



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 08:44 AM UTC

PDB ID : 7EG9 / pdb_00007eg9
EMDB ID : EMD-31109
Title : TFIID-based intermediate PIC on SCP promoter
Authors : Chen, X.; Qi, Y.; Wang, X.; Wu, Z.; Li, J.; Xu, Y.
Deposited on : 2021-03-24
Resolution : 3.70 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:

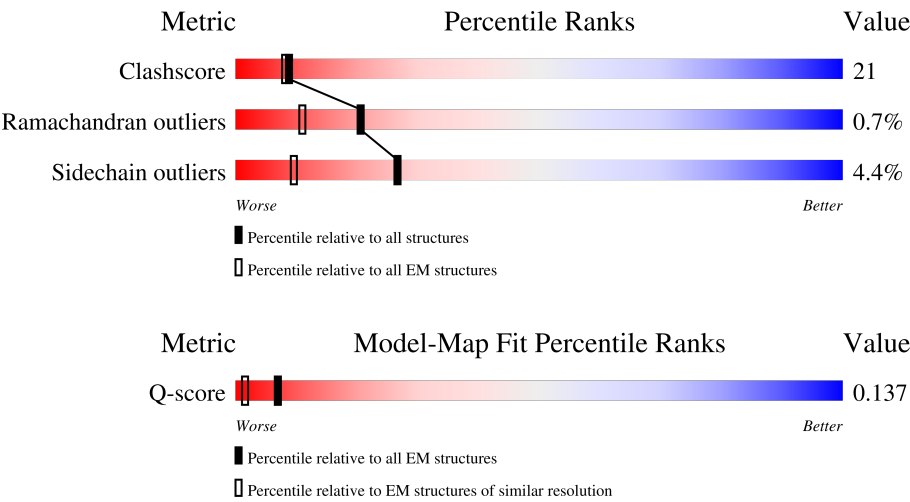
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	A	1872	
2	B	1199	
3	D	1085	
3	d	1085	

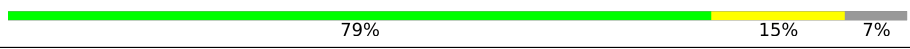
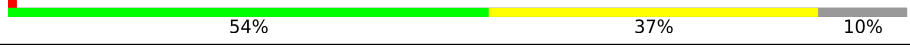
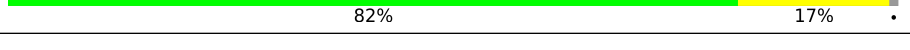
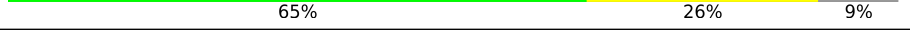
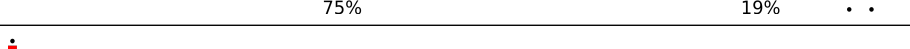
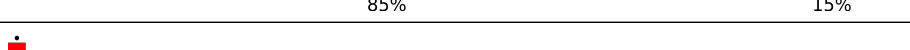
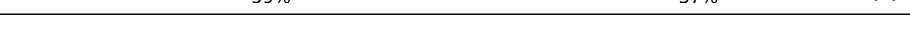
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	E	800	
4	e	800	
5	F	677	
5	f	677	
6	G	349	
7	H	310	
8	I	264	
8	i	264	
9	J	218	
9	j	218	
10	L	161	
10	l	161	
11	O	109	
12	P	339	
13	Q	376	
14	R	316	
15	S	517	
16	T	249	
17	U	439	
18	V	291	
19	X	79	
20	Y	79	
21	c	929	
22	k	211	
23	m	124	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
24	o	1970	
25	p	1174	
26	q	275	
27	r	142	
28	s	210	
29	t	127	
30	v	150	
31	w	125	
32	x	67	
33	y	117	
34	z	58	
35	u	172	

2 Entry composition

There are 37 unique types of molecules in this entry. The entry contains 84318 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 Transcription initiation factor TFIID subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	602	Total	C	N	O	S	0	0
			4927	3142	858	899	28		

- Molecule 2 is a protein called Transcription initiation factor TFIID subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	963	Total	C	N	O	S	0	0
			7796	5011	1315	1412	58		

- Molecule 3 is a protein called Transcription initiation factor TFIID subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	163	Total	C	N	O	S	0	0
			1361	848	255	254	4		
3	d	158	Total	C	N	O	S	0	0
			1307	814	238	252	3		

- Molecule 4 is a protein called Transcription initiation factor TFIID subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	546	Total	C	N	O	S	0	0
			4364	2766	757	820	21		
4	e	539	Total	C	N	O	S	0	0
			4327	2746	748	814	19		

- Molecule 5 is a protein called Transcription initiation factor TFIID subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	404	Total	C	N	O	S	0	0
			3081	1954	537	572	18		
5	f	403	Total	C	N	O	S	0	0
			3081	1954	533	576	18		

- Molecule 6 is a protein called Transcription initiation factor TFIID subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	145	Total	C	N	O	S	0	0
			1180	748	217	211	4		

- Molecule 7 is a protein called Transcription initiation factor TFIID subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	209	Total	C	N	O	S	0	0
			1633	1034	283	311	5		

- Molecule 8 is a protein called Transcription initiation factor TFIID subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	120	Total	C	N	O	S	0	0
			959	610	166	177	6		
8	i	121	Total	C	N	O	S	0	0
			967	615	167	178	7		

- Molecule 9 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	89	Total	C	N	O	S	0	0
			709	457	114	134	4		
9	j	95	Total	C	N	O	S	0	0
			759	488	124	143	4		

- Molecule 10 is a protein called Transcription initiation factor TFIID subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	76	Total	C	N	O	S	0	0
			622	388	109	122	3		
10	l	107	Total	C	N	O	S	0	0
			876	547	158	166	5		

- Molecule 11 is a protein called Transcription initiation factor IIA subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	97	Total	C	N	O	S	0	0
			771	491	133	145	2		

- Molecule 12 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	177	Total	C	N	O	S	0	0
			1412	918	249	238	7		

- Molecule 13 is a protein called Transcription initiation factor IIA subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	122	Total	C	N	O	S	0	0
			996	623	162	207	4		

- Molecule 14 is a protein called Transcription initiation factor IIB.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	248	Total	C	N	O	S	0	0
			1913	1200	338	358	17		

- Molecule 15 is a protein called General transcription factor IIF subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	134	Total	C	N	O	S	0	0
			1101	698	199	202	2		

- Molecule 16 is a protein called General transcription factor IIF subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	103	Total	C	N	O	S	0	0
			789	492	142	154	1		

- Molecule 17 is a protein called General transcription factor IIE subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	179	Total	C	N	O	S	0	0
			1476	932	261	272	11		

- Molecule 18 is a protein called Transcription initiation factor IIE subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	172	Total	C	N	O	S	0	0
			1400	890	242	264	4		

- Molecule 19 is a DNA chain called DNA (79-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
19	X	71	Total	C	N	O	P	0	0
			1470	691	287	421	71		

- Molecule 20 is a DNA chain called DNA (79-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	71	Total	C	N	O	P	0	0
			1441	683	256	431	71		

- Molecule 21 is a protein called Transcription initiation factor TFIID subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	c	127	Total	C	N	O	S	0	0
			1011	638	174	193	6		

- Molecule 22 is a protein called Transcription initiation factor TFIID subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	k	98	Total	C	N	O	S	0	0
			785	499	142	139	5		

- Molecule 23 is a protein called Transcription initiation factor TFIID subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	m	87	Total	C	N	O	S	0	0
			724	456	131	131	6		

- Molecule 24 is a protein called RPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	o	1427	Total	C	N	O	S	0	0
			11308	7114	2023	2099	72		

- Molecule 25 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	p	1134	Total	C	N	O	S	0	0
			9062	5732	1595	1671	64		

- Molecule 26 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	q	257	Total	C	N	O	S	0	0
			2059	1294	351	408	6		

- Molecule 27 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	r	128	Total	C	N	O	S	0	0
			1005	632	172	197	4		

- Molecule 28 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	s	209	Total	C	N	O	S	0	0
			1720	1089	300	323	8		

- Molecule 29 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	t	79	Total	C	N	O	S	0	0
			635	406	108	116	5		

- Molecule 30 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	v	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 31 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	w	114	Total	C	N	O	S	0	0
			927	571	166	179	11		

- Molecule 32 is a protein called RPB10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	x	64	Total	C	N	O	S	0	0
			507	328	86	87	6		

- Molecule 33 is a protein called RNA_pol_L_2 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	y	117	Total	C	N	O	S	0	0
			937	604	154	177	2		

- Molecule 34 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	z	44	Total	C	N	O	S	0	0
			372	231	72	63	6		

- Molecule 35 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	u	171	Total	C	N	O	S	0	0
			1351	875	219	249	8		

- Molecule 36 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
36	R	1	Total	Zn	0
			1	1	
36	U	1	Total	Zn	0
			1	1	
36	o	2	Total	Zn	0
			2	2	
36	p	1	Total	Zn	0
			1	1	
36	q	1	Total	Zn	0
			1	1	
36	w	2	Total	Zn	0
			2	2	
36	x	1	Total	Zn	0
			1	1	
36	z	1	Total	Zn	0
			1	1	

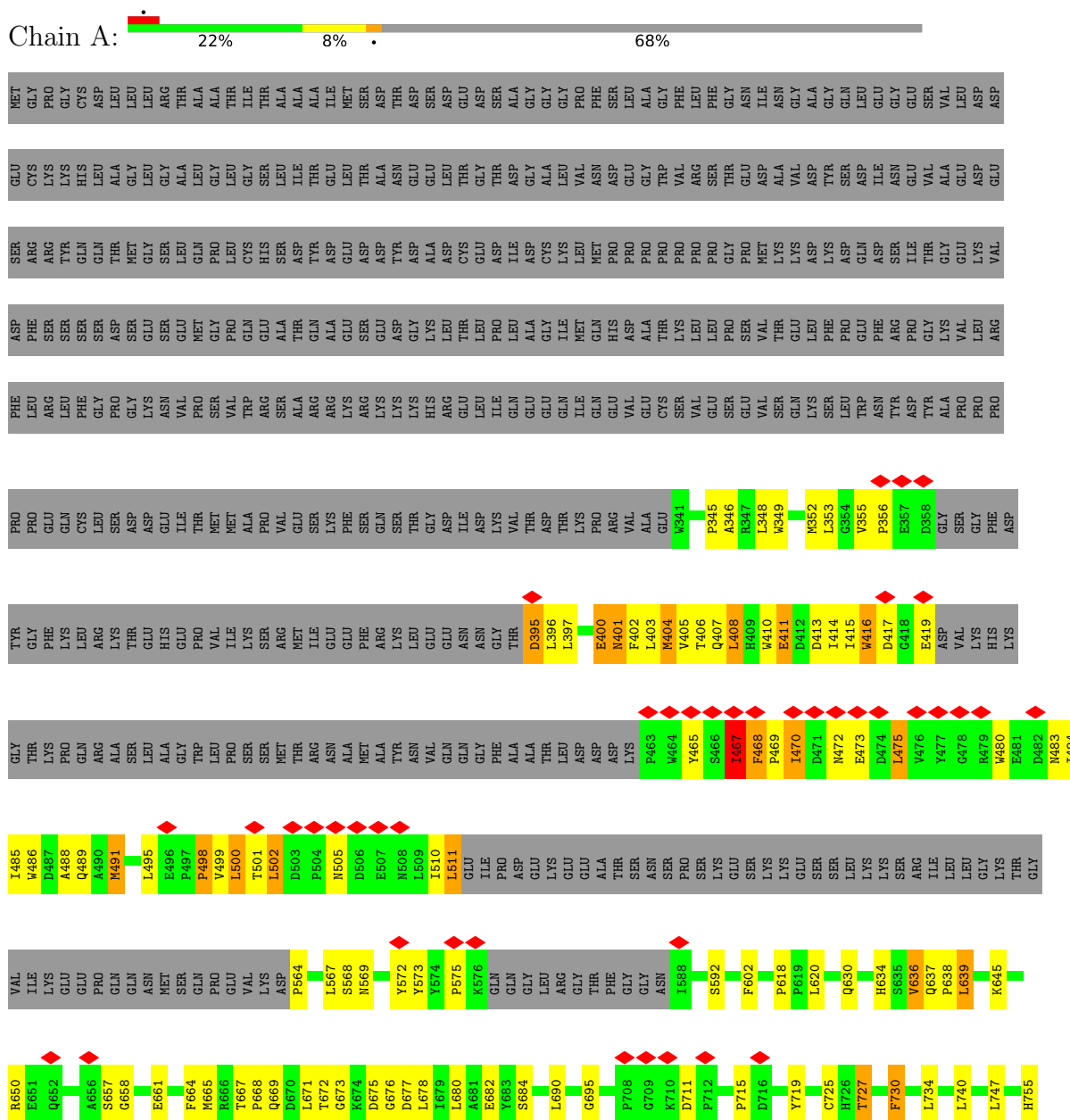
- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	o	1	Total	Mg	0
			1	1	

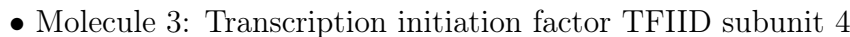
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

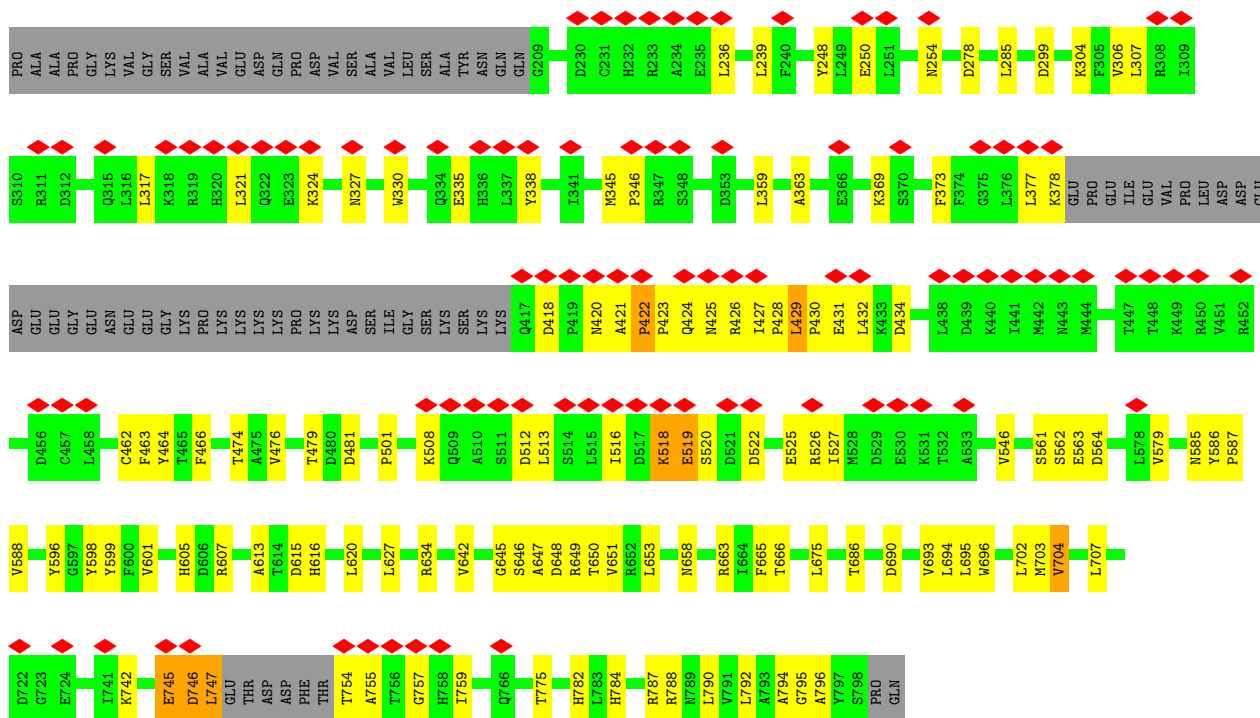
- Molecule 1: Transcription initiation factor TFIID subunit 1



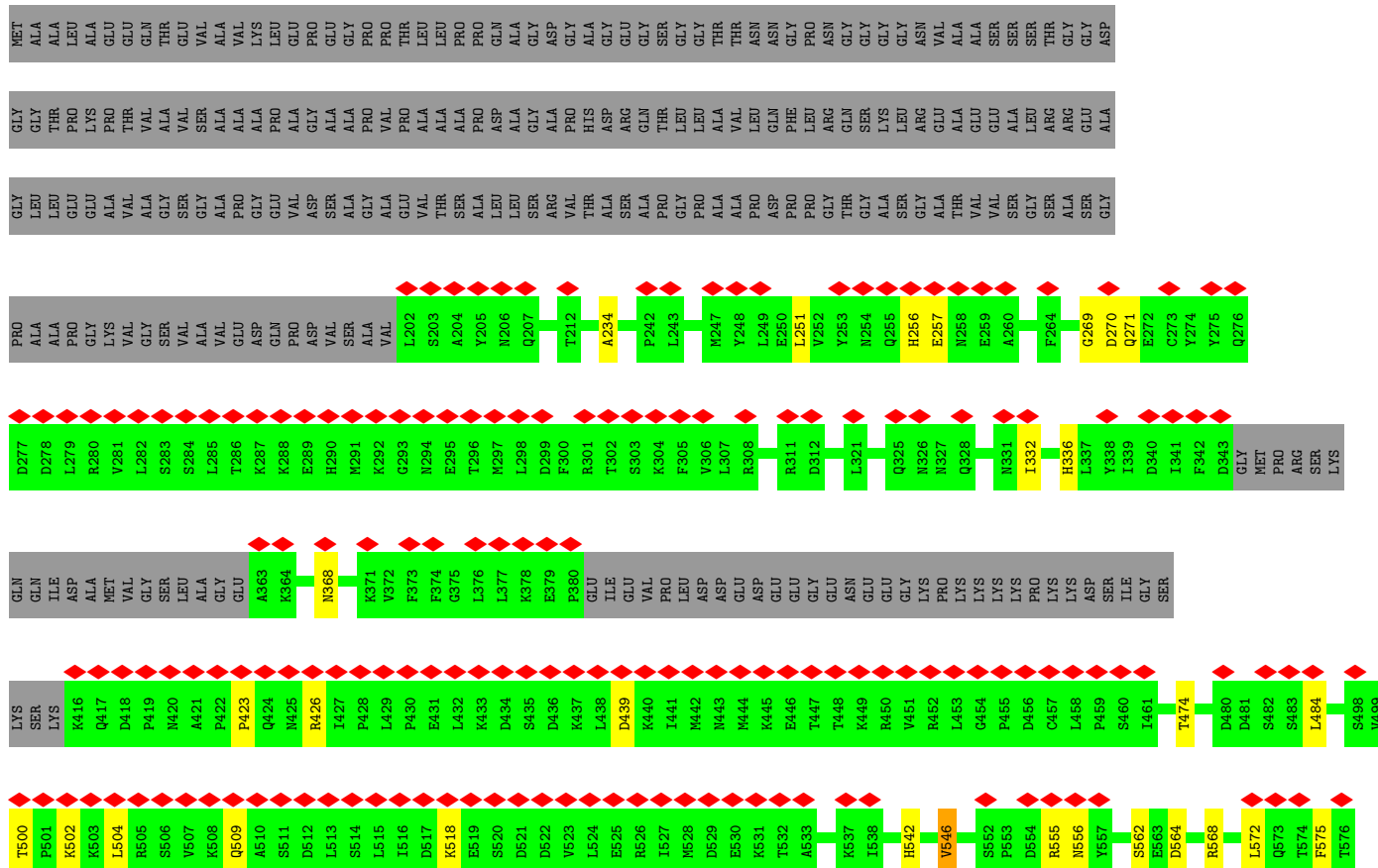


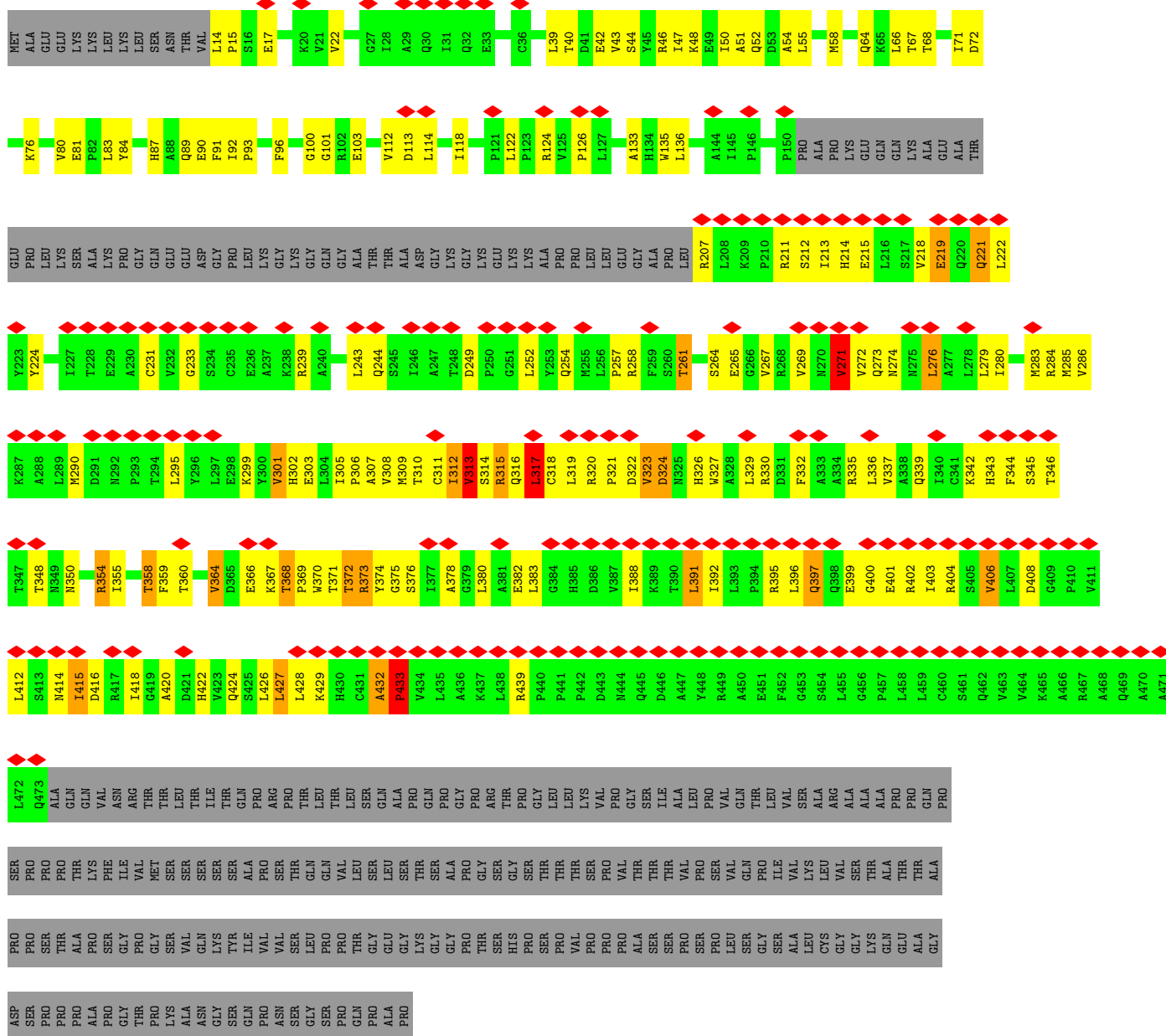
[illegible]

[illegible]

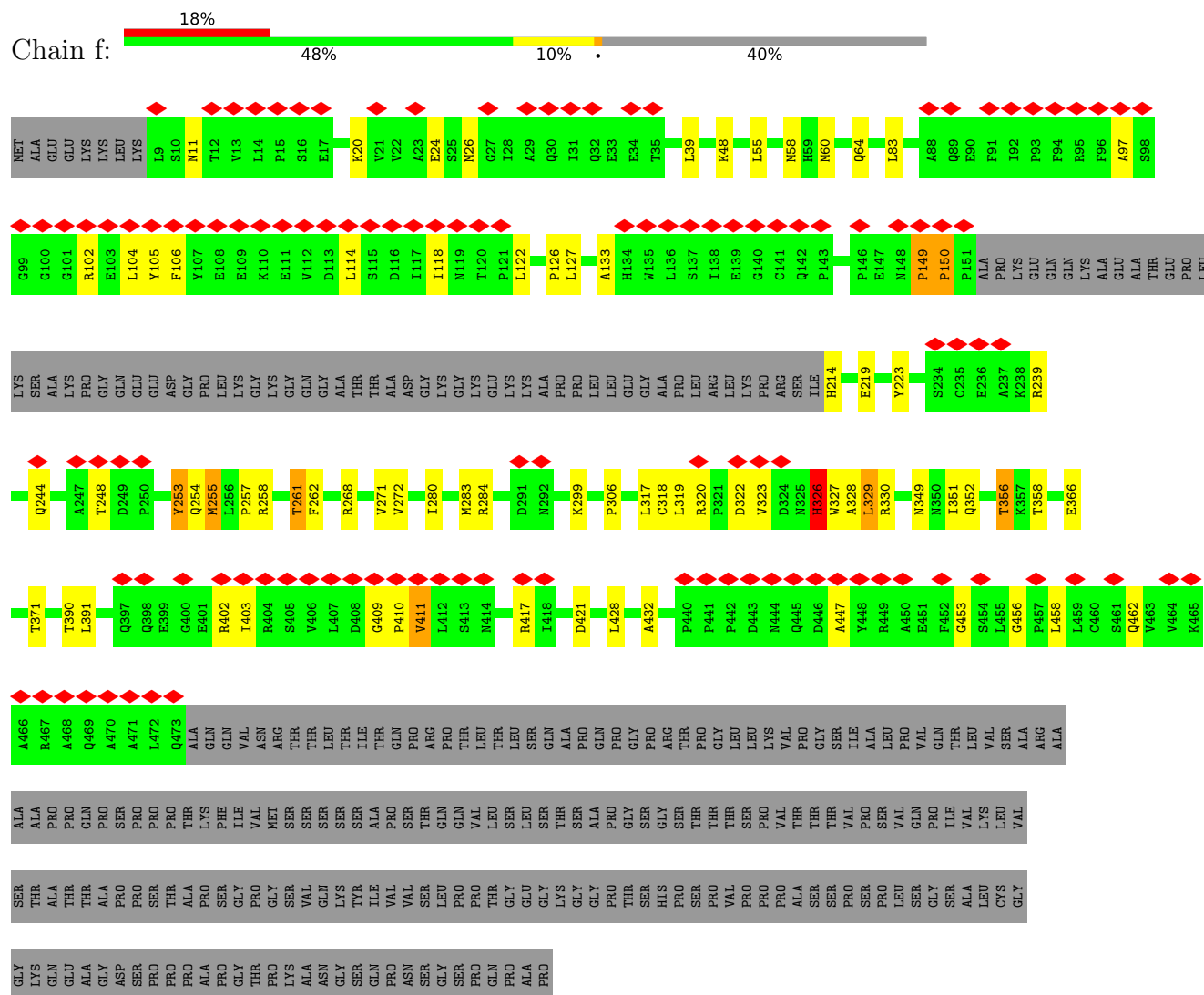


- Molecule 4: Transcription initiation factor TFIID subunit 5

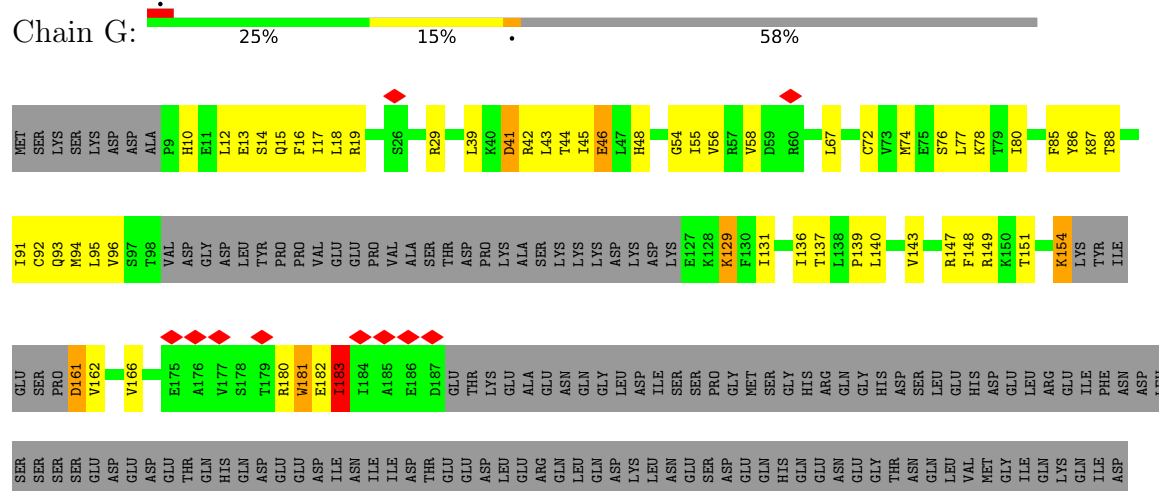




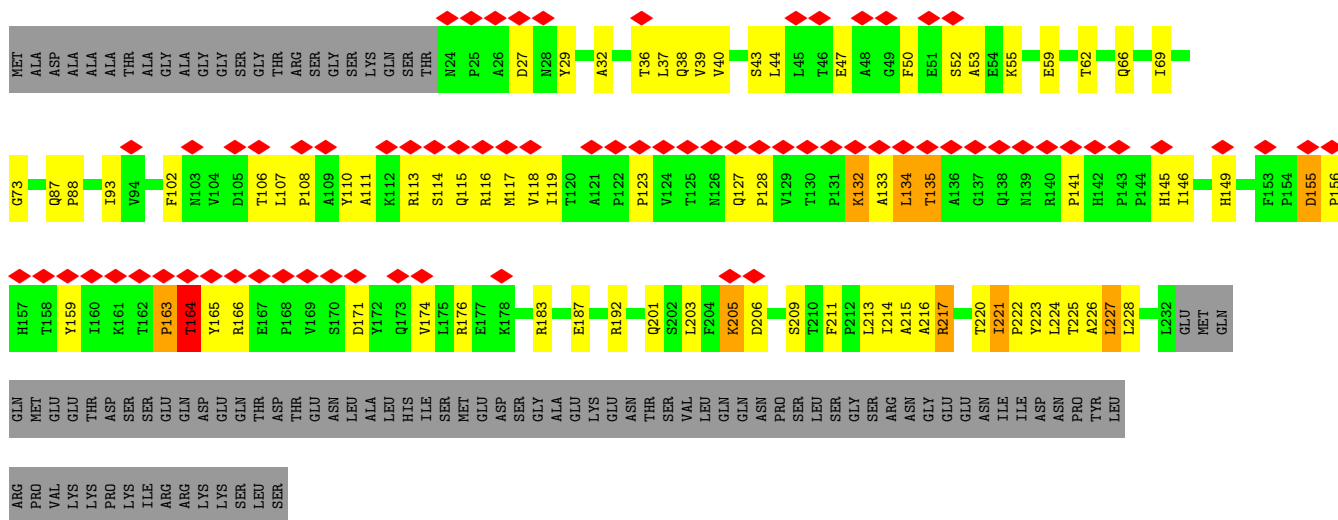
Chain f:



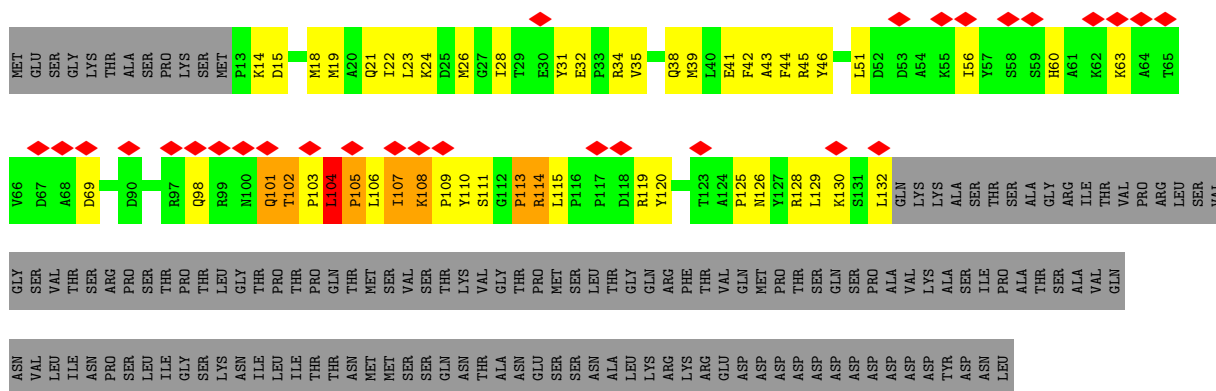
Chain G:



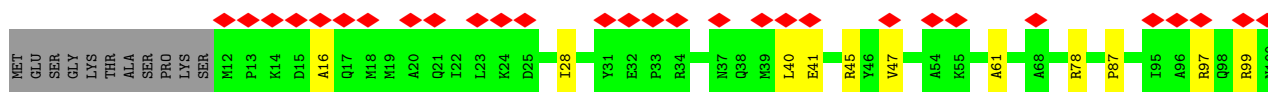
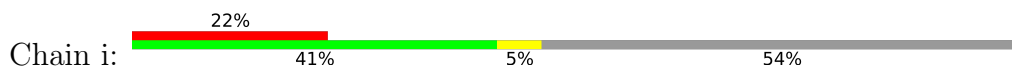
- Molecule 7: Transcription initiation factor TFIID subunit 8

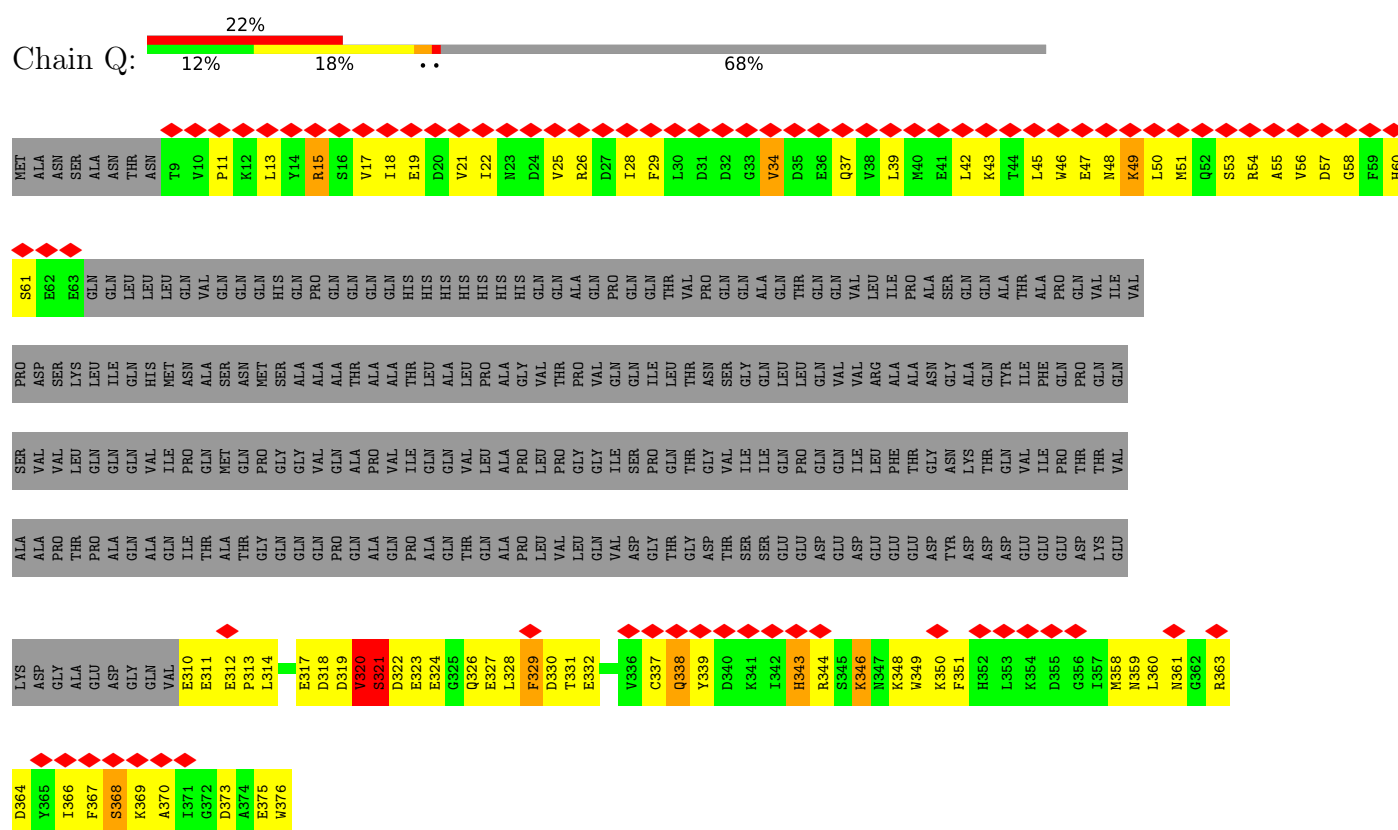


- Molecule 8: Transcription initiation factor TFIID subunit 9

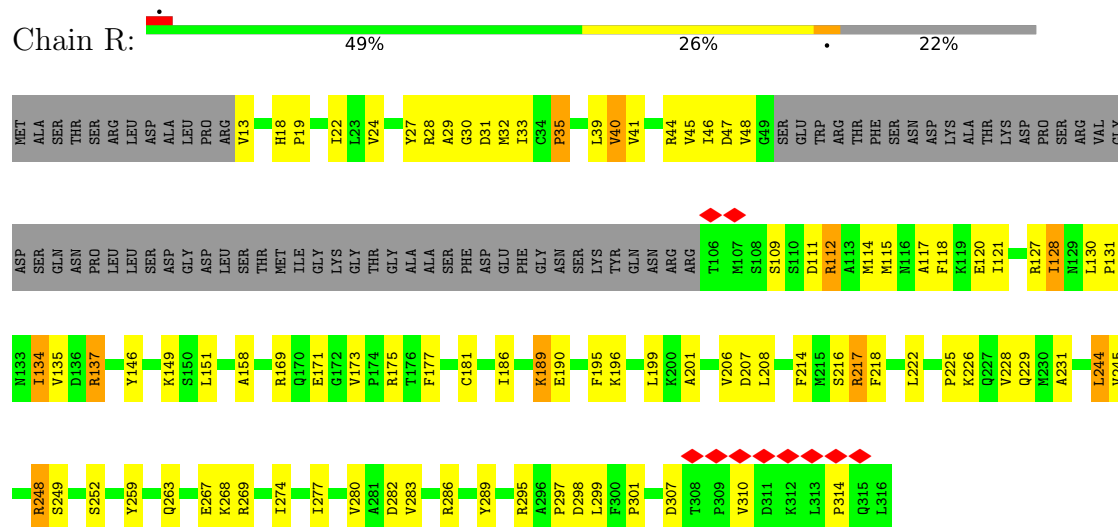


- Molecule 8: Transcription initiation factor TFIID subunit 9

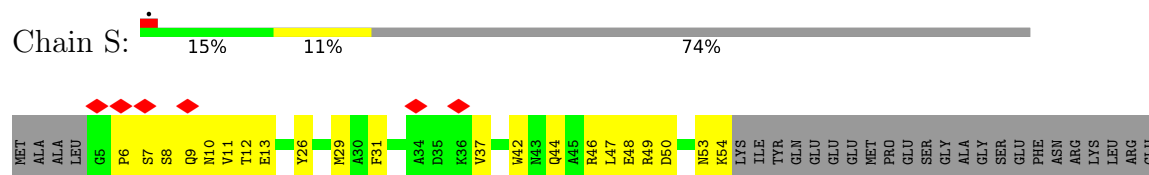


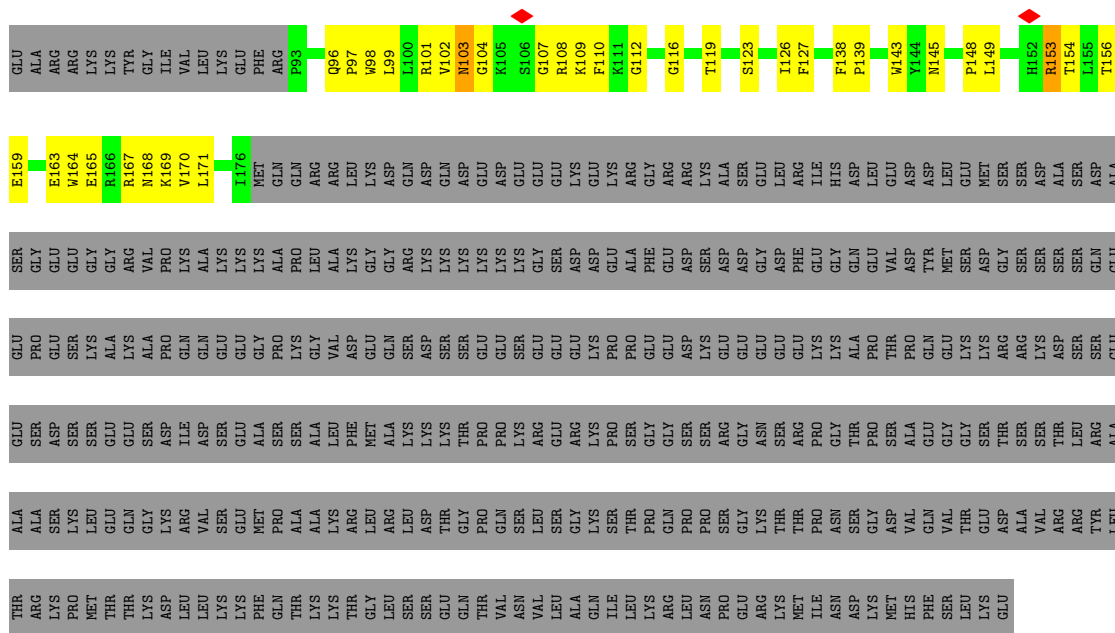


• Molecule 14: Transcription initiation factor IIB

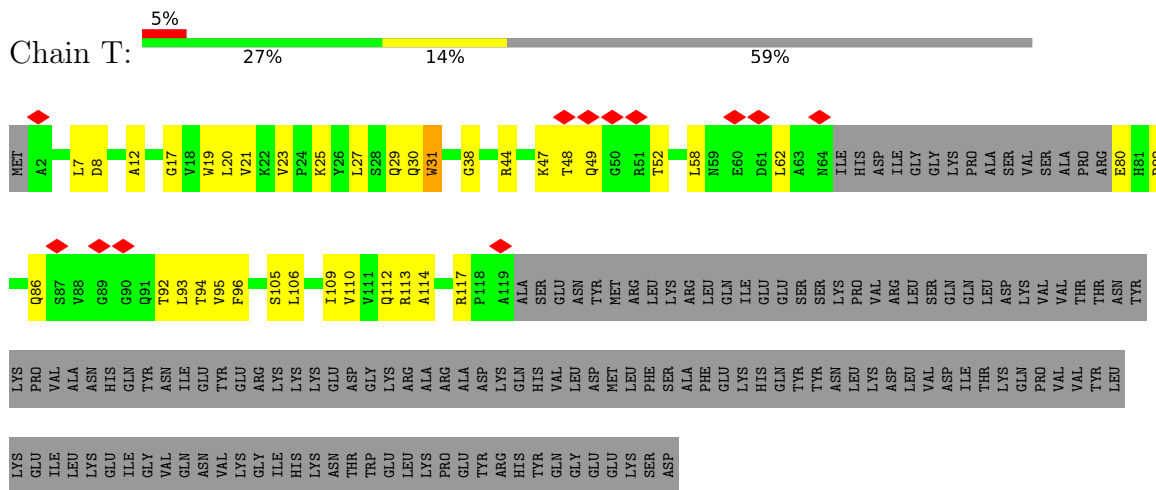


• Molecule 15: General transcription factor IIF subunit 1

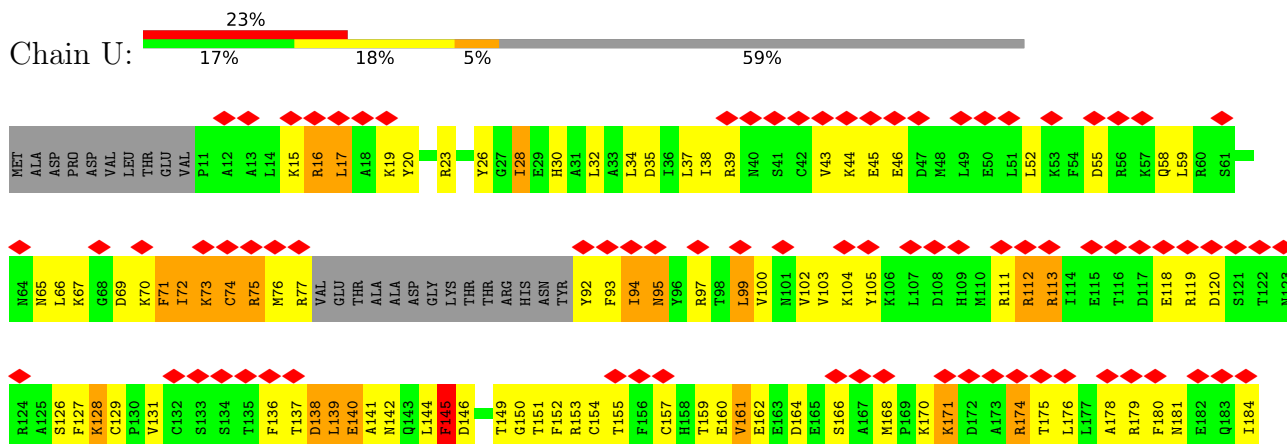


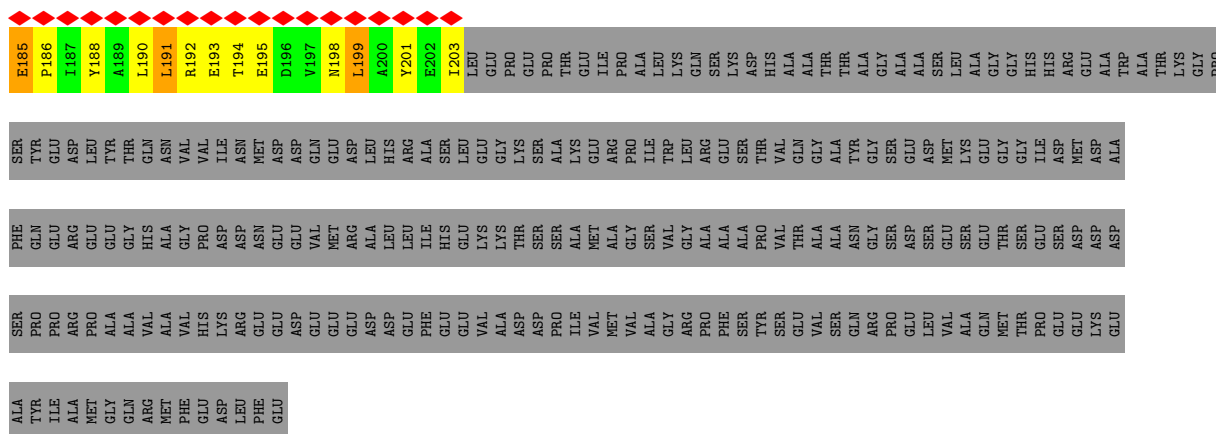


- Molecule 16: General transcription factor IIF subunit 2

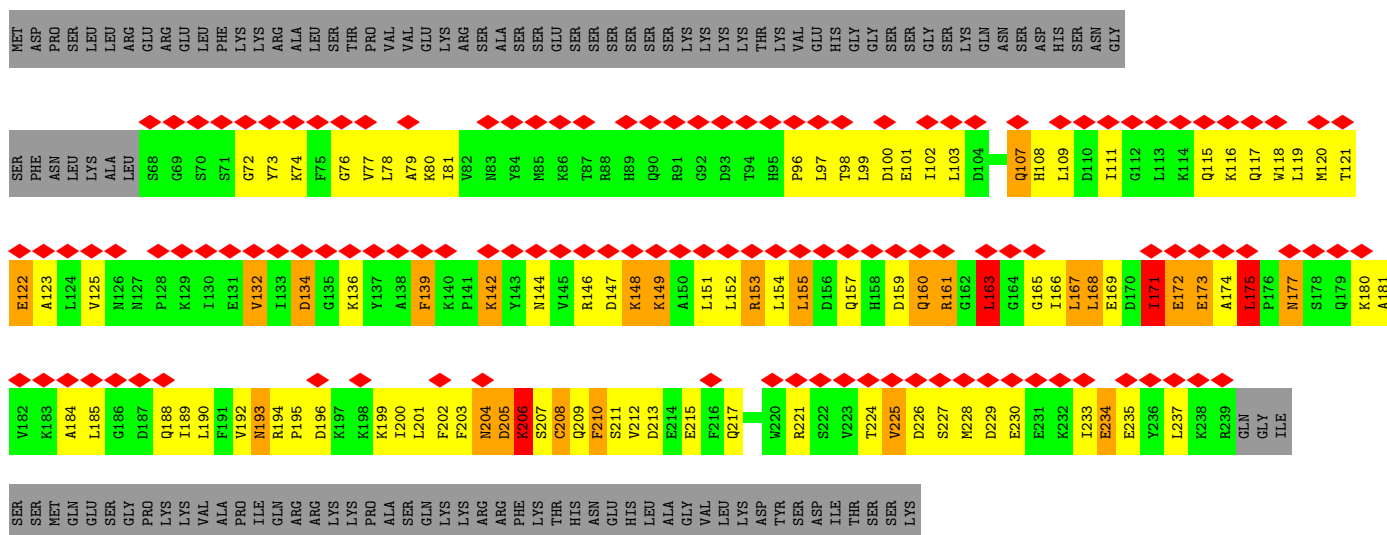
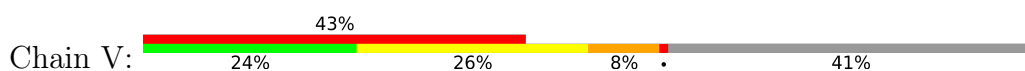


- Molecule 17: General transcription factor IIE subunit 1





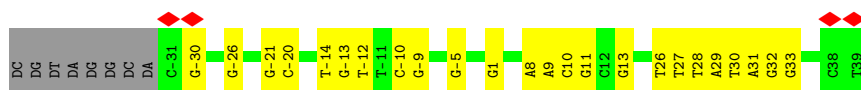
- Molecule 18: Transcription initiation factor IIE subunit beta



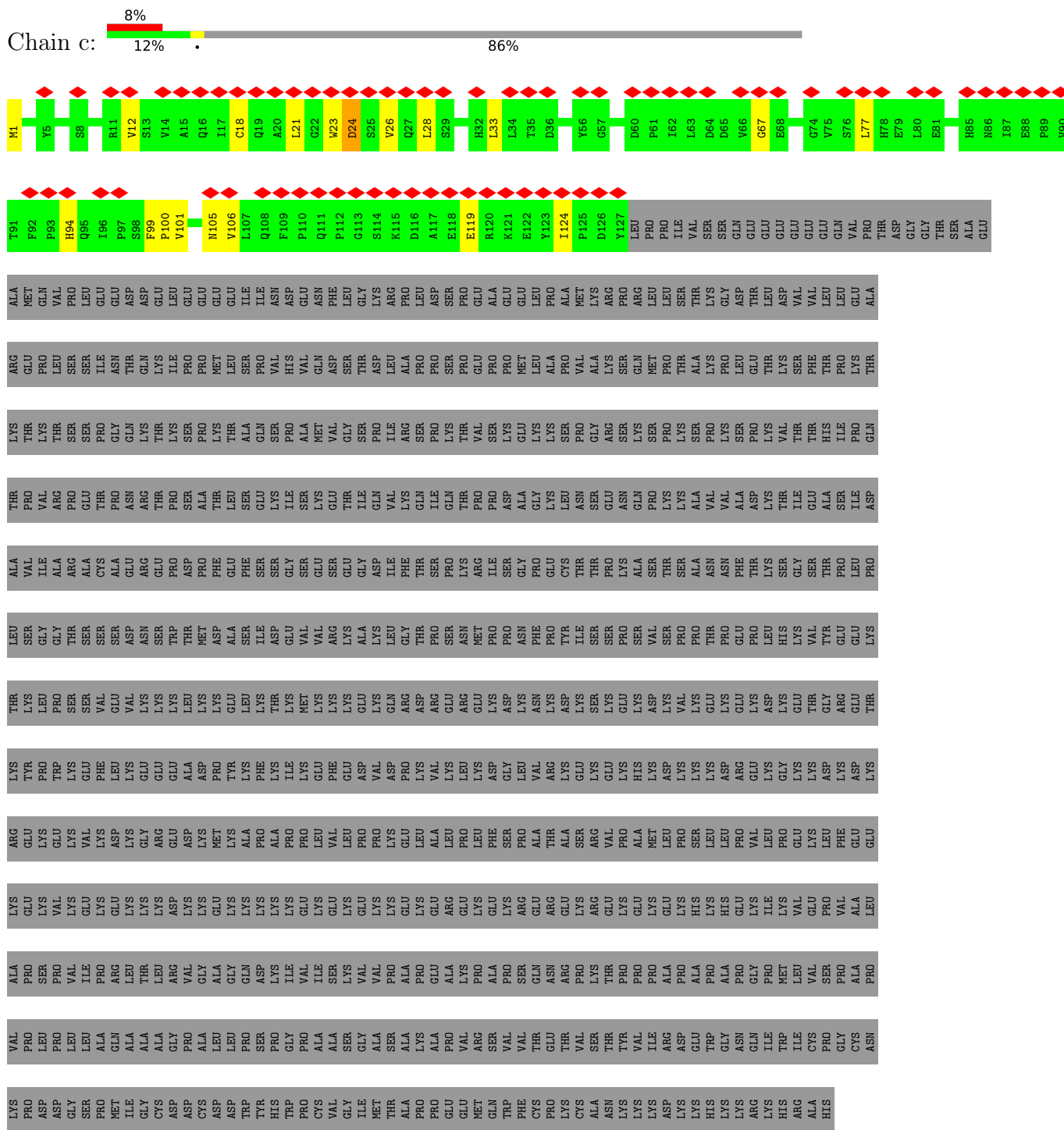
- Molecule 19: DNA (79-MER)



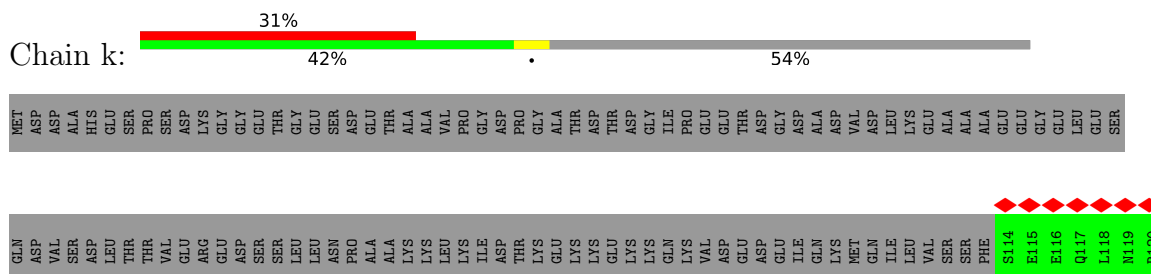
- Molecule 20: DNA (79-MER)

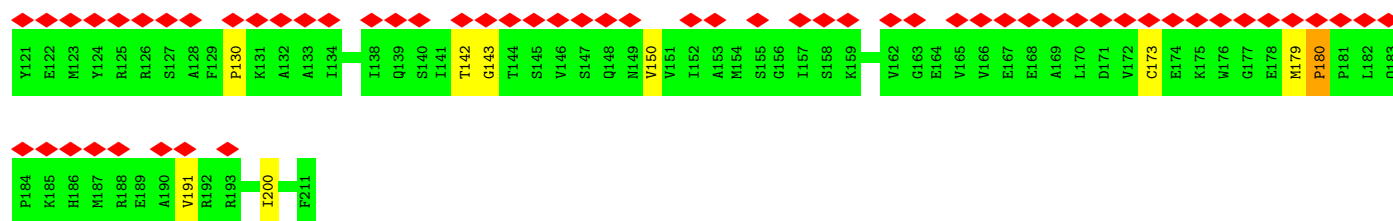


- Molecule 21: Transcription initiation factor TFIID subunit 3

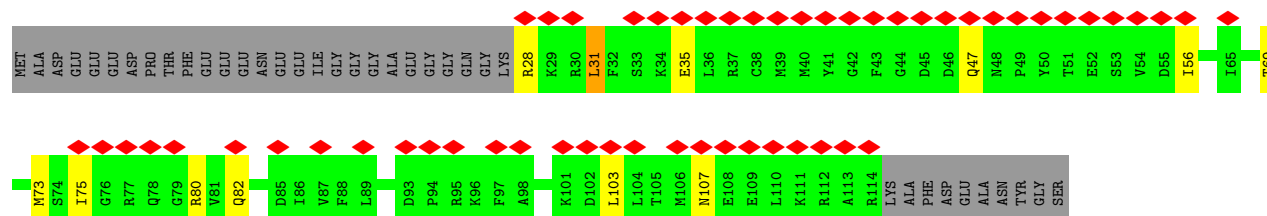
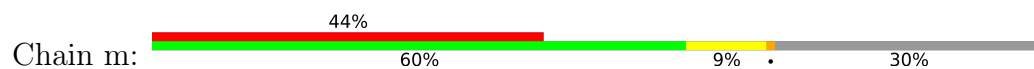


- Molecule 22: Transcription initiation factor TFIID subunit 11

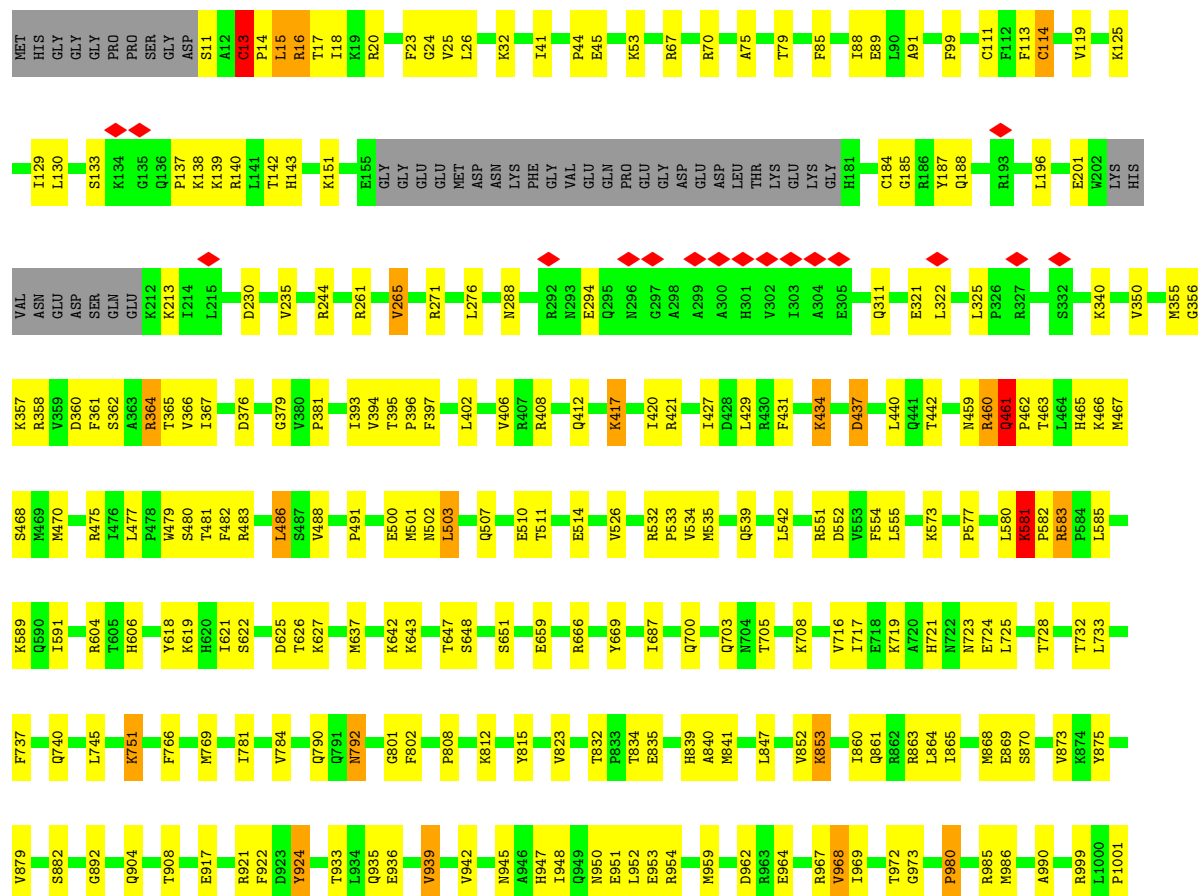




• Molecule 23: Transcription initiation factor TFIID subunit 13

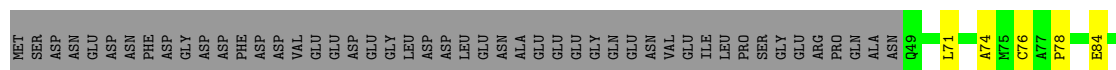


• Molecule 24: RPB1

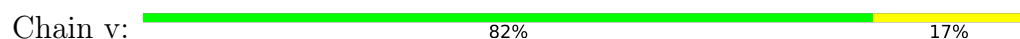




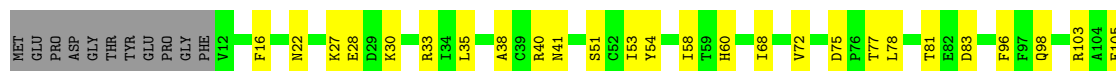
- Molecule 29: DNA-directed RNA polymerase II subunit F



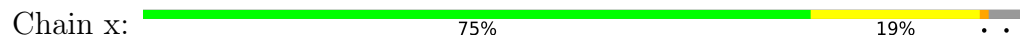
- Molecule 30: DNA-directed RNA polymerases I, II, and III subunit RPABC3



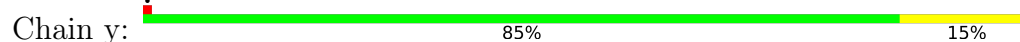
- Molecule 31: DNA-directed RNA polymerase II subunit RPB9



- Molecule 32: RPB10



- Molecule 33: RNA_pol_L_2 domain-containing protein

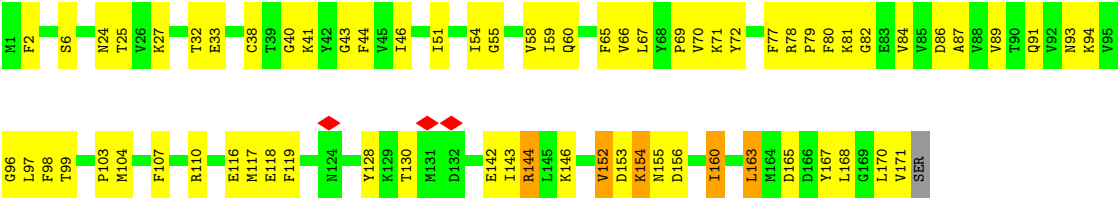


- Molecule 34: RPB12





• Molecule 35: DNA-directed RNA polymerase II subunit RPB7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57889	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.158	Depositor
Minimum map value	-0.399	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.13	Depositor
Map size ($\text{\AA}$)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.70	1/5046 (0.0%)	0.98	10/6810 (0.1%)
2	B	0.48	1/7993 (0.0%)	0.72	11/10836 (0.1%)
3	D	0.59	0/1374	0.90	0/1836
3	d	0.21	0/1321	0.44	0/1772
4	E	0.38	0/4469	0.63	3/6050 (0.0%)
4	e	0.28	0/4433	0.53	0/6004
5	F	0.69	1/3139 (0.0%)	1.09	9/4264 (0.2%)
5	f	0.46	0/3140	0.80	6/4268 (0.1%)
6	G	0.69	0/1199	0.96	1/1612 (0.1%)
7	H	0.57	0/1673	0.80	2/2285 (0.1%)
8	I	0.43	0/981	0.69	5/1332 (0.4%)
8	i	0.21	0/989	0.40	0/1343
9	J	0.28	0/724	0.49	0/982
9	j	0.22	0/775	0.44	0/1049
10	L	0.40	0/630	0.75	1/852 (0.1%)
10	l	0.43	0/888	0.75	0/1194
11	O	0.87	1/781 (0.1%)	1.25	9/1061 (0.8%)
12	P	0.95	0/1438	1.25	5/1935 (0.3%)
13	Q	0.60	0/1013	1.17	13/1366 (1.0%)
14	R	0.54	0/1941	1.07	4/2622 (0.2%)
15	S	0.44	0/1130	0.86	1/1528 (0.1%)
16	T	0.38	0/799	0.90	1/1077 (0.1%)
17	U	0.76	0/1499	1.24	9/2012 (0.4%)
18	V	0.72	0/1424	1.23	10/1913 (0.5%)
19	X	0.41	0/1653	0.67	3/2552 (0.1%)
20	Y	0.36	0/1611	0.61	1/2481 (0.0%)
21	c	0.48	0/1035	0.67	0/1406
22	k	0.29	0/799	0.53	1/1070 (0.1%)
23	m	0.30	0/733	0.55	0/977
24	o	0.60	1/11516 (0.0%)	0.91	24/15548 (0.2%)
25	p	0.31	0/9243	0.48	2/12475 (0.0%)
26	q	0.32	0/2102	0.44	0/2857

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	r	0.17	0/1019	0.45	0/1374
28	s	0.22	0/1751	0.46	0/2366
29	t	0.29	0/645	0.47	0/871
30	v	0.28	0/1207	0.46	0/1628
31	w	0.22	0/948	0.45	0/1284
32	x	0.59	0/516	1.05	0/696
33	y	0.36	0/956	0.53	0/1294
34	z	0.27	0/377	0.43	0/500
35	u	0.42	0/1382	0.82	3/1874 (0.2%)
All	All	0.50	5/86292 (0.0%)	0.79	134/117256 (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
11	O	0	1
17	U	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	762	PHE	C-O	-7.30	1.14	1.23
2	B	61	ASN	C-O	-6.17	1.18	1.24
24	o	964	GLU	C-O	5.75	1.30	1.24
5	F	395	ARG	C-O	5.72	1.32	1.24
11	O	59	ARG	N-CA	5.05	1.52	1.45

All (134) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	883	PHE	CA-C-N	-9.96	104.04	121.97
2	B	883	PHE	C-N-CA	-9.96	104.04	121.97
2	B	491	HIS	N-CA-C	-9.53	100.89	111.28
17	U	94	ILE	O-C-N	9.53	133.29	123.10
5	f	149	PRO	O-C-N	9.22	125.55	121.31
14	R	112	ARG	N-CA-C	-9.20	101.25	111.28
13	Q	331	THR	N-CA-C	-8.40	102.59	112.92
19	X	-30	DA	C2'-C3'-O3'	-8.36	98.97	111.50
5	F	373	ARG	N-CA-C	-8.31	103.30	113.19

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	U	138	ASP	N-CA-C	-8.29	102.24	111.28
5	F	317	LEU	N-CA-C	-8.08	103.40	113.18
1	A	762	PHE	CA-C-O	-7.94	112.17	121.46
1	A	356	PRO	N-CA-C	7.88	124.76	114.68
18	V	234	GLU	CB-CA-C	-7.80	98.94	110.96
18	V	108	HIS	N-CA-C	-7.74	104.27	112.93
18	V	174	ALA	N-CA-C	-7.63	103.99	113.38
7	H	163	PRO	N-CA-C	7.49	124.18	113.47
17	U	140	GLU	CB-CA-C	-7.17	99.63	110.88
24	o	13	CYS	CA-C-N	7.16	127.12	120.03
24	o	13	CYS	C-N-CA	7.16	127.12	120.03
2	B	495	GLN	N-CA-C	-7.14	104.57	113.28
1	A	715	PRO	N-CA-C	-7.09	100.12	111.03
11	O	29	THR	CB-CA-C	7.01	123.99	110.17
5	F	271	VAL	N-CA-C	-6.99	106.19	112.90
5	F	219	GLU	N-CA-C	-6.85	103.26	111.69
5	F	371	THR	N-CA-C	-6.80	103.93	111.82
22	k	180	PRO	N-CA-C	6.78	118.97	110.70
24	o	950	ASN	CB-CA-C	-6.74	100.31	110.88
5	f	326	HIS	N-CA-C	-6.73	104.17	112.38
13	Q	329	PHE	N-CA-C	-6.70	104.27	113.18
8	I	114	ARG	CA-C-O	-6.69	113.67	121.16
1	A	396	LEU	N-CA-C	-6.62	104.96	113.16
5	f	319	LEU	N-CA-C	-6.61	103.90	112.68
17	U	198	ASN	CB-CA-C	-6.50	100.67	110.88
25	p	249	LYS	N-CA-C	-6.49	104.46	112.38
7	H	114	SER	N-CA-C	-6.46	105.43	113.38
24	o	1102	MET	N-CA-C	6.42	119.54	110.23
8	I	114	ARG	CB-CA-C	6.39	120.58	109.65
24	o	1433	GLU	N-CA-CB	-6.39	106.89	114.17
18	V	210	PHE	CA-CB-CG	6.34	120.14	113.80
18	V	139	PHE	CB-CA-C	-6.30	97.88	110.42
1	A	848	LEU	CA-C-O	-6.28	113.21	120.49
17	U	178	ALA	N-CA-C	-6.27	105.63	113.28
35	u	152	VAL	N-CA-C	6.26	117.76	107.24
13	Q	330	ASP	CB-CA-C	6.24	122.82	110.65
17	U	199	LEU	CA-C-N	-6.24	109.67	122.58
17	U	199	LEU	C-N-CA	-6.24	109.67	122.58
20	Y	-30	DG	C2'-C3'-O3'	-6.22	102.16	111.50
14	R	217	ARG	N-CA-C	6.16	117.99	111.28
10	L	72	PRO	N-CA-C	-6.12	106.09	113.98
18	V	139	PHE	CA-CB-CG	6.08	119.88	113.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	U	26	TYR	N-CA-C	6.08	118.61	110.35
13	Q	319	ASP	N-CA-C	6.06	117.33	107.32
11	O	60	GLY	N-CA-C	6.02	120.43	110.55
13	Q	368	SER	N-CA-C	-6.01	105.03	112.90
2	B	181	GLY	CA-C-O	-5.99	118.00	122.37
5	f	255	MET	N-CA-C	-5.98	104.82	114.09
24	o	1063	GLU	N-CA-C	-5.98	104.76	111.28
18	V	168	LEU	N-CA-C	-5.96	104.67	113.61
25	p	1135	TYR	CB-CA-C	5.95	121.23	111.23
1	A	762	PHE	CA-C-N	5.94	131.37	123.05
1	A	762	PHE	C-N-CA	5.94	131.37	123.05
15	S	103	ASN	N-CA-C	5.92	119.73	111.74
11	O	58	PHE	N-CA-C	5.91	116.39	108.23
5	F	324	ASP	N-CA-C	-5.90	105.19	112.38
24	o	1355	VAL	N-CA-C	5.84	116.62	110.72
13	Q	338	GLN	CA-C-N	-5.82	114.49	122.93
13	Q	338	GLN	C-N-CA	-5.82	114.49	122.93
11	O	61	SER	CA-C-O	-5.77	114.35	121.11
18	V	122	GLU	N-CA-C	5.73	120.30	112.68
12	P	298	PRO	N-CA-C	-5.67	100.78	112.47
2	B	583	GLU	CB-CA-C	-5.66	101.39	110.79
11	O	6	TYR	N-CA-C	5.58	119.18	112.93
2	B	264	GLU	N-CA-C	-5.56	106.16	113.17
2	B	846	TYR	CA-C-O	-5.56	114.81	120.71
13	Q	321	SER	CA-C-N	-5.54	111.54	122.02
13	Q	321	SER	C-N-CA	-5.54	111.54	122.02
5	f	150	PRO	N-CA-C	5.54	117.46	110.70
1	A	468	PHE	CA-CB-CG	-5.51	108.29	113.80
4	E	428	PRO	CA-C-O	-5.45	115.56	121.77
19	X	6	DG	C4'-C3'-O3'	5.41	118.12	110.00
5	f	329	LEU	N-CA-C	-5.40	106.39	112.87
24	o	113	PHE	CA-CB-CG	5.40	119.20	113.80
12	P	207	PRO	N-CA-C	-5.37	101.40	112.47
14	R	307	ASP	N-CA-C	-5.37	107.10	113.97
8	I	114	ARG	N-CA-CB	-5.37	102.08	109.97
1	A	843	ARG	CG-CD-NE	5.36	123.79	112.00
17	U	128	LYS	N-CA-CB	5.36	119.62	110.57
6	G	183	ILE	N-CA-C	-5.35	102.61	109.30
24	o	1019	LYS	N-CA-C	5.32	116.88	111.14
16	T	31	TRP	N-CA-C	5.31	117.82	111.71
2	B	491	HIS	CB-CA-C	5.30	119.59	110.79
5	F	272	VAL	N-CA-C	-5.29	105.23	110.62

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	V	163	LEU	N-CA-C	5.28	118.87	111.74
11	O	7	ARG	N-CA-C	-5.26	106.37	112.89
11	O	55	ARG	N-CA-C	5.25	118.28	110.14
12	P	205	ARG	CB-CA-C	-5.25	101.09	110.70
24	o	1477	ALA	O-C-N	-5.25	115.13	122.37
24	o	1482	TYR	CA-C-N	-5.24	117.62	122.29
24	o	1482	TYR	C-N-CA	-5.24	117.62	122.29
24	o	724	GLU	N-CA-C	5.23	118.68	112.72
13	Q	321	SER	N-CA-C	-5.20	99.72	110.80
18	V	175	LEU	N-CA-C	5.19	121.48	108.40
24	o	1482	TYR	CB-CA-C	5.18	119.95	110.36
19	X	-12	DG	C2'-C3'-O3'	-5.18	103.73	111.50
12	P	305	PHE	CA-C-N	-5.18	112.80	120.82
12	P	305	PHE	C-N-CA	-5.18	112.80	120.82
35	u	160	ILE	N-CA-C	5.16	115.90	108.48
24	o	1019	LYS	CA-C-O	-5.15	115.40	120.70
2	B	882	HIS	CA-C-O	-5.13	115.76	121.81
11	O	60	GLY	CA-C-O	-5.11	116.64	121.60
13	Q	320	VAL	CA-C-O	-5.11	115.14	120.76
11	O	21	GLU	N-CA-C	-5.11	105.89	111.82
24	o	968	VAL	CA-C-O	-5.11	114.40	120.78
1	A	498	PRO	N-CA-CB	5.10	108.61	103.25
5	F	313	VAL	N-CA-C	-5.10	105.44	111.00
8	I	101	GLN	N-CA-C	-5.10	107.44	113.97
24	o	1482	TYR	N-CA-C	-5.09	107.09	113.15
8	I	104	LEU	CA-C-O	-5.09	116.19	120.26
24	o	1001	PRO	CB-CA-C	-5.08	104.99	113.06
4	E	795	GLY	N-CA-C	5.07	125.19	113.18
13	Q	15	ARG	N-CA-C	-5.07	105.65	111.07
24	o	967	ARG	CA-C-N	-5.07	112.85	121.97
24	o	967	ARG	C-N-CA	-5.07	112.85	121.97
35	u	96	GLY	N-CA-C	5.06	117.67	110.74
4	E	423	PRO	N-CA-C	5.06	122.90	112.47
24	o	1013	VAL	N-CA-C	-5.05	105.57	110.42
13	Q	346	LYS	CB-CA-C	-5.05	110.78	116.63
24	o	1432	PHE	CA-C-O	-5.04	113.47	121.94
5	F	358	THR	CB-CA-C	-5.04	102.97	110.88
14	R	35	PRO	N-CA-C	5.04	122.86	112.47
2	B	541	ARG	CB-CA-C	-5.02	101.70	110.09
24	o	1097	GLU	CA-C-N	5.01	125.04	119.32
24	o	1097	GLU	C-N-CA	5.01	125.04	119.32

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	O	17	GLU	Mainchain
17	U	161	VAL	Mainchain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4927	0	4871	439	0
2	B	7796	0	7751	184	0
3	D	1361	0	1384	269	0
3	d	1307	0	1318	18	0
4	E	4364	0	4244	138	0
4	e	4327	0	4197	45	0
5	F	3081	0	3018	444	0
5	f	3081	0	3012	89	0
6	G	1180	0	1235	254	0
7	H	1633	0	1621	196	0
8	I	959	0	968	220	0
8	i	967	0	977	13	0
9	J	709	0	710	101	0
9	j	759	0	759	17	0
10	L	622	0	620	155	0
10	l	876	0	893	15	0
11	O	771	0	764	125	0
12	P	1412	0	1506	140	0
13	Q	996	0	926	173	0
14	R	1913	0	1957	160	0
15	S	1101	0	1065	112	0
16	T	789	0	795	38	0
17	U	1476	0	1488	121	0
18	V	1400	0	1413	128	0
19	X	1470	0	792	19	0
20	Y	1441	0	797	50	0
21	c	1011	0	975	26	0
22	k	785	0	818	8	0
23	m	724	0	744	12	0
24	o	11308	0	11429	596	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	p	9062	0	9107	300	0
26	q	2059	0	2008	30	0
27	r	1005	0	964	87	0
28	s	1720	0	1737	55	0
29	t	635	0	665	18	0
30	v	1186	0	1147	20	0
31	w	927	0	859	43	0
32	x	507	0	523	7	0
33	y	937	0	959	17	0
34	z	372	0	379	16	0
35	u	1351	0	1358	133	0
36	R	1	0	0	0	0
36	U	1	0	0	1	0
36	o	2	0	0	0	0
36	p	1	0	0	0	0
36	q	1	0	0	0	0
36	w	2	0	0	0	0
36	x	1	0	0	0	0
36	z	1	0	0	0	0
37	o	1	0	0	0	0
All	All	84318	0	82753	3508	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 21.

All (3508) 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)
27:r:60:VAL:HG11	35:u:44:PHE:CZ	1.19	1.69
5:F:47:ILE:HG21	8:I:19:MET:SD	1.09	1.65
27:r:60:VAL:CG1	35:u:44:PHE:HZ	1.12	1.63
4:E:694:LEU:CD1	4:E:703:MET:HE1	1.27	1.62
15:S:116:GLY:HA2	25:p:356:PHE:CD1	1.33	1.61
3:D:871:THR:CG2	10:L:66:LEU:HD22	1.31	1.59
14:R:44:ARG:CB	25:p:1067:ILE:HD13	1.31	1.59
14:R:44:ARG:HB3	25:p:1067:ILE:CD1	1.21	1.58
12:P:203:ARG:HB2	13:Q:376:TRP:CH2	1.34	1.57
8:I:60:HIS:CE1	10:L:118:LEU:CD2	1.84	1.56
5:F:48:LYS:CG	8:I:22:ILE:HG23	1.17	1.56
5:F:48:LYS:HG3	8:I:22:ILE:CG2	1.11	1.56
1:A:680:LEU:HD23	6:G:74:MET:SD	1.46	1.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:694:LEU:HD13	4:E:703:MET:CE	1.31	1.54
3:D:1000:ARG:HH22	11:O:5:LEU:CD1	1.17	1.54
5:F:47:ILE:CD1	8:I:19:MET:HE1	1.11	1.54
12:P:203:ARG:CB	13:Q:376:TRP:CH2	1.88	1.53
8:I:60:HIS:CE1	10:L:118:LEU:HD22	1.36	1.51
24:o:1060:LEU:HD11	24:o:1064:ALA:CB	1.39	1.50
5:F:47:ILE:HD13	8:I:19:MET:CE	1.04	1.49
17:U:145:PHE:CZ	35:u:98:PHE:HE2	1.28	1.48
3:D:881:ARG:NH2	10:L:57:VAL:CG2	1.75	1.47
1:A:410:TRP:CH2	5:F:305:ILE:HG21	1.50	1.47
5:F:15:PRO:CB	8:I:14:LYS:HZ1	1.22	1.47
3:D:881:ARG:NH2	10:L:57:VAL:HG22	1.15	1.46
10:L:106:ARG:HH11	10:L:114:LYS:NZ	1.00	1.46
3:D:957:ARG:NH2	4:E:434:ASP:CB	1.79	1.46
3:D:1000:ARG:NH2	11:O:5:LEU:HD11	1.24	1.45
5:F:211:ARG:CG	7:H:165:TYR:HD2	1.29	1.45
27:r:103:LEU:HD23	35:u:144:ARG:NH1	1.17	1.45
5:F:211:ARG:HG2	7:H:165:TYR:CD2	1.51	1.44
5:F:47:ILE:CG2	8:I:19:MET:SD	2.02	1.44
27:r:16:ASP:CG	35:u:81:LYS:HZ2	1.22	1.44
1:A:602:PHE:CD1	6:G:12:LEU:HD21	1.53	1.43
5:F:267:VAL:HG12	5:F:310:THR:CG2	1.46	1.43
5:F:15:PRO:CB	8:I:14:LYS:NZ	1.75	1.42
3:D:1000:ARG:NH2	11:O:5:LEU:CD1	1.77	1.42
10:L:106:ARG:NH1	10:L:114:LYS:HZ3	1.16	1.41
3:D:871:THR:CG2	10:L:66:LEU:CD2	1.99	1.41
4:E:696:TRP:CE3	4:E:703:MET:HB3	1.53	1.41
3:D:957:ARG:NH2	4:E:434:ASP:HB3	1.09	1.40
27:r:16:ASP:HB2	35:u:81:LYS:CE	1.48	1.40
27:r:16:ASP:CB	35:u:81:LYS:NZ	1.85	1.40
17:U:145:PHE:CE2	35:u:98:PHE:CE2	2.06	1.40
3:D:871:THR:CA	10:L:66:LEU:HD13	1.49	1.40
13:Q:47:GLU:OE2	13:Q:60:HIS:CE1	1.75	1.40
1:A:410:TRP:CZ3	5:F:305:ILE:HG21	1.55	1.39
10:L:106:ARG:HH12	10:L:114:LYS:CD	1.35	1.39
27:r:16:ASP:HB2	35:u:81:LYS:NZ	1.38	1.39
1:A:1077:LEU:HD11	6:G:147:ARG:NH2	1.09	1.39
5:F:68:THR:HG21	8:I:34:ARG:NH1	1.37	1.38
5:F:279:LEU:HD23	5:F:330:ARG:NH1	1.09	1.38
12:P:188:ARG:NH2	13:Q:326:GLN:HB2	1.36	1.38
5:F:279:LEU:HD23	5:F:330:ARG:CZ	1.52	1.38

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:u:40:GLY:HA2	35:u:152:VAL:CG2	1.54	1.37
5:F:309:MET:CA	5:F:312:ILE:HD11	1.54	1.37
12:P:203:ARG:HB3	13:Q:376:TRP:CZ3	1.59	1.37
1:A:1077:LEU:CD1	6:G:147:ARG:NH2	1.85	1.37
5:F:43:VAL:CG2	8:I:43:ALA:HB1	1.55	1.37
5:F:299:LYS:O	5:F:302:HIS:CE1	1.77	1.36
24:o:1486:ILE:CG1	24:o:1487:PRO:HD3	1.55	1.35
3:D:1000:ARG:NH1	11:O:5:LEU:HD12	1.37	1.35
14:R:44:ARG:O	25:p:1067:ILE:CD1	1.73	1.35
1:A:602:PHE:CE1	6:G:12:LEU:HD21	1.61	1.35
5:F:211:ARG:CG	7:H:165:TYR:CD2	2.09	1.34
3:D:1000:ARG:CZ	11:O:5:LEU:HD12	1.56	1.34
5:F:71:ILE:HB	8:I:38:GLN:NE2	1.38	1.34
1:A:650:ARG:HH22	6:G:78:LYS:NZ	1.22	1.33
5:F:271:VAL:CG2	5:F:311:CYS:SG	2.15	1.33
5:F:271:VAL:HG21	5:F:311:CYS:SG	1.69	1.32
11:O:79:VAL:O	11:O:90:VAL:CG1	1.76	1.32
3:D:949:GLN:O	3:D:953:ILE:HG12	1.20	1.32
24:o:1158:LEU:HD21	24:o:1307:VAL:CG1	1.60	1.32
1:A:1077:LEU:HD11	6:G:147:ARG:CZ	1.60	1.31
5:F:67:THR:HA	8:I:32:GLU:CD	1.53	1.31
24:o:1158:LEU:CD2	24:o:1307:VAL:CG1	2.06	1.31
5:F:309:MET:HA	5:F:312:ILE:CD1	1.61	1.30
12:P:167:ASN:OD1	20:Y:27:DT:H4'	1.19	1.30
5:F:15:PRO:HB3	8:I:14:LYS:NZ	0.97	1.30
5:F:279:LEU:CD2	5:F:330:ARG:HH12	1.45	1.29
24:o:1485:GLU:HB3	29:t:78:PRO:CB	1.60	1.29
27:r:16:ASP:CB	35:u:81:LYS:HZ1	1.40	1.29
1:A:682:GLU:OE2	6:G:140:LEU:HD12	1.24	1.29
1:A:1077:LEU:CD1	6:G:147:ARG:HH22	1.41	1.29
1:A:620:LEU:HD22	6:G:67:LEU:CD2	1.62	1.28
17:U:145:PHE:CZ	35:u:98:PHE:CE2	2.17	1.28
24:o:716:VAL:HG12	24:o:737:PHE:CE2	1.65	1.28
10:L:101:GLN:O	10:L:105:HIS:CD2	1.87	1.27
1:A:410:TRP:CZ3	5:F:305:ILE:CG2	2.16	1.27
1:A:488:ALA:HB1	5:f:271:VAL:CG2	1.65	1.26
2:B:762:ASP:OD1	2:B:768:PRO:HG3	1.27	1.26
1:A:779:ILE:CG2	6:G:137:THR:HG22	1.65	1.26
5:F:267:VAL:HG11	5:F:310:THR:CB	1.66	1.25
10:L:106:ARG:NH1	10:L:114:LYS:HD2	1.48	1.25
14:R:47:ASP:OD1	25:p:1075:MET:CE	1.84	1.25

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:S:44:GLN:NE2	15:S:104:GLY:HA3	1.50	1.25
5:F:267:VAL:CG1	5:F:310:THR:HB	1.66	1.25
27:r:16:ASP:CG	35:u:81:LYS:NZ	1.84	1.25
3:D:891:ILE:CG2	10:L:111:LEU:HB2	1.65	1.25
15:S:116:GLY:CA	25:p:356:PHE:CD1	2.20	1.24
24:o:1486:ILE:HG13	24:o:1487:PRO:CD	1.67	1.24
10:L:106:ARG:NH1	10:L:114:LYS:CD	1.98	1.24
5:F:87:HIS:HB3	9:J:212:LYS:NZ	1.49	1.24
5:F:299:LYS:O	5:F:302:HIS:HE1	0.97	1.24
5:F:213:ILE:HB	7:H:163:PRO:O	1.38	1.23
5:F:279:LEU:CD2	5:F:330:ARG:NH1	2.00	1.23
3:D:881:ARG:HH21	10:L:57:VAL:CG1	1.50	1.23
24:o:461:GLN:HB3	24:o:462:PRO:CD	1.68	1.22
1:A:665:MET:HG3	6:G:86:TYR:CD2	1.74	1.22
15:S:6:PRO:O	15:S:10:ASN:CB	1.86	1.22
18:V:121:THR:O	18:V:125:VAL:HG21	1.39	1.22
14:R:46:ILE:HA	24:o:67:ARG:NH2	1.53	1.22
27:r:110:GLU:OE2	35:u:167:TYR:CD1	1.93	1.22
27:r:103:LEU:CD2	35:u:144:ARG:HH11	1.52	1.21
5:F:267:VAL:CG1	5:F:310:THR:CG2	2.18	1.21
1:A:680:LEU:CD2	6:G:74:MET:SD	2.29	1.21
5:F:68:THR:N	8:I:32:GLU:OE1	1.73	1.21
18:V:181:ALA:O	18:V:185:LEU:N	1.72	1.21
3:D:946:PHE:CD2	4:E:513:LEU:HD13	1.75	1.20
15:S:116:GLY:HA2	25:p:356:PHE:CE1	1.75	1.20
3:D:871:THR:N	10:L:66:LEU:CD1	2.03	1.20
12:P:248:ALA:C	13:Q:314:LEU:HD12	1.67	1.20
1:A:956:PRO:O	6:G:149:ARG:HB3	1.40	1.20
5:F:279:LEU:CD2	5:F:330:ARG:HH22	1.54	1.20
24:o:1050:CYS:SG	24:o:1053:ARG:CB	2.30	1.20
11:O:79:VAL:O	11:O:90:VAL:HG12	1.33	1.20
12:P:167:ASN:OD1	20:Y:27:DT:C4'	1.88	1.20
12:P:203:ARG:CB	13:Q:376:TRP:CZ3	2.18	1.19
17:U:145:PHE:CE2	35:u:98:PHE:CZ	2.29	1.19
1:A:650:ARG:NH2	6:G:78:LYS:NZ	1.90	1.19
2:B:834:THR:HG23	7:H:213:LEU:HD23	1.25	1.19
5:F:267:VAL:CG1	5:F:310:THR:CB	2.19	1.19
1:A:564:PRO:HG2	2:B:744:PHE:CE2	1.79	1.18
1:A:602:PHE:CE1	6:G:12:LEU:CD2	2.26	1.18
1:A:620:LEU:CD2	6:G:67:LEU:HD22	1.73	1.18
17:U:145:PHE:CE2	35:u:98:PHE:HE2	1.47	1.18

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:889:HIS:HA	10:L:104:ARG:NH2	1.57	1.18
14:R:30:GLY:HA3	25:p:1066:PRO:HB3	1.24	1.18
24:o:1158:LEU:HD23	24:o:1336:LEU:HD22	1.21	1.18
1:A:764:ILE:CD1	6:G:18:LEU:HB3	1.74	1.18
13:Q:346:LYS:HE2	20:Y:27:DT:P	1.84	1.18
3:D:871:THR:HA	10:L:66:LEU:HD13	1.17	1.17
3:D:889:HIS:C	10:L:104:ARG:HH21	1.51	1.17
3:D:1000:ARG:NH1	11:O:5:LEU:CD1	2.08	1.17
15:S:6:PRO:O	15:S:10:ASN:HB2	1.36	1.17
14:R:47:ASP:OD1	25:p:1075:MET:HE1	0.99	1.17
24:o:393:ILE:HD11	29:t:74:ALA:HB1	1.22	1.16
5:F:213:ILE:HG21	7:H:163:PRO:CB	1.75	1.16
15:S:164:TRP:CH2	25:p:307:GLU:O	1.98	1.16
14:R:44:ARG:C	25:p:1067:ILE:HD11	1.70	1.16
27:r:16:ASP:OD2	35:u:81:LYS:NZ	1.75	1.16
27:r:110:GLU:OE2	35:u:167:TYR:CE1	1.98	1.16
3:D:1000:ARG:CZ	11:O:5:LEU:CD1	2.18	1.16
12:P:203:ARG:C	13:Q:376:TRP:HH2	1.52	1.16
13:Q:344:ARG:NH2	20:Y:26:DT:OP1	1.79	1.16
1:A:764:ILE:HG13	6:G:18:LEU:HB2	1.19	1.15
1:A:1053:PHE:O	1:A:1057:GLU:CB	1.94	1.15
5:F:320:ARG:HD2	5:F:321:PRO:HD3	1.17	1.15
5:F:71:ILE:CB	8:I:38:GLN:HE21	1.59	1.15
24:o:1158:LEU:HD21	24:o:1307:VAL:CB	1.76	1.15
35:u:38:CYS:SG	35:u:44:PHE:HA	1.86	1.15
5:F:279:LEU:CD2	5:F:330:ARG:NH2	2.07	1.15
5:F:15:PRO:CG	8:I:14:LYS:HZ2	1.59	1.15
1:A:672:THR:HA	6:G:13:GLU:OE1	1.45	1.14
24:o:1060:LEU:HD11	24:o:1064:ALA:HB3	1.24	1.14
24:o:1485:GLU:HB3	29:t:78:PRO:HB2	1.20	1.14
1:A:650:ARG:HD3	6:G:80:ILE:HD12	1.24	1.14
3:D:1000:ARG:HH12	11:O:5:LEU:CG	1.59	1.14
10:L:106:ARG:NH1	10:L:114:LYS:CE	2.10	1.14
5:F:213:ILE:HG21	7:H:163:PRO:HB3	1.15	1.14
14:R:111:ASP:HB3	14:R:114:MET:HB2	1.26	1.14
24:o:1060:LEU:CD1	24:o:1064:ALA:CB	2.26	1.14
1:A:575:PRO:HD3	2:B:608:ASN:HD22	0.98	1.14
1:A:1053:PHE:O	1:A:1057:GLU:HB3	1.48	1.14
11:O:10:THR:CG2	13:Q:50:LEU:HD21	1.78	1.14
24:o:365:THR:CG2	24:o:482:PHE:CG	2.30	1.14
5:F:267:VAL:CG1	5:F:310:THR:HG21	1.76	1.13

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1083:PHE:HE2	4:E:585:ASN:ND2	1.47	1.13
5:F:43:VAL:CG2	8:I:43:ALA:CB	2.26	1.13
24:o:15:LEU:HA	25:p:1148:LEU:O	1.48	1.13
35:u:40:GLY:CA	35:u:152:VAL:HG21	1.79	1.13
5:F:43:VAL:HG21	8:I:43:ALA:HB1	1.21	1.13
3:D:1000:ARG:HH12	11:O:5:LEU:CD1	1.60	1.12
24:o:461:GLN:HB3	24:o:462:PRO:HD3	1.25	1.12
1:A:650:ARG:CD	6:G:80:ILE:HD12	1.80	1.12
1:A:766:ARG:HB3	6:G:16:PHE:HE1	1.13	1.12
35:u:44:PHE:CE2	35:u:46:ILE:HG13	1.82	1.12
3:D:871:THR:HG22	10:L:66:LEU:CD2	1.70	1.12
7:H:116:ARG:HD3	9:J:126:TYR:HE1	1.09	1.12
12:P:166:GLN:CB	20:Y:28:DT:H5"	1.79	1.12
18:V:224:THR:CG2	18:V:227:SER:HB2	1.80	1.11
24:o:1050:CYS:SG	24:o:1053:ARG:HB2	1.87	1.11
5:F:14:LEU:HD13	8:I:15:ASP:OD1	1.47	1.11
5:F:320:ARG:HH21	5:F:415:ILE:HB	0.96	1.11
15:S:44:GLN:HE21	15:S:103:ASN:C	1.58	1.11
27:r:16:ASP:HB2	35:u:81:LYS:HE3	1.27	1.11
27:r:103:LEU:CD2	35:u:144:ARG:NH1	2.08	1.11
35:u:44:PHE:CD2	35:u:46:ILE:HG13	1.85	1.11
5:F:320:ARG:NH2	5:F:415:ILE:HB	1.65	1.11
3:D:871:THR:HG23	10:L:66:LEU:CD2	1.78	1.10
1:A:488:ALA:HB1	5:f:271:VAL:HG23	1.24	1.10
1:A:672:THR:HA	6:G:13:GLU:CD	1.75	1.10
3:D:891:ILE:HG21	10:L:111:LEU:HD22	1.31	1.10
14:R:47:ASP:HB2	25:p:1069:ILE:HG12	1.31	1.10
1:A:650:ARG:NH2	6:G:78:LYS:HZ1	1.43	1.10
5:F:51:ALA:CB	8:I:23:LEU:CD2	2.28	1.10
17:U:46:GLU:OE2	17:U:93:PHE:HE2	1.33	1.10
18:V:121:THR:O	18:V:125:VAL:CG2	1.99	1.10
5:F:14:LEU:HD23	8:I:18:MET:HB3	1.23	1.10
14:R:30:GLY:CA	25:p:1066:PRO:HB3	1.81	1.10
15:S:164:TRP:HH2	25:p:307:GLU:CA	1.64	1.10
17:U:32:LEU:HD22	18:V:161:ARG:NH2	1.64	1.10
5:F:90:GLU:OE1	9:J:208:GLY:O	1.71	1.09
12:P:188:ARG:HH22	13:Q:326:GLN:CB	1.63	1.09
13:Q:47:GLU:OE2	13:Q:60:HIS:ND1	1.85	1.09
5:F:67:THR:HA	8:I:32:GLU:CG	1.82	1.09
5:F:244:GLN:OE1	7:H:133:ALA:HB3	1.48	1.09
1:A:775:GLU:OE1	6:G:29:ARG:NH1	1.85	1.09

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:LEU:CD2	6:G:67:LEU:CD2	2.28	1.09
12:P:188:ARG:CZ	13:Q:323:GLU:O	2.00	1.09
24:o:480:SER:CB	33:y:2:ASN:HD22	1.65	1.09
24:o:705:THR:OG1	24:o:751:LYS:HD2	1.52	1.09
24:o:1050:CYS:SG	24:o:1053:ARG:HB3	1.91	1.09
5:F:51:ALA:HB1	8:I:23:LEU:HD22	1.33	1.08
11:O:39:GLN:OE1	13:Q:28:ILE:HD11	1.50	1.08
1:A:900:ASP:HB3	6:G:154:LYS:HD2	1.34	1.08
15:S:11:VAL:O	15:S:12:THR:HG23	1.51	1.08
24:o:463:THR:HB	24:o:468:SER:HB2	1.35	1.08
1:A:779:ILE:HG21	6:G:137:THR:HG22	1.33	1.08
5:F:279:LEU:HD22	5:F:330:ARG:HH22	0.94	1.08
10:L:106:ARG:NH1	10:L:114:LYS:NZ	1.81	1.08
1:A:764:ILE:HD11	6:G:18:LEU:CB	1.82	1.08
27:r:103:LEU:HA	35:u:144:ARG:HH12	1.18	1.08
1:A:779:ILE:HD13	6:G:137:THR:HG23	1.29	1.08
5:F:415:ILE:HG13	5:F:418:ILE:HD13	1.26	1.08
14:R:111:ASP:CB	14:R:114:MET:HB2	1.82	1.07
1:A:764:ILE:N	6:G:16:PHE:O	1.87	1.07
1:A:573:TYR:HA	2:B:657:ARG:HD3	1.34	1.07
3:D:933:ARG:HD2	9:J:117:VAL:HG11	1.14	1.07
14:R:29:ALA:HA	25:p:1066:PRO:HD3	1.34	1.07
11:O:39:GLN:CD	13:Q:28:ILE:HD11	1.77	1.07
15:S:153:ARG:NE	31:w:41:ASN:OD1	1.87	1.07
11:O:39:GLN:HG2	13:Q:28:ILE:HD12	1.13	1.07
24:o:16:ARG:HB3	24:o:16:ARG:HH11	1.18	1.07
24:o:137:PRO:CG	24:o:1445:HIS:HB3	1.84	1.07
1:A:486:TRP:HH2	5:f:358:THR:HB	1.17	1.06
5:F:279:LEU:CD2	5:F:330:ARG:CZ	2.31	1.06
1:A:765:ILE:HG23	6:G:15:GLN:HG2	1.29	1.06
3:D:917:ILE:CD1	3:D:1058:VAL:HG21	1.84	1.06
5:F:17:GLU:OE2	8:I:14:LYS:HE3	1.54	1.06
5:F:279:LEU:HD22	5:F:330:ARG:NH2	1.69	1.06
11:O:79:VAL:O	11:O:90:VAL:HG13	1.54	1.06
12:P:189:ASN:HB3	13:Q:376:TRP:HZ2	1.07	1.06
3:D:881:ARG:HH21	10:L:57:VAL:HG13	1.06	1.06
5:F:68:THR:CG2	8:I:34:ARG:NH1	2.18	1.06
5:F:89:GLN:CD	9:J:210:ASN:HD22	1.62	1.06
1:A:956:PRO:HA	6:G:149:ARG:NE	1.71	1.06
3:D:881:ARG:HH22	10:L:57:VAL:CG2	1.47	1.06
14:R:46:ILE:HA	24:o:67:ARG:HH22	1.10	1.06

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:o:1158:LEU:CD2	24:o:1307:VAL:HG11	1.80	1.06
1:A:764:ILE:CG1	6:G:18:LEU:CB	2.33	1.06
21:c:67:GLY:HA3	9:j:116:LEU:CD1	1.84	1.06
5:F:369:PRO:HB2	5:F:372:THR:HB	1.37	1.05
18:V:181:ALA:HA	18:V:184:ALA:HB3	1.08	1.05
7:H:116:ARG:HD3	9:J:126:TYR:CE1	1.91	1.05
11:O:39:GLN:CG	13:Q:28:ILE:HD12	1.86	1.05
13:Q:346:LYS:CE	20:Y:27:DT:OP2	2.03	1.05
1:A:764:ILE:CG1	6:G:18:LEU:HB2	1.86	1.05
1:A:900:ASP:CB	6:G:154:LYS:HD2	1.87	1.05
5:F:15:PRO:CG	8:I:14:LYS:HG3	1.85	1.05
14:R:24:VAL:HG21	24:o:431:PHE:CE2	1.91	1.05
15:S:164:TRP:CH2	25:p:307:GLU:HA	1.92	1.05
3:D:957:ARG:HH21	4:E:434:ASP:CB	1.48	1.05
7:H:111:ALA:O	9:J:126:TYR:CZ	2.09	1.05
5:F:68:THR:HG21	8:I:34:ARG:CZ	1.87	1.05
24:o:25:VAL:HA	25:p:1166:SER:O	1.55	1.05
5:F:15:PRO:HG3	8:I:14:LYS:HG3	1.11	1.04
24:o:1060:LEU:CD1	24:o:1064:ALA:HB3	1.85	1.04
1:A:673:GLY:N	6:G:13:GLU:OE1	1.89	1.04
5:F:271:VAL:HG23	5:F:311:CYS:SG	1.91	1.04
15:S:10:ASN:O	16:T:47:LYS:HB2	1.55	1.04
24:o:365:THR:HG22	24:o:482:PHE:CD2	1.92	1.04
1:A:575:PRO:HD3	2:B:608:ASN:ND2	1.73	1.04
3:D:871:THR:CA	10:L:66:LEU:CD1	2.35	1.04
15:S:164:TRP:HH2	25:p:307:GLU:HA	1.18	1.04
24:o:393:ILE:CD1	29:t:74:ALA:HB1	1.87	1.04
24:o:480:SER:HB2	33:y:2:ASN:HD22	1.14	1.04
5:F:67:THR:CA	8:I:32:GLU:CD	2.31	1.03
11:O:10:THR:HG22	13:Q:50:LEU:HD21	1.36	1.03
15:S:44:GLN:NE2	15:S:104:GLY:CA	2.20	1.03
24:o:1060:LEU:HD11	24:o:1064:ALA:HB1	1.10	1.03
15:S:156:THR:OG1	15:S:159:GLU:HB2	1.58	1.03
1:A:779:ILE:CD1	6:G:137:THR:HG23	1.88	1.03
3:D:881:ARG:CG	10:L:57:VAL:HG11	1.87	1.03
5:F:43:VAL:HG22	8:I:43:ALA:HB1	1.35	1.03
12:P:166:GLN:HB3	20:Y:28:DT:H5"	1.40	1.03
12:P:303:LEU:CD1	20:Y:29:DA:H2	1.70	1.03
11:O:10:THR:CG2	13:Q:50:LEU:CD2	2.36	1.03
24:o:365:THR:CG2	24:o:482:PHE:CD1	2.42	1.03
3:D:889:HIS:CA	10:L:104:ARG:NH2	2.21	1.03

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:14:LEU:HD13	8:I:15:ASP:CG	1.84	1.03
18:V:181:ALA:CA	18:V:184:ALA:HB3	1.89	1.03
10:L:106:ARG:HH11	10:L:114:LYS:CE	1.68	1.02
24:o:1485:GLU:HB3	29:t:78:PRO:HB3	1.38	1.02
24:o:355:MET:CE	24:o:1459:MET:SD	2.46	1.02
27:r:110:GLU:CD	35:u:167:TYR:CD1	2.37	1.02
1:A:650:ARG:HD3	6:G:80:ILE:CD1	1.90	1.02
2:B:883:PHE:HA	7:H:222:PRO:HB2	1.40	1.02
17:U:32:LEU:HD22	18:V:161:ARG:HH21	1.21	1.01
24:o:834:THR:CG2	25:p:677:MET:HE1	1.89	1.01
17:U:32:LEU:HD22	18:V:161:ARG:CZ	1.89	1.01
1:A:764:ILE:HD11	6:G:18:LEU:HB3	1.07	1.01
13:Q:346:LYS:HE3	20:Y:27:DT:OP2	1.61	1.00
18:V:77:VAL:HG21	18:V:111:ILE:HD11	1.41	1.00
1:A:682:GLU:OE2	6:G:140:LEU:CD1	2.08	1.00
3:D:949:GLN:O	3:D:953:ILE:CG1	2.08	1.00
14:R:24:VAL:HG21	24:o:431:PHE:HE2	1.22	1.00
2:B:735:ILE:CG2	7:H:176:ARG:NH1	2.24	1.00
11:O:39:GLN:CG	13:Q:28:ILE:CD1	2.40	1.00
18:V:181:ALA:HA	18:V:184:ALA:CB	1.91	1.00
1:A:672:THR:CA	6:G:13:GLU:OE1	2.10	1.00
3:D:1000:ARG:NH1	11:O:5:LEU:CA	2.25	1.00
11:O:39:GLN:HG2	13:Q:28:ILE:CD1	1.91	1.00
15:S:44:GLN:HG2	15:S:103:ASN:HA	1.39	1.00
24:o:1158:LEU:HD21	24:o:1307:VAL:HB	1.42	1.00
1:A:764:ILE:O	6:G:16:PHE:N	1.95	0.99
1:A:765:ILE:HA	6:G:15:GLN:HA	1.42	0.99
4:E:696:TRP:CE3	4:E:703:MET:CB	2.44	0.99
4:E:696:TRP:CZ3	4:E:703:MET:HB3	1.97	0.99
24:o:716:VAL:CG1	24:o:740:GLN:HE21	1.76	0.99
24:o:1102:MET:HE2	24:o:1120:GLY:HA2	1.43	0.99
24:o:1158:LEU:CD2	24:o:1307:VAL:HG12	1.85	0.99
12:P:189:ASN:HB3	13:Q:376:TRP:CZ2	1.96	0.99
24:o:463:THR:HG22	24:o:468:SER:HB3	1.44	0.99
24:o:1160:ARG:CZ	24:o:1349:GLU:OE2	2.09	0.99
1:A:779:ILE:HG23	6:G:137:THR:HG22	1.42	0.99
5:F:87:HIS:HB3	9:J:212:LYS:HZ1	1.09	0.99
24:o:1045:LEU:O	24:o:1049:LEU:HB2	1.59	0.99
27:r:114:LEU:HD21	35:u:167:TYR:HD2	1.26	0.99
5:F:211:ARG:HB3	7:H:165:TYR:HE2	1.26	0.99
35:u:40:GLY:CA	35:u:152:VAL:CG2	2.39	0.99

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:575:PRO:HG3	2:B:610:GLU:HG2	1.41	0.98
11:O:15:LEU:HD12	13:Q:42:LEU:HD11	1.43	0.98
17:U:32:LEU:HD22	18:V:161:ARG:NE	1.78	0.98
4:E:694:LEU:HD12	4:E:703:MET:HE1	1.45	0.98
10:L:106:ARG:HH12	10:L:114:LYS:HD2	0.82	0.98
24:o:1485:GLU:CB	29:t:78:PRO:HB3	1.92	0.98
3:D:1000:ARG:HH12	11:O:5:LEU:CB	1.76	0.98
11:O:10:THR:HG21	13:Q:50:LEU:CD2	1.92	0.98
1:A:486:TRP:CH2	5:f:358:THR:HB	1.97	0.98
14:R:44:ARG:O	25:p:1067:ILE:HD11	0.82	0.98
14:R:47:ASP:H	25:p:1069:ILE:HD11	1.26	0.98
3:D:871:THR:HG22	10:L:66:LEU:HD22	0.99	0.98
5:F:321:PRO:HA	5:F:415:ILE:HD12	1.44	0.98
15:S:44:GLN:CG	15:S:103:ASN:HA	1.93	0.98
3:D:957:ARG:CZ	4:E:434:ASP:HB2	1.91	0.98
24:o:365:THR:HG22	24:o:482:PHE:CE2	1.98	0.98
24:o:716:VAL:HG12	24:o:737:PHE:HE2	1.16	0.98
1:A:618:PRO:HD2	6:G:92:CYS:SG	2.04	0.98
5:F:15:PRO:HG3	8:I:14:LYS:CG	1.94	0.98
1:A:725:CYS:SG	1:A:725:CYS:O	2.22	0.97
3:D:917:ILE:HD12	3:D:1058:VAL:HG21	1.43	0.97
14:R:30:GLY:HA3	25:p:1066:PRO:CB	1.94	0.97
27:r:103:LEU:HA	35:u:144:ARG:NH1	1.77	0.97
35:u:38:CYS:N	35:u:155:ASN:OD1	1.98	0.97
7:H:119:ILE:O	9:J:131:PRO:HG3	1.63	0.97
12:P:248:ALA:HB1	13:Q:314:LEU:HD13	1.43	0.97
4:E:696:TRP:HA	4:E:703:MET:HA	1.47	0.97
5:F:48:LYS:HG3	8:I:22:ILE:HG21	1.44	0.97
5:F:412:LEU:HD23	5:F:412:LEU:H	1.28	0.97
17:U:46:GLU:OE2	17:U:93:PHE:CE2	2.16	0.97
5:F:89:GLN:OE1	9:J:210:ASN:ND2	1.96	0.97
24:o:792:ASN:HD22	24:o:792:ASN:N	1.62	0.97
2:B:781:TYR:HB3	7:H:176:ARG:NH2	1.80	0.97
24:o:802:PHE:HE1	25:p:504:THR:HA	1.29	0.97
3:D:957:ARG:CZ	4:E:434:ASP:CB	2.43	0.96
24:o:461:GLN:CB	24:o:462:PRO:CD	2.43	0.96
24:o:1029:LEU:CD1	28:s:162:ARG:HG2	1.94	0.96
5:F:66:LEU:HB3	8:I:31:TYR:HA	1.46	0.96
5:F:51:ALA:HB1	8:I:23:LEU:CD2	1.95	0.96
12:P:303:LEU:HD12	20:Y:29:DA:H2	1.29	0.96
1:A:1077:LEU:HD21	6:G:147:ARG:CZ	1.95	0.96

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:320:ARG:CD	5:F:321:PRO:HD3	1.95	0.96
4:E:513:LEU:O	4:E:516:ILE:HG12	1.65	0.96
15:S:164:TRP:HH2	25:p:307:GLU:C	1.73	0.96
3:D:891:ILE:HG13	10:L:100:CYS:SG	2.05	0.96
1:A:755:HIS:ND1	6:G:139:PRO:HD3	1.81	0.96
3:D:889:HIS:O	10:L:104:ARG:NH2	1.98	0.96
5:F:15:PRO:HG3	8:I:14:LYS:HZ2	1.28	0.96
5:F:211:ARG:HG3	7:H:165:TYR:CD2	1.96	0.96
7:H:106:THR:OG1	9:J:161:LYS:NZ	1.98	0.96
13:Q:47:GLU:CD	13:Q:60:HIS:ND1	2.23	0.96
21:c:77:LEU:CD1	9:j:116:LEU:HD23	1.94	0.96
2:B:735:ILE:CG2	7:H:176:ARG:CZ	2.43	0.96
5:F:71:ILE:HB	8:I:38:GLN:HE21	0.81	0.96
1:A:668:PRO:HB2	6:G:10:HIS:CD2	2.01	0.96
24:o:1158:LEU:CD2	24:o:1336:LEU:HD22	1.96	0.96
8:I:60:HIS:CE1	10:L:118:LEU:HD21	1.97	0.95
24:o:1482:TYR:OH	29:t:101:LYS:NZ	1.99	0.95
12:P:203:ARG:C	13:Q:376:TRP:CH2	2.43	0.95
24:o:396:PRO:HD3	24:o:442:THR:CG2	1.95	0.95
14:R:27:TYR:CD2	25:p:1078:ARG:HB2	2.01	0.95
24:o:15:LEU:CA	25:p:1148:LEU:O	2.13	0.95
1:A:564:PRO:HG2	2:B:744:PHE:CD2	2.00	0.95
24:o:137:PRO:HG3	24:o:1445:HIS:HB3	1.49	0.95
8:I:60:HIS:CE1	10:L:118:LEU:HD23	1.99	0.95
21:c:67:GLY:HA3	9:j:116:LEU:HD11	1.48	0.95
24:o:1158:LEU:HD21	24:o:1307:VAL:HG12	1.35	0.95
3:D:881:ARG:HB2	10:L:57:VAL:CG1	1.96	0.95
3:D:1000:ARG:NH1	11:O:5:LEU:HA	1.81	0.95
5:F:14:LEU:CD1	8:I:15:ASP:OD1	2.14	0.95
11:O:39:GLN:OE1	13:Q:28:ILE:CD1	2.14	0.95
14:R:48:VAL:HG11	25:p:1077:GLY:HA2	1.46	0.95
14:R:29:ALA:CA	25:p:1066:PRO:HD3	1.96	0.95
4:E:694:LEU:HB3	4:E:703:MET:CE	1.97	0.95
24:o:716:VAL:HG13	24:o:740:GLN:NE2	1.81	0.95
5:F:14:LEU:HD22	8:I:15:ASP:OD1	1.66	0.95
1:A:1077:LEU:CG	6:G:147:ARG:NH2	2.29	0.95
5:F:286:VAL:HG11	5:F:308:VAL:HG11	1.48	0.95
1:A:763:LEU:HA	6:G:17:ILE:HD13	1.49	0.94
3:D:901:TYR:HE1	10:L:128:ILE:O	1.49	0.94
5:F:211:ARG:HG2	7:H:165:TYR:HD2	0.80	0.94
10:L:93:GLU:O	10:L:97:THR:HG23	1.66	0.94

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:63:ASN:O	12:P:189:ASN:OD1	1.83	0.94
24:o:942:VAL:HA	24:o:948:ILE:HD12	1.49	0.94
2:B:834:THR:HG23	7:H:213:LEU:CD2	1.95	0.94
3:D:935:GLU:N	8:I:128:ARG:O	1.99	0.94
1:A:349:TRP:CZ2	5:f:262:PHE:CE1	2.55	0.94
3:D:901:TYR:CE1	10:L:128:ILE:HB	2.01	0.94
27:r:16:ASP:CB	35:u:81:LYS:CE	2.37	0.94
1:A:956:PRO:HA	6:G:149:ARG:CZ	1.98	0.94
3:D:917:ILE:HD12	3:D:1058:VAL:HG11	1.46	0.94
24:o:16:ARG:HD3	25:p:1147:SER:HB3	1.47	0.94
3:D:881:ARG:CB	10:L:57:VAL:HG11	1.96	0.94
5:F:67:THR:HA	8:I:32:GLU:HG3	1.49	0.94
3:D:901:TYR:CE1	10:L:128:ILE:O	2.20	0.94
5:F:66:LEU:HD23	8:I:31:TYR:CB	1.98	0.94
15:S:8:SER:O	16:T:48:THR:C	2.11	0.94
17:U:52:LEU:HD23	18:V:161:ARG:NH1	1.82	0.94
17:U:151:THR:HB	17:U:160:GLU:OE2	1.68	0.94
2:B:310:ASP:CG	7:H:223:TYR:HE2	1.75	0.94
5:F:52:GLN:HE21	8:I:26:MET:HB3	1.32	0.94
1:A:620:LEU:HD22	6:G:67:LEU:HD22	1.33	0.94
3:D:871:THR:CG2	10:L:66:LEU:HD13	1.98	0.94
12:P:203:ARG:CA	13:Q:376:TRP:HH2	1.81	0.94
3:D:871:THR:HG21	10:L:66:LEU:HD22	1.46	0.93
1:A:956:PRO:C	6:G:149:ARG:HB3	1.94	0.93
5:F:15:PRO:CG	8:I:14:LYS:NZ	2.25	0.93
24:o:23:PHE:CE2	24:o:1439:LEU:HD23	2.03	0.93
1:A:779:ILE:CG2	6:G:137:THR:CG2	2.46	0.93
4:E:704:VAL:HG12	4:E:759:ILE:HD13	1.50	0.93
5:F:43:VAL:HG22	8:I:43:ALA:CB	1.91	0.93
1:A:665:MET:HG3	6:G:86:TYR:CG	2.03	0.93
3:D:898:VAL:HG22	10:L:113:VAL:HG23	1.50	0.93
11:O:39:GLN:CD	13:Q:28:ILE:CD1	2.42	0.93
1:A:766:ARG:HB3	6:G:16:PHE:CE1	2.03	0.93
5:F:320:ARG:HD2	5:F:321:PRO:CD	1.96	0.93
1:A:488:ALA:CB	5:f:271:VAL:HG23	1.98	0.93
1:A:620:LEU:HD22	6:G:67:LEU:HD21	1.49	0.93
11:O:56:VAL:HG11	11:O:84:VAL:H	1.34	0.93
18:V:81:ILE:HG23	18:V:102:ILE:HD13	1.51	0.93
1:A:755:HIS:CE1	6:G:139:PRO:HD3	2.03	0.93
24:o:1485:GLU:CB	29:t:78:PRO:CB	2.46	0.93
11:O:76:LEU:HB3	11:O:79:VAL:HG21	1.51	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:P:303:LEU:HD12	20:Y:29:DA:C2	2.02	0.92
24:o:355:MET:HE1	24:o:1459:MET:SD	2.07	0.92
24:o:716:VAL:CG1	24:o:740:GLN:NE2	2.32	0.92
5:F:48:LYS:HG2	8:I:22:ILE:HG23	1.51	0.92
5:F:213:ILE:HA	7:H:164:THR:O	1.68	0.92
24:o:355:MET:HE2	24:o:1459:MET:SD	2.07	0.92
24:o:460:ARG:HG2	24:o:460:ARG:HH11	1.34	0.92
3:D:871:THR:CG2	10:L:66:LEU:CD1	2.47	0.92
7:H:118:VAL:HG21	9:J:127:THR:CG2	2.00	0.92
14:R:47:ASP:N	25:p:1069:ILE:HD11	1.84	0.92
3:D:1000:ARG:HG2	3:D:1000:ARG:HH11	1.31	0.92
35:u:38:CYS:SG	35:u:43:GLY:O	2.28	0.92
3:D:933:ARG:CD	9:J:117:VAL:HG11	1.99	0.92
2:B:780:LYS:O	7:H:183:ARG:NH1	2.01	0.92
14:R:175:ARG:NH2	25:p:102:ASP:HA	1.83	0.92
24:o:465:HIS:HD2	24:o:467:MET:H	1.18	0.92
1:A:620:LEU:HD23	6:G:67:LEU:HD22	1.50	0.91
3:D:891:ILE:HG22	10:L:111:LEU:HB2	1.48	0.91
5:F:71:ILE:HD11	8:I:35:VAL:HG13	1.52	0.91
1:A:755:HIS:CD2	6:G:139:PRO:HG3	2.05	0.91
1:A:410:TRP:CH2	5:F:305:ILE:CG2	2.45	0.91
1:A:488:ALA:HB1	5:f:271:VAL:HG21	1.52	0.91
4:E:696:TRP:CH2	4:E:703:MET:SD	2.64	0.91
5:F:276:LEU:HD21	5:F:327:TRP:HB3	1.53	0.91
14:R:114:MET:SD	14:R:146:TYR:CD1	2.63	0.91
1:A:763:LEU:CA	6:G:17:ILE:HD13	2.01	0.91
4:E:694:LEU:HB3	4:E:703:MET:HE3	1.53	0.91
12:P:240:VAL:HG22	13:Q:321:SER:HB3	1.53	0.91
14:R:44:ARG:CB	25:p:1067:ILE:CD1	2.10	0.91
7:H:110:TYR:OH	9:J:160:GLN:HB3	1.70	0.91
1:A:764:ILE:CD1	6:G:18:LEU:CB	2.42	0.90
24:o:716:VAL:CG1	24:o:737:PHE:CE2	2.54	0.90
24:o:716:VAL:HG11	24:o:740:GLN:HE21	1.32	0.90
3:D:871:THR:N	10:L:66:LEU:HD11	1.85	0.90
5:F:211:ARG:HG3	7:H:165:TYR:HD2	1.31	0.90
35:u:40:GLY:HA2	35:u:152:VAL:HG21	0.92	0.90
3:D:917:ILE:HD12	3:D:1058:VAL:CB	2.01	0.90
3:D:917:ILE:HD12	3:D:1058:VAL:CG2	2.00	0.90
13:Q:55:ALA:O	13:Q:56:VAL:HG23	1.71	0.90
1:A:410:TRP:CZ3	5:F:305:ILE:HG22	2.05	0.90
3:D:917:ILE:CD1	3:D:1058:VAL:HG11	2.00	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:o:1158:LEU:HD23	24:o:1336:LEU:CD2	2.01	0.90
3:D:917:ILE:HD12	3:D:1058:VAL:CG1	2.02	0.90
3:D:1000:ARG:NH1	11:O:5:LEU:CG	2.30	0.90
24:o:137:PRO:HB2	24:o:1445:HIS:ND1	1.85	0.90
24:o:365:THR:HG23	24:o:482:PHE:CG	2.07	0.90
4:E:694:LEU:CD1	4:E:703:MET:CE	2.11	0.89
12:P:167:ASN:CG	20:Y:27:DT:H4'	1.96	0.89
1:A:495:LEU:HD13	5:f:268:ARG:NH2	1.86	0.89
5:F:66:LEU:HD23	8:I:31:TYR:HB2	1.54	0.89
1:A:763:LEU:HA	6:G:17:ILE:HA	1.55	0.89
2:B:735:ILE:HG22	7:H:176:ARG:NH1	1.86	0.89
3:D:917:ILE:HB	3:D:1058:VAL:CG1	2.03	0.89
7:H:37:LEU:HD11	9:J:138:TYR:CE2	2.07	0.89
3:D:871:THR:HA	10:L:66:LEU:CD1	2.02	0.89
24:o:1307:VAL:CG1	24:o:1336:LEU:HB3	2.02	0.89
2:B:310:ASP:CG	7:H:223:TYR:CE2	2.50	0.89
24:o:365:THR:HG21	24:o:482:PHE:CD1	2.05	0.89
27:r:60:VAL:CG1	35:u:44:PHE:CZ	2.03	0.89
12:P:203:ARG:HB3	13:Q:376:TRP:HZ3	1.28	0.89
13:Q:47:GLU:CD	13:Q:60:HIS:CG	2.50	0.89
3:D:881:ARG:NH2	10:L:57:VAL:CG1	2.30	0.88
12:P:303:LEU:HD11	19:X:-29:DT:O2	1.73	0.88
13:Q:346:LYS:CE	20:Y:27:DT:P	2.60	0.88
8:I:60:HIS:ND1	10:L:118:LEU:CD2	2.36	0.88
12:P:188:ARG:NH2	13:Q:323:GLU:O	2.05	0.88
27:r:114:LEU:HD21	35:u:167:TYR:CD2	2.09	0.88
3:D:889:HIS:C	10:L:104:ARG:NH2	2.32	0.88
5:F:415:ILE:CG1	5:F:418:ILE:HD13	2.02	0.88
1:A:764:ILE:HG13	6:G:18:LEU:CB	1.98	0.88
1:A:602:PHE:HE1	6:G:12:LEU:CD2	1.81	0.88
5:F:14:LEU:N	8:I:18:MET:HG2	1.89	0.88
5:F:279:LEU:HD23	5:F:330:ARG:NH2	1.76	0.88
15:S:164:TRP:CH2	25:p:307:GLU:CA	2.52	0.88
17:U:32:LEU:CD2	18:V:161:ARG:HH21	1.87	0.88
3:D:941:ARG:O	3:D:944:LEU:HG	1.74	0.88
24:o:137:PRO:HG2	24:o:1445:HIS:CB	2.03	0.88
1:A:511:LEU:H	1:A:511:LEU:HD22	1.37	0.88
1:A:484:ILE:HA	5:f:306:PRO:HB3	1.56	0.88
1:A:678:LEU:CD2	6:G:76:SER:HB3	2.04	0.88
2:B:762:ASP:OD1	2:B:768:PRO:CG	2.19	0.87
3:D:871:THR:N	10:L:66:LEU:HD13	1.74	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:211:ARG:HB3	7:H:165:TYR:CE2	2.08	0.87
17:U:30:HIS:NE2	17:U:65:ASN:OD1	2.05	0.87
3:D:914:VAL:HG12	10:L:70:VAL:HG11	1.55	0.87
17:U:52:LEU:CD2	18:V:161:ARG:NH1	2.38	0.87
1:A:1022:ARG:HA	1:A:1025:VAL:HB	1.54	0.87
12:P:203:ARG:HB2	13:Q:376:TRP:CZ2	2.09	0.87
14:R:27:TYR:HD2	25:p:1078:ARG:HB2	1.38	0.87
15:S:164:TRP:CD1	15:S:168:ASN:HD21	1.92	0.87
35:u:44:PHE:CE2	35:u:46:ILE:CG1	2.57	0.87
1:A:900:ASP:HB3	6:G:154:LYS:CD	2.04	0.87
3:D:946:PHE:HD2	4:E:513:LEU:HD13	1.16	0.87
15:S:11:VAL:O	15:S:12:THR:CG2	2.23	0.87
1:A:650:ARG:NH2	6:G:78:LYS:HZ3	1.71	0.87
4:E:694:LEU:HD13	4:E:703:MET:HE2	1.52	0.87
5:F:51:ALA:O	8:I:28:ILE:HD11	1.74	0.87
1:A:620:LEU:CB	6:G:67:LEU:HD21	2.04	0.87
1:A:956:PRO:O	6:G:149:ARG:CB	2.21	0.87
3:D:934:TYR:CG	8:I:129:LEU:HD23	2.10	0.87
5:F:14:LEU:CD2	8:I:18:MET:HB3	2.04	0.87
10:L:102:LEU:HA	10:L:105:HIS:HD2	1.36	0.87
1:A:673:GLY:HA3	6:G:15:GLN:NE2	1.90	0.87
3:D:935:GLU:O	8:I:128:ARG:O	1.91	0.87
3:D:995:GLU:OE2	12:P:181:LYS:NZ	2.08	0.87
5:F:87:HIS:CB	9:J:212:LYS:NZ	2.38	0.87
24:o:705:THR:OG1	24:o:751:LYS:CD	2.22	0.87
5:F:48:LYS:CG	8:I:22:ILE:CG2	2.01	0.86
5:F:87:HIS:HB3	9:J:212:LYS:HZ3	1.39	0.86
5:F:415:ILE:HG12	5:F:418:ILE:HB	1.57	0.86
1:A:410:TRP:CZ2	5:F:305:ILE:HD13	2.11	0.86
5:F:279:LEU:HB3	5:F:330:ARG:CZ	2.05	0.86
17:U:157:CYS:SG	36:U:501:ZN:ZN	1.64	0.86
5:F:48:LYS:HE3	8:I:22:ILE:HG12	1.56	0.86
24:o:365:THR:HG22	24:o:482:PHE:CG	2.05	0.86
24:o:491:PRO:HG2	24:o:535:MET:HE2	1.55	0.86
15:S:44:GLN:HG3	15:S:104:GLY:N	1.91	0.86
5:F:15:PRO:HB3	8:I:14:LYS:CE	2.05	0.86
11:O:18:SER:HA	13:Q:45:LEU:HD13	1.58	0.86
1:A:672:THR:HB	6:G:13:GLU:OE2	1.76	0.86
3:D:889:HIS:HA	10:L:104:ARG:HH22	1.36	0.86
17:U:32:LEU:HD22	18:V:161:ARG:HE	1.37	0.86
24:o:1158:LEU:HD23	24:o:1307:VAL:CG1	2.05	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1077:LEU:HD11	6:G:147:ARG:NH1	1.90	0.86
18:V:224:THR:HG22	18:V:227:SER:HB2	1.57	0.86
2:B:835:ARG:CD	7:H:187:GLU:OE2	2.23	0.85
7:H:111:ALA:HB1	9:J:126:TYR:CE2	2.11	0.85
12:P:188:ARG:HH22	13:Q:326:GLN:HB2	0.76	0.85
24:o:364:ARG:CB	24:o:364:ARG:HH11	1.88	0.85
24:o:14:PRO:O	25:p:1148:LEU:N	2.09	0.85
24:o:1343:LEU:HB3	24:o:1364:GLU:OE2	1.75	0.85
3:D:1000:ARG:HH12	11:O:5:LEU:CA	1.85	0.85
5:F:71:ILE:HD11	8:I:35:VAL:HG22	1.57	0.85
1:A:410:TRP:CZ2	5:F:305:ILE:CD1	2.60	0.85
18:V:77:VAL:HG11	18:V:119:LEU:CD1	2.07	0.85
24:o:1307:VAL:HG22	24:o:1338:THR:HG22	1.57	0.85
1:A:672:THR:C	6:G:13:GLU:OE1	2.19	0.85
3:D:881:ARG:NH2	10:L:57:VAL:CB	2.38	0.85
5:F:71:ILE:CD1	8:I:35:VAL:HA	2.07	0.85
5:F:267:VAL:HG11	5:F:310:THR:HB	0.87	0.85
18:V:117:GLN:HE21	18:V:121:THR:HG23	1.39	0.85
1:A:763:LEU:CB	6:G:17:ILE:HD13	2.07	0.85
5:F:17:GLU:OE2	8:I:14:LYS:CE	2.24	0.85
24:o:1451:MET:HE2	24:o:1451:MET:HA	1.57	0.85
35:u:86:ASP:OD2	35:u:171:VAL:HG21	1.75	0.85
3:D:881:ARG:NH2	10:L:57:VAL:HG13	1.90	0.85
3:D:934:TYR:CE1	8:I:129:LEU:HG	2.11	0.85
14:R:175:ARG:NH2	25:p:102:ASP:CA	2.39	0.85
24:o:137:PRO:HG2	24:o:1445:HIS:HB3	1.59	0.85
5:F:286:VAL:HG21	5:F:308:VAL:HG12	1.59	0.85
5:F:320:ARG:HH21	5:F:415:ILE:CB	1.87	0.85
3:D:917:ILE:HB	3:D:1058:VAL:HG13	1.59	0.85
1:A:486:TRP:HH2	5:f:358:THR:CB	1.89	0.84
1:A:765:ILE:CG2	6:G:15:GLN:HG2	2.06	0.84
1:A:1052:ARG:HG2	1:A:1057:GLU:HG2	1.58	0.84
5:F:51:ALA:HB2	8:I:23:LEU:HD21	1.58	0.84
3:D:891:ILE:HG23	10:L:111:LEU:HB2	1.57	0.84
5:F:267:VAL:HG12	5:F:310:THR:CB	1.98	0.84
12:P:203:ARG:HB3	13:Q:376:TRP:CH2	1.82	0.84
18:V:117:GLN:HE21	18:V:121:THR:CG2	1.90	0.84
12:P:249:LYS:N	13:Q:314:LEU:HD12	1.93	0.84
2:B:735:ILE:HG21	7:H:176:ARG:NH1	1.92	0.84
3:D:871:THR:HG23	10:L:66:LEU:CD1	2.07	0.84
11:O:15:LEU:CD1	13:Q:42:LEU:HD11	2.08	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:LEU:HB2	6:G:67:LEU:HD21	1.58	0.84
1:A:764:ILE:HB	6:G:16:PHE:CE2	2.13	0.84
2:B:835:ARG:HD3	7:H:187:GLU:HG3	1.58	0.84
3:D:871:THR:HG23	10:L:66:LEU:HD21	1.57	0.84
3:D:901:TYR:HE1	10:L:128:ILE:C	1.85	0.84
17:U:150:GLY:O	35:u:93:ASN:ND2	2.11	0.84
1:A:602:PHE:HD1	6:G:12:LEU:HD21	1.37	0.84
1:A:1053:PHE:O	1:A:1057:GLU:HB2	1.78	0.84
3:D:995:GLU:CD	12:P:181:LYS:NZ	2.36	0.84
24:o:861:GLN:HG3	24:o:1096:GLY:HA3	1.57	0.84
1:A:572:TYR:CD2	2:B:689:GLN:HB2	2.13	0.84
5:F:321:PRO:HA	5:F:415:ILE:CD1	2.08	0.84
24:o:802:PHE:CE1	25:p:504:THR:HG22	2.13	0.84
5:F:286:VAL:HG11	5:F:308:VAL:CG1	2.08	0.83
24:o:23:PHE:HE2	24:o:1439:LEU:HD23	1.43	0.83
2:B:310:ASP:OD1	7:H:223:TYR:CE2	2.31	0.83
5:F:48:LYS:CD	8:I:22:ILE:HG23	2.08	0.83
17:U:20:TYR:HB3	17:U:191:LEU:HD22	1.59	0.83
3:D:957:ARG:HH22	4:E:434:ASP:HB3	1.39	0.83
15:S:164:TRP:CH2	25:p:307:GLU:C	2.53	0.83
21:c:67:GLY:HA3	9:j:116:LEU:HD13	1.60	0.83
24:o:13:CYS:HB2	24:o:14:PRO:HD2	1.60	0.83
24:o:1063:GLU:OE1	24:o:1063:GLU:HA	1.77	0.83
27:r:16:ASP:CB	35:u:81:LYS:HE3	2.04	0.83
1:A:1077:LEU:HD21	6:G:147:ARG:NE	1.93	0.83
8:I:60:HIS:ND1	10:L:118:LEU:HD21	1.92	0.83
24:o:1160:ARG:NH1	24:o:1349:GLU:OE2	2.12	0.83
1:A:416:TRP:HE1	5:F:313:VAL:HB	1.43	0.83
3:D:871:THR:CB	10:L:66:LEU:HD13	2.08	0.83
7:H:111:ALA:O	9:J:126:TYR:CE1	2.31	0.83
12:P:239:ARG:HH21	13:Q:318:ASP:H	1.27	0.83
24:o:15:LEU:HD23	24:o:15:LEU:O	1.78	0.83
24:o:15:LEU:CB	25:p:1148:LEU:O	2.26	0.83
24:o:365:THR:CG2	24:o:482:PHE:CD2	2.58	0.83
24:o:1177:TYR:OH	31:w:28:GLU:OE1	1.96	0.83
3:D:871:THR:HG22	10:L:66:LEU:CG	2.08	0.83
18:V:190:LEU:HD12	18:V:204:ASN:HA	1.61	0.83
3:D:891:ILE:CG2	10:L:111:LEU:CB	2.54	0.83
5:F:14:LEU:CG	8:I:15:ASP:OD1	2.26	0.83
5:F:47:ILE:CD1	8:I:19:MET:CE	1.97	0.82
24:o:196:LEU:HD13	24:o:311:GLN:HG3	1.60	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:S:44:GLN:HE21	15:S:104:GLY:N	1.78	0.82
24:o:16:ARG:HB3	24:o:16:ARG:NH1	1.94	0.82
2:B:883:PHE:H	2:B:886:ILE:HD12	1.42	0.82
5:F:214:HIS:H	7:H:164:THR:HG22	1.42	0.82
24:o:365:THR:HG22	24:o:482:PHE:CZ	2.15	0.82
5:F:89:GLN:CD	9:J:210:ASN:ND2	2.37	0.82
5:F:211:ARG:CG	7:H:165:TYR:CE2	2.62	0.82
12:P:248:ALA:C	13:Q:314:LEU:CD1	2.49	0.82
14:R:44:ARG:HG2	25:p:1067:ILE:HG23	1.59	0.82
17:U:32:LEU:HD13	18:V:161:ARG:NH2	1.94	0.82
1:A:569:ASN:CG	2:B:689:GLN:HA	2.04	0.82
3:D:901:TYR:CE1	10:L:128:ILE:CB	2.62	0.82
7:H:111:ALA:HB2	9:J:157:LEU:CD1	2.09	0.82
2:B:883:PHE:CA	7:H:222:PRO:HB2	2.10	0.82
5:F:15:PRO:CB	8:I:14:LYS:CE	2.57	0.82
24:o:379:GLY:HA2	24:o:475:ARG:O	1.80	0.82
4:E:747:LEU:HD22	4:E:747:LEU:H	1.44	0.82
5:F:14:LEU:CD2	8:I:15:ASP:OD1	2.27	0.82
5:F:244:GLN:OE1	7:H:133:ALA:CB	2.26	0.82
5:F:322:ASP:C	5:F:324:ASP:H	1.86	0.82
14:R:47:ASP:HB2	25:p:1069:ILE:CG1	2.09	0.82
15:S:6:PRO:O	15:S:10:ASN:HB3	1.76	0.82
1:A:763:LEU:CD1	6:G:91:ILE:HD13	2.10	0.82
1:A:779:ILE:HD13	6:G:137:THR:CG2	2.09	0.82
7:H:73:GLY:HA3	9:J:142:ALA:HB3	1.60	0.82
10:L:101:GLN:C	10:L:105:HIS:CD2	2.57	0.82
15:S:44:GLN:NE2	15:S:103:ASN:C	2.36	0.82
4:E:429:LEU:HB3	4:E:432:LEU:HD13	1.62	0.82
12:P:203:ARG:CA	13:Q:376:TRP:CH2	2.60	0.82
24:o:397:PHE:HZ	24:o:1486:ILE:CD1	1.93	0.82
1:A:682:GLU:HG3	6:G:72:CYS:CB	2.10	0.81
5:F:80:VAL:CG1	8:I:45:ARG:HH12	1.93	0.81
5:F:415:ILE:HG13	5:F:418:ILE:CD1	2.10	0.81
18:V:73:TYR:HB2	18:V:115:GLN:HG2	1.61	0.81
24:o:196:LEU:HD13	24:o:311:GLN:CG	2.10	0.81
12:P:301:VAL:HG21	19:X:-28:DA:H4'	1.62	0.81
24:o:1058:PHE:O	24:o:1059:ARG:O	1.96	0.81
3:D:905:ALA:O	10:L:126:MET:HE1	1.80	0.81
24:o:1115:LYS:HE3	24:o:1337:GLU:HG2	1.63	0.81
1:A:564:PRO:CG	2:B:744:PHE:CE2	2.62	0.81
8:I:132:LEU:HG	9:J:121:MET:HE2	1.61	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:P:203:ARG:O	13:Q:376:TRP:CH2	2.33	0.81
18:V:117:GLN:NE2	18:V:121:THR:HG23	1.96	0.81
5:F:290:MET:HE1	5:F:337:VAL:HB	1.63	0.81
1:A:602:PHE:CD1	6:G:12:LEU:CD2	2.50	0.81
3:D:914:VAL:HG11	10:L:70:VAL:HG21	1.62	0.81
15:S:109:LYS:HD2	15:S:149:LEU:CD2	2.11	0.81
24:o:15:LEU:HB2	25:p:1148:LEU:O	1.80	0.81
1:A:682:GLU:CD	6:G:140:LEU:HD12	2.06	0.81
5:F:267:VAL:HG12	5:F:310:THR:HG21	0.81	0.81
14:R:24:VAL:CG2	24:o:431:PHE:HE2	1.94	0.81
4:E:704:VAL:HG11	4:E:747:LEU:HG	1.63	0.80
24:o:23:PHE:CE2	24:o:1439:LEU:CD2	2.65	0.80
24:o:396:PRO:HD3	24:o:442:THR:HG21	1.62	0.80
3:D:891:ILE:CG2	10:L:111:LEU:HD22	2.12	0.80
3:d:1082:ALA:HB2	10:l:83:MET:HE2	1.63	0.80
5:f:447:ALA:HA	5:f:456:GLY:HA3	1.61	0.80
24:o:802:PHE:CE1	25:p:504:THR:HA	2.15	0.80
2:B:159:LEU:HD23	2:B:159:LEU:H	1.46	0.80
3:D:881:ARG:HG2	10:L:57:VAL:HG11	1.62	0.80
3:D:1000:ARG:NH1	11:O:5:LEU:O	2.14	0.80
1:A:779:ILE:HG12	6:G:137:THR:HG21	1.63	0.80
21:c:77:LEU:HD13	9:j:116:LEU:HD23	1.62	0.80
24:o:463:THR:CB	24:o:468:SER:HB2	2.11	0.80
24:o:973:GLY:HA2	24:o:1328:PHE:CE2	2.16	0.80
24:o:1147:SER:CA	24:o:1153:ARG:HD2	2.12	0.80
1:A:665:MET:CG	6:G:86:TYR:CD2	2.63	0.80
3:D:889:HIS:CA	10:L:104:ARG:HH21	1.86	0.80
17:U:145:PHE:CE2	35:u:98:PHE:HZ	1.96	0.80
1:A:650:ARG:CD	6:G:80:ILE:CD1	2.53	0.80
1:A:779:ILE:HG12	6:G:137:THR:CG2	2.11	0.80
8:I:132:LEU:HG	9:J:121:MET:CE	2.12	0.80
24:o:1310:HIS:NE2	24:o:1335:ILE:HD11	1.97	0.80
24:o:1310:HIS:CE1	24:o:1335:ILE:HD11	2.16	0.80
1:A:763:LEU:HB2	6:G:17:ILE:HD13	1.64	0.80
1:A:1009:LYS:HE2	24:o:187:TYR:CD2	2.17	0.80
3:D:881:ARG:NH2	10:L:57:VAL:HG21	1.92	0.80
5:F:89:GLN:NE2	9:J:210:ASN:HD22	1.79	0.80
5:F:271:VAL:HG21	5:F:311:CYS:HG	1.47	0.80
1:A:620:LEU:CD2	6:G:67:LEU:HD21	2.07	0.79
1:A:779:ILE:CG1	6:G:137:THR:CG2	2.60	0.79
2:B:781:TYR:HB3	7:H:176:ARG:HH21	1.47	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:835:ARG:HD2	7:H:187:GLU:OE2	1.82	0.79
11:O:88:ILE:HG21	13:Q:360:LEU:HD13	1.63	0.79
1:A:672:THR:CA	6:G:13:GLU:CD	2.53	0.79
5:F:332:PHE:HA	5:F:335:ARG:HD3	1.64	0.79
24:o:137:PRO:HG2	24:o:1445:HIS:CG	2.17	0.79
3:D:934:TYR:HA	8:I:129:LEU:HA	1.63	0.79
23:m:31:LEU:HD23	23:m:31:LEU:H	1.47	0.79
1:A:1009:LYS:CE	24:o:187:TYR:CD2	2.65	0.79
3:D:949:GLN:N	3:D:949:GLN:HE21	1.81	0.79
1:A:1009:LYS:NZ	24:o:187:TYR:CD2	2.50	0.79
1:A:764:ILE:CG1	6:G:18:LEU:HB3	2.03	0.79
3:D:871:THR:CG2	10:L:66:LEU:CG	2.61	0.79
35:u:44:PHE:CD2	35:u:46:ILE:CG1	2.65	0.79
1:A:1009:LYS:HE2	24:o:187:TYR:CG	2.18	0.79
24:o:396:PRO:HD3	24:o:442:THR:HG23	1.62	0.79
1:A:602:PHE:CE1	6:G:12:LEU:HD23	2.17	0.79
3:D:963:ARG:O	3:D:963:ARG:HD3	1.83	0.79
24:o:868:MET:SD	24:o:1401:LEU:CD1	2.71	0.79
5:F:309:MET:C	5:F:312:ILE:HD11	2.06	0.79
13:Q:358:MET:HE2	13:Q:367:PHE:HD2	1.46	0.79
24:o:24:GLY:O	25:p:1167:ILE:HA	1.83	0.79
27:r:110:GLU:HG3	35:u:167:TYR:HB2	1.65	0.79
3:D:891:ILE:HG21	10:L:111:LEU:CD2	2.11	0.78
24:o:364:ARG:NH2	24:o:500:GLU:OE1	2.16	0.78
5:F:51:ALA:HB2	8:I:23:LEU:CD2	2.12	0.78
5:F:320:ARG:HD3	5:F:415:ILE:CG2	2.12	0.78
24:o:1147:SER:HB2	24:o:1153:ARG:CD	2.13	0.78
12:P:203:ARG:HB2	13:Q:376:TRP:CZ3	1.99	0.78
18:V:190:LEU:HB2	18:V:203:PHE:O	1.83	0.78
1:A:755:HIS:NE2	6:G:139:PRO:HG3	1.98	0.78
3:D:1000:ARG:NH1	11:O:5:LEU:C	2.41	0.78
14:R:175:ARG:NH2	25:p:102:ASP:CB	2.46	0.78
24:o:1177:TYR:OH	31:w:28:GLU:CD	2.27	0.78
25:p:68:GLN:HB3	25:p:83:ARG:HB3	1.64	0.78
27:r:110:GLU:OE2	35:u:167:TYR:CG	2.36	0.78
2:B:735:ILE:HG22	7:H:176:ARG:HH12	1.46	0.78
24:o:1158:LEU:CD2	24:o:1307:VAL:HB	2.11	0.78
1:A:682:GLU:HG2	6:G:140:LEU:CD1	2.14	0.78
5:F:273:GLN:NE2	5:F:273:GLN:H	1.81	0.78
4:e:747:LEU:HD23	4:e:747:LEU:H	1.47	0.78
24:o:1101:GLN:NE2	24:o:1101:GLN:H	1.81	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:901:TYR:CD1	10:L:128:ILE:HG22	2.19	0.78
5:F:47:ILE:HD13	8:I:19:MET:SD	2.24	0.78
12:P:249:LYS:N	13:Q:314:LEU:CD1	2.45	0.78
3:D:935:GLU:HB2	8:I:130:LYS:HG3	1.64	0.78
12:P:303:LEU:CD1	20:Y:29:DA:C2	2.61	0.78
14:R:226:LYS:NZ	34:z:40:GLY:N	2.32	0.78
5:F:320:ARG:NH2	5:F:415:ILE:CB	2.47	0.77
27:r:115:ILE:HG22	27:r:117:SER:H	1.49	0.77
3:D:946:PHE:HZ	4:E:527:ILE:HD12	1.50	0.77
3:D:1083:PHE:CE2	4:E:585:ASN:ND2	2.38	0.77
13:Q:43:LYS:O	13:Q:47:GLU:HG3	1.84	0.77
10:l:93:GLU:O	10:l:97:THR:HG23	1.83	0.77
24:o:480:SER:HB2	33:y:2:ASN:ND2	1.96	0.77
5:F:342:LYS:HE2	5:F:383:LEU:O	1.84	0.77
24:o:1013:VAL:HG13	24:o:1049:LEU:HD13	1.65	0.77
5:F:71:ILE:HD11	8:I:35:VAL:CG1	2.13	0.77
5:F:80:VAL:HG11	8:I:42:PHE:CE1	2.19	0.77
14:R:109:SER:O	14:R:112:ARG:HG3	1.85	0.77
24:o:461:GLN:HB3	24:o:462:PRO:HD2	1.62	0.77
19:X:-30:DA:H2'	19:X:-30:DA:OP2	1.83	0.77
24:o:507:GLN:HB2	25:p:1105:GLU:OE2	1.85	0.77
27:r:60:VAL:HG11	35:u:44:PHE:CE1	2.12	0.77
1:A:900:ASP:CA	6:G:154:LYS:HD2	2.14	0.77
24:o:1098:PRO:HG3	24:o:1393:VAL:HG21	1.65	0.77
17:U:92:TYR:CE2	17:U:94:ILE:HD11	2.20	0.77
1:A:665:MET:HE1	6:G:78:LYS:HD3	1.66	0.77
3:D:946:PHE:HZ	4:E:527:ILE:CD1	1.97	0.77
5:F:71:ILE:HD11	8:I:35:VAL:CB	2.15	0.77
5:F:71:ILE:CD1	8:I:35:VAL:HG13	2.15	0.77
5:F:213:ILE:HD13	7:H:163:PRO:HB3	1.67	0.77
24:o:924:TYR:OH	24:o:952:LEU:HB2	1.85	0.77
24:o:20:ARG:HD2	24:o:1448:SER:OG	1.84	0.76
7:H:117:MET:O	9:J:129:THR:HA	1.84	0.76
12:P:239:ARG:HH21	13:Q:318:ASP:N	1.82	0.76
15:S:50:ASP:HB3	15:S:97:PRO:HG2	1.66	0.76
24:o:1486:ILE:CB	24:o:1487:PRO:HD3	2.13	0.76
25:p:83:ARG:HG3	25:p:133:ILE:HG23	1.68	0.76
24:o:1013:VAL:HG22	24:o:1049:LEU:HD22	1.67	0.76
14:R:44:ARG:HG2	25:p:1067:ILE:CG2	2.14	0.76
15:S:10:ASN:HB3	16:T:47:LYS:HD2	1.67	0.76
18:V:77:VAL:HG11	18:V:119:LEU:HD11	1.64	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1052:ARG:O	1:A:1052:ARG:NE	2.19	0.76
5:F:14:LEU:CA	8:I:18:MET:HG2	2.15	0.76
5:F:211:ARG:CB	7:H:165:TYR:CE2	2.69	0.76
7:H:102:PHE:CZ	9:J:158:ALA:HA	2.20	0.76
15:S:44:GLN:NE2	15:S:104:GLY:N	2.33	0.76
15:S:44:GLN:O	15:S:103:ASN:N	2.16	0.76
24:o:792:ASN:N	24:o:792:ASN:ND2	2.33	0.76
35:u:86:ASP:CG	35:u:171:VAL:HG21	2.10	0.76
3:D:1085:LYS:HZ3	10:L:83:MET:HE1	1.51	0.76
5:F:321:PRO:CA	5:F:415:ILE:HD12	2.15	0.76
11:O:82:ARG:HH21	11:O:87:LEU:HB2	1.51	0.76
1:A:671:LEU:HD22	6:G:87:LYS:O	1.84	0.76
15:S:6:PRO:C	15:S:10:ASN:HB2	2.10	0.76
24:o:834:THR:HG23	25:p:677:MET:HE1	1.64	0.76
3:D:995:GLU:OE1	12:P:181:LYS:NZ	2.19	0.76
7:H:118:VAL:HG21	9:J:127:THR:HG23	1.67	0.76
1:A:410:TRP:CH2	5:F:305:ILE:HD13	2.21	0.76
4:E:518:LYS:HD2	4:E:518:LYS:O	1.85	0.76
5:F:51:ALA:CB	8:I:23:LEU:HD21	2.15	0.76
27:r:26:PHE:HE2	35:u:80:PHE:HZ	1.32	0.76
1:A:665:MET:HE2	6:G:86:TYR:CB	2.15	0.76
10:L:106:ARG:HH12	10:L:114:LYS:CG	1.99	0.76
24:o:1060:LEU:CD1	24:o:1064:ALA:HB1	2.03	0.76
25:p:953:ASP:OD1	26:q:36:ARG:NH2	2.19	0.76
1:A:779:ILE:HG23	6:G:137:THR:CG2	2.12	0.75
17:U:32:LEU:CD2	18:V:161:ARG:NH2	2.44	0.75
5:F:412:LEU:H	5:F:412:LEU:CD2	1.98	0.75
1:A:1009:LYS:HZ3	24:o:187:TYR:HB2	1.51	0.75
7:H:36:THR:HG21	9:J:134:VAL:HG21	1.67	0.75
12:P:166:GLN:HB2	20:Y:28:DT:H5''	1.69	0.75
14:R:30:GLY:N	25:p:1066:PRO:HB3	2.01	0.75
15:S:44:GLN:HE21	15:S:104:GLY:CA	1.89	0.75
15:S:44:GLN:CG	15:S:103:ASN:C	2.59	0.75
24:o:1029:LEU:HD11	28:s:162:ARG:HG2	1.69	0.75
18:V:81:ILE:HG23	18:V:102:ILE:CD1	2.17	0.75
1:A:1077:LEU:CD1	6:G:147:ARG:CZ	2.43	0.75
5:F:274:ASN:HB2	5:F:317:LEU:H	1.52	0.75
17:U:32:LEU:CD2	18:V:161:ARG:HE	1.99	0.75
24:o:1160:ARG:NH2	24:o:1349:GLU:HG3	2.01	0.75
2:B:835:ARG:HD3	7:H:187:GLU:CG	2.16	0.75
21:c:77:LEU:HD12	9:j:116:LEU:HD23	1.68	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:650:ARG:HD2	6:G:80:ILE:HD12	1.68	0.75
5:F:43:VAL:HG21	8:I:43:ALA:CB	2.03	0.75
17:U:164:ASP:OD2	17:U:166:SER:O	2.04	0.75
24:o:868:MET:SD	24:o:1401:LEU:HD13	2.27	0.75
24:o:745:LEU:HD13	24:o:790:GLN:OE1	1.87	0.74
24:o:1177:TYR:HH	31:w:28:GLU:CD	1.94	0.74
4:E:359:LEU:HD12	4:E:359:LEU:O	1.87	0.74
5:F:71:ILE:HD11	8:I:35:VAL:CG2	2.16	0.74
14:R:146:TYR:O	14:R:149:LYS:HG3	1.86	0.74
24:o:321:GLU:OE2	24:o:340:LYS:NZ	2.20	0.74
1:A:682:GLU:HG2	6:G:140:LEU:HD13	1.69	0.74
3:D:934:TYR:CE2	8:I:129:LEU:HD21	2.22	0.74
5:F:213:ILE:HG22	7:H:164:THR:O	1.87	0.74
14:R:29:ALA:C	25:p:1066:PRO:HD3	2.11	0.74
24:o:79:THR:HG23	25:p:1072:ARG:NH1	2.00	0.74
1:A:675:ASP:OD1	6:G:78:LYS:NZ	2.21	0.74
2:B:792:ASN:ND2	2:B:846:TYR:HB3	2.03	0.74
24:o:491:PRO:HG2	24:o:535:MET:CE	2.17	0.74
8:I:60:HIS:HE1	10:L:118:LEU:HD22	0.92	0.74
14:R:44:ARG:CA	25:p:1067:ILE:CD1	2.65	0.74
14:R:171:GLU:HB3	25:p:101:ARG:NH1	2.02	0.74
27:r:26:PHE:CE2	35:u:80:PHE:HZ	2.04	0.74
3:D:881:ARG:HH21	10:L:57:VAL:CB	1.98	0.74
3:D:901:TYR:CE1	10:L:128:ILE:HG22	2.22	0.74
4:E:377:LEU:HD22	4:E:426:ARG:HA	1.69	0.74
14:R:175:ARG:HH22	25:p:102:ASP:CB	2.01	0.74
15:S:164:TRP:CD1	15:S:168:ASN:ND2	2.54	0.74
17:U:35:ASP:O	17:U:38:ILE:HG12	1.87	0.74
24:o:1486:ILE:HG13	24:o:1487:PRO:HD3	0.77	0.74
1:A:764:ILE:HB	6:G:16:PHE:CD2	2.23	0.74
1:A:764:ILE:HG12	6:G:18:LEU:N	2.02	0.74
3:D:935:GLU:HB2	8:I:130:LYS:CG	2.17	0.74
6:G:43:LEU:HD13	6:G:58:VAL:HG22	1.69	0.74
14:R:175:ARG:HH21	25:p:102:ASP:HA	1.49	0.74
10:L:102:LEU:HA	10:L:105:HIS:CD2	2.21	0.74
24:o:461:GLN:CB	24:o:462:PRO:HD2	2.15	0.74
31:w:30:LYS:HA	31:w:33:ARG:HH21	1.53	0.74
3:D:941:ARG:O	3:D:944:LEU:CG	2.36	0.74
5:F:211:ARG:CB	7:H:165:TYR:HE2	2.00	0.74
15:S:116:GLY:CA	25:p:356:PHE:HD1	1.95	0.74
15:S:126:ILE:HB	15:S:138:PHE:HB2	1.70	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:672:THR:CB	6:G:13:GLU:OE2	2.36	0.73
1:A:682:GLU:CG	6:G:140:LEU:CD1	2.66	0.73
1:A:671:LEU:O	6:G:88:THR:HB	1.89	0.73
1:A:682:GLU:HG3	6:G:72:CYS:HB2	1.69	0.73
5:F:66:LEU:HD23	8:I:31:TYR:HB3	1.68	0.73
5:F:309:MET:HA	5:F:312:ILE:HD11	0.78	0.73
11:O:89:LYS:H	13:Q:361:ASN:HD21	1.36	0.73
3:D:946:PHE:CZ	4:E:527:ILE:HD12	2.23	0.73
5:F:322:ASP:O	5:F:324:ASP:N	2.21	0.73
12:P:188:ARG:NH1	13:Q:322:ASP:OD2	2.16	0.73
5:F:313:VAL:HG13	5:F:376:SER:H	1.53	0.73
5:F:114:LEU:HD13	7:H:53:ALA:HB3	1.71	0.73
11:O:58:PHE:CD1	11:O:58:PHE:N	2.57	0.73
16:T:47:LYS:HG2	16:T:52:THR:HG23	1.69	0.73
24:o:1210:TRP:HD1	24:o:1281:ASP:OD2	1.72	0.73
24:o:463:THR:HG22	24:o:468:SER:CB	2.18	0.73
24:o:864:LEU:O	24:o:864:LEU:HD23	1.88	0.73
1:A:673:GLY:HA3	6:G:15:GLN:HE22	1.53	0.72
5:F:66:LEU:O	8:I:32:GLU:HG3	1.88	0.72
14:R:28:ARG:CG	25:p:1078:ARG:HH11	2.01	0.72
14:R:226:LYS:NZ	34:z:39:CYS:C	2.47	0.72
31:w:81:THR:HG22	31:w:83:ASP:H	1.54	0.72
24:o:847:LEU:HD11	25:p:516:GLU:HG3	1.72	0.72
2:B:241:PRO:HG2	2:B:496:MET:HE1	1.72	0.72
3:D:940:VAL:HG13	3:D:943:GLN:CD	2.14	0.72
3:D:1000:ARG:HH11	11:O:5:LEU:HA	1.55	0.72
15:S:44:GLN:HG3	15:S:103:ASN:C	2.14	0.72
1:A:573:TYR:CD2	2:B:657:ARG:HA	2.24	0.72
12:P:188:ARG:NH2	13:Q:326:GLN:CB	2.31	0.72
12:P:259:VAL:HG11	20:Y:28:DT:O2	1.90	0.72
1:A:572:TYR:CE2	2:B:689:GLN:HB2	2.25	0.72
3:D:957:ARG:HH21	4:E:434:ASP:CG	1.98	0.72
5:F:68:THR:OG1	8:I:32:GLU:OE1	2.05	0.72
35:u:40:GLY:HA2	35:u:152:VAL:HG22	1.66	0.72
2:B:735:ILE:HG21	7:H:176:ARG:CZ	2.18	0.72
13:Q:55:ALA:O	13:Q:56:VAL:CG2	2.38	0.72
24:o:460:ARG:HB2	24:o:501:MET:HE3	1.69	0.72
1:A:567:LEU:HD22	2:B:745:GLN:CG	2.19	0.72
3:D:901:TYR:CE1	10:L:128:ILE:CG2	2.73	0.72
5:F:67:THR:HB	8:I:32:GLU:OE2	1.89	0.72
8:I:132:LEU:HD21	9:J:121:MET:HE1	1.72	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:R:44:ARG:NH2	25:p:1067:ILE:CG2	2.53	0.72
1:A:620:LEU:H	6:G:93:GLN:HE22	1.38	0.71
3:D:891:ILE:HG22	10:L:111:LEU:CB	2.19	0.71
12:P:203:ARG:O	13:Q:376:TRP:HH2	1.67	0.71
24:o:463:THR:CG2	24:o:468:SER:CB	2.68	0.71
24:o:1210:TRP:CE2	24:o:1282:ASP:OD1	2.43	0.71
24:o:1347:LEU:HD21	24:o:1357:THR:HB	1.71	0.71
25:p:133:ILE:HA	25:p:139:GLN:HE22	1.55	0.71
25:p:274:ARG:HG2	25:p:279:VAL:HA	1.70	0.71
25:p:344:GLN:NE2	25:p:353:VAL:O	2.22	0.71
5:F:418:ILE:H	5:F:418:ILE:HD12	1.54	0.71
7:H:66:GLN:HG3	9:J:138:TYR:CE1	2.25	0.71
14:R:27:TYR:HD2	25:p:1078:ARG:CB	2.03	0.71
1:A:678:LEU:HD21	6:G:76:SER:HB3	1.71	0.71
1:A:779:ILE:HG21	6:G:137:THR:CG2	2.18	0.71
4:E:696:TRP:CZ3	4:E:703:MET:SD	2.83	0.71
6:G:129:LYS:O	6:G:129:LYS:NZ	2.23	0.71
14:R:44:ARG:NH2	25:p:1067:ILE:HG21	2.04	0.71
18:V:163:LEU:O	18:V:163:LEU:HD13	1.91	0.71
27:r:16:ASP:HA	35:u:81:LYS:HB3	1.72	0.71
3:D:881:ARG:HB2	10:L:57:VAL:HG12	1.71	0.71
11:O:61:SER:H	11:O:79:VAL:HG22	1.55	0.71
12:P:248:ALA:HB1	13:Q:314:LEU:CD1	2.18	0.71
14:R:175:ARG:NH2	25:p:102:ASP:HB2	2.04	0.71
3:D:939:ASP:HA	8:I:125:PRO:HA	1.69	0.71
5:F:319:LEU:H	5:F:319:LEU:HD23	1.56	0.71
7:H:111:ALA:HB2	9:J:157:LEU:HD11	1.72	0.71
12:P:248:ALA:CB	13:Q:314:LEU:HD13	2.20	0.71
24:o:1029:LEU:HD11	28:s:162:ARG:CG	2.21	0.71
1:A:1077:LEU:CD2	6:G:147:ARG:CZ	2.68	0.71
3:D:963:ARG:HD3	3:D:963:ARG:C	2.16	0.71
14:R:111:ASP:HB3	14:R:114:MET:CB	2.15	0.71
14:R:297:PRO:HB3	14:R:310:VAL:HG21	1.73	0.71
27:r:108:ALA:HB2	27:r:128:GLN:HB2	1.71	0.71
35:u:110:ARG:NH2	35:u:118:GLU:OE2	2.24	0.71
1:A:763:LEU:HB2	6:G:17:ILE:CD1	2.20	0.71
3:D:917:ILE:CG1	3:D:1058:VAL:HG21	2.21	0.71
13:Q:346:LYS:HE2	20:Y:27:DT:OP2	1.74	0.71
24:o:463:THR:CG2	24:o:468:SER:HB3	2.20	0.71
24:o:463:THR:OG1	25:p:1093:CYS:SG	2.48	0.71
24:o:784:VAL:HG22	25:p:978:ILE:HD11	1.72	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:r:87:LEU:HD22	27:r:97:LEU:HB2	1.71	0.71
1:A:1009:LYS:NZ	24:o:187:TYR:HB2	2.06	0.71
5:F:213:ILE:HB	7:H:163:PRO:C	2.15	0.71
24:o:1158:LEU:HD22	24:o:1307:VAL:HG11	1.70	0.71
7:H:110:TYR:CZ	9:J:160:GLN:HB3	2.26	0.71
1:A:779:ILE:CD1	6:G:137:THR:CG2	2.66	0.70
7:H:93:ILE:HD13	9:J:155:ILE:HD11	1.72	0.70
24:o:551:ARG:HG3	30:v:121:LEU:HD23	1.73	0.70
1:A:763:LEU:HD11	6:G:91:ILE:HD13	1.72	0.70
15:S:44:GLN:CG	15:S:103:ASN:CA	2.68	0.70
15:S:44:GLN:HG3	15:S:103:ASN:HA	1.73	0.70
17:U:145:PHE:CD2	35:u:98:PHE:CZ	2.78	0.70
1:A:568:SER:HB2	2:B:389:ASN:HB2	1.74	0.70
3:D:917:ILE:CB	3:D:1058:VAL:HG11	2.21	0.70
4:E:694:LEU:CB	4:E:703:MET:CE	2.69	0.70
5:F:344:PHE:O	5:F:346:THR:N	2.24	0.70
7:H:119:ILE:HD13	9:J:129:THR:O	1.91	0.70
11:O:80:GLU:HG2	11:O:89:LYS:HA	1.72	0.70
14:R:146:TYR:O	14:R:149:LYS:CG	2.39	0.70
24:o:137:PRO:HB2	24:o:1445:HIS:HD1	1.53	0.70
24:o:365:THR:HG22	24:o:482:PHE:CD1	2.22	0.70
27:r:16:ASP:HB2	35:u:81:LYS:HZ1	1.14	0.70
27:r:63:LYS:HE3	35:u:103:PRO:HB3	1.73	0.70
27:r:110:GLU:OE2	35:u:167:TYR:CZ	2.44	0.70
5:F:87:HIS:CB	9:J:212:LYS:HZ3	2.00	0.70
7:H:36:THR:CG2	9:J:134:VAL:HG21	2.22	0.70
14:R:27:TYR:O	14:R:48:VAL:HG21	1.91	0.70
24:o:868:MET:SD	24:o:1401:LEU:HD12	2.31	0.70
11:O:55:ARG:HB2	13:Q:369:LYS:HB2	1.73	0.70
27:r:110:GLU:HG3	35:u:167:TYR:CB	2.21	0.70
30:v:104:THR:HG22	30:v:105:SER:H	1.57	0.70
5:F:14:LEU:HD13	8:I:15:ASP:OD2	1.91	0.70
12:P:300:ILE:HD11	12:P:320:GLU:HB3	1.73	0.70
24:o:355:MET:CE	24:o:1459:MET:CG	2.69	0.70
2:B:877:TYR:CE2	7:H:216:ALA:HB2	2.26	0.70
3:D:995:GLU:OE1	12:P:181:LYS:CE	2.39	0.70
24:o:1166:LEU:HB2	24:o:1296:MET:HG2	1.73	0.70
15:S:156:THR:OG1	15:S:159:GLU:CB	2.38	0.70
24:o:397:PHE:HZ	24:o:1486:ILE:HD11	1.55	0.70
1:A:764:ILE:O	6:G:16:PHE:O	2.09	0.70
1:A:956:PRO:CA	6:G:149:ARG:CZ	2.70	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:898:VAL:CG2	10:L:113:VAL:HG23	2.22	0.70
14:R:226:LYS:HZ2	34:z:40:GLY:N	1.90	0.70
1:A:410:TRP:CZ2	5:F:305:ILE:HD12	2.27	0.69
12:P:239:ARG:NH1	13:Q:320:VAL:HB	2.06	0.69
24:o:535:MET:O	24:o:669:TYR:OH	2.08	0.69
1:A:620:LEU:HD22	6:G:67:LEU:CD1	2.21	0.69
1:A:673:GLY:H	6:G:13:GLU:CD	2.00	0.69
1:A:682:GLU:CD	6:G:140:LEU:CD1	2.64	0.69
28:s:172:ARG:NH2	28:s:210:GLN:O	2.25	0.69
5:F:22:VAL:HG13	8:I:44:PHE:HE1	1.56	0.69
5:F:67:THR:HA	8:I:32:GLU:OE2	1.91	0.69
24:o:480:SER:CB	33:y:2:ASN:ND2	2.49	0.69
5:F:66:LEU:CD2	8:I:31:TYR:HB3	2.22	0.69
15:S:44:GLN:HE22	15:S:104:GLY:HA3	1.54	0.69
18:V:99:LEU:HD13	18:V:120:MET:HB2	1.74	0.69
24:o:365:THR:HG22	24:o:482:PHE:CE1	2.27	0.69
27:r:29:ALA:O	27:r:94:LYS:NZ	2.18	0.69
27:r:103:LEU:HD23	35:u:144:ARG:CZ	2.15	0.69
24:o:20:ARG:HA	24:o:1449:ASP:O	1.93	0.69
24:o:801:GLY:HA3	25:p:503:ASN:HB2	1.74	0.69
24:o:1485:GLU:HB2	29:t:78:PRO:HB3	1.73	0.69
2:B:835:ARG:HD3	7:H:187:GLU:OE2	1.92	0.69
3:D:881:ARG:CZ	10:L:57:VAL:HG22	2.16	0.69
5:F:71:ILE:HD12	8:I:35:VAL:HA	1.73	0.69
24:o:99:PHE:HE1	24:o:1440:MET:HB3	1.58	0.69
24:o:751:LYS:HB2	24:o:751:LYS:NZ	2.07	0.69
24:o:792:ASN:HD22	24:o:792:ASN:H	1.37	0.69
5:F:52:GLN:HG2	8:I:26:MET:HG3	1.74	0.69
5:F:80:VAL:HG13	8:I:45:ARG:HH12	1.58	0.69
5:F:81:GLU:C	5:F:83:LEU:H	1.99	0.69
12:P:248:ALA:O	13:Q:314:LEU:HD12	1.93	0.69
14:R:44:ARG:HH21	25:p:1067:ILE:HG21	1.55	0.69
5:F:100:GLY:O	8:I:34:ARG:NH2	2.26	0.69
12:P:303:LEU:CD1	19:X:-29:DT:O2	2.41	0.69
17:U:52:LEU:HD23	18:V:161:ARG:HH12	1.55	0.69
18:V:224:THR:HG23	18:V:227:SER:HB2	1.72	0.69
5:F:322:ASP:C	5:F:324:ASP:N	2.49	0.68
13:Q:47:GLU:OE2	13:Q:60:HIS:CG	2.45	0.68
16:T:8:ASP:HB3	16:T:105:SER:HA	1.75	0.68
24:o:839:HIS:CD2	25:p:719:SER:HB2	2.29	0.68
24:o:1190:GLN:O	24:o:1194:ASN:HB2	1.93	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:P:238:ALA:HB1	13:Q:314:LEU:HD22	1.75	0.68
14:R:44:ARG:O	25:p:1067:ILE:CG1	2.41	0.68
15:S:10:ASN:O	16:T:47:LYS:CB	2.39	0.68
1:A:575:PRO:HG3	2:B:610:GLU:CG	2.22	0.68
1:A:575:PRO:CD	2:B:608:ASN:HD22	1.92	0.68
24:o:1158:LEU:HD23	24:o:1307:VAL:HG12	1.68	0.68
24:o:1158:LEU:HD13	24:o:1158:LEU:C	2.17	0.68
24:o:1177:TYR:OH	31:w:28:GLU:OE2	2.12	0.68
35:u:38:CYS:O	35:u:155:ASN:HA	1.93	0.68
35:u:44:PHE:HE2	35:u:46:ILE:CG1	2.03	0.68
15:S:153:ARG:CZ	31:w:41:ASN:OD1	2.42	0.68
3:D:996:LEU:HD23	3:D:996:LEU:C	2.19	0.68
12:P:166:GLN:HB3	20:Y:28:DT:C5'	2.19	0.68
15:S:49:ARG:NH1	15:S:96:GLN:O	2.25	0.68
22:k:191:VAL:HG13	22:k:200:ILE:HD13	1.74	0.68
3:D:941:ARG:HG2	3:D:944:LEU:CD1	2.23	0.68
24:o:461:GLN:OE1	24:o:461:GLN:N	2.26	0.68
35:u:38:CYS:O	35:u:155:ASN:OD1	2.12	0.68
5:F:329:LEU:O	5:F:329:LEU:HD23	1.94	0.68
5:F:366:GLU:N	5:F:366:GLU:OE2	2.26	0.68
3:D:946:PHE:CD2	4:E:513:LEU:CD1	2.67	0.68
5:F:369:PRO:HB2	5:F:372:THR:CB	2.20	0.68
24:o:532:ARG:NH1	24:o:647:THR:OG1	2.27	0.68
35:u:99:THR:HG21	35:u:143:ILE:HD11	1.76	0.68
3:D:955:LYS:C	3:D:955:LYS:HD3	2.19	0.67
5:F:329:LEU:HD23	5:F:329:LEU:C	2.19	0.67
12:P:189:ASN:CB	13:Q:376:TRP:HZ2	1.94	0.67
5:f:447:ALA:CA	5:f:456:GLY:HA3	2.23	0.67
24:o:1307:VAL:HG11	24:o:1336:LEU:HB3	1.77	0.67
25:p:320:PHE:O	25:p:324:ARG:NH1	2.27	0.67
35:u:93:ASN:OD1	35:u:94:LYS:N	2.26	0.67
2:B:310:ASP:OD2	7:H:223:TYR:HE2	1.77	0.67
3:D:957:ARG:HH21	4:E:434:ASP:HB3	0.85	0.67
4:E:359:LEU:HD13	4:E:627:LEU:HD12	1.76	0.67
12:P:249:LYS:O	13:Q:314:LEU:HD11	1.93	0.67
24:o:802:PHE:HE1	25:p:504:THR:CA	2.06	0.67
24:o:1155:LYS:HA	24:o:1309:MET:HE1	1.74	0.67
27:r:80:ILE:HA	27:r:83:VAL:HG12	1.75	0.67
1:A:1022:ARG:HD2	1:A:1026:ILE:HB	1.75	0.67
5:F:213:ILE:CG2	7:H:163:PRO:CB	2.64	0.67
1:A:602:PHE:HE1	6:G:12:LEU:HD23	1.53	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1000:ARG:NH1	3:D:1000:ARG:HG2	2.08	0.67
14:R:44:ARG:C	25:p:1067:ILE:CD1	2.43	0.67
17:U:32:LEU:CD2	18:V:161:ARG:NE	2.55	0.67
3:D:881:ARG:CZ	10:L:57:VAL:CG2	2.69	0.67
5:F:51:ALA:O	8:I:28:ILE:CD1	2.42	0.67
24:o:230:ASP:OD1	24:o:244:ARG:NH1	2.27	0.67
2:B:877:TYR:CZ	7:H:216:ALA:HB2	2.29	0.67
3:D:917:ILE:HB	3:D:1058:VAL:HG11	1.75	0.67
5:F:14:LEU:HA	8:I:18:MET:HG2	1.76	0.67
14:R:114:MET:SD	14:R:146:TYR:CE1	2.87	0.67
24:o:13:CYS:CB	24:o:14:PRO:HD2	2.22	0.67
1:A:495:LEU:HD13	5:f:268:ARG:CZ	2.24	0.67
1:A:567:LEU:HD22	2:B:745:GLN:HG2	1.76	0.67
1:A:665:MET:HE2	6:G:86:TYR:HB2	1.74	0.67
1:A:954:ALA:O	6:G:149:ARG:NH2	2.25	0.67
3:D:914:VAL:CG1	10:L:70:VAL:HG21	2.24	0.67
3:D:955:LYS:HD3	3:D:955:LYS:O	1.93	0.67
5:F:46:ARG:HB3	8:I:42:PHE:HE2	1.60	0.67
5:F:319:LEU:HD23	5:F:319:LEU:N	2.10	0.67
18:V:117:GLN:NE2	18:V:121:THR:CG2	2.55	0.67
2:B:402:ILE:HD12	2:B:455:LEU:HD12	1.77	0.67
5:F:80:VAL:HG11	8:I:42:PHE:HE1	1.58	0.67
6:G:19:ARG:HD2	6:G:96:VAL:HG13	1.77	0.67
7:H:111:ALA:HA	9:J:126:TYR:OH	1.95	0.67
31:w:105:GLU:HG2	31:w:106:ASP:H	1.58	0.67
1:A:758:PRO:CG	6:G:136:ILE:O	2.43	0.67
3:D:941:ARG:HG2	3:D:944:LEU:HD11	1.76	0.67
7:H:108:PRO:HG3	9:J:119:PHE:CD2	2.30	0.67
11:O:10:THR:HG21	13:Q:50:LEU:HD22	1.73	0.67
1:A:658:GLY:HA3	2:B:475:LYS:HG2	1.76	0.67
14:R:175:ARG:HH21	25:p:102:ASP:CA	2.04	0.67
15:S:11:VAL:C	15:S:12:THR:HG23	2.20	0.67
27:r:87:LEU:HD13	27:r:97:LEU:HD22	1.77	0.67
1:A:468:PHE:HB3	5:F:214:HIS:CD2	2.30	0.66
1:A:673:GLY:CA	6:G:15:GLN:NE2	2.58	0.66
35:u:153:ASP:O	35:u:155:ASN:N	2.27	0.66
1:A:764:ILE:HD11	6:G:18:LEU:CD2	2.23	0.66
3:D:1000:ARG:HD2	11:O:8:ASN:HB3	1.76	0.66
14:R:46:ILE:CA	24:o:67:ARG:NH2	2.47	0.66
5:f:239:ARG:HD3	5:f:284:ARG:HH11	1.60	0.66
24:o:1158:LEU:CD2	24:o:1307:VAL:CB	2.53	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:p:1120:ASN:HD22	25:p:1145:GLN:HB2	1.60	0.66
1:A:673:GLY:CA	6:G:15:GLN:HE22	2.08	0.66
3:D:1000:ARG:HH22	11:O:5:LEU:CG	2.04	0.66
24:o:853:LYS:NZ	24:o:853:LYS:HB3	2.11	0.66
24:o:1210:TRP:CD2	24:o:1282:ASP:OD1	2.47	0.66
24:o:1428:MET:HB2	24:o:1456:GLU:OE2	1.95	0.66
26:q:154:ARG:HD3	32:x:64:PRO:HD3	1.77	0.66
31:w:109:ARG:NH2	31:w:125:GLU:O	2.28	0.66
12:P:240:VAL:HG22	13:Q:321:SER:CB	2.24	0.66
24:o:11:SER:N	25:p:1117:HIS:HE2	1.93	0.66
25:p:690:CYS:SG	25:p:691:SER:N	2.69	0.66
3:D:1000:ARG:HH11	11:O:5:LEU:CA	2.08	0.66
7:H:111:ALA:HB2	9:J:157:LEU:HD13	1.76	0.66
3:d:1082:ALA:HB2	10:l:83:MET:CE	2.24	0.66
4:e:645:GLY:H	4:e:675:LEU:HD11	1.59	0.66
24:o:15:LEU:HD23	24:o:15:LEU:C	2.20	0.66
24:o:1147:SER:HA	24:o:1153:ARG:HD2	1.76	0.66
3:D:933:ARG:HD2	9:J:117:VAL:CG1	2.09	0.66
5:F:283:MET:HE1	5:F:308:VAL:HB	1.76	0.66
18:V:78:LEU:C	18:V:80:LYS:H	2.02	0.66
24:o:393:ILE:HD11	29:t:74:ALA:CB	2.13	0.66
24:o:716:VAL:HG11	24:o:740:GLN:NE2	2.05	0.66
3:D:910:LEU:HB2	10:L:66:LEU:HD21	1.77	0.66
5:F:43:VAL:CG2	8:I:43:ALA:CA	2.73	0.66
7:H:118:VAL:CG2	9:J:127:THR:HG23	2.25	0.66
3:D:1085:LYS:HZ3	10:L:83:MET:CE	2.09	0.66
5:F:113:ASP:HA	7:H:52:SER:HA	1.76	0.66
5:F:372:THR:C	5:F:374:TYR:H	2.02	0.66
12:P:204:ILE:HG13	12:P:207:PRO:HD2	1.78	0.66
15:S:102:VAL:HG12	15:S:103:ASN:OD1	1.96	0.66
17:U:128:LYS:O	17:U:162:GLU:N	2.28	0.66
35:u:167:TYR:CD2	35:u:167:TYR:O	2.48	0.66
7:H:108:PRO:HG3	9:J:119:PHE:CG	2.30	0.66
14:R:109:SER:HA	14:R:112:ARG:HD2	1.76	0.66
16:T:20:LEU:N	16:T:112:GLN:O	2.28	0.66
4:E:518:LYS:HD2	4:E:518:LYS:C	2.20	0.66
5:F:213:ILE:CG2	7:H:163:PRO:HB3	2.10	0.66
1:A:349:TRP:HE1	5:f:262:PHE:HA	1.60	0.65
1:A:472:ASN:N	5:f:299:LYS:HZ3	1.94	0.65
1:A:766:ARG:HD2	6:G:16:PHE:CE1	2.31	0.65
5:F:67:THR:CB	8:I:32:GLU:OE2	2.44	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:102:LEU:CA	10:L:105:HIS:HD2	2.08	0.65
14:R:46:ILE:HA	24:o:67:ARG:HH21	1.56	0.65
25:p:1022:LEU:HD12	25:p:1023:ARG:HG2	1.78	0.65
26:q:36:ARG:HH12	33:y:40:HIS:HB2	1.61	0.65
1:A:1168:TYR:HB2	6:G:180:ARG:HB3	1.78	0.65
5:F:90:GLU:CD	9:J:208:GLY:HA3	2.20	0.65
11:O:3:TYR:C	11:O:5:LEU:H	2.04	0.65
14:R:137:ARG:CZ	14:R:137:ARG:HB3	2.24	0.65
18:V:203:PHE:O	18:V:203:PHE:CG	2.50	0.65
24:o:67:ARG:HH12	25:p:1069:ILE:HD12	1.59	0.65
24:o:1312:PRO:HG3	24:o:1317:LYS:O	1.96	0.65
26:q:15:THR:HG22	26:q:16:ASP:H	1.62	0.65
12:P:188:ARG:HD2	13:Q:322:ASP:OD1	1.96	0.65
24:o:1029:LEU:CD1	28:s:162:ARG:CG	2.74	0.65
27:r:62:MET:HA	27:r:65:LEU:HB3	1.78	0.65
5:F:213:ILE:CB	7:H:163:PRO:O	2.31	0.65
7:H:69:ILE:HG21	9:J:138:TYR:HB2	1.79	0.65
7:H:102:PHE:CE1	9:J:158:ALA:O	2.49	0.65
7:H:111:ALA:CB	9:J:157:LEU:HD11	2.26	0.65
15:S:44:GLN:NE2	15:S:103:ASN:O	2.28	0.65
24:o:365:THR:CG2	24:o:482:PHE:CE1	2.79	0.65
2:B:827:ARG:NE	7:H:211:PHE:HZ	1.95	0.65
7:H:107:LEU:HD11	9:J:157:LEU:C	2.21	0.65
18:V:77:VAL:HG11	18:V:119:LEU:HD13	1.78	0.65
28:s:51:GLY:O	28:s:54:ARG:NH2	2.29	0.65
1:A:1009:LYS:HZ3	24:o:187:TYR:HD2	1.43	0.65
4:E:788:ARG:O	7:H:145:HIS:HB2	1.97	0.65
11:O:60:GLY:HA2	11:O:79:VAL:HG13	1.78	0.65
15:S:44:GLN:HG2	15:S:103:ASN:CA	2.22	0.65
18:V:173:GLU:HG3	18:V:175:LEU:H	1.62	0.65
3:D:940:VAL:HG13	3:D:943:GLN:NE2	2.12	0.65
14:R:47:ASP:CB	25:p:1069:ILE:HG12	2.20	0.65
15:S:8:SER:HB3	16:T:49:GLN:HA	1.79	0.65
21:c:67:GLY:CA	9:j:116:LEU:CD1	2.70	0.65
1:A:650:ARG:HH22	6:G:78:LYS:HZ1	0.65	0.65
11:O:58:PHE:CD2	11:O:81:PHE:HD2	2.15	0.65
18:V:97:LEU:HD22	18:V:102:ILE:HG13	1.78	0.65
24:o:863:ARG:HH21	24:o:1128:ILE:HG21	1.62	0.65
3:D:937:ALA:HB2	8:I:128:ARG:HD3	1.79	0.65
24:o:465:HIS:CD2	24:o:467:MET:H	2.07	0.65
1:A:417:ASP:HA	5:F:315:ARG:HG2	1.77	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:668:PRO:HB2	6:G:10:HIS:CG	2.31	0.65
3:D:1000:ARG:HH11	11:O:5:LEU:C	2.04	0.65
4:E:746:ASP:OD1	4:E:746:ASP:N	2.29	0.65
5:F:101:GLY:HA3	8:I:34:ARG:NH2	2.12	0.65
13:Q:26:ARG:HH21	13:Q:39:LEU:HD23	1.61	0.65
18:V:99:LEU:HB2	18:V:120:MET:SD	2.37	0.65
18:V:121:THR:O	18:V:125:VAL:HG23	1.91	0.65
26:q:19:VAL:HG23	26:q:241:PRO:HB2	1.79	0.65
5:F:48:LYS:HE3	8:I:22:ILE:HA	1.78	0.64
5:F:414:ASN:C	5:F:416:ASP:H	2.05	0.64
5:F:415:ILE:CG1	5:F:418:ILE:HB	2.27	0.64
7:H:132:LYS:HE2	7:H:134:LEU:H	1.62	0.64
8:I:60:HIS:NE2	10:L:118:LEU:CD2	2.55	0.64
13:Q:48:ASN:HA	13:Q:51:MET:HE2	1.78	0.64
14:R:48:VAL:CG1	25:p:1077:GLY:HA2	2.26	0.64
17:U:141:ALA:HB1	17:U:152:PHE:HB3	1.79	0.64
24:o:1210:TRP:HB3	24:o:1285:LEU:HD13	1.79	0.64
28:s:17:ILE:HD11	28:s:135:LEU:HD13	1.78	0.64
35:u:38:CYS:SG	35:u:44:PHE:CA	2.75	0.64
35:u:91:GLN:HB2	35:u:98:PHE:HD2	1.62	0.64
1:A:416:TRP:NE1	5:F:313:VAL:HB	2.13	0.64
12:P:303:LEU:HD13	20:Y:29:DA:H2	1.56	0.64
14:R:29:ALA:O	25:p:1066:PRO:N	2.31	0.64
24:o:395:THR:HG23	24:o:397:PHE:H	1.62	0.64
24:o:716:VAL:HG13	24:o:740:GLN:HE22	1.61	0.64
2:B:583:GLU:CD	2:B:583:GLU:H	2.06	0.64
3:D:995:GLU:CD	12:P:181:LYS:HZ2	1.98	0.64
12:P:278:GLN:CD	12:P:278:GLN:H	2.04	0.64
5:f:320:ARG:NH1	5:f:320:ARG:HB3	2.12	0.64
35:u:32:THR:OG1	35:u:33:GLU:OE1	2.14	0.64
2:B:883:PHE:HB3	2:B:886:ILE:HG13	1.78	0.64
3:D:881:ARG:CD	10:L:57:VAL:HG11	2.28	0.64
5:F:313:VAL:HG12	5:F:372:THR:CA	2.26	0.64
1:A:1053:PHE:C	1:A:1057:GLU:HB3	2.22	0.64
4:E:694:LEU:HD13	4:E:703:MET:HE1	0.65	0.64
15:S:44:GLN:HG3	15:S:103:ASN:CA	2.27	0.64
17:U:28:ILE:H	17:U:28:ILE:HD13	1.63	0.64
1:A:678:LEU:CG	6:G:76:SER:HB3	2.28	0.64
5:F:68:THR:N	8:I:32:GLU:CD	2.55	0.64
5:F:313:VAL:HG12	5:F:372:THR:HA	1.79	0.64
15:S:126:ILE:N	15:S:138:PHE:O	2.22	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:o:659:GLU:OE2	24:o:985:ARG:NH1	2.29	0.64
1:A:511:LEU:HD22	1:A:511:LEU:N	2.10	0.64
17:U:52:LEU:CD2	18:V:161:ARG:HH12	2.10	0.64
2:B:361:ARG:HD2	2:B:367:GLU:HB2	1.80	0.64
24:o:364:ARG:HH11	24:o:364:ARG:CG	2.09	0.64
25:p:677:MET:H	25:p:682:LEU:HD12	1.62	0.64
27:r:103:LEU:CA	35:u:144:ARG:HH12	2.04	0.64
1:A:1009:LYS:HZ3	24:o:187:TYR:CB	2.10	0.64
24:o:1303:GLN:HB2	24:o:1342:SER:HB3	1.79	0.64
25:p:854:ILE:HD12	25:p:866:ILE:HG22	1.77	0.64
1:A:349:TRP:NE1	5:f:262:PHE:CD1	2.66	0.64
3:D:881:ARG:CB	10:L:57:VAL:CG1	2.64	0.64
4:E:462:CYS:HB2	5:F:135:TRP:CZ3	2.33	0.64
14:R:28:ARG:HG3	25:p:1078:ARG:HH11	1.63	0.64
15:S:153:ARG:HH21	31:w:41:ASN:CG	2.05	0.64
21:c:67:GLY:CA	9:j:116:LEU:HD11	2.25	0.64
3:D:948:GLU:O	3:D:952:GLN:HB3	1.98	0.63
3:D:1083:PHE:HE2	4:E:585:ASN:HD21	0.73	0.63
4:E:616:HIS:CE1	11:O:24:GLN:HB2	2.33	0.63
15:S:164:TRP:HD1	15:S:168:ASN:ND2	1.95	0.63
17:U:185:GLU:N	17:U:186:PRO:CD	2.60	0.63
24:o:125:LYS:O	24:o:129:ILE:HB	1.98	0.63
1:A:575:PRO:CD	2:B:608:ASN:HB2	2.28	0.63
5:F:319:LEU:H	5:F:319:LEU:CD2	2.11	0.63
14:R:111:ASP:O	14:R:115:MET:HB2	1.98	0.63
24:o:511:THR:HG21	25:p:1105:GLU:OE1	1.98	0.63
24:o:581:LYS:C	24:o:581:LYS:HD3	2.23	0.63
27:r:16:ASP:HB3	35:u:81:LYS:HZ1	1.54	0.63
2:B:490:SER:HA	2:B:493:TRP:HB2	1.78	0.63
3:D:901:TYR:CD1	10:L:128:ILE:CG2	2.80	0.63
5:F:84:TYR:HB3	8:I:41:GLU:OE1	1.99	0.63
5:F:392:ILE:O	5:F:392:ILE:HG22	1.99	0.63
24:o:721:HIS:HA	31:w:108:MET:O	1.98	0.63
24:o:863:ARG:HH21	24:o:1128:ILE:CG2	2.11	0.63
35:u:40:GLY:CA	35:u:152:VAL:HG22	2.22	0.63
3:D:958:LYS:NZ	3:D:958:LYS:HB3	2.13	0.63
3:D:995:GLU:CD	12:P:181:LYS:HZ1	2.06	0.63
24:o:1160:ARG:NH2	24:o:1349:GLU:CG	2.62	0.63
24:o:1211:LEU:HD11	24:o:1258:ARG:HE	1.63	0.63
2:B:883:PHE:HA	7:H:222:PRO:CB	2.23	0.63
3:D:934:TYR:CD1	8:I:129:LEU:HD23	2.34	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:412:LEU:HD23	5:F:412:LEU:N	2.07	0.63
11:O:59:ARG:HG3	13:Q:373:ASP:HB2	1.80	0.63
14:R:248:ARG:NH2	20:Y:33:DG:OP2	2.32	0.63
3:D:950:LEU:C	3:D:950:LEU:HD13	2.23	0.63
4:E:359:LEU:HD11	4:E:648:ASP:HB2	1.80	0.63
5:F:14:LEU:HB3	8:I:15:ASP:OD1	1.98	0.63
5:F:213:ILE:HG21	7:H:163:PRO:HB2	1.75	0.63
1:A:484:ILE:CA	5:f:306:PRO:HB3	2.27	0.63
1:A:678:LEU:HG	6:G:76:SER:HB3	1.81	0.63
1:A:1063:LYS:HD3	1:A:1063:LYS:C	2.24	0.63
5:F:313:VAL:HG12	5:F:372:THR:CB	2.28	0.63
14:R:40:VAL:HG11	25:p:1064:ARG:HH22	1.64	0.63
15:S:164:TRP:CZ3	25:p:307:GLU:O	2.50	0.63
25:p:313:GLU:HG3	25:p:316:VAL:HG12	1.79	0.63
5:F:372:THR:C	5:F:374:TYR:N	2.55	0.63
11:O:20:ASP:HA	11:O:23:ILE:HB	1.81	0.63
15:S:44:GLN:CG	15:S:104:GLY:N	2.62	0.63
16:T:31:TRP:HD1	16:T:62:LEU:HD21	1.64	0.63
1:A:762:PHE:O	6:G:17:ILE:HG23	1.99	0.63
1:A:1077:LEU:CD1	6:G:147:ARG:NH1	2.60	0.63
3:D:881:ARG:HD3	10:L:57:VAL:CG1	2.29	0.63
12:P:305:PHE:HB2	20:Y:30:DT:H4'	1.81	0.63
27:r:16:ASP:OD1	35:u:81:LYS:O	2.16	0.63
27:r:103:LEU:HD23	35:u:144:ARG:HH11	0.82	0.63
1:A:468:PHE:HB3	5:F:214:HIS:NE2	2.14	0.62
1:A:765:ILE:HG23	6:G:15:GLN:CG	2.17	0.62
1:A:843:ARG:HD3	20:Y:-26:DG:C8	2.34	0.62
5:F:114:LEU:HD13	7:H:53:ALA:CB	2.29	0.62
11:O:39:GLN:CG	13:Q:25:VAL:HG12	2.29	0.62
13:Q:47:GLU:OE1	13:Q:60:HIS:ND1	2.30	0.62
24:o:137:PRO:CG	24:o:1445:HIS:CB	2.60	0.62
24:o:364:ARG:HH11	24:o:364:ARG:HB2	1.63	0.62
1:A:355:VAL:O	1:A:355:VAL:HG23	1.97	0.62
11:O:29:THR:HB	11:O:30:PRO:HD3	1.80	0.62
14:R:114:MET:HE2	14:R:146:TYR:CG	2.34	0.62
5:F:320:ARG:O	5:F:324:ASP:HB2	1.98	0.62
11:O:72:TRP:HD1	13:Q:339:TYR:CE2	2.16	0.62
24:o:1475:LEU:HB2	35:u:59:ILE:HD11	1.80	0.62
14:R:28:ARG:HG3	25:p:1078:ARG:NH1	2.14	0.62
15:S:8:SER:O	16:T:48:THR:O	2.18	0.62
26:q:2:PRO:HB3	33:y:54:PRO:HD2	1.81	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:745:GLU:OE1	4:E:745:GLU:HA	1.98	0.62
13:Q:47:GLU:OE2	13:Q:60:HIS:NE2	2.27	0.62
24:o:868:MET:HE1	24:o:1401:LEU:HA	1.81	0.62
24:o:364:ARG:CZ	24:o:500:GLU:OE1	2.47	0.62
24:o:802:PHE:CE1	25:p:504:THR:CG2	2.82	0.62
24:o:860:ILE:HA	24:o:863:ARG:HH12	1.64	0.62
24:o:1063:GLU:OE1	24:o:1063:GLU:CA	2.42	0.62
24:o:1306:LYS:O	24:o:1338:THR:HA	1.99	0.62
4:E:373:PHE:HB3	4:E:421:ALA:HA	1.81	0.62
14:R:29:ALA:C	25:p:1066:PRO:CD	2.72	0.62
17:U:145:PHE:HE2	35:u:98:PHE:CZ	2.06	0.62
5:F:213:ILE:CD1	7:H:163:PRO:HB3	2.30	0.62
24:o:1147:SER:HB2	24:o:1153:ARG:HD3	1.80	0.62
1:A:664:PHE:CD2	6:G:80:ILE:HG13	2.35	0.62
1:A:755:HIS:CE1	6:G:139:PRO:CD	2.81	0.62
3:D:1000:ARG:HH22	11:O:5:LEU:HD11	0.47	0.62
5:F:415:ILE:HG12	5:F:415:ILE:O	2.00	0.62
7:H:118:VAL:HG21	9:J:127:THR:HG21	1.82	0.62
24:o:397:PHE:HZ	24:o:1486:ILE:HD12	1.61	0.62
1:A:1019:LYS:C	1:A:1021:SER:H	2.06	0.61
3:D:914:VAL:HG11	10:L:70:VAL:CG2	2.30	0.61
5:F:71:ILE:CD1	8:I:35:VAL:HG22	2.30	0.61
7:H:108:PRO:HA	9:J:119:PHE:CE1	2.34	0.61
12:P:188:ARG:NE	13:Q:323:GLU:O	2.32	0.61
27:r:26:PHE:HE2	35:u:80:PHE:CZ	2.17	0.61
1:A:779:ILE:CG1	6:G:137:THR:HG23	2.26	0.61
4:E:613:ALA:HB2	4:E:620:LEU:HD11	1.81	0.61
2:B:735:ILE:CG2	7:H:176:ARG:NH2	2.62	0.61
3:D:940:VAL:O	3:D:943:GLN:HG3	1.99	0.61
18:V:148:LYS:HB3	18:V:149:LYS:NZ	2.16	0.61
24:o:1399:ALA:O	24:o:1403:ASP:HB2	2.00	0.61
25:p:407:MET:HE1	25:p:444:LEU:HG	1.81	0.61
35:u:167:TYR:CG	35:u:167:TYR:O	2.54	0.61
14:R:297:PRO:HA	14:R:310:VAL:HG11	1.82	0.61
18:V:177:ASN:HD21	18:V:202:PHE:HZ	1.46	0.61
24:o:1029:LEU:HD13	28:s:162:ARG:HG2	1.80	0.61
5:F:48:LYS:CE	8:I:22:ILE:HG12	2.30	0.61
12:P:249:LYS:C	13:Q:314:LEU:HD11	2.24	0.61
24:o:1375:ARG:NH1	24:o:1379:GLU:OE1	2.33	0.61
25:p:111:ASN:HD21	25:p:742:VAL:HG11	1.65	0.61
27:r:110:GLU:CD	35:u:167:TYR:CG	2.78	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:102:PHE:HZ	9:J:158:ALA:HA	1.65	0.61
8:I:60:HIS:NE2	10:L:118:LEU:HD23	2.16	0.61
15:S:156:THR:OG1	15:S:159:GLU:OE1	2.15	0.61
17:U:46:GLU:CD	17:U:93:PHE:HE2	2.05	0.61
21:c:18:CYS:O	21:c:23:TRP:HB2	2.00	0.61
26:q:193:ARG:HD3	26:q:220:TYR:HD1	1.65	0.61
4:E:703:MET:O	4:E:703:MET:HG3	2.00	0.61
5:f:330:ARG:HH22	5:f:371:THR:HB	1.66	0.61
24:o:138:LYS:HA	24:o:1445:HIS:NE2	2.15	0.61
25:p:312:GLN:HE21	31:w:22:ASN:HD21	1.49	0.61
3:D:881:ARG:HD3	10:L:57:VAL:HG13	1.83	0.61
13:Q:56:VAL:HG12	13:Q:57:ASP:N	2.16	0.61
14:R:289:TYR:OH	14:R:314:PRO:O	2.17	0.61
27:r:73:ARG:HH12	35:u:144:ARG:HH22	1.47	0.61
35:u:24:ASN:HA	35:u:27:LYS:HG3	1.82	0.61
1:A:620:LEU:HB2	6:G:93:GLN:OE1	1.99	0.61
3:D:916:LYS:HE2	3:D:1066:CYS:SG	2.41	0.61
4:E:463:PHE:HB2	5:F:136:LEU:HG	1.81	0.61
14:R:111:ASP:CG	14:R:114:MET:HB2	2.26	0.61
17:U:136:PHE:HB3	17:U:140:GLU:CB	2.31	0.61
24:o:581:LYS:HB2	30:v:91:VAL:HG23	1.83	0.61
24:o:581:LYS:HB3	24:o:582:PRO:HD3	1.81	0.61
31:w:35:LEU:HD12	31:w:51:SER:HA	1.83	0.61
2:B:203:LYS:HD3	2:B:237:MET:HE3	1.83	0.61
2:B:873:LEU:HD12	7:H:201:GLN:HE22	1.64	0.61
4:E:696:TRP:CZ3	4:E:703:MET:CB	2.78	0.61
7:H:93:ILE:HD11	9:J:144:PHE:CZ	2.36	0.61
7:H:192:ARG:NH1	7:H:209:SER:O	2.34	0.61
24:o:1102:MET:HE2	24:o:1120:GLY:CA	2.25	0.61
25:p:311:ILE:HD11	25:p:317:ALA:HA	1.81	0.61
3:D:938:SER:O	8:I:125:PRO:O	2.17	0.60
13:Q:15:ARG:HH21	13:Q:58:GLY:HA2	1.65	0.60
14:R:48:VAL:O	14:R:48:VAL:HG13	2.01	0.60
15:S:153:ARG:NH2	31:w:41:ASN:OD1	2.33	0.60
18:V:97:LEU:HD22	18:V:102:ILE:CG1	2.31	0.60
24:o:577:PRO:HG2	24:o:580:LEU:HG	1.83	0.60
24:o:1311:LEU:HD12	24:o:1332:GLN:HB3	1.83	0.60
25:p:82:PRO:HB3	25:p:134:LYS:HB3	1.81	0.60
7:H:40:VAL:HG11	9:J:130:ILE:HG12	1.83	0.60
7:H:93:ILE:HD11	9:J:144:PHE:HZ	1.65	0.60
25:p:988:LYS:O	25:p:992:ASN:ND2	2.31	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:TRP:CE3	5:F:305:ILE:CG2	2.81	0.60
1:A:684:SER:O	6:G:148:PHE:CE1	2.54	0.60
2:B:873:LEU:HD12	7:H:201:GLN:NE2	2.16	0.60
5:F:274:ASN:ND2	5:F:316:GLN:HA	2.16	0.60
14:R:173:VAL:HB	14:R:175:ARG:HH12	1.64	0.60
25:p:584:MET:HE3	25:p:605:ARG:HB2	1.83	0.60
27:r:16:ASP:HB3	27:r:19:GLN:HG2	1.83	0.60
1:A:485:ILE:CD1	5:f:268:ARG:HG2	2.32	0.60
1:A:1077:LEU:HD11	6:G:147:ARG:HH22	0.78	0.60
5:F:90:GLU:OE1	9:J:208:GLY:C	2.44	0.60
15:S:109:LYS:HD2	15:S:149:LEU:HD22	1.84	0.60
24:o:853:LYS:HB3	24:o:853:LYS:HZ2	1.66	0.60
5:F:52:GLN:HG2	8:I:26:MET:CG	2.32	0.60
5:F:68:THR:CB	8:I:34:ARG:NH1	2.65	0.60
17:U:191:LEU:H	17:U:191:LEU:HD23	1.66	0.60
8:I:132:LEU:CG	9:J:121:MET:CE	2.79	0.60
12:P:311:VAL:HB	20:Y:29:DA:H1'	1.84	0.60
3:d:884:GLU:HA	3:d:887:LYS:HE3	1.82	0.60
24:o:355:MET:HE1	24:o:1459:MET:CG	2.31	0.60
3:D:1085:LYS:NZ	10:L:83:MET:CE	2.65	0.60
5:F:211:ARG:HG2	7:H:165:TYR:CE2	2.25	0.60
12:P:305:PHE:CG	20:Y:30:DT:H4'	2.36	0.60
17:U:118:GLU:HG2	17:U:174:ARG:HA	1.84	0.60
24:o:864:LEU:HD23	24:o:864:LEU:C	2.27	0.60
25:p:565:THR:HG21	25:p:580:PRO:HG3	1.83	0.60
1:A:682:GLU:CG	6:G:72:CYS:SG	2.90	0.60
3:D:941:ARG:O	3:D:944:LEU:CB	2.50	0.60
3:D:1080:TYR:CD1	4:E:585:ASN:OD1	2.55	0.60
5:F:51:ALA:CB	8:I:23:LEU:HD23	2.30	0.60
5:F:218:VAL:HA	5:F:221:GLN:HG2	1.84	0.60
13:Q:26:ARG:NH2	13:Q:39:LEU:CD2	2.65	0.60
14:R:114:MET:HE2	14:R:146:TYR:HB2	1.84	0.60
2:B:159:LEU:HD23	2:B:159:LEU:N	2.17	0.59
13:Q:324:GLU:CD	13:Q:324:GLU:H	2.10	0.59
16:T:20:LEU:O	16:T:114:ALA:N	2.34	0.59
24:o:79:THR:CG2	25:p:1072:ARG:NH1	2.65	0.59
24:o:111:CYS:SG	24:o:188:GLN:NE2	2.75	0.59
12:P:287:LEU:HD22	20:Y:33:DG:H5'	1.84	0.59
18:V:181:ALA:C	18:V:184:ALA:HB3	2.27	0.59
1:A:484:ILE:HG12	5:f:306:PRO:HB3	1.84	0.59
3:D:893:GLU:OE2	10:L:110:THR:OG1	2.18	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:48:LYS:HE3	8:I:22:ILE:CG1	2.31	0.59
5:F:68:THR:HG21	8:I:34:ARG:HH11	1.56	0.59
12:P:167:ASN:OD1	20:Y:27:DT:O4'	2.19	0.59
17:U:131:VAL:HG21	17:U:159:THR:HG21	1.85	0.59
24:o:91:ALA:HB1	24:o:294:GLU:OE2	2.02	0.59
27:r:73:ARG:HH12	35:u:144:ARG:NH2	1.99	0.59
1:A:763:LEU:HD13	6:G:91:ILE:HD13	1.83	0.59
11:O:14:SER:HG	13:Q:46:TRP:CD1	2.20	0.59
18:V:118:TRP:NE1	18:V:122:GLU:OE1	2.35	0.59
18:V:175:LEU:HD21	18:V:180:LYS:CB	2.33	0.59
24:o:510:GLU:OE2	29:t:71:LEU:HD13	2.02	0.59
24:o:1022:ILE:H	24:o:1034:GLN:HE22	1.51	0.59
24:o:1027:ASP:OD2	28:s:162:ARG:HD3	2.02	0.59
24:o:1312:PRO:HD2	24:o:1333:GLU:H	1.67	0.59
25:p:607:ILE:HG21	31:w:72:VAL:HA	1.85	0.59
1:A:489:GLN:NE2	1:A:489:GLN:H	2.01	0.59
3:D:934:TYR:CG	8:I:129:LEU:CD2	2.83	0.59
17:U:145:PHE:HE2	35:u:98:PHE:CE2	2.06	0.59
21:c:99:PHE:HB2	21:c:100:PRO:HD3	1.83	0.59
24:o:23:PHE:CZ	24:o:1439:LEU:CD2	2.85	0.59
24:o:847:LEU:HD11	25:p:516:GLU:CG	2.32	0.59
1:A:405:VAL:CA	5:F:302:HIS:HB3	2.32	0.59
3:D:996:LEU:HD23	3:D:996:LEU:O	2.03	0.59
5:F:320:ARG:N	5:F:321:PRO:HD2	2.18	0.59
26:q:44:ILE:HD12	26:q:178:PRO:HB3	1.84	0.59
1:A:954:ALA:C	6:G:149:ARG:HH22	2.11	0.59
5:F:71:ILE:CG2	8:I:38:GLN:HE21	2.15	0.59
13:Q:15:ARG:HH21	13:Q:58:GLY:CA	2.15	0.59
17:U:52:LEU:HD23	18:V:161:ARG:HH11	1.62	0.59
5:f:349:ASN:HB3	5:f:351:ILE:HG13	1.84	0.59
23:m:31:LEU:HD23	23:m:31:LEU:N	2.16	0.59
2:B:848:HIS:CD2	2:B:886:ILE:HD11	2.38	0.59
5:F:214:HIS:N	7:H:164:THR:HG22	2.16	0.59
24:o:356:GLY:HA3	25:p:1085:ARG:NH2	2.18	0.59
25:p:591:ARG:NH1	25:p:601:VAL:O	2.36	0.59
17:U:92:TYR:HE2	17:U:94:ILE:HD11	1.64	0.59
18:V:171:ILE:HG12	18:V:177:ASN:H	1.68	0.59
25:p:820:LYS:HE3	25:p:826:GLU:HB2	1.85	0.59
3:D:1000:ARG:NH1	11:O:5:LEU:HG	2.14	0.59
12:P:188:ARG:HH11	13:Q:322:ASP:CG	2.10	0.59
18:V:99:LEU:HD13	18:V:120:MET:CB	2.32	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:r:132:ASP:HA	27:r:135:GLN:HG2	1.85	0.59
1:A:468:PHE:CE1	5:F:258:ARG:HG3	2.38	0.58
1:A:680:LEU:HG	6:G:74:MET:HB3	1.85	0.58
3:D:940:VAL:O	3:D:943:GLN:HB2	2.02	0.58
5:F:207:ARG:HD2	5:F:207:ARG:N	2.18	0.58
5:F:320:ARG:HD3	5:F:415:ILE:HG21	1.84	0.58
6:G:154:LYS:HG2	6:G:162:VAL:HB	1.84	0.58
24:o:751:LYS:HB2	24:o:751:LYS:HZ2	1.68	0.58
1:A:1010:PHE:CE1	24:o:187:TYR:OH	2.57	0.58
18:V:226:ASP:O	18:V:227:SER:C	2.44	0.58
21:c:21:LEU:HD12	21:c:21:LEU:C	2.29	0.58
24:o:397:PHE:CZ	24:o:1486:ILE:HD12	2.38	0.58
24:o:904:GLN:NE2	24:o:980:PRO:O	2.37	0.58
24:o:1244:ASN:O	24:o:1259:ILE:HA	2.03	0.58
1:A:564:PRO:CG	2:B:744:PHE:CD2	2.82	0.58
1:A:620:LEU:CG	6:G:67:LEU:HD21	2.33	0.58
1:A:764:ILE:HG12	6:G:18:LEU:CB	2.30	0.58
3:D:935:GLU:O	8:I:128:ARG:N	2.36	0.58
17:U:32:LEU:CD1	18:V:161:ARG:NH2	2.65	0.58
24:o:705:THR:HG1	24:o:751:LYS:HD2	1.66	0.58
24:o:784:VAL:CG2	25:p:976:MET:HG2	2.33	0.58
24:o:870:SER:HB3	24:o:882:SER:HB3	1.85	0.58
11:O:58:PHE:CG	11:O:81:PHE:CD2	2.91	0.58
17:U:136:PHE:HB3	17:U:140:GLU:HB2	1.85	0.58
18:V:77:VAL:HG21	18:V:111:ILE:CD1	2.24	0.58
24:o:1027:ASP:OD1	24:o:1027:ASP:N	2.36	0.58
24:o:1231:ILE:HG12	24:o:1298:LEU:HD11	1.83	0.58
24:o:1482:TYR:CD1	24:o:1482:TYR:C	2.81	0.58
2:B:769:LYS:O	2:B:769:LYS:HG3	2.04	0.58
2:B:883:PHE:O	2:B:884:VAL:C	2.45	0.58
3:D:940:VAL:O	3:D:943:GLN:CB	2.51	0.58
4:E:501:PRO:HD3	7:H:149:HIS:HB3	1.83	0.58
17:U:141:ALA:O	17:U:145:PHE:N	2.36	0.58
24:o:1309:MET:HG2	24:o:1334:TRP:CE3	2.39	0.58
3:D:940:VAL:O	3:D:943:GLN:CG	2.51	0.58
5:F:14:LEU:CB	8:I:15:ASP:OD1	2.50	0.58
15:S:116:GLY:CA	25:p:356:PHE:CE1	2.66	0.58
21:c:12:VAL:HG23	5:f:118:ILE:HA	1.85	0.58
5:f:219:GLU:OE1	5:f:219:GLU:N	2.26	0.58
1:A:956:PRO:HB3	6:G:149:ARG:NH1	2.18	0.58
3:D:917:ILE:HG13	3:D:1058:VAL:HG21	1.86	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:14:LEU:HD22	8:I:15:ASP:O	2.03	0.58
8:I:56:ILE:HG21	10:L:122:ARG:HH21	1.68	0.58
11:O:10:THR:HG21	13:Q:50:LEU:HD21	1.62	0.58
15:S:31:PHE:HB2	16:T:92:THR:HB	1.86	0.58
24:o:622:SER:HB3	24:o:637:MET:CE	2.34	0.58
1:A:620:LEU:CB	6:G:67:LEU:CD2	2.79	0.58
2:B:877:TYR:CZ	7:H:216:ALA:CB	2.87	0.58
3:D:957:ARG:NE	4:E:434:ASP:HB2	2.18	0.58
5:F:114:LEU:HB2	7:H:52:SER:N	2.18	0.58
15:S:47:LEU:HD22	16:T:7:LEU:HD22	1.84	0.58
24:o:364:ARG:NE	24:o:500:GLU:OE1	2.37	0.58
24:o:463:THR:CG2	24:o:468:SER:HB2	2.33	0.58
1:A:620:LEU:HD22	6:G:67:LEU:CG	2.32	0.58
1:A:764:ILE:HD11	6:G:18:LEU:HD23	1.85	0.58
1:A:781:VAL:HG13	6:G:140:LEU:HD11	1.86	0.58
4:E:378:LYS:HZ1	4:E:418:ASP:H	1.51	0.58
5:F:335:ARG:HE	5:F:382:GLU:HB2	1.69	0.58
13:Q:29:PHE:HD2	13:Q:34:VAL:HG11	1.69	0.58
2:B:560:TYR:CD2	2:B:581:ILE:HD11	2.39	0.58
18:V:148:LYS:HB3	18:V:149:LYS:HZ3	1.68	0.58
4:e:562:SER:OG	4:e:564:ASP:OD1	2.21	0.58
24:o:393:ILE:HD13	29:t:74:ALA:HB1	1.84	0.58
27:r:128:GLN:O	27:r:132:ASP:N	2.34	0.58
2:B:489:GLN:OE1	2:B:489:GLN:N	2.34	0.57
5:F:319:LEU:HG	5:F:319:LEU:O	2.02	0.57
15:S:112:GLY:HA2	15:S:145:ASN:O	2.04	0.57
24:o:1155:LYS:HA	24:o:1309:MET:CE	2.34	0.57
24:o:1430:CYS:HB2	24:o:1435:THR:HG23	1.85	0.57
27:r:130:ILE:HA	27:r:133:ASP:HB2	1.86	0.57
30:v:27:ARG:HD2	30:v:40:ILE:HG23	1.86	0.57
1:A:929:THR:HG22	1:A:954:ALA:HA	1.86	0.57
3:D:905:ALA:O	10:L:126:MET:CE	2.51	0.57
11:O:18:SER:HB3	13:Q:45:LEU:HD12	1.86	0.57
18:V:175:LEU:HD21	18:V:180:LYS:HB2	1.86	0.57
24:o:366:VAL:HB	24:o:481:THR:HG22	1.86	0.57
31:w:105:GLU:HG2	31:w:106:ASP:N	2.19	0.57
35:u:38:CYS:CA	35:u:155:ASN:OD1	2.52	0.57
5:F:279:LEU:CG	5:F:330:ARG:NH1	2.67	0.57
17:U:32:LEU:HD21	18:V:203:PHE:CD2	2.39	0.57
5:f:320:ARG:CB	5:f:320:ARG:HH11	2.18	0.57
24:o:1097:GLU:C	24:o:1101:GLN:HE22	2.12	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:474:THR:OG1	4:E:546:VAL:O	2.19	0.57
14:R:214:PHE:HB3	14:R:218:PHE:CE2	2.40	0.57
15:S:153:ARG:NE	31:w:41:ASN:HA	2.19	0.57
15:S:171:LEU:HD22	25:p:248:LYS:HG3	1.86	0.57
16:T:12:ALA:HA	16:T:109:ILE:HD11	1.85	0.57
24:o:621:ILE:HD11	30:v:124:ARG:NH1	2.19	0.57
24:o:1210:TRP:CB	24:o:1285:LEU:HD13	2.34	0.57
17:U:136:PHE:HA	17:U:140:GLU:HG3	1.86	0.57
4:e:484:LEU:HD21	4:e:504:LEU:HD21	1.86	0.57
25:p:312:GLN:NE2	31:w:22:ASN:ND2	2.53	0.57
28:s:100:THR:HG23	28:s:125:TYR:H	1.69	0.57
1:A:764:ILE:C	6:G:16:PHE:O	2.48	0.57
24:o:465:HIS:NE2	24:o:467:MET:HB2	2.19	0.57
24:o:1029:LEU:HD11	28:s:162:ARG:CD	2.35	0.57
3:D:947:PHE:HB2	8:I:113:PRO:HD2	1.85	0.57
4:E:464:TYR:CE2	5:F:133:ALA:HB2	2.39	0.57
4:E:742:LYS:HA	4:E:745:GLU:HG2	1.85	0.57
5:F:71:ILE:HD11	8:I:35:VAL:HA	1.85	0.57
12:P:249:LYS:N	13:Q:314:LEU:HD11	2.20	0.57
17:U:152:PHE:O	17:U:160:GLU:OE1	2.22	0.57
1:A:575:PRO:HD2	2:B:608:ASN:HB2	1.87	0.57
1:A:684:SER:O	6:G:148:PHE:HE1	1.86	0.57
4:E:586:TYR:HB3	4:E:605:HIS:HB3	1.85	0.57
5:F:44:SER:HB3	8:I:22:ILE:HD11	1.85	0.57
5:F:279:LEU:HD23	5:F:330:ARG:HH12	0.75	0.57
6:G:45:ILE:HG12	6:G:56:VAL:HG13	1.86	0.57
7:H:108:PRO:HA	9:J:119:PHE:CZ	2.40	0.57
12:P:263:ASP:HB2	12:P:309:LYS:HG2	1.86	0.57
17:U:100:VAL:HG12	17:U:103:VAL:HG23	1.86	0.57
25:p:124:LEU:HD22	25:p:152:ILE:HD11	1.85	0.57
25:p:685:LYS:NZ	25:p:686:GLU:O	2.38	0.57
1:A:472:ASN:N	5:f:299:LYS:NZ	2.53	0.57
1:A:1009:LYS:CE	24:o:187:TYR:CG	2.85	0.57
14:R:169:ARG:NH1	14:R:207:ASP:O	2.37	0.57
17:U:144:LEU:HB3	17:U:153:ARG:O	2.05	0.57
3:d:1082:ALA:CB	10:l:83:MET:HE2	2.31	0.57
24:o:1309:MET:HG2	24:o:1334:TRP:HE3	1.70	0.57
35:u:55:GLY:HA3	35:u:69:PRO:HG2	1.86	0.57
7:H:73:GLY:HA3	9:J:142:ALA:CB	2.31	0.57
21:c:67:GLY:CA	9:j:116:LEU:HD13	2.33	0.57
27:r:78:GLU:HA	27:r:81:ALA:HB3	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1052:ARG:CG	1:A:1057:GLU:HG2	2.34	0.56
12:P:227:GLU:OE1	12:P:227:GLU:N	2.37	0.56
12:P:305:PHE:CB	20:Y:30:DT:H4'	2.34	0.56
1:A:402:PHE:HA	1:A:407:GLN:NE2	2.20	0.56
1:A:484:ILE:CG1	5:f:306:PRO:HB3	2.34	0.56
1:A:485:ILE:HD12	5:f:268:ARG:HG2	1.87	0.56
3:D:934:TYR:CD1	8:I:129:LEU:CD2	2.88	0.56
3:D:1000:ARG:HG2	11:O:5:LEU:O	2.05	0.56
4:E:429:LEU:HA	4:E:596:TYR:HB3	1.87	0.56
18:V:78:LEU:O	18:V:80:LYS:N	2.39	0.56
1:A:468:PHE:HD2	5:F:221:GLN:HB3	1.69	0.56
1:A:678:LEU:CD2	6:G:76:SER:CB	2.81	0.56
2:B:735:ILE:HG23	7:H:176:ARG:NH2	2.21	0.56
4:E:694:LEU:CG	4:E:703:MET:CE	2.81	0.56
5:F:335:ARG:HD2	5:F:378:ALA:HB1	1.86	0.56
5:F:418:ILE:HD12	5:F:418:ILE:N	2.20	0.56
7:H:171:ASP:HB3	7:H:174:VAL:HG12	1.86	0.56
13:Q:344:ARG:CZ	20:Y:26:DT:OP1	2.52	0.56
15:S:127:PHE:HB2	16:T:19:TRP:HB2	1.87	0.56
15:S:165:GLU:O	15:S:169:LYS:HG3	2.06	0.56
3:d:917:ILE:HD11	3:d:1063:LEU:HD13	1.87	0.56
24:o:367:ILE:HA	24:o:482:PHE:O	2.03	0.56
24:o:1038:THR:O	24:o:1042:ASN:ND2	2.38	0.56
24:o:1130:ILE:HG21	24:o:1411:LEU:HB3	1.87	0.56
24:o:1158:LEU:CG	24:o:1336:LEU:HD22	2.36	0.56
24:o:1243:LEU:HD11	24:o:1288:ILE:HD12	1.86	0.56
24:o:1309:MET:HA	24:o:1335:ILE:O	2.05	0.56
24:o:1476:ASP:HB3	29:t:105:ILE:HD12	1.87	0.56
25:p:625:LEU:HD13	25:p:675:LEU:HD21	1.88	0.56
28:s:11:TRP:NE1	28:s:35:GLN:O	2.33	0.56
1:A:668:PRO:CB	6:G:10:HIS:CG	2.87	0.56
1:A:900:ASP:CB	6:G:154:LYS:CD	2.69	0.56
2:B:259:ASP:HB3	2:B:262:MET:O	2.05	0.56
3:D:949:GLN:HE21	3:D:949:GLN:CA	2.19	0.56
17:U:129:CYS:SG	17:U:159:THR:OG1	2.62	0.56
18:V:76:GLY:O	18:V:80:LYS:CB	2.53	0.56
5:f:280:ILE:O	5:f:284:ARG:HG3	2.05	0.56
24:o:13:CYS:SG	25:p:1117:HIS:HD2	2.27	0.56
24:o:1243:LEU:HD11	24:o:1288:ILE:CD1	2.35	0.56
5:F:265:GLU:OE2	5:F:265:GLU:HA	2.06	0.56
11:O:90:VAL:HG22	11:O:92:LYS:H	1.71	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:V:180:LYS:O	18:V:184:ALA:N	2.36	0.56
2:B:310:ASP:OD1	7:H:223:TYR:CD2	2.58	0.56
5:F:55:LEU:HD13	8:I:28:ILE:HG23	1.88	0.56
6:G:46:GLU:N	6:G:55:ILE:O	2.37	0.56
12:P:239:ARG:HH11	13:Q:320:VAL:HB	1.70	0.56
24:o:261:ARG:HB3	24:o:276:LEU:HD12	1.87	0.56
24:o:1158:LEU:HD13	24:o:1158:LEU:O	2.05	0.56
24:o:1210:TRP:CD1	24:o:1281:ASP:CG	2.84	0.56
1:A:564:PRO:HB2	2:B:744:PHE:CE2	2.41	0.56
1:A:1157:ASN:O	1:A:1159:SER:N	2.36	0.56
14:R:226:LYS:HZ3	34:z:39:CYS:CA	2.19	0.56
4:E:615:ASP:OD1	8:I:114:ARG:HB3	2.05	0.56
8:I:132:LEU:HG	9:J:121:MET:SD	2.45	0.56
12:P:248:ALA:CB	13:Q:314:LEU:CD1	2.82	0.56
14:R:173:VAL:O	14:R:175:ARG:NH1	2.39	0.56
1:A:766:ARG:O	6:G:14:SER:O	2.24	0.56
7:H:40:VAL:HG21	9:J:130:ILE:HG23	1.88	0.56
10:L:101:GLN:O	10:L:105:HIS:CG	2.52	0.56
10:L:119:HIS:NE2	10:L:123:GLN:OE1	2.38	0.56
20:Y:-5:DG:OP2	20:Y:-5:DG:H2'	2.06	0.56
5:f:223:TYR:HD2	5:f:255:MET:HE1	1.70	0.56
5:f:253:TYR:O	5:f:254:GLN:HB3	2.06	0.56
24:o:526:VAL:HA	24:o:533:PRO:HA	1.87	0.56
2:B:544:LEU:HD23	2:B:590:ILE:HD11	1.88	0.56
5:F:264:SER:HA	5:F:307:ALA:HB2	1.87	0.56
10:L:80:VAL:O	10:L:84:LEU:HG	2.06	0.56
12:P:253:PHE:CD2	12:P:253:PHE:O	2.59	0.56
25:p:1046:THR:HG22	25:p:1047:TYR:H	1.70	0.56
28:s:56:THR:HG22	28:s:57:ASP:H	1.71	0.56
1:A:410:TRP:HH2	5:F:355:ILE:CG2	2.19	0.55
1:A:665:MET:CG	6:G:86:TYR:CE2	2.89	0.55
2:B:883:PHE:CE1	7:H:223:TYR:HB3	2.41	0.55
3:D:871:THR:HG22	10:L:66:LEU:HD13	1.85	0.55
4:E:345:MET:HE3	4:E:346:PRO:HD2	1.87	0.55
5:F:15:PRO:CG	8:I:14:LYS:CG	2.69	0.55
5:F:43:VAL:HG23	8:I:43:ALA:HA	1.88	0.55
7:H:69:ILE:CG2	9:J:138:TYR:HB2	2.35	0.55
7:H:110:TYR:CE2	9:J:160:GLN:HB3	2.41	0.55
11:O:47:ALA:O	11:O:51:ARG:CB	2.54	0.55
14:R:114:MET:HE2	14:R:146:TYR:CB	2.36	0.55
14:R:295:ARG:HG2	14:R:299:LEU:HG	1.86	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:V:192:VAL:O	18:V:192:VAL:HG13	2.05	0.55
18:V:193:ASN:HB3	18:V:196:ASP:HA	1.88	0.55
24:o:733:LEU:CB	31:w:106:ASP:HA	2.36	0.55
25:p:313:GLU:OE2	25:p:316:VAL:N	2.36	0.55
35:u:38:CYS:HG	35:u:44:PHE:HA	1.66	0.55
1:A:763:LEU:HD11	6:G:91:ILE:CD1	2.37	0.55
2:B:61:ASN:O	2:B:130:VAL:HG23	2.06	0.55
3:D:947:PHE:C	3:D:947:PHE:CD1	2.85	0.55
3:D:1000:ARG:NH2	11:O:5:LEU:CG	2.63	0.55
5:F:67:THR:CA	8:I:32:GLU:OE2	2.52	0.55
6:G:45:ILE:HG12	6:G:56:VAL:HG22	1.88	0.55
12:P:192:TYR:HB2	12:P:200:VAL:HG22	1.87	0.55
14:R:47:ASP:OD1	25:p:1075:MET:SD	2.63	0.55
24:o:1050:CYS:HG	24:o:1053:ARG:HB3	1.70	0.55
24:o:1130:ILE:HG12	24:o:1413:ALA:HB2	1.87	0.55
25:p:570:ASN:ND2	25:p:616:THR:OG1	2.39	0.55
1:A:1077:LEU:HG	6:G:147:ARG:NH2	2.18	0.55
3:D:1000:ARG:CZ	11:O:5:LEU:CG	2.81	0.55
16:T:30:GLN:HG2	16:T:62:LEU:HG	1.89	0.55
24:o:769:MET:SD	25:p:973:PRO:HG3	2.46	0.55
24:o:1098:PRO:C	24:o:1100:THR:N	2.64	0.55
35:u:67:LEU:HD12	35:u:67:LEU:O	2.07	0.55
1:A:349:TRP:CE2	5:f:262:PHE:CD1	2.94	0.55
1:A:668:PRO:CB	6:G:10:HIS:CD2	2.85	0.55
3:D:871:THR:HG23	10:L:66:LEU:CG	2.33	0.55
3:D:871:THR:HG23	10:L:66:LEU:HD11	1.89	0.55
3:D:934:TYR:CD2	8:I:129:LEU:CD2	2.89	0.55
3:D:946:PHE:CE2	4:E:513:LEU:HD13	2.39	0.55
4:E:790:LEU:HD13	7:H:146:ILE:HG12	1.87	0.55
5:F:114:LEU:HB2	7:H:52:SER:H	1.72	0.55
5:F:429:LYS:O	5:F:433:PRO:HD2	2.05	0.55
14:R:44:ARG:NH2	25:p:1067:ILE:HG22	2.22	0.55
16:T:31:TRP:CD1	16:T:62:LEU:HD21	2.41	0.55
24:o:503:LEU:O	24:o:503:LEU:HG	2.05	0.55
1:A:349:TRP:CZ2	5:f:262:PHE:CD1	2.95	0.55
2:B:158:GLY:HA2	2:B:188:PHE:HB3	1.88	0.55
5:F:406:VAL:HG11	5:F:420:ALA:HB2	1.88	0.55
7:H:50:PHE:CZ	9:J:195:LEU:HB2	2.42	0.55
13:Q:55:ALA:C	13:Q:56:VAL:HG23	2.30	0.55
17:U:71:PHE:HA	17:U:99:LEU:H	1.71	0.55
17:U:185:GLU:H	17:U:186:PRO:CD	2.18	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:o:583:ARG:NH1	30:v:47:ILE:HD11	2.21	0.55
1:A:355:VAL:O	1:A:355:VAL:CG2	2.54	0.55
1:A:665:MET:HE2	6:G:86:TYR:HB3	1.89	0.55
3:D:871:THR:HG22	10:L:66:LEU:CD1	2.30	0.55
4:E:561:SER:HB2	4:E:588:VAL:HB	1.88	0.55
4:E:696:TRP:CZ2	4:E:703:MET:HE3	2.41	0.55
5:F:67:THR:CA	8:I:32:GLU:HG3	2.29	0.55
11:O:56:VAL:HG11	11:O:84:VAL:N	2.14	0.55
25:p:1136:GLU:HG2	25:p:1143:LYS:HE3	1.89	0.55
27:r:33:LEU:HD13	27:r:101:ALA:HB1	1.87	0.55
1:A:665:MET:HG3	6:G:86:TYR:CE2	2.35	0.55
4:E:775:THR:HG23	5:F:136:LEU:HD21	1.89	0.55
5:F:276:LEU:HD22	5:F:323:VAL:HG22	1.88	0.55
5:F:313:VAL:HG13	5:F:376:SER:N	2.21	0.55
13:Q:346:LYS:HE2	20:Y:27:DT:O5'	2.07	0.55
17:U:137:THR:H	17:U:140:GLU:HG3	1.72	0.55
18:V:166:ILE:HA	18:V:200:ILE:O	2.07	0.55
24:o:1147:SER:N	24:o:1153:ARG:HD2	2.22	0.55
2:B:827:ARG:NE	7:H:211:PHE:CZ	2.75	0.55
5:F:43:VAL:HG22	8:I:43:ALA:HB2	1.83	0.55
5:F:219:GLU:HB2	7:H:156:PRO:HB2	1.89	0.55
12:P:188:ARG:NH1	13:Q:326:GLN:OE1	2.36	0.55
18:V:72:GLY:HA3	18:V:115:GLN:HG3	1.88	0.55
1:A:401:ASN:H	1:A:401:ASN:HD22	1.53	0.55
1:A:486:TRP:HH2	5:f:358:THR:CG2	2.18	0.55
1:A:639:LEU:HD11	1:A:774:ARG:HG2	1.88	0.55
3:D:948:GLU:O	3:D:952:GLN:CB	2.54	0.55
5:F:47:ILE:HG23	8:I:39:MET:SD	2.47	0.55
5:F:279:LEU:CB	5:F:330:ARG:CZ	2.81	0.55
5:F:313:VAL:HA	5:F:375:GLY:HA3	1.89	0.55
14:R:47:ASP:CB	25:p:1069:ILE:CG1	2.83	0.55
28:s:189:GLN:O	28:s:209:VAL:HG12	2.07	0.55
35:u:44:PHE:HD2	35:u:46:ILE:HG13	1.63	0.55
14:R:111:ASP:O	14:R:115:MET:CB	2.54	0.55
14:R:225:PRO:HG2	14:R:228:VAL:HG23	1.89	0.55
17:U:20:TYR:CB	17:U:191:LEU:HB3	2.37	0.55
18:V:81:ILE:CG2	18:V:102:ILE:CD1	2.85	0.55
24:o:808:PRO:HG2	25:p:675:LEU:HD12	1.87	0.55
25:p:387:HIS:NE2	25:p:671:GLU:OE2	2.35	0.55
3:D:934:TYR:CZ	8:I:129:LEU:HD21	2.42	0.54
14:R:226:LYS:HZ3	34:z:39:CYS:C	2.13	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:V:195:PRO:HG2	18:V:199:LYS:HB2	1.89	0.54
4:e:251:LEU:O	4:e:256:HIS:HB2	2.08	0.54
24:o:1175:ILE:HB	31:w:54:TYR:HB3	1.88	0.54
25:p:113:ALA:HA	25:p:118:LEU:HB2	1.89	0.54
1:A:1077:LEU:HD21	6:G:147:ARG:NH2	2.21	0.54
5:F:14:LEU:HA	8:I:18:MET:CB	2.36	0.54
7:H:111:ALA:HA	9:J:157:LEU:HD21	1.88	0.54
10:L:106:ARG:HH11	10:L:114:LYS:HZ3	0.57	0.54
11:O:39:GLN:HG3	13:Q:25:VAL:HG12	1.89	0.54
13:Q:43:LYS:NZ	13:Q:60:HIS:HE1	2.06	0.54
15:S:119:THR:HG22	15:S:123:SER:HA	1.89	0.54
15:S:126:ILE:O	15:S:138:PHE:N	2.35	0.54
4:e:610:ARG:HD3	4:e:619:PRO:HG3	1.89	0.54
24:o:1021:VAL:HA	24:o:1034:GLN:NE2	2.22	0.54
25:p:627:ILE:HD11	25:p:663:GLU:HB2	1.88	0.54
2:B:248:SER:OG	2:B:322:MET:SD	2.65	0.54
12:P:166:GLN:CB	20:Y:28:DT:C5'	2.71	0.54
17:U:188:TYR:HA	17:U:191:LEU:HD21	1.89	0.54
18:V:76:GLY:O	18:V:80:LYS:HB3	2.06	0.54
24:o:460:ARG:HG2	24:o:460:ARG:NH1	2.13	0.54
24:o:460:ARG:HH11	24:o:460:ARG:CG	2.10	0.54
24:o:1173:THR:HG22	24:o:1214:VAL:HG22	1.90	0.54
24:o:1343:LEU:CB	24:o:1364:GLU:OE2	2.50	0.54
4:E:278:ASP:OD2	4:E:649:ARG:NH2	2.40	0.54
5:F:71:ILE:HB	8:I:38:GLN:HE22	1.59	0.54
5:F:71:ILE:HD11	8:I:35:VAL:CA	2.37	0.54
7:H:47:GLU:OE1	7:H:113:ARG:NH2	2.40	0.54
13:Q:15:ARG:NH2	13:Q:58:GLY:HA3	2.22	0.54
25:p:629:GLU:OE1	25:p:630:LYS:N	2.40	0.54
1:A:1077:LEU:CD2	6:G:147:ARG:NH2	2.68	0.54
5:F:309:MET:CA	5:F:312:ILE:CD1	2.46	0.54
12:P:188:ARG:CD	13:Q:322:ASP:OD1	2.55	0.54
12:P:191:GLU:OE2	13:Q:349:TRP:CZ2	2.60	0.54
14:R:27:TYR:CD2	25:p:1078:ARG:CB	2.80	0.54
14:R:27:TYR:CE2	25:p:1078:ARG:HG3	2.41	0.54
14:R:214:PHE:O	14:R:218:PHE:HD2	1.90	0.54
15:S:8:SER:O	16:T:48:THR:CA	2.54	0.54
24:o:542:LEU:HD21	24:o:642:LYS:HB3	1.90	0.54
3:D:881:ARG:CD	10:L:57:VAL:CG1	2.85	0.54
5:F:47:ILE:CD1	8:I:19:MET:HE3	2.23	0.54
14:R:13:VAL:HG22	14:R:13:VAL:O	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:645:GLY:H	4:E:675:LEU:HD11	1.73	0.54
5:F:71:ILE:CD1	8:I:35:VAL:CA	2.83	0.54
13:Q:26:ARG:NH2	13:Q:39:LEU:HD23	2.23	0.54
24:o:1009:VAL:O	24:o:1013:VAL:HG23	2.06	0.54
27:r:132:ASP:OD1	27:r:135:GLN:NE2	2.41	0.54
5:F:369:PRO:O	5:F:373:ARG:N	2.41	0.54
24:o:802:PHE:CD1	25:p:504:THR:HG22	2.42	0.54
4:E:377:LEU:HD23	4:E:426:ARG:HH11	1.73	0.54
4:E:430:PRO:HG3	4:E:598:TYR:HB2	1.90	0.54
4:E:653:LEU:HB2	4:E:663:ARG:HB2	1.90	0.54
5:F:81:GLU:C	5:F:83:LEU:N	2.63	0.54
7:H:73:GLY:C	9:J:142:ALA:HB1	2.32	0.54
12:P:167:ASN:ND2	20:Y:28:DT:H5'	2.23	0.54
12:P:306:VAL:HG13	20:Y:31:DA:OP1	2.08	0.54
15:S:110:PHE:CD1	15:S:148:PRO:HA	2.42	0.54
3:d:911:GLN:NE2	10:l:69:GLU:OE2	2.40	0.54
24:o:863:ARG:NH2	24:o:1128:ILE:HG21	2.22	0.54
26:q:9:VAL:HG11	33:y:105:PHE:HD1	1.72	0.54
27:r:110:GLU:O	27:r:114:LEU:N	2.39	0.54
5:F:68:THR:H	8:I:32:GLU:CD	2.10	0.54
3:d:943:GLN:NE2	4:e:509:GLN:O	2.41	0.54
5:f:390:THR:HG23	5:f:391:LEU:HD22	1.90	0.54
24:o:1115:LYS:HE3	24:o:1337:GLU:CG	2.33	0.54
25:p:357:CYS:HB2	25:p:360:LYS:HE2	1.88	0.54
25:p:910:THR:OG1	34:z:42:ARG:O	2.24	0.54
27:r:123:GLU:HG2	27:r:126:GLU:HB2	1.90	0.54
2:B:629:ARG:NH1	2:B:658:ASP:OD2	2.37	0.53
4:E:563:GLU:HG2	4:E:587:PRO:HG3	1.90	0.53
4:E:694:LEU:HB3	4:E:703:MET:HE2	1.88	0.53
7:H:118:VAL:CG2	9:J:127:THR:CG2	2.80	0.53
18:V:81:ILE:CG2	18:V:102:ILE:HD13	2.30	0.53
5:f:352:GLN:O	5:f:356:THR:OG1	2.25	0.53
24:o:265:VAL:HG13	24:o:271:ARG:HG2	1.89	0.53
1:A:349:TRP:CZ2	5:f:262:PHE:CZ	2.96	0.53
2:B:571:LEU:HD21	2:B:619:MET:HE1	1.89	0.53
2:B:838:ASN:CG	7:H:214:ILE:HG13	2.32	0.53
5:F:55:LEU:HD13	8:I:28:ILE:HG12	1.90	0.53
5:F:342:LYS:O	5:F:346:THR:OG1	2.26	0.53
5:F:403:ILE:O	5:F:406:VAL:HG22	2.08	0.53
14:R:44:ARG:CG	25:p:1067:ILE:HG21	2.39	0.53
4:e:368:ASN:ND2	4:e:701:GLY:HA3	2.23	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:o:1030:SER:HB2	28:s:162:ARG:HE	1.74	0.53
30:v:8:ASP:OD1	30:v:9:ILE:N	2.39	0.53
35:u:51:ILE:HG22	35:u:72:TYR:HB3	1.90	0.53
1:A:567:LEU:HD22	2:B:745:GLN:NE2	2.23	0.53
1:A:764:ILE:CB	6:G:16:PHE:CE2	2.88	0.53
2:B:152:LEU:HD23	2:B:155:PRO:HB3	1.91	0.53
2:B:808:PRO:HA	2:B:864:ASN:HB3	1.90	0.53
3:D:934:TYR:CD2	8:I:129:LEU:HD21	2.42	0.53
14:R:151:LEU:HD11	14:R:201:ALA:HB2	1.90	0.53
24:o:1013:VAL:HG22	24:o:1049:LEU:CD2	2.35	0.53
24:o:1147:SER:CB	24:o:1153:ARG:CD	2.86	0.53
25:p:892:CYS:SG	25:p:893:SER:N	2.82	0.53
17:U:34:LEU:HA	17:U:37:LEU:HD12	1.89	0.53
18:V:99:LEU:HD21	18:V:116:LYS:HG3	1.90	0.53
27:r:125:GLU:HA	27:r:128:GLN:HB3	1.90	0.53
1:A:678:LEU:HA	6:G:77:LEU:O	2.09	0.53
1:A:1068:ARG:HD2	1:A:1068:ARG:C	2.33	0.53
5:F:22:VAL:CG1	8:I:44:PHE:HE1	2.21	0.53
5:F:67:THR:C	8:I:32:GLU:CD	2.77	0.53
12:P:271:GLU:OE2	14:R:208:LEU:CD1	2.57	0.53
17:U:72:ILE:HA	17:U:97:ARG:H	1.74	0.53
18:V:194:ARG:O	18:V:194:ARG:HD3	2.09	0.53
4:e:636:HIS:HD2	4:e:638:ASN:H	1.53	0.53
24:o:18:ILE:H	24:o:1462:GLN:HE22	1.57	0.53
24:o:1484:MET:C	24:o:1485:GLU:HG3	2.34	0.53
25:p:242:ARG:HB2	25:p:254:GLN:HE21	1.74	0.53
1:A:572:TYR:CE1	2:B:689:GLN:OE1	2.62	0.53
1:A:1193:ALA:HB3	6:G:166:VAL:HG21	1.88	0.53
3:D:940:VAL:CG1	3:D:943:GLN:CD	2.80	0.53
5:F:276:LEU:HD22	5:F:323:VAL:CG2	2.39	0.53
14:R:111:ASP:O	14:R:115:MET:N	2.33	0.53
14:R:267:GLU:OE1	14:R:269:ARG:NH2	2.41	0.53
18:V:165:GLY:O	18:V:201:LEU:HA	2.07	0.53
24:o:16:ARG:O	25:p:1149:VAL:HG23	2.09	0.53
24:o:397:PHE:CZ	24:o:1486:ILE:CD1	2.83	0.53
24:o:1068:LEU:O	24:o:1072:ILE:HG12	2.09	0.53
35:u:119:PHE:HB2	35:u:128:TYR:HE1	1.73	0.53
1:A:569:ASN:ND2	2:B:689:GLN:HA	2.24	0.53
7:H:107:LEU:HD11	9:J:157:LEU:O	2.09	0.53
7:H:118:VAL:CG2	9:J:127:THR:OG1	2.56	0.53
9:J:130:ILE:HG13	9:J:160:GLN:HE21	1.74	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:S:46:ARG:HB2	15:S:101:ARG:HB2	1.91	0.53
17:U:75:ARG:HB2	17:U:95:ASN:O	2.09	0.53
18:V:117:GLN:HE21	18:V:121:THR:HG21	1.72	0.53
3:d:963:ARG:NH2	3:d:964:GLU:OE2	2.42	0.53
24:o:1243:LEU:HG	24:o:1292:MET:HE1	1.90	0.53
27:r:115:ILE:HD12	27:r:118:LEU:HD12	1.91	0.53
1:A:395:ASP:OD1	1:A:395:ASP:N	2.41	0.53
1:A:669:GLN:HE21	6:G:10:HIS:HD2	1.55	0.53
2:B:628:ILE:O	2:B:644:GLN:NE2	2.41	0.53
5:F:273:GLN:H	5:F:273:GLN:CD	2.17	0.53
12:P:167:ASN:HD21	20:Y:28:DT:H5'	1.74	0.53
18:V:160:GLN:OE1	18:V:163:LEU:HD23	2.08	0.53
4:e:646:SER:OG	4:e:647:ALA:N	2.40	0.53
24:o:1155:LYS:CA	24:o:1309:MET:HE1	2.39	0.53
26:q:190:ASN:O	26:q:193:ARG:NH1	2.42	0.53
1:A:763:LEU:CD1	6:G:17:ILE:CD1	2.87	0.53
1:A:764:ILE:CG2	6:G:16:PHE:CZ	2.92	0.53
2:B:66:ASN:HD21	2:B:119:PRO:HB3	1.73	0.53
3:D:955:LYS:HG2	3:D:958:LYS:HZ1	1.74	0.53
4:E:658:ASN:OD1	13:Q:37:GLN:OE1	2.26	0.53
5:F:213:ILE:CA	7:H:164:THR:O	2.51	0.53
14:R:226:LYS:HZ3	34:z:39:CYS:N	2.07	0.53
25:p:830:GLU:OE2	25:p:870:THR:OG1	2.23	0.53
28:s:55:ARG:HH22	28:s:107:GLN:HG3	1.74	0.53
35:u:59:ILE:HG12	35:u:66:VAL:HG22	1.90	0.53
14:R:44:ARG:CG	25:p:1067:ILE:CG2	2.86	0.53
17:U:171:LYS:HA	17:U:174:ARG:HB3	1.90	0.53
18:V:181:ALA:O	18:V:184:ALA:C	2.50	0.53
21:c:33:LEU:HD13	9:j:197:MET:HE1	1.91	0.53
24:o:865:ILE:HD13	24:o:1092:ALA:HB3	1.90	0.53
27:r:129:GLN:O	27:r:133:ASP:N	2.38	0.53
35:u:119:PHE:HB2	35:u:128:TYR:CE1	2.44	0.53
2:B:217:ASN:ND2	2:B:320:ALA:O	2.35	0.52
2:B:883:PHE:CD1	2:B:884:VAL:N	2.77	0.52
7:H:37:LEU:CD1	9:J:138:TYR:CE2	2.87	0.52
12:P:176:CYS:SG	12:P:247:PRO:O	2.60	0.52
13:Q:26:ARG:NH2	13:Q:39:LEU:HD21	2.25	0.52
16:T:30:GLN:NE2	16:T:62:LEU:O	2.28	0.52
5:f:318:CYS:SG	5:f:326:HIS:HB3	2.49	0.52
24:o:13:CYS:CB	24:o:14:PRO:CD	2.88	0.52
2:B:781:TYR:HB3	7:H:176:ARG:HH22	1.67	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:324:LYS:HG2	4:E:327:ASN:HD22	1.74	0.52
14:R:146:TYR:O	14:R:149:LYS:HG2	2.09	0.52
15:S:9:GLN:O	15:S:9:GLN:HG2	2.07	0.52
17:U:34:LEU:HD23	17:U:37:LEU:HD12	1.92	0.52
24:o:463:THR:HB	24:o:468:SER:CB	2.25	0.52
24:o:733:LEU:HB3	31:w:106:ASP:HA	1.91	0.52
24:o:1316:ASN:OD1	24:o:1316:ASN:N	2.43	0.52
1:A:764:ILE:CA	6:G:16:PHE:O	2.56	0.52
1:A:1009:LYS:NZ	24:o:187:TYR:CG	2.75	0.52
1:A:1163:ARG:HB3	6:G:183:ILE:HG22	1.91	0.52
3:D:946:PHE:HZ	4:E:527:ILE:HD13	1.74	0.52
9:J:137:TYR:OH	9:J:141:ARG:NH2	2.43	0.52
10:L:67:VAL:HG12	10:L:74:GLU:HB3	1.92	0.52
14:R:218:PHE:HD1	14:R:277:ILE:HG22	1.74	0.52
4:e:423:PRO:HG2	4:e:426:ARG:HB2	1.91	0.52
5:f:283:MET:HG3	5:f:329:LEU:HD11	1.91	0.52
24:o:137:PRO:HA	24:o:140:ARG:HE	1.75	0.52
24:o:1304:ILE:HD11	24:o:1346:VAL:HG21	1.90	0.52
34:z:36:CYS:SG	34:z:37:ARG:N	2.82	0.52
1:A:564:PRO:CB	2:B:744:PHE:CE2	2.92	0.52
5:F:67:THR:C	8:I:32:GLU:OE1	2.47	0.52
11:O:14:SER:HB2	13:Q:46:TRP:HA	1.92	0.52
11:O:57:ASN:O	11:O:57:ASN:ND2	2.42	0.52
18:V:99:LEU:HD13	18:V:120:MET:CA	2.40	0.52
18:V:103:LEU:HB3	18:V:109:LEU:HA	1.90	0.52
27:r:17:ALA:N	35:u:81:LYS:O	2.37	0.52
27:r:100:LEU:HA	27:r:103:LEU:HB2	1.89	0.52
1:A:671:LEU:CD2	6:G:87:LYS:O	2.57	0.52
4:E:304:LYS:NZ	4:E:335:GLU:O	2.42	0.52
4:E:696:TRP:CD2	4:E:703:MET:CB	2.92	0.52
4:E:704:VAL:HG12	4:E:759:ILE:CD1	2.33	0.52
11:O:78:ASP:HA	11:O:91:ASP:HA	1.91	0.52
16:T:94:THR:HG22	16:T:109:ILE:HG23	1.91	0.52
24:o:366:VAL:O	24:o:482:PHE:N	2.41	0.52
1:A:472:ASN:HB2	5:f:299:LYS:HD3	1.90	0.52
1:A:763:LEU:HD12	6:G:17:ILE:HG12	1.90	0.52
1:A:950:VAL:HG13	1:A:1062:TYR:HE2	1.74	0.52
2:B:202:TRP:HB2	2:B:238:LEU:HB3	1.91	0.52
2:B:345:CYS:HA	2:B:348:GLN:HE21	1.73	0.52
2:B:735:ILE:HG23	7:H:176:ARG:CZ	2.38	0.52
2:B:848:HIS:CG	2:B:886:ILE:HD11	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:914:VAL:CG1	10:L:70:VAL:HG11	2.35	0.52
7:H:107:LEU:HD11	9:J:157:LEU:HB3	1.90	0.52
14:R:27:TYR:CD2	25:p:1078:ARG:HG3	2.44	0.52
18:V:167:LEU:HB2	18:V:200:ILE:HB	1.91	0.52
5:f:447:ALA:O	5:f:453:GLY:HA2	2.09	0.52
24:o:44:PRO:HD3	24:o:288:ASN:ND2	2.25	0.52
24:o:1102:MET:CE	24:o:1385:VAL:O	2.57	0.52
24:o:1158:LEU:HD23	24:o:1307:VAL:HG11	1.70	0.52
6:G:181:TRP:CE3	6:G:181:TRP:O	2.63	0.52
14:R:226:LYS:HZ2	34:z:39:CYS:C	2.15	0.52
17:U:102:VAL:HB	17:U:105:TYR:HD2	1.74	0.52
17:U:144:LEU:HD21	17:U:155:THR:HG22	1.92	0.52
4:e:747:LEU:HG	4:e:747:LEU:O	2.09	0.52
24:o:868:MET:CE	24:o:1401:LEU:HA	2.40	0.52
24:o:1436:VAL:HG22	24:o:1440:MET:HE2	1.92	0.52
26:q:31:ALA:O	26:q:231:TYR:OH	2.23	0.52
27:r:42:GLU:O	27:r:46:GLN:N	2.40	0.52
4:E:754:THR:OG1	4:E:755:ALA:N	2.43	0.52
10:L:71:ASP:HB2	10:L:74:GLU:HB2	1.90	0.52
14:R:263:GLN:HA	14:R:268:LYS:HG2	1.92	0.52
18:V:103:LEU:HD12	18:V:116:LYS:HE3	1.92	0.52
2:B:66:ASN:OD1	2:B:187:ARG:NH1	2.42	0.52
5:F:412:LEU:O	5:F:412:LEU:HG	2.09	0.52
7:H:102:PHE:CZ	9:J:158:ALA:CA	2.91	0.52
12:P:302:LEU:HD12	12:P:302:LEU:N	2.24	0.52
18:V:77:VAL:O	18:V:81:ILE:HG13	2.09	0.52
25:p:666:ASP:OD1	25:p:667:THR:N	2.36	0.52
28:s:94:MET:HE2	28:s:125:TYR:HD2	1.75	0.52
1:A:406:THR:C	5:F:354:ARG:HH22	2.17	0.52
12:P:166:GLN:CG	20:Y:28:DT:H5''	2.40	0.52
14:R:29:ALA:HA	25:p:1066:PRO:CD	2.22	0.52
15:S:6:PRO:O	15:S:10:ASN:N	2.43	0.52
4:e:269:GLY:O	8:i:97:ARG:NH2	2.43	0.52
3:D:881:ARG:HH22	10:L:57:VAL:HG22	0.53	0.51
5:F:55:LEU:CD1	8:I:28:ILE:HG23	2.40	0.51
14:R:30:GLY:HA3	25:p:1066:PRO:CA	2.40	0.51
15:S:48:GLU:O	15:S:99:LEU:N	2.38	0.51
17:U:146:ASP:HB3	17:U:149:THR:HG22	1.90	0.51
24:o:463:THR:CB	24:o:468:SER:CB	2.87	0.51
24:o:606:HIS:HB3	24:o:626:THR:HG23	1.92	0.51
24:o:751:LYS:NZ	24:o:751:LYS:CB	2.73	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:o:1158:LEU:HD23	24:o:1336:LEU:CG	2.40	0.51
27:r:73:ARG:NH1	35:u:144:ARG:HH22	2.08	0.51
28:s:64:HIS:HD2	28:s:66:ASP:H	1.58	0.51
35:u:86:ASP:OD1	35:u:143:ILE:O	2.28	0.51
1:A:349:TRP:HZ2	5:f:262:PHE:CE1	2.24	0.51
1:A:472:ASN:HD22	5:f:299:LYS:HA	1.75	0.51
2:B:90:THR:O	2:B:968:ARG:NH2	2.43	0.51
2:B:835:ARG:HD3	7:H:187:GLU:CD	2.34	0.51
5:F:15:PRO:HG3	8:I:14:LYS:NZ	2.04	0.51
5:F:17:GLU:CD	8:I:14:LYS:HE3	2.30	0.51
5:F:52:GLN:NE2	8:I:26:MET:O	2.43	0.51
11:O:60:GLY:N	13:Q:373:ASP:O	2.42	0.51
24:o:840:ALA:HA	25:p:719:SER:OG	2.10	0.51
24:o:1344:MET:HE2	28:s:134:GLU:HA	1.92	0.51
27:r:103:LEU:HA	35:u:144:ARG:CZ	2.39	0.51
1:A:650:ARG:CZ	6:G:78:LYS:HZ1	2.19	0.51
2:B:983:ARG:HH11	2:B:983:ARG:HG3	1.75	0.51
3:D:940:VAL:CG1	3:D:943:GLN:OE1	2.59	0.51
4:E:501:PRO:HD3	7:H:149:HIS:CB	2.40	0.51
4:E:562:SER:OG	4:E:564:ASP:OD1	2.28	0.51
10:L:76:LEU:HD13	10:L:84:LEU:HD12	1.91	0.51
14:R:35:PRO:HG3	24:o:431:PHE:CD2	2.46	0.51
4:e:500:THR:HG22	4:e:502:LYS:H	1.76	0.51
5:f:320:ARG:NH1	5:f:320:ARG:CB	2.73	0.51
24:o:1098:PRO:C	24:o:1100:THR:H	2.18	0.51
25:p:134:LYS:O	25:p:135:GLU:HG3	2.10	0.51
34:z:16:ILE:HD11	34:z:25:GLU:HB3	1.93	0.51
1:A:410:TRP:CE3	5:F:305:ILE:HG22	2.42	0.51
1:A:510:ILE:HB	1:A:511:LEU:HD13	1.93	0.51
1:A:843:ARG:HD3	20:Y:-26:DG:N7	2.25	0.51
1:A:950:VAL:CG1	1:A:1062:TYR:HE2	2.23	0.51
1:A:1009:LYS:NZ	24:o:187:TYR:CB	2.70	0.51
2:B:529:VAL:HG11	2:B:560:TYR:HB2	1.92	0.51
2:B:937:THR:HG23	2:B:939:ASN:H	1.74	0.51
4:E:378:LYS:HD3	4:E:426:ARG:HG3	1.92	0.51
5:F:76:LYS:HG3	5:F:96:PHE:HB3	1.91	0.51
24:o:376:ASP:HB2	24:o:666:ARG:HD2	1.91	0.51
28:s:26:TYR:HD1	28:s:64:HIS:HA	1.75	0.51
1:A:828:GLU:HA	1:A:831:LYS:HB2	1.92	0.51
3:D:891:ILE:HG21	10:L:111:LEU:HB2	1.80	0.51
4:E:601:VAL:HG21	4:E:642:VAL:HG11	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:110:TYR:HD2	9:J:157:LEU:HD22	1.75	0.51
13:Q:18:ILE:O	13:Q:22:ILE:HG12	2.10	0.51
14:R:131:PRO:HD2	25:p:101:ARG:HA	1.93	0.51
17:U:152:PHE:O	17:U:160:GLU:CD	2.54	0.51
24:o:717:ILE:HD11	24:o:815:TYR:O	2.10	0.51
24:o:1374:VAL:O	24:o:1378:LEU:HB2	2.10	0.51
1:A:665:MET:CG	6:G:86:TYR:CG	2.85	0.51
2:B:274:LEU:HG	2:B:278:LYS:HE2	1.93	0.51
2:B:983:ARG:HG3	2:B:983:ARG:NH1	2.26	0.51
5:F:51:ALA:HB1	8:I:28:ILE:HD12	1.92	0.51
5:F:52:GLN:NE2	8:I:26:MET:HB3	2.15	0.51
5:F:118:ILE:HA	7:H:39:VAL:HG13	1.91	0.51
5:F:243:LEU:HD21	5:F:284:ARG:HB3	1.92	0.51
5:F:257:PRO:O	5:F:261:THR:OG1	2.26	0.51
9:J:128:PRO:HB2	9:J:160:GLN:HE22	1.74	0.51
17:U:137:THR:H	17:U:140:GLU:CG	2.23	0.51
4:e:595:PRO:HD2	4:e:639:SER:HB3	1.91	0.51
24:o:1058:PHE:O	24:o:1059:ARG:C	2.53	0.51
24:o:1357:THR:O	28:s:142:HIS:NE2	2.42	0.51
1:A:900:ASP:HA	6:G:154:LYS:HD2	1.89	0.51
7:H:32:ALA:O	7:H:36:THR:OG1	2.29	0.51
14:R:46:ILE:HG23	14:R:46:ILE:O	2.09	0.51
14:R:231:ALA:HA	14:R:301:PRO:HG3	1.93	0.51
15:S:31:PHE:O	16:T:92:THR:N	2.44	0.51
24:o:322:LEU:HD22	24:o:325:LEU:HD12	1.93	0.51
27:r:105:PRO:HG2	27:r:131:LEU:HD11	1.92	0.51
27:r:132:ASP:O	27:r:136:THR:OG1	2.14	0.51
3:D:901:TYR:CZ	10:L:128:ILE:HB	2.44	0.51
4:E:324:LYS:O	4:E:327:ASN:ND2	2.44	0.51
5:F:370:TRP:CH2	5:F:402:ARG:HB3	2.45	0.51
21:c:21:LEU:HD12	21:c:21:LEU:O	2.11	0.51
4:e:607:ARG:NH1	8:i:87:PRO:O	2.43	0.51
24:o:32:LYS:HE3	24:o:89:GLU:OE2	2.10	0.51
3:D:891:ILE:CG2	10:L:111:LEU:CD2	2.82	0.51
5:F:114:LEU:H	7:H:52:SER:HA	1.76	0.51
5:F:286:VAL:HG21	5:F:308:VAL:CG1	2.33	0.51
5:F:313:VAL:HG12	5:F:372:THR:HG23	1.93	0.51
5:F:359:PHE:HB3	5:F:380:LEU:HG	1.92	0.51
5:F:367:LYS:HD2	5:F:367:LYS:O	2.09	0.51
7:H:116:ARG:NH1	9:J:126:TYR:CE1	2.76	0.51
17:U:52:LEU:CD2	18:V:161:ARG:HH11	2.22	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:m:69:THR:HG23	23:m:80:ARG:HE	1.76	0.51
24:o:922:PHE:HB2	24:o:1052:ARG:HB2	1.93	0.51
24:o:1281:ASP:HA	24:o:1284:PHE:HB3	1.93	0.51
25:p:132:VAL:HG22	25:p:140:LEU:HB3	1.93	0.51
25:p:888:THR:HG23	25:p:889:LYS:H	1.76	0.51
1:A:763:LEU:HD13	6:G:17:ILE:HD11	1.91	0.51
1:A:765:ILE:HG12	6:G:15:GLN:HB3	1.92	0.51
2:B:656:GLU:HG2	2:B:661:ALA:HB3	1.93	0.51
2:B:827:ARG:CG	7:H:211:PHE:HZ	2.23	0.51
2:B:883:PHE:C	2:B:885:ASP:N	2.69	0.51
6:G:181:TRP:CD2	6:G:181:TRP:C	2.87	0.51
8:I:132:LEU:CD2	9:J:121:MET:CE	2.89	0.51
9:J:139:LEU:HB3	9:J:144:PHE:HB3	1.93	0.51
15:S:103:ASN:HB2	15:S:107:GLY:HA3	1.93	0.51
17:U:113:ARG:HH21	18:V:217:GLN:HB3	1.76	0.51
24:o:873:VAL:HG22	24:o:879:VAL:HG22	1.92	0.51
24:o:1318:LYS:HE2	24:o:1332:GLN:HG2	1.93	0.51
28:s:46:ASP:OD1	28:s:52:ARG:NH2	2.44	0.51
1:A:406:THR:HG22	5:F:350:ASN:HD22	1.76	0.50
1:A:927:VAL:O	1:A:933:ASN:ND2	2.44	0.50
2:B:338:GLU:HG2	2:B:846:TYR:OH	2.09	0.50
5:F:360:THR:O	5:F:364:VAL:HG22	2.12	0.50
11:O:76:LEU:HB3	11:O:79:VAL:CG2	2.30	0.50
13:Q:15:ARG:NH2	13:Q:58:GLY:CA	2.74	0.50
18:V:200:ILE:N	18:V:200:ILE:HD12	2.26	0.50
24:o:1139:LEU:HD11	24:o:1343:LEU:HD13	1.93	0.50
24:o:1347:LEU:HB3	28:s:137:ILE:HD13	1.91	0.50
3:D:898:VAL:HG22	10:L:113:VAL:CG2	2.33	0.50
17:U:144:LEU:O	17:U:145:PHE:C	2.55	0.50
18:V:78:LEU:C	18:V:80:LYS:N	2.62	0.50
19:X:-39:DA:H2'	19:X:-39:DA:OP2	2.11	0.50
23:m:28:ARG:HH21	23:m:31:LEU:HD21	1.76	0.50
24:o:1210:TRP:CD1	24:o:1281:ASP:OD2	2.60	0.50
25:p:311:ILE:HG13	25:p:316:VAL:HG13	1.93	0.50
1:A:657:SER:HB2	2:B:509:ASN:HB3	1.93	0.50
2:B:877:TYR:CE2	7:H:216:ALA:CB	2.93	0.50
12:P:235:ARG:HB3	13:Q:317:GLU:HG2	1.92	0.50
17:U:32:LEU:HD13	18:V:161:ARG:HH22	1.73	0.50
21:c:1:MET:HG3	5:f:126:PRO:HB3	1.93	0.50
22:k:191:VAL:HG13	22:k:200:ILE:CD1	2.41	0.50
25:p:563:ASP:OD1	25:p:563:ASP:N	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:u:54:ILE:HG13	35:u:70:VAL:HG23	1.93	0.50
1:A:638:PRO:HB3	6:G:39:LEU:HD23	1.93	0.50
3:D:1000:ARG:HH11	3:D:1000:ARG:CG	2.10	0.50
3:D:1085:LYS:NZ	10:L:83:MET:HE2	2.26	0.50
7:H:36:THR:HG21	9:J:134:VAL:CG2	2.38	0.50
12:P:207:PRO:HD2	12:P:207:PRO:O	2.11	0.50
13:Q:358:MET:HE2	13:Q:367:PHE:CD2	2.37	0.50
3:d:916:LYS:NZ	3:d:1070:GLU:OE2	2.42	0.50
24:o:480:SER:OG	33:y:2:ASN:ND2	2.44	0.50
24:o:619:LYS:NZ	24:o:627:LYS:HE3	2.26	0.50
25:p:647:GLU:H	25:p:647:GLU:CD	2.20	0.50
30:v:65:TYR:O	30:v:66:GLU:HG2	2.11	0.50
31:w:96:PHE:HD2	31:w:110:LEU:HD11	1.75	0.50
1:A:484:ILE:HG12	5:f:306:PRO:CB	2.42	0.50
1:A:755:HIS:NE2	6:G:139:PRO:CG	2.73	0.50
3:D:898:VAL:HG23	10:L:113:VAL:HB	1.94	0.50
5:F:273:GLN:CD	5:F:273:GLN:N	2.70	0.50
5:F:320:ARG:NH2	5:F:415:ILE:CA	2.74	0.50
7:H:116:ARG:NH1	9:J:126:TYR:CD1	2.79	0.50
12:P:192:TYR:O	12:P:192:TYR:CG	2.65	0.50
12:P:239:ARG:CD	13:Q:320:VAL:H	2.25	0.50
14:R:169:ARG:HD3	14:R:207:ASP:H	1.77	0.50
17:U:145:PHE:C	17:U:145:PHE:CD1	2.89	0.50
3:d:910:LEU:HD11	10:l:88:ALA:HB2	1.92	0.50
3:D:934:TYR:CE1	8:I:129:LEU:CG	2.89	0.50
4:e:693:VAL:HB	4:e:707:LEU:HB2	1.94	0.50
24:o:1359:SER:O	24:o:1365:ILE:HD11	2.11	0.50
25:p:502:HIS:ND1	25:p:504:THR:OG1	2.33	0.50
1:A:405:VAL:N	5:F:302:HIS:HB3	2.27	0.50
1:A:676:GLY:HA3	6:G:78:LYS:HB2	1.92	0.50
1:A:771:TYR:CD1	6:G:16:PHE:HZ	2.30	0.50
3:D:1085:LYS:NZ	10:L:83:MET:HE1	2.25	0.50
5:F:80:VAL:HG12	8:I:45:ARG:HH12	1.71	0.50
11:O:5:LEU:HD23	11:O:6:TYR:CZ	2.46	0.50
14:R:44:ARG:HB3	25:p:1067:ILE:CG1	2.23	0.50
14:R:44:ARG:CG	25:p:1067:ILE:HD13	2.28	0.50
17:U:105:TYR:HA	18:V:234:GLU:HG2	1.92	0.50
24:o:85:PHE:HE1	25:p:1164:SER:OG	1.95	0.50
24:o:1372:GLU:OE1	28:s:195:ARG:NH1	2.45	0.50
27:r:36:GLU:HG3	27:r:39:MET:HE2	1.93	0.50
35:u:44:PHE:HD2	35:u:46:ILE:CG1	2.19	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:567:LEU:HD22	2:B:745:GLN:HE21	1.77	0.50
1:A:1007:LEU:HD11	1:A:1025:VAL:HG13	1.94	0.50
1:A:1077:LEU:HD11	6:G:147:ARG:HH12	1.74	0.50
7:H:110:TYR:CE2	9:J:160:GLN:CB	2.95	0.50
8:I:56:ILE:HG21	10:L:122:ARG:NH2	2.27	0.50
13:Q:47:GLU:OE2	13:Q:60:HIS:CD2	2.65	0.50
14:R:109:SER:C	14:R:112:ARG:HG3	2.36	0.50
16:T:27:LEU:HD11	16:T:58:LEU:HD21	1.93	0.50
24:o:26:LEU:HB2	25:p:1166:SER:HA	1.94	0.50
24:o:137:PRO:CG	24:o:1445:HIS:CG	2.90	0.50
4:E:481:ASP:HB3	4:E:787:ARG:HH22	1.77	0.50
10:L:93:GLU:O	10:L:97:THR:CG2	2.52	0.50
14:R:111:ASP:CA	14:R:114:MET:HB2	2.40	0.50
4:e:234:ALA:HB2	4:e:648:ASP:HB2	1.94	0.50
24:o:13:CYS:SG	25:p:1117:HIS:CD2	3.04	0.50
24:o:129:ILE:HD11	24:o:143:HIS:HB3	1.93	0.50
2:B:739:ASN:ND2	2:B:782:ASN:OD1	2.44	0.49
3:D:897:ASP:OD2	10:L:130:GLY:O	2.29	0.49
14:R:29:ALA:O	25:p:1066:PRO:CA	2.60	0.49
16:T:93:LEU:HB2	16:T:110:VAL:HB	1.93	0.49
24:o:366:VAL:O	24:o:481:THR:HB	2.11	0.49
24:o:511:THR:HA	24:o:514:GLU:HG2	1.94	0.49
24:o:618:TYR:HD1	24:o:621:ILE:HD12	1.77	0.49
25:p:513:GLU:CD	25:p:525:ASN:HD22	2.20	0.49
1:A:775:GLU:CB	6:G:29:ARG:HH12	2.25	0.49
1:A:1053:PHE:O	1:A:1057:GLU:N	2.42	0.49
4:E:466:PHE:HB2	4:E:796:ALA:HA	1.94	0.49
4:E:634:ARG:HG3	4:E:675:LEU:HB2	1.95	0.49
12:P:269:ARG:HG3	12:P:337:LYS:HE2	1.94	0.49
24:o:16:ARG:NH1	24:o:16:ARG:CB	2.72	0.49
24:o:861:GLN:HG3	24:o:1096:GLY:CA	2.36	0.49
24:o:1045:LEU:O	24:o:1049:LEU:CB	2.48	0.49
24:o:1304:ILE:HG23	24:o:1338:THR:HB	1.94	0.49
24:o:1416:ARG:O	24:o:1420:ASN:HB2	2.12	0.49
25:p:230:ARG:HB2	25:p:231:PRO:HD3	1.92	0.49
26:q:183:ALA:HB3	26:q:232:ASN:HB3	1.94	0.49
2:B:560:TYR:HD2	2:B:581:ILE:HD11	1.77	0.49
3:D:941:ARG:O	3:D:944:LEU:HB2	2.10	0.49
3:D:955:LYS:C	3:D:955:LYS:CD	2.86	0.49
4:E:651:VAL:HB	4:E:665:PHE:HB2	1.95	0.49
4:E:696:TRP:CZ2	4:E:703:MET:CE	2.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:276:LEU:CD2	5:F:327:TRP:HB3	2.35	0.49
9:J:126:TYR:HE2	9:J:157:LEU:HD11	1.77	0.49
12:P:263:ASP:HA	12:P:309:LYS:HA	1.92	0.49
14:R:24:VAL:CG2	24:o:431:PHE:CE2	2.75	0.49
14:R:295:ARG:NH2	14:R:298:ASP:OD2	2.45	0.49
17:U:23:ARG:HD2	18:V:209:GLN:HB2	1.94	0.49
21:c:77:LEU:HD23	21:c:77:LEU:O	2.12	0.49
4:e:650:THR:HG22	4:e:666:THR:HG22	1.93	0.49
24:o:360:ASP:HB3	25:p:1062:ARG:HE	1.77	0.49
24:o:365:THR:HG23	24:o:482:PHE:CB	2.42	0.49
24:o:589:LYS:NZ	24:o:625:ASP:OD2	2.40	0.49
25:p:845:TYR:CD1	25:p:865:VAL:HG11	2.47	0.49
28:s:56:THR:O	28:s:57:ASP:HB3	2.13	0.49
1:A:564:PRO:HB2	2:B:744:PHE:HE2	1.76	0.49
3:D:1085:LYS:HZ2	10:L:83:MET:HE2	1.78	0.49
4:E:693:VAL:HB	4:E:707:LEU:HB2	1.94	0.49
5:F:42:GLU:OE2	8:I:46:TYR:HE2	1.94	0.49
5:F:302:HIS:CD2	5:F:303:GLU:HG3	2.47	0.49
7:H:50:PHE:CE1	9:J:195:LEU:HB2	2.47	0.49
7:H:135:THR:HG22	7:H:135:THR:O	2.13	0.49
14:R:44:ARG:C	25:p:1067:ILE:CG1	2.85	0.49
15:S:153:ARG:HH22	25:p:312:GLN:CD	2.21	0.49
18:V:73:TYR:CD2	18:V:74:LYS:HG2	2.47	0.49
24:o:604:ARG:HH21	24:o:643:LYS:HE2	1.78	0.49
25:p:1144:THR:HG21	35:u:41:LYS:HB2	1.94	0.49
27:r:125:GLU:O	27:r:129:GLN:N	2.39	0.49
1:A:664:PHE:CE2	6:G:80:ILE:HG21	2.47	0.49
1:A:998:LEU:HB3	1:A:1003:ALA:HB2	1.95	0.49
2:B:27:LYS:HE3	2:B:490:SER:HB3	1.95	0.49
5:F:124:ARG:HA	7:H:123:PRO:O	2.12	0.49
8:I:132:LEU:CD2	9:J:121:MET:HE1	2.41	0.49
14:R:214:PHE:HB3	14:R:218:PHE:HE2	1.75	0.49
15:S:153:ARG:NH2	31:w:41:ASN:CG	2.70	0.49
15:S:164:TRP:CZ2	25:p:307:GLU:HB2	2.47	0.49
17:U:137:THR:N	17:U:140:GLU:HB2	2.27	0.49
19:X:-10:DG:OP2	19:X:-10:DG:H2'	2.12	0.49
24:o:364:ARG:CG	24:o:364:ARG:NH1	2.72	0.49
24:o:1177:TYR:CD1	31:w:35:LEU:HD21	2.48	0.49
25:p:1137:CYS:HB3	25:p:1142:ASN:HB3	1.95	0.49
3:D:934:TYR:HA	8:I:129:LEU:HD23	1.93	0.49
5:F:47:ILE:HG23	8:I:19:MET:SD	2.37	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:211:ARG:O	7:H:165:TYR:CE2	2.65	0.49
17:U:32:LEU:CG	18:V:161:ARG:NH2	2.75	0.49
5:f:39:LEU:HD22	8:i:47:VAL:HG13	1.94	0.49
5:f:97:ALA:HB2	5:f:106:PHE:HE1	1.77	0.49
24:o:573:LYS:HD2	30:v:74:GLU:CD	2.38	0.49
24:o:864:LEU:C	24:o:864:LEU:CD2	2.86	0.49
24:o:1147:SER:CB	24:o:1153:ARG:HD2	2.42	0.49
24:o:1347:LEU:CD2	24:o:1357:THR:HB	2.41	0.49
25:p:497:LYS:HG3	25:p:498:PRO:HD3	1.95	0.49
1:A:673:GLY:N	6:G:15:GLN:NE2	2.61	0.49
1:A:758:PRO:HG3	6:G:136:ILE:O	2.12	0.49
13:Q:56:VAL:CG1	13:Q:57:ASP:N	2.76	0.49
24:o:801:GLY:HA3	25:p:503:ASN:CB	2.41	0.49
24:o:1050:CYS:SG	24:o:1053:ARG:CD	3.01	0.49
25:p:359:THR:HG21	25:p:554:GLU:HG3	1.94	0.49
28:s:64:HIS:CD2	28:s:66:ASP:H	2.31	0.49
28:s:103:LEU:HG	28:s:128:GLU:HB2	1.95	0.49
2:B:834:THR:CG2	7:H:213:LEU:HD23	2.17	0.49
3:D:901:TYR:HE1	10:L:128:ILE:CB	2.17	0.49
3:D:938:SER:O	8:I:126:ASN:HB3	2.13	0.49
3:D:996:LEU:C	3:D:996:LEU:CD2	2.85	0.49
5:F:39:LEU:HD11	8:I:51:LEU:HD11	1.94	0.49
5:F:264:SER:HA	5:F:307:ALA:CB	2.43	0.49
5:F:329:LEU:C	5:F:329:LEU:CD2	2.86	0.49
13:Q:348:LYS:HZ2	13:Q:375:GLU:CD	2.20	0.49
17:U:19:LYS:HB3	17:U:23:ARG:HH21	1.78	0.49
18:V:78:LEU:HD13	18:V:123:ALA:HB1	1.95	0.49
8:i:61:ALA:HA	10:l:106:ARG:HG2	1.93	0.49
24:o:358:ARG:H	25:p:1073:GLN:HE21	1.59	0.49
25:p:312:GLN:NE2	31:w:22:ASN:HD21	2.09	0.49
28:s:102:ALA:HB3	28:s:127:LEU:HG	1.95	0.49
28:s:188:GLY:N	28:s:210:GLN:OE1	2.45	0.49
1:A:762:PHE:O	6:G:18:LEU:N	2.45	0.49
2:B:367:GLU:OE2	2:B:371:LYS:NZ	2.39	0.49
2:B:570:GLU:HA	2:B:625:LEU:HA	1.95	0.49
5:f:24:GLU:HG2	10:l:145:THR:HG21	1.93	0.49
24:o:1453:GLY:HA3	24:o:1456:GLU:OE1	2.13	0.49
2:B:598:ARG:HH11	2:B:619:MET:HE3	1.77	0.49
5:F:215:GLU:O	5:F:254:GLN:NE2	2.39	0.49
12:P:203:ARG:O	13:Q:376:TRP:CZ2	2.65	0.49
24:o:466:LYS:HG3	24:o:467:MET:HE2	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:p:380:ARG:HG2	25:p:608:ARG:HH22	1.78	0.49
25:p:1119:CYS:SG	25:p:1120:ASN:N	2.85	0.49
26:q:77:ASP:OD1	26:q:77:ASP:N	2.46	0.49
27:r:60:VAL:HG11	35:u:44:PHE:HZ	0.33	0.49
4:E:747:LEU:HD22	4:E:747:LEU:N	2.20	0.48
11:O:92:LYS:NZ	13:Q:329:PHE:HB2	2.28	0.48
11:O:97:ALA:HA	13:Q:337:CYS:O	2.13	0.48
4:e:439:ASP:OD1	4:e:555:ARG:NH2	2.44	0.48
4:e:651:VAL:HG13	4:e:665:PHE:HB2	1.95	0.48
1:A:636:VAL:HG11	6:G:45:ILE:HG13	1.96	0.48
1:A:1014:GLU:O	1:A:1018:LYS:HB2	2.13	0.48
13:Q:17:VAL:O	13:Q:21:VAL:HG23	2.14	0.48
14:R:177:PHE:O	14:R:181:CYS:N	2.38	0.48
14:R:222:LEU:HD22	14:R:269:ARG:HG3	1.94	0.48
17:U:32:LEU:HB3	18:V:161:ARG:CZ	2.43	0.48
4:e:586:TYR:HB3	4:e:605:HIS:HB3	1.94	0.48
1:A:954:ALA:C	6:G:149:ARG:NH2	2.70	0.48
5:F:219:GLU:CB	7:H:156:PRO:HB2	2.43	0.48
7:H:40:VAL:CG1	9:J:130:ILE:HG12	2.43	0.48
24:o:394:VAL:HG22	24:o:402:LEU:HD13	1.94	0.48
24:o:397:PHE:CZ	24:o:1486:ILE:HD11	2.44	0.48
24:o:1122:PRO:HA	24:o:1125:LYS:HG2	1.95	0.48
24:o:1347:LEU:CB	28:s:137:ILE:HD13	2.42	0.48
1:A:755:HIS:CG	6:G:139:PRO:CD	2.97	0.48
4:E:516:ILE:O	4:E:516:ILE:HG13	2.13	0.48
14:R:114:MET:CE	14:R:146:TYR:HB2	2.43	0.48
17:U:145:PHE:CD2	35:u:98:PHE:HZ	2.21	0.48
24:o:1029:LEU:HD11	28:s:162:ARG:HD3	1.96	0.48
26:q:197:TYR:HD2	26:q:217:GLN:HE21	1.62	0.48
1:A:781:VAL:HG21	6:G:139:PRO:CG	2.44	0.48
1:A:824:ARG:HB3	1:A:863:VAL:HG12	1.95	0.48
1:A:1019:LYS:C	1:A:1021:SER:N	2.72	0.48
7:H:43:SER:CB	7:H:119:ILE:HD11	2.43	0.48
12:P:249:LYS:CA	13:Q:314:LEU:CD1	2.91	0.48
12:P:297:LYS:HB3	12:P:298:PRO:HD3	1.94	0.48
15:S:153:ARG:HD3	31:w:41:ASN:O	2.12	0.48
17:U:152:PHE:HB2	17:U:161:VAL:CG2	2.44	0.48
18:V:132:VAL:O	18:V:132:VAL:HG12	2.14	0.48
18:V:175:LEU:HD23	18:V:175:LEU:C	2.39	0.48
22:k:173:CYS:SG	22:k:179:MET:O	2.72	0.48
24:o:137:PRO:HB3	24:o:140:ARG:HH21	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:o:832:THR:OG1	24:o:835:GLU:OE1	2.30	0.48
25:p:933:ASP:OD2	25:p:1050:ARG:NH2	2.41	0.48
28:s:61:LEU:HD12	28:s:73:PHE:HD2	1.79	0.48
31:w:68:ILE:HG13	31:w:122:ARG:HD2	1.95	0.48
32:x:3:ILE:HD12	32:x:4:PRO:HD2	1.96	0.48
1:A:592:SER:OG	1:A:695:GLY:O	2.31	0.48
1:A:854:ARG:HB3	19:X:30:DC:H5'	1.95	0.48
5:F:81:GLU:HB3	5:F:83:LEU:HD13	1.96	0.48
12:P:251:LEU:HD23	13:Q:311:GLU:HB3	1.94	0.48
13:Q:359:ASN:HA	13:Q:363:ARG:O	2.14	0.48
17:U:72:ILE:HG13	17:U:74:CYS:H	1.79	0.48
21:c:26:VAL:HG23	9:j:195:LEU:HB3	1.96	0.48
4:e:474:THR:OG1	4:e:546:VAL:O	2.28	0.48
5:f:254:GLN:O	5:f:258:ARG:NH2	2.47	0.48
24:o:362:SER:HB2	25:p:1084:LEU:HD12	1.96	0.48
3:D:940:VAL:HG13	3:D:943:GLN:OE1	2.13	0.48
11:O:5:LEU:HD22	11:O:98:CYS:SG	2.53	0.48
18:V:155:LEU:HD21	18:V:189:ILE:HG12	1.94	0.48
24:o:865:ILE:HA	24:o:1092:ALA:HB1	1.95	0.48
24:o:945:ASN:HB3	24:o:948:ILE:HG13	1.96	0.48
24:o:1310:HIS:O	24:o:1335:ILE:N	2.47	0.48
25:p:265:GLN:HG2	25:p:266:GLU:N	2.29	0.48
27:r:128:GLN:HA	27:r:131:LEU:HB2	1.95	0.48
1:A:1022:ARG:O	1:A:1023:TRP:C	2.55	0.48
2:B:329:LEU:HB3	2:B:342:THR:HG23	1.96	0.48
5:F:14:LEU:HA	8:I:18:MET:CG	2.40	0.48
17:U:142:ASN:O	17:U:145:PHE:HB3	2.14	0.48
20:Y:-14:DT:H2''	20:Y:-13:DG:C8	2.49	0.48
24:o:951:GLU:HA	24:o:954:ARG:HH11	1.79	0.48
24:o:959:MET:HA	24:o:962:ASP:OD2	2.13	0.48
25:p:384:ASP:HB3	25:p:387:HIS:HB2	1.96	0.48
25:p:851:ASP:H	34:z:15:MET:HE1	1.77	0.48
35:u:97:LEU:HD13	35:u:128:TYR:CD2	2.48	0.48
1:A:956:PRO:HA	6:G:149:ARG:CD	2.44	0.48
4:E:299:ASP:OD2	4:E:607:ARG:NH2	2.38	0.48
8:I:98:GLN:O	8:I:102:THR:HB	2.13	0.48
15:S:156:THR:OG1	15:S:159:GLU:CD	2.57	0.48
20:Y:-13:DG:H2''	20:Y:-12:DT:H72	1.94	0.48
4:e:724:GLU:OE1	4:e:789:ASN:ND2	2.46	0.48
24:o:1310:HIS:O	24:o:1334:TRP:HA	2.13	0.48
24:o:1428:MET:HB2	24:o:1456:GLU:CD	2.39	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:PRO:HG2	2:B:744:PHE:CZ	2.40	0.48
1:A:844:LYS:O	1:A:847:LYS:HB3	2.14	0.48
1:A:997:ARG:HG3	20:Y:1:DG:H5"	1.96	0.48
2:B:135:TRP:HA	2:B:138:VAL:HG12	1.95	0.48
3:D:898:VAL:CG2	10:L:113:VAL:HA	2.44	0.48
3:D:937:ALA:HB2	8:I:128:ARG:CD	2.41	0.48
15:S:127:PHE:HB2	16:T:19:TRP:CB	2.42	0.48
15:S:164:TRP:NE1	15:S:168:ASN:HD21	2.11	0.48
15:S:167:ARG:O	15:S:171:LEU:HG	2.13	0.48
17:U:120:ASP:HB2	17:U:170:LYS:HE3	1.95	0.48
21:c:119:GLU:HG3	4:e:790:LEU:HD11	1.95	0.48
3:d:922:GLN:NE2	10:l:71:ASP:OD2	2.47	0.48
24:o:869:GLU:OE2	25:p:1095:ILE:HD13	2.14	0.48
24:o:972:THR:O	24:o:1320:ILE:HG21	2.14	0.48
29:t:88:ASP:HB3	29:t:91:LEU:HB2	1.96	0.48
30:v:64:LEU:HB3	30:v:84:ARG:HB2	1.96	0.48
1:A:575:PRO:HD3	2:B:608:ASN:HB2	1.95	0.47
1:A:682:GLU:CG	6:G:140:LEU:HD13	2.37	0.47
3:D:889:HIS:O	10:L:104:ARG:CZ	2.61	0.47
4:E:369:LYS:HA	4:E:369:LYS:HD3	1.74	0.47
5:F:214:HIS:CB	7:H:164:THR:CG2	2.92	0.47
5:F:309:MET:O	5:F:312:ILE:HG12	2.14	0.47
6:G:94:MET:HE3	6:G:96:VAL:HG22	1.94	0.47
16:T:82:PRO:HD2	16:T:117:ARG:O	2.14	0.47
17:U:17:LEU:HG	17:U:195:GLU:CD	2.38	0.47
17:U:55:ASP:HB3	17:U:58:GLN:HB2	1.96	0.47
18:V:81:ILE:HG23	18:V:102:ILE:HG21	1.96	0.47
24:o:13:CYS:HB2	24:o:14:PRO:CD	2.38	0.47
24:o:555:LEU:HD12	24:o:591:ILE:HG13	1.95	0.47
24:o:1005:HIS:HB3	24:o:1008:LYS:HG2	1.96	0.47
35:u:97:LEU:HD13	35:u:128:TYR:HD2	1.79	0.47
1:A:678:LEU:HD21	6:G:76:SER:CB	2.43	0.47
1:A:764:ILE:O	6:G:16:PHE:CA	2.63	0.47
2:B:953:LEU:HD12	2:B:979:PHE:HE2	1.79	0.47
4:E:696:TRP:CH2	4:E:703:MET:CE	2.97	0.47
5:F:309:MET:C	5:F:312:ILE:CD1	2.83	0.47
6:G:48:HIS:HD2	6:G:54:GLY:HA2	1.78	0.47
7:H:224:LEU:O	7:H:228:LEU:HB2	2.14	0.47
11:O:54:ASN:O	13:Q:367:PHE:HA	2.13	0.47
12:P:239:ARG:CZ	13:Q:317:GLU:HB3	2.43	0.47
14:R:29:ALA:O	25:p:1065:GLY:C	2.56	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:720:SER:OG	4:e:721:ARG:N	2.46	0.47
24:o:85:PHE:HE1	25:p:1164:SER:HG	1.62	0.47
24:o:130:LEU:HD21	24:o:235:VAL:HG12	1.96	0.47
24:o:1472:ASP:OD1	24:o:1472:ASP:N	2.43	0.47
28:s:18:MET:HE2	28:s:32:GLU:HG2	1.95	0.47
30:v:14:ASP:OD1	30:v:15:ILE:N	2.43	0.47
3:D:996:LEU:HB2	11:O:69:ASP:CB	2.44	0.47
7:H:27:ASP:OD1	7:H:27:ASP:N	2.46	0.47
17:U:44:LYS:HA	17:U:94:ILE:O	2.14	0.47
3:d:941:ARG:NH2	8:i:123:THR:O	2.48	0.47
24:o:1474:LEU:CD2	35:u:58:VAL:HG22	2.45	0.47
27:r:16:ASP:CA	35:u:81:LYS:HE3	2.43	0.47
27:r:124:ASP:OD1	27:r:125:GLU:N	2.47	0.47
4:E:788:ARG:HB3	7:H:145:HIS:HA	1.96	0.47
8:I:63:LYS:NZ	8:I:69:ASP:OD1	2.47	0.47
11:O:98:CYS:O	13:Q:338:GLN:HA	2.15	0.47
18:V:221:ARG:C	18:V:221:ARG:HD3	2.39	0.47
19:X:-30:DA:C8	19:X:-29:DT:H71	2.49	0.47
4:e:556:ASN:HA	4:e:572:LEU:HB2	1.96	0.47
24:o:460:ARG:NH1	24:o:460:ARG:CG	2.72	0.47
24:o:463:THR:HG21	24:o:468:SER:O	2.13	0.47
24:o:1177:TYR:CD2	31:w:35:LEU:HG	2.50	0.47
25:p:341:GLU:O	25:p:345:LYS:N	2.41	0.47
1:A:349:TRP:CE2	5:f:262:PHE:CE1	3.01	0.47
3:D:1057:ARG:NH2	10:L:77:ASP:OD1	2.47	0.47
5:F:103:GLU:HB3	7:H:59:GLU:HG2	1.96	0.47
5:F:320:ARG:HD3	5:F:415:ILE:HB	1.95	0.47
11:O:57:ASN:HD22	11:O:57:ASN:N	2.11	0.47
13:Q:43:LYS:HE2	13:Q:47:GLU:OE2	2.13	0.47
13:Q:312:GLU:HB2	13:Q:313:PRO:HD3	1.96	0.47
17:U:32:LEU:HD21	18:V:203:PHE:CG	2.49	0.47
3:d:1061:ARG:NH1	8:i:119:ARG:O	2.48	0.47
24:o:356:GLY:HA3	25:p:1085:ARG:HH22	1.78	0.47
24:o:719:LYS:HG3	24:o:725:LEU:HD11	1.96	0.47
25:p:131:THR:HA	25:p:141:GLN:HA	1.95	0.47
5:F:15:PRO:CB	8:I:14:LYS:HE3	2.42	0.47
5:F:48:LYS:CE	8:I:22:ILE:HG23	2.45	0.47
11:O:18:SER:HA	13:Q:45:LEU:CD1	2.34	0.47
17:U:139:LEU:H	17:U:139:LEU:HG	1.45	0.47
18:V:77:VAL:HG13	18:V:81:ILE:HD11	1.96	0.47
24:o:1171:ALA:O	31:w:58:ILE:HB	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:o:1365:ILE:HG23	24:o:1369:LEU:HD12	1.95	0.47
25:p:59:VAL:HG11	25:p:91:ILE:HD11	1.97	0.47
28:s:120:ASP:OD1	28:s:120:ASP:N	2.44	0.47
1:A:468:PHE:CD2	5:F:221:GLN:HB3	2.47	0.47
1:A:573:TYR:HD2	2:B:657:ARG:C	2.23	0.47
1:A:618:PRO:CD	6:G:92:CYS:SG	2.91	0.47
1:A:672:THR:CA	6:G:13:GLU:OE2	2.62	0.47
1:A:677:ASP:O	6:G:77:LEU:O	2.33	0.47
3:D:947:PHE:HB2	8:I:113:PRO:CD	2.45	0.47
3:D:958:LYS:HB3	3:D:958:LYS:HZ2	1.79	0.47
5:F:219:GLU:CG	7:H:156:PRO:HB2	2.45	0.47
5:F:320:ARG:HD3	5:F:415:ILE:CB	2.45	0.47
5:F:388:ILE:HG22	5:F:392:ILE:HG13	1.95	0.47
10:L:71:ASP:C	10:L:73:ASN:N	2.73	0.47
11:O:39:GLN:HG2	13:Q:25:VAL:HG12	1.97	0.47
11:O:58:PHE:CG	11:O:81:PHE:HD2	2.31	0.47
11:O:79:VAL:N	11:O:90:VAL:O	2.48	0.47
12:P:239:ARG:NH2	13:Q:317:GLU:HB3	2.30	0.47
12:P:299:ARG:C	12:P:300:ILE:HG12	2.38	0.47
14:R:29:ALA:C	25:p:1066:PRO:N	2.72	0.47
14:R:35:PRO:HB3	24:o:431:PHE:HB3	1.96	0.47
14:R:132:ARG:HB3	14:R:135:VAL:HG21	1.97	0.47
15:S:156:THR:HG1	15:S:159:GLU:CD	2.20	0.47
4:e:633:THR:O	4:e:634:ARG:NH2	2.45	0.47
24:o:648:SER:OG	24:o:651:SER:OG	2.32	0.47
24:o:721:HIS:HE1	31:w:98:GLN:HE21	1.62	0.47
24:o:861:GLN:CG	24:o:1096:GLY:HA3	2.38	0.47
24:o:1060:LEU:CG	24:o:1064:ALA:HB3	2.44	0.47
24:o:1310:HIS:CE1	24:o:1335:ILE:CD1	2.93	0.47
25:p:28:ILE:HD11	25:p:644:LYS:HB3	1.97	0.47
25:p:371:ARG:NH1	25:p:609:GLU:OE1	2.47	0.47
31:w:27:LYS:HD2	31:w:38:ALA:HB2	1.95	0.47
2:B:636:VAL:HG23	2:B:638:ARG:HB3	1.96	0.47
3:D:935:GLU:C	8:I:128:ARG:O	2.56	0.47
3:D:1080:TYR:HD1	4:E:585:ASN:OD1	1.97	0.47
5:F:44:SER:O	8:I:22:ILE:HD13	2.15	0.47
5:F:51:ALA:C	8:I:28:ILE:HD11	2.37	0.47
7:H:118:VAL:HG22	9:J:127:THR:OG1	2.15	0.47
12:P:263:ASP:CB	12:P:309:LYS:HG2	2.44	0.47
18:V:190:LEU:CD1	18:V:204:ASN:HA	2.40	0.47
5:f:330:ARG:NH1	5:f:371:THR:O	2.47	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:o:1208:SER:O	24:o:1260:ARG:NH2	2.35	0.47
1:A:567:LEU:HA	2:B:745:GLN:NE2	2.30	0.47
5:F:424:GLN:O	5:F:428:LEU:HG	2.15	0.47
13:Q:45:LEU:O	13:Q:49:LYS:HD2	2.15	0.47
18:V:181:ALA:O	18:V:184:ALA:HB3	2.14	0.47
4:e:270:ASP:OD1	4:e:271:GLN:NE2	2.41	0.47
5:f:102:ARG:HD3	10:l:151:ARG:HG3	1.96	0.47
24:o:201:GLU:HG3	24:o:213:LYS:HG2	1.97	0.47
24:o:812:LYS:HE3	31:w:77:THR:HG21	1.96	0.47
24:o:1173:THR:HG21	24:o:1293:LEU:HD21	1.96	0.47
1:A:755:HIS:CE1	6:G:139:PRO:CG	2.98	0.47
5:F:214:HIS:H	7:H:164:THR:CG2	2.20	0.47
7:H:110:TYR:HD2	9:J:157:LEU:CD2	2.28	0.47
15:S:49:ARG:HB3	15:S:96:GLN:HB3	1.96	0.47
24:o:1158:LEU:C	24:o:1158:LEU:CD1	2.86	0.47
26:q:91:GLU:HG3	26:q:92:GLU:H	1.80	0.47
26:q:189:ASP:O	26:q:191:ALA:N	2.41	0.47
32:x:10:CYS:SG	32:x:42:ARG:NE	2.86	0.47
1:A:467:ILE:H	1:A:467:ILE:HG13	1.55	0.46
1:A:569:ASN:HB3	1:A:572:TYR:HD2	1.78	0.46
2:B:184:ASN:N	2:B:184:ASN:ND2	2.63	0.46
5:F:43:VAL:CG2	8:I:43:ALA:HA	2.44	0.46
6:G:41:ASP:OD1	6:G:41:ASP:N	2.48	0.46
14:R:111:ASP:O	14:R:115:MET:HG3	2.15	0.46
17:U:127:PHE:HB3	17:U:161:VAL:HB	1.97	0.46
24:o:823:VAL:HG22	24:o:835:GLU:HG3	1.96	0.46
24:o:1155:LYS:C	24:o:1155:LYS:HD3	2.40	0.46
25:p:853:LEU:HB2	34:z:46:LYS:NZ	2.30	0.46
30:v:32:SER:HB3	30:v:37:MET:H	1.78	0.46
2:B:27:LYS:CE	2:B:490:SER:HB3	2.45	0.46
7:H:205:LYS:HA	7:H:205:LYS:HD3	1.77	0.46
19:X:-30:DA:H1'	19:X:-29:DT:H5'	1.97	0.46
24:o:875:TYR:CE2	29:t:108:ARG:HB3	2.49	0.46
26:q:193:ARG:HD3	26:q:220:TYR:CD1	2.47	0.46
28:s:107:GLN:HG2	28:s:108:GLN:OE1	2.15	0.46
30:v:136:GLU:OE1	30:v:136:GLU:N	2.48	0.46
2:B:475:LYS:HB2	2:B:475:LYS:HE3	1.64	0.46
5:F:15:PRO:HG3	8:I:14:LYS:CD	2.43	0.46
7:H:111:ALA:O	9:J:126:TYR:OH	2.33	0.46
14:R:27:TYR:CE2	25:p:1078:ARG:HB2	2.49	0.46
17:U:154:CYS:SG	17:U:155:THR:N	2.88	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:j:176:MET:HE1	23:m:75:ILE:HD11	1.97	0.46
24:o:20:ARG:HG3	24:o:1449:ASP:O	2.15	0.46
25:p:323:SER:OG	25:p:324:ARG:NH1	2.48	0.46
25:p:625:LEU:HD12	25:p:665:ILE:HG13	1.98	0.46
25:p:856:PRO:HG2	34:z:48:ARG:HA	1.97	0.46
28:s:85:LYS:HD2	28:s:88:LYS:HD2	1.96	0.46
2:B:71:ARG:HD3	2:B:73:TYR:CE1	2.51	0.46
2:B:564:LEU:HB2	2:B:581:ILE:HD13	1.97	0.46
5:F:58:MET:HG3	5:F:66:LEU:H	1.79	0.46
5:F:279:LEU:CD2	5:F:311:CYS:HB2	2.46	0.46
5:F:318:CYS:HB3	5:F:319:LEU:HD23	1.96	0.46
8:I:108:LYS:HD3	8:I:108:LYS:HA	1.47	0.46
11:O:30:PRO:HB2	11:O:31:GLN:H	1.60	0.46
11:O:58:PHE:CD2	11:O:81:PHE:CD2	2.99	0.46
17:U:92:TYR:HE2	17:U:94:ILE:CD1	2.27	0.46
3:d:1080:TYR:OH	4:e:606:ASP:OD2	2.26	0.46
4:e:589:TRP:HB3	5:f:60:MET:HE3	1.96	0.46
24:o:1101:GLN:H	24:o:1101:GLN:HE21	1.62	0.46
24:o:1158:LEU:HD23	24:o:1336:LEU:HD13	1.98	0.46
24:o:1205:ALA:HB1	24:o:1267:ASN:HB2	1.98	0.46
24:o:1482:TYR:CD1	24:o:1482:TYR:O	2.68	0.46
25:p:276:LEU:HG	25:p:343:LEU:HD21	1.97	0.46
25:p:773:PRO:HG3	32:x:53:VAL:HG11	1.97	0.46
25:p:809:VAL:HG22	25:p:810:PHE:H	1.80	0.46
26:q:193:ARG:NH2	26:q:217:GLN:OE1	2.49	0.46
1:A:730:PHE:CD1	1:A:730:PHE:N	2.82	0.46
4:E:321:LEU:HB3	4:E:330:TRP:HB2	1.97	0.46
5:F:414:ASN:C	5:F:416:ASP:N	2.73	0.46
7:H:217:ARG:HE	7:H:217:ARG:HB2	1.33	0.46
12:P:238:ALA:HB1	13:Q:314:LEU:CD2	2.43	0.46
17:U:73:LYS:HE2	17:U:73:LYS:HB3	1.53	0.46
18:V:96:PRO:HB2	18:V:136:LYS:HD3	1.98	0.46
5:f:317:LEU:HD12	5:f:329:LEU:HD23	1.98	0.46
24:o:406:VAL:HG21	24:o:440:LEU:HD11	1.98	0.46
24:o:1173:THR:OG1	24:o:1289:GLU:OE2	2.27	0.46
25:p:84:TYR:CD2	25:p:132:VAL:HG12	2.50	0.46
25:p:898:THR:OG1	25:p:1079:SER:HA	2.15	0.46
3:D:917:ILE:CD1	3:D:1058:VAL:CG2	2.68	0.46
3:D:934:TYR:CD2	8:I:129:LEU:HD23	2.50	0.46
5:F:90:GLU:OE2	9:J:208:GLY:HA3	2.16	0.46
5:F:213:ILE:CG2	7:H:164:THR:O	2.63	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:412:LEU:CD2	5:F:412:LEU:N	2.73	0.46
7:H:111:ALA:CB	9:J:126:TYR:CE2	2.93	0.46
8:I:119:ARG:NH1	8:I:120:TYR:OH	2.48	0.46
10:L:71:ASP:C	10:L:73:ASN:H	2.23	0.46
12:P:256:GLN:HA	12:P:256:GLN:OE1	2.16	0.46
15:S:44:GLN:HG3	15:S:104:GLY:H	1.75	0.46
18:V:72:GLY:CA	18:V:115:GLN:HG3	2.45	0.46
18:V:228:MET:HE3	18:V:228:MET:HB2	1.83	0.46
24:o:1231:ILE:HG23	24:o:1296:MET:HE1	1.96	0.46
24:o:1312:PRO:HG2	24:o:1318:LYS:HG2	1.97	0.46
25:p:260:LEU:HD22	25:p:347:MET:HE1	1.97	0.46
25:p:446:TYR:O	25:p:450:THR:HG22	2.16	0.46
25:p:606:ASP:OD1	25:p:606:ASP:N	2.44	0.46
27:r:103:LEU:CG	35:u:144:ARG:NH1	2.75	0.46
28:s:11:TRP:HB2	28:s:40:PHE:CD2	2.51	0.46
28:s:47:LYS:O	28:s:51:GLY:HA3	2.16	0.46
30:v:96:VAL:HG22	30:v:116:VAL:HG22	1.96	0.46
1:A:636:VAL:CG1	6:G:45:ILE:HG13	2.45	0.46
1:A:682:GLU:HG2	6:G:72:CYS:SG	2.55	0.46
1:A:773:ILE:HD12	6:G:18:LEU:HD23	1.98	0.46
5:F:80:VAL:CG1	8:I:45:ARG:NH1	2.73	0.46
5:F:267:VAL:HG21	5:F:307:ALA:O	2.15	0.46
5:F:313:VAL:CG1	5:F:372:THR:HG23	2.46	0.46
8:I:38:GLN:HA	8:I:41:GLU:HB2	1.98	0.46
10:L:106:ARG:NH1	10:L:114:LYS:CG	2.70	0.46
12:P:239:ARG:HD2	13:Q:320:VAL:H	1.81	0.46
12:P:309:LYS:HB2	20:Y:30:DT:OP1	2.15	0.46
14:R:175:ARG:HH22	25:p:102:ASP:HA	1.69	0.46
16:T:30:GLN:O	16:T:62:LEU:HD11	2.16	0.46
17:U:32:LEU:CD1	18:V:161:ARG:HH21	2.29	0.46
3:d:1084:LEU:HB3	8:i:99:ARG:HH21	1.81	0.46
24:o:355:MET:HE2	24:o:1459:MET:CG	2.42	0.46
24:o:687:ILE:HD12	25:p:969:PRO:O	2.15	0.46
24:o:834:THR:HG21	25:p:677:MET:HE1	1.89	0.46
24:o:922:PHE:HA	24:o:1052:ARG:HD3	1.97	0.46
25:p:908:MET:HE3	25:p:910:THR:HG22	1.98	0.46
26:q:123:ASN:OD1	26:q:124:SER:N	2.48	0.46
28:s:75:PHE:HB2	28:s:104:ILE:HG22	1.96	0.46
33:y:37:LYS:HD3	33:y:37:LYS:HA	1.69	0.46
1:A:719:TYR:HD1	6:G:85:PHE:HZ	1.63	0.46
1:A:995:LEU:HA	1:A:998:LEU:HG	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:901:TYR:HD1	10:L:128:ILE:HG22	1.77	0.46
4:E:646:SER:OG	4:E:647:ALA:N	2.49	0.46
5:F:324:ASP:HA	5:F:327:TRP:NE1	2.31	0.46
12:P:271:GLU:CD	14:R:208:LEU:HD11	2.40	0.46
14:R:117:ALA:O	14:R:121:ILE:N	2.45	0.46
17:U:185:GLU:N	17:U:186:PRO:HD2	2.31	0.46
24:o:350:VAL:HG23	24:o:1459:MET:HE3	1.98	0.46
24:o:477:LEU:HB2	24:o:483:ARG:HH21	1.81	0.46
24:o:534:VAL:HG23	24:o:535:MET:HG3	1.97	0.46
24:o:1220:HIS:HB3	24:o:1224:ARG:HH12	1.79	0.46
24:o:1281:ASP:O	24:o:1285:LEU:HB2	2.15	0.46
24:o:1347:LEU:HD21	24:o:1357:THR:CB	2.41	0.46
35:u:6:SER:HB3	35:u:71:LYS:NZ	2.31	0.46
1:A:1165:LEU:HB2	1:A:1191:ILE:HG12	1.97	0.46
2:B:559:LYS:HB2	2:B:559:LYS:NZ	2.31	0.46
3:D:871:THR:HG21	3:D:910:LEU:HD12	1.98	0.46
3:D:941:ARG:HG2	3:D:944:LEU:HD12	1.95	0.46
5:F:112:VAL:O	7:H:53:ALA:O	2.33	0.46
5:F:276:LEU:HD13	5:F:323:VAL:HG11	1.97	0.46
10:L:106:ARG:CZ	10:L:114:LYS:HD2	2.37	0.46
11:O:57:ASN:HD22	11:O:57:ASN:H	1.64	0.46
15:S:46:ARG:N	15:S:101:ARG:O	2.38	0.46
20:Y:13:DG:OP2	20:Y:13:DG:H8	1.99	0.46
5:f:257:PRO:O	5:f:261:THR:OG1	2.31	0.46
24:o:381:PRO:HB3	24:o:479:TRP:O	2.16	0.46
24:o:461:GLN:HB2	24:o:462:PRO:HD2	1.95	0.46
24:o:839:HIS:HE2	25:p:719:SER:H	1.61	0.46
24:o:1377:ALA:HB2	28:s:144:LEU:HD13	1.97	0.46
24:o:1451:MET:HA	24:o:1451:MET:CE	2.38	0.46
25:p:626:LEU:HD23	25:p:662:VAL:HG12	1.98	0.46
35:u:84:VAL:HG12	35:u:144:ARG:HD3	1.98	0.46
5:F:426:LEU:C	5:F:426:LEU:HD23	2.41	0.46
12:P:191:GLU:OE2	13:Q:349:TRP:HZ2	1.99	0.46
12:P:271:GLU:OE2	14:R:208:LEU:HD11	2.16	0.46
15:S:164:TRP:HZ2	25:p:307:GLU:HB2	1.81	0.46
9:j:149:PRO:O	9:j:153:ARG:NH1	2.46	0.46
25:p:794:VAL:HG12	25:p:967:ILE:HG22	1.98	0.46
25:p:1035:ARG:NH1	25:p:1036:LYS:O	2.48	0.46
3:D:881:ARG:CZ	10:L:57:VAL:HG21	2.43	0.45
3:D:917:ILE:CG1	3:D:1058:VAL:HG11	2.44	0.45
3:D:935:GLU:O	8:I:128:ARG:HG2	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:15:PRO:HD2	8:I:15:ASP:HA	1.96	0.45
5:F:214:HIS:HB3	7:H:164:THR:HG21	1.98	0.45
8:I:103:PRO:HB2	11:O:21:GLU:OE1	2.16	0.45
14:R:45:VAL:O	24:o:67:ARG:NH2	2.48	0.45
15:S:156:THR:OG1	15:S:159:GLU:CG	2.64	0.45
5:f:326:HIS:ND1	5:f:326:HIS:N	2.64	0.45
5:f:327:TRP:O	5:f:330:ARG:HB2	2.15	0.45
24:o:460:ARG:HD3	24:o:501:MET:HG2	1.97	0.45
24:o:552:ASP:OD1	24:o:552:ASP:N	2.45	0.45
24:o:784:VAL:HG13	25:p:978:ILE:CD1	2.45	0.45
24:o:784:VAL:HG13	25:p:978:ILE:HD11	1.97	0.45
28:s:70:ASP:OD1	28:s:70:ASP:N	2.49	0.45
31:w:124:THR:OG1	31:w:125:GLU:N	2.49	0.45
35:u:43:GLY:HA2	35:u:78:ARG:HD3	1.98	0.45
1:A:405:VAL:HG21	5:F:301:VAL:CG1	2.46	0.45
11:O:58:PHE:N	11:O:58:PHE:HD1	2.13	0.45
18:V:193:ASN:N	18:V:193:ASN:HD22	2.14	0.45
4:e:717:LEU:HD22	4:e:726:LEU:HD11	1.97	0.45
24:o:619:LYS:HZ2	24:o:627:LYS:HE3	1.81	0.45
25:p:309:PHE:HZ	31:w:40:ARG:HB3	1.81	0.45
25:p:371:ARG:HH22	25:p:380:ARG:HH22	1.63	0.45
26:q:266:GLU:HG2	33:y:21:ILE:HG12	1.97	0.45
1:A:1010:PHE:CD1	24:o:187:TYR:OH	2.69	0.45
4:E:324:LYS:HA	4:E:327:ASN:HB3	1.97	0.45
15:S:26:TYR:HB2	15:S:139:PRO:O	2.16	0.45
16:T:44:ARG:HH22	16:T:80:GLU:CD	2.25	0.45
24:o:365:THR:HG21	24:o:482:PHE:CE1	2.47	0.45
24:o:717:ILE:CD1	24:o:815:TYR:O	2.65	0.45
24:o:1037:ALA:O	24:o:1039:LEU:N	2.42	0.45
29:t:84:GLU:O	29:t:84:GLU:HG2	2.16	0.45
1:A:401:ASN:HD22	1:A:401:ASN:N	2.14	0.45
1:A:404:MET:O	1:A:408:LEU:HB2	2.17	0.45
1:A:473:GLU:CD	5:F:212:SER:HB2	2.41	0.45
3:D:1000:ARG:NH1	3:D:1000:ARG:CG	2.73	0.45
11:O:55:ARG:CB	13:Q:369:LYS:HB2	2.43	0.45
17:U:141:ALA:HA	17:U:144:LEU:HD12	1.98	0.45
24:o:44:PRO:HD3	24:o:288:ASN:HD22	1.81	0.45
24:o:721:HIS:CE1	31:w:98:GLN:HE21	2.34	0.45
28:s:55:ARG:HA	28:s:58:LEU:HD12	1.98	0.45
4:E:694:LEU:CB	4:E:703:MET:HE3	2.33	0.45
16:T:23:VAL:HG21	16:T:31:TRP:CZ3	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:X:-39:DA:H2'	19:X:-39:DA:P	2.56	0.45
20:Y:-10:DC:H2''	20:Y:-9:DG:C8	2.52	0.45
5:f:326:HIS:O	5:f:330:ARG:HG2	2.15	0.45
24:o:465:HIS:CD2	24:o:467:MET:HB2	2.51	0.45
25:p:65:ILE:HD11	25:p:86:LEU:HD12	1.99	0.45
25:p:591:ARG:NH2	25:p:663:GLU:OE2	2.50	0.45
35:u:38:CYS:HB2	35:u:44:PHE:CD1	2.51	0.45
1:A:475:LEU:HD23	1:A:480:TRP:HE1	1.82	0.45
2:B:882:HIS:O	2:B:887:ARG:HG3	2.16	0.45
4:E:702:LEU:HD22	4:E:757:GLY:C	2.42	0.45
7:H:221:ILE:H	7:H:221:ILE:HG12	1.65	0.45
11:O:11:LEU:HG	13:Q:46:TRP:HE1	1.81	0.45
12:P:249:LYS:C	13:Q:314:LEU:CD1	2.89	0.45
14:R:189:LYS:HZ1	14:R:190:GLU:HB2	1.82	0.45
15:S:54:LYS:HE2	15:S:54:LYS:HB2	1.84	0.45
17:U:23:ARG:HD3	18:V:206:LYS:HB2	1.97	0.45
5:f:223:TYR:CD2	5:f:255:MET:HE1	2.52	0.45
24:o:1482:TYR:C	24:o:1482:TYR:HD1	2.24	0.45
25:p:1141:ARG:HE	25:p:1143:LYS:HZ1	1.64	0.45
1:A:572:TYR:CD1	2:B:689:GLN:CD	2.95	0.45
1:A:620:LEU:HB2	6:G:93:GLN:CD	2.42	0.45
1:A:764:ILE:O	6:G:16:PHE:C	2.60	0.45
3:D:969:ALA:HB1	3:D:990:GLU:HG3	1.99	0.45
5:F:344:PHE:C	5:F:346:THR:N	2.73	0.45
15:S:29:MET:HB2	16:T:96:PHE:CD1	2.52	0.45
19:X:-2:DT:H2'	19:X:-2:DT:OP2	2.17	0.45
24:o:622:SER:HB3	24:o:637:MET:HE3	1.98	0.45
24:o:1019:LYS:O	24:o:1021:VAL:HG23	2.16	0.45
1:A:470:ILE:HD12	7:H:166:ARG:HB2	1.99	0.45
1:A:1077:LEU:CD1	6:G:147:ARG:HH12	2.30	0.45
2:B:883:PHE:N	7:H:222:PRO:HB2	2.31	0.45
3:D:905:ALA:CB	10:L:120:LEU:HD21	2.46	0.45
3:D:917:ILE:CG2	3:D:1058:VAL:HG11	2.47	0.45
3:D:950:LEU:C	3:D:950:LEU:CD1	2.90	0.45
4:E:250:GLU:O	4:E:254:ASN:ND2	2.50	0.45
5:F:50:ILE:O	5:F:54:ALA:N	2.47	0.45
5:F:114:LEU:N	7:H:52:SER:HA	2.32	0.45
10:L:101:GLN:C	10:L:105:HIS:HD2	2.17	0.45
12:P:228:GLU:OE1	12:P:228:GLU:HA	2.16	0.45
12:P:271:GLU:OE1	14:R:208:LEU:HD11	2.16	0.45
14:R:248:ARG:CZ	20:Y:32:DG:H3'	2.47	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:V:153:ARG:HD3	18:V:153:ARG:HA	1.74	0.45
18:V:172:GLU:O	18:V:173:GLU:C	2.59	0.45
20:Y:-21:DG:H2"	20:Y:-20:DC:C6	2.52	0.45
24:o:1218:ARG:HA	24:o:1221:MET:HB2	1.98	0.45
24:o:1374:VAL:O	24:o:1378:LEU:CB	2.65	0.45
25:p:329:GLY:HA3	25:p:335:ARG:HG3	1.98	0.45
25:p:1108:PHE:HZ	25:p:1150:ARG:HG2	1.81	0.45
27:r:87:LEU:H	27:r:87:LEU:HG	1.64	0.45
33:y:42:LEU:O	33:y:45:ILE:HG22	2.17	0.45
35:u:24:ASN:OD1	35:u:25:THR:N	2.50	0.45
1:A:680:LEU:CG	6:G:74:MET:SD	3.02	0.45
1:A:968:ILE:HD12	1:A:968:ILE:HA	1.79	0.45
5:F:112:VAL:HG11	7:H:55:LYS:HD3	1.98	0.45
7:H:73:GLY:CA	9:J:142:ALA:HB3	2.39	0.45
11:O:88:ILE:HG21	13:Q:360:LEU:CD1	2.39	0.45
12:P:249:LYS:CA	13:Q:314:LEU:HD12	2.46	0.45
12:P:252:ASP:OD1	12:P:252:ASP:N	2.49	0.45
15:S:102:VAL:O	15:S:107:GLY:HA3	2.16	0.45
18:V:142:LYS:HD2	18:V:142:LYS:HA	1.59	0.45
24:o:417:LYS:HE2	24:o:417:LYS:HB2	1.62	0.45
24:o:551:ARG:HG3	30:v:121:LEU:CD2	2.46	0.45
24:o:745:LEU:CD1	24:o:790:GLN:OE1	2.62	0.45
24:o:852:VAL:HG13	25:p:494:LYS:HE3	1.99	0.45
25:p:1119:CYS:HA	25:p:1146:ILE:HD13	1.98	0.45
26:q:9:VAL:HG11	33:y:105:PHE:CD1	2.51	0.45
35:u:86:ASP:OD2	35:u:171:VAL:CG2	2.55	0.45
1:A:400:GLU:HG3	1:A:401:ASN:N	2.32	0.45
4:E:599:TYR:HE2	11:O:28:ILE:HD13	1.81	0.45
5:F:323:VAL:HG22	5:F:326:HIS:HB3	1.98	0.45
5:f:83:LEU:HD22	8:i:41:GLU:HG2	1.99	0.45
25:p:50:PHE:HA	25:p:54:SER:HB3	1.97	0.45
25:p:552:ASN:OD1	25:p:553:LEU:N	2.49	0.45
1:A:411:GLU:H	1:A:411:GLU:HG3	1.55	0.44
2:B:639:LYS:NZ	2:B:641:GLU:OE2	2.42	0.44
6:G:149:ARG:HG3	6:G:151:THR:HG23	2.00	0.44
11:O:28:ILE:H	11:O:28:ILE:HG12	1.48	0.44
11:O:53:ARG:CB	13:Q:368:SER:HB3	2.47	0.44
21:c:24:ASP:CB	9:j:192:LYS:HD2	2.48	0.44
24:o:834:THR:HG22	25:p:677:MET:HE1	1.91	0.44
24:o:1097:GLU:O	24:o:1100:THR:N	2.42	0.44
25:p:961:ILE:HD11	32:x:42:ARG:HD2	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:575:PRO:HD3	2:B:608:ASN:CB	2.48	0.44
1:A:755:HIS:CG	6:G:139:PRO:HD3	2.49	0.44
2:B:827:ARG:CG	7:H:211:PHE:CZ	3.00	0.44
3:D:935:GLU:CB	8:I:130:LYS:HG3	2.43	0.44
4:E:373:PHE:HB3	4:E:422:PRO:HD3	1.99	0.44
5:F:92:ILE:HG13	5:F:93:PRO:HD3	1.98	0.44
5:F:400:GLY:O	5:F:404:ARG:HG2	2.18	0.44
7:H:43:SER:HB2	7:H:119:ILE:HD11	1.98	0.44
11:O:30:PRO:HD2	11:O:31:GLN:HG2	1.99	0.44
12:P:207:PRO:O	12:P:207:PRO:CD	2.66	0.44
13:Q:367:PHE:C	13:Q:367:PHE:CD1	2.95	0.44
14:R:134:ILE:H	14:R:134:ILE:HG12	1.19	0.44
17:U:127:PHE:CE2	17:U:138:ASP:HA	2.51	0.44
19:X:12:DA:H2"	19:X:13:DC:C6	2.52	0.44
3:d:860:VAL:HA	23:m:47:GLN:HG2	1.98	0.44
5:f:58:MET:HE3	5:f:64:GLN:HA	1.97	0.44
5:f:149:PRO:HA	5:f:150:PRO:HD3	1.83	0.44
10:l:113:VAL:O	10:l:113:VAL:HG22	2.18	0.44
23:m:103:LEU:O	23:m:107:ASN:ND2	2.51	0.44
24:o:70:ARG:HD2	24:o:75:ALA:HB1	2.00	0.44
24:o:1054:MET:HG3	24:o:1058:PHE:HD2	1.82	0.44
25:p:371:ARG:NH2	25:p:380:ARG:HH22	2.16	0.44
27:r:18:SER:OG	35:u:82:GLY:HA3	2.18	0.44
27:r:50:SER:OG	27:r:51:ALA:N	2.50	0.44
31:w:75:ASP:HB3	31:w:78:LEU:HD12	1.99	0.44
31:w:103:ARG:O	31:w:103:ARG:HD3	2.18	0.44
35:u:60:GLN:NE2	35:u:65:PHE:HB2	2.32	0.44
3:D:934:TYR:CD1	8:I:129:LEU:HG	2.52	0.44
5:F:14:LEU:CD2	8:I:15:ASP:O	2.65	0.44
12:P:236:LYS:HG2	12:P:239:ARG:HH12	1.81	0.44
15:S:143:TRP:CD1	15:S:143:TRP:C	2.95	0.44
15:S:153:ARG:CZ	31:w:41:ASN:HA	2.47	0.44
24:o:20:ARG:CD	24:o:1448:SER:OG	2.59	0.44
24:o:99:PHE:CE1	24:o:1440:MET:SD	3.10	0.44
24:o:716:VAL:HA	24:o:719:LYS:HE2	2.00	0.44
24:o:990:ALA:HB2	24:o:1067:TRP:CZ3	2.52	0.44
24:o:1050:CYS:SG	24:o:1053:ARG:HD2	2.57	0.44
24:o:1313:GLN:C	24:o:1318:LYS:HE3	2.43	0.44
25:p:486:ASN:OD1	25:p:491:ARG:NH2	2.50	0.44
25:p:603:MET:HE3	25:p:603:MET:HB2	1.85	0.44
25:p:1046:THR:HG22	25:p:1047:TYR:N	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:q:101:PHE:CE1	26:q:122:SER:HB3	2.53	0.44
28:s:88:LYS:HA	28:s:91:CYS:HB2	1.99	0.44
1:A:416:TRP:HE1	5:F:313:VAL:CB	2.23	0.44
1:A:781:VAL:HG21	6:G:139:PRO:HG2	1.99	0.44
2:B:492:MET:HE3	2:B:492:MET:HB2	1.85	0.44
3:D:957:ARG:NE	4:E:434:ASP:CB	2.78	0.44
5:F:47:ILE:CG1	8:I:19:MET:CE	2.86	0.44
5:F:319:LEU:N	5:F:319:LEU:CD2	2.75	0.44
5:F:391:LEU:HD12	5:F:391:LEU:HA	1.78	0.44
7:H:116:ARG:HG3	7:H:116:ARG:O	2.16	0.44
14:R:268:LYS:O	14:R:269:ARG:NH1	2.37	0.44
17:U:16:ARG:HD2	17:U:16:ARG:HA	1.41	0.44
17:U:137:THR:H	17:U:140:GLU:HB2	1.81	0.44
4:e:703:MET:HE2	4:e:703:MET:HB3	1.83	0.44
28:s:4:GLU:HA	28:s:7:THR:HG22	1.98	0.44
28:s:154:GLU:O	28:s:157:THR:HG22	2.17	0.44
35:u:116:GLU:O	35:u:130:THR:HA	2.16	0.44
1:A:618:PRO:O	6:G:92:CYS:SG	2.75	0.44
1:A:669:GLN:NE2	6:G:10:HIS:HD2	2.16	0.44
2:B:568:VAL:HG22	2:B:628:ILE:HG23	1.98	0.44
5:F:233:GLY:HA2	5:F:239:ARG:HE	1.82	0.44
11:O:61:SER:H	11:O:79:VAL:CG2	2.28	0.44
16:T:17:GLY:HA2	16:T:109:ILE:O	2.17	0.44
20:Y:10:DC:H2"	20:Y:11:DG:C8	2.53	0.44
4:e:718:ARG:HA	4:e:718:ARG:HD3	1.77	0.44
5:f:11:ASN:OD1	5:f:48:LYS:NZ	2.51	0.44
24:o:1212:LEU:HD11	24:o:1289:GLU:HG2	1.99	0.44
25:p:110:PRO:HG2	25:p:163:LEU:HD11	2.00	0.44
25:p:256:ILE:HD11	25:p:373:LEU:HD21	2.00	0.44
1:A:758:PRO:HG2	6:G:136:ILE:O	2.14	0.44
1:A:764:ILE:HG21	6:G:16:PHE:CZ	2.52	0.44
5:F:15:PRO:HG2	8:I:14:LYS:HG3	1.91	0.44
5:F:90:GLU:OE1	9:J:208:GLY:HA3	2.18	0.44
7:H:110:TYR:CD2	9:J:157:LEU:CD2	3.01	0.44
8:I:132:LEU:CD1	9:J:121:MET:SD	3.06	0.44
11:O:36:VAL:HG13	13:Q:29:PHE:HE1	1.82	0.44
18:V:175:LEU:HD21	18:V:180:LYS:HB3	1.98	0.44
20:Y:28:DT:H2"	20:Y:29:DA:C8	2.53	0.44
24:o:769:MET:HE2	25:p:970:HIS:CD2	2.52	0.44
24:o:1013:VAL:HG11	24:o:1046:ARG:HG2	2.00	0.44
24:o:1034:GLN:OE1	24:o:1034:GLN:HA	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:p:1117:HIS:NE2	25:p:1135:TYR:HE2	2.16	0.44
1:A:345:PRO:HG3	1:A:500:LEU:HG	1.99	0.44
1:A:567:LEU:CD2	2:B:745:GLN:HE21	2.30	0.44
1:A:573:TYR:CD1	2:B:657:ARG:NH1	2.85	0.44
3:D:871:THR:HG22	10:L:66:LEU:CB	2.47	0.44
3:D:905:ALA:HB2	10:L:120:LEU:HD21	2.00	0.44
6:G:45:ILE:HD13	6:G:95:LEU:HD23	2.00	0.44
7:H:127:GLN:N	7:H:128:PRO:HD2	2.32	0.44
13:Q:369:LYS:HB3	13:Q:369:LYS:HE2	1.71	0.44
17:U:32:LEU:CD2	18:V:161:ARG:CZ	2.79	0.44
24:o:18:ILE:H	24:o:1462:GLN:NE2	2.16	0.44
24:o:841:MET:HG2	25:p:501:LEU:HD23	1.98	0.44
24:o:1422:GLN:O	24:o:1422:GLN:HG2	2.17	0.44
25:p:526:LEU:H	25:p:526:LEU:HD23	1.83	0.44
33:y:26:LYS:HG3	33:y:27:VAL:HG22	2.00	0.44
5:F:48:LYS:HE3	8:I:22:ILE:CB	2.48	0.44
7:H:59:GLU:HA	7:H:62:THR:HG22	1.99	0.44
15:S:127:PHE:CB	16:T:19:TRP:HB2	2.48	0.44
24:o:459:ASN:OD1	24:o:459:ASN:C	2.60	0.44
24:o:860:ILE:HA	24:o:863:ARG:NH1	2.29	0.44
24:o:1087:VAL:HG12	24:o:1400:LEU:HD22	2.00	0.44
24:o:1312:PRO:HG3	24:o:1317:LYS:C	2.43	0.44
25:p:787:GLY:HA2	25:p:790:GLN:HE21	1.82	0.44
26:q:240:ARG:HB2	26:q:243:THR:HG22	1.99	0.44
27:r:114:LEU:HD11	35:u:167:TYR:CD2	2.53	0.44
32:x:19:GLU:H	32:x:19:GLU:HG3	1.53	0.44
2:B:766:LEU:HA	2:B:807:THR:HG21	2.00	0.44
2:B:845:SER:HB3	2:B:846:TYR:H	1.66	0.44
2:B:925:LYS:HD3	2:B:925:LYS:HA	1.78	0.44
4:E:464:TYR:CD2	5:F:133:ALA:HB2	2.52	0.44
12:P:220:VAL:HG21	19:X:-25:DA:HI'	1.99	0.44
13:Q:321:SER:O	13:Q:321:SER:OG	2.32	0.44
14:R:45:VAL:O	14:R:45:VAL:HG22	2.18	0.44
16:T:95:VAL:O	16:T:106:LEU:HD12	2.17	0.44
17:U:32:LEU:HD13	18:V:161:ARG:HH21	1.80	0.44
4:e:542:HIS:CE1	4:e:568:ARG:HG3	2.53	0.44
22:k:150:VAL:HG22	23:m:82:GLN:HB3	1.98	0.44
24:o:802:PHE:CD1	25:p:504:THR:CG2	3.00	0.44
24:o:1179:PRO:HA	24:o:1209:PRO:HB3	2.00	0.44
24:o:1196:TYR:OH	24:o:1201:ASP:O	2.35	0.44
24:o:1210:TRP:CZ3	31:w:53:ILE:HD12	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:p:171:LEU:HD23	25:p:171:LEU:HA	1.89	0.44
26:q:190:ASN:HD21	26:q:195:THR:HG23	1.81	0.44
27:r:94:LYS:O	27:r:97:LEU:HG	2.16	0.44
34:z:19:CYS:SG	34:z:20:GLY:N	2.91	0.44
1:A:848:LEU:H	1:A:848:LEU:HG	1.37	0.43
1:A:1182:CYS:O	1:A:1182:CYS:SG	2.75	0.43
2:B:839:MET:HE1	2:B:843:LEU:HD13	2.00	0.43
4:E:463:PHE:CD2	5:F:136:LEU:HD11	2.53	0.43
4:E:650:THR:HG22	4:E:666:THR:HG22	1.99	0.43
4:E:704:VAL:HG11	4:E:747:LEU:CG	2.41	0.43
4:E:784:HIS:HB3	4:E:792:LEU:HB2	1.99	0.43
5:F:368:THR:HB	5:F:373:ARG:CZ	2.48	0.43
11:O:39:GLN:CB	13:Q:28:ILE:CD1	2.96	0.43
18:V:76:GLY:O	18:V:80:LYS:HB2	2.18	0.43
5:f:411:VAL:O	5:f:417:ARG:NH2	2.51	0.43
24:o:986:MET:HE1	24:o:1075:LYS:HG3	1.99	0.43
24:o:1160:ARG:CZ	24:o:1349:GLU:CD	2.88	0.43
24:o:1218:ARG:NH2	24:o:1253:GLU:OE1	2.41	0.43
25:p:458:LYS:NZ	25:p:461:GLN:HB3	2.33	0.43
25:p:937:SER:OG	25:p:938:ARG:N	2.51	0.43
26:q:116:THR:HB	26:q:147:ASP:HB3	1.99	0.43
35:u:86:ASP:OD1	35:u:87:ALA:N	2.51	0.43
35:u:107:PHE:O	35:u:160:ILE:HG13	2.17	0.43
1:A:639:LEU:H	1:A:639:LEU:HD12	1.83	0.43
1:A:766:ARG:N	6:G:14:SER:O	2.50	0.43
3:D:901:TYR:CE2	10:L:120:LEU:HD22	2.52	0.43
3:D:933:ARG:NH1	9:J:117:VAL:HG21	2.32	0.43
7:H:44:LEU:HD11	9:J:160:GLN:HG2	1.99	0.43
17:U:180:PHE:HB3	17:U:181:ASN:H	1.58	0.43
24:o:45:GLU:HB3	24:o:53:LYS:HE2	1.99	0.43
24:o:119:VAL:HG22	24:o:151:LYS:NZ	2.33	0.43
24:o:1160:ARG:HE	24:o:1161:LEU:HD22	1.82	0.43
24:o:1287:CYS:HA	25:p:251:ALA:HB2	2.00	0.43
25:p:628:VAL:HG12	25:p:629:GLU:O	2.18	0.43
25:p:849:ASP:HB3	34:z:15:MET:HE3	2.00	0.43
28:s:173:ILE:O	28:s:209:VAL:HA	2.18	0.43
35:u:40:GLY:O	35:u:152:VAL:HG11	2.17	0.43
3:D:917:ILE:HG21	3:D:1058:VAL:HG11	2.00	0.43
4:E:429:LEU:HG	4:E:596:TYR:O	2.19	0.43
5:F:66:LEU:C	8:I:32:GLU:HG3	2.43	0.43
5:F:427:LEU:HD12	5:F:427:LEU:HA	1.71	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:102:THR:HG23	8:I:104:LEU:H	1.83	0.43
9:J:123:LEU:O	9:J:153:ARG:NH1	2.50	0.43
17:U:70:LYS:HD3	17:U:70:LYS:HA	1.71	0.43
5:f:20:LYS:HE2	5:f:20:LYS:HB3	1.83	0.43
24:o:138:LYS:HD2	24:o:1441:GLU:OE1	2.17	0.43
24:o:434:LYS:HG2	24:o:437:ASP:H	1.83	0.43
25:p:840:MET:HB3	25:p:891:ASP:OD2	2.18	0.43
25:p:1128:ALA:HB1	25:p:1135:TYR:CE2	2.53	0.43
1:A:349:TRP:HE1	5:f:262:PHE:CA	2.28	0.43
1:A:468:PHE:CZ	5:F:224:TYR:CD2	3.05	0.43
1:A:573:TYR:OH	2:B:662:GLN:OE1	2.31	0.43
3:D:934:TYR:CE1	8:I:129:LEU:CD2	3.01	0.43
4:E:695:LEU:O	4:E:703:MET:HA	2.18	0.43
7:H:155:ASP:OD1	7:H:155:ASP:N	2.51	0.43
12:P:257:ASN:ND2	19:X:-27:DA:N3	2.65	0.43
15:S:47:LEU:HG	15:S:98:TRP:CE3	2.53	0.43
8:i:45:ARG:HG3	9:j:212:LYS:HB3	2.01	0.43
24:o:1013:VAL:CG2	24:o:1049:LEU:HD22	2.44	0.43
24:o:1049:LEU:HD23	24:o:1049:LEU:O	2.18	0.43
27:r:26:PHE:CE2	35:u:80:PHE:CZ	2.95	0.43
30:v:71:ASP:O	30:v:72:ASP:HB3	2.17	0.43
1:A:469:PRO:HA	7:H:166:ARG:NH1	2.33	0.43
1:A:755:HIS:ND1	6:G:139:PRO:CD	2.64	0.43
1:A:925:ASP:N	1:A:925:ASP:OD1	2.52	0.43
1:A:1022:ARG:HB3	19:X:2:DT:OP1	2.18	0.43
3:D:961:GLN:OE1	3:D:961:GLN:HA	2.19	0.43
5:F:14:LEU:HA	8:I:18:MET:HB3	1.99	0.43
5:F:320:ARG:CD	5:F:415:ILE:HB	2.48	0.43
11:O:54:ASN:O	13:Q:368:SER:N	2.43	0.43
13:Q:47:GLU:OE1	13:Q:60:HIS:CG	2.71	0.43
13:Q:310:GLU:C	13:Q:313:PRO:HD2	2.43	0.43
13:Q:346:LYS:HD3	20:Y:27:DT:OP1	2.19	0.43
17:U:55:ASP:O	17:U:59:LEU:N	2.42	0.43
5:f:105:TYR:O	9:j:217:PHE:N	2.51	0.43
5:f:317:LEU:HG	5:f:330:ARG:HE	1.83	0.43
24:o:500:GLU:OE2	25:p:1058:LYS:HD3	2.18	0.43
24:o:801:GLY:HA3	25:p:503:ASN:CG	2.43	0.43
25:p:891:ASP:OD1	25:p:891:ASP:N	2.50	0.43
35:u:165:ASP:HB2	35:u:168:LEU:HD11	1.98	0.43
1:A:502:LEU:HD22	1:A:502:LEU:HA	1.80	0.43
1:A:638:PRO:HD3	6:G:39:LEU:HD23	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:950:VAL:CG1	1:A:1062:TYR:CE2	3.01	0.43
1:A:956:PRO:O	6:G:149:ARG:N	2.52	0.43
2:B:653:LEU:HG	2:B:684:ILE:HG13	2.00	0.43
2:B:780:LYS:HA	7:H:183:ARG:HH12	1.83	0.43
4:E:616:HIS:HE1	11:O:24:GLN:HB2	1.79	0.43
5:F:48:LYS:HG3	8:I:22:ILE:HG23	0.50	0.43
5:F:312:ILE:HD13	5:F:312:ILE:N	2.33	0.43
6:G:181:TRP:O	6:G:181:TRP:CD2	2.72	0.43
8:I:23:LEU:HD22	8:I:28:ILE:HD12	2.00	0.43
11:O:57:ASN:C	11:O:58:PHE:CD1	2.96	0.43
14:R:44:ARG:HG2	25:p:1067:ILE:HG21	1.96	0.43
21:c:21:LEU:HD11	21:c:23:TRP:CD1	2.54	0.43
24:o:355:MET:HE1	24:o:1459:MET:HG3	2.00	0.43
24:o:1102:MET:HE1	24:o:1385:VAL:O	2.18	0.43
24:o:1158:LEU:HB2	24:o:1336:LEU:HD21	2.00	0.43
25:p:143:GLN:N	25:p:143:GLN:OE1	2.52	0.43
25:p:912:ASN:HB3	25:p:918:PHE:CD1	2.54	0.43
26:q:103:LEU:HD12	26:q:120:LEU:HD22	2.00	0.43
30:v:8:ASP:OD2	30:v:32:SER:OG	2.36	0.43
35:u:94:LYS:O	35:u:110:ARG:HD2	2.18	0.43
1:A:690:LEU:HD22	1:A:747:LEU:HD22	1.99	0.43
1:A:764:ILE:CD1	6:G:18:LEU:CD2	2.93	0.43
2:B:603:LYS:H	2:B:603:LYS:HG2	1.64	0.43
4:E:599:TYR:CE2	11:O:28:ILE:HD13	2.53	0.43
6:G:129:LYS:HD2	6:G:129:LYS:HA	1.76	0.43
8:I:21:GLN:HE22	8:I:24:LYS:HE2	1.84	0.43
11:O:77:ASN:O	11:O:79:VAL:HG23	2.19	0.43
12:P:278:GLN:CD	12:P:278:GLN:N	2.76	0.43
15:S:6:PRO:O	15:S:10:ASN:CA	2.62	0.43
17:U:17:LEU:HD23	17:U:191:LEU:HB2	2.01	0.43
10:l:129:PRO:HB2	23:m:56:ILE:HG23	2.01	0.43
1:A:727:THR:HG23	1:A:727:THR:O	2.19	0.43
1:A:1007:LEU:HD22	1:A:1012:VAL:HG21	2.01	0.43
2:B:819:LEU:HD13	2:B:819:LEU:HA	1.80	0.43
5:F:244:GLN:CD	7:H:133:ALA:HB3	2.36	0.43
10:L:106:ARG:HD2	10:L:114:LYS:NZ	2.34	0.43
11:O:62:LEU:O	12:P:205:ARG:NH2	2.52	0.43
12:P:304:ILE:HG13	12:P:310:VAL:HG13	2.00	0.43
13:Q:348:LYS:NZ	13:Q:375:GLU:CD	2.76	0.43
17:U:69:ASP:HB3	17:U:71:PHE:HD1	1.83	0.43
18:V:98:THR:H	18:V:101:GLU:HB3	1.84	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:f:320:ARG:HH11	5:f:320:ARG:HB2	1.83	0.43
24:o:16:ARG:HD3	25:p:1147:SER:CB	2.33	0.43
24:o:1004:LEU:HD12	24:o:1004:LEU:HA	1.84	0.43
24:o:1262:MET:HE3	24:o:1264:SER:HB2	2.00	0.43
35:u:2:PHE:CE1	35:u:77:PHE:HB2	2.54	0.43
2:B:216:SER:OG	2:B:217:ASN:N	2.52	0.43
2:B:414:LEU:HB2	2:B:523:VAL:HG13	1.99	0.43
2:B:562:GLY:O	2:B:581:ILE:HG12	2.19	0.43
5:F:332:PHE:HE1	5:F:336:LEU:HD11	1.84	0.43
11:O:58:PHE:CD2	11:O:82:ARG:O	2.71	0.43
12:P:301:VAL:HG21	19:X:-28:DA:C4'	2.41	0.43
13:Q:351:PHE:CD1	13:Q:351:PHE:N	2.87	0.43
14:R:18:HIS:HB2	14:R:19:PRO:HD2	2.00	0.43
17:U:46:GLU:CD	17:U:93:PHE:CE2	2.88	0.43
21:c:101:VAL:HG22	5:f:127:LEU:HA	2.00	0.43
4:e:777:SER:O	4:e:777:SER:OG	2.34	0.43
24:o:1303:GLN:CB	24:o:1342:SER:HB3	2.47	0.43
28:s:94:MET:HE2	28:s:125:TYR:CD2	2.52	0.43
1:A:410:TRP:CH2	5:F:355:ILE:CG2	3.02	0.43
2:B:559:LYS:HB2	2:B:559:LYS:HZ3	1.83	0.43
2:B:831:GLU:OE1	2:B:835:ARG:NH2	2.52	0.43
12:P:197:PHE:CZ	12:P:212:LEU:HD13	2.53	0.43
16:T:86:GLN:OE1	16:T:86:GLN:HA	2.18	0.43
4:e:332:ILE:HA	4:e:336:HIS:HD2	1.84	0.43
5:f:219:GLU:H	5:f:219:GLU:CD	2.21	0.43
26:q:44:ILE:HD11	26:q:238:SER:CB	2.49	0.43
33:y:63:VAL:HG22	33:y:71:ILE:HG22	2.00	0.43
3:D:935:GLU:O	8:I:128:ARG:C	2.62	0.42
4:E:476:VAL:HB	4:E:782:HIS:HB2	2.01	0.42
12:P:264:VAL:HG23	12:P:266:PHE:H	1.84	0.42
13:Q:29:PHE:CD2	13:Q:34:VAL:HG11	2.52	0.42
14:R:169:ARG:HD3	14:R:206:VAL:HB	1.99	0.42
17:U:37:LEU:HD11	17:U:66:LEU:HD13	1.99	0.42
17:U:92:TYR:CE2	17:U:94:ILE:CD1	2.98	0.42
21:c:124:ILE:HD11	5:f:133:ALA:HB1	2.00	0.42
5:f:428:LEU:HD13	5:f:458:LEU:CB	2.49	0.42
8:i:16:ALA:HB2	8:i:40:LEU:HD11	2.00	0.42
24:o:865:ILE:HA	24:o:1092:ALA:CB	2.47	0.42
24:o:1158:LEU:CD2	24:o:1336:LEU:HD13	2.49	0.42
24:o:1347:LEU:CD2	24:o:1357:THR:CB	2.97	0.42
25:p:799:SER:HB2	26:q:174:ALA:HB2	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:877:TYR:HA	2:B:882:HIS:CD2	2.54	0.42
5:F:418:ILE:CD1	5:F:418:ILE:H	2.26	0.42
5:F:432:ALA:HB3	5:F:433:PRO:HD2	2.00	0.42
12:P:191:GLU:OE2	13:Q:349:TRP:CH2	2.72	0.42
12:P:278:GLN:N	12:P:278:GLN:OE1	2.48	0.42
13:Q:366:ILE:HG22	13:Q:367:PHE:N	2.33	0.42
15:S:108:ARG:HD3	15:S:108:ARG:HA	1.93	0.42
16:T:21:VAL:HA	16:T:114:ALA:O	2.18	0.42
18:V:203:PHE:O	18:V:203:PHE:CD2	2.73	0.42
4:e:747:LEU:H	4:e:747:LEU:CD2	2.22	0.42
5:f:432:ALA:HB1	5:f:462:GLN:CB	2.50	0.42
22:k:179:MET:HB3	22:k:180:PRO:HD2	2.01	0.42
24:o:1082:HIS:HA	24:o:1083:PRO:HD3	1.87	0.42
25:p:551:GLU:OE1	25:p:551:GLU:N	2.45	0.42
25:p:634:LEU:HD23	25:p:634:LEU:HA	1.86	0.42
33:y:114:GLU:OE1	33:y:114:GLU:N	2.40	0.42
2:B:203:LYS:HZ3	2:B:235:HIS:HB3	1.84	0.42
2:B:847:ARG:H	7:H:227:LEU:HA	1.84	0.42
4:E:613:ALA:HB3	4:E:616:HIS:HD2	1.83	0.42
4:E:651:VAL:HG21	4:E:686:THR:HG21	2.01	0.42
14:R:45:VAL:O	25:p:1069:ILE:CD1	2.67	0.42
14:R:214:PHE:HA	14:R:217:ARG:NH1	2.34	0.42
15:S:13:GLU:HG3	16:T:44:ARG:HA	2.00	0.42
19:X:-39:DA:OP2	19:X:-39:DA:H8	2.01	0.42
5:f:26:MET:HE3	5:f:26:MET:HB3	1.77	0.42
24:o:196:LEU:CD1	24:o:311:GLN:HG3	2.40	0.42
24:o:908:THR:OG1	24:o:1047:SER:OG	2.31	0.42
25:p:225:LEU:H	25:p:225:LEU:HD23	1.84	0.42
26:q:69:GLY:HA3	34:z:57:ALA:HB1	2.01	0.42
1:A:405:VAL:HB	5:F:302:HIS:HB3	2.01	0.42
3:D:1006:LEU:HD12	3:D:1006:LEU:HA	1.85	0.42
5:F:313:VAL:HG12	5:F:372:THR:CG2	2.48	0.42
7:H:87:GLN:HA	7:H:88:PRO:HD3	1.82	0.42
11:O:27:GLN:HG3	11:O:32:LEU:HB3	2.01	0.42
14:R:158:ALA:HA	14:R:186:ILE:HG13	2.01	0.42
5:f:328:ALA:C	5:f:330:ARG:N	2.72	0.42
24:o:869:GLU:OE2	25:p:1095:ILE:CD1	2.68	0.42
24:o:1160:ARG:HD2	24:o:1160:ARG:C	2.44	0.42
25:p:36:GLU:OE1	25:p:653:TRP:HB3	2.20	0.42
30:v:32:SER:OG	30:v:33:GLU:N	2.52	0.42
1:A:485:ILE:HG12	1:A:491:MET:HE3	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:949:GLN:N	3:D:949:GLN:NE2	2.60	0.42
3:D:1000:ARG:HH12	11:O:5:LEU:HD12	1.21	0.42
8:I:132:LEU:CG	9:J:121:MET:HE2	2.38	0.42
11:O:39:GLN:CB	13:Q:28:ILE:HD12	2.47	0.42
14:R:111:ASP:CG	14:R:114:MET:CB	2.92	0.42
5:f:447:ALA:CB	5:f:456:GLY:HA3	2.49	0.42
24:o:581:LYS:HB2	30:v:91:VAL:CG2	2.47	0.42
24:o:823:VAL:HG13	24:o:835:GLU:OE2	2.20	0.42
24:o:935:GLN:O	24:o:939:VAL:HG12	2.19	0.42
25:p:309:PHE:CZ	31:w:40:ARG:CB	3.03	0.42
25:p:628:VAL:HG22	25:p:633:LEU:HD23	2.00	0.42
1:A:658:GLY:HA3	2:B:475:LYS:CG	2.47	0.42
1:A:1073:GLN:HG2	1:A:1077:LEU:HD12	2.02	0.42
5:F:320:ARG:H	5:F:320:ARG:HG3	1.61	0.42
5:F:370:TRP:HH2	5:F:402:ARG:HB3	1.85	0.42
10:L:120:LEU:O	10:L:125:ASN:N	2.52	0.42
11:O:76:LEU:CB	11:O:79:VAL:HG21	2.35	0.42
12:P:166:GLN:HB2	20:Y:28:DT:C5'	2.46	0.42
17:U:145:PHE:HD1	17:U:145:PHE:O	2.03	0.42
18:V:107:GLN:C	18:V:109:LEU:H	2.27	0.42
3:d:871:THR:O	10:l:62:LYS:NZ	2.42	0.42
4:e:667:GLY:O	4:e:692:ARG:NH2	2.52	0.42
24:o:621:ILE:O	24:o:621:ILE:HG22	2.19	0.42
25:p:629:GLU:O	25:p:630:LYS:C	2.61	0.42
27:r:36:GLU:HA	27:r:39:MET:HE2	2.02	0.42
2:B:159:LEU:N	2:B:159:LEU:CD2	2.82	0.42
3:D:1055:ILE:HA	10:L:73:ASN:HB2	2.01	0.42
4:E:564:ASP:OD1	4:E:564:ASP:N	2.51	0.42
5:F:72:ASP:OD1	5:F:84:TYR:OH	2.33	0.42
5:F:402:ARG:O	5:F:406:VAL:HG13	2.19	0.42
11:O:39:GLN:OE1	13:Q:28:ILE:HD13	2.09	0.42
14:R:22:ILE:HG23	14:R:35:PRO:HG2	2.01	0.42
14:R:175:ARG:HH21	25:p:102:ASP:C	2.28	0.42
14:R:244:LEU:HD22	14:R:244:LEU:HA	1.86	0.42
18:V:119:LEU:O	18:V:123:ALA:HB3	2.20	0.42
10:l:139:TYR:HD2	23:m:73:MET:HE3	1.84	0.42
24:o:1152:GLU:H	24:o:1152:GLU:HG3	1.69	0.42
24:o:1227:THR:HG23	24:o:1229:GLU:H	1.84	0.42
25:p:824:ASP:OD1	25:p:825:GLN:N	2.53	0.42
35:u:38:CYS:C	35:u:155:ASN:OD1	2.62	0.42
1:A:349:TRP:HZ2	5:f:262:PHE:CZ	2.36	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:690:ASP:OD1	4:E:690:ASP:N	2.43	0.42
5:F:15:PRO:HB2	8:I:14:LYS:HE3	2.00	0.42
5:F:350:ASN:OD1	5:F:350:ASN:N	2.51	0.42
7:H:111:ALA:HB1	9:J:126:TYR:HE2	1.78	0.42
10:L:106:ARG:CD	10:L:114:LYS:NZ	2.83	0.42
13:Q:51:MET:HG2	13:Q:61:SER:HB3	0.90	0.42
15:S:44:GLN:CD	15:S:104:GLY:N	2.78	0.42
15:S:53:ASN:HB2	15:S:96:GLN:OE1	2.19	0.42
17:U:129:CYS:HB2	17:U:154:CYS:HB2	2.02	0.42
5:f:402:ARG:HH22	5:f:403:ILE:HD12	1.85	0.42
22:k:130:PRO:HD3	23:m:35:GLU:HG2	2.02	0.42
24:o:1315:ASP:HB3	24:o:1320:ILE:HD11	2.01	0.42
28:s:49:SER:C	28:s:50:GLU:HG3	2.44	0.42
28:s:185:ILE:HG22	28:s:209:VAL:HG11	2.02	0.42
35:u:117:MET:HE1	35:u:163:LEU:HD22	2.02	0.42
1:A:486:TRP:CH2	5:f:358:THR:CG2	3.01	0.42
1:A:763:LEU:CD1	6:G:91:ILE:CD1	2.90	0.42
5:F:249:ASP:HB3	5:F:252:LEU:HB2	2.02	0.42
11:O:58:PHE:CE1	13:Q:370:ALA:HB1	2.54	0.42
12:P:203:ARG:NH2	13:Q:344:ARG:CZ	2.83	0.42
14:R:216:SER:HA	14:R:229:GLN:NE2	2.35	0.42
16:T:25:LYS:O	16:T:29:GLN:N	2.47	0.42
24:o:184:CYS:SG	24:o:185:GLY:N	2.93	0.42
24:o:618:TYR:CD1	24:o:621:ILE:HD12	2.54	0.42
25:p:296:GLU:CD	25:p:296:GLU:H	2.27	0.42
27:r:82:SER:O	27:r:86:LEU:N	2.51	0.42
1:A:620:LEU:HD11	1:A:766:ARG:HD3	2.02	0.42
1:A:825:ILE:HD12	1:A:830:ILE:HD11	2.02	0.42
2:B:669:LEU:HD23	2:B:669:LEU:HA	1.92	0.42
3:D:881:ARG:NH1	10:L:89:ASP:HA	2.35	0.42
5:F:213:ILE:CG2	7:H:163:PRO:C	2.93	0.42
6:G:161:ASP:OD1	6:G:161:ASP:N	2.53	0.42
24:o:486:LEU:C	24:o:488:VAL:N	2.77	0.42
24:o:1307:VAL:HG13	24:o:1336:LEU:HB3	1.94	0.42
25:p:177:CYS:SG	25:p:738:THR:OG1	2.59	0.42
35:u:78:ARG:HG3	35:u:80:PHE:CE1	2.54	0.42
2:B:176:HIS:HE1	2:B:310:ASP:H	1.68	0.41
3:D:910:LEU:HB2	10:L:66:LEU:CD2	2.45	0.41
5:F:401:GLU:C	5:F:401:GLU:CD	2.87	0.41
7:H:227:LEU:H	7:H:227:LEU:HG	1.62	0.41
12:P:179:ASP:C	12:P:179:ASP:OD1	2.62	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:P:329:TYR:N	12:P:330:PRO:HD2	2.35	0.41
13:Q:19:GLU:OE1	13:Q:19:GLU:HA	2.19	0.41
15:S:110:PHE:HD1	15:S:148:PRO:HA	1.85	0.41
18:V:99:LEU:HD21	18:V:116:LYS:CG	2.49	0.41
21:c:94:HIS:CD2	5:f:122:LEU:HD22	2.55	0.41
24:o:1310:HIS:O	24:o:1335:ILE:HG12	2.19	0.41
25:p:368:MET:HE3	25:p:368:MET:HB2	1.85	0.41
27:r:76:ASN:O	27:r:80:ILE:HD12	2.19	0.41
35:u:79:PRO:HG3	35:u:104:MET:SD	2.60	0.41
1:A:1065:GLU:OE1	1:A:1065:GLU:HA	2.20	0.41
2:B:594:SER:OG	2:B:595:LYS:N	2.51	0.41
3:D:955:LYS:HA	3:D:958:LYS:HZ2	1.85	0.41
3:D:1071:ARG:HB2	5:F:91:PHE:CD2	2.55	0.41
5:F:43:VAL:HG21	8:I:43:ALA:CA	2.46	0.41
11:O:67:PHE:HE2	12:P:195:LYS:NZ	2.18	0.41
17:U:67:LYS:HG2	17:U:72:ILE:HG12	2.02	0.41
24:o:357:LYS:HD2	25:p:1107:LEU:O	2.19	0.41
24:o:396:PRO:HD2	29:t:76:CYS:SG	2.61	0.41
24:o:700:GLN:OE1	24:o:700:GLN:HA	2.20	0.41
1:A:645:LYS:HD2	1:A:645:LYS:HA	1.77	0.41
1:A:771:TYR:CD1	6:G:16:PHE:CZ	3.07	0.41
2:B:55:PRO:HB3	2:B:60:LEU:HD22	2.02	0.41
2:B:887:ARG:NH2	2:B:917:ASP:OD2	2.49	0.41
4:E:359:LEU:HD12	4:E:359:LEU:C	2.46	0.41
4:E:519:GLU:HB3	4:E:520:SER:H	1.76	0.41
4:E:579:VAL:CG2	8:I:115:LEU:HD22	2.49	0.41
5:F:231:CYS:HB3	5:F:285:MET:HE2	2.03	0.41
14:R:27:TYR:O	14:R:48:VAL:CG2	2.66	0.41
15:S:143:TRP:NE1	15:S:145:ASN:OD1	2.37	0.41
5:f:104:LEU:HD22	9:j:216:TYR:HB2	2.02	0.41
24:o:361:PHE:HA	25:p:1062:ARG:O	2.19	0.41
24:o:622:SER:HB2	24:o:625:ASP:HA	2.01	0.41
24:o:917:GLU:O	24:o:921:ARG:HB2	2.20	0.41
24:o:942:VAL:HG22	24:o:948:ILE:HG21	2.02	0.41
24:o:1311:LEU:HD22	24:o:1334:TRP:CZ2	2.54	0.41
24:o:1429:LYS:HB2	24:o:1438:VAL:HG11	2.01	0.41
25:p:90:GLN:HG3	25:p:91:ILE:N	2.34	0.41
25:p:840:MET:HE2	25:p:891:ASP:OD2	2.20	0.41
2:B:749:LEU:HA	2:B:752:THR:HG22	2.03	0.41
3:D:935:GLU:CA	8:I:128:ARG:O	2.68	0.41
5:F:14:LEU:O	5:F:40:THR:OG1	2.35	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:218:VAL:HA	5:F:221:GLN:CG	2.51	0.41
7:H:116:ARG:CD	9:J:126:TYR:CE1	2.82	0.41
13:Q:53:SER:O	13:Q:54:ARG:HB2	2.20	0.41
17:U:152:PHE:HB2	17:U:161:VAL:HG21	2.03	0.41
18:V:155:LEU:HD12	18:V:155:LEU:HA	1.86	0.41
24:o:1163:HIS:CE1	24:o:1302:GLU:HG3	2.55	0.41
25:p:100:GLU:HG3	25:p:101:ARG:H	1.85	0.41
25:p:193:VAL:O	25:p:467:SER:HA	2.20	0.41
25:p:957:THR:HG22	25:p:1028:LEU:CD2	2.51	0.41
25:p:1021:HIS:HD2	25:p:1025:ASN:HB2	1.85	0.41
35:u:27:LYS:HD3	35:u:51:ILE:HD11	2.02	0.41
1:A:771:TYR:CE1	6:G:16:PHE:HZ	2.37	0.41
4:E:239:LEU:HB3	4:E:307:LEU:HD21	2.03	0.41
5:F:290:MET:CE	5:F:337:VAL:HB	2.40	0.41
5:f:55:LEU:HD13	8:i:28:ILE:HG12	2.01	0.41
22:k:179:MET:HB3	22:k:180:PRO:CD	2.50	0.41
24:o:948:ILE:HG23	24:o:1007:ILE:HG23	2.01	0.41
24:o:973:GLY:HA2	24:o:1328:PHE:CD2	2.54	0.41
24:o:1226:LEU:HA	24:o:1230:GLN:HE21	1.86	0.41
24:o:1359:SER:O	24:o:1365:ILE:CD1	2.67	0.41
27:r:109:GLU:O	27:r:113:ALA:N	2.49	0.41
2:B:496:MET:HE3	2:B:496:MET:HB2	1.84	0.41
3:D:1056:THR:O	10:L:74:GLU:HA	2.20	0.41
4:E:479:THR:OG1	4:E:481:ASP:O	2.31	0.41
5:F:396:LEU:HA	5:F:399:GLU:CD	2.46	0.41
5:F:426:LEU:O	5:F:429:LYS:HG2	2.21	0.41
6:G:74:MET:HE1	6:G:136:ILE:HD12	2.02	0.41
17:U:104:LYS:O	17:U:104:LYS:HG2	2.21	0.41
24:o:1018:LYS:HE3	24:o:1018:LYS:HB2	1.92	0.41
24:o:1476:ASP:HB3	29:t:105:ILE:CD1	2.49	0.41
25:p:109:MET:HB2	25:p:112:GLU:OE1	2.20	0.41
25:p:718:GLN:HG2	25:p:720:PRO:HD2	2.01	0.41
27:r:36:GLU:OE1	27:r:36:GLU:N	2.53	0.41
35:u:89:VAL:HA	35:u:99:THR:HA	2.03	0.41
35:u:154:LYS:HG3	35:u:155:ASN:H	1.86	0.41
35:u:163:LEU:O	35:u:163:LEU:HD23	2.21	0.41
1:A:573:TYR:HD2	2:B:657:ARG:HA	1.81	0.41
1:A:740:LEU:HD22	1:A:1070:PHE:HZ	1.86	0.41
2:B:464:ILE:HG12	2:B:513:LYS:HE2	2.02	0.41
4:E:747:LEU:N	4:E:747:LEU:HD13	2.35	0.41
5:F:90:GLU:OE1	9:J:208:GLY:CA	2.69	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:305:ILE:N	5:F:306:PRO:HD2	2.35	0.41
7:H:38:GLN:NE2	7:H:59:GLU:OE2	2.54	0.41
8:I:114:ARG:O	8:I:115:LEU:HD23	2.20	0.41
14:R:128:ILE:H	14:R:128:ILE:HG12	1.45	0.41
14:R:259:TYR:HD1	14:R:274:ILE:HD12	1.86	0.41
16:T:23:VAL:HG13	16:T:27:LEU:HD23	2.02	0.41
17:U:201:TYR:C	17:U:203:ILE:H	2.27	0.41
18:V:221:ARG:HD3	18:V:221:ARG:O	2.21	0.41
20:Y:8:DA:H2"	20:Y:9:DA:C8	2.56	0.41
4:e:518:LYS:HE2	4:e:518:LYS:HB2	1.95	0.41
23:m:80:ARG:HA	23:m:80:ARG:HD2	1.85	0.41
24:o:129:ILE:O	24:o:133:SER:OG	2.27	0.41
24:o:583:ARG:HH11	30:v:47:ILE:CD1	2.33	0.41
24:o:933:THR:HA	24:o:1059:ARG:HH12	1.85	0.41
24:o:1098:PRO:O	24:o:1100:THR:N	2.54	0.41
24:o:1212:LEU:HD11	24:o:1289:GLU:HA	2.02	0.41
25:p:991:ALA:O	32:x:46:ARG:NE	2.53	0.41
28:s:56:THR:HG22	28:s:57:ASP:N	2.36	0.41
1:A:345:PRO:O	1:A:346:ALA:HB3	2.21	0.41
1:A:352:MET:HB3	1:A:352:MET:HE3	1.82	0.41
1:A:500:LEU:HD23	1:A:500:LEU:HA	1.81	0.41
5:F:67:THR:CA	8:I:32:GLU:CG	2.75	0.41
7:H:224:LEU:HD23	7:H:224:LEU:HA	1.82	0.41
11:O:60:GLY:CA	11:O:79:VAL:HG13	2.49	0.41
11:O:67:PHE:HE1	13:Q:339:TYR:OH	2.04	0.41
11:O:75:VAL:HG21	13:Q:327:GLU:HG3	2.01	0.41
12:P:193:ASN:HD22	12:P:194:PRO:HD2	1.86	0.41
12:P:206:GLU:HB3	12:P:207:PRO:HD3	2.03	0.41
17:U:136:PHE:HD1	17:U:140:GLU:CD	2.28	0.41
18:V:181:ALA:O	18:V:184:ALA:CA	2.69	0.41
5:f:244:GLN:O	5:f:248:THR:OG1	2.34	0.41
24:o:766:PHE:HB3	24:o:781:ILE:HD12	2.03	0.41
24:o:1020:LEU:H	24:o:1020:LEU:HG	1.60	0.41
24:o:1097:GLU:O	24:o:1101:GLN:NE2	2.47	0.41
1:A:405:VAL:HA	5:F:302:HIS:HB3	2.02	0.41
1:A:511:LEU:N	1:A:511:LEU:HD13	2.36	0.41
1:A:673:GLY:N	6:G:13:GLU:CD	2.68	0.41
1:A:740:LEU:HD22	1:A:1070:PHE:CZ	2.56	0.41
1:A:764:ILE:HD11	6:G:18:LEU:CG	2.43	0.41
1:A:950:VAL:HG11	1:A:1062:TYR:CE2	2.56	0.41
1:A:1063:LYS:C	1:A:1063:LYS:CD	2.91	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:298:ARG:HH11	2:B:298:ARG:HD3	1.69	0.41
2:B:463:ARG:HD2	2:B:515:ILE:HG22	2.03	0.41
2:B:984:PRO:HG2	2:B:987:LEU:HD22	2.02	0.41
2:B:987:LEU:HG	2:B:988:PRO:HD2	2.03	0.41
4:E:508:LYS:HB3	4:E:512:ASP:HB2	2.02	0.41
5:F:48:LYS:HE3	8:I:22:ILE:HG23	2.03	0.41
10:L:76:LEU:HD13	10:L:84:LEU:CD1	2.50	0.41
10:L:122:ARG:HA	10:L:122:ARG:HD2	1.88	0.41
14:R:189:LYS:NZ	14:R:190:GLU:HB2	2.35	0.41
15:S:37:VAL:HG11	15:S:42:TRP:CZ2	2.55	0.41
15:S:116:GLY:HA3	25:p:356:PHE:CD1	2.42	0.41
18:V:77:VAL:HG13	18:V:81:ILE:CD1	2.50	0.41
8:i:78:ARG:HD3	8:i:78:ARG:HA	1.78	0.41
24:o:999:ARG:HA	24:o:999:ARG:HD3	1.49	0.41
25:p:267:VAL:HG12	25:p:268:PRO:O	2.20	0.41
25:p:334:LYS:HA	25:p:334:LYS:HD3	1.83	0.41
25:p:516:GLU:HA	25:p:520:VAL:HG22	2.02	0.41
25:p:639:HIS:O	25:p:643:LEU:HB2	2.21	0.41
25:p:794:VAL:HG22	25:p:944:THR:O	2.20	0.41
25:p:1088:GLU:OE1	25:p:1091:ARG:NH1	2.53	0.41
26:q:225:LYS:HG3	26:q:226:PRO:HD2	2.03	0.41
28:s:43:GLN:NE2	28:s:44:PHE:CZ	2.89	0.41
3:D:898:VAL:HG22	10:L:113:VAL:HA	2.01	0.41
4:E:306:VAL:HA	4:E:338:TYR:HB3	2.03	0.41
5:F:214:HIS:CB	7:H:164:THR:HG21	2.51	0.41
15:S:159:GLU:O	15:S:163:GLU:HG3	2.21	0.41
16:T:20:LEU:O	16:T:113:ARG:HA	2.21	0.41
17:U:112:ARG:HD2	17:U:112:ARG:HA	1.33	0.41
17:U:145:PHE:CD1	17:U:145:PHE:O	2.74	0.41
17:U:164:ASP:CG	17:U:166:SER:O	2.63	0.41
5:f:114:LEU:HD23	5:f:114:LEU:HA	1.95	0.41
24:o:139:LYS:HA	24:o:142:THR:HG22	2.03	0.41
24:o:365:THR:HG23	24:o:482:PHE:N	2.36	0.41
24:o:470:MET:HE1	24:o:535:MET:CE	2.51	0.41
24:o:1160:ARG:NH2	24:o:1349:GLU:OE2	2.47	0.41
24:o:1210:TRP:CZ2	24:o:1282:ASP:OD1	2.74	0.41
25:p:341:GLU:HG2	25:p:342:VAL:N	2.34	0.41
28:s:81:LYS:HA	28:s:109:GLY:O	2.21	0.41
28:s:193:ILE:HB	28:s:205:THR:HG23	2.03	0.41
31:w:60:HIS:O	31:w:60:HIS:ND1	2.54	0.41
33:y:82:SER:OG	33:y:84:GLN:OE1	2.38	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:630:GLN:O	1:A:634:HIS:HE1	2.04	0.40
4:E:236:LEU:HD21	4:E:317:LEU:HB2	2.03	0.40
4:E:248:TYR:OH	4:E:285:LEU:O	2.34	0.40
4:E:525:GLU:HB3	18:V:107:GLN:NE2	2.36	0.40
13:Q:43:LYS:HE2	13:Q:60:HIS:CE1	2.56	0.40
14:R:118:PHE:HA	14:R:121:ILE:HB	2.02	0.40
18:V:237:LEU:O	18:V:237:LEU:HG	2.21	0.40
21:c:105:ASN:OD1	21:c:105:ASN:N	2.54	0.40
4:e:668:HIS:NE2	4:e:686:THR:OG1	2.39	0.40
22:k:142:THR:OG1	22:k:143:GLY:N	2.55	0.40
24:o:408:ARG:HH21	24:o:412:GLN:HB3	1.86	0.40
24:o:542:LEU:HD21	24:o:642:LYS:CB	2.49	0.40
24:o:990:ALA:HB2	24:o:1067:TRP:HZ3	1.86	0.40
28:s:81:LYS:HB3	28:s:81:LYS:HE2	1.82	0.40
1:A:410:TRP:CH2	5:F:355:ILE:HG22	2.55	0.40
1:A:413:ASP:O	1:A:414:ILE:C	2.63	0.40
1:A:725:CYS:SG	1:A:734:LEU:HD12	2.61	0.40
1:A:996:ARG:HG3	19:X:3:DC:H5"	2.04	0.40
2:B:371:LYS:HA	2:B:371:LYS:HD3	1.87	0.40
5:F:68:THR:CB	8:I:34:ARG:HH11	2.32	0.40
5:F:374:TYR:CE1	5:F:422:HIS:HB3	2.56	0.40
7:H:166:ARG:HA	7:H:166:ARG:HD2	1.87	0.40
7:H:201:GLN:HG3	7:H:215:ALA:HA	2.04	0.40
11:O:7:ARG:CZ	11:O:37:LEU:HB3	2.52	0.40
11:O:9:THR:O	11:O:10:THR:C	2.64	0.40
14:R:195:PHE:CZ	14:R:199:LEU:HD11	2.57	0.40
4:e:256:HIS:O	4:e:257:GLU:HB2	2.21	0.40
4:e:504:LEU:HD22	4:e:575:PHE:HZ	1.85	0.40
4:e:620:LEU:HD13	8:i:104:LEU:HD22	2.03	0.40
24:o:41:ILE:HB	24:o:88:ILE:HG12	2.03	0.40
24:o:892:GLY:HA3	24:o:1396:ARG:HH11	1.85	0.40
25:p:374:LEU:HD23	25:p:374:LEU:HA	1.85	0.40
25:p:837:CYS:HA	25:p:889:LYS:O	2.21	0.40
25:p:914:GLU:HG3	25:p:914:GLU:O	2.21	0.40
27:r:103:LEU:CA	35:u:144:ARG:NH1	2.65	0.40
28:s:55:ARG:O	28:s:76:PHE:HB2	2.21	0.40
33:y:11:LEU:HD12	33:y:11:LEU:HA	1.93	0.40
35:u:142:GLU:O	35:u:170:LEU:HA	2.20	0.40
35:u:146:LYS:HD3	35:u:165:ASP:OD2	2.21	0.40
1:A:763:LEU:HD12	6:G:17:ILE:CD1	2.51	0.40
1:A:839:GLU:HB2	1:A:843:ARG:NH2	2.36	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:882:HIS:HB3	2:B:886:ILE:HB	2.03	0.40
2:B:957:MET:O	2:B:968:ARG:NH1	2.52	0.40
3:D:1006:LEU:HG	13:Q:328:LEU:HD21	2.02	0.40
5:F:286:VAL:HG11	5:F:308:VAL:HG12	1.97	0.40
5:F:302:HIS:HD2	5:F:303:GLU:HG3	1.87	0.40
11:O:5:LEU:CD2	11:O:98:CYS:SG	3.09	0.40
11:O:59:ARG:HA	13:Q:373:ASP:H	1.86	0.40
12:P:235:ARG:HB3	13:Q:317:GLU:CG	2.52	0.40
12:P:312:LEU:N	12:P:312:LEU:HD12	2.36	0.40
17:U:203:ILE:O	17:U:203:ILE:HG22	2.22	0.40
18:V:152:LEU:HD12	18:V:152:LEU:HA	1.88	0.40
20:Y:28:DT:H6	20:Y:28:DT:H2'	1.60	0.40
24:o:26:LEU:H	25:p:1166:SER:C	2.29	0.40
25:p:728:MET:HE2	25:p:942:LYS:HD3	2.02	0.40
25:p:968:ASN:OD1	25:p:969:PRO:HD2	2.21	0.40
25:p:980:HIS:ND1	25:p:980:HIS:O	2.54	0.40
25:p:1120:ASN:ND2	25:p:1145:GLN:HB2	2.33	0.40
2:B:77:ILE:HG12	2:B:146:ILE:HG23	2.03	0.40
2:B:490:SER:O	2:B:491:HIS:C	2.63	0.40
2:B:877:TYR:O	2:B:882:HIS:HB2	2.21	0.40
2:B:908:GLN:HE22	2:B:952:GLN:HE22	1.69	0.40
5:F:369:PRO:HB2	5:F:372:THR:CG2	2.51	0.40
5:F:396:LEU:HA	5:F:399:GLU:OE1	2.20	0.40
13:Q:310:GLU:HB3	13:Q:313:PRO:CD	2.51	0.40
13:Q:343:HIS:HD2	13:Q:350:LYS:HB2	1.87	0.40
14:R:218:PHE:CD1	14:R:277:ILE:HG22	2.55	0.40
18:V:132:VAL:HG13	18:V:134:ASP:N	2.36	0.40
18:V:204:ASN:O	18:V:205:ASP:HB3	2.21	0.40
19:X:-1:DC:H2''	19:X:0:DA:C8	2.56	0.40
3:d:1060:LEU:HD11	10:l:83:MET:HG3	2.02	0.40
4:e:607:ARG:HE	4:e:607:ARG:HB2	1.68	0.40
5:f:284:ARG:HH21	5:f:284:ARG:HD2	1.76	0.40
5:f:409:GLY:HA3	5:f:410:PRO:HA	1.96	0.40
24:o:554:PHE:HB3	24:o:585:LEU:HD23	2.04	0.40
24:o:1004:LEU:O	24:o:1005:HIS:C	2.65	0.40
24:o:1094:SER:O	24:o:1098:PRO:HD2	2.22	0.40
1:A:573:TYR:O	2:B:657:ARG:HB3	2.22	0.40
1:A:797:LYS:HE2	1:A:797:LYS:HB3	1.89	0.40
2:B:847:ARG:HG2	2:B:885:ASP:OD2	2.20	0.40
4:E:306:VAL:HG21	4:E:363:ALA:HA	2.04	0.40
4:E:466:PHE:HE1	4:E:794:ALA:HB1	1.85	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:122:LEU:CD1	7:H:36:THR:HG23	2.52	0.40
5:F:126:PRO:CD	7:H:29:TYR:HA	2.51	0.40
5:F:350:ASN:O	5:F:354:ARG:HB2	2.22	0.40
5:F:397:GLN:H	5:F:397:GLN:HG3	1.61	0.40
13:Q:11:PRO:O	13:Q:15:ARG:HG2	2.22	0.40
21:c:28:LEU:HD23	21:c:28:LEU:HA	1.89	0.40
24:o:1048:THR:HG22	24:o:1048:THR:O	2.20	0.40
24:o:1102:MET:SD	24:o:1385:VAL:O	2.80	0.40
25:p:281:ASP:O	31:w:16:PHE:HE2	2.05	0.40
35:u:153:ASP:O	35:u:156:ASP:N	2.53	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	A	584/1872 (31%)	553 (95%)	27 (5%)	4 (1%)	18	50
2	B	959/1199 (80%)	908 (95%)	50 (5%)	1 (0%)	48	78
3	D	157/1085 (14%)	150 (96%)	7 (4%)	0	100	100
3	d	154/1085 (14%)	150 (97%)	4 (3%)	0	100	100
4	E	540/800 (68%)	497 (92%)	40 (7%)	3 (1%)	21	52
4	e	531/800 (66%)	484 (91%)	47 (9%)	0	100	100
5	F	400/677 (59%)	367 (92%)	24 (6%)	9 (2%)	5	30
5	f	399/677 (59%)	377 (94%)	22 (6%)	0	100	100
6	G	139/349 (40%)	134 (96%)	5 (4%)	0	100	100
7	H	207/310 (67%)	188 (91%)	15 (7%)	4 (2%)	6	33
8	I	118/264 (45%)	109 (92%)	5 (4%)	4 (3%)	3	25
8	i	119/264 (45%)	115 (97%)	4 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	J	85/218 (39%)	82 (96%)	3 (4%)	0	100	100
9	j	91/218 (42%)	89 (98%)	2 (2%)	0	100	100
10	L	74/161 (46%)	69 (93%)	5 (7%)	0	100	100
10	l	105/161 (65%)	100 (95%)	5 (5%)	0	100	100
11	O	95/109 (87%)	76 (80%)	13 (14%)	6 (6%)	1	14
12	P	175/339 (52%)	164 (94%)	8 (5%)	3 (2%)	7	34
13	Q	118/376 (31%)	108 (92%)	9 (8%)	1 (1%)	16	48
14	R	244/316 (77%)	228 (93%)	15 (6%)	1 (0%)	30	60
15	S	130/517 (25%)	127 (98%)	2 (2%)	1 (1%)	16	48
16	T	99/249 (40%)	95 (96%)	3 (3%)	1 (1%)	12	43
17	U	175/439 (40%)	155 (89%)	16 (9%)	4 (2%)	5	30
18	V	170/291 (58%)	133 (78%)	25 (15%)	12 (7%)	1	12
21	c	125/929 (14%)	116 (93%)	9 (7%)	0	100	100
22	k	96/211 (46%)	91 (95%)	5 (5%)	0	100	100
23	m	85/124 (68%)	79 (93%)	6 (7%)	0	100	100
24	o	1417/1970 (72%)	1280 (90%)	124 (9%)	13 (1%)	14	45
25	p	1128/1174 (96%)	1052 (93%)	76 (7%)	0	100	100
26	q	253/275 (92%)	226 (89%)	27 (11%)	0	100	100
27	r	126/142 (89%)	119 (94%)	7 (6%)	0	100	100
28	s	207/210 (99%)	196 (95%)	11 (5%)	0	100	100
29	t	77/127 (61%)	74 (96%)	3 (4%)	0	100	100
30	v	146/150 (97%)	132 (90%)	14 (10%)	0	100	100
31	w	112/125 (90%)	103 (92%)	9 (8%)	0	100	100
32	x	62/67 (92%)	60 (97%)	2 (3%)	0	100	100
33	y	115/117 (98%)	108 (94%)	6 (5%)	1 (1%)	14	45
34	z	42/58 (72%)	38 (90%)	4 (10%)	0	100	100
35	u	169/172 (98%)	156 (92%)	12 (7%)	1 (1%)	21	52
All	All	10028/18627 (54%)	9288 (93%)	671 (7%)	69 (1%)	20	50

All (69) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1158	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	F	323	VAL
5	F	345	SER
5	F	415	ILE
7	H	141	PRO
8	I	105	PRO
8	I	109	PRO
11	O	28	ILE
11	O	29	THR
11	O	30	PRO
11	O	52	VAL
13	Q	321	SER
17	U	71	PHE
17	U	119	ARG
18	V	171	ILE
18	V	205	ASP
24	o	461	GLN
24	o	1059	ARG
35	u	154	LYS
1	A	849	CYS
7	H	226	ALA
12	P	285	PRO
18	V	79	ALA
18	V	173	GLU
24	o	114	CYS
24	o	723	ASN
24	o	969	ILE
24	o	1038	THR
24	o	1103	THR
4	E	422	PRO
5	F	64	GLN
12	P	207	PRO
18	V	134	ASP
24	o	17	THR
24	o	1037	ALA
4	E	429	LEU
5	F	439	ARG
11	O	56	VAL
11	O	84	VAL
16	T	38	GLY
17	U	145	PHE
18	V	139	PHE
18	V	172	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
18	V	206	LYS
18	V	208	CYS
18	V	225	VAL
24	o	581	LYS
24	o	1099	ALA
2	B	880	TYR
7	H	134	LEU
7	H	164	THR
8	I	107	ILE
15	S	153	ARG
17	U	74	CYS
18	V	212	VAL
5	F	314	SER
5	F	432	ALA
12	P	298	PRO
18	V	177	ASN
24	o	968	VAL
33	y	4	PRO
8	I	113	PRO
5	F	433	PRO
1	A	467	ILE
1	A	498	PRO
4	E	704	VAL
5	F	364	VAL
14	R	280	VAL
24	o	980	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	536/1665 (32%)	475 (89%)	61 (11%)	5	24
2	B	876/1083 (81%)	860 (98%)	16 (2%)	51	67
3	D	147/815 (18%)	131 (89%)	16 (11%)	6	26
3	d	146/815 (18%)	146 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	478/657 (73%)	466 (98%)	12 (2%)	42	61
4	e	475/657 (72%)	473 (100%)	2 (0%)	84	81
5	F	320/574 (56%)	294 (92%)	26 (8%)	11	36
5	f	322/574 (56%)	311 (97%)	11 (3%)	32	55
6	G	133/322 (41%)	121 (91%)	12 (9%)	9	33
7	H	181/270 (67%)	167 (92%)	14 (8%)	12	38
8	I	106/235 (45%)	97 (92%)	9 (8%)	10	35
8	i	107/235 (46%)	107 (100%)	0	100	100
9	J	78/154 (51%)	78 (100%)	0	100	100
9	j	83/154 (54%)	83 (100%)	0	100	100
10	L	71/141 (50%)	70 (99%)	1 (1%)	59	70
10	l	98/141 (70%)	95 (97%)	3 (3%)	35	57
11	O	84/98 (86%)	68 (81%)	16 (19%)	1	10
12	P	153/293 (52%)	133 (87%)	20 (13%)	4	20
13	Q	111/324 (34%)	104 (94%)	7 (6%)	16	43
14	R	211/268 (79%)	188 (89%)	23 (11%)	6	26
15	S	117/448 (26%)	114 (97%)	3 (3%)	40	60
16	T	85/218 (39%)	85 (100%)	0	100	100
17	U	163/373 (44%)	129 (79%)	34 (21%)	1	7
18	V	154/261 (59%)	116 (75%)	38 (25%)	1	5
21	c	113/833 (14%)	111 (98%)	2 (2%)	51	67
22	k	87/182 (48%)	87 (100%)	0	100	100
23	m	80/106 (76%)	79 (99%)	1 (1%)	61	71
24	o	1257/1748 (72%)	1205 (96%)	52 (4%)	27	52
25	p	993/1027 (97%)	990 (100%)	3 (0%)	86	83
26	q	234/252 (93%)	234 (100%)	0	100	100
27	r	106/126 (84%)	106 (100%)	0	100	100
28	s	191/192 (100%)	191 (100%)	0	100	100
29	t	69/111 (62%)	69 (100%)	0	100	100
30	v	129/131 (98%)	129 (100%)	0	100	100
31	w	103/112 (92%)	103 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	x	53/56 (95%)	46 (87%)	7 (13%)	4	20
33	y	106/106 (100%)	106 (100%)	0	100	100
34	z	41/55 (74%)	41 (100%)	0	100	100
35	u	152/153 (99%)	150 (99%)	2 (1%)	61	71
All	All	8949/15965 (56%)	8558 (96%)	391 (4%)	27	50

All (391) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	348	LEU
1	A	353	LEU
1	A	395	ASP
1	A	397	LEU
1	A	400	GLU
1	A	401	ASN
1	A	403	LEU
1	A	404	MET
1	A	408	LEU
1	A	411	GLU
1	A	415	ILE
1	A	416	TRP
1	A	419	GLU
1	A	465	TYR
1	A	467	ILE
1	A	470	ILE
1	A	475	LEU
1	A	483	ASN
1	A	491	MET
1	A	499	VAL
1	A	500	LEU
1	A	501	THR
1	A	502	LEU
1	A	505	ASN
1	A	511	LEU
1	A	636	VAL
1	A	637	GLN
1	A	639	LEU
1	A	661	GLU
1	A	667	THR
1	A	711	ASP
1	A	727	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	730	PHE
1	A	804	ARG
1	A	828	GLU
1	A	842	ILE
1	A	848	LEU
1	A	853	LYS
1	A	855	THR
1	A	859	SER
1	A	869	ARG
1	A	925	ASP
1	A	943	LYS
1	A	968	ILE
1	A	970	ASN
1	A	971	LYS
1	A	994	ASP
1	A	996	ARG
1	A	999	SER
1	A	1019	LYS
1	A	1020	LEU
1	A	1021	SER
1	A	1022	ARG
1	A	1024	GLU
1	A	1026	ILE
1	A	1029	VAL
1	A	1052	ARG
1	A	1055	VAL
1	A	1165	LEU
1	A	1181	ARG
1	A	1203	GLU
2	B	21	GLU
2	B	71	ARG
2	B	140	GLU
2	B	184	ASN
2	B	262	MET
2	B	266	THR
2	B	293	GLU
2	B	475	LYS
2	B	559	LYS
2	B	603	LYS
2	B	640	VAL
2	B	746	SER
2	B	771	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	819	LEU
2	B	820	ASP
2	B	987	LEU
3	D	947	PHE
3	D	949	GLN
3	D	958	LYS
3	D	963	ARG
3	D	964	GLU
3	D	966	LEU
3	D	968	ARG
3	D	986	GLN
3	D	990	GLU
3	D	991	MET
3	D	992	GLN
3	D	993	GLN
3	D	1000	ARG
3	D	1006	LEU
3	D	1054	ARG
3	D	1055	ILE
4	E	420	ASN
4	E	424	GLN
4	E	425	ASN
4	E	427	ILE
4	E	431	GLU
4	E	518	LYS
4	E	519	GLU
4	E	522	ASP
4	E	526	ARG
4	E	745	GLU
4	E	746	ASP
4	E	747	LEU
5	F	221	GLN
5	F	222	LEU
5	F	261	THR
5	F	269	VAL
5	F	271	VAL
5	F	276	LEU
5	F	280	ILE
5	F	295	LEU
5	F	301	VAL
5	F	312	ILE
5	F	313	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	F	315	ARG
5	F	317	LEU
5	F	339	GLN
5	F	343	HIS
5	F	348	THR
5	F	354	ARG
5	F	358	THR
5	F	368	THR
5	F	372	THR
5	F	391	LEU
5	F	397	GLN
5	F	406	VAL
5	F	408	ASP
5	F	427	LEU
5	F	433	PRO
6	G	41	ASP
6	G	42	ARG
6	G	44	THR
6	G	46	GLU
6	G	129	LYS
6	G	131	ILE
6	G	143	VAL
6	G	154	LYS
6	G	161	ASP
6	G	181	TRP
6	G	182	GLU
6	G	183	ILE
7	H	115	GLN
7	H	132	LYS
7	H	135	THR
7	H	155	ASP
7	H	159	TYR
7	H	164	THR
7	H	203	LEU
7	H	205	LYS
7	H	206	ASP
7	H	217	ARG
7	H	220	THR
7	H	221	ILE
7	H	225	THR
7	H	227	LEU
8	I	101	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	I	102	THR
8	I	104	LEU
8	I	105	PRO
8	I	106	LEU
8	I	107	ILE
8	I	108	LYS
8	I	110	TYR
8	I	111	SER
10	L	73	ASN
11	O	11	LEU
11	O	23	ILE
11	O	28	ILE
11	O	29	THR
11	O	32	LEU
11	O	52	VAL
11	O	56	VAL
11	O	57	ASN
11	O	58	PHE
11	O	61	SER
11	O	65	TYR
11	O	66	ARG
11	O	76	LEU
11	O	84	VAL
11	O	88	ILE
11	O	89	LYS
12	P	172	VAL
12	P	196	ARG
12	P	209	THR
12	P	216	SER
12	P	218	LYS
12	P	219	MET
12	P	221	CYS
12	P	252	ASP
12	P	268	ILE
12	P	269	ARG
12	P	274	VAL
12	P	278	GLN
12	P	286	GLU
12	P	288	PHE
12	P	294	ARG
12	P	300	ILE
12	P	306	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
12	P	311	VAL
12	P	317	VAL
12	P	328	ILE
13	Q	13	LEU
13	Q	34	VAL
13	Q	49	LYS
13	Q	320	VAL
13	Q	332	GLU
13	Q	343	HIS
13	Q	364	ASP
14	R	31	ASP
14	R	32	MET
14	R	33	ILE
14	R	39	LEU
14	R	40	VAL
14	R	41	VAL
14	R	120	GLU
14	R	127	ARG
14	R	128	ILE
14	R	130	LEU
14	R	132	ARG
14	R	134	ILE
14	R	137	ARG
14	R	189	LYS
14	R	196	LYS
14	R	244	LEU
14	R	245	VAL
14	R	248	ARG
14	R	249	SER
14	R	252	SER
14	R	282	ASP
14	R	283	VAL
14	R	286	ARG
15	S	7	SER
15	S	154	THR
15	S	170	VAL
17	U	15	LYS
17	U	16	ARG
17	U	17	LEU
17	U	28	ILE
17	U	39	ARG
17	U	43	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
17	U	45	GLU
17	U	72	ILE
17	U	73	LYS
17	U	75	ARG
17	U	76	MET
17	U	77	ARG
17	U	95	ASN
17	U	99	LEU
17	U	111	ARG
17	U	112	ARG
17	U	113	ARG
17	U	126	SER
17	U	139	LEU
17	U	145	PHE
17	U	168	MET
17	U	171	LYS
17	U	174	ARG
17	U	175	THR
17	U	176	LEU
17	U	179	ARG
17	U	184	ILE
17	U	185	GLU
17	U	190	LEU
17	U	191	LEU
17	U	192	ARG
17	U	193	GLU
17	U	194	THR
17	U	199	LEU
18	V	100	ASP
18	V	107	GLN
18	V	132	VAL
18	V	142	LYS
18	V	144	ASN
18	V	146	ARG
18	V	147	ASP
18	V	148	LYS
18	V	149	LYS
18	V	151	LEU
18	V	153	ARG
18	V	154	LEU
18	V	155	LEU
18	V	157	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
18	V	159	ASP
18	V	160	GLN
18	V	161	ARG
18	V	163	LEU
18	V	167	LEU
18	V	168	LEU
18	V	169	GLU
18	V	171	ILE
18	V	175	LEU
18	V	188	GLN
18	V	193	ASN
18	V	204	ASN
18	V	206	LYS
18	V	207	SER
18	V	208	CYS
18	V	210	PHE
18	V	211	SER
18	V	213	ASP
18	V	215	GLU
18	V	225	VAL
18	V	229	ASP
18	V	230	GLU
18	V	233	ILE
18	V	235	GLU
21	c	24	ASP
21	c	106	VAL
4	e	546	VAL
4	e	579	VAL
5	f	214	HIS
5	f	253	TYR
5	f	261	THR
5	f	272	VAL
5	f	322	ASP
5	f	323	VAL
5	f	326	HIS
5	f	356	THR
5	f	366	GLU
5	f	411	VAL
5	f	421	ASP
10	l	84	LEU
10	l	104	ARG
10	l	106	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
23	m	31	LEU
24	o	13	CYS
24	o	15	LEU
24	o	16	ARG
24	o	114	CYS
24	o	265	VAL
24	o	364	ARG
24	o	417	LYS
24	o	420	ILE
24	o	421	ARG
24	o	427	ILE
24	o	429	LEU
24	o	434	LYS
24	o	437	ASP
24	o	460	ARG
24	o	461	GLN
24	o	486	LEU
24	o	502	ASN
24	o	503	LEU
24	o	539	GLN
24	o	581	LYS
24	o	583	ARG
24	o	703	GLN
24	o	708	LYS
24	o	728	THR
24	o	732	THR
24	o	751	LYS
24	o	792	ASN
24	o	853	LYS
24	o	924	TYR
24	o	936	GLU
24	o	939	VAL
24	o	947	HIS
24	o	953	GLU
24	o	1007	ILE
24	o	1027	ASP
24	o	1032	GLN
24	o	1063	GLU
24	o	1075	LYS
24	o	1095	LEU
24	o	1101	GLN
24	o	1142	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
24	o	1156	ASP
24	o	1296	MET
24	o	1298	LEU
24	o	1316	ASN
24	o	1356	ARG
24	o	1479	LYS
24	o	1481	LYS
24	o	1482	TYR
24	o	1484	MET
24	o	1485	GLU
24	o	1486	ILE
25	p	248	LYS
25	p	249	LYS
25	p	841	ARG
32	x	14	VAL
32	x	19	GLU
32	x	26	GLN
32	x	28	GLU
32	x	30	THR
32	x	31	GLU
32	x	40	LEU
35	u	144	ARG
35	u	163	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (166) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	401	ASN
1	A	489	GLN
1	A	569	ASN
1	A	634	HIS
1	A	669	GLN
1	A	693	GLN
1	A	702	ASN
1	A	837	HIS
1	A	896	GLN
1	A	1058	HIS
1	A	1073	GLN
2	B	30	HIS
2	B	36	ASN
2	B	137	HIS
2	B	160	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	176	HIS
2	B	183	GLN
2	B	235	HIS
2	B	348	GLN
2	B	439	HIS
2	B	450	GLN
2	B	509	ASN
2	B	577	HIS
2	B	644	GLN
2	B	652	GLN
2	B	663	GLN
2	B	745	GLN
2	B	750	GLN
2	B	813	ASN
2	B	864	ASN
2	B	882	HIS
2	B	908	GLN
2	B	912	ASN
2	B	963	HIS
3	D	875	GLN
3	D	912	ASN
3	D	925	ASN
3	D	949	GLN
3	D	992	GLN
3	D	993	GLN
4	E	254	ASN
4	E	290	HIS
4	E	326	ASN
4	E	327	ASN
4	E	351	GLN
4	E	425	ASN
4	E	616	HIS
4	E	733	ASN
5	F	37	GLN
5	F	52	GLN
5	F	59	HIS
5	F	79	ASN
5	F	119	ASN
5	F	221	GLN
5	F	270	ASN
5	F	273	GLN
5	F	274	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	F	275	ASN
5	F	302	HIS
5	F	316	GLN
6	G	10	HIS
6	G	15	GLN
6	G	48	HIS
6	G	133	ASN
6	G	142	ASN
7	H	66	GLN
7	H	145	HIS
7	H	201	GLN
8	I	21	GLN
8	I	38	GLN
8	I	60	HIS
8	I	98	GLN
9	J	160	GLN
9	J	173	HIS
9	J	210	ASN
10	L	105	HIS
10	L	117	GLN
11	O	13	ASN
11	O	57	ASN
12	P	189	ASN
13	Q	37	GLN
13	Q	60	HIS
13	Q	343	HIS
13	Q	352	HIS
13	Q	361	ASN
14	R	116	ASN
14	R	133	ASN
14	R	229	GLN
15	S	44	GLN
16	T	14	GLN
17	U	109	HIS
17	U	123	ASN
18	V	95	HIS
18	V	108	HIS
18	V	117	GLN
18	V	177	ASN
18	V	193	ASN
21	c	27	GLN
21	c	50	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	d	844	ASN
3	d	912	ASN
4	e	256	HIS
4	e	320	HIS
4	e	368	ASN
4	e	420	ASN
4	e	424	GLN
4	e	660	ASN
4	e	733	ASN
5	f	30	GLN
5	f	119	ASN
5	f	134	HIS
5	f	214	HIS
5	f	325	ASN
22	k	186	HIS
22	k	205	HIS
10	l	73	ASN
10	l	105	HIS
23	m	107	ASN
24	o	267	GLN
24	o	341	GLN
24	o	353	ASN
24	o	410	ASN
24	o	432	HIS
24	o	465	HIS
24	o	507	GLN
24	o	539	GLN
24	o	673	GLN
24	o	721	HIS
24	o	739	ASN
24	o	740	GLN
24	o	792	ASN
24	o	861	GLN
24	o	1101	GLN
24	o	1230	GLN
24	o	1462	GLN
25	p	68	GLN
25	p	111	ASN
25	p	254	GLN
25	p	287	HIS
25	p	370	HIS
25	p	525	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
25	p	537	GLN
25	p	570	ASN
25	p	741	HIS
25	p	755	GLN
25	p	777	ASN
25	p	1021	HIS
25	p	1073	GLN
25	p	1120	ASN
26	q	6	GLN
26	q	83	GLN
26	q	114	HIS
27	r	19	GLN
27	r	129	GLN
28	s	22	HIS
28	s	71	GLN
28	s	132	GLN
30	v	130	ASN
30	v	131	ASN
31	w	22	ASN
31	w	45	GLN
33	y	2	ASN
33	y	29	ASN
33	y	69	HIS
33	y	89	ASN
35	u	60	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 11 ligands modelled in this entry, 11 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

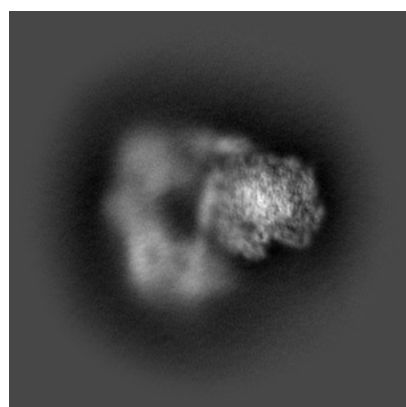
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31109. These allow visual inspection of the internal detail of the map and identification of artifacts.

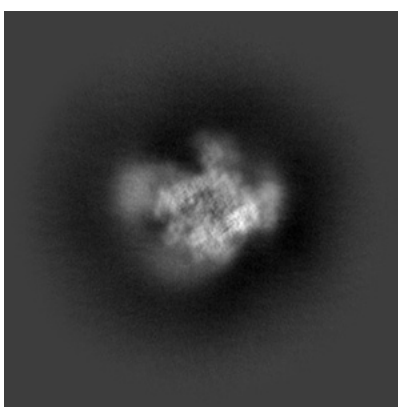
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

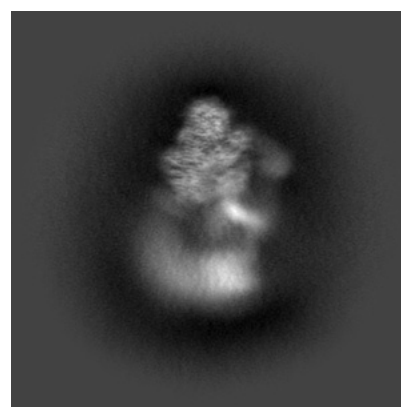
6.1.1 Primary map



X



Y

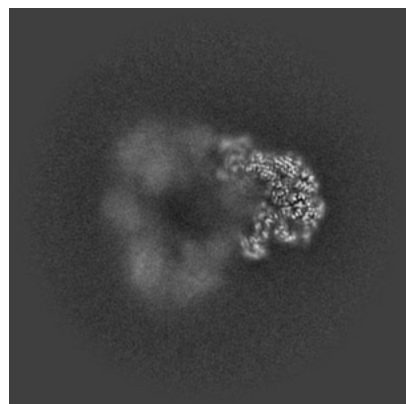


Z

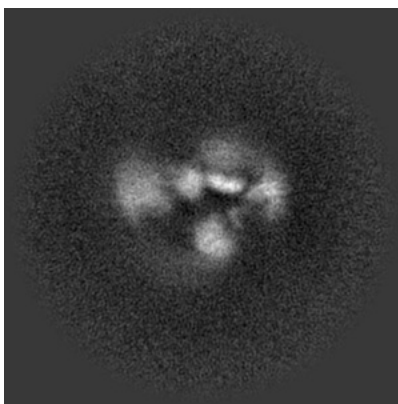
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

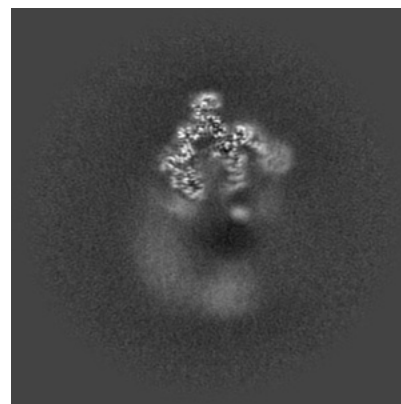
6.2.1 Primary map



X Index: 240



Y Index: 240

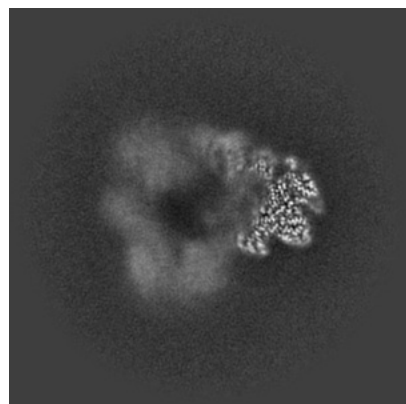


Z Index: 240

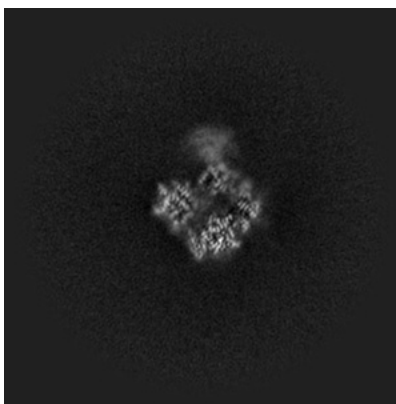
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

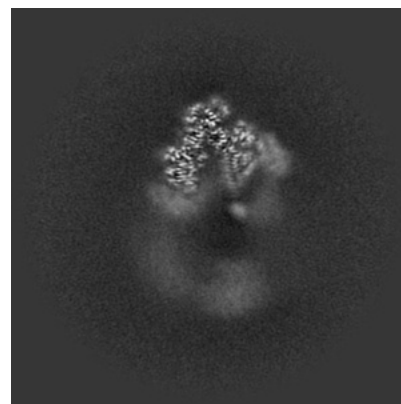
6.3.1 Primary map



X Index: 250



Y Index: 299

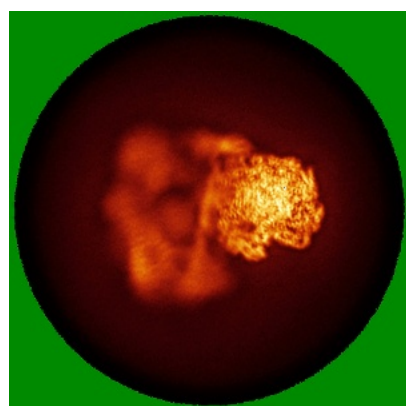


Z Index: 252

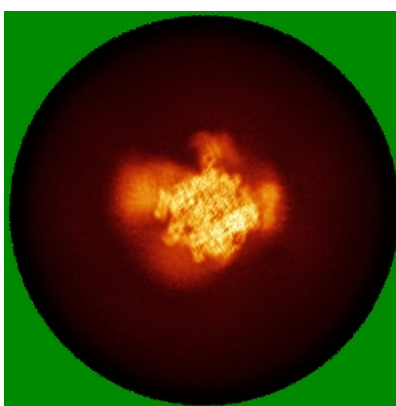
The images above show the largest variance slices of the map in three orthogonal directions.

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

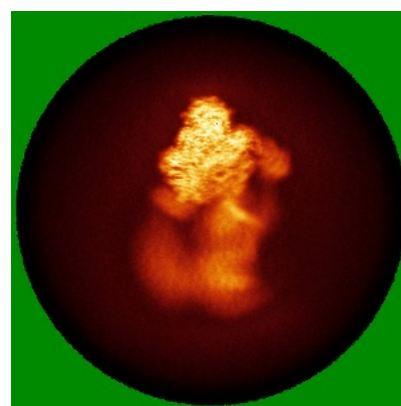
6.4.1 Primary map



X



Y

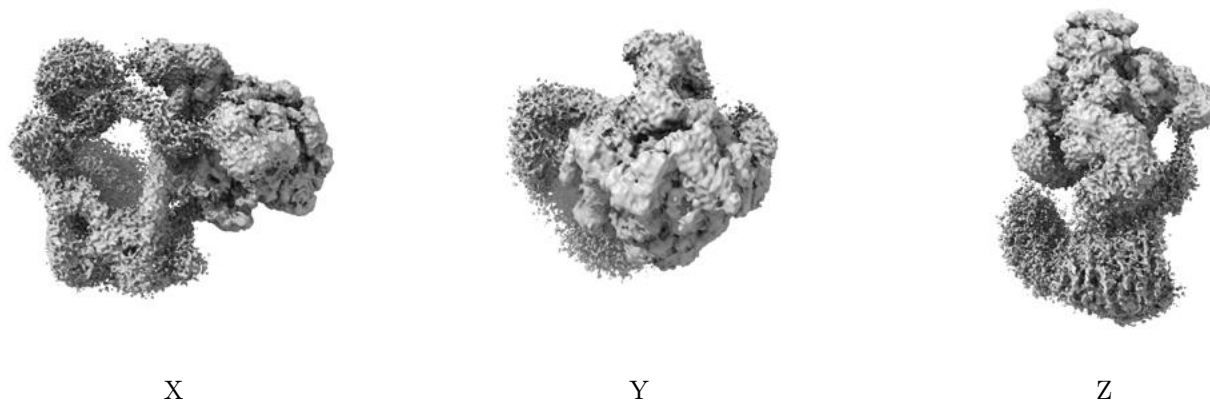


Z

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 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

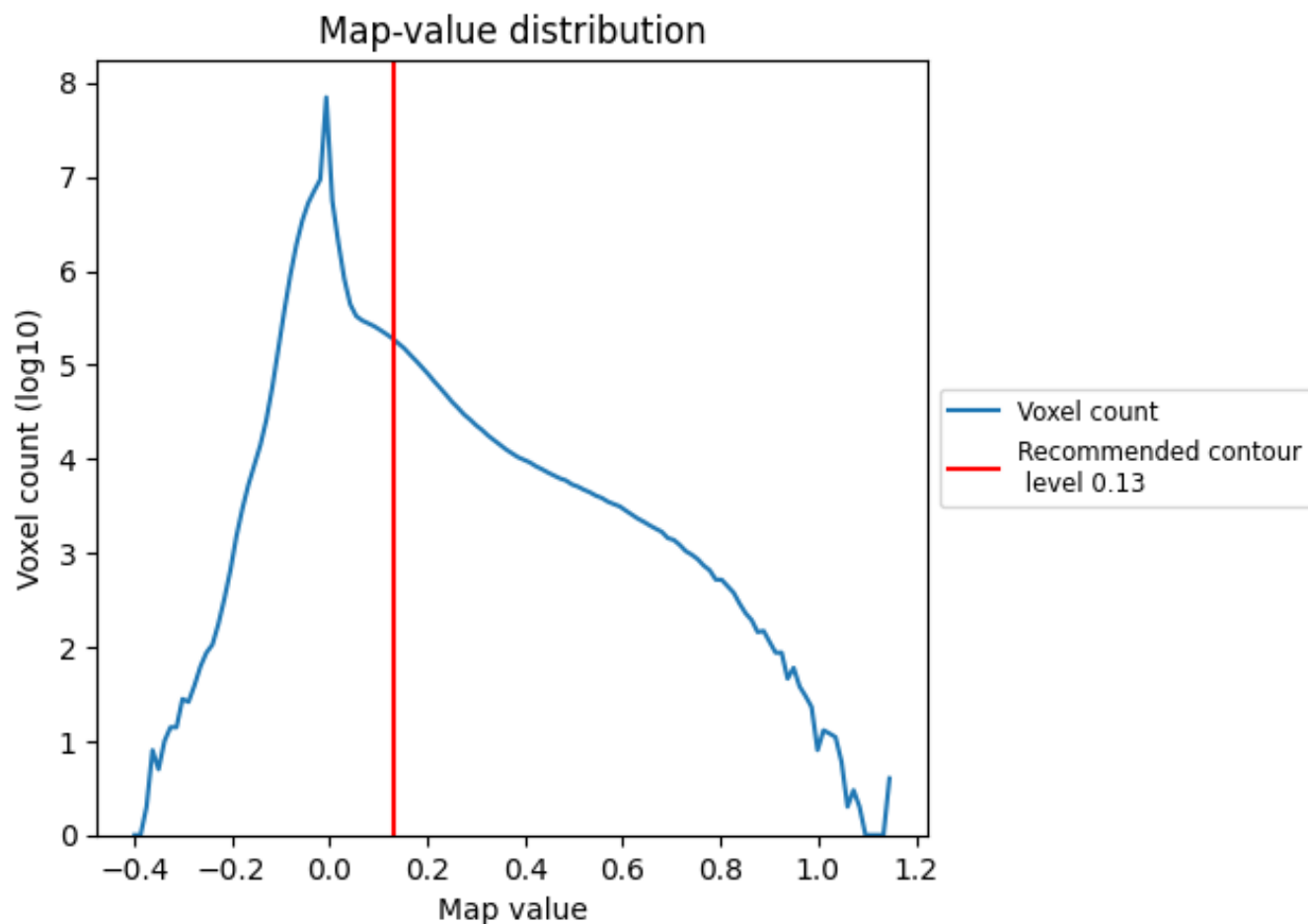
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

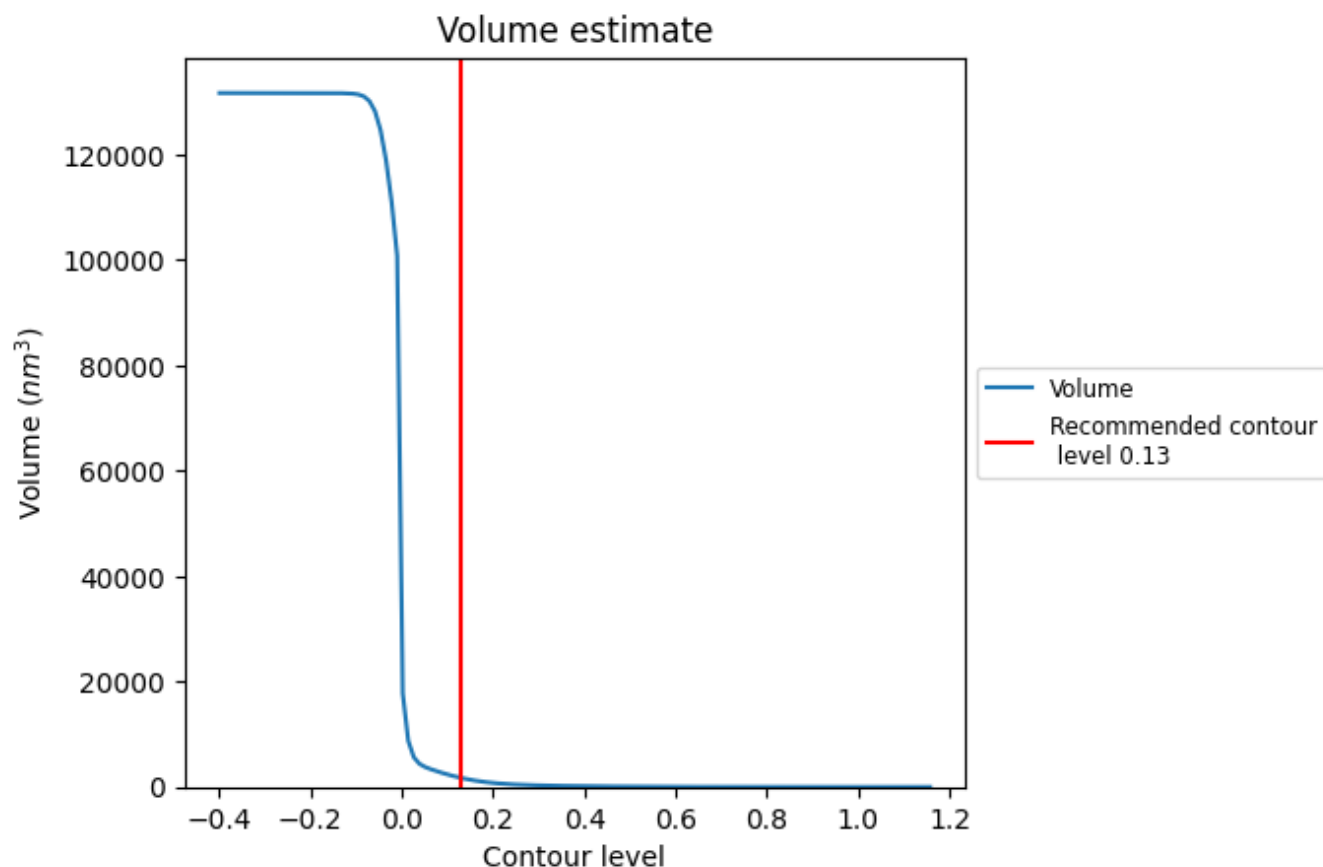
This section contains the results of statistical analysis of the map.

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.

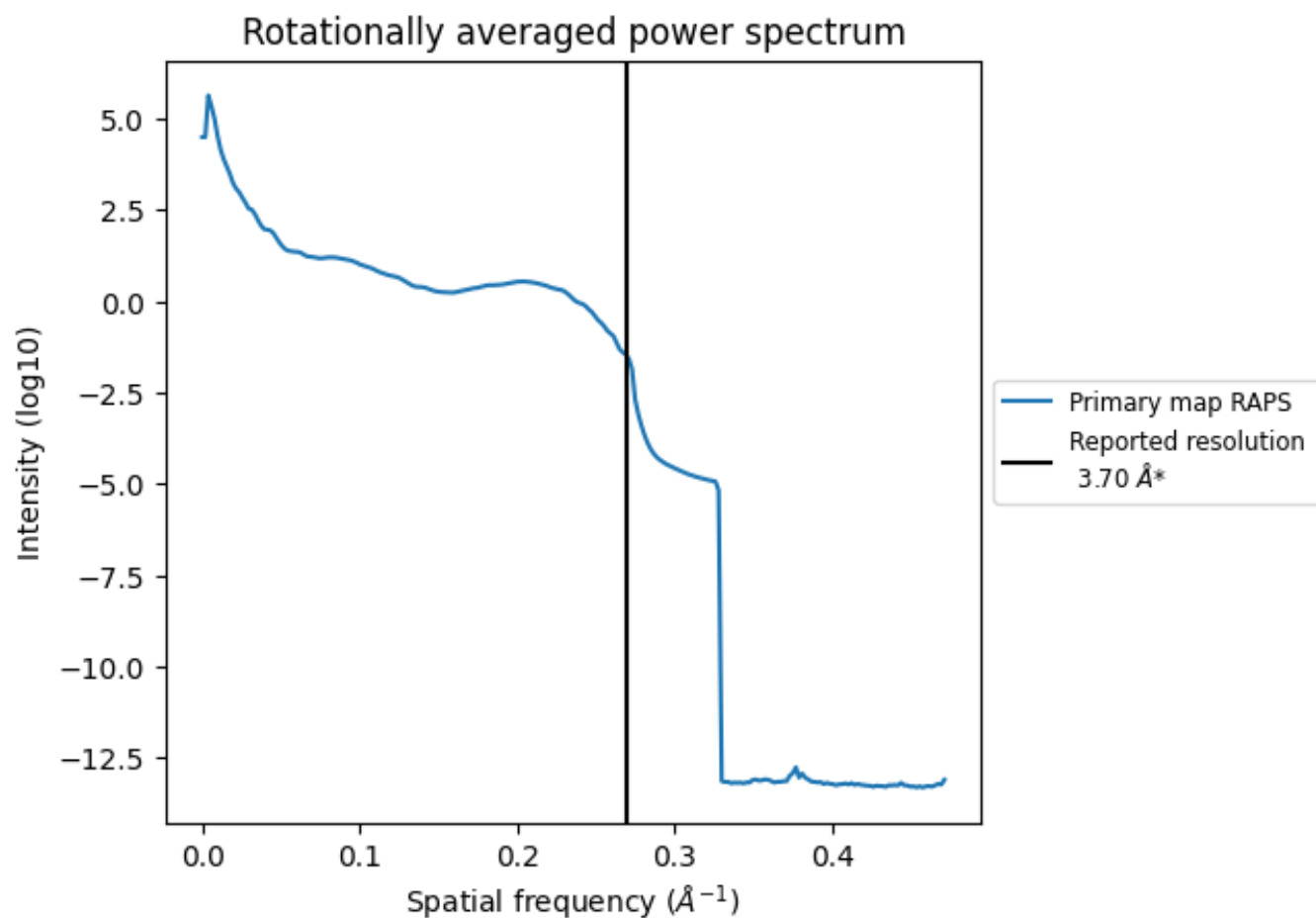
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1729 nm^3 ; this corresponds to an approximate mass of 1562 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

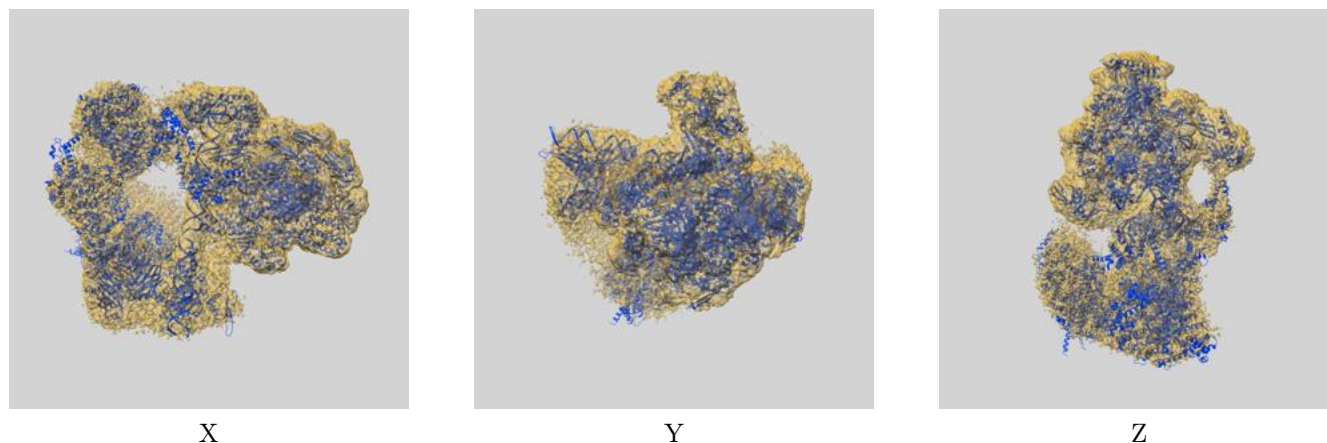
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

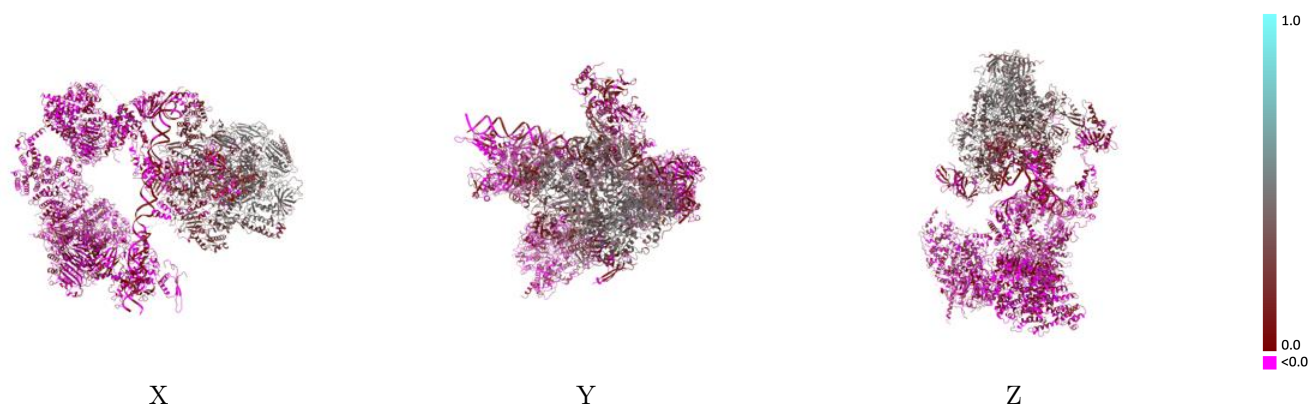
This section contains information regarding the fit between EMDB map EMD-31109 and PDB model 7EG9. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



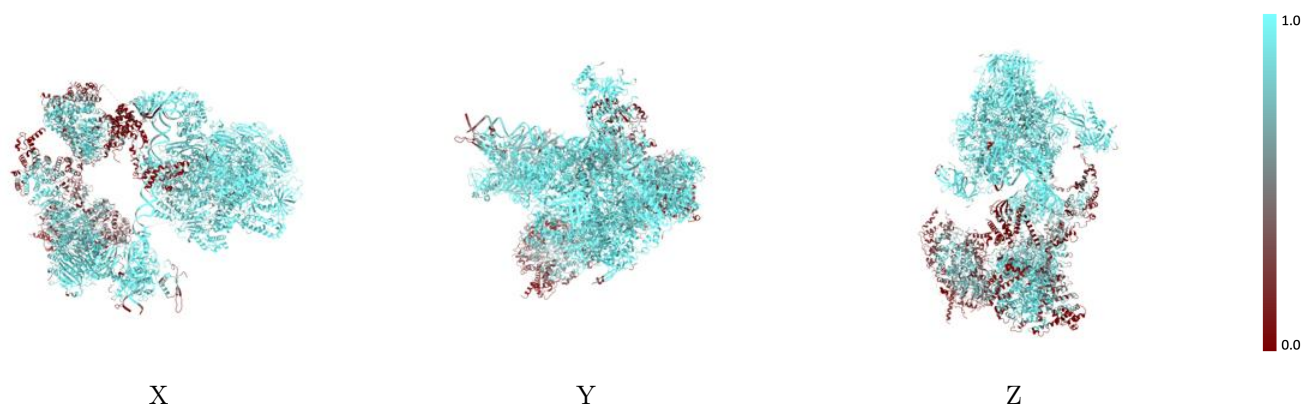
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



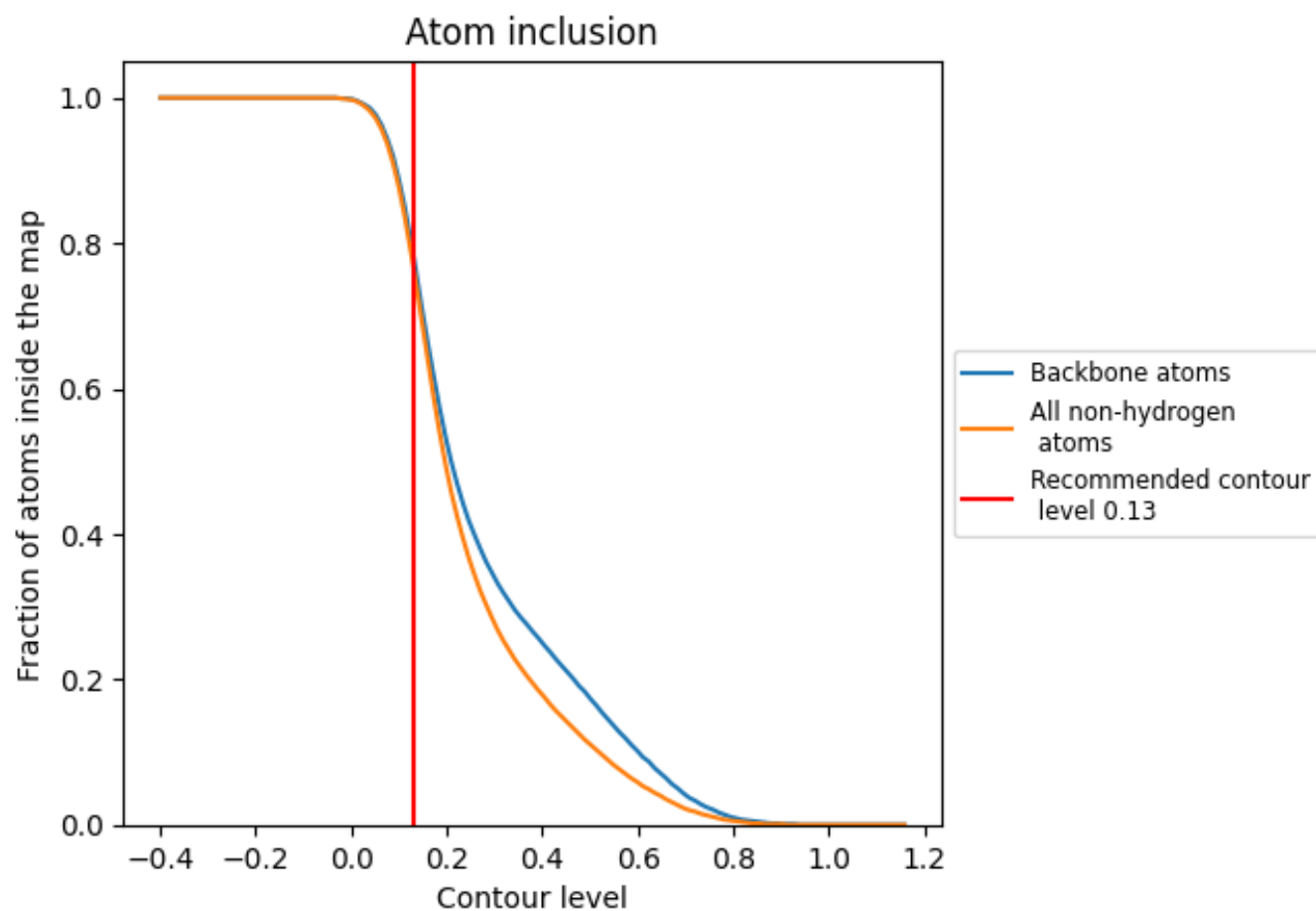
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 77% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7680	 0.1370
A	 0.8320	 0.0160
B	 0.9040	 0.0370
D	 0.2970	 0.0010
E	 0.7600	 0.0140
F	 0.5210	 0.0090
G	 0.8760	 -0.0040
H	 0.6060	 -0.0030
I	 0.7100	 0.0160
J	 0.6810	 -0.0010
L	 0.2210	 -0.0060
O	 0.3060	 -0.0150
P	 0.9460	 0.0130
Q	 0.3010	 0.0030
R	 0.9090	 0.1460
S	 0.8920	 0.0820
T	 0.8840	 0.0670
U	 0.4200	 -0.0010
V	 0.2480	 0.0100
X	 0.8830	 0.0620
Y	 0.8220	 0.0720
c	 0.4010	 -0.0170
d	 0.3100	 0.0110
e	 0.4380	 -0.0020
f	 0.6670	 0.0200
i	 0.4870	 -0.0100
j	 0.4170	 -0.0160
k	 0.3100	 -0.0000
l	 0.5020	 0.0270
m	 0.2930	 -0.0060
o	 0.9340	 0.3050
p	 0.9620	 0.3760
q	 0.9920	 0.4220
r	 0.9510	 0.1150
s	 0.9820	 0.3140



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
t	 0.9970	 0.4100
u	 0.9720	 0.1760
v	 0.9920	 0.3870
w	 0.9880	 0.3280
x	 0.9880	 0.4410
y	 0.9680	 0.3950
z	 0.9780	 0.3530