



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:59 PM UTC

PDB ID : 3J97 / pdb_00003j97
EMDB ID : EMD-6207
Title : Structure of 20S supercomplex determined by single particle cryoelectron microscopy (State II)
Authors : Zhao, M.; Wu, S.; Cheng, Y.; Brunger, A.T.
Deposited on : 2014-12-05
Resolution : 7.80 Å (reported)
Based on initial models : 1QCS, 1N7S, 1NSF

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

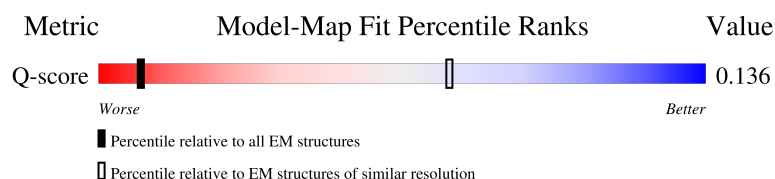
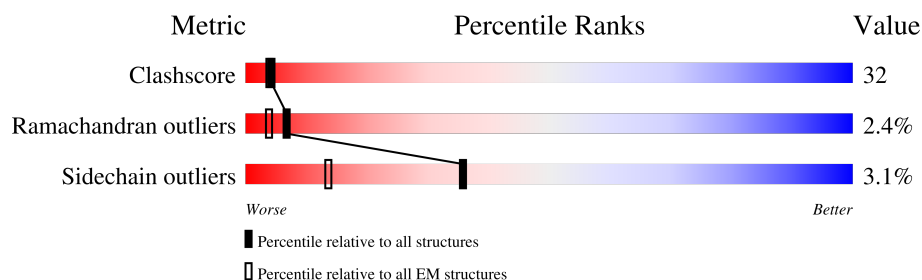
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.80 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	370 (7.30 - 8.30)

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	747	
1	B	747	
1	C	747	
1	D	747	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	E	747	
1	F	747	
2	G	297	
2	H	297	
2	I	297	
2	J	297	
3	K	63	
4	L	67	
5	M	198	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 41095 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 Vesicle-fusing ATPase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	678	Total	C	N	O	S	0	0
			5044	3201	874	946	23		
1	B	672	Total	C	N	O	S	0	0
			5015	3184	868	939	24		
1	C	676	Total	C	N	O	S	0	0
			5028	3189	869	947	23		
1	D	673	Total	C	N	O	S	0	0
			4986	3169	854	939	24		
1	E	670	Total	C	N	O	S	0	0
			5020	3185	871	940	24		
1	F	654	Total	C	N	O	S	0	0
			4932	3135	852	922	23		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P18708
A	-1	ALA	-	expression tag	UNP P18708
A	0	HIS	-	expression tag	UNP P18708
B	-2	GLY	-	expression tag	UNP P18708
B	-1	ALA	-	expression tag	UNP P18708
B	0	HIS	-	expression tag	UNP P18708
C	-2	GLY	-	expression tag	UNP P18708
C	-1	ALA	-	expression tag	UNP P18708
C	0	HIS	-	expression tag	UNP P18708
D	-2	GLY	-	expression tag	UNP P18708
D	-1	ALA	-	expression tag	UNP P18708
D	0	HIS	-	expression tag	UNP P18708
E	-2	GLY	-	expression tag	UNP P18708
E	-1	ALA	-	expression tag	UNP P18708
E	0	HIS	-	expression tag	UNP P18708
F	-2	GLY	-	expression tag	UNP P18708
F	-1	ALA	-	expression tag	UNP P18708
F	0	HIS	-	expression tag	UNP P18708

- Molecule 2 is a protein called Alpha-soluble NSF attachment protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		
2	I	286	Total	C	N	O	S	0	0
			2246	1416	373	441	16		
2	J	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		
2	G	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-1	GLY	-	expression tag	UNP P54921
H	0	SER	-	expression tag	UNP P54921
I	-1	GLY	-	expression tag	UNP P54921
I	0	SER	-	expression tag	UNP P54921
J	-1	GLY	-	expression tag	UNP P54921
J	0	SER	-	expression tag	UNP P54921
G	-1	GLY	-	expression tag	UNP P54921
G	0	SER	-	expression tag	UNP P54921

- Molecule 3 is a protein called Vesicle-associated membrane protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	K	61	Total	C	N	O	S	0	0
			494	300	94	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	27	GLY	-	expression tag	UNP P63045

- Molecule 4 is a protein called Syntaxin-1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	66	Total	C	N	O	S	0	0
			536	331	91	109	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	190	MET	-	expression tag	UNP P32851

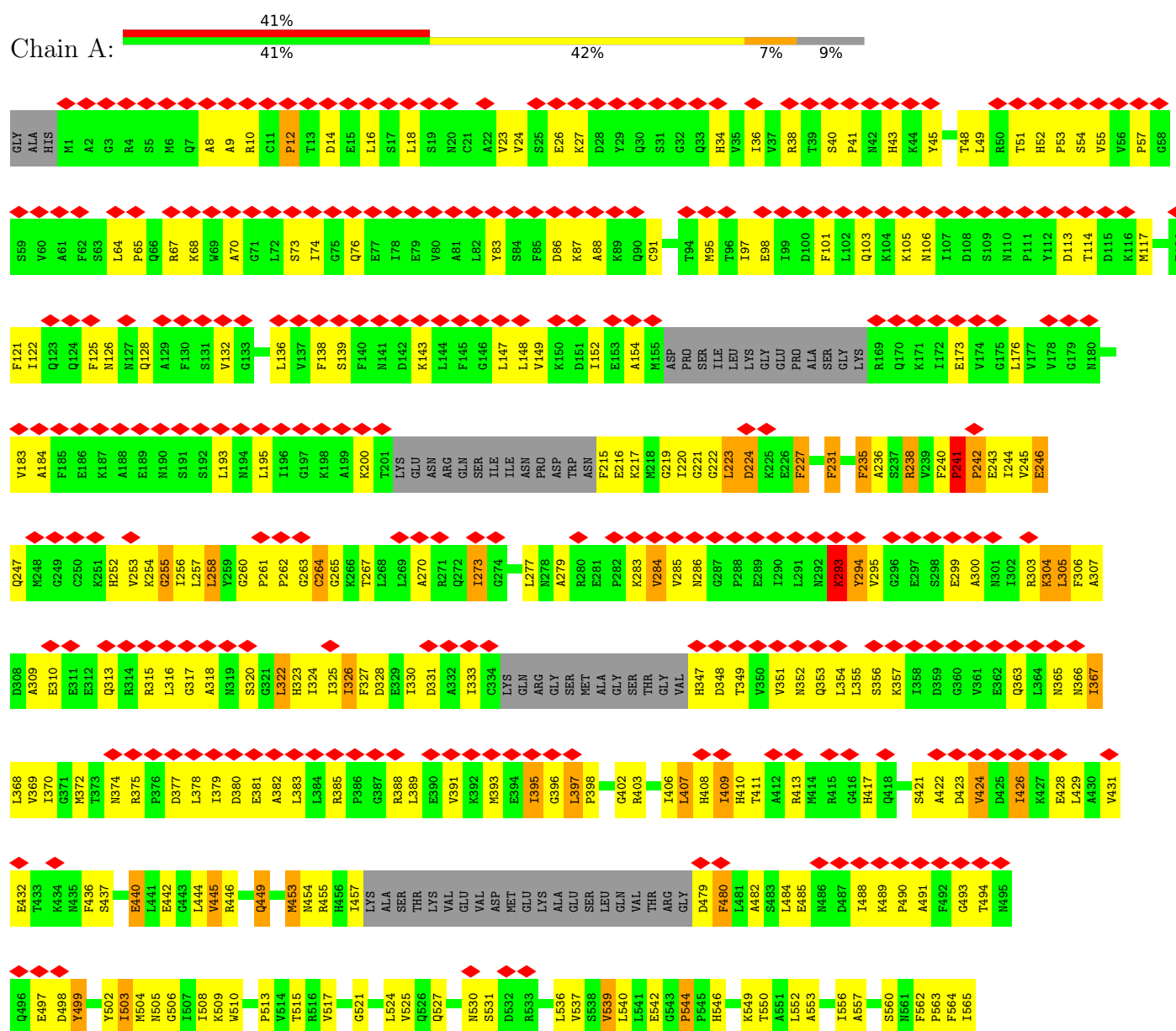
- Molecule 5 is a protein called Synaptosomal-associated protein 25.

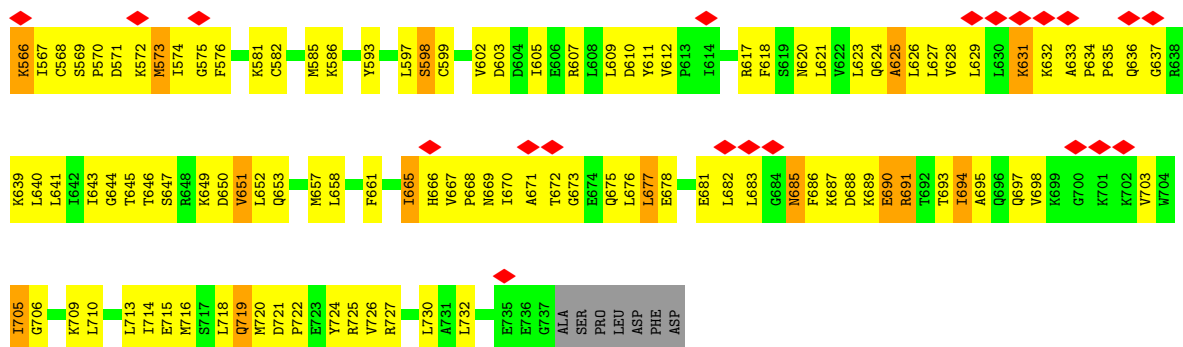
Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	131	Total	C	N	O	S	0	0
			1029	609	191	220	9		

3 Residue-property plots

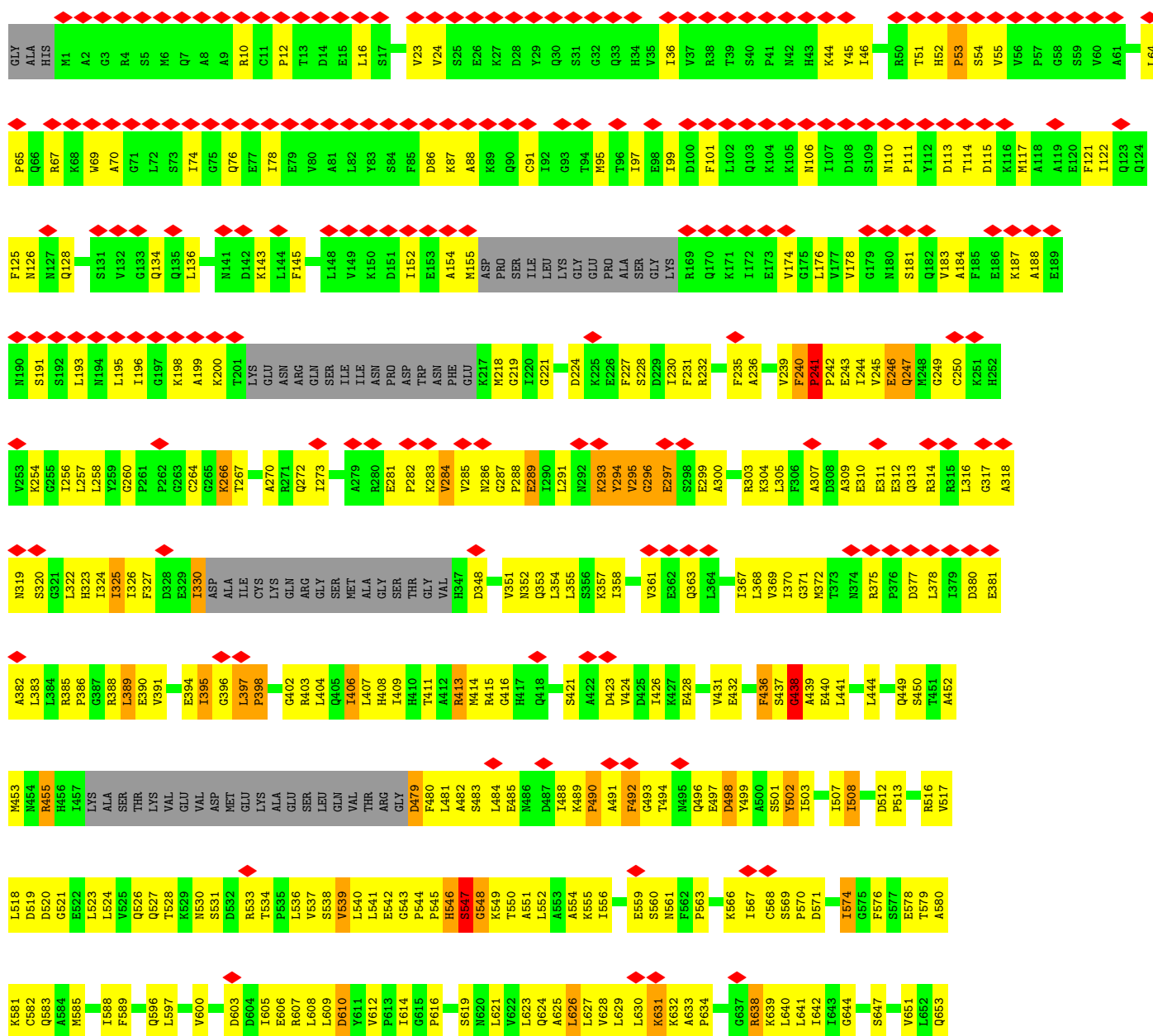
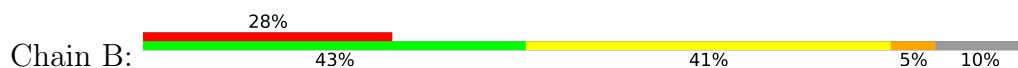
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Vesicle-fusing ATPase





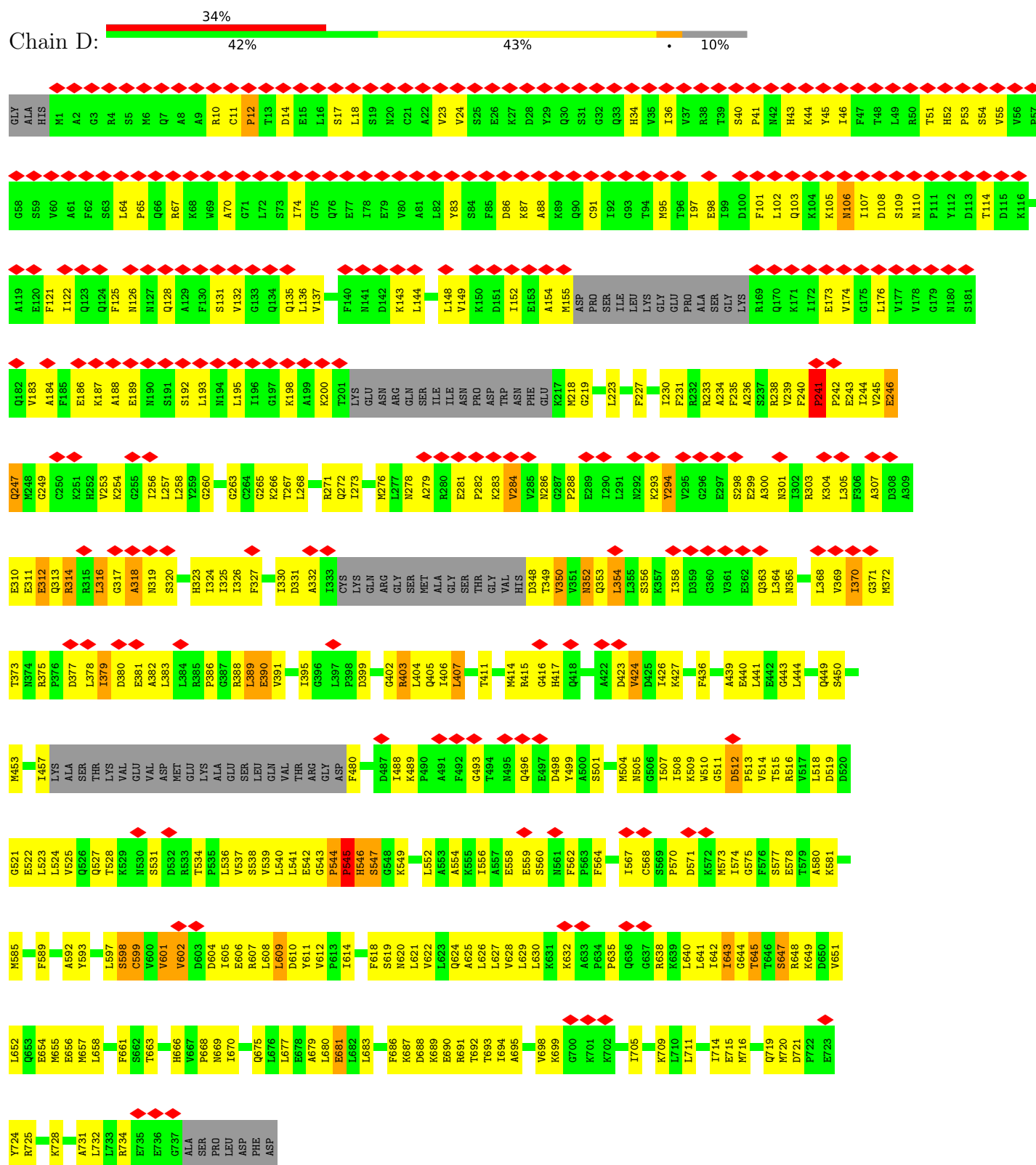
• Molecule 1: Vesicle-fusing ATPase





• Molecule 1: Vesicle-fusing ATPase

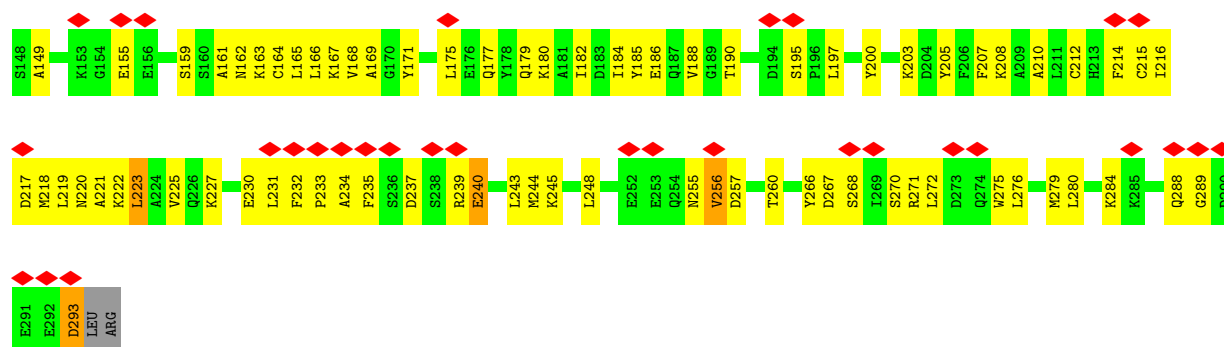
Chain D:



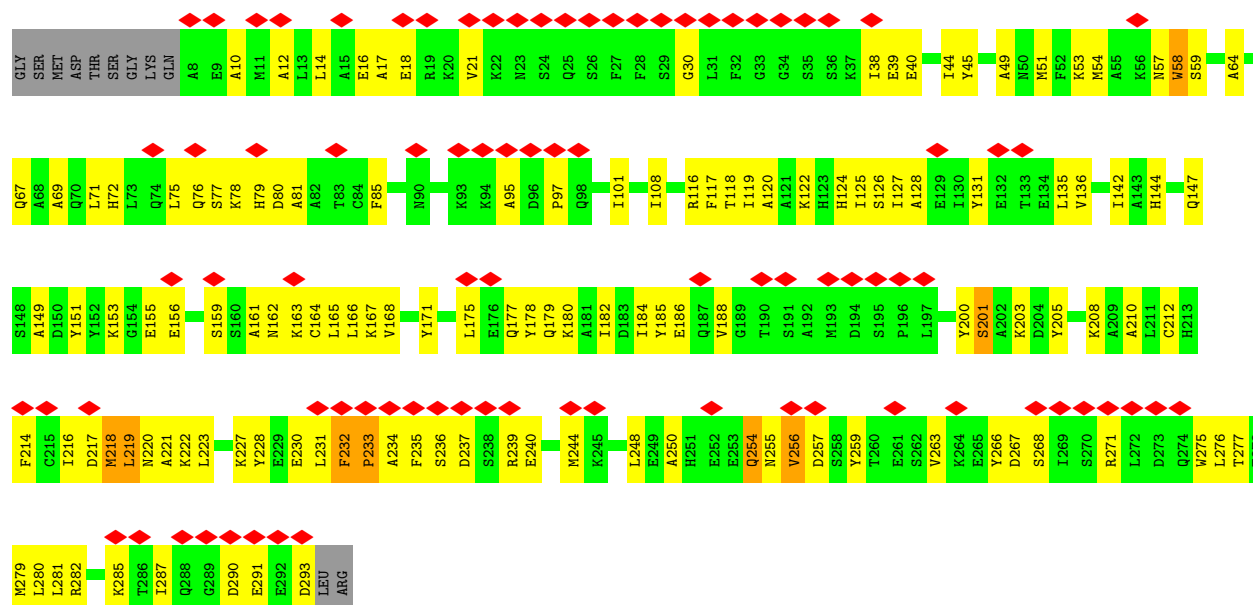
• Molecule 1: Vesicle-fusing ATPase

Chain E:

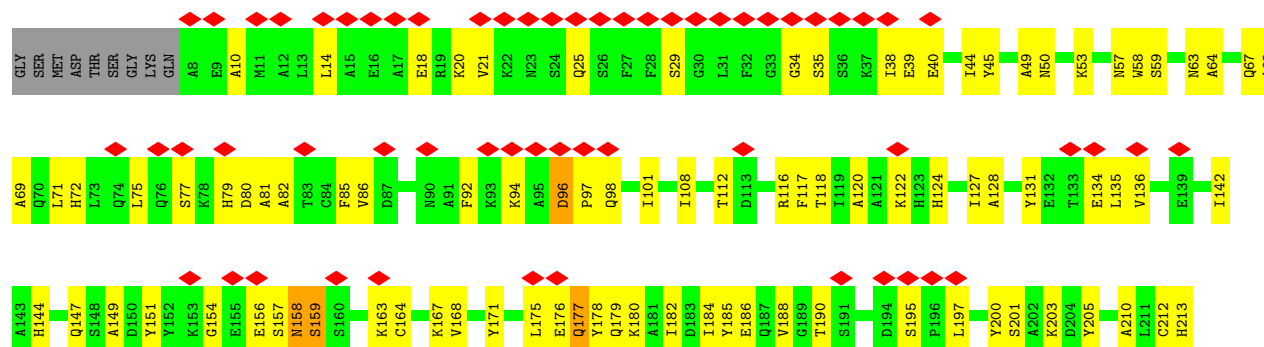


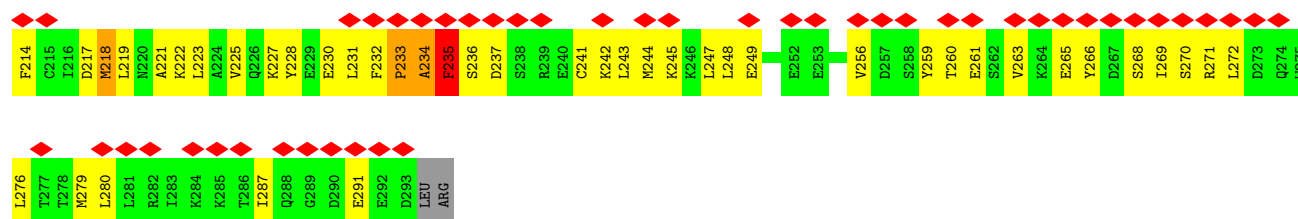


• Molecule 2: Alpha-soluble NSF attachment protein

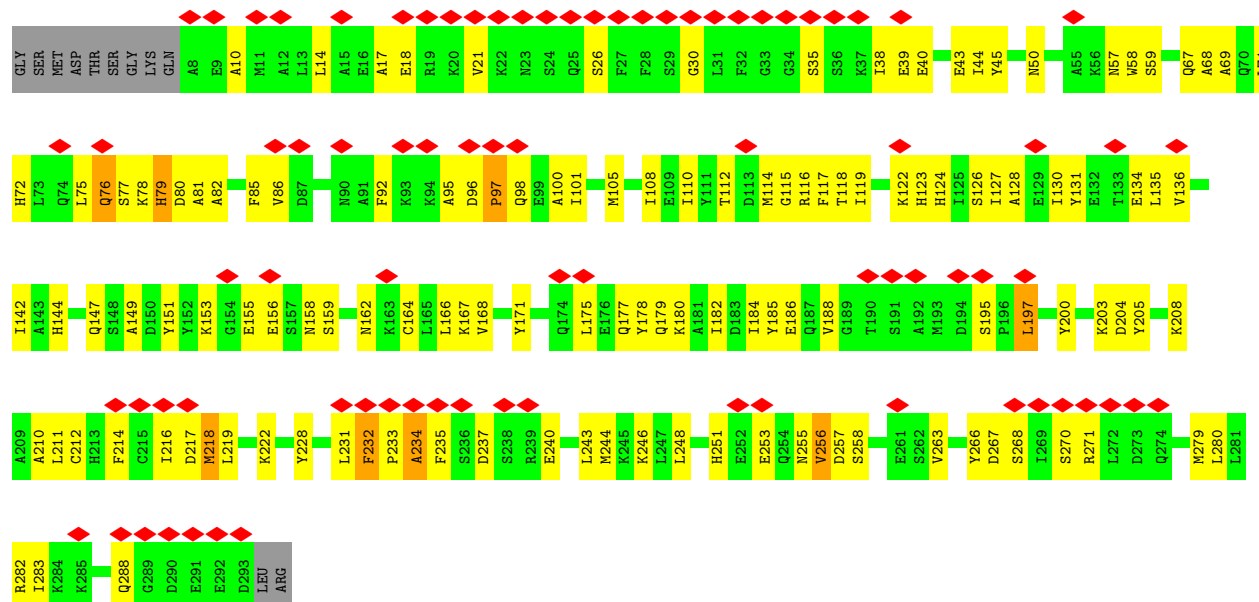


• Molecule 2: Alpha-soluble NSF attachment protein

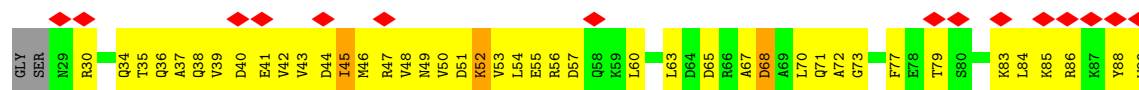




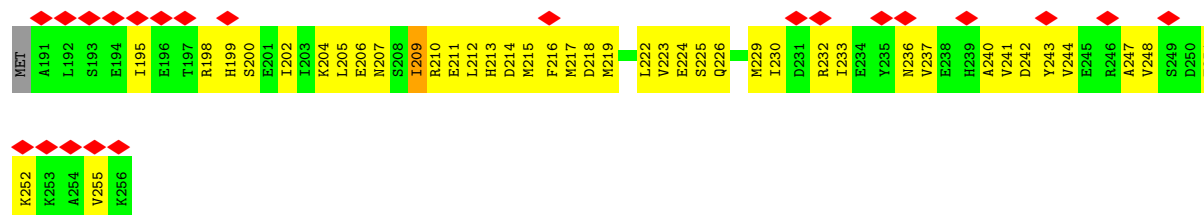
• Molecule 2: Alpha-soluble NSF attachment protein



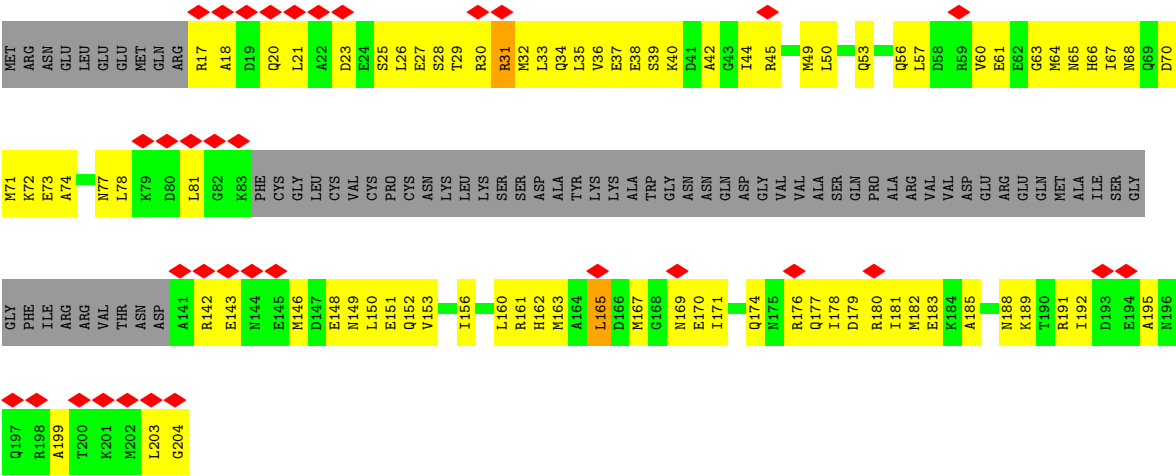
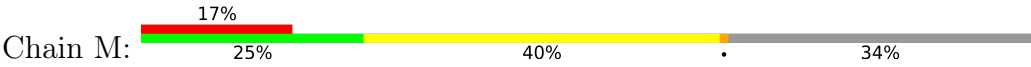
• Molecule 3: Vesicle-associated membrane protein 2



• Molecule 4: Syntaxin-1A



• Molecule 5: Synaptosomal-associated protein 25



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21489	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	-1800	Depositor
Maximum defocus (nm)	-2800	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	11.321	Depositor
Minimum map value	-4.152	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5	Depositor
Map size ($\text{\AA}$)	311.1936, 311.1936, 311.1936	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.4312, 2.4312, 2.4312	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.63	1/5120 (0.0%)	1.28	50/6930 (0.7%)
1	B	0.57	1/5091 (0.0%)	1.24	56/6887 (0.8%)
1	C	0.51	0/5104	1.13	32/6910 (0.5%)
1	D	0.57	1/5061 (0.0%)	1.20	43/6854 (0.6%)
1	E	0.63	3/5095 (0.1%)	1.26	52/6890 (0.8%)
1	F	0.57	0/5007	1.16	36/6767 (0.5%)
2	G	0.44	1/2295 (0.0%)	0.89	3/3086 (0.1%)
2	H	0.46	0/2295	0.93	4/3086 (0.1%)
2	I	0.44	0/2285	0.93	4/3074 (0.1%)
2	J	0.44	0/2295	0.91	5/3086 (0.2%)
3	K	0.28	0/497	0.77	0/665
4	L	0.27	0/541	0.72	0/723
5	M	0.27	0/1029	0.88	1/1369 (0.1%)
All	All	0.54	7/41715 (0.0%)	1.14	286/56327 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	E	0	2
1	F	0	1
2	J	0	1
All	All	0	6

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	547	SER	C-O	7.84	1.33	1.24
1	E	544	PRO	CA-C	6.45	1.55	1.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	232	ARG	CB-CG	-5.67	1.35	1.52
2	G	234	ALA	CA-CB	-5.60	1.45	1.53
1	D	545	PRO	CA-C	-5.48	1.44	1.52
1	A	330	ILE	CA-CB	5.42	1.61	1.54
1	E	231	PHE	CA-C	-5.15	1.46	1.52

All (286) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	287	GLY	CA-C-N	14.24	134.85	119.05
1	B	287	GLY	C-N-CA	14.24	134.85	119.05
1	A	236	ALA	N-CA-C	-13.40	96.73	111.07
1	B	544	PRO	N-CA-C	-11.45	99.47	110.47
1	F	396	GLY	N-CA-C	11.45	126.35	112.49
1	A	261	PRO	CA-C-N	10.66	133.16	119.84
1	A	261	PRO	C-N-CA	10.66	133.16	119.84
1	A	241	PRO	N-CA-C	10.46	123.47	110.70
1	D	416	GLY	N-CA-C	-10.15	100.21	112.49
1	D	547	SER	CA-C-N	-10.05	103.92	121.00
1	D	547	SER	C-N-CA	-10.05	103.92	121.00
1	F	241	PRO	N-CA-C	9.94	122.82	110.70
1	F	294	TYR	N-CA-C	9.86	122.10	111.36
1	C	543	GLY	CA-C-N	9.72	126.75	119.66
1	C	543	GLY	C-N-CA	9.72	126.75	119.66
1	E	231	PHE	N-CA-C	-9.68	100.72	111.07
1	D	544	PRO	CA-C-N	9.62	131.87	119.84
1	D	544	PRO	C-N-CA	9.62	131.87	119.84
1	E	413	ARG	N-CA-C	-9.54	100.88	111.28
1	C	413	ARG	N-CA-C	-9.44	101.00	111.28
1	E	316	LEU	N-CA-C	9.40	124.05	112.59
1	E	545	PRO	CA-C-O	-9.20	110.85	121.34
1	C	241	PRO	N-CA-C	9.19	121.91	110.70
1	B	241	PRO	N-CA-C	9.11	121.81	110.70
1	B	231	PHE	N-CA-C	-8.97	101.47	111.07
1	A	426	ILE	N-CA-C	8.77	118.84	110.42
1	A	216	GLU	N-CA-C	-8.71	96.56	109.62
1	B	493	GLY	N-CA-C	-8.69	103.92	115.21
1	A	273	ILE	N-CA-C	-8.58	102.46	110.53
1	F	416	GLY	N-CA-C	-8.57	102.56	112.50
1	E	315	ARG	N-CA-C	-8.26	102.28	111.28
1	A	238	ARG	N-CA-C	8.14	119.93	111.14
1	A	231	PHE	N-CA-C	-8.13	102.42	111.28

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	287	GLY	CA-C-N	8.09	128.03	119.05
1	E	287	GLY	C-N-CA	8.09	128.03	119.05
1	B	289	GLU	N-CA-C	-7.91	102.61	111.07
1	C	620	ASN	N-CA-C	7.84	119.83	111.28
1	E	241	PRO	N-CA-C	7.82	120.24	110.70
1	B	544	PRO	CB-CA-C	7.82	118.74	111.39
1	C	231	PHE	N-CA-C	-7.82	102.76	111.28
1	A	277	LEU	N-CA-C	7.81	119.88	111.36
1	B	530	ASN	N-CA-C	7.63	119.60	111.28
1	D	241	PRO	N-CA-C	7.58	119.95	110.70
1	C	632	LYS	N-CA-C	7.50	120.55	110.35
1	A	685	ASN	N-CA-C	7.45	119.48	111.36
1	B	498	ASP	N-CA-C	-7.41	103.20	111.28
1	A	694	ILE	N-CA-C	-7.41	103.24	110.72
1	E	295	VAL	N-CA-C	7.40	118.17	110.62
1	A	304	LYS	N-CA-C	7.36	118.94	111.07
1	D	316	LEU	CA-CB-CG	7.30	141.84	116.30
1	C	688	ASP	N-CA-C	7.29	118.87	111.07
1	B	416	GLY	N-CA-C	-7.26	103.71	112.49
1	D	312	GLU	CA-C-N	7.23	130.29	120.38
1	D	312	GLU	C-N-CA	7.23	130.29	120.38
1	A	499	TYR	N-CA-C	-7.18	102.26	111.02
1	E	294	TYR	N-CA-C	7.17	119.17	111.36
1	B	406	ILE	CB-CA-C	-7.16	102.33	112.22
1	C	691	ARG	N-CA-C	-7.15	103.49	111.28
1	D	512	ASP	N-CA-C	-7.09	103.09	113.16
1	D	316	LEU	CB-CA-C	-7.07	99.64	111.02
1	E	232	ARG	CB-CG-CD	-7.07	95.04	111.30
1	C	689	LYS	N-CA-C	7.05	118.62	111.07
1	E	603	ASP	N-CA-C	7.03	120.97	109.72
1	D	643	ILE	CB-CA-C	-7.02	100.24	110.63
1	E	314	ARG	N-CA-C	-7.00	103.65	111.28
1	B	543	GLY	N-CA-C	-6.97	98.12	112.34
1	A	625	ALA	N-CA-C	-6.96	103.69	111.28
1	E	649	LYS	N-CA-C	6.93	118.62	111.14
1	A	598	SER	N-CA-C	6.92	120.46	108.76
1	E	512	ASP	N-CA-C	-6.88	103.39	113.16
1	F	525	VAL	CB-CA-C	-6.85	103.21	111.97
1	B	479	ASP	N-CA-C	-6.84	91.86	111.00
1	F	563	PRO	N-CA-C	-6.76	104.34	113.40
1	B	651	VAL	CB-CA-C	-6.76	103.02	112.14
1	B	610	ASP	N-CA-CB	-6.75	101.94	112.13

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	312	GLU	N-CA-C	6.75	119.20	111.11
1	F	231	PHE	N-CA-C	-6.74	103.86	111.07
1	A	424	VAL	N-CA-C	6.72	117.70	109.30
1	F	295	VAL	N-CA-C	6.65	117.40	110.62
1	C	598	SER	N-CA-C	6.61	118.26	108.60
1	B	438	GLY	N-CA-C	6.58	128.78	113.18
1	B	484	LEU	N-CA-C	-6.57	104.12	111.28
1	E	248	MET	N-CA-C	6.57	118.44	111.28
1	A	260	GLY	CA-C-N	6.51	127.09	120.38
1	A	260	GLY	C-N-CA	6.51	127.09	120.38
1	F	598	SER	N-CA-C	6.50	118.73	108.79
1	C	387	GLY	N-CA-C	-6.49	97.79	113.18
1	C	726	VAL	N-CA-C	6.45	117.20	110.62
1	B	294	TYR	N-CA-C	6.44	118.38	111.36
1	E	670	ILE	CB-CA-C	-6.42	101.13	111.59
1	D	546	HIS	CA-C-N	-6.41	111.96	122.54
1	D	546	HIS	C-N-CA	-6.41	111.96	122.54
1	E	247	GLN	CA-C-N	6.41	128.86	120.28
1	E	247	GLN	C-N-CA	6.41	128.86	120.28
1	D	609	LEU	CA-C-N	6.38	131.41	122.36
1	D	609	LEU	C-N-CA	6.38	131.41	122.36
1	F	526	GLN	N-CA-C	-6.36	104.26	111.07
1	B	548	GLY	N-CA-C	-6.36	98.11	113.18
1	D	547	SER	N-CA-C	-6.34	105.18	113.17
1	C	406	ILE	CB-CA-C	-6.34	103.72	112.02
1	D	314	ARG	N-CA-C	-6.33	104.46	111.36
1	E	246	GLU	N-CA-C	-6.30	104.41	111.28
1	B	539	VAL	N-CA-C	6.29	117.19	108.12
1	D	647	SER	N-CA-C	6.29	118.14	111.28
2	G	159	SER	N-CA-C	6.23	118.62	111.02
1	F	514	VAL	N-CA-C	-6.22	104.45	110.42
1	A	480	PHE	N-CA-C	6.21	118.58	108.08
1	D	546	HIS	N-CA-C	-6.17	104.34	112.24
1	C	694	ILE	N-CA-C	-6.13	104.37	110.62
1	F	710	LEU	N-CA-C	-6.12	104.53	111.07
1	B	492	PHE	N-CA-C	-6.11	104.62	111.28
2	I	218	MET	CA-C-N	6.10	133.20	121.54
2	I	218	MET	C-N-CA	6.10	133.20	121.54
1	A	484	LEU	N-CA-C	-6.07	104.67	111.28
1	B	550	THR	N-CA-C	-6.07	104.75	111.36
1	E	235	PHE	N-CA-C	6.06	119.15	111.69
1	E	348	ASP	CB-CA-C	-6.06	109.60	116.63

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	453	MET	CB-CG-SD	6.06	130.88	112.70
1	A	258	LEU	CA-C-N	-6.05	114.46	122.99
1	A	258	LEU	C-N-CA	-6.05	114.46	122.99
1	A	530	ASN	N-CA-C	6.04	120.78	113.17
2	I	290	ASP	N-CA-C	-6.04	106.05	113.41
2	H	293	ASP	CA-C-O	-6.02	110.56	120.80
1	A	391	VAL	N-CA-C	6.01	116.53	108.11
1	E	585	MET	N-CA-C	-6.00	104.73	111.28
1	B	413	ARG	N-CA-C	-5.99	104.75	111.28
1	A	363	GLN	CB-CA-C	-5.98	109.69	116.63
1	E	416	GLY	N-CA-C	-5.98	105.25	112.49
1	E	438	GLY	N-CA-C	5.96	127.32	113.18
1	E	544	PRO	CA-C-O	-5.96	116.61	120.90
1	E	435	ASN	N-CA-C	5.95	117.85	111.36
1	E	299	GLU	N-CA-C	-5.94	104.81	111.28
1	E	718	LEU	N-CA-C	5.94	117.75	111.28
1	B	547	SER	O-C-N	5.92	130.46	122.59
2	J	234	ALA	N-CA-C	-5.91	103.45	111.55
1	B	299	GLU	N-CA-C	-5.89	104.86	111.28
1	C	363	GLN	CB-CA-C	-5.89	109.80	116.63
2	G	26	SER	CB-CA-C	-5.88	109.77	116.54
5	M	31	ARG	N-CA-C	-5.86	106.11	113.20
1	C	436	PHE	N-CA-C	5.82	118.67	110.23
1	F	348	ASP	CB-CA-C	-5.81	109.89	116.63
1	D	294	TYR	N-CA-C	5.79	119.44	112.38
1	B	348	ASP	CB-CA-C	-5.78	109.92	116.63
1	B	266	LYS	N-CA-C	-5.77	104.99	111.28
1	B	488	ILE	N-CA-C	5.77	120.98	113.07
1	D	352	ASN	N-CA-C	-5.76	105.00	111.28
1	A	407	LEU	N-CA-C	-5.76	105.00	111.28
1	D	363	GLN	CB-CA-C	-5.76	109.95	116.63
1	C	239	VAL	N-CA-C	5.75	116.53	110.72
1	D	642	ILE	N-CA-C	5.75	116.16	108.11
1	A	422	ALA	N-CA-C	-5.74	105.03	111.28
1	C	480	PHE	CB-CA-C	-5.71	110.00	116.63
1	F	529	LYS	N-CA-C	5.71	117.58	111.36
1	D	599	CYS	N-CA-C	5.71	117.71	108.41
1	A	235	PHE	CA-CB-CG	-5.70	108.10	113.80
1	C	234	ALA	N-CA-C	5.69	117.29	111.14
1	B	560	SER	N-CA-C	5.69	117.48	111.28
1	E	522	GLU	CA-CB-CG	5.69	125.48	114.10
1	B	574	ILE	N-CA-C	5.68	116.74	109.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	628	VAL	CB-CA-C	-5.68	104.70	111.97
1	F	363	GLN	CB-CA-C	-5.67	110.05	116.63
1	C	348	ASP	CB-CA-C	-5.67	110.05	116.63
1	E	240	PHE	CA-C-N	5.64	126.19	120.38
1	E	240	PHE	C-N-CA	5.64	126.19	120.38
1	E	363	GLN	CB-CA-C	-5.64	110.09	116.63
1	F	545	PRO	N-CA-C	5.63	119.85	111.41
1	A	691	ARG	CA-C-N	5.61	127.80	120.28
1	A	691	ARG	C-N-CA	5.61	127.80	120.28
1	A	279	ALA	N-CA-C	-5.58	100.87	109.52
1	E	629	LEU	N-CA-C	5.57	117.35	111.28
2	H	215	CYS	N-CA-C	-5.54	106.47	113.23
1	C	416	GLY	N-CA-C	-5.54	105.79	112.49
1	F	299	GLU	N-CA-C	-5.53	105.25	111.28
1	D	247	GLN	CA-C-N	5.53	127.69	120.28
1	D	247	GLN	C-N-CA	5.53	127.69	120.28
1	E	519	ASP	N-CA-CB	5.52	118.24	110.12
1	B	415	ARG	CA-C-N	5.52	125.95	119.94
1	B	415	ARG	C-N-CA	5.52	125.95	119.94
1	A	440	GLU	N-CA-C	-5.51	105.17	111.07
1	D	390	GLU	N-CA-C	5.51	117.29	111.28
1	C	230	ILE	CA-C-N	5.51	127.66	120.28
1	C	230	ILE	C-N-CA	5.51	127.66	120.28
1	B	240	PHE	CA-C-N	5.51	126.05	120.38
1	B	240	PHE	C-N-CA	5.51	126.05	120.38
1	F	227	PHE	N-CA-C	-5.50	105.28	111.28
1	A	330	ILE	N-CA-C	-5.50	105.01	110.62
1	A	455	ARG	N-CA-C	5.50	117.27	111.28
2	J	235	PHE	N-CA-C	5.50	122.51	110.80
1	A	719	GLN	N-CA-C	5.50	117.98	111.33
1	E	629	LEU	CB-CG-CD1	-5.49	94.24	110.70
1	A	227	PHE	N-CA-C	-5.47	105.31	111.28
1	B	363	GLN	CB-CA-C	-5.47	110.28	116.63
1	E	707	ILE	CB-CA-C	-5.46	104.78	112.14
1	B	455	ARG	CG-CD-NE	-5.44	100.03	112.00
1	A	273	ILE	N-CA-CB	5.43	117.52	110.57
2	I	201	SER	N-CA-C	5.42	118.68	111.75
1	B	544	PRO	CA-C-O	-5.41	117.00	120.90
1	C	388	ARG	N-CA-C	5.41	117.17	111.28
1	B	227	PHE	N-CA-C	-5.41	105.39	111.28
1	F	612	VAL	CA-C-N	-5.40	113.06	119.05
1	F	612	VAL	C-N-CA	-5.40	113.06	119.05

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	403	ARG	N-CA-C	-5.39	105.40	111.28
1	B	247	GLN	CA-C-N	5.38	127.48	120.28
1	B	247	GLN	C-N-CA	5.38	127.48	120.28
1	D	238	ARG	N-CA-C	5.36	117.20	111.36
1	D	276	MET	N-CA-C	5.35	117.19	111.36
1	B	295	VAL	N-CA-C	5.35	115.56	110.42
2	H	67	GLN	N-CA-C	-5.35	105.35	111.07
1	B	235	PHE	N-CA-C	5.34	118.26	111.69
2	J	235	PHE	N-CA-CB	-5.34	101.47	110.49
1	A	224	ASP	N-CA-C	5.31	117.07	111.28
1	B	544	PRO	O-C-N	5.29	123.74	121.31
1	F	232	ARG	N-CA-C	-5.29	105.41	111.07
1	D	316	LEU	N-CA-C	5.29	119.04	112.59
1	B	638	ARG	N-CA-C	5.27	118.04	109.24
1	B	543	GLY	CA-C-N	5.25	123.49	119.66
1	B	543	GLY	C-N-CA	5.25	123.49	119.66
1	E	480	PHE	CB-CA-C	-5.24	110.55	116.63
1	F	518	LEU	CD1-CG-CD2	-5.24	99.26	110.80
1	D	598	SER	N-CA-C	5.24	117.22	108.99
1	D	233	ARG	N-CA-C	5.24	118.14	111.69
1	E	629	LEU	CB-CA-C	-5.24	102.09	110.79
1	A	349	THR	N-CA-C	5.23	116.98	111.28
1	F	524	LEU	N-CA-C	-5.23	105.58	111.28
1	A	453	MET	N-CA-C	-5.22	105.59	111.28
1	E	706	GLY	N-CA-C	5.22	118.87	112.14
1	A	255	GLY	N-CA-C	5.21	118.87	110.90
1	E	594	LYS	N-CA-C	5.20	116.95	111.28
1	B	709	LYS	N-CA-C	-5.20	105.61	111.28
1	D	443	GLY	N-CA-C	-5.20	106.49	112.73
1	A	293	LYS	CA-C-N	5.19	131.46	121.54
1	A	293	LYS	C-N-CA	5.19	131.46	121.54
1	F	518	LEU	CB-CG-CD1	-5.19	95.12	110.70
1	E	277	LEU	N-CA-C	5.19	116.94	111.28
1	F	407	LEU	N-CA-C	-5.19	105.62	111.28
1	C	312	GLU	N-CA-C	-5.19	105.52	111.07
1	E	489	LYS	N-CA-C	5.17	121.24	109.81
2	G	197	LEU	CA-CB-CG	5.17	134.39	116.30
1	A	544	PRO	CA-C-N	-5.17	114.44	119.76
1	A	544	PRO	C-N-CA	-5.17	114.44	119.76
1	E	296	GLY	CA-C-N	5.17	131.00	121.70
1	E	296	GLY	C-N-CA	5.17	131.00	121.70
1	A	354	LEU	N-CA-C	-5.16	105.55	111.07

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	619	SER	N-CA-C	5.16	117.14	108.73
1	F	246	GLU	N-CA-C	-5.16	105.66	111.28
1	A	424	VAL	CB-CA-C	-5.15	103.66	111.33
1	B	574	ILE	CB-CA-C	-5.15	103.58	111.71
1	F	500	ALA	N-CA-C	5.14	116.97	111.36
1	B	521	GLY	N-CA-C	-5.13	106.58	112.73
1	F	709	LYS	N-CA-C	-5.12	105.82	111.71
1	E	640	LEU	N-CA-C	5.11	117.02	108.99
1	B	518	LEU	N-CA-C	5.11	116.85	111.28
1	F	533	ARG	N-CA-C	5.11	116.85	111.28
1	A	503	ILE	N-CA-C	-5.10	105.57	110.72
1	C	544	PRO	CA-C-O	-5.10	117.23	120.90
1	E	714	ILE	CB-CA-C	-5.10	105.44	111.97
1	F	296	GLY	CA-C-N	5.10	130.88	121.70
1	F	296	GLY	C-N-CA	5.10	130.88	121.70
1	C	447	ALA	N-CA-C	-5.09	105.81	111.36
1	B	436	PHE	CA-C-N	5.09	130.24	120.97
1	B	436	PHE	C-N-CA	5.09	130.24	120.97
1	C	385	ARG	CG-CD-NE	-5.09	100.80	112.00
1	E	570	PRO	N-CA-C	-5.09	106.45	113.53
1	D	414	MET	CA-C-N	5.08	127.51	120.29
1	D	414	MET	C-N-CA	5.08	127.51	120.29
1	D	379	ILE	N-CA-C	5.08	115.95	110.21
1	D	415	ARG	CA-C-N	5.07	125.47	119.94
1	D	415	ARG	C-N-CA	5.07	125.47	119.94
1	B	296	GLY	CA-C-N	5.07	130.82	121.70
1	B	296	GLY	C-N-CA	5.07	130.82	121.70
1	A	488	ILE	N-CA-C	5.06	118.62	112.80
1	F	562	PHE	CA-C-N	5.06	124.36	118.85
1	F	562	PHE	C-N-CA	5.06	124.36	118.85
1	C	556	ILE	N-CA-C	-5.05	105.57	110.42
1	D	354	LEU	N-CA-C	-5.05	105.77	111.28
2	H	223	LEU	N-CA-C	-5.04	106.30	112.90
1	E	727	ARG	N-CA-C	-5.03	105.50	111.69
1	E	643	ILE	CA-C-N	-5.03	118.66	122.33
1	E	643	ILE	C-N-CA	-5.03	118.66	122.33
1	F	235	PHE	N-CA-C	5.03	116.84	111.36
1	B	406	ILE	N-CA-CB	5.03	118.12	110.58
2	J	234	ALA	CA-C-N	5.02	131.13	121.54
2	J	234	ALA	C-N-CA	5.02	131.13	121.54
1	C	296	GLY	CA-C-N	5.01	130.72	121.70
1	C	296	GLY	C-N-CA	5.01	130.72	121.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	705	ILE	N-CA-C	5.01	115.86	108.45

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	PRO	Peptide
1	B	438	GLY	Peptide
1	E	315	ARG	Mainchain
1	E	438	GLY	Peptide
1	F	438	GLY	Peptide
2	J	233	PRO	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	5044	0	4963	361	0
1	B	5015	0	4953	311	0
1	C	5028	0	4939	353	0
1	D	4986	0	4905	358	0
1	E	5020	0	4974	397	0
1	F	4932	0	4914	343	0
2	G	2255	0	2199	136	0
2	H	2255	0	2199	145	0
2	I	2246	0	2185	114	0
2	J	2255	0	2199	138	0
3	K	494	0	488	84	0
4	L	536	0	527	76	0
5	M	1029	0	996	148	0
All	All	41095	0	40441	2627	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 32.

All (2627) 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)
1:F:518:LEU:HD23	1:F:555:LYS:HG2	1.21	1.10
2:H:219:LEU:HB2	2:H:222:LYS:HB3	1.34	1.08
2:I:201:SER:HA	3:K:47:ARG:HH12	1.11	1.08
1:E:593:TYR:O	1:E:638:ARG:NH1	1.90	1.04
1:B:264:CYS:HA	1:B:437:SER:HB2	1.38	1.04
1:B:240:PHE:HD2	1:B:244:ILE:HG21	1.22	1.03
3:K:43:VAL:HA	4:L:212:LEU:HD13	1.36	1.03
2:J:201:SER:HG	2:J:205:TYR:HE1	1.05	1.02
1:C:507:ILE:CD1	1:C:555:LYS:HG2	1.87	1.02
1:B:258:LEU:HB3	1:B:395:ILE:HD11	1.37	1.01
1:E:528:THR:HG21	1:E:641:LEU:HD23	1.41	0.99
5:M:203:LEU:HD23	5:M:204:GLY:H	1.25	0.99
1:A:424:VAL:HG13	1:A:482:ALA:HB2	1.44	0.99
1:A:685:ASN:OD1	1:F:533:ARG:NH1	1.97	0.98
3:K:53:VAL:HG22	4:L:226:GLN:HE22	1.26	0.98
1:C:327:PHE:HB3	1:C:330:ILE:HD11	1.42	0.98
1:C:257:LEU:HB2	1:C:389:LEU:HD13	1.44	0.97
2:J:159:SER:HB2	5:M:169:ASN:HB3	1.46	0.97
1:E:596:GLN:HA	1:E:638:ARG:HG2	1.46	0.97
1:C:507:ILE:HD11	1:C:555:LYS:HB2	1.42	0.96
1:E:540:LEU:HD11	1:E:646:THR:HG22	1.45	0.96
1:A:715:GLU:HG3	1:F:527:GLN:HE21	1.30	0.96
2:G:219:LEU:HB2	2:G:222:LYS:HB3	1.47	0.95
1:A:331:ASP:HA	1:A:379:ILE:HD11	1.46	0.95
1:E:232:ARG:HH22	1:F:451:THR:HA	1.28	0.95
1:D:628:VAL:HG11	1:E:574:ILE:HG21	1.49	0.95
1:C:507:ILE:CD1	1:C:555:LYS:CG	2.45	0.94
1:E:232:ARG:HE	1:F:454:ASN:HB2	1.29	0.94
1:E:528:THR:HG22	1:E:537:VAL:HG21	1.50	0.94
3:K:83:LYS:HD3	5:M:203:LEU:HD11	1.49	0.94
1:D:509:LYS:HG2	1:D:515:THR:HG23	1.47	0.93
1:C:618:PHE:HE2	1:D:614:ILE:HD11	1.31	0.92
1:D:406:ILE:HG22	1:D:441:LEU:HD22	1.48	0.92
1:F:521:GLY:HA2	1:F:524:LEU:HD12	1.49	0.92
1:A:569:SER:OG	1:A:571:ASP:OD1	1.86	0.92
1:D:256:ILE:HG13	1:D:370:ILE:HG22	1.51	0.92
1:A:264:CYS:SG	1:A:265:GLY:N	2.41	0.91
1:C:240:PHE:HD2	1:C:244:ILE:HG21	1.34	0.91
3:K:36:GLN:HA	4:L:205:LEU:HD13	1.52	0.91
2:J:201:SER:HB2	5:M:165:LEU:HD11	1.53	0.91
1:A:497:GLU:O	1:A:499:TYR:N	2.04	0.91
1:C:490:PRO:HA	1:C:491:ALA:HB3	1.52	0.91

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:72:HIS:CE1	2:G:80:ASP:HB2	2.07	0.90
1:B:327:PHE:HB2	1:B:330:ILE:HG22	1.54	0.89
1:D:240:PHE:HD2	1:D:244:ILE:HG21	1.37	0.89
2:J:219:LEU:HB2	2:J:222:LYS:HB3	1.54	0.89
1:A:295:VAL:HB	1:B:294:TYR:HB2	1.55	0.89
5:M:73:GLU:HG3	5:M:77:ASN:HD21	1.36	0.88
2:G:218:MET:HG2	2:G:219:LEU:H	1.36	0.88
2:H:218:MET:HG2	2:H:219:LEU:H	1.35	0.88
1:B:266:LYS:HG2	1:B:395:ILE:HG12	1.52	0.87
1:A:542:GLU:HG2	1:A:649:LYS:HD2	1.56	0.87
1:A:502:TYR:HE2	1:A:567:ILE:HG21	1.40	0.87
1:A:562:PHE:CD2	1:A:597:LEU:HD21	2.09	0.86
1:F:327:PHE:HB2	1:F:330:ILE:HG22	1.55	0.86
1:B:95:MET:HE3	1:B:97:ILE:HD11	1.57	0.86
1:B:566:LYS:HD2	1:B:588:ILE:HG23	1.57	0.86
1:E:625:ALA:HA	1:F:574:ILE:HD11	1.55	0.86
1:C:507:ILE:HD11	1:C:555:LYS:CB	2.03	0.86
1:D:313:GLN:HE22	1:D:364:LEU:HA	1.40	0.86
1:C:497:GLU:O	1:C:499:TYR:N	2.07	0.86
1:E:256:ILE:HG13	1:E:370:ILE:HG22	1.56	0.86
1:E:327:PHE:HB2	1:E:330:ILE:HG22	1.55	0.86
1:F:545:PRO:HA	1:F:547:SER:H	1.39	0.86
1:A:421:SER:HB3	1:A:424:VAL:HG23	1.56	0.86
1:D:606:GLU:HA	1:D:609:LEU:HG	1.57	0.85
1:F:538:SER:HB3	1:F:662:SER:H	1.40	0.85
5:M:40:LYS:HD3	5:M:156:ILE:HG23	1.58	0.85
1:C:386:PRO:HA	1:C:390:GLU:HA	1.57	0.85
3:K:43:VAL:HG22	4:L:212:LEU:HB2	1.59	0.85
1:E:64:LEU:HA	1:E:67:ARG:HE	1.39	0.84
1:F:538:SER:HG	1:F:661:PHE:HD1	1.23	0.84
2:G:38:ILE:HD11	2:G:71:LEU:HB3	1.57	0.84
1:F:539:VAL:HB	1:F:643:ILE:HG12	1.60	0.84
1:A:305:LEU:HD23	1:A:325:ILE:HG21	1.58	0.84
1:E:232:ARG:HH22	1:F:451:THR:CA	1.89	0.84
1:E:490:PRO:HA	1:E:491:ALA:HB3	1.59	0.84
1:E:618:PHE:HZ	1:F:612:VAL:HG11	1.39	0.83
1:D:510:TRP:CD2	1:D:670:ILE:HG22	2.14	0.83
1:F:525:VAL:HG13	1:F:562:PHE:CE1	2.12	0.83
1:A:705:ILE:HD13	1:A:710:LEU:HD12	1.60	0.83
1:E:720:MET:HG3	1:E:728:LYS:HE3	1.60	0.83
1:B:64:LEU:HB2	2:H:293:ASP:O	1.78	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:ILE:HG13	1:B:370:ILE:HG22	1.59	0.83
1:D:510:TRP:HE3	1:D:675:GLN:HG2	1.44	0.83
1:C:687:LYS:N	1:C:690:GLU:OE2	2.11	0.83
1:E:585:MET:HG3	1:E:589:PHE:CZ	2.13	0.83
1:E:527:GLN:O	1:E:531:SER:OG	1.95	0.83
1:F:256:ILE:HG13	1:F:370:ILE:HG22	1.58	0.83
2:J:200:TYR:OH	3:K:41:GLU:O	1.96	0.83
2:I:201:SER:CA	3:K:47:ARG:HH12	1.91	0.82
1:C:256:ILE:HG13	1:C:370:ILE:HG22	1.58	0.82
2:J:271:ARG:NH2	2:G:234:ALA:HB2	1.94	0.82
1:A:686:PHE:HE2	1:A:714:ILE:HG12	1.43	0.82
2:I:38:ILE:HG23	2:I:75:LEU:HD12	1.61	0.82
1:A:624:GLN:HG3	1:B:610:ASP:OD2	1.80	0.82
1:F:544:PRO:O	1:F:547:SER:OG	1.96	0.82
2:J:235:PHE:HB3	3:K:38:GLN:HG2	1.62	0.82
2:G:232:PHE:HB2	2:G:233:PRO:HD3	1.59	0.82
1:B:490:PRO:HA	1:B:491:ALA:HB3	1.62	0.82
2:J:228:TYR:OH	2:J:237:ASP:OD1	1.98	0.81
1:A:428:GLU:HG2	1:A:479:ASP:HA	1.62	0.81
1:B:111:PRO:HB2	1:B:196:ILE:HD13	1.61	0.81
1:B:10:ARG:HE	2:H:293:ASP:CG	1.89	0.81
1:E:232:ARG:NE	1:F:454:ASN:HB2	1.95	0.81
1:F:555:LYS:NZ	1:F:559:GLU:OE2	2.11	0.81
1:C:627:LEU:HD12	1:D:607:ARG:HH12	1.46	0.81
1:F:536:LEU:HD11	1:F:634:PRO:HD3	1.61	0.81
1:D:518:LEU:HD21	1:D:552:LEU:HD22	1.63	0.81
2:I:201:SER:HA	3:K:47:ARG:NH1	1.95	0.81
2:J:218:MET:HG2	2:J:219:LEU:H	1.44	0.81
1:A:285:VAL:HG13	1:A:326:ILE:HD11	1.63	0.80
1:F:386:PRO:HA	1:F:390:GLU:HA	1.63	0.80
1:A:713:LEU:HD21	1:A:732:LEU:HB3	1.63	0.80
3:K:48:VAL:HG12	3:K:52:LYS:HE3	1.61	0.80
1:A:557:ALA:O	1:A:560:SER:OG	1.99	0.80
1:E:549:LYS:HA	1:E:552:LEU:HD12	1.62	0.80
1:C:676:LEU:HD12	1:C:705:ILE:HG21	1.64	0.80
1:F:538:SER:H	1:F:662:SER:HB3	1.45	0.80
2:J:235:PHE:HE2	3:K:37:ALA:HB3	1.42	0.80
1:C:313:GLN:O	1:C:317:GLY:N	2.15	0.80
1:E:586:LYS:NZ	1:F:574:ILE:O	2.14	0.80
1:E:589:PHE:CZ	1:E:629:LEU:HD11	2.16	0.80
1:C:618:PHE:CE2	1:D:614:ILE:HD11	2.16	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:568:CYS:SG	1:D:585:MET:HE1	2.21	0.79
1:E:386:PRO:HA	1:E:390:GLU:HA	1.63	0.79
1:B:526:GLN:HE21	1:C:719:GLN:HB3	1.47	0.79
1:E:95:MET:HE3	1:E:97:ILE:HD11	1.65	0.79
1:E:627:LEU:HG	1:E:657:MET:HE1	1.63	0.79
1:C:98:GLU:HB3	1:C:148:LEU:HB3	1.65	0.79
1:C:407:LEU:HD11	1:C:426:ILE:HG23	1.64	0.79
1:E:190:ASN:HD21	1:E:316:LEU:HG	1.49	0.78
1:E:563:PRO:HG2	1:E:595:SER:OG	1.83	0.78
1:A:562:PHE:HD2	1:A:597:LEU:HD21	1.46	0.78
2:J:235:PHE:CB	3:K:38:GLN:HG2	2.12	0.78
1:A:490:PRO:HA	1:A:491:ALA:HB3	1.65	0.78
1:E:686:PHE:HE1	1:E:714:ILE:HG23	1.49	0.78
1:E:526:GLN:NE2	1:F:719:GLN:O	2.17	0.78
1:D:654:GLU:HB3	1:E:614:ILE:HD11	1.66	0.78
1:E:510:TRP:HE1	1:E:707:ILE:HD11	1.48	0.78
1:B:111:PRO:HD3	1:B:316:LEU:HG	1.66	0.78
2:J:201:SER:HB2	5:M:165:LEU:CD1	2.14	0.78
1:D:720:MET:HE3	1:D:724:TYR:HE1	1.47	0.78
1:D:353:GLN:HE22	1:E:288:PRO:HG2	1.47	0.78
1:A:502:TYR:CE2	1:A:567:ILE:HG21	2.19	0.77
1:B:386:PRO:HA	1:B:390:GLU:HA	1.64	0.77
1:C:652:LEU:HD22	1:C:657:MET:HG2	1.66	0.77
1:A:67:ARG:HD2	2:H:218:MET:HG3	1.64	0.77
1:A:525:VAL:HG13	1:A:562:PHE:CZ	2.20	0.77
3:K:39:VAL:HG11	4:L:209:ILE:HD13	1.66	0.77
2:H:289:GLY:O	2:H:293:ASP:HB2	1.84	0.77
1:C:690:GLU:HB2	1:C:726:VAL:HG21	1.66	0.77
1:F:407:LEU:HD11	1:F:426:ILE:HG23	1.66	0.77
1:E:587:LYS:O	1:E:587:LYS:NZ	2.15	0.77
1:D:240:PHE:CD2	1:D:244:ILE:HG21	2.19	0.77
1:E:234:ALA:HA	1:F:446:ARG:NH2	1.99	0.77
1:B:589:PHE:HE1	1:B:600:VAL:HG11	1.49	0.77
1:C:540:LEU:HB3	1:C:664:THR:HG22	1.64	0.77
1:C:691:ARG:HA	1:C:694:ILE:HD12	1.67	0.77
1:A:48:THR:HG21	1:A:128:GLN:HG2	1.66	0.77
1:E:653:GLN:HA	1:E:658:LEU:HB2	1.66	0.76
1:B:540:LEU:HD23	1:B:661:PHE:CD1	2.21	0.76
1:C:544:PRO:O	1:C:547:SER:OG	2.01	0.76
1:B:581:LYS:NZ	1:B:608:LEU:O	2.18	0.76
1:C:40:SER:HB2	1:C:41:PRO:HD2	1.65	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:549:LYS:NZ	1:A:647:SER:OG	2.16	0.76
1:C:496:GLN:O	1:C:498:ASP:N	2.18	0.76
1:C:507:ILE:HD12	1:C:555:LYS:CD	2.16	0.76
1:E:407:LEU:HD11	1:E:426:ILE:HG23	1.66	0.76
1:E:190:ASN:OD1	1:E:315:ARG:C	2.29	0.76
1:F:240:PHE:CD2	1:F:244:ILE:HG21	2.20	0.76
1:F:570:PRO:HG2	1:F:604:ASP:HB2	1.68	0.76
5:M:61:GLU:HG2	5:M:65:ASN:HD21	1.50	0.76
1:A:95:MET:HE3	1:A:97:ILE:HD11	1.67	0.75
1:E:585:MET:HA	1:E:588:ILE:HD12	1.68	0.75
1:F:564:PHE:O	1:F:598:SER:OG	2.04	0.75
1:F:569:SER:OG	1:F:571:ASP:OD2	2.04	0.75
1:A:453:MET:O	1:F:232:ARG:NH2	2.19	0.75
1:D:310:GLU:O	1:D:313:GLN:HG2	1.86	0.75
1:E:311:GLU:OE1	1:E:314:ARG:NE	2.19	0.75
1:A:626:LEU:HD21	1:A:657:MET:HE1	1.67	0.75
2:G:72:HIS:HE1	2:G:80:ASP:HB2	1.51	0.75
2:G:21:VAL:HG21	2:G:71:LEU:HD22	1.68	0.75
1:D:728:LYS:HE3	1:D:732:LEU:HD11	1.67	0.75
1:B:240:PHE:CD2	1:B:244:ILE:HG21	2.15	0.75
1:E:313:GLN:O	1:E:317:GLY:N	2.20	0.75
4:L:209:ILE:HG21	5:M:32:MET:HG3	1.69	0.75
1:A:677:LEU:HD21	1:A:695:ALA:HA	1.68	0.74
1:A:397:LEU:HB3	1:A:398:PRO:CD	2.17	0.74
1:C:507:ILE:HD12	1:C:555:LYS:HG2	1.69	0.74
1:F:12:PRO:HG2	1:F:23:VAL:HG11	1.69	0.74
1:F:95:MET:HE3	1:F:97:ILE:HD11	1.70	0.74
1:E:300:ALA:O	1:E:304:LYS:HG2	1.87	0.74
1:A:553:ALA:HA	1:A:556:ILE:HD12	1.68	0.74
1:A:262:PRO:HG2	1:A:374:ASN:OD1	1.87	0.74
1:D:95:MET:HE3	1:D:97:ILE:HD11	1.69	0.74
1:E:349:THR:HA	1:E:352:ASN:HD22	1.52	0.74
1:C:578:GLU:HB3	1:C:621:LEU:HB3	1.67	0.74
5:M:31:ARG:O	5:M:35:LEU:HG	1.88	0.74
1:B:524:LEU:HD21	1:B:663:THR:HG21	1.69	0.74
1:C:630:LEU:HD11	1:C:661:PHE:CE1	2.23	0.74
1:C:724:TYR:HD2	1:C:727:ARG:HH21	1.35	0.74
1:E:686:PHE:HB3	1:E:690:GLU:HB2	1.69	0.74
2:G:228:TYR:OH	2:G:237:ASP:OD1	2.05	0.74
1:F:397:LEU:HD22	1:F:398:PRO:HD3	1.69	0.73
1:A:352:ASN:HB3	1:B:288:PRO:HB2	1.68	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:301:ASN:HA	1:D:304:LYS:HD3	1.70	0.73
1:C:318:ALA:O	1:C:319:ASN:ND2	2.21	0.73
1:C:513:PRO:O	1:C:516:ARG:HG2	1.88	0.73
1:B:300:ALA:O	1:B:304:LYS:HG2	1.88	0.73
1:E:106:ASN:HB3	1:E:143:LYS:NZ	2.03	0.73
1:B:621:LEU:HD11	1:C:575:GLY:HA2	1.70	0.73
1:A:67:ARG:NH1	2:H:217:ASP:O	2.20	0.73
1:F:73:SER:O	1:F:76:GLN:HG2	1.89	0.73
1:D:399:ASP:O	1:D:403:ARG:N	2.22	0.73
1:F:536:LEU:HD21	1:F:632:LYS:O	1.89	0.73
1:F:609:LEU:HD13	1:F:655:MET:HE1	1.70	0.73
1:F:634:PRO:HB2	1:F:638:ARG:HG3	1.68	0.73
1:E:670:ILE:HG22	1:E:672:THR:H	1.54	0.72
1:F:300:ALA:O	1:F:304:LYS:HG2	1.87	0.72
1:D:46:ILE:HD12	1:D:174:VAL:HG21	1.71	0.72
1:E:553:ALA:HA	1:E:556:ILE:HD12	1.72	0.72
1:B:187:LYS:HB2	1:B:191:SER:HB3	1.70	0.72
1:B:585:MET:HE1	1:B:626:LEU:HG	1.71	0.72
1:B:533:ARG:HG3	1:B:534:THR:H	1.54	0.72
1:E:538:SER:OG	1:E:661:PHE:HA	1.90	0.72
2:H:94:LYS:HE3	2:I:153:LYS:HG3	1.70	0.72
1:B:407:LEU:HD11	1:B:426:ILE:HG23	1.71	0.72
1:B:563:PRO:HD2	1:B:597:LEU:HB2	1.69	0.72
1:C:236:ALA:HB1	1:D:453:MET:HB3	1.72	0.72
1:C:596:GLN:HA	1:C:638:ARG:HD3	1.72	0.72
1:A:10:ARG:HB2	2:H:217:ASP:OD2	1.90	0.72
1:E:236:ALA:HB1	1:F:453:MET:HG3	1.72	0.72
1:D:98:GLU:HB3	1:D:148:LEU:HB3	1.72	0.71
1:D:544:PRO:O	1:D:547:SER:HB3	1.90	0.71
1:B:496:GLN:O	1:B:498:ASP:N	2.22	0.71
1:D:513:PRO:HA	1:D:516:ARG:HG2	1.72	0.71
1:A:417:HIS:ND1	1:F:246:GLU:O	2.23	0.71
1:A:602:VAL:HG12	1:A:605:ILE:HG12	1.73	0.71
1:E:303:ARG:HG3	1:E:357:LYS:HE2	1.72	0.71
1:C:507:ILE:HD11	1:C:555:LYS:CG	2.17	0.71
1:F:517:VAL:HG13	1:F:665:ILE:HG21	1.72	0.71
5:M:36:VAL:HG21	5:M:153:VAL:HG13	1.72	0.71
1:A:258:LEU:HA	1:A:393:MET:O	1.90	0.71
1:F:311:GLU:OE1	1:F:314:ARG:NE	2.24	0.71
1:A:309:ALA:HB1	1:A:367:ILE:HG21	1.73	0.71
1:B:538:SER:HB3	1:B:661:PHE:HD2	1.55	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:105:LYS:HZ3	2:I:291:GLU:HB3	1.55	0.71
1:E:9:ALA:HA	1:E:74:ILE:HG23	1.72	0.71
1:E:680:LEU:HD13	1:E:694:ILE:HD13	1.70	0.71
1:D:310:GLU:O	1:D:313:GLN:CG	2.39	0.71
1:D:605:ILE:HD11	1:D:644:GLY:HA3	1.72	0.71
2:H:93:LYS:NZ	2:I:156:GLU:OE2	2.21	0.71
1:D:711:LEU:HA	1:D:714:ILE:HD12	1.72	0.71
1:B:627:LEU:HD21	1:B:657:MET:HG3	1.73	0.70
1:B:249:GLY:HA3	1:C:414:MET:HE3	1.72	0.70
1:B:361:VAL:O	1:C:271:ARG:HD2	1.91	0.70
1:C:564:PHE:O	1:C:598:SER:OG	2.07	0.70
1:B:624:GLN:NE2	1:C:610:ASP:O	2.24	0.70
1:C:611:TYR:CE1	1:C:616:PRO:HB2	2.26	0.70
3:K:39:VAL:O	3:K:43:VAL:HG23	1.91	0.70
1:A:423:ASP:HB3	1:A:480:PHE:CB	2.22	0.70
1:C:236:ALA:HB1	1:D:453:MET:CB	2.21	0.70
1:E:527:GLN:HE22	1:F:716:MET:HG2	1.57	0.70
1:D:620:ASN:O	1:D:624:GLN:HG2	1.91	0.70
1:E:190:ASN:OD1	1:E:315:ARG:O	2.09	0.70
1:E:513:PRO:HA	1:E:516:ARG:HG2	1.74	0.70
2:I:51:MET:HA	2:I:54:MET:HG2	1.74	0.70
1:A:562:PHE:HD2	1:A:597:LEU:CD2	2.05	0.70
1:E:589:PHE:CD2	1:E:629:LEU:HD21	2.26	0.70
1:D:10:ARG:NH2	2:I:293:ASP:OD1	2.24	0.70
2:J:213:HIS:HE1	2:J:221:ALA:HB2	1.55	0.70
1:A:503:ILE:O	1:A:505:ASN:N	2.25	0.70
1:E:190:ASN:HD21	1:E:316:LEU:CG	2.03	0.70
1:E:232:ARG:HH21	1:F:454:ASN:HB3	1.56	0.70
1:F:713:LEU:HD22	1:F:732:LEU:HB3	1.74	0.70
2:J:235:PHE:HD1	3:K:34:GLN:NE2	1.89	0.70
1:A:125:PHE:HA	1:A:128:GLN:NE2	2.06	0.70
1:A:353:GLN:HE21	1:A:357:LYS:HG2	1.57	0.70
1:C:240:PHE:CD2	1:C:244:ILE:HG21	2.24	0.70
1:F:535:PRO:HA	1:F:639:LYS:HG2	1.74	0.70
1:F:125:PHE:HA	1:F:128:GLN:NE2	2.06	0.69
5:M:152:GLN:O	5:M:156:ILE:HG13	1.91	0.69
1:C:125:PHE:HA	1:C:128:GLN:NE2	2.07	0.69
1:D:353:GLN:HE22	1:E:288:PRO:CG	2.04	0.69
1:F:606:GLU:OE1	1:F:606:GLU:N	2.22	0.69
2:J:235:PHE:CE2	3:K:37:ALA:HB3	2.25	0.69
1:A:231:PHE:CD1	1:A:235:PHE:HE2	2.10	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:718:LEU:O	1:C:725:ARG:NH1	2.26	0.69
1:E:606:GLU:OE2	1:E:646:THR:OG1	2.09	0.69
1:E:234:ALA:HA	1:F:446:ARG:HH21	1.57	0.69
1:F:721:ASP:HB2	1:F:724:TYR:HD1	1.57	0.69
1:C:331:ASP:HA	1:C:379:ILE:HD11	1.75	0.69
1:E:232:ARG:NH2	1:F:450:SER:O	2.25	0.69
1:F:545:PRO:HA	1:F:547:SER:N	2.05	0.69
1:B:125:PHE:HA	1:B:128:GLN:NE2	2.08	0.69
1:C:247:GLN:HA	1:D:417:HIS:CD2	2.26	0.69
1:D:230:ILE:HD11	1:D:256:ILE:HD13	1.73	0.69
1:D:245:VAL:O	1:D:249:GLY:N	2.26	0.69
1:D:386:PRO:HA	1:D:390:GLU:HA	1.74	0.69
1:E:592:ALA:HB1	1:E:640:LEU:HD22	1.73	0.69
1:F:670:ILE:HG23	1:F:675:GLN:HB2	1.74	0.69
4:L:205:LEU:O	4:L:209:ILE:HG12	1.93	0.69
5:M:179:ASP:HA	5:M:182:MET:HE3	1.75	0.69
2:I:116:ARG:NH2	5:M:183:GLU:OE1	2.25	0.69
1:B:538:SER:HB3	1:B:661:PHE:CD2	2.28	0.69
1:E:604:ASP:HB3	1:E:607:ARG:HB3	1.74	0.69
1:B:303:ARG:HG3	1:B:357:LYS:HE2	1.74	0.68
1:B:489:LYS:O	1:B:491:ALA:HB3	1.94	0.68
1:C:507:ILE:HD12	1:C:555:LYS:CG	2.20	0.68
1:F:589:PHE:HD2	1:F:629:LEU:HD13	1.57	0.68
1:D:125:PHE:HA	1:D:128:GLN:NE2	2.07	0.68
1:F:303:ARG:HG3	1:F:357:LYS:HE2	1.74	0.68
1:A:453:MET:C	1:F:232:ARG:HH22	2.01	0.68
1:E:640:LEU:HD12	1:E:641:LEU:N	2.09	0.68
1:A:564:PHE:CE1	1:A:566:LYS:HB2	2.28	0.68
1:C:358:ILE:CB	1:C:388:ARG:HG3	2.23	0.68
1:D:539:VAL:HG23	1:D:663:THR:HG23	1.75	0.68
2:I:228:TYR:OH	2:I:237:ASP:OD1	2.09	0.68
1:F:358:ILE:HD12	1:F:388:ARG:HB3	1.75	0.68
5:M:73:GLU:HG3	5:M:77:ASN:ND2	2.09	0.68
1:A:351:VAL:O	1:A:355:LEU:HG	1.93	0.68
1:A:521:GLY:O	1:A:525:VAL:HG23	1.94	0.68
1:D:543:GLY:H	1:D:549:LYS:HD3	1.59	0.68
1:E:685:ASN:HB3	1:E:718:LEU:HD11	1.74	0.68
1:B:311:GLU:OE1	1:B:314:ARG:NE	2.26	0.68
1:C:533:ARG:O	1:D:505:ASN:ND2	2.27	0.68
1:E:358:ILE:HD12	1:E:388:ARG:HB3	1.75	0.68
1:F:550:THR:HA	1:F:645:THR:HG21	1.76	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:42:VAL:HG13	3:K:45:ILE:HD11	1.76	0.68
1:C:649:LYS:HE2	1:C:658:LEU:HD13	1.75	0.68
2:J:50:ASN:HD21	2:G:115:GLY:CA	2.05	0.67
1:C:95:MET:HE3	1:C:97:ILE:HD11	1.76	0.67
1:D:527:GLN:NE2	1:E:715:GLU:O	2.27	0.67
1:E:246:GLU:HG3	1:F:417:HIS:HE1	1.59	0.67
1:A:326:ILE:HG22	1:A:370:ILE:HG12	1.74	0.67
1:B:295:VAL:C	1:C:294:TYR:HB2	2.19	0.67
5:M:170:GLU:HG3	5:M:174:GLN:NE2	2.09	0.67
1:A:612:VAL:HG11	1:F:618:PHE:HZ	1.59	0.67
1:E:510:TRP:CZ3	1:E:670:ILE:HG13	2.29	0.67
3:K:34:GLN:O	3:K:38:GLN:HG3	1.94	0.67
1:C:64:LEU:HB3	1:C:65:PRO:HD3	1.75	0.67
1:B:358:ILE:HD12	1:B:388:ARG:HB3	1.76	0.67
1:A:683:LEU:HB3	1:A:685:ASN:ND2	2.09	0.67
1:E:525:VAL:O	1:E:528:THR:OG1	2.11	0.67
1:D:407:LEU:HG	1:D:441:LEU:HD11	1.76	0.67
1:F:518:LEU:H	1:F:518:LEU:HD12	1.59	0.67
1:A:247:GLN:O	1:B:413:ARG:NH1	2.28	0.67
1:B:240:PHE:CE1	1:C:457:ILE:HD11	2.29	0.67
2:H:35:SER:HB3	2:H:75:LEU:HD12	1.76	0.67
4:L:223:VAL:HG12	5:M:49:MET:HE3	1.75	0.67
1:A:720:MET:O	1:A:725:ARG:NE	2.24	0.67
1:E:232:ARG:HH21	1:F:454:ASN:H	1.41	0.67
1:B:224:ASP:O	1:B:228:SER:HB2	1.95	0.66
1:C:542:GLU:CB	1:C:649:LYS:HD3	2.25	0.66
1:D:527:GLN:HE22	1:E:715:GLU:C	2.03	0.66
1:E:398:PRO:HG3	1:E:436:PHE:O	1.94	0.66
1:E:540:LEU:HD11	1:E:646:THR:CG2	2.21	0.66
1:A:563:PRO:HD2	1:A:597:LEU:HD22	1.77	0.66
1:F:538:SER:O	1:F:663:THR:HG22	1.95	0.66
5:M:27:GLU:O	5:M:31:ARG:HG3	1.96	0.66
1:E:232:ARG:NH2	1:F:451:THR:HA	2.07	0.66
1:E:602:VAL:O	1:E:644:GLY:HA2	1.95	0.66
1:A:653:GLN:NE2	1:A:653:GLN:O	2.29	0.66
1:E:534:THR:HG23	1:F:715:GLU:HG3	1.77	0.66
1:F:518:LEU:CD2	1:F:555:LYS:HG2	2.13	0.66
1:F:695:ALA:HB1	1:F:699:LYS:HE3	1.77	0.66
2:G:149:ALA:HB2	2:G:164:CYS:HB2	1.76	0.66
1:B:713:LEU:HD22	1:B:732:LEU:HB3	1.76	0.66
1:A:671:ALA:HA	1:A:703:VAL:O	1.96	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:528:THR:O	1:B:639:LYS:HD2	1.96	0.66
1:D:627:LEU:HD21	1:D:657:MET:HG3	1.77	0.66
1:E:253:VAL:H	1:F:446:ARG:HH12	1.41	0.66
1:D:319:ASN:HB3	1:D:320:SER:HB2	1.78	0.66
4:L:198:ARG:O	4:L:202:ILE:HG13	1.95	0.66
1:A:657:MET:HE3	1:A:661:PHE:CE1	2.31	0.66
1:E:625:ALA:O	1:E:629:LEU:HG	1.95	0.66
1:F:224:ASP:O	1:F:228:SER:HB2	1.96	0.66
2:H:230:GLU:HG3	2:H:237:ASP:HB3	1.78	0.66
4:L:255:VAL:HG11	5:M:77:ASN:HB3	1.78	0.66
1:B:67:ARG:NH1	1:B:74:ILE:HD11	2.11	0.66
1:C:533:ARG:HB2	1:D:715:GLU:OE1	1.96	0.66
1:E:544:PRO:O	1:E:547:SER:HB3	1.96	0.66
2:H:72:HIS:HE1	2:H:80:ASP:HB2	1.61	0.66
1:A:687:LYS:N	1:A:690:GLU:OE1	2.27	0.66
1:B:245:VAL:O	1:B:249:GLY:N	2.28	0.66
1:E:603:ASP:OD2	1:E:645:THR:OG1	2.10	0.66
2:G:197:LEU:HD23	5:M:162:HIS:NE2	2.10	0.66
1:E:91:CYS:HB3	1:E:155:MET:HE2	1.78	0.65
1:E:547:SER:OG	1:E:549:LYS:HD3	1.96	0.65
1:D:510:TRP:CE3	1:D:670:ILE:HG22	2.31	0.65
5:M:26:LEU:HD13	5:M:146:MET:HG3	1.77	0.65
1:A:550:THR:HA	1:A:645:THR:HG21	1.76	0.65
1:B:424:VAL:N	1:B:479:ASP:N	2.44	0.65
1:D:573:MET:SD	1:D:581:LYS:HD3	2.36	0.65
2:H:57:ASN:O	2:H:59:SER:N	2.29	0.65
2:G:112:THR:HG23	2:G:117:PHE:HE1	1.61	0.65
1:B:589:PHE:CE1	1:B:600:VAL:HG11	2.30	0.65
1:D:358:ILE:HD12	1:D:388:ARG:HB3	1.78	0.65
1:D:234:ALA:HA	1:D:253:VAL:HG11	1.79	0.65
1:E:640:LEU:HD12	1:E:641:LEU:H	1.61	0.65
2:G:175:LEU:HD23	2:G:177:GLN:HE21	1.61	0.65
1:A:356:SER:CB	1:B:288:PRO:HD3	2.27	0.65
1:A:686:PHE:CE2	1:A:714:ILE:HG12	2.31	0.65
1:E:232:ARG:HH21	1:F:454:ASN:CB	2.09	0.65
1:A:620:ASN:ND2	1:B:610:ASP:OD1	2.30	0.65
1:B:501:SER:O	1:B:503:ILE:N	2.29	0.65
1:F:565:ILE:HG23	1:F:599:CYS:HB3	1.77	0.65
2:G:235:PHE:CD1	5:M:152:GLN:HG2	2.31	0.65
1:A:597:LEU:C	1:A:597:LEU:HD23	2.22	0.65
1:B:449:GLN:O	1:B:453:MET:HG2	1.97	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:125:PHE:HA	1:E:128:GLN:NE2	2.11	0.65
1:A:64:LEU:HB3	1:A:65:PRO:HD3	1.77	0.64
1:A:527:GLN:HB2	1:B:719:GLN:HG3	1.78	0.64
1:A:670:ILE:HG23	1:A:675:GLN:HB2	1.79	0.64
1:C:711:LEU:HA	1:C:714:ILE:HD12	1.79	0.64
1:F:240:PHE:HD2	1:F:244:ILE:HG21	1.58	0.64
1:D:286:ASN:HB2	1:D:327:PHE:HD1	1.62	0.64
1:E:89:LYS:HB3	1:E:89:LYS:HZ3	1.62	0.64
1:E:536:LEU:HD12	1:E:640:LEU:O	1.97	0.64
1:F:245:VAL:O	1:F:249:GLY:N	2.29	0.64
1:C:711:LEU:O	1:C:715:GLU:HG2	1.97	0.64
1:F:513:PRO:O	1:F:517:VAL:HG23	1.97	0.64
2:H:200:TYR:CE2	5:M:38:GLU:HG3	2.32	0.64
2:G:158:ASN:OD1	2:G:162:ASN:ND2	2.30	0.64
1:F:73:SER:HA	2:G:218:MET:SD	2.38	0.64
1:F:307:ALA:O	1:F:311:GLU:HG2	1.97	0.64
1:A:408:HIS:HA	1:A:426:ILE:HD12	1.80	0.64
1:B:496:GLN:O	1:B:499:TYR:N	2.25	0.64
1:E:652:LEU:CD2	1:E:657:MET:HB3	2.28	0.64
2:G:210:ALA:HB3	2:G:244:MET:HE3	1.78	0.64
1:D:546:HIS:ND1	1:D:709:LYS:HD3	2.11	0.64
2:J:39:GLU:HB2	2:J:75:LEU:HD13	1.78	0.64
1:F:544:PRO:HD2	1:F:547:SER:OG	1.96	0.64
2:I:232:PHE:HB2	2:I:233:PRO:HD3	1.80	0.64
5:M:188:ASN:O	5:M:192:ILE:HG13	1.98	0.64
1:D:534:THR:OG1	1:E:715:GLU:HG2	1.98	0.64
1:D:695:ALA:HB1	1:D:699:LYS:HE3	1.79	0.64
3:K:56:ARG:HD2	5:M:171:ILE:HG23	1.80	0.64
1:D:284:VAL:HG23	1:D:324:ILE:O	1.97	0.64
2:J:128:ALA:HB2	2:J:144:HIS:HB2	1.79	0.64
2:H:210:ALA:HB3	2:H:244:MET:HE3	1.81	0.63
3:K:63:LEU:HD22	5:M:178:ILE:HG23	1.79	0.63
1:A:256:ILE:HG13	1:A:370:ILE:HG22	1.79	0.63
1:C:375:ARG:HH12	1:C:378:LEU:HG	1.64	0.63
1:D:64:LEU:HA	1:D:67:ARG:HE	1.63	0.63
2:H:101:ILE:HG21	2:H:135:LEU:HD11	1.80	0.63
4:L:226:GLN:HA	4:L:229:MET:HE3	1.80	0.63
1:B:295:VAL:O	1:C:294:TYR:HB2	1.99	0.63
1:D:256:ILE:CG1	1:D:370:ILE:HG22	2.27	0.63
1:D:404:LEU:HA	1:D:407:LEU:HD12	1.79	0.63
2:I:38:ILE:HD11	2:I:71:LEU:HB3	1.79	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:612:VAL:HG12	1:F:617:ARG:HB2	1.81	0.63
2:H:216:ILE:HG12	2:H:220:ASN:HB2	1.80	0.63
2:J:72:HIS:CE1	2:J:80:ASP:HB2	2.34	0.63
1:A:710:LEU:O	1:A:714:ILE:HG13	1.98	0.63
1:B:307:ALA:O	1:B:311:GLU:HG2	1.98	0.63
1:C:614:ILE:C	1:C:616:PRO:HA	2.24	0.63
1:E:232:ARG:NH2	1:F:454:ASN:HB3	2.13	0.63
1:E:307:ALA:O	1:E:311:GLU:HG2	1.97	0.63
5:M:167:MET:O	5:M:171:ILE:HG13	1.99	0.63
5:M:176:ARG:O	5:M:176:ARG:HD3	1.99	0.63
1:B:397:LEU:HB3	1:B:398:PRO:CD	2.29	0.63
1:B:526:GLN:NE2	1:C:719:GLN:HB3	2.11	0.63
1:E:63:SER:O	1:E:67:ARG:HG3	1.99	0.63
1:E:437:SER:O	1:E:440:GLU:HB2	1.98	0.63
1:E:674:GLU:HA	1:E:677:LEU:HD12	1.81	0.63
2:H:231:LEU:HD13	2:G:271:ARG:HG2	1.80	0.63
2:J:57:ASN:O	2:J:59:SER:N	2.32	0.63
2:G:69:ALA:HB1	2:G:85:PHE:CE1	2.33	0.63
1:B:503:ILE:HG12	1:B:551:ALA:HA	1.80	0.63
1:F:635:PRO:O	1:F:638:ARG:HG2	1.98	0.63
4:L:229:MET:HG2	4:L:232:ARG:HH22	1.63	0.63
5:M:34:GLN:HA	5:M:37:GLU:HB2	1.81	0.63
1:A:313:GLN:NE2	1:A:365:ASN:O	2.30	0.63
1:A:449:GLN:NE2	1:F:248:MET:O	2.31	0.63
1:B:64:LEU:HB3	1:B:65:PRO:HD3	1.80	0.63
1:B:548:GLY:O	1:B:552:LEU:HD23	1.99	0.63
1:E:289:GLU:C	1:E:291:LEU:H	2.05	0.63
1:E:670:ILE:H	1:E:670:ILE:HD12	1.64	0.63
1:A:657:MET:HE3	1:A:661:PHE:HE1	1.63	0.62
1:B:101:PHE:CZ	1:B:193:LEU:HD13	2.34	0.62
1:B:380:ASP:OD1	1:B:382:ALA:N	2.32	0.62
1:F:64:LEU:HB3	1:F:65:PRO:HD3	1.79	0.62
2:H:232:PHE:HB2	2:H:233:PRO:HD3	1.80	0.62
2:I:210:ALA:HB3	2:I:244:MET:HE3	1.79	0.62
2:J:235:PHE:CD1	3:K:34:GLN:NE2	2.67	0.62
1:D:256:ILE:HG22	1:D:391:VAL:HG12	1.80	0.62
1:E:581:LYS:NZ	1:E:610:ASP:OD1	2.31	0.62
1:B:326:ILE:HG22	1:B:370:ILE:HG13	1.82	0.62
1:B:394:GLU:O	1:B:396:GLY:N	2.32	0.62
1:C:624:GLN:NE2	1:D:610:ASP:HB2	2.14	0.62
1:C:728:LYS:O	1:C:732:LEU:HG	1.99	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:686:PHE:CE1	1:E:714:ILE:HG23	2.34	0.62
2:G:38:ILE:HG23	2:G:75:LEU:HD12	1.81	0.62
1:B:46:ILE:HD12	1:B:174:VAL:HG21	1.80	0.62
1:D:521:GLY:O	1:D:525:VAL:HG23	1.98	0.62
1:F:326:ILE:HG22	1:F:370:ILE:HG13	1.81	0.62
1:F:404:LEU:O	1:F:408:HIS:HB2	1.99	0.62
1:A:549:LYS:HE3	1:A:646:THR:C	2.24	0.62
1:D:604:ASP:HB3	1:D:607:ARG:CB	2.29	0.62
1:E:380:ASP:OD1	1:E:382:ALA:N	2.33	0.62
1:E:706:GLY:O	1:E:710:LEU:N	2.24	0.62
1:C:383:LEU:O	1:C:389:LEU:HB2	1.98	0.62
1:D:12:PRO:HG2	1:D:23:VAL:HG11	1.81	0.62
1:D:648:ARG:HG3	1:D:651:VAL:HG23	1.82	0.62
1:F:549:LYS:HE2	1:F:645:THR:HB	1.80	0.62
2:H:115:GLY:HA2	2:G:50:ASN:HD21	1.64	0.62
2:J:269:ILE:HA	5:M:151:GLU:OE1	1.99	0.62
1:A:607:ARG:HD3	1:F:624:GLN:NE2	2.13	0.62
1:C:624:GLN:O	1:C:628:VAL:HG23	1.99	0.62
1:D:267:THR:HA	1:D:372:MET:SD	2.40	0.62
1:D:312:GLU:CG	1:D:313:GLN:H	2.12	0.62
1:D:651:VAL:O	1:D:655:MET:HG2	1.99	0.62
2:J:159:SER:CB	5:M:169:ASN:HB3	2.25	0.62
1:C:490:PRO:HB2	1:C:492:PHE:N	2.15	0.62
1:C:546:HIS:HA	1:C:708:LYS:HD3	1.82	0.62
1:D:91:CYS:HB3	1:D:155:MET:HE2	1.81	0.62
1:E:349:THR:HG21	1:F:294:TYR:HE1	1.63	0.62
1:F:27:LYS:HD2	1:F:57:PRO:HG3	1.81	0.62
1:F:570:PRO:HG2	1:F:604:ASP:CB	2.29	0.62
1:A:12:PRO:HG2	1:A:23:VAL:HG11	1.80	0.62
1:A:617:ARG:HH11	1:A:617:ARG:HG3	1.63	0.62
1:C:311:GLU:HA	1:C:314:ARG:HG2	1.81	0.62
1:D:240:PHE:HB3	1:D:244:ILE:HD13	1.80	0.62
1:D:652:LEU:HB3	1:D:658:LEU:HB2	1.82	0.62
2:J:210:ALA:HB3	2:J:244:MET:HE3	1.81	0.62
2:G:128:ALA:HB2	2:G:144:HIS:HB2	1.80	0.62
2:G:218:MET:HG2	2:G:219:LEU:N	2.11	0.62
5:M:74:ALA:O	5:M:78:LEU:HG	2.00	0.62
1:C:285:VAL:HG13	1:C:326:ILE:HD11	1.80	0.61
1:D:105:LYS:NZ	2:I:291:GLU:HB3	2.13	0.61
1:E:624:GLN:HA	1:E:624:GLN:OE1	2.00	0.61
2:H:93:LYS:HE2	2:H:130:ILE:HD11	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:25:SER:O	5:M:29:THR:HG23	1.98	0.61
1:D:512:ASP:O	1:D:515:THR:OG1	2.15	0.61
1:D:528:THR:OG1	1:D:641:LEU:HD12	2.00	0.61
1:D:545:PRO:HD3	1:D:647:SER:OG	2.00	0.61
1:E:64:LEU:HB3	1:E:65:PRO:HD3	1.80	0.61
1:E:652:LEU:HD23	1:E:657:MET:HB3	1.82	0.61
1:F:524:LEU:HD13	1:F:539:VAL:HG22	1.82	0.61
2:J:35:SER:HB3	2:J:75:LEU:HD12	1.81	0.61
5:M:203:LEU:CD2	5:M:204:GLY:H	2.06	0.61
1:D:36:ILE:HD11	1:D:44:LYS:HB3	1.82	0.61
1:A:9:ALA:HA	1:A:74:ILE:HG23	1.81	0.61
1:C:334:CYS:HA	1:C:351:VAL:HG22	1.82	0.61
1:C:407:LEU:CD1	1:C:426:ILE:HG23	2.30	0.61
1:D:236:ALA:HB1	1:E:453:MET:HG3	1.82	0.61
1:E:349:THR:HG21	1:F:294:TYR:CE1	2.35	0.61
1:F:91:CYS:HB3	1:F:155:MET:HE2	1.82	0.61
2:H:218:MET:HG2	2:H:219:LEU:N	2.13	0.61
3:K:46:MET:HE2	4:L:216:PHE:HA	1.81	0.61
4:L:216:PHE:HB3	5:M:39:SER:HB2	1.82	0.61
5:M:174:GLN:O	5:M:178:ILE:HG13	2.01	0.61
5:M:177:GLN:HG3	5:M:180:ARG:HH21	1.65	0.61
1:B:383:LEU:O	1:B:389:LEU:HB2	2.01	0.61
1:C:511:GLY:HA3	1:C:513:PRO:HD2	1.82	0.61
1:C:590:ASP:HA	1:C:593:TYR:CD2	2.35	0.61
1:E:326:ILE:HG22	1:E:370:ILE:HG13	1.81	0.61
1:E:404:LEU:O	1:E:408:HIS:HB2	2.00	0.61
1:F:562:PHE:CD1	1:F:599:CYS:HB2	2.36	0.61
1:F:570:PRO:HA	1:F:573:MET:HE2	1.82	0.61
2:G:80:ASP:OD1	4:L:243:TYR:CE1	2.52	0.61
1:A:598:SER:OG	1:A:640:LEU:HD12	2.00	0.61
1:E:672:THR:OG1	1:E:675:GLN:HB2	2.00	0.61
1:F:650:ASP:O	1:F:653:GLN:HG3	2.01	0.61
1:A:231:PHE:CE1	1:A:235:PHE:HE2	2.19	0.61
1:B:625:ALA:O	1:B:629:LEU:HG	2.01	0.61
1:C:12:PRO:HG2	1:C:23:VAL:HG11	1.82	0.61
1:C:254:LYS:O	1:C:368:LEU:HA	2.01	0.61
1:D:239:VAL:HG13	1:D:240:PHE:CD1	2.36	0.61
1:D:606:GLU:O	1:D:610:ASP:N	2.34	0.61
1:D:632:LYS:NZ	1:E:571:ASP:HB3	2.16	0.61
1:E:710:LEU:O	1:E:714:ILE:HG13	2.00	0.61
1:F:258:LEU:HB3	1:F:395:ILE:HD11	1.82	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:670:ILE:HG23	1:B:675:GLN:HB2	1.83	0.61
1:C:579:THR:O	1:C:583:GLN:HG2	2.00	0.61
1:D:554:ALA:O	1:D:558:GLU:HG2	2.01	0.61
1:E:224:ASP:O	1:E:228:SER:HB2	2.01	0.61
1:E:407:LEU:CD1	1:E:426:ILE:HG23	2.31	0.61
1:F:612:VAL:CG1	1:F:617:ARG:HB2	2.31	0.61
1:D:348:ASP:O	1:D:352:ASN:ND2	2.34	0.60
1:E:513:PRO:O	1:E:517:VAL:HG23	2.01	0.60
1:E:552:LEU:HD11	1:E:667:VAL:HG11	1.82	0.60
3:K:84:LEU:HD21	5:M:199:ALA:HB1	1.83	0.60
1:B:95:MET:HG3	1:B:152:ILE:HG12	1.82	0.60
1:B:437:SER:O	1:B:440:GLU:HB2	2.01	0.60
1:C:404:LEU:O	1:C:408:HIS:HB2	2.01	0.60
1:E:64:LEU:O	1:E:68:LYS:HG3	2.01	0.60
2:H:231:LEU:HD13	2:G:271:ARG:HE	1.65	0.60
1:A:610:ASP:HA	1:F:624:GLN:NE2	2.16	0.60
1:D:599:CYS:SG	1:D:641:LEU:HD22	2.42	0.60
3:K:83:LYS:HG2	3:K:86:ARG:HH22	1.64	0.60
1:A:678:GLU:O	1:A:682:LEU:HD12	2.01	0.60
1:C:689:LYS:O	1:C:692:THR:OG1	2.19	0.60
1:F:380:ASP:OD1	1:F:382:ALA:N	2.32	0.60
2:H:115:GLY:HA2	2:G:50:ASN:ND2	2.17	0.60
2:H:142:ILE:HG23	2:H:168:VAL:HG13	1.83	0.60
1:C:73:SER:O	1:C:76:GLN:HG2	2.00	0.60
1:D:436:PHE:HE2	1:D:444:LEU:HD12	1.66	0.60
1:E:264:CYS:SG	1:E:395:ILE:HG21	2.41	0.60
1:F:521:GLY:O	1:F:525:VAL:HG23	2.01	0.60
1:F:525:VAL:HG13	1:F:562:PHE:HE1	1.62	0.60
2:G:234:ALA:HB3	2:G:237:ASP:HB2	1.84	0.60
1:B:404:LEU:O	1:B:408:HIS:HB2	2.02	0.60
1:D:585:MET:O	1:D:589:PHE:HD2	1.84	0.60
1:A:413:ARG:NH1	1:F:249:GLY:O	2.27	0.60
1:E:383:LEU:O	1:E:389:LEU:HB2	2.02	0.60
1:F:655:MET:O	1:F:656:GLU:HG2	2.01	0.60
1:A:582:CYS:SG	1:A:621:LEU:HG	2.42	0.60
1:B:289:GLU:C	1:B:291:LEU:H	2.09	0.60
1:D:256:ILE:O	1:D:370:ILE:HA	2.01	0.60
1:D:527:GLN:NE2	1:E:716:MET:HA	2.16	0.60
1:D:547:SER:OG	1:D:549:LYS:HG3	2.02	0.60
1:E:705:ILE:HD13	1:E:710:LEU:HD13	1.84	0.60
1:F:407:LEU:CD1	1:F:426:ILE:HG23	2.32	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:128:ALA:HB2	2:I:144:HIS:HB2	1.84	0.60
3:K:79:THR:HG22	3:K:83:LYS:HE3	1.84	0.60
5:M:203:LEU:HD23	5:M:204:GLY:N	2.07	0.60
1:A:508:ILE:HB	1:A:682:LEU:HD22	1.83	0.60
1:C:695:ALA:HB1	1:C:699:LYS:HE3	1.83	0.60
1:D:64:LEU:HB3	1:D:65:PRO:HD3	1.82	0.60
1:D:513:PRO:HB3	1:D:516:ARG:HE	1.66	0.60
1:E:289:GLU:O	1:E:291:LEU:N	2.24	0.60
2:H:128:ALA:HB2	2:H:144:HIS:HB2	1.84	0.60
1:A:270:ALA:O	1:A:273:ILE:HG22	2.02	0.60
1:B:36:ILE:HD11	1:B:44:LYS:HB3	1.84	0.60
1:B:533:ARG:HG3	1:B:534:THR:HG23	1.84	0.60
1:D:513:PRO:O	1:D:516:ARG:HG2	2.02	0.60
1:E:671:ALA:HA	1:E:703:VAL:O	2.02	0.60
5:M:64:MET:HE3	5:M:181:ILE:HG23	1.84	0.60
1:A:628:VAL:HG11	1:B:571:ASP:HA	1.83	0.59
1:A:687:LYS:HB2	1:A:690:GLU:HG3	1.83	0.59
1:B:240:PHE:HB3	1:B:244:ILE:HB	1.84	0.59
1:C:383:LEU:HD22	1:C:388:ARG:HD2	1.84	0.59
2:I:57:ASN:O	2:I:59:SER:N	2.35	0.59
1:B:407:LEU:CD1	1:B:426:ILE:HG23	2.31	0.59
2:I:21:VAL:HG21	2:I:71:LEU:HD22	1.82	0.59
2:I:101:ILE:HG21	2:I:135:LEU:HD11	1.84	0.59
2:I:287:ILE:O	2:I:291:GLU:HG3	2.02	0.59
2:J:233:PRO:HA	2:J:235:PHE:CE1	2.37	0.59
1:A:627:LEU:HD13	1:B:607:ARG:HH12	1.66	0.59
1:A:676:LEU:CD1	1:A:710:LEU:HD11	2.33	0.59
1:B:284:VAL:HG23	1:B:324:ILE:O	2.02	0.59
1:E:284:VAL:HG23	1:E:324:ILE:O	2.02	0.59
3:K:56:ARG:HH11	5:M:171:ILE:HG23	1.67	0.59
4:L:212:LEU:HA	4:L:215:MET:HE3	1.83	0.59
1:C:507:ILE:HD13	1:C:555:LYS:HG2	1.77	0.59
1:C:606:GLU:HG2	1:C:607:ARG:N	2.18	0.59
1:D:618:PHE:CE2	1:E:614:ILE:HD12	2.37	0.59
1:E:532:ASP:OD2	1:E:533:ARG:N	2.35	0.59
5:M:40:LYS:O	5:M:44:ILE:HG13	2.03	0.59
1:A:694:ILE:O	1:A:698:VAL:HG13	2.02	0.59
1:B:540:LEU:HA	1:B:644:GLY:O	2.02	0.59
1:B:589:PHE:HE2	1:B:629:LEU:HB3	1.67	0.59
1:C:540:LEU:HB2	1:C:661:PHE:CD2	2.37	0.59
1:C:542:GLU:HB3	1:C:649:LYS:HD3	1.82	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:69:ALA:HB1	2:I:85:PHE:CE1	2.36	0.59
5:M:17:ARG:O	5:M:21:LEU:HG	2.02	0.59
1:B:121:PHE:CD2	1:B:183:VAL:HG21	2.37	0.59
1:D:18:LEU:HA	1:D:137:VAL:CG2	2.32	0.59
1:D:310:GLU:O	1:D:313:GLN:NE2	2.36	0.59
1:E:713:LEU:HD22	1:E:732:LEU:HD13	1.85	0.59
1:F:236:ALA:HA	1:F:239:VAL:HG12	1.83	0.59
2:H:200:TYR:CE2	5:M:42:ALA:HB2	2.38	0.59
2:H:235:PHE:CD2	5:M:31:ARG:HA	2.37	0.59
1:C:540:LEU:HD12	1:C:644:GLY:O	2.02	0.59
1:F:437:SER:O	1:F:440:GLU:HB2	2.02	0.59
2:H:18:GLU:HA	2:H:21:VAL:HG12	1.85	0.59
2:H:289:GLY:O	2:H:293:ASP:CB	2.51	0.59
1:A:449:GLN:O	1:A:453:MET:HG2	2.03	0.59
1:E:502:TYR:OH	1:E:569:SER:OG	2.19	0.59
1:E:510:TRP:NE1	1:E:707:ILE:HD11	2.18	0.59
1:E:586:LYS:HA	1:E:589:PHE:CD2	2.37	0.59
4:L:199:HIS:CE1	5:M:21:LEU:HD22	2.38	0.59
1:B:64:LEU:HB2	2:H:293:ASP:C	2.28	0.59
1:B:571:ASP:OD2	1:B:571:ASP:N	2.35	0.59
1:D:312:GLU:HG2	1:D:313:GLN:H	1.68	0.59
2:G:101:ILE:HG21	2:G:135:LEU:HD11	1.85	0.59
1:B:67:ARG:NH2	2:H:293:ASP:O	2.36	0.59
1:B:662:SER:HB3	1:C:712:MET:HE3	1.85	0.59
1:C:577:SER:O	1:C:580:ALA:N	2.34	0.59
1:D:383:LEU:O	1:D:389:LEU:HB2	2.03	0.59
1:F:589:PHE:CD2	1:F:629:LEU:HD22	2.37	0.59
1:A:238:ARG:HA	1:A:252:HIS:CE1	2.37	0.58
1:A:307:ALA:O	1:A:310:GLU:HG3	2.02	0.58
1:A:397:LEU:HB3	1:A:398:PRO:HD3	1.84	0.58
1:A:716:MET:HG2	1:A:732:LEU:HD11	1.85	0.58
1:E:190:ASN:ND2	1:E:316:LEU:HA	2.18	0.58
1:E:506:GLY:O	1:E:508:ILE:N	2.36	0.58
5:M:148:GLU:O	5:M:152:GLN:HG3	2.03	0.58
1:A:411:THR:OG1	1:A:426:ILE:HD11	2.03	0.58
1:A:503:ILE:HG23	1:A:506:GLY:HA2	1.83	0.58
1:C:527:GLN:HB2	1:D:719:GLN:HG3	1.85	0.58
1:D:11:CYS:SG	1:D:17:SER:HB2	2.43	0.58
1:F:383:LEU:O	1:F:389:LEU:HB2	2.02	0.58
2:G:235:PHE:CZ	5:M:151:GLU:HG2	2.38	0.58
2:H:218:MET:CG	2:H:219:LEU:H	2.06	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:167:LYS:HE2	2:J:171:TYR:HE2	1.67	0.58
1:A:382:ALA:O	1:A:385:ARG:HG2	2.02	0.58
1:B:596:GLN:HA	1:B:638:ARG:HG2	1.86	0.58
1:D:527:GLN:HE21	1:E:715:GLU:HG3	1.68	0.58
5:M:49:MET:HG2	5:M:53:GLN:HE21	1.68	0.58
1:A:585:MET:HE1	1:A:626:LEU:HD12	1.84	0.58
1:B:578:GLU:HG3	1:B:619:SER:HB2	1.85	0.58
1:C:377:ASP:OD2	1:C:377:ASP:N	2.36	0.58
1:E:310:GLU:OE2	1:E:357:LYS:NZ	2.36	0.58
2:J:18:GLU:HA	2:J:21:VAL:HG12	1.85	0.58
3:K:35:THR:HA	3:K:38:GLN:OE1	2.03	0.58
5:M:34:GLN:O	5:M:38:GLU:N	2.35	0.58
5:M:191:ARG:HH11	5:M:191:ARG:HG3	1.67	0.58
1:B:605:ILE:HD11	1:B:644:GLY:HA3	1.85	0.58
1:E:628:VAL:O	1:E:632:LYS:N	2.35	0.58
2:H:231:LEU:HD13	2:G:271:ARG:NE	2.18	0.58
1:C:621:LEU:HD11	1:D:575:GLY:HA2	1.85	0.58
1:D:312:GLU:OE1	1:D:323:HIS:ND1	2.33	0.58
2:G:218:MET:CG	2:G:219:LEU:H	2.05	0.58
1:A:353:GLN:HA	1:B:288:PRO:CG	2.34	0.58
1:B:236:ALA:HA	1:B:239:VAL:HG12	1.86	0.58
1:B:631:LYS:NZ	1:C:604:ASP:OD2	2.36	0.58
1:D:242:PRO:HD2	1:D:243:GLU:H	1.69	0.58
1:F:284:VAL:HG23	1:F:324:ILE:O	2.03	0.58
2:H:21:VAL:HG21	2:H:71:LEU:HD22	1.84	0.58
2:I:108:ILE:HD12	2:I:127:ILE:HD12	1.85	0.58
5:M:26:LEU:HB2	5:M:146:MET:HE2	1.86	0.58
1:A:257:LEU:HG	1:A:389:LEU:HD12	1.86	0.58
1:C:289:GLU:O	1:C:291:LEU:N	2.31	0.58
1:E:296:GLY:H	1:E:297:GLU:CB	2.17	0.58
2:I:232:PHE:C	2:I:234:ALA:H	2.12	0.58
1:B:64:LEU:HA	1:B:67:ARG:HE	1.69	0.58
1:C:490:PRO:HA	1:C:491:ALA:CB	2.28	0.58
1:D:313:GLN:O	1:D:317:GLY:N	2.36	0.58
1:E:270:ALA:O	1:E:273:ILE:HG22	2.04	0.58
1:F:566:LYS:HD2	1:F:567:ILE:N	2.19	0.58
1:F:715:GLU:O	1:F:719:GLN:HG2	2.04	0.58
1:A:18:LEU:HD13	1:A:139:SER:HB2	1.84	0.57
1:A:428:GLU:HG2	1:A:479:ASP:CA	2.31	0.57
1:A:571:ASP:HA	1:A:574:ILE:HG23	1.86	0.57
1:A:726:VAL:O	1:A:730:LEU:HG	2.04	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:507:ILE:CD1	1:C:555:LYS:CD	2.79	0.57
1:D:18:LEU:HA	1:D:137:VAL:HG23	1.85	0.57
1:D:687:LYS:O	1:D:691:ARG:HG3	2.05	0.57
2:H:94:LYS:CE	2:I:153:LYS:HG3	2.34	0.57
5:M:170:GLU:HG3	5:M:174:GLN:HE21	1.68	0.57
1:B:423:ASP:HB2	1:B:479:ASP:N	2.19	0.57
1:B:695:ALA:HB1	1:B:699:LYS:HE3	1.85	0.57
1:C:658:LEU:HD11	1:C:664:THR:HG21	1.86	0.57
1:E:171:LYS:HB3	1:E:171:LYS:NZ	2.20	0.57
1:E:664:THR:C	1:E:665:ILE:HD13	2.29	0.57
1:F:106:ASN:HB3	1:F:143:LYS:NZ	2.18	0.57
1:F:604:ASP:HB3	1:F:607:ARG:HB2	1.85	0.57
2:J:201:SER:OG	2:J:205:TYR:HE1	1.81	0.57
4:L:218:ASP:O	4:L:222:LEU:HG	2.03	0.57
1:C:510:TRP:CE3	1:C:670:ILE:HG12	2.39	0.57
1:C:688:ASP:OD1	1:C:691:ARG:NH2	2.26	0.57
1:F:606:GLU:OE2	1:F:647:SER:HB2	2.04	0.57
2:H:271:ARG:HH22	2:I:231:LEU:HB2	1.69	0.57
1:D:303:ARG:HD3	1:D:353:GLN:CD	2.28	0.57
2:I:235:PHE:CB	4:L:207:ASN:HB3	2.35	0.57
2:G:235:PHE:CD2	5:M:152:GLN:HA	2.40	0.57
1:A:299:GLU:HG2	1:A:353:GLN:HG2	1.86	0.57
1:A:536:LEU:HD23	1:A:633:ALA:HA	1.86	0.57
1:A:542:GLU:OE2	1:A:666:HIS:NE2	2.37	0.57
1:C:256:ILE:HG22	1:C:391:VAL:HG11	1.84	0.57
1:D:380:ASP:OD1	1:D:382:ALA:N	2.36	0.57
1:E:267:THR:HA	1:E:372:MET:SD	2.44	0.57
1:E:697:GLN:HG3	1:E:730:LEU:HD11	1.84	0.57
2:H:149:ALA:HB2	2:H:164:CYS:HB2	1.86	0.57
5:M:178:ILE:HG22	5:M:182:MET:HE2	1.86	0.57
1:A:445:VAL:O	1:A:449:GLN:HG2	2.04	0.57
1:B:289:GLU:O	1:B:291:LEU:N	2.28	0.57
1:E:721:ASP:O	1:E:725:ARG:HG3	2.05	0.57
1:A:560:SER:HB2	1:A:562:PHE:CE1	2.40	0.57
1:A:678:GLU:O	1:A:681:GLU:HG2	2.04	0.57
1:B:589:PHE:CE2	1:B:629:LEU:HB3	2.39	0.57
1:D:604:ASP:HB3	1:D:607:ARG:HB3	1.86	0.57
1:E:550:THR:HA	1:E:645:THR:HG21	1.85	0.57
1:D:223:LEU:HD12	1:D:395:ILE:HG23	1.87	0.57
1:D:404:LEU:HD11	1:D:427:LYS:HE3	1.85	0.57
1:D:528:THR:OG1	1:D:537:VAL:HG21	2.05	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:628:VAL:HG13	1:E:571:ASP:OD1	2.02	0.57
1:F:242:PRO:HD2	1:F:243:GLU:H	1.69	0.57
1:F:653:GLN:HB3	1:F:658:LEU:HD23	1.86	0.57
2:H:116:ARG:NH2	3:K:68:ASP:HB3	2.20	0.57
2:G:256:VAL:HG11	2:G:288:GLN:HG2	1.87	0.57
4:L:199:HIS:CD2	5:M:21:LEU:HD13	2.39	0.57
1:A:352:ASN:HA	1:A:355:LEU:HD12	1.87	0.57
1:B:110:ASN:HB3	1:B:111:PRO:HD2	1.85	0.57
1:C:540:LEU:HD23	1:C:649:LYS:HE3	1.86	0.57
1:D:625:ALA:O	1:D:629:LEU:HG	2.04	0.57
1:E:27:LYS:N	1:E:27:LYS:HD2	2.20	0.57
1:A:267:THR:OG1	1:A:328:ASP:OD2	2.23	0.57
1:B:542:GLU:HG3	1:B:542:GLU:O	2.05	0.57
1:C:436:PHE:HB3	1:C:440:GLU:OE1	2.05	0.57
1:C:677:LEU:HD11	1:C:698:VAL:HG21	1.87	0.57
1:E:397:LEU:HD22	1:E:398:PRO:HD2	1.86	0.57
1:E:673:GLY:HA3	1:E:698:VAL:HB	1.87	0.57
1:F:296:GLY:H	1:F:297:GLU:CB	2.17	0.57
1:F:562:PHE:HE2	1:F:597:LEU:HD12	1.69	0.57
2:J:96:ASP:H	2:J:97:PRO:HD2	1.70	0.57
2:J:231:LEU:O	2:J:234:ALA:N	2.19	0.57
1:A:489:LYS:N	1:A:490:PRO:HD2	2.19	0.56
1:B:296:GLY:H	1:B:297:GLU:CB	2.18	0.56
1:E:190:ASN:ND2	1:E:316:LEU:HG	2.17	0.56
1:F:562:PHE:HB2	1:F:565:ILE:HG12	1.86	0.56
2:G:267:ASP:CG	2:G:271:ARG:HH11	2.13	0.56
1:A:106:ASN:HB3	1:A:143:LYS:HZ2	1.69	0.56
1:A:295:VAL:HB	1:B:294:TYR:CB	2.34	0.56
1:A:513:PRO:O	1:A:517:VAL:HG23	2.05	0.56
1:A:568:CYS:O	1:A:603:ASP:HB3	2.04	0.56
1:B:404:LEU:HG	1:B:426:ILE:HG22	1.87	0.56
1:B:654:GLU:O	1:C:613:PRO:HG3	2.04	0.56
1:D:300:ALA:O	1:D:303:ARG:HB3	2.05	0.56
1:D:686:PHE:HB2	1:D:691:ARG:HG2	1.87	0.56
1:A:544:PRO:HB2	1:A:669:ASN:ND2	2.21	0.56
1:A:565:ILE:HG13	1:A:599:CYS:HB3	1.88	0.56
1:A:690:GLU:O	1:A:694:ILE:HG13	2.04	0.56
1:B:559:GLU:O	1:B:561:ASN:ND2	2.38	0.56
1:C:375:ARG:NH2	1:C:377:ASP:OD1	2.38	0.56
1:C:555:LYS:HA	1:C:558:GLU:OE1	2.05	0.56
1:D:312:GLU:CG	1:D:313:GLN:N	2.67	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:493:GLY:HA2	1:D:496:GLN:CB	2.36	0.56
1:D:656:GLU:OE1	1:E:613:PRO:HB3	2.05	0.56
1:E:693:THR:O	1:E:697:GLN:NE2	2.20	0.56
1:F:632:LYS:HD2	1:F:633:ALA:H	1.71	0.56
3:K:63:LEU:HD13	5:M:182:MET:HG2	1.87	0.56
4:L:199:HIS:CG	5:M:21:LEU:HD13	2.40	0.56
2:H:230:GLU:HG2	2:H:231:LEU:N	2.20	0.56
1:D:284:VAL:HB	1:D:325:ILE:HA	1.87	0.56
2:J:266:TYR:CZ	2:J:270:SER:HB2	2.40	0.56
4:L:202:ILE:O	4:L:205:LEU:HB3	2.05	0.56
1:A:64:LEU:HA	1:A:67:ARG:HE	1.71	0.56
1:A:539:VAL:HG13	1:A:643:ILE:HA	1.87	0.56
1:C:694:ILE:O	1:C:698:VAL:HG22	2.05	0.56
1:D:299:GLU:OE1	1:D:350:VAL:HG13	2.06	0.56
1:E:352:ASN:HA	1:E:355:LEU:HD12	1.87	0.56
1:F:542:GLU:HB2	1:F:666:HIS:HA	1.87	0.56
2:J:53:LYS:HE3	2:G:117:PHE:CE2	2.40	0.56
1:B:242:PRO:HD2	1:B:243:GLU:H	1.71	0.56
1:B:327:PHE:HB2	1:B:330:ILE:CG2	2.33	0.56
1:B:545:PRO:O	1:B:546:HIS:HB2	2.05	0.56
1:C:245:VAL:O	1:C:249:GLY:N	2.36	0.56
1:C:503:ILE:HG22	1:C:506:GLY:HA2	1.86	0.56
1:E:98:GLU:HB3	1:E:148:LEU:HB3	1.87	0.56
1:E:502:TYR:CZ	1:E:567:ILE:HG21	2.40	0.56
1:E:648:ARG:NE	1:E:650:ASP:OD1	2.32	0.56
1:F:609:LEU:CD1	1:F:655:MET:HE1	2.35	0.56
1:A:73:SER:O	1:A:76:GLN:HG2	2.06	0.56
1:A:223:LEU:CD1	1:A:227:PHE:HB2	2.36	0.56
1:C:330:ILE:HG22	1:C:379:ILE:CD1	2.36	0.56
1:C:653:GLN:HG3	1:C:658:LEU:HD23	1.86	0.56
1:D:40:SER:OG	1:D:41:PRO:HD2	2.06	0.56
1:E:490:PRO:HA	1:E:491:ALA:CB	2.33	0.56
1:F:267:THR:HA	1:F:372:MET:SD	2.45	0.56
2:H:256:VAL:HG21	2:H:288:GLN:HG3	1.88	0.56
2:I:200:TYR:CE2	4:L:211:GLU:HG3	2.41	0.56
1:A:525:VAL:HG13	1:A:562:PHE:CE1	2.40	0.56
1:A:540:LEU:HD11	1:A:646:THR:HG22	1.86	0.56
1:C:375:ARG:NH1	1:C:378:LEU:HG	2.20	0.56
2:H:179:GLN:HB3	2:H:214:PHE:HB3	1.88	0.56
2:H:271:ARG:HH22	2:I:231:LEU:CB	2.17	0.56
2:I:127:ILE:HG23	2:I:131:TYR:CE1	2.41	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:40:SER:OG	1:C:43:HIS:HB2	2.05	0.56
1:D:627:LEU:HD13	1:E:607:ARG:HH12	1.70	0.56
1:F:270:ALA:O	1:F:273:ILE:HG22	2.06	0.56
1:F:559:GLU:HA	1:F:559:GLU:OE1	2.06	0.56
1:F:602:VAL:N	1:F:643:ILE:O	2.23	0.56
2:I:67:GLN:O	2:I:71:LEU:HG	2.06	0.56
2:J:69:ALA:HB1	2:J:85:PHE:CE1	2.41	0.56
5:M:42:ALA:HA	5:M:45:ARG:CZ	2.36	0.56
1:A:536:LEU:HD23	1:A:634:PRO:HD3	1.88	0.55
1:B:10:ARG:NE	2:H:293:ASP:OD2	2.34	0.55
1:C:688:ASP:O	1:C:692:THR:HG23	2.07	0.55
1:E:354:LEU:O	1:E:358:ILE:HG12	2.06	0.55
1:E:681:GLU:HA	1:E:691:ARG:HE	1.71	0.55
2:J:218:MET:CG	2:J:219:LEU:H	2.14	0.55
1:A:67:ARG:HD2	2:H:218:MET:CG	2.35	0.55
1:B:398:PRO:HG3	1:B:436:PHE:O	2.06	0.55
1:C:106:ASN:HB3	1:C:143:LYS:NZ	2.21	0.55
1:E:528:THR:HG21	1:E:641:LEU:CD2	2.27	0.55
1:E:705:ILE:HG13	1:E:709:LYS:HG3	1.88	0.55
2:J:243:LEU:HD22	2:J:266:TYR:CG	2.41	0.55
2:G:57:ASN:O	2:G:59:SER:N	2.39	0.55
4:L:233:ILE:O	4:L:237:VAL:HG23	2.06	0.55
5:M:50:LEU:HD12	5:M:167:MET:HG2	1.88	0.55
1:A:549:LYS:HG3	1:A:550:THR:N	2.21	0.55
1:A:709:LYS:HE2	1:A:709:LYS:HA	1.89	0.55
1:B:198:LYS:N	1:B:198:LYS:HD2	2.21	0.55
1:E:242:PRO:HD2	1:E:243:GLU:H	1.70	0.55
1:E:573:MET:SD	1:E:581:LYS:HG2	2.46	0.55
1:F:69:TRP:NE1	1:F:134:GLN:HA	2.21	0.55
1:A:531:SER:O	1:A:639:LYS:HE2	2.07	0.55
1:B:270:ALA:O	1:B:273:ILE:HG22	2.06	0.55
1:E:232:ARG:NH2	1:F:454:ASN:H	2.03	0.55
1:F:554:ALA:O	1:F:558:GLU:HG3	2.06	0.55
2:H:119:ILE:HD13	3:K:65:ASP:OD1	2.06	0.55
5:M:56:GLN:O	5:M:60:VAL:HG23	2.05	0.55
1:A:383:LEU:O	1:A:389:LEU:HB2	2.07	0.55
1:A:724:TYR:HD1	1:A:727:ARG:HH12	1.54	0.55
1:C:128:GLN:O	1:C:176:LEU:HD12	2.07	0.55
1:F:91:CYS:O	1:F:154:ALA:HA	2.07	0.55
2:J:175:LEU:HD23	2:J:177:GLN:HE21	1.70	0.55
2:J:182:ILE:O	2:J:186:GLU:HG2	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:LEU:HB3	1:A:388:ARG:NH1	2.21	0.55
1:C:95:MET:HG3	1:C:152:ILE:HG12	1.87	0.55
1:C:256:ILE:HA	1:C:391:VAL:HG13	1.87	0.55
1:C:507:ILE:HD12	1:C:555:LYS:HD3	1.89	0.55
1:D:510:TRP:CE3	1:D:675:GLN:HG2	2.34	0.55
2:I:175:LEU:HD23	2:I:177:GLN:HE21	1.72	0.55
3:K:70:LEU:HD13	5:M:185:ALA:O	2.07	0.55
1:B:354:LEU:O	1:B:358:ILE:HG12	2.05	0.55
1:B:552:LEU:O	1:B:556:ILE:HG13	2.07	0.55
1:C:327:PHE:CB	1:C:330:ILE:HD11	2.28	0.55
1:F:354:LEU:O	1:F:358:ILE:HG12	2.07	0.55
2:H:72:HIS:CE1	2:H:80:ASP:HB2	2.42	0.55
4:L:211:GLU:HA	4:L:214:ASP:OD2	2.07	0.55
1:A:242:PRO:HD2	1:A:243:GLU:CD	2.32	0.55
1:A:688:ASP:OD1	1:A:689:LYS:N	2.40	0.55
1:A:705:ILE:HD13	1:A:710:LEU:CD1	2.34	0.55
1:C:284:VAL:HG11	1:C:305:LEU:HD11	1.88	0.55
1:D:681:GLU:HG2	1:D:691:ARG:NH1	2.21	0.55
2:H:182:ILE:O	2:H:186:GLU:HG2	2.06	0.55
2:J:266:TYR:C	2:J:268:SER:H	2.15	0.55
4:L:213:HIS:CD2	5:M:35:LEU:HB3	2.42	0.55
1:A:40:SER:OG	1:A:41:PRO:HD2	2.07	0.55
1:A:485:GLU:O	1:A:489:LYS:CB	2.54	0.55
1:E:449:GLN:O	1:E:453:MET:HG2	2.05	0.55
1:E:604:ASP:O	1:E:608:LEU:N	2.38	0.55
3:K:37:ALA:HA	3:K:40:ASP:OD2	2.06	0.55
1:A:286:ASN:HB2	1:A:327:PHE:CB	2.37	0.55
1:B:421:SER:HB3	1:B:424:VAL:HG23	1.87	0.55
1:D:40:SER:HB3	1:D:43:HIS:HB2	1.88	0.55
1:D:313:GLN:HG3	1:D:314:ARG:N	2.20	0.55
1:F:617:ARG:HH11	1:F:617:ARG:HG3	1.72	0.55
2:J:101:ILE:HG21	2:J:135:LEU:HD11	1.89	0.55
5:M:149:ASN:O	5:M:153:VAL:HG23	2.07	0.55
1:A:406:ILE:O	1:A:409:ILE:HG22	2.06	0.54
1:A:562:PHE:CD2	1:A:597:LEU:CD2	2.83	0.54
1:B:267:THR:HA	1:B:372:MET:SD	2.47	0.54
1:D:720:MET:HE3	1:D:724:TYR:CE1	2.36	0.54
3:K:52:LYS:HB2	3:K:52:LYS:NZ	2.23	0.54
1:A:247:GLN:O	1:B:414:MET:HE3	2.08	0.54
1:A:293:LYS:O	1:A:294:TYR:CG	2.60	0.54
1:A:315:ARG:HG2	1:A:316:LEU:CD1	2.37	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:PRO:HG3	1:A:437:SER:HA	1.90	0.54
1:D:690:GLU:O	1:D:693:THR:OG1	2.21	0.54
1:E:587:LYS:HZ1	1:E:591:ASP:CG	2.15	0.54
1:F:538:SER:OG	1:F:661:PHE:HD1	1.88	0.54
4:L:202:ILE:CG2	5:M:25:SER:HB3	2.37	0.54
1:A:563:PRO:HG2	1:A:597:LEU:O	2.06	0.54
1:B:570:PRO:HG3	1:B:608:LEU:HD23	1.88	0.54
1:C:355:LEU:O	1:C:388:ARG:NH2	2.34	0.54
1:C:577:SER:O	1:C:579:THR:N	2.40	0.54
1:D:423:ASP:HB2	1:D:480:PHE:CB	2.37	0.54
1:D:686:PHE:CE1	1:D:714:ILE:HG23	2.42	0.54
1:E:508:ILE:HB	1:E:682:LEU:HD13	1.89	0.54
1:F:89:LYS:O	1:F:172:ILE:HG21	2.07	0.54
1:F:721:ASP:HB2	1:F:724:TYR:CD1	2.41	0.54
2:I:231:LEU:O	2:I:234:ALA:N	2.40	0.54
1:A:625:ALA:O	1:A:629:LEU:HG	2.08	0.54
1:A:677:LEU:HG	1:A:695:ALA:HB2	1.88	0.54
1:B:570:PRO:HD3	1:B:603:ASP:HB3	1.90	0.54
1:B:571:ASP:O	1:B:574:ILE:HG13	2.08	0.54
2:J:243:LEU:HD13	2:J:266:TYR:HB2	1.88	0.54
5:M:78:LEU:CD1	5:M:195:ALA:HB1	2.37	0.54
1:A:457:ILE:HG13	1:F:240:PHE:HE1	1.73	0.54
1:A:570:PRO:HD3	1:A:603:ASP:OD2	2.08	0.54
1:B:527:GLN:NE2	1:C:716:MET:SD	2.69	0.54
1:C:281:GLU:CB	1:C:324:ILE:HD13	2.38	0.54
1:D:353:GLN:NE2	1:E:288:PRO:HG2	2.21	0.54
1:E:587:LYS:HZ3	1:E:587:LYS:C	2.10	0.54
1:C:570:PRO:HG2	1:C:604:ASP:HB2	1.90	0.54
1:C:589:PHE:CD2	1:C:629:LEU:HD13	2.42	0.54
1:D:657:MET:HG2	1:D:661:PHE:CE2	2.42	0.54
1:E:590:ASP:O	1:E:593:TYR:HB2	2.08	0.54
1:F:686:PHE:HE1	1:F:714:ILE:HG23	1.73	0.54
2:J:112:THR:HG23	2:J:117:PHE:HE1	1.73	0.54
1:A:565:ILE:HA	1:A:599:CYS:O	2.08	0.54
1:A:672:THR:OG1	1:A:675:GLN:OE1	2.14	0.54
1:A:686:PHE:CE2	1:A:714:ILE:HG23	2.43	0.54
1:E:8:ALA:HB3	1:E:73:SER:O	2.08	0.54
2:H:124:HIS:HE1	2:H:147:GLN:HB3	1.73	0.54
2:I:124:HIS:HE1	2:I:147:GLN:HB3	1.72	0.54
2:G:142:ILE:HG23	2:G:168:VAL:HG13	1.89	0.54
1:A:286:ASN:HB2	1:A:327:PHE:HB3	1.90	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:388:ARG:NH1	1:C:388:ARG:HB2	2.23	0.54
1:C:690:GLU:CB	1:C:726:VAL:HG21	2.36	0.54
1:D:356:SER:HB2	1:E:288:PRO:HG3	1.90	0.54
1:E:516:ARG:O	1:E:519:ASP:OD1	2.25	0.54
5:M:156:ILE:HG22	5:M:160:LEU:HG	1.89	0.54
1:A:407:LEU:HD12	1:A:426:ILE:HG23	1.90	0.54
1:A:610:ASP:OD1	1:F:624:GLN:HG3	2.06	0.54
1:C:34:HIS:HB2	1:C:83:TYR:O	2.08	0.54
1:C:63:SER:O	1:C:67:ARG:HG3	2.08	0.54
1:C:399:ASP:O	1:C:402:GLY:N	2.41	0.54
1:D:260:GLY:N	1:D:266:LYS:HD3	2.23	0.54
1:E:236:ALA:O	1:E:239:VAL:HG12	2.08	0.54
1:F:40:SER:HB2	1:F:41:PRO:HD2	1.90	0.54
2:H:98:GLN:H	2:H:98:GLN:CD	2.15	0.54
4:L:229:MET:O	4:L:233:ILE:HG13	2.08	0.54
1:B:539:VAL:HG21	1:B:665:ILE:HD12	1.88	0.53
1:C:46:ILE:HD12	1:C:174:VAL:HG21	1.89	0.53
1:D:657:MET:HE2	1:D:661:PHE:CZ	2.43	0.53
1:E:232:ARG:HH22	1:F:451:THR:C	2.16	0.53
1:F:113:ASP:O	1:F:117:MET:HG3	2.08	0.53
2:J:116:ARG:HH22	5:M:65:ASN:CG	2.16	0.53
5:M:61:GLU:HG2	5:M:65:ASN:ND2	2.19	0.53
1:A:122:ILE:O	1:A:126:ASN:HB3	2.08	0.53
1:B:452:ALA:HA	1:B:455:ARG:NH2	2.23	0.53
1:C:242:PRO:HD2	1:C:243:GLU:H	1.73	0.53
1:E:149:VAL:HG11	1:E:152:ILE:HD11	1.89	0.53
1:E:585:MET:HG3	1:E:589:PHE:HZ	1.70	0.53
1:F:289:GLU:C	1:F:291:LEU:H	2.16	0.53
1:F:522:GLU:OE2	1:F:526:GLN:HG2	2.09	0.53
1:F:535:PRO:HB2	1:F:536:LEU:HD13	1.90	0.53
2:J:179:GLN:HB3	2:J:214:PHE:CG	2.43	0.53
2:J:201:SER:HA	5:M:161:ARG:HD2	1.90	0.53
5:M:29:THR:HB	5:M:150:LEU:HD21	1.89	0.53
5:M:143:GLU:HA	5:M:146:MET:HB3	1.89	0.53
1:A:521:GLY:HA2	1:A:524:LEU:HD12	1.89	0.53
1:C:347:HIS:O	1:C:350:VAL:HG22	2.08	0.53
1:D:593:TYR:O	1:D:638:ARG:HG2	2.08	0.53
2:H:20:LYS:HE2	2:H:37:LYS:HA	1.89	0.53
1:C:612:VAL:HG12	1:C:617:ARG:HB3	1.90	0.53
1:D:86:ASP:C	1:D:88:ALA:H	2.16	0.53
1:E:313:GLN:HE21	1:E:317:GLY:HA3	1.72	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:585:MET:HE1	1:E:602:VAL:HG13	1.90	0.53
1:E:585:MET:HE2	1:E:626:LEU:HD21	1.90	0.53
1:F:555:LYS:HE2	1:F:555:LYS:HA	1.90	0.53
2:J:218:MET:HG2	2:J:219:LEU:N	2.19	0.53
1:B:101:PHE:HZ	1:B:193:LEU:HD13	1.72	0.53
1:C:536:LEU:HD12	1:C:640:LEU:HB3	1.89	0.53
2:H:95:ALA:HB1	2:H:97:PRO:HD2	1.91	0.53
2:I:120:ALA:O	2:I:124:HIS:HB2	2.08	0.53
1:B:246:GLU:O	1:C:414:MET:HE1	2.09	0.53
1:F:26:GLU:HG2	1:F:51:THR:HB	1.91	0.53
1:F:184:ALA:HB1	1:F:200:LYS:O	2.09	0.53
1:F:503:ILE:HG22	1:F:506:GLY:H	1.73	0.53
1:F:710:LEU:O	1:F:714:ILE:HG13	2.09	0.53
3:K:68:ASP:O	3:K:71:GLN:HG3	2.09	0.53
1:B:184:ALA:HB1	1:B:200:LYS:O	2.07	0.53
1:B:576:PHE:HB2	1:B:581:LYS:HG3	1.90	0.53
1:D:136:LEU:HD23	1:D:136:LEU:H	1.73	0.53
1:D:510:TRP:HB3	1:D:679:ALA:HB2	1.90	0.53
1:D:731:ALA:HA	1:D:734:ARG:NH1	2.23	0.53
1:F:106:ASN:HB3	1:F:143:LYS:HZ2	1.73	0.53
1:F:525:VAL:HG11	1:F:560:SER:CB	2.38	0.53
2:I:179:GLN:O	2:I:182:ILE:HG12	2.08	0.53
2:I:254:GLN:HB2	2:I:291:GLU:HG2	1.89	0.53
5:M:67:ILE:O	5:M:71:MET:HG2	2.08	0.53
1:B:546:HIS:O	1:B:549:LYS:HE3	2.09	0.53
1:B:569:SER:HA	1:B:603:ASP:HB3	1.91	0.53
1:D:14:ASP:O	1:D:18:LEU:HG	2.08	0.53
1:D:263:GLY:O	1:D:439:ALA:N	2.38	0.53
1:D:522:GLU:OE2	1:D:556:ILE:HA	2.08	0.53
1:D:686:PHE:HB3	1:D:690:GLU:HG3	1.91	0.53
1:F:525:VAL:HG11	1:F:560:SER:HB2	1.91	0.53
1:A:300:ALA:HA	1:A:303:ARG:HG2	1.91	0.53
1:A:306:PHE:CD1	1:A:357:LYS:HB3	2.44	0.53
1:A:347:HIS:N	1:A:348:ASP:HA	2.23	0.53
1:A:421:SER:HB3	1:A:424:VAL:CG2	2.33	0.53
1:B:310:GLU:OE2	1:B:357:LYS:NZ	2.41	0.53
1:C:38:ARG:HB3	1:C:79:GLU:HB2	1.91	0.53
1:E:89:LYS:HB3	1:E:89:LYS:NZ	2.23	0.53
1:E:307:ALA:HA	1:E:310:GLU:HG2	1.91	0.53
1:F:34:HIS:HB2	1:F:83:TYR:O	2.08	0.53
5:M:33:LEU:HA	5:M:153:VAL:HG22	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:GLY:HA3	1:A:389:LEU:HD13	1.90	0.53
1:C:606:GLU:HB2	1:C:648:ARG:HD2	1.90	0.53
1:D:101:PHE:CD2	1:D:107:ILE:HA	2.44	0.53
1:F:605:ILE:HD11	1:F:644:GLY:HA3	1.89	0.53
1:A:550:THR:HG23	1:A:603:ASP:OD1	2.08	0.52
1:D:67:ARG:NH1	1:D:74:ILE:HD11	2.24	0.52
1:D:528:THR:HG22	1:D:597:LEU:HD11	1.90	0.52
1:F:635:PRO:HD2	1:F:638:ARG:HD2	1.90	0.52
2:I:219:LEU:HA	2:I:222:LYS:HB3	1.91	0.52
2:G:179:GLN:O	2:G:182:ILE:HG12	2.09	0.52
1:D:527:GLN:HE22	1:E:716:MET:HA	1.73	0.52
1:D:680:LEU:HB2	1:D:691:ARG:HH21	1.73	0.52
1:E:540:LEU:HD12	1:E:541:LEU:N	2.24	0.52
1:F:508:ILE:C	1:F:509:LYS:HD3	2.34	0.52
1:F:517:VAL:HG13	1:F:665:ILE:CG2	2.38	0.52
1:F:612:VAL:HG13	1:F:614:ILE:O	2.10	0.52
2:H:235:PHE:HB3	5:M:31:ARG:HB3	1.91	0.52
2:J:225:VAL:HG23	2:J:241:CYS:HB2	1.91	0.52
3:K:73:GLY:HA3	5:M:189:LYS:HE2	1.91	0.52
1:A:68:LYS:HD2	2:H:219:LEU:CD2	2.39	0.52
1:A:437:SER:OG	1:A:440:GLU:HG2	2.09	0.52
1:D:604:ASP:HB3	1:D:607:ARG:HB2	1.91	0.52
4:L:210:ARG:HG2	4:L:210:ARG:HH11	1.75	0.52
5:M:177:GLN:O	5:M:181:ILE:HG13	2.09	0.52
1:A:611:TYR:CE2	1:A:651:VAL:HG11	2.44	0.52
1:B:402:GLY:O	1:B:406:ILE:HD12	2.10	0.52
1:B:656:GLU:OE1	1:C:648:ARG:NH2	2.42	0.52
1:C:308:ASP:OD1	1:C:309:ALA:N	2.42	0.52
1:F:720:MET:HB3	1:F:724:TYR:HB2	1.90	0.52
2:H:127:ILE:HG23	2:H:131:TYR:CE1	2.44	0.52
1:C:45:TYR:CE2	1:C:70:ALA:HA	2.44	0.52
1:C:677:LEU:HD21	1:C:695:ALA:CB	2.40	0.52
1:F:315:ARG:HG3	1:F:316:LEU:HD12	1.90	0.52
1:F:515:THR:HA	1:F:518:LEU:CD1	2.39	0.52
2:H:69:ALA:HB1	2:H:85:PHE:CE1	2.44	0.52
2:I:39:GLU:HB2	2:I:75:LEU:CD1	2.39	0.52
2:I:149:ALA:HB2	2:I:164:CYS:HB2	1.92	0.52
2:I:159:SER:OG	3:K:55:GLU:HG2	2.09	0.52
2:J:127:ILE:HG23	2:J:131:TYR:CE1	2.43	0.52
5:M:68:ASN:O	5:M:72:LYS:HG3	2.10	0.52
1:C:538:SER:O	1:C:662:SER:OG	2.27	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:310:GLU:OE2	1:F:357:LYS:NZ	2.42	0.52
3:K:83:LYS:HB3	5:M:203:LEU:HD21	1.92	0.52
1:B:479:ASP:O	1:B:480:PHE:C	2.51	0.52
1:B:503:ILE:HD11	1:B:554:ALA:HB3	1.90	0.52
1:E:128:GLN:O	1:E:176:LEU:HD12	2.10	0.52
1:E:696:GLN:HB3	1:E:697:GLN:NE2	2.25	0.52
2:H:126:SER:O	2:H:130:ILE:HG13	2.09	0.52
2:G:127:ILE:HG23	2:G:131:TYR:CE1	2.44	0.52
1:A:64:LEU:O	1:A:68:LYS:HG2	2.10	0.52
1:A:454:ASN:HA	1:F:232:ARG:CZ	2.39	0.52
1:B:728:LYS:HE3	1:B:732:LEU:HD21	1.90	0.52
1:C:227:PHE:O	1:C:231:PHE:HB2	2.09	0.52
1:C:231:PHE:O	1:C:235:PHE:HB2	2.10	0.52
1:D:136:LEU:HD23	1:D:136:LEU:N	2.25	0.52
1:D:326:ILE:HG22	1:D:370:ILE:HG13	1.92	0.52
1:E:527:GLN:HA	1:F:719:GLN:CD	2.34	0.52
1:E:536:LEU:HD22	1:E:634:PRO:HD3	1.92	0.52
2:H:244:MET:O	2:H:248:LEU:HG	2.10	0.52
2:G:40:GLU:O	2:G:44:ILE:HG12	2.09	0.52
2:G:243:LEU:HD13	2:G:266:TYR:HB2	1.92	0.52
4:L:216:PHE:CE2	5:M:160:LEU:HD22	2.45	0.52
5:M:26:LEU:O	5:M:30:ARG:HG3	2.10	0.52
1:A:73:SER:HA	2:H:218:MET:SD	2.49	0.52
1:A:223:LEU:HD12	1:A:227:PHE:HB2	1.91	0.52
1:A:356:SER:HB2	1:B:288:PRO:HD3	1.91	0.52
1:B:533:ARG:HG3	1:B:534:THR:N	2.23	0.52
1:C:596:GLN:HA	1:C:638:ARG:CD	2.38	0.52
1:C:611:TYR:HE1	1:C:616:PRO:HB2	1.75	0.52
1:C:686:PHE:CE1	1:C:714:ILE:HG23	2.45	0.52
1:D:187:LYS:NZ	1:D:316:LEU:HD11	2.25	0.52
1:E:612:VAL:HG11	1:E:617:ARG:HH21	1.74	0.52
1:B:122:ILE:O	1:B:126:ASN:HB3	2.09	0.52
1:D:512:ASP:N	1:D:513:PRO:CD	2.73	0.52
1:E:689:LYS:O	1:E:692:THR:OG1	2.26	0.52
2:H:179:GLN:O	2:H:182:ILE:HG12	2.10	0.52
1:A:136:LEU:N	1:A:136:LEU:HD23	2.25	0.51
1:A:227:PHE:CE1	1:A:273:ILE:HD13	2.45	0.51
1:A:247:GLN:C	1:B:413:ARG:HH12	2.18	0.51
1:A:258:LEU:O	1:A:372:MET:HA	2.09	0.51
1:B:91:CYS:HB3	1:B:155:MET:HE2	1.92	0.51
1:D:18:LEU:HD13	1:D:144:LEU:HD21	1.90	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:24:VAL:O	1:D:51:THR:HA	2.10	0.51
1:D:184:ALA:HB1	1:D:200:LYS:O	2.10	0.51
1:E:618:PHE:CZ	1:F:612:VAL:HG11	2.31	0.51
1:F:188:ALA:O	1:F:189:GLU:C	2.53	0.51
2:G:244:MET:O	2:G:248:LEU:HG	2.10	0.51
1:C:64:LEU:O	1:C:68:LYS:HG3	2.10	0.51
1:C:285:VAL:HA	1:C:326:ILE:HG13	1.92	0.51
1:D:539:VAL:HG23	1:D:663:THR:CG2	2.41	0.51
1:E:45:TYR:CE2	1:E:70:ALA:HA	2.45	0.51
2:I:40:GLU:O	2:I:44:ILE:HG12	2.11	0.51
2:J:149:ALA:HB2	2:J:164:CYS:HB2	1.91	0.51
2:G:78:LYS:HB3	2:G:110:ILE:HG23	1.92	0.51
3:K:49:ASN:HB3	4:L:219:MET:CE	2.39	0.51
3:K:84:LEU:HD13	5:M:78:LEU:HD22	1.91	0.51
1:A:489:LYS:H	1:A:490:PRO:HD2	1.75	0.51
1:B:421:SER:HG	1:B:479:ASP:N	2.09	0.51
1:B:626:LEU:O	1:B:630:LEU:HG	2.10	0.51
1:C:616:PRO:HG2	1:D:614:ILE:HD13	1.92	0.51
1:C:632:LYS:HG3	1:D:571:ASP:CG	2.36	0.51
1:D:657:MET:HG2	1:D:661:PHE:HE2	1.75	0.51
1:E:106:ASN:HB3	1:E:143:LYS:HZ1	1.73	0.51
1:F:327:PHE:HB2	1:F:330:ILE:CG2	2.33	0.51
2:H:195:SER:C	2:H:197:LEU:H	2.18	0.51
3:K:88:TYR:HB2	5:M:81:LEU:HD11	1.91	0.51
5:M:156:ILE:O	5:M:160:LEU:HG	2.09	0.51
1:C:399:ASP:O	1:C:403:ARG:N	2.39	0.51
1:C:612:VAL:CG1	1:C:617:ARG:HB3	2.40	0.51
1:C:686:PHE:HE1	1:C:714:ILE:HG23	1.75	0.51
1:D:528:THR:CB	1:D:641:LEU:HD12	2.40	0.51
1:E:136:LEU:N	1:E:136:LEU:HD23	2.25	0.51
1:E:666:HIS:CD2	1:E:668:PRO:HD3	2.45	0.51
3:K:83:LYS:CD	5:M:203:LEU:HD11	2.33	0.51
1:A:184:ALA:HB1	1:A:200:LYS:O	2.10	0.51
1:A:607:ARG:NH1	1:F:624:GLN:OE1	2.44	0.51
1:C:121:PHE:CD2	1:C:183:VAL:HG21	2.46	0.51
1:C:270:ALA:O	1:C:273:ILE:HG22	2.10	0.51
1:C:521:GLY:HA3	1:C:556:ILE:HD13	1.91	0.51
1:C:728:LYS:HE3	1:C:732:LEU:HD21	1.91	0.51
1:D:254:LYS:O	1:D:368:LEU:HA	2.11	0.51
1:D:325:ILE:O	1:D:369:VAL:HA	2.10	0.51
1:E:540:LEU:HD12	1:E:541:LEU:H	1.76	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:235:PHE:CD1	5:M:31:ARG:HG2	2.45	0.51
2:J:50:ASN:HD21	2:G:115:GLY:HA2	1.75	0.51
1:A:106:ASN:HB3	1:A:143:LYS:NZ	2.24	0.51
1:B:236:ALA:O	1:B:239:VAL:HG12	2.10	0.51
1:B:327:PHE:CZ	1:B:369:VAL:HG21	2.46	0.51
1:B:395:ILE:H	1:B:395:ILE:HD12	1.75	0.51
1:C:511:GLY:C	1:C:513:PRO:HD2	2.35	0.51
1:E:121:PHE:HD2	1:E:183:VAL:HG21	1.75	0.51
1:E:510:TRP:CE3	1:E:511:GLY:HA3	2.45	0.51
1:E:674:GLU:O	1:E:677:LEU:HB2	2.11	0.51
1:F:122:ILE:O	1:F:126:ASN:HB3	2.10	0.51
2:I:208:LYS:HG2	2:I:275:TRP:CZ3	2.45	0.51
2:G:267:ASP:OD2	2:G:271:ARG:NH1	2.42	0.51
1:C:411:THR:O	1:C:414:MET:HB2	2.10	0.51
1:E:327:PHE:CZ	1:E:369:VAL:HG21	2.46	0.51
2:J:233:PRO:HA	2:J:235:PHE:CZ	2.45	0.51
5:M:160:LEU:HA	5:M:163:MET:HE3	1.91	0.51
1:B:397:LEU:HD11	1:B:638:ARG:HH21	1.76	0.51
1:C:86:ASP:C	1:C:88:ALA:H	2.18	0.51
1:D:507:ILE:HG21	1:D:509:LYS:HZ1	1.74	0.51
1:E:545:PRO:O	1:E:546:HIS:HB2	2.10	0.51
1:A:222:GLY:O	1:A:224:ASP:N	2.44	0.51
1:B:313:GLN:O	1:B:317:GLY:N	2.43	0.51
1:C:322:LEU:HD12	1:C:324:ILE:HD11	1.93	0.51
1:C:356:SER:HB3	1:D:288:PRO:HG3	1.92	0.51
1:D:524:LEU:HD13	1:D:663:THR:HG21	1.93	0.51
1:D:602:VAL:O	1:D:644:GLY:HA2	2.11	0.51
2:I:119:ILE:HD12	2:I:122:LYS:HB2	1.93	0.51
2:G:21:VAL:HG23	2:G:38:ILE:HD13	1.92	0.51
5:M:26:LEU:HD22	5:M:146:MET:HE3	1.92	0.51
1:A:270:ALA:HA	1:A:273:ILE:HG22	1.92	0.51
1:C:136:LEU:N	1:C:136:LEU:HD23	2.26	0.51
1:C:691:ARG:HH11	1:C:691:ARG:HB2	1.77	0.51
1:D:330:ILE:HD12	1:D:331:ASP:N	2.25	0.51
1:D:508:ILE:HG12	1:D:683:LEU:HD21	1.92	0.51
1:D:560:SER:HB2	1:D:562:PHE:CD1	2.45	0.51
1:E:652:LEU:HD22	1:E:658:LEU:HD13	1.91	0.51
1:E:666:HIS:HD2	1:E:668:PRO:HD3	1.76	0.51
1:F:512:ASP:OD1	1:F:513:PRO:HD3	2.10	0.51
1:F:542:GLU:O	1:F:666:HIS:ND1	2.44	0.51
1:F:609:LEU:HD13	1:F:655:MET:CE	2.41	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:658:LEU:HA	1:F:661:PHE:HD2	1.76	0.51
2:I:39:GLU:HB2	2:I:75:LEU:HD11	1.92	0.51
1:A:489:LYS:N	1:A:490:PRO:CD	2.74	0.50
1:B:249:GLY:HA3	1:C:414:MET:CE	2.40	0.50
1:C:542:GLU:HB2	1:C:649:LYS:HD3	1.93	0.50
1:D:108:ASP:OD2	1:D:143:LYS:HE2	2.10	0.50
1:D:257:LEU:HG	1:D:371:GLY:O	2.11	0.50
1:D:313:GLN:OE1	1:D:365:ASN:O	2.29	0.50
1:D:589:PHE:CE2	1:D:629:LEU:HD13	2.46	0.50
1:D:677:LEU:O	1:D:691:ARG:NH2	2.44	0.50
1:E:24:VAL:O	1:E:51:THR:HA	2.11	0.50
1:F:136:LEU:N	1:F:136:LEU:HD23	2.26	0.50
1:A:16:LEU:HD11	1:A:52:HIS:HD2	1.75	0.50
1:A:300:ALA:O	1:A:304:LYS:HG3	2.10	0.50
1:C:121:PHE:HD2	1:C:183:VAL:HG21	1.76	0.50
1:C:560:SER:HB2	1:C:562:PHE:CE1	2.46	0.50
1:C:688:ASP:HA	1:C:691:ARG:NH1	2.26	0.50
1:D:128:GLN:O	1:D:176:LEU:HD12	2.12	0.50
1:D:511:GLY:HA3	1:D:675:GLN:HE21	1.76	0.50
1:E:327:PHE:HB2	1:E:330:ILE:CG2	2.33	0.50
1:E:654:GLU:CD	1:F:614:ILE:HD11	2.36	0.50
2:H:185:TYR:HA	2:H:188:VAL:HG12	1.93	0.50
2:G:235:PHE:CG	5:M:152:GLN:HG2	2.46	0.50
3:K:39:VAL:HG21	4:L:209:ILE:CD1	2.39	0.50
1:A:103:GLN:C	1:A:105:LYS:H	2.19	0.50
1:A:264:CYS:HG	1:A:265:GLY:N	2.08	0.50
1:C:611:TYR:CZ	1:C:651:VAL:HG11	2.46	0.50
1:D:356:SER:OG	1:E:288:PRO:HB3	2.12	0.50
1:D:686:PHE:HE1	1:D:714:ILE:HG23	1.76	0.50
1:E:232:ARG:CZ	1:F:450:SER:O	2.58	0.50
2:J:40:GLU:O	2:J:44:ILE:HG12	2.11	0.50
1:A:326:ILE:HG22	1:A:370:ILE:CG1	2.40	0.50
1:B:492:PHE:C	1:B:494:THR:H	2.19	0.50
1:C:576:PHE:HB2	1:C:581:LYS:HE3	1.94	0.50
1:D:540:LEU:HD12	1:D:661:PHE:CE1	2.46	0.50
1:E:549:LYS:HG2	1:E:550:THR:N	2.26	0.50
1:E:563:PRO:HD2	1:E:597:LEU:O	2.12	0.50
2:I:116:ARG:HH22	5:M:183:GLU:HA	1.75	0.50
3:K:68:ASP:OD2	4:L:236:ASN:ND2	2.45	0.50
1:A:18:LEU:HD13	1:A:139:SER:CB	2.41	0.50
1:B:576:PHE:HB3	1:B:580:ALA:HB3	1.92	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:404:LEU:HG	1:C:426:ILE:HG22	1.94	0.50
1:C:730:LEU:O	1:C:734:ARG:HG3	2.12	0.50
1:D:198:LYS:O	1:D:198:LYS:HD3	2.12	0.50
1:D:298:SER:O	1:D:301:ASN:HB3	2.11	0.50
1:D:593:TYR:OH	1:D:632:LYS:HD2	2.12	0.50
1:E:232:ARG:NH2	1:F:454:ASN:CB	2.74	0.50
1:F:289:GLU:O	1:F:291:LEU:N	2.33	0.50
1:F:327:PHE:CZ	1:F:369:VAL:HG21	2.46	0.50
2:I:18:GLU:HA	2:I:21:VAL:HG12	1.93	0.50
2:J:72:HIS:CE1	2:J:77:SER:HB2	2.46	0.50
2:J:223:LEU:O	2:J:227:LYS:HG3	2.11	0.50
1:B:669:ASN:CG	1:B:706:GLY:HA2	2.36	0.50
1:C:703:VAL:O	1:C:704:TRP:HD1	1.95	0.50
1:D:375:ARG:NH2	1:D:377:ASP:OD2	2.42	0.50
1:D:632:LYS:HZ3	1:E:571:ASP:HB3	1.75	0.50
1:E:232:ARG:HH21	1:F:454:ASN:N	2.07	0.50
1:E:596:GLN:O	1:E:638:ARG:HA	2.12	0.50
1:F:188:ALA:O	1:F:191:SER:HB2	2.12	0.50
1:F:529:LYS:HG3	1:F:597:LEU:HD11	1.93	0.50
2:I:72:HIS:CE1	2:I:80:ASP:HB2	2.47	0.50
2:J:53:LYS:HE3	2:G:117:PHE:CD2	2.47	0.50
2:G:118:THR:O	2:G:122:LYS:HG2	2.12	0.50
2:G:243:LEU:HD22	2:G:266:TYR:CD2	2.47	0.50
5:M:36:VAL:HG23	5:M:156:ILE:HD12	1.94	0.50
1:A:612:VAL:HG12	1:A:617:ARG:HB2	1.93	0.50
1:B:23:VAL:HG12	1:B:55:VAL:HG21	1.93	0.50
1:B:428:GLU:O	1:B:432:GLU:HG2	2.12	0.50
1:C:428:GLU:O	1:C:432:GLU:HG2	2.12	0.50
1:C:445:VAL:HG12	1:C:449:GLN:HE22	1.76	0.50
1:C:568:CYS:HB2	1:C:602:VAL:HA	1.93	0.50
1:C:721:ASP:O	1:C:725:ARG:HG3	2.11	0.50
1:E:256:ILE:O	1:E:370:ILE:HA	2.12	0.50
1:E:538:SER:OG	1:E:662:SER:N	2.40	0.50
2:H:79:HIS:CE1	3:K:72:ALA:HB1	2.46	0.50
2:I:244:MET:O	2:I:248:LEU:HG	2.12	0.50
2:G:180:LYS:O	2:G:184:ILE:HG13	2.12	0.50
3:K:56:ARG:HD2	5:M:171:ILE:HG12	1.94	0.50
4:L:209:ILE:HG21	5:M:32:MET:CG	2.40	0.50
1:A:128:GLN:O	1:A:176:LEU:HD12	2.12	0.50
1:A:149:VAL:HG11	1:A:152:ILE:HD11	1.94	0.50
1:C:618:PHE:HE1	1:C:620:ASN:OD1	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:CYS:O	1:D:154:ALA:HA	2.11	0.50
1:D:402:GLY:HA2	1:D:405:GLN:OE1	2.12	0.50
2:I:53:LYS:HE3	2:J:117:PHE:CE2	2.46	0.50
1:A:14:ASP:O	1:A:18:LEU:HG	2.12	0.50
1:A:353:GLN:HA	1:B:288:PRO:HG3	1.94	0.50
1:B:106:ASN:HB3	1:B:143:LYS:NZ	2.26	0.50
1:B:395:ILE:HD12	1:B:395:ILE:N	2.27	0.50
1:B:490:PRO:HA	1:B:491:ALA:CB	2.31	0.50
1:C:507:ILE:CD1	1:C:555:LYS:HD3	2.42	0.50
1:C:525:VAL:HG13	1:C:562:PHE:CZ	2.47	0.50
1:D:109:SER:O	1:D:110:ASN:C	2.54	0.50
1:D:331:ASP:HA	1:D:379:ILE:HD11	1.92	0.50
1:D:539:VAL:HG13	1:D:643:ILE:HG13	1.93	0.50
1:E:47:PHE:HE2	1:E:66:GLN:HB3	1.76	0.50
1:F:303:ARG:CG	1:F:357:LYS:HE2	2.40	0.50
2:H:266:TYR:CZ	2:H:270:SER:HB2	2.47	0.50
2:I:179:GLN:HB3	2:I:214:PHE:HB3	1.93	0.50
3:K:70:LEU:HD22	5:M:185:ALA:HA	1.94	0.50
1:A:454:ASN:HA	1:F:232:ARG:NH2	2.27	0.49
1:A:598:SER:O	1:A:640:LEU:HA	2.11	0.49
1:B:516:ARG:O	1:B:519:ASP:OD1	2.29	0.49
1:E:428:GLU:O	1:E:432:GLU:HG2	2.12	0.49
1:F:428:GLU:O	1:F:432:GLU:HG2	2.12	0.49
2:H:233:PRO:CG	2:G:268:SER:HA	2.42	0.49
2:J:231:LEU:O	2:J:232:PHE:C	2.55	0.49
2:G:67:GLN:O	2:G:71:LEU:HG	2.11	0.49
1:B:256:ILE:O	1:B:370:ILE:HA	2.12	0.49
1:C:361:VAL:HA	1:D:267:THR:CG2	2.43	0.49
1:C:677:LEU:HD11	1:C:698:VAL:CG2	2.41	0.49
1:D:95:MET:HG3	1:D:152:ILE:HG12	1.94	0.49
1:D:628:VAL:O	1:D:632:LYS:N	2.45	0.49
1:E:236:ALA:HA	1:E:239:VAL:HG12	1.94	0.49
1:E:524:LEU:HD11	1:E:663:THR:HG21	1.93	0.49
1:F:450:SER:O	1:F:453:MET:HB2	2.12	0.49
2:I:167:LYS:HE2	2:I:171:TYR:HE2	1.77	0.49
1:B:45:TYR:CE2	1:B:70:ALA:HA	2.46	0.49
1:C:533:ARG:HD2	1:D:505:ASN:OD1	2.12	0.49
1:D:609:LEU:CD1	1:D:611:TYR:HB2	2.42	0.49
2:J:118:THR:O	2:J:122:LYS:HG2	2.13	0.49
3:K:88:TYR:CB	5:M:81:LEU:HD11	2.41	0.49
1:A:687:LYS:NZ	1:A:722:PRO:HB3	2.27	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:LEU:N	1:B:136:LEU:HD23	2.26	0.49
1:C:149:VAL:HG11	1:C:152:ILE:HD11	1.93	0.49
1:C:256:ILE:O	1:C:370:ILE:HA	2.13	0.49
1:D:694:ILE:O	1:D:698:VAL:HG22	2.12	0.49
2:I:95:ALA:HB1	2:I:97:PRO:HD2	1.93	0.49
2:J:142:ILE:HG23	2:J:168:VAL:HG13	1.94	0.49
2:J:233:PRO:O	2:J:235:PHE:CE2	2.66	0.49
1:A:540:LEU:HD12	1:A:644:GLY:O	2.12	0.49
1:B:499:TYR:HA	1:B:502:TYR:CE2	2.48	0.49
1:B:578:GLU:CG	1:B:619:SER:HB2	2.42	0.49
1:C:589:PHE:CE1	1:C:600:VAL:HG11	2.46	0.49
1:C:614:ILE:O	1:C:616:PRO:HA	2.11	0.49
1:F:311:GLU:O	1:F:314:ARG:HG2	2.13	0.49
5:M:34:GLN:O	5:M:37:GLU:HB2	2.13	0.49
1:A:610:ASP:OD1	1:F:620:ASN:ND2	2.45	0.49
1:B:113:ASP:OD1	1:B:115:ASP:HB2	2.12	0.49
1:B:303:ARG:CG	1:B:357:LYS:HE2	2.41	0.49
1:B:406:ILE:HB	1:B:441:LEU:HD13	1.94	0.49
1:B:479:ASP:O	1:B:482:ALA:N	2.45	0.49
1:C:593:TYR:CE2	1:C:632:LYS:NZ	2.80	0.49
1:D:312:GLU:HG3	1:D:313:GLN:N	2.28	0.49
1:E:303:ARG:CG	1:E:357:LYS:HE2	2.39	0.49
1:F:536:LEU:HD11	1:F:633:ALA:HA	1.94	0.49
2:H:94:LYS:HG3	2:H:94:LYS:O	2.12	0.49
1:A:113:ASP:O	1:A:117:MET:HG3	2.11	0.49
1:A:571:ASP:OD1	1:A:572:LYS:N	2.46	0.49
1:B:606:GLU:OE1	1:B:606:GLU:N	2.45	0.49
1:B:710:LEU:O	1:B:714:ILE:HG13	2.13	0.49
1:C:311:GLU:O	1:C:314:ARG:HG2	2.13	0.49
1:C:407:LEU:O	1:C:411:THR:OG1	2.27	0.49
1:E:101:PHE:HE1	1:E:193:LEU:HB2	1.78	0.49
1:E:540:LEU:HD12	1:E:644:GLY:O	2.12	0.49
1:E:562:PHE:CD1	1:E:597:LEU:HG	2.48	0.49
2:G:18:GLU:HA	2:G:21:VAL:HG12	1.95	0.49
2:G:182:ILE:O	2:G:186:GLU:HG2	2.13	0.49
3:K:44:ASP:O	3:K:47:ARG:HB3	2.13	0.49
4:L:247:ALA:O	4:L:251:THR:HG23	2.13	0.49
1:A:231:PHE:CE2	1:A:235:PHE:HD2	2.31	0.49
1:A:283:LYS:HA	1:A:324:ILE:O	2.13	0.49
1:A:313:GLN:OE1	1:A:317:GLY:HA2	2.13	0.49
1:A:517:VAL:HG13	1:A:665:ILE:HG21	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:617:ARG:HG3	1:A:617:ARG:NH1	2.28	0.49
1:B:653:GLN:OE1	1:B:658:LEU:HD22	2.12	0.49
1:C:512:ASP:N	1:C:513:PRO:CD	2.76	0.49
2:G:266:TYR:C	2:G:268:SER:H	2.21	0.49
1:A:626:LEU:CD2	1:A:657:MET:HE1	2.42	0.49
1:B:121:PHE:HD2	1:B:183:VAL:HG21	1.77	0.49
1:D:114:THR:HG21	1:D:200:LYS:HG2	1.95	0.49
1:E:64:LEU:HB2	1:E:67:ARG:HH21	1.77	0.49
1:F:236:ALA:O	1:F:239:VAL:HG12	2.12	0.49
2:H:162:ASN:O	2:H:166:LEU:HG	2.13	0.49
2:J:94:LYS:HE3	2:G:153:LYS:HG3	1.94	0.49
2:G:175:LEU:HD23	2:G:177:GLN:NE2	2.26	0.49
3:K:70:LEU:HA	5:M:189:LYS:HD3	1.94	0.49
1:A:67:ARG:CD	2:H:218:MET:HG3	2.38	0.49
1:A:95:MET:HG3	1:A:152:ILE:HG12	1.95	0.49
1:A:636:GLN:HA	1:A:637:GLY:HA2	1.49	0.49
1:B:128:GLN:O	1:B:176:LEU:HD12	2.13	0.49
1:B:193:LEU:HG	1:B:195:LEU:HG	1.94	0.49
1:D:249:GLY:HA3	1:E:414:MET:HE3	1.95	0.49
1:D:511:GLY:CA	1:D:675:GLN:HE21	2.26	0.49
1:E:46:ILE:HD12	1:E:174:VAL:HG21	1.93	0.49
2:H:130:ILE:C	2:H:132:GLU:H	2.21	0.49
2:H:237:ASP:C	2:H:239:ARG:H	2.20	0.49
1:A:315:ARG:C	1:A:316:LEU:HD12	2.38	0.48
1:B:523:LEU:HA	1:B:526:GLN:HG2	1.95	0.48
1:C:16:LEU:HD11	1:C:52:HIS:HD2	1.78	0.48
1:D:681:GLU:HG2	1:D:691:ARG:CZ	2.42	0.48
1:E:254:LYS:O	1:E:368:LEU:HA	2.13	0.48
1:E:684:GLY:HA2	1:E:691:ARG:HH21	1.78	0.48
2:J:287:ILE:O	2:J:291:GLU:HG3	2.13	0.48
2:G:72:HIS:HE1	2:G:80:ASP:CB	2.23	0.48
1:B:258:LEU:HB3	1:B:395:ILE:CD1	2.27	0.48
1:C:18:LEU:HD13	1:C:139:SER:OG	2.12	0.48
1:E:95:MET:HG3	1:E:152:ILE:HG12	1.94	0.48
1:E:281:GLU:N	1:E:282:PRO:HA	2.28	0.48
1:E:411:THR:O	1:E:414:MET:HB2	2.13	0.48
1:F:395:ILE:HD12	1:F:395:ILE:N	2.29	0.48
2:G:101:ILE:HD13	2:G:135:LEU:HD11	1.95	0.48
2:G:218:MET:CG	2:G:219:LEU:N	2.75	0.48
1:A:45:TYR:CE2	1:A:70:ALA:HA	2.49	0.48
1:C:299:GLU:OE2	1:C:349:THR:OG1	2.26	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:330:ILE:HB	1:C:373:THR:HB	1.94	0.48
1:C:584:ALA:O	1:C:588:ILE:HG13	2.12	0.48
1:D:552:LEU:O	1:D:556:ILE:HG13	2.12	0.48
1:D:592:ALA:HB1	1:D:640:LEU:HD13	1.93	0.48
1:D:670:ILE:HD11	1:D:705:ILE:HG23	1.95	0.48
1:E:670:ILE:HG22	1:E:672:THR:N	2.25	0.48
1:F:313:GLN:O	1:F:317:GLY:N	2.46	0.48
1:F:319:ASN:HB3	1:F:320:SER:HB2	1.95	0.48
2:H:72:HIS:O	2:H:75:LEU:HB3	2.13	0.48
2:H:180:LYS:O	2:H:184:ILE:HG13	2.13	0.48
2:J:67:GLN:O	2:J:71:LEU:HG	2.13	0.48
4:L:198:ARG:HG2	4:L:202:ILE:HD11	1.95	0.48
5:M:33:LEU:HD12	5:M:149:ASN:CB	2.44	0.48
1:A:627:LEU:O	1:A:631:LYS:NZ	2.46	0.48
1:B:193:LEU:HD21	1:B:195:LEU:HD21	1.95	0.48
1:B:281:GLU:N	1:B:282:PRO:HA	2.28	0.48
1:C:681:GLU:HG3	1:C:691:ARG:HD2	1.96	0.48
1:E:16:LEU:HD11	1:E:52:HIS:HD2	1.79	0.48
1:E:243:GLU:O	1:E:246:GLU:HG2	2.13	0.48
1:E:404:LEU:HG	1:E:426:ILE:HG22	1.94	0.48
1:F:36:ILE:HD11	1:F:44:LYS:HD2	1.95	0.48
2:H:207:PHE:HB2	2:H:240:GLU:HG2	1.96	0.48
1:C:89:LYS:O	1:C:89:LYS:HG2	2.12	0.48
1:C:325:ILE:HG13	1:C:369:VAL:HG23	1.95	0.48
1:C:386:PRO:HD2	1:D:440:GLU:OE1	2.13	0.48
1:D:310:GLU:O	1:D:313:GLN:CD	2.55	0.48
1:D:326:ILE:HG22	1:D:370:ILE:CG1	2.44	0.48
1:E:526:GLN:HA	1:E:529:LYS:HG2	1.95	0.48
2:I:178:TYR:OH	2:I:282:ARG:HG2	2.14	0.48
2:J:49:ALA:HB2	2:J:64:ALA:HB3	1.95	0.48
2:J:271:ARG:HD2	2:G:231:LEU:HD12	1.96	0.48
2:G:59:SER:OG	2:G:97:PRO:HD3	2.13	0.48
3:K:51:ASP:O	3:K:55:GLU:HG3	2.14	0.48
1:A:193:LEU:HD21	1:A:195:LEU:HD21	1.96	0.48
1:A:353:GLN:HA	1:B:288:PRO:HG2	1.95	0.48
1:B:609:LEU:HD23	1:B:609:LEU:HA	1.67	0.48
1:C:540:LEU:HD22	1:C:661:PHE:CD2	2.49	0.48
1:C:609:LEU:O	1:C:610:ASP:HB2	2.13	0.48
1:D:257:LEU:HB2	1:D:389:LEU:HD13	1.95	0.48
1:F:230:ILE:HD11	1:F:391:VAL:HG11	1.95	0.48
1:F:256:ILE:O	1:F:370:ILE:HA	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:195:SER:C	2:G:197:LEU:H	2.21	0.48
1:A:8:ALA:HB3	1:A:73:SER:O	2.13	0.48
1:A:240:PHE:HE2	1:B:453:MET:SD	2.37	0.48
1:C:613:PRO:HD3	1:C:648:ARG:NH2	2.29	0.48
1:D:103:GLN:C	1:D:105:LYS:H	2.20	0.48
1:D:286:ASN:HB2	1:D:327:PHE:CD1	2.46	0.48
1:D:581:LYS:O	1:D:585:MET:HG2	2.13	0.48
1:D:635:PRO:O	1:D:638:ARG:HB2	2.14	0.48
1:E:658:LEU:HD12	1:E:658:LEU:HA	1.64	0.48
1:F:635:PRO:HB2	1:F:638:ARG:NH1	2.29	0.48
2:I:38:ILE:CD1	2:I:71:LEU:HB3	2.43	0.48
2:I:212:CYS:SG	2:I:279:MET:HE1	2.53	0.48
2:J:235:PHE:CG	3:K:38:GLN:HG2	2.48	0.48
3:K:39:VAL:HA	3:K:42:VAL:HG23	1.96	0.48
5:M:53:GLN:HA	5:M:56:GLN:HG2	1.96	0.48
1:A:407:LEU:CD1	1:A:426:ILE:HG23	2.44	0.48
1:C:380:ASP:OD1	1:C:382:ALA:N	2.43	0.48
1:D:536:LEU:HD21	1:D:630:LEU:O	2.14	0.48
1:E:184:ALA:HB1	1:E:200:LYS:O	2.14	0.48
1:E:440:GLU:O	1:E:444:LEU:HG	2.14	0.48
1:F:601:VAL:HG22	1:F:643:ILE:HD12	1.95	0.48
2:H:233:PRO:HB3	2:G:268:SER:O	2.14	0.48
3:K:83:LYS:HG2	3:K:86:ARG:NH2	2.29	0.48
1:A:562:PHE:CE1	1:A:641:LEU:HD21	2.49	0.48
1:B:106:ASN:HB3	1:B:143:LYS:HZ1	1.79	0.48
1:B:589:PHE:HD2	1:B:629:LEU:HD22	1.78	0.48
1:C:64:LEU:HG	1:C:68:LYS:HD2	1.96	0.48
1:C:322:LEU:HD22	1:C:366:ASN:O	2.14	0.48
1:C:538:SER:OG	1:C:662:SER:N	2.40	0.48
1:D:564:PHE:HB3	1:D:598:SER:HB3	1.95	0.48
1:E:314:ARG:HG3	1:E:315:ARG:N	2.29	0.48
1:E:653:GLN:OE1	1:E:658:LEU:HD23	2.13	0.48
1:F:113:ASP:HA	1:F:196:ILE:HG13	1.96	0.48
1:F:517:VAL:HG21	1:F:667:VAL:HG22	1.95	0.48
2:H:81:ALA:O	2:H:85:PHE:HD1	1.97	0.48
2:J:185:TYR:HA	2:J:188:VAL:HG12	1.96	0.48
1:C:544:PRO:HG2	1:C:669:ASN:CG	2.39	0.48
1:C:657:MET:HE3	1:C:661:PHE:CZ	2.49	0.48
1:D:721:ASP:O	1:D:725:ARG:HG3	2.13	0.48
1:E:445:VAL:O	1:E:449:GLN:HG2	2.14	0.48
1:F:286:ASN:OD1	1:F:327:PHE:HD1	1.97	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:40:GLU:O	2:H:44:ILE:HG12	2.14	0.48
2:J:276:LEU:O	2:J:280:LEU:HG	2.14	0.48
2:G:79:HIS:CG	4:L:242:ASP:OD2	2.67	0.48
5:M:191:ARG:HG3	5:M:191:ARG:NH1	2.29	0.48
1:A:388:ARG:O	1:A:389:LEU:HD22	2.14	0.47
1:B:640:LEU:CD2	1:B:642:ILE:HG13	2.44	0.47
1:F:14:ASP:O	1:F:18:LEU:HG	2.13	0.47
1:F:236:ALA:HA	1:F:239:VAL:CG1	2.44	0.47
1:F:327:PHE:CE2	1:F:369:VAL:HG21	2.49	0.47
1:F:428:GLU:O	1:F:431:VAL:HG12	2.14	0.47
1:F:436:PHE:HB3	1:F:440:GLU:CB	2.44	0.47
2:J:212:CYS:SG	2:J:279:MET:HE1	2.54	0.47
2:J:222:LYS:HA	2:J:225:VAL:HG12	1.96	0.47
1:A:673:GLY:O	1:A:677:LEU:HD22	2.12	0.47
1:A:719:GLN:HG2	1:F:523:LEU:HG	1.96	0.47
1:C:618:PHE:HZ	1:D:612:VAL:HG11	1.79	0.47
1:D:242:PRO:HD2	1:D:243:GLU:N	2.28	0.47
1:D:281:GLU:N	1:D:282:PRO:HA	2.30	0.47
1:E:257:LEU:HG	1:E:371:GLY:O	2.14	0.47
1:E:436:PHE:HB3	1:E:440:GLU:CB	2.44	0.47
1:F:653:GLN:HA	1:F:658:LEU:HB3	1.95	0.47
2:I:17:ALA:O	2:I:21:VAL:HG12	2.13	0.47
2:I:281:LEU:O	2:I:285:LYS:HG3	2.14	0.47
1:A:331:ASP:CA	1:A:379:ILE:HD11	2.32	0.47
1:B:76:GLN:HE21	1:B:78:ILE:CG2	2.26	0.47
1:B:257:LEU:HB2	1:B:389:LEU:HD13	1.95	0.47
1:C:331:ASP:HA	1:C:379:ILE:CD1	2.41	0.47
1:C:355:LEU:HA	1:C:388:ARG:NE	2.30	0.47
1:D:407:LEU:O	1:D:411:THR:HG23	2.14	0.47
1:F:557:ALA:HB2	1:F:601:VAL:HG21	1.97	0.47
2:J:268:SER:HA	2:G:233:PRO:HB2	1.97	0.47
1:B:436:PHE:CD2	1:B:444:LEU:HD11	2.49	0.47
1:C:36:ILE:O	1:C:36:ILE:HG23	2.15	0.47
1:D:149:VAL:HG11	1:D:152:ILE:HD11	1.95	0.47
1:E:23:VAL:HG12	1:E:55:VAL:CG2	2.44	0.47
1:E:428:GLU:O	1:E:431:VAL:HG12	2.14	0.47
1:F:307:ALA:HA	1:F:310:GLU:HG2	1.96	0.47
1:A:242:PRO:O	1:A:246:GLU:OE1	2.33	0.47
1:A:411:THR:HG21	1:A:426:ILE:HD11	1.96	0.47
1:A:609:LEU:O	1:A:610:ASP:HB3	2.13	0.47
1:B:307:ALA:HA	1:B:310:GLU:HG2	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:436:PHE:N	1:B:436:PHE:CD1	2.82	0.47
1:B:537:VAL:HG12	1:C:712:MET:HE1	1.96	0.47
1:C:193:LEU:HD21	1:C:195:LEU:HD21	1.96	0.47
1:D:284:VAL:HG21	1:D:325:ILE:HG22	1.95	0.47
1:E:573:MET:O	1:E:576:PHE:HB2	2.15	0.47
1:F:87:LYS:HA	1:F:91:CYS:SG	2.55	0.47
2:J:163:LYS:O	2:J:167:LYS:HG2	2.15	0.47
2:J:186:GLU:O	2:J:190:THR:HG23	2.14	0.47
1:C:533:ARG:C	1:D:505:ASN:HD21	2.22	0.47
1:C:582:CYS:SG	1:C:621:LEU:HG	2.55	0.47
1:D:318:ALA:O	1:D:319:ASN:ND2	2.47	0.47
1:D:531:SER:OG	1:D:534:THR:OG1	2.30	0.47
1:D:567:ILE:HG23	1:D:601:VAL:HB	1.96	0.47
1:E:86:ASP:C	1:E:88:ALA:H	2.21	0.47
1:F:149:VAL:HG11	1:F:152:ILE:HD11	1.95	0.47
1:F:281:GLU:N	1:F:282:PRO:HA	2.29	0.47
2:I:188:VAL:HG13	2:I:205:TYR:HD2	1.80	0.47
2:J:45:TYR:HB2	2:J:68:ALA:HB2	1.96	0.47
2:J:124:HIS:HE1	2:J:147:GLN:HB3	1.79	0.47
2:J:219:LEU:HD12	2:J:223:LEU:HB2	1.97	0.47
1:A:23:VAL:HG12	1:A:55:VAL:HG21	1.95	0.47
1:A:34:HIS:HB2	1:A:83:TYR:O	2.14	0.47
1:A:98:GLU:HB3	1:A:148:LEU:HB3	1.97	0.47
1:A:240:PHE:CE2	1:B:453:MET:SD	3.08	0.47
1:A:429:LEU:HG	1:A:482:ALA:HB1	1.96	0.47
1:A:650:ASP:OD1	1:A:650:ASP:N	2.46	0.47
1:A:683:LEU:HB3	1:A:685:ASN:HD22	1.76	0.47
1:B:295:VAL:HB	1:C:294:TYR:CG	2.50	0.47
1:B:414:MET:HE2	1:B:414:MET:HA	1.96	0.47
1:B:428:GLU:O	1:B:431:VAL:HG12	2.14	0.47
1:C:122:ILE:O	1:C:126:ASN:HB3	2.14	0.47
1:C:318:ALA:C	1:C:319:ASN:HD22	2.21	0.47
1:C:510:TRP:CZ3	1:C:670:ILE:HG12	2.50	0.47
1:D:52:HIS:C	1:D:54:SER:H	2.23	0.47
1:D:122:ILE:O	1:D:126:ASN:HB3	2.14	0.47
1:D:246:GLU:HG2	1:D:247:GLN:N	2.29	0.47
1:D:570:PRO:HA	1:D:573:MET:HB3	1.97	0.47
1:D:609:LEU:O	1:D:610:ASP:OD1	2.32	0.47
1:D:652:LEU:HD13	1:D:657:MET:HB3	1.95	0.47
1:D:688:ASP:O	1:D:692:THR:HG23	2.14	0.47
1:E:23:VAL:HG12	1:E:55:VAL:HG21	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:67:ARG:HB3	2:J:217:ASP:OD2	2.14	0.47
1:E:241:PRO:HA	1:E:242:PRO:HA	1.54	0.47
1:F:64:LEU:HA	1:F:67:ARG:HE	1.79	0.47
1:F:404:LEU:HG	1:F:426:ILE:HG22	1.96	0.47
1:F:415:ARG:O	1:F:417:HIS:O	2.33	0.47
2:H:243:LEU:HD22	2:H:266:TYR:CG	2.50	0.47
2:I:58:TRP:HB3	2:I:95:ALA:HB2	1.96	0.47
2:J:92:PHE:HB3	2:J:98:GLN:O	2.15	0.47
4:L:237:VAL:HG11	5:M:60:VAL:HG13	1.96	0.47
4:L:240:ALA:O	4:L:244:VAL:HG23	2.14	0.47
1:A:86:ASP:C	1:A:88:ALA:H	2.22	0.47
1:B:246:GLU:HG3	1:C:417:HIS:CE1	2.50	0.47
1:B:272:GLN:OE1	1:B:272:GLN:HA	2.15	0.47
1:C:106:ASN:HB3	1:C:143:LYS:HZ1	1.80	0.47
1:C:539:VAL:HG23	1:C:663:THR:HG23	1.95	0.47
1:D:519:ASP:O	1:D:523:LEU:HG	2.15	0.47
1:E:318:ALA:O	1:E:319:ASN:ND2	2.48	0.47
1:F:257:LEU:HG	1:F:371:GLY:O	2.14	0.47
1:F:570:PRO:CG	1:F:604:ASP:HB2	2.41	0.47
2:J:21:VAL:HG21	2:J:71:LEU:HD22	1.96	0.47
2:G:81:ALA:O	2:G:85:PHE:HD1	1.98	0.47
2:G:267:ASP:OD1	2:G:271:ARG:NH1	2.48	0.47
1:B:52:HIS:C	1:B:54:SER:H	2.23	0.47
1:B:247:GLN:O	1:C:414:MET:SD	2.73	0.47
1:B:327:PHE:CE2	1:B:369:VAL:HG21	2.50	0.47
1:B:568:CYS:SG	1:B:588:ILE:HD12	2.55	0.47
1:B:614:ILE:O	1:B:616:PRO:HA	2.15	0.47
1:B:627:LEU:CD2	1:B:657:MET:HG3	2.42	0.47
1:C:233:ARG:CZ	1:C:233:ARG:HB2	2.44	0.47
1:C:499:TYR:HB3	1:C:558:GLU:OE2	2.15	0.47
1:D:527:GLN:HA	1:E:719:GLN:HG3	1.97	0.47
1:F:613:PRO:HD3	1:F:648:ARG:HH12	1.80	0.47
2:I:200:TYR:H	2:I:200:TYR:HD1	1.63	0.47
2:I:228:TYR:CE2	2:I:230:GLU:HB2	2.49	0.47
2:J:195:SER:C	2:J:197:LEU:H	2.23	0.47
1:C:511:GLY:CA	1:C:513:PRO:HD2	2.45	0.47
1:D:407:LEU:HA	1:D:441:LEU:HD21	1.96	0.47
1:E:436:PHE:N	1:E:436:PHE:CD1	2.83	0.47
1:E:612:VAL:HG22	1:E:613:PRO:HD2	1.97	0.47
1:E:627:LEU:HD13	1:F:607:ARG:NE	2.30	0.47
2:H:39:GLU:HB2	2:H:75:LEU:HD13	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:23:ASP:O	5:M:27:GLU:N	2.44	0.47
1:A:24:VAL:O	1:A:51:THR:HA	2.16	0.46
1:A:36:ILE:HG23	1:A:36:ILE:O	2.15	0.46
1:A:517:VAL:HG13	1:A:665:ILE:CG2	2.45	0.46
1:A:690:GLU:HB3	1:A:726:VAL:HG22	1.97	0.46
1:B:319:ASN:HB3	1:B:320:SER:HB2	1.97	0.46
1:B:353:GLN:HA	1:C:288:PRO:HG3	1.97	0.46
1:C:513:PRO:HA	1:C:516:ARG:HG2	1.97	0.46
1:E:106:ASN:HB3	1:E:143:LYS:HZ2	1.79	0.46
1:E:289:GLU:C	1:E:291:LEU:N	2.69	0.46
1:E:628:VAL:HB	1:F:574:ILE:CD1	2.44	0.46
2:H:219:LEU:HD12	2:H:223:LEU:HB2	1.97	0.46
2:J:244:MET:O	2:J:248:LEU:HG	2.14	0.46
1:A:611:TYR:HD1	1:A:618:PHE:HB3	1.81	0.46
1:C:240:PHE:HB3	1:C:244:ILE:HB	1.97	0.46
1:C:428:GLU:O	1:C:431:VAL:HG12	2.14	0.46
1:E:122:ILE:O	1:E:126:ASN:HB3	2.14	0.46
2:H:186:GLU:O	2:H:190:THR:HG23	2.15	0.46
2:H:243:LEU:HD22	2:H:266:TYR:CD2	2.51	0.46
2:J:112:THR:HG23	2:J:117:PHE:CE1	2.50	0.46
2:J:179:GLN:O	2:J:182:ILE:HG12	2.15	0.46
2:G:108:ILE:HD12	2:G:127:ILE:HD12	1.96	0.46
2:G:219:LEU:HB2	2:G:222:LYS:CB	2.33	0.46
1:A:428:GLU:O	1:A:431:VAL:HG12	2.15	0.46
1:A:593:TYR:HB3	1:A:635:PRO:HD3	1.97	0.46
1:B:230:ILE:HD11	1:B:391:VAL:HG11	1.97	0.46
1:B:311:GLU:O	1:B:314:ARG:HG2	2.15	0.46
1:B:385:ARG:NH1	1:C:263:GLY:HA2	2.29	0.46
1:B:479:ASP:C	1:B:483:SER:H	2.23	0.46
1:C:16:LEU:HD11	1:C:52:HIS:CD2	2.51	0.46
1:C:385:ARG:NH2	1:D:263:GLY:HA3	2.30	0.46
1:C:555:LYS:O	1:C:559:GLU:HG2	2.15	0.46
1:C:573:MET:HB3	1:C:576:PHE:CD2	2.49	0.46
1:D:36:ILE:HG23	1:D:36:ILE:O	2.15	0.46
1:D:627:LEU:CD2	1:D:657:MET:HG3	2.44	0.46
1:E:73:SER:HB2	1:E:76:GLN:HG2	1.96	0.46
1:F:189:GLU:O	1:F:190:ASN:HB2	2.15	0.46
2:H:45:TYR:HB2	2:H:68:ALA:HB2	1.96	0.46
2:I:21:VAL:HG23	2:I:38:ILE:CD1	2.44	0.46
2:J:45:TYR:HE2	2:J:71:LEU:HD11	1.79	0.46
3:K:79:THR:O	3:K:83:LYS:HG3	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:216:PHE:HE2	5:M:160:LEU:HD22	1.81	0.46
1:A:121:PHE:HD2	1:A:183:VAL:HG21	1.81	0.46
1:A:493:GLY:HA2	1:A:494:THR:CB	2.45	0.46
1:B:236:ALA:HA	1:B:239:VAL:CG1	2.45	0.46
1:B:540:LEU:HD12	1:B:540:LEU:O	2.16	0.46
1:C:612:VAL:CG2	1:C:613:PRO:HD2	2.46	0.46
1:D:436:PHE:CE2	1:D:444:LEU:HD12	2.48	0.46
1:D:573:MET:CE	1:D:585:MET:HE3	2.45	0.46
1:E:73:SER:HB2	1:E:76:GLN:CG	2.46	0.46
1:E:246:GLU:CG	1:F:417:HIS:HE1	2.27	0.46
1:E:327:PHE:CE2	1:E:369:VAL:HG21	2.50	0.46
1:F:272:GLN:OE1	1:F:272:GLN:HA	2.15	0.46
2:H:276:LEU:O	2:H:280:LEU:HG	2.16	0.46
2:G:167:LYS:HE2	2:G:171:TYR:HE2	1.80	0.46
3:K:46:MET:CE	4:L:216:PHE:HA	2.45	0.46
1:B:99:ILE:HD11	1:B:145:PHE:CD2	2.50	0.46
1:C:48:THR:HG21	1:C:128:GLN:HG2	1.97	0.46
1:C:326:ILE:HB	1:C:370:ILE:HD11	1.96	0.46
1:D:18:LEU:HD23	1:D:137:VAL:HG21	1.98	0.46
1:D:657:MET:HE2	1:D:661:PHE:HZ	1.81	0.46
1:E:272:GLN:OE1	1:E:272:GLN:HA	2.15	0.46
1:E:677:LEU:HD11	1:E:695:ALA:HA	1.96	0.46
1:E:721:ASP:HB2	1:E:724:TYR:CD2	2.51	0.46
1:F:549:LYS:HE3	1:F:646:THR:C	2.40	0.46
1:F:552:LEU:O	1:F:556:ILE:HG13	2.15	0.46
3:K:39:VAL:HG21	4:L:209:ILE:HD11	1.97	0.46
3:K:56:ARG:HD2	5:M:171:ILE:CG2	2.45	0.46
3:K:57:ASP:OD2	4:L:229:MET:HE1	2.16	0.46
5:M:33:LEU:HD23	5:M:33:LEU:C	2.40	0.46
1:D:589:PHE:CD2	1:D:629:LEU:HD13	2.50	0.46
1:E:36:ILE:HG23	1:E:36:ILE:O	2.16	0.46
1:E:198:LYS:HG2	1:E:198:LYS:O	2.16	0.46
1:F:128:GLN:O	1:F:176:LEU:HD12	2.15	0.46
1:F:325:ILE:HG13	1:F:369:VAL:HB	1.98	0.46
2:H:200:TYR:CZ	5:M:42:ALA:HB2	2.51	0.46
2:J:263:VAL:HG23	2:J:280:LEU:HD13	1.97	0.46
4:L:199:HIS:ND1	5:M:21:LEU:HB3	2.31	0.46
5:M:32:MET:HA	5:M:35:LEU:HD12	1.97	0.46
5:M:42:ALA:HA	5:M:45:ARG:NH2	2.31	0.46
5:M:57:LEU:HD12	5:M:174:GLN:OE1	2.16	0.46
1:A:315:ARG:O	1:A:316:LEU:HD12	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:536:LEU:CD1	1:C:640:LEU:HB3	2.45	0.46
1:C:690:GLU:HB2	1:C:726:VAL:CG2	2.42	0.46
1:D:132:VAL:HG23	1:D:173:GLU:HA	1.97	0.46
1:D:524:LEU:O	1:D:527:GLN:HB3	2.15	0.46
1:E:232:ARG:HE	1:F:454:ASN:CB	2.15	0.46
1:E:240:PHE:HA	1:E:241:PRO:HD3	1.69	0.46
1:E:314:ARG:CG	1:E:315:ARG:N	2.78	0.46
1:E:527:GLN:HG3	1:F:719:GLN:HG3	1.98	0.46
1:E:527:GLN:NE2	1:F:716:MET:HG2	2.27	0.46
1:E:628:VAL:HB	1:F:574:ILE:HD12	1.98	0.46
1:F:246:GLU:HG2	1:F:247:GLN:N	2.31	0.46
1:F:579:THR:O	1:F:583:GLN:HG2	2.15	0.46
2:H:219:LEU:CD1	2:H:223:LEU:HB2	2.45	0.46
2:J:147:GLN:HG2	2:J:151:TYR:CE2	2.51	0.46
3:K:43:VAL:HA	4:L:212:LEU:CD1	2.25	0.46
1:A:215:PHE:N	1:A:231:PHE:CE2	2.84	0.46
1:B:352:ASN:HA	1:B:355:LEU:HD12	1.98	0.46
1:B:536:LEU:HD12	1:B:640:LEU:O	2.16	0.46
1:C:236:ALA:HB1	1:D:453:MET:HB2	1.98	0.46
1:D:268:LEU:HA	1:D:271:ARG:HD2	1.97	0.46
1:F:352:ASN:HA	1:F:355:LEU:HD12	1.98	0.46
1:F:540:LEU:O	1:F:665:ILE:HB	2.16	0.46
1:F:686:PHE:CE1	1:F:714:ILE:HG23	2.50	0.46
2:H:51:MET:O	2:H:54:MET:HB3	2.16	0.46
4:L:219:MET:O	4:L:223:VAL:HG23	2.16	0.46
1:A:64:LEU:HA	1:A:67:ARG:HH21	1.81	0.46
1:B:91:CYS:O	1:B:154:ALA:HA	2.16	0.46
1:B:240:PHE:HA	1:B:241:PRO:HD3	1.73	0.46
1:B:539:VAL:HA	1:B:663:THR:O	2.16	0.46
1:D:571:ASP:O	1:D:574:ILE:HG13	2.15	0.46
1:D:578:GLU:OE1	1:D:621:LEU:HD13	2.15	0.46
1:D:711:LEU:O	1:D:715:GLU:HG2	2.15	0.46
1:E:595:SER:HB3	1:E:598:SER:HB3	1.96	0.46
1:F:8:ALA:HB3	1:F:73:SER:O	2.16	0.46
1:F:241:PRO:HA	1:F:242:PRO:HA	1.60	0.46
1:F:436:PHE:N	1:F:436:PHE:CD1	2.83	0.46
2:H:256:VAL:HG21	2:H:288:GLN:CG	2.44	0.46
2:I:185:TYR:HA	2:I:188:VAL:HG12	1.97	0.46
2:J:72:HIS:O	2:J:75:LEU:HB3	2.16	0.46
2:J:80:ASP:OD1	5:M:66:HIS:CD2	2.69	0.46
2:G:162:ASN:OD1	2:G:188:VAL:HG23	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:236:ASN:O	4:L:240:ALA:HB2	2.16	0.46
1:A:322:LEU:HD12	1:A:323:HIS:H	1.81	0.46
1:A:410:HIS:NE2	1:A:442:GLU:HG2	2.31	0.46
1:C:705:ILE:HD11	1:C:710:LEU:HA	1.97	0.46
1:D:198:LYS:HD3	1:D:198:LYS:C	2.41	0.46
1:D:218:MET:HA	1:D:219:GLY:HA2	1.72	0.46
1:D:618:PHE:CD2	1:D:655:MET:HE1	2.51	0.46
1:E:24:VAL:HG11	1:E:49:LEU:HD22	1.96	0.46
1:E:611:TYR:CE1	1:E:616:PRO:HB2	2.51	0.46
1:F:121:PHE:HD2	1:F:183:VAL:HG21	1.81	0.46
2:G:10:ALA:O	2:G:14:LEU:HG	2.16	0.46
2:G:45:TYR:HB2	2:G:68:ALA:HB2	1.97	0.46
4:L:212:LEU:HA	4:L:215:MET:CE	2.46	0.46
1:A:240:PHE:HA	1:A:241:PRO:HD3	1.81	0.45
1:A:542:GLU:OE2	1:A:666:HIS:CD2	2.68	0.45
1:C:104:LYS:HA	1:C:107:ILE:HG13	1.98	0.45
1:D:40:SER:HB3	1:D:43:HIS:CG	2.50	0.45
1:D:135:GLN:HG2	1:D:148:LEU:HD13	1.97	0.45
1:E:104:LYS:HA	1:E:107:ILE:HD11	1.97	0.45
1:F:95:MET:HG3	1:F:152:ILE:HG12	1.97	0.45
2:H:233:PRO:HB3	2:G:268:SER:HA	1.98	0.45
2:J:266:TYR:HD2	2:J:272:LEU:HD21	1.80	0.45
3:K:54:LEU:HD21	4:L:222:LEU:HD22	1.98	0.45
1:A:356:SER:OG	1:B:288:PRO:HD3	2.16	0.45
1:B:254:LYS:O	1:B:368:LEU:HA	2.16	0.45
1:C:349:THR:O	1:C:352:ASN:HB3	2.15	0.45
1:C:507:ILE:HD12	1:C:555:LYS:HE2	1.98	0.45
1:D:542:GLU:OE2	1:D:649:LYS:HD2	2.16	0.45
1:D:669:ASN:OD1	1:D:669:ASN:N	2.44	0.45
1:E:286:ASN:OD1	1:E:327:PHE:HD1	1.99	0.45
1:E:714:ILE:O	1:E:718:LEU:HG	2.15	0.45
2:I:142:ILE:HG23	2:I:168:VAL:HG13	1.99	0.45
1:D:303:ARG:HD2	1:D:353:GLN:NE2	2.32	0.45
1:E:438:GLY:O	1:E:441:LEU:N	2.39	0.45
2:H:38:ILE:HD11	2:H:71:LEU:HB3	1.98	0.45
3:K:52:LYS:HZ2	3:K:52:LYS:CB	2.28	0.45
3:K:85:LYS:O	3:K:89:TRP:HB3	2.15	0.45
5:M:17:ARG:CB	5:M:20:GLN:HB3	2.46	0.45
1:A:721:ASP:O	1:A:725:ARG:HG3	2.17	0.45
1:B:528:THR:HG21	1:B:641:LEU:HD13	1.98	0.45
1:B:531:SER:HA	1:B:639:LYS:HD3	1.98	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:221:GLY:HA3	1:C:406:ILE:HG13	1.97	0.45
1:C:414:MET:HE2	1:C:414:MET:HA	1.99	0.45
1:C:671:ALA:HA	1:C:703:VAL:O	2.17	0.45
1:D:187:LYS:HZ2	1:D:316:LEU:HD11	1.80	0.45
1:E:399:ASP:O	1:E:403:ARG:N	2.42	0.45
1:E:519:ASP:O	1:E:522:GLU:HB2	2.17	0.45
1:E:593:TYR:CD2	1:E:635:PRO:HD3	2.50	0.45
2:J:243:LEU:O	2:J:247:LEU:HG	2.17	0.45
1:B:307:ALA:O	1:B:310:GLU:HG2	2.17	0.45
1:D:193:LEU:HD21	1:D:195:LEU:HD21	1.97	0.45
1:E:246:GLU:HG3	1:F:417:HIS:CE1	2.46	0.45
1:F:307:ALA:O	1:F:310:GLU:HG2	2.16	0.45
1:F:602:VAL:O	1:F:644:GLY:HA2	2.17	0.45
2:H:266:TYR:C	2:H:268:SER:H	2.25	0.45
2:I:223:LEU:O	2:I:227:LYS:HG3	2.16	0.45
5:M:36:VAL:O	5:M:40:LYS:HB2	2.16	0.45
1:A:27:LYS:HD2	1:A:57:PRO:HG2	1.99	0.45
1:A:242:PRO:HD2	1:A:243:GLU:OE1	2.17	0.45
1:A:402:GLY:O	1:A:406:ILE:HD12	2.15	0.45
1:A:546:HIS:CE1	1:A:709:LYS:HE3	2.52	0.45
1:A:575:GLY:HA3	1:F:586:LYS:CE	2.45	0.45
1:C:143:LYS:HB3	1:C:145:PHE:HE1	1.81	0.45
1:C:327:PHE:HB3	1:C:330:ILE:CD1	2.31	0.45
1:C:707:ILE:O	1:C:711:LEU:HG	2.16	0.45
1:D:424:VAL:HG22	1:D:480:PHE:N	2.32	0.45
1:E:16:LEU:HD11	1:E:52:HIS:CD2	2.52	0.45
1:E:143:LYS:HB3	1:E:145:PHE:HE1	1.81	0.45
1:E:325:ILE:HG13	1:E:369:VAL:HB	1.98	0.45
1:E:618:PHE:CD1	1:E:618:PHE:C	2.95	0.45
2:H:53:LYS:HE3	2:I:117:PHE:CE2	2.52	0.45
2:H:200:TYR:HD2	4:L:217:MET:SD	2.40	0.45
2:I:125:ILE:HD12	2:I:126:SER:N	2.32	0.45
2:I:230:GLU:HG2	2:I:231:LEU:N	2.31	0.45
2:G:204:ASP:OD2	2:G:208:LYS:HE2	2.17	0.45
5:M:33:LEU:HD12	5:M:149:ASN:HB3	1.99	0.45
1:A:421:SER:CB	1:A:424:VAL:HG23	2.39	0.45
1:A:446:ARG:HA	1:A:449:GLN:HG3	1.98	0.45
1:A:624:GLN:HG3	1:B:610:ASP:CG	2.39	0.45
1:B:36:ILE:HG23	1:B:36:ILE:O	2.16	0.45
1:B:507:ILE:CG1	1:B:555:LYS:HD3	2.47	0.45
1:B:508:ILE:HD13	1:B:683:LEU:HD21	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:531:SER:CB	1:B:639:LYS:HD3	2.47	0.45
1:C:388:ARG:O	1:C:389:LEU:HD23	2.17	0.45
1:C:677:LEU:O	1:C:681:GLU:OE1	2.35	0.45
1:E:397:LEU:HD13	1:E:398:PRO:HD2	1.99	0.45
2:I:182:ILE:O	2:I:186:GLU:HG2	2.17	0.45
2:I:182:ILE:CG2	2:I:212:CYS:HB2	2.47	0.45
2:I:216:ILE:HG12	2:I:217:ASP:N	2.31	0.45
2:I:276:LEU:O	2:I:280:LEU:HG	2.17	0.45
2:J:50:ASN:HD21	2:G:115:GLY:HA3	1.82	0.45
2:J:134:GLU:O	2:J:136:VAL:HG23	2.17	0.45
2:J:175:LEU:HD23	2:J:177:GLN:NE2	2.32	0.45
5:M:50:LEU:HD13	5:M:167:MET:HB3	1.99	0.45
1:A:219:GLY:O	1:A:220:ILE:HG13	2.16	0.45
1:A:403:ARG:O	1:A:407:LEU:HG	2.16	0.45
1:C:441:LEU:O	1:C:444:LEU:HG	2.17	0.45
1:D:286:ASN:CB	1:D:327:PHE:HD1	2.29	0.45
1:D:406:ILE:CG2	1:D:441:LEU:HD22	2.34	0.45
1:E:64:LEU:CA	1:E:67:ARG:HE	2.20	0.45
1:E:598:SER:OG	1:E:639:LYS:O	2.20	0.45
1:F:242:PRO:CD	1:F:243:GLU:H	2.30	0.45
1:F:615:GLY:HA3	1:F:616:PRO:C	2.41	0.45
1:F:694:ILE:O	1:F:698:VAL:HG22	2.17	0.45
2:I:118:THR:O	2:I:122:LYS:HG2	2.16	0.45
2:I:214:PHE:HD1	2:I:214:PHE:H	1.62	0.45
2:I:255:ASN:C	2:I:257:ASP:H	2.24	0.45
2:J:176:GLU:O	2:J:178:TYR:N	2.49	0.45
2:G:263:VAL:O	2:G:267:ASP:HB2	2.16	0.45
1:A:263:GLY:C	1:A:437:SER:HB3	2.42	0.45
1:A:607:ARG:NH2	1:F:627:LEU:HD22	2.31	0.45
1:B:246:GLU:HB2	1:C:413:ARG:HH22	1.80	0.45
1:C:324:ILE:HD12	1:C:324:ILE:N	2.32	0.45
1:D:223:LEU:HD23	1:D:223:LEU:O	2.17	0.45
1:E:612:VAL:CG2	1:E:613:PRO:HD2	2.47	0.45
1:E:641:LEU:HD12	1:E:641:LEU:O	2.16	0.45
2:I:219:LEU:O	2:I:221:ALA:N	2.46	0.45
1:A:219:GLY:C	1:A:220:ILE:HG13	2.42	0.45
1:A:355:LEU:HD22	1:A:388:ARG:NH1	2.32	0.45
1:A:357:LYS:HA	1:A:357:LYS:HE3	1.97	0.45
1:B:284:VAL:O	1:B:326:ILE:HG12	2.17	0.45
1:C:24:VAL:HG11	1:C:49:LEU:HD22	1.99	0.45
1:C:330:ILE:HA	1:C:330:ILE:HD13	1.60	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:453:MET:O	1:D:457:ILE:HG13	2.17	0.45
1:D:626:LEU:O	1:D:630:LEU:HG	2.17	0.45
1:D:626:LEU:HD23	1:D:626:LEU:HA	1.72	0.45
1:E:25:SER:HB3	1:E:28:ASP:OD2	2.17	0.45
1:E:114:THR:HG21	1:E:200:LYS:HG2	1.99	0.45
1:E:319:ASN:HB3	1:E:320:SER:HB2	1.99	0.45
1:E:527:GLN:HA	1:F:719:GLN:HG3	1.99	0.45
1:E:605:ILE:HA	1:E:608:LEU:HB3	1.99	0.45
1:F:525:VAL:CG1	1:F:560:SER:HB2	2.46	0.45
2:G:82:ALA:O	2:G:86:VAL:HG23	2.17	0.45
2:G:101:ILE:HB	2:G:131:TYR:CZ	2.51	0.45
2:G:243:LEU:HD22	2:G:266:TYR:CG	2.52	0.45
3:K:43:VAL:HG22	4:L:212:LEU:HD22	1.98	0.45
3:K:51:ASP:OD2	3:K:55:GLU:OE2	2.35	0.45
4:L:216:PHE:CB	5:M:39:SER:HB2	2.45	0.45
5:M:142:ARG:HG2	5:M:143:GLU:N	2.32	0.45
1:B:523:LEU:O	1:B:526:GLN:HG2	2.16	0.44
1:C:677:LEU:CD1	1:C:698:VAL:HG21	2.47	0.44
1:C:715:GLU:OE1	1:C:715:GLU:HA	2.16	0.44
1:D:300:ALA:O	1:D:304:LYS:HG3	2.17	0.44
1:D:510:TRP:HZ2	1:D:668:PRO:O	2.00	0.44
1:D:573:MET:HE1	1:D:585:MET:HE3	1.98	0.44
1:E:596:GLN:HA	1:E:638:ARG:CG	2.32	0.44
1:E:696:GLN:OE1	1:E:696:GLN:HA	2.17	0.44
2:J:21:VAL:HG23	2:J:38:ILE:HD12	2.00	0.44
2:G:185:TYR:HA	2:G:188:VAL:HG12	1.98	0.44
5:M:33:LEU:HA	5:M:153:VAL:CG2	2.47	0.44
1:B:424:VAL:H	1:B:479:ASP:N	2.15	0.44
1:B:626:LEU:HD23	1:B:626:LEU:HA	1.52	0.44
1:C:562:PHE:O	1:C:565:ILE:HD11	2.16	0.44
1:D:564:PHE:HD2	1:D:598:SER:HB2	1.83	0.44
1:E:596:GLN:CA	1:E:638:ARG:HG2	2.31	0.44
1:E:717:SER:OG	1:E:729:PHE:HB2	2.17	0.44
1:F:375:ARG:NH2	1:F:377:ASP:OD2	2.50	0.44
1:F:552:LEU:HD12	1:F:667:VAL:HG21	1.98	0.44
1:F:707:ILE:O	1:F:710:LEU:HB3	2.17	0.44
2:J:180:LYS:O	2:J:184:ILE:HG13	2.18	0.44
2:G:40:GLU:O	2:G:43:GLU:HG3	2.17	0.44
2:G:72:HIS:NE2	2:G:77:SER:HB2	2.32	0.44
1:B:114:THR:OG1	1:B:199:ALA:HB3	2.17	0.44
1:B:260:GLY:CA	1:B:395:ILE:HB	2.48	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:523:LEU:HD22	1:B:526:GLN:NE2	2.32	0.44
1:C:113:ASP:O	1:C:117:MET:HG3	2.17	0.44
1:C:114:THR:OG1	1:C:199:ALA:HB3	2.17	0.44
1:C:540:LEU:HD22	1:C:661:PHE:CE2	2.53	0.44
1:D:304:LYS:HA	1:D:307:ALA:HB3	1.99	0.44
1:D:626:LEU:HD13	1:D:657:MET:HE1	1.98	0.44
1:E:510:TRP:CE3	1:E:670:ILE:HG13	2.51	0.44
1:F:67:ARG:HH12	2:G:217:ASP:CG	2.24	0.44
1:F:284:VAL:O	1:F:326:ILE:HG12	2.17	0.44
2:H:95:ALA:CB	2:H:97:PRO:HD2	2.47	0.44
2:H:161:ALA:O	2:H:165:LEU:HG	2.17	0.44
2:H:203:LYS:HB3	2:H:240:GLU:HG3	1.99	0.44
2:G:17:ALA:O	2:G:21:VAL:HG12	2.16	0.44
1:B:325:ILE:HG13	1:B:369:VAL:HB	1.98	0.44
1:C:295:VAL:O	1:D:294:TYR:HB2	2.17	0.44
1:C:518:LEU:HD23	1:C:518:LEU:HA	1.84	0.44
1:C:543:GLY:O	1:C:647:SER:OG	2.30	0.44
1:D:18:LEU:HD13	1:D:144:LEU:CD2	2.48	0.44
1:D:510:TRP:NE1	1:D:514:VAL:HG21	2.33	0.44
1:E:27:LYS:HD2	1:E:27:LYS:H	1.82	0.44
1:E:697:GLN:HG3	1:E:730:LEU:CD1	2.45	0.44
1:F:242:PRO:HD2	1:F:243:GLU:N	2.33	0.44
1:F:449:GLN:O	1:F:453:MET:HG2	2.18	0.44
2:J:38:ILE:HD11	2:J:71:LEU:HB3	1.98	0.44
4:L:211:GLU:O	4:L:214:ASP:HB2	2.18	0.44
1:A:101:PHE:CE1	1:A:193:LEU:HD13	2.53	0.44
1:A:132:VAL:HG23	1:A:173:GLU:O	2.18	0.44
1:A:295:VAL:HG12	1:B:293:LYS:N	2.32	0.44
1:B:258:LEU:CB	1:B:395:ILE:HD11	2.27	0.44
1:B:628:VAL:HG13	1:C:571:ASP:OD1	2.16	0.44
1:C:721:ASP:HB2	1:C:724:TYR:CD1	2.52	0.44
1:E:69:TRP:CE2	1:E:134:GLN:HA	2.52	0.44
1:E:91:CYS:O	1:E:154:ALA:HA	2.17	0.44
1:E:520:ASP:OD2	1:E:665:ILE:HD12	2.18	0.44
1:E:585:MET:HG3	1:E:589:PHE:CE2	2.51	0.44
1:E:676:LEU:O	1:E:680:LEU:HG	2.17	0.44
1:E:726:VAL:O	1:E:730:LEU:HG	2.17	0.44
1:F:218:MET:HA	1:F:219:GLY:HA2	1.78	0.44
1:F:399:ASP:N	1:F:399:ASP:OD1	2.49	0.44
2:H:164:CYS:O	2:H:168:VAL:HG23	2.17	0.44
2:J:108:ILE:HD12	2:J:127:ILE:HD12	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:245:LYS:O	2:J:249:GLU:HG3	2.16	0.44
3:K:43:VAL:CG2	4:L:212:LEU:HD22	2.48	0.44
5:M:63:GLY:O	5:M:67:ILE:HG13	2.16	0.44
1:A:380:ASP:OD1	1:A:381:GLU:N	2.51	0.44
1:A:624:GLN:OE1	1:A:624:GLN:HA	2.17	0.44
1:B:507:ILE:HG13	1:B:555:LYS:HD3	1.98	0.44
1:B:513:PRO:O	1:B:517:VAL:HG23	2.17	0.44
1:D:564:PHE:HB3	1:D:598:SER:CB	2.47	0.44
1:D:670:ILE:HG12	1:D:705:ILE:O	2.18	0.44
1:D:686:PHE:HB2	1:D:691:ARG:CG	2.47	0.44
1:E:8:ALA:HA	1:E:60:VAL:O	2.18	0.44
1:E:589:PHE:CE2	1:E:629:LEU:HD21	2.52	0.44
1:F:45:TYR:CE2	1:F:70:ALA:HA	2.53	0.44
4:L:200:SER:O	4:L:204:LYS:HG3	2.17	0.44
4:L:206:GLU:O	4:L:209:ILE:HB	2.18	0.44
4:L:225:SER:OG	4:L:229:MET:HE2	2.18	0.44
1:B:297:GLU:O	1:B:300:ALA:HB3	2.18	0.44
1:B:541:LEU:HA	1:B:665:ILE:O	2.18	0.44
1:B:576:PHE:HB2	1:B:581:LYS:CG	2.48	0.44
1:C:24:VAL:O	1:C:51:THR:HA	2.18	0.44
1:D:23:VAL:HG12	1:D:55:VAL:CG2	2.48	0.44
1:D:268:LEU:HA	1:D:271:ARG:CD	2.48	0.44
1:D:689:LYS:O	1:D:692:THR:OG1	2.32	0.44
1:E:24:VAL:CG1	1:E:49:LEU:HD22	2.48	0.44
2:J:120:ALA:O	2:J:124:HIS:HB2	2.18	0.44
3:K:77:PHE:HB2	5:M:192:ILE:CG2	2.47	0.44
4:L:209:ILE:HG13	5:M:32:MET:CE	2.46	0.44
1:A:121:PHE:CD2	1:A:183:VAL:HG21	2.52	0.44
1:A:573:MET:HA	1:A:576:PHE:CD2	2.53	0.44
1:B:450:SER:O	1:B:453:MET:HB2	2.16	0.44
1:B:669:ASN:OD1	1:B:706:GLY:HA2	2.17	0.44
1:E:102:LEU:HD22	1:E:137:VAL:HG12	2.00	0.44
1:E:190:ASN:HD21	1:E:316:LEU:CB	2.30	0.44
1:F:36:ILE:HG23	1:F:36:ILE:O	2.16	0.44
2:I:232:PHE:C	2:I:234:ALA:N	2.76	0.44
2:J:20:LYS:NZ	2:J:40:GLU:HG2	2.33	0.44
2:G:182:ILE:CG2	2:G:212:CYS:HB2	2.47	0.44
2:G:182:ILE:HG22	2:G:212:CYS:HB2	1.99	0.44
2:G:263:VAL:HG23	2:G:280:LEU:HD13	2.00	0.44
3:K:52:LYS:HB2	3:K:52:LYS:HZ2	1.81	0.44
5:M:29:THR:O	5:M:32:MET:HB3	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:142:ARG:HG2	5:M:143:GLU:H	1.82	0.44
1:B:260:GLY:HA3	1:B:266:LYS:HD3	2.00	0.44
1:B:582:CYS:SG	1:C:574:ILE:HG22	2.58	0.44
1:C:590:ASP:HA	1:C:593:TYR:HD2	1.81	0.44
1:C:603:ASP:HA	1:C:645:THR:OG1	2.18	0.44
1:C:613:PRO:HD3	1:C:648:ARG:HH22	1.83	0.44
1:C:686:PHE:HB3	1:C:690:GLU:OE2	2.18	0.44
1:D:231:PHE:HA	1:D:235:PHE:CD2	2.52	0.44
1:D:527:GLN:NE2	1:E:715:GLU:C	2.72	0.44
1:E:24:VAL:C	1:E:55:VAL:HG11	2.43	0.44
1:F:48:THR:HG22	1:F:49:LEU:N	2.33	0.44
1:F:562:PHE:CE2	1:F:597:LEU:HD12	2.51	0.44
2:H:134:GLU:O	2:H:136:VAL:HG23	2.18	0.44
2:H:223:LEU:O	2:H:227:LYS:HG3	2.18	0.44
2:H:256:VAL:HG11	2:H:288:GLN:HG2	2.00	0.44
2:I:45:TYR:HE2	2:I:71:LEU:HD11	1.83	0.44
2:J:243:LEU:HD22	2:J:266:TYR:CD2	2.53	0.44
1:A:240:PHE:HB3	1:A:244:ILE:HD11	1.99	0.43
1:A:632:LYS:HE3	1:A:633:ALA:O	2.18	0.43
1:B:569:SER:OG	1:B:571:ASP:OD2	2.33	0.43
1:C:132:VAL:HG23	1:C:173:GLU:O	2.18	0.43
1:D:121:PHE:HD2	1:D:183:VAL:HG21	1.83	0.43
1:D:303:ARG:HD3	1:D:353:GLN:CG	2.48	0.43
1:E:12:PRO:HG2	1:E:23:VAL:HG11	1.98	0.43
2:H:92:PHE:HB3	2:H:98:GLN:O	2.17	0.43
2:H:119:ILE:HD11	2:H:123:HIS:CE1	2.53	0.43
2:H:182:ILE:CG2	2:H:212:CYS:HB2	2.48	0.43
2:I:81:ALA:O	2:I:85:PHE:HD1	2.01	0.43
2:G:119:ILE:HD11	2:G:123:HIS:HE1	1.82	0.43
2:G:251:HIS:C	2:G:253:GLU:H	2.26	0.43
1:A:255:GLY:C	1:A:389:LEU:HD13	2.44	0.43
1:A:300:ALA:O	1:A:303:ARG:HG2	2.19	0.43
1:C:507:ILE:HD12	1:C:555:LYS:CE	2.47	0.43
1:D:354:LEU:HD23	1:D:354:LEU:HA	1.77	0.43
1:E:7:GLN:O	1:E:59:SER:HB2	2.18	0.43
1:E:512:ASP:N	1:E:513:PRO:CD	2.81	0.43
1:E:713:LEU:CD2	1:E:732:LEU:HD13	2.47	0.43
1:F:589:PHE:O	1:F:593:TYR:CD1	2.71	0.43
1:F:657:MET:SD	1:F:661:PHE:CE2	3.10	0.43
1:F:712:MET:O	1:F:716:MET:HG3	2.18	0.43
2:I:182:ILE:HG22	2:I:212:CYS:HB2	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:266:TYR:C	2:I:268:SER:H	2.26	0.43
2:G:124:HIS:HE1	2:G:147:GLN:HB3	1.83	0.43
2:G:179:GLN:HG3	2:G:180:LYS:N	2.33	0.43
1:A:262:PRO:CG	1:A:374:ASN:OD1	2.64	0.43
1:B:69:TRP:NE1	1:B:134:GLN:HA	2.33	0.43
1:B:221:GLY:HA3	1:B:406:ILE:HD12	1.99	0.43
1:B:241:PRO:HA	1:B:242:PRO:HA	1.55	0.43
1:B:677:LEU:O	1:B:681:GLU:HG3	2.18	0.43
1:C:402:GLY:O	1:C:406:ILE:HD12	2.18	0.43
1:C:688:ASP:HA	1:C:691:ARG:CZ	2.48	0.43
1:E:375:ARG:NH2	1:E:377:ASP:OD2	2.51	0.43
1:E:655:MET:C	1:E:656:GLU:HG3	2.44	0.43
2:H:118:THR:O	2:H:122:LYS:HG2	2.18	0.43
2:H:188:VAL:HG13	2:H:205:TYR:HD2	1.83	0.43
2:H:222:LYS:HA	2:H:225:VAL:HG12	2.00	0.43
2:G:112:THR:HG23	2:G:117:PHE:CE1	2.47	0.43
3:K:50:VAL:O	3:K:53:VAL:HG12	2.19	0.43
4:L:223:VAL:HG12	5:M:49:MET:CE	2.46	0.43
1:A:67:ARG:HD2	2:H:218:MET:SD	2.58	0.43
1:A:68:LYS:HD2	2:H:219:LEU:HD23	2.00	0.43
1:A:242:PRO:HD2	1:A:243:GLU:H	1.82	0.43
1:A:258:LEU:O	1:A:258:LEU:HD12	2.18	0.43
1:A:395:ILE:HD12	1:A:395:ILE:N	2.32	0.43
1:A:395:ILE:HG22	1:A:396:GLY:N	2.33	0.43
1:A:502:TYR:N	1:A:502:TYR:HD1	2.17	0.43
1:B:86:ASP:C	1:B:88:ALA:H	2.25	0.43
1:B:440:GLU:O	1:B:444:LEU:HG	2.18	0.43
1:D:241:PRO:HA	1:D:242:PRO:HA	1.68	0.43
1:E:231:PHE:O	1:E:235:PHE:CD2	2.71	0.43
1:F:74:ILE:HB	2:G:216:ILE:CD1	2.48	0.43
1:F:101:PHE:CD2	1:F:107:ILE:HA	2.53	0.43
2:H:203:LYS:NZ	2:H:239:ARG:HH21	2.15	0.43
2:H:230:GLU:HG2	2:H:231:LEU:H	1.83	0.43
2:I:162:ASN:O	2:I:166:LEU:HG	2.18	0.43
2:I:219:LEU:C	2:I:221:ALA:N	2.76	0.43
2:J:203:LYS:HE3	2:J:203:LYS:HB2	1.85	0.43
2:G:266:TYR:C	2:G:268:SER:N	2.76	0.43
1:A:457:ILE:HD12	1:F:232:ARG:HH21	1.83	0.43
1:A:510:TRP:CE3	1:A:675:GLN:HG2	2.54	0.43
1:A:718:LEU:O	1:A:725:ARG:NE	2.51	0.43
1:B:455:ARG:NH2	1:B:481:LEU:CB	2.81	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:ASP:C	1:C:88:ALA:N	2.77	0.43
1:C:504:MET:HE3	1:C:504:MET:HB3	1.80	0.43
1:D:34:HIS:HB2	1:D:83:TYR:O	2.18	0.43
1:D:498:ASP:O	1:D:501:SER:HB3	2.19	0.43
1:F:72:LEU:O	2:G:218:MET:SD	2.77	0.43
2:J:167:LYS:HE2	2:J:171:TYR:CE2	2.49	0.43
2:J:235:PHE:HD1	3:K:34:GLN:HE21	1.62	0.43
4:L:209:ILE:CG2	5:M:32:MET:HG3	2.45	0.43
1:A:256:ILE:CG1	1:A:370:ILE:HG22	2.47	0.43
1:A:612:VAL:CG1	1:A:617:ARG:HB2	2.49	0.43
1:A:646:THR:HG21	1:A:652:LEU:HD22	1.99	0.43
1:B:549:LYS:NZ	1:B:647:SER:HA	2.34	0.43
1:B:715:GLU:O	1:B:719:GLN:HG2	2.18	0.43
1:C:241:PRO:HA	1:C:242:PRO:HA	1.66	0.43
1:C:265:GLY:O	1:C:268:LEU:HG	2.18	0.43
1:D:102:LEU:HD22	1:D:137:VAL:CG1	2.48	0.43
1:D:331:ASP:CA	1:D:379:ILE:HD11	2.48	0.43
1:E:531:SER:HB3	1:E:534:THR:O	2.18	0.43
1:E:676:LEU:HD22	1:E:703:VAL:HG11	2.01	0.43
1:E:732:LEU:HA	1:E:732:LEU:HD23	1.73	0.43
1:F:555:LYS:HD3	1:F:559:GLU:HG2	2.00	0.43
1:F:629:LEU:O	1:F:632:LYS:HB3	2.18	0.43
2:H:231:LEU:HD13	2:G:271:ARG:CG	2.48	0.43
2:J:21:VAL:HG23	2:J:38:ILE:CD1	2.48	0.43
4:L:210:ARG:HG2	4:L:210:ARG:NH1	2.32	0.43
5:M:49:MET:O	5:M:53:GLN:HG3	2.19	0.43
1:A:377:ASP:OD2	1:A:378:LEU:HD23	2.19	0.43
1:A:436:PHE:CD2	1:A:444:LEU:HD11	2.54	0.43
1:A:457:ILE:HD12	1:F:232:ARG:NH2	2.33	0.43
1:A:564:PHE:CZ	1:A:566:LYS:HB2	2.53	0.43
1:C:508:ILE:HD13	1:C:683:LEU:HD21	2.01	0.43
1:C:526:GLN:OE1	1:C:530:ASN:ND2	2.52	0.43
1:D:655:MET:O	1:D:656:GLU:HB2	2.18	0.43
1:E:684:GLY:HA2	1:E:691:ARG:NH2	2.33	0.43
1:F:597:LEU:HA	1:F:639:LYS:O	2.18	0.43
2:H:82:ALA:HB2	2:H:110:ILE:HG21	2.00	0.43
2:H:98:GLN:C	2:H:100:ALA:H	2.27	0.43
2:H:175:LEU:C	2:H:177:GLN:H	2.26	0.43
2:J:197:LEU:CD2	3:K:48:VAL:HG11	2.48	0.43
2:G:96:ASP:N	2:G:97:PRO:HD2	2.34	0.43
2:G:255:ASN:C	2:G:257:ASP:H	2.26	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:46:MET:O	3:K:50:VAL:HG23	2.19	0.43
4:L:248:VAL:HB	5:M:70:ASP:HB3	1.99	0.43
1:A:114:THR:HG21	1:A:200:LYS:HG2	2.00	0.43
1:A:713:LEU:CD2	1:A:732:LEU:HB3	2.40	0.43
1:B:388:ARG:O	1:B:389:LEU:HD23	2.19	0.43
1:B:485:GLU:O	1:B:489:LYS:CB	2.67	0.43
1:B:541:LEU:HD12	1:B:541:LEU:O	2.19	0.43
1:B:547:SER:HA	1:B:707:ILE:HG22	2.00	0.43
1:C:12:PRO:HB3	1:C:54:SER:OG	2.18	0.43
1:C:709:LYS:HA	1:C:709:LYS:HD2	1.84	0.43
1:D:105:LYS:O	1:D:106:ASN:ND2	2.51	0.43
1:E:242:PRO:CD	1:E:243:GLU:H	2.32	0.43
1:E:530:ASN:O	1:E:639:LYS:HE3	2.19	0.43
1:E:625:ALA:HA	1:F:574:ILE:CD1	2.39	0.43
1:F:76:GLN:HE21	1:F:78:ILE:CG2	2.32	0.43
1:F:571:ASP:HA	1:F:574:ILE:HB	2.00	0.43
1:F:677:LEU:O	1:F:681:GLU:HG3	2.18	0.43
2:I:72:HIS:ND1	2:I:81:ALA:HB2	2.34	0.43
2:J:10:ALA:O	2:J:14:LEU:HG	2.19	0.43
2:J:101:ILE:HB	2:J:131:TYR:OH	2.18	0.43
2:G:45:TYR:HE2	2:G:71:LEU:HD11	1.83	0.43
2:G:147:GLN:HG2	2:G:151:TYR:CE2	2.53	0.43
4:L:248:VAL:O	4:L:252:LYS:HG3	2.18	0.43
1:A:247:GLN:CA	1:B:413:ARG:HH12	2.32	0.43
1:B:218:MET:HA	1:B:219:GLY:HA2	1.70	0.43
1:B:549:LYS:HZ3	1:B:647:SER:HA	1.84	0.43
1:C:24:VAL:HG12	1:C:60:VAL:HG13	1.99	0.43
1:D:227:PHE:O	1:D:230:ILE:HG22	2.18	0.43
1:D:247:GLN:O	1:E:414:MET:SD	2.77	0.43
1:D:327:PHE:HB2	1:D:330:ILE:CG2	2.48	0.43
1:D:522:GLU:CD	1:D:559:GLU:HB2	2.44	0.43
1:F:24:VAL:HG21	1:F:29:TYR:HB2	2.00	0.43
1:F:254:LYS:O	1:F:368:LEU:HA	2.18	0.43
1:F:263:GLY:HA3	1:F:437:SER:HB2	2.01	0.43
1:F:408:HIS:O	1:F:408:HIS:ND1	2.45	0.43
1:F:524:LEU:HD13	1:F:539:VAL:CG2	2.49	0.43
1:F:560:SER:HB2	1:F:562:PHE:CD1	2.54	0.43
2:H:231:LEU:HB2	2:H:234:ALA:CB	2.49	0.43
2:I:12:ALA:O	2:I:16:GLU:HG3	2.19	0.43
2:I:147:GLN:HG2	2:I:151:TYR:CE2	2.53	0.43
2:I:200:TYR:O	2:I:203:LYS:NZ	2.45	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:21:VAL:HG13	2:J:21:VAL:O	2.19	0.43
2:J:63:ASN:O	2:J:67:GLN:HG3	2.19	0.43
2:G:35:SER:HA	2:G:38:ILE:HG22	2.01	0.43
2:G:179:GLN:HB3	2:G:214:PHE:HB3	2.00	0.43
1:A:231:PHE:CE1	1:A:235:PHE:CE2	3.04	0.43
1:A:313:GLN:NE2	1:A:365:ASN:OD1	2.52	0.43
1:B:288:PRO:HG2	1:B:289:GLU:H	1.83	0.43
1:B:375:ARG:NH2	1:B:377:ASP:OD2	2.51	0.43
1:C:289:GLU:C	1:C:291:LEU:H	2.25	0.43
1:D:406:ILE:HD12	1:D:406:ILE:HG23	1.70	0.43
1:E:586:LYS:O	1:E:589:PHE:HB2	2.19	0.43
2:H:67:GLN:O	2:H:71:LEU:HG	2.19	0.43
2:H:169:ALA:HB2	2:H:184:ILE:HB	2.01	0.43
2:I:45:TYR:CE2	2:I:71:LEU:HD11	2.54	0.43
2:I:167:LYS:HE2	2:I:171:TYR:CE2	2.53	0.43
2:I:263:VAL:HG21	2:I:280:LEU:HD13	2.01	0.43
2:J:271:ARG:CZ	2:G:234:ALA:HB2	2.48	0.43
2:G:167:LYS:HE2	2:G:171:TYR:CE2	2.54	0.43
2:G:212:CYS:SG	2:G:279:MET:HE1	2.59	0.43
3:K:48:VAL:HG12	3:K:52:LYS:CE	2.40	0.43
3:K:48:VAL:O	3:K:52:LYS:HG3	2.18	0.43
1:A:86:ASP:C	1:A:88:ALA:N	2.77	0.42
1:B:286:ASN:OD1	1:B:327:PHE:HD1	2.02	0.42
1:C:620:ASN:O	1:C:624:GLN:HG2	2.20	0.42
1:E:67:ARG:HH11	1:E:74:ILE:HD11	1.84	0.42
1:E:242:PRO:HD2	1:E:243:GLU:N	2.34	0.42
1:E:564:PHE:HB3	1:E:595:SER:HB2	2.01	0.42
1:F:518:LEU:HD23	1:F:555:LYS:CG	2.16	0.42
2:I:17:ALA:HB2	2:I:44:ILE:HG21	2.01	0.42
2:I:161:ALA:O	2:I:165:LEU:HG	2.18	0.42
2:J:230:GLU:HG2	2:J:231:LEU:N	2.34	0.42
2:J:266:TYR:C	2:J:268:SER:N	2.76	0.42
2:J:269:ILE:HG22	5:M:151:GLU:OE1	2.19	0.42
2:G:95:ALA:HB1	2:G:97:PRO:HD2	2.00	0.42
5:M:167:MET:HA	5:M:170:GLU:HB3	2.00	0.42
1:A:12:PRO:HB3	1:A:54:SER:OG	2.19	0.42
1:A:407:LEU:O	1:A:411:THR:HG23	2.19	0.42
1:A:453:MET:HA	1:F:240:PHE:CE2	2.54	0.42
1:B:671:ALA:HA	1:B:703:VAL:O	2.19	0.42
1:D:236:ALA:HA	1:D:239:VAL:HG12	2.00	0.42
1:D:690:GLU:O	1:D:694:ILE:HG13	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:73:SER:O	1:E:76:GLN:HG2	2.19	0.42
1:E:297:GLU:O	1:E:300:ALA:HB3	2.19	0.42
1:E:608:LEU:HD23	1:E:626:LEU:HD11	2.01	0.42
1:F:440:GLU:O	1:F:444:LEU:HG	2.18	0.42
2:H:58:TRP:HB3	2:H:95:ALA:HB2	2.00	0.42
2:I:17:ALA:HB2	2:I:44:ILE:CG2	2.50	0.42
2:I:267:ASP:OD2	2:I:271:ARG:NH2	2.52	0.42
2:G:266:TYR:CZ	2:G:270:SER:HB2	2.55	0.42
1:A:73:SER:HB2	1:A:76:GLN:OE1	2.18	0.42
1:A:235:PHE:N	1:A:235:PHE:CD1	2.81	0.42
1:B:612:VAL:HG13	1:B:614:ILE:O	2.19	0.42
1:D:86:ASP:C	1:D:88:ALA:N	2.77	0.42
1:D:131:SER:HA	1:D:173:GLU:O	2.20	0.42
1:D:518:LEU:HA	1:D:518:LEU:HD23	1.86	0.42
1:E:705:ILE:CD1	1:E:713:LEU:HD12	2.49	0.42
1:F:436:PHE:CD2	1:F:444:LEU:HD11	2.55	0.42
1:F:503:ILE:HD11	1:F:554:ALA:HB3	2.02	0.42
1:F:721:ASP:O	1:F:725:ARG:HG3	2.20	0.42
2:H:75:LEU:O	2:H:76:GLN:HB2	2.19	0.42
2:G:134:GLU:O	2:G:136:VAL:HG23	2.19	0.42
2:G:246:LYS:HZ1	2:G:258:SER:HB3	1.84	0.42
3:K:60:LEU:HD23	5:M:178:ILE:HD13	2.01	0.42
3:K:67:ALA:HB1	4:L:237:VAL:HG22	2.01	0.42
3:K:77:PHE:HB2	5:M:192:ILE:HG23	2.02	0.42
1:A:611:TYR:HA	1:A:618:PHE:HB3	2.00	0.42
1:B:24:VAL:O	1:B:51:THR:HA	2.19	0.42
1:B:436:PHE:CE2	1:B:444:LEU:HD11	2.54	0.42
1:C:386:PRO:HA	1:C:390:GLU:CA	2.39	0.42
1:C:490:PRO:HB2	1:C:492:PHE:H	1.83	0.42
1:C:517:VAL:HG13	1:C:665:ILE:HG21	2.02	0.42
1:C:629:LEU:HD23	1:C:629:LEU:HA	1.74	0.42
1:C:691:ARG:HB2	1:C:691:ARG:NH1	2.35	0.42
1:D:388:ARG:O	1:D:389:LEU:HD23	2.19	0.42
1:D:510:TRP:CB	1:D:679:ALA:HB2	2.50	0.42
1:D:543:GLY:N	1:D:549:LYS:HD3	2.30	0.42
1:E:388:ARG:O	1:E:389:LEU:HD23	2.20	0.42
1:E:691:ARG:HA	1:E:694:ILE:HD12	2.01	0.42
1:F:618:PHE:HE1	1:F:620:ASN:HA	1.85	0.42
1:F:653:GLN:CB	1:F:658:LEU:HD23	2.49	0.42
2:H:179:GLN:HB3	2:H:214:PHE:CB	2.50	0.42
2:H:230:GLU:C	2:H:231:LEU:HG	2.44	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:188:VAL:HG13	2:J:205:TYR:CD2	2.55	0.42
2:J:200:TYR:O	2:J:203:LYS:HG3	2.19	0.42
2:J:260:THR:HA	2:J:263:VAL:HG12	2.01	0.42
2:G:166:LEU:HD21	2:G:205:TYR:CE2	2.54	0.42
2:G:232:PHE:CB	2:G:233:PRO:HD3	2.40	0.42
2:G:235:PHE:CG	5:M:152:GLN:HA	2.53	0.42
1:A:231:PHE:CE2	1:A:235:PHE:CD2	3.08	0.42
1:A:322:LEU:HD13	1:A:366:ASN:O	2.20	0.42
1:A:502:TYR:N	1:A:502:TYR:CD1	2.86	0.42
1:A:687:LYS:HZ3	1:A:722:PRO:HB3	1.82	0.42
1:B:23:VAL:HG12	1:B:55:VAL:CG2	2.50	0.42
1:B:232:ARG:O	1:B:236:ALA:HB3	2.19	0.42
1:C:220:ILE:HD11	1:C:272:GLN:HG3	2.01	0.42
1:C:499:TYR:OH	1:C:565:ILE:HB	2.20	0.42
1:C:519:ASP:O	1:C:523:LEU:HG	2.20	0.42
1:C:560:SER:HB2	1:C:562:PHE:CZ	2.54	0.42
1:D:331:ASP:O	1:D:332:ALA:HB3	2.19	0.42
1:D:407:LEU:HB2	1:D:426:ILE:HG23	2.02	0.42
1:D:538:SER:OG	1:D:661:PHE:HA	2.19	0.42
1:E:245:VAL:HG13	1:E:246:GLU:N	2.34	0.42
1:F:38:ARG:HG2	1:F:38:ARG:HH11	1.84	0.42
2:H:101:ILE:HB	2:H:131:TYR:OH	2.20	0.42
2:H:163:LYS:O	2:H:167:LYS:HG2	2.19	0.42
2:I:277:THR:O	2:I:281:LEU:HD13	2.20	0.42
2:J:184:ILE:O	2:J:188:VAL:HG12	2.20	0.42
1:A:220:ILE:HG22	1:A:221:GLY:N	2.34	0.42
1:B:64:LEU:HA	1:B:67:ARG:HH21	1.84	0.42
1:B:242:PRO:HD2	1:B:243:GLU:N	2.34	0.42
1:D:499:TYR:CD1	1:D:499:TYR:N	2.86	0.42
1:D:549:LYS:HB3	1:D:645:THR:HB	2.01	0.42
1:E:122:ILE:HD11	1:E:183:VAL:CG2	2.50	0.42
1:E:406:ILE:O	1:E:409:ILE:HG22	2.19	0.42
1:E:648:ARG:NE	1:E:651:VAL:HG13	2.33	0.42
1:F:91:CYS:HB3	1:F:155:MET:CE	2.49	0.42
1:F:388:ARG:O	1:F:389:LEU:HD23	2.20	0.42
1:F:524:LEU:HD11	1:F:665:ILE:HD11	2.01	0.42
2:H:118:THR:HG22	2:H:155:GLU:HG3	2.00	0.42
2:H:266:TYR:HD2	2:H:272:LEU:HD21	1.85	0.42
2:I:118:THR:HG22	2:I:155:GLU:HG3	2.02	0.42
5:M:28:SER:O	5:M:32:MET:N	2.53	0.42
1:A:315:ARG:HG2	1:A:316:LEU:HD12	2.00	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:552:LEU:HD22	1:A:556:ILE:HD11	2.00	0.42
1:C:576:PHE:HB3	1:C:580:ALA:HB3	2.01	0.42
1:D:240:PHE:HA	1:D:241:PRO:HD3	1.89	0.42
1:D:709:LYS:HA	1:D:709:LYS:HD2	1.85	0.42
1:E:313:GLN:HE21	1:E:317:GLY:CA	2.32	0.42
1:E:643:ILE:N	1:E:643:ILE:HD12	2.35	0.42
1:F:408:HIS:HD1	1:F:408:HIS:C	2.27	0.42
1:F:589:PHE:N	1:F:589:PHE:CD1	2.84	0.42
2:H:219:LEU:HD12	2:H:219:LEU:O	2.19	0.42
2:I:49:ALA:HB2	2:I:64:ALA:HB3	2.02	0.42
2:I:216:ILE:HG12	2:I:217:ASP:H	1.85	0.42
5:M:49:MET:HG2	5:M:53:GLN:NE2	2.33	0.42
1:A:676:LEU:HD12	1:A:710:LEU:HD11	2.01	0.42
1:A:706:GLY:O	1:A:710:LEU:N	2.53	0.42
1:B:250:CYS:HB2	1:C:449:GLN:CD	2.45	0.42
1:C:24:VAL:CG1	1:C:49:LEU:HD22	2.49	0.42
1:C:26:GLU:HG2	1:C:51:THR:HB	2.01	0.42
1:C:521:GLY:O	1:C:525:VAL:HG23	2.20	0.42
1:D:186:GLU:HG3	1:D:186:GLU:O	2.19	0.42
1:D:268:LEU:O	1:D:271:ARG:HG2	2.19	0.42
1:D:670:ILE:HD13	1:D:670:ILE:HG21	1.75	0.42
1:E:284:VAL:O	1:E:326:ILE:HG12	2.19	0.42
1:E:307:ALA:O	1:E:310:GLU:HG2	2.20	0.42
1:E:377:ASP:OD1	1:E:378:LEU:N	2.53	0.42
1:E:714:ILE:HG12	1:E:729:PHE:HE1	1.84	0.42
1:F:12:PRO:HD2	1:F:23:VAL:HG21	2.01	0.42
1:F:74:ILE:HB	2:G:216:ILE:HD11	2.01	0.42
2:H:45:TYR:HE2	2:H:71:LEU:HD11	1.84	0.42
2:I:163:LYS:O	2:I:167:LYS:HG2	2.20	0.42
2:J:25:GLN:N	2:J:29:SER:HB2	2.35	0.42
2:J:81:ALA:O	2:J:85:PHE:HD1	2.02	0.42
2:J:175:LEU:C	2:J:177:GLN:H	2.27	0.42
2:J:203:LYS:HD3	2:J:236:SER:HB3	2.02	0.42
2:J:265:GLU:O	2:J:268:SER:HB2	2.20	0.42
5:M:23:ASP:O	5:M:27:GLU:HB2	2.20	0.42
1:A:16:LEU:HD11	1:A:52:HIS:CD2	2.54	0.42
1:A:38:ARG:HG2	1:A:38:ARG:HH11	1.85	0.42
1:A:247:GLN:HA	1:B:413:ARG:HH12	1.85	0.42
1:A:542:GLU:HA	1:A:646:THR:O	2.19	0.42
1:A:575:GLY:HA3	1:F:586:LYS:HZ1	1.85	0.42
1:B:579:THR:O	1:B:583:GLN:HG2	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:545:PRO:CD	1:D:647:SER:OG	2.68	0.42
1:D:627:LEU:HA	1:D:627:LEU:HD23	1.65	0.42
1:E:534:THR:HG21	1:F:712:MET:HA	2.01	0.42
1:F:545:PRO:HB3	1:F:546:HIS:HA	2.01	0.42
2:I:95:ALA:CB	2:I:97:PRO:HD2	2.50	0.42
1:A:240:PHE:CG	1:A:244:ILE:HD11	2.55	0.42
1:B:452:ALA:HA	1:B:455:ARG:CZ	2.50	0.42
1:B:520:ASP:OD2	1:B:665:ILE:HG12	2.20	0.42
1:C:284:VAL:HB	1:C:325:ILE:HA	2.01	0.42
1:C:508:ILE:HD11	1:C:707:ILE:HD11	2.02	0.42
1:C:562:PHE:HD2	1:C:599:CYS:CB	2.33	0.42
1:D:573:MET:SD	1:D:608:LEU:HD22	2.59	0.42
1:E:545:PRO:HG3	1:E:647:SER:OG	2.20	0.42
1:E:568:CYS:HB3	1:E:601:VAL:O	2.20	0.42
2:H:237:ASP:C	2:H:239:ARG:N	2.76	0.42
2:I:250:ALA:HB1	2:I:259:TYR:HB2	2.02	0.42
2:G:75:LEU:O	2:G:76:GLN:HB3	2.19	0.42
2:G:92:PHE:HD1	2:G:97:PRO:HG2	1.84	0.42
2:G:164:CYS:O	2:G:168:VAL:HG23	2.20	0.42
4:L:195:ILE:HG21	5:M:18:ALA:HB1	2.02	0.42
1:B:295:VAL:HB	1:C:294:TYR:CB	2.50	0.41
1:B:539:VAL:CG2	1:B:665:ILE:HD12	2.50	0.41
1:C:218:MET:HA	1:C:219:GLY:HA2	1.76	0.41
1:D:278:ASN:O	1:D:279:ALA:C	2.63	0.41
1:E:670:ILE:HG21	1:E:675:GLN:HB3	2.02	0.41
1:F:438:GLY:O	1:F:441:LEU:N	2.45	0.41
2:H:208:LYS:HG2	2:H:275:TRP:CZ3	2.55	0.41
2:J:82:ALA:O	2:J:86:VAL:HG23	2.20	0.41
2:J:117:PHE:HA	2:J:120:ALA:HB3	2.01	0.41
2:J:157:SER:O	2:J:158:ASN:C	2.62	0.41
2:J:247:LEU:HD22	2:J:259:TYR:CE1	2.55	0.41
4:L:241:VAL:HG21	5:M:63:GLY:HA3	2.01	0.41
5:M:36:VAL:HA	5:M:39:SER:OG	2.20	0.41
1:A:10:ARG:HD2	2:H:217:ASP:HB2	2.02	0.41
1:A:97:ILE:HG21	1:A:147:LEU:HD22	2.03	0.41
1:A:220:ILE:HD11	1:A:227:PHE:CZ	2.54	0.41
1:A:235:PHE:HD1	1:A:235:PHE:HA	1.58	0.41
1:A:509:LYS:HG2	1:A:515:THR:OG1	2.20	0.41
1:A:686:PHE:O	1:A:691:ARG:NH2	2.52	0.41
1:B:377:ASP:OD1	1:B:378:LEU:N	2.53	0.41
1:C:113:ASP:HA	1:C:196:ILE:HG13	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:624:GLN:OE1	1:C:624:GLN:HA	2.20	0.41
1:D:122:ILE:HD11	1:D:183:VAL:CG2	2.50	0.41
1:D:349:THR:HA	1:D:352:ASN:HD22	1.84	0.41
1:D:377:ASP:OD1	1:D:378:LEU:N	2.53	0.41
1:D:570:PRO:O	1:D:573:MET:HB3	2.20	0.41
1:E:99:ILE:HD11	1:E:145:PHE:CD2	2.55	0.41
1:E:190:ASN:HB2	1:E:315:ARG:HH12	1.85	0.41
1:E:533:ARG:HB2	1:F:715:GLU:CD	2.45	0.41
1:F:18:LEU:HD13	1:F:139:SER:OG	2.21	0.41
1:F:377:ASP:OD1	1:F:378:LEU:N	2.53	0.41
1:F:400:GLU:OE2	1:F:434:LYS:HA	2.21	0.41
1:F:542:GLU:N	1:F:665:ILE:O	2.52	0.41
1:F:629:LEU:C	1:F:629:LEU:HD23	2.45	0.41
2:I:236:SER:HA	2:I:239:ARG:NH1	2.35	0.41
3:K:35:THR:O	3:K:35:THR:HG22	2.20	0.41
4:L:202:ILE:HG22	5:M:25:SER:HB3	2.01	0.41
5:M:36:VAL:CG2	5:M:156:ILE:HD12	2.51	0.41
1:B:536:LEU:HD22	1:B:632:LYS:O	2.19	0.41
1:C:125:PHE:CD2	1:C:130:PHE:HZ	2.39	0.41
1:C:232:ARG:O	1:C:236:ALA:HB3	2.21	0.41
1:C:233:ARG:HA	1:D:450:SER:HB2	2.02	0.41
1:D:541:LEU:HD12	1:D:541:LEU:O	2.21	0.41
1:E:242:PRO:O	1:E:245:VAL:HG12	2.20	0.41
1:E:539:VAL:HG13	1:E:643:ILE:HA	2.02	0.41
1:E:670:ILE:CG2	1:E:672:THR:H	2.29	0.41
1:F:263:GLY:HA3	1:F:437:SER:CB	2.50	0.41
1:F:324:ILE:HG12	1:F:368:LEU:HD11	2.03	0.41
1:F:624:GLN:O	1:F:628:VAL:HG23	2.21	0.41
2:H:21:VAL:HG23	2:H:38:ILE:CD1	2.50	0.41
2:H:256:VAL:O	2:H:256:VAL:HG22	2.19	0.41
2:I:219:LEU:O	2:I:220:ASN:HB3	2.21	0.41
2:J:154:GLY:C	2:J:156:GLU:H	2.27	0.41
2:J:271:ARG:NH2	2:G:231:LEU:HB2	2.35	0.41
3:K:54:LEU:HD21	4:L:222:LEU:HD13	2.02	0.41
1:A:24:VAL:HG11	1:A:49:LEU:HD22	2.02	0.41
1:A:138:PHE:HB2	1:A:147:LEU:HD11	2.01	0.41
1:A:215:PHE:C	1:A:217:LYS:N	2.75	0.41
1:A:254:LYS:O	1:A:368:LEU:HA	2.20	0.41
1:C:67:ARG:CZ	2:I:217:ASP:OD1	2.69	0.41
1:D:256:ILE:HG22	1:D:391:VAL:CG1	2.48	0.41
1:D:331:ASP:HA	1:D:379:ILE:CD1	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:203:LYS:HD2	2:I:237:ASP:HA	2.03	0.41
2:J:188:VAL:HG13	2:J:205:TYR:HD2	1.86	0.41
2:J:232:PHE:CZ	2:J:242:LYS:HD3	2.55	0.41
2:G:39:GLU:HB2	2:G:75:LEU:HD11	2.01	0.41
1:A:242:PRO:O	1:A:245:VAL:HG12	2.20	0.41
1:A:510:TRP:CE3	1:A:675:GLN:HB3	2.56	0.41
1:B:69:TRP:CE2	1:B:134:GLN:HA	2.56	0.41
1:C:38:ARG:HH11	1:C:38:ARG:HG2	1.85	0.41
1:C:436:PHE:N	1:C:436:PHE:CD1	2.84	0.41
1:C:528:THR:O	1:C:639:LYS:HD3	2.20	0.41
1:C:633:ALA:HB1	1:D:504:MET:HE1	2.02	0.41
1:D:11:CYS:HA	1:D:12:PRO:HD3	1.92	0.41
1:D:45:TYR:CE2	1:D:70:ALA:HA	2.56	0.41
1:D:272:GLN:OE1	1:D:272:GLN:HA	2.21	0.41
1:E:230:ILE:HD11	1:E:391:VAL:HG11	2.02	0.41
1:E:586:LYS:NZ	1:F:574:ILE:HG23	2.35	0.41
1:F:101:PHE:HD1	1:F:101:PHE:H	1.67	0.41
1:F:520:ASP:O	1:F:524:LEU:HG	2.20	0.41
2:H:9:GLU:O	2:H:13:LEU:HG	2.20	0.41
2:G:116:ARG:HB3	2:G:119:ILE:HG22	2.02	0.41
2:G:118:THR:HG22	2:G:155:GLU:HG3	2.03	0.41
2:G:195:SER:C	2:G:197:LEU:N	2.78	0.41
2:G:211:LEU:HG	2:G:244:MET:HE1	2.03	0.41
5:M:64:MET:HE3	5:M:181:ILE:CG2	2.50	0.41
1:A:693:THR:O	1:A:697:GLN:OE1	2.38	0.41
1:B:143:LYS:HB3	1:B:145:PHE:HE1	1.84	0.41
1:B:512:ASP:N	1:B:513:PRO:CD	2.83	0.41
1:B:631:LYS:HB2	1:B:631:LYS:HE3	1.67	0.41
1:C:320:SER:O	1:C:320:SER:OG	2.31	0.41
1:C:552:LEU:HD23	1:C:552:LEU:HA	1.78	0.41
1:D:247:GLN:HA	1:E:417:HIS:ND1	2.35	0.41
1:D:604:ASP:O	1:D:607:ARG:N	2.54	0.41
1:D:627:LEU:CD1	1:E:607:ARG:HH12	2.32	0.41
1:E:441:LEU:O	1:E:445:VAL:HG23	2.21	0.41
1:E:593:TYR:OH	1:E:632:LYS:NZ	2.31	0.41
1:E:721:ASP:HB2	1:E:724:TYR:HD2	1.85	0.41
1:F:323:HIS:HB2	1:F:367:ILE:HG22	2.01	0.41
1:F:670:ILE:O	1:F:704:TRP:HA	2.20	0.41
2:I:164:CYS:O	2:I:168:VAL:HG23	2.20	0.41
2:I:180:LYS:O	2:I:184:ILE:HG13	2.20	0.41
2:J:219:LEU:O	2:J:223:LEU:N	2.52	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:179:GLN:HG3	2:G:180:LYS:H	1.85	0.41
3:K:53:VAL:HB	4:L:219:MET:HE1	2.02	0.41
3:K:84:LEU:HD21	5:M:199:ALA:CB	2.50	0.41
4:L:223:VAL:O	5:M:49:MET:HE3	2.19	0.41
1:A:241:PRO:HA	1:A:242:PRO:HA	1.62	0.41
1:B:143:LYS:HB3	1:B:145:PHE:CE1	2.56	0.41
1:B:407:LEU:O	1:B:411:THR:OG1	2.27	0.41
1:C:272:GLN:OE1	1:C:272:GLN:HA	2.20	0.41
1:C:297:GLU:O	1:C:301:ASN:N	2.32	0.41
1:C:604:ASP:HB3	1:C:607:ARG:HB3	2.02	0.41
1:C:626:LEU:HA	1:C:626:LEU:HD23	1.87	0.41
1:D:258:LEU:HB2	1:D:395:ILE:HD11	2.02	0.41
1:D:265:GLY:O	1:D:268:LEU:HG	2.20	0.41
1:D:509:LYS:HE2	1:D:515:THR:HG22	2.03	0.41
1:E:562:PHE:HE2	1:E:641:LEU:CD2	2.34	0.41
1:E:640:LEU:HG	1:E:642:ILE:CD1	2.50	0.41
1:E:659:ASN:HD21	1:F:545:PRO:HB2	1.86	0.41
1:E:709:LYS:O	1:E:709:LYS:HD3	2.20	0.41
1:F:510:TRP:HZ3	1:F:675:GLN:NE2	2.18	0.41
1:F:709:LYS:HG3	1:F:713:LEU:HG	2.02	0.41
2:H:112:THR:HG23	2:H:117:PHE:CE1	2.56	0.41
2:H:175:LEU:HD23	2:H:177:GLN:HE21	1.85	0.41
2:H:217:ASP:OD1	2:H:217:ASP:N	2.50	0.41
3:K:52:LYS:NZ	3:K:52:LYS:CB	2.84	0.41
1:A:215:PHE:N	1:A:231:PHE:CZ	2.89	0.41
1:A:673:GLY:O	1:A:676:LEU:HB3	2.21	0.41
1:B:257:LEU:HG	1:B:371:GLY:O	2.21	0.41
1:C:240:PHE:HA	1:C:241:PRO:HD3	1.94	0.41
1:C:649:LYS:HE2	1:C:658:LEU:CD1	2.45	0.41
1:D:527:GLN:HE22	1:E:716:MET:CA	2.33	0.41
1:D:562:PHE:CD2	1:D:597:LEU:HG	2.55	0.41
1:E:395:ILE:H	1:E:395:ILE:HD12	1.86	0.41
1:E:451:THR:O	1:E:454:ASN:HB3	2.21	0.41
2:I:124:HIS:CE1	2:I:147:GLN:HB3	2.55	0.41
2:G:78:LYS:HB2	2:G:114:MET:HE2	2.02	0.41
2:G:95:ALA:CB	2:G:97:PRO:HD2	2.51	0.41
2:G:200:TYR:O	2:G:203:LYS:HE2	2.21	0.41
4:L:224:GLU:HA	5:M:49:MET:HE1	2.02	0.41
4:L:237:VAL:O	4:L:241:VAL:HG23	2.21	0.41
1:A:26:GLU:HG2	1:A:51:THR:HB	2.03	0.41
1:A:27:LYS:HD2	1:A:57:PRO:CG	2.51	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:SER:HB3	1:A:43:HIS:ND1	2.36	0.41
1:A:91:CYS:O	1:A:154:ALA:HA	2.21	0.41
1:A:457:ILE:HB	1:F:232:ARG:HH21	1.86	0.41
1:B:16:LEU:HD11	1:B:52:HIS:HD2	1.86	0.41
1:B:406:ILE:O	1:B:409:ILE:HG22	2.20	0.41
1:B:501:SER:C	1:B:503:ILE:N	2.78	0.41
1:C:257:LEU:HG	1:C:371:GLY:O	2.21	0.41
1:C:653:GLN:HA	1:C:658:LEU:HB3	2.02	0.41
1:D:40:SER:HB3	1:D:43:HIS:CB	2.51	0.41
1:D:330:ILE:CD1	1:D:373:THR:HB	2.50	0.41
1:D:449:GLN:O	1:D:453:MET:HG2	2.21	0.41
1:D:560:SER:HB2	1:D:562:PHE:CE1	2.55	0.41
1:D:608:LEU:O	1:D:622:VAL:HG11	2.20	0.41
1:E:455:ARG:HH21	1:E:481:LEU:H	1.69	0.41
1:E:598:SER:O	1:E:640:LEU:HA	2.21	0.41
1:E:604:ASP:HB3	1:E:607:ARG:CB	2.49	0.41
1:F:98:GLU:HB3	1:F:148:LEU:HB3	2.02	0.41
1:F:121:PHE:CD2	1:F:183:VAL:HG21	2.56	0.41
1:F:230:ILE:HD13	1:F:391:VAL:HG21	2.03	0.41
1:F:503:ILE:HD11	1:F:551:ALA:HA	2.02	0.41
1:F:658:LEU:HD12	1:F:658:LEU:O	2.20	0.41
1:F:705:ILE:HG12	1:F:706:GLY:O	2.20	0.41
1:F:709:LYS:HB2	1:F:709:LYS:HE2	1.82	0.41
2:H:167:LYS:HE2	2:H:171:TYR:HE2	1.85	0.41
2:H:255:ASN:C	2:H:257:ASP:H	2.29	0.41
2:H:260:THR:HG21	2:H:284:LYS:HE3	2.02	0.41
2:J:213:HIS:CE1	2:J:221:ALA:HB2	2.44	0.41
2:G:178:TYR:OH	2:G:282:ARG:HG2	2.20	0.41
3:K:39:VAL:CG1	4:L:209:ILE:HD13	2.46	0.41
4:L:209:ILE:HG21	5:M:32:MET:HE2	2.02	0.41
5:M:174:GLN:O	5:M:177:GLN:HB3	2.21	0.41
1:A:243:GLU:O	1:A:246:GLU:HG2	2.21	0.41
1:B:178:VAL:HG22	1:B:181:SER:OG	2.20	0.41
1:B:633:ALA:HA	1:B:634:PRO:HD3	1.94	0.41
1:C:379:ILE:HD13	1:C:379:ILE:HA	1.74	0.41
1:C:402:GLY:O	1:C:405:GLN:HB2	2.22	0.41
1:C:696:GLN:NE2	1:C:696:GLN:O	2.54	0.41
1:D:188:ALA:O	1:D:189:GLU:C	2.64	0.41
1:D:507:ILE:HG21	1:D:509:LYS:NZ	2.36	0.41
1:D:577:SER:O	1:D:580:ALA:N	2.54	0.41
1:D:609:LEU:HD12	1:D:611:TYR:H	1.86	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:553:ALA:HB1	1:E:643:ILE:HG21	2.03	0.41
1:F:257:LEU:HB2	1:F:389:LEU:HD13	2.03	0.41
1:F:297:GLU:O	1:F:300:ALA:HB3	2.21	0.41
1:F:309:ALA:HA	1:F:312:GLU:OE1	2.21	0.41
2:I:236:SER:HA	2:I:239:ARG:HH12	1.86	0.41
2:G:101:ILE:O	2:G:105:MET:HG3	2.20	0.41
4:L:226:GLN:O	4:L:230:ILE:HG13	2.20	0.41
1:A:24:VAL:C	1:A:55:VAL:HG11	2.46	0.40
1:A:352:ASN:CB	1:B:288:PRO:HB2	2.44	0.40
1:A:429:LEU:CD2	1:A:482:ALA:HB1	2.51	0.40
1:A:623:LEU:O	1:A:626:LEU:HB3	2.22	0.40
1:B:67:ARG:HH12	1:B:74:ILE:HD11	1.84	0.40
1:B:309:ALA:HA	1:B:312:GLU:OE1	2.22	0.40
1:C:449:GLN:O	1:C:453:MET:HG2	2.21	0.40
1:C:577:SER:O	1:C:578:GLU:C	2.64	0.40
1:D:192:SER:O	1:D:193:LEU:C	2.63	0.40
1:E:190:ASN:HB2	1:E:315:ARG:NH1	2.36	0.40
1:E:323:HIS:HB2	1:E:367:ILE:HG22	2.03	0.40
1:E:324:ILE:HG12	1:E:368:LEU:HD11	2.03	0.40
2:H:130:ILE:C	2:H:132:GLU:N	2.79	0.40
2:H:221:ALA:O	2:H:225:VAL:N	2.53	0.40
2:G:279:MET:O	2:G:283:ILE:HG13	2.21	0.40
5:M:165:LEU:O	5:M:169:ASN:ND2	2.48	0.40
1:A:428:GLU:O	1:A:432:GLU:HG2	2.21	0.40
1:B:501:SER:O	1:B:502:TYR:C	2.65	0.40
1:B:655:MET:C	1:B:656:GLU:HG3	2.47	0.40
1:C:331:ASP:CA	1:C:379:ILE:HD11	2.46	0.40
1:F:437:SER:OG	1:F:440:GLU:HG2	2.20	0.40
2:H:116:ARG:HG3	2:H:116:ARG:NH1	2.37	0.40
1:A:231:PHE:CD2	1:A:235:PHE:HD2	2.38	0.40
1:A:255:GLY:HA2	1:A:369:VAL:O	2.22	0.40
1:A:607:ARG:HH11	1:F:624:GLN:CD	2.29	0.40
1:B:113:ASP:O	1:B:117:MET:HG3	2.21	0.40
1:B:721:ASP:HB2	1:B:724:TYR:CD1	2.57	0.40
1:C:36:ILE:HD11	1:C:44:LYS:HB3	2.03	0.40
1:C:65:PRO:HG2	1:C:137:VAL:HG13	2.03	0.40
1:C:98:GLU:HG2	1:C:188:ALA:HB2	2.04	0.40
1:C:98:GLU:O	1:C:147:LEU:HA	2.21	0.40
1:C:630:LEU:HD23	1:C:630:LEU:HA	1.94	0.40
1:E:86:ASP:C	1:E:88:ALA:N	2.79	0.40
1:E:236:ALA:HA	1:E:239:VAL:CG1	2.50	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:502:TYR:HD2	1:F:503:ILE:HG13	1.86	0.40
1:F:678:GLU:O	1:F:682:LEU:HG	2.22	0.40
2:I:10:ALA:O	2:I:14:LEU:HG	2.20	0.40
2:I:231:LEU:O	2:I:232:PHE:C	2.63	0.40
2:J:235:PHE:CG	3:K:38:GLN:CG	3.04	0.40
2:G:17:ALA:HB2	2:G:44:ILE:HG21	2.04	0.40
5:M:30:ARG:C	5:M:32:MET:H	2.28	0.40
1:A:284:VAL:O	1:A:326:ILE:HG13	2.21	0.40
1:A:564:PHE:CD1	1:A:564:PHE:C	3.00	0.40
1:B:52:HIS:HA	1:B:53:PRO:HD3	1.91	0.40
1:B:221:GLY:HA3	1:B:406:ILE:CD1	2.52	0.40
1:B:323:HIS:HB2	1:B:367:ILE:HG22	2.02	0.40
1:B:403:ARG:O	1:B:407:LEU:HG	2.22	0.40
1:C:99:ILE:HD11	1:C:145:PHE:CD2	2.57	0.40
1:C:237:SER:OG	1:C:252:HIS:ND1	2.49	0.40
1:D:18:LEU:HD21	1:D:144:LEU:HD13	2.02	0.40
1:E:242:PRO:CD	1:E:243:GLU:N	2.85	0.40
1:E:641:LEU:CD1	1:E:643:ILE:HD11	2.51	0.40
1:F:219:GLY:C	1:F:220:ILE:HD12	2.46	0.40
1:F:242:PRO:CD	1:F:243:GLU:N	2.84	0.40
1:F:652:LEU:O	1:F:655:MET:HB2	2.22	0.40
2:H:212:CYS:SG	2:H:279:MET:HE1	2.60	0.40
2:I:256:VAL:HG22	2:I:256:VAL:O	2.21	0.40
2:J:45:TYR:CE2	2:J:71:LEU:HD11	2.56	0.40
2:J:59:SER:OG	2:J:97:PRO:HD3	2.21	0.40
2:G:98:GLN:C	2:G:100:ALA:H	2.29	0.40
2:G:126:SER:O	2:G:130:ILE:HG13	2.22	0.40
1:A:694:ILE:HA	1:A:697:GLN:OE1	2.22	0.40
1:B:540:LEU:HD12	1:B:540:LEU:C	2.47	0.40
1:C:246:GLU:HG2	1:C:247:GLN:N	2.37	0.40
1:D:312:GLU:CD	1:D:323:HIS:ND1	2.80	0.40
1:D:379:ILE:HD13	1:D:379:ILE:HA	1.74	0.40
1:E:64:LEU:HA	1:E:67:ARG:NE	2.21	0.40
1:E:190:ASN:ND2	1:E:316:LEU:CA	2.85	0.40
1:E:253:VAL:H	1:F:446:ARG:NH1	2.15	0.40
1:E:257:LEU:HB2	1:E:389:LEU:HD13	2.02	0.40
1:E:544:PRO:O	1:E:547:SER:CB	2.68	0.40
1:E:686:PHE:O	1:E:691:ARG:NH1	2.54	0.40
2:H:216:ILE:HG21	2:H:220:ASN:HB3	2.03	0.40
2:I:175:LEU:HD23	2:I:177:GLN:NE2	2.37	0.40
2:I:232:PHE:O	2:I:234:ALA:N	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:261:GLU:O	2:J:265:GLU:HG3	2.21	0.40
4:L:209:ILE:HG22	4:L:210:ARG:N	2.35	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	668/747 (89%)	613 (92%)	39 (6%)	16 (2%)	4	27
1	B	662/747 (89%)	589 (89%)	54 (8%)	19 (3%)	3	23
1	C	666/747 (89%)	616 (92%)	37 (6%)	13 (2%)	6	31
1	D	663/747 (89%)	601 (91%)	52 (8%)	10 (2%)	8	40
1	E	658/747 (88%)	603 (92%)	42 (6%)	13 (2%)	6	31
1	F	644/747 (86%)	585 (91%)	46 (7%)	13 (2%)	6	31
2	G	284/297 (96%)	227 (80%)	47 (16%)	10 (4%)	3	20
2	H	284/297 (96%)	230 (81%)	44 (16%)	10 (4%)	3	20
2	I	284/297 (96%)	229 (81%)	41 (14%)	14 (5%)	1	16
2	J	284/297 (96%)	229 (81%)	45 (16%)	10 (4%)	3	20
3	K	59/63 (94%)	56 (95%)	2 (3%)	1 (2%)	7	36
4	L	64/67 (96%)	58 (91%)	5 (8%)	1 (2%)	7	38
5	M	127/198 (64%)	119 (94%)	7 (6%)	1 (1%)	16	54
All	All	5347/5998 (89%)	4755 (89%)	461 (9%)	131 (2%)	7	27

All (131) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	293	LYS
1	A	294	TYR
1	A	318	ALA
1	A	320	SER
1	A	333	ILE
1	A	498	ASP
1	A	504	MET
1	B	283	LYS
1	B	297	GLU
1	B	318	ALA
1	B	395	ILE
1	B	439	ALA
1	B	497	GLU
1	B	502	TYR
1	C	297	GLU
1	C	318	ALA
1	C	497	GLU
1	C	498	ASP
1	C	578	GLU
1	D	283	LYS
1	D	318	ALA
1	D	489	LYS
1	E	283	LYS
1	E	297	GLU
1	E	318	ALA
1	E	439	ALA
1	E	489	LYS
1	F	12	PRO
1	F	283	LYS
1	F	297	GLU
1	F	318	ALA
1	F	439	ALA
2	H	58	TRP
2	H	76	GLN
2	I	58	TRP
2	I	77	SER
2	I	219	LEU
2	J	58	TRP
2	J	218	MET
2	J	235	PHE
2	G	58	TRP
1	A	397	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	12	PRO
1	B	188	ALA
1	C	12	PRO
1	C	89	LYS
1	C	293	LYS
1	C	610	ASP
1	D	12	PRO
1	E	507	ILE
1	F	189	GLU
2	H	33	GLY
2	H	79	HIS
2	I	136	VAL
2	I	218	MET
2	I	254	GLN
2	I	256	VAL
2	G	76	GLN
3	K	30	ARG
4	L	209	ILE
1	A	12	PRO
1	A	241	PRO
1	A	264	CYS
1	B	241	PRO
1	B	293	LYS
1	B	546	HIS
1	C	87	LYS
1	C	241	PRO
1	D	87	LYS
1	D	293	LYS
1	E	87	LYS
1	E	241	PRO
1	E	293	LYS
1	F	241	PRO
1	F	293	LYS
2	H	159	SER
2	H	240	GLU
2	H	256	VAL
2	I	78	LYS
2	J	158	ASN
2	J	159	SER
2	G	79	HIS
2	G	156	GLU
2	G	232	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	G	240	GLU
5	M	165	LEU
1	A	87	LYS
1	A	242	PRO
1	E	71	GLY
2	H	267	ASP
2	I	30	GLY
2	I	76	GLN
2	I	79	HIS
2	I	240	GLU
2	J	79	HIS
2	J	177	GLN
2	J	256	VAL
2	G	218	MET
1	A	668	PRO
1	B	87	LYS
1	B	397	LEU
1	B	547	SER
1	D	53	PRO
1	D	241	PRO
1	E	438	GLY
1	F	398	PRO
2	H	26	SER
2	I	232	PHE
2	I	233	PRO
2	J	96	ASP
2	G	97	PRO
2	G	256	VAL
1	B	53	PRO
1	B	438	GLY
1	B	490	PRO
1	E	490	PRO
1	F	397	LEU
1	F	668	PRO
1	B	398	PRO
1	D	488	ILE
1	F	438	GLY
1	F	684	GLY
2	G	30	GLY
1	C	490	PRO
1	D	545	PRO
1	E	12	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	H	34	GLY
1	A	53	PRO
2	J	34	GLY
1	C	3	GLY

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	514/638 (81%)	488 (95%)	26 (5%)	21	42
1	B	514/638 (81%)	499 (97%)	15 (3%)	37	58
1	C	513/638 (80%)	489 (95%)	24 (5%)	23	45
1	D	509/638 (80%)	491 (96%)	18 (4%)	32	53
1	E	518/638 (81%)	495 (96%)	23 (4%)	25	47
1	F	513/638 (80%)	492 (96%)	21 (4%)	27	49
2	G	235/244 (96%)	235 (100%)	0	100	100
2	H	235/244 (96%)	234 (100%)	1 (0%)	84	84
2	I	233/244 (96%)	233 (100%)	0	100	100
2	J	235/244 (96%)	235 (100%)	0	100	100
3	K	52/54 (96%)	49 (94%)	3 (6%)	18	40
4	L	60/61 (98%)	60 (100%)	0	100	100
5	M	111/171 (65%)	111 (100%)	0	100	100
All	All	4242/5090 (83%)	4111 (97%)	131 (3%)	36	56

All (131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	246	GLU
1	A	253	VAL
1	A	284	VAL
1	A	305	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	322	LEU
1	A	326	ILE
1	A	367	ILE
1	A	375	ARG
1	A	395	ILE
1	A	409	ILE
1	A	445	VAL
1	A	449	GLN
1	A	537	VAL
1	A	539	VAL
1	A	566	LYS
1	A	573	MET
1	A	581	LYS
1	A	586	LYS
1	A	631	LYS
1	A	651	VAL
1	A	658	LEU
1	A	665	ILE
1	A	667	VAL
1	A	677	LEU
1	A	690	GLU
1	A	705	ILE
1	B	246	GLU
1	B	284	VAL
1	B	285	VAL
1	B	305	LEU
1	B	322	LEU
1	B	325	ILE
1	B	330	ILE
1	B	351	VAL
1	B	381	GLU
1	B	389	LEU
1	B	508	ILE
1	B	567	ILE
1	B	623	LEU
1	B	626	LEU
1	B	631	LYS
1	C	246	GLU
1	C	256	ILE
1	C	268	LEU
1	C	273	ILE
1	C	305	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	312	GLU
1	C	316	LEU
1	C	322	LEU
1	C	324	ILE
1	C	326	ILE
1	C	330	ILE
1	C	367	ILE
1	C	541	LEU
1	C	573	MET
1	C	587	LYS
1	C	602	VAL
1	C	609	LEU
1	C	623	LEU
1	C	632	LYS
1	C	651	VAL
1	C	676	LEU
1	C	682	LEU
1	C	691	ARG
1	C	711	LEU
1	D	106	ASN
1	D	246	GLU
1	D	273	ILE
1	D	284	VAL
1	D	305	LEU
1	D	311	GLU
1	D	350	VAL
1	D	370	ILE
1	D	381	GLU
1	D	389	LEU
1	D	407	LEU
1	D	424	VAL
1	D	601	VAL
1	D	602	VAL
1	D	645	THR
1	D	666	HIS
1	D	681	GLU
1	D	716	MET
1	E	246	GLU
1	E	284	VAL
1	E	285	VAL
1	E	305	LEU
1	E	322	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	325	ILE
1	E	330	ILE
1	E	351	VAL
1	E	381	GLU
1	E	389	LEU
1	E	457	ILE
1	E	508	ILE
1	E	522	GLU
1	E	537	VAL
1	E	540	LEU
1	E	549	LYS
1	E	586	LYS
1	E	588	ILE
1	E	602	VAL
1	E	626	LEU
1	E	658	LEU
1	E	689	LYS
1	E	693	THR
1	F	246	GLU
1	F	284	VAL
1	F	285	VAL
1	F	305	LEU
1	F	322	LEU
1	F	325	ILE
1	F	330	ILE
1	F	351	VAL
1	F	381	GLU
1	F	389	LEU
1	F	395	ILE
1	F	397	LEU
1	F	399	ASP
1	F	519	ASP
1	F	524	LEU
1	F	536	LEU
1	F	537	VAL
1	F	578	GLU
1	F	606	GLU
1	F	614	ILE
1	F	651	VAL
2	H	245	LYS
3	K	45	ILE
3	K	52	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	K	68	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (68) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	ASN
1	A	353	GLN
1	A	408	HIS
1	A	418	GLN
1	A	449	GLN
1	A	527	GLN
1	A	583	GLN
1	A	653	GLN
1	B	180	ASN
1	B	405	GLN
1	B	418	GLN
1	B	454	ASN
1	B	526	GLN
1	B	527	GLN
1	B	620	ASN
1	B	675	GLN
1	C	319	ASN
1	C	405	GLN
1	C	418	GLN
1	D	313	GLN
1	D	319	ASN
1	D	352	ASN
1	D	353	GLN
1	D	526	GLN
1	D	527	GLN
1	D	596	GLN
1	D	675	GLN
1	E	170	GLN
1	E	313	GLN
1	E	319	ASN
1	E	352	ASN
1	E	405	GLN
1	E	418	GLN
1	E	527	GLN
1	E	546	HIS
1	E	659	ASN
1	E	666	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	106	ASN
1	F	182	GLN
1	F	405	GLN
1	F	418	GLN
1	F	456	HIS
1	F	527	GLN
2	H	50	ASN
2	H	72	HIS
2	H	179	GLN
2	H	187	GLN
2	I	72	HIS
2	I	123	HIS
2	I	187	GLN
2	J	50	ASN
2	J	179	GLN
2	J	187	GLN
2	J	226	GLN
2	J	288	GLN
2	G	79	HIS
2	G	123	HIS
2	G	179	GLN
2	G	187	GLN
3	K	34	GLN
4	L	199	HIS
4	L	213	HIS
4	L	226	GLN
5	M	53	GLN
5	M	56	GLN
5	M	65	ASN
5	M	77	ASN
5	M	188	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

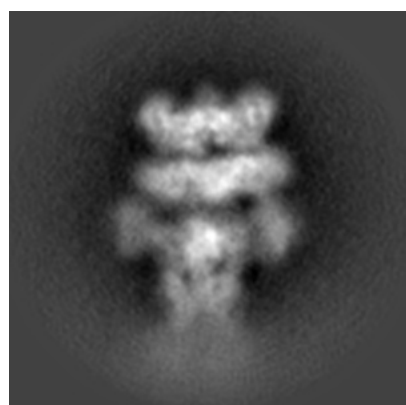
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6207. These allow visual inspection of the internal detail of the map and identification of artifacts.

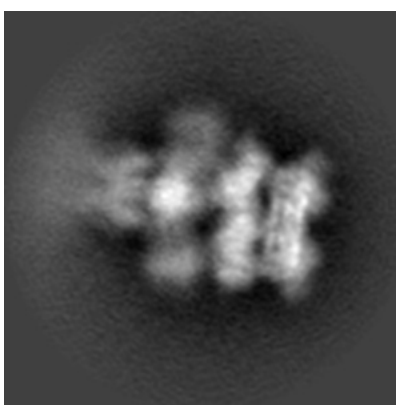
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

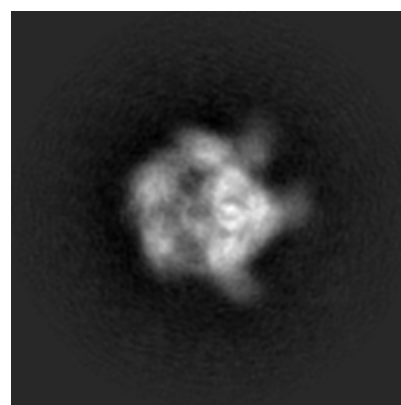
6.1.1 Primary map



X



Y

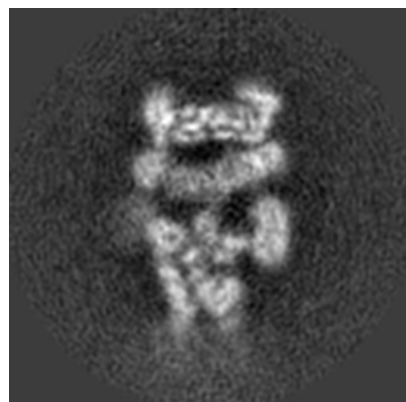


Z

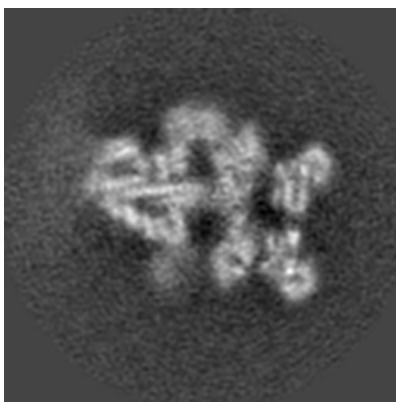
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

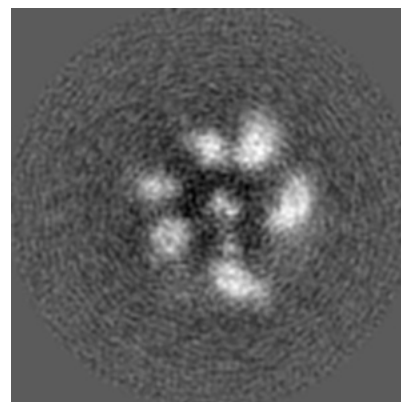
6.2.1 Primary map



X Index: 64



Y Index: 64



Z Index: 64

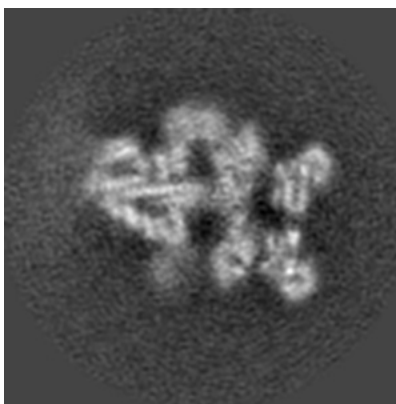
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

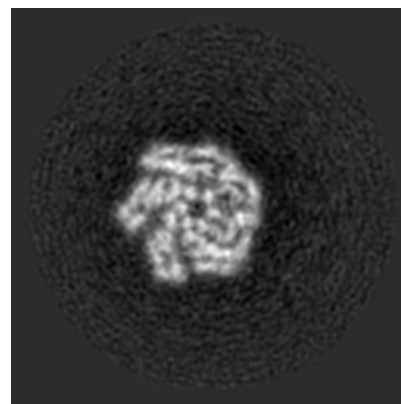
6.3.1 Primary map



X Index: 70



Y Index: 64

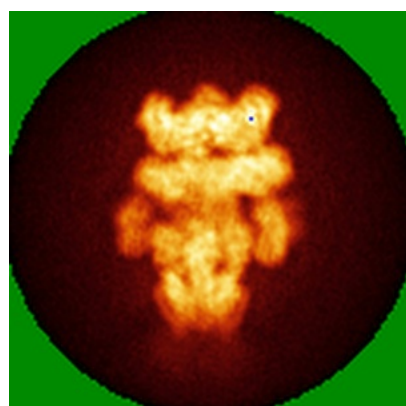


Z Index: 93

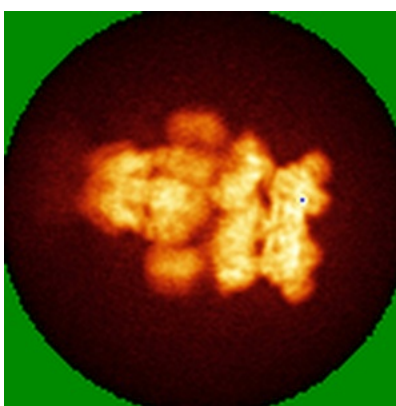
The images above show the largest variance slices of the map in three orthogonal directions.

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

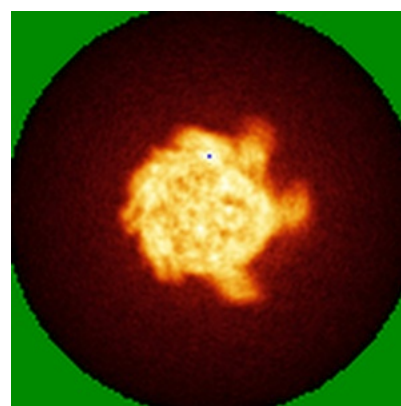
6.4.1 Primary map



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

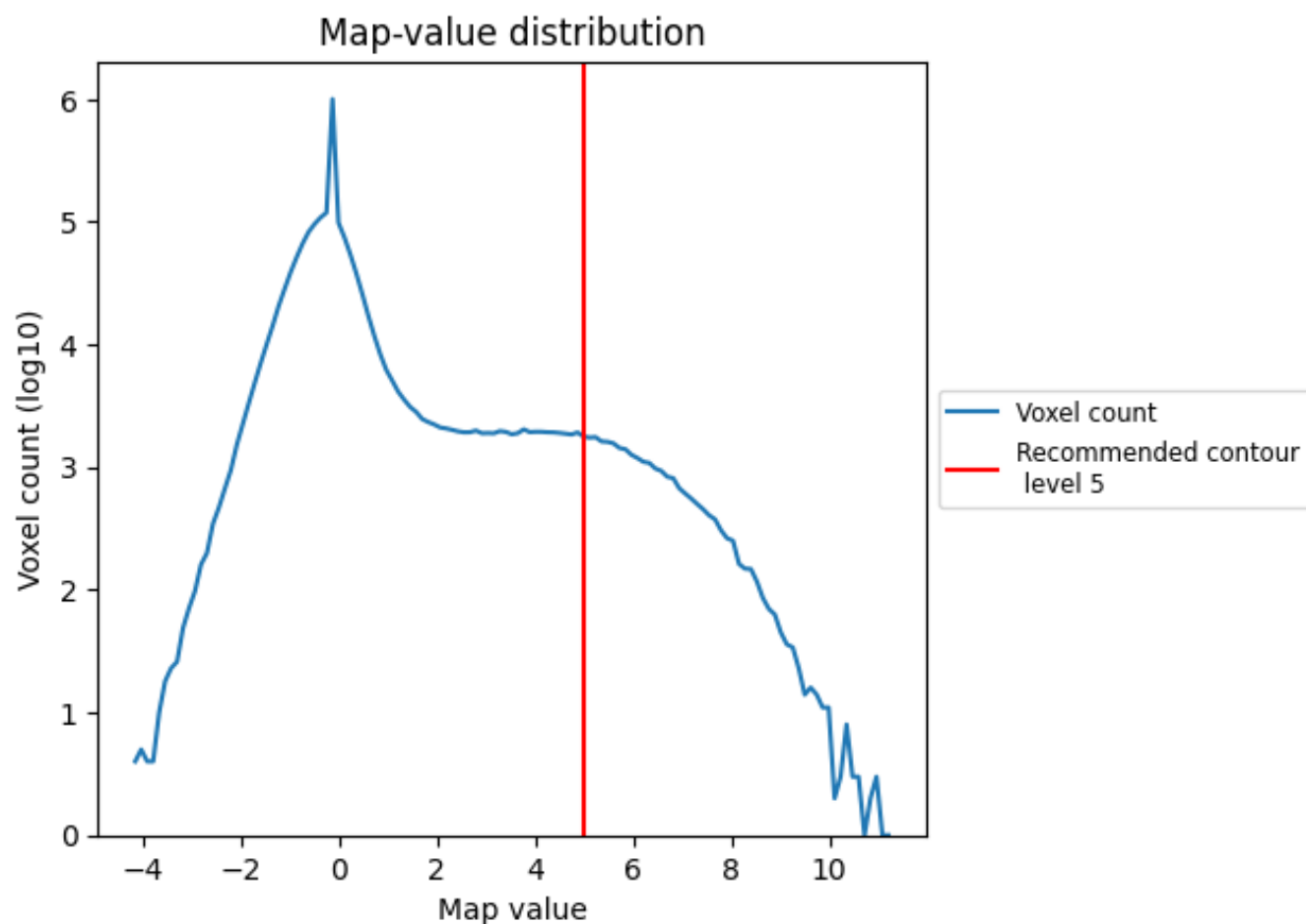
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

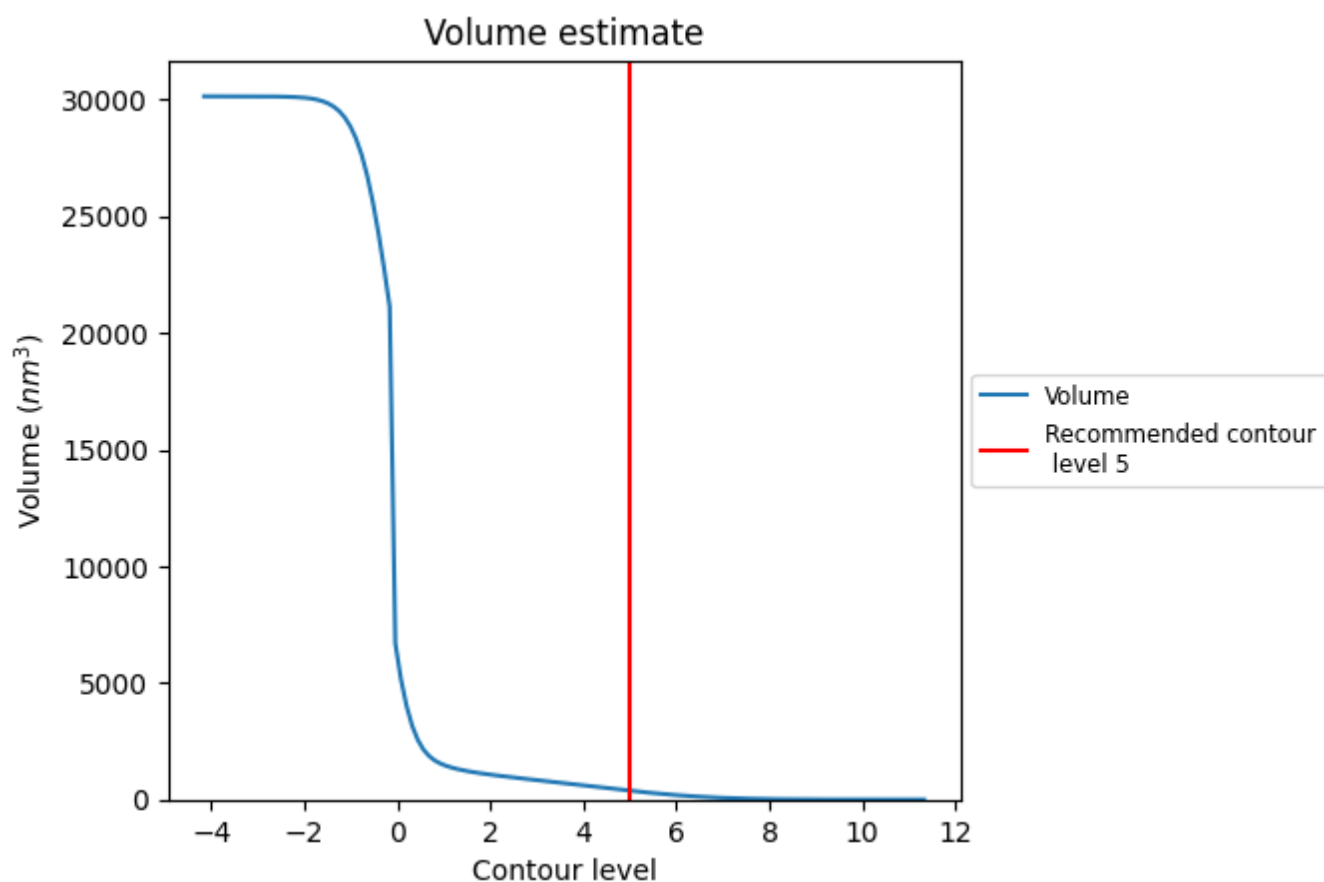
This section contains the results of statistical analysis of the map.

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.

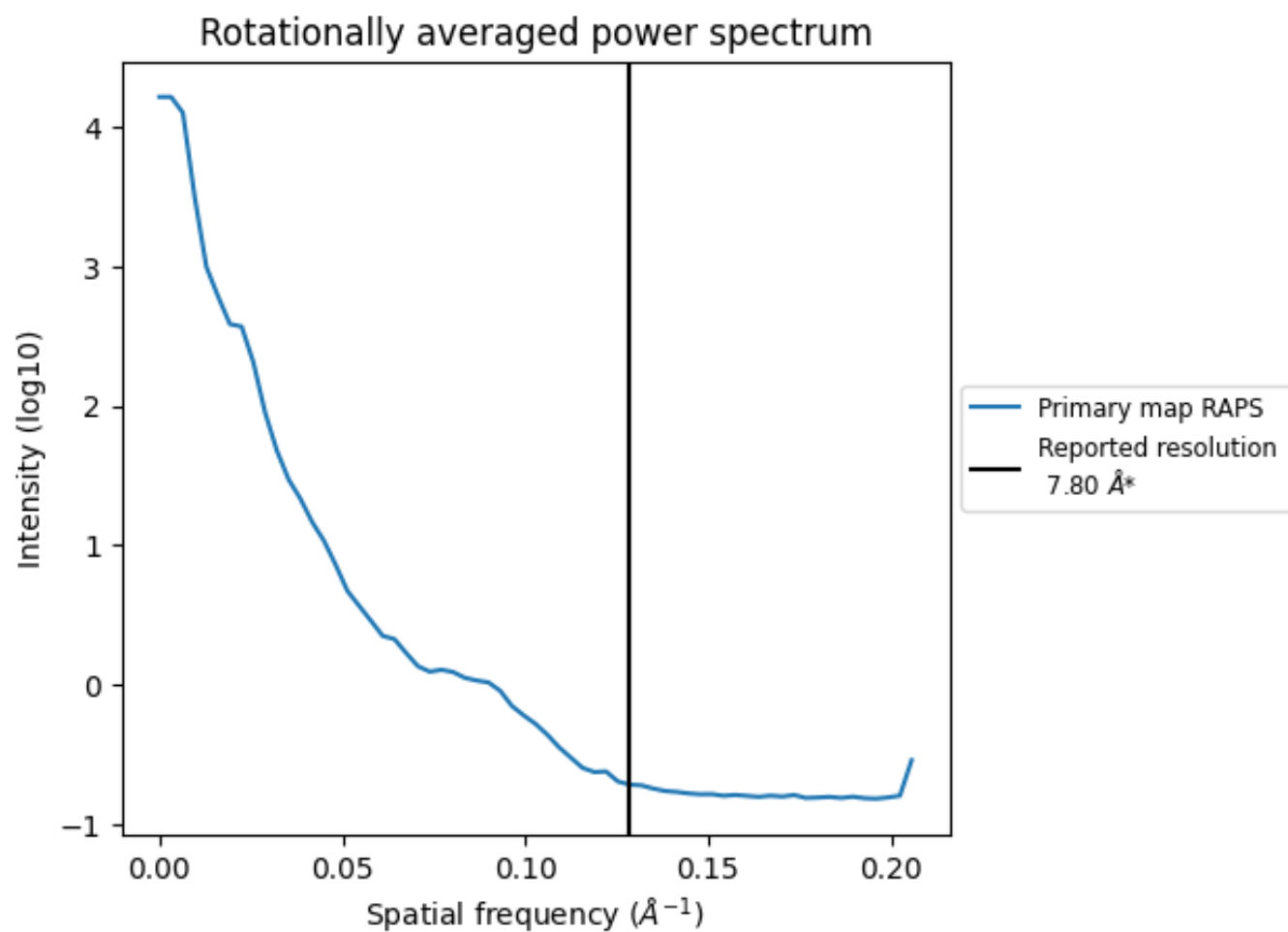
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 379 nm³; this corresponds to an approximate mass of 342 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 0.128 Å⁻¹

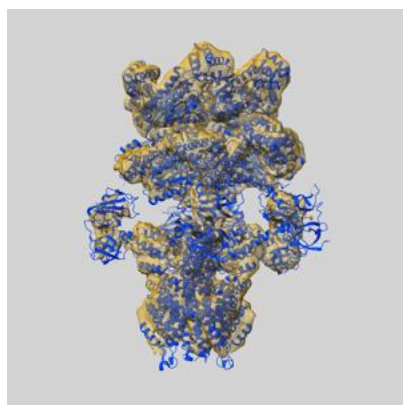
8 Fourier-Shell correlation

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

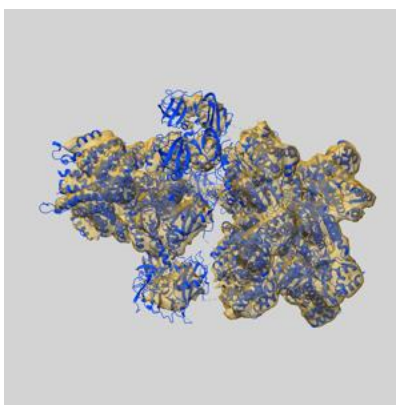
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6207 and PDB model 3J97. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

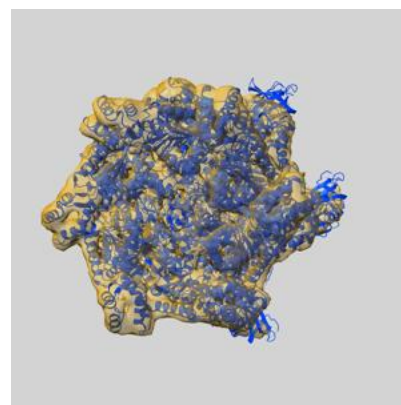
9.1 Map-model overlay [i](#)



X



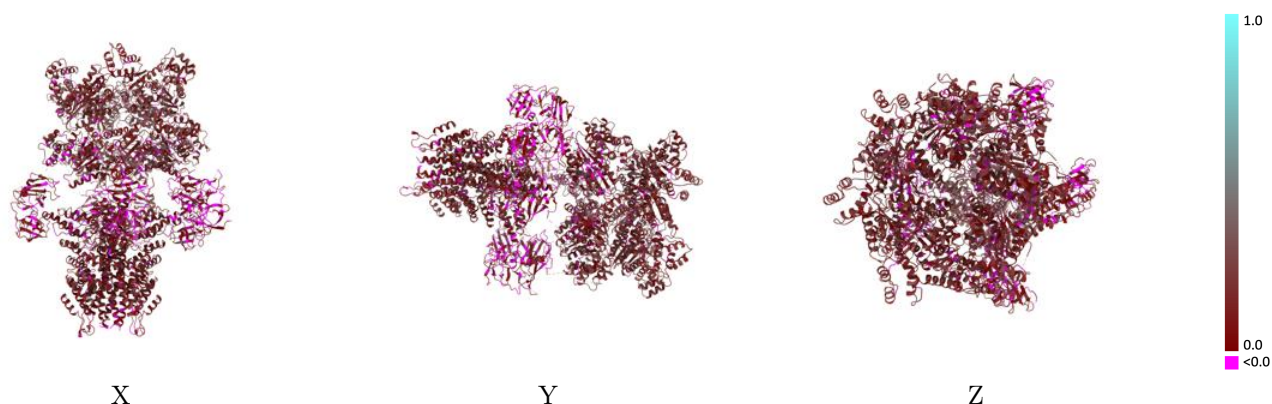
Y



Z

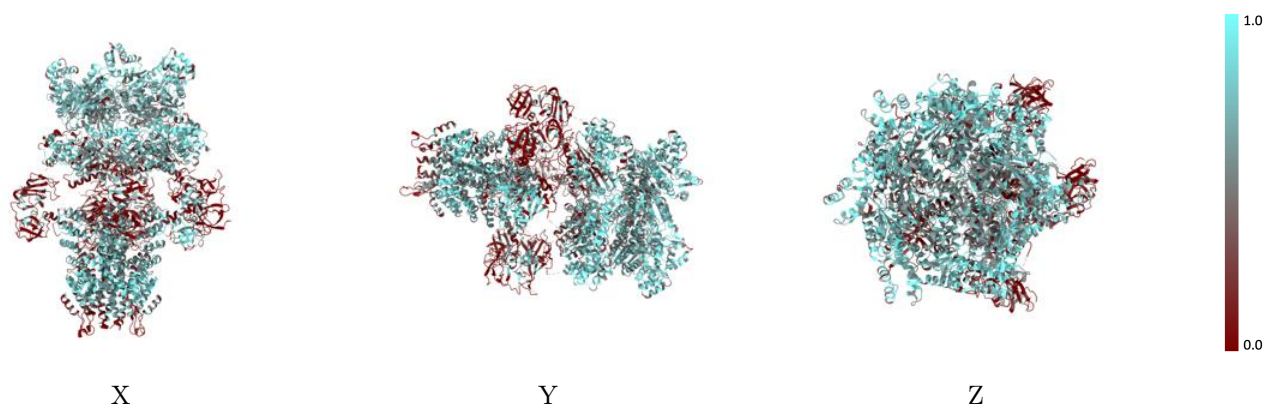
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



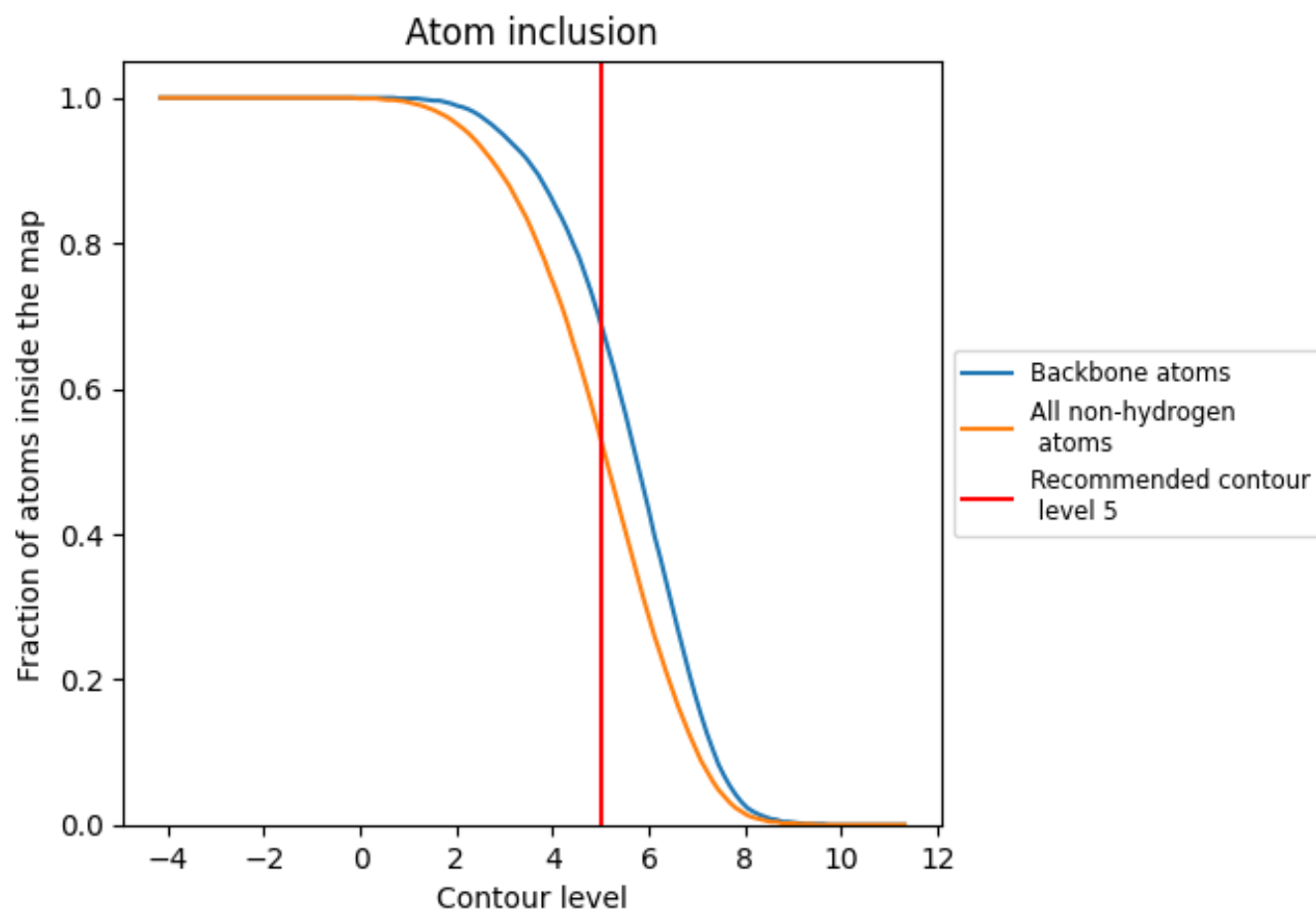
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 53% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5310	0.1360
A	0.4590	0.1350
B	0.5500	0.1330
C	0.6490	0.1550
D	0.5020	0.1270
E	0.4920	0.1380
F	0.4700	0.1310
G	0.5560	0.1370
H	0.5950	0.1370
I	0.5720	0.1340
J	0.5360	0.1320
K	0.5350	0.1320
L	0.4960	0.1300
M	0.5520	0.1350

1.0

0.0

<0.0