	12:KC:313:PHE:CD2	3.00	0.50
12:KF:212:LEU:HD11	12:KF:294:ARG:HD2	1.92	0.50
12:KG:593:HIS:HB2	12:KG:707:GLU:HB3	1.93	0.50
13:LI:429:GLU:HA	13:LI:432:THR:HG22	1.92	0.50
14:MF:330:LEU:HD13	14:MF:333:LEU:HD12	1.92	0.50
15:NB:1422:VAL:HB	20:SC:108:HIS:CE1	2.46	0.50
20:SC:73:MET:HA	20:SC:77:MET:HE3	1.93	0.50
1:AA:240:MET:HE1	1:AA:265:VAL:HG11	1.93	0.50
1:AA:241:CYS:HB3	1:AA:243:VAL:HG23	1.92	0.50
1:AA:648:ARG:HE	1:AA:688:PHE:HE2	1.59	0.50
1:AL:62:ASP:HA	1:AL:228:PRO:HB3	1.93	0.50
3:BA:724:GLN:HG3	3:BA:725:GLN:H	1.77	0.50
3:CE:1237:VAL:HG21	3:CE:4468:LYS:HD2	1.92	0.50
4:DA:315:LEU:HD21	14:MB:239:GLU:HB3	1.93	0.50
4:DD:28:LEU:HG	4:DD:29:LEU:HG	1.92	0.50
4:DE:308:GLN:HE22	4:DE:315:LEU:HD21	1.76	0.50
5:EA:4539:MET:HB2	5:EA:4685:PRO:HA	1.93	0.50
5:EB:3265:LEU:HA	5:EB:3510:LEU:HD21	1.93	0.50
6:FE:846:CYS:HB3	12:KB:305:HIS:NE2	2.25	0.50
7:GC:518:LEU:HB3	7:GC:520:ILE:HG12	1.94	0.50
7:GE:276:ARG:HB3	7:GE:276:ARG:CZ	2.41	0.50
7:GE:372:GLY:HA3	7:GE:403:VAL:HG11	1.91	0.50
8:GH:773:ASP:HB2	8:GL:346:LYS:HD3	1.93	0.50
7:GI:309:LEU:HB3	7:GI:402:PHE:HE1	1.76	0.50
7:GI:919:VAL:HB	12:KC:684:LEU:HD22	1.92	0.50
7:GK:544:PRO:HG3	9:HC:596:TYR:HA	1.93	0.50
7:GK:843:LEU:HD13	7:GK:935:VAL:HG13	1.94	0.50
10:IA:922:ALA:HB2	10:IA:942:PHE:HD2	1.75	0.50
11:JB:1169:ARG:HH21	11:JB:1665:GLN:HA	1.77	0.50
12:KA:599:GLU:HA	12:KA:606:ARG:NH2	2.26	0.50
12:KC:305:HIS:HB2	12:KC:309:GLN:HB2	1.93	0.50
12:KC:376:ALA:HB2	12:KC:725:ILE:HD11	1.93	0.50
15:NB:467:ASP:HB2	15:NB:469:PHE:CZ	2.47	0.50
15:NC:801:ALA:HA	15:NC:804:VAL:HG12	1.93	0.50
15:NC:894:LEU:H	15:NC:1153:ALA:H	1.59	0.50
2:AG:53:PRO:HB2	5:EC:4290:GLY:HA2	1.94	0.50
2:AG:548:ARG:HD2	5:EB:4620:LYS:NZ	2.27	0.50
1:AI:1046:THR:HG22	1:AI:1048:ALA:H	1.75	0.50
3:CB:920:ARG:HH12	3:CB:957:ALA:HA	1.75	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FB:1647:LEU:HD22	6:FB:1797:VAL:HG23	1.94	0.50
6:FC:1845:PRO:HB2	6:FC:1848:PRO:HD2	1.94	0.50
6:FE:910:ILE:HD11	6:FE:965:TRP:CD1	2.46	0.50
6:FF:861:LEU:HA	6:FF:864:LEU:HD12	1.94	0.50
7:GA:536:THR:HA	9:HB:553:TYR:HB2	1.93	0.50
8:GD:154:ASP:HA	8:GD:157:MET:HG2	1.93	0.50
7:GK:531:GLY:HA2	9:HC:530:LYS:HB2	1.93	0.50
9:HB:856:GLU:HA	9:HB:859:LYS:HD2	1.93	0.50
10:IB:1087:THR:HG21	10:IB:1091:LEU:HD12	1.92	0.50
11:JB:786:PHE:HB3	11:JB:814:ASP:HB2	1.93	0.50
11:JC:131:LEU:HD11	11:JC:1821:LEU:HD13	1.94	0.50
12:KA:285:ILE:HG21	12:KA:293:ILE:HG12	1.92	0.50
12:KE:530:ASP:HA	12:KE:550:ARG:HD2	1.94	0.50
15:NA:368:GLU:HG2	15:NA:428:ARG:HH21	1.76	0.50
1:AA:266:HIS:HA	1:AA:272:LEU:HD12	1.94	0.50
1:AA:731:SER:H	1:AA:735:LEU:HD23	1.77	0.50
2:AG:376:ARG:HH22	5:EC:4405:ILE:CD1	2.25	0.50
2:AJ:140:LYS:HD3	2:AJ:143:ARG:NH2	2.26	0.50
2:AK:63:THR:HG21	2:AK:170:GLY:HA3	1.93	0.50
3:CG:1133:VAL:HG11	10:IC:1094:ASN:ND2	2.26	0.50
5:EA:4724:LEU:HG	5:EA:4812:LEU:HD11	1.93	0.50
5:EC:4217:LEU:HD13	5:EC:4254:MET:HE2	1.94	0.50
5:EC:4403:LEU:HD12	5:EC:4428:MET:HE1	1.93	0.50
6:FB:1653:ARG:HH12	6:FB:1733:ARG:HH21	1.57	0.50
6:FC:1755:VAL:HG21	6:FC:1934:LEU:HB3	1.93	0.50
7:GA:418:THR:HG21	8:GF:192:VAL:HG21	1.94	0.50
8:GD:526:ILE:HG21	14:MA:317:THR:HB	1.94	0.50
8:GL:661:PRO:HB2	8:GL:680:LEU:H	1.77	0.50
9:HA:854:ASN:HA	9:HA:857:ARG:HE	1.77	0.50
10:IC:929:GLY:H	10:IC:963:ARG:HE	1.60	0.50
11:JA:836:MET:HG3	11:JA:966:LEU:HD13	1.93	0.50
11:JC:1803:ARG:HA	11:JC:1806:MET:HB3	1.92	0.50
12:KC:534:VAL:HB	12:KC:536:ARG:HG2	1.93	0.50
15:NB:1532:ARG:HA	15:NB:1535:MET:HE2	1.94	0.50
15:ND:885:LEU:HA	15:ND:888:ARG:HB2	1.94	0.50
16:OB:70:THR:HG22	16:OB:71:SER:H	1.76	0.50
18:QB:144:GLU:HB3	18:QB:150:ALA:HB2	1.93	0.50
1:AA:382:ILE:HG23	2:AB:460:LEU:HD12	1.94	0.50
2:AB:303:CYS:HB2	2:AB:323:CYS:HB3	1.94	0.50
1:AD:131:ARG:HG2	1:AD:205:ARG:HH12	1.76	0.50
1:AD:231:ILE:HA	10:IB:825:LEU:HD11	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:967:ARG:HD3	14:MC:94:LEU:HD13	1.92	0.50
3:BB:810:PRO:HA	17:PB:278:TRP:CZ3	2.47	0.50
4:DA:329:ARG:HA	4:DA:332:LEU:HB2	1.94	0.50
4:DB:304:THR:HG22	4:DB:307:LEU:HD12	1.93	0.50
4:DC:134:LEU:HA	4:DC:148:ARG:HH22	1.76	0.50
4:DE:88:CYS:HB2	4:DE:172:ARG:HH22	1.77	0.50
6:FB:2044:CYS:HB3	9:HD:826:ARG:HH21	1.76	0.50
6:FF:1217:GLU:O	6:FF:1219:GLU:N	2.44	0.50
8:GF:61:CYS:CB	8:GF:78:CYS:SG	2.99	0.50
7:GG:494:LEU:HB3	7:GG:814:THR:HG21	1.93	0.50
11:JC:1427:LEU:HD12	11:JC:1462:ILE:HD11	1.94	0.50
12:KA:621:GLY:HA3	12:KA:633:ARG:HE	1.77	0.50
12:KB:498:ARG:HE	12:KE:507:LEU:HD22	1.76	0.50
16:OA:7:ARG:HD2	16:OA:12:GLU:HB2	1.94	0.50
16:OA:1046:MET:HG3	16:OA:1047:GLY:H	1.77	0.50
19:RD:22:ARG:HH21	19:RD:177:ALA:HB2	1.77	0.50
1:AD:908:ARG:HB3	13:LA:490:MET:HB3	1.94	0.50
2:AF:207:GLU:HG2	2:AF:208:GLU:HG3	1.93	0.50
1:AH:99:ASN:HD21	1:AH:134:PHE:HB3	1.75	0.50
2:AK:263:TYR:HD1	1:AL:423:THR:HB	1.76	0.50
4:DB:110:LEU:HG	4:DB:114:VAL:HG13	1.94	0.50
5:EA:3304:LYS:HD3	5:EA:4163:MET:HB2	1.92	0.50
5:EC:3836:GLU:HG2	5:EC:3863:SER:HA	1.94	0.50
6:FA:2063:GLN:OE1	9:HA:751:SER:HB2	2.12	0.50
6:FB:1850:GLN:HA	6:FB:1923:PHE:HE1	1.77	0.50
6:FB:2037:LEU:HD23	9:HD:816:LEU:HD22	1.93	0.50
6:FD:852:VAL:HG12	6:FD:880:VAL:HG22	1.93	0.50
6:FD:1441:ILE:O	6:FD:1444:ARG:N	2.44	0.50
6:FE:829:ARG:HB2	6:FE:976:HIS:CD2	2.46	0.50
6:FF:895:ILE:HG12	7:GI:967:PHE:CE2	2.46	0.50
6:FF:981:HIS:NE2	12:KC:667:SER:HB2	2.27	0.50
8:GF:316:VAL:HG23	8:GF:341:VAL:HG12	1.94	0.50
8:GL:379:VAL:HA	8:GL:382:GLU:HG2	1.94	0.50
11:JC:138:THR:HA	11:JC:162:PRO:HA	1.94	0.50
12:KF:414:TRP:HE3	12:KF:415:LEU:HD22	1.77	0.50
13:LF:489:LEU:HB3	14:MH:113:VAL:HG21	1.92	0.50
13:LJ:464:ASP:HA	13:LJ:467:GLN:HB3	1.93	0.50
15:NA:575:LEU:HD12	15:NA:581:LEU:HD21	1.94	0.50
15:NA:1005:VAL:H	15:NA:1008:SER:HB3	1.77	0.50
15:NB:864:GLU:HA	15:NB:867:ARG:HE	1.77	0.50
16:OA:891:ARG:HH12	16:OA:924:VAL:HG22	1.76	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:259:VAL:HG21	2:AB:307:PRO:HB3	1.93	0.50
1:AE:429:ARG:HE	2:AF:417:ALA:HB1	1.77	0.50
2:AF:72:PHE:HB3	2:AF:164:TYR:HD2	1.76	0.50
1:AI:303:MET:HB2	1:AI:328:PRO:HG2	1.94	0.50
2:AK:373:ARG:HE	2:AK:374:LEU:HD22	1.77	0.50
2:AK:495:SER:HB2	2:AK:518:HIS:HE1	1.76	0.50
3:BA:812:MET:HA	16:OA:196:TRP:HZ3	1.76	0.50
3:CL:1152:LEU:HD23	10:IC:397:VAL:HG13	1.94	0.50
4:DD:174:THR:HA	4:DD:177:LYS:HZ2	1.77	0.50
5:EA:4454:ARG:HD2	5:EA:4507:ASP:HB2	1.94	0.50
5:EC:3426:ARG:HH22	5:EC:3804:ILE:HG13	1.77	0.50
6:FD:909:PRO:O	6:FD:911:SER:N	2.45	0.50
6:FE:1285:CYS:O	6:FE:1286:LEU:C	2.53	0.50
6:FF:886:THR:HG22	6:FF:900:ALA:HB2	1.92	0.50
7:GC:620:HIS:CD2	7:GC:720:GLN:HB3	2.47	0.50
8:GD:283:LEU:HD21	8:GD:303:LEU:HD22	1.94	0.50
8:GH:374:LEU:HB2	8:GH:613:ASP:HA	1.93	0.50
9:HD:779:PRO:O	9:HD:780:PHE:C	2.54	0.50
10:IA:827:ARG:HE	11:JA:2055:TRP:HE1	1.60	0.50
11:JA:107:PRO:HB3	11:JA:186:SER:HA	1.94	0.50
11:JA:1679:ALA:HB2	11:JA:1714:CYS:HB2	1.94	0.50
11:JB:131:LEU:HD21	11:JB:1821:LEU:HA	1.94	0.50
11:JB:841:VAL:HG13	11:JB:1424:ARG:HB2	1.94	0.50
11:JC:761:LYS:HD2	11:JC:768:ASP:HA	1.94	0.50
11:JC:1542:PRO:HD2	11:JC:1545:HIS:CD2	2.47	0.50
11:JC:1569:ASN:HB2	11:JC:1572:LEU:HG	1.94	0.50
15:NA:864:GLU:HA	15:NA:867:ARG:HD2	1.93	0.50
15:NA:1508:PHE:HB2	20:SA:19:LEU:HD11	1.94	0.50
15:NC:980:LEU:HD13	15:NC:983:ILE:HD12	1.94	0.50
2:AG:332:ARG:HH12	2:AG:336:ARG:HE	1.60	0.49
3:BB:790:ASN:HB3	3:BB:811:ILE:HG22	1.94	0.49
3:BB:825:SER:HB2	16:OB:291:VAL:HG12	1.92	0.49
3:CC:680:PRO:HA	3:CC:683:GLN:HB2	1.94	0.49
4:DF:285:ARG:HE	4:DF:345:ALA:HB2	1.77	0.49
5:EB:3488:THR:HG22	5:EB:3559:VAL:HG22	1.94	0.49
6:FD:834:VAL:O	6:FD:835:SER:C	2.55	0.49
8:GH:336:ASN:HA	8:GL:219:ALA:HA	1.93	0.49
9:HA:552:ASP:HB2	9:HA:576:LYS:HG3	1.94	0.49
9:HA:761:CYS:HA	9:HA:765:TRP:CE2	2.47	0.49
9:HB:801:VAL:HA	13:LE:532:LEU:O	2.11	0.49
11:JA:139:ARG:HH11	11:JA:160:LEU:HD11	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:KA:314:LEU:HD13	12:KA:317:ALA:HB3	1.92	0.49
12:KC:503:ASP:H	12:KC:506:LEU:HD23	1.77	0.49
12:KF:398:ASP:HA	12:KF:522:ARG:HD2	1.94	0.49
13:LE:513:LEU:HA	13:LE:516:VAL:HG12	1.94	0.49
15:NA:1503:PHE:HD1	15:NA:1506:ARG:HH22	1.59	0.49
15:NB:608:ALA:H	15:NB:676:ARG:HH22	1.60	0.49
15:NB:1036:LEU:HD11	15:NB:1097:ILE:HB	1.94	0.49
15:ND:1140:LEU:HD12	15:ND:1143:LEU:HD22	1.94	0.49
16:OB:184:ASN:HA	16:OB:295:LEU:HD11	1.93	0.49
18:QA:165:ARG:HE	18:QA:172:GLN:HA	1.77	0.49
18:QC:55:VAL:HA	18:QC:58:LEU:HB3	1.94	0.49
1:AA:399:ARG:HD2	6:FA:1672:LEU:HD11	1.94	0.49
1:AH:389:LEU:HA	5:EB:4619:VAL:HG11	1.93	0.49
1:AI:44:LEU:HD22	17:PB:268:PRO:HB2	1.94	0.49
2:AK:12:SER:HB2	6:FC:1911:PRO:HD2	1.95	0.49
5:EA:4727:SER:HB2	5:EA:4817:LEU:HD12	1.94	0.49
5:EB:4397:ASP:OD1	5:EB:4402:PRO:HD3	2.12	0.49
6:FA:2012:ARG:HH21	6:FA:2012:ARG:HB3	1.77	0.49
6:FE:841:TYR:C	7:GE:957:ARG:HH21	2.20	0.49
6:FF:917:TRP:O	6:FF:918:GLN:C	2.55	0.49
6:FF:923:ALA:C	6:FF:928:SER:H	2.20	0.49
7:GA:604:ALA:HB3	7:GA:633:LEU:HB2	1.95	0.49
7:GC:884:LEU:HD21	7:GC:969:GLN:HB2	1.94	0.49
8:GH:251:CYS:HA	8:GH:254:LYS:HE2	1.93	0.49
10:IC:374:PHE:HB3	10:IC:393:LEU:HD12	1.94	0.49
11:JB:769:LEU:HD12	11:JB:794:ALA:HB1	1.93	0.49
11:JB:1125:ILE:HG22	11:JB:1156:ILE:HD11	1.95	0.49
11:JC:1138:PRO:HA	11:JC:1670:ARG:HH12	1.76	0.49
13:LO:404:LEU:HA	13:LO:407:ARG:HG2	1.94	0.49
15:NA:545:VAL:HG22	15:NA:1195:SER:HA	1.94	0.49
2:AB:408:LYS:HA	2:AB:411:GLN:HE21	1.76	0.49
1:AE:443:LYS:HG2	2:AF:27:ALA:HB1	1.94	0.49
2:AG:145:LYS:HA	2:AG:148:ASP:HB2	1.94	0.49
3:BA:904:PRO:HG3	3:BA:941:ARG:HG2	1.94	0.49
5:EB:3273:LEU:HD23	5:EB:3494:VAL:HG11	1.94	0.49
6:FF:800:ALA:HB3	6:FF:910:ILE:HG23	1.94	0.49
6:FF:895:ILE:C	7:GI:878:GLN:HE22	2.19	0.49
6:FF:1001:ASN:O	6:FF:1009:VAL:HA	2.12	0.49
7:GC:372:GLY:HA3	7:GC:403:VAL:HG11	1.94	0.49
7:GG:959:GLY:HA2	9:HA:689:LYS:NZ	2.27	0.49
11:JA:1594:ARG:HD3	11:JA:1624:VAL:HG11	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JB:1703:ASN:HA	11:JB:1706:ASP:HB2	1.94	0.49
11:JC:882:ALA:HA	11:JC:891:VAL:HG12	1.94	0.49
12:KF:212:LEU:HD22	12:KF:290:PRO:HB2	1.94	0.49
14:MF:308:GLU:HA	14:MF:311:ILE:HG22	1.95	0.49
15:NB:1518:ARG:HG3	18:QC:167:LEU:HB3	1.94	0.49
16:OA:190:LEU:HD23	16:OA:229:LEU:HD13	1.93	0.49
17:PA:124:ILE:HG23	17:PA:128:GLU:HB2	1.94	0.49
19:RA:136:ALA:HA	19:RA:139:LEU:HB2	1.95	0.49
1:AE:289:SER:H	17:PC:271:ASN:HD22	1.60	0.49
3:CJ:1212:GLU:HB2	3:CJ:1222:ARG:HH22	1.76	0.49
4:DA:48:TYR:HE1	4:DA:128:ALA:HB3	1.78	0.49
4:DB:48:TYR:CD1	4:DB:125:GLU:HA	2.47	0.49
4:DD:150:SER:HA	4:DD:153:PHE:HB3	1.94	0.49
4:DF:105:CYS:H	4:DF:260:GLY:H	1.60	0.49
5:EA:4667:PRO:HA	5:EA:4670:TRP:HB3	1.92	0.49
5:EC:3273:LEU:HD12	5:EC:3305:GLU:HG3	1.93	0.49
6:FA:2059:VAL:HG23	9:HA:754:LEU:CB	2.43	0.49
6:FD:1212:VAL:HG23	6:FD:1264:ILE:HD12	1.94	0.49
6:FD:1244:LEU:HB3	6:FD:1249:ILE:HG12	1.95	0.49
6:FE:1064:TYR:O	6:FE:1065:LEU:C	2.55	0.49
6:FF:1186:TRP:CE3	6:FF:1269:CYS:HB2	2.47	0.49
8:GD:184:GLY:H	8:GD:254:LYS:HG3	1.76	0.49
9:HD:782:ALA:O	9:HD:783:SER:C	2.55	0.49
10:IA:740:ARG:HH12	10:IA:777:GLY:HA3	1.77	0.49
10:IA:791:VAL:HG11	10:IA:812:LEU:HD22	1.94	0.49
10:IB:1307:ASN:HA	10:IB:1383:LEU:HD13	1.93	0.49
10:IC:1196:VAL:HG12	10:IC:1305:GLU:HG2	1.94	0.49
11:JA:1686:LEU:HD12	11:JA:1707:VAL:HG13	1.94	0.49
11:JB:533:ILE:HG21	11:JB:888:PHE:HE2	1.77	0.49
12:KA:574:LEU:HD12	12:KA:699:PHE:HB3	1.95	0.49
13:LI:482:LEU:HD13	13:LJ:482:LEU:HD22	1.93	0.49
15:NB:884:LYS:HD3	15:NB:1127:LEU:HD12	1.93	0.49
15:ND:950:VAL:HA	15:ND:954:PHE:HD2	1.77	0.49
1:AA:146:VAL:HB	1:AA:224:PHE:HE2	1.78	0.49
1:AD:470:SER:HB3	11:JA:1019:ARG:HH21	1.78	0.49
1:AE:203:ALA:HB2	3:BC:804:ARG:HB2	1.94	0.49
1:AE:648:ARG:HD2	1:AE:688:PHE:HE1	1.76	0.49
2:AK:427:ARG:HB2	1:AL:418:ILE:HD13	1.94	0.49
3:CJ:1237:VAL:HA	3:CJ:1244:PRO:HA	1.94	0.49
4:DF:310:LEU:HB3	4:DF:339:ALA:HB2	1.94	0.49
6:FF:1184:ALA:O	6:FF:1424:CYS:SG	2.69	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GB:541:MET:HE2	8:GB:564:LYS:HG2	1.94	0.49
7:GG:731:ILE:HD13	7:GG:821:TRP:HZ2	1.77	0.49
8:GL:68:ALA:HB3	8:GL:76:TRP:HA	1.94	0.49
9:HA:835:LYS:O	9:HA:838:LYS:HB2	2.11	0.49
9:HB:676:ALA:HB2	9:HB:682:ILE:HG12	1.93	0.49
9:HB:773:ALA:HB3	13:LF:527:VAL:HG13	1.94	0.49
9:HB:792:ARG:HD3	13:LG:529:PRO:HD3	1.94	0.49
9:HB:809:LEU:O	9:HB:813:THR:HG23	2.12	0.49
11:JC:162:PRO:HD2	11:JC:170:ILE:H	1.76	0.49
11:JC:414:ILE:HD13	11:JC:417:LEU:HD12	1.93	0.49
12:KA:299:TYR:CE2	12:KA:330:LEU:HD13	2.47	0.49
12:KB:576:ASN:HB2	12:KB:699:PHE:HE1	1.78	0.49
12:KF:405:PRO:HD3	12:KF:489:MET:HE1	1.95	0.49
12:KF:684:LEU:HD13	12:KF:688:VAL:H	1.77	0.49
13:LA:374:HIS:CE1	13:LB:370:MET:HB2	2.45	0.49
14:MA:211:MET:HE3	14:MB:210:LEU:HD22	1.94	0.49
15:NA:562:GLU:O	15:NA:566:GLN:HG2	2.12	0.49
15:NA:1539:ILE:HA	15:NA:1542:LEU:HD12	1.93	0.49
1:AA:415:MET:HE3	2:AB:431:LEU:HD11	1.95	0.49
2:AC:180:GLU:HA	2:AC:183:ALA:HB3	1.93	0.49
2:AF:143:ARG:HD3	2:AF:210:LEU:HD11	1.93	0.49
1:AH:139:ASN:HD21	10:IA:874:ASN:HD21	1.59	0.49
3:BB:827:ALA:HB2	3:BB:842:PHE:HB2	1.93	0.49
5:EB:3717:ILE:HG12	5:EB:3743:ARG:HH22	1.77	0.49
5:EC:3700:PHE:HA	5:EC:3706:VAL:HG22	1.94	0.49
6:FA:1850:GLN:HA	6:FA:1923:PHE:HE1	1.78	0.49
6:FD:1095:LEU:O	6:FD:1096:LEU:C	2.56	0.49
6:FD:1103:SER:HB2	9:HB:393:VAL:HG21	1.94	0.49
6:FD:1442:GLU:HG3	6:FD:1444:ARG:HB2	1.93	0.49
7:GC:311:LEU:HD23	7:GC:453:LEU:HD13	1.95	0.49
7:GG:551:LEU:HB2	9:HA:666:LYS:HD3	1.94	0.49
7:GG:612:ARG:HH21	7:GG:662:VAL:HG13	1.78	0.49
8:GH:135:LEU:HB3	8:GH:299:ALA:HA	1.93	0.49
9:HA:497:ALA:HB2	9:HA:627:GLY:HA3	1.95	0.49
9:HC:722:SER:HA	9:HC:724:PHE:H	1.78	0.49
9:HD:810:ARG:HA	9:HD:813:THR:HG23	1.93	0.49
10:IA:412:ALA:HA	10:IA:415:ARG:HE	1.78	0.49
11:JA:1285:SER:HA	11:JA:1288:ARG:HH11	1.77	0.49
11:JB:473:ASN:HB3	11:JB:876:GLN:HE21	1.76	0.49
12:KF:250:SER:HB2	12:KF:327:MET:HE1	1.95	0.49
12:KG:210:VAL:HG12	12:KG:283:TYR:H	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LJ:422:GLN:HG3	13:LJ:425:LYS:HZ3	1.77	0.49
14:MA:304:ARG:NH1	14:MB:237:ARG:HH12	2.09	0.49
15:NA:1476:LEU:HA	15:NA:1479:GLU:HG2	1.94	0.49
15:NA:1533:LYS:O	15:NA:1537:LYS:HG2	2.13	0.49
15:NC:891:TRP:CD1	15:NC:1151:ASN:HA	2.47	0.49
15:NC:891:TRP:H	15:NC:1154:ASP:C	2.20	0.49
15:NC:1521:SER:HA	18:QD:60:ARG:HD3	1.95	0.49
15:ND:741:ILE:HG23	15:ND:793:THR:HG22	1.93	0.49
18:QA:113:LYS:HE3	20:SA:22:LYS:HE2	1.93	0.49
1:AE:176:ILE:HG21	1:AE:211:LYS:HG3	1.94	0.49
1:AE:243:VAL:HG12	1:AE:244:LEU:HB2	1.93	0.49
2:AF:92:LEU:HD23	2:AF:277:VAL:HG11	1.95	0.49
1:AI:395:ALA:HB2	6:FC:1669:LYS:HG3	1.95	0.49
3:CA:715:ARG:HH12	3:CA:756:GLU:HG2	1.78	0.49
3:CJ:4466:ILE:HD11	3:CJ:4487:LEU:HB3	1.94	0.49
4:DE:320:ILE:HD12	4:DE:323:ASP:HB3	1.95	0.49
5:EA:3399:PHE:HB3	5:EA:3418:SER:HB3	1.94	0.49
5:EB:3520:VAL:HG21	5:EB:3595:LEU:HD23	1.95	0.49
6:FA:1755:VAL:HB	6:FA:1759:GLU:HG3	1.93	0.49
6:FB:1771:GLU:HG2	6:FB:1776:GLY:HA3	1.94	0.49
6:FB:1885:ILE:HD13	6:FB:1888:LEU:HD12	1.93	0.49
6:FC:2034:ARG:HD2	9:HB:772:PRO:O	2.13	0.49
6:FE:809:ILE:HD11	6:FE:812:LEU:HD22	1.95	0.49
6:FE:1105:ARG:O	6:FE:1106:LEU:C	2.55	0.49
6:FF:1189:ILE:HG23	6:FF:1417:ILE:HD11	1.95	0.49
7:GA:325:GLU:HG3	7:GA:581:ARG:HD2	1.93	0.49
7:GC:294:ALA:HB3	7:GC:687:ARG:HB3	1.94	0.49
8:GF:76:TRP:HZ3	8:GF:79:PRO:HD3	1.77	0.49
7:GG:237:TYR:HE1	7:GG:607:ARG:HH22	1.60	0.49
8:GH:756:ALA:HB3	8:GL:333:LYS:HD2	1.94	0.49
7:GI:249:ARG:HH22	7:GI:267:MET:HA	1.77	0.49
8:GL:741:PRO:HB3	8:GL:770:ILE:HB	1.95	0.49
11:JA:2110:LEU:HD12	11:JA:2113:PHE:HB3	1.94	0.49
11:JB:1522:ILE:HD13	11:JB:1557:LEU:HD22	1.94	0.49
11:JC:128:THR:HG21	11:JC:2086:PRO:HB2	1.94	0.49
12:KB:700:LEU:HD22	12:KB:702:ILE:HG22	1.94	0.49
12:KC:395:LEU:HD12	12:KC:484:ILE:HA	1.94	0.49
12:KE:521:PRO:HB2	12:KE:523:VAL:HG12	1.94	0.49
13:LI:401:LEU:HD13	13:LI:404:LEU:HD23	1.95	0.49
15:NB:614:LYS:HE3	15:NB:678:LEU:HB2	1.95	0.49
15:NB:925:ARG:HH22	15:NB:1111:ARG:HD2	1.78	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:RC:20:PRO:HD2	19:RC:101:ASP:HA	1.94	0.49
1:AD:168:ASP:HA	1:AD:185:ARG:HH22	1.77	0.49
2:AF:259:VAL:HG11	2:AF:307:PRO:HG3	1.95	0.49
1:AI:270:ARG:NH2	16:OA:746:LEU:H	2.11	0.49
1:AL:741:SER:O	1:AL:745:GLN:HG3	2.13	0.49
4:DA:48:TYR:CD1	4:DA:125:GLU:HA	2.47	0.49
4:DA:267:ARG:HH12	4:DA:271:ALA:HB2	1.77	0.49
4:DE:19:ARG:HH22	4:DE:156:ASP:HB3	1.76	0.49
5:EA:4035:THR:HG22	5:EA:4037:ASP:H	1.78	0.49
5:EA:4213:LYS:HB3	5:EA:4232:MET:SD	2.53	0.49
5:EC:3395:TYR:HE1	5:EC:3510:LEU:HD12	1.77	0.49
6:FA:2072:ILE:HD12	9:HA:855:ARG:N	2.27	0.49
6:FE:1255:SER:C	6:FE:1257:ASP:H	2.21	0.49
6:FF:878:LEU:HD12	6:FF:906:LEU:HA	1.95	0.49
7:GA:171:GLN:HG3	7:GA:172:PHE:CD2	2.48	0.49
8:GF:638:LEU:HD11	8:GF:665:LEU:HB3	1.94	0.49
7:GG:472:LEU:HB3	7:GG:494:LEU:HD11	1.95	0.49
7:GI:676:ALA:HB3	7:GI:692:HIS:HB2	1.95	0.49
7:GK:768:PRO:HG2	7:GK:773:VAL:HG22	1.94	0.49
9:HB:674:VAL:HG13	9:HB:712:ILE:HG12	1.95	0.49
9:HB:676:ALA:HB1	9:HB:681:LYS:HA	1.94	0.49
9:HB:765:TRP:HE3	9:HB:765:TRP:H	1.59	0.49
10:IB:947:HIS:HB3	10:IB:951:GLY:H	1.78	0.49
11:JA:519:PHE:HE2	11:JA:1473:LEU:HD13	1.78	0.49
12:KF:289:HIS:CE1	12:KF:317:ALA:HB1	2.48	0.49
13:LO:424:LEU:HD11	13:LP:421:VAL:HG13	1.94	0.49
14:ME:235:ASP:HA	14:ME:238:THR:HG22	1.95	0.49
15:NA:1518:ARG:HG3	18:QA:167:LEU:HB3	1.95	0.49
15:ND:883:LEU:HD23	15:ND:1123:ALA:HB1	1.93	0.49
19:RD:74:LEU:HG	19:RD:91:VAL:HG11	1.95	0.49
1:AE:670:ASP:HB3	1:AE:673:GLN:HB2	1.94	0.49
1:AH:99:ASN:HA	1:AH:104:PRO:HB3	1.95	0.49
2:AK:483:LEU:HD13	1:AL:158:ALA:H	1.78	0.49
3:CE:1231:ARG:HD2	3:CE:1234:LEU:HB3	1.95	0.49
5:EC:3877:ILE:HG13	5:EC:3881:ARG:HE	1.78	0.49
5:EC:4658:ASP:HA	5:EC:4690:CYS:SG	2.53	0.49
6:FB:2059:VAL:HG12	6:FB:2063:GLN:HE22	1.78	0.49
6:FC:2085:GLU:O	6:FC:2089:PRO:CD	2.61	0.49
6:FD:850:CYS:HB3	6:FD:973:ILE:CG1	2.41	0.49
6:FD:1294:LEU:O	6:FD:1295:ALA:C	2.56	0.49
7:GA:196:LEU:HB3	7:GA:198:LEU:HD23	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GE:746:LEU:HD21	7:GE:989:VAL:HG23	1.94	0.49
7:GE:809:VAL:HG12	7:GE:817:ARG:HH22	1.78	0.49
8:GJ:123:PRO:HD2	8:GJ:238:ARG:HH12	1.78	0.49
8:GL:519:ARG:HE	8:GL:520:PHE:N	2.11	0.49
10:IB:621:VAL:HG11	10:IB:704:ASN:HD22	1.77	0.49
10:IB:1394:VAL:HG22	10:IB:1396:ASP:H	1.78	0.49
10:IC:910:LEU:HD12	10:IC:913:LEU:HD13	1.93	0.49
11:JA:840:ILE:HD13	11:JA:875:LEU:HD23	1.95	0.49
12:KA:405:PRO:HD3	12:KA:489:MET:HE1	1.95	0.49
12:KG:381:MET:HE3	12:KG:722:VAL:HG11	1.95	0.49
15:NB:1391:LEU:HD12	15:NB:1394:LEU:HD11	1.94	0.49
16:OA:158:ARG:HA	16:OA:163:TYR:HB2	1.95	0.49
1:AA:915:TRP:CZ2	13:LK:355:LYS:HG3	2.48	0.49
1:AE:743:LEU:HA	1:AE:746:VAL:HG22	1.95	0.49
2:AG:68:LEU:HD13	1:AH:457:ARG:HD3	1.94	0.49
3:BA:689:LEU:HB3	17:PA:258:PRO:HG2	1.94	0.49
3:CC:943:TYR:HE2	10:IB:1405:PRO:HD3	1.77	0.49
4:DA:327:PHE:HE1	14:MA:259:MET:HE2	1.78	0.49
4:DC:20:LEU:HB3	4:DC:98:ARG:HH22	1.77	0.49
6:FC:1951:TYR:CE2	9:HB:844:GLY:HA3	2.48	0.49
6:FF:981:HIS:HA	12:KC:656:ARG:NH1	2.28	0.49
8:GB:439:PRO:HD2	8:GB:474:VAL:HG22	1.95	0.49
8:GF:300:ARG:HD2	8:GF:361:ALA:HB3	1.95	0.49
8:GH:276:MET:HE1	8:GH:319:LEU:HB2	1.95	0.49
8:GH:534:GLN:HG3	8:GH:591:ILE:HB	1.93	0.49
7:GI:453:LEU:HD23	7:GI:518:LEU:HG	1.95	0.49
7:GI:706:VAL:HG11	7:GI:752:VAL:HG21	1.95	0.49
8:GJ:50:GLU:HB3	8:GJ:112:ILE:HB	1.95	0.49
7:GK:841:LEU:HB3	7:GK:866:PRO:HG2	1.94	0.49
8:GL:638:LEU:HD11	8:GL:665:LEU:HB3	1.95	0.49
11:JA:2098:THR:HG23	11:JA:2109:ALA:HB2	1.94	0.49
12:KF:209:VAL:HG13	12:KF:239:LYS:HA	1.95	0.49
13:LC:356:LEU:HD13	13:LD:356:LEU:HD11	1.94	0.49
15:NB:600:LEU:HD13	15:NB:917:MET:HB2	1.94	0.49
15:NB:725:ILE:HG13	15:NB:799:ILE:HG21	1.95	0.49
15:NC:797:ARG:HD3	15:NC:859:LEU:HD13	1.94	0.49
15:ND:542:LEU:HD23	15:ND:1190:ILE:HD12	1.95	0.49
15:ND:598:PHE:HB2	15:ND:1185:PRO:HB2	1.95	0.49
15:ND:864:GLU:CD	15:ND:865:SER:H	2.21	0.49
19:RB:112:LEU:HD11	19:RB:170:VAL:HG21	1.94	0.49
1:AD:665:LEU:HB3	1:AD:1019:TYR:HE2	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:169:VAL:HG23	2:AJ:277:VAL:HG22	1.94	0.48
3:BA:955:VAL:HG13	3:BA:978:VAL:HG22	1.94	0.48
3:CA:762:LEU:HD11	3:CA:822:VAL:HG23	1.95	0.48
3:CF:1264:VAL:HG13	3:CF:1265:ILE:HD12	1.94	0.48
3:CL:4452:HIS:CE1	3:CL:4454:ASP:HB2	2.48	0.48
4:DC:300:GLN:HG3	4:DC:354:TRP:CE2	2.48	0.48
4:DF:384:ILE:HG22	4:DF:386:VAL:HG23	1.94	0.48
5:EA:3237:LEU:HD21	5:EA:3243:VAL:HG12	1.95	0.48
5:EB:4031:ARG:HG3	5:EB:4032:PHE:CD1	2.48	0.48
5:EB:4064:ALA:HB1	5:EB:4180:TYR:HE2	1.77	0.48
5:EC:4724:LEU:HD23	5:EC:4812:LEU:HD21	1.94	0.48
6:FD:1293:THR:O	6:FD:1295:ALA:N	2.46	0.48
6:FE:846:CYS:HB3	12:KB:305:HIS:HE1	1.72	0.48
6:FE:860:PRO:C	6:FE:862:GLU:H	2.21	0.48
8:GB:184:GLY:HA2	8:GB:254:LYS:HG3	1.95	0.48
8:GF:741:PRO:HB3	8:GF:770:ILE:HB	1.95	0.48
8:GH:664:ILE:HD12	8:GH:677:HIS:HD2	1.78	0.48
7:GI:881:ALA:HA	7:GI:894:ILE:HA	1.95	0.48
8:GJ:420:ASN:HB2	8:GJ:503:LEU:HD23	1.95	0.48
8:GJ:431:PHE:HE1	8:GJ:494:SER:HB3	1.77	0.48
8:GL:545:ALA:HB1	8:GL:605:LEU:HD21	1.95	0.48
10:IA:916:LYS:HE3	11:JA:2042:SER:HA	1.94	0.48
11:JC:463:ILE:H	11:JC:466:ARG:NH2	2.11	0.48
11:JC:760:LEU:HB2	11:JC:1491:ALA:HB1	1.95	0.48
12:KF:403:ASP:HB3	12:KF:541:TYR:CZ	2.48	0.48
15:NA:597:GLN:HB2	15:NA:914:ILE:HG22	1.95	0.48
15:NA:611:ASN:HA	15:NA:614:LYS:HG2	1.95	0.48
15:NB:893:LEU:HB3	15:NB:1153:ALA:HB3	1.95	0.48
15:NB:1120:VAL:HA	15:NB:1123:ALA:HB2	1.95	0.48
2:AC:502:LEU:HA	2:AC:505:VAL:HG12	1.94	0.48
1:AD:157:LEU:HB2	1:AD:180:PHE:CD2	2.48	0.48
2:AG:452:GLU:HA	2:AG:455:ARG:HG2	1.94	0.48
1:AH:381:ARG:HH22	5:EB:4625:SER:HA	1.79	0.48
1:AI:660:ILE:HG13	1:AI:661:PRO:HD3	1.94	0.48
4:DA:84:ILE:HD13	4:DA:169:GLY:HA3	1.95	0.48
5:EC:3768:VAL:HG11	5:EC:4003:THR:HA	1.93	0.48
6:FD:860:PRO:O	6:FD:862:GLU:N	2.46	0.48
6:FE:814:THR:O	6:FE:815:SER:C	2.56	0.48
6:FF:813:GLN:O	6:FF:814:THR:C	2.56	0.48
6:FF:975:ILE:O	6:FF:976:HIS:C	2.56	0.48
6:FF:990:PHE:HB2	12:KC:313:PHE:CE2	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:1122:LEU:HD22	6:FF:1122:LEU:HA	1.71	0.48
7:GA:537:GLY:H	9:HB:554:ASP:H	1.59	0.48
7:GE:798:LEU:HD13	7:GE:985:PHE:CG	2.48	0.48
11:JA:547:PRO:HB3	11:JA:1286:LEU:HD23	1.95	0.48
11:JA:1868:LEU:HD22	11:JA:2270:MET:HG2	1.94	0.48
11:JB:437:LEU:HD11	11:JB:1461:PHE:HB3	1.95	0.48
11:JB:1190:LEU:HD11	11:JB:1327:LEU:HD23	1.95	0.48
11:JC:1731:PRO:HB3	11:JC:1778:PHE:HZ	1.76	0.48
12:KB:389:LYS:HA	12:KB:392:GLN:HE22	1.78	0.48
12:KC:583:GLU:HG2	12:KC:718:ALA:HA	1.95	0.48
13:LE:473:LYS:O	13:LE:476:GLY:HA3	2.13	0.48
14:ME:225:VAL:HG21	14:ME:315:TRP:HE1	1.78	0.48
15:NA:347:LEU:HD22	15:NA:491:PRO:HG2	1.95	0.48
15:NB:709:ILE:HA	15:NB:714:ARG:HD3	1.95	0.48
15:NB:819:GLY:H	15:NB:842:THR:HA	1.77	0.48
15:ND:812:ARG:HH21	15:ND:870:TYR:HD2	1.60	0.48
15:ND:891:TRP:H	15:ND:1155:GLU:N	2.11	0.48
2:AB:298:PRO:HG2	2:AB:318:ARG:HD2	1.95	0.48
1:AD:157:LEU:HB2	1:AD:180:PHE:HD2	1.79	0.48
1:AE:850:ILE:HG22	1:AE:895:ARG:HH22	1.78	0.48
2:AK:448:ASN:C	2:AK:448:ASN:ND2	2.71	0.48
1:AL:656:ASP:HA	9:HC:514:PHE:CE1	2.48	0.48
3:BC:816:LYS:HE2	3:BC:849:LEU:HD11	1.94	0.48
3:CE:1269:ILE:HA	3:CE:1272:TYR:HB3	1.96	0.48
4:DB:356:TYR:CZ	4:DB:385:LYS:HG2	2.47	0.48
4:DD:66:ARG:HG3	4:DD:71:LEU:HA	1.96	0.48
5:EA:3689:LEU:HD13	5:EA:3713:GLN:HG3	1.95	0.48
5:EB:4147:PHE:HE1	5:EB:4182:LEU:HA	1.78	0.48
6:FA:1962:GLN:HG2	9:HA:834:LEU:HD21	1.95	0.48
6:FB:1892:ILE:HG22	6:FB:1894:THR:H	1.77	0.48
6:FD:888:PRO:HD3	12:KA:305:HIS:CE1	2.49	0.48
6:FD:1212:VAL:O	6:FD:1233:ILE:HD12	2.14	0.48
6:FD:1217:GLU:O	6:FD:1219:GLU:N	2.46	0.48
6:FD:1244:LEU:O	6:FD:1246:ILE:N	2.41	0.48
6:FE:824:TYR:N	6:FE:825:PRO:HD3	2.28	0.48
6:FE:1201:THR:O	6:FE:1202:PHE:C	2.56	0.48
6:FF:1064:TYR:O	6:FF:1065:LEU:HB2	2.13	0.48
6:FF:1216:TRP:CZ3	6:FF:1300:LEU:HD13	2.48	0.48
8:GF:75:GLN:HG2	8:GF:84:ARG:HE	1.78	0.48
7:GG:354:ARG:HA	7:GG:404:ASN:HD21	1.79	0.48
7:GG:371:LEU:HD13	7:GG:412:VAL:HG22	1.94	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GI:496:LYS:HB2	7:GI:496:LYS:HE3	1.59	0.48
7:GK:264:GLN:HA	7:GK:267:MET:HE3	1.95	0.48
7:GK:397:LEU:HD12	8:GL:177:MET:HE3	1.94	0.48
10:IB:414:ALA:HB2	10:IB:424:VAL:HG11	1.95	0.48
10:IB:910:LEU:HA	10:IB:913:LEU:HD13	1.94	0.48
10:IC:612:ARG:HD3	10:IC:797:VAL:HG23	1.95	0.48
12:KC:226:ALA:HB1	12:KC:232:THR:HG23	1.96	0.48
15:NA:950:VAL:HG13	15:NA:954:PHE:HD2	1.77	0.48
15:ND:925:ARG:HE	15:ND:926:ARG:H	1.60	0.48
15:ND:1407:MET:HG3	15:ND:1469:PHE:HB3	1.94	0.48
2:AB:481:ARG:HE	2:AB:537:ARG:HH22	1.61	0.48
1:AD:99:ASN:HA	1:AD:104:PRO:HB3	1.94	0.48
2:AG:441:MET:HE2	1:AH:404:LEU:HD11	1.93	0.48
2:AK:14:LYS:HG2	6:FC:1911:PRO:HD3	1.95	0.48
3:CA:679:SER:HB3	17:PA:250:VAL:HG21	1.94	0.48
3:CG:1267:PRO:HA	3:CG:1270:LEU:HG	1.95	0.48
3:CG:4460:PRO:HA	3:CG:4463:LEU:HG	1.95	0.48
3:CJ:1280:VAL:HG13	3:CJ:1284:LYS:HD2	1.95	0.48
4:DA:98:ARG:HH22	4:DA:102:LEU:HD22	1.79	0.48
5:EA:4316:ILE:HG22	5:EA:4317:MET:HE2	1.95	0.48
5:EA:4438:LEU:HD11	5:EA:4709:PHE:HE1	1.78	0.48
5:EB:3269:TRP:HD1	5:EB:3409:SER:HB2	1.78	0.48
6:FA:2059:VAL:CG2	9:HA:754:LEU:CB	2.91	0.48
6:FD:1075:VAL:HG13	6:FD:1105:ARG:HB2	1.94	0.48
6:FE:1439:LEU:O	6:FE:1441:ILE:N	2.46	0.48
6:FF:1223:ALA:HA	6:FF:1226:LEU:HD12	1.95	0.48
8:GB:333:LYS:HE2	8:GB:335:ASN:HD21	1.78	0.48
8:GF:168:MET:HE1	8:GF:247:PRO:HG3	1.95	0.48
8:GH:54:VAL:HG11	8:GH:88:PRO:HD3	1.95	0.48
8:GH:303:LEU:HD11	8:GH:305:VAL:HB	1.96	0.48
8:GH:545:ALA:HA	8:GH:548:LYS:HZ1	1.78	0.48
8:GJ:172:ILE:HG12	8:GJ:180:LEU:HA	1.95	0.48
7:GK:535:PRO:HB2	9:HC:553:TYR:N	2.27	0.48
9:HB:777:TYR:N	13:LE:521:ASN:HD21	2.11	0.48
10:IC:328:ALA:HB3	10:IC:570:GLY:H	1.79	0.48
11:JA:1675:LEU:HD21	11:JA:1717:TRP:HE3	1.79	0.48
11:JB:499:THR:HG23	11:JB:502:TRP:H	1.78	0.48
12:KG:473:GLN:HA	12:KG:476:MET:HE2	1.95	0.48
15:NA:866:LEU:HD23	15:NA:869:PHE:HD2	1.79	0.48
15:ND:1542:LEU:HA	15:ND:1545:VAL:HG23	1.96	0.48
17:PC:268:PRO:HG2	17:PC:269:ILE:HD12	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:32:LEU:HD11	1:AD:451:ILE:HD11	1.95	0.48
2:AG:50:ILE:HD11	2:AG:282:PHE:HB2	1.94	0.48
1:AI:629:LEU:HA	1:AI:632:LEU:HD23	1.95	0.48
2:AJ:145:LYS:HA	2:AJ:148:ASP:HB3	1.95	0.48
2:AK:553:THR:HB	1:AL:471:GLU:HG3	1.95	0.48
3:CF:1187:GLU:HB3	3:CF:1192:HIS:HB3	1.96	0.48
3:CF:4459:ALA:HB3	3:CF:4462:VAL:HG23	1.94	0.48
3:CJ:1226:LEU:HG	3:CJ:1231:ARG:HH21	1.77	0.48
3:CL:4487:LEU:HB2	3:CL:4496:ALA:HB3	1.95	0.48
6:FB:2023:ILE:CG2	9:HD:778:PRO:HB3	2.43	0.48
6:FE:809:ILE:HG23	6:FE:900:ALA:O	2.14	0.48
6:FE:1441:ILE:O	6:FE:1444:ARG:N	2.36	0.48
6:FF:1431:MET:O	6:FF:1432:THR:C	2.57	0.48
8:GF:25:GLU:HA	8:GF:28:LYS:HE3	1.94	0.48
8:GL:14:PHE:HZ	8:GL:496:LEU:HD11	1.78	0.48
8:GL:693:PRO:HA	8:GL:696:GLU:HG3	1.94	0.48
9:HD:792:ARG:HD3	13:LK:529:PRO:HD3	1.95	0.48
10:IC:1128:VAL:HG11	10:IC:1180:VAL:HG11	1.94	0.48
11:JA:443:ILE:HG23	11:JA:444:PHE:HD2	1.79	0.48
11:JB:1292:LEU:HD21	11:JB:1299:ALA:HB1	1.94	0.48
11:JC:161:LEU:HD12	11:JC:169:PHE:HB3	1.96	0.48
11:JC:543:ILE:HD11	11:JC:546:LEU:HD12	1.96	0.48
14:MA:233:LEU:HA	14:MA:236:GLU:HG2	1.96	0.48
1:AA:403:TYR:HE1	2:AB:193:GLU:HB3	1.78	0.48
1:AA:507:LEU:HD11	6:FA:1826:LEU:HB3	1.95	0.48
1:AH:234:ARG:HG3	10:IA:778:GLN:HB2	1.95	0.48
2:AJ:29:LEU:HD13	2:AJ:283:LEU:HD21	1.94	0.48
1:AL:421:MET:HB3	1:AL:444:PHE:HE1	1.79	0.48
3:BB:990:HIS:HB3	3:BB:993:THR:HG23	1.94	0.48
3:CF:1269:ILE:HA	3:CF:1272:TYR:HB3	1.96	0.48
3:CL:1239:PRO:HB3	3:CL:4470:LYS:HE2	1.95	0.48
4:DA:66:ARG:HH22	4:DA:74:LYS:HD2	1.79	0.48
4:DD:251:LEU:HD11	8:GD:755:MET:HG2	1.95	0.48
5:EB:4403:LEU:H	5:EB:4440:ILE:HD13	1.79	0.48
5:EC:4150:PHE:HE2	5:EC:4181:VAL:HG21	1.77	0.48
6:FB:1640:VAL:HG12	6:FB:1651:ALA:HB3	1.94	0.48
6:FC:1787:ALA:N	6:FC:1932:ARG:HH12	2.12	0.48
6:FD:1004:GLY:O	6:FD:1005:PRO:C	2.56	0.48
6:FE:998:GLN:C	12:KB:229:SER:OG	2.57	0.48
8:GD:594:GLN:HG3	8:GD:777:LEU:HD21	1.95	0.48
7:GE:188:HIS:HA	7:GE:661:LEU:HD22	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GG:372:GLY:H	7:GG:400:ASP:HB3	1.77	0.48
8:GH:200:GLY:HA2	8:GH:281:LEU:HD23	1.96	0.48
7:GI:232:LYS:HB3	7:GI:258:TYR:HE2	1.78	0.48
7:GI:894:ILE:HD11	7:GI:912:LEU:HD11	1.95	0.48
8:GJ:1:MET:HE1	8:GJ:531:GLY:HA2	1.94	0.48
11:JB:1720:ASP:HB3	16:OB:930:ALA:HA	1.95	0.48
11:JC:1414:ALA:HB2	11:JC:1504:ARG:HE	1.77	0.48
11:JC:2094:ILE:HD11	11:JC:2110:LEU:HD13	1.96	0.48
12:KA:251:SER:HB3	12:KA:254:TRP:HB2	1.94	0.48
12:KC:688:VAL:HG22	12:KC:689:CYS:H	1.78	0.48
12:KG:248:ARG:HD2	12:KG:258:LEU:HD13	1.95	0.48
13:LA:510:ILE:HD13	13:LA:513:LEU:HD12	1.95	0.48
13:LJ:398:ARG:HA	13:LJ:401:LEU:HG	1.96	0.48
15:NA:614:LYS:HE3	15:NA:678:LEU:HB2	1.94	0.48
15:NA:1500:TRP:CZ2	20:SA:124:GLU:HG3	2.48	0.48
15:NB:511:LEU:HD11	15:NB:1472:LYS:HD3	1.94	0.48
15:NC:806:ASP:HB3	15:NC:882:SER:HB2	1.95	0.48
15:NC:1100:GLN:HG3	15:NC:1113:ASP:HB3	1.96	0.48
15:ND:468:ARG:HH11	15:ND:469:PHE:HB3	1.79	0.48
15:ND:893:LEU:H	15:ND:1154:ASP:N	2.10	0.48
1:AA:425:PHE:HA	1:AA:428:LEU:HD23	1.96	0.48
2:AB:427:ARG:HA	2:AB:430:GLU:HB3	1.94	0.48
2:AC:332:ARG:HH12	11:JA:2284:LYS:HG3	1.77	0.48
2:AF:548:ARG:HE	2:AF:551:ILE:HG21	1.79	0.48
2:AG:332:ARG:HH22	11:JC:2285:ASP:HB2	1.79	0.48
2:AJ:177:VAL:HG21	2:AJ:183:ALA:HB2	1.94	0.48
2:AK:44:LEU:HD12	2:AK:285:PHE:HB3	1.94	0.48
4:DF:174:THR:HA	4:DF:177:LYS:HE3	1.96	0.48
5:EA:3400:GLU:H	5:EA:3418:SER:HB3	1.78	0.48
6:FA:1958:LEU:HD22	6:FA:2054:PHE:HD2	1.77	0.48
6:FC:2037:LEU:HD21	9:HB:820:SER:HB3	1.95	0.48
6:FE:1066:GLN:N	6:FE:1114:VAL:O	2.47	0.48
6:FE:1293:THR:O	6:FE:1294:LEU:C	2.56	0.48
6:FF:1210:LEU:HD23	6:FF:1286:LEU:HA	1.95	0.48
7:GA:537:GLY:H	9:HB:554:ASP:N	2.12	0.48
8:GB:336:ASN:HA	8:GF:219:ALA:HA	1.95	0.48
7:GE:451:ILE:HB	7:GE:516:VAL:HG23	1.95	0.48
7:GE:870:ARG:HG2	7:GE:872:THR:HG23	1.95	0.48
7:GG:206:PRO:HB2	7:GG:678:LEU:HD22	1.96	0.48
8:GJ:741:PRO:HB3	8:GJ:770:ILE:HB	1.96	0.48
10:IC:477:ALA:CB	10:IC:494:HIS:HE1	2.26	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:477:ALA:HB3	10:IC:494:HIS:HE1	1.79	0.48
11:JA:444:PHE:HE2	11:JA:512:SER:HB2	1.79	0.48
11:JC:1116:ARG:HA	11:JC:1119:GLY:H	1.79	0.48
12:KF:569:LEU:HD13	12:KF:703:TRP:HE3	1.77	0.48
14:MB:210:LEU:HD12	14:MB:330:LEU:HD13	1.96	0.48
15:NA:350:ARG:HE	15:NA:486:ARG:HD3	1.79	0.48
15:NC:661:ARG:HB3	15:NC:677:CYS:HB2	1.96	0.48
18:QD:120:LYS:HB3	18:QD:123:VAL:HG23	1.95	0.48
19:RA:23:LEU:HD12	19:RA:30:LEU:HD12	1.95	0.48
1:AD:892:GLU:HA	1:AD:895:ARG:HH12	1.77	0.48
1:AE:915:TRP:HB3	13:LM:355:LYS:NZ	2.29	0.48
3:CL:4462:VAL:HG13	3:CL:4495:LEU:HD13	1.95	0.48
3:CL:4466:ILE:HG12	3:CL:4487:LEU:HD23	1.95	0.48
5:EB:3519:ASN:HB2	5:EB:3522:LYS:H	1.79	0.48
5:EC:3843:THR:HG23	5:EC:3852:PHE:CE1	2.49	0.48
6:FC:1611:ARG:HG2	6:FC:1617:GLU:H	1.78	0.48
6:FC:2089:PRO:O	6:FC:2092:GLU:HG3	2.14	0.48
6:FD:1079:MET:HG2	6:FD:1102:TYR:HD2	1.77	0.48
7:GC:199:PRO:HB2	7:GC:717:LEU:HD13	1.96	0.48
7:GE:314:VAL:HG23	7:GE:363:ASP:HB3	1.96	0.48
9:HA:575:ARG:H	9:HA:578:THR:HG23	1.79	0.48
9:HA:765:TRP:N	9:HA:765:TRP:CE3	2.81	0.48
9:HC:554:ASP:HB2	9:HC:557:ALA:HB3	1.95	0.48
9:HD:773:ALA:HB3	13:LJ:527:VAL:CG1	2.43	0.48
11:JA:1745:PHE:HE2	11:JA:1858:ILE:HG21	1.78	0.48
11:JB:878:HIS:HB2	11:JB:962:VAL:HB	1.96	0.48
11:JC:192:LEU:HA	11:JC:195:LEU:HD23	1.96	0.48
11:JC:1553:LEU:HD11	11:JC:1597:LEU:HD22	1.95	0.48
11:JC:2078:LYS:H	11:JC:2264:SER:HB3	1.79	0.48
12:KC:375:TYR:O	12:KC:379:SER:HB3	2.13	0.48
12:KE:395:LEU:HD21	12:KE:484:ILE:HG13	1.95	0.48
12:KF:327:MET:HB3	12:KF:330:LEU:HB2	1.95	0.48
14:MK:104:LYS:HA	14:MK:107:SER:HB3	1.96	0.48
15:NA:666:ILE:HG23	15:NA:721:PRO:HG2	1.96	0.48
15:NB:1420:TYR:HE2	15:NB:1478:LEU:HD23	1.78	0.48
15:NC:768:GLU:OE1	15:NC:769:GLU:HG2	2.13	0.48
16:OB:198:ASP:HB3	17:PB:290:PHE:CD1	2.49	0.48
1:AD:60:THR:HG22	1:AD:62:ASP:H	1.78	0.48
1:AD:747:MET:HE1	1:AD:784:PHE:HE1	1.79	0.48
1:AE:1025:ARG:HG2	1:AE:1025:ARG:HH11	1.78	0.48
1:AH:745:GLN:NE2	7:GG:916:HIS:HB2	2.29	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:908:ARG:HH12	13:LI:497:LEU:HD12	1.78	0.48
3:CG:1168:ARG:HH11	3:CG:4483:PRO:HD2	1.79	0.48
3:CJ:1229:HIS:HB2	3:CJ:4463:LEU:HB3	1.96	0.48
3:CL:1171:LEU:HD11	3:CL:1258:PRO:HD3	1.96	0.48
4:DB:312:ASN:HD21	4:DB:315:LEU:HD23	1.77	0.48
4:DC:21:ASP:HB3	14:MI:277:VAL:HG13	1.94	0.48
5:EB:3306:ILE:O	5:EB:3310:THR:HG23	2.14	0.48
6:FA:1647:LEU:HD22	6:FA:1797:VAL:HG23	1.96	0.48
6:FD:1216:TRP:CZ2	6:FD:1272:VAL:HG22	2.49	0.48
6:FD:1289:HIS:O	6:FD:1290:ILE:C	2.57	0.48
6:FE:983:LEU:HA	12:KB:726:ASP:CG	2.39	0.48
6:FF:1182:ALA:CB	6:FF:1429:LEU:HB2	2.38	0.48
6:FF:1393:LEU:O	6:FF:1394:ARG:C	2.57	0.48
8:GB:18:VAL:HG13	8:GB:520:PHE:HA	1.96	0.48
8:GD:345:LEU:HD23	8:GD:376:GLU:HA	1.96	0.48
7:GG:544:PRO:HD3	9:HA:596:TYR:HA	1.96	0.48
8:GH:42:ASP:HB3	8:GH:470:LYS:HZ1	1.78	0.48
8:GH:698:LEU:HA	8:GH:701:LEU:HB3	1.96	0.48
7:GI:450:LYS:HG3	7:GI:635:THR:HG21	1.95	0.48
7:GI:636:VAL:HG11	7:GI:678:LEU:HD21	1.94	0.48
8:GL:398:VAL:HA	8:GL:719:VAL:HG13	1.94	0.48
10:IC:1294:ILE:HD12	10:IC:1358:LEU:HD11	1.96	0.48
11:JB:160:LEU:HD22	11:JB:171:LYS:HD2	1.96	0.48
11:JB:440:PRO:HB3	11:JB:1474:TRP:CE2	2.48	0.48
11:JB:913:LEU:HD21	11:JB:950:LEU:HD13	1.95	0.48
11:JC:157:GLU:HB3	11:JC:172:LEU:HD11	1.96	0.48
11:JC:190:TRP:HB3	11:JC:195:LEU:HD21	1.94	0.48
11:JC:973:MET:HB2	11:JC:1118:ALA:HB2	1.95	0.48
11:JC:1474:TRP:HA	11:JC:1477:TRP:HB2	1.96	0.48
11:JC:2069:GLU:HA	11:JC:2072:GLN:HB3	1.96	0.48
12:KC:313:PHE:HA	12:KC:316:VAL:HG12	1.94	0.48
12:KG:403:ASP:HB3	12:KG:541:TYR:CZ	2.48	0.48
13:LE:532:LEU:HD21	13:LF:530:VAL:HG23	1.95	0.48
15:NB:682:ARG:HH22	15:NB:1172:LEU:HG	1.78	0.48
15:NC:1488:ARG:HH12	15:NC:1491:PRO:HG2	1.78	0.48
15:ND:931:TRP:CD1	15:ND:934:LEU:HB2	2.48	0.48
15:ND:1514:TRP:HA	15:ND:1517:VAL:HG12	1.96	0.48
2:AB:209:SER:HB3	2:AB:259:VAL:HA	1.95	0.48
2:AG:492:MET:HE1	1:AH:354:ARG:HE	1.79	0.48
1:AI:181:THR:HB	1:AI:215:GLN:HE22	1.78	0.48
1:AI:238:CYS:HB3	1:AI:242:GLU:H	1.78	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:259:VAL:HB	2:AJ:297:VAL:HB	1.95	0.48
1:AL:804:LEU:HD22	1:AL:837:CYS:HB2	1.94	0.48
4:DA:384:ILE:HG21	13:LA:457:GLN:HE22	1.78	0.48
6:FD:1293:THR:O	6:FD:1294:LEU:C	2.57	0.48
6:FE:1393:LEU:HD12	6:FE:1393:LEU:HA	1.78	0.48
8:GB:15:SER:HG	8:GB:16:TRP:CD1	2.32	0.48
8:GB:586:SER:HB3	14:ME:320:ARG:HH12	1.78	0.48
7:GC:201:GLY:HA3	7:GC:717:LEU:HD11	1.95	0.48
7:GG:663:THR:HG23	7:GG:668:GLY:HA2	1.96	0.48
7:GI:273:LYS:HE2	7:GI:279:ARG:HH21	1.79	0.48
7:GK:663:THR:HG23	7:GK:668:GLY:HA2	1.95	0.48
9:HB:777:TYR:N	13:LE:521:ASN:ND2	2.61	0.48
10:IA:782:GLN:HA	10:IA:785:LEU:HD13	1.96	0.48
10:IB:740:ARG:HD3	10:IB:771:LEU:HB3	1.96	0.48
10:IB:864:GLN:HG3	10:IB:1240:PRO:HB2	1.96	0.48
10:IC:438:ARG:HH22	10:IC:448:LEU:HB3	1.78	0.48
11:JA:194:VAL:HG23	11:JA:197:ARG:HH11	1.78	0.48
12:KA:671:LEU:HD21	12:KA:725:ILE:HG22	1.95	0.48
12:KB:206:CYS:HA	12:KB:243:HIS:HA	1.96	0.48
12:KB:526:TRP:CD1	12:KB:706:ILE:HG12	2.49	0.48
12:KF:263:ALA:HA	12:KF:266:ARG:HG2	1.96	0.48
13:LA:481:GLU:HG3	13:LB:482:LEU:HD11	1.96	0.48
16:OA:190:LEU:HB3	16:OA:241:ALA:HB1	1.96	0.48
16:OB:1089:LEU:HB3	16:OB:1092:ARG:HH21	1.79	0.48
1:AA:715:LEU:HB3	13:LK:364:ASN:ND2	2.29	0.47
2:AC:49:HIS:HE2	2:AC:51:ALA:HB3	1.79	0.47
1:AE:49:GLN:HG2	2:AF:520:ARG:NH2	2.29	0.47
1:AE:757:ILE:HD11	1:AE:779:PRO:HB2	1.96	0.47
1:AI:289:SER:N	17:PB:271:ASN:HD22	2.12	0.47
1:AI:1004:VAL:HG13	1:AI:1006:ARG:HH22	1.79	0.47
2:AJ:113:LEU:HD22	2:AJ:208:GLU:HG2	1.96	0.47
2:AJ:314:ALA:HB3	2:AJ:337:HIS:HD2	1.78	0.47
2:AK:494:TRP:HZ2	1:AL:57:SER:HA	1.79	0.47
1:AL:298:ILE:HG22	1:AL:332:THR:HG21	1.95	0.47
3:CJ:1123:LEU:HG	10:IB:811:GLN:HG3	1.95	0.47
4:DD:60:ILE:HG21	4:DD:81:GLY:HA2	1.96	0.47
5:EB:3710:LEU:HD12	5:EB:3717:ILE:HD12	1.97	0.47
5:EB:4332:LEU:HD13	5:EB:4336:VAL:HG11	1.96	0.47
6:FC:2015:LYS:HE2	6:FC:2015:LYS:HB2	1.42	0.47
6:FC:2101:LEU:O	6:FC:2104:GLN:HG3	2.14	0.47
6:FD:895:ILE:HG12	7:GC:876:MET:HE2	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1231:ARG:HE	6:FE:1231:ARG:HB3	1.50	0.47
7:GA:180:ARG:HD3	7:GA:829:VAL:HG21	1.95	0.47
7:GC:406:ALA:HA	7:GC:409:ARG:HB2	1.96	0.47
7:GI:645:LEU:HG	7:GI:717:LEU:HD12	1.95	0.47
8:GL:432:LYS:HB2	8:GL:451:SER:HB3	1.96	0.47
9:HB:674:VAL:HG22	9:HB:712:ILE:HG23	1.95	0.47
9:HB:674:VAL:HG11	9:HB:695:VAL:HG21	1.94	0.47
10:IC:1113:ILE:HD12	10:IC:1119:VAL:HG22	1.96	0.47
11:JB:2078:LYS:HB2	11:JB:2083:ILE:HD13	1.96	0.47
11:JC:1306:ILE:HA	11:JC:1309:LEU:HB2	1.95	0.47
12:KB:365:GLU:HG2	12:KB:368:ARG:HH12	1.79	0.47
12:KE:335:LEU:HD23	12:KE:338:LEU:HD21	1.94	0.47
15:NC:609:GLN:HG3	15:NC:1192:SER:HB3	1.95	0.47
1:AA:289:SER:N	17:PA:271:ASN:HD22	2.12	0.47
2:AG:379:HIS:HB3	2:AG:382:ALA:HB2	1.96	0.47
1:AI:310:CYS:H	1:AI:313:CYS:HB2	1.78	0.47
1:AI:841:LEU:HA	1:AI:845:PHE:HD2	1.79	0.47
1:AL:157:LEU:HB2	1:AL:180:PHE:CD2	2.49	0.47
1:AL:908:ARG:HH12	13:LE:497:LEU:HD12	1.78	0.47
3:BB:812:MET:HG3	3:BB:814:VAL:HG22	1.95	0.47
3:CB:781:LEU:HD22	3:CB:833:TYR:HD2	1.79	0.47
3:CE:1263:SER:HB2	3:CE:4458:VAL:HB	1.94	0.47
3:CF:4479:LEU:HD11	3:CF:4482:LEU:HD22	1.96	0.47
4:DA:10:GLU:HA	4:DA:13:VAL:HG12	1.96	0.47
4:DB:130:ARG:HD3	4:DB:134:LEU:HG	1.96	0.47
6:FC:1850:GLN:HA	6:FC:1923:PHE:HE1	1.79	0.47
6:FD:814:THR:O	6:FD:815:SER:C	2.57	0.47
6:FE:834:VAL:O	6:FE:835:SER:C	2.56	0.47
6:FE:863:ILE:HA	6:FE:866:PHE:CE2	2.49	0.47
6:FE:1213:VAL:HG11	6:FE:1226:LEU:HA	1.95	0.47
6:FE:1222:CYS:O	6:FE:1224:ALA:N	2.47	0.47
6:FF:962:PHE:HE2	6:FF:965:TRP:HB2	1.79	0.47
6:FF:1244:LEU:HD13	6:FF:1257:ASP:HB2	1.96	0.47
6:FF:1300:LEU:HB3	6:FF:1430:PHE:CE2	2.49	0.47
7:GC:662:VAL:HG21	7:GC:672:VAL:HA	1.95	0.47
7:GI:677:ALA:HB1	7:GI:689:ILE:HD11	1.96	0.47
7:GI:823:ARG:HG2	7:GI:827:LEU:HD11	1.96	0.47
7:GI:824:LEU:HD21	7:GI:835:TYR:HD1	1.79	0.47
7:GK:545:GLY:O	9:HC:497:ALA:HB2	2.13	0.47
9:HA:487:VAL:HG12	9:HA:505:ILE:HG12	1.96	0.47
11:JA:1013:ASP:HA	11:JA:1016:LEU:HB2	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:1571:ARG:NH2	15:NA:346:SER:HB2	2.29	0.47
12:KE:370:LEU:HD22	12:KE:377:LEU:HD13	1.96	0.47
13:LE:413:GLU:HA	13:LE:416:ARG:HB2	1.96	0.47
14:MG:111:ALA:HA	14:MG:114:ARG:HB2	1.95	0.47
15:NA:1506:ARG:HA	15:NA:1509:ARG:HB3	1.96	0.47
15:NC:555:PHE:HA	15:NC:559:PHE:HD2	1.79	0.47
15:NC:582:LEU:HG	15:NC:585:ARG:HH21	1.79	0.47
15:NC:735:HIS:CD2	15:NC:768:GLU:HG2	2.49	0.47
15:ND:1529:CYS:HA	15:ND:1532:ARG:HG2	1.96	0.47
16:OB:190:LEU:HD11	16:OB:234:ALA:HB1	1.95	0.47
1:AA:799:THR:HB	1:AA:1000:PHE:HE2	1.79	0.47
2:AB:421:HIS:CE1	2:AB:423:VAL:HG12	2.49	0.47
1:AD:830:THR:HG23	1:AD:833:ALA:H	1.79	0.47
1:AE:237:VAL:HG12	17:PC:247:LEU:HD21	1.95	0.47
1:AE:367:GLN:HE22	1:AE:371:LEU:HD22	1.79	0.47
1:AE:668:ALA:HB1	1:AE:1032:PHE:HZ	1.79	0.47
1:AE:683:ASN:HD21	1:AE:1008:ALA:HB1	1.80	0.47
1:AI:246:ALA:HA	1:AI:258:CYS:SG	2.54	0.47
3:CE:1172:PRO:HA	3:CE:4503:ASP:HB3	1.97	0.47
3:CG:1181:ARG:CZ	10:IC:452:LEU:HB2	2.45	0.47
4:DB:32:SER:HB2	4:DB:122:ILE:HA	1.96	0.47
5:EA:4407:ASP:O	5:EA:4409:GLU:N	2.47	0.47
5:EC:3763:ARG:HB2	5:EC:3764:LYS:NZ	2.29	0.47
5:EC:4733:GLU:HA	5:EC:4736:ILE:HG12	1.97	0.47
6:FE:1283:TYR:CD1	6:FE:1293:THR:HB	2.49	0.47
7:GC:341:PRO:HD3	7:GC:597:THR:HA	1.96	0.47
8:GD:261:GLU:HA	8:GD:263:ARG:NH1	2.30	0.47
8:GF:46:LEU:HD11	8:GF:110:GLU:HB2	1.96	0.47
7:GG:738:LEU:HD22	7:GG:797:ILE:HD12	1.96	0.47
8:GH:604:PHE:HE1	8:GH:622:LEU:HD13	1.79	0.47
9:HA:763:GLN:HG2	9:HA:764:LYS:H	1.78	0.47
10:IB:506:GLN:HB3	10:IB:594:PRO:HD2	1.95	0.47
11:JA:520:VAL:HA	11:JA:523:ASN:HB2	1.96	0.47
11:JA:885:TYR:HD1	11:JA:1413:PRO:HB3	1.78	0.47
11:JB:1039:VAL:HG21	11:JB:1059:ARG:HH12	1.79	0.47
11:JB:2022:VAL:HG13	11:JB:2055:TRP:HH2	1.79	0.47
11:JB:2073:HIS:HB2	11:JB:2248:ILE:HD12	1.95	0.47
12:KA:658:SER:HB2	12:KA:665:HIS:HB2	1.97	0.47
15:NB:1017:GLN:HE22	15:NB:1098:LEU:HB3	1.78	0.47
15:NC:891:TRP:HD1	15:NC:1151:ASN:HA	1.79	0.47
15:ND:614:LYS:HB3	15:ND:678:LEU:HD22	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:ND:707:GLU:HG2	15:ND:883:LEU:HD11	1.95	0.47
2:AC:361:GLU:HB2	5:EB:4406:MET:SD	2.55	0.47
1:AH:716:HIS:CG	13:LI:493:GLN:HE22	2.32	0.47
1:AH:878:ARG:HD3	1:AH:881:LEU:HD23	1.95	0.47
3:BB:791:THR:HG22	3:BB:812:MET:H	1.79	0.47
4:DA:297:ARG:HA	4:DA:300:GLN:HB2	1.97	0.47
4:DC:245:LEU:HD12	4:DC:248:ARG:HD2	1.96	0.47
5:EA:3764:LYS:HG3	5:EA:3765:VAL:HG13	1.95	0.47
5:EA:4443:MET:HE1	17:PB:143:ILE:HD13	1.97	0.47
5:EC:3642:PRO:HD3	5:EC:3673:LEU:HD23	1.96	0.47
6:FA:2062:LEU:O	6:FA:2063:GLN:C	2.54	0.47
6:FC:1976:LYS:HB2	6:FC:1976:LYS:HE2	1.70	0.47
6:FD:912:ILE:HG21	6:FD:1425:PRO:O	2.14	0.47
6:FD:922:LEU:O	6:FD:925:GLU:HB2	2.14	0.47
6:FD:1097:SER:O	6:FD:1101:ALA:N	2.47	0.47
6:FD:1285:CYS:O	6:FD:1286:LEU:C	2.57	0.47
6:FE:1008:ARG:O	6:FE:1009:VAL:C	2.57	0.47
7:GA:184:ALA:HB3	7:GA:708:SER:HB2	1.96	0.47
7:GC:309:LEU:HD23	7:GC:309:LEU:H	1.78	0.47
7:GC:952:ARG:HA	7:GC:952:ARG:HD3	1.75	0.47
7:GE:518:LEU:HD12	7:GE:520:ILE:HD11	1.96	0.47
7:GG:464:LEU:HB3	7:GG:502:TYR:CE1	2.47	0.47
9:HA:561:ASN:HB2	9:HA:564:ARG:HB2	1.97	0.47
9:HB:644:PHE:HD2	9:HB:726:PRO:HB2	1.78	0.47
9:HD:804:THR:O	9:HD:805:THR:C	2.56	0.47
10:IB:800:ILE:HD12	16:OB:1062:ARG:HG2	1.97	0.47
10:IB:1222:VAL:HG13	10:IB:1223:LEU:HD12	1.96	0.47
11:JA:1689:LEU:HB3	11:JA:1698:PHE:HB3	1.96	0.47
11:JB:1501:LEU:HB3	15:NB:440:LEU:HD11	1.96	0.47
11:JC:1374:LEU:HG	11:JC:1378:MET:HE1	1.96	0.47
11:JC:1584:LYS:HA	11:JC:1588:GLU:HA	1.95	0.47
11:JC:1598:LEU:HD13	11:JC:1621:ALA:HA	1.97	0.47
12:KA:365:GLU:HG3	12:KA:368:ARG:HH12	1.79	0.47
12:KC:206:CYS:H	12:KC:244:SER:HB3	1.80	0.47
15:NC:779:VAL:HG12	15:NC:783:GLN:HE22	1.79	0.47
15:NC:1537:LYS:HA	19:RA:114:GLU:HG2	1.96	0.47
16:OB:7:ARG:HD2	16:OB:12:GLU:HB2	1.97	0.47
19:RD:20:PRO:HB2	19:RD:22:ARG:HG2	1.97	0.47
3:CA:691:LEU:HD22	3:CA:710:ILE:HD13	1.97	0.47
4:DF:168:SER:HA	4:DF:171:ASP:HB3	1.94	0.47
5:EA:3731:VAL:HG21	5:EA:4249:LEU:HB2	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EA:4011:VAL:HB	5:EA:4166:SER:HB2	1.96	0.47
5:EB:3609:LEU:HD22	5:EB:3612:LEU:HD13	1.94	0.47
6:FA:1871:PRO:HD2	6:FA:1874:PHE:CE2	2.49	0.47
6:FA:2030:ILE:HD13	6:FA:2030:ILE:HA	1.69	0.47
6:FE:922:LEU:O	6:FE:925:GLU:HB2	2.15	0.47
6:FF:854:TRP:CD1	6:FF:854:TRP:H	2.32	0.47
6:FF:1186:TRP:HE3	6:FF:1267:GLN:HB2	1.79	0.47
7:GC:636:VAL:HG21	7:GC:678:LEU:HD21	1.96	0.47
7:GE:201:GLY:HA3	7:GE:717:LEU:HD21	1.95	0.47
7:GE:709:MET:HG2	7:GE:714:VAL:HG21	1.96	0.47
8:GJ:354:GLN:HA	8:GJ:357:ARG:HG2	1.95	0.47
8:GL:300:ARG:HD2	8:GL:419:PHE:HE1	1.79	0.47
9:HA:771:PRO:HG3	9:HA:819:TYR:CE1	2.49	0.47
10:IA:1326:THR:HG23	10:IA:1328:LYS:H	1.79	0.47
10:IC:398:ARG:H	10:IC:398:ARG:HG2	1.51	0.47
11:JA:1372:PRO:HB2	11:JA:1390:ALA:HB1	1.96	0.47
11:JC:62:ALA:HB3	11:JC:124:VAL:HB	1.96	0.47
12:KE:656:ARG:HB3	12:KE:667:SER:HB3	1.95	0.47
15:NA:627:ASP:HB2	15:NA:904:ARG:HB2	1.96	0.47
15:NC:891:TRP:HA	15:NC:1152:GLU:O	2.15	0.47
15:ND:1454:ILE:HD12	15:ND:1478:LEU:HD11	1.96	0.47
1:AA:768:ILE:HA	1:AA:776:LEU:HD21	1.95	0.47
2:AB:113:LEU:HD23	11:JA:1649:LEU:HD21	1.96	0.47
1:AI:650:LEU:HD22	1:AI:1013:THR:HG23	1.97	0.47
3:CB:956:LEU:HB2	3:CB:978:VAL:HG21	1.97	0.47
3:CL:1121:ARG:HH12	3:CL:1131:LEU:HD13	1.79	0.47
4:DB:249:GLY:HA3	4:DB:287:ALA:HB2	1.97	0.47
4:DC:277:ARG:HD2	4:DC:278:ALA:H	1.79	0.47
6:FC:2079:MET:HE3	6:FC:2083:GLN:HG2	1.95	0.47
6:FE:814:THR:OG1	6:FE:815:SER:N	2.46	0.47
6:FF:913:LEU:HD12	6:FF:913:LEU:HA	1.70	0.47
6:FF:1098:VAL:C	6:FF:1101:ALA:H	2.23	0.47
7:GA:891:LEU:HB3	7:GA:956:ILE:HD12	1.97	0.47
7:GE:583:GLN:HG2	7:GE:584:HIS:ND1	2.30	0.47
8:GF:25:GLU:HA	8:GF:28:LYS:HG2	1.97	0.47
8:GL:401:ASP:HB2	8:GL:719:VAL:HG11	1.96	0.47
10:IC:881:VAL:HA	16:OC:1045:LEU:HD13	1.96	0.47
10:IC:889:VAL:HA	10:IC:892:ILE:HB	1.97	0.47
11:JB:1856:ARG:NH1	11:JB:1988:SER:H	2.13	0.47
11:JC:2277:GLN:NE2	11:JC:2281:ARG:HH12	2.12	0.47
12:KA:524:PHE:H	12:KA:525:PRO:CD	2.27	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LA:468:HIS:HA	13:LA:471:THR:HG22	1.97	0.47
14:MA:292:ALA:HA	14:MA:295:GLU:HG2	1.97	0.47
15:NB:818:ILE:HB	15:NB:842:THR:HA	1.96	0.47
15:ND:806:ASP:HA	15:ND:809:GLU:HG2	1.96	0.47
15:ND:1120:VAL:HA	15:ND:1123:ALA:HB2	1.96	0.47
19:RD:30:LEU:HD13	19:RD:33:ILE:HD12	1.97	0.47
1:AA:56:LEU:HD22	2:AB:521:LEU:HD21	1.97	0.47
1:AA:107:LEU:HD13	1:AA:221:VAL:HG11	1.96	0.47
1:AA:816:ARG:HH22	1:AA:828:HIS:H	1.61	0.47
2:AB:52:THR:HG22	2:AB:54:HIS:H	1.79	0.47
1:AE:1021:LEU:HB3	14:ML:85:PRO:HG3	1.97	0.47
1:AH:38:VAL:HG11	11:JA:2031:MET:HE1	1.97	0.47
1:AH:603:THR:HB	1:AH:608:LEU:HD11	1.97	0.47
1:AI:787:ARG:HG3	1:AI:790:ARG:HH21	1.78	0.47
1:AL:703:LEU:HA	1:AL:706:VAL:HG12	1.96	0.47
3:BB:988:VAL:HG13	3:BB:989:THR:HG23	1.95	0.47
3:CA:956:LEU:HB2	3:CA:978:VAL:HG21	1.97	0.47
3:CF:1123:LEU:HD11	10:IB:997:PRO:HA	1.95	0.47
3:CJ:4452:HIS:CE1	3:CJ:4499:PRO:HG3	2.50	0.47
4:DB:385:LYS:NZ	13:LF:462:GLN:HA	2.30	0.47
4:DC:300:GLN:NE2	4:DC:354:TRP:HA	2.28	0.47
4:DE:256:LEU:HD11	4:DE:268:ARG:HG2	1.96	0.47
5:EA:3274:GLN:HE22	5:EA:3492:LEU:HB3	1.79	0.47
5:EA:4098:PRO:HG3	9:HB:797:TYR:CE2	2.49	0.47
5:EB:4405:ILE:HD13	5:EB:4431:ARG:HD3	1.96	0.47
6:FA:2061:ARG:NH1	6:FA:2065:THR:HB	2.30	0.47
6:FB:2038:LEU:HD13	6:FB:2038:LEU:HA	1.76	0.47
6:FC:1978:LEU:HD11	9:HB:817:VAL:CG2	2.42	0.47
6:FC:2037:LEU:HD13	6:FC:2037:LEU:HA	1.73	0.47
6:FC:2099:ILE:HA	6:FC:2102:PHE:CD2	2.50	0.47
6:FD:818:VAL:O	6:FD:821:ARG:N	2.46	0.47
6:FD:834:VAL:O	6:FD:840:ALA:HB3	2.15	0.47
6:FD:1285:CYS:HB2	6:FD:1289:HIS:H	1.80	0.47
6:FE:963:THR:O	6:FE:964:LEU:C	2.57	0.47
6:FE:1067:ALA:HB1	6:FE:1111:GLU:OE2	2.14	0.47
6:FE:1393:LEU:HD22	6:FE:1417:ILE:HB	1.96	0.47
6:FF:980:SER:HA	12:KC:343:ASN:HB2	1.96	0.47
8:GB:777:LEU:HD23	8:GB:781:MET:HE2	1.96	0.47
7:GC:252:SER:HB2	7:GC:259:VAL:HG12	1.97	0.47
7:GE:746:LEU:HA	7:GE:749:LEU:HD12	1.97	0.47
8:GF:56:CYS:SG	8:GF:61:CYS:HB2	2.55	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GG:422:LEU:HD11	8:GJ:192:VAL:HG11	1.95	0.47
7:GG:790:GLY:HA2	7:GG:793:VAL:HG12	1.96	0.47
8:GH:439:PRO:HD2	8:GH:474:VAL:HG22	1.96	0.47
7:GI:357:VAL:HG13	7:GI:371:LEU:HD11	1.96	0.47
8:GJ:294:TRP:CE3	8:GJ:297:LEU:HD23	2.50	0.47
8:GJ:314:GLY:HA2	8:GJ:344:ALA:HA	1.96	0.47
7:GK:372:GLY:H	7:GK:400:ASP:HB3	1.79	0.47
8:GL:661:PRO:HB2	8:GL:680:LEU:HB2	1.96	0.47
9:HA:758:ALA:HA	9:HA:761:CYS:HB2	1.97	0.47
9:HA:766:SER:O	9:HA:767:GLN:C	2.58	0.47
9:HB:758:ALA:O	9:HB:761:CYS:HB2	2.15	0.47
9:HB:813:THR:OG1	9:HB:814:LYS:N	2.47	0.47
9:HD:765:TRP:O	9:HD:766:SER:C	2.58	0.47
9:HD:807:GLU:OE2	9:HD:807:GLU:N	2.44	0.47
10:IA:561:ARG:HH22	10:IA:853:GLY:HA2	1.79	0.47
10:IA:893:PHE:HZ	10:IA:907:ASP:HA	1.80	0.47
10:IA:1143:MET:HE1	10:IA:1207:LYS:HE2	1.97	0.47
10:IB:351:LEU:HD21	10:IB:355:GLN:HB2	1.96	0.47
10:IC:346:CYS:HB3	10:IC:532:VAL:HG12	1.97	0.47
11:JB:843:LEU:HD21	11:JB:916:GLU:HB3	1.97	0.47
11:JC:1667:THR:HG22	11:JC:1671:MET:HE3	1.97	0.47
12:KA:327:MET:HB3	12:KA:330:LEU:HB3	1.96	0.47
12:KE:534:VAL:HG13	12:KE:536:ARG:HH12	1.79	0.47
12:KF:212:LEU:HD12	12:KF:236:LYS:HB2	1.97	0.47
12:KG:669:GLN:HB3	12:KG:677:ARG:HH11	1.79	0.47
13:LB:486:ARG:HH12	13:LB:490:MET:HE2	1.79	0.47
15:NA:564:ARG:HH12	15:NA:619:TYR:HB2	1.80	0.47
15:NA:943:GLU:HA	15:NA:946:LEU:HB2	1.97	0.47
15:NA:1531:GLN:HA	15:NA:1534:GLU:HG3	1.95	0.47
15:NB:627:ASP:HB2	15:NB:904:ARG:HB2	1.96	0.47
15:NC:572:ILE:HG23	15:NC:581:LEU:HD22	1.96	0.47
15:NC:1479:GLU:HA	15:NC:1482:ARG:HG2	1.97	0.47
15:ND:733:VAL:HG21	15:ND:747:LEU:HD13	1.97	0.47
15:ND:1125:TYR:HE1	15:ND:1156:LEU:HD13	1.79	0.47
20:SC:100:PHE:HE1	20:SC:138:ASN:HB3	1.79	0.47
1:AA:393:LEU:HD11	1:AA:475:LEU:HD13	1.97	0.47
2:AB:415:HIS:HA	2:AB:418:LYS:HE3	1.96	0.47
2:AC:182:GLU:HA	2:AC:187:ARG:HD2	1.97	0.47
2:AC:190:LEU:HD21	2:AC:195:ASP:HA	1.97	0.47
1:AE:185:ARG:HB3	1:AE:207:LEU:HB2	1.97	0.47
2:AF:44:LEU:HD21	2:AF:47:ALA:HB2	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:830:THR:HG23	1:AH:833:ALA:H	1.80	0.47
1:AL:1025:ARG:O	1:AL:1029:GLU:HG3	2.14	0.47
3:CC:899:PHE:HE1	3:CC:934:ILE:HB	1.79	0.47
3:CL:4486:ILE:HG22	3:CL:4497:ARG:HE	1.77	0.47
4:DA:357:GLU:HA	4:DA:386:VAL:HB	1.96	0.47
4:DF:19:ARG:HD3	4:DF:19:ARG:HA	1.75	0.47
5:EA:3746:LYS:HA	5:EA:3831:LEU:HD13	1.96	0.47
5:EB:4520:LEU:HD11	5:EB:4691:PHE:HE2	1.80	0.47
6:FA:2010:LYS:HE2	6:FA:2010:LYS:HB2	1.44	0.47
6:FC:1636:GLN:HB2	6:FC:1666:VAL:HG13	1.97	0.47
6:FC:1798:VAL:HG21	6:FC:1900:VAL:HG11	1.97	0.47
6:FC:2055:THR:HA	9:HB:837:LEU:HD21	1.97	0.47
6:FD:1297:PRO:C	6:FD:1299:ASN:H	2.23	0.47
7:GC:706:VAL:HG11	7:GC:752:VAL:HG11	1.96	0.47
8:GD:563:ARG:HA	8:GD:566:ILE:HG22	1.97	0.47
7:GE:163:GLN:HA	7:GE:166:LEU:HG	1.97	0.47
7:GE:893:TRP:HE1	7:GE:958:GLN:HB2	1.80	0.47
7:GG:185:ARG:HB2	7:GG:705:ILE:HD13	1.97	0.47
7:GG:262:THR:HG23	7:GG:266:TYR:HD2	1.79	0.47
8:GH:238:ARG:HH11	8:GH:240:ALA:HB3	1.79	0.47
7:GI:311:LEU:HD11	7:GI:436:ALA:HB1	1.96	0.47
8:GL:362:VAL:HG11	8:GL:380:MET:HG2	1.97	0.47
10:IA:226:ARG:HG2	10:IA:226:ARG:HH11	1.80	0.47
10:IB:841:MET:HB3	10:IB:866:LEU:HD13	1.96	0.47
11:JC:1745:PHE:HB2	11:JC:1795:LEU:HD21	1.97	0.47
11:JC:1786:LEU:HD12	11:JC:1812:VAL:HG13	1.97	0.47
12:KC:304:ARG:NH2	12:KC:308:LEU:HD23	2.29	0.47
12:KE:488:SER:C	12:KE:489:MET:HE2	2.39	0.47
13:LI:506:GLN:HE22	13:LJ:507:ARG:HE	1.63	0.47
15:NA:983:ILE:HG12	15:NA:989:ILE:HD12	1.97	0.47
15:NB:717:TYR:HE1	15:NB:927:LEU:HD22	1.79	0.47
15:NC:947:ASN:HA	15:NC:950:VAL:HB	1.97	0.47
15:ND:468:ARG:NH1	15:ND:469:PHE:HB3	2.30	0.47
2:AB:284:LEU:HD22	5:EA:4533:LEU:HD11	1.96	0.47
2:AC:114:MET:HE2	16:OA:135:VAL:HG21	1.96	0.47
1:AE:131:ARG:N	1:AE:205:ARG:HH12	2.12	0.47
1:AE:132:PRO:HA	1:AE:133:PRO:HD3	1.84	0.47
3:CI:1181:ARG:HB2	3:CI:4512:SER:HA	1.97	0.47
5:EA:3859:PRO:HA	5:EA:3862:LEU:HD13	1.96	0.47
5:EB:4539:MET:HE3	5:EB:4688:LEU:HD21	1.97	0.47
6:FA:1699:PRO:HA	6:FA:1722:PHE:HB3	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FA:1898:ILE:HB	6:FA:1912:PHE:HB2	1.96	0.47
6:FD:1030:ILE:HG13	6:FD:1116:LEU:HB2	1.96	0.47
6:FE:971:SER:HA	6:FE:1022:THR:HA	1.96	0.47
6:FF:864:LEU:O	6:FF:865:GLY:C	2.57	0.47
6:FF:1075:VAL:HG13	6:FF:1105:ARG:HB2	1.97	0.47
8:GD:326:ARG:HH21	8:GD:373:GLY:HA2	1.79	0.47
8:GD:419:PHE:HB2	8:GD:503:LEU:HB3	1.97	0.47
7:GI:633:LEU:HD23	7:GI:636:VAL:HB	1.96	0.47
7:GI:903:LEU:HD11	7:GI:912:LEU:HD13	1.97	0.47
7:GI:910:HIS:HE1	12:KC:340:ALA:HA	1.80	0.47
8:GJ:437:ILE:HB	8:GJ:475:ALA:HB3	1.97	0.47
7:GK:534:PRO:HA	7:GK:535:PRO:HD3	1.64	0.47
8:GL:46:LEU:HD11	8:GL:110:GLU:HG2	1.97	0.47
8:GL:638:LEU:HD21	8:GL:665:LEU:HD13	1.97	0.47
11:JA:1079:TYR:HB3	11:JA:1428:LEU:HD12	1.97	0.47
11:JB:107:PRO:HB3	11:JB:186:SER:HA	1.97	0.47
11:JC:1051:LEU:HA	11:JC:1055:GLN:HB2	1.96	0.47
12:KC:532:PHE:HB2	12:KC:547:ARG:HA	1.97	0.47
12:KF:329:GLN:HA	12:KF:332:LYS:HE3	1.95	0.47
13:LC:336:VAL:HG13	13:LC:340:LYS:HE2	1.96	0.47
13:LF:425:LYS:HA	13:LF:428:VAL:HG12	1.95	0.47
15:NA:947:ASN:HA	15:NA:950:VAL:HB	1.95	0.47
15:NB:644:MET:HE3	15:NB:648:ASN:HD21	1.80	0.47
15:NB:794:GLU:HA	15:NB:797:ARG:HB2	1.96	0.47
16:OA:215:ALA:HA	16:OA:218:LYS:HE3	1.97	0.47
1:AA:497:PRO:HG3	6:FA:1789:LEU:HD13	1.97	0.47
1:AE:421:MET:HE1	1:AE:451:ILE:HG21	1.96	0.47
2:AF:177:VAL:HG21	2:AF:197:ALA:HB1	1.97	0.47
1:AL:730:SER:HB3	1:AL:852:ARG:HD2	1.96	0.47
1:AL:793:LEU:HB3	1:AL:801:ARG:HG3	1.96	0.47
3:CA:870:LEU:HD22	17:PA:311:PHE:HE2	1.80	0.47
3:CB:784:LEU:HD22	3:CB:826:LEU:HD13	1.97	0.47
3:CG:4486:ILE:HG22	3:CG:4497:ARG:HA	1.97	0.47
4:DA:385:LYS:HZ1	13:LB:462:GLN:HG3	1.79	0.47
4:DE:137:LYS:HG3	4:DE:138:LYS:H	1.80	0.47
4:DE:343:LEU:HB3	4:DE:374:VAL:HG21	1.97	0.47
6:FA:2061:ARG:HH11	6:FA:2065:THR:HB	1.80	0.47
6:FB:2098:TYR:CG	9:HD:879:ILE:HG12	2.50	0.47
6:FE:965:TRP:CD1	6:FE:965:TRP:H	2.33	0.47
6:FE:1441:ILE:O	6:FE:1442:GLU:C	2.58	0.47
6:FE:1441:ILE:C	6:FE:1442:GLU:HG3	2.39	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:804:LEU:HD13	6:FF:804:LEU:HA	1.74	0.47
6:FF:814:THR:O	6:FF:815:SER:C	2.57	0.47
6:FF:1009:VAL:CG2	6:FF:1219:GLU:HA	2.44	0.47
7:GI:662:VAL:HG21	7:GI:672:VAL:HA	1.96	0.47
7:GK:341:PRO:HD3	7:GK:597:THR:HA	1.96	0.47
8:GL:294:TRP:CD1	8:GL:299:ALA:HB2	2.49	0.47
10:IA:581:PHE:CE2	10:IA:759:PHE:HA	2.50	0.47
10:IC:486:PRO:HA	10:IC:489:TYR:CZ	2.50	0.47
11:JA:1677:LEU:HD21	11:JA:1833:ASP:HB2	1.97	0.47
11:JB:1873:ARG:HG3	11:JB:1874:ARG:HG2	1.96	0.47
11:JC:76:CYS:HB3	11:JC:84:PHE:HZ	1.80	0.47
13:LJ:403:SER:HA	13:LJ:406:GLN:HG2	1.96	0.47
15:NA:754:PHE:HB3	15:NA:847:ALA:HB2	1.97	0.47
15:NB:891:TRP:HA	15:NB:1152:GLU:O	2.15	0.47
15:NC:866:LEU:HD22	15:NC:878:ILE:HG12	1.96	0.47
15:ND:627:ASP:HB2	15:ND:904:ARG:HB2	1.97	0.47
2:AB:415:HIS:CB	6:FC:2077:HIS:HB2	2.38	0.46
2:AC:558:ARG:HH11	5:EB:3787:GLU:HB3	1.79	0.46
1:AD:139:ASN:HD21	10:IB:874:ASN:HD21	1.63	0.46
2:AF:208:GLU:OE2	11:JC:1649:LEU:HD11	2.15	0.46
2:AG:428:ARG:HH12	1:AH:419:GLU:HG3	1.79	0.46
1:AH:654:LEU:HG	1:AH:662:LEU:HB2	1.97	0.46
1:AI:446:LEU:HD21	2:AJ:24:ASP:HA	1.97	0.46
2:AK:169:VAL:HG12	2:AK:171:VAL:HG23	1.95	0.46
3:CB:810:PRO:HB2	3:CB:813:ARG:HG3	1.97	0.46
3:CL:4466:ILE:HD11	3:CL:4487:LEU:HB3	1.97	0.46
5:EA:3649:TRP:HZ2	5:EA:3655:GLU:HG3	1.80	0.46
5:EB:4401:PRO:HD2	5:EB:4702:ILE:HG21	1.96	0.46
5:EB:4667:PRO:HA	5:EB:4670:TRP:HB3	1.97	0.46
6:FB:2030:ILE:HD13	6:FB:2030:ILE:HA	1.74	0.46
6:FC:1971:LYS:HG2	6:FC:1972:GLU:N	2.31	0.46
6:FC:2086:ASN:O	6:FC:2087:LEU:C	2.58	0.46
6:FD:1249:ILE:HG13	6:FD:1250:GLU:N	2.27	0.46
6:FE:1103:SER:O	6:FE:1105:ARG:N	2.47	0.46
6:FE:1203:ARG:HB2	11:JC:901:ARG:HH12	1.76	0.46
7:GA:294:ALA:HB1	7:GA:298:TYR:HD2	1.80	0.46
8:GB:200:GLY:HA2	8:GB:281:LEU:HD22	1.96	0.46
7:GE:243:HIS:CE1	7:GE:252:SER:HB3	2.50	0.46
7:GE:984:GLU:HA	7:GE:987:GLN:HB2	1.97	0.46
7:GG:211:ARG:HE	7:GG:212:PRO:HD2	1.79	0.46
7:GI:433:MET:HE3	7:GI:453:LEU:HD21	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GI:727:LEU:HD13	7:GI:821:TRP:HZ3	1.80	0.46
7:GK:518:LEU:HD21	7:GK:562:ILE:HG13	1.96	0.46
10:IB:900:LEU:HD12	10:IB:902:ARG:HH21	1.80	0.46
10:IC:455:LEU:HD21	10:IC:535:ARG:HH12	1.80	0.46
10:IC:882:VAL:HA	16:OC:1044:ARG:HH21	1.81	0.46
11:JB:139:ARG:HG2	11:JB:140:LEU:H	1.80	0.46
11:JC:1431:VAL:HG22	11:JC:1462:ILE:HG23	1.97	0.46
12:KB:359:VAL:HG12	12:KB:362:LEU:H	1.79	0.46
12:KB:622:THR:HG22	12:KB:632:TYR:HB2	1.96	0.46
12:KC:582:ILE:HB	12:KC:653:VAL:HG13	1.98	0.46
13:LD:367:VAL:HA	13:LD:370:MET:HG2	1.97	0.46
14:MI:284:LEU:HG	14:MJ:283:GLN:HE22	1.80	0.46
16:OB:742:PHE:HA	18:QC:89:ARG:NH2	2.30	0.46
20:SC:106:LEU:HD23	20:SC:126:ILE:HG12	1.98	0.46
1:AD:667:LYS:HD3	1:AD:1036:THR:HG21	1.95	0.46
1:AE:107:LEU:HD22	1:AE:145:HIS:CE1	2.50	0.46
2:AF:75:THR:HG23	2:AF:84:LEU:HD21	1.97	0.46
2:AG:332:ARG:HH21	11:JC:2281:ARG:HG3	1.80	0.46
1:AH:157:LEU:HB2	1:AH:180:PHE:CD2	2.51	0.46
2:AK:265:PHE:HZ	2:AK:267:HIS:CE1	2.33	0.46
1:AL:799:THR:HG22	1:AL:998:LEU:HA	1.97	0.46
3:BB:865:LEU:HD12	3:BB:884:LEU:HG	1.97	0.46
3:CJ:1172:PRO:HD3	3:CJ:1202:LEU:HD13	1.98	0.46
4:DA:301:LEU:HD22	4:DA:357:GLU:HG2	1.98	0.46
4:DB:170:ARG:HH12	4:DE:173:PHE:HD2	1.63	0.46
4:DF:100:GLU:HG2	4:DF:103:LEU:HD12	1.95	0.46
4:DF:296:ASN:H	4:DF:299:ARG:HB2	1.79	0.46
5:EB:3532:MET:HG3	5:EB:3535:TYR:HB3	1.98	0.46
5:EB:4443:MET:HE2	17:PA:143:ILE:HD12	1.97	0.46
6:FC:1974:VAL:CG2	6:FC:2036:LEU:HB3	2.45	0.46
6:FC:2070:LEU:HD22	6:FC:2070:LEU:HA	1.73	0.46
6:FD:817:VAL:HG11	6:FD:826:LEU:HD12	1.98	0.46
6:FE:911:SER:C	6:FE:912:ILE:HG23	2.40	0.46
6:FF:926:LEU:H	6:FF:926:LEU:HG	1.56	0.46
6:FF:990:PHE:C	12:KC:313:PHE:CE2	2.93	0.46
7:GA:210:ILE:HD13	7:GA:216:THR:HA	1.96	0.46
7:GC:233:ARG:HE	7:GC:258:TYR:HB2	1.80	0.46
7:GC:606:MET:HB3	7:GC:631:PHE:HB2	1.97	0.46
7:GC:680:TYR:HE1	7:GC:682:ASN:HB3	1.79	0.46
7:GC:758:LEU:HD22	7:GC:787:LEU:HD22	1.95	0.46
8:GF:326:ARG:HB3	8:GF:338:ALA:HB2	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GH:46:LEU:HD13	8:GH:512:ARG:HH12	1.80	0.46
8:GL:667:LEU:HB3	8:GL:674:VAL:HB	1.97	0.46
9:HD:773:ALA:CB	13:LJ:527:VAL:HG13	2.45	0.46
10:IA:889:VAL:HG12	10:IA:893:PHE:HE1	1.80	0.46
10:IA:889:VAL:H	10:IA:911:ARG:NH2	2.14	0.46
11:JC:1679:ALA:HB2	11:JC:1714:CYS:HB2	1.98	0.46
12:KA:596:ILE:HD13	12:KA:657:VAL:HG11	1.97	0.46
12:KB:567:TRP:HZ3	12:KB:569:LEU:HB2	1.80	0.46
13:LE:523:GLU:HG2	13:LH:522:ARG:HD2	1.97	0.46
13:LI:523:GLU:C	13:LI:525:SER:N	2.72	0.46
14:MJ:227:GLN:HA	14:MJ:230:VAL:HG12	1.97	0.46
15:NC:545:VAL:HG22	15:NC:1195:SER:HA	1.97	0.46
15:NC:1545:VAL:HG11	19:RA:139:LEU:HG	1.96	0.46
2:AC:68:LEU:HD13	1:AD:457:ARG:HD3	1.97	0.46
1:AE:728:VAL:HG23	1:AE:734:MET:HE2	1.98	0.46
1:AI:237:VAL:HG23	1:AI:238:CYS:H	1.80	0.46
3:BB:807:LEU:HD23	17:PB:279:ARG:HH22	1.80	0.46
3:CA:765:VAL:HG13	3:CA:833:TYR:HE1	1.81	0.46
6:FE:994:PRO:HB3	12:KB:382:ARG:HD3	1.97	0.46
6:FF:1213:VAL:HG11	6:FF:1226:LEU:HA	1.97	0.46
7:GA:494:LEU:HB3	7:GA:814:THR:HG21	1.98	0.46
7:GE:616:ILE:HG23	7:GE:644:ILE:HG23	1.96	0.46
7:GE:703:GLN:HG3	7:GE:752:VAL:HG13	1.97	0.46
8:GF:283:LEU:HD11	8:GF:303:LEU:HD22	1.97	0.46
8:GF:692:MET:HE1	8:GF:694:GLU:HB2	1.97	0.46
7:GI:220:VAL:HG22	7:GI:283:ALA:HB3	1.98	0.46
7:GK:715:THR:HG21	7:GK:796:PHE:HB3	1.97	0.46
7:GK:916:HIS:HD2	7:GK:917:PRO:HD2	1.80	0.46
8:GL:35:CYS:C	8:GL:36:MET:HE2	2.40	0.46
8:GL:171:ILE:HG22	8:GL:183:LEU:HD21	1.97	0.46
9:HB:783:SER:O	9:HB:784:GLU:C	2.58	0.46
10:IB:348:PRO:HB3	10:IB:364:LEU:HD11	1.97	0.46
11:JB:1803:ARG:NH2	16:OB:4:ARG:HH12	2.13	0.46
11:JC:154:ARG:HG3	11:JC:174:ALA:HB3	1.98	0.46
12:KE:335:LEU:HD13	12:KE:697:ARG:HH22	1.79	0.46
14:MF:294:ALA:HA	14:MF:297:VAL:HG12	1.97	0.46
15:ND:866:LEU:HD23	15:ND:869:PHE:HD2	1.80	0.46
16:OB:1096:MET:HE3	16:OB:1096:MET:HB3	1.82	0.46
19:RA:20:PRO:HB3	19:RA:22:ARG:HD3	1.98	0.46
20:SA:139:TYR:HA	20:SA:142:PHE:HB3	1.97	0.46
1:AA:705:TRP:HZ2	1:AA:1037:PRO:HD2	1.80	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:331:ASN:HD21	1:AH:265:VAL:HG13	1.80	0.46
1:AE:465:MET:HG2	1:AE:469:MET:HG3	1.97	0.46
3:CG:4470:LYS:HB2	3:CG:4486:ILE:HG13	1.97	0.46
4:DD:28:LEU:HD11	4:DD:154:LEU:HD13	1.96	0.46
6:FA:1657:MET:HE1	6:FA:1698:ARG:HD3	1.98	0.46
6:FD:813:GLN:O	6:FD:815:SER:N	2.48	0.46
6:FD:1189:ILE:CD1	6:FD:1233:ILE:HD13	2.45	0.46
6:FF:1191:LYS:HG3	6:FF:1418:GLU:HG3	1.96	0.46
6:FF:1439:LEU:O	6:FF:1440:ASN:HB3	2.15	0.46
7:GG:979:LEU:HB3	9:HA:650:PHE:HB2	1.97	0.46
8:GL:417:MET:HG3	8:GL:469:ASP:HB3	1.98	0.46
9:HA:650:PHE:HE1	13:LL:486:ARG:HH21	1.63	0.46
9:HA:779:PRO:O	9:HA:780:PHE:C	2.58	0.46
10:IB:888:THR:HA	15:NC:566:GLN:NE2	2.29	0.46
11:JC:1790:LEU:HD21	11:JC:1859:GLN:HG3	1.96	0.46
12:KE:207:ASP:HB2	12:KE:281:MET:HG3	1.97	0.46
12:KG:613:PRO:HG3	12:KG:643:TRP:HZ3	1.81	0.46
13:LA:360:LEU:HD22	13:LB:356:LEU:HD22	1.98	0.46
13:LI:523:GLU:O	13:LI:525:SER:N	2.46	0.46
14:MC:93:SER:HA	14:MC:96:ASP:HB3	1.98	0.46
14:ME:253:GLU:HG2	14:ME:254:ILE:HD12	1.97	0.46
15:NC:564:ARG:HA	15:NC:580:PHE:CZ	2.50	0.46
15:NC:1550:MET:HE2	19:RA:29:GLU:HB3	1.96	0.46
16:OB:729:SER:HA	16:OB:732:ASN:HB2	1.96	0.46
1:AA:419:GLU:HB3	16:OA:76:PHE:HD1	1.81	0.46
1:AA:801:ARG:HD2	1:AA:996:SER:HB2	1.98	0.46
2:AC:190:LEU:HD22	2:AC:272:TYR:HD2	1.80	0.46
1:AE:314:ILE:HD12	1:AE:319:HIS:HB3	1.97	0.46
1:AE:1036:THR:HG21	1:AE:1039:LEU:HD23	1.96	0.46
3:BC:754:GLU:HA	17:PC:278:TRP:HH2	1.80	0.46
3:BC:793:ILE:HG21	3:BC:807:LEU:HA	1.98	0.46
3:BC:904:PRO:HG2	3:BC:941:ARG:HG2	1.97	0.46
3:CI:1156:GLU:HA	10:IA:398:ARG:NH2	2.30	0.46
4:DA:159:GLU:HA	4:DA:162:VAL:HG22	1.98	0.46
4:DF:90:LEU:HA	4:DF:93:ILE:HG22	1.98	0.46
5:EB:4143:ARG:HD2	5:EB:4143:ARG:HA	1.72	0.46
6:FA:1817:VAL:HG11	6:FA:1838:VAL:HG11	1.98	0.46
6:FD:803:ARG:CG	6:FD:1118:GLN:NE2	2.69	0.46
6:FD:1078:GLU:O	6:FD:1081:SER:HB3	2.15	0.46
6:FD:1103:SER:OG	6:FD:1104:GLY:N	2.48	0.46
6:FE:832:GLY:HA3	6:FE:844:ALA:HB2	1.95	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GC:570:GLY:HA3	7:GC:633:LEU:HD11	1.98	0.46
7:GE:570:GLY:HA2	7:GE:622:ARG:HB3	1.96	0.46
7:GK:233:ARG:HE	7:GK:258:TYR:HB2	1.81	0.46
7:GK:543:LYS:N	9:HC:596:TYR:HB3	2.30	0.46
8:GL:341:VAL:HG13	8:GL:342:LYS:HD3	1.97	0.46
9:HB:762:HIS:CD2	9:HB:763:GLN:NE2	2.83	0.46
10:IB:455:LEU:HD21	10:IB:535:ARG:HH12	1.80	0.46
11:JA:191:ASP:HB3	11:JA:194:VAL:HG12	1.97	0.46
11:JB:889:ARG:HH21	11:JB:1416:ARG:HH12	1.64	0.46
11:JC:171:LYS:HG2	11:JC:172:LEU:H	1.81	0.46
11:JC:202:LEU:HD23	11:JC:1043:ALA:HB3	1.98	0.46
11:JC:2011:ARG:HH12	11:JC:2290:VAL:HG12	1.81	0.46
12:KA:618:PHE:HD2	12:KA:639:GLY:HA2	1.79	0.46
13:LK:532:LEU:HD23	13:LL:530:VAL:HG23	1.98	0.46
13:LP:392:GLU:HA	13:LP:395:ILE:HG12	1.98	0.46
14:MF:227:GLN:HA	14:MF:230:VAL:HG12	1.98	0.46
15:NA:682:ARG:HD2	15:NA:917:MET:HE1	1.96	0.46
15:NA:1498:ARG:CZ	20:SA:38:ARG:HD2	2.46	0.46
15:NA:1528:SER:HA	15:NA:1531:GLN:HG3	1.96	0.46
15:NB:512:TYR:HA	15:NB:1473:ARG:NH2	2.31	0.46
15:NC:937:MET:HA	15:NC:940:TYR:HB3	1.96	0.46
1:AA:265:VAL:HB	2:AF:331:ASN:HD21	1.81	0.46
1:AA:431:SER:HB2	2:AB:296:ALA:H	1.80	0.46
1:AD:918:VAL:HB	1:AD:982:VAL:HG21	1.97	0.46
1:AD:1030:GLY:HA3	8:GD:84:ARG:HH21	1.79	0.46
2:AG:446:ARG:HD2	2:AG:450:ARG:HH21	1.80	0.46
1:AI:397:LYS:HD2	1:AI:397:LYS:HA	1.77	0.46
3:BA:792:LEU:HD13	3:BA:845:LYS:HG2	1.97	0.46
3:BC:825:SER:HB3	16:OC:291:VAL:HG12	1.96	0.46
3:CE:1263:SER:HA	3:CE:4457:PRO:HB3	1.96	0.46
4:DC:28:LEU:HD13	4:DC:154:LEU:HD11	1.97	0.46
5:EC:3270:HIS:CE1	5:EC:3603:LEU:HD11	2.51	0.46
5:EC:4047:MET:HG3	13:LK:516:VAL:HG21	1.97	0.46
6:FA:1759:GLU:HB3	6:FA:1934:LEU:HG	1.98	0.46
6:FA:1962:GLN:O	6:FA:2047:ARG:HD2	2.16	0.46
6:FA:2034:ARG:HE	9:HA:774:LEU:HG	1.80	0.46
6:FC:1946:LEU:HD11	6:FC:2054:PHE:CE1	2.51	0.46
6:FD:993:ALA:CB	12:KA:230:GLN:HB2	2.46	0.46
6:FD:1008:ARG:HD3	6:FD:1008:ARG:HA	1.35	0.46
6:FD:1190:ARG:NH2	6:FD:1418:GLU:HB3	2.30	0.46
6:FE:819:PRO:HG3	6:FE:895:ILE:HB	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:864:LEU:HD11	6:FF:973:ILE:HD12	1.97	0.46
6:FF:1184:ALA:H	6:FF:1424:CYS:HB3	1.79	0.46
7:GC:522:PRO:HG3	7:GC:575:TYR:HE1	1.80	0.46
7:GE:862:GLU:HG3	7:GE:864:ILE:HG23	1.96	0.46
8:GF:63:LEU:HD21	8:GF:87:PHE:HE1	1.81	0.46
8:GF:667:LEU:HB3	8:GF:674:VAL:HB	1.98	0.46
7:GG:374:ALA:HB2	7:GG:380:ARG:HB2	1.98	0.46
8:GH:152:LEU:HB2	8:GH:394:PHE:CD2	2.50	0.46
8:GH:681:ILE:HG22	8:GH:685:ARG:HH21	1.81	0.46
7:GI:458:PRO:HB2	7:GI:467:LYS:NZ	2.30	0.46
7:GK:891:LEU:HB3	7:GK:956:ILE:HD12	1.96	0.46
8:GL:168:MET:HE1	8:GL:247:PRO:HG3	1.97	0.46
9:HA:807:GLU:HG3	9:HA:810:ARG:HH21	1.80	0.46
10:IC:372:ARG:HD2	10:IC:1217:ARG:HH21	1.81	0.46
10:IC:473:LEU:HD13	10:IC:501:MET:HE2	1.98	0.46
11:JA:1731:PRO:HB3	11:JA:1778:PHE:HZ	1.80	0.46
11:JC:159:LEU:HD21	11:JC:169:PHE:HB2	1.97	0.46
11:JC:1090:LEU:HB2	11:JC:1128:LYS:HZ3	1.81	0.46
12:KA:376:ALA:HB2	12:KA:579:LEU:HD11	1.97	0.46
12:KA:594:PHE:H	12:KA:611:LEU:HB3	1.80	0.46
14:MC:122:LEU:HD22	14:MD:122:LEU:HB3	1.97	0.46
15:NB:885:LEU:HD23	15:NB:888:ARG:HD3	1.98	0.46
15:NC:1148:GLY:HA2	15:NC:1157:PRO:HA	1.97	0.46
15:ND:1125:TYR:CE1	15:ND:1156:LEU:HD13	2.49	0.46
15:ND:1423:LEU:HB3	15:ND:1424:VAL:H	1.57	0.46
16:OA:1033:ALA:HA	16:OA:1034:PRO:HD3	1.83	0.46
2:AC:371:VAL:HG12	2:AC:379:HIS:CE1	2.51	0.46
1:AE:157:LEU:HB2	1:AE:180:PHE:HD2	1.80	0.46
2:AF:481:ARG:HH22	2:AF:532:PRO:HB2	1.80	0.46
2:AG:354:ARG:HG3	2:AG:355:HIS:CE1	2.51	0.46
3:CA:906:ALA:HB2	3:CA:942:ILE:HG12	1.97	0.46
3:CC:755:GLY:HA2	3:CC:810:PRO:HG3	1.97	0.46
5:EA:3436:TYR:CE1	5:EA:4014:VAL:HG22	2.49	0.46
5:EA:3720:LEU:HD23	5:EA:3740:MET:HG3	1.97	0.46
5:EA:3821:PRO:HG2	5:EA:4242:PHE:CZ	2.51	0.46
6:FD:1208:ALA:HB3	6:FD:1286:LEU:HD22	1.98	0.46
6:FD:1443:GLY:O	6:FD:1444:ARG:C	2.59	0.46
6:FE:1247:SER:HB2	11:JC:795:ARG:HD2	1.97	0.46
6:FF:843:LEU:HB3	7:GI:958:GLN:OE1	2.15	0.46
6:FF:1198:TYR:O	6:FF:1199:GLY:C	2.59	0.46
6:FF:1429:LEU:HD22	6:FF:1429:LEU:N	2.30	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GD:396:ILE:HG23	8:GD:398:VAL:HG12	1.98	0.46
8:GD:424:GLU:HB3	8:GD:499:GLN:HB2	1.96	0.46
8:GF:604:PHE:HE1	8:GF:618:TYR:HB3	1.80	0.46
7:GI:243:HIS:CE1	7:GI:252:SER:HB3	2.51	0.46
7:GK:433:MET:HE3	7:GK:459:PRO:HD3	1.97	0.46
9:HD:774:LEU:C	13:LJ:526:LEU:HD23	2.40	0.46
10:IB:1196:VAL:HG12	10:IB:1305:GLU:HG2	1.97	0.46
10:IC:537:LEU:HD22	10:IC:558:VAL:HG11	1.97	0.46
11:JA:476:LEU:HA	11:JA:479:VAL:HG12	1.97	0.46
11:JA:1328:LEU:HD21	11:JA:1408:LEU:HD11	1.98	0.46
11:JA:1676:ARG:NH2	11:JA:1833:ASP:HA	2.31	0.46
11:JA:1716:GLN:NE2	16:OA:890:THR:HG23	2.31	0.46
11:JB:1735:GLY:HA2	11:JB:1774:ARG:HH22	1.81	0.46
11:JC:55:LEU:HD12	11:JC:56:PRO:HD2	1.98	0.46
12:KA:212:LEU:HB2	12:KA:238:PHE:HB2	1.97	0.46
12:KA:513:LYS:HE2	12:KA:513:LYS:HB2	1.74	0.46
12:KC:402:LEU:HD13	12:KC:406:GLN:HG3	1.97	0.46
12:KF:208:LEU:HB2	12:KF:281:MET:HE3	1.97	0.46
13:LF:423:GLN:HG3	13:LF:427:ARG:HH22	1.81	0.46
15:ND:890:ARG:C	15:ND:1153:ALA:HA	2.40	0.46
16:OB:152:THR:HG22	16:OB:156:GLU:HB3	1.98	0.46
20:SD:106:LEU:HB3	20:SD:110:MET:HE2	1.98	0.46
2:AB:323:CYS:O	2:AB:327:ILE:HG12	2.16	0.46
2:AG:14:LYS:HG3	6:FB:1911:PRO:HD3	1.98	0.46
2:AG:114:MET:HE1	16:OC:143:VAL:HG13	1.97	0.46
1:AH:965:ALA:HB1	1:AH:967:ARG:NH1	2.31	0.46
5:EB:3651:ALA:H	9:HB:499:ARG:HD2	1.80	0.46
5:EB:3842:LYS:H	11:JA:1041:LYS:HE3	1.81	0.46
5:EB:4540:ASP:H	5:EB:4685:PRO:HD3	1.80	0.46
5:EB:4674:LEU:HD21	5:EB:4690:CYS:HB3	1.98	0.46
6:FD:888:PRO:HB3	7:GC:896:ARG:HG3	1.97	0.46
6:FF:1201:THR:O	6:FF:1202:PHE:C	2.59	0.46
6:FF:1210:LEU:HD23	6:FF:1286:LEU:HD23	1.98	0.46
7:GA:397:LEU:HD21	8:GF:176:ALA:HB3	1.97	0.46
7:GA:548:ALA:HB3	9:HB:626:PRO:HG2	1.98	0.46
8:GB:22:THR:H	8:GB:25:GLU:HB2	1.81	0.46
7:GC:323:LEU:HA	7:GC:579:PHE:HE2	1.80	0.46
7:GC:619:ARG:HD3	7:GC:631:PHE:CE1	2.51	0.46
8:GF:504:HIS:CD2	8:GF:505:PRO:HD2	2.51	0.46
7:GI:311:LEU:HD23	7:GI:453:LEU:HD13	1.98	0.46
7:GK:276:ARG:HD3	7:GK:285:LEU:HD21	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:HA:777:TYR:O	9:HA:778:PRO:C	2.58	0.46
10:IC:1068:ARG:HH22	10:IC:1072:ARG:HD3	1.81	0.46
11:JA:1669:LEU:HD11	11:JA:1726:LEU:HD13	1.98	0.46
11:JB:970:PHE:HD1	11:JB:1008:PHE:HD2	1.64	0.46
11:JB:1745:PHE:HE2	11:JB:1858:ILE:HG12	1.81	0.46
12:KC:413:ALA:HA	12:KC:416:ALA:HB3	1.98	0.46
12:KC:582:ILE:HG21	12:KC:594:PHE:HE2	1.81	0.46
12:KC:600:ASP:HB2	12:KC:685:ARG:HB2	1.97	0.46
12:KE:219:LEU:HD22	12:KE:223:ALA:HA	1.98	0.46
13:LI:520:LEU:O	13:LI:523:GLU:N	2.49	0.46
15:NC:355:LEU:HB3	15:NC:434:VAL:HG11	1.96	0.46
15:NC:503:LEU:HB2	15:NC:514:SER:HB2	1.97	0.46
15:ND:903:CYS:SG	15:ND:904:ARG:HG2	2.56	0.46
16:OA:1109:LYS:HA	16:OA:1112:LYS:HE2	1.98	0.46
2:AC:145:LYS:HA	2:AC:148:ASP:HB2	1.98	0.46
2:AC:147:LEU:HA	2:AC:150:ALA:HB3	1.98	0.46
3:BC:875:THR:HB	16:OC:154:ALA:HA	1.97	0.46
5:EA:4431:ARG:HH11	5:EA:4432:PRO:HD2	1.81	0.46
5:EB:3690:VAL:HG11	5:EB:3726:ARG:HG3	1.98	0.46
5:EB:4348:LEU:HA	5:EB:4351:VAL:HG12	1.97	0.46
6:FB:1684:THR:HG22	6:FB:1685:GLU:H	1.80	0.46
6:FC:2052:HIS:CE1	9:HB:762:HIS:HB2	2.47	0.46
6:FD:865:GLY:HA2	6:FD:868:GLN:HE21	1.81	0.46
6:FD:963:THR:HA	6:FD:1028:LYS:HD3	1.98	0.46
6:FD:1182:ALA:HB1	6:FD:1424:CYS:SG	2.56	0.46
6:FE:1001:ASN:HD22	6:FE:1001:ASN:H	1.62	0.46
7:GA:298:TYR:HB3	7:GA:679:LEU:HD11	1.97	0.46
8:GB:716:ARG:HH11	8:GB:720:PRO:HG3	1.81	0.46
7:GE:916:HIS:HB3	7:GE:919:VAL:HG12	1.98	0.46
7:GG:438:LYS:HE2	7:GG:464:LEU:HG	1.98	0.46
7:GG:690:ARG:HA	7:GG:690:ARG:HD3	1.74	0.46
9:HC:676:ALA:HB2	9:HC:682:ILE:HG12	1.98	0.46
10:IA:561:ARG:HH12	10:IA:853:GLY:HA2	1.80	0.46
10:IA:947:HIS:HB3	10:IA:951:GLY:H	1.81	0.46
11:JA:123:ILE:HB	11:JA:135:ILE:HB	1.98	0.46
11:JA:1584:LYS:HA	11:JA:1588:GLU:HA	1.97	0.46
11:JA:1838:THR:HG22	11:JA:1839:LEU:HD12	1.97	0.46
11:JB:529:ILE:HG21	11:JB:885:TYR:HD2	1.81	0.46
11:JC:1152:HIS:CE1	11:JC:1158:MET:HB2	2.51	0.46
13:LI:510:ILE:HD13	13:LI:513:LEU:HD12	1.98	0.46
13:LK:483:ARG:HA	13:LK:486:ARG:HG2	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NA:542:LEU:HB3	15:NA:1190:ILE:HG13	1.98	0.46
15:NA:548:PRO:HA	15:NA:551:ARG:HE	1.81	0.46
15:NA:657:VAL:HG21	15:NA:897:ILE:HD12	1.97	0.46
15:NC:537:LYS:NZ	15:NC:578:HIS:H	2.13	0.46
15:NC:1526:ILE:HG21	18:QD:146:ILE:HD13	1.98	0.46
15:NC:1550:MET:HE1	19:RA:26:HIS:HA	1.97	0.46
15:ND:468:ARG:HG2	15:ND:469:PHE:H	1.80	0.46
15:ND:1498:ARG:HH12	20:SB:44:PRO:HD3	1.80	0.46
20:SB:11:ALA:HA	20:SB:14:LYS:HE3	1.98	0.46
20:SD:33:LEU:HD13	20:SD:64:ILE:HG12	1.98	0.46
1:AA:777:PHE:HB3	1:AA:780:ALA:HB3	1.96	0.46
1:AH:811:VAL:HG21	1:AH:836:THR:HG21	1.98	0.46
1:AI:1026:ASP:HB3	1:AI:1032:PHE:HB2	1.97	0.46
3:CA:850:THR:HG23	3:CA:861:VAL:HG23	1.97	0.46
3:CG:1126:GLU:HB3	10:IC:995:PRO:HG2	1.97	0.46
4:DA:19:ARG:HH12	4:DA:156:ASP:CG	2.24	0.46
4:DB:395:MET:HA	14:MF:320:ARG:NH2	2.31	0.46
4:DC:3:TRP:CH2	14:MJ:293:LEU:HD22	2.51	0.46
5:EA:3445:VAL:HG11	5:EA:3566:ILE:HA	1.98	0.46
5:EA:3881:ARG:HG2	5:EA:4004:PHE:HE2	1.81	0.46
5:EC:3246:LYS:HB3	5:EC:3301:LEU:HD21	1.98	0.46
6:FA:2037:LEU:HD13	6:FA:2037:LEU:HA	1.70	0.46
6:FC:1974:VAL:HG21	6:FC:2040:LEU:HD23	1.98	0.46
6:FC:2064:LEU:HD12	6:FC:2064:LEU:HA	1.73	0.46
6:FE:821:ARG:O	6:FE:823:GLY:N	2.49	0.46
6:FE:1190:ARG:CZ	6:FE:1388:PHE:HB3	2.46	0.46
8:GD:69:ILE:HD11	8:GD:104:LEU:HD21	1.98	0.46
7:GG:292:PHE:HB2	7:GG:689:ILE:HB	1.98	0.46
7:GK:506:ALA:HA	7:GK:509:LEU:HD12	1.98	0.46
8:GL:63:LEU:HD21	8:GL:104:LEU:HD22	1.98	0.46
9:HA:496:GLU:HG3	9:HA:499:ARG:HD2	1.98	0.46
10:IC:1223:LEU:HD23	10:IC:1387:LEU:HD22	1.98	0.46
11:JA:1556:PHE:HA	11:JA:1575:LEU:HD13	1.98	0.46
11:JB:837:ASN:HA	11:JB:840:ILE:HG22	1.98	0.46
11:JB:1412:LEU:HB3	11:JB:1504:ARG:HB2	1.98	0.46
11:JC:1765:ARG:HH22	16:OC:893:PRO:HD2	1.81	0.46
12:KB:261:VAL:HA	12:KB:264:LYS:HG2	1.98	0.46
12:KF:312:PRO:HA	12:KF:315:GLN:HB2	1.98	0.46
13:LB:497:LEU:HD11	14:MD:114:ARG:HD3	1.98	0.46
13:LI:380:MET:HE3	13:LI:384:LEU:HB2	1.98	0.46
15:NB:780:GLN:HA	15:NB:783:GLN:NE2	2.31	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NB:891:TRP:H	15:NB:1154:ASP:C	2.24	0.46
15:ND:1441:ARG:HA	15:ND:1441:ARG:HD2	1.83	0.46
19:RD:53:PHE:HE1	19:RD:139:LEU:HD21	1.80	0.46
1:AA:389:LEU:HD11	2:AB:549:VAL:HG11	1.97	0.45
2:AC:200:GLU:HG3	2:AC:201:LYS:H	1.80	0.45
3:CG:4462:VAL:HG12	3:CG:4465:LYS:HD3	1.98	0.45
3:CL:1131:LEU:O	3:CL:1132:MET:HE2	2.16	0.45
4:DB:393:LEU:HD13	14:MF:316:GLN:HG3	1.98	0.45
4:DC:343:LEU:HD13	4:DC:374:VAL:HG11	1.97	0.45
4:DE:173:PHE:HA	4:DE:176:ILE:HG12	1.98	0.45
5:EA:4408:GLY:O	5:EA:4410:ASP:N	2.47	0.45
5:EB:4072:ASN:HB3	5:EB:4293:TRP:HH2	1.81	0.45
6:FC:2083:GLN:HG3	6:FC:2084:GLN:H	1.80	0.45
6:FE:1193:VAL:HG12	6:FE:1194:ASN:HD22	1.81	0.45
6:FF:976:HIS:O	6:FF:987:ASN:ND2	2.49	0.45
6:FF:1216:TRP:CZ2	6:FF:1272:VAL:HG22	2.51	0.45
6:FF:1216:TRP:O	6:FF:1217:GLU:C	2.59	0.45
7:GA:294:ALA:HB2	7:GA:689:ILE:HG12	1.97	0.45
8:GB:664:ILE:HD11	8:GB:681:ILE:HG21	1.97	0.45
7:GE:276:ARG:HH22	7:GE:279:ARG:HG2	1.81	0.45
7:GE:839:ARG:HA	7:GE:839:ARG:HD3	1.83	0.45
7:GG:715:THR:HG21	7:GG:796:PHE:HB3	1.97	0.45
7:GI:898:ILE:HG23	7:GI:903:LEU:HD21	1.98	0.45
9:HA:872:MET:HB2	9:HA:872:MET:HE2	1.58	0.45
9:HB:854:ASN:HA	9:HB:857:ARG:HE	1.80	0.45
10:IB:649:VAL:HA	10:IB:652:LYS:HG2	1.98	0.45
10:IB:1095:GLY:H	10:IB:1098:HIS:CD2	2.34	0.45
10:IC:615:ARG:HD3	10:IC:629:PRO:HG3	1.97	0.45
10:IC:1059:LEU:HD22	10:IC:1111:GLN:HG3	1.97	0.45
10:IC:1278:VAL:HG23	10:IC:1279:GLU:H	1.81	0.45
11:JA:64:ALA:HB2	11:JA:82:VAL:HG23	1.98	0.45
11:JA:1437:ILE:HA	11:JA:1438:PRO:HD3	1.81	0.45
11:JB:1515:LEU:HD22	11:JB:1554:LEU:HD22	1.98	0.45
11:JC:162:PRO:HD2	11:JC:169:PHE:HA	1.98	0.45
11:JC:945:LEU:HD23	11:JC:947:LYS:H	1.81	0.45
11:JC:1687:LEU:HG	11:JC:1854:HIS:CE1	2.50	0.45
12:KA:495:GLN:NE2	12:KA:496:VAL:HG23	2.31	0.45
15:NC:504:GLU:HA	15:NC:514:SER:H	1.81	0.45
15:NC:1163:THR:HA	15:NC:1166:VAL:HG22	1.98	0.45
15:ND:508:GLY:HA3	15:ND:577:PRO:HG3	1.97	0.45
19:RC:108:LEU:HD22	19:RC:171:GLN:HE21	1.82	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:SB:52:MET:HG2	20:SB:72:LEU:HD11	1.98	0.45
1:AA:289:SER:H	17:PA:271:ASN:HD22	1.63	0.45
2:AF:502:LEU:HD23	2:AF:514:ALA:HB1	1.99	0.45
1:AH:291:PRO:HB3	10:IA:826:SER:HA	1.97	0.45
1:AL:795:ASP:HB3	7:GK:582:LEU:HD22	1.98	0.45
5:EB:3729:GLY:HA2	5:EB:4288:PRO:HD3	1.98	0.45
5:EB:3881:ARG:HA	5:EB:4004:PHE:HE2	1.82	0.45
5:EB:4229:MET:HE1	5:EB:4261:VAL:HG21	1.97	0.45
5:EC:4256:LEU:HD12	5:EC:4278:VAL:HG11	1.97	0.45
6:FA:1946:LEU:HD22	6:FA:2054:PHE:CE1	2.51	0.45
6:FB:1643:PRO:HG2	6:FB:1652:TYR:HD2	1.81	0.45
6:FF:912:ILE:H	6:FF:912:ILE:HG12	1.43	0.45
8:GB:565:LEU:HD22	8:GB:596:MET:HG2	1.98	0.45
8:GD:133:PRO:HB2	8:GD:167:ALA:HA	1.98	0.45
8:GD:674:VAL:HG12	8:GD:723:VAL:HB	1.98	0.45
7:GI:641:THR:HG21	7:GI:828:PRO:HA	1.99	0.45
7:GI:885:GLU:HA	7:GI:890:MET:HG3	1.98	0.45
8:GJ:565:LEU:HD13	8:GJ:596:MET:HE3	1.98	0.45
7:GK:535:PRO:HB3	9:HC:551:GLU:O	2.16	0.45
10:IA:506:GLN:HB3	10:IA:594:PRO:HD2	1.98	0.45
10:IA:893:PHE:O	10:IA:897:ARG:HG2	2.17	0.45
13:LA:526:LEU:HD11	13:LB:525:SER:HB3	1.97	0.45
13:LM:353:ASN:HD22	13:LN:349:TYR:HE1	1.63	0.45
14:ME:285:ARG:HH22	14:MF:257:LYS:HD2	1.81	0.45
15:NA:361:VAL:HG11	15:NA:445:ILE:HD11	1.96	0.45
15:NA:812:ARG:CZ	15:NA:870:TYR:HA	2.45	0.45
15:NA:893:LEU:HG	15:NA:1154:ASP:CG	2.42	0.45
15:NA:1487:ARG:HB3	15:NA:1488:ARG:H	1.52	0.45
15:NB:629:ALA:HB2	15:NB:646:GLU:HG3	1.99	0.45
15:ND:536:THR:HB	15:ND:543:ILE:HB	1.98	0.45
15:ND:1412:THR:HG22	15:ND:1467:LEU:HG	1.98	0.45
15:ND:1488:ARG:NH1	15:ND:1491:PRO:HD2	2.28	0.45
19:RA:37:ILE:HG22	19:RA:53:PHE:CD1	2.52	0.45
1:AA:237:VAL:HG11	17:PA:249:LEU:HD13	1.97	0.45
1:AE:850:ILE:HG21	1:AE:904:ASP:HB2	1.98	0.45
2:AG:521:LEU:HD21	1:AH:56:LEU:HD22	1.99	0.45
3:BA:952:GLN:HA	3:BA:955:VAL:HG12	1.97	0.45
3:CB:776:ARG:HD2	3:CB:776:ARG:HA	1.73	0.45
4:DB:300:GLN:HG3	4:DB:355:CYS:HB2	1.98	0.45
4:DB:354:TRP:HB2	4:DB:381:MET:HE2	1.98	0.45
4:DC:267:ARG:NH2	14:MI:294:ALA:HA	2.26	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DC:269:LEU:HD13	4:DC:284:ILE:HD12	1.98	0.45
4:DE:103:LEU:HB2	4:DE:106:ASN:ND2	2.31	0.45
5:EA:3631:ARG:HH21	5:EA:4057:LEU:HD13	1.81	0.45
5:EA:4247:LEU:HD11	5:EA:4284:LEU:HB3	1.97	0.45
5:EB:4888:TRP:O	5:EB:4889:ILE:C	2.60	0.45
5:EC:4024:THR:HG23	9:HA:438:TYR:HD2	1.81	0.45
6:FE:851:THR:HG23	6:FE:972:VAL:HG13	1.98	0.45
6:FE:1000:GLN:HG3	6:FE:1444:ARG:HG2	1.98	0.45
8:GD:580:PRO:HG3	8:GD:789:VAL:HG11	1.98	0.45
7:GE:322:GLY:HA3	7:GE:581:ARG:HD3	1.98	0.45
8:GH:501:SER:HB3	8:GH:511:LEU:HD13	1.99	0.45
7:GI:871:LEU:O	7:GI:972:GLU:HG2	2.16	0.45
10:IC:1128:VAL:HG12	10:IC:1131:HIS:ND1	2.31	0.45
11:JA:2071:LEU:HD13	11:JA:2266:LEU:HB3	1.97	0.45
11:JB:1765:ARG:NH2	16:OB:893:PRO:HD2	2.32	0.45
12:KA:511:LEU:H	12:KA:514:PHE:HD2	1.65	0.45
12:KB:377:LEU:HD12	12:KB:386:LEU:HD11	1.99	0.45
12:KC:319:TYR:HE1	12:KC:331:GLN:HE22	1.64	0.45
12:KG:633:ARG:HH22	12:KG:635:VAL:HG23	1.81	0.45
15:NB:693:GLY:HA2	15:NB:901:LEU:HD23	1.97	0.45
15:NB:801:ALA:HA	15:NB:804:VAL:HG12	1.99	0.45
15:NB:805:ALA:HB2	15:NB:885:LEU:HD12	1.98	0.45
15:NB:1156:LEU:HD13	15:NB:1160:LEU:HD21	1.98	0.45
16:OA:1075:TYR:HE2	16:OA:1077:LYS:HB3	1.82	0.45
19:RA:20:PRO:HB3	19:RA:22:ARG:HB2	1.98	0.45
19:RA:116:PHE:HE1	19:RA:166:PHE:HB3	1.82	0.45
19:RC:51:MET:HA	19:RC:54:MET:HE2	1.98	0.45
2:AB:373:ARG:HG3	2:AB:374:LEU:HD12	1.97	0.45
2:AC:273:ASP:HB3	2:AC:276:GLN:HG3	1.97	0.45
1:AE:654:LEU:HB3	1:AE:662:LEU:HB2	1.99	0.45
2:AF:61:ARG:HG2	6:FB:1711:LEU:HD11	1.99	0.45
1:AH:966:LEU:HD12	1:AH:971:GLU:HB3	1.98	0.45
2:AK:164:TYR:HB2	2:AK:285:PHE:HE1	1.82	0.45
1:AL:725:LEU:HA	1:AL:728:VAL:HG12	1.98	0.45
3:CC:835:GLN:HB3	3:CC:838:ASP:HB2	1.99	0.45
3:CE:1228:LYS:HE3	3:CE:1228:LYS:HB3	1.83	0.45
4:DB:103:LEU:HB3	4:DB:106:ASN:HB3	1.97	0.45
4:DB:352:LYS:HZ3	13:LE:454:VAL:HG23	1.80	0.45
4:DD:163:GLU:HA	4:DD:166:VAL:HG23	1.97	0.45
5:EB:3223:TRP:HZ2	5:EB:4182:LEU:HD21	1.80	0.45
5:EB:3258:GLY:HA2	5:EB:3262:VAL:HG13	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:3648:PRO:HB2	7:GA:543:LYS:NZ	2.31	0.45
5:EC:3498:VAL:HG23	5:EC:3505:ILE:HB	1.98	0.45
5:EC:3874:PHE:HD1	5:EC:4009:PRO:HD3	1.82	0.45
5:EC:3881:ARG:HA	5:EC:4004:PHE:CZ	2.51	0.45
5:EC:4035:THR:HG22	5:EC:4037:ASP:H	1.82	0.45
6:FA:1951:TYR:CE2	9:HA:844:GLY:HA3	2.51	0.45
6:FA:2038:LEU:HD22	9:HA:771:PRO:HG2	1.99	0.45
6:FB:1880:GLU:HA	6:FB:1883:GLU:HB2	1.98	0.45
6:FB:1951:TYR:CE1	9:HD:844:GLY:HA3	2.51	0.45
6:FC:1828:VAL:HG13	6:FC:1838:VAL:HG22	1.97	0.45
6:FC:1936:GLY:HA2	6:FC:1939:VAL:HB	1.99	0.45
6:FC:2042:LYS:HZ2	6:FC:2042:LYS:HG3	1.68	0.45
6:FD:845:PRO:N	7:GC:896:ARG:NH1	2.64	0.45
6:FD:860:PRO:HG2	6:FD:861:LEU:HD22	1.98	0.45
6:FE:1230:SER:C	6:FE:1232:LYS:H	2.24	0.45
6:FE:1233:ILE:HG12	6:FE:1268:VAL:HG22	1.98	0.45
6:FF:811:ASN:O	6:FF:1110:GLY:HA2	2.17	0.45
6:FF:912:ILE:HD11	6:FF:965:TRP:HZ2	1.81	0.45
8:GB:261:GLU:HG3	8:GB:263:ARG:HH22	1.81	0.45
7:GC:185:ARG:NH2	7:GC:704:ASP:HB2	2.31	0.45
7:GC:280:PHE:HE1	12:KE:626:GLU:HB3	1.82	0.45
8:GD:151:GLN:HB3	8:GD:400:LYS:HZ3	1.82	0.45
7:GE:706:VAL:HG21	7:GE:752:VAL:HG21	1.98	0.45
7:GG:575:TYR:HE1	7:GG:577:SER:HB2	1.80	0.45
7:GG:607:ARG:HD2	7:GG:609:ARG:NH2	2.31	0.45
7:GK:397:LEU:HB3	8:GL:267:TRP:HE1	1.81	0.45
12:KA:545:LEU:HD12	12:KA:715:LEU:HD11	1.98	0.45
12:KB:339:SER:HA	12:KB:697:ARG:HD3	1.98	0.45
15:NA:357:CYS:O	15:NA:471:TYR:HB3	2.17	0.45
15:NA:564:ARG:NH2	15:NA:619:TYR:HA	2.31	0.45
15:NA:1138:THR:HG21	15:NA:1143:LEU:HB3	1.99	0.45
15:NB:685:PHE:HB3	15:NB:912:THR:HG23	1.98	0.45
15:NC:893:LEU:HB2	15:NC:1154:ASP:CG	2.41	0.45
15:ND:1521:SER:HB3	18:QB:60:ARG:NH2	2.32	0.45
18:QB:55:VAL:HG23	18:QB:58:LEU:HD23	1.98	0.45
1:AE:423:THR:HG21	2:AF:263:TYR:HD1	1.80	0.45
2:AG:176:VAL:HG13	16:OC:27:LEU:HA	1.99	0.45
1:AH:416:LEU:HD12	16:OC:17:PHE:HB3	1.97	0.45
1:AI:203:ALA:HB2	3:BB:804:ARG:HB2	1.97	0.45
1:AI:628:ASN:HB2	1:AI:630:PRO:HD2	1.99	0.45
1:AI:709:LEU:HD21	1:AI:1037:PRO:HG2	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:338:MET:HE2	1:AL:344:SER:HB2	1.99	0.45
3:BA:875:THR:HB	16:OA:154:ALA:HA	1.98	0.45
3:CA:1014:ASP:HA	3:CA:1017:ARG:HG2	1.97	0.45
3:CJ:1116:SER:HA	3:CJ:1119:ARG:HG2	1.98	0.45
3:CL:1239:PRO:HA	3:CL:4470:LYS:HD3	1.98	0.45
5:EC:4222:LYS:HE2	5:EC:4222:LYS:HB3	1.86	0.45
5:EC:4404:LYS:H	5:EC:4404:LYS:HG2	1.65	0.45
6:FA:1681:VAL:HG22	6:FA:1692:VAL:HG22	1.98	0.45
6:FA:1730:GLU:HA	6:FA:1907:ILE:HA	1.98	0.45
6:FA:1962:GLN:HG2	9:HA:834:LEU:CD2	2.47	0.45
6:FB:1699:PRO:HA	6:FB:1722:PHE:HB3	1.99	0.45
6:FC:2063:GLN:NE2	9:HB:751:SER:HB2	2.32	0.45
6:FD:887:ARG:CZ	6:FD:889:SER:HA	2.46	0.45
6:FD:992:PRO:O	12:KA:230:GLN:HB3	2.17	0.45
6:FD:1098:VAL:C	6:FD:1101:ALA:H	2.25	0.45
6:FE:841:TYR:N	7:GE:957:ARG:NH2	2.64	0.45
6:FE:1260:LEU:HG	6:FE:1261:SER:N	2.32	0.45
6:FF:1105:ARG:H	6:FF:1105:ARG:HG2	1.43	0.45
6:FF:1210:LEU:HD23	6:FF:1210:LEU:HA	1.77	0.45
8:GB:317:VAL:HB	8:GB:325:ILE:HG13	1.99	0.45
7:GC:268:ARG:HB2	7:GC:276:ARG:CZ	2.47	0.45
7:GC:370:ALA:HB3	7:GC:383:GLN:HB2	1.99	0.45
8:GD:626:SER:HB3	8:GD:629:ASN:HB2	1.99	0.45
7:GG:730:LYS:HA	7:GG:730:LYS:HE3	1.99	0.45
8:GH:40:LEU:HG	8:GH:470:LYS:HD3	1.98	0.45
8:GH:708:ASP:O	8:GH:712:ILE:HG12	2.16	0.45
7:GI:872:THR:HG22	7:GI:972:GLU:HG3	1.98	0.45
8:GJ:667:LEU:HB3	8:GJ:674:VAL:HB	1.99	0.45
7:GK:607:ARG:HH22	7:GK:609:ARG:HH21	1.64	0.45
8:GL:383:LYS:HE2	8:GL:441:THR:HG22	1.97	0.45
9:HA:722:SER:HA	9:HA:724:PHE:H	1.81	0.45
9:HB:783:SER:O	9:HB:786:ALA:N	2.49	0.45
9:HC:566:PRO:HA	9:HC:569:ARG:HB3	1.98	0.45
11:JB:783:PHE:HD1	11:JB:807:LEU:HD11	1.82	0.45
11:JC:837:ASN:HB3	11:JC:1419:ILE:HD11	1.98	0.45
11:JC:1161:LEU:HB2	11:JC:1357:PHE:HB3	1.98	0.45
11:JC:1388:PRO:HG3	11:JC:1407:HIS:HD2	1.81	0.45
11:JC:1722:TYR:HB3	11:JC:1733:THR:HG22	1.98	0.45
12:KE:414:TRP:HE3	12:KE:415:LEU:HD23	1.80	0.45
14:MA:320:ARG:HH22	14:MA:327:ARG:HH21	1.64	0.45
15:NC:948:LEU:HD21	15:NC:1173:MET:HE1	1.97	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:88:LYS:HD3	2:AB:535:LEU:HD13	1.98	0.45
1:AA:148:VAL:HG23	1:AA:219:THR:HB	1.98	0.45
1:AD:245:PRO:HG3	10:IB:776:PRO:HG2	1.98	0.45
1:AE:507:LEU:HD21	6:FB:1826:LEU:HD13	1.97	0.45
1:AH:663:LEU:HD21	1:AH:698:LEU:HA	1.98	0.45
2:AK:190:LEU:HD22	2:AK:272:TYR:HD2	1.82	0.45
1:AL:600:GLU:CD	13:LH:511:GLN:HE22	2.25	0.45
1:AL:851:LEU:HD23	1:AL:896:VAL:HG11	1.99	0.45
3:CF:1127:GLU:HB2	3:CF:1128:TRP:CE3	2.51	0.45
3:CL:4478:GLN:HG2	3:CL:4479:LEU:HG	1.98	0.45
4:DA:103:LEU:HB2	4:DA:106:ASN:HB2	1.99	0.45
4:DB:266:TRP:CD1	4:DB:316:ARG:HH22	2.35	0.45
4:DE:301:LEU:HD11	4:DE:357:GLU:HB2	1.97	0.45
4:DF:16:LEU:HD13	4:DF:160:PHE:CD2	2.52	0.45
5:EA:4403:LEU:HD13	5:EA:4405:ILE:HD11	1.98	0.45
6:FC:2009:SER:HA	6:FC:2012:ARG:CZ	2.47	0.45
6:FC:2027:TRP:HB2	9:HB:778:PRO:HD3	1.98	0.45
6:FC:2085:GLU:O	6:FC:2086:ASN:C	2.59	0.45
6:FD:860:PRO:CD	6:FD:861:LEU:HD23	2.47	0.45
6:FD:1028:LYS:HA	6:FD:1028:LYS:HD2	1.55	0.45
6:FE:1075:VAL:O	6:FE:1076:ILE:C	2.58	0.45
6:FE:1276:LEU:O	6:FE:1277:ASP:C	2.60	0.45
8:GB:432:LYS:HE2	8:GB:451:SER:HB3	1.99	0.45
7:GG:706:VAL:HG11	7:GG:752:VAL:HG11	1.99	0.45
8:GH:56:CYS:HB3	8:GH:61:CYS:HB2	1.36	0.45
8:GH:184:GLY:HA2	8:GH:254:LYS:HE3	1.98	0.45
8:GH:236:LEU:HB3	8:GH:294:TRP:HE1	1.80	0.45
9:HD:800:VAL:O	13:LI:534:PRO:HD2	2.17	0.45
10:IA:172:GLN:HB3	10:IA:173:GLN:H	1.59	0.45
10:IB:1121:LYS:HA	10:IB:1121:LYS:HD3	1.79	0.45
10:IC:938:ILE:HA	16:OC:1040:PHE:HE1	1.82	0.45
11:JA:1393:LEU:HA	11:JA:1396:MET:HE2	1.98	0.45
11:JB:1584:LYS:HB2	11:JB:1584:LYS:HE2	1.77	0.45
12:KG:486:PHE:HA	12:KG:489:MET:HE1	1.98	0.45
13:LA:401:LEU:HD23	13:LA:404:LEU:HD21	1.99	0.45
13:LA:513:LEU:HD21	13:LB:514:TYR:CD1	2.52	0.45
13:LJ:503:VAL:O	13:LJ:507:ARG:HG2	2.16	0.45
13:LJ:506:GLN:O	13:LJ:510:ILE:HG12	2.17	0.45
15:NA:676:ARG:O	15:NA:676:ARG:HD2	2.17	0.45
15:NB:503:LEU:HB3	15:NB:512:TYR:HB3	1.99	0.45
15:NC:898:ASN:HA	15:NC:901:LEU:HB3	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NC:1412:THR:HG23	15:NC:1415:GLU:H	1.80	0.45
19:RA:58:VAL:HA	19:RA:118:TYR:OH	2.17	0.45
20:SD:76:LYS:HZ1	20:SD:78:LYS:HG3	1.82	0.45
1:AE:815:LEU:HD23	1:AE:830:THR:HG21	1.98	0.45
2:AG:94:ILE:HG12	2:AG:274:SER:HA	1.99	0.45
2:AK:515:TRP:HE3	2:AK:516:LEU:HD22	1.81	0.45
1:AL:593:GLU:HG2	1:AL:594:TYR:HD2	1.82	0.45
3:BA:693:ARG:HB2	17:PA:258:PRO:HG3	1.97	0.45
3:BA:731:MET:HE2	3:BA:776:ARG:HH12	1.82	0.45
3:BA:845:LYS:HB2	3:BA:845:LYS:HE2	1.70	0.45
4:DB:28:LEU:HD13	4:DB:154:LEU:HD11	1.98	0.45
4:DC:103:LEU:HB2	4:DC:106:ASN:HB2	1.99	0.45
4:DD:275:LEU:HB2	4:DD:280:ALA:HB2	1.99	0.45
5:EA:4505:MET:HE1	5:EA:4694:MET:HB3	1.99	0.45
6:FB:1817:VAL:HG11	6:FB:1838:VAL:HG11	1.99	0.45
6:FB:2031:HIS:CE1	13:LJ:519:SER:HG	2.35	0.45
6:FC:2038:LEU:HD13	9:HB:771:PRO:HG2	1.99	0.45
6:FD:843:LEU:HB3	7:GC:896:ARG:CZ	2.47	0.45
6:FD:1119:LEU:HD12	6:FD:1119:LEU:HA	1.87	0.45
6:FE:983:LEU:HA	12:KB:726:ASP:OD2	2.16	0.45
6:FE:1245:ASN:HB3	6:FE:1249:ILE:HG23	1.98	0.45
6:FE:1293:THR:HG22	6:FE:1396:PHE:HB2	1.99	0.45
6:FF:990:PHE:CB	12:KC:313:PHE:HE2	2.30	0.45
7:GA:543:LYS:HA	7:GA:544:PRO:HD3	1.92	0.45
8:GB:674:VAL:HG12	8:GB:723:VAL:HB	1.99	0.45
8:GD:681:ILE:HA	8:GD:684:TRP:CD1	2.51	0.45
8:GF:276:MET:SD	8:GF:311:SER:HB3	2.57	0.45
7:GG:318:ALA:HB1	7:GG:323:LEU:HB3	1.99	0.45
7:GG:626:ARG:HH12	7:GG:632:VAL:HG21	1.82	0.45
9:HA:808:HIS:O	9:HA:812:THR:HG23	2.17	0.45
9:HA:865:ILE:HD12	9:HA:865:ILE:HA	1.83	0.45
10:IA:829:GLY:HA2	11:JA:2037:ARG:HH12	1.82	0.45
10:IB:1077:LYS:HG3	10:IB:1080:ASP:H	1.82	0.45
11:JA:467:SER:O	11:JA:471:VAL:HG23	2.17	0.45
11:JA:1867:LEU:HB3	11:JA:2273:ARG:HH12	1.82	0.45
11:JC:552:THR:HG21	11:JC:1203:GLY:HA3	1.99	0.45
12:KA:664:ILE:HB	12:KA:682:LEU:HB3	1.98	0.45
12:KE:658:SER:HB3	12:KE:665:HIS:HB2	1.99	0.45
12:KF:215:PRO:HB3	12:KF:286:GLU:HB3	1.98	0.45
13:LP:417:LEU:HA	13:LP:420:GLU:HG2	1.99	0.45
15:NA:890:ARG:O	15:NA:891:TRP:HD1	2.00	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NB:679:ASP:HB2	15:NB:696:PHE:HB3	1.99	0.45
15:NB:698:PRO:HB3	15:NB:890:ARG:NH2	2.31	0.45
15:NB:937:MET:HE1	15:NB:1162:ARG:HH22	1.81	0.45
15:NB:1499:ALA:HA	20:SC:38:ARG:CZ	2.47	0.45
15:ND:609:GLN:HA	15:ND:612:ILE:HG22	1.99	0.45
15:ND:884:LYS:HZ3	15:ND:1127:LEU:HD13	1.80	0.45
15:ND:1391:LEU:HG	15:ND:1396:VAL:HB	1.97	0.45
16:OA:1075:TYR:CE2	16:OA:1077:LYS:HB3	2.51	0.45
16:OB:1077:LYS:NZ	16:OB:1079:ALA:H	2.15	0.45
1:AA:834:ILE:HG23	1:AA:985:CYS:HB2	1.98	0.45
1:AD:993:ARG:HD3	1:AD:993:ARG:HA	1.68	0.45
3:CE:1168:ARG:HH21	3:CE:4482:LEU:HD22	1.82	0.45
4:DC:357:GLU:HA	4:DC:386:VAL:HB	1.98	0.45
6:FD:813:GLN:O	6:FD:816:GLY:N	2.49	0.45
6:FD:818:VAL:O	6:FD:819:PRO:C	2.60	0.45
6:FD:819:PRO:HG3	6:FD:895:ILE:HD13	1.98	0.45
6:FD:829:ARG:HB2	6:FD:976:HIS:CD2	2.51	0.45
6:FD:1196:PRO:O	6:FD:1197:ILE:C	2.58	0.45
6:FD:1251:ARG:HD3	6:FD:1252:MET:HE1	1.97	0.45
6:FF:1429:LEU:HD23	6:FF:1430:PHE:CE2	2.52	0.45
7:GA:319:VAL:HG12	7:GA:324:VAL:HG11	1.98	0.45
8:GB:717:PHE:CD2	8:GB:718:PRO:HD3	2.52	0.45
8:GD:19:TRP:H	8:GD:520:PHE:HB2	1.82	0.45
8:GF:454:ILE:HD11	8:GF:459:MET:HE3	1.98	0.45
8:GH:600:ARG:NH2	8:GH:605:LEU:HD22	2.32	0.45
8:GJ:150:ASP:HA	8:GJ:153:ARG:HB3	1.97	0.45
7:GK:544:PRO:HD3	9:HC:596:TYR:HD1	1.81	0.45
8:GL:615:THR:O	8:GL:619:ARG:HG2	2.17	0.45
8:GL:631:LEU:HA	8:GL:634:ILE:HG22	1.99	0.45
9:HA:699:ILE:HD12	9:HA:708:VAL:HG21	1.98	0.45
9:HC:680:ALA:HB2	9:HC:708:VAL:HG13	1.99	0.45
10:IA:1307:ASN:HA	10:IA:1383:LEU:HD13	1.99	0.45
10:IB:765:HIS:HD2	10:IB:786:TYR:HA	1.82	0.45
10:IC:363:CYS:O	10:IC:365:ARG:HG3	2.17	0.45
10:IC:427:PHE:HD1	10:IC:504:VAL:HG21	1.81	0.45
11:JB:75:VAL:HB	11:JB:81:ARG:HD2	1.99	0.45
11:JB:1138:PRO:HG3	11:JB:1837:GLN:HB3	1.99	0.45
11:JC:1475:ARG:HG3	11:JC:1476:VAL:HG13	1.98	0.45
12:KB:215:PRO:HA	12:KB:286:GLU:OE2	2.17	0.45
12:KB:587:THR:HG23	12:KB:589:LYS:H	1.81	0.45
14:MA:258:ILE:HA	14:MA:264:LEU:HD23	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:OA:263:ALA:HB1	16:OA:267:GLU:HB2	1.98	0.45
19:RC:22:ARG:HE	19:RC:174:LEU:HB3	1.81	0.45
20:SB:48:GLU:HA	20:SB:51:ASP:HB3	1.99	0.45
1:AA:1021:LEU:HB3	14:MD:85:PRO:HG3	1.99	0.45
1:AE:403:TYR:HE1	1:AE:466:PRO:HD2	1.81	0.45
1:AE:424:PHE:CD2	2:AF:35:MET:HG3	2.52	0.45
3:CE:1168:ARG:HE	3:CE:4483:PRO:HD2	1.82	0.45
4:DD:333:LYS:HE2	4:DD:334:GLN:HE22	1.82	0.45
5:EB:4519:ARG:HA	5:EB:4519:ARG:HD2	1.75	0.45
5:EC:4093:SER:OG	5:EC:4094:LEU:N	2.49	0.45
6:FA:2034:ARG:HD2	9:HA:772:PRO:O	2.15	0.45
6:FB:2052:HIS:CE1	9:HD:762:HIS:HB2	2.51	0.45
6:FD:838:ASN:O	6:FD:839:GLY:C	2.59	0.45
6:FD:997:THR:HG21	12:KA:230:GLN:HE22	1.81	0.45
6:FD:1088:LYS:HD3	6:FD:1233:ILE:HG23	1.97	0.45
6:FD:1106:LEU:HD23	6:FD:1106:LEU:HA	1.84	0.45
6:FE:805:HIS:O	6:FE:806:ILE:C	2.60	0.45
6:FE:989:PRO:HG2	6:FE:990:PHE:CE2	2.52	0.45
6:FE:1229:LYS:H	6:FE:1229:LYS:HG3	1.62	0.45
6:FF:891:ARG:O	6:FF:892:PRO:C	2.59	0.45
6:FF:1196:PRO:O	6:FF:1197:ILE:C	2.60	0.45
6:FF:1216:TRP:HZ3	6:FF:1300:LEU:HD13	1.80	0.45
7:GA:380:ARG:HD2	8:GF:263:ARG:HH22	1.82	0.45
8:GF:549:THR:HG22	8:GF:554:SER:HA	1.98	0.45
8:GH:259:LEU:HA	8:GH:262:LEU:HD23	1.99	0.45
7:GI:607:ARG:HB3	7:GI:609:ARG:NH1	2.32	0.45
8:GL:50:GLU:HB3	8:GL:112:ILE:HG23	1.97	0.45
10:IB:1070:ASP:HB3	10:IB:1077:LYS:NZ	2.31	0.45
10:IC:216:TRP:NE1	10:IC:232:LEU:HD11	2.31	0.45
10:IC:630:PHE:HE2	10:IC:698:GLN:HB3	1.82	0.45
10:IC:1232:ARG:H	10:IC:1302:ARG:HH22	1.65	0.45
11:JB:1756:ALA:HA	11:JB:1759:LEU:HD23	1.99	0.45
11:JC:1077:ASN:HB3	11:JC:1084:VAL:HG22	1.98	0.45
12:KA:378:PHE:HA	12:KA:383:HIS:HD2	1.81	0.45
12:KB:321:GLU:HB3	12:KB:325:LEU:HD12	1.97	0.45
12:KE:665:HIS:CD2	12:KE:681:MET:HE1	2.50	0.45
12:KF:576:ASN:ND2	12:KF:697:ARG:HB3	2.32	0.45
12:KF:658:SER:HB3	12:KF:665:HIS:HB3	1.98	0.45
13:LM:359:HIS:HD2	13:LN:360:LEU:HD11	1.82	0.45
14:ME:264:LEU:HD23	14:ME:267:LYS:HG3	1.98	0.45
14:MJ:320:ARG:HA	14:MJ:323:GLN:HB2	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NA:599:ILE:HB	15:NA:916:LEU:HG	1.99	0.45
15:NC:528:ARG:NH2	15:NC:577:PRO:HG2	2.32	0.45
15:ND:854:VAL:O	15:ND:858:ILE:HG12	2.17	0.45
16:OB:1085:ARG:H	16:OB:1085:ARG:HG2	1.61	0.45
18:QC:137:ALA:HA	18:QC:140:TRP:HB3	1.99	0.45
1:AA:290:CYS:HA	1:AA:298:ILE:HD11	1.99	0.45
2:AB:425:ALA:HA	2:AB:428:ARG:HB3	1.98	0.45
2:AC:505:VAL:HG22	10:IB:1255:LEU:HD23	1.99	0.45
1:AI:39:SER:HB3	1:AI:70:ASN:HB3	1.98	0.45
1:AL:622:ALA:HA	1:AL:625:ARG:HB2	1.99	0.45
1:AL:692:PRO:HG3	1:AL:998:LEU:HD12	1.99	0.45
3:CA:967:HIS:HB3	3:CA:970:ALA:HB3	1.99	0.45
4:DD:103:LEU:HD13	4:DD:106:ASN:HB3	1.98	0.45
4:DF:29:LEU:HD21	4:DF:126:LEU:HG	1.98	0.45
5:EB:3490:TYR:HE2	5:EB:3562:LYS:HB3	1.81	0.45
6:FA:2059:VAL:HG23	9:HA:754:LEU:HB3	1.98	0.45
6:FE:921:MET:HG3	6:FE:1092:PRO:HG3	1.97	0.45
6:FE:1197:ILE:HG13	6:FE:1260:LEU:HD22	1.98	0.45
6:FE:1289:HIS:O	6:FE:1291:TYR:N	2.50	0.45
6:FF:840:ALA:HB2	12:KC:665:HIS:HE1	1.82	0.45
7:GA:472:LEU:HB3	7:GA:494:LEU:HD21	1.99	0.45
8:GB:171:ILE:HG23	8:GB:181:HIS:HB2	1.97	0.45
8:GB:348:TYR:HD2	8:GB:376:GLU:HB3	1.82	0.45
8:GH:135:LEU:HD12	8:GH:168:MET:HE3	1.99	0.45
8:GH:541:MET:HE1	8:GH:544:LEU:HD22	1.99	0.45
7:GI:719:ILE:HD11	7:GI:800:VAL:HG21	1.99	0.45
8:GJ:168:MET:HE1	8:GJ:247:PRO:HG3	1.98	0.45
10:IA:742:ILE:HA	10:IA:745:ASP:HB3	1.99	0.45
10:IB:181:LEU:HD12	10:IB:201:LEU:HD22	1.98	0.45
10:IB:240:LEU:HD13	10:IB:792:ILE:HG13	1.99	0.45
10:IB:616:GLY:H	10:IB:758:ASN:ND2	2.11	0.45
11:JB:87:VAL:HG22	11:JB:90:ARG:HH12	1.81	0.45
11:JB:1689:LEU:HB3	11:JB:1698:PHE:HB3	1.98	0.45
13:LJ:403:SER:HB2	13:LJ:407:ARG:HH12	1.82	0.45
13:LN:384:LEU:HA	13:LN:387:THR:HG22	1.99	0.45
15:NA:1411:LEU:HD23	15:NA:1470:PHE:HE2	1.82	0.45
15:NC:735:HIS:HD2	15:NC:768:GLU:HG2	1.82	0.45
15:NC:881:LEU:HD12	15:NC:884:LYS:HB2	1.99	0.45
15:NC:1420:TYR:HE1	15:NC:1478:LEU:HB3	1.81	0.45
15:ND:624:ALA:O	15:ND:626:ARG:HG3	2.17	0.45
1:AA:121:ARG:HB3	1:AA:213:ALA:HB2	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:141:SER:HA	1:AA:226:MET:HB3	1.99	0.44
2:AB:63:THR:HA	2:AB:66:ARG:HD2	1.98	0.44
2:AB:506:LEU:HD13	2:AB:510:ASP:HB3	1.99	0.44
1:AD:133:PRO:O	1:AD:136:PHE:HB2	2.17	0.44
1:AE:316:ILE:HD13	9:HD:872:MET:HG2	1.99	0.44
1:AE:403:TYR:CZ	1:AE:465:MET:HG3	2.52	0.44
1:AI:127:SER:HB3	1:AI:206:VAL:HG23	1.98	0.44
3:BA:920:ARG:HH22	16:OA:177:THR:HG21	1.82	0.44
3:BC:937:ASP:HA	3:BC:940:MET:HB2	1.99	0.44
3:CG:1209:ALA:HB3	3:CG:1223:GLU:HA	1.99	0.44
4:DA:3:TRP:CD1	4:DA:3:TRP:H	2.35	0.44
4:DC:93:ILE:HD11	4:DC:168:SER:HB2	1.99	0.44
4:DD:86:ASP:HB3	4:DD:89:ASN:HB2	2.00	0.44
5:EB:4341:ARG:HG2	5:EB:4364:ALA:HB2	1.98	0.44
5:EB:4405:ILE:O	5:EB:4406:MET:C	2.60	0.44
5:EB:4500:THR:HG21	5:EB:4667:PRO:HG2	1.99	0.44
5:EB:4658:ASP:HB3	5:EB:4670:TRP:HZ2	1.83	0.44
5:EC:3373:LYS:HG3	5:EC:3378:GLY:HA2	1.98	0.44
6:FA:2098:TYR:CZ	9:HA:875:THR:HG22	2.51	0.44
6:FB:2062:LEU:HG	9:HD:750:PRO:HG2	1.98	0.44
6:FD:843:LEU:C	7:GC:896:ARG:NH1	2.75	0.44
6:FD:1089:ARG:O	6:FD:1090:LEU:C	2.60	0.44
6:FD:1434:ALA:O	6:FD:1435:GLU:C	2.60	0.44
6:FE:1198:TYR:O	6:FE:1199:GLY:C	2.59	0.44
6:FE:1232:LYS:C	6:FE:1233:ILE:HG13	2.42	0.44
8:GB:267:TRP:CZ2	7:GC:397:LEU:HA	2.52	0.44
8:GH:11:GLY:HA3	8:GH:41:ARG:HG2	1.98	0.44
7:GI:614:TRP:CE3	7:GI:646:MET:HG2	2.51	0.44
9:HC:553:TYR:HD1	9:HC:575:ARG:HE	1.66	0.44
10:IC:698:GLN:NE2	10:IC:703:GLY:HA2	2.32	0.44
11:JA:2131:ARG:HH11	11:JA:2136:GLU:HG2	1.82	0.44
12:KC:364:LEU:O	12:KC:368:ARG:HG2	2.17	0.44
12:KC:405:PRO:HA	12:KC:408:TYR:HB3	1.99	0.44
12:KE:342:MET:SD	12:KE:346:PRO:HB2	2.57	0.44
13:LJ:422:GLN:HA	13:LJ:425:LYS:NZ	2.32	0.44
13:LM:336:VAL:O	13:LM:340:LYS:HG2	2.17	0.44
15:NA:745:THR:HB	15:NA:858:ILE:HG23	1.99	0.44
15:NC:854:VAL:O	15:NC:858:ILE:HG12	2.17	0.44
15:NC:1524:ARG:HH21	18:QD:57:ASN:CG	2.25	0.44
15:ND:1032:VAL:HG23	15:ND:1104:ARG:HB3	1.99	0.44
16:OB:195:LEU:HB2	16:OB:284:GLU:HG2	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:RC:22:ARG:HE	19:RC:174:LEU:HD22	1.82	0.44
1:AD:799:THR:HG22	1:AD:998:LEU:HA	1.98	0.44
2:AF:61:ARG:NH1	6:FB:1586:GLN:HE22	2.16	0.44
1:AH:73:THR:HG22	1:AH:75:ALA:H	1.82	0.44
2:AK:176:VAL:HG11	16:OB:25:ALA:HB1	1.99	0.44
1:AL:364:LYS:HD3	1:AL:364:LYS:HA	1.80	0.44
3:CE:4468:LYS:HE2	3:CE:4490:ASP:HA	1.99	0.44
3:CJ:1123:LEU:HA	10:IB:770:GLY:HA3	1.98	0.44
3:CL:1158:PHE:CE1	3:CL:4504:ILE:HG23	2.52	0.44
3:CL:1274:ARG:HH22	3:CL:4447:CYS:N	2.15	0.44
4:DB:76:MET:HB3	4:DE:9:PHE:HZ	1.81	0.44
4:DF:20:LEU:O	4:DF:24:LYS:HG2	2.17	0.44
5:EA:4348:LEU:HA	5:EA:4351:VAL:HG12	2.00	0.44
5:EB:3636:ILE:HG23	5:EB:4055:ARG:NH2	2.32	0.44
5:EB:4817:LEU:HD23	5:EB:4817:LEU:H	1.81	0.44
6:FA:1746:PRO:HB3	6:FA:1926:TYR:HE2	1.81	0.44
6:FA:2053:LYS:HE3	6:FA:2053:LYS:HB3	1.30	0.44
6:FB:2033:LEU:HD23	9:HD:816:LEU:HD13	2.00	0.44
6:FC:1699:PRO:HA	6:FC:1722:PHE:HB3	1.98	0.44
6:FC:2072:ILE:HG12	9:HB:855:ARG:HG3	2.00	0.44
6:FD:911:SER:C	6:FD:912:ILE:HG23	2.42	0.44
6:FD:916:PRO:O	6:FD:917:TRP:C	2.60	0.44
6:FD:1294:LEU:HD11	6:FD:1391:TYR:CD1	2.53	0.44
6:FD:1441:ILE:O	6:FD:1443:GLY:N	2.50	0.44
6:FE:800:ALA:HB3	6:FE:910:ILE:O	2.17	0.44
6:FE:813:GLN:O	6:FE:815:SER:N	2.50	0.44
6:FE:1217:GLU:O	6:FE:1219:GLU:N	2.50	0.44
6:FE:1293:THR:O	6:FE:1295:ALA:N	2.50	0.44
6:FF:800:ALA:HB2	6:FF:913:LEU:HD11	1.99	0.44
7:GA:833:CYS:HA	7:GA:836:VAL:HG22	1.98	0.44
7:GC:454:PHE:HZ	7:GC:592:ILE:HD12	1.81	0.44
8:GD:215:LEU:HA	8:GD:240:ALA:HB1	1.99	0.44
7:GE:309:LEU:HD11	7:GE:360:VAL:HG23	1.99	0.44
7:GE:510:THR:HB	7:GE:632:VAL:HG11	1.98	0.44
8:GH:163:MET:HE3	8:GH:164:PRO:HD2	1.98	0.44
8:GH:192:VAL:HG21	7:GI:422:LEU:HD11	1.99	0.44
7:GI:176:ARG:HE	7:GI:180:ARG:HH12	1.64	0.44
7:GI:515:SER:HA	7:GI:569:THR:HB	1.98	0.44
7:GI:620:HIS:HB2	7:GI:643:SER:HB3	1.99	0.44
9:HA:858:LEU:HD23	9:HA:858:LEU:HA	1.78	0.44
9:HB:526:VAL:HB	9:HB:579:LEU:HB2	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IB:890:GLY:HA2	10:IB:893:PHE:CZ	2.53	0.44
10:IB:1109:CYS:HA	10:IB:1112:LEU:HD12	1.99	0.44
11:JC:1004:ARG:HH12	11:JC:1152:HIS:CG	2.36	0.44
12:KG:521:PRO:O	12:KG:522:ARG:HD3	2.17	0.44
13:LA:513:LEU:HD21	13:LB:514:TYR:CE1	2.53	0.44
13:LI:395:ILE:HD12	13:LJ:398:ARG:HH22	1.80	0.44
14:MI:262:PRO:HA	14:MI:265:SER:HB3	1.98	0.44
15:NB:605:LEU:HB2	15:NB:923:ASP:HB2	2.00	0.44
15:NB:937:MET:HA	15:NB:940:TYR:HB3	1.99	0.44
15:ND:922:LEU:HD11	15:ND:1105:HIS:CD2	2.52	0.44
3:BC:790:ASN:HB3	3:BC:811:ILE:HG22	1.99	0.44
3:BC:795:GLU:HB2	3:BC:816:LYS:HE3	1.99	0.44
3:CA:687:GLU:HA	3:CA:690:MET:HE3	1.99	0.44
3:CB:891:ILE:HA	3:CB:894:LYS:HE2	1.98	0.44
3:CL:1152:LEU:HD21	10:IC:377:PRO:HG3	1.99	0.44
4:DD:359:GLU:HA	4:DD:362:LYS:NZ	2.32	0.44
6:FC:1745:SER:HB3	6:FC:1792:TYR:H	1.82	0.44
6:FC:2066:GLU:HG3	6:FC:2067:MET:N	2.32	0.44
6:FD:962:PHE:HE2	6:FD:965:TRP:HB2	1.78	0.44
6:FE:886:THR:HA	6:FE:900:ALA:HB2	1.98	0.44
6:FE:1079:MET:HG2	6:FE:1102:TYR:HD2	1.82	0.44
6:FF:1203:ARG:HA	6:FF:1203:ARG:HD2	1.67	0.44
7:GA:536:THR:CA	9:HB:553:TYR:H	2.30	0.44
7:GG:275:LYS:HB3	7:GG:279:ARG:NH2	2.32	0.44
8:GH:367:CYS:HB3	8:GH:394:PHE:CE1	2.52	0.44
8:GH:676:TRP:HB2	8:GH:735:LEU:HD13	2.00	0.44
7:GI:365:ALA:HB1	7:GI:388:PRO:HA	1.99	0.44
7:GI:368:PHE:HZ	7:GI:439:ALA:HB1	1.83	0.44
7:GK:438:LYS:HE2	7:GK:464:LEU:HG	1.98	0.44
9:HB:800:VAL:O	13:LE:533:ALA:HA	2.16	0.44
10:IB:991:MET:HE1	10:IB:1108:LEU:HD11	1.99	0.44
10:IC:167:LYS:HB3	10:IC:167:LYS:HE2	1.81	0.44
11:JA:1130:LEU:O	11:JA:1134:GLU:HG2	2.18	0.44
11:JA:1414:ALA:HB2	11:JA:1504:ARG:HE	1.82	0.44
11:JC:442:ARG:HA	11:JC:445:GLN:HB3	1.99	0.44
11:JC:1591:HIS:CE1	11:JC:1593:VAL:HG13	2.52	0.44
12:KA:581:GLY:HA2	12:KA:654:ILE:HG22	2.00	0.44
12:KA:668:ILE:HB	12:KA:678:ALA:HB3	1.99	0.44
12:KC:405:PRO:HD3	12:KC:489:MET:HG3	1.99	0.44
12:KC:579:LEU:HD21	12:KC:726:ASP:OD2	2.18	0.44
12:KF:270:LYS:HD2	12:KF:270:LYS:HA	1.83	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LO:384:LEU:HB3	13:LP:384:LEU:HD22	1.98	0.44
14:MB:227:GLN:HA	14:MB:230:VAL:HG12	1.98	0.44
14:MG:83:TYR:HB3	14:MG:87:LEU:HD23	1.99	0.44
14:MJ:246:ASN:O	14:MJ:249:GLU:HB2	2.17	0.44
15:NB:698:PRO:HG2	15:NB:890:ARG:O	2.18	0.44
15:NB:1332:MET:HA	15:NB:1335:TYR:HD2	1.81	0.44
15:NC:545:VAL:HG23	15:NC:1193:VAL:HG23	1.98	0.44
15:NC:952:TRP:HZ2	15:NC:1177:LEU:HD13	1.82	0.44
15:ND:1508:PHE:O	15:ND:1512:MET:HG3	2.18	0.44
1:AD:243:VAL:HG12	10:IB:738:PRO:HG3	1.98	0.44
1:AE:728:VAL:HA	1:AE:734:MET:HG2	1.99	0.44
3:BA:785:ARG:HD2	3:BA:804:ARG:HH12	1.83	0.44
3:BB:787:ILE:HG12	3:BB:810:PRO:HB2	1.99	0.44
3:CC:830:CYS:HB2	3:CC:839:ALA:HB2	2.00	0.44
5:EA:4406:MET:N	5:EA:4406:MET:SD	2.91	0.44
5:EA:4817:LEU:HD23	5:EA:4817:LEU:H	1.82	0.44
5:EB:4665:LEU:HD23	5:EB:4665:LEU:HA	1.82	0.44
5:EC:4416:PHE:HZ	5:EC:4723:SER:HA	1.83	0.44
6:FE:822:GLY:O	6:FE:824:TYR:N	2.50	0.44
6:FE:1295:ALA:HB3	6:FE:1392:LYS:HB3	2.00	0.44
6:FF:1208:ALA:HB3	6:FF:1286:LEU:HD22	1.98	0.44
7:GI:322:GLY:HA3	7:GI:581:ARG:HD2	1.99	0.44
8:GJ:300:ARG:HD2	8:GJ:419:PHE:HE1	1.81	0.44
8:GL:75:GLN:HG3	8:GL:86:ALA:HA	1.98	0.44
9:HA:400:ALA:HA	9:HA:402:ARG:NH1	2.33	0.44
10:IA:886:LEU:HD12	16:OA:1040:PHE:HE1	1.82	0.44
10:IA:897:ARG:HB2	10:IA:903:HIS:HA	1.99	0.44
10:IA:1221:THR:H	10:IA:1224:HIS:HB2	1.82	0.44
10:IB:1221:THR:H	10:IB:1224:HIS:HB2	1.82	0.44
10:IC:897:ARG:HD2	10:IC:903:HIS:HA	1.98	0.44
11:JA:756:SER:HB3	11:JA:1491:ALA:HA	2.00	0.44
11:JA:843:LEU:HD21	11:JA:916:GLU:HB2	1.99	0.44
11:JB:1667:THR:HG23	11:JB:1671:MET:HE3	1.98	0.44
11:JC:874:VAL:O	11:JC:875:LEU:HD12	2.17	0.44
12:KA:524:PHE:HZ	12:KA:704:PRO:HD2	1.82	0.44
12:KB:352:LYS:HE3	12:KB:386:LEU:HA	2.00	0.44
15:NA:685:PHE:CE2	15:NA:689:ASN:HA	2.53	0.44
15:NB:702:LEU:HD12	15:NB:703:GLU:HB3	1.99	0.44
1:AH:666:LEU:HD23	1:AH:720:LEU:HD13	2.00	0.44
1:AI:829:VAL:HG11	1:AI:989:LEU:HB3	2.00	0.44
2:AJ:160:ARG:HD2	2:AJ:160:ARG:HA	1.78	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:1031:THR:O	1:AL:1032:PHE:C	2.60	0.44
5:EA:3661:PHE:HD1	5:EA:3664:THR:H	1.66	0.44
5:EC:4094:LEU:HD13	5:EC:4094:LEU:HA	1.73	0.44
5:EC:4167:ASP:HB3	5:EC:4170:LYS:HG2	2.00	0.44
6:FA:1764:ILE:HG12	6:FA:1767:ARG:HH21	1.82	0.44
6:FD:1094:SER:O	6:FD:1095:LEU:C	2.60	0.44
6:FD:1225:ILE:HG23	6:FD:1231:ARG:HD3	1.99	0.44
6:FD:1242:GLN:HB3	6:FD:1243:PRO:HD2	2.00	0.44
6:FE:1095:LEU:HD13	6:FE:1095:LEU:HA	1.79	0.44
6:FF:854:TRP:CD2	6:FF:860:PRO:HD3	2.53	0.44
6:FF:1185:VAL:O	6:FF:1186:TRP:C	2.61	0.44
6:FF:1390:ALA:HA	6:FF:1416:GLN:HG2	1.99	0.44
8:GB:138:LEU:HB2	8:GB:171:ILE:HD12	1.99	0.44
8:GB:300:ARG:HH11	8:GB:467:ALA:HB3	1.81	0.44
8:GD:756:ALA:HB3	8:GJ:333:LYS:HD2	1.98	0.44
8:GF:56:CYS:O	8:GF:57:ARG:HD3	2.17	0.44
7:GI:230:ARG:HE	7:GI:235:ARG:HB3	1.81	0.44
8:GJ:183:LEU:HA	8:GJ:254:LYS:HD2	1.99	0.44
8:GJ:692:MET:HA	8:GJ:693:PRO:HD3	1.87	0.44
8:GL:638:LEU:HD22	8:GL:654:LEU:HD23	2.00	0.44
10:IB:362:HIS:HD2	10:IB:429:ARG:HH22	1.65	0.44
11:JB:2094:ILE:HD11	11:JB:2110:LEU:HB2	1.99	0.44
11:JB:2254:LEU:HA	11:JB:2254:LEU:HD23	1.80	0.44
12:KA:591:ARG:HB2	12:KA:709:VAL:HB	1.98	0.44
12:KB:370:LEU:HD22	12:KB:377:LEU:HD21	2.00	0.44
12:KB:531:GLN:HE22	12:KB:551:SER:H	1.64	0.44
12:KC:321:GLU:HA	12:KC:324:ARG:HB3	1.99	0.44
12:KC:526:TRP:HB3	12:KC:545:LEU:HD13	1.99	0.44
12:KF:521:PRO:HD3	12:KF:540:LEU:HD23	1.99	0.44
13:LB:376:ARG:O	13:LB:380:MET:HG3	2.17	0.44
15:NA:622:THR:HG23	15:NA:650:ARG:HH12	1.81	0.44
15:NA:843:ASN:HB3	15:NA:845:LEU:HD23	1.98	0.44
15:NA:1456:PHE:HE2	15:NA:1461:TYR:HB2	1.82	0.44
15:NB:564:ARG:HH22	15:NB:622:THR:HB	1.82	0.44
15:NB:591:TRP:HB3	15:NB:592:LEU:HD12	2.00	0.44
15:NC:891:TRP:HA	15:NC:1152:GLU:C	2.43	0.44
16:OA:743:PRO:HD2	18:QD:89:ARG:HH12	1.83	0.44
16:OB:263:ALA:HB1	16:OB:267:GLU:HB2	1.99	0.44
16:OC:263:ALA:HB1	16:OC:267:GLU:HB2	2.00	0.44
19:RA:34:PHE:HA	19:RA:37:ILE:HG12	1.99	0.44
1:AA:915:TRP:CE2	13:LK:359:HIS:HB2	2.51	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:171:PHE:HB2	1:AD:185:ARG:HH21	1.82	0.44
1:AE:715:LEU:HD12	1:AE:715:LEU:HA	1.89	0.44
2:AF:428:ARG:HH21	2:AF:432:GLU:CD	2.25	0.44
2:AF:502:LEU:HG	2:AF:506:LEU:HD12	1.98	0.44
2:AJ:44:LEU:HD23	2:AJ:285:PHE:HB3	1.99	0.44
2:AK:147:LEU:HA	2:AK:150:ALA:HB3	1.99	0.44
2:AK:190:LEU:HD11	2:AK:195:ASP:HA	2.00	0.44
2:AK:509:ALA:HB1	1:AL:231:ILE:HD11	1.99	0.44
3:BB:706:GLU:OE1	10:IB:1378:GLN:HG2	2.18	0.44
3:CB:775:ASP:HA	3:CB:778:GLN:HB2	1.99	0.44
3:CI:1237:VAL:HG21	3:CI:4468:LYS:HG2	2.00	0.44
3:CI:4473:VAL:HG23	3:CI:4474:GLU:H	1.82	0.44
3:CJ:1258:PRO:HA	3:CJ:1261:TYR:HB2	1.98	0.44
4:DA:16:LEU:HD11	4:DA:161:LEU:HD23	2.00	0.44
4:DC:64:LEU:HD23	4:DC:64:LEU:HA	1.87	0.44
4:DC:119:LEU:HA	4:DC:122:ILE:HD12	1.99	0.44
5:EA:4154:LEU:HD22	5:EA:4174:ILE:HD11	1.98	0.44
5:EC:3841:GLN:HE22	11:JC:1045:THR:HG21	1.81	0.44
6:FC:2101:LEU:HD22	6:FC:2104:GLN:HE21	1.82	0.44
6:FE:1089:ARG:O	6:FE:1090:LEU:C	2.61	0.44
6:FE:1389:ARG:HE	6:FE:1389:ARG:HB3	1.53	0.44
7:GA:193:GLN:HA	7:GA:196:LEU:HD12	2.00	0.44
7:GG:906:VAL:HG22	7:GG:932:GLY:HA2	2.00	0.44
8:GH:560:TRP:CZ2	8:GH:564:LYS:HD2	2.53	0.44
8:GJ:639:LEU:HB3	8:GJ:649:PRO:HB2	2.00	0.44
7:GK:185:ARG:HG2	7:GK:697:PRO:HG2	2.00	0.44
7:GK:764:LEU:HD13	7:GK:870:ARG:HD3	1.98	0.44
10:IA:315:PHE:HZ	10:IA:536:ARG:HH21	1.66	0.44
10:IA:551:ASN:ND2	10:IA:803:ARG:HH21	2.14	0.44
11:JA:750:ALA:O	11:JA:754:ARG:HG2	2.18	0.44
11:JA:825:LEU:HD12	11:JA:825:LEU:HA	1.85	0.44
11:JC:195:LEU:HD12	11:JC:1036:LEU:HG	1.99	0.44
11:JC:489:VAL:HG22	11:JC:490:THR:H	1.83	0.44
12:KC:379:SER:HA	12:KC:720:LEU:HB3	1.98	0.44
12:KC:523:VAL:HG23	12:KC:525:PRO:HG3	1.99	0.44
12:KE:479:ALA:HA	12:KE:482:ARG:HG2	1.98	0.44
15:NB:683:ALA:HB3	15:NB:915:VAL:HA	2.00	0.44
15:NB:721:PRO:HD3	15:NB:762:GLN:HE21	1.81	0.44
15:NC:565:TRP:HZ2	16:OB:1039:ILE:HA	1.82	0.44
15:NC:666:ILE:HA	15:NC:724:ASN:HB2	1.99	0.44
15:ND:626:ARG:HD3	15:ND:690:TYR:HA	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:OB:1047:GLY:HA2	16:OB:1053:THR:HG22	2.00	0.44
19:RD:38:ASP:HB3	19:RD:41:GLY:H	1.82	0.44
20:SC:11:ALA:HA	20:SC:14:LYS:HD3	1.99	0.44
2:AC:558:ARG:HA	11:JA:1116:ARG:NH2	2.33	0.44
1:AD:41:ILE:HG22	1:AD:47:LEU:HG	2.00	0.44
1:AE:419:GLU:HB3	16:OC:76:PHE:HD2	1.83	0.44
2:AF:507:PRO:HG3	3:BC:752:PRO:HD3	1.99	0.44
1:AI:274:ARG:HG3	1:AI:275:HIS:H	1.83	0.44
1:AL:38:VAL:HG23	1:AL:39:SER:H	1.83	0.44
3:BB:845:LYS:HA	3:BB:848:ILE:HG22	1.99	0.44
3:CI:1186:LEU:HD21	10:IA:1423:PRO:HG3	2.00	0.44
4:DD:319:LYS:HA	4:DD:324:VAL:HG22	1.98	0.44
4:DE:9:PHE:CD2	4:DE:12:LEU:HD12	2.53	0.44
4:DF:34:ASP:HB3	4:DF:104:GLU:OE2	2.18	0.44
5:EA:4049:ALA:HA	6:FC:1905:GLN:HG2	2.00	0.44
5:EB:4653:GLU:HB3	5:EB:4654:ASP:H	1.66	0.44
5:EC:3651:ALA:H	9:HA:499:ARG:HG2	1.83	0.44
5:EC:3860:ALA:HA	5:EC:4002:ARG:HH12	1.82	0.44
5:EC:4403:LEU:HD23	5:EC:4403:LEU:HA	1.82	0.44
6:FB:2062:LEU:HD13	6:FB:2062:LEU:HA	1.76	0.44
6:FC:1828:VAL:HG22	6:FC:1838:VAL:HG13	1.98	0.44
6:FD:1027:LEU:O	6:FD:1028:LYS:C	2.60	0.44
6:FD:1098:VAL:O	6:FD:1101:ALA:N	2.50	0.44
6:FE:1016:PRO:HG2	6:FE:1017:VAL:HG12	1.99	0.44
6:FF:832:GLY:HA3	6:FF:844:ALA:HB2	1.99	0.44
7:GA:424:ARG:HD2	7:GA:424:ARG:HA	1.85	0.44
7:GC:423:TRP:HB3	7:GC:426:ASN:ND2	2.32	0.44
7:GC:764:LEU:HD21	7:GC:767:LEU:HD11	2.00	0.44
8:GD:59:SER:HA	14:MD:138:LEU:HD21	2.00	0.44
8:GD:192:VAL:HG22	7:GE:382:PRO:HG2	1.98	0.44
7:GE:524:SER:HB3	7:GE:555:PRO:HD3	1.99	0.44
8:GF:321:LEU:HD11	13:LA:415:GLU:HG3	1.98	0.44
8:GF:380:MET:O	8:GF:384:THR:HG22	2.17	0.44
7:GG:535:PRO:HB2	9:HA:553:TYR:N	2.32	0.44
8:GH:192:VAL:HG22	7:GI:381:ARG:HH12	1.81	0.44
8:GL:423:ILE:HG12	8:GL:500:THR:HG23	2.00	0.44
9:HA:754:LEU:HD21	9:HA:840:HIS:HB2	2.00	0.44
9:HB:566:PRO:HB3	9:HB:569:ARG:HH22	1.83	0.44
9:HB:762:HIS:O	9:HB:763:GLN:C	2.59	0.44
10:IC:208:PHE:HB2	10:IC:239:LEU:HD13	2.00	0.44
11:JB:57:GLU:HB3	11:JB:90:ARG:HE	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JB:782:VAL:HG21	11:JB:900:PRO:HB2	1.99	0.44
11:JC:1554:LEU:HD23	11:JC:1554:LEU:HA	1.86	0.44
11:JC:2250:LEU:HD12	11:JC:2251:PRO:HD2	2.00	0.44
13:LE:482:LEU:HD13	13:LF:482:LEU:HD22	2.00	0.44
13:LI:391:ALA:O	13:LI:395:ILE:HG12	2.18	0.44
15:NA:931:TRP:CD1	15:NA:934:LEU:HB2	2.53	0.44
15:NA:966:VAL:HA	15:NA:1462:GLN:NE2	2.32	0.44
15:NB:808:ILE:HA	15:NB:811:GLU:HB2	2.00	0.44
15:NC:1387:VAL:HA	15:NC:1391:LEU:HD23	1.98	0.44
15:ND:895:GLY:HA3	15:ND:1152:GLU:HG3	2.00	0.44
19:RA:58:VAL:HG12	19:RA:60:PHE:H	1.82	0.44
1:AA:381:ARG:HD2	1:AA:381:ARG:HA	1.83	0.44
2:AC:49:HIS:CD2	2:AC:51:ALA:H	2.35	0.44
1:AD:266:HIS:HA	1:AD:272:LEU:HB3	2.00	0.44
1:AI:715:LEU:HB2	13:LC:364:ASN:ND2	2.33	0.44
1:AI:715:LEU:HB2	13:LC:364:ASN:HD21	1.82	0.44
2:AK:66:ARG:NH1	2:AK:173:ARG:HD3	2.33	0.44
3:CB:827:ALA:HB1	3:CB:843:TYR:CE1	2.53	0.44
3:CI:1219:VAL:HB	3:CI:1254:MET:HE3	1.99	0.44
5:EA:3300:LEU:HD13	5:EA:4160:LEU:HD12	2.00	0.44
5:EC:3651:ALA:O	9:HA:499:ARG:HD3	2.18	0.44
5:EC:4089:HIS:CG	5:EC:4090:CYS:H	2.35	0.44
6:FE:837:ALA:O	6:FE:839:GLY:N	2.51	0.44
6:FE:964:LEU:HB2	6:FE:965:TRP:H	1.62	0.44
6:FF:1011:TYR:O	6:FF:1012:PRO:C	2.60	0.44
7:GA:676:ALA:HB3	7:GA:692:HIS:HB2	1.99	0.44
7:GC:205:ARG:HD2	7:GC:828:PRO:HB3	2.00	0.44
8:GF:138:LEU:HD13	8:GF:156:LEU:HD22	2.00	0.44
8:GJ:138:LEU:HD13	8:GJ:156:LEU:HD22	2.00	0.44
8:GL:74:LYS:HG2	8:GL:95:ILE:HG21	2.00	0.44
9:HB:403:ASP:HA	9:HB:406:ALA:HB3	2.00	0.44
9:HD:868:LEU:HD22	9:HD:868:LEU:HA	1.68	0.44
10:IA:991:MET:HE1	10:IA:1108:LEU:HD11	2.00	0.44
10:IC:208:PHE:HB3	10:IC:239:LEU:HB2	2.00	0.44
11:JA:437:LEU:HD11	11:JA:1461:PHE:HB3	1.99	0.44
11:JB:1742:MET:HE2	11:JB:1791:LEU:HD22	2.00	0.44
11:JB:1968:ARG:HH22	11:JB:1971:TYR:HB3	1.83	0.44
11:JC:1523:ARG:HH11	11:JC:1524:PHE:HE2	1.66	0.44
12:KB:228:GLU:HB2	12:KB:230:GLN:HG2	2.00	0.44
12:KE:531:GLN:HG3	12:KE:566:ALA:HB1	2.00	0.44
12:KG:565:TRP:CE3	12:KG:709:VAL:HG23	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NA:808:ILE:HG22	15:NA:878:ILE:HG21	1.98	0.44
15:NC:1325:ALA:HB3	15:NC:1328:VAL:HB	1.99	0.44
16:OA:742:PHE:HA	18:QD:89:ARG:NH1	2.31	0.44
19:RA:127:LEU:HB3	19:RA:132:LEU:HD11	1.98	0.44
19:RB:51:MET:HE2	19:RB:67:VAL:HG11	2.00	0.44
1:AA:893:ARG:CZ	1:AA:894:SER:HB3	2.47	0.44
2:AB:72:PHE:HB3	2:AB:164:TYR:HD2	1.83	0.44
1:AE:338:MET:HA	1:AE:341:GLN:HG3	1.99	0.44
2:AF:361:GLU:HG3	2:AF:373:ARG:HB3	1.99	0.44
2:AF:501:TYR:HD2	2:AF:502:LEU:HD12	1.83	0.44
3:CJ:1121:ARG:CZ	3:CJ:1131:LEU:HD22	2.48	0.44
3:CL:4504:ILE:HD12	3:CL:4524:LEU:HD21	1.99	0.44
4:DA:12:LEU:HB3	4:DA:164:PHE:CZ	2.53	0.44
4:DB:162:VAL:O	4:DB:166:VAL:HG23	2.18	0.44
4:DC:181:ILE:HG22	4:DC:182:LEU:HG	2.00	0.44
4:DC:329:ARG:HB3	4:DC:333:LYS:NZ	2.33	0.44
5:EA:3596:TRP:CD1	5:EA:3607:ARG:HG3	2.53	0.44
5:EA:4230:VAL:HA	5:EA:4233:TYR:HB3	2.00	0.44
5:EC:4221:ALA:HB2	5:EC:4229:MET:HE1	1.99	0.44
5:EC:4886:LYS:HB2	5:EC:4887:GLY:H	1.65	0.44
6:FD:1238:ARG:HA	6:FD:1238:ARG:HD3	1.67	0.44
6:FD:1441:ILE:O	6:FD:1442:GLU:C	2.59	0.44
6:FE:907:ASN:HD22	6:FE:907:ASN:HA	1.71	0.44
6:FE:1075:VAL:HG13	6:FE:1105:ARG:HB2	2.00	0.44
6:FE:1231:ARG:HB3	6:FE:1270:LEU:HD21	1.99	0.44
6:FE:1294:LEU:HD22	6:FE:1294:LEU:HA	1.86	0.44
6:FE:1443:GLY:C	6:FE:1445:SER:H	2.26	0.44
6:FF:917:TRP:CG	6:FF:918:GLN:N	2.85	0.44
6:FF:1219:GLU:H	6:FF:1219:GLU:HG2	1.42	0.44
7:GC:807:ARG:HB3	7:GC:812:VAL:HG21	1.98	0.44
7:GE:715:THR:HG21	7:GE:796:PHE:HB3	2.00	0.44
7:GE:850:GLY:HA3	7:GE:934:ARG:HE	1.83	0.44
7:GG:308:TYR:CE1	7:GG:450:LYS:HD3	2.53	0.44
7:GG:612:ARG:HB2	7:GG:662:VAL:HG22	2.00	0.44
7:GI:780:ASN:HD22	7:GI:788:GLU:HG2	1.82	0.44
7:GK:543:LYS:HD3	9:HC:661:HIS:CD2	2.52	0.44
7:GK:604:ALA:HB1	7:GK:678:LEU:HD11	2.00	0.44
8:GL:132:PRO:HD3	8:GL:236:LEU:HD22	2.00	0.44
9:HA:852:LYS:HA	9:HA:852:LYS:HD3	1.73	0.44
9:HB:528:PRO:HB3	9:HB:603:HIS:CE1	2.52	0.44
9:HC:496:GLU:HG3	9:HC:499:ARG:HD2	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IA:1003:VAL:HB	10:IA:1043:PHE:HB2	2.00	0.44
10:IC:368:PRO:HD3	10:IC:388:CYS:HB2	2.00	0.44
11:JA:1499:HIS:CE1	11:JA:1501:LEU:HD23	2.53	0.44
11:JB:1372:PRO:HA	11:JB:1375:TYR:HB3	1.99	0.44
11:JC:746:VAL:HA	11:JC:749:LYS:HG2	1.99	0.44
12:KB:520:LYS:HD2	12:KB:521:PRO:HD2	1.99	0.44
12:KC:319:TYR:CE2	12:KC:353:ALA:HB1	2.53	0.44
12:KG:375:TYR:HE1	12:KG:719:GLU:HA	1.83	0.44
12:KG:525:PRO:HA	12:KG:542:PRO:HG3	1.99	0.44
13:LL:376:ARG:HA	13:LL:379:LYS:HE2	1.99	0.44
14:MD:81:ARG:HG3	14:MD:83:TYR:HD1	1.83	0.44
15:NA:694:MET:HE3	15:NA:694:MET:HB2	1.87	0.44
15:NB:726:CYS:HB3	15:NB:803:LEU:HD12	2.00	0.44
15:NB:745:THR:HB	15:NB:858:ILE:HG13	1.99	0.44
15:NC:528:ARG:HH22	15:NC:577:PRO:HG2	1.82	0.44
15:NC:600:LEU:HD11	15:NC:945:PHE:HB3	2.00	0.44
15:ND:866:LEU:HD22	15:ND:878:ILE:HG12	2.00	0.44
17:PB:124:ILE:HG23	17:PB:128:GLU:HB3	2.00	0.44
18:QC:52:LYS:HD2	18:QC:75:PHE:HE2	1.83	0.44
19:RC:58:VAL:HG22	19:RC:60:PHE:HD2	1.83	0.44
2:AB:327:ILE:HD13	1:AI:271:MET:HE2	2.00	0.43
2:AC:45:LEU:HD23	2:AC:286:GLU:HB2	2.00	0.43
2:AC:438:VAL:HG22	1:AD:460:VAL:HG21	2.00	0.43
2:AC:542:ASP:HA	5:EA:4627:PRO:HB3	1.99	0.43
1:AE:749:PRO:HB2	1:AE:787:ARG:HD2	2.00	0.43
2:AG:188:PHE:HD1	2:AG:190:LEU:H	1.66	0.43
2:AG:355:HIS:CE1	2:AG:375:CYS:HB3	2.53	0.43
2:AG:528:LEU:HD22	1:AH:91:ILE:HB	1.99	0.43
1:AH:212:ARG:HH12	11:JC:1338:SER:HA	1.82	0.43
2:AJ:319:LEU:HD13	2:AJ:324:ASP:HA	1.98	0.43
1:AL:993:ARG:HD3	1:AL:993:ARG:HA	1.70	0.43
3:BA:694:ARG:HD2	17:PA:290:PHE:CE1	2.50	0.43
3:BC:832:LEU:HD22	16:OC:164:THR:HG23	2.00	0.43
4:DA:172:ARG:HH12	4:DD:190:PRO:HD3	1.83	0.43
4:DF:16:LEU:HD13	4:DF:160:PHE:HD2	1.82	0.43
5:EA:3277:PHE:HE1	5:EA:3447:TYR:HD1	1.65	0.43
5:EB:3737:LEU:HD11	5:EB:3813:VAL:HG21	2.00	0.43
5:EB:4011:VAL:HB	5:EB:4166:SER:HB2	1.99	0.43
5:EB:4374:GLU:HA	5:EB:4379:THR:HG21	2.00	0.43
5:EB:4882:ARG:HH12	5:EB:4888:TRP:HE3	1.65	0.43
5:EC:4849:TYR:HB2	15:ND:1319:LEU:HD21	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FD:803:ARG:HH11	6:FD:905:GLU:HB3	1.82	0.43
6:FD:837:ALA:HA	12:KA:640:ASP:OD2	2.18	0.43
6:FD:1014:LYS:HB2	6:FD:1014:LYS:HE2	1.41	0.43
6:FD:1267:GLN:HB3	6:FD:1267:GLN:HE21	1.61	0.43
6:FF:924:LEU:HB3	6:FF:1092:PRO:HD2	2.00	0.43
7:GE:448:GLY:HA2	7:GE:514:VAL:HG22	2.00	0.43
8:GF:417:MET:HG2	8:GF:469:ASP:HB3	2.00	0.43
7:GK:441:LEU:HD13	7:GK:509:LEU:HD23	2.00	0.43
7:GK:855:ARG:HA	7:GK:855:ARG:HD3	1.84	0.43
8:GL:328:HIS:CG	8:GL:607:THR:HB	2.53	0.43
8:GL:426:LEU:HD13	8:GL:499:GLN:HE22	1.83	0.43
9:HA:604:SER:HB2	9:HA:619:PRO:HB2	1.99	0.43
9:HB:633:ASN:HA	9:HB:720:LYS:HE2	1.99	0.43
9:HB:759:GLU:O	9:HB:760:LYS:C	2.61	0.43
10:IB:884:TYR:HB2	10:IB:942:PHE:HE1	1.82	0.43
11:JA:882:ALA:HA	11:JA:891:VAL:HG12	2.00	0.43
11:JA:884:ASP:HB2	11:JA:1414:ALA:HB3	2.00	0.43
11:JA:2076:ASN:HD21	11:JA:2255:ARG:NH1	2.15	0.43
11:JC:164:MET:HA	11:JC:165:GLU:HA	1.82	0.43
11:JC:902:LEU:HB3	11:JC:935:TRP:CD1	2.53	0.43
12:KA:572:SER:HA	12:KA:703:TRP:CD1	2.53	0.43
12:KB:501:LEU:HD22	12:KB:502:LEU:HD23	2.00	0.43
12:KB:579:LEU:HD12	12:KB:656:ARG:HB2	2.00	0.43
12:KC:385:GLU:H	12:KC:385:GLU:HG2	1.70	0.43
12:KC:597:ALA:O	12:KC:703:TRP:HB2	2.18	0.43
12:KE:322:ALA:HA	12:KE:325:LEU:HD12	1.99	0.43
13:LO:381:LEU:O	13:LO:385:THR:HG23	2.18	0.43
15:NC:564:ARG:NH2	15:NC:622:THR:HB	2.33	0.43
16:OB:119:TRP:HB2	16:OB:149:ILE:HB	2.00	0.43
16:OC:1067:GLU:HG3	16:OC:1068:GLY:H	1.83	0.43
19:RA:71:LEU:HD23	19:RA:74:LEU:HD12	2.00	0.43
1:AA:236:PRO:HG2	1:AA:256:GLN:HG3	2.00	0.43
1:AA:238:CYS:HB3	1:AA:242:GLU:H	1.84	0.43
2:AC:296:ALA:H	1:AD:431:SER:HB2	1.83	0.43
1:AE:338:MET:HA	1:AE:341:GLN:HE21	1.83	0.43
2:AF:355:HIS:HA	2:AF:356:PRO:HD3	1.86	0.43
2:AG:19:VAL:HB	2:AG:47:ALA:HB3	2.00	0.43
1:AH:878:ARG:HH22	6:FB:2036:LEU:HD21	1.83	0.43
1:AI:636:LEU:HD11	7:GK:857:LEU:HD13	2.00	0.43
2:AK:178:GLU:CD	2:AK:179:ASP:H	2.25	0.43
3:CB:832:LEU:HA	17:PC:295:GLN:HE21	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DD:303:PHE:HB3	4:DD:354:TRP:HZ2	1.82	0.43
5:EA:3698:VAL:HG23	5:EA:3699:ASN:H	1.82	0.43
5:EA:4637:THR:HG22	5:EA:4708:LEU:HD13	1.99	0.43
5:EC:4405:ILE:HG22	5:EC:4406:MET:H	1.83	0.43
6:FA:2038:LEU:HD13	6:FA:2038:LEU:HA	1.73	0.43
6:FB:1580:ALA:HA	6:FB:1618:VAL:HG12	1.99	0.43
6:FC:1984:LYS:HA	6:FC:1984:LYS:HD2	1.65	0.43
6:FC:2088:MET:O	6:FC:2089:PRO:C	2.61	0.43
6:FD:809:ILE:HD11	6:FD:812:LEU:HD22	1.99	0.43
6:FD:1291:TYR:HD1	6:FD:1291:TYR:HA	1.75	0.43
6:FF:859:ASP:N	6:FF:859:ASP:OD2	2.51	0.43
6:FF:1300:LEU:O	6:FF:1302:ALA:N	2.50	0.43
6:FF:1390:ALA:O	6:FF:1391:TYR:C	2.62	0.43
7:GC:842:PRO:HA	7:GC:882:TYR:CD1	2.53	0.43
7:GC:843:LEU:HG	7:GC:846:LEU:HD11	2.01	0.43
8:GD:641:TYR:HB2	8:GD:664:ILE:HB	2.00	0.43
7:GE:323:LEU:HA	7:GE:579:PHE:HE2	1.83	0.43
8:GH:326:ARG:HH22	8:GH:376:GLU:N	2.17	0.43
7:GI:309:LEU:HD11	7:GI:440:ALA:HB1	2.00	0.43
8:GJ:276:MET:HE3	8:GJ:311:SER:HB3	2.01	0.43
7:GK:230:ARG:HD3	7:GK:235:ARG:NH2	2.33	0.43
7:GK:279:ARG:HG2	7:GK:280:PHE:HD1	1.82	0.43
10:IB:1070:ASP:HB3	10:IB:1077:LYS:HZ3	1.83	0.43
10:IB:1405:PRO:HG2	10:IB:1410:LEU:HD11	2.00	0.43
10:IC:698:GLN:HG3	16:OC:1081:ILE:HD11	1.99	0.43
10:IC:795:GLU:HG3	10:IC:805:LYS:NZ	2.33	0.43
11:JA:1803:ARG:HA	11:JA:1806:MET:HB2	1.99	0.43
11:JB:65:VAL:HG12	11:JB:121:ILE:HG12	2.00	0.43
11:JB:1584:LYS:HA	11:JB:1588:GLU:HA	1.99	0.43
12:KA:664:ILE:HD11	12:KA:700:LEU:HD13	2.00	0.43
12:KF:404:GLU:HA	12:KF:407:ILE:HB	2.00	0.43
12:KG:720:LEU:HD23	12:KG:720:LEU:HA	1.85	0.43
13:LL:378:GLU:HA	13:LL:381:LEU:HG	1.99	0.43
15:NB:613:GLN:HG3	15:NB:918:ALA:HB2	2.00	0.43
15:NB:702:LEU:HB3	15:NB:937:MET:SD	2.58	0.43
15:NB:922:LEU:HD23	15:NB:1394:LEU:HD22	2.00	0.43
15:ND:787:LEU:HD21	15:ND:896:ARG:HG3	1.99	0.43
17:PC:138:ARG:HG2	17:PC:142:TYR:CZ	2.53	0.43
19:RB:89:SER:HA	19:RB:90:PRO:HD3	1.90	0.43
1:AA:705:TRP:HE1	1:AA:1036:THR:HG23	1.83	0.43
1:AD:65:ILE:HD11	1:AD:222:LEU:HD22	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AD:261:CYS:HA	1:AD:264:ARG:HG2	1.99	0.43
1:AD:831:SER:HB3	1:AD:918:VAL:HG22	1.99	0.43
1:AE:131:ARG:HB2	1:AE:205:ARG:HH22	1.83	0.43
2:AF:259:VAL:HG23	2:AF:297:VAL:HB	1.99	0.43
2:AG:311:TRP:CD2	2:AG:345:MET:HG3	2.53	0.43
1:AH:231:ILE:HG22	10:IA:825:LEU:HD11	2.00	0.43
1:AH:282:HIS:CE1	10:IA:1359:ALA:HB2	2.53	0.43
1:AH:882:VAL:HG11	13:LJ:518:GLU:HG2	2.00	0.43
3:CE:1137:ALA:HA	10:IA:1184:ARG:HH21	1.83	0.43
3:CL:1156:GLU:HA	10:IC:398:ARG:HH12	1.83	0.43
4:DA:13:VAL:HG23	4:DA:97:LEU:HD13	2.00	0.43
5:EB:4717:ARG:NH1	5:EB:4720:LEU:HB2	2.33	0.43
5:EC:3395:TYR:HE2	5:EC:3607:ARG:HD3	1.81	0.43
5:EC:3787:GLU:HG2	5:EC:3790:ARG:NH1	2.33	0.43
5:EC:3798:LEU:HD11	5:EC:3813:VAL:HB	1.99	0.43
5:EC:4896:ARG:HH11	5:EC:4899:GLY:HA2	1.83	0.43
6:FA:1955:THR:HG21	9:HA:838:LYS:CA	2.48	0.43
6:FC:1683:LYS:HG3	6:FC:1690:TYR:CZ	2.53	0.43
6:FC:1907:ILE:HD11	6:FC:1912:PHE:HZ	1.84	0.43
6:FC:2018:ARG:HE	6:FC:2018:ARG:HB2	1.59	0.43
6:FD:1201:THR:O	6:FD:1202:PHE:C	2.61	0.43
6:FE:895:ILE:HG21	7:GE:967:PHE:CZ	2.52	0.43
6:FF:1213:VAL:HG12	6:FF:1231:ARG:HB2	2.00	0.43
6:FF:1392:LYS:HE3	6:FF:1392:LYS:HB3	1.82	0.43
7:GA:843:LEU:HD13	7:GA:935:VAL:HG13	2.00	0.43
8:GB:18:VAL:HG11	8:GB:527:ASP:HB3	2.01	0.43
8:GB:325:ILE:HD13	8:GB:371:GLN:HB2	2.00	0.43
8:GD:639:LEU:HD12	8:GD:649:PRO:HB2	2.00	0.43
7:GE:306:PRO:HG3	7:GE:342:GLY:HA3	2.00	0.43
7:GE:873:ALA:HA	7:GE:876:MET:HG2	2.00	0.43
8:GF:599:LEU:HA	8:GF:634:ILE:HD11	2.00	0.43
8:GH:182:GLU:HB3	8:GH:194:LYS:HB2	1.99	0.43
7:GI:890:MET:HE1	7:GI:951:MET:HB2	2.00	0.43
7:GK:576:TYR:HB3	7:GK:584:HIS:ND1	2.33	0.43
9:HB:779:PRO:O	9:HB:780:PHE:C	2.60	0.43
9:HD:761:CYS:HB3	9:HD:765:TRP:NE1	2.34	0.43
9:HD:762:HIS:O	9:HD:763:GLN:C	2.61	0.43
10:IB:618:ARG:HB2	10:IB:753:ARG:HA	1.99	0.43
10:IC:730:ARG:HB3	10:IC:739:ALA:HB2	2.00	0.43
11:JA:114:SER:HB3	11:JA:190:TRP:HH2	1.82	0.43
11:JB:1181:VAL:HG23	11:JB:1357:PHE:HD2	1.82	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LI:475:LEU:HD22	13:LJ:471:THR:HG22	2.01	0.43
14:MA:251:LEU:HD21	14:MB:250:ARG:HH21	1.83	0.43
14:ME:291:LEU:HD21	14:MF:290:ARG:NH1	2.33	0.43
14:MJ:308:GLU:HA	14:MJ:311:ILE:HG22	2.00	0.43
15:NA:881:LEU:HD22	15:NA:1131:LEU:HD21	2.00	0.43
15:NB:548:PRO:HG3	15:NB:551:ARG:HH21	1.82	0.43
15:NB:1525:ARG:HE	18:QC:60:ARG:NH1	2.16	0.43
15:NC:1094:LYS:HB3	15:NC:1098:LEU:HD13	2.00	0.43
15:NC:1498:ARG:NH1	20:SD:38:ARG:HB3	2.33	0.43
15:ND:1498:ARG:NH1	20:SB:44:PRO:HD3	2.33	0.43
16:OB:265:LEU:HB3	16:OB:266:GLN:H	1.66	0.43
19:RD:18:LYS:HB2	19:RD:105:MET:HB2	2.00	0.43
2:AB:160:ARG:HB3	5:EA:4624:SER:HB2	2.00	0.43
2:AB:501:TYR:CZ	2:AB:505:VAL:HG21	2.53	0.43
1:AH:993:ARG:HA	1:AH:993:ARG:HD3	1.74	0.43
1:AI:153:LEU:HB2	1:AI:182:ALA:HB2	1.99	0.43
1:AL:248:LEU:HD21	1:AL:277:ARG:HG2	1.99	0.43
1:AL:405:LEU:HD12	1:AL:405:LEU:HA	1.80	0.43
1:AL:906:LEU:HD11	1:AL:973:PHE:HE2	1.84	0.43
3:CF:1131:LEU:HB3	10:IB:1091:LEU:HD11	2.00	0.43
3:CG:1156:GLU:HG2	10:IC:411:MET:HE2	2.00	0.43
3:CI:1146:VAL:HG22	10:IA:381:HIS:HE1	1.83	0.43
4:DA:332:LEU:HB3	8:GF:411:SER:HB2	2.01	0.43
4:DC:395:MET:HA	14:MJ:320:ARG:HH12	1.82	0.43
4:DF:303:PHE:HB3	4:DF:354:TRP:HZ2	1.83	0.43
5:EA:4407:ASP:O	5:EA:4408:GLY:C	2.62	0.43
5:EB:3323:THR:HB	5:EB:3377:ALA:HB2	2.00	0.43
5:EB:4505:MET:HG3	5:EB:4699:PHE:CE1	2.54	0.43
5:EC:3821:PRO:HG2	5:EC:4242:PHE:CZ	2.53	0.43
6:FA:2072:ILE:HG21	9:HA:855:ARG:HG3	2.01	0.43
6:FC:1649:VAL:HG12	6:FC:1735:ILE:HD13	2.00	0.43
6:FC:2076:HIS:HE1	9:HB:857:ARG:HB3	1.82	0.43
6:FD:888:PRO:O	6:FD:889:SER:C	2.61	0.43
6:FD:965:TRP:CD1	6:FD:965:TRP:H	2.36	0.43
6:FD:1229:LYS:H	6:FD:1229:LYS:HG3	1.54	0.43
6:FE:850:CYS:HB3	6:FE:973:ILE:HG12	1.99	0.43
6:FE:864:LEU:HD11	6:FE:973:ILE:HD12	2.00	0.43
6:FE:992:PRO:CA	12:KB:230:GLN:O	2.58	0.43
6:FE:1251:ARG:HD3	6:FE:1252:MET:HE1	2.01	0.43
6:FE:1253:SER:O	6:FE:1254:GLY:C	2.60	0.43
6:FE:1389:ARG:O	6:FE:1390:ALA:C	2.61	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:962:PHE:CE2	6:FF:965:TRP:HB2	2.53	0.43
6:FF:1244:LEU:C	6:FF:1246:ILE:H	2.27	0.43
8:GH:326:ARG:HH22	8:GH:376:GLU:H	1.64	0.43
8:GJ:200:GLY:HA2	8:GJ:281:LEU:HD22	2.01	0.43
8:GL:171:ILE:HG23	8:GL:181:HIS:HB2	2.00	0.43
8:GL:499:GLN:HB2	8:GL:511:LEU:HD11	2.00	0.43
8:GL:777:LEU:HG	8:GL:781:MET:HE1	2.01	0.43
9:HA:564:ARG:HD2	9:HA:564:ARG:HA	1.78	0.43
9:HD:795:LEU:HD23	9:HD:795:LEU:HA	1.83	0.43
10:IA:830:VAL:HG22	11:JA:2040:GLN:HB2	1.99	0.43
10:IA:839:GLU:HA	10:IA:842:TYR:HD2	1.82	0.43
10:IA:1236:VAL:HG22	10:IA:1285:VAL:HG22	2.00	0.43
10:IA:1249:ALA:HB1	10:IA:1253:MET:HE2	2.01	0.43
10:IB:821:MET:HE1	10:IB:1251:VAL:HG21	2.00	0.43
10:IC:393:LEU:O	10:IC:397:VAL:HB	2.19	0.43
10:IC:455:LEU:HB3	10:IC:507:TYR:HE2	1.83	0.43
11:JA:2270:MET:HE2	11:JA:2275:PHE:HB2	1.99	0.43
12:KC:375:TYR:CD2	12:KC:725:ILE:HD13	2.54	0.43
13:LI:398:ARG:HA	13:LI:401:LEU:HB2	2.00	0.43
15:NC:884:LYS:HZ3	15:NC:1127:LEU:HD12	1.83	0.43
15:NC:1197:ARG:HA	15:NC:1386:HIS:ND1	2.33	0.43
18:QD:113:LYS:HE3	20:SD:22:LYS:HE2	1.99	0.43
1:AA:249:TYR:HE2	1:AA:284:PRO:HD2	1.83	0.43
2:AB:53:PRO:HA	2:AB:56:VAL:HG12	2.00	0.43
1:AE:424:PHE:CG	2:AF:35:MET:HG3	2.53	0.43
1:AE:660:ILE:HD13	1:AE:663:LEU:HD21	2.00	0.43
2:AF:63:THR:HG21	2:AF:170:GLY:HA3	2.01	0.43
1:AI:105:GLN:HG2	1:AI:109:ASN:HB3	1.99	0.43
1:AI:301:VAL:HG11	1:AI:335:ALA:HB2	1.99	0.43
2:AJ:203:ALA:HB1	2:AJ:266:ARG:HE	1.83	0.43
3:CC:812:MET:HB3	3:CC:814:VAL:HG22	2.00	0.43
3:CI:1229:HIS:HE2	3:CI:1260:VAL:HG13	1.82	0.43
4:DA:388:ARG:HA	4:DA:391:ILE:HG12	1.98	0.43
4:DE:97:LEU:HG	4:DE:99:VAL:HG23	2.00	0.43
4:DE:258:ASN:HA	4:DE:299:ARG:HD2	1.98	0.43
4:DF:318:GLY:HA2	4:DF:324:VAL:HG22	2.01	0.43
5:EB:4173:LYS:HA	5:EB:4176:THR:HG22	2.00	0.43
5:EC:4150:PHE:HD2	5:EC:4181:VAL:HG11	1.82	0.43
6:FC:1898:ILE:HB	6:FC:1912:PHE:HB2	2.00	0.43
6:FE:978:LYS:NZ	6:FE:984:THR:H	2.16	0.43
6:FE:1294:LEU:O	6:FE:1295:ALA:C	2.61	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FF:841:TYR:C	6:FF:841:TYR:CD2	2.95	0.43
7:GA:896:ARG:HG2	7:GA:958:GLN:HB3	2.00	0.43
8:GB:62:ILE:HG21	8:GB:111:TYR:HE2	1.82	0.43
8:GF:147:GLU:HG3	13:LA:423:GLN:HG3	2.00	0.43
8:GF:356:VAL:HG23	8:GF:357:ARG:HD2	1.99	0.43
7:GG:301:ARG:HE	7:GG:304:GLN:HG2	1.84	0.43
7:GG:619:ARG:HG3	7:GG:644:ILE:HG22	2.00	0.43
7:GG:749:LEU:HD23	7:GG:749:LEU:HA	1.81	0.43
7:GI:671:VAL:HG22	7:GI:697:PRO:HA	2.00	0.43
7:GI:870:ARG:HH21	7:GI:874:GLU:HG2	1.83	0.43
7:GI:912:LEU:HD12	7:GI:912:LEU:HA	1.75	0.43
7:GI:920:ALA:HB3	7:GI:955:VAL:HG11	2.01	0.43
7:GK:468:ARG:HH12	7:GK:494:LEU:HA	1.83	0.43
9:HD:774:LEU:O	13:LJ:526:LEU:HD23	2.19	0.43
9:HD:854:ASN:HA	9:HD:857:ARG:HE	1.84	0.43
10:IA:823:ASP:HB2	11:JA:2056:LEU:HD22	2.00	0.43
10:IB:185:LEU:HD21	10:IB:624:ARG:HG3	2.00	0.43
10:IC:1068:ARG:HH21	10:IC:1069:ARG:HG2	1.84	0.43
11:JA:459:GLU:HG2	11:JA:460:GLY:H	1.84	0.43
11:JA:841:VAL:HG13	11:JA:1424:ARG:HB3	2.01	0.43
11:JB:805:CYS:HB2	11:JB:895:LEU:HD22	1.99	0.43
11:JC:67:TYR:CE1	11:JC:106:LEU:HD23	2.53	0.43
12:KA:522:ARG:HD2	12:KA:522:ARG:HA	1.88	0.43
12:KE:590:GLY:HA3	12:KE:646:ARG:HG2	2.00	0.43
13:LE:480:GLN:HE21	14:MH:102:LYS:NZ	2.17	0.43
13:LJ:410:LYS:HB3	13:LJ:413:GLU:OE1	2.18	0.43
14:MF:218:LEU:HD21	14:MF:323:GLN:HB3	2.00	0.43
15:NA:1032:VAL:HG22	15:NA:1104:ARG:HB3	1.99	0.43
15:NB:884:LYS:HZ3	15:NB:1127:LEU:HG	1.83	0.43
15:NB:1147:MET:O	15:NB:1157:PRO:HA	2.19	0.43
19:RC:45:LEU:HD12	19:RC:91:VAL:HB	2.01	0.43
19:RD:22:ARG:HH12	19:RD:174:LEU:HB3	1.83	0.43
2:AF:374:LEU:HD11	5:EB:4439:GLU:HA	1.99	0.43
2:AG:5:VAL:HG12	2:AG:84:LEU:HD23	2.01	0.43
1:AI:249:TYR:HD1	1:AI:256:GLN:HG2	1.83	0.43
1:AI:269:THR:OG1	1:AI:271:MET:HB2	2.18	0.43
3:CG:1181:ARG:NH1	10:IC:452:LEU:HB2	2.33	0.43
3:CJ:1176:VAL:HG13	3:CJ:1194:VAL:HG13	2.00	0.43
5:EA:3223:TRP:HH2	5:EA:4182:LEU:HD21	1.83	0.43
5:EA:3332:ALA:HB3	5:EA:3766:LEU:HA	2.00	0.43
5:EA:4405:ILE:H	5:EA:4405:ILE:HG12	1.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:3240:TYR:O	5:EB:3242:LEU:HD12	2.18	0.43
5:EB:3524:LEU:HD21	5:EB:3559:VAL:HG11	1.99	0.43
5:EB:3700:PHE:HA	5:EB:3706:VAL:HG22	2.01	0.43
5:EC:4900:ARG:HD2	5:EC:4900:ARG:HA	1.79	0.43
6:FA:2098:TYR:CE1	9:HA:878:SER:HB2	2.52	0.43
6:FC:1675:LEU:HD12	6:FC:1696:HIS:HE2	1.84	0.43
6:FC:1857:LEU:HB3	6:FC:1919:PHE:HB3	2.00	0.43
6:FD:820:LYS:O	6:FD:821:ARG:NH1	2.52	0.43
6:FD:1298:LEU:O	6:FD:1299:ASN:C	2.61	0.43
6:FF:1098:VAL:O	6:FF:1099:ILE:C	2.62	0.43
6:FF:1289:HIS:O	6:FF:1290:ILE:C	2.61	0.43
7:GA:843:LEU:HD21	7:GA:938:VAL:HG11	1.98	0.43
8:GD:574:ASP:HB2	8:GD:584:HIS:HB3	2.01	0.43
7:GE:450:LYS:HB3	7:GE:635:THR:HG21	2.00	0.43
8:GH:422:LYS:HD2	8:GH:464:GLN:HA	2.01	0.43
8:GH:781:MET:O	8:GH:785:ILE:HG13	2.18	0.43
7:GI:664:PRO:HD2	7:GI:669:ASP:HB2	2.00	0.43
7:GI:735:ARG:HG3	7:GI:801:LEU:HD11	1.99	0.43
9:HA:868:LEU:HA	9:HA:868:LEU:HD22	1.67	0.43
10:IA:806:ILE:HG21	10:IA:858:LEU:HD21	2.01	0.43
10:IC:313:PRO:HA	10:IC:314:PRO:HD3	1.82	0.43
10:IC:451:VAL:HG12	10:IC:503:LEU:HD13	2.01	0.43
11:JB:805:CYS:HB2	11:JB:895:LEU:HB3	2.01	0.43
11:JC:527:GLU:HB2	11:JC:531:ARG:HD3	2.00	0.43
11:JC:885:TYR:CD2	11:JC:886:LYS:HG2	2.53	0.43
11:JC:1541:TYR:HD1	11:JC:1545:HIS:HD2	1.66	0.43
12:KA:523:VAL:HG12	12:KA:524:PHE:HD1	1.83	0.43
12:KB:354:ALA:HA	12:KB:357:MET:HG2	1.99	0.43
12:KC:567:TRP:CD2	12:KC:627:PRO:HA	2.54	0.43
12:KG:499:ASP:HA	12:KG:500:PRO:HD3	1.90	0.43
13:LN:392:GLU:HA	13:LN:395:ILE:HD12	2.00	0.43
14:MA:203:CYS:HB2	14:MB:203:CYS:HB3	1.49	0.43
15:NA:926:ARG:HG3	15:NA:1111:ARG:HB2	2.00	0.43
15:NB:1422:VAL:HG23	15:NB:1423:LEU:H	1.82	0.43
15:NC:685:PHE:HB2	15:NC:914:ILE:HG12	1.99	0.43
15:NC:966:VAL:HG22	15:NC:1462:GLN:HE22	1.84	0.43
16:OC:119:TRP:CZ3	16:OC:121:PRO:HG3	2.53	0.43
16:OC:156:GLU:O	16:OC:160:LEU:HG	2.19	0.43
1:AA:632:LEU:HD12	7:GA:857:LEU:HD12	2.01	0.43
2:AC:89:ARG:HG3	2:AC:90:ARG:HG3	2.01	0.43
2:AC:330:GLN:HG2	2:AC:331:ASN:H	1.82	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:285:LEU:HD22	1:AE:297:MET:HB2	2.01	0.43
1:AE:315:LEU:HD12	1:AE:316:ILE:HB	2.01	0.43
1:AE:698:LEU:HA	1:AE:701:TYR:CE1	2.53	0.43
2:AG:540:PHE:HE2	5:EB:4818:ILE:HD11	1.83	0.43
3:CC:711:ARG:HH12	3:CC:756:GLU:HB2	1.84	0.43
3:CE:1138:ILE:HG22	10:IA:1184:ARG:HH22	1.83	0.43
3:CE:4456:PRO:HA	3:CE:4457:PRO:HD3	1.84	0.43
3:CJ:1111:LYS:HA	3:CJ:1111:LYS:HD2	1.87	0.43
4:DB:318:GLY:H	14:MF:243:LYS:HZ2	1.65	0.43
4:DD:172:ARG:O	4:DD:176:ILE:HG12	2.19	0.43
4:DD:349:SER:HB3	4:DD:351:VAL:HG23	2.01	0.43
5:EA:4021:ILE:HB	5:EA:4160:LEU:HD22	2.00	0.43
5:EA:4043:LYS:HD3	5:EA:4053:LEU:HD21	2.01	0.43
5:EA:4084:TYR:CE1	5:EA:4184:GLN:HG3	2.53	0.43
5:EC:3746:LYS:HA	5:EC:3831:LEU:HD21	2.00	0.43
6:FC:1974:VAL:HG23	6:FC:2036:LEU:HB3	2.00	0.43
6:FC:2048:GLU:OE2	9:HB:765:TRP:CD2	2.71	0.43
6:FD:1030:ILE:HD12	6:FD:1030:ILE:HA	1.75	0.43
6:FD:1205:ILE:HG22	6:FD:1260:LEU:HD13	2.01	0.43
6:FD:1270:LEU:HD22	6:FD:1270:LEU:HA	1.79	0.43
6:FD:1301:ALA:HA	6:FD:1430:PHE:CB	2.47	0.43
6:FD:1429:LEU:O	6:FD:1430:PHE:HB2	2.18	0.43
8:GB:133:PRO:HG2	8:GB:168:MET:HE2	2.00	0.43
7:GC:207:LEU:HD13	7:GC:599:THR:HG22	2.01	0.43
7:GC:809:VAL:HG12	7:GC:817:ARG:HH22	1.84	0.43
7:GE:169:ILE:O	7:GE:173:ASN:HB2	2.19	0.43
7:GE:271:ASP:HB3	7:GE:277:GLU:HA	2.01	0.43
7:GE:833:CYS:HA	7:GE:836:VAL:HG22	1.99	0.43
8:GF:431:PHE:HE1	8:GF:494:SER:HB3	1.83	0.43
8:GH:113:LEU:HD12	8:GH:113:LEU:HA	1.82	0.43
8:GL:664:ILE:HG21	8:GL:705:PRO:HG3	1.99	0.43
9:HB:861:TYR:HD1	9:HB:861:TYR:HA	1.69	0.43
9:HD:860:GLN:OE1	9:HD:860:GLN:HA	2.18	0.43
10:IA:1128:VAL:HG11	10:IA:1180:VAL:HG11	2.00	0.43
10:IB:300:LEU:HD23	10:IB:302:THR:H	1.83	0.43
10:IC:509:PRO:HB2	10:IC:550:TYR:CZ	2.54	0.43
10:IC:1190:MET:HG2	10:IC:1222:VAL:HA	2.01	0.43
11:JA:1717:TRP:HZ3	16:OA:940:LEU:HD12	1.82	0.43
11:JB:476:LEU:HD23	11:JB:476:LEU:HA	1.88	0.43
11:JC:117:PRO:HG3	11:JC:146:TYR:HD1	1.84	0.43
12:KC:376:ALA:HB2	12:KC:579:LEU:HD23	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LA:469:ARG:HH21	13:LB:460:ARG:HH22	1.65	0.43
13:LL:372:THR:HA	13:LL:375:ILE:HD12	2.00	0.43
14:ME:261:ASP:HA	14:ME:262:PRO:HD2	1.71	0.43
15:NA:982:ILE:O	15:NA:988:GLY:HA3	2.19	0.43
15:ND:563:ASN:HA	15:ND:566:GLN:NE2	2.33	0.43
15:ND:693:GLY:HA2	15:ND:901:LEU:O	2.19	0.43
15:ND:867:ARG:HA	15:ND:870:TYR:CE1	2.53	0.43
16:OB:931:PRO:HB2	16:OB:936:VAL:HB	2.00	0.43
16:OC:876:GLU:HG2	16:OC:939:MET:HB3	1.99	0.43
19:RB:36:ARG:HH12	19:RB:140:GLY:H	1.66	0.43
1:AA:715:LEU:HD22	13:LK:364:ASN:HD21	1.83	0.43
1:AE:716:HIS:HB3	1:AE:1037:PRO:HD3	2.01	0.43
1:AE:892:GLU:HA	1:AE:895:ARG:HB3	1.99	0.43
1:AE:1010:ASP:HA	1:AE:1013:THR:HG22	2.01	0.43
2:AG:506:LEU:HD13	10:IA:1255:LEU:HD11	2.01	0.43
1:AL:609:PRO:HG3	13:LH:497:LEU:HD12	2.00	0.43
4:DA:84:ILE:HA	4:DA:169:GLY:HA3	2.00	0.43
4:DA:384:ILE:HD11	13:LA:461:VAL:HG11	2.00	0.43
4:DC:161:LEU:O	4:DC:165:ILE:HG12	2.19	0.43
5:EA:3573:PHE:CZ	5:EA:3650:THR:HB	2.54	0.43
5:EA:4665:LEU:HD23	5:EA:4665:LEU:HA	1.91	0.43
5:EB:3274:GLN:NE2	5:EB:3491:ALA:HB1	2.34	0.43
5:EB:3388:LEU:HB3	5:EB:3391:VAL:HB	2.00	0.43
5:EC:4170:LYS:O	5:EC:4174:ILE:HG12	2.18	0.43
6:FC:2019:GLU:O	6:FC:2023:ILE:HG12	2.18	0.43
6:FD:821:ARG:HA	6:FD:821:ARG:HD3	1.60	0.43
6:FD:1241:VAL:HG22	6:FD:1260:LEU:HD12	2.00	0.43
6:FD:1392:LYS:HE3	6:FD:1392:LYS:HB3	1.43	0.43
6:FE:856:PRO:HA	6:FE:1080:ILE:HD11	2.01	0.43
6:FE:1181:VAL:O	6:FE:1425:PRO:HG2	2.18	0.43
6:FE:1295:ALA:HA	6:FE:1394:ARG:NE	2.34	0.43
6:FF:808:SER:O	6:FF:809:ILE:C	2.60	0.43
6:FF:1027:LEU:O	6:FF:1028:LYS:C	2.61	0.43
6:FF:1186:TRP:CD2	6:FF:1269:CYS:HB2	2.53	0.43
6:FF:1393:LEU:HD13	6:FF:1393:LEU:HA	1.77	0.43
7:GC:186:VAL:HG21	7:GC:672:VAL:HG21	2.01	0.43
7:GC:423:TRP:HB3	7:GC:426:ASN:HD22	1.84	0.43
8:GD:681:ILE:HD13	8:GD:684:TRP:HE1	1.84	0.43
8:GH:425:VAL:HG23	8:GH:498:PHE:HE1	1.84	0.43
7:GI:614:TRP:HE1	7:GI:661:LEU:HD13	1.83	0.43
8:GJ:294:TRP:CD1	8:GJ:299:ALA:HB2	2.54	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GK:544:PRO:HB3	9:HC:597:CYS:H	1.84	0.43
8:GL:636:PRO:HB2	8:GL:654:LEU:HD11	1.99	0.43
9:HB:432:LEU:HD13	9:HB:435:LEU:HD12	2.01	0.43
9:HB:765:TRP:N	9:HB:765:TRP:CE3	2.85	0.43
10:IB:188:PHE:HE1	11:JB:1883:ARG:HE	1.66	0.43
10:IB:450:ASN:O	10:IB:454:GLU:HB3	2.18	0.43
10:IC:462:VAL:HG12	10:IC:470:ARG:HG3	2.00	0.43
10:IC:581:PHE:CE2	10:IC:759:PHE:HA	2.54	0.43
11:JA:531:ARG:HG3	11:JA:532:HIS:CD2	2.54	0.43
11:JA:1084:VAL:HG11	11:JA:1153:LEU:HD23	2.00	0.43
11:JA:2109:ALA:HA	11:JA:2112:ARG:HE	1.84	0.43
11:JB:1790:LEU:HD13	11:JB:1812:VAL:HG11	2.01	0.43
11:JB:2110:LEU:O	11:JB:2114:ILE:HG12	2.18	0.43
11:JB:2280:ARG:O	11:JB:2284:LYS:HG2	2.19	0.43
12:KG:311:ASP:HB2	12:KG:314:LEU:HG	2.01	0.43
13:LE:473:LYS:O	13:LE:477:LEU:HD23	2.19	0.43
13:LE:530:VAL:HG11	13:LF:530:VAL:HB	2.00	0.43
13:LI:460:ARG:HG2	13:LI:463:ARG:HE	1.84	0.43
13:LJ:425:LYS:HA	13:LJ:428:VAL:HG12	2.01	0.43
13:LP:374:HIS:HA	13:LP:377:GLN:HB3	2.01	0.43
14:MG:93:SER:HA	14:MG:96:ASP:HB2	2.01	0.43
15:NA:600:LEU:HD11	15:NA:945:PHE:HB3	2.01	0.43
15:ND:364:ARG:HB2	15:ND:488:GLU:HG2	2.01	0.43
16:OC:882:ARG:NE	16:OC:885:GLN:HE21	2.00	0.43
18:QD:71:VAL:HG12	18:QD:90:PHE:HZ	1.83	0.43
19:RB:18:LYS:HB3	19:RB:105:MET:HA	2.01	0.43
20:SB:76:LYS:NZ	20:SB:78:LYS:HG2	2.33	0.43
1:AA:98:LEU:HD23	1:AA:145:HIS:HB3	2.01	0.43
1:AA:350:LEU:HD13	2:AB:522:ARG:HD3	2.01	0.43
2:AF:87:ILE:HD11	2:AF:279:PRO:HG3	2.01	0.43
1:AH:133:PRO:O	1:AH:136:PHE:HB2	2.19	0.43
1:AI:107:LEU:HD12	1:AI:221:VAL:HG11	2.00	0.43
1:AI:768:ILE:HA	1:AI:776:LEU:HD13	2.01	0.43
3:BA:873:PHE:HD2	3:BA:918:LEU:HD21	1.84	0.43
3:BC:845:LYS:HA	3:BC:848:ILE:HG22	2.01	0.43
3:CA:695:LEU:HD22	3:CA:743:SER:HB2	2.00	0.43
3:CC:858:SER:H	3:CC:891:ILE:HD11	1.84	0.43
3:CF:1156:GLU:HA	10:IB:415:ARG:HH22	1.84	0.43
4:DB:145:ASN:HA	4:DB:148:ARG:HG2	2.00	0.43
4:DE:90:LEU:HB3	4:DE:119:LEU:HD23	2.00	0.43
4:DF:180:LEU:HB2	4:DF:181:ILE:HD12	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EA:4030:GLU:HB2	5:EA:4058:PRO:HB3	2.00	0.43
5:EA:4212:ALA:HA	5:EA:4215:LEU:HD23	2.00	0.43
5:EB:4213:LYS:HB3	5:EB:4236:LEU:HD21	2.00	0.43
5:EC:4071:LEU:HD21	5:EC:4222:LYS:HG2	2.01	0.43
6:FE:1205:ILE:HG23	6:FE:1286:LEU:HD11	2.01	0.43
6:FF:806:ILE:HG23	6:FF:1112:ILE:HD11	2.00	0.43
6:FF:1065:LEU:HA	6:FF:1115:THR:CA	2.49	0.43
6:FF:1066:GLN:O	6:FF:1114:VAL:N	2.46	0.43
6:FF:1071:PHE:HD1	6:FF:1108:PRO:HA	1.84	0.43
8:GB:193:MET:HG3	7:GC:381:ARG:HH12	1.82	0.43
7:GC:719:ILE:HD11	7:GC:800:VAL:HG21	2.01	0.43
8:GD:707:GLU:HA	8:GD:710:LYS:HD2	1.99	0.43
7:GI:271:ASP:HB3	7:GI:277:GLU:HG3	2.01	0.43
7:GI:298:TYR:HB3	7:GI:679:LEU:HD21	2.00	0.43
9:HA:432:LEU:HD13	9:HA:435:LEU:HD12	2.01	0.43
9:HB:524:VAL:HG22	9:HB:607:VAL:HG22	2.01	0.43
9:HB:526:VAL:HB	9:HB:579:LEU:HD22	2.00	0.43
10:IA:551:ASN:ND2	10:IA:852:CYS:HA	2.32	0.43
10:IB:1278:VAL:HG23	10:IB:1279:GLU:H	1.83	0.43
11:JB:138:THR:HG22	11:JB:162:PRO:HG3	2.00	0.43
11:JC:1480:VAL:HG13	15:NA:440:LEU:HD11	2.00	0.43
11:JC:1765:ARG:HH12	16:OC:893:PRO:HD2	1.84	0.43
12:KE:593:HIS:HB2	12:KE:707:GLU:HB3	1.99	0.43
13:LN:428:VAL:HA	13:LN:431:LEU:HD12	2.01	0.43
14:ME:315:TRP:CZ3	14:MF:315:TRP:HA	2.54	0.43
15:NA:529:PHE:CD2	15:NA:1382:PHE:HB2	2.54	0.43
15:NA:685:PHE:HE2	15:NA:689:ASN:HA	1.83	0.43
15:NB:599:ILE:HB	15:NB:916:LEU:HG	2.01	0.43
15:NC:617:PHE:O	15:NC:620:ILE:HG12	2.19	0.43
15:NC:1487:ARG:HB3	15:NC:1488:ARG:H	1.62	0.43
19:RC:116:PHE:CE2	19:RC:163:PHE:HA	2.53	0.43
19:RC:132:LEU:HD21	19:RC:152:LEU:HD11	2.00	0.43
1:AA:73:THR:HG22	1:AA:75:ALA:H	1.83	0.43
1:AD:488:VAL:HG12	1:AD:490:SER:H	1.84	0.43
1:AL:71:LEU:HD11	1:AL:218:PRO:HB2	2.01	0.43
3:BA:963:HIS:HE1	16:OA:125:SER:HB3	1.83	0.43
4:DD:267:ARG:NH1	4:DD:268:ARG:HB2	2.34	0.43
4:DE:19:ARG:HD2	4:DE:22:ILE:HD11	2.01	0.43
5:EA:4522:VAL:HA	5:EA:4525:VAL:HG12	2.01	0.43
5:EB:3521:GLU:HB3	5:EB:3546:TYR:CE1	2.54	0.43
5:EB:3784:GLY:HA2	5:EB:3855:LEU:HD21	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:4880:ASP:OD1	5:EB:4880:ASP:N	2.52	0.43
5:EC:3648:PRO:HB2	7:GG:543:LYS:HZ2	1.84	0.43
6:FD:1068:CYS:HB3	6:FD:1112:ILE:HG23	2.01	0.43
6:FD:1089:ARG:HD2	6:FD:1089:ARG:HA	1.71	0.43
6:FE:1270:LEU:HD22	6:FE:1270:LEU:HA	1.81	0.43
6:FF:1065:LEU:HA	6:FF:1115:THR:HA	2.01	0.43
7:GA:872:THR:HB	7:GA:972:GLU:HB2	2.01	0.43
7:GC:724:ASP:HB3	7:GC:728:ARG:HH21	1.83	0.43
8:GH:664:ILE:HD11	8:GH:681:ILE:HG21	2.00	0.43
7:GK:211:ARG:HD3	7:GK:212:PRO:HD2	2.00	0.43
8:GL:142:THR:HA	8:GL:149:LEU:HD21	2.00	0.43
9:HA:761:CYS:SG	9:HA:765:TRP:CZ2	3.10	0.43
9:HB:487:VAL:HG21	9:HB:620:TYR:CZ	2.53	0.43
10:IA:457:SER:HB3	10:IA:503:LEU:HD21	2.01	0.43
10:IA:743:TYR:CD2	10:IA:764:ALA:HA	2.54	0.43
10:IB:344:TYR:CZ	10:IB:433:ARG:HG2	2.54	0.43
10:IB:893:PHE:HZ	10:IB:907:ASP:HA	1.83	0.43
10:IC:963:ARG:HD3	10:IC:963:ARG:HA	1.80	0.43
10:IC:1232:ARG:H	10:IC:1302:ARG:NH2	2.16	0.43
11:JA:812:LEU:HA	11:JA:819:ILE:HG23	2.00	0.43
11:JA:1447:LEU:HD11	11:JA:1976:HIS:HD2	1.84	0.43
11:JB:1385:SER:HB2	11:JB:1409:ARG:NH2	2.33	0.43
12:KC:536:ARG:NH2	12:KC:544:LEU:H	2.16	0.43
15:NC:808:ILE:HG22	15:NC:878:ILE:HG21	1.99	0.43
15:NC:915:VAL:HG12	15:NC:917:MET:HE3	2.01	0.43
18:QB:52:LYS:HA	18:QB:75:PHE:CE1	2.54	0.43
2:AC:161:ILE:HD11	6:FA:1874:PHE:HA	2.01	0.42
1:AD:282:HIS:CE1	10:IB:1359:ALA:HB2	2.53	0.42
1:AE:419:GLU:HG3	16:OC:79:LEU:HD11	2.00	0.42
1:AH:393:LEU:HA	1:AH:393:LEU:HD12	1.89	0.42
3:BA:850:THR:HA	3:BA:853:VAL:HG12	2.01	0.42
3:BB:689:LEU:HD23	17:PB:258:PRO:HB2	2.00	0.42
3:BB:755:GLY:HA2	3:BB:787:ILE:HD13	2.00	0.42
3:BB:873:PHE:HZ	16:OB:174:VAL:HG22	1.82	0.42
3:CJ:1116:SER:HB2	10:IB:512:ARG:HH22	1.84	0.42
3:CJ:1154:LEU:HD13	3:CJ:4516:ILE:HD12	2.01	0.42
3:CL:1186:LEU:HD13	10:IC:1423:PRO:HG3	2.00	0.42
4:DD:118:VAL:O	4:DD:122:ILE:HG12	2.19	0.42
5:EA:4308:GLU:H	5:EA:4308:GLU:HG2	1.69	0.42
5:EC:3242:LEU:HD23	5:EC:3249:ALA:HA	2.01	0.42
5:EC:3306:ILE:O	5:EC:3310:THR:HG23	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FA:2075:GLU:CB	9:HA:858:LEU:HD11	2.40	0.42
6:FC:1852:ILE:HD11	6:FC:1891:PRO:HD2	2.01	0.42
6:FD:854:TRP:CD1	6:FD:854:TRP:N	2.87	0.42
6:FD:993:ALA:HB1	12:KA:228:GLU:HG3	2.01	0.42
6:FD:1202:PHE:HE1	6:FD:1243:PRO:HA	1.84	0.42
6:FE:917:TRP:HA	6:FE:1422:PHE:HE2	1.84	0.42
6:FF:980:SER:C	6:FF:982:SER:N	2.77	0.42
6:FF:1246:ILE:HG23	6:FF:1247:SER:N	2.34	0.42
7:GA:311:LEU:HD11	7:GA:440:ALA:HB2	2.01	0.42
8:GB:532:PHE:HB3	8:GB:589:PHE:HE2	1.83	0.42
7:GC:792:LEU:HG	7:GC:796:PHE:HE2	1.83	0.42
8:GD:333:LYS:HE2	8:GD:335:ASN:HD21	1.83	0.42
8:GF:112:ILE:HD12	8:GF:510:ARG:HG2	2.00	0.42
8:GH:196:HIS:HA	7:GI:386:VAL:HB	2.01	0.42
8:GH:401:ASP:HA	8:GH:404:ARG:HG2	2.01	0.42
9:HA:836:SER:O	9:HA:839:ALA:N	2.51	0.42
9:HD:760:LYS:O	9:HD:761:CYS:C	2.61	0.42
10:IB:366:GLU:HB3	10:IB:516:PRO:HD2	2.01	0.42
10:IB:580:LEU:HG	10:IB:603:ARG:HH12	1.84	0.42
11:JA:138:THR:HG22	11:JA:162:PRO:HG3	2.01	0.42
11:JA:1824:PRO:HB2	11:JA:1973:PHE:CE1	2.54	0.42
11:JB:781:ASN:HD21	11:JB:939:VAL:HG11	1.84	0.42
12:KA:404:GLU:HA	12:KA:407:ILE:HD12	2.01	0.42
12:KA:652:ILE:HG22	12:KA:654:ILE:HG23	1.99	0.42
12:KE:567:TRP:HB3	12:KE:707:GLU:HG3	2.01	0.42
13:LI:398:ARG:HH21	13:LJ:395:ILE:HD13	1.83	0.42
14:MA:285:ARG:NH1	14:MB:257:LYS:HA	2.34	0.42
15:NA:630:LYS:HA	15:NA:637:PRO:HD3	2.00	0.42
15:NB:806:ASP:HB3	15:NB:882:SER:HB2	2.01	0.42
15:NB:993:LEU:HB3	15:NB:1121:ASN:HD21	1.84	0.42
15:NB:1010:LEU:HD22	15:NB:1093:LYS:HB2	2.01	0.42
15:NC:513:LEU:HB2	15:NC:1404:HIS:CD2	2.54	0.42
15:ND:1525:ARG:NH2	18:QB:60:ARG:HG3	2.34	0.42
16:OA:288:LEU:HD23	16:OA:288:LEU:HA	1.93	0.42
16:OB:10:ARG:HA	16:OB:10:ARG:HD3	1.77	0.42
16:OB:1077:LYS:HZ3	16:OB:1079:ALA:H	1.66	0.42
18:QD:128:PHE:HB2	18:QD:140:TRP:CH2	2.54	0.42
20:SA:55:GLU:HA	20:SA:58:ALA:HB2	2.00	0.42
20:SA:86:LEU:HD12	20:SA:89:ALA:HB3	2.00	0.42
1:AA:368:LEU:HB3	2:AC:153:GLN:HE21	1.84	0.42
2:AC:16:LEU:HD13	2:AC:50:ILE:HG22	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:176:VAL:HG11	16:OA:25:ALA:HB1	2.02	0.42
2:AC:364:CYS:SG	2:AC:381:HIS:HB2	2.58	0.42
2:AC:538:ASN:HB3	5:EA:4818:ILE:HD12	2.00	0.42
2:AF:559:ARG:HH21	13:LK:483:ARG:HB3	1.85	0.42
1:AI:418:ILE:HG23	2:AJ:424:LEU:HD22	2.01	0.42
2:AJ:288:ASP:HB3	2:AJ:291:LEU:HG	2.01	0.42
3:BC:907:ARG:CZ	16:OC:184:ASN:HD21	2.32	0.42
3:CE:4486:ILE:HG21	3:CE:4497:ARG:HH11	1.83	0.42
3:CJ:1168:ARG:HH12	3:CJ:4482:LEU:HB3	1.83	0.42
4:DC:363:LEU:HD21	8:GJ:161:ALA:HB1	2.00	0.42
5:EA:3743:ARG:HE	5:EA:3830:HIS:CE1	2.37	0.42
5:EB:3653:LYS:HD3	5:EB:3653:LYS:HA	1.81	0.42
5:EC:3314:ARG:HH22	5:EC:4166:SER:HA	1.84	0.42
6:FA:1759:GLU:OE2	6:FA:1964:MET:HG2	2.19	0.42
6:FB:1804:MET:HE2	6:FB:1804:MET:HB3	1.86	0.42
6:FC:1738:GLY:HA3	6:FC:1796:PHE:HB3	2.02	0.42
6:FD:993:ALA:HB1	12:KA:230:GLN:OE1	2.19	0.42
6:FD:1067:ALA:HB1	6:FD:1111:GLU:OE2	2.19	0.42
6:FD:1442:GLU:C	6:FD:1444:ARG:N	2.76	0.42
6:FE:811:ASN:HD21	6:FE:891:ARG:HD2	1.84	0.42
6:FF:830:ALA:HB1	6:FF:843:LEU:HD21	2.01	0.42
6:FF:975:ILE:H	6:FF:975:ILE:HG12	1.59	0.42
8:GB:326:ARG:NH1	8:GB:375:TYR:HB3	2.31	0.42
8:GD:431:PHE:HZ	8:GD:496:LEU:HD13	1.83	0.42
8:GF:88:PRO:HG2	8:GF:91:TYR:HB2	2.01	0.42
8:GF:348:TYR:HB3	8:GF:380:MET:SD	2.59	0.42
7:GG:699:SER:HB3	7:GG:705:ILE:HD11	2.01	0.42
7:GK:305:PRO:HA	7:GK:354:ARG:HH21	1.84	0.42
10:IA:930:LEU:H	10:IA:966:LEU:HD12	1.84	0.42
10:IC:1207:LYS:HD3	10:IC:1207:LYS:HA	1.83	0.42
11:JB:84:PHE:CE2	11:JB:2096:HIS:HB3	2.53	0.42
12:KF:247:LEU:HB3	12:KF:258:LEU:HD12	2.00	0.42
13:LE:483:ARG:O	13:LE:487:MET:HG2	2.19	0.42
13:LO:403:SER:HB2	13:LO:407:ARG:HH21	1.84	0.42
14:MK:80:ALA:HA	14:MK:88:ALA:HB2	2.00	0.42
15:NA:598:PHE:HB3	15:NA:1187:CYS:HA	2.01	0.42
15:NB:599:ILE:HD13	15:NB:1188:HIS:HB2	2.01	0.42
15:NC:946:LEU:HA	15:NC:949:PHE:CE1	2.53	0.42
2:AC:552:LEU:HD13	2:AC:557:LEU:HB2	2.01	0.42
1:AD:287:PHE:CZ	10:IB:1356:LEU:HD11	2.53	0.42
2:AF:300:CYS:HB2	2:AF:320:CYS:H	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AJ:32:LEU:HD23	2:AJ:166:LEU:HD11	2.02	0.42
2:AJ:68:LEU:HB3	2:AJ:168:GLN:HE21	1.84	0.42
2:AK:267:HIS:HB3	2:AK:269:TYR:CE1	2.54	0.42
3:CB:1014:ASP:HA	3:CB:1017:ARG:HG2	2.01	0.42
3:CC:677:LYS:HB2	17:PB:249:LEU:HD22	2.01	0.42
3:CF:1213:VAL:HG22	3:CF:1219:VAL:HG12	2.01	0.42
3:CJ:4455:VAL:HA	3:CJ:4456:PRO:HD3	1.81	0.42
5:EA:3269:TRP:HD1	5:EA:3409:SER:HB2	1.84	0.42
5:EB:3660:LYS:NZ	5:EB:4055:ARG:HH22	2.18	0.42
5:EB:3746:LYS:HA	5:EB:3831:LEU:HD13	2.00	0.42
5:EB:4296:VAL:HG13	5:EB:4340:ASN:HD21	1.84	0.42
6:FA:1640:VAL:HG13	6:FA:1643:PRO:HB3	2.01	0.42
6:FD:799:GLN:HG3	6:FD:912:ILE:H	1.84	0.42
6:FD:855:PHE:C	6:FD:857:GLU:H	2.27	0.42
6:FE:830:ALA:HA	6:FE:847:PHE:CE1	2.53	0.42
6:FE:1008:ARG:HH11	6:FE:1009:VAL:HG23	1.84	0.42
7:GC:739:GLN:HB3	7:GC:992:ARG:HH22	1.83	0.42
7:GC:939:VAL:O	7:GC:943:GLN:HG2	2.19	0.42
7:GE:371:LEU:HD12	7:GE:412:VAL:HG22	2.00	0.42
7:GG:533:VAL:O	7:GG:535:PRO:HD3	2.20	0.42
7:GG:950:ALA:O	7:GG:951:MET:HE2	2.19	0.42
8:GH:661:PRO:HB2	8:GH:680:LEU:H	1.84	0.42
7:GK:433:MET:HE3	7:GK:433:MET:HB3	1.94	0.42
7:GK:548:ALA:HB1	9:HC:666:LYS:HG3	2.01	0.42
8:GL:101:PRO:HD2	8:GL:104:LEU:HD23	2.01	0.42
9:HA:786:ALA:HB1	9:HA:801:VAL:HG11	2.01	0.42
9:HA:825:ASN:O	9:HA:829:THR:HG23	2.20	0.42
9:HB:749:ASN:C	9:HB:751:SER:N	2.73	0.42
9:HB:786:ALA:HB1	9:HB:801:VAL:HG11	2.02	0.42
9:HC:552:ASP:HB2	9:HC:576:LYS:HB2	2.02	0.42
9:HD:771:PRO:HG3	9:HD:819:TYR:CZ	2.54	0.42
9:HD:816:LEU:HD23	9:HD:816:LEU:HA	1.89	0.42
10:IB:845:TYR:CZ	10:IB:863:LEU:HD22	2.55	0.42
10:IB:902:ARG:HH12	10:IB:910:LEU:HB3	1.84	0.42
11:JA:440:PRO:HG3	11:JA:1474:TRP:CZ3	2.54	0.42
11:JB:764:TRP:CD2	11:JB:1501:LEU:HD21	2.53	0.42
11:JC:78:GLN:HA	11:JC:79:PRO:HD3	1.92	0.42
11:JC:450:PHE:O	11:JC:451:MET:HE2	2.19	0.42
11:JC:1122:ARG:HG3	11:JC:1123:THR:HG23	2.01	0.42
12:KC:212:LEU:HD11	12:KC:293:ILE:HD11	2.01	0.42
12:KC:393:LEU:O	12:KC:397:GLN:HG2	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:ML:140:ARG:HB2	14:ML:144:ARG:NH1	2.31	0.42
15:NB:893:LEU:HB2	15:NB:1154:ASP:CG	2.44	0.42
15:ND:510:LEU:O	15:ND:513:LEU:HG	2.19	0.42
15:ND:1407:MET:HE1	15:ND:1471:ARG:HD2	2.01	0.42
15:ND:1508:PHE:HZ	18:QB:110:VAL:HG11	1.84	0.42
17:PA:267:ASP:HB3	17:PA:269:ILE:HG22	2.00	0.42
18:QD:144:GLU:HB3	18:QD:149:LEU:C	2.45	0.42
1:AA:707:GLY:HA2	13:LK:354:ARG:HH12	1.83	0.42
1:AD:905:LYS:O	1:AD:909:GLN:HG3	2.19	0.42
2:AF:86:ASP:HB3	2:AF:90:ARG:NH1	2.35	0.42
1:AI:999:LYS:HE2	7:GK:860:GLN:HB3	2.02	0.42
2:AK:331:ASN:C	2:AK:331:ASN:ND2	2.77	0.42
3:BA:686:ALA:HA	3:BA:689:LEU:HD13	1.99	0.42
3:BA:754:GLU:HG2	17:PA:284:PRO:HB2	2.01	0.42
3:CF:4479:LEU:HD12	3:CF:4481:GLU:H	1.83	0.42
4:DB:170:ARG:HG2	4:DE:170:ARG:NH2	2.35	0.42
4:DC:312:ASN:O	4:DC:316:ARG:HG2	2.20	0.42
5:EA:4653:GLU:HB3	5:EA:4654:ASP:H	1.70	0.42
5:EB:3280:VAL:HG13	5:EB:3281:VAL:HG13	2.01	0.42
5:EB:3435:ASP:HA	5:EB:3610:GLN:HA	2.01	0.42
6:FB:2024:ARG:HH21	9:HD:779:PRO:HG2	1.84	0.42
6:FC:1647:LEU:HD22	6:FC:1797:VAL:HG23	2.01	0.42
6:FD:1108:PRO:HG3	9:HB:394:LEU:HG	2.00	0.42
6:FE:827:PRO:O	6:FE:829:ARG:N	2.48	0.42
6:FE:844:ALA:O	6:FE:845:PRO:C	2.62	0.42
6:FE:1106:LEU:HD23	6:FE:1106:LEU:HA	1.83	0.42
6:FE:1203:ARG:O	6:FE:1204:GLN:C	2.62	0.42
6:FF:807:ALA:HB2	6:FF:903:GLN:HA	1.99	0.42
7:GA:257:GLY:HA3	7:GA:612:ARG:HH21	1.84	0.42
7:GA:612:ARG:HB2	7:GA:662:VAL:HG22	2.01	0.42
8:GB:160:LEU:HA	8:GB:163:MET:HG2	2.01	0.42
7:GC:231:CYS:HB3	7:GC:236:THR:H	1.85	0.42
8:GH:177:MET:HB3	8:GH:198:PHE:O	2.19	0.42
9:HD:776:PRO:O	9:HD:777:TYR:C	2.62	0.42
10:IA:451:VAL:HG12	10:IA:503:LEU:HD13	2.01	0.42
10:IA:618:ARG:HH12	10:IA:752:SER:HB2	1.85	0.42
10:IA:886:LEU:HD12	16:OA:1040:PHE:CE1	2.54	0.42
10:IA:1296:PRO:HB3	10:IA:1373:TRP:CE2	2.54	0.42
11:JA:164:MET:HA	11:JA:165:GLU:HA	1.82	0.42
11:JC:1449:VAL:HG23	11:JC:1452:SER:HA	2.01	0.42
14:MA:313:ARG:HD2	14:MA:316:GLN:HE22	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:MA:326:LEU:HD23	14:MA:326:LEU:HA	1.93	0.42
14:MF:243:LYS:HD3	14:MF:243:LYS:HA	1.74	0.42
15:NA:349:ARG:HG3	15:NA:351:SER:H	1.84	0.42
15:NA:537:LYS:HB3	15:NA:577:PRO:HB2	2.00	0.42
15:NA:697:VAL:HG21	15:NA:1169:PHE:CE2	2.54	0.42
15:NB:891:TRP:HA	15:NB:1152:GLU:C	2.44	0.42
15:NB:1441:ARG:HB3	15:NB:1442:LYS:H	1.71	0.42
15:NB:1525:ARG:HG2	18:QC:60:ARG:NH1	2.34	0.42
15:NC:578:HIS:HD1	15:NC:580:PHE:HD2	1.68	0.42
15:ND:582:LEU:HD21	15:ND:599:ILE:HG23	2.01	0.42
15:ND:892:TRP:HE3	15:ND:1154:ASP:HB2	1.85	0.42
15:ND:1391:LEU:HD23	15:ND:1397:LEU:HG	2.00	0.42
16:OA:226:GLU:HB3	16:OA:249:LEU:HD11	2.01	0.42
17:PA:138:ARG:HB3	17:PA:142:TYR:CD2	2.54	0.42
18:QB:58:LEU:HA	18:QB:61:TYR:CD2	2.54	0.42
19:RA:119:VAL:O	19:RA:131:GLU:HG3	2.19	0.42
19:RB:22:ARG:HD2	19:RB:174:LEU:HD22	2.01	0.42
1:AA:243:VAL:HG12	17:PA:247:LEU:HB3	2.00	0.42
2:AB:19:VAL:HB	2:AB:47:ALA:HB3	2.01	0.42
1:AE:49:GLN:HG2	2:AF:520:ARG:HH21	1.84	0.42
1:AE:229:LEU:HB2	17:PC:273:GLU:O	2.20	0.42
2:AF:206:PRO:HD3	2:AF:266:ARG:HB2	2.00	0.42
1:AH:364:LYS:HD3	1:AH:364:LYS:HA	1.78	0.42
1:AH:783:LEU:HD21	7:GG:926:ASP:HB3	2.02	0.42
2:AK:446:ARG:HD2	2:AK:450:ARG:HH21	1.84	0.42
4:DA:374:VAL:HG13	4:DA:375:SER:H	1.82	0.42
4:DD:262:ILE:HA	4:DD:265:ILE:HG12	2.00	0.42
5:EA:3809:LEU:HD13	5:EA:3813:VAL:HG11	2.01	0.42
5:EC:3414:VAL:HG12	5:EC:3505:ILE:HD12	2.02	0.42
6:FB:1981:LEU:O	6:FB:1985:GLN:HG2	2.20	0.42
6:FD:844:ALA:C	7:GC:896:ARG:NH1	2.76	0.42
6:FD:978:LYS:NZ	6:FD:984:THR:H	2.17	0.42
6:FD:1088:LYS:C	6:FD:1090:LEU:H	2.27	0.42
6:FD:1217:GLU:HB3	6:FD:1218:ALA:H	1.58	0.42
6:FD:1218:ALA:HB3	6:FD:1276:LEU:HD13	2.02	0.42
6:FE:839:GLY:CA	12:KB:681:MET:HE3	2.49	0.42
6:FE:917:TRP:HA	6:FE:1422:PHE:CE2	2.54	0.42
6:FE:1230:SER:OG	6:FE:1231:ARG:N	2.53	0.42
6:FE:1293:THR:HG23	6:FE:1394:ARG:CG	2.49	0.42
6:FF:1391:TYR:HE2	6:FF:1419:LEU:HB3	1.84	0.42
7:GC:213:GLY:HA3	12:KE:685:ARG:HH12	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GC:232:LYS:HD3	7:GC:235:ARG:HH12	1.85	0.42
7:GC:827:LEU:HB3	7:GC:831:ARG:HB2	2.01	0.42
7:GE:572:GLU:HA	7:GE:622:ARG:NH2	2.34	0.42
9:HB:579:LEU:HD21	9:HB:597:CYS:HB3	2.01	0.42
9:HB:754:LEU:HD23	9:HB:754:LEU:HA	1.75	0.42
9:HB:761:CYS:HB3	9:HB:765:TRP:CE2	2.54	0.42
9:HC:579:LEU:HA	9:HC:579:LEU:HD23	1.85	0.42
10:IA:876:ALA:HB1	10:IA:947:HIS:HE2	1.84	0.42
10:IA:964:LEU:O	10:IA:968:ARG:HG2	2.19	0.42
10:IB:1186:GLU:HA	10:IB:1190:MET:HE3	2.01	0.42
10:IC:1094:ASN:HA	10:IC:1123:ASN:ND2	2.33	0.42
11:JA:102:ARG:HH21	11:JA:104:PHE:HE1	1.66	0.42
11:JA:1775:THR:HG23	11:JA:1780:ARG:HG2	2.00	0.42
11:JA:1987:PRO:HG2	11:JA:1992:LEU:HD21	2.00	0.42
11:JC:895:LEU:HD12	11:JC:896:PRO:HD2	2.01	0.42
12:KA:525:PRO:HD2	12:KA:541:TYR:CE2	2.55	0.42
12:KF:369:ILE:HD11	12:KF:697:ARG:HH21	1.84	0.42
13:LI:372:THR:HA	13:LI:375:ILE:HG12	2.00	0.42
13:LL:484:VAL:HA	13:LL:487:MET:HE2	2.00	0.42
14:MB:254:ILE:O	14:MB:257:LYS:HB2	2.20	0.42
14:ME:233:LEU:HA	14:ME:236:GLU:HG2	2.01	0.42
15:NA:644:MET:HE2	16:OA:1042:PRO:HD2	2.01	0.42
15:NA:686:ASN:HD21	15:NA:908:PHE:HA	1.85	0.42
15:NA:852:VAL:HG11	15:NA:867:ARG:HG3	2.02	0.42
15:NB:510:LEU:O	15:NB:513:LEU:HG	2.19	0.42
15:NC:564:ARG:CZ	15:NC:622:THR:HB	2.49	0.42
15:NC:1516:ALA:HB1	18:QD:135:LEU:HD21	2.01	0.42
15:ND:946:LEU:HA	15:ND:949:PHE:CE1	2.54	0.42
15:ND:1505:ALA:HA	20:SB:19:LEU:HD11	2.01	0.42
16:OC:226:GLU:HB3	16:OC:245:LEU:HD21	2.01	0.42
18:QA:165:ARG:HE	18:QA:172:GLN:HG2	1.84	0.42
18:QC:39:PHE:HD1	18:QC:58:LEU:HD21	1.84	0.42
19:RB:100:VAL:HA	19:RB:103:GLN:NE2	2.35	0.42
1:AA:246:ALA:HA	1:AA:258:CYS:SG	2.59	0.42
2:AB:44:LEU:HD21	2:AB:47:ALA:HB2	2.01	0.42
2:AB:366:ILE:HD12	2:AB:381:HIS:CG	2.55	0.42
1:AD:298:ILE:HG22	1:AD:332:THR:HG21	2.01	0.42
1:AI:465:MET:HE3	1:AI:465:MET:HB2	1.76	0.42
2:AJ:213:HIS:CD2	2:AJ:293:GLU:HB3	2.55	0.42
1:AL:967:ARG:H	1:AL:967:ARG:HG2	1.68	0.42
3:BA:793:ILE:HG21	3:BA:807:LEU:HA	1.99	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BC:952:GLN:HA	3:BC:955:VAL:HG12	2.02	0.42
3:CF:1146:VAL:HG13	3:CJ:1137:ALA:HB2	2.02	0.42
3:CF:4482:LEU:HA	3:CF:4483:PRO:HD3	1.88	0.42
3:CI:4452:HIS:CE1	3:CI:4454:ASP:HB2	2.54	0.42
3:CJ:4486:ILE:HA	3:CJ:4497:ARG:HH12	1.84	0.42
3:CL:1255:VAL:HG21	3:CL:4469:LEU:HD22	2.01	0.42
4:DA:93:ILE:HD11	4:DA:168:SER:HB2	2.02	0.42
4:DE:164:PHE:HA	4:DE:167:GLU:OE1	2.20	0.42
5:EA:3235:SER:HB2	9:HC:413:ARG:NH2	2.35	0.42
5:EB:4032:PHE:CD2	5:EB:4146:ILE:HG12	2.55	0.42
5:EB:4145:LEU:HD23	5:EB:4145:LEU:HA	1.91	0.42
5:EC:3304:LYS:HG2	9:HA:416:PHE:HE1	1.84	0.42
6:FA:1845:PRO:HB2	6:FA:1848:PRO:HD2	2.01	0.42
6:FD:800:ALA:HB2	6:FD:913:LEU:HD11	2.01	0.42
6:FD:1182:ALA:HB2	6:FD:1430:PHE:N	2.31	0.42
6:FE:877:GLY:HA3	6:FE:909:PRO:HG3	2.01	0.42
6:FE:1087:LEU:O	6:FE:1088:LYS:C	2.62	0.42
6:FE:1190:ARG:NH2	6:FE:1418:GLU:OE2	2.53	0.42
6:FF:810:THR:HB	6:FF:1113:PHE:HE2	1.84	0.42
6:FF:1181:VAL:O	6:FF:1425:PRO:HG3	2.19	0.42
7:GA:205:ARG:HH12	7:GA:947:LEU:HD11	1.85	0.42
7:GA:979:LEU:HB3	9:HB:650:PHE:HB2	2.00	0.42
7:GC:633:LEU:HD22	7:GC:642:PHE:HZ	1.85	0.42
8:GF:50:GLU:HB3	8:GF:112:ILE:CG2	2.50	0.42
9:HB:752:ASP:OD1	9:HB:752:ASP:N	2.53	0.42
10:IB:374:PHE:HB2	10:IB:387:PHE:HB2	2.00	0.42
10:IB:963:ARG:HD3	10:IB:963:ARG:HA	1.89	0.42
10:IC:720:VAL:HB	10:IC:760:LEU:HD13	2.01	0.42
10:IC:947:HIS:HB3	10:IC:951:GLY:H	1.84	0.42
10:IC:1246:ASP:HB3	10:IC:1249:ALA:H	1.85	0.42
11:JA:170:ILE:O	11:JA:171:LYS:HG2	2.19	0.42
11:JA:1682:LYS:HB2	11:JA:1711:ALA:HB2	2.01	0.42
11:JB:162:PRO:HD2	11:JB:170:ILE:H	1.84	0.42
11:JC:1197:LEU:HD12	11:JC:1197:LEU:HA	1.92	0.42
12:KE:312:PRO:HB3	12:KE:350:LEU:HB3	2.01	0.42
13:LM:377:GLN:NE2	13:LM:378:GLU:HG3	2.35	0.42
14:ME:227:GLN:HA	14:ME:230:VAL:HG22	2.02	0.42
14:MI:304:ARG:O	14:MI:308:GLU:HB3	2.18	0.42
15:NA:891:TRP:HA	15:NA:1152:GLU:C	2.43	0.42
15:NA:908:PHE:HD1	15:NA:911:ARG:HD3	1.85	0.42
15:NB:902:ARG:HA	15:NB:902:ARG:HD3	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NC:893:LEU:H	15:NC:1153:ALA:C	2.27	0.42
15:NC:1136:SER:HB2	15:NC:1144:ARG:HG2	2.01	0.42
15:ND:578:HIS:HB3	15:ND:580:PHE:HD1	1.84	0.42
15:ND:1548:PHE:N	19:RD:142:ASN:HA	2.34	0.42
18:QB:64:LEU:HD23	18:QB:64:LEU:HA	1.85	0.42
18:QC:159:PRO:HB2	18:QC:162:PRO:HD2	2.02	0.42
1:AA:298:ILE:HG22	1:AA:332:THR:HG21	2.00	0.42
1:AA:398:GLU:HA	1:AA:401:THR:HG22	2.01	0.42
1:AD:747:MET:HE1	1:AD:784:PHE:CE1	2.54	0.42
1:AE:186:ARG:HH21	1:AE:204:TYR:HE1	1.67	0.42
1:AE:384:GLU:OE1	6:FB:1654:MET:HE2	2.20	0.42
2:AF:150:ALA:HB2	2:AF:212:VAL:HG11	2.02	0.42
2:AF:161:ILE:HB	5:EB:4626:LEU:HD22	2.02	0.42
1:AH:798:CYS:HB2	1:AH:997:PRO:HD2	2.02	0.42
1:AI:279:PRO:HG3	16:OA:751:VAL:HB	2.02	0.42
1:AI:360:GLU:HB3	2:AJ:485:LEU:HD21	2.02	0.42
2:AK:24:ASP:HB2	1:AL:446:LEU:HG	2.02	0.42
3:BB:1018:PHE:HB2	16:OB:912:TRP:NE1	2.35	0.42
3:CA:819:LEU:HA	3:CA:822:VAL:HG12	2.02	0.42
3:CB:976:LYS:HG3	10:IC:382:THR:HG22	2.01	0.42
3:CI:4467:THR:HG22	3:CI:4489:ASP:HA	2.01	0.42
4:DD:300:GLN:HE21	4:DD:354:TRP:HA	1.85	0.42
4:DF:80:LEU:O	4:DF:84:ILE:HD12	2.18	0.42
5:EA:3496:THR:HG22	5:EA:3498:VAL:H	1.83	0.42
5:EB:3578:PRO:HD3	5:EB:3612:LEU:HD12	2.01	0.42
5:EB:4405:ILE:H	5:EB:4405:ILE:HG12	1.50	0.42
5:EB:4492:ARG:HA	5:EB:4492:ARG:HD2	1.76	0.42
5:EC:3421:HIS:CE1	5:EC:3588:CYS:HA	2.54	0.42
6:FB:1639:PHE:CE1	6:FB:1654:MET:HE1	2.55	0.42
6:FB:1991:ALA:HA	6:FB:1994:ARG:HG2	2.01	0.42
6:FD:968:LEU:HB2	6:FD:1027:LEU:HD11	2.01	0.42
6:FE:1184:ALA:H	6:FE:1424:CYS:HB3	1.85	0.42
6:FE:1429:LEU:O	6:FE:1430:PHE:HB2	2.20	0.42
6:FE:1434:ALA:O	6:FE:1435:GLU:C	2.61	0.42
6:FF:1223:ALA:O	6:FF:1224:ALA:C	2.62	0.42
8:GB:179:MET:HG3	8:GB:197:VAL:HG22	2.02	0.42
8:GF:274:ARG:NH1	8:GF:321:LEU:HA	2.35	0.42
8:GF:383:LYS:HE3	8:GF:441:THR:HG21	2.02	0.42
8:GF:629:ASN:HB3	8:GF:670:PHE:CE1	2.55	0.42
8:GH:64:ASN:C	8:GH:64:ASN:ND2	2.76	0.42
8:GH:152:LEU:HB2	8:GH:394:PHE:HD2	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GI:974:ARG:HB2	7:GI:979:LEU:HA	2.01	0.42
8:GJ:454:ILE:HG23	8:GJ:458:GLY:HA3	2.01	0.42
8:GJ:549:THR:HG22	8:GJ:554:SER:HA	2.02	0.42
10:IA:300:LEU:HD23	10:IA:302:THR:H	1.85	0.42
10:IB:875:VAL:HG13	10:IB:948:LEU:HD23	2.02	0.42
10:IC:927:ARG:HH12	10:IC:961:GLN:HE22	1.68	0.42
10:IC:1221:THR:HB	10:IC:1321:LEU:HD11	2.01	0.42
11:JA:973:MET:HG3	11:JA:1003:ILE:HG23	2.00	0.42
11:JA:1689:LEU:HD12	11:JA:1699:SER:HB2	2.02	0.42
11:JB:2122:GLN:NE2	11:JB:2126:ILE:HG12	2.35	0.42
12:KA:325:LEU:HD23	12:KA:327:MET:HE3	2.00	0.42
12:KB:299:TYR:HE1	12:KB:304:ARG:HG3	1.85	0.42
12:KF:372:GLY:HA2	12:KF:401:GLN:HE22	1.84	0.42
12:KF:402:LEU:HD21	12:KF:406:GLN:HB3	2.01	0.42
12:KG:688:VAL:HG23	12:KG:698:PRO:HB3	2.01	0.42
13:LJ:423:GLN:HA	13:LJ:426:CYS:HB3	2.02	0.42
13:LJ:500:GLN:HA	13:LJ:503:VAL:HG12	2.02	0.42
13:LM:421:VAL:HG21	13:LN:417:LEU:HD22	2.00	0.42
15:NB:626:ARG:HB3	15:NB:690:TYR:HA	2.01	0.42
15:NC:548:PRO:HD3	15:NC:1194:ASN:HB2	2.00	0.42
15:NC:1125:TYR:HB3	15:NC:1160:LEU:H	1.85	0.42
15:NC:1407:MET:O	15:NC:1469:PHE:HB3	2.19	0.42
16:OC:198:ASP:HB3	17:PC:290:PHE:CD2	2.54	0.42
18:QA:122:ARG:HH11	18:QA:126:MET:HE1	1.84	0.42
18:QB:59:ALA:HB3	18:QB:66:PRO:HG3	2.00	0.42
1:AA:39:SER:HB3	1:AA:70:ASN:HB3	2.01	0.42
2:AC:332:ARG:NH1	11:JA:2284:LYS:HG3	2.34	0.42
1:AD:774:ALA:HA	1:AD:906:LEU:HD13	2.00	0.42
1:AI:161:SER:HB3	1:AI:185:ARG:CZ	2.50	0.42
1:AI:746:VAL:HG13	1:AI:747:MET:HG2	2.02	0.42
2:AJ:312:CYS:HB3	2:AJ:315:ASP:HB2	2.02	0.42
3:BA:738:TYR:HD2	3:BA:739:LEU:HD22	1.84	0.42
3:BA:892:ARG:O	3:BA:896:LEU:HB2	2.20	0.42
3:BB:945:THR:HG23	16:OB:314:GLY:HA2	2.02	0.42
3:CI:1123:LEU:HA	10:IA:770:GLY:HA3	2.02	0.42
4:DA:355:CYS:HA	4:DA:384:ILE:O	2.20	0.42
4:DA:385:LYS:NZ	13:LB:461:VAL:HG23	2.34	0.42
4:DC:130:ARG:HH21	4:DC:151:ALA:HA	1.84	0.42
4:DF:273:PHE:HZ	4:DF:338:ILE:HD13	1.84	0.42
5:EA:3781:ILE:HD12	5:EA:3781:ILE:HA	1.91	0.42
5:EB:4044:ILE:HA	5:EB:4047:MET:HG3	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:4687:ASP:HA	5:EB:4690:CYS:SG	2.60	0.42
5:EB:4734:LEU:HD21	5:EB:4828:LEU:HB3	2.02	0.42
5:EC:4173:LYS:HA	5:EC:4173:LYS:HD3	1.84	0.42
6:FC:2040:LEU:HA	6:FC:2040:LEU:HD13	1.68	0.42
6:FD:819:PRO:HA	6:FD:824:TYR:OH	2.20	0.42
6:FD:866:PHE:HB3	6:FD:1274:PRO:HD2	2.02	0.42
6:FD:910:ILE:HD11	6:FD:965:TRP:CD1	2.55	0.42
6:FD:1298:LEU:HD23	6:FD:1298:LEU:HA	1.91	0.42
6:FE:1004:GLY:O	6:FE:1005:PRO:C	2.63	0.42
6:FE:1095:LEU:HB3	6:FE:1099:ILE:HG12	2.02	0.42
8:GB:569:VAL:HG21	8:GB:784:LEU:HD21	2.02	0.42
7:GC:719:ILE:HD12	7:GC:800:VAL:HG11	2.00	0.42
7:GE:276:ARG:HH12	7:GE:279:ARG:HA	1.85	0.42
7:GG:980:LEU:HD21	7:GG:988:LYS:HE2	2.02	0.42
8:GH:168:MET:HG2	8:GH:247:PRO:HA	2.02	0.42
7:GI:279:ARG:HA	7:GI:285:LEU:HB3	2.01	0.42
8:GJ:283:LEU:HD11	8:GJ:303:LEU:HD22	2.02	0.42
7:GK:738:LEU:HD22	7:GK:797:ILE:HD12	2.01	0.42
8:GL:56:CYS:HB3	8:GL:59:SER:HB2	2.01	0.42
9:HA:760:LYS:HA	9:HA:763:GLN:CD	2.44	0.42
9:HB:764:LYS:HB2	9:HB:765:TRP:HE3	1.85	0.42
9:HD:757:LEU:O	9:HD:761:CYS:SG	2.75	0.42
9:HD:820:SER:O	9:HD:824:LEU:HG	2.20	0.42
9:HD:851:GLU:HB3	9:HD:855:ARG:CZ	2.50	0.42
10:IC:186:ASP:HB2	16:OC:1095:ARG:HH22	1.84	0.42
10:IC:916:LYS:HB2	11:JC:2042:SER:HB2	2.02	0.42
11:JA:419:SER:O	11:JA:490:THR:HG22	2.20	0.42
11:JB:1765:ARG:HH22	16:OB:891:ARG:HA	1.84	0.42
11:JB:1996:LEU:HG	11:JB:2000:TYR:CZ	2.54	0.42
11:JC:1206:GLN:HE21	11:JC:1211:ARG:HG2	1.85	0.42
11:JC:1335:LEU:HD21	11:JC:1375:TYR:HB2	2.02	0.42
11:JC:1437:ILE:HG22	11:JC:1439:LEU:HG	2.02	0.42
13:LA:394:GLY:O	13:LA:398:ARG:HG2	2.20	0.42
13:LA:531:VAL:HG23	13:LD:531:VAL:HG23	2.02	0.42
13:LF:430:LYS:HD3	13:LF:431:LEU:HD12	2.02	0.42
14:MJ:223:ARG:HE	14:MJ:223:ARG:HB2	1.75	0.42
15:NC:511:LEU:HD13	15:NC:539:GLY:HA3	2.01	0.42
15:NC:548:PRO:HA	15:NC:551:ARG:HE	1.85	0.42
16:OA:876:GLU:HG2	16:OA:939:MET:HB3	2.01	0.42
18:QC:64:LEU:HD11	18:QC:91:CYS:HA	2.00	0.42
19:RA:68:LYS:HA	19:RA:68:LYS:HD2	1.81	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:RC:50:VAL:HG12	19:RC:54:MET:HE1	2.02	0.42
20:SB:141:GLU:HA	20:SB:144:LYS:HG3	2.02	0.42
2:AC:176:VAL:HG13	16:OA:27:LEU:HA	2.01	0.42
1:AH:612:THR:HG22	13:LL:501:LYS:HG3	2.02	0.42
1:AI:410:GLU:HG2	2:AJ:67:LEU:HD22	2.00	0.42
1:AI:491:LEU:HB3	6:FC:1791:ASN:HB2	2.02	0.42
1:AI:507:LEU:HD11	6:FC:1826:LEU:HB3	2.01	0.42
2:AJ:481:ARG:HD3	2:AJ:537:ARG:HH22	1.85	0.42
2:AK:9:VAL:HG21	6:FC:1909:GLY:HA3	2.02	0.42
2:AK:296:ALA:H	1:AL:431:SER:HB2	1.84	0.42
1:AL:663:LEU:HD21	1:AL:698:LEU:HA	2.02	0.42
1:AL:967:ARG:HD3	14:MG:94:LEU:HD13	2.02	0.42
3:CE:1237:VAL:HG21	3:CE:4468:LYS:HB3	2.02	0.42
3:CG:1194:VAL:HG22	3:CG:1195:LEU:H	1.85	0.42
3:CG:1235:PRO:HB2	3:CG:1244:PRO:HB3	2.01	0.42
3:CI:1236:LEU:HA	3:CI:4469:LEU:HB3	2.02	0.42
4:DB:267:ARG:HD2	14:ME:297:VAL:HG11	2.01	0.42
5:EB:3244:GLY:H	9:HB:409:GLU:HG3	1.83	0.42
5:EC:4520:LEU:HD11	5:EC:4692:ILE:HD11	2.02	0.42
6:FA:2012:ARG:HB3	6:FA:2012:ARG:NH2	2.35	0.42
6:FB:1814:ARG:NH1	13:LL:511:GLN:HA	2.35	0.42
6:FD:805:HIS:O	6:FD:806:ILE:C	2.62	0.42
6:FD:894:ALA:HB1	6:FD:897:LEU:HB2	2.01	0.42
6:FD:922:LEU:HD22	6:FD:922:LEU:HA	1.75	0.42
6:FD:976:HIS:CE1	6:FD:1018:THR:HG23	2.55	0.42
6:FE:824:TYR:HB2	7:GE:964:GLN:NE2	2.35	0.42
6:FE:1227:ARG:O	6:FE:1228:ARG:C	2.61	0.42
6:FF:830:ALA:HB1	6:FF:843:LEU:CD2	2.50	0.42
6:FF:975:ILE:HG21	6:FF:989:PRO:HD3	2.02	0.42
6:FF:1096:LEU:HD13	6:FF:1096:LEU:HA	1.90	0.42
6:FF:1217:GLU:HB3	6:FF:1218:ALA:H	1.69	0.42
6:FF:1218:ALA:O	6:FF:1220:ARG:N	2.53	0.42
6:FF:1296:SER:O	6:FF:1297:PRO:C	2.63	0.42
7:GA:441:LEU:HD22	7:GA:505:PHE:HE1	1.83	0.42
7:GC:605:VAL:HG13	7:GC:630:LEU:HD11	2.02	0.42
7:GC:794:ALA:HA	7:GC:797:ILE:HG22	2.02	0.42
7:GC:910:HIS:CE1	12:KA:340:ALA:HA	2.55	0.42
8:GD:171:ILE:HG23	8:GD:181:HIS:HB2	2.00	0.42
7:GE:341:PRO:HD3	7:GE:597:THR:HA	2.02	0.42
7:GE:454:PHE:HZ	7:GE:592:ILE:HD12	1.85	0.42
8:GH:133:PRO:HG2	8:GH:168:MET:HE2	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GH:535:GLU:HB3	8:GH:631:LEU:HD11	2.01	0.42
7:GI:390:ILE:HG22	7:GI:462:GLY:HA3	2.02	0.42
7:GI:870:ARG:HE	7:GI:872:THR:HG21	1.84	0.42
9:HA:771:PRO:HG3	9:HA:819:TYR:CZ	2.55	0.42
9:HA:836:SER:O	9:HA:837:LEU:C	2.63	0.42
9:HB:400:ALA:HA	9:HB:402:ARG:NH1	2.35	0.42
9:HB:782:ALA:O	9:HB:783:SER:C	2.62	0.42
9:HB:795:LEU:HD23	9:HB:795:LEU:HA	1.78	0.42
10:IB:500:LEU:HA	10:IB:503:LEU:HD12	2.01	0.42
10:IB:821:MET:HE2	10:IB:821:MET:HB2	1.97	0.42
10:IC:300:LEU:HD23	10:IC:302:THR:H	1.83	0.42
12:KC:308:LEU:HA	12:KC:337:ALA:HB2	2.01	0.42
12:KF:212:LEU:HD13	12:KF:290:PRO:HB2	2.02	0.42
13:LI:526:LEU:HD23	13:LI:526:LEU:HA	1.80	0.42
14:MJ:207:LEU:HD23	14:MJ:207:LEU:HA	1.95	0.42
15:NA:558:GLU:HB2	15:NA:578:HIS:NE2	2.32	0.42
15:NA:883:LEU:HD23	15:NA:1123:ALA:HB1	2.02	0.42
15:NB:996:LEU:HD13	15:NB:1015:ALA:HB1	2.02	0.42
15:NB:1180:ASP:HB3	15:NB:1181:SER:H	1.61	0.42
15:NC:1407:MET:HB3	15:NC:1469:PHE:HB3	2.02	0.42
15:NC:1521:SER:O	15:NC:1525:ARG:HG2	2.20	0.42
19:RB:26:HIS:CE1	19:RB:29:GLU:HB3	2.55	0.42
20:SD:106:LEU:O	20:SD:110:MET:HG2	2.19	0.42
2:AB:328:HIS:CD2	2:AB:337:HIS:HB2	2.55	0.42
1:AD:988:GLN:HA	1:AD:988:GLN:NE2	2.35	0.42
1:AE:655:SER:HA	1:AE:659:PHE:HD1	1.84	0.42
2:AG:105:ASN:HB2	2:AG:264:THR:HG23	2.02	0.42
1:AI:265:VAL:HG23	1:AI:266:HIS:CD2	2.55	0.42
1:AI:1004:VAL:HG23	1:AI:1008:ALA:HB3	2.01	0.42
1:AL:894:SER:O	13:LE:502:MET:HE1	2.20	0.42
3:CC:976:LYS:HA	3:CC:976:LYS:HD2	1.86	0.42
3:CF:1129:ARG:HD3	10:IB:1264:ILE:HD11	2.01	0.42
4:DA:175:TYR:HE2	4:DD:186:THR:OG1	2.03	0.42
4:DB:130:ARG:CZ	4:DB:151:ALA:HA	2.50	0.42
4:DC:365:ILE:HG21	4:DC:378:ILE:HG21	2.02	0.42
4:DE:299:ARG:HD3	4:DE:299:ARG:HA	1.81	0.42
5:EA:4282:SER:HA	5:EA:4285:THR:HG22	2.01	0.42
5:EB:3320:LEU:HD13	5:EB:3412:LEU:HD22	2.02	0.42
5:EB:3433:ALA:O	5:EB:3436:TYR:HB3	2.20	0.42
5:EB:4465:PHE:HD2	5:EB:4666:VAL:HG12	1.84	0.42
5:EB:4487:ASP:HA	5:EB:4490:THR:HG22	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EC:3704:SER:HB2	5:EC:3829:PHE:CE1	2.55	0.42
5:EC:4403:LEU:CB	5:EC:4405:ILE:HD11	2.50	0.42
5:EC:4405:ILE:HG22	5:EC:4406:MET:N	2.35	0.42
6:FA:1962:GLN:O	6:FA:1966:ASP:HB2	2.20	0.42
6:FD:824:TYR:HB2	7:GC:964:GLN:NE2	2.34	0.42
6:FD:841:TYR:CD2	6:FD:841:TYR:C	2.98	0.42
6:FE:895:ILE:HG12	7:GE:967:PHE:CZ	2.55	0.42
6:FE:1218:ALA:HB3	6:FE:1276:LEU:HD13	2.02	0.42
6:FF:1003:ILE:HG21	6:FF:1444:ARG:HH12	1.84	0.42
6:FF:1027:LEU:O	6:FF:1030:ILE:N	2.48	0.42
7:GA:538:THR:H	9:HB:554:ASP:C	2.28	0.42
8:GD:656:ALA:HB3	8:GD:742:SER:H	1.84	0.42
7:GE:239:ASN:HB2	7:GE:693:THR:HG21	2.01	0.42
7:GE:765:PRO:HB3	7:GE:791:ARG:HG3	2.02	0.42
7:GI:340:LEU:HA	7:GI:597:THR:HG22	2.00	0.42
7:GK:421:SER:HA	7:GK:424:ARG:NE	2.34	0.42
8:GL:29:ILE:HG22	8:GL:31:LEU:H	1.85	0.42
8:GL:342:LYS:HE2	8:GL:342:LYS:HB2	1.79	0.42
9:HA:674:VAL:HG13	9:HA:712:ILE:HG12	2.01	0.42
9:HA:843:VAL:O	9:HA:846:VAL:HB	2.20	0.42
9:HD:808:HIS:O	9:HD:812:THR:HG23	2.20	0.42
10:IA:588:LYS:HE2	10:IA:604:CYS:HB3	2.02	0.42
10:IB:893:PHE:CZ	10:IB:907:ASP:HA	2.55	0.42
10:IB:1223:LEU:HD23	10:IB:1387:LEU:HD22	2.02	0.42
11:JA:1991:ASP:HA	11:JA:1994:GLU:HB3	2.02	0.42
11:JB:83:VAL:HG21	11:JB:100:ILE:HD11	2.02	0.42
11:JB:472:CYS:HB3	11:JB:879:LEU:HD11	2.02	0.42
11:JB:1387:LEU:HG	11:JB:1409:ARG:HB2	2.02	0.42
11:JC:191:ASP:HB3	11:JC:194:VAL:HB	2.02	0.42
11:JC:533:ILE:HG22	11:JC:534:TYR:CD1	2.55	0.42
11:JC:1158:MET:HE2	11:JC:1161:LEU:HD21	2.02	0.42
12:KA:526:TRP:CE2	12:KA:582:ILE:HD13	2.54	0.42
12:KE:579:LEU:HD23	12:KE:656:ARG:HA	2.02	0.42
12:KF:279:VAL:HG11	12:KF:282:LYS:HD3	2.02	0.42
13:LI:527:VAL:HG11	13:LJ:528:PRO:HG3	2.01	0.42
15:NA:601:THR:HG23	15:NA:1190:ILE:HG23	2.01	0.42
15:NA:647:GLN:HE21	15:NA:647:GLN:HB3	1.74	0.42
15:NB:1116:ASP:HB2	15:NB:1119:SER:HB2	2.00	0.42
15:NC:1536:GLN:HE22	19:RA:113:ARG:HH21	1.68	0.42
15:ND:1548:PHE:HB3	19:RD:136:ALA:HA	2.02	0.42
16:OC:171:PHE:CG	16:OC:180:LYS:HD3	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:PC:128:GLU:HG3	17:PC:132:LEU:HD12	2.01	0.42
1:AA:683:ASN:C	1:AA:683:ASN:HD22	2.28	0.41
2:AC:528:LEU:HD22	1:AD:91:ILE:HB	2.01	0.41
1:AE:653:LEU:HD23	1:AE:653:LEU:HA	1.90	0.41
1:AE:1004:VAL:HG13	1:AE:1006:ARG:HH22	1.85	0.41
2:AF:45:LEU:HD13	5:EB:4525:VAL:HG11	2.01	0.41
3:CA:731:MET:HE2	3:CA:731:MET:HB2	1.93	0.41
3:CC:742:LYS:HA	3:CC:746:THR:HB	2.01	0.41
4:DB:75:TYR:HD1	4:DB:78:LYS:HZ3	1.68	0.41
5:EA:3610:GLN:HG2	5:EA:3611:GLU:HG2	2.00	0.41
5:EB:4156:LEU:HD12	9:HB:431:TYR:CE1	2.55	0.41
5:EB:4759:LYS:HB2	5:EB:4759:LYS:HE3	1.77	0.41
5:EC:4465:PHE:HD2	5:EC:4666:VAL:HG12	1.85	0.41
6:FA:2097:GLN:HA	6:FA:2100:SER:HB3	2.01	0.41
6:FC:2023:ILE:CG2	9:HB:778:PRO:HB3	2.49	0.41
6:FD:819:PRO:HG3	6:FD:895:ILE:CD1	2.50	0.41
6:FF:818:VAL:O	6:FF:821:ARG:HB2	2.19	0.41
7:GA:491:GLU:HA	7:GA:494:LEU:HD23	2.02	0.41
8:GB:135:LEU:HB2	8:GB:294:TRP:CZ3	2.55	0.41
7:GC:619:ARG:HH12	7:GC:629:ASP:HA	1.84	0.41
7:GE:176:ARG:HA	7:GE:176:ARG:HD2	1.93	0.41
10:IC:635:LEU:HD12	10:IC:638:ARG:HD3	2.02	0.41
11:JA:57:GLU:HB3	11:JA:90:ARG:HE	1.85	0.41
11:JA:1409:ARG:HG3	11:JA:1410:LEU:H	1.85	0.41
11:JA:1734:VAL:HG11	11:JA:1774:ARG:HG3	2.02	0.41
11:JB:838:ASP:OD1	11:JB:1423:PRO:HD2	2.20	0.41
11:JC:2255:ARG:HD3	11:JC:2255:ARG:HA	1.87	0.41
12:KB:258:LEU:HA	12:KB:261:VAL:HG12	2.01	0.41
12:KC:586:ARG:HH21	12:KC:712:GLY:HA2	1.84	0.41
13:LI:473:LYS:O	13:LI:476:GLY:HA3	2.20	0.41
13:LK:421:VAL:HG11	13:LL:421:VAL:HG22	2.02	0.41
14:MB:294:ALA:HA	14:MB:297:VAL:HG12	2.02	0.41
15:NA:622:THR:HG23	15:NA:650:ARG:HH22	1.85	0.41
15:NB:676:ARG:HA	15:NB:676:ARG:HD3	1.82	0.41
15:NC:1193:VAL:HG11	15:NC:1391:LEU:HD21	2.02	0.41
15:ND:525:LEU:HD21	15:ND:545:VAL:HG11	2.02	0.41
15:ND:542:LEU:HB3	15:ND:1190:ILE:HA	2.02	0.41
15:ND:568:TYR:HE2	16:OC:1038:ARG:HE	1.68	0.41
16:OC:1055:ARG:NH1	16:OC:1059:LEU:HD23	2.35	0.41
18:QB:119:LEU:HD22	18:QB:123:VAL:HG11	2.02	0.41
19:RA:20:PRO:HD2	19:RA:101:ASP:HA	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:89:GLY:HA3	1:AA:154:GLY:HA2	2.02	0.41
1:AA:418:ILE:O	1:AA:421:MET:HB2	2.20	0.41
1:AD:132:PRO:HA	1:AD:133:PRO:HD3	1.96	0.41
2:AF:29:LEU:HD13	2:AF:283:LEU:HD21	2.02	0.41
2:AG:428:ARG:HH11	1:AH:415:MET:HE3	1.85	0.41
2:AK:450:ARG:HD2	11:JB:1724:PHE:HE1	1.85	0.41
3:CB:765:VAL:HG12	3:CB:829:LEU:HD22	2.02	0.41
3:CF:1179:ILE:HD13	3:CF:4517:LEU:HD22	2.00	0.41
3:CL:1237:VAL:HA	3:CL:1244:PRO:HA	2.02	0.41
4:DA:310:LEU:HD23	4:DA:310:LEU:HA	1.87	0.41
5:EA:4209:HIS:O	5:EA:4213:LYS:HG2	2.20	0.41
5:EC:3446:ILE:HD12	5:EC:3490:TYR:HB3	2.01	0.41
6:FA:1823:ALA:HA	6:FA:1842:VAL:HA	2.01	0.41
6:FC:2042:LYS:HA	6:FC:2042:LYS:HD2	1.86	0.41
6:FC:2073:LEU:HD12	6:FC:2073:LEU:HA	1.75	0.41
6:FD:864:LEU:HD11	6:FD:973:ILE:HD12	2.02	0.41
6:FE:1241:VAL:HG22	6:FE:1260:LEU:HD12	2.01	0.41
6:FF:965:TRP:N	6:FF:965:TRP:CD1	2.88	0.41
6:FF:1194:ASN:HD22	6:FF:1194:ASN:HA	1.59	0.41
6:FF:1253:SER:O	6:FF:1254:GLY:C	2.62	0.41
7:GA:548:ALA:HB1	9:HB:666:LYS:HB2	2.02	0.41
8:GB:326:ARG:HH22	8:GB:375:TYR:H	1.68	0.41
8:GB:563:ARG:HA	8:GB:566:ILE:HG22	2.01	0.41
8:GD:200:GLY:HA2	8:GD:281:LEU:HD22	2.01	0.41
8:GD:689:PHE:HA	8:GD:692:MET:SD	2.60	0.41
7:GE:190:SER:HA	7:GE:648:LEU:HD13	2.02	0.41
7:GI:916:HIS:NE2	12:KC:663:ALA:HB2	2.35	0.41
8:GJ:348:TYR:HB3	8:GJ:380:MET:SD	2.60	0.41
7:GK:719:ILE:HG12	7:GK:800:VAL:HG11	2.02	0.41
8:GL:56:CYS:HB2	8:GL:61:CYS:HB2	2.02	0.41
9:HB:764:LYS:H	9:HB:764:LYS:HG2	1.61	0.41
9:HD:826:ARG:O	9:HD:830:ILE:HG13	2.21	0.41
10:IC:551:ASN:ND2	10:IC:852:CYS:HA	2.35	0.41
11:JA:1298:ILE:HG12	11:JA:1348:PHE:HB2	2.01	0.41
11:JA:1756:ALA:HA	11:JA:1759:LEU:HD23	2.02	0.41
11:JB:428:GLU:HA	11:JB:431:ALA:HB3	2.02	0.41
11:JB:1464:HIS:HD1	11:JB:1464:HIS:C	2.28	0.41
11:JC:48:GLN:HA	11:JC:95:PRO:HB3	2.02	0.41
11:JC:519:PHE:HE1	11:JC:1473:LEU:HD13	1.84	0.41
11:JC:2005:ILE:HD13	11:JC:2005:ILE:HA	1.91	0.41
12:KB:520:LYS:HG3	12:KB:522:ARG:H	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LF:509:GLU:HG2	13:LF:512:ARG:NH2	2.35	0.41
13:LJ:424:LEU:HA	13:LJ:427:ARG:NH1	2.35	0.41
15:NC:529:PHE:CD2	15:NC:1382:PHE:HB2	2.55	0.41
15:NC:898:ASN:HB3	15:NC:902:ARG:HE	1.85	0.41
15:NC:1426:PRO:HG2	16:OA:949:PRO:HB2	2.02	0.41
1:AA:315:LEU:HD12	1:AA:316:ILE:HB	2.03	0.41
2:AB:113:LEU:HG	11:JA:1649:LEU:HD11	2.01	0.41
2:AB:355:HIS:HA	2:AB:356:PRO:HD3	1.90	0.41
1:AE:51:GLU:HG3	1:AE:64:HIS:HA	2.03	0.41
1:AE:998:LEU:HD12	1:AE:998:LEU:HA	1.84	0.41
2:AG:263:TYR:CE1	16:OC:11:GLY:HA3	2.55	0.41
4:DB:281:GLN:HG3	4:DB:285:ARG:HH22	1.85	0.41
5:EA:3239:SER:HB2	5:EA:3268:ASN:HB3	2.02	0.41
5:EA:3382:GLU:OE1	5:EA:3384:LYS:HG2	2.20	0.41
5:EA:4446:ARG:NH2	17:PB:143:ILE:HD11	2.35	0.41
5:EA:4744:GLN:HA	5:EA:4747:MET:HG2	2.00	0.41
5:EB:3534:PHE:O	5:EB:3538:GLN:HG3	2.19	0.41
5:EB:4024:THR:HG21	9:HB:435:LEU:HD23	2.03	0.41
5:EB:4307:MET:HE3	5:EB:4350:LYS:HG3	2.03	0.41
6:FA:2040:LEU:HD23	6:FA:2040:LEU:HA	1.74	0.41
6:FC:2038:LEU:HD13	6:FC:2038:LEU:HA	1.87	0.41
6:FF:1203:ARG:HH22	11:JB:957:ASP:HA	1.85	0.41
7:GA:293:VAL:HG22	7:GA:688:ARG:HH12	1.85	0.41
8:GB:29:ILE:HG21	8:GB:528:VAL:HG21	2.01	0.41
8:GB:294:TRP:CG	8:GB:297:LEU:HD12	2.55	0.41
8:GB:725:CYS:HA	8:GB:730:SER:HB3	2.02	0.41
8:GD:22:THR:HG23	8:GD:25:GLU:H	1.85	0.41
7:GE:169:ILE:HD13	7:GE:697:PRO:HG3	2.02	0.41
7:GE:289:SER:HA	7:GE:691:VAL:O	2.20	0.41
7:GE:402:PHE:HE2	7:GE:447:VAL:HB	1.85	0.41
7:GE:446:HIS:CD2	7:GE:447:VAL:HG23	2.56	0.41
8:GF:149:LEU:HD12	8:GF:149:LEU:HA	1.90	0.41
8:GH:183:LEU:HD21	8:GH:245:ILE:HA	2.02	0.41
8:GH:710:LYS:HA	8:GH:710:LYS:HD3	1.69	0.41
7:GK:543:LYS:HA	7:GK:544:PRO:HD3	1.97	0.41
9:HA:526:VAL:O	9:HA:578:THR:HA	2.20	0.41
9:HA:824:LEU:O	9:HA:827:ASP:N	2.53	0.41
9:HD:758:ALA:O	9:HD:759:GLU:C	2.63	0.41
10:IA:486:PRO:HA	10:IA:489:TYR:CZ	2.56	0.41
10:IA:616:GLY:H	10:IA:758:ASN:ND2	2.14	0.41
10:IA:751:ASN:HB3	10:IA:752:SER:H	1.68	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IA:882:VAL:HB	10:IA:884:TYR:CE1	2.55	0.41
10:IB:230:ARG:HD3	11:JB:2054:ARG:HD2	2.02	0.41
10:IB:837:VAL:HB	10:IB:873:LEU:HD11	2.00	0.41
10:IC:740:ARG:HH12	10:IC:777:GLY:HA3	1.85	0.41
10:IC:789:ARG:HA	10:IC:792:ILE:HG22	2.02	0.41
11:JA:1514:VAL:HA	11:JA:1517:ILE:HG22	2.01	0.41
11:JB:1090:LEU:HD12	11:JB:1090:LEU:HA	1.92	0.41
11:JC:83:VAL:HG11	11:JC:100:ILE:HD11	2.01	0.41
12:KC:391:LEU:HA	12:KC:391:LEU:HD12	1.71	0.41
12:KE:633:ARG:HH12	12:KE:635:VAL:HG22	1.85	0.41
13:LF:530:VAL:HG21	13:LH:532:LEU:HD22	2.01	0.41
14:MA:247:LEU:HD11	14:MB:248:SER:HA	2.02	0.41
14:MF:292:ALA:HA	14:MF:295:GLU:HB2	2.02	0.41
15:NA:600:LEU:HD13	15:NA:917:MET:HB3	2.02	0.41
15:NB:729:VAL:HG11	15:NB:800:SER:HB3	2.03	0.41
15:NB:1552:ILE:HD12	19:RB:143:LEU:HA	2.02	0.41
15:NC:587:LEU:HA	15:NC:590:VAL:HB	2.03	0.41
15:NC:602:PHE:HD2	15:NC:1191:ALA:HB2	1.85	0.41
15:NC:1498:ARG:HD3	20:SD:41:GLY:HA2	2.01	0.41
15:ND:735:HIS:CE1	15:ND:768:GLU:HA	2.55	0.41
18:QB:120:LYS:HB2	18:QB:123:VAL:HG23	2.02	0.41
2:AB:374:LEU:HD23	5:EA:4442:GLU:HG3	2.02	0.41
1:AD:656:ASP:HA	9:HB:514:PHE:CD1	2.55	0.41
2:AF:169:VAL:HG12	2:AF:171:VAL:HG13	2.02	0.41
1:AL:987:LEU:HD13	7:GK:424:ARG:NH2	2.29	0.41
3:BA:731:MET:HE1	3:BA:768:CYS:SG	2.60	0.41
3:CC:689:LEU:HD12	3:CC:736:HIS:NE2	2.35	0.41
3:CF:1170:THR:HA	3:CF:4501:GLN:HB2	2.03	0.41
3:CG:1262:HIS:CE1	3:CG:4454:ASP:HA	2.54	0.41
3:CG:1264:VAL:HG13	3:CG:1265:ILE:HD12	2.01	0.41
3:CG:4521:ARG:HD3	3:CG:4521:ARG:HA	1.83	0.41
3:CI:4522:LEU:HB3	3:CI:4524:LEU:HD13	2.01	0.41
3:CJ:1236:LEU:HD11	3:CJ:4502:VAL:HG11	2.02	0.41
4:DC:66:ARG:HA	4:DC:66:ARG:HD2	1.87	0.41
4:DE:298:LEU:HD23	4:DE:298:LEU:HA	1.93	0.41
5:EA:3564:ARG:HA	5:EA:3564:ARG:HD3	1.83	0.41
5:EB:3720:LEU:HD12	5:EB:3805:PHE:HE2	1.85	0.41
5:EB:4401:PRO:O	5:EB:4402:PRO:C	2.63	0.41
5:EC:4892:ARG:O	5:EC:4893:THR:C	2.61	0.41
6:FA:1712:GLU:HG2	6:FA:1716:SER:HB2	2.02	0.41
6:FA:2023:ILE:HG22	9:HA:778:PRO:HB3	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FB:2069:ASN:O	6:FB:2072:ILE:N	2.53	0.41
6:FC:2055:THR:OG1	6:FC:2056:LEU:N	2.53	0.41
6:FC:2080:GLN:HB3	9:HB:861:TYR:CE2	2.51	0.41
6:FE:927:GLY:O	6:FE:928:SER:C	2.62	0.41
6:FE:1219:GLU:H	6:FE:1219:GLU:HG2	1.51	0.41
6:FF:925:GLU:CG	6:FF:1092:PRO:HB2	2.46	0.41
6:FF:1187:ILE:O	6:FF:1267:GLN:HA	2.21	0.41
6:FF:1215:MET:HG2	6:FF:1219:GLU:HG3	2.01	0.41
8:GB:263:ARG:HE	7:GC:380:ARG:NH2	2.18	0.41
8:GB:283:LEU:HD21	8:GB:303:LEU:HD22	2.01	0.41
7:GC:165:VAL:HB	7:GC:697:PRO:HG3	2.02	0.41
7:GC:340:LEU:HA	7:GC:597:THR:HG22	2.03	0.41
7:GC:451:ILE:HD11	7:GC:516:VAL:HG23	2.02	0.41
7:GC:607:ARG:HG3	7:GC:677:ALA:HB3	2.02	0.41
8:GD:638:LEU:HD22	8:GD:654:LEU:HA	2.02	0.41
8:GH:189:ASN:HD21	7:GI:422:LEU:HA	1.85	0.41
7:GK:974:ARG:HB3	7:GK:979:LEU:HA	2.02	0.41
9:HA:482:ALA:HB2	9:HA:613:ILE:HD12	2.02	0.41
9:HB:865:ILE:HA	9:HB:865:ILE:HD12	1.57	0.41
9:HD:769:LYS:HE2	9:HD:826:ARG:HD2	2.03	0.41
10:IA:614:LEU:HD21	10:IA:759:PHE:HB3	2.02	0.41
10:IA:1309:ILE:HA	10:IA:1312:ILE:HG22	2.03	0.41
10:IB:172:GLN:HB3	10:IB:173:GLN:H	1.58	0.41
10:IB:537:LEU:HD22	10:IB:558:VAL:HG11	2.01	0.41
10:IC:452:LEU:HD23	10:IC:503:LEU:HD12	2.03	0.41
10:IC:735:LYS:HG3	10:IC:738:PRO:HD2	2.02	0.41
10:IC:994:MET:HE2	10:IC:994:MET:HB2	1.80	0.41
11:JA:473:ASN:ND2	11:JA:876:GLN:HB3	2.35	0.41
11:JA:489:VAL:HG22	11:JA:490:THR:H	1.84	0.41
11:JB:123:ILE:HG13	11:JB:135:ILE:HB	2.02	0.41
11:JB:536:ILE:HD12	11:JB:551:PRO:HG2	2.01	0.41
11:JB:1587:TRP:HB3	11:JB:1591:HIS:HB2	2.02	0.41
11:JB:2009:LEU:HD23	11:JB:2009:LEU:HA	1.94	0.41
11:JC:1110:PRO:HA	11:JC:1114:ALA:HB3	2.02	0.41
12:KA:476:MET:O	12:KA:480:VAL:HG13	2.20	0.41
12:KB:486:PHE:HE2	12:KB:506:LEU:HD13	1.86	0.41
12:KC:361:GLN:HA	12:KC:364:LEU:HD23	2.01	0.41
12:KC:377:LEU:HD12	12:KC:383:HIS:CE1	2.54	0.41
12:KE:547:ARG:HG3	12:KE:711:ILE:HD13	2.01	0.41
12:KG:367:ILE:HG23	12:KG:397:GLN:NE2	2.35	0.41
13:LH:506:GLN:O	13:LH:510:ILE:HG12	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:LJ:457:GLN:HA	13:LJ:460:ARG:NH1	2.35	0.41
13:LO:399:ASP:HA	13:LO:402:LEU:HB2	2.02	0.41
14:MG:98:ASN:O	14:MG:102:LYS:HG3	2.21	0.41
15:NA:682:ARG:NH1	15:NA:915:VAL:HG13	2.34	0.41
15:NA:739:HIS:HB3	15:NA:742:LEU:HB2	2.02	0.41
15:NA:1533:LYS:HA	15:NA:1536:GLN:HE21	1.84	0.41
15:NC:926:ARG:HD3	15:NC:1111:ARG:HB2	2.02	0.41
16:OB:1089:LEU:HD22	16:OB:1092:ARG:HH21	1.85	0.41
19:RA:62:LEU:HD23	19:RA:67:VAL:HG12	2.01	0.41
2:AB:108:LEU:HA	2:AB:108:LEU:HD23	1.77	0.41
2:AC:32:LEU:HD21	1:AD:451:ILE:HD11	2.01	0.41
1:AD:389:LEU:HD12	5:EA:4619:VAL:HG21	2.02	0.41
1:AE:399:ARG:HG2	1:AE:400:LYS:HG3	2.02	0.41
1:AE:669:SER:HB2	1:AE:674:ARG:HE	1.85	0.41
2:AG:90:ARG:HE	2:AG:90:ARG:HB2	1.70	0.41
1:AI:284:PRO:HA	1:AI:333:LEU:HD23	2.02	0.41
2:AJ:271:VAL:HG12	2:AJ:273:ASP:H	1.85	0.41
3:BA:880:GLN:O	3:BA:884:LEU:HD23	2.21	0.41
3:CE:1235:PRO:HA	3:CE:1254:MET:HA	2.01	0.41
3:CE:1264:VAL:HG13	3:CE:1265:ILE:HD12	2.03	0.41
3:CJ:4470:LYS:HB2	3:CJ:4470:LYS:HE3	1.84	0.41
4:DB:254:GLU:HB2	4:DB:291:GLN:NE2	2.35	0.41
4:DC:172:ARG:O	4:DC:176:ILE:HG12	2.21	0.41
4:DC:272:LEU:HD23	4:DC:272:LEU:HA	1.94	0.41
4:DE:253:LEU:HA	4:DE:256:LEU:HG	2.01	0.41
4:DF:59:TYR:CE2	4:DF:166:VAL:HG11	2.56	0.41
5:EA:3304:LYS:HG2	9:HC:416:PHE:HE1	1.86	0.41
5:EA:4223:THR:O	5:EA:4225:LYS:HG2	2.21	0.41
5:EC:4521:TYR:HB2	5:EC:4711:LEU:HD21	2.02	0.41
6:FB:1946:LEU:HD22	6:FB:1954:ALA:HB1	2.01	0.41
6:FC:2069:ASN:HB2	9:HB:851:GLU:CD	2.45	0.41
6:FD:1075:VAL:O	6:FD:1076:ILE:C	2.64	0.41
6:FE:882:SER:N	6:FE:904:GLN:OE1	2.51	0.41
6:FF:802:LEU:HD21	6:FF:968:LEU:HD22	2.01	0.41
6:FF:910:ILE:O	6:FF:910:ILE:HG13	2.19	0.41
6:FF:1095:LEU:O	6:FF:1096:LEU:C	2.64	0.41
6:FF:1096:LEU:O	6:FF:1099:ILE:HB	2.20	0.41
6:FF:1389:ARG:CZ	6:FF:1391:TYR:HA	2.50	0.41
6:FF:1394:ARG:O	6:FF:1396:PHE:N	2.53	0.41
6:FF:1420:ARG:O	6:FF:1421:VAL:C	2.63	0.41
8:GB:522:GLU:OE2	8:GB:524:ASN:HB2	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GC:827:LEU:HD12	7:GC:832:ILE:HD13	2.03	0.41
8:GD:401:ASP:HA	8:GD:404:ARG:HG2	2.02	0.41
8:GD:723:VAL:HG11	8:GD:731:GLN:HB2	2.02	0.41
7:GG:873:ALA:HA	7:GG:876:MET:HE3	2.02	0.41
8:GH:137:PHE:CE1	8:GH:245:ILE:HG21	2.55	0.41
8:GL:172:ILE:HG12	8:GL:180:LEU:HA	2.03	0.41
9:HA:822:ASP:O	9:HA:823:ILE:C	2.63	0.41
9:HD:877:LYS:HD3	9:HD:877:LYS:HA	1.60	0.41
10:IA:1079:LYS:HE3	10:IA:1083:MET:HE3	2.03	0.41
10:IB:238:ARG:HD3	11:JB:2050:TYR:HB3	2.03	0.41
11:JA:1996:LEU:HD23	11:JA:1996:LEU:HA	1.93	0.41
11:JB:1484:LEU:HB3	11:JB:1488:ASN:HB2	2.02	0.41
11:JB:1728:SER:HA	11:JB:1733:THR:HG21	2.02	0.41
11:JC:1068:ASP:HA	11:JC:1069:PRO:HD3	1.94	0.41
11:JC:1404:GLN:HB2	11:JC:1407:HIS:CE1	2.55	0.41
11:JC:1437:ILE:HA	11:JC:1438:PRO:HD3	1.89	0.41
12:KA:547:ARG:HB3	12:KA:712:GLY:H	1.85	0.41
12:KA:597:ALA:HB2	12:KA:608:VAL:HG12	2.02	0.41
12:KC:234:PRO:O	12:KC:235:PRO:C	2.64	0.41
12:KE:322:ALA:HA	12:KE:325:LEU:HB2	2.02	0.41
13:LA:513:LEU:HD23	13:LA:513:LEU:HA	1.80	0.41
13:LI:388:LEU:HD11	13:LJ:384:LEU:HD13	2.02	0.41
14:MI:225:VAL:HG21	14:MI:315:TRP:NE1	2.35	0.41
15:NA:867:ARG:HA	15:NA:870:TYR:CE1	2.55	0.41
15:NA:874:GLN:HB3	15:NA:877:GLN:HB2	2.01	0.41
15:NA:966:VAL:HG22	15:NA:1462:GLN:HE21	1.84	0.41
15:ND:686:ASN:ND2	15:ND:905:ASP:HB3	2.36	0.41
1:AA:835:ALA:HB1	1:AA:915:TRP:CZ3	2.55	0.41
2:AB:475:MET:HE3	2:AB:475:MET:HB3	1.76	0.41
1:AE:66:VAL:HG11	17:PC:266:HIS:HB3	2.02	0.41
1:AI:62:ASP:HB2	1:AI:228:PRO:HB3	2.02	0.41
2:AK:265:PHE:HD1	16:OB:140:THR:HG22	1.85	0.41
1:AL:615:ILE:HD13	1:AL:618:ARG:HE	1.85	0.41
3:CC:1014:ASP:HA	3:CC:1017:ARG:HG2	2.02	0.41
4:DB:272:LEU:HD23	4:DB:272:LEU:HA	1.92	0.41
4:DB:297:ARG:HH22	13:LE:460:ARG:NH2	2.18	0.41
4:DD:367:ARG:HD2	4:DD:367:ARG:HA	1.86	0.41
4:DF:97:LEU:HD21	4:DF:164:PHE:HE2	1.85	0.41
4:DF:163:GLU:O	4:DF:166:VAL:HG22	2.20	0.41
5:EA:3672:GLU:HA	5:EA:3675:GLU:HB2	2.02	0.41
5:EA:3822:SER:HB3	5:EA:4243:PHE:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EB:3681:LEU:HD11	5:EB:3715:VAL:HA	2.01	0.41
5:EB:4658:ASP:HA	5:EB:4690:CYS:SG	2.60	0.41
6:FA:1866:ILE:HG23	6:FA:1867:THR:HG23	2.03	0.41
6:FB:2040:LEU:HA	6:FB:2040:LEU:HD23	1.79	0.41
6:FC:1991:ALA:HA	6:FC:1994:ARG:NE	2.33	0.41
6:FD:842:GLY:O	6:FD:843:LEU:C	2.62	0.41
6:FD:1388:PHE:CE1	6:FD:1390:ALA:HA	2.56	0.41
6:FE:1181:VAL:HG22	6:FE:1182:ALA:H	1.86	0.41
6:FF:854:TRP:NE1	6:FF:971:SER:OG	2.50	0.41
8:GB:274:ARG:HH12	8:GB:308:ALA:HB3	1.85	0.41
8:GB:301:VAL:HB	8:GB:362:VAL:HG12	2.02	0.41
7:GC:309:LEU:HD21	7:GC:451:ILE:HG22	2.01	0.41
7:GC:946:HIS:CE1	7:GC:948:CYS:HB2	2.55	0.41
7:GG:535:PRO:HB2	9:HA:552:ASP:C	2.46	0.41
8:GL:667:LEU:HD22	8:GL:735:LEU:HA	2.02	0.41
9:HC:561:ASN:HD21	9:HC:570:ALA:HB3	1.85	0.41
10:IB:469:LEU:HA	10:IB:472:LYS:NZ	2.35	0.41
10:IC:337:LEU:HD13	10:IC:561:ARG:HE	1.84	0.41
11:JB:1122:ARG:HG3	11:JB:1123:THR:HG23	2.02	0.41
11:JB:1479:ALA:HA	11:JB:1482:LYS:HG2	2.02	0.41
11:JC:929:LEU:HD21	11:JC:966:LEU:HD11	2.02	0.41
11:JC:1150:PHE:HE1	11:JC:1154:ARG:HH21	1.68	0.41
11:JC:1553:LEU:HD23	11:JC:1553:LEU:HA	1.93	0.41
12:KA:345:GLY:HA3	12:KA:346:PRO:HD3	1.95	0.41
12:KC:236:LYS:C	12:KC:238:PHE:N	2.78	0.41
12:KF:322:ALA:HB1	12:KF:327:MET:HB2	2.03	0.41
13:LA:483:ARG:HH11	13:LA:483:ARG:HG3	1.85	0.41
13:LE:377:GLN:HA	13:LE:380:MET:HG2	2.02	0.41
13:LN:372:THR:HA	13:LN:375:ILE:HG22	2.01	0.41
15:NA:605:LEU:HB2	15:NA:923:ASP:HB2	2.02	0.41
15:NC:570:GLY:HA3	15:NC:575:LEU:HD21	2.02	0.41
15:NC:578:HIS:ND1	15:NC:580:PHE:HD2	2.19	0.41
15:NC:722:VAL:HG13	15:NC:726:CYS:HB2	2.03	0.41
15:ND:1541:PHE:O	15:ND:1545:VAL:HG23	2.21	0.41
19:RA:46:SER:H	19:RA:49:ASP:HB2	1.84	0.41
20:SC:143:VAL:O	20:SC:146:MET:HB2	2.21	0.41
1:AA:64:HIS:NE2	17:PA:268:PRO:HD2	2.36	0.41
2:AF:46:GLN:HB3	2:AF:48:TRP:CZ3	2.56	0.41
1:AI:91:ILE:HD12	1:AI:91:ILE:HG23	1.79	0.41
2:AK:380:LEU:HG	5:EA:4351:VAL:O	2.21	0.41
1:AL:628:ASN:HB3	13:LH:512:ARG:HG2	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AL:661:PRO:HB3	1:AL:1052:LEU:HD11	2.03	0.41
3:BB:727:TYR:HE1	3:BB:770:LEU:HD13	1.85	0.41
3:BB:812:MET:HA	16:OB:196:TRP:CZ3	2.56	0.41
3:BC:836:PRO:HG3	16:OC:155:SER:HB3	2.02	0.41
3:CB:905:HIS:NE2	3:CB:907:ARG:HG2	2.36	0.41
3:CL:1237:VAL:HG11	3:CL:4468:LYS:HD3	2.01	0.41
4:DA:53:LYS:HD2	4:DA:53:LYS:HA	1.87	0.41
4:DE:43:PRO:HG3	8:GB:680:LEU:HD22	2.03	0.41
4:DE:247:ARG:HD2	4:DE:290:ARG:NH1	2.35	0.41
4:DF:105:CYS:H	4:DF:260:GLY:N	2.19	0.41
5:EB:3289:ILE:HD11	9:HB:432:LEU:HB3	2.03	0.41
5:EB:3841:GLN:HB3	11:JA:1041:LYS:NZ	2.36	0.41
5:EB:4892:ARG:O	5:EB:4893:THR:C	2.63	0.41
5:EC:3393:ARG:HH21	5:EC:3516:GLU:HB3	1.86	0.41
5:EC:3415:VAL:HB	5:EC:3504:ARG:HB3	2.02	0.41
5:EC:4011:VAL:HG11	5:EC:4166:SER:HB2	2.01	0.41
6:FA:1892:ILE:HG22	6:FA:1894:THR:H	1.84	0.41
6:FA:2049:SER:O	6:FA:2050:LEU:C	2.64	0.41
6:FB:1612:ASN:HD22	6:FB:1618:VAL:HG13	1.85	0.41
6:FC:2087:LEU:HD22	6:FC:2087:LEU:HA	1.76	0.41
6:FE:804:LEU:HG	6:FE:1114:VAL:HG11	2.02	0.41
6:FE:1122:LEU:HD22	6:FE:1122:LEU:HA	1.82	0.41
6:FE:1427:ASN:C	6:FE:1429:LEU:HD13	2.46	0.41
6:FF:826:LEU:O	6:FF:831:ARG:NH2	2.53	0.41
6:FF:1081:SER:HA	6:FF:1084:ARG:HE	1.86	0.41
7:GA:860:GLN:H	7:GA:860:GLN:HG2	1.69	0.41
7:GC:770:TYR:OH	7:GC:839:ARG:HG2	2.19	0.41
7:GE:850:GLY:HA2	7:GE:934:ARG:HH21	1.86	0.41
8:GH:81:SER:HA	8:GH:429:LYS:HG2	2.02	0.41
7:GI:598:ARG:NH2	7:GI:637:ASN:HD22	2.18	0.41
7:GI:844:HIS:HB2	7:GI:881:ALA:H	1.85	0.41
8:GJ:364:ILE:HD13	8:GJ:377:MET:HG3	2.02	0.41
7:GK:609:ARG:HG3	7:GK:675:GLN:HE21	1.84	0.41
8:GL:3:VAL:HG23	8:GL:13:ARG:HH21	1.85	0.41
8:GL:400:LYS:HE2	8:GL:400:LYS:HB2	1.96	0.41
10:IB:623:LEU:HD12	10:IB:623:LEU:HA	1.86	0.41
10:IC:580:LEU:HD12	10:IC:587:ARG:HH12	1.85	0.41
10:IC:923:THR:O	10:IC:927:ARG:HG3	2.21	0.41
11:JA:1722:TYR:CD1	11:JA:1732:LEU:HB3	2.56	0.41
11:JB:39:ALA:HB3	11:JB:175:ARG:HB2	2.03	0.41
11:JB:2110:LEU:HD11	11:JB:2114:ILE:HG23	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JC:1777:LEU:HD23	11:JC:1777:LEU:HA	1.93	0.41
12:KC:319:TYR:CD2	12:KC:353:ALA:HB1	2.55	0.41
12:KF:208:LEU:HB3	12:KF:242:VAL:HG23	2.03	0.41
12:KG:381:MET:HE2	12:KG:383:HIS:HE1	1.86	0.41
12:KG:523:VAL:HA	12:KG:573:ARG:HH21	1.86	0.41
13:LA:380:MET:HE3	13:LA:384:LEU:HG	2.02	0.41
13:LE:517:ILE:HD12	13:LF:516:VAL:HG12	2.02	0.41
13:LJ:416:ARG:HA	13:LJ:419:SER:HB3	2.01	0.41
13:LP:398:ARG:HA	13:LP:401:LEU:HB2	2.03	0.41
15:NA:958:GLU:HA	15:NA:961:TYR:HD2	1.85	0.41
15:NA:1498:ARG:HB3	20:SA:38:ARG:HG3	2.01	0.41
15:NB:347:LEU:HD22	15:NB:491:PRO:HG2	2.03	0.41
15:NB:515:ALA:HB3	15:NB:520:ALA:HB2	2.03	0.41
15:NB:666:ILE:HG23	15:NB:721:PRO:HG2	2.02	0.41
15:NB:667:THR:HG23	15:NB:673:ILE:HG12	2.03	0.41
15:NB:685:PHE:HB2	15:NB:914:ILE:HG12	2.02	0.41
15:NB:892:TRP:CA	15:NB:1152:GLU:HB2	2.51	0.41
15:NC:682:ARG:HD2	15:NC:1169:PHE:CZ	2.56	0.41
15:ND:589:ASN:HB3	15:ND:593:LYS:HE2	2.03	0.41
15:ND:614:LYS:HE3	15:ND:678:LEU:HB2	2.02	0.41
15:ND:755:ILE:HD12	15:ND:846:PHE:CE2	2.55	0.41
18:QA:66:PRO:HB3	18:QA:94:LEU:HD21	2.02	0.41
20:SB:87:ILE:HD13	20:SB:143:VAL:HG21	2.01	0.41
2:AB:90:ARG:HH21	2:AB:93:LYS:HB3	1.85	0.41
2:AB:153:GLN:HE22	2:AB:155:LEU:HB2	1.85	0.41
2:AB:405:PRO:HG3	17:PB:131:ALA:HB3	2.02	0.41
2:AC:49:HIS:HD2	2:AC:51:ALA:H	1.69	0.41
2:AC:541:PRO:HG3	1:AD:370:GLN:HB3	2.02	0.41
1:AD:330:ILE:HD13	5:EA:4909:PHE:CZ	2.56	0.41
1:AD:892:GLU:HA	1:AD:895:ARG:NH1	2.35	0.41
1:AE:73:THR:HB	1:AE:76:GLN:HG3	2.02	0.41
2:AG:450:ARG:HD2	11:JC:1724:PHE:CE2	2.55	0.41
2:AJ:166:LEU:HD22	2:AJ:281:PHE:HD2	1.85	0.41
2:AK:300:CYS:HB2	2:AK:320:CYS:HB3	2.02	0.41
2:AK:543:MET:HE3	2:AK:543:MET:HB2	1.89	0.41
3:BA:873:PHE:CZ	16:OA:174:VAL:HG22	2.54	0.41
3:CE:1236:LEU:O	3:CE:1244:PRO:HA	2.21	0.41
3:CL:1229:HIS:HD2	3:CL:1260:VAL:HG23	1.86	0.41
4:DA:96:ILE:HG23	4:DA:97:LEU:HD22	2.02	0.41
4:DA:268:ARG:HD2	4:DA:268:ARG:HA	1.76	0.41
4:DB:69:LEU:HG	4:DE:9:PHE:HE2	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DC:392:ASP:HA	14:MJ:313:ARG:NH1	2.36	0.41
5:EB:4896:ARG:H	5:EB:4896:ARG:HG2	1.73	0.41
6:FA:2027:TRP:NE1	9:HA:775:SER:O	2.54	0.41
6:FB:1866:ILE:HG23	6:FB:1867:THR:HG23	2.02	0.41
6:FC:2061:ARG:HA	6:FC:2061:ARG:HD2	1.78	0.41
6:FD:1294:LEU:HD22	6:FD:1294:LEU:HA	1.80	0.41
6:FE:818:VAL:O	6:FE:820:LYS:N	2.53	0.41
6:FE:842:GLY:O	6:FE:843:LEU:C	2.64	0.41
6:FE:1427:ASN:HD22	6:FE:1427:ASN:HA	1.55	0.41
6:FF:854:TRP:CE2	6:FF:860:PRO:HD3	2.56	0.41
7:GA:590:ASN:HA	7:GA:593:VAL:HG12	2.01	0.41
7:GA:618:ALA:HB3	7:GA:645:LEU:HD22	2.03	0.41
8:GB:15:SER:HB3	8:GB:540:LEU:HD12	2.03	0.41
7:GC:459:PRO:HB2	7:GC:465:VAL:HG22	2.03	0.41
8:GD:210:GLN:HG2	8:GD:292:ALA:HB2	2.01	0.41
7:GE:298:TYR:HB3	7:GE:679:LEU:HD21	2.02	0.41
8:GH:431:PHE:HA	8:GH:480:VAL:HA	2.03	0.41
8:GH:721:LYS:HB3	8:GH:723:VAL:HG23	2.02	0.41
7:GI:872:THR:HA	7:GI:972:GLU:HB2	2.02	0.41
7:GK:543:LYS:HG2	9:HC:498:GLY:HA2	2.02	0.41
7:GK:857:LEU:HD21	7:GK:863:VAL:HA	2.00	0.41
8:GL:12:CYS:SG	8:GL:516:LEU:HD11	2.61	0.41
9:HA:487:VAL:HG21	9:HA:620:TYR:CZ	2.56	0.41
9:HA:762:HIS:O	9:HA:763:GLN:C	2.61	0.41
9:HD:754:LEU:HG	9:HD:840:HIS:CD2	2.55	0.41
10:IA:743:TYR:HD2	10:IA:764:ALA:HA	1.84	0.41
10:IA:971:LEU:HD22	10:IA:1065:GLU:HG2	2.03	0.41
10:IA:1120:SER:HA	10:IA:1128:VAL:HG23	2.03	0.41
10:IA:1233:THR:HG23	10:IA:1293:PHE:HZ	1.86	0.41
10:IC:580:LEU:HG	10:IC:603:ARG:HH12	1.86	0.41
10:IC:1224:HIS:HD1	10:IC:1326:THR:HB	1.85	0.41
11:JA:1036:LEU:HD12	11:JA:1036:LEU:HA	1.89	0.41
11:JA:1845:ALA:HA	11:JA:1848:TYR:HD2	1.86	0.41
12:KE:684:LEU:HD13	12:KE:688:VAL:H	1.86	0.41
13:LE:380:MET:HA	13:LE:383:GLN:HB2	2.01	0.41
13:LL:353:ASN:HA	13:LL:356:LEU:HD12	2.03	0.41
13:LO:414:ASN:O	13:LO:418:LYS:HG2	2.20	0.41
15:NA:1004:PHE:HA	15:NA:1008:SER:HB3	2.02	0.41
15:NB:686:ASN:HA	15:NB:911:ARG:HA	2.01	0.41
15:NC:486:ARG:HH11	15:NC:489:VAL:HG23	1.85	0.41
15:NC:660:LEU:HA	15:NC:778:PHE:HE2	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:ND:983:ILE:HG12	15:ND:989:ILE:HD12	2.03	0.41
15:ND:1411:LEU:HB3	15:ND:1470:PHE:CE2	2.56	0.41
1:AA:176:ILE:HA	1:AA:177:PRO:HD3	1.84	0.41
1:AA:791:LEU:HD13	1:AA:796:PHE:HE1	1.85	0.41
1:AA:897:PRO:HD2	1:AA:900:TYR:HD2	1.86	0.41
2:AB:72:PHE:HB3	2:AB:164:TYR:CD2	2.56	0.41
1:AD:62:ASP:OD1	1:AD:228:PRO:HG3	2.21	0.41
2:AG:328:HIS:CD2	2:AG:339:ARG:HD3	2.55	0.41
1:AI:381:ARG:HH21	6:FC:1641:ALA:HA	1.84	0.41
1:AI:497:PRO:HG3	6:FC:1789:LEU:HD13	2.03	0.41
2:AJ:263:TYR:CE2	16:OB:73:ALA:HA	2.55	0.41
3:BA:693:ARG:NH1	17:PA:256:ARG:HG2	2.34	0.41
3:BB:776:ARG:HH11	3:BB:780:TYR:HE2	1.67	0.41
3:CB:949:SER:HA	3:CB:981:PHE:HE2	1.84	0.41
3:CI:1182:GLY:H	3:CI:4512:SER:HB2	1.85	0.41
3:CI:1185:VAL:HG23	3:CI:1188:GLN:H	1.84	0.41
3:CI:1255:VAL:HG21	3:CI:4469:LEU:HD22	2.02	0.41
3:CJ:1130:SER:O	3:CJ:1131:LEU:HD23	2.21	0.41
3:CJ:1239:PRO:HA	3:CJ:4470:LYS:HE2	2.02	0.41
3:CJ:1258:PRO:HB2	3:CJ:4498:LEU:HD23	2.02	0.41
4:DD:148:ARG:HA	4:DD:148:ARG:CZ	2.51	0.41
4:DD:358:SER:H	4:DD:361:GLN:HE22	1.69	0.41
4:DE:187:PRO:HA	4:DE:188:PRO:HD3	1.92	0.41
5:EA:4156:LEU:HD21	9:HC:422:VAL:HG11	2.03	0.41
5:EB:3650:THR:HG23	9:HB:499:ARG:HA	2.03	0.41
5:EC:4737:ASP:O	5:EC:4741:LYS:HG2	2.21	0.41
6:FA:1993:LYS:HD2	6:FA:1993:LYS:HA	1.76	0.41
6:FA:2048:GLU:HG3	9:HA:830:ILE:HG12	2.02	0.41
6:FB:1745:SER:HB3	6:FB:1792:TYR:H	1.84	0.41
6:FB:1966:ASP:HA	6:FB:2047:ARG:NH1	2.35	0.41
6:FC:2017:ARG:HH12	6:FC:2018:ARG:HG3	1.86	0.41
6:FD:803:ARG:HA	6:FD:906:LEU:O	2.21	0.41
6:FD:925:GLU:HG2	6:FD:1092:PRO:HG2	2.03	0.41
6:FD:1260:LEU:HG	6:FD:1261:SER:N	2.35	0.41
6:FD:1281:VAL:O	6:FD:1282:LEU:C	2.62	0.41
6:FD:1388:PHE:CD1	6:FD:1418:GLU:HA	2.50	0.41
6:FE:840:ALA:N	12:KB:681:MET:HE3	2.35	0.41
6:FE:845:PRO:HA	7:GE:896:ARG:HH12	1.86	0.41
6:FE:1075:VAL:HG11	6:FE:1106:LEU:N	2.36	0.41
6:FE:1094:SER:O	6:FE:1095:LEU:C	2.64	0.41
6:FE:1229:LYS:HB2	6:FE:1229:LYS:HE2	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FE:1297:PRO:O	6:FE:1299:ASN:N	2.47	0.41
6:FE:1435:GLU:O	6:FE:1436:PHE:C	2.63	0.41
6:FF:839:GLY:O	7:GI:957:ARG:NH2	2.50	0.41
6:FF:1075:VAL:O	6:FF:1076:ILE:C	2.64	0.41
6:FF:1116:LEU:HB2	6:FF:1117:ASN:H	1.64	0.41
7:GC:163:GLN:HA	7:GC:166:LEU:HG	2.03	0.41
7:GC:764:LEU:HD13	7:GC:870:ARG:HE	1.85	0.41
8:GD:21:ALA:HB2	8:GD:521:ALA:HB1	2.03	0.41
8:GD:192:VAL:HG21	7:GE:418:THR:HG21	2.01	0.41
8:GD:254:LYS:HD2	8:GD:254:LYS:HA	1.86	0.41
7:GE:345:ASP:HA	7:GE:349:GLY:HA2	2.03	0.41
7:GE:843:LEU:HD11	7:GE:883:LEU:HB2	2.03	0.41
8:GF:171:ILE:HG23	8:GF:181:HIS:HB2	2.02	0.41
8:GF:350:GLN:HA	8:GF:353:ASN:HB2	2.02	0.41
7:GG:211:ARG:NE	7:GG:212:PRO:HD2	2.36	0.41
7:GG:388:PRO:HB2	8:GJ:212:GLN:HB3	2.02	0.41
8:GH:135:LEU:HD11	8:GH:245:ILE:HD12	2.03	0.41
8:GH:650:GLN:HA	8:GH:651:PRO:HD3	1.93	0.41
8:GH:679:GLU:N	8:GH:727:SER:HB2	2.35	0.41
7:GI:393:VAL:HG11	7:GI:438:LYS:HB2	2.02	0.41
8:GJ:661:PRO:HA	8:GJ:679:GLU:H	1.85	0.41
7:GK:562:ILE:HD12	7:GK:562:ILE:HA	1.95	0.41
8:GL:65:PRO:HA	8:GL:104:LEU:HD12	2.03	0.41
8:GL:364:ILE:HD13	8:GL:377:MET:HB3	2.03	0.41
9:HB:708:VAL:HG12	9:HB:726:PRO:HG2	2.02	0.41
10:IA:845:TYR:CZ	10:IA:863:LEU:HD22	2.56	0.41
10:IA:913:LEU:HA	10:IA:916:LYS:NZ	2.36	0.41
10:IA:963:ARG:HD3	10:IA:963:ARG:HA	1.84	0.41
10:IB:476:LEU:HD23	10:IB:501:MET:HE3	2.03	0.41
10:IB:891:VAL:HG11	15:NC:566:GLN:O	2.21	0.41
10:IB:1118:ASN:HB3	10:IB:1121:LYS:HB2	2.02	0.41
10:IC:445:LYS:HA	10:IC:449:TYR:CD2	2.56	0.41
10:IC:751:ASN:HB3	10:IC:752:SER:H	1.64	0.41
11:JA:136:ALA:HB1	11:JA:162:PRO:HB3	2.03	0.41
11:JA:761:LYS:HD2	11:JA:768:ASP:HA	2.03	0.41
11:JA:833:GLN:HB2	11:JA:1418:THR:HG21	2.03	0.41
11:JA:1161:LEU:HD23	11:JA:1164:MET:HE3	2.03	0.41
11:JA:2034:THR:HA	11:JA:2037:ARG:HG2	2.03	0.41
11:JC:875:LEU:HD23	11:JC:963:PHE:HE2	1.86	0.41
11:JC:1785:THR:HA	11:JC:1788:THR:HG22	2.02	0.41
12:KB:266:ARG:CZ	12:KB:269:MET:HE3	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:KE:299:TYR:HB2	12:KE:307:VAL:HG21	2.03	0.41
12:KF:565:TRP:CE3	12:KF:709:VAL:HG13	2.55	0.41
12:KG:352:LYS:HE3	12:KG:352:LYS:HB2	1.86	0.41
12:KG:523:VAL:O	12:KG:525:PRO:HD3	2.20	0.41
13:LA:461:VAL:O	13:LA:465:ILE:HG12	2.21	0.41
13:LF:475:LEU:HD12	13:LF:479:PHE:CE2	2.56	0.41
13:LI:481:GLU:HA	13:LI:484:VAL:HG12	2.02	0.41
13:LI:514:TYR:HE1	13:LJ:513:LEU:HD11	1.86	0.41
13:LJ:528:PRO:HA	13:LJ:529:PRO:HD3	1.94	0.41
13:LL:370:MET:HA	13:LL:373:VAL:HG12	2.03	0.41
14:ME:258:ILE:HG12	14:MF:258:ILE:HD11	2.02	0.41
14:MI:285:ARG:NH1	14:MJ:257:LYS:HA	2.23	0.41
15:NB:987:GLN:HG3	15:NB:1026:LEU:HD13	2.02	0.41
15:NB:1488:ARG:CZ	15:NB:1491:PRO:HG2	2.51	0.41
15:NC:434:VAL:HA	15:NC:445:ILE:HD12	2.03	0.41
15:NC:798:LEU:HD13	15:NC:885:LEU:HD12	2.03	0.41
15:NC:983:ILE:HG12	15:NC:989:ILE:HD12	2.01	0.41
15:NC:1329:PRO:HD2	15:NC:1332:MET:HE1	2.03	0.41
15:NC:1546:VAL:HG21	19:RA:23:LEU:HD11	2.03	0.41
15:NC:1552:ILE:HB	19:RA:143:LEU:HD23	2.03	0.41
15:ND:468:ARG:HD3	15:ND:469:PHE:CD1	2.51	0.41
15:ND:891:TRP:C	15:ND:1152:GLU:H	2.29	0.41
15:ND:1143:LEU:HD12	15:ND:1143:LEU:HA	1.91	0.41
15:ND:1503:PHE:CD1	20:SB:146:MET:HB3	2.56	0.41
15:ND:1512:MET:HB3	18:QB:107:LEU:HD22	2.03	0.41
1:AA:915:TRP:CZ2	13:LK:359:HIS:HB2	2.56	0.41
1:AD:418:ILE:HG22	1:AD:452:PHE:CE2	2.56	0.41
1:AE:1025:ARG:NE	1:AE:1025:ARG:HA	2.36	0.41
1:AH:747:MET:HE2	1:AH:850:ILE:HD11	2.03	0.41
1:AI:238:CYS:HB3	1:AI:241:CYS:H	1.86	0.41
1:AL:878:ARG:HH12	6:FC:2039:ARG:HE	1.69	0.41
3:CC:921:LEU:HD23	3:CC:921:LEU:HA	1.92	0.41
3:CE:1126:GLU:CD	3:CE:1129:ARG:HH21	2.28	0.41
3:CF:1184:ALA:HB2	3:CF:4517:LEU:HB2	2.03	0.41
3:CG:1208:VAL:HG22	3:CG:1209:ALA:H	1.86	0.41
3:CI:1212:GLU:HG2	3:CI:1222:ARG:HH12	1.86	0.41
4:DA:23:ALA:HB1	4:DA:29:LEU:HD23	2.02	0.41
4:DB:246:TYR:CZ	4:DE:189:ARG:HB3	2.56	0.41
5:EA:3412:LEU:HG	5:EA:3507:VAL:HG22	2.03	0.41
5:EA:3421:HIS:CE1	5:EA:3588:CYS:HA	2.55	0.41
5:EA:3614:PRO:HG2	5:EA:3628:MET:HE3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EA:4061:TYR:HB3	5:EA:4174:ILE:HD13	2.01	0.41
5:EA:4643:PRO:HA	5:EA:4644:PRO:HD3	1.92	0.41
5:EB:4344:LEU:HD23	5:EB:4360:GLU:HG2	2.03	0.41
5:EC:4513:GLN:HG2	5:EC:4707:PHE:HD1	1.86	0.41
6:FA:1655:ASP:OD1	6:FA:1657:MET:HG2	2.21	0.41
6:FA:1759:GLU:HA	6:FA:1964:MET:CE	2.51	0.41
6:FA:1764:ILE:HA	6:FA:1767:ARG:HG2	2.03	0.41
6:FC:1951:TYR:HE2	9:HB:844:GLY:HA3	1.86	0.41
7:GA:535:PRO:C	9:HB:550:GLU:HG2	2.46	0.41
7:GA:575:TYR:HE2	7:GA:577:SER:HB2	1.86	0.41
7:GA:702:ILE:HA	7:GA:705:ILE:HG12	2.03	0.41
8:GB:132:PRO:HA	8:GB:133:PRO:HD2	1.96	0.41
7:GC:960:ASP:HA	7:GC:961:PRO:HD3	1.95	0.41
8:GD:713:LEU:HD21	8:GD:722:TYR:HB2	2.02	0.41
8:GD:769:PHE:HB3	8:GJ:551:SER:HA	2.03	0.41
7:GE:664:PRO:HD2	7:GE:669:ASP:HB2	2.03	0.41
8:GF:305:VAL:HG11	8:GF:377:MET:HE1	2.03	0.41
7:GG:302:PRO:HA	7:GG:303:PRO:HD3	1.94	0.41
8:GH:754:ALA:H	8:GL:333:LYS:HE2	1.87	0.41
7:GI:232:LYS:HA	7:GI:232:LYS:HD3	1.91	0.41
7:GI:268:ARG:HD2	7:GI:268:ARG:HA	1.86	0.41
7:GI:584:HIS:HA	7:GI:952:ARG:HH12	1.86	0.41
7:GI:841:LEU:HD13	7:GI:865:LEU:HD12	2.03	0.41
9:HA:579:LEU:HA	9:HA:579:LEU:HD23	1.87	0.41
9:HC:433:GLY:HA2	9:HC:436:ASN:HD22	1.86	0.41
10:IA:968:ARG:NE	10:IA:1061:LEU:HD21	2.35	0.41
10:IC:1139:VAL:HG13	10:IC:1203:LEU:HD22	2.03	0.41
11:JA:925:ASN:HB3	11:JA:1012:ARG:HH12	1.85	0.41
11:JA:1308:TYR:HD1	11:JA:1405:PRO:HD3	1.86	0.41
11:JB:48:GLN:HG3	11:JB:50:GLU:OE1	2.21	0.41
11:JB:195:LEU:HG	11:JB:1036:LEU:HD11	2.02	0.41
11:JC:411:ASP:HB3	11:JC:412:CYS:H	1.66	0.41
11:JC:1121:VAL:HA	11:JC:1125:ILE:HB	2.03	0.41
11:JC:1304:ASP:H	11:JC:1329:ASN:HD21	1.69	0.41
12:KA:523:VAL:HG12	12:KA:524:PHE:CD1	2.56	0.41
12:KB:641:VAL:HG12	12:KB:678:ALA:HB1	2.02	0.41
12:KC:231:PHE:CZ	12:KC:313:PHE:CD2	3.09	0.41
12:KC:645:ARG:HH12	12:KC:647:LEU:HA	1.86	0.41
13:LA:413:GLU:HA	13:LA:416:ARG:HG2	2.02	0.41
15:NA:995:ARG:HH22	15:NA:1018:GLN:HG2	1.85	0.41
15:NB:933:LEU:O	15:NB:937:MET:HG3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:NB:1552:ILE:HG13	15:NB:1555:TYR:HD2	1.86	0.41
15:NC:598:PHE:HD1	15:NC:915:VAL:HB	1.86	0.41
15:NC:785:ILE:HD13	15:NC:785:ILE:HA	1.96	0.41
15:NC:1397:LEU:HA	15:NC:1400:CYS:HB2	2.03	0.41
15:ND:898:ASN:HA	15:ND:901:LEU:HB3	2.02	0.41
15:ND:1545:VAL:HA	19:RD:141:LEU:HD22	2.03	0.41
16:OC:1098:VAL:HG13	16:OC:1099:PHE:H	1.85	0.41
2:AB:92:LEU:HD23	2:AB:277:VAL:HG11	2.02	0.40
2:AB:327:ILE:HA	1:AI:271:MET:HE2	2.02	0.40
1:AD:712:SER:HA	1:AD:915:TRP:CE2	2.56	0.40
1:AE:65:ILE:HG13	1:AE:224:PHE:HB3	2.03	0.40
1:AE:71:LEU:H	1:AE:220:ALA:HA	1.86	0.40
1:AI:120:TRP:CH2	1:AI:218:PRO:HG3	2.56	0.40
2:AJ:499:LEU:HD22	2:AJ:518:HIS:CD2	2.56	0.40
2:AK:471:THR:O	2:AK:475:MET:HG2	2.22	0.40
3:CA:790:ASN:C	3:CA:790:ASN:HD22	2.29	0.40
3:CB:851:LYS:HB2	3:CB:851:LYS:HE3	1.84	0.40
3:CC:790:ASN:C	3:CC:790:ASN:HD22	2.29	0.40
3:CE:1137:ALA:HB1	3:CE:1139:LEU:HD13	2.03	0.40
3:CG:1231:ARG:HG3	3:CG:1233:PHE:H	1.86	0.40
3:CI:4448:TYR:HE1	3:CI:4453:MET:HG2	1.87	0.40
4:DC:384:ILE:HD13	13:LI:457:GLN:HB3	2.03	0.40
5:EA:4187:ASP:OD1	5:EA:4190:GLN:HB2	2.21	0.40
5:EC:3650:THR:HG22	9:HA:500:LEU:HD22	2.03	0.40
6:FA:1783:PRO:HA	6:FA:1784:PRO:HD3	1.98	0.40
6:FB:1600:VAL:HB	6:FB:1724:ARG:HA	2.03	0.40
6:FB:1896:ALA:HB3	6:FB:1914:VAL:HG23	2.02	0.40
6:FC:1866:ILE:HD13	6:FC:1866:ILE:HA	1.96	0.40
6:FE:1027:LEU:O	6:FE:1028:LYS:C	2.64	0.40
6:FF:990:PHE:C	12:KC:313:PHE:HE2	2.29	0.40
6:FF:1002:ALA:HB2	6:FF:1009:VAL:HG13	2.03	0.40
8:GB:641:TYR:HB2	8:GB:664:ILE:HB	2.03	0.40
7:GC:796:PHE:HD1	7:GC:836:VAL:HG23	1.86	0.40
8:GF:456:GLY:HA2	8:GF:547:PHE:CZ	2.56	0.40
7:GI:433:MET:HB3	7:GI:459:PRO:HD3	2.04	0.40
7:GI:827:LEU:HB3	7:GI:831:ARG:HB3	2.02	0.40
9:HB:564:ARG:HD2	9:HB:564:ARG:HA	1.81	0.40
9:HC:565:PRO:HA	9:HC:566:PRO:HD3	1.77	0.40
9:HD:825:ASN:O	9:HD:829:THR:HG23	2.22	0.40
10:IA:185:LEU:HD21	10:IA:624:ARG:HB2	2.04	0.40
10:IB:908:ARG:HH21	10:IB:911:ARG:HH11	1.69	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IB:1330:TYR:HB3	10:IB:1335:LEU:HB2	2.03	0.40
10:IC:369:VAL:HB	10:IC:372:ARG:HB3	2.03	0.40
10:IC:868:MET:HE2	10:IC:868:MET:HB2	1.96	0.40
10:IC:1130:LEU:HD11	10:IC:1142:VAL:HG13	2.03	0.40
11:JA:207:GLU:HB3	11:JA:1051:LEU:HD11	2.04	0.40
11:JC:1292:LEU:HD21	11:JC:1299:ALA:HB1	2.03	0.40
11:JC:1489:LEU:HD22	15:NA:444:LEU:HD13	2.03	0.40
11:JC:1490:LEU:O	11:JC:1494:VAL:HG23	2.20	0.40
11:JC:1713:ASN:O	11:JC:1716:GLN:HB3	2.20	0.40
13:LD:364:ASN:HA	13:LD:367:VAL:HG12	2.02	0.40
13:LE:516:VAL:HG13	13:LF:517:ILE:HD13	2.03	0.40
14:MG:81:ARG:HG2	14:MG:82:ARG:H	1.86	0.40
15:NA:547:PRO:HG2	15:NA:549:LYS:HG2	2.04	0.40
15:NA:600:LEU:HB3	15:NA:1189:PHE:CE1	2.56	0.40
15:NB:933:LEU:HD13	15:NB:1120:VAL:HG21	2.03	0.40
15:ND:564:ARG:HH22	15:ND:618:ARG:HB2	1.86	0.40
15:ND:1549:GLY:H	19:RD:142:ASN:HB3	1.85	0.40
1:AA:132:PRO:HB3	3:BA:807:LEU:HD11	2.03	0.40
1:AA:408:LYS:HB2	2:AB:438:VAL:HG11	2.03	0.40
1:AA:793:LEU:HD23	1:AA:793:LEU:HA	1.91	0.40
1:AD:271:MET:HE2	1:AD:271:MET:HB2	1.99	0.40
1:AE:692:PRO:HG3	1:AE:998:LEU:HD23	2.02	0.40
2:AF:447:ARG:HD2	2:AF:450:ARG:HH21	1.87	0.40
1:AH:631:THR:HG23	13:LL:512:ARG:NH2	2.35	0.40
1:AI:775:LYS:HB3	1:AI:970:GLU:HG2	2.02	0.40
2:AJ:300:CYS:HB2	2:AJ:319:LEU:HA	2.02	0.40
1:AL:908:ARG:HH22	13:LE:497:LEU:HD12	1.85	0.40
3:BC:815:GLU:OE2	16:OC:240:ARG:HD3	2.21	0.40
3:CC:880:GLN:H	3:CC:880:GLN:HG3	1.71	0.40
3:CJ:4462:VAL:HG13	3:CJ:4495:LEU:HB3	2.04	0.40
4:DC:320:ILE:HG23	4:DC:323:ASP:HB2	2.03	0.40
4:DF:249:GLY:HA3	4:DF:287:ALA:HB2	2.02	0.40
5:EA:4147:PHE:HB2	5:EA:4185:HIS:CE1	2.56	0.40
5:EA:4405:ILE:HG13	5:EA:4428:MET:HE1	2.03	0.40
5:EA:4760:ARG:NH1	11:JA:743:PHE:HA	2.24	0.40
6:FC:1587:MET:HE2	6:FC:1587:MET:HB2	1.92	0.40
6:FC:1683:LYS:HD3	6:FC:1684:THR:O	2.21	0.40
6:FE:966:PRO:O	6:FE:1027:LEU:HB2	2.21	0.40
6:FF:923:ALA:O	6:FF:927:GLY:N	2.54	0.40
6:FF:1003:ILE:H	6:FF:1003:ILE:HG12	1.73	0.40
6:FF:1225:ILE:C	6:FF:1227:ARG:H	2.28	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GA:715:THR:HG21	7:GA:796:PHE:HB3	2.02	0.40
8:GB:426:LEU:HD23	8:GB:426:LEU:HA	1.87	0.40
8:GB:526:ILE:HD11	14:ME:324:ARG:HH11	1.85	0.40
7:GC:390:ILE:HD12	7:GC:390:ILE:HG23	1.78	0.40
7:GC:515:SER:HB2	7:GC:634:PRO:HB2	2.03	0.40
7:GC:583:GLN:HB3	7:GC:584:HIS:ND1	2.36	0.40
8:GF:598:HIS:HA	8:GF:601:ARG:HG2	2.02	0.40
7:GG:205:ARG:HB2	7:GG:208:ALA:HB2	2.04	0.40
8:GH:658:ALA:HB1	8:GH:665:LEU:HD21	2.03	0.40
8:GH:661:PRO:O	8:GH:681:ILE:HG12	2.21	0.40
7:GI:238:ILE:HG23	7:GI:284:GLU:HG3	2.04	0.40
8:GL:158:GLN:HE22	13:LE:433:ARG:HH12	1.68	0.40
9:HA:877:LYS:HA	9:HA:877:LYS:HD3	1.41	0.40
10:IA:893:PHE:CZ	10:IA:907:ASP:HA	2.56	0.40
10:IB:362:HIS:CD2	10:IB:429:ARG:HH22	2.38	0.40
10:IB:496:GLU:HA	10:IB:499:ARG:HG3	2.04	0.40
10:IB:1110:ARG:HB2	10:IB:1144:VAL:HG21	2.02	0.40
10:IC:921:LEU:O	10:IC:925:ILE:HG12	2.20	0.40
12:KA:721:GLN:NE2	12:KA:725:ILE:HG23	2.34	0.40
12:KC:485:ARG:HH21	12:KC:522:ARG:HG2	1.86	0.40
12:KC:536:ARG:NE	12:KC:542:PRO:HA	2.36	0.40
14:MB:218:LEU:HD21	14:MB:323:GLN:HB3	2.02	0.40
14:MI:229:GLN:HG3	14:MI:311:ILE:HD12	2.03	0.40
14:MK:90:ALA:O	14:MK:94:LEU:HD23	2.20	0.40
15:NA:864:GLU:HB3	15:NA:865:SER:H	1.70	0.40
15:NA:1321:TRP:HB3	15:NA:1322:LYS:H	1.72	0.40
15:NA:1490:MET:HA	15:NA:1493:VAL:HG22	2.02	0.40
15:NA:1508:PHE:HZ	18:QA:110:VAL:HG21	1.86	0.40
15:NC:737:PRO:HG2	15:NC:749:PRO:HD3	2.03	0.40
15:NC:992:GLN:HE22	15:NC:1022:ASP:HB2	1.86	0.40
15:ND:891:TRP:CD1	15:ND:1156:LEU:HD21	2.56	0.40
15:ND:943:GLU:HA	15:ND:946:LEU:HB2	2.03	0.40
17:PB:138:ARG:HB3	17:PB:142:TYR:CD2	2.56	0.40
19:RA:51:MET:HB3	19:RA:55:LYS:NZ	2.35	0.40
19:RA:74:LEU:HB3	19:RA:91:VAL:HG11	2.02	0.40
20:SC:37:MET:HE2	20:SC:44:PRO:HB3	2.03	0.40
1:AA:345:PRO:HA	1:AA:348:GLU:HB2	2.03	0.40
1:AA:437:PHE:CB	2:AB:410:TYR:HE1	2.33	0.40
2:AB:41:ARG:HH21	2:AB:293:GLU:HG3	1.86	0.40
2:AC:66:ARG:NH2	2:AC:173:ARG:HH21	2.20	0.40
1:AD:376:LEU:HA	1:AD:379:GLN:HB3	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:915:TRP:CE3	13:LM:359:HIS:HB2	2.56	0.40
1:AH:629:LEU:C	13:LL:512:ARG:HH12	2.29	0.40
1:AI:442:HIS:HB2	2:AJ:368:HIS:HB2	2.04	0.40
1:AI:458:VAL:HB	2:AJ:434:ARG:HH11	1.86	0.40
1:AI:507:LEU:HD13	6:FC:1827:GLN:HE21	1.85	0.40
2:AJ:499:LEU:HD21	2:AJ:515:TRP:HD1	1.85	0.40
2:AK:494:TRP:CZ2	1:AL:56:LEU:HG	2.57	0.40
3:CA:824:SER:HB2	3:CA:846:TYR:CE1	2.56	0.40
3:CA:829:LEU:HA	3:CA:832:LEU:HB3	2.04	0.40
4:DB:33:LEU:HB2	4:DB:103:LEU:HD23	2.04	0.40
4:DB:257:LEU:HD23	4:DB:265:ILE:HD13	2.02	0.40
4:DF:260:GLY:HA2	4:DF:299:ARG:HH12	1.87	0.40
5:EA:3577:PHE:HB2	5:EA:3579:PHE:CE2	2.57	0.40
5:EB:3497:LEU:HD12	5:EB:3504:ARG:HD2	2.03	0.40
5:EB:4438:LEU:HD11	5:EB:4709:PHE:CE2	2.52	0.40
5:EC:3294:LYS:HA	5:EC:3297:ASP:OD1	2.21	0.40
5:EC:3516:GLU:HA	5:EC:3517:PRO:HD3	1.85	0.40
5:EC:4401:PRO:O	5:EC:4402:PRO:C	2.63	0.40
6:FB:2061:ARG:O	6:FB:2065:THR:HG23	2.22	0.40
6:FC:2080:GLN:HE21	6:FC:2080:GLN:HB2	1.57	0.40
6:FD:824:TYR:C	6:FD:826:LEU:H	2.29	0.40
6:FD:891:ARG:HB2	6:FD:891:ARG:NH1	2.36	0.40
6:FD:1095:LEU:HA	6:FD:1095:LEU:HD13	1.79	0.40
6:FD:1203:ARG:HA	6:FD:1203:ARG:HD2	1.35	0.40
6:FE:912:ILE:HG21	6:FE:1425:PRO:O	2.21	0.40
6:FF:1064:TYR:HB3	6:FF:1065:LEU:H	1.75	0.40
6:FF:1089:ARG:HA	6:FF:1089:ARG:HD2	1.78	0.40
7:GA:841:LEU:HD13	7:GA:865:LEU:HD22	2.02	0.40
8:GB:396:ILE:HG23	8:GB:398:VAL:HG12	2.02	0.40
7:GC:758:LEU:HB3	7:GC:787:LEU:HD22	2.04	0.40
7:GE:311:LEU:HD23	7:GE:453:LEU:HD13	2.02	0.40
7:GE:418:THR:HG22	7:GE:422:LEU:HB2	2.03	0.40
7:GG:563:LEU:HD11	7:GG:818:VAL:HG13	2.04	0.40
7:GG:840:MET:HE1	7:GG:970:LEU:HD11	2.03	0.40
8:GH:633:MET:HE1	8:GH:670:PHE:HB2	2.03	0.40
7:GI:195:LYS:NZ	7:GI:702:ILE:HD12	2.36	0.40
8:GJ:692:MET:HE1	8:GJ:694:GLU:HB2	2.02	0.40
8:GL:542:THR:HG22	8:GL:622:LEU:HD21	2.03	0.40
9:HA:575:ARG:HB2	9:HA:578:THR:HG23	2.03	0.40
10:IA:635:LEU:HD12	10:IA:638:ARG:HD3	2.03	0.40
11:JB:1587:TRP:HE3	11:JB:1590:THR:HG23	1.87	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JB:1808:LEU:HD12	11:JB:1808:LEU:HA	1.89	0.40
11:JB:2026:LYS:HB3	11:JB:2028:TYR:CZ	2.56	0.40
11:JC:970:PHE:HA	11:JC:971:PRO:HD3	1.92	0.40
11:JC:1145:ILE:HD11	11:JC:1380:HIS:HB3	2.03	0.40
11:JC:1161:LEU:HD11	11:JC:1184:ARG:HH11	1.87	0.40
11:JC:1581:ARG:NH2	15:NA:354:PHE:HB3	2.35	0.40
12:KG:247:LEU:HA	12:KG:250:SER:HB3	2.03	0.40
13:LE:523:GLU:OE2	13:LH:523:GLU:HA	2.20	0.40
15:NA:941:LEU:HD23	15:NA:941:LEU:HA	1.92	0.40
15:NB:444:LEU:HD21	15:NB:481:LEU:HD13	2.04	0.40
15:NB:702:LEU:HA	15:NB:934:LEU:HA	2.03	0.40
15:NB:885:LEU:HA	15:NB:888:ARG:HB2	2.04	0.40
15:NB:1522:GLN:HB3	18:QC:167:LEU:HD23	2.02	0.40
15:NC:690:TYR:HB2	15:NC:905:ASP:CG	2.45	0.40
19:RD:113:ARG:HH11	19:RD:114:GLU:HB3	1.85	0.40
20:SC:13:PHE:HD1	20:SC:40:LEU:HD11	1.86	0.40
2:AC:108:LEU:HB3	2:AC:162:PHE:HE2	1.86	0.40
2:AC:319:LEU:HD11	2:AC:327:ILE:HD11	2.03	0.40
2:AC:434:ARG:O	2:AC:438:VAL:HG23	2.20	0.40
1:AD:736:LEU:HA	1:AD:737:PRO:HD3	1.97	0.40
2:AF:64:GLN:H	2:AF:66:ARG:NH1	2.20	0.40
2:AF:159:ARG:O	5:EB:4626:LEU:HB3	2.22	0.40
1:AH:649:ARG:HA	1:AH:649:ARG:HD2	1.85	0.40
2:AJ:475:MET:HG3	2:AK:145:LYS:HB2	2.02	0.40
3:CA:692:LEU:HD23	3:CA:692:LEU:HA	1.97	0.40
3:CA:968:PHE:HB3	3:CA:1007:LEU:HD13	2.04	0.40
3:CB:907:ARG:HH22	17:PC:314:LYS:HB3	1.87	0.40
3:CB:920:ARG:NH1	3:CB:957:ALA:HA	2.37	0.40
3:CE:4470:LYS:HB2	3:CE:4486:ILE:HG13	2.03	0.40
3:CI:4470:LYS:HB2	3:CI:4470:LYS:HE3	1.87	0.40
4:DB:172:ARG:O	4:DB:176:ILE:HG12	2.22	0.40
5:EA:4403:LEU:CD1	5:EA:4405:ILE:HD11	2.51	0.40
5:EA:4880:ASP:CG	5:EA:4888:TRP:CZ3	3.00	0.40
5:EB:3591:PRO:HB2	5:EB:3608:ASN:ND2	2.36	0.40
5:EB:3760:LYS:HA	5:EB:3760:LYS:HD3	1.94	0.40
5:EB:4147:PHE:CE1	5:EB:4182:LEU:HA	2.56	0.40
5:EB:4282:SER:HA	5:EB:4285:THR:HG22	2.04	0.40
5:EC:3277:PHE:HE1	5:EC:3447:TYR:HD1	1.69	0.40
5:EC:3869:ARG:HD3	5:EC:4209:HIS:CE1	2.56	0.40
5:EC:4397:ASP:OD2	5:EC:4402:PRO:HD3	2.22	0.40
6:FC:2024:ARG:O	6:FC:2028:GLU:HG2	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FC:2103:ARG:O	6:FC:2106:THR:OG1	2.40	0.40
6:FD:859:ASP:OD2	6:FD:859:ASP:N	2.54	0.40
6:FD:1297:PRO:C	6:FD:1299:ASN:N	2.80	0.40
6:FD:1424:CYS:SG	6:FD:1429:LEU:HG	2.62	0.40
6:FE:1103:SER:OG	6:FE:1104:GLY:N	2.54	0.40
6:FE:1285:CYS:HB2	6:FE:1289:HIS:H	1.87	0.40
6:FE:1442:GLU:C	6:FE:1444:ARG:H	2.29	0.40
6:FF:803:ARG:CB	6:FF:907:ASN:HA	2.51	0.40
6:FF:1089:ARG:O	6:FF:1090:LEU:C	2.65	0.40
6:FF:1216:TRP:O	6:FF:1218:ALA:N	2.55	0.40
6:FF:1251:ARG:NE	11:JB:774:LEU:H	2.15	0.40
7:GA:592:ILE:HD13	7:GA:592:ILE:HA	1.89	0.40
8:GF:69:ILE:HB	8:GF:71:PHE:CE2	2.56	0.40
8:GF:150:ASP:HA	8:GF:153:ARG:HH11	1.86	0.40
8:GF:432:LYS:HD2	8:GF:449:GLN:HA	2.03	0.40
8:GJ:14:PHE:HZ	8:GJ:496:LEU:HD11	1.87	0.40
8:GJ:400:LYS:HE2	8:GJ:400:LYS:HB2	1.95	0.40
9:HA:752:ASP:OD1	9:HA:752:ASP:N	2.50	0.40
10:IA:868:MET:HE3	10:IA:1249:ALA:HB2	2.03	0.40
10:IB:165:ILE:HD13	10:IB:168:LEU:HD12	2.03	0.40
10:IC:1432:LYS:HA	10:IC:1432:LYS:HD3	1.91	0.40
11:JA:1518:VAL:O	11:JA:1522:ILE:HG12	2.21	0.40
11:JC:1686:LEU:HD11	11:JC:1704:ARG:HD3	2.02	0.40
12:KB:209:VAL:HG22	12:KB:241:PRO:HB3	2.02	0.40
12:KB:569:LEU:HD11	12:KB:703:TRP:HE3	1.86	0.40
12:KC:317:ALA:HA	12:KC:320:LYS:HE2	2.03	0.40
12:KC:723:GLU:H	12:KC:723:GLU:HG2	1.77	0.40
12:KE:213:VAL:HG12	12:KE:237:VAL:HG22	2.03	0.40
12:KE:268:LYS:HA	12:KE:268:LYS:HD3	1.81	0.40
13:LF:518:GLU:OE2	13:LF:522:ARG:HD3	2.21	0.40
13:LH:515:LYS:HE3	13:LH:515:LYS:HB2	1.93	0.40
13:LI:522:ARG:HB2	13:LL:523:GLU:OE2	2.21	0.40
13:LM:425:LYS:HZ3	13:LN:424:LEU:HD12	1.86	0.40
14:MA:219:LYS:O	14:MA:223:ARG:HG2	2.22	0.40
14:MC:102:LYS:HB2	14:MC:102:LYS:HE2	1.84	0.40
15:NB:801:ALA:HB2	15:NB:859:LEU:HD21	2.03	0.40
15:NB:1502:THR:HA	15:NB:1505:ALA:HB3	2.04	0.40
15:NC:794:GLU:HA	15:NC:797:ARG:HD2	2.02	0.40
15:NC:1539:ILE:HD11	19:RA:100:VAL:HA	2.03	0.40
16:OB:1096:MET:SD	16:OB:1101:PHE:HB2	2.61	0.40
16:OC:891:ARG:HH12	16:OC:924:VAL:HB	1.85	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:QD:108:PHE:HD1	18:QD:119:LEU:HD12	1.86	0.40
19:RA:128:THR:HG22	19:RA:160:CYS:HB3	2.02	0.40
1:AA:368:LEU:HB3	2:AC:153:GLN:NE2	2.37	0.40
2:AB:65:GLY:H	2:AB:66:ARG:HH11	1.69	0.40
2:AC:441:MET:HE2	1:AD:404:LEU:HD21	2.02	0.40
1:AE:289:SER:N	17:PC:271:ASN:HD22	2.19	0.40
1:AE:1026:ASP:HB3	1:AE:1032:PHE:HB2	2.04	0.40
1:AI:1058:ARG:HD3	14:MG:90:ALA:HB1	2.03	0.40
2:AJ:502:LEU:HA	2:AJ:505:VAL:HG12	2.04	0.40
3:CG:1223:GLU:HB3	3:CG:1224:ALA:H	1.67	0.40
4:DB:179:ALA:HB3	4:DE:189:ARG:NH1	2.35	0.40
4:DB:389:GLY:O	4:DB:393:LEU:HB2	2.22	0.40
4:DD:321:LYS:HD2	4:DD:321:LYS:HA	1.95	0.40
4:DE:20:LEU:O	4:DE:24:LYS:HG2	2.21	0.40
4:DE:257:LEU:HB3	4:DE:303:PHE:HZ	1.86	0.40
4:DF:33:LEU:HD12	4:DF:33:LEU:HA	1.91	0.40
4:DF:305:ARG:HH11	4:DF:308:GLN:HG2	1.86	0.40
5:EB:3409:SER:HA	5:EB:3510:LEU:HD22	2.02	0.40
5:EB:3756:LEU:HD22	5:EB:3770:LEU:HD21	2.03	0.40
5:EB:4285:THR:HG23	5:EB:4286:VAL:HG23	2.03	0.40
5:EC:4508:LEU:HD23	5:EC:4508:LEU:HA	1.95	0.40
6:FC:1782:GLU:HA	6:FC:1783:PRO:HD3	1.95	0.40
6:FC:2081:ARG:O	6:FC:2082:LEU:C	2.65	0.40
6:FD:843:LEU:HD22	6:FD:847:PHE:HZ	1.85	0.40
6:FD:1011:TYR:O	6:FD:1012:PRO:C	2.64	0.40
6:FD:1393:LEU:HD13	6:FD:1393:LEU:HA	1.86	0.40
6:FE:1001:ASN:HD22	6:FE:1001:ASN:N	2.19	0.40
6:FE:1298:LEU:HD23	6:FE:1298:LEU:HA	1.88	0.40
6:FF:1088:LYS:C	6:FF:1090:LEU:H	2.30	0.40
7:GA:842:PRO:HD2	7:GA:867:PRO:HG2	2.04	0.40
8:GB:604:PHE:HE2	8:GB:634:ILE:HD13	1.86	0.40
8:GB:685:ARG:HA	8:GB:690:HIS:CD2	2.57	0.40
8:GB:692:MET:HA	8:GB:693:PRO:HD3	1.84	0.40
7:GC:557:CYS:HB3	7:GC:815:ASP:OD2	2.21	0.40
7:GC:843:LEU:HD11	7:GC:938:VAL:HG11	2.04	0.40
8:GD:95:ILE:HD12	8:GD:95:ILE:HA	2.00	0.40
7:GI:943:GLN:HE22	7:GI:951:MET:H	1.69	0.40
8:GL:67:CYS:SG	8:GL:79:PRO:HD3	2.62	0.40
9:HC:688:MET:HB2	9:HC:692:THR:O	2.22	0.40
10:IA:765:HIS:HD2	10:IA:786:TYR:HA	1.87	0.40
10:IB:995:PRO:HA	10:IB:1103:ARG:HD2	2.04	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:IC:1187:THR:HG23	10:IC:1190:MET:HE2	2.04	0.40
10:IC:1307:ASN:HA	10:IC:1383:LEU:HD13	2.03	0.40
11:JB:556:LEU:HD23	11:JB:790:ARG:HG3	2.04	0.40
11:JB:1731:PRO:HB3	11:JB:1778:PHE:HZ	1.85	0.40
11:JB:2126:ILE:HD13	11:JB:2126:ILE:HA	1.89	0.40
11:JC:440:PRO:HG3	11:JC:1474:TRP:CZ3	2.57	0.40
11:JC:2002:ASN:O	11:JC:2274:ILE:HG12	2.22	0.40
11:JC:2013:LEU:HD23	11:JC:2013:LEU:HA	1.96	0.40
12:KA:383:HIS:HE1	12:KA:413:ALA:HB3	1.87	0.40
12:KC:383:HIS:C	12:KC:386:LEU:HD23	2.47	0.40
12:KE:208:LEU:HD12	12:KE:242:VAL:HG23	2.04	0.40
12:KF:264:LYS:HD3	12:KF:264:LYS:HA	1.85	0.40
12:KF:626:GLU:HA	12:KF:627:PRO:HD3	1.90	0.40
12:KF:720:LEU:HD23	12:KF:720:LEU:HA	1.77	0.40
13:LE:422:GLN:HA	13:LE:425:LYS:HE2	2.04	0.40
15:NA:737:PRO:HG2	15:NA:749:PRO:HD3	2.02	0.40
15:NC:700:THR:HG21	15:NC:890:ARG:HD2	2.02	0.40
15:ND:1155:GLU:O	15:ND:1156:LEU:HG	2.20	0.40
15:ND:1550:MET:N	19:RD:142:ASN:HB3	2.29	0.40
20:SA:11:ALA:HA	20:SA:14:LYS:NZ	2.36	0.40
20:SB:110:MET:HE2	20:SB:110:MET:HB3	1.88	0.40
20:SC:125:MET:HB2	20:SC:125:MET:HE3	1.79	0.40
20:SD:43:ASN:HA	20:SD:44:PRO:HD3	1.90	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	AA	817/1073 (76%)	730 (89%)	81 (10%)	6 (1%)	18 52
1	AD	851/1073 (79%)	782 (92%)	64 (8%)	5 (1%)	21 55

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AE	817/1073 (76%)	731 (90%)	82 (10%)	4 (0%)	24	58
1	AH	851/1073 (79%)	781 (92%)	65 (8%)	5 (1%)	21	55
1	AI	817/1073 (76%)	725 (89%)	88 (11%)	4 (0%)	24	58
1	AL	851/1073 (79%)	779 (92%)	65 (8%)	7 (1%)	16	50
2	AB	465/603 (77%)	406 (87%)	53 (11%)	6 (1%)	9	40
2	AC	471/603 (78%)	439 (93%)	30 (6%)	2 (0%)	30	61
2	AF	465/603 (77%)	411 (88%)	50 (11%)	4 (1%)	14	47
2	AG	471/603 (78%)	427 (91%)	43 (9%)	1 (0%)	43	73
2	AJ	465/603 (77%)	417 (90%)	46 (10%)	2 (0%)	30	61
2	AK	471/603 (78%)	427 (91%)	42 (9%)	2 (0%)	30	61
3	BA	344/5051 (7%)	313 (91%)	30 (9%)	1 (0%)	36	66
3	BB	344/5051 (7%)	308 (90%)	35 (10%)	1 (0%)	36	66
3	BC	344/5051 (7%)	312 (91%)	31 (9%)	1 (0%)	36	66
3	CA	342/5051 (7%)	313 (92%)	29 (8%)	0	100	100
3	CB	342/5051 (7%)	312 (91%)	29 (8%)	1 (0%)	36	66
3	CC	342/5051 (7%)	306 (90%)	35 (10%)	1 (0%)	36	66
3	CE	238/5051 (5%)	195 (82%)	42 (18%)	1 (0%)	30	61
3	CF	238/5051 (5%)	188 (79%)	48 (20%)	2 (1%)	16	50
3	CG	238/5051 (5%)	190 (80%)	43 (18%)	5 (2%)	5	31
3	CI	255/5051 (5%)	228 (89%)	24 (9%)	3 (1%)	10	42
3	CJ	255/5051 (5%)	224 (88%)	28 (11%)	3 (1%)	10	42
3	CL	255/5051 (5%)	222 (87%)	30 (12%)	3 (1%)	10	42
4	DA	343/505 (68%)	317 (92%)	21 (6%)	5 (2%)	8	37
4	DB	343/505 (68%)	322 (94%)	16 (5%)	5 (2%)	8	37
4	DC	343/505 (68%)	318 (93%)	22 (6%)	3 (1%)	14	47
4	DD	328/505 (65%)	317 (97%)	11 (3%)	0	100	100
4	DE	328/505 (65%)	316 (96%)	12 (4%)	0	100	100
4	DF	328/505 (65%)	316 (96%)	11 (3%)	1 (0%)	36	66
5	EA	1333/4956 (27%)	1186 (89%)	130 (10%)	17 (1%)	9	40
5	EB	1333/4956 (27%)	1175 (88%)	142 (11%)	16 (1%)	10	42
5	EC	1333/4956 (27%)	1168 (88%)	151 (11%)	14 (1%)	11	44

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	FA	529/2777 (19%)	484 (92%)	42 (8%)	3 (1%)	21	55
6	FB	529/2777 (19%)	477 (90%)	50 (10%)	2 (0%)	30	61
6	FC	529/2777 (19%)	472 (89%)	53 (10%)	4 (1%)	16	50
6	FD	409/2777 (15%)	236 (58%)	112 (27%)	61 (15%)	0	2
6	FE	409/2777 (15%)	214 (52%)	133 (32%)	62 (15%)	0	2
6	FF	397/2777 (14%)	215 (54%)	137 (34%)	45 (11%)	0	4
7	GA	835/1019 (82%)	784 (94%)	47 (6%)	4 (0%)	24	58
7	GC	775/1019 (76%)	712 (92%)	59 (8%)	4 (0%)	24	58
7	GE	775/1019 (76%)	702 (91%)	67 (9%)	6 (1%)	16	50
7	GG	835/1019 (82%)	781 (94%)	52 (6%)	2 (0%)	43	73
7	GI	775/1019 (76%)	706 (91%)	65 (8%)	4 (0%)	24	58
7	GK	835/1019 (82%)	781 (94%)	52 (6%)	2 (0%)	43	73
8	GB	752/791 (95%)	667 (89%)	80 (11%)	5 (1%)	18	52
8	GD	752/791 (95%)	661 (88%)	87 (12%)	4 (0%)	24	58
8	GF	789/791 (100%)	746 (95%)	43 (5%)	0	100	100
8	GH	728/791 (92%)	650 (89%)	75 (10%)	3 (0%)	30	61
8	GJ	789/791 (100%)	744 (94%)	45 (6%)	0	100	100
8	GL	789/791 (100%)	743 (94%)	44 (6%)	2 (0%)	36	66
9	HA	424/1192 (36%)	359 (85%)	56 (13%)	9 (2%)	5	31
9	HB	424/1192 (36%)	360 (85%)	54 (13%)	10 (2%)	4	29
9	HC	290/1192 (24%)	242 (83%)	43 (15%)	5 (2%)	7	35
9	HD	134/1192 (11%)	114 (85%)	15 (11%)	5 (4%)	2	21
10	IA	1146/1599 (72%)	1045 (91%)	94 (8%)	7 (1%)	21	55
10	IB	1146/1599 (72%)	1046 (91%)	93 (8%)	7 (1%)	21	55
10	IC	1146/1599 (72%)	1054 (92%)	84 (7%)	8 (1%)	18	52
11	JA	1573/2316 (68%)	1374 (87%)	182 (12%)	17 (1%)	11	44
11	JB	1573/2316 (68%)	1357 (86%)	199 (13%)	17 (1%)	11	44
11	JC	1573/2316 (68%)	1368 (87%)	191 (12%)	14 (1%)	14	47
12	KA	458/728 (63%)	355 (78%)	92 (20%)	11 (2%)	4	29
12	KB	458/728 (63%)	365 (80%)	84 (18%)	9 (2%)	6	32
12	KC	458/728 (63%)	334 (73%)	101 (22%)	23 (5%)	1	15

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	KE	437/728 (60%)	408 (93%)	27 (6%)	2 (0%)	24	58
12	KF	437/728 (60%)	408 (93%)	28 (6%)	1 (0%)	43	73
12	KG	437/728 (60%)	409 (94%)	27 (6%)	1 (0%)	43	73
13	LA	186/1322 (14%)	184 (99%)	2 (1%)	0	100	100
13	LB	187/1322 (14%)	184 (98%)	2 (1%)	1 (0%)	24	58
13	LC	158/1322 (12%)	158 (100%)	0	0	100	100
13	LD	157/1322 (12%)	155 (99%)	2 (1%)	0	100	100
13	LE	145/1322 (11%)	138 (95%)	5 (3%)	2 (1%)	9	38
13	LF	146/1322 (11%)	137 (94%)	7 (5%)	2 (1%)	9	38
13	LG	55/1322 (4%)	54 (98%)	1 (2%)	0	100	100
13	LH	53/1322 (4%)	52 (98%)	1 (2%)	0	100	100
13	LI	186/1322 (14%)	176 (95%)	7 (4%)	3 (2%)	7	36
13	LJ	187/1322 (14%)	179 (96%)	6 (3%)	2 (1%)	11	44
13	LK	159/1322 (12%)	156 (98%)	3 (2%)	0	100	100
13	LL	157/1322 (12%)	156 (99%)	1 (1%)	0	100	100
13	LM	104/1322 (8%)	104 (100%)	0	0	100	100
13	LN	104/1322 (8%)	104 (100%)	0	0	100	100
13	LO	103/1322 (8%)	102 (99%)	1 (1%)	0	100	100
13	LP	108/1322 (8%)	106 (98%)	2 (2%)	0	100	100
14	MA	140/2736 (5%)	128 (91%)	11 (8%)	1 (1%)	18	52
14	MB	116/2736 (4%)	109 (94%)	6 (5%)	1 (1%)	14	47
14	MC	71/2736 (3%)	65 (92%)	6 (8%)	0	100	100
14	MD	63/2736 (2%)	63 (100%)	0	0	100	100
14	ME	140/2736 (5%)	125 (89%)	13 (9%)	2 (1%)	9	38
14	MF	116/2736 (4%)	112 (97%)	4 (3%)	0	100	100
14	MG	71/2736 (3%)	65 (92%)	5 (7%)	1 (1%)	9	38
14	MH	63/2736 (2%)	60 (95%)	3 (5%)	0	100	100
14	MI	140/2736 (5%)	126 (90%)	13 (9%)	1 (1%)	18	52
14	MJ	116/2736 (4%)	108 (93%)	6 (5%)	2 (2%)	7	35
14	MK	71/2736 (3%)	66 (93%)	5 (7%)	0	100	100
14	ML	63/2736 (2%)	63 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	NA	879/2484 (35%)	763 (87%)	107 (12%)	9 (1%)	12	45
15	NB	879/2484 (35%)	757 (86%)	107 (12%)	15 (2%)	7	35
15	NC	879/2484 (35%)	758 (86%)	110 (12%)	11 (1%)	9	40
15	ND	879/2484 (35%)	757 (86%)	111 (13%)	11 (1%)	9	40
16	OA	432/2333 (18%)	369 (85%)	51 (12%)	12 (3%)	4	25
16	OB	432/2333 (18%)	373 (86%)	45 (10%)	14 (3%)	3	24
16	OC	432/2333 (18%)	373 (86%)	46 (11%)	13 (3%)	3	25
17	PA	97/1822 (5%)	77 (79%)	19 (20%)	1 (1%)	12	45
17	PB	97/1822 (5%)	75 (77%)	20 (21%)	2 (2%)	5	31
17	PC	97/1822 (5%)	81 (84%)	15 (16%)	1 (1%)	12	45
18	QA	139/172 (81%)	136 (98%)	3 (2%)	0	100	100
18	QB	139/172 (81%)	137 (99%)	2 (1%)	0	100	100
18	QC	139/172 (81%)	135 (97%)	4 (3%)	0	100	100
18	QD	139/172 (81%)	135 (97%)	4 (3%)	0	100	100
19	RA	144/179 (80%)	135 (94%)	9 (6%)	0	100	100
19	RB	144/179 (80%)	130 (90%)	14 (10%)	0	100	100
19	RC	144/179 (80%)	135 (94%)	9 (6%)	0	100	100
19	RD	144/179 (80%)	136 (94%)	8 (6%)	0	100	100
20	SA	142/149 (95%)	133 (94%)	9 (6%)	0	100	100
20	SB	142/149 (95%)	137 (96%)	5 (4%)	0	100	100
20	SC	142/149 (95%)	138 (97%)	4 (3%)	0	100	100
20	SD	142/149 (95%)	138 (97%)	4 (3%)	0	100	100
All	All	51874/215354 (24%)	46217 (89%)	5060 (10%)	597 (1%)	13	42

All (597) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AA	174	CYS
1	AD	136	PHE
1	AD	460	VAL
1	AD	588	ILE
1	AE	137	GLU
1	AE	174	CYS
1	AE	829	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	AF	259	VAL
1	AH	136	PHE
1	AH	460	VAL
1	AI	174	CYS
1	AI	344	SER
1	AL	136	PHE
1	AL	460	VAL
1	AL	798	CYS
3	BB	686	ALA
3	CE	4451	PRO
3	CF	4451	PRO
3	CF	4474	GLU
3	CG	1117	VAL
3	CG	4451	PRO
3	CG	4459	ALA
3	CG	4474	GLU
4	DA	309	VAL
4	DA	327	PHE
4	DA	374	VAL
4	DB	309	VAL
4	DB	327	PHE
4	DB	369	MET
4	DB	374	VAL
4	DB	386	VAL
4	DC	369	MET
5	EA	3330	ASP
5	EA	3454	ASP
5	EA	3699	ASN
5	EB	3330	ASP
5	EB	3645	ALA
5	EB	3699	ASN
5	EB	3886	ASN
5	EB	4894	SER
5	EC	3330	ASP
5	EC	3454	ASP
5	EC	3645	ALA
5	EC	3699	ASN
5	EC	3886	ASN
5	EC	4653	GLU
6	FA	1580	ALA
6	FA	1640	VAL
6	FB	1640	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FC	1640	VAL
6	FD	808	SER
6	FD	809	ILE
6	FD	814	THR
6	FD	845	PRO
6	FD	981	HIS
6	FD	1185	VAL
6	FD	1218	ALA
6	FD	1269	CYS
6	FD	1442	GLU
6	FE	808	SER
6	FE	809	ILE
6	FE	981	HIS
6	FE	1003	ILE
6	FE	1121	PRO
6	FE	1185	VAL
6	FE	1218	ALA
6	FE	1243	PRO
6	FE	1246	ILE
6	FE	1290	ILE
6	FE	1424	CYS
6	FF	808	SER
6	FF	857	GLU
6	FF	1185	VAL
6	FF	1218	ALA
6	FF	1246	ILE
6	FF	1301	ALA
6	FF	1425	PRO
6	FF	1434	ALA
7	GA	856	VAL
8	GB	190	VAL
8	GB	252	GLU
8	GB	526	ILE
7	GC	949	ASN
8	GD	526	ILE
7	GE	864	ILE
7	GE	949	ASN
7	GI	864	ILE
7	GI	949	ASN
8	GL	57	ARG
8	GL	755	MET
9	HA	482	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HA	767	GLN
9	HB	482	ALA
9	HB	767	GLN
9	HB	778	PRO
9	HC	482	ALA
9	HD	767	GLN
9	HD	778	PRO
10	IA	780	VAL
10	IA	1273	TYR
10	IA	1278	VAL
10	IB	780	VAL
10	IB	1273	TYR
10	IB	1407	ARG
10	IC	780	VAL
10	IC	1273	TYR
10	IC	1278	VAL
11	JA	451	MET
11	JA	463	ILE
11	JA	742	VAL
11	JA	944	ILE
11	JA	1093	THR
11	JA	2005	ILE
11	JB	179	PHE
11	JB	181	ASP
11	JB	451	MET
11	JB	463	ILE
11	JB	742	VAL
11	JB	1093	THR
11	JB	1283	ARG
11	JB	1866	ALA
11	JC	463	ILE
11	JC	742	VAL
11	JC	973	MET
11	JC	1093	THR
12	KA	379	SER
12	KA	503	ASP
12	KA	524	PHE
12	KA	625	ASN
12	KA	686	SER
12	KA	721	GLN
12	KB	292	ALA
12	KB	375	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	KB	524	PHE
12	KC	234	PRO
12	KC	235	PRO
12	KC	357	MET
12	KC	360	ASP
12	KC	507	LEU
12	KC	511	LEU
12	KC	688	VAL
12	KC	726	ASP
12	KE	698	PRO
13	LE	465	ILE
13	LE	477	LEU
13	LF	522	ARG
13	LI	477	LEU
13	LJ	522	ARG
14	MB	259	MET
14	ME	262	PRO
14	MG	82	ARG
15	NA	469	PHE
15	NA	1180	ASP
15	NB	469	PHE
15	NB	1422	VAL
15	NC	469	PHE
15	NC	1180	ASP
15	ND	469	PHE
15	ND	1123	ALA
15	ND	1180	ASP
16	OA	266	GLN
16	OA	949	PRO
16	OA	1098	VAL
16	OB	266	GLN
16	OB	949	PRO
16	OC	26	VAL
16	OC	949	PRO
16	OC	1076	VAL
16	OC	1098	VAL
17	PA	141	GLU
17	PB	141	GLU
1	AA	137	GLU
1	AA	829	VAL
2	AB	208	GLU
2	AB	343	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AD	15	THR
1	AH	15	THR
1	AI	137	GLU
1	AL	15	THR
1	AL	588	ILE
3	BA	945	THR
3	BC	945	THR
3	CJ	4490	ASP
3	CJ	4499	PRO
3	CL	4490	ASP
4	DC	309	VAL
4	DF	181	ILE
5	EA	4408	GLY
5	EA	4653	GLU
5	EB	3703	SER
5	EC	3264	LEU
5	EC	3703	SER
5	EC	4408	GLY
6	FA	1892	ILE
6	FB	1892	ILE
6	FC	1892	ILE
6	FC	2001	CYS
6	FC	2086	ASN
6	FD	823	GLY
6	FD	860	PRO
6	FD	910	ILE
6	FD	1103	SER
6	FD	1104	GLY
6	FD	1186	TRP
6	FD	1217	GLU
6	FD	1223	ALA
6	FD	1243	PRO
6	FD	1246	ILE
6	FD	1294	LEU
6	FE	814	THR
6	FE	822	GLY
6	FE	823	GLY
6	FE	838	ASN
6	FE	841	TYR
6	FE	912	ILE
6	FE	1097	SER
6	FE	1104	GLY

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	1186	TRP
6	FE	1197	ILE
6	FE	1199	GLY
6	FE	1217	GLU
6	FE	1223	ALA
6	FE	1245	ASN
6	FE	1269	CYS
6	FE	1294	LEU
6	FE	1300	LEU
6	FE	1428	GLY
6	FE	1439	LEU
6	FF	987	ASN
6	FF	1002	ALA
6	FF	1005	PRO
6	FF	1104	GLY
6	FF	1199	GLY
6	FF	1217	GLU
6	FF	1264	ILE
6	FF	1298	LEU
6	FF	1299	ASN
6	FF	1395	SER
6	FF	1421	VAL
6	FF	1433	ALA
6	FF	1439	LEU
6	FF	1442	GLU
7	GC	864	ILE
8	GD	252	GLU
8	GH	252	GLU
7	GI	782	ALA
9	HA	402	ARG
9	HA	555	SER
9	HA	761	CYS
9	HA	778	PRO
9	HB	555	SER
9	HC	632	GLU
10	IA	644	VAL
10	IB	644	VAL
10	IB	751	ASN
10	IB	1278	VAL
11	JA	181	ASP
11	JA	1283	ARG
11	JC	768	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	JC	944	ILE
11	JC	1283	ARG
12	KA	244	SER
12	KA	292	ALA
12	KA	344	ILE
12	KA	478	MET
12	KB	376	ALA
12	KB	721	GLN
12	KC	237	VAL
12	KC	379	SER
12	KC	478	MET
12	KE	210	VAL
12	KG	237	VAL
13	LJ	454	VAL
14	MJ	287	ALA
15	NB	572	ILE
15	NB	724	ASN
15	NB	1117	PHE
15	NB	1123	ALA
15	NB	1408	THR
15	NC	1123	ALA
15	NC	1472	LYS
15	ND	1422	VAL
16	OA	73	ALA
16	OA	319	GLU
16	OA	1043	VAL
16	OA	1076	VAL
16	OA	1090	GLN
16	OB	73	ALA
16	OB	1076	VAL
16	OC	73	ALA
16	OC	266	GLN
16	OC	1043	VAL
16	OC	1090	GLN
2	AB	305	ASP
2	AB	418	LYS
2	AC	359	VAL
2	AC	534	MET
1	AD	39	SER
2	AF	115	ARG
2	AF	343	ASN
2	AG	359	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	AK	359	VAL
2	AK	534	MET
3	CJ	4452	HIS
4	DA	369	MET
5	EA	3487	ARG
5	EA	3664	THR
5	EA	3703	SER
5	EA	3886	ASN
5	EA	4407	ASP
5	EB	4407	ASP
5	EB	4408	GLY
5	EB	4410	ASP
5	EC	3269	TRP
5	EC	4402	PRO
6	FD	822	GLY
6	FD	827	PRO
6	FD	861	LEU
6	FD	883	ALA
6	FD	1121	PRO
6	FD	1210	LEU
6	FD	1300	LEU
6	FD	1424	CYS
6	FD	1426	ALA
6	FD	1439	LEU
6	FE	1009	VAL
6	FE	1012	PRO
6	FE	1070	LEU
6	FE	1268	VAL
6	FE	1426	ALA
6	FE	1442	GLU
6	FF	912	ILE
6	FF	1106	LEU
6	FF	1243	PRO
6	FF	1286	LEU
6	FF	1294	LEU
8	GB	89	ASN
7	GC	158	THR
8	GD	89	ASN
9	HA	632	GLU
9	HB	402	ARG
9	HB	632	GLU
9	HB	761	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HB	763	GLN
9	HC	402	ARG
9	HC	553	TYR
9	HC	555	SER
9	HD	766	SER
10	IA	1407	ARG
10	IC	226	ARG
10	IC	644	VAL
10	IC	751	ASN
11	JA	43	SER
11	JB	70	GLU
11	JB	2005	ILE
11	JC	2005	ILE
11	JC	2105	ASN
12	KB	233	PRO
12	KC	381	MET
12	KC	389	LYS
12	KC	567	TRP
12	KC	686	SER
12	KF	217	GLU
13	LF	454	VAL
13	LI	521	ASN
14	MJ	259	MET
15	NA	865	SER
15	NA	1123	ALA
15	NA	1422	VAL
15	NB	905	ASP
15	NC	865	SER
15	NC	1117	PHE
15	ND	1117	PHE
15	ND	1549	GLY
16	OA	1089	LEU
16	OB	319	GLU
16	OB	1043	VAL
16	OB	1090	GLN
1	AA	898	PRO
2	AF	208	GLU
1	AH	39	SER
1	AL	1034	SER
3	CI	4452	HIS
3	CL	4452	HIS
5	EA	3697	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	EA	4409	GLU
5	EA	4410	ASP
5	EA	4411	THR
5	EB	4168	ILE
5	EB	4405	ILE
5	EB	4406	MET
5	EC	3266	SER
6	FD	826	LEU
6	FD	828	GLN
6	FD	841	TYR
6	FD	890	ALA
6	FD	912	ILE
6	FD	963	THR
6	FD	1097	SER
6	FD	1200	LEU
6	FD	1296	SER
6	FE	1103	SER
6	FE	1106	LEU
6	FE	1183	HIS
6	FE	1200	LEU
6	FE	1209	GLU
6	FE	1219	GLU
6	FE	1255	SER
6	FE	1264	ILE
6	FE	1388	PHE
6	FF	835	SER
6	FF	856	PRO
6	FF	1216	TRP
6	FF	1219	GLU
6	FF	1440	ASN
7	GE	158	THR
7	GE	774	ALA
7	GE	782	ALA
10	IA	751	ASN
11	JA	763	GLN
11	JA	973	MET
11	JA	1047	ASN
11	JB	768	ASP
11	JB	973	MET
11	JC	763	GLN
12	KA	502	LEU
12	KB	507	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	KC	238	PHE
13	LB	532	LEU
15	NA	572	ILE
15	NA	1472	LYS
15	NB	624	ALA
15	NB	768	GLU
15	NB	864	GLU
15	NB	1423	LEU
15	NC	572	ILE
15	NC	864	GLU
15	ND	572	ILE
16	OA	26	VAL
16	OA	950	VAL
16	OC	950	VAL
1	AH	588	ILE
3	CI	4490	ASP
5	EB	3490	TYR
5	EC	4889	ILE
6	FD	919	GLN
6	FD	1003	ILE
6	FD	1219	GLU
6	FD	1388	PHE
6	FD	1440	ASN
6	FD	1441	ILE
6	FE	919	GLN
6	FE	963	THR
6	FE	1198	TYR
6	FE	1208	ALA
6	FE	1210	LEU
6	FE	1262	CYS
6	FE	1296	SER
6	FE	1441	ILE
6	FF	920	ARG
6	FF	1223	ALA
6	FF	1432	THR
7	GC	662	VAL
7	GE	662	VAL
7	GI	662	VAL
9	HA	762	HIS
9	HD	782	ALA
11	JA	70	GLU
11	JA	768	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	JA	1589	ASP
11	JB	141	ASP
11	JB	436	PRO
11	JB	1047	ASN
12	KC	206	CYS
12	KC	210	VAL
12	KC	226	ALA
12	KC	231	PHE
12	KC	530	ASP
15	NA	624	ALA
15	NB	865	SER
15	NC	468	ARG
15	ND	436	ASP
15	ND	864	GLU
15	ND	1472	LYS
16	OA	29	PRO
16	OB	26	VAL
16	OB	72	SER
16	OB	950	VAL
16	OB	1089	LEU
16	OC	211	LYS
16	OC	319	GLU
1	AA	260	THR
2	AB	259	VAL
1	AI	829	VAL
2	AJ	343	ASN
1	AL	39	SER
3	CG	4490	ASP
3	CI	4499	PRO
3	CL	4499	PRO
5	EB	4268	TYR
5	EC	4168	ILE
6	FD	999	PRO
6	FD	1106	LEU
6	FD	1224	ALA
6	FD	1248	ALA
6	FD	1290	ILE
6	FD	1298	LEU
6	FE	828	GLN
6	FE	1023	ALA
6	FE	1024	ILE
6	FE	1256	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	892	PRO
6	FF	1008	ARG
6	FF	1103	SER
6	FF	1121	PRO
8	GD	190	VAL
9	HB	782	ALA
10	IC	1407	ARG
11	JA	2105	ASN
11	JB	763	GLN
11	JB	2105	ASN
11	JC	70	GLU
11	JC	1047	ASN
12	KB	234	PRO
12	KB	324	ARG
12	KC	579	LEU
14	ME	273	THR
15	NA	724	ASN
15	NB	930	SER
15	NC	724	ASN
15	NC	1422	VAL
15	ND	865	SER
16	OB	29	PRO
16	OB	154	ALA
16	OC	70	THR
2	AJ	259	VAL
5	EB	4402	PRO
6	FD	994	PRO
6	FD	1428	GLY
6	FE	806	ILE
9	HD	779	PRO
11	JC	436	PRO
12	KC	727	ILE
14	MI	273	THR
2	AB	541	PRO
5	EA	4168	ILE
6	FD	1443	GLY
6	FE	1005	PRO
9	HB	779	PRO
10	IA	1196	VAL
10	IC	1196	VAL
16	OB	1033	ALA
1	AE	898	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	CB	752	PRO
4	DA	386	VAL
5	EB	4889	ILE
6	FD	806	ILE
6	FD	839	GLY
6	FD	1264	ILE
6	FD	1268	VAL
6	FD	1274	PRO
6	FF	845	PRO
6	FF	1012	PRO
6	FF	1254	GLY
6	FF	1278	PRO
7	GA	662	VAL
8	GB	718	PRO
9	HA	779	PRO
17	PB	281	PRO
17	PC	281	PRO
1	AA	344	SER
3	CC	772	GLY
4	DC	386	VAL
6	FD	1005	PRO
6	FD	1109	VAL
6	FE	845	PRO
6	FE	910	ILE
6	FF	1274	PRO
6	FF	1296	SER
7	GA	351	GLY
7	GG	662	VAL
8	GH	190	VAL
7	GK	349	GLY
7	GK	662	VAL
10	IB	1196	VAL
11	JA	436	PRO
11	JC	435	VAL
14	MA	273	THR
15	NB	843	ASN
5	EA	4405	ILE
5	EA	4656	ILE
6	FE	892	PRO
7	GA	349	GLY
7	GG	349	GLY
8	GH	113	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	LI	476	GLY
16	OC	1033	ALA

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	AA	718/908 (79%)	718 (100%)	0	100	100
1	AD	740/908 (82%)	739 (100%)	1 (0%)	88	87
1	AE	718/908 (79%)	718 (100%)	0	100	100
1	AH	740/908 (82%)	740 (100%)	0	100	100
1	AI	718/908 (79%)	717 (100%)	1 (0%)	88	87
1	AL	740/908 (82%)	736 (100%)	4 (0%)	81	81
2	AB	415/516 (80%)	410 (99%)	5 (1%)	63	73
2	AC	418/516 (81%)	418 (100%)	0	100	100
2	AF	415/516 (80%)	415 (100%)	0	100	100
2	AG	418/516 (81%)	418 (100%)	0	100	100
2	AJ	414/516 (80%)	414 (100%)	0	100	100
2	AK	418/516 (81%)	415 (99%)	3 (1%)	76	78
3	BA	286/4189 (7%)	286 (100%)	0	100	100
3	BB	286/4189 (7%)	286 (100%)	0	100	100
3	BC	286/4189 (7%)	286 (100%)	0	100	100
3	CA	284/4189 (7%)	284 (100%)	0	100	100
3	CB	284/4189 (7%)	283 (100%)	1 (0%)	84	81
3	CC	284/4189 (7%)	283 (100%)	1 (0%)	84	81
3	CE	206/4189 (5%)	206 (100%)	0	100	100
3	CF	206/4189 (5%)	206 (100%)	0	100	100
3	CG	206/4189 (5%)	206 (100%)	0	100	100
3	CI	221/4189 (5%)	221 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	CJ	221/4189 (5%)	221 (100%)	0	100	100
3	CL	221/4189 (5%)	221 (100%)	0	100	100
4	DA	297/435 (68%)	297 (100%)	0	100	100
4	DB	297/435 (68%)	297 (100%)	0	100	100
4	DC	297/435 (68%)	297 (100%)	0	100	100
4	DD	285/435 (66%)	285 (100%)	0	100	100
4	DE	285/435 (66%)	285 (100%)	0	100	100
4	DF	285/435 (66%)	285 (100%)	0	100	100
5	EA	1150/4160 (28%)	1147 (100%)	3 (0%)	86	83
5	EB	1150/4160 (28%)	1135 (99%)	15 (1%)	61	72
5	EC	1149/4160 (28%)	1135 (99%)	14 (1%)	63	73
6	FA	453/2343 (19%)	435 (96%)	18 (4%)	28	53
6	FB	453/2343 (19%)	436 (96%)	17 (4%)	29	56
6	FC	453/2343 (19%)	391 (86%)	62 (14%)	3	20
6	FD	356/2343 (15%)	189 (53%)	167 (47%)	0	0
6	FE	357/2343 (15%)	192 (54%)	165 (46%)	0	0
6	FF	348/2343 (15%)	184 (53%)	164 (47%)	0	0
7	GA	680/807 (84%)	680 (100%)	0	100	100
7	GC	647/807 (80%)	647 (100%)	0	100	100
7	GE	647/807 (80%)	647 (100%)	0	100	100
7	GG	680/807 (84%)	680 (100%)	0	100	100
7	GI	647/807 (80%)	647 (100%)	0	100	100
7	GK	680/807 (84%)	680 (100%)	0	100	100
8	GB	647/665 (97%)	646 (100%)	1 (0%)	87	85
8	GD	647/665 (97%)	645 (100%)	2 (0%)	86	83
8	GF	665/665 (100%)	665 (100%)	0	100	100
8	GH	629/665 (95%)	628 (100%)	1 (0%)	87	85
8	GJ	665/665 (100%)	665 (100%)	0	100	100
8	GL	665/665 (100%)	664 (100%)	1 (0%)	87	85
9	HA	353/1003 (35%)	306 (87%)	47 (13%)	4	21
9	HB	353/1003 (35%)	309 (88%)	44 (12%)	4	22

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	HC	234/1003 (23%)	234 (100%)	0	100	100
9	HD	119/1003 (12%)	77 (65%)	42 (35%)	0	1
10	IA	978/1309 (75%)	978 (100%)	0	100	100
10	IB	978/1309 (75%)	977 (100%)	1 (0%)	88	87
10	IC	978/1309 (75%)	978 (100%)	0	100	100
11	JA	1388/1993 (70%)	1388 (100%)	0	100	100
11	JB	1388/1993 (70%)	1387 (100%)	1 (0%)	88	87
11	JC	1388/1993 (70%)	1388 (100%)	0	100	100
12	KA	401/626 (64%)	401 (100%)	0	100	100
12	KB	401/626 (64%)	401 (100%)	0	100	100
12	KC	400/626 (64%)	388 (97%)	12 (3%)	36	60
12	KE	385/626 (62%)	385 (100%)	0	100	100
12	KF	385/626 (62%)	385 (100%)	0	100	100
12	KG	385/626 (62%)	385 (100%)	0	100	100
13	LA	165/1137 (14%)	164 (99%)	1 (1%)	78	80
13	LB	167/1137 (15%)	167 (100%)	0	100	100
13	LC	146/1137 (13%)	146 (100%)	0	100	100
13	LD	146/1137 (13%)	146 (100%)	0	100	100
13	LE	132/1137 (12%)	132 (100%)	0	100	100
13	LF	134/1137 (12%)	134 (100%)	0	100	100
13	LG	54/1137 (5%)	54 (100%)	0	100	100
13	LH	53/1137 (5%)	53 (100%)	0	100	100
13	LI	165/1137 (14%)	161 (98%)	4 (2%)	43	64
13	LJ	167/1137 (15%)	167 (100%)	0	100	100
13	LK	147/1137 (13%)	147 (100%)	0	100	100
13	LL	146/1137 (13%)	146 (100%)	0	100	100
13	LM	93/1137 (8%)	93 (100%)	0	100	100
13	LN	93/1137 (8%)	93 (100%)	0	100	100
13	LO	90/1137 (8%)	90 (100%)	0	100	100
13	LP	95/1137 (8%)	95 (100%)	0	100	100
14	MA	123/2310 (5%)	123 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	MB	107/2310 (5%)	107 (100%)	0	100	100
14	MC	63/2310 (3%)	63 (100%)	0	100	100
14	MD	51/2310 (2%)	51 (100%)	0	100	100
14	ME	123/2310 (5%)	123 (100%)	0	100	100
14	MF	107/2310 (5%)	107 (100%)	0	100	100
14	MG	63/2310 (3%)	63 (100%)	0	100	100
14	MH	51/2310 (2%)	51 (100%)	0	100	100
14	MI	123/2310 (5%)	123 (100%)	0	100	100
14	MJ	107/2310 (5%)	107 (100%)	0	100	100
14	MK	63/2310 (3%)	63 (100%)	0	100	100
14	ML	51/2310 (2%)	51 (100%)	0	100	100
15	NA	785/2093 (38%)	785 (100%)	0	100	100
15	NB	785/2093 (38%)	785 (100%)	0	100	100
15	NC	785/2093 (38%)	785 (100%)	0	100	100
15	ND	785/2093 (38%)	785 (100%)	0	100	100
16	OA	370/1912 (19%)	370 (100%)	0	100	100
16	OB	370/1912 (19%)	370 (100%)	0	100	100
16	OC	370/1912 (19%)	370 (100%)	0	100	100
17	PA	88/1558 (6%)	88 (100%)	0	100	100
17	PB	88/1558 (6%)	88 (100%)	0	100	100
17	PC	88/1558 (6%)	88 (100%)	0	100	100
18	QA	120/150 (80%)	120 (100%)	0	100	100
18	QB	120/150 (80%)	120 (100%)	0	100	100
18	QC	120/150 (80%)	120 (100%)	0	100	100
18	QD	120/150 (80%)	120 (100%)	0	100	100
19	RA	123/139 (88%)	123 (100%)	0	100	100
19	RB	123/139 (88%)	123 (100%)	0	100	100
19	RC	123/139 (88%)	123 (100%)	0	100	100
19	RD	123/139 (88%)	122 (99%)	1 (1%)	73	77
20	SA	123/127 (97%)	123 (100%)	0	100	100
20	SB	123/127 (97%)	123 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	SC	123/127 (97%)	123 (100%)	0	100	100
20	SD	123/127 (97%)	123 (100%)	0	100	100
All	All	44894/180824 (25%)	44095 (98%)	799 (2%)	51	69

All (799) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AB	329	GLN
2	AB	408	LYS
2	AB	411	GLN
2	AB	414	LEU
2	AB	419	LYS
1	AD	988	GLN
1	AI	341	GLN
2	AK	331	ASN
2	AK	343	ASN
2	AK	448	ASN
1	AL	1027	MET
1	AL	1028	ARG
1	AL	1031	THR
1	AL	1033	GLN
3	CB	880	GLN
3	CC	724	GLN
5	EA	3335	GLN
5	EA	4405	ILE
5	EA	4406	MET
5	EB	4069	HIS
5	EB	4403	LEU
5	EB	4404	LYS
5	EB	4405	ILE
5	EB	4406	MET
5	EB	4407	ASP
5	EB	4879	THR
5	EB	4880	ASP
5	EB	4881	ARG
5	EB	4883	LEU
5	EB	4884	LEU
5	EB	4886	LYS
5	EB	4889	ILE
5	EB	4892	ARG
5	EB	4896	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	EC	4093	SER
5	EC	4094	LEU
5	EC	4099	THR
5	EC	4403	LEU
5	EC	4404	LYS
5	EC	4406	MET
5	EC	4879	THR
5	EC	4880	ASP
5	EC	4881	ARG
5	EC	4882	ARG
5	EC	4886	LYS
5	EC	4889	ILE
5	EC	4892	ARG
5	EC	4898	MET
6	FA	2010	LYS
6	FA	2013	GLU
6	FA	2014	GLU
6	FA	2015	LYS
6	FA	2016	ARG
6	FA	2017	ARG
6	FA	2018	ARG
6	FA	2024	ARG
6	FA	2030	ILE
6	FA	2037	LEU
6	FA	2038	LEU
6	FA	2042	LYS
6	FA	2044	CYS
6	FA	2046	ASP
6	FA	2050	LEU
6	FA	2053	LYS
6	FA	2056	LEU
6	FA	2059	VAL
6	FB	2030	ILE
6	FB	2037	LEU
6	FB	2038	LEU
6	FB	2042	LYS
6	FB	2046	ASP
6	FB	2047	ARG
6	FB	2048	GLU
6	FB	2050	LEU
6	FB	2053	LYS
6	FB	2056	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FB	2057	SER
6	FB	2061	ARG
6	FB	2062	LEU
6	FB	2063	GLN
6	FB	2064	LEU
6	FB	2067	MET
6	FB	2068	CYS
6	FC	1968	LYS
6	FC	1970	LEU
6	FC	1971	LYS
6	FC	1972	GLU
6	FC	1973	GLU
6	FC	1976	LYS
6	FC	1978	LEU
6	FC	1979	GLU
6	FC	1983	ARG
6	FC	1984	LYS
6	FC	1989	GLU
6	FC	1993	LYS
6	FC	1994	ARG
6	FC	1995	GLU
6	FC	1997	GLU
6	FC	1998	GLU
6	FC	2001	CYS
6	FC	2007	GLU
6	FC	2008	THR
6	FC	2010	LYS
6	FC	2012	ARG
6	FC	2013	GLU
6	FC	2014	GLU
6	FC	2015	LYS
6	FC	2017	ARG
6	FC	2018	ARG
6	FC	2021	GLU
6	FC	2022	GLU
6	FC	2024	ARG
6	FC	2030	ILE
6	FC	2034	ARG
6	FC	2037	LEU
6	FC	2038	LEU
6	FC	2040	LEU
6	FC	2042	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FC	2046	ASP
6	FC	2047	ARG
6	FC	2051	VAL
6	FC	2053	LYS
6	FC	2057	SER
6	FC	2058	MET
6	FC	2061	ARG
6	FC	2064	LEU
6	FC	2066	GLU
6	FC	2070	LEU
6	FC	2072	ILE
6	FC	2073	LEU
6	FC	2079	MET
6	FC	2080	GLN
6	FC	2082	LEU
6	FC	2083	GLN
6	FC	2084	GLN
6	FC	2087	LEU
6	FC	2088	MET
6	FC	2089	PRO
6	FC	2090	LEU
6	FC	2094	LEU
6	FC	2095	GLN
6	FC	2097	GLN
6	FC	2099	ILE
6	FC	2101	LEU
6	FC	2109	ILE
6	FD	801	THR
6	FD	802	LEU
6	FD	803	ARG
6	FD	804	LEU
6	FD	808	SER
6	FD	809	ILE
6	FD	810	THR
6	FD	811	ASN
6	FD	813	GLN
6	FD	814	THR
6	FD	818	VAL
6	FD	820	LYS
6	FD	821	ARG
6	FD	826	LEU
6	FD	828	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FD	829	ARG
6	FD	834	VAL
6	FD	835	SER
6	FD	838	ASN
6	FD	841	TYR
6	FD	843	LEU
6	FD	848	THR
6	FD	849	ILE
6	FD	851	THR
6	FD	858	GLU
6	FD	861	LEU
6	FD	862	GLU
6	FD	863	ILE
6	FD	866	PHE
6	FD	878	LEU
6	FD	882	SER
6	FD	887	ARG
6	FD	891	ARG
6	FD	896	CYS
6	FD	897	LEU
6	FD	898	ASP
6	FD	901	GLU
6	FD	903	GLN
6	FD	905	GLU
6	FD	912	ILE
6	FD	913	LEU
6	FD	915	SER
6	FD	918	GLN
6	FD	920	ARG
6	FD	921	MET
6	FD	922	LEU
6	FD	924	LEU
6	FD	925	GLU
6	FD	926	LEU
6	FD	929	ASN
6	FD	964	LEU
6	FD	969	LEU
6	FD	970	VAL
6	FD	973	ILE
6	FD	978	LYS
6	FD	984	THR
6	FD	985	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FD	988	SER
6	FD	990	PHE
6	FD	991	ARG
6	FD	995	VAL
6	FD	997	THR
6	FD	1000	GLN
6	FD	1001	ASN
6	FD	1003	ILE
6	FD	1008	ARG
6	FD	1009	VAL
6	FD	1010	ARG
6	FD	1014	LYS
6	FD	1017	VAL
6	FD	1018	THR
6	FD	1024	ILE
6	FD	1028	LYS
6	FD	1029	GLN
6	FD	1030	ILE
6	FD	1064	TYR
6	FD	1065	LEU
6	FD	1066	GLN
6	FD	1068	CYS
6	FD	1077	ARG
6	FD	1078	GLU
6	FD	1080	ILE
6	FD	1084	ARG
6	FD	1089	ARG
6	FD	1091	GLU
6	FD	1093	VAL
6	FD	1095	LEU
6	FD	1098	VAL
6	FD	1100	GLU
6	FD	1107	SER
6	FD	1109	VAL
6	FD	1114	VAL
6	FD	1116	LEU
6	FD	1119	LEU
6	FD	1120	LYS
6	FD	1122	LEU
6	FD	1123	THR
6	FD	1124	ILE
6	FD	1183	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FD	1185	VAL
6	FD	1187	ILE
6	FD	1188	GLU
6	FD	1190	ARG
6	FD	1191	LYS
6	FD	1192	VAL
6	FD	1193	VAL
6	FD	1194	ASN
6	FD	1195	VAL
6	FD	1200	LEU
6	FD	1201	THR
6	FD	1203	ARG
6	FD	1206	CYS
6	FD	1209	GLU
6	FD	1210	LEU
6	FD	1215	MET
6	FD	1217	GLU
6	FD	1219	GLU
6	FD	1220	ARG
6	FD	1225	ILE
6	FD	1229	LYS
6	FD	1231	ARG
6	FD	1232	LYS
6	FD	1233	ILE
6	FD	1238	ARG
6	FD	1239	CYS
6	FD	1244	LEU
6	FD	1246	ILE
6	FD	1249	ILE
6	FD	1252	MET
6	FD	1255	SER
6	FD	1256	GLU
6	FD	1257	ASP
6	FD	1258	SER
6	FD	1259	LEU
6	FD	1260	LEU
6	FD	1261	SER
6	FD	1262	CYS
6	FD	1264	ILE
6	FD	1267	GLN
6	FD	1268	VAL
6	FD	1270	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FD	1277	ASP
6	FD	1279	SER
6	FD	1281	VAL
6	FD	1284	LEU
6	FD	1289	HIS
6	FD	1291	TYR
6	FD	1294	LEU
6	FD	1298	LEU
6	FD	1300	LEU
6	FD	1388	PHE
6	FD	1389	ARG
6	FD	1391	TYR
6	FD	1392	LYS
6	FD	1393	LEU
6	FD	1416	GLN
6	FD	1419	LEU
6	FD	1420	ARG
6	FD	1421	VAL
6	FD	1422	PHE
6	FD	1424	CYS
6	FD	1427	ASN
6	FD	1429	LEU
6	FD	1431	MET
6	FD	1438	LYS
6	FD	1439	LEU
6	FD	1444	ARG
6	FE	801	THR
6	FE	802	LEU
6	FE	803	ARG
6	FE	804	LEU
6	FE	809	ILE
6	FE	810	THR
6	FE	813	GLN
6	FE	814	THR
6	FE	818	VAL
6	FE	821	ARG
6	FE	824	TYR
6	FE	828	GLN
6	FE	829	ARG
6	FE	835	SER
6	FE	841	TYR
6	FE	843	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	849	ILE
6	FE	851	THR
6	FE	858	GLU
6	FE	861	LEU
6	FE	862	GLU
6	FE	866	PHE
6	FE	878	LEU
6	FE	879	ARG
6	FE	882	SER
6	FE	884	VAL
6	FE	891	ARG
6	FE	895	ILE
6	FE	897	LEU
6	FE	898	ASP
6	FE	901	GLU
6	FE	905	GLU
6	FE	907	ASN
6	FE	912	ILE
6	FE	913	LEU
6	FE	915	SER
6	FE	918	GLN
6	FE	920	ARG
6	FE	921	MET
6	FE	922	LEU
6	FE	924	LEU
6	FE	926	LEU
6	FE	929	ASN
6	FE	964	LEU
6	FE	969	LEU
6	FE	972	VAL
6	FE	973	ILE
6	FE	975	ILE
6	FE	978	LYS
6	FE	981	HIS
6	FE	982	SER
6	FE	985	ILE
6	FE	987	ASN
6	FE	988	SER
6	FE	997	THR
6	FE	1000	GLN
6	FE	1001	ASN
6	FE	1003	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	1007	GLN
6	FE	1008	ARG
6	FE	1010	ARG
6	FE	1014	LYS
6	FE	1015	SER
6	FE	1017	VAL
6	FE	1018	THR
6	FE	1020	VAL
6	FE	1024	ILE
6	FE	1028	LYS
6	FE	1029	GLN
6	FE	1030	ILE
6	FE	1065	LEU
6	FE	1068	CYS
6	FE	1069	ARG
6	FE	1077	ARG
6	FE	1078	GLU
6	FE	1080	ILE
6	FE	1084	ARG
6	FE	1087	LEU
6	FE	1089	ARG
6	FE	1090	LEU
6	FE	1091	GLU
6	FE	1093	VAL
6	FE	1095	LEU
6	FE	1098	VAL
6	FE	1099	ILE
6	FE	1100	GLU
6	FE	1105	ARG
6	FE	1109	VAL
6	FE	1114	VAL
6	FE	1116	LEU
6	FE	1119	LEU
6	FE	1120	LYS
6	FE	1122	LEU
6	FE	1123	THR
6	FE	1124	ILE
6	FE	1183	HIS
6	FE	1185	VAL
6	FE	1187	ILE
6	FE	1188	GLU
6	FE	1190	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	1191	LYS
6	FE	1192	VAL
6	FE	1195	VAL
6	FE	1200	LEU
6	FE	1201	THR
6	FE	1210	LEU
6	FE	1217	GLU
6	FE	1219	GLU
6	FE	1220	ARG
6	FE	1225	ILE
6	FE	1229	LYS
6	FE	1231	ARG
6	FE	1232	LYS
6	FE	1233	ILE
6	FE	1238	ARG
6	FE	1239	CYS
6	FE	1242	GLN
6	FE	1244	LEU
6	FE	1246	ILE
6	FE	1249	ILE
6	FE	1252	MET
6	FE	1255	SER
6	FE	1257	ASP
6	FE	1258	SER
6	FE	1259	LEU
6	FE	1260	LEU
6	FE	1261	SER
6	FE	1262	CYS
6	FE	1263	TYR
6	FE	1264	ILE
6	FE	1265	ARG
6	FE	1267	GLN
6	FE	1268	VAL
6	FE	1270	LEU
6	FE	1272	VAL
6	FE	1277	ASP
6	FE	1279	SER
6	FE	1281	VAL
6	FE	1284	LEU
6	FE	1285	CYS
6	FE	1289	HIS
6	FE	1293	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	1294	LEU
6	FE	1298	LEU
6	FE	1300	LEU
6	FE	1388	PHE
6	FE	1389	ARG
6	FE	1392	LYS
6	FE	1394	ARG
6	FE	1397	VAL
6	FE	1416	GLN
6	FE	1417	ILE
6	FE	1418	GLU
6	FE	1419	LEU
6	FE	1420	ARG
6	FE	1421	VAL
6	FE	1422	PHE
6	FE	1424	CYS
6	FE	1427	ASN
6	FE	1429	LEU
6	FE	1431	MET
6	FE	1438	LYS
6	FE	1439	LEU
6	FE	1442	GLU
6	FE	1444	ARG
6	FF	801	THR
6	FF	802	LEU
6	FF	803	ARG
6	FF	804	LEU
6	FF	809	ILE
6	FF	810	THR
6	FF	813	GLN
6	FF	814	THR
6	FF	817	VAL
6	FF	818	VAL
6	FF	821	ARG
6	FF	826	LEU
6	FF	828	GLN
6	FF	829	ARG
6	FF	834	VAL
6	FF	835	SER
6	FF	838	ASN
6	FF	841	TYR
6	FF	843	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	846	CYS
6	FF	849	ILE
6	FF	852	VAL
6	FF	857	GLU
6	FF	858	GLU
6	FF	859	ASP
6	FF	861	LEU
6	FF	863	ILE
6	FF	868	GLN
6	FF	878	LEU
6	FF	879	ARG
6	FF	887	ARG
6	FF	889	SER
6	FF	891	ARG
6	FF	895	ILE
6	FF	897	LEU
6	FF	901	GLU
6	FF	905	GLU
6	FF	910	ILE
6	FF	912	ILE
6	FF	913	LEU
6	FF	917	TRP
6	FF	920	ARG
6	FF	922	LEU
6	FF	924	LEU
6	FF	926	LEU
6	FF	929	ASN
6	FF	962	PHE
6	FF	969	LEU
6	FF	971	SER
6	FF	973	ILE
6	FF	975	ILE
6	FF	979	LEU
6	FF	982	SER
6	FF	988	SER
6	FF	990	PHE
6	FF	1003	ILE
6	FF	1008	ARG
6	FF	1010	ARG
6	FF	1014	LYS
6	FF	1017	VAL
6	FF	1018	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	1019	VAL
6	FF	1020	VAL
6	FF	1024	ILE
6	FF	1028	LYS
6	FF	1029	GLN
6	FF	1030	ILE
6	FF	1065	LEU
6	FF	1066	GLN
6	FF	1068	CYS
6	FF	1069	ARG
6	FF	1080	ILE
6	FF	1081	SER
6	FF	1084	ARG
6	FF	1085	GLU
6	FF	1090	LEU
6	FF	1091	GLU
6	FF	1093	VAL
6	FF	1094	SER
6	FF	1096	LEU
6	FF	1098	VAL
6	FF	1100	GLU
6	FF	1105	ARG
6	FF	1112	ILE
6	FF	1114	VAL
6	FF	1115	THR
6	FF	1116	LEU
6	FF	1119	LEU
6	FF	1120	LYS
6	FF	1122	LEU
6	FF	1124	ILE
6	FF	1183	HIS
6	FF	1185	VAL
6	FF	1187	ILE
6	FF	1188	GLU
6	FF	1189	ILE
6	FF	1190	ARG
6	FF	1191	LYS
6	FF	1192	VAL
6	FF	1194	ASN
6	FF	1195	VAL
6	FF	1200	LEU
6	FF	1201	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	1203	ARG
6	FF	1205	ILE
6	FF	1207	GLU
6	FF	1209	GLU
6	FF	1210	LEU
6	FF	1212	VAL
6	FF	1213	VAL
6	FF	1215	MET
6	FF	1217	GLU
6	FF	1219	GLU
6	FF	1225	ILE
6	FF	1227	ARG
6	FF	1229	LYS
6	FF	1230	SER
6	FF	1231	ARG
6	FF	1232	LYS
6	FF	1233	ILE
6	FF	1234	THR
6	FF	1238	ARG
6	FF	1240	GLU
6	FF	1241	VAL
6	FF	1242	GLN
6	FF	1244	LEU
6	FF	1245	ASN
6	FF	1246	ILE
6	FF	1249	ILE
6	FF	1250	GLU
6	FF	1251	ARG
6	FF	1252	MET
6	FF	1256	GLU
6	FF	1257	ASP
6	FF	1258	SER
6	FF	1261	SER
6	FF	1262	CYS
6	FF	1264	ILE
6	FF	1267	GLN
6	FF	1268	VAL
6	FF	1270	LEU
6	FF	1272	VAL
6	FF	1279	SER
6	FF	1281	VAL
6	FF	1284	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FF	1289	HIS
6	FF	1294	LEU
6	FF	1298	LEU
6	FF	1389	ARG
6	FF	1393	LEU
6	FF	1394	ARG
6	FF	1416	GLN
6	FF	1421	VAL
6	FF	1427	ASN
6	FF	1429	LEU
6	FF	1431	MET
6	FF	1432	THR
6	FF	1438	LYS
6	FF	1439	LEU
6	FF	1441	ILE
6	FF	1442	GLU
6	FF	1444	ARG
6	FF	1445	SER
6	FF	1446	ASN
8	GB	683	GLN
8	GD	629	ASN
8	GD	703	GLN
8	GH	64	ASN
8	GL	83	GLN
9	HA	747	VAL
9	HA	752	ASP
9	HA	753	SER
9	HA	755	MET
9	HA	757	LEU
9	HA	760	LYS
9	HA	762	HIS
9	HA	765	TRP
9	HA	768	THR
9	HA	769	LYS
9	HA	770	ASN
9	HA	775	SER
9	HA	779	PRO
9	HA	780	PHE
9	HA	784	GLU
9	HA	790	LEU
9	HA	791	GLN
9	HA	795	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HA	796	ASP
9	HA	798	ASP
9	HA	800	VAL
9	HA	802	MET
9	HA	810	ARG
9	HA	814	LYS
9	HA	820	SER
9	HA	832	SER
9	HA	834	LEU
9	HA	838	LYS
9	HA	842	HIS
9	HA	848	ASP
9	HA	851	GLU
9	HA	852	LYS
9	HA	855	ARG
9	HA	856	GLU
9	HA	858	LEU
9	HA	859	LYS
9	HA	861	TYR
9	HA	862	LEU
9	HA	865	ILE
9	HA	868	LEU
9	HA	869	GLN
9	HA	871	GLU
9	HA	872	MET
9	HA	874	VAL
9	HA	877	LYS
9	HA	878	SER
9	HA	880	HIS
9	HB	747	VAL
9	HB	752	ASP
9	HB	753	SER
9	HB	754	LEU
9	HB	755	MET
9	HB	757	LEU
9	HB	760	LYS
9	HB	764	LYS
9	HB	765	TRP
9	HB	768	THR
9	HB	769	LYS
9	HB	770	ASN
9	HB	775	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HB	776	PRO
9	HB	784	GLU
9	HB	790	LEU
9	HB	791	GLN
9	HB	795	LEU
9	HB	796	ASP
9	HB	798	ASP
9	HB	800	VAL
9	HB	802	MET
9	HB	810	ARG
9	HB	812	THR
9	HB	814	LYS
9	HB	832	SER
9	HB	834	LEU
9	HB	835	LYS
9	HB	838	LYS
9	HB	842	HIS
9	HB	848	ASP
9	HB	851	GLU
9	HB	852	LYS
9	HB	855	ARG
9	HB	858	LEU
9	HB	859	LYS
9	HB	861	TYR
9	HB	865	ILE
9	HB	868	LEU
9	HB	869	GLN
9	HB	872	MET
9	HB	877	LYS
9	HB	879	ILE
9	HB	880	HIS
9	HD	747	VAL
9	HD	749	ASN
9	HD	752	ASP
9	HD	753	SER
9	HD	757	LEU
9	HD	760	LYS
9	HD	763	GLN
9	HD	764	LYS
9	HD	768	THR
9	HD	769	LYS
9	HD	770	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
9	HD	775	SER
9	HD	776	PRO
9	HD	779	PRO
9	HD	784	GLU
9	HD	790	LEU
9	HD	791	GLN
9	HD	792	ARG
9	HD	798	ASP
9	HD	800	VAL
9	HD	802	MET
9	HD	804	THR
9	HD	810	ARG
9	HD	814	LYS
9	HD	823	ILE
9	HD	834	LEU
9	HD	838	LYS
9	HD	842	HIS
9	HD	848	ASP
9	HD	851	GLU
9	HD	852	LYS
9	HD	855	ARG
9	HD	858	LEU
9	HD	859	LYS
9	HD	860	GLN
9	HD	865	ILE
9	HD	868	LEU
9	HD	869	GLN
9	HD	872	MET
9	HD	875	THR
9	HD	877	LYS
9	HD	880	HIS
10	IB	1179	ASN
11	JB	2122	GLN
12	KC	227	THR
12	KC	228	GLU
12	KC	229	SER
12	KC	230	GLN
12	KC	231	PHE
12	KC	236	LYS
12	KC	237	VAL
12	KC	381	MET
12	KC	384	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	KC	385	GLU
12	KC	722	VAL
12	KC	723	GLU
13	LA	480	GLN
13	LI	520	LEU
13	LI	526	LEU
13	LI	530	VAL
13	LI	532	LEU
19	RD	142	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (520) such sidechains are listed below:

Mol	Chain	Res	Type
1	AA	76	GLN
1	AA	232	GLN
1	AA	256	GLN
1	AA	275	HIS
1	AA	372	HIS
1	AA	442	HIS
1	AA	673	GLN
1	AA	683	ASN
2	AB	153	GLN
2	AB	168	GLN
2	AB	267	HIS
2	AB	329	GLN
2	AB	415	HIS
2	AB	466	GLN
2	AB	518	HIS
2	AC	46	GLN
2	AC	82	ASN
2	AC	153	GLN
2	AC	415	HIS
1	AD	370	GLN
1	AD	716	HIS
1	AD	814	GLN
1	AD	909	GLN
1	AD	988	GLN
1	AE	442	HIS
1	AE	744	HIS
1	AE	909	GLN
2	AF	64	GLN
2	AF	136	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	AF	262	GLN
2	AF	304	GLN
2	AF	368	HIS
2	AF	381	HIS
2	AF	466	GLN
2	AF	482	GLN
2	AG	46	GLN
2	AG	49	HIS
2	AG	304	GLN
2	AG	355	HIS
2	AG	448	ASN
2	AG	518	HIS
1	AH	27	HIS
1	AH	232	GLN
1	AH	256	GLN
1	AH	450	ASN
1	AH	652	ASN
1	AI	145	HIS
1	AI	215	GLN
1	AI	379	GLN
1	AI	476	GLN
1	AI	504	ASN
1	AI	652	ASN
1	AI	686	ASN
2	AJ	168	GLN
2	AJ	213	HIS
2	AJ	304	GLN
2	AJ	337	HIS
2	AJ	411	GLN
2	AJ	518	HIS
2	AK	262	GLN
2	AK	329	GLN
2	AK	439	GLN
2	AK	518	HIS
1	AL	76	GLN
1	AL	145	HIS
1	AL	293	HIS
1	AL	628	ASN
1	AL	683	ASN
1	AL	762	HIS
1	AL	968	ASN
3	BA	725	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	BA	733	GLN
3	BA	817	HIS
3	BA	964	GLN
3	BA	967	HIS
3	BA	995	ASN
3	BB	736	HIS
3	BB	778	GLN
3	BB	952	GLN
3	BB	962	GLN
3	BB	995	ASN
3	BB	1012	GLN
3	BC	683	GLN
3	BC	708	GLN
3	BC	749	GLN
3	BC	790	ASN
3	BC	995	ASN
3	BC	1010	GLN
3	CA	733	GLN
3	CA	835	GLN
3	CB	790	ASN
3	CB	817	HIS
3	CC	683	GLN
3	CC	790	ASN
3	CC	895	HIS
3	CC	944	GLN
3	CC	962	GLN
3	CF	1192	HIS
3	CG	1178	GLN
3	CG	1192	HIS
3	CG	1257	ASN
3	CI	1242	ASN
3	CJ	1178	GLN
3	CJ	1205	GLN
3	CJ	1243	GLN
3	CJ	4511	GLN
3	CL	1221	ASN
3	CL	1242	ASN
3	CL	4492	ASN
4	DA	308	GLN
4	DA	334	GLN
4	DA	361	GLN
4	DB	63	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	DB	72	GLN
4	DB	291	GLN
4	DB	312	ASN
4	DB	361	GLN
4	DC	312	ASN
4	DC	361	GLN
4	DD	334	GLN
4	DE	281	GLN
4	DE	308	GLN
4	DF	252	GLN
4	DF	300	GLN
5	EA	3274	GLN
5	EA	3440	GLN
5	EA	3519	ASN
5	EA	3581	HIS
5	EA	3820	HIS
5	EA	3864	HIS
5	EA	3882	ASN
5	EA	4069	HIS
5	EA	4177	GLN
5	EA	4340	ASN
5	EA	4830	ASN
5	EB	3279	GLN
5	EB	3416	HIS
5	EB	3503	GLN
5	EB	3713	GLN
5	EB	3820	HIS
5	EB	3864	HIS
5	EB	4264	GLN
5	EB	4280	HIS
5	EB	4340	ASN
5	EB	4455	GLN
5	EB	4631	HIS
5	EB	4703	GLN
5	EB	4748	ASN
5	EB	4756	GLN
5	EB	4829	GLN
5	EB	4878	HIS
5	EC	3448	GLN
5	EC	3626	HIS
5	EC	3725	ASN
5	EC	3820	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	EC	4161	HIS
5	EC	4267	GLN
5	EC	4287	ASN
5	EC	4376	HIS
5	EC	4391	GLN
5	EC	4479	GLN
5	EC	4762	GLN
5	EC	4824	ASN
5	EC	4878	HIS
6	FA	1612	ASN
6	FA	1806	ASN
6	FA	1850	GLN
6	FA	1893	HIS
6	FA	1937	GLN
6	FA	2043	ASN
6	FA	2095	GLN
6	FB	1612	ASN
6	FB	1790	ASN
6	FB	1851	GLN
6	FB	2043	ASN
6	FB	2052	HIS
6	FB	2063	GLN
6	FB	2076	HIS
6	FB	2080	GLN
6	FC	1599	HIS
6	FC	1791	ASN
6	FC	1827	GLN
6	FC	1985	GLN
6	FC	2031	HIS
6	FC	2052	HIS
6	FC	2076	HIS
6	FC	2097	GLN
6	FC	2107	GLN
6	FD	799	GLN
6	FD	907	ASN
6	FD	1001	ASN
6	FD	1242	GLN
6	FD	1267	GLN
6	FD	1427	ASN
6	FE	811	ASN
6	FE	885	ASN
6	FE	903	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	FE	907	ASN
6	FE	918	GLN
6	FE	1001	ASN
6	FE	1007	GLN
6	FE	1117	ASN
6	FE	1194	ASN
6	FE	1204	GLN
6	FE	1242	GLN
6	FE	1267	GLN
6	FE	1416	GLN
6	FE	1427	ASN
6	FF	811	ASN
6	FF	828	GLN
6	FF	907	ASN
6	FF	918	GLN
6	FF	919	GLN
6	FF	1007	GLN
6	FF	1194	ASN
6	FF	1242	GLN
6	FF	1245	ASN
7	GA	239	ASN
7	GA	721	GLN
7	GA	958	GLN
8	GB	47	GLN
8	GB	99	ASN
8	GB	336	ASN
7	GC	171	GLN
7	GC	260	ASN
7	GC	426	ASN
7	GC	586	GLN
7	GC	590	ASN
7	GC	670	ASN
7	GC	848	ASN
7	GC	964	GLN
8	GD	371	GLN
8	GD	484	GLN
8	GD	677	HIS
8	GD	731	GLN
8	GD	771	ASN
7	GE	197	HIS
7	GE	426	ASN
7	GE	590	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	GE	675	GLN
7	GE	878	GLN
7	GE	964	GLN
7	GE	969	GLN
8	GF	85	ASN
8	GF	90	HIS
8	GF	98	GLN
8	GF	158	GLN
8	GF	196	HIS
8	GF	328	HIS
8	GF	629	ASN
7	GG	173	ASN
7	GG	586	GLN
7	GG	845	ASN
7	GG	910	HIS
7	GG	943	GLN
8	GH	47	GLN
8	GH	115	GLN
8	GH	350	GLN
8	GH	484	GLN
8	GH	672	HIS
8	GH	683	GLN
8	GH	724	GLN
7	GI	620	HIS
7	GI	637	ASN
7	GI	670	ASN
7	GI	675	GLN
7	GI	848	ASN
7	GI	878	GLN
7	GI	910	HIS
8	GJ	115	GLN
8	GJ	211	GLN
8	GJ	327	HIS
8	GJ	336	ASN
8	GJ	397	ASN
8	GJ	482	ASN
8	GJ	724	GLN
7	GK	532	ASN
7	GK	837	HIS
7	GK	910	HIS
7	GK	969	GLN
8	GL	98	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	GL	196	HIS
8	GL	534	GLN
8	GL	683	GLN
8	GL	690	HIS
9	HA	603	HIS
9	HA	661	HIS
9	HA	791	GLN
9	HA	808	HIS
9	HA	840	HIS
9	HA	860	GLN
9	HB	401	GLN
9	HB	410	ASN
9	HB	661	HIS
9	HB	749	ASN
9	HB	762	HIS
9	HB	763	GLN
9	HB	791	GLN
9	HB	821	GLN
9	HB	860	GLN
9	HC	610	ASN
9	HC	612	GLN
9	HD	791	GLN
9	HD	808	HIS
10	IA	173	GLN
10	IA	311	GLN
10	IA	323	GLN
10	IA	336	GLN
10	IA	381	HIS
10	IA	494	HIS
10	IA	551	ASN
10	IA	757	ASN
10	IA	765	HIS
10	IA	874	ASN
10	IA	898	HIS
10	IA	943	ASN
10	IA	1123	ASN
10	IA	1212	ASN
10	IA	1237	GLN
10	IA	1257	HIS
10	IA	1320	GLN
10	IA	1411	GLN
10	IA	1417	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	IB	202	ASN
10	IB	205	GLN
10	IB	336	GLN
10	IB	396	ASN
10	IB	698	GLN
10	IB	757	ASN
10	IB	778	GLN
10	IB	864	GLN
10	IB	874	ASN
10	IB	943	ASN
10	IB	1055	GLN
10	IB	1098	HIS
10	IB	1123	ASN
10	IB	1179	ASN
10	IB	1212	ASN
10	IB	1417	GLN
10	IC	323	GLN
10	IC	355	GLN
10	IC	362	HIS
10	IC	400	HIS
10	IC	494	HIS
10	IC	765	HIS
10	IC	811	GLN
10	IC	943	ASN
10	IC	1094	ASN
10	IC	1111	GLN
10	IC	1123	ASN
10	IC	1212	ASN
10	IC	1245	GLN
10	IC	1266	ASN
10	IC	1378	GLN
11	JA	473	ASN
11	JA	915	GLN
11	JA	1072	HIS
11	JA	1213	GLN
11	JA	1539	ASN
11	JA	1591	HIS
11	JA	1638	ASN
11	JA	1781	GLN
11	JA	1799	GLN
11	JA	1854	HIS
11	JA	1871	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	JA	2003	HIS
11	JA	2076	ASN
11	JB	469	GLN
11	JB	503	HIS
11	JB	1468	GLN
11	JB	1604	HIS
11	JB	1656	GLN
11	JB	1657	GLN
11	JB	1781	GLN
11	JB	1799	GLN
11	JB	1802	HIS
11	JB	1870	HIS
11	JB	2072	GLN
11	JB	2122	GLN
11	JB	2268	HIS
11	JC	41	ASN
11	JC	101	ASN
11	JC	503	HIS
11	JC	523	ASN
11	JC	763	GLN
11	JC	1152	HIS
11	JC	1202	HIS
11	JC	1355	GLN
11	JC	1407	HIS
11	JC	1545	HIS
11	JC	1550	GLN
11	JC	1604	HIS
11	JC	1606	HIS
11	JC	1713	ASN
11	JC	1852	HIS
11	JC	1984	HIS
12	KA	216	GLN
12	KA	230	GLN
12	KA	298	GLN
12	KA	343	ASN
12	KA	383	HIS
12	KA	401	GLN
12	KA	593	HIS
12	KA	636	GLN
12	KA	696	GLN
12	KA	721	GLN
12	KB	669	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	KB	710	ASN
12	KC	331	GLN
12	KC	383	HIS
12	KC	665	HIS
12	KE	298	GLN
12	KE	392	GLN
12	KE	473	GLN
12	KE	516	HIS
12	KE	636	GLN
12	KE	665	HIS
12	KE	710	ASN
12	KF	516	HIS
12	KF	604	GLN
12	KF	636	GLN
12	KF	696	GLN
12	KG	397	GLN
12	KG	418	GLN
12	KG	531	GLN
12	KG	576	ASN
12	KG	636	GLN
13	LA	374	HIS
13	LA	422	GLN
13	LA	467	GLN
13	LA	480	GLN
13	LA	493	GLN
13	LA	506	GLN
13	LB	377	GLN
13	LB	491	GLN
13	LC	353	ASN
13	LC	491	GLN
13	LC	493	GLN
13	LE	480	GLN
13	LE	521	ASN
13	LF	374	HIS
13	LG	491	GLN
13	LH	493	GLN
13	LI	343	GLN
13	LI	422	GLN
13	LI	468	HIS
13	LI	493	GLN
13	LI	506	GLN
13	LJ	521	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	LK	506	GLN
13	LL	343	GLN
13	LL	364	ASN
13	LL	493	GLN
13	LN	364	ASN
13	LO	374	HIS
14	MA	241	GLN
14	ME	208	GLN
14	ME	224	ASN
14	MF	229	GLN
14	MF	283	GLN
14	MF	323	GLN
14	MI	227	GLN
14	MJ	246	ASN
14	MJ	316	GLN
15	NA	589	ASN
15	NA	597	GLN
15	NA	686	ASN
15	NA	744	GLN
15	NA	810	GLN
15	NA	1158	HIS
15	NB	480	ASN
15	NB	609	GLN
15	NB	724	ASN
15	NB	735	HIS
15	NB	736	GLN
15	NB	1121	ASN
15	NB	1188	HIS
15	NB	1398	ASN
15	NB	1536	GLN
15	NB	1540	ASN
15	NC	566	GLN
15	NC	609	GLN
15	NC	758	GLN
15	NC	783	GLN
15	NC	810	GLN
15	NC	871	GLN
15	NC	1018	GLN
15	NC	1398	ASN
15	NC	1462	GLN
15	ND	540	ASN
15	ND	810	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	ND	871	GLN
15	ND	1105	HIS
15	ND	1403	GLN
15	ND	1452	GLN
16	OA	131	ASN
16	OA	197	HIS
16	OA	217	GLN
16	OA	266	GLN
16	OA	745	ASN
16	OB	308	GLN
16	OB	310	ASN
16	OB	745	ASN
16	OB	1086	GLN
16	OC	184	ASN
16	OC	745	ASN
16	OC	1060	GLN
17	PC	266	HIS
18	QA	172	GLN
18	QB	172	GLN
18	QD	76	HIS
19	RA	171	GLN
19	RB	26	HIS
19	RC	26	HIS
19	RC	133	GLN
19	RC	171	GLN
19	RD	133	GLN
20	SA	9	GLN
20	SB	112	ASN
20	SC	108	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

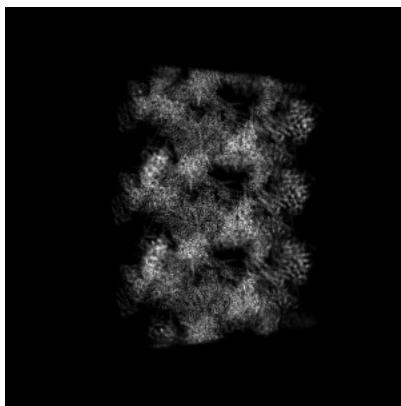
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72716. These allow visual inspection of the internal detail of the map and identification of artifacts.

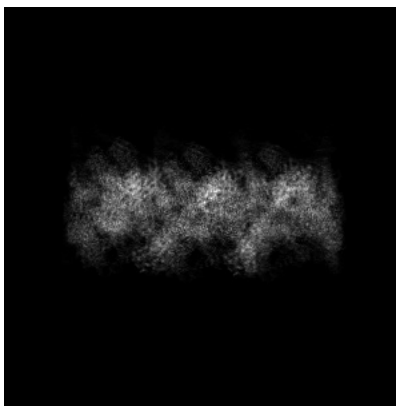
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

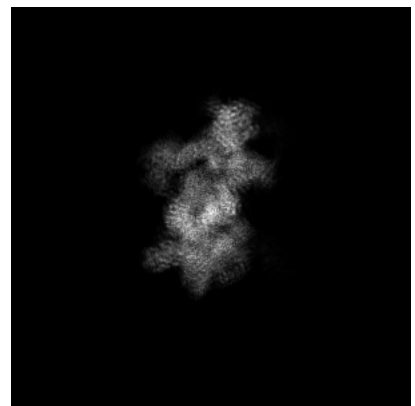
6.1.1 Primary map



X

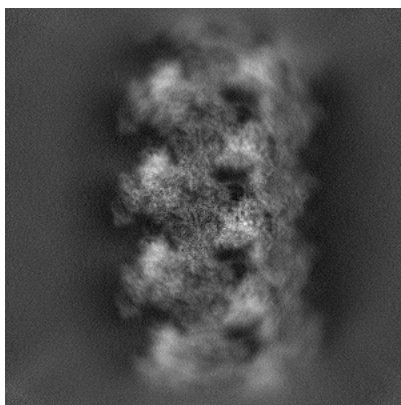


Y

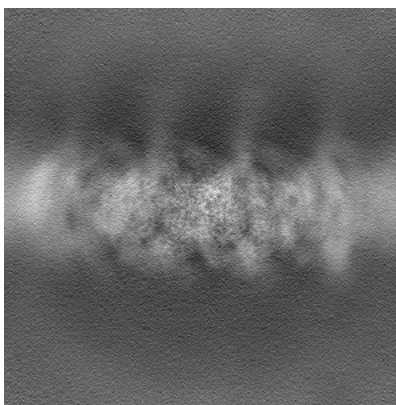


Z

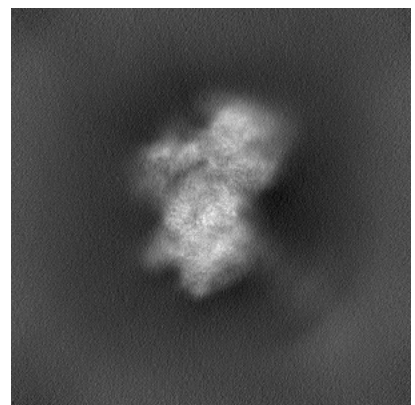
6.1.2 Raw map



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: 256

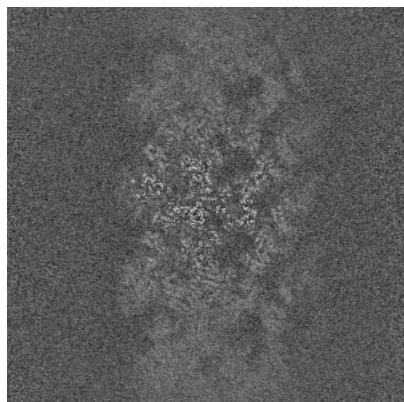


Y Index: 256

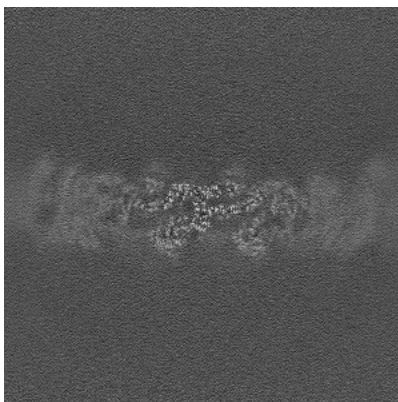


Z Index: 256

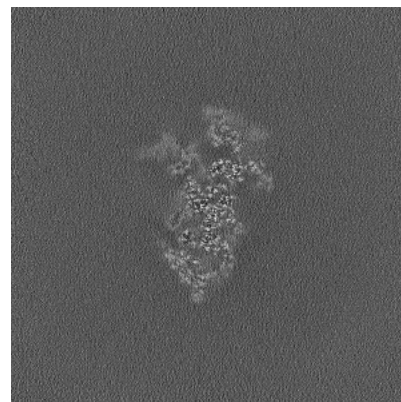
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

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

6.3 Largest variance slices [i](#)

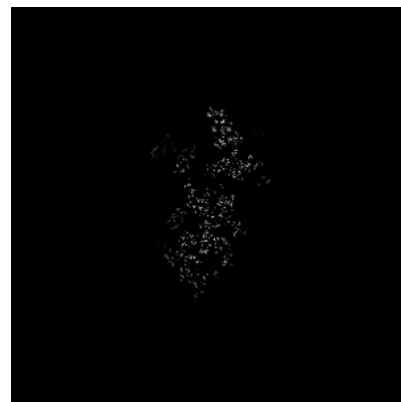
6.3.1 Primary map



X Index: 279

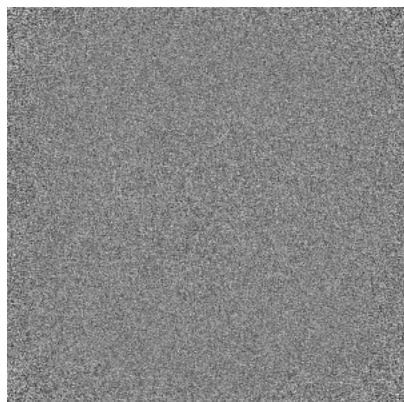


Y Index: 249

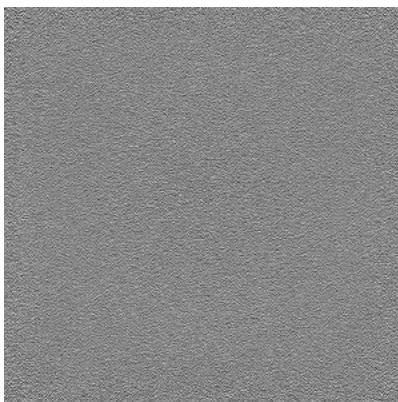


Z Index: 258

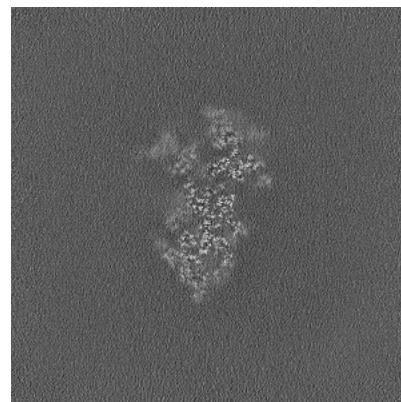
6.3.2 Raw map



X Index: 0



Y Index: 0

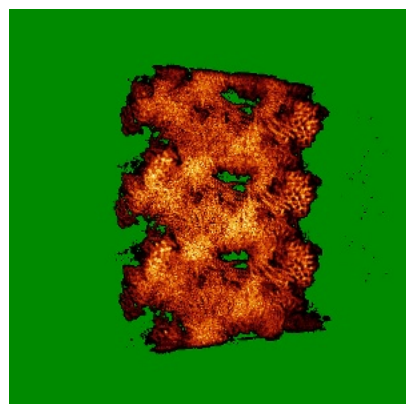


Z Index: 258

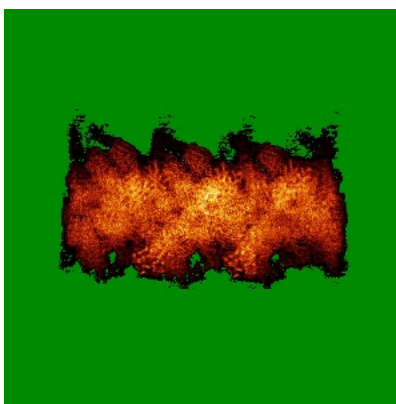
The images above show the largest variance slices of the map in three orthogonal directions.

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

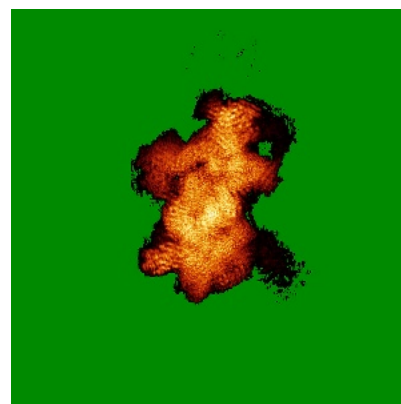
6.4.1 Primary map



X

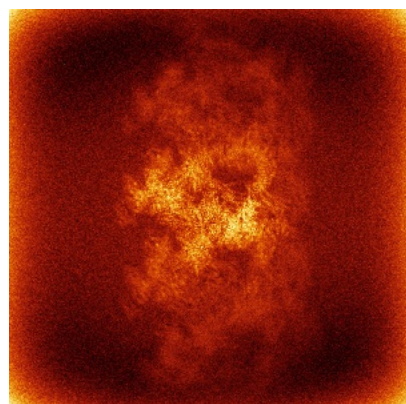


Y

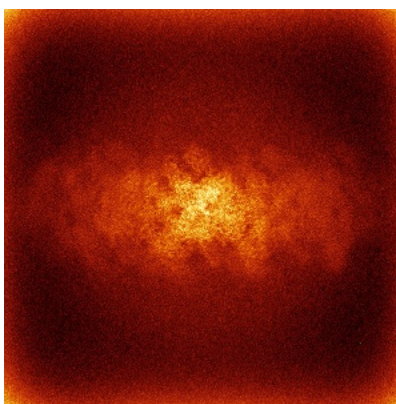


Z

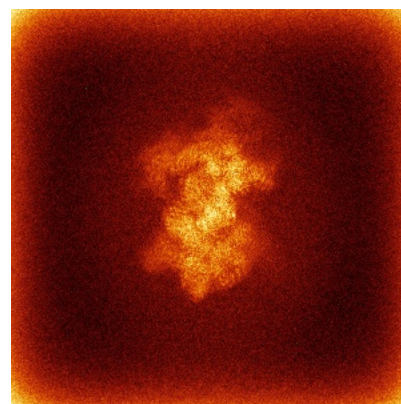
6.4.2 Raw map



X



Y

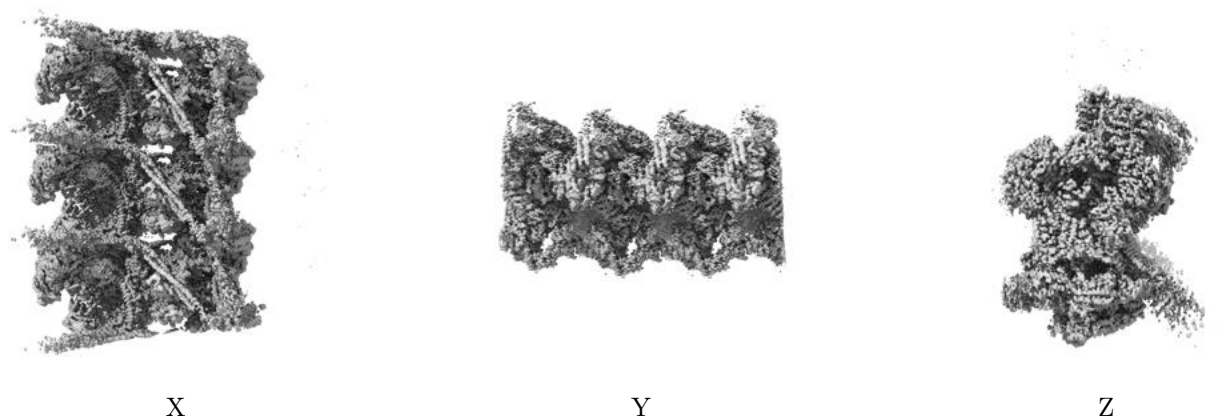


Z

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.

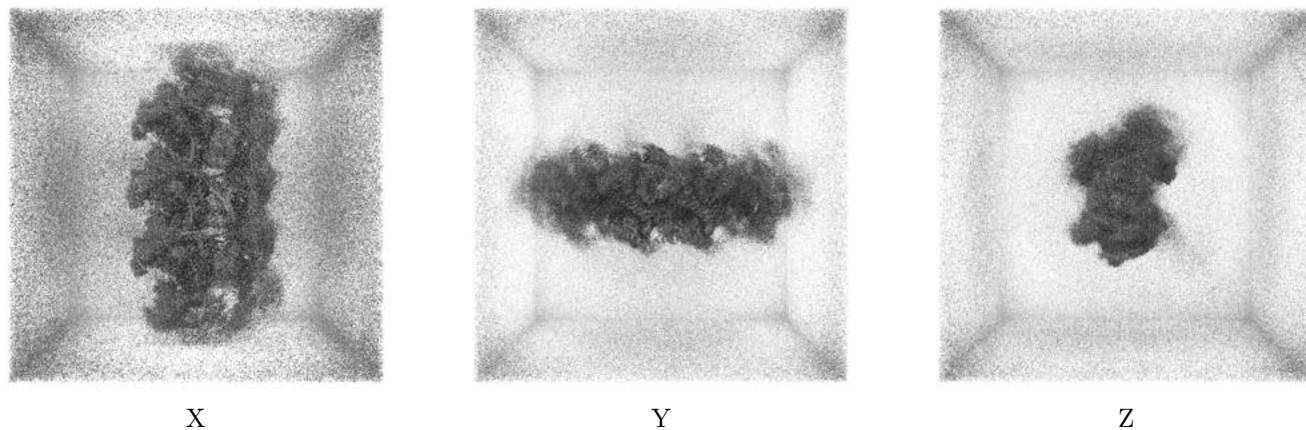
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

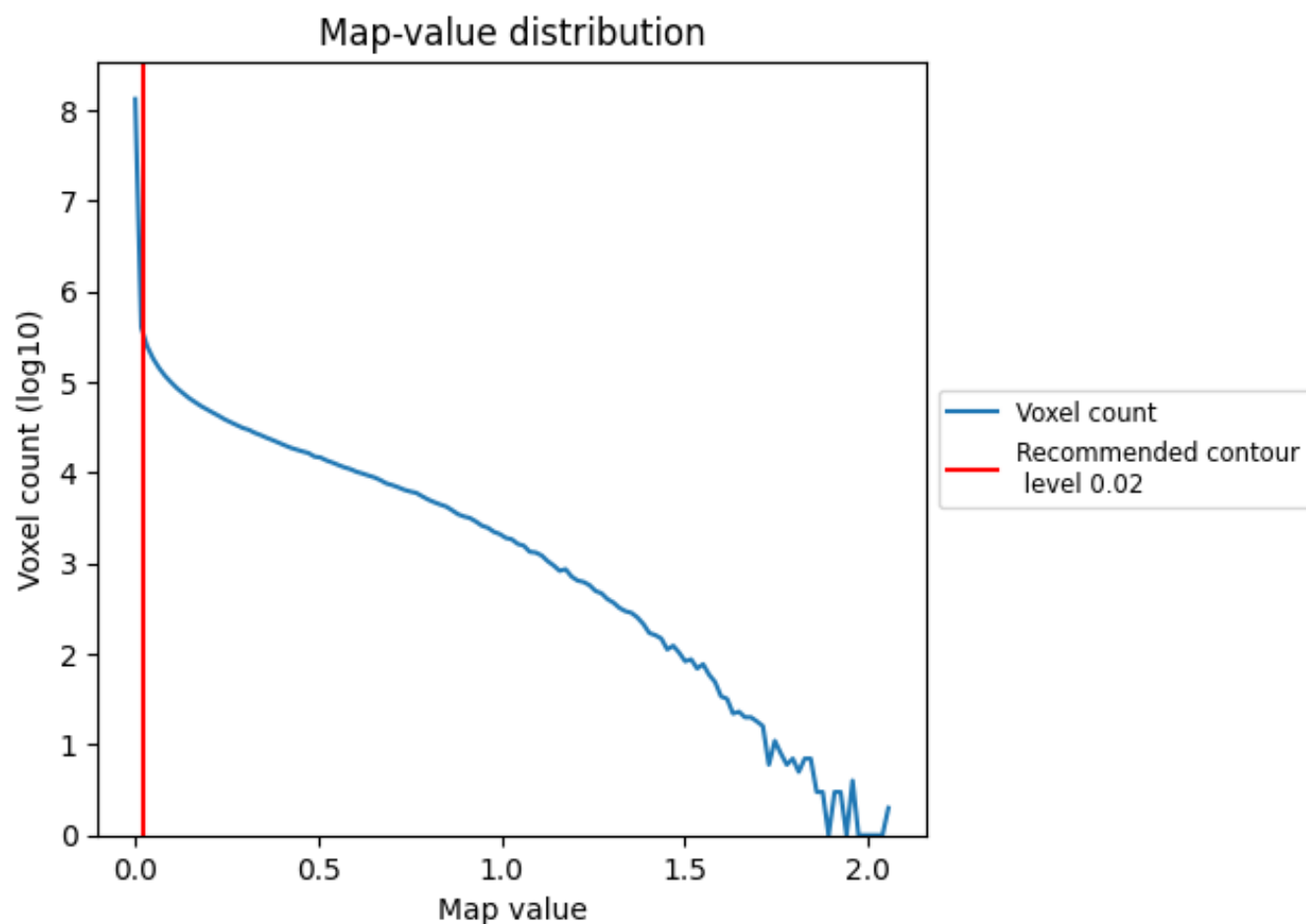
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

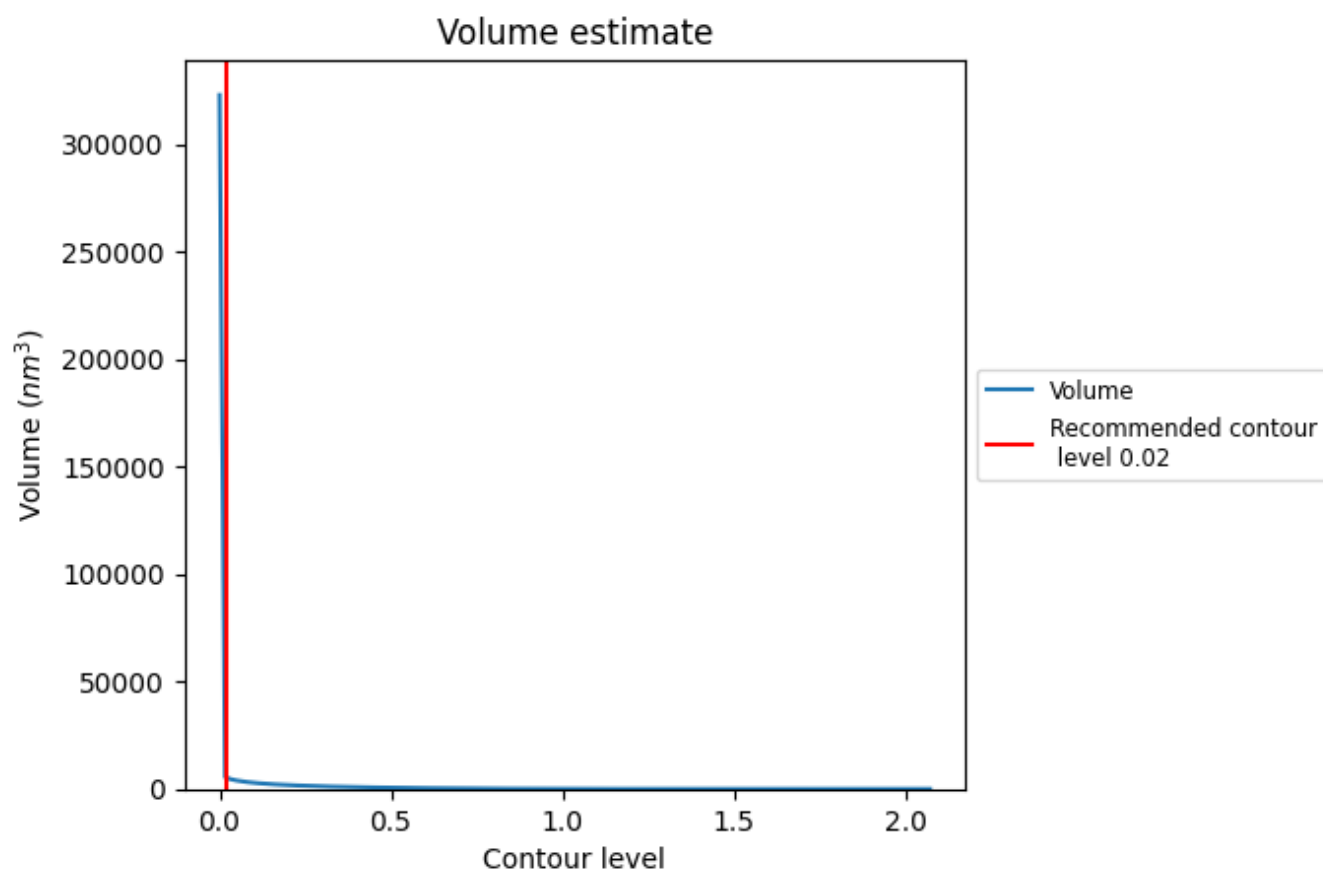
This section contains the results of statistical analysis of the map.

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.

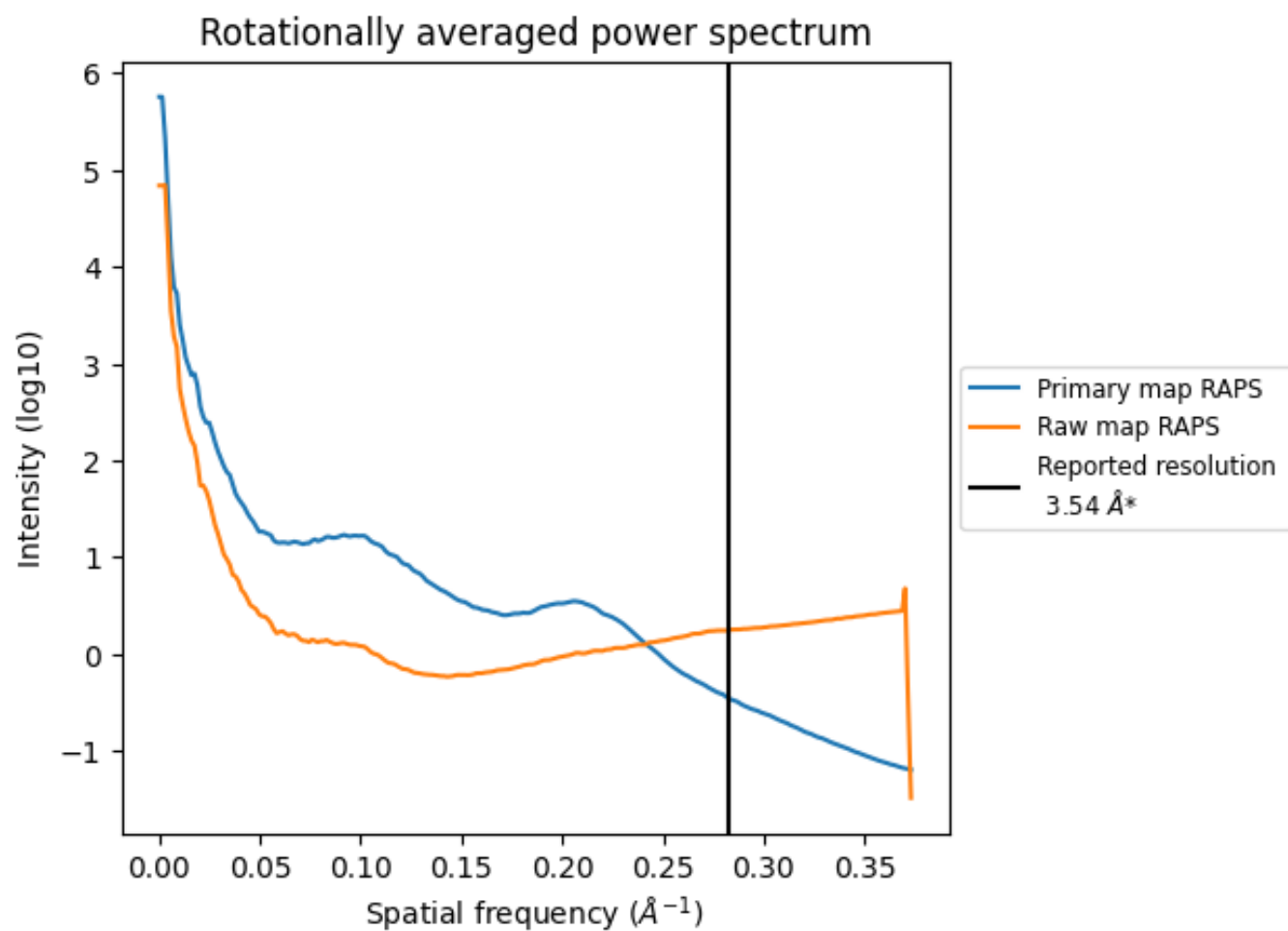
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5300 nm^3 ; this corresponds to an approximate mass of 4787 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

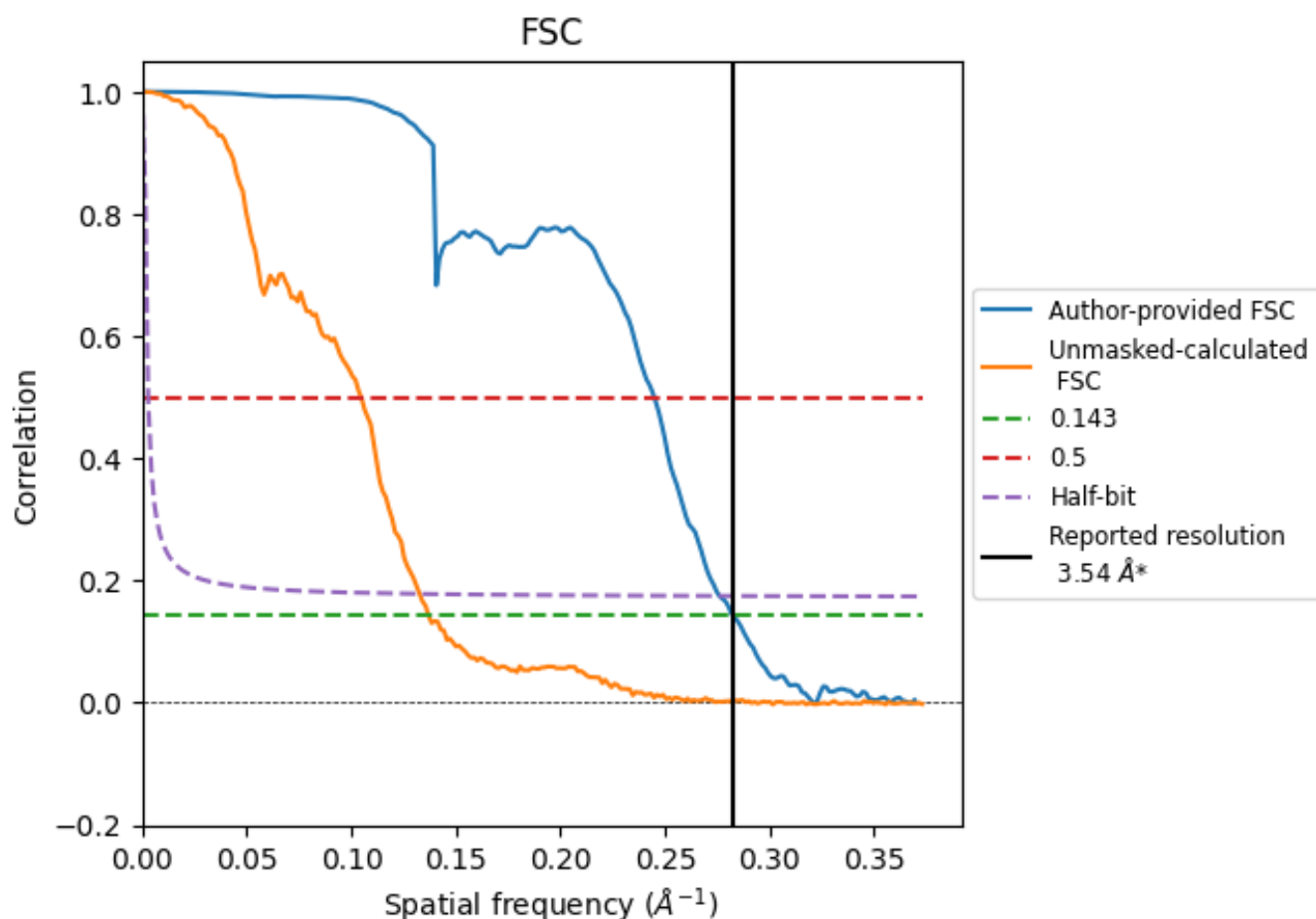


*Reported resolution corresponds to spatial frequency of 0.282 $\text{\AA}^{-1}$

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 0.282 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

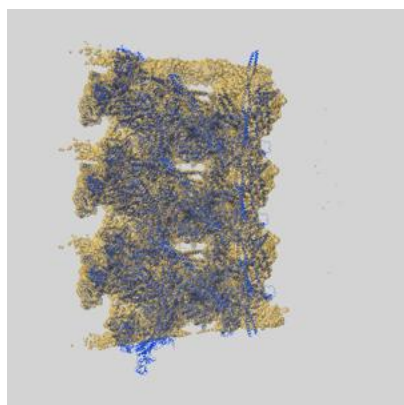
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	3.54	4.08	3.62
Unmasked-calculated*	7.30	9.55	7.53

*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 7.30 differs from the reported value 3.54 by more than 10 %

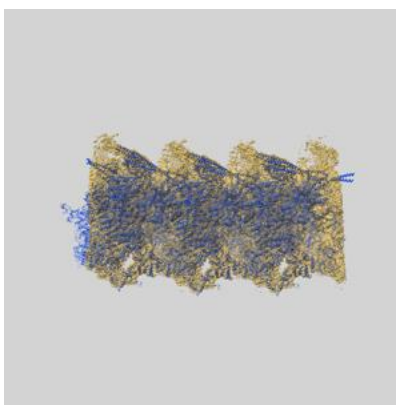
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72716 and PDB model 9YA0. Per-residue inclusion information can be found in section [3](#) on page [21](#).

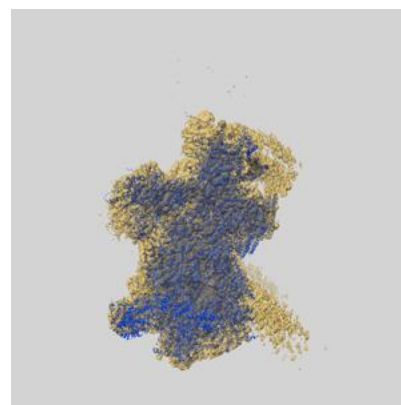
9.1 Map-model overlay [i](#)



X



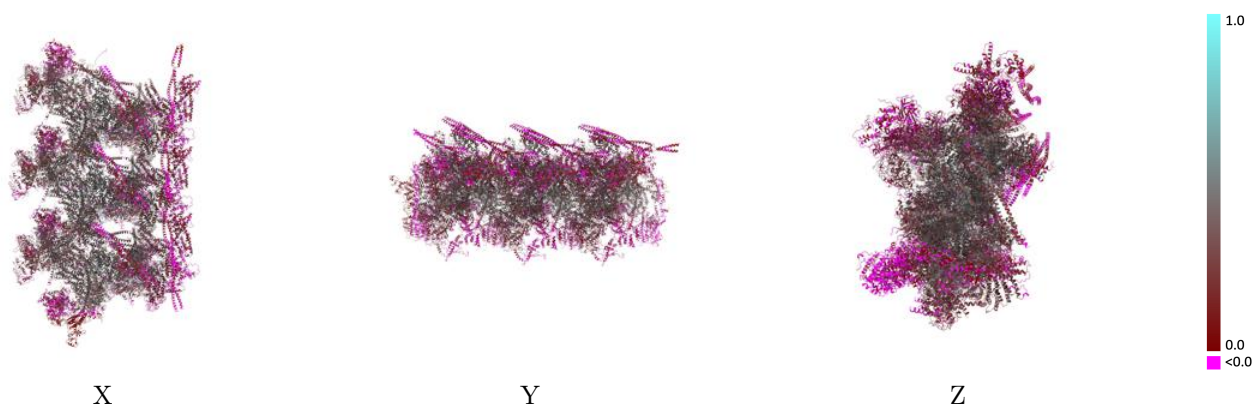
Y



Z

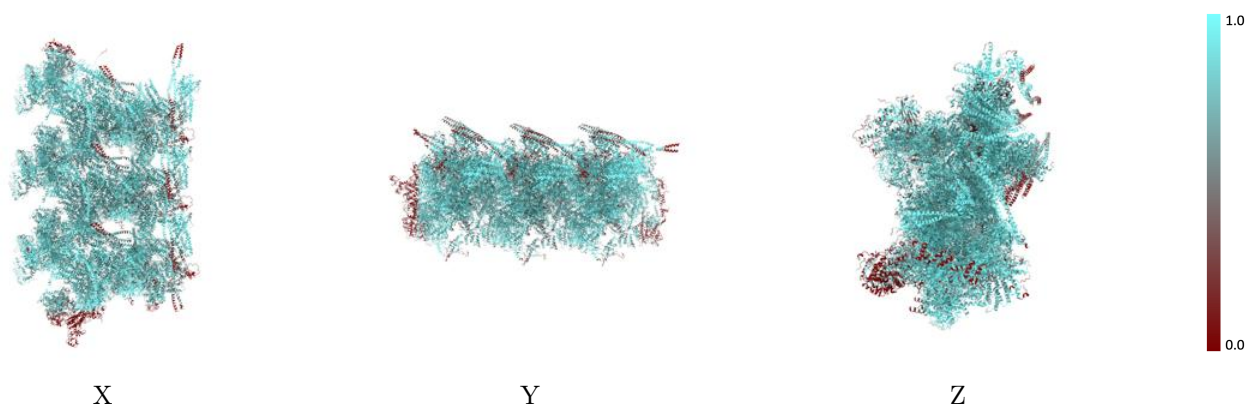
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



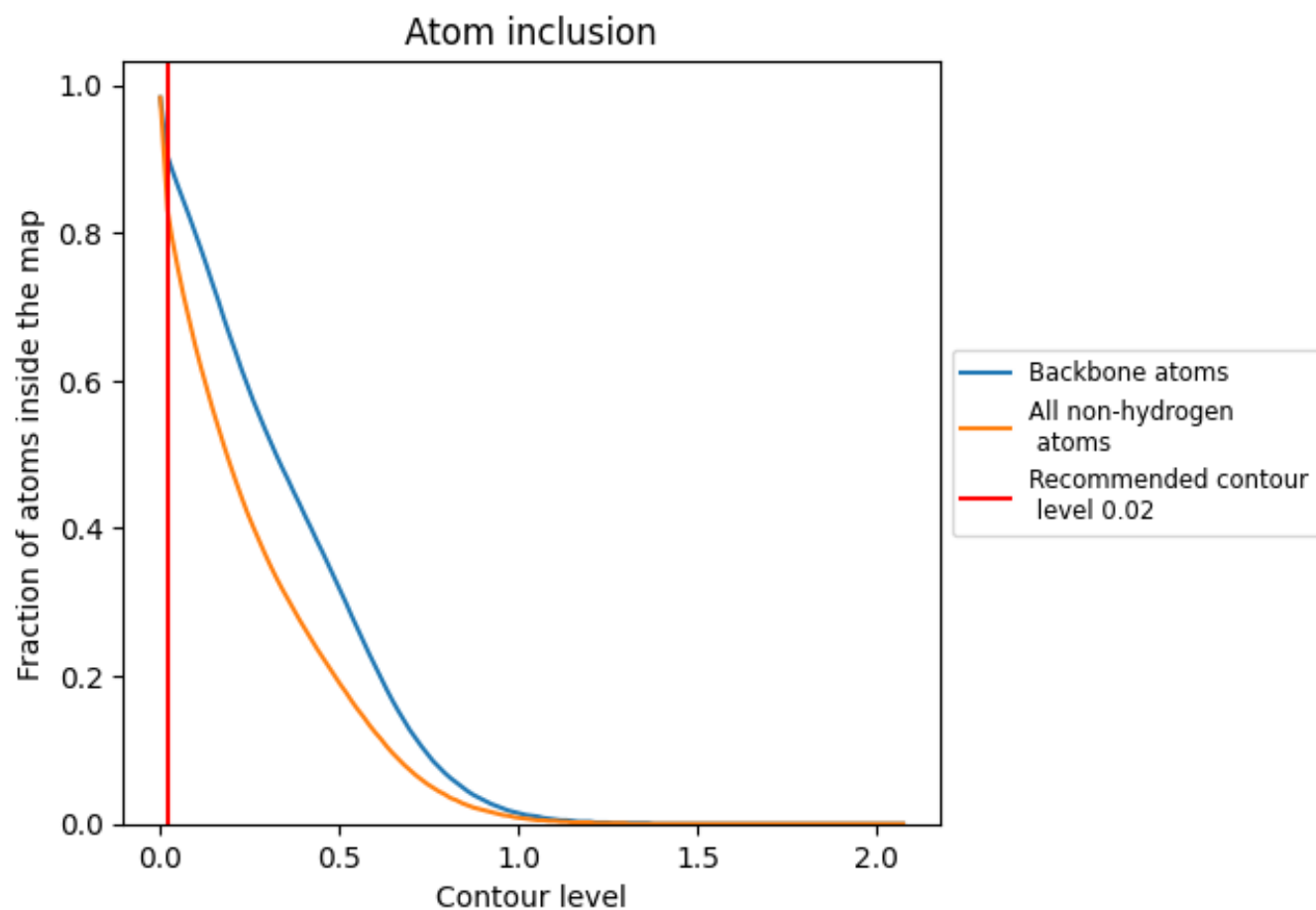
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 83% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8310	 0.2630
AA	 0.8810	 0.3180
AB	 0.9330	 0.3690
AC	 0.9200	 0.3960
AD	 0.9530	 0.4090
AE	 0.9020	 0.3070
AF	 0.9380	 0.3630
AG	 0.9310	 0.3870
AH	 0.9530	 0.4060
AI	 0.9070	 0.3080
AJ	 0.8560	 0.3270
AK	 0.8170	 0.3280
AL	 0.6320	 0.2580
BA	 0.9260	 0.3830
BB	 0.9490	 0.3730
BC	 0.9490	 0.3730
CA	 0.8220	 0.2550
CB	 0.8550	 0.2550
CC	 0.8530	 0.2500
CE	 0.7720	 0.1770
CF	 0.8240	 0.1880
CG	 0.8280	 0.1920
CI	 0.8090	 0.2280
CJ	 0.8350	 0.2300
CL	 0.8540	 0.2330
DA	 0.8870	 0.1810
DB	 0.9220	 0.1760
DC	 0.9110	 0.1670
DD	 0.8820	 0.1360
DE	 0.9150	 0.1430
DF	 0.9040	 0.1420
EA	 0.9520	 0.3910
EB	 0.9290	 0.3910
EC	 0.9460	 0.3880
FA	 0.9000	 0.3750



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
FB	 0.9120	 0.3640
FC	 0.9200	 0.3610
FD	 0.8650	 0.2500
FE	 0.8780	 0.2470
FF	 0.8540	 0.2580
GA	 0.8260	 0.3120
GB	 0.8810	 0.2880
GC	 0.8020	 0.2430
GD	 0.8730	 0.2910
GE	 0.8360	 0.2410
GF	 0.6990	 0.1670
GG	 0.8400	 0.3030
GH	 0.6860	 0.1480
GI	 0.8290	 0.2390
GJ	 0.7230	 0.1710
GK	 0.8290	 0.3120
GL	 0.7020	 0.1710
HA	 0.9060	 0.3390
HB	 0.8960	 0.3370
HC	 0.9100	 0.3600
HD	 0.8810	 0.2960
IA	 0.9190	 0.3510
IB	 0.9380	 0.3420
IC	 0.9350	 0.3450
JA	 0.8950	 0.3330
JB	 0.8520	 0.3040
JC	 0.9080	 0.3230
KA	 0.8400	 0.1560
KB	 0.8560	 0.1610
KC	 0.7530	 0.1260
KE	 0.5630	 0.0310
KF	 0.6210	 0.0460
KG	 0.6070	 0.0470
LA	 0.7380	 0.1890
LB	 0.7550	 0.1940
LC	 0.6430	 0.1780
LD	 0.6610	 0.1620
LE	 0.7910	 0.2390
LF	 0.7300	 0.2010
LG	 0.8930	 0.3760
LH	 0.9610	 0.4310
LI	 0.7700	 0.1980

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
LJ	 0.7510	 0.1710
LK	 0.6280	 0.1670
LL	 0.6600	 0.1590
LM	 0.5200	 0.0610
LN	 0.5370	 0.0240
LO	 0.5640	 0.0570
LP	 0.5260	 0.0490
MA	 0.9030	 0.2890
MB	 0.9190	 0.2890
MC	 0.7890	 0.3380
MD	 0.9200	 0.3960
ME	 0.9190	 0.2600
MF	 0.9420	 0.2670
MG	 0.8140	 0.3300
MH	 0.9440	 0.3720
MI	 0.9240	 0.2660
MJ	 0.9220	 0.2580
MK	 0.8260	 0.3310
ML	 0.9420	 0.3690
NA	 0.8300	 0.0930
NB	 0.3040	 0.0020
NC	 0.8310	 0.0940
ND	 0.3900	 0.0160
OA	 0.8440	 0.2900
OB	 0.8390	 0.2790
OC	 0.8640	 0.2850
PA	 0.7550	 0.2530
PB	 0.7980	 0.2450
PC	 0.8120	 0.2690
QA	 0.8610	 0.2020
QB	 0.5000	 0.1140
QC	 0.8330	 0.1740
QD	 0.8350	 0.2000
RA	 0.7650	 0.0940
RB	 0.6230	 0.0540
RC	 0.7670	 0.0940
RD	 0.6930	 0.1060
SA	 0.8170	 0.1530
SB	 0.4520	 0.0920
SC	 0.7500	 0.1340
SD	 0.8090	 0.1560