



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 09:11 AM UTC

PDB ID : 3J96 / pdb_00003j96
EMDB ID : EMD-6206
Title : Structure of 20S supercomplex determined by single particle cryoelectron microscopy (State I)
Authors : Zhao, M.; Wu, S.; Cheng, Y.; Brunger, A.T.
Deposited on : 2014-12-05
Resolution : 7.60 Å (reported)
Based on initial models : 1NSF, 1N7S, 1QCS

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

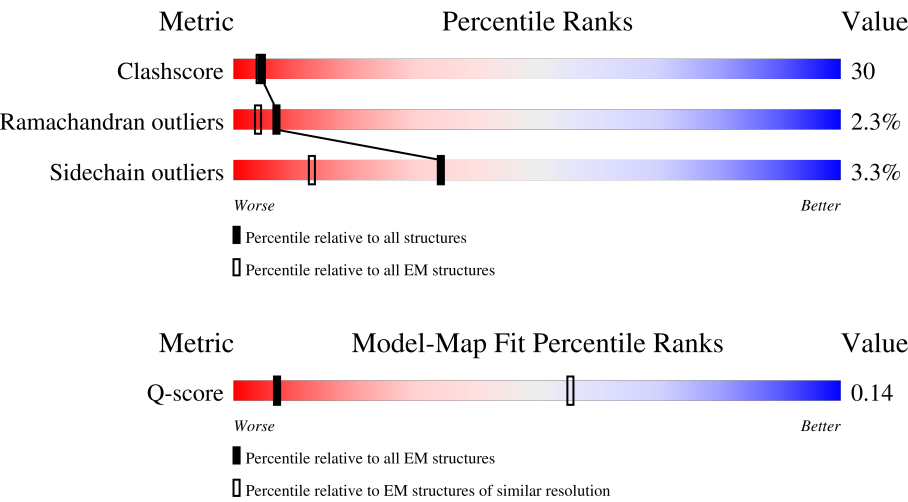
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 7.60 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	389 (7.10 - 8.10)

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	35% 42%40%7%9%
1	B	747	18% 42%44%10%
1	C	747	28% 44%41%5%10%
1	D	747	30% 43%42%5%10%

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Mol	Chain	Length	Quality of chain
1	E	747	28%42%41%7%10%
1	F	747	36%41%42%5%12%
2	G	297	26%46%46%. .
2	H	297	28%51%42%. .
2	I	297	28%55%40%. .
2	J	297	29%51%43%. .
3	K	63	22%38%57%. .
4	L	67	22%49%45%. .
5	M	188	16%29%40%30%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 41139 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
			5048	3203	876	946	23		
1	B	672	Total	C	N	O	S	0	0
			5037	3197	872	944	24		
1	C	676	Total	C	N	O	S	0	0
			5039	3196	872	948	23		
1	D	673	Total	C	N	O	S	0	0
			4994	3174	857	939	24		
1	E	670	Total	C	N	O	S	0	0
			5012	3183	866	939	24		
1	F	654	Total	C	N	O	S	0	0
			4926	3130	849	923	24		

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	G	286	Total	C	N	O	S	0	0
			2255	1424	373	441	17		
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
			2251	1421	372	441	17		
2	J	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
G	-1	GLY	-	expression tag	UNP P54921
G	0	SER	-	expression tag	UNP P54921
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

- 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
			493	301	93	98	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

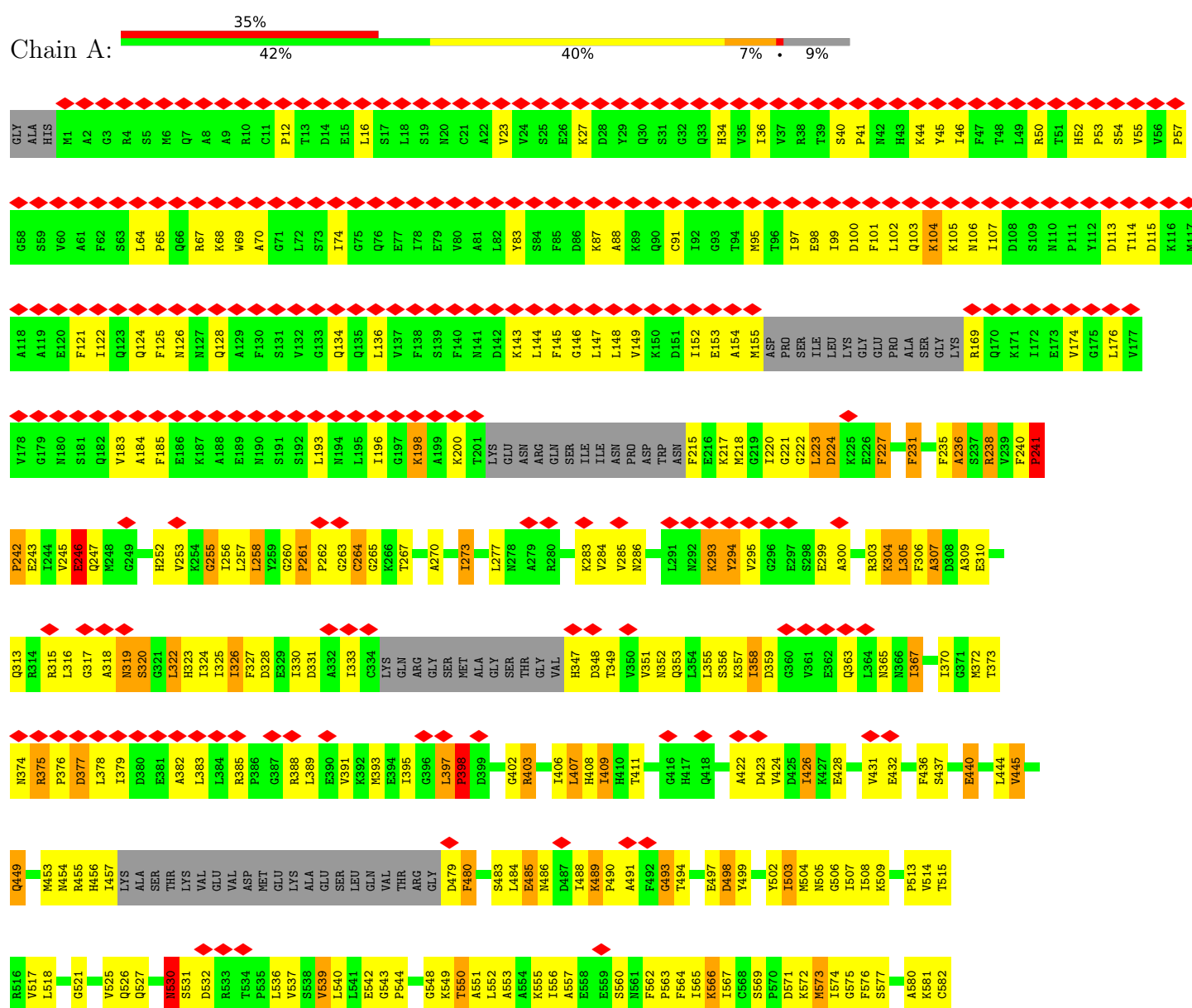
- Molecule 5 is a protein called Synaptosomal-associated protein 25.

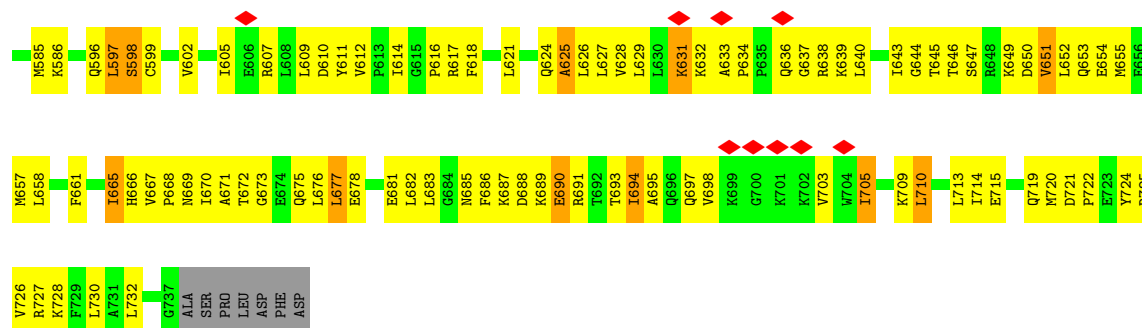
Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	131	Total	C	N	O	S	0	0
			1038	614	194	221	9		

3 Residue-property plots

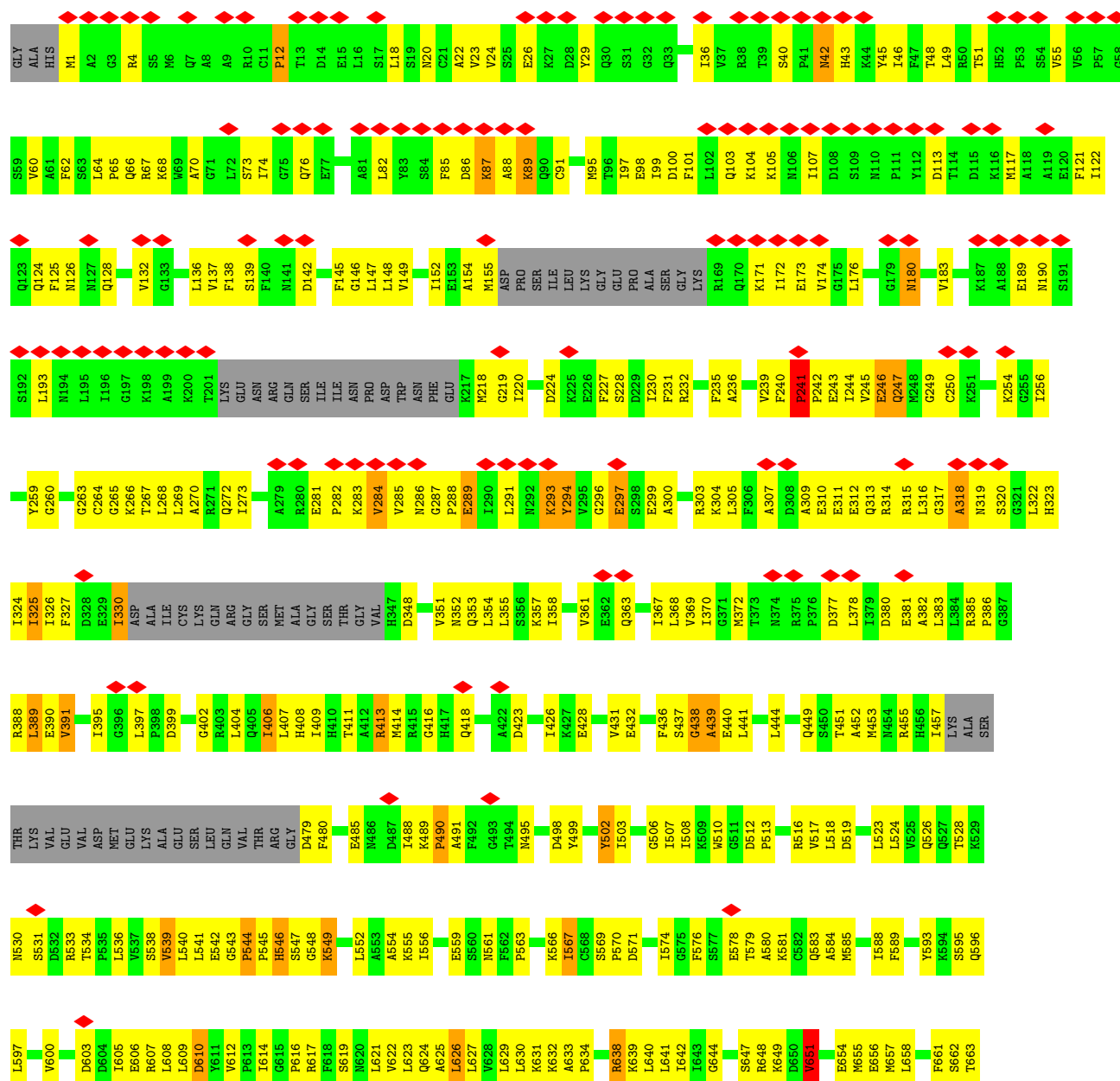
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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



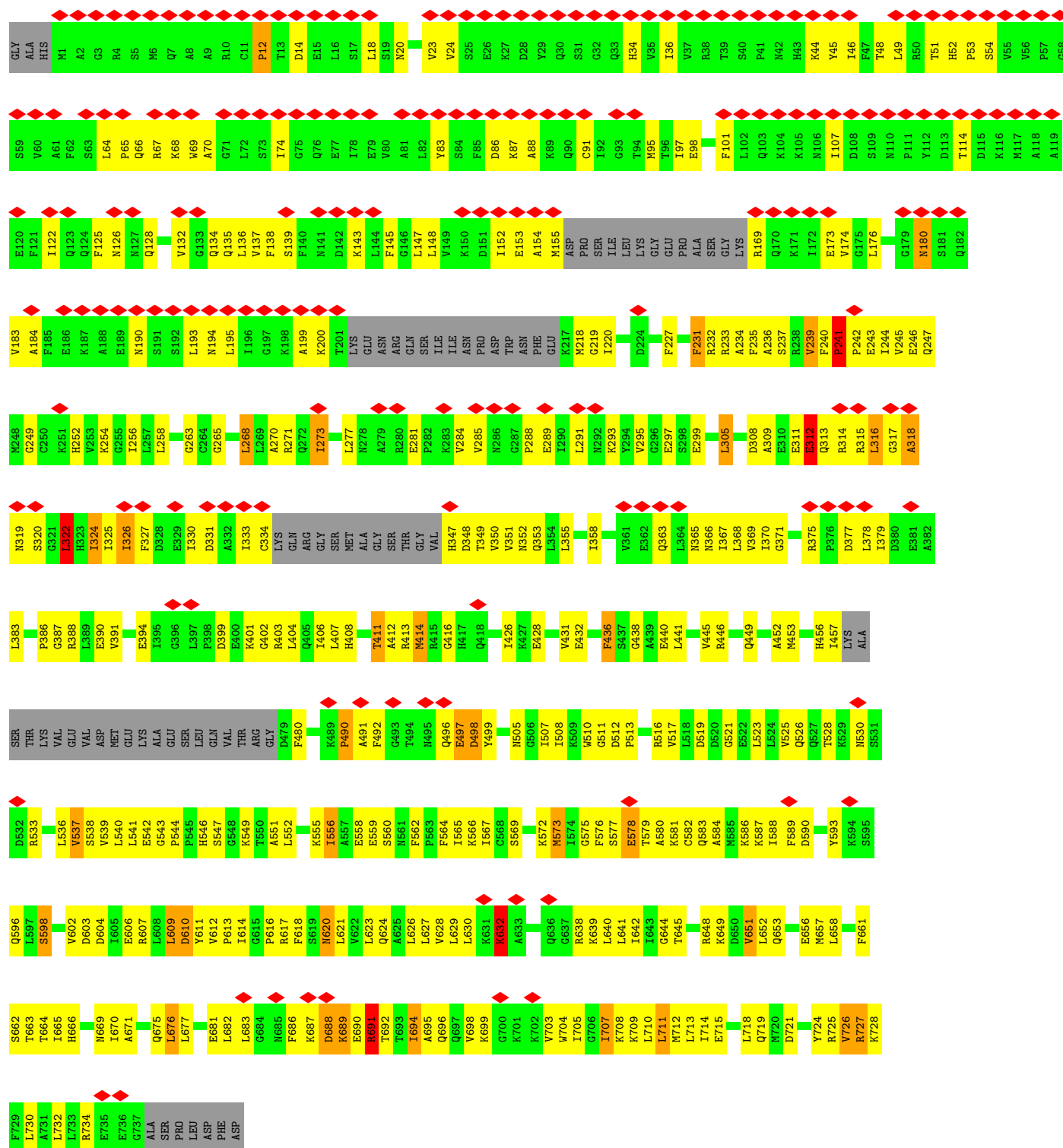
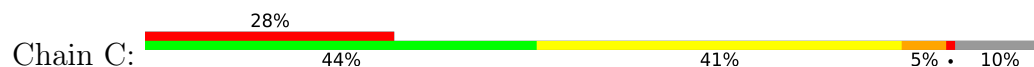


• Molecule 1: Vesicle-fusing ATPase



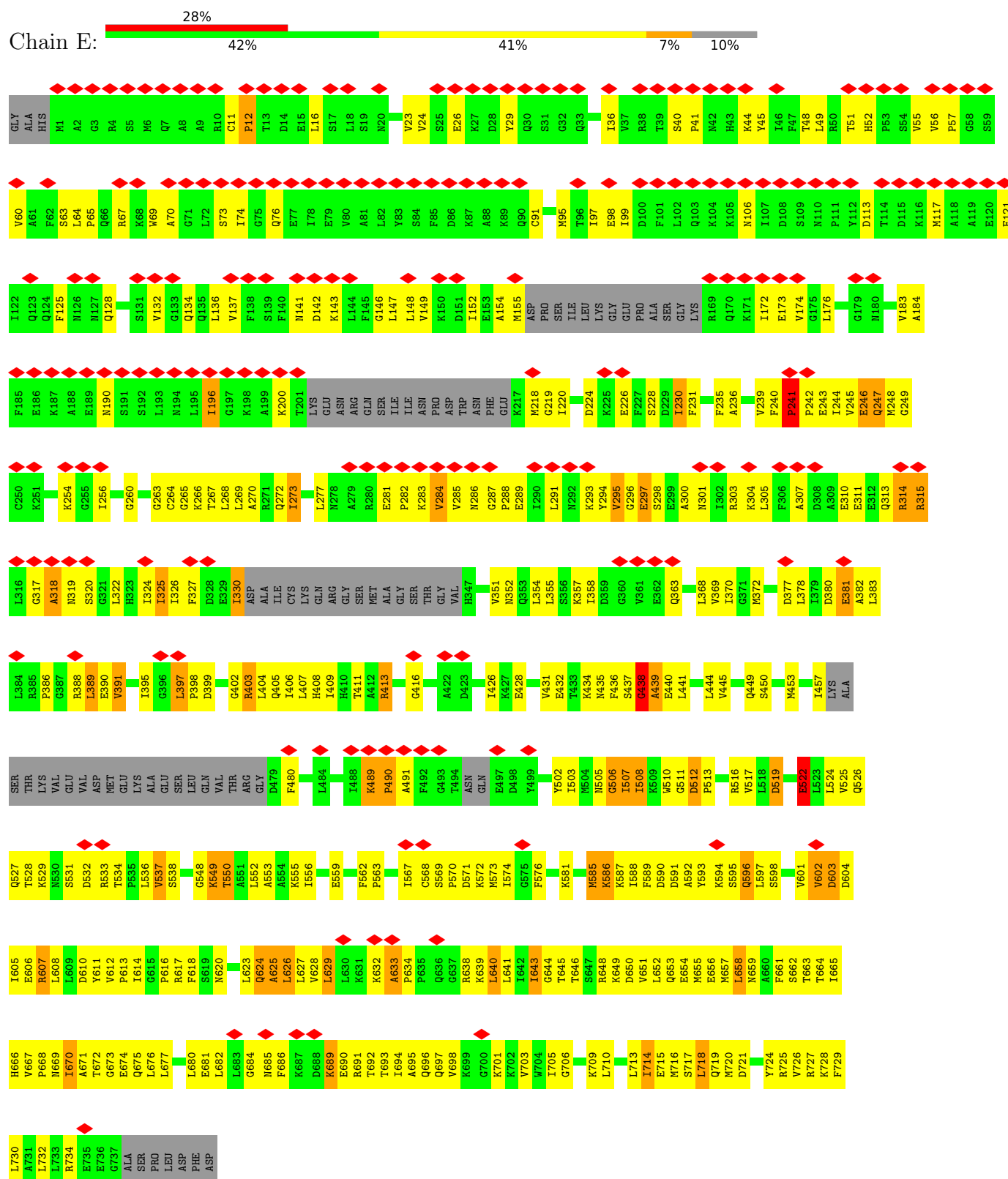


• Molecule 1: Vesicle-fusing ATPase



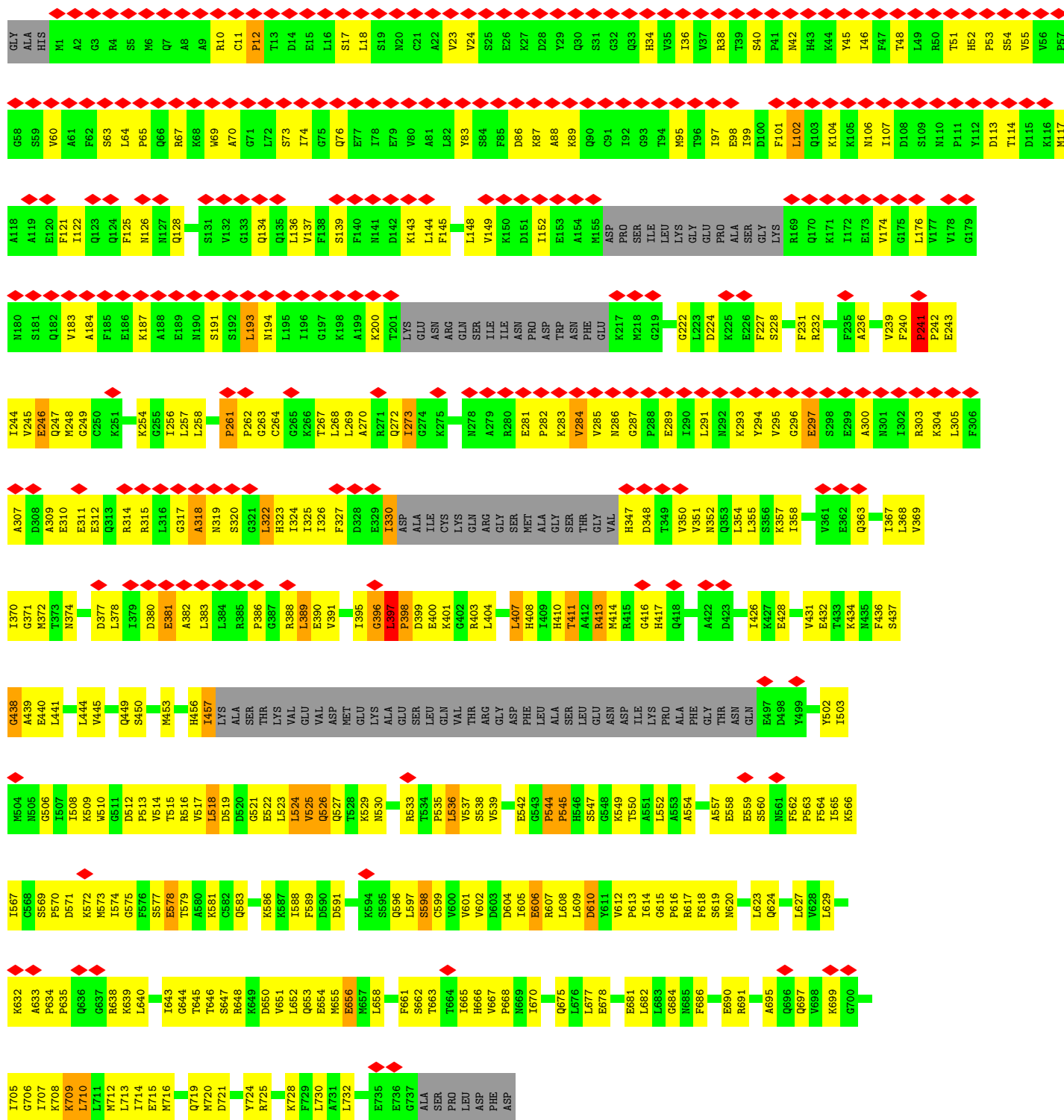
Chain D: 30% 43% 42% 5% 10%



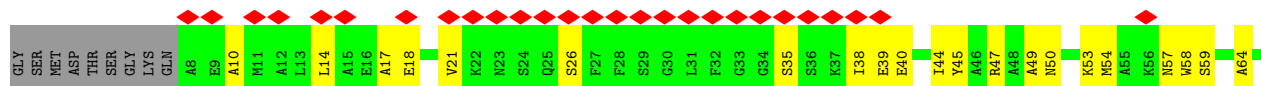


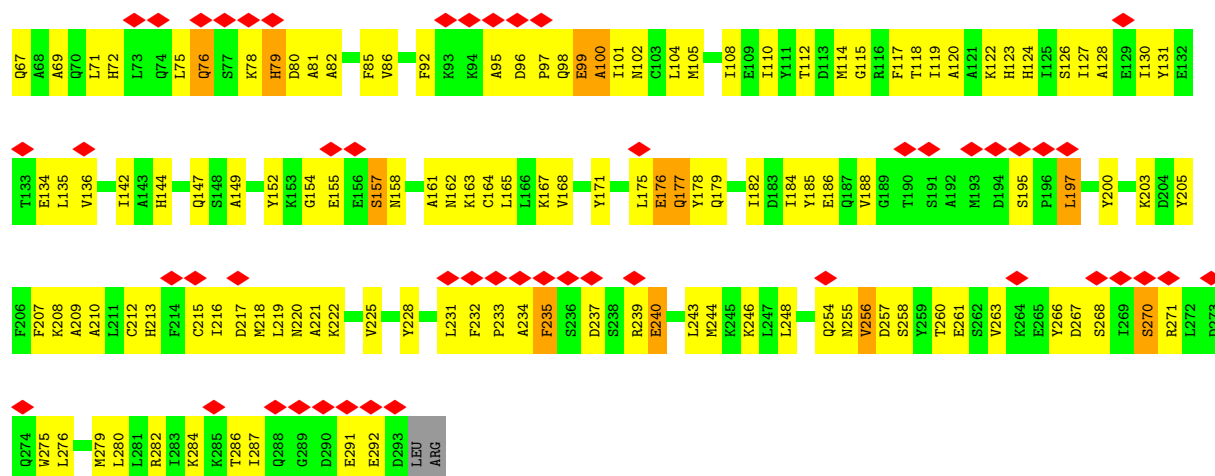
• Molecule 1: Vesicle-fusing ATPase



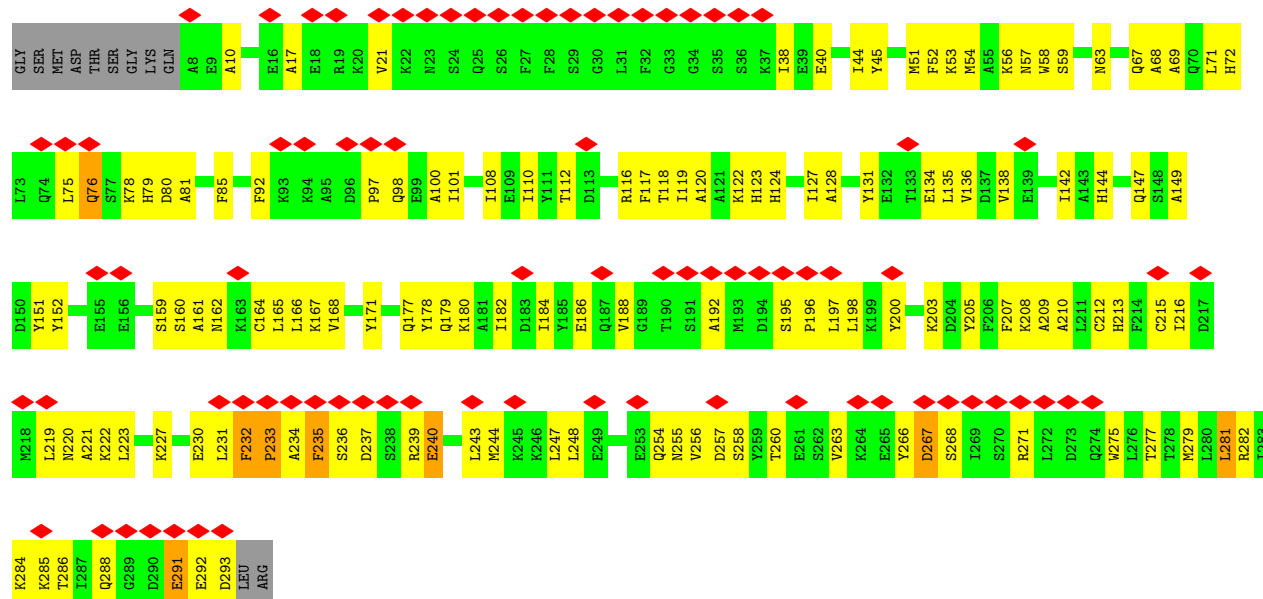


• Molecule 2: Alpha-soluble NSF attachment protein

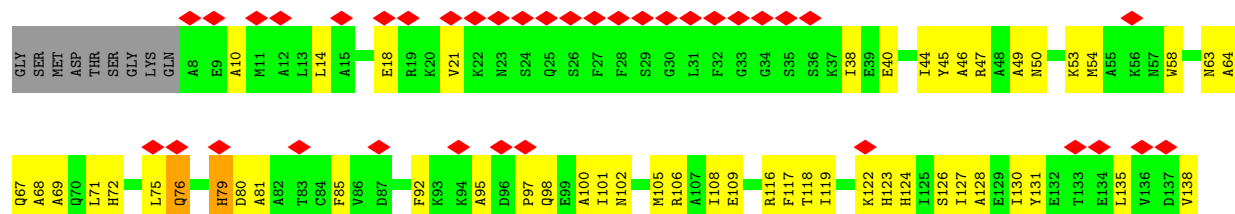


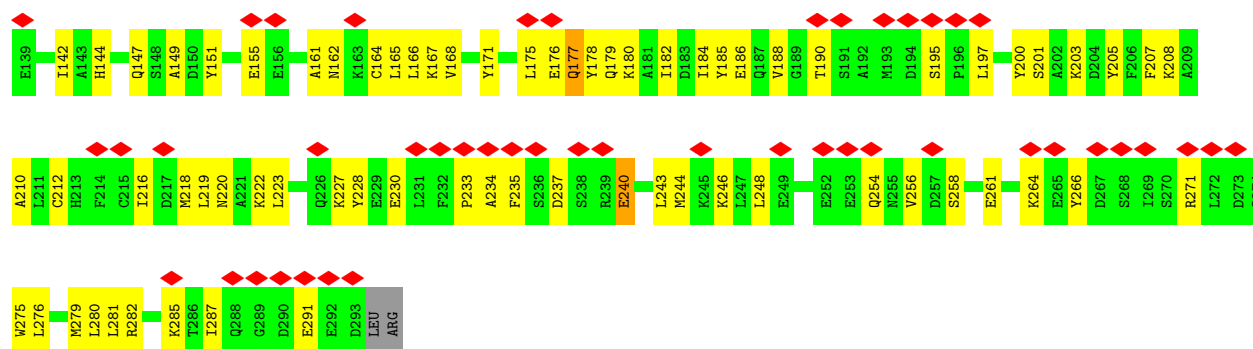


• Molecule 2: Alpha-soluble NSF attachment protein

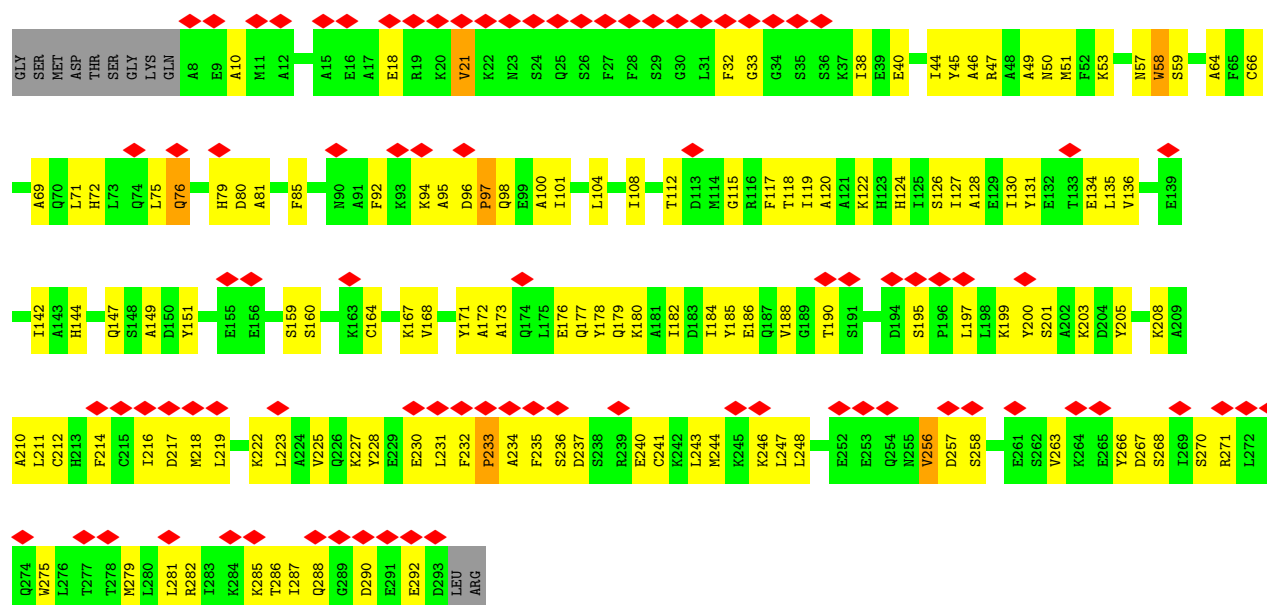


• Molecule 2: Alpha-soluble NSF attachment protein

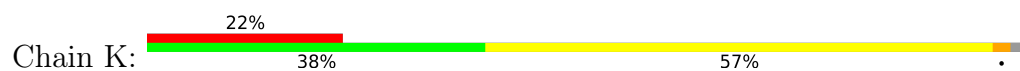




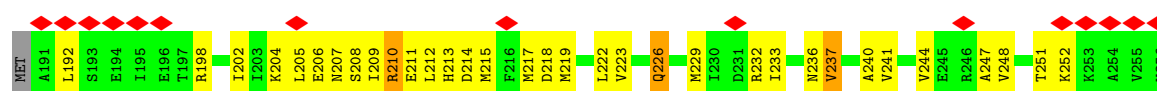
• Molecule 2: Alpha-soluble NSF attachment protein



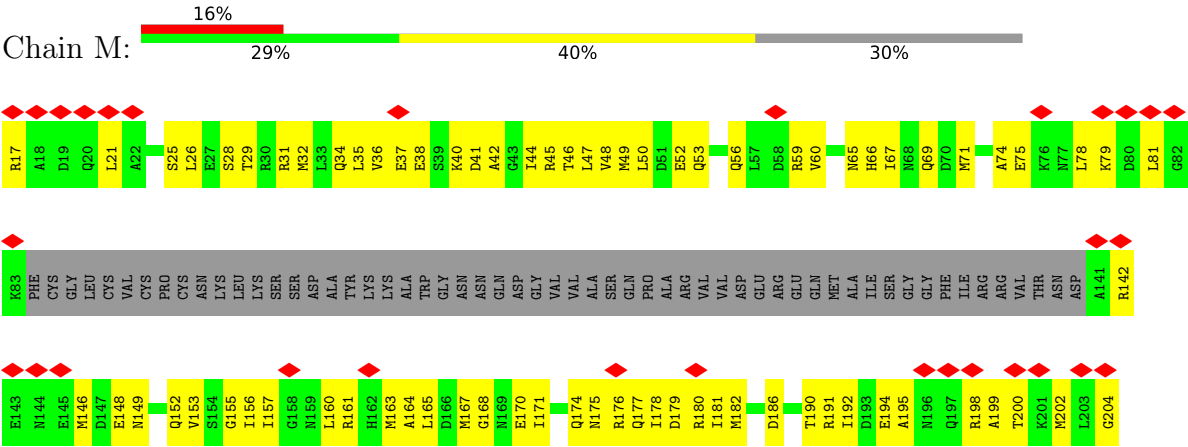
• Molecule 3: Vesicle-associated membrane protein 2



• 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	29717	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	12.118	Depositor
Minimum map value	-4.498	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	2/5124 (0.0%)	1.31	52/6935 (0.7%)
1	B	0.55	0/5113	1.20	36/6915 (0.5%)
1	C	0.52	0/5115	1.17	31/6922 (0.4%)
1	D	0.58	1/5069 (0.0%)	1.22	46/6864 (0.7%)
1	E	0.60	0/5088	1.27	58/6881 (0.8%)
1	F	0.60	3/5001 (0.1%)	1.21	34/6760 (0.5%)
2	G	0.47	0/2295	0.96	4/3086 (0.1%)
2	H	0.46	0/2295	0.98	7/3086 (0.2%)
2	I	0.46	0/2291	0.92	0/3082
2	J	0.46	0/2295	0.93	0/3086
3	K	0.27	0/496	0.78	0/664
4	L	0.28	0/541	0.84	1/723 (0.1%)
5	M	0.27	0/1038	0.79	0/1381
All	All	0.55	6/41761 (0.0%)	1.16	269/56385 (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	1
1	F	0	1
All	All	0	4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	503	ILE	C-O	6.23	1.31	1.24
1	F	544	PRO	C-N	5.42	1.41	1.33
1	F	518	LEU	CG-CD1	-5.32	1.35	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	545	PRO	CA-C	-5.31	1.44	1.52
1	F	545	PRO	N-CD	5.28	1.55	1.47
1	A	485	GLU	C-O	-5.04	1.17	1.24

All (269) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	236	ALA	N-CA-C	-13.98	96.11	111.07
1	D	504	MET	CA-C-N	-13.29	101.87	122.60
1	D	504	MET	C-N-CA	-13.29	101.87	122.60
1	E	231	PHE	N-CA-C	-13.23	96.91	111.07
1	A	261	PRO	CA-C-N	12.62	135.61	119.84
1	A	261	PRO	C-N-CA	12.62	135.61	119.84
1	F	294	TYR	N-CA-C	11.81	124.23	111.36
1	B	549	LYS	N-CA-C	-11.57	98.19	111.03
1	D	416	GLY	N-CA-C	-11.35	98.76	112.49
1	F	396	GLY	N-CA-C	10.73	124.94	112.50
1	B	708	LYS	CD-CE-NZ	10.44	145.29	111.90
1	A	231	PHE	N-CA-C	-10.24	100.12	111.28
1	A	273	ILE	N-CA-C	-10.19	100.95	110.53
1	A	238	ARG	N-CA-C	9.81	121.74	111.14
1	B	231	PHE	N-CA-C	-9.53	100.87	111.07
1	B	543	GLY	CA-C-N	9.49	126.59	119.66
1	B	543	GLY	C-N-CA	9.49	126.59	119.66
1	F	241	PRO	N-CA-C	9.41	122.19	110.70
1	B	287	GLY	CA-C-N	9.29	129.36	119.05
1	B	287	GLY	C-N-CA	9.29	129.36	119.05
1	A	241	PRO	N-CA-C	9.00	121.68	110.70
1	F	231	PHE	N-CA-C	-8.82	101.63	111.07
1	B	294	TYR	N-CA-C	8.78	120.93	111.36
1	C	231	PHE	N-CA-C	-8.64	101.86	111.28
1	C	413	ARG	N-CA-C	-8.58	101.93	111.28
1	E	241	PRO	N-CA-C	8.48	121.05	110.70
1	C	241	PRO	N-CA-C	8.41	120.96	110.70
1	B	530	ASN	N-CA-C	8.40	120.44	111.28
2	H	235	PHE	N-CA-C	-8.33	103.98	114.56
1	A	484	LEU	N-CA-C	-8.27	102.27	111.28
1	E	294	TYR	N-CA-C	8.21	120.30	111.36
1	A	277	LEU	N-CA-C	8.13	120.22	111.36
1	E	570	PRO	N-CA-C	-8.11	102.25	113.53
1	E	549	LYS	CB-CG-CD	8.09	129.90	111.30
1	E	603	ASP	N-CA-C	8.05	122.59	109.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	620	ASN	N-CA-C	7.98	119.98	111.28
1	A	480	PHE	CB-CA-C	-7.92	107.44	116.54
1	E	314	ARG	N-CA-C	-7.78	102.80	111.28
1	C	691	ARG	N-CA-C	-7.76	102.82	111.28
1	E	287	GLY	CA-C-N	7.76	127.66	119.05
1	E	287	GLY	C-N-CA	7.76	127.66	119.05
1	B	413	ARG	N-CA-C	-7.75	102.83	111.28
1	F	413	ARG	N-CA-C	-7.75	102.83	111.28
1	B	241	PRO	N-CA-C	7.59	119.97	110.70
1	C	543	GLY	CA-C-N	7.56	125.18	119.66
1	C	543	GLY	C-N-CA	7.56	125.18	119.66
1	B	544	PRO	N-CA-C	-7.52	103.25	110.47
1	A	625	ALA	N-CA-C	-7.50	103.11	111.28
1	E	413	ARG	N-CA-C	-7.43	103.19	111.28
1	A	260	GLY	CA-C-N	7.39	127.99	120.38
1	A	260	GLY	C-N-CA	7.39	127.99	120.38
1	C	632	LYS	N-CA-C	7.37	120.38	110.35
1	E	549	LYS	CG-CD-CE	-7.34	94.41	111.30
1	C	726	VAL	N-CA-C	7.32	118.09	110.62
1	B	544	PRO	CB-CA-C	7.22	118.18	111.39
1	D	512	ASP	N-CA-C	-7.21	102.93	113.16
1	D	643	ILE	CB-CA-C	-7.20	99.97	110.63
1	D	537	VAL	N-CA-C	7.20	118.19	108.11
2	H	292	GLU	CA-C-N	-7.16	108.81	121.70
2	H	292	GLU	C-N-CA	-7.16	108.81	121.70
1	D	609	LEU	CA-C-N	7.12	132.47	122.36
1	D	609	LEU	C-N-CA	7.12	132.47	122.36
1	E	548	GLY	CA-C-N	6.99	129.65	120.28
1	E	548	GLY	C-N-CA	6.99	129.65	120.28
1	A	598	SER	N-CA-C	6.88	120.39	108.76
1	E	718	LEU	N-CA-C	6.88	118.78	111.28
1	A	224	ASP	N-CA-C	6.85	118.75	111.28
1	F	563	PRO	N-CA-C	-6.82	104.26	113.40
1	A	530	ASN	N-CA-C	6.78	121.71	113.17
1	A	349	THR	N-CA-C	6.78	118.67	111.28
1	C	688	ASP	N-CA-C	6.75	118.30	111.07
1	B	651	VAL	CB-CA-C	-6.67	103.14	112.14
1	D	238	ARG	N-CA-C	6.66	118.62	111.36
1	A	363	GLN	CB-CA-C	-6.64	108.92	116.63
1	A	694	ILE	N-CA-C	-6.61	104.04	110.72
1	C	689	LYS	N-CA-C	6.61	118.14	111.07
1	D	725	ARG	N-CA-C	-6.60	105.36	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	416	GLY	N-CA-C	-6.58	104.53	112.49
1	A	304	LYS	N-CA-C	6.58	118.11	111.07
1	A	258	LEU	CA-C-N	-6.56	113.74	122.99
1	A	258	LEU	C-N-CA	-6.56	113.74	122.99
1	C	277	LEU	N-CA-C	6.55	118.42	111.28
1	F	544	PRO	CA-C-N	-6.55	113.03	119.78
1	F	544	PRO	C-N-CA	-6.55	113.03	119.78
1	F	518	LEU	CD1-CG-CD2	-6.55	96.39	110.80
1	A	320	SER	N-CA-C	6.54	119.74	111.69
1	C	598	SER	N-CA-C	6.54	118.15	108.60
1	E	625	ALA	N-CA-C	-6.48	104.22	111.28
1	C	363	GLN	CB-CA-C	-6.40	109.20	116.63
2	G	261	GLU	N-CA-C	-6.40	105.12	113.12
1	E	381	GLU	N-CA-C	6.40	118.33	111.36
1	A	241	PRO	C-N-CD	6.37	134.62	120.60
1	B	381	GLU	N-CA-C	6.36	118.29	111.36
1	E	435	ASN	N-CA-C	6.34	118.28	111.36
1	F	514	VAL	N-CA-C	-6.33	104.34	110.42
1	D	598	SER	N-CA-C	6.32	118.91	108.99
1	C	239	VAL	N-CA-C	6.31	117.09	110.72
1	D	508	ILE	N-CA-C	-6.30	99.04	108.12
1	E	649	LYS	N-CA-C	6.30	117.95	111.14
1	D	363	GLN	CB-CA-C	-6.30	109.32	116.63
1	E	633	ALA	CA-C-N	6.28	126.85	120.38
1	E	633	ALA	C-N-CA	6.28	126.85	120.38
1	D	544	PRO	CA-C-N	6.28	127.69	119.84
1	D	544	PRO	C-N-CA	6.28	127.69	119.84
1	C	387	GLY	N-CA-C	-6.27	98.31	113.18
1	E	277	LEU	N-CA-C	6.25	118.09	111.28
1	A	319	ASN	N-CA-C	-6.23	97.05	107.32
1	E	624	GLN	N-CA-C	6.20	118.04	111.28
1	B	539	VAL	N-CA-C	6.20	117.04	108.12
1	E	549	LYS	CA-CB-CG	-6.19	101.71	114.10
1	D	647	SER	N-CA-C	6.19	118.03	111.28
1	A	227	PHE	N-CA-C	-6.15	104.58	111.28
1	A	391	VAL	N-CA-C	6.14	116.70	108.11
1	E	506	GLY	N-CA-C	-6.14	104.18	111.36
1	F	363	GLN	CB-CA-C	-6.12	109.53	116.63
1	C	416	GLY	N-CA-C	-6.12	105.09	112.49
1	E	438	GLY	N-CA-C	6.09	127.62	113.18
1	C	694	ILE	N-CA-C	-6.08	104.42	110.62
1	D	276	MET	N-CA-C	6.08	118.87	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	548	GLY	N-CA-C	-6.04	106.38	115.32
1	D	241	PRO	N-CA-C	6.04	118.07	110.70
1	D	599	CYS	N-CA-C	6.04	118.26	108.41
1	B	348	ASP	CB-CA-C	-6.01	109.66	116.63
1	A	577	SER	N-CA-C	-6.00	102.62	110.53
1	C	312	GLU	N-CA-C	-5.99	104.66	111.07
1	E	550	THR	N-CA-C	5.97	117.86	111.36
2	H	232	PHE	CA-C-N	5.97	127.30	119.84
2	H	232	PHE	C-N-CA	5.97	127.30	119.84
1	E	295	VAL	N-CA-C	5.96	117.41	110.62
1	F	598	SER	N-CA-C	5.96	117.90	108.79
1	F	708	LYS	N-CA-C	5.95	117.76	111.28
1	B	299	GLU	N-CA-C	-5.94	104.80	111.28
1	A	218	MET	N-CA-C	5.94	117.75	111.28
1	B	363	GLN	CB-CA-C	-5.91	109.78	116.63
1	F	656	GLU	CA-CB-CG	5.89	125.87	114.10
1	E	512	ASP	N-CA-C	-5.88	104.81	113.16
1	D	414	MET	CA-C-N	5.86	128.61	120.29
1	D	414	MET	C-N-CA	5.86	128.61	120.29
1	D	403	ARG	N-CA-C	-5.85	104.90	111.28
1	F	518	LEU	CB-CG-CD1	-5.84	93.17	110.70
1	F	640	LEU	N-CA-C	5.84	118.29	109.23
2	H	291	GLU	N-CA-C	5.84	123.25	110.80
1	B	416	GLY	N-CA-C	-5.84	105.42	112.49
1	B	543	GLY	N-CA-C	-5.84	100.43	112.34
1	E	363	GLN	CB-CA-C	-5.84	109.86	116.63
1	E	235	PHE	N-CA-C	5.80	118.83	111.69
1	B	495	ASN	N-CA-C	5.80	117.68	111.36
1	F	525	VAL	CB-CA-C	-5.79	104.56	111.97
1	D	642	ILE	N-CA-C	5.78	116.20	108.11
1	D	569	SER	CA-C-N	5.78	125.63	119.28
1	D	569	SER	C-N-CA	5.78	125.63	119.28
1	F	348	ASP	CB-CA-C	-5.77	109.94	116.63
1	B	638	ARG	N-CA-C	5.75	118.85	109.24
1	E	640	LEU	N-CA-C	5.75	118.03	108.99
1	F	416	GLY	N-CA-C	-5.75	105.53	112.49
1	C	727	ARG	N-CA-C	-5.75	105.02	111.28
1	F	397	LEU	CA-CB-CG	5.72	136.32	116.30
1	A	407	LEU	N-CA-C	-5.72	105.05	111.28
1	A	403	ARG	N-CA-C	-5.71	105.06	111.28
1	A	455	ARG	N-CA-C	5.68	117.47	111.28
1	F	287	GLY	CA-C-N	5.68	125.36	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	287	GLY	C-N-CA	5.68	125.36	119.05
1	C	436	PHE	N-CA-C	5.66	118.44	110.23
1	F	709	LYS	N-CA-C	-5.66	105.11	111.28
1	F	381	GLU	N-CA-C	5.64	117.51	111.36
1	B	247	GLN	CA-C-N	5.63	127.82	120.28
1	B	247	GLN	C-N-CA	5.63	127.82	120.28
1	A	488	ILE	N-CA-C	5.62	119.27	112.80
1	E	273	ILE	N-CA-C	-5.61	104.90	110.62
1	D	312	GLU	CA-C-N	5.61	128.06	120.38
1	D	312	GLU	C-N-CA	5.61	128.06	120.38
1	A	597	LEU	CB-CG-CD2	-5.60	93.91	110.70
1	C	394	GLU	CA-C-N	-5.59	115.74	122.90
1	C	394	GLU	C-N-CA	-5.59	115.74	122.90
1	E	670	ILE	CB-CA-C	-5.59	102.48	111.59
1	E	391	VAL	N-CA-C	5.58	115.98	108.17
1	F	227	PHE	N-CA-C	-5.58	105.19	111.28
1	A	562	PHE	N-CA-C	-5.58	102.17	110.20
1	B	518	LEU	N-CA-C	5.57	117.35	111.28
1	F	710	LEU	N-CA-C	-5.56	105.12	111.07
1	D	277	LEU	N-CA-C	5.55	117.33	111.28
1	C	348	ASP	CB-CA-C	-5.55	110.19	116.63
1	A	480	PHE	N-CA-C	5.54	116.74	108.31
1	A	426	ILE	N-CA-C	5.53	115.73	110.42
1	D	542	GLU	N-CA-C	5.52	117.90	108.90
1	B	544	PRO	O-C-N	5.52	123.85	121.31
1	E	226	GLU	N-CA-C	-5.51	105.18	111.07
1	A	273	ILE	N-CA-CB	5.50	117.61	110.57
1	E	596	GLN	N-CA-C	5.50	117.36	111.36
1	E	403	ARG	N-CA-C	-5.50	105.29	111.28
1	F	391	VAL	N-CA-C	5.50	115.86	108.17
1	A	440	GLU	N-CA-C	-5.49	105.19	111.07
1	A	398	PRO	CA-N-CD	-5.49	104.32	112.00
1	B	406	ILE	CB-CA-C	-5.47	104.86	112.02
1	B	235	PHE	N-CA-C	5.46	118.41	111.69
1	D	312	GLU	N-CA-C	5.46	117.67	111.11
1	E	230	ILE	CA-C-N	5.46	127.54	120.44
1	E	230	ILE	C-N-CA	5.46	127.54	120.44
1	E	629	LEU	N-CA-C	5.46	117.23	111.28
1	E	643	ILE	CA-C-N	-5.45	118.35	122.33
1	E	643	ILE	C-N-CA	-5.45	118.35	122.33
1	E	318	ALA	N-CA-C	-5.45	99.20	110.80
1	B	498	ASP	N-CA-C	-5.44	105.35	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	489	LYS	N-CA-C	5.44	121.84	109.81
1	A	489	LYS	CA-C-N	-5.43	114.33	119.76
1	A	489	LYS	C-N-CA	-5.43	114.33	119.76
1	D	320	SER	CA-C-N	-5.43	117.04	122.20
1	D	320	SER	C-N-CA	-5.43	117.04	122.20
1	E	480	PHE	CB-CA-C	-5.43	110.33	116.63
2	H	257	ASP	N-CA-C	-5.43	107.20	113.88
1	B	418	GLN	N-CA-C	5.43	117.20	111.28
1	D	592	ALA	N-CA-C	5.40	117.87	111.33
1	D	508	ILE	CA-C-N	-5.39	115.83	122.84
1	D	508	ILE	C-N-CA	-5.39	115.83	122.84
1	F	295	VAL	N-CA-C	5.39	116.12	110.62
1	D	663	THR	N-CA-C	5.38	117.36	109.24
1	E	549	LYS	N-CA-C	-5.36	105.43	111.28
1	A	217	LYS	N-CA-C	5.35	117.19	111.36
1	B	595	SER	N-CA-C	5.34	118.02	110.50
1	C	406	ILE	CB-CA-C	-5.33	105.03	112.02
1	D	227	PHE	N-CA-C	-5.33	105.47	111.28
1	D	381	GLU	N-CA-C	5.32	117.16	111.36
1	E	585	MET	N-CA-C	-5.32	105.48	111.28
2	G	270	SER	N-CA-C	5.31	116.09	107.23
1	E	727	ARG	N-CA-C	-5.29	105.18	111.69
1	D	233	ARG	N-CA-C	5.28	118.19	111.69
1	D	294	TYR	N-CA-C	5.27	118.97	112.54
1	C	234	ALA	N-CA-C	5.27	116.83	111.14
1	B	480	PHE	CB-CA-C	-5.26	110.49	116.54
1	A	532	ASP	N-CA-C	5.25	117.08	111.36
1	F	526	GLN	N-CA-C	-5.25	105.46	111.07
1	C	707	ILE	N-CA-C	5.24	115.45	110.42
1	A	246	GLU	N-CA-CB	5.24	117.82	110.12
1	E	714	ILE	CB-CA-C	-5.24	105.27	111.97
1	D	434	LYS	N-CA-C	-5.23	107.27	113.97
1	F	261	PRO	N-CA-C	-5.23	104.98	110.58
1	E	522	GLU	CA-CB-CG	5.22	124.55	114.10
1	A	493	GLY	CA-C-N	5.21	131.08	121.70
1	A	493	GLY	C-N-CA	5.21	131.08	121.70
1	D	415	ARG	CA-C-N	5.21	125.62	119.94
1	D	415	ARG	C-N-CA	5.21	125.62	119.94
1	F	403	ARG	N-CA-C	-5.19	105.62	111.28
1	A	307	ALA	N-CA-C	-5.19	105.53	111.14
1	A	255	GLY	N-CA-C	5.18	118.83	110.90
1	A	377	ASP	N-CA-C	5.18	117.00	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	519	ASP	N-CA-CB	5.17	117.72	110.12
1	D	286	ASN	N-CA-C	5.17	116.95	108.52
1	B	289	GLU	N-CA-C	-5.17	105.54	111.07
1	C	480	PHE	CB-CA-C	-5.17	110.64	116.63
1	E	639	LYS	N-CA-C	5.16	117.53	109.52
1	C	556	ILE	N-CA-C	-5.15	105.48	110.42
1	E	315	ARG	N-CA-C	5.14	116.88	111.28
1	C	322	LEU	CA-CB-CG	5.12	134.21	116.30
1	D	379	ILE	N-CA-C	5.12	115.99	110.21
1	F	407	LEU	N-CA-C	-5.08	105.74	111.28
4	L	208	SER	N-CA-C	-5.08	106.19	112.38
1	B	227	PHE	N-CA-C	-5.07	105.76	111.28
1	B	391	VAL	N-CA-C	5.06	115.26	108.17
1	E	607	ARG	CB-CG-CD	-5.06	99.67	111.30
1	F	610	ASP	N-CA-CB	-5.06	104.49	112.13
1	E	247	GLN	CA-C-N	5.04	127.04	120.28
1	E	247	GLN	C-N-CA	5.04	127.04	120.28
1	A	422	ALA	N-CA-C	5.04	116.77	111.28
1	E	405	GLN	N-CA-C	5.04	116.46	111.07
1	D	648	ARG	N-CA-C	5.03	116.61	108.41
2	G	197	LEU	N-CA-C	-5.03	106.39	112.88
1	C	414	MET	N-CA-C	5.03	117.49	111.71
2	G	215	CYS	N-CA-C	-5.02	106.45	112.58
1	F	273	ILE	N-CA-C	-5.02	105.50	110.62

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	PRO	Peptide
1	B	438	GLY	Peptide
1	E	438	GLY	Peptide
1	F	438	GLY	Peptide

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	5048	0	4974	355	0
1	B	5037	0	4996	329	0
1	C	5039	0	4965	323	0
1	D	4994	0	4923	345	0
1	E	5012	0	4954	353	0
1	F	4926	0	4896	321	0
2	G	2255	0	2199	154	0
2	H	2255	0	2199	122	0
2	I	2251	0	2188	122	0
2	J	2255	0	2199	130	0
3	K	493	0	491	63	0
4	L	536	0	527	59	0
5	M	1038	0	1011	120	0
All	All	41139	0	40522	2490	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 30.

All (2490) 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:263:GLY:HA3	1:F:437:SER:HB2	1.29	1.14
1:A:549:LYS:NZ	1:A:647:SER:OG	1.93	1.01
2:H:271:ARG:HH11	2:I:234:ALA:HB2	1.28	0.98
2:I:200:TYR:HB3	5:M:161:ARG:HD2	1.43	0.97
2:H:219:LEU:HB2	2:H:222:LYS:HB3	1.46	0.97
2:J:219:LEU:HB2	2:J:222:LYS:HB3	1.48	0.96
1:E:528:THR:HG22	1:E:537:VAL:HG21	1.49	0.94
1:C:327:PHE:HB3	1:C:330:ILE:HD11	1.44	0.94
1:D:509:LYS:HG2	1:D:515:THR:HG23	1.49	0.94
1:E:720:MET:HG3	1:E:728:LYS:HE3	1.49	0.94
1:D:406:ILE:HG22	1:D:441:LEU:HD22	1.50	0.93
1:A:490:PRO:HA	1:A:491:ALA:HB3	1.49	0.93
3:K:39:VAL:HG22	5:M:157:ILE:HG12	1.50	0.92
2:J:228:TYR:OH	2:J:237:ASP:OD1	1.88	0.92
1:C:386:PRO:HA	1:C:390:GLU:HA	1.52	0.91
1:C:407:LEU:HD11	1:C:426:ILE:HG23	1.50	0.91
1:B:649:LYS:HE3	1:B:658:LEU:HD11	1.53	0.91
1:C:724:TYR:HD2	1:C:727:ARG:HH21	1.19	0.91
5:M:40:LYS:HG3	5:M:163:MET:HE1	1.53	0.90
1:B:256:ILE:HG13	1:B:370:ILE:HG22	1.53	0.90
1:A:331:ASP:HA	1:A:379:ILE:HD11	1.53	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:618:PHE:HE2	1:D:614:ILE:HD11	1.38	0.89
1:E:627:LEU:HG	1:E:657:MET:HE1	1.52	0.89
1:E:585:MET:HG3	1:E:589:PHE:CZ	2.08	0.89
1:C:497:GLU:O	1:C:499:TYR:N	2.06	0.89
1:E:596:GLN:HA	1:E:638:ARG:HG2	1.52	0.89
1:F:386:PRO:HA	1:F:390:GLU:HA	1.54	0.89
1:A:569:SER:OG	1:A:571:ASP:OD1	1.89	0.89
1:B:490:PRO:HA	1:B:491:ALA:HB3	1.55	0.89
1:E:240:PHE:HZ	1:F:456:HIS:HB2	1.35	0.88
1:F:256:ILE:HG13	1:F:370:ILE:HG22	1.53	0.88
1:B:240:PHE:HD2	1:B:244:ILE:HG21	1.34	0.88
1:E:95:MET:HE3	1:E:97:ILE:HD11	1.55	0.88
1:A:264:CYS:SG	1:A:265:GLY:N	2.46	0.88
1:A:685:ASN:OD1	1:F:533:ARG:NH1	2.07	0.87
2:G:219:LEU:HB2	2:G:222:LYS:HB3	1.56	0.87
1:A:449:GLN:NE2	1:F:248:MET:O	2.08	0.87
1:E:256:ILE:HG13	1:E:370:ILE:HG22	1.56	0.87
3:K:52:LYS:HB3	5:M:171:ILE:HG21	1.53	0.87
1:A:295:VAL:HB	1:B:294:TYR:HB2	1.55	0.87
1:C:313:GLN:O	1:C:317:GLY:N	2.07	0.87
2:G:231:LEU:HB3	2:J:271:ARG:HG3	1.56	0.87
2:H:213:HIS:HE1	2:H:221:ALA:HB2	1.38	0.86
1:A:503:ILE:HG23	1:A:506:GLY:HA2	1.57	0.86
5:M:29:THR:HA	5:M:32:MET:HE3	1.56	0.86
2:G:271:ARG:HH22	2:H:234:ALA:HB2	1.40	0.86
1:E:686:PHE:HE1	1:E:714:ILE:HG23	1.41	0.86
2:G:38:ILE:HD11	2:G:71:LEU:HB3	1.57	0.86
1:A:353:GLN:HA	1:B:288:PRO:HG3	1.58	0.85
1:F:263:GLY:HA3	1:F:437:SER:CB	2.07	0.85
1:F:521:GLY:HA2	1:F:524:LEU:HD12	1.55	0.85
5:M:26:LEU:HB2	5:M:146:MET:HE2	1.58	0.85
1:B:407:LEU:HD11	1:B:426:ILE:HG23	1.58	0.85
1:B:526:GLN:HE21	1:C:719:GLN:HB3	1.40	0.84
1:C:240:PHE:HD2	1:C:244:ILE:HG21	1.42	0.84
1:F:240:PHE:HD2	1:F:244:ILE:HG21	1.43	0.84
1:B:541:LEU:HD11	1:B:549:LYS:HA	1.57	0.84
1:D:256:ILE:HG13	1:D:370:ILE:HG22	1.59	0.84
2:H:119:ILE:HD12	2:H:122:LYS:HB2	1.59	0.84
1:B:566:LYS:HD2	1:B:588:ILE:HG23	1.59	0.83
5:M:49:MET:HB3	5:M:53:GLN:HE21	1.43	0.83
1:D:606:GLU:HA	1:D:609:LEU:HG	1.59	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:10:ARG:HG3	1:F:67:ARG:HH22	1.44	0.83
1:C:627:LEU:HD12	1:D:607:ARG:HH12	1.41	0.83
1:E:624:GLN:NE2	1:F:610:ASP:OD1	2.11	0.83
1:A:686:PHE:HE2	1:A:714:ILE:HG12	1.44	0.82
2:G:268:SER:HA	2:H:233:PRO:HG3	1.61	0.82
1:F:545:PRO:HA	1:F:547:SER:H	1.44	0.82
1:E:589:PHE:CZ	1:E:629:LEU:HD11	2.15	0.82
1:E:603:ASP:OD2	1:E:645:THR:OG1	1.97	0.82
1:E:240:PHE:HD2	1:E:244:ILE:HG21	1.45	0.82
1:E:386:PRO:HA	1:E:390:GLU:HA	1.61	0.82
5:M:50:LEU:HB3	5:M:170:GLU:HG2	1.63	0.81
1:B:386:PRO:HA	1:B:390:GLU:HA	1.60	0.81
2:I:235:PHE:CE1	3:K:34:GLN:HA	2.15	0.81
1:E:527:GLN:O	1:E:531:SER:OG	1.99	0.81
1:E:593:TYR:O	1:E:638:ARG:NH1	2.13	0.81
1:A:497:GLU:O	1:A:499:TYR:N	2.14	0.81
1:A:502:TYR:HE2	1:A:567:ILE:HG21	1.46	0.81
1:F:536:LEU:HD11	1:F:634:PRO:HD3	1.61	0.81
1:F:570:PRO:HG2	1:F:604:ASP:HB2	1.61	0.81
1:F:327:PHE:HB2	1:F:330:ILE:HG22	1.60	0.81
1:A:542:GLU:HG2	1:A:649:LYS:HD2	1.63	0.80
1:A:705:ILE:HD13	1:A:710:LEU:HD12	1.62	0.80
1:C:490:PRO:HA	1:C:491:ALA:HB3	1.60	0.80
1:D:386:PRO:HA	1:D:390:GLU:HA	1.64	0.80
1:D:720:MET:HE3	1:D:724:TYR:HE1	1.47	0.80
1:A:624:GLN:HG3	1:B:610:ASP:HB2	1.62	0.80
1:A:305:LEU:HD23	1:A:325:ILE:HG21	1.64	0.80
1:E:587:LYS:NZ	1:E:587:LYS:O	2.13	0.80
1:F:240:PHE:CD2	1:F:244:ILE:HG21	2.16	0.79
1:D:95:MET:HE3	1:D:97:ILE:HD11	1.64	0.79
1:D:510:TRP:HE3	1:D:675:GLN:HG2	1.45	0.79
2:G:235:PHE:CG	5:M:31:ARG:HG2	2.17	0.79
1:E:653:GLN:HA	1:E:658:LEU:HB2	1.63	0.79
2:H:38:ILE:HD11	2:H:71:LEU:HB3	1.63	0.79
1:E:528:THR:HG21	1:E:641:LEU:HD23	1.64	0.79
1:A:309:ALA:HB1	1:A:367:ILE:HG21	1.64	0.79
1:D:312:GLU:OE1	1:D:323:HIS:ND1	2.15	0.79
1:E:625:ALA:HA	1:F:574:ILE:HD11	1.64	0.79
1:B:656:GLU:OE1	1:C:648:ARG:NH2	2.16	0.79
3:K:43:VAL:HA	4:L:212:LEU:HD13	1.65	0.79
1:C:540:LEU:HB3	1:C:664:THR:HG22	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:618:PHE:CE2	1:D:614:ILE:HD11	2.18	0.79
1:E:490:PRO:HA	1:E:491:ALA:HB3	1.62	0.79
1:F:564:PHE:O	1:F:598:SER:OG	2.00	0.79
1:E:407:LEU:HD11	1:E:426:ILE:HG23	1.64	0.78
1:E:606:GLU:OE2	1:E:646:THR:OG1	1.99	0.78
1:F:569:SER:OG	1:F:571:ASP:OD2	2.01	0.78
1:B:581:LYS:NZ	1:B:608:LEU:O	2.16	0.78
1:D:518:LEU:HD21	1:D:552:LEU:HD22	1.64	0.78
1:E:73:SER:HA	2:G:218:MET:SD	2.24	0.77
2:G:216:ILE:HD13	2:G:220:ASN:HB3	1.65	0.77
1:D:240:PHE:HD2	1:D:244:ILE:HG21	1.47	0.77
1:A:398:PRO:HG3	1:A:436:PHE:O	1.83	0.77
1:B:648:ARG:NH1	1:B:651:VAL:HG22	1.99	0.77
1:E:686:PHE:HB3	1:E:690:GLU:HB2	1.65	0.77
1:F:539:VAL:HB	1:F:643:ILE:HG12	1.65	0.77
2:G:158:ASN:O	2:G:162:ASN:ND2	2.17	0.77
2:I:203:LYS:HE2	5:M:161:ARG:HH12	1.48	0.77
1:D:399:ASP:O	1:D:403:ARG:N	2.17	0.76
1:B:300:ALA:O	1:B:304:LYS:HG2	1.85	0.76
1:C:236:ALA:HB1	1:D:453:MET:HB3	1.67	0.76
1:C:496:GLN:O	1:C:498:ASP:N	2.19	0.76
1:C:544:PRO:O	1:C:547:SER:OG	2.03	0.76
1:E:618:PHE:HZ	1:F:612:VAL:HG11	1.49	0.76
1:B:311:GLU:OE1	1:B:314:ARG:NE	2.15	0.76
1:E:196:ILE:HD13	1:E:196:ILE:H	1.51	0.76
1:E:300:ALA:O	1:E:304:LYS:HG2	1.86	0.76
1:E:652:LEU:HD23	1:E:657:MET:HB3	1.68	0.75
4:L:212:LEU:HA	4:L:215:MET:HE3	1.67	0.75
1:A:196:ILE:HG22	1:A:319:ASN:ND2	2.01	0.75
1:C:718:LEU:O	1:C:725:ARG:NH1	2.19	0.75
1:D:711:LEU:HA	1:D:714:ILE:HD12	1.68	0.75
1:A:557:ALA:O	1:A:560:SER:OG	2.03	0.75
1:C:256:ILE:HG13	1:C:370:ILE:HG22	1.67	0.75
1:F:300:ALA:O	1:F:304:LYS:HG2	1.87	0.75
1:A:549:LYS:HE3	1:A:646:THR:C	2.12	0.74
1:D:527:GLN:HE21	1:E:715:GLU:HG3	1.52	0.74
1:B:624:GLN:NE2	1:C:610:ASP:O	2.20	0.74
1:D:240:PHE:HB3	1:D:244:ILE:HD13	1.68	0.74
1:D:510:TRP:CD2	1:D:670:ILE:HG22	2.21	0.74
1:C:18:LEU:HD13	1:C:139:SER:HB2	1.68	0.74
1:F:437:SER:OG	1:F:440:GLU:HG2	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:672:THR:OG1	1:A:675:GLN:OE1	2.05	0.74
1:B:540:LEU:HD23	1:B:661:PHE:CD1	2.23	0.74
1:C:687:LYS:N	1:C:690:GLU:OE2	2.20	0.74
1:D:543:GLY:H	1:D:549:LYS:HD3	1.52	0.74
1:E:246:GLU:O	1:F:413:ARG:NH1	2.19	0.74
1:E:624:GLN:HG3	1:F:610:ASP:OD2	1.86	0.74
2:G:268:SER:HA	2:H:233:PRO:CG	2.18	0.74
1:A:564:PHE:CE1	1:A:566:LYS:HB2	2.22	0.74
1:D:573:MET:SD	1:D:581:LYS:HD3	2.28	0.74
1:F:613:PRO:HD3	1:F:648:ARG:HH12	1.52	0.74
1:A:262:PRO:HG2	1:A:374:ASN:OD1	1.87	0.73
2:G:128:ALA:HB2	2:G:144:HIS:HB2	1.69	0.73
1:B:627:LEU:HD21	1:B:657:MET:HG3	1.70	0.73
1:B:713:LEU:HD22	1:B:732:LEU:HB3	1.70	0.73
1:D:301:ASN:HA	1:D:304:LYS:HD3	1.69	0.73
1:E:585:MET:HA	1:E:588:ILE:HD12	1.68	0.73
1:C:596:GLN:HA	1:C:638:ARG:HD3	1.69	0.73
1:D:358:ILE:HD12	1:D:388:ARG:HB3	1.71	0.73
1:D:545:PRO:HD3	1:D:647:SER:OG	1.88	0.73
1:B:67:ARG:HH11	2:I:218:MET:HG2	1.54	0.73
1:A:285:VAL:HG13	1:A:326:ILE:HD11	1.70	0.73
1:E:240:PHE:CZ	1:F:456:HIS:HB2	2.23	0.72
1:E:240:PHE:HZ	1:F:456:HIS:CB	2.01	0.72
1:E:624:GLN:HA	1:E:624:GLN:OE1	1.89	0.72
5:M:177:GLN:HA	5:M:180:ARG:NH1	2.04	0.72
1:C:691:ARG:HA	1:C:694:ILE:HD12	1.71	0.72
1:A:423:ASP:HB2	1:A:480:PHE:CB	2.19	0.72
1:B:12:PRO:HG2	1:B:23:VAL:HG11	1.72	0.72
1:F:194:ASN:ND2	1:F:312:GLU:HG2	2.05	0.72
1:F:565:ILE:HG23	1:F:599:CYS:HB3	1.71	0.72
1:A:713:LEU:HD21	1:A:732:LEU:HB3	1.69	0.72
1:E:549:LYS:HA	1:E:552:LEU:HD12	1.71	0.72
1:F:264:CYS:SG	1:F:395:ILE:HG22	2.29	0.72
1:F:311:GLU:OE1	1:F:314:ARG:NE	2.21	0.72
1:F:517:VAL:HG13	1:F:665:ILE:HG21	1.69	0.72
2:G:228:TYR:OH	2:G:237:ASP:OD1	2.07	0.72
1:E:706:GLY:O	1:E:710:LEU:N	2.19	0.72
1:B:240:PHE:CD2	1:B:244:ILE:HG21	2.23	0.72
1:E:586:LYS:NZ	1:F:574:ILE:O	2.21	0.72
1:A:326:ILE:HG22	1:A:370:ILE:HG12	1.71	0.71
2:G:200:TYR:HB3	4:L:217:MET:HE1	1.70	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:456:HIS:HB2	1:F:240:PHE:CZ	2.26	0.71
2:J:246:LYS:NZ	2:J:258:SER:OG	2.22	0.71
1:C:513:PRO:O	1:C:516:ARG:HG2	1.90	0.71
1:C:564:PHE:O	1:C:598:SER:OG	2.08	0.71
1:D:527:GLN:HE22	1:E:715:GLU:C	1.98	0.71
1:E:307:ALA:O	1:E:311:GLU:HG2	1.90	0.71
1:F:721:ASP:HB2	1:F:724:TYR:HD1	1.54	0.71
1:C:676:LEU:HD12	1:C:705:ILE:HG21	1.71	0.71
1:D:73:SER:OG	2:J:217:ASP:OD1	2.08	0.71
1:E:620:ASN:O	1:E:624:GLN:HG2	1.89	0.71
3:K:59:LYS:HB3	5:M:178:ILE:HG21	1.71	0.71
1:D:627:LEU:HD21	1:D:657:MET:HG3	1.71	0.71
1:F:10:ARG:HG3	1:F:67:ARG:NH2	2.04	0.71
1:C:331:ASP:HA	1:C:379:ILE:HD11	1.72	0.71
1:E:628:VAL:HB	1:F:574:ILE:HD12	1.72	0.71
1:F:525:VAL:HG13	1:F:562:PHE:CE1	2.25	0.71
1:D:568:CYS:SG	1:D:585:MET:HE1	2.30	0.71
1:C:576:PHE:HB2	1:C:581:LYS:HE3	1.72	0.71
2:G:207:PHE:HB2	2:G:240:GLU:HG2	1.71	0.71
3:K:50:VAL:O	3:K:54:LEU:HD23	1.90	0.71
1:D:513:PRO:HA	1:D:516:ARG:HG2	1.71	0.71
1:E:327:PHE:HB2	1:E:330:ILE:HG22	1.73	0.71
1:F:125:PHE:HA	1:F:128:GLN:NE2	2.05	0.70
2:G:200:TYR:CB	4:L:217:MET:HE1	2.21	0.70
1:A:95:MET:HE3	1:A:97:ILE:HD11	1.74	0.70
1:E:437:SER:O	1:E:440:GLU:HB2	1.91	0.70
1:D:125:PHE:HA	1:D:128:GLN:NE2	2.06	0.70
1:E:526:GLN:NE2	1:F:719:GLN:O	2.23	0.70
1:F:317:GLY:O	1:F:318:ALA:CB	2.39	0.70
1:F:549:LYS:HE2	1:F:645:THR:HB	1.72	0.70
1:B:533:ARG:HG3	1:B:534:THR:H	1.57	0.70
1:D:64:LEU:HB3	1:D:65:PRO:HD3	1.74	0.70
1:B:585:MET:HE1	1:B:626:LEU:HG	1.73	0.70
1:E:240:PHE:CD2	1:E:244:ILE:HG21	2.25	0.70
1:A:236:ALA:HB1	1:B:453:MET:HB3	1.74	0.70
1:C:695:ALA:HB1	1:C:699:LYS:HE3	1.74	0.70
1:F:263:GLY:CA	1:F:437:SER:HB2	2.18	0.70
1:F:606:GLU:OE1	1:F:606:GLU:N	2.22	0.70
2:G:235:PHE:CD1	5:M:31:ARG:HG2	2.27	0.69
1:D:240:PHE:CD2	1:D:244:ILE:HG21	2.26	0.69
1:A:113:ASP:OD2	1:A:316:LEU:HD21	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:201:SER:HB3	5:M:165:LEU:HD13	1.72	0.69
1:F:695:ALA:HB1	1:F:699:LYS:HE3	1.75	0.69
1:C:318:ALA:O	1:C:319:ASN:ND2	2.26	0.69
1:A:316:LEU:O	1:A:320:SER:OG	2.10	0.69
1:B:18:LEU:HD13	1:B:139:SER:HB3	1.74	0.69
1:B:526:GLN:NE2	1:C:719:GLN:HB3	2.07	0.69
1:C:125:PHE:HA	1:C:128:GLN:NE2	2.07	0.69
1:D:632:LYS:HZ1	1:E:571:ASP:HB3	1.57	0.69
2:G:72:HIS:HE1	2:G:80:ASP:HB2	1.58	0.69
1:A:351:VAL:O	1:A:355:LEU:HG	1.92	0.69
1:A:353:GLN:HA	1:B:288:PRO:CG	2.21	0.69
1:D:510:TRP:CE3	1:D:670:ILE:HG22	2.27	0.69
1:F:187:LYS:HB2	1:F:191:SER:HB3	1.72	0.69
1:A:657:MET:HE3	1:A:661:PHE:CE1	2.28	0.69
1:E:326:ILE:HG22	1:E:370:ILE:HG13	1.75	0.69
1:E:625:ALA:O	1:E:629:LEU:HG	1.92	0.69
1:F:303:ARG:HG3	1:F:357:LYS:HE2	1.74	0.69
2:G:108:ILE:HD11	2:G:127:ILE:HG13	1.73	0.69
1:A:677:LEU:HD21	1:A:695:ALA:HA	1.73	0.68
1:B:538:SER:HB3	1:B:661:PHE:CD2	2.27	0.68
1:A:50:ARG:NH1	2:H:293:ASP:O	2.26	0.68
1:A:247:GLN:O	1:B:414:MET:HE1	1.93	0.68
1:E:510:TRP:CZ3	1:E:670:ILE:HG13	2.28	0.68
1:E:563:PRO:HG2	1:E:595:SER:OG	1.94	0.68
1:F:397:LEU:HB3	1:F:398:PRO:CD	2.22	0.68
2:I:101:ILE:HG21	2:I:135:LEU:HD11	1.74	0.68
1:C:64:LEU:HA	1:C:67:ARG:HE	1.58	0.68
1:F:95:MET:HE3	1:F:97:ILE:HD11	1.75	0.68
1:D:528:THR:OG1	1:D:537:VAL:HG21	1.94	0.68
2:H:235:PHE:HD1	4:L:204:LYS:HG3	1.58	0.68
1:A:125:PHE:HA	1:A:128:GLN:NE2	2.08	0.68
1:C:624:GLN:NE2	1:D:610:ASP:HB2	2.09	0.68
1:A:610:ASP:OD1	1:F:620:ASN:ND2	2.26	0.68
1:D:686:PHE:HE1	1:D:714:ILE:HG23	1.59	0.68
1:B:303:ARG:HG3	1:B:357:LYS:HE2	1.74	0.68
1:E:586:LYS:HA	1:E:589:PHE:CD2	2.28	0.68
1:F:538:SER:HB3	1:F:662:SER:H	1.57	0.68
1:F:538:SER:HG	1:F:661:PHE:HD1	1.40	0.68
1:A:50:ARG:CZ	2:H:293:ASP:OD1	2.42	0.67
3:K:39:VAL:HG11	4:L:209:ILE:HG12	1.74	0.67
1:A:627:LEU:HD13	1:B:607:ARG:HH12	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:683:LEU:HB3	1:A:685:ASN:ND2	2.08	0.67
1:B:528:THR:O	1:B:639:LYS:HD2	1.93	0.67
1:D:326:ILE:HG22	1:D:370:ILE:HG13	1.75	0.67
1:D:620:ASN:O	1:D:624:GLN:HG2	1.93	0.67
1:A:242:PRO:HD2	1:A:243:GLU:CD	2.19	0.67
1:A:553:ALA:HA	1:A:556:ILE:HD12	1.77	0.67
2:G:54:MET:HE1	2:H:112:THR:HG22	1.75	0.67
1:A:602:VAL:HG12	1:A:605:ILE:HG12	1.76	0.67
1:C:386:PRO:HD2	1:D:440:GLU:OE1	1.94	0.67
1:E:106:ASN:HB3	1:E:143:LYS:NZ	2.09	0.67
2:G:243:LEU:HD13	2:G:266:TYR:HB2	1.75	0.67
2:H:72:HIS:HE1	2:H:80:ASP:HB2	1.59	0.67
2:J:149:ALA:HB2	2:J:164:CYS:HB2	1.77	0.67
1:A:607:ARG:HD3	1:F:624:GLN:HE22	1.60	0.67
1:B:245:VAL:O	1:B:249:GLY:N	2.27	0.67
1:C:611:TYR:CE1	1:C:616:PRO:HB2	2.29	0.67
1:D:12:PRO:HG2	1:D:23:VAL:HG11	1.74	0.67
3:K:50:VAL:O	3:K:53:VAL:HG12	1.94	0.67
1:C:630:LEU:HD11	1:C:661:PHE:CE1	2.30	0.67
1:C:690:GLU:HB2	1:C:726:VAL:HG21	1.76	0.67
1:E:508:ILE:HB	1:E:682:LEU:HD13	1.76	0.67
1:B:546:HIS:O	1:B:547:SER:OG	2.13	0.67
1:F:634:PRO:HB2	1:F:638:ARG:HG3	1.77	0.67
2:G:231:LEU:HB2	2:G:234:ALA:HB3	1.76	0.67
1:A:12:PRO:HG2	1:A:23:VAL:HG11	1.77	0.67
1:D:632:LYS:NZ	1:E:571:ASP:HB3	2.10	0.67
1:E:553:ALA:HA	1:E:556:ILE:HD12	1.76	0.67
1:F:258:LEU:HB3	1:F:395:ILE:HD11	1.75	0.67
1:E:64:LEU:N	1:E:67:ARG:HH21	1.93	0.67
1:A:313:GLN:NE2	1:A:365:ASN:O	2.28	0.67
1:C:358:ILE:CB	1:C:388:ARG:HG3	2.25	0.67
1:E:686:PHE:CE1	1:E:714:ILE:HG23	2.28	0.67
2:I:124:HIS:HE1	2:I:147:GLN:HB3	1.60	0.67
1:A:626:LEU:HD21	1:A:657:MET:HE1	1.76	0.66
1:D:544:PRO:O	1:D:547:SER:HB3	1.95	0.66
1:A:508:ILE:HB	1:A:682:LEU:HD22	1.76	0.66
1:A:585:MET:HE1	1:A:626:LEU:HD12	1.77	0.66
1:C:285:VAL:HG13	1:C:326:ILE:HD11	1.76	0.66
1:D:319:ASN:HB3	1:D:320:SER:HB2	1.77	0.66
1:E:604:ASP:HB3	1:E:607:ARG:HB3	1.78	0.66
1:F:245:VAL:O	1:F:249:GLY:N	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:64:LEU:HB3	1:B:65:PRO:HD3	1.77	0.66
1:B:549:LYS:HZ2	1:B:647:SER:HA	1.60	0.66
1:D:533:ARG:HD2	1:E:505:ASN:ND2	2.10	0.66
2:G:233:PRO:HB3	2:J:268:SER:O	1.94	0.66
4:L:237:VAL:HG21	5:M:60:VAL:HG13	1.76	0.66
1:D:513:PRO:HB3	1:D:516:ARG:HE	1.59	0.66
1:D:695:ALA:HB1	1:D:699:LYS:HE3	1.78	0.66
2:H:38:ILE:HG23	2:H:75:LEU:HD12	1.76	0.66
1:B:67:ARG:HD2	2:I:218:MET:HE2	1.76	0.66
1:B:307:ALA:O	1:B:311:GLU:HG2	1.94	0.66
1:B:449:GLN:O	1:B:453:MET:HG2	1.95	0.66
1:D:605:ILE:HD11	1:D:644:GLY:HA3	1.78	0.66
1:B:73:SER:O	1:B:76:GLN:HG2	1.96	0.66
1:E:64:LEU:HB3	1:E:65:PRO:HD3	1.78	0.66
1:F:224:ASP:O	1:F:228:SER:HB2	1.95	0.66
2:J:200:TYR:HB3	5:M:40:LYS:HZ2	1.60	0.66
1:A:653:GLN:NE2	1:A:653:GLN:O	2.29	0.66
1:C:616:PRO:HG2	1:D:614:ILE:HD13	1.77	0.66
1:B:125:PHE:HA	1:B:128:GLN:NE2	2.10	0.66
1:B:326:ILE:HG22	1:B:370:ILE:HG13	1.77	0.66
1:C:48:THR:HG21	1:C:128:GLN:HG2	1.78	0.66
1:C:618:PHE:HZ	1:D:612:VAL:HG11	1.61	0.66
1:D:245:VAL:O	1:D:249:GLY:N	2.29	0.66
2:J:201:SER:HB2	5:M:44:ILE:HD13	1.78	0.66
1:A:628:VAL:HG11	1:B:571:ASP:HA	1.78	0.66
1:F:518:LEU:H	1:F:518:LEU:HD12	1.61	0.66
1:E:681:GLU:HA	1:E:691:ARG:HE	1.59	0.65
4:L:202:ILE:HD12	5:M:25:SER:HB3	1.78	0.65
1:D:230:ILE:HD11	1:D:256:ILE:HD13	1.78	0.65
1:E:670:ILE:HG22	1:E:672:THR:H	1.60	0.65
1:F:12:PRO:HG2	1:F:23:VAL:HG11	1.78	0.65
1:F:317:GLY:O	1:F:318:ALA:HB2	1.96	0.65
1:F:535:PRO:HA	1:F:639:LYS:HG2	1.78	0.65
2:G:188:VAL:HG13	2:G:205:TYR:HD2	1.61	0.65
2:I:216:ILE:HG12	2:I:220:ASN:HB2	1.77	0.65
1:F:106:ASN:HB3	1:F:143:LYS:HZ1	1.60	0.65
1:A:64:LEU:HB3	1:A:65:PRO:HD3	1.78	0.65
1:A:710:LEU:O	1:A:714:ILE:HG13	1.96	0.65
1:C:436:PHE:HB3	1:C:440:GLU:OE1	1.96	0.65
1:E:680:LEU:HD13	1:E:694:ILE:HD13	1.77	0.65
1:A:327:PHE:CD1	1:A:330:ILE:HG22	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:549:LYS:HE3	1:A:646:THR:O	1.97	0.65
1:C:711:LEU:O	1:C:715:GLU:HG2	1.97	0.65
1:D:686:PHE:CE1	1:D:714:ILE:HG23	2.32	0.65
2:G:235:PHE:CD2	5:M:31:ARG:HA	2.31	0.65
2:J:72:HIS:HE1	2:J:80:ASP:HB2	1.61	0.65
5:M:56:GLN:O	5:M:60:VAL:HG23	1.97	0.65
1:B:67:ARG:NH1	2:I:218:MET:HG2	2.12	0.65
1:B:249:GLY:HA3	1:C:414:MET:HE3	1.79	0.65
1:E:527:GLN:HE22	1:F:716:MET:HG2	1.60	0.65
1:A:720:MET:O	1:A:725:ARG:NE	2.22	0.65
1:D:299:GLU:OE1	1:D:350:VAL:HG13	1.97	0.65
1:E:513:PRO:HA	1:E:516:ARG:HG2	1.77	0.65
1:B:589:PHE:HD2	1:B:629:LEU:HD22	1.62	0.65
1:C:649:LYS:HE2	1:C:658:LEU:HD13	1.78	0.65
1:A:521:GLY:O	1:A:525:VAL:HG23	1.97	0.65
1:A:550:THR:HA	1:A:645:THR:HG21	1.79	0.65
1:B:224:ASP:O	1:B:228:SER:HB2	1.97	0.65
1:E:12:PRO:HG2	1:E:23:VAL:HG11	1.79	0.65
1:E:648:ARG:NE	1:E:650:ASP:OD1	2.26	0.65
1:E:697:GLN:HG3	1:E:730:LEU:HD11	1.79	0.65
1:A:503:ILE:CG2	1:A:506:GLY:HA2	2.27	0.64
1:A:539:VAL:HG13	1:A:643:ILE:HA	1.78	0.64
1:F:410:HIS:O	1:F:414:MET:HG2	1.96	0.64
1:F:635:PRO:O	1:F:638:ARG:HG2	1.96	0.64
1:A:124:GLN:HE21	1:A:125:PHE:HE1	1.43	0.64
1:B:358:ILE:HD12	1:B:388:ARG:HB3	1.79	0.64
1:B:563:PRO:HD2	1:B:597:LEU:HB2	1.79	0.64
1:C:728:LYS:O	1:C:732:LEU:HG	1.97	0.64
2:H:101:ILE:HG21	2:H:135:LEU:HD11	1.79	0.64
1:B:540:LEU:HD11	1:B:649:LYS:NZ	2.12	0.64
3:K:70:LEU:HD11	5:M:192:ILE:HD12	1.77	0.64
1:A:678:GLU:O	1:A:682:LEU:HD12	1.98	0.64
1:A:502:TYR:CE2	1:A:567:ILE:HG21	2.31	0.64
1:C:590:ASP:HA	1:C:593:TYR:CD2	2.33	0.64
1:D:713:LEU:HD21	1:D:732:LEU:HB2	1.79	0.64
2:J:232:PHE:C	2:J:234:ALA:H	2.05	0.64
1:B:240:PHE:CE1	1:C:457:ILE:HD11	2.33	0.64
1:B:361:VAL:O	1:C:271:ARG:HD2	1.98	0.64
1:F:326:ILE:HG22	1:F:370:ILE:HG13	1.80	0.64
1:E:602:VAL:O	1:E:644:GLY:HA2	1.98	0.64
1:F:554:ALA:O	1:F:558:GLU:HG3	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:ILE:HB	1:A:319:ASN:O	1.98	0.64
1:D:256:ILE:CG1	1:D:370:ILE:HG22	2.28	0.64
1:F:612:VAL:HG12	1:F:617:ARG:HB2	1.80	0.64
2:H:267:ASP:O	2:I:233:PRO:HB3	1.98	0.64
1:B:289:GLU:C	1:B:291:LEU:H	2.05	0.63
1:C:18:LEU:HA	1:C:137:VAL:HG23	1.79	0.63
1:C:240:PHE:CD2	1:C:244:ILE:HG21	2.30	0.63
1:D:105:LYS:O	1:D:105:LYS:HD2	1.98	0.63
1:F:589:PHE:HD2	1:F:629:LEU:HD13	1.63	0.63
2:I:155:GLU:O	5:M:176:ARG:NH2	2.31	0.63
2:J:235:PHE:CD1	5:M:152:GLN:HG2	2.33	0.63
1:A:196:ILE:HG22	1:A:319:ASN:HD22	1.63	0.63
1:A:353:GLN:HE21	1:A:357:LYS:HG2	1.63	0.63
1:A:617:ARG:HH11	1:A:617:ARG:HG3	1.63	0.63
1:C:375:ARG:HH12	1:C:378:LEU:HG	1.64	0.63
1:D:680:LEU:HB2	1:D:691:ARG:HH21	1.63	0.63
1:D:720:MET:HE3	1:D:724:TYR:CE1	2.30	0.63
1:B:289:GLU:O	1:B:291:LEU:N	2.26	0.63
1:B:589:PHE:HE1	1:B:600:VAL:HG11	1.63	0.63
1:C:614:ILE:C	1:C:616:PRO:HA	2.22	0.63
1:D:713:LEU:HD21	1:D:732:LEU:CB	2.27	0.63
1:E:284:VAL:HG23	1:E:324:ILE:O	1.98	0.63
1:F:407:LEU:HD11	1:F:426:ILE:HG23	1.81	0.63
1:A:457:ILE:HD12	1:F:232:ARG:HH21	1.64	0.63
1:C:245:VAL:O	1:C:249:GLY:N	2.30	0.63
1:E:125:PHE:HA	1:E:128:GLN:NE2	2.14	0.63
2:G:175:LEU:HD23	2:G:177:GLN:HE21	1.63	0.63
3:K:46:MET:O	3:K:50:VAL:HG23	1.97	0.63
1:A:258:LEU:HA	1:A:393:MET:O	1.99	0.63
1:A:330:ILE:HG13	1:A:373:THR:HB	1.78	0.63
1:D:651:VAL:O	1:D:655:MET:HG2	1.99	0.63
2:I:175:LEU:HD23	2:I:177:GLN:HE21	1.63	0.63
1:A:355:LEU:HA	1:A:358:ILE:HD11	1.80	0.63
1:D:547:SER:OG	1:D:549:LYS:HG3	1.99	0.63
1:E:311:GLU:OE1	1:E:314:ARG:NE	2.29	0.63
1:E:654:GLU:HG2	1:F:614:ILE:HD11	1.81	0.63
1:E:685:ASN:HB3	1:E:718:LEU:HD11	1.78	0.63
2:G:271:ARG:NH2	2:H:234:ALA:HB2	2.13	0.63
1:D:40:SER:HB2	1:D:41:PRO:HD2	1.81	0.63
1:E:91:CYS:HB3	1:E:155:MET:HE2	1.81	0.63
1:E:536:LEU:HD12	1:E:640:LEU:O	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:106:ASN:HB3	1:F:143:LYS:NZ	2.13	0.63
1:F:525:VAL:HG13	1:F:562:PHE:HE1	1.63	0.63
2:H:236:SER:OG	4:L:211:GLU:HG2	1.99	0.63
1:D:67:ARG:HH12	1:D:74:ILE:HD11	1.63	0.63
1:D:593:TYR:O	1:D:638:ARG:HG2	1.98	0.63
1:E:264:CYS:SG	1:E:395:ILE:HG21	2.39	0.63
1:C:377:ASP:OD2	1:C:377:ASP:N	2.32	0.62
1:F:542:GLU:HB2	1:F:666:HIS:HA	1.80	0.62
1:F:545:PRO:HA	1:F:547:SER:N	2.14	0.62
1:F:550:THR:HA	1:F:645:THR:HG21	1.80	0.62
1:A:267:THR:OG1	1:A:328:ASP:OD2	2.16	0.62
1:C:521:GLY:HA3	1:C:556:ILE:HD13	1.80	0.62
1:C:546:HIS:HA	1:C:708:LYS:HD3	1.81	0.62
1:D:527:GLN:NE2	1:E:715:GLU:O	2.28	0.62
1:F:327:PHE:HB2	1:F:330:ILE:CG2	2.29	0.62
2:G:213:HIS:ND1	2:G:216:ILE:HD12	2.13	0.62
1:A:382:ALA:O	1:A:385:ARG:HG2	1.99	0.62
1:D:657:MET:HG2	1:D:661:PHE:CE2	2.34	0.62
1:D:677:LEU:O	1:D:691:ARG:NH2	2.32	0.62
1:B:327:PHE:HB2	1:B:330:ILE:HG22	1.81	0.62
1:E:240:PHE:HE1	1:F:457:ILE:HD12	1.64	0.62
1:E:398:PRO:HG3	1:E:436:PHE:O	2.00	0.62
1:D:436:PHE:HE2	1:D:444:LEU:HD12	1.64	0.62
1:F:404:LEU:O	1:F:408:HIS:HB2	1.99	0.62
1:A:503:ILE:HG23	1:A:506:GLY:CA	2.30	0.62
1:B:670:ILE:HG23	1:B:675:GLN:HB2	1.80	0.62
1:E:538:SER:OG	1:E:661:PHE:HA	1.99	0.62
1:A:104:LYS:HA	1:A:107:ILE:CD1	2.29	0.62
1:A:540:LEU:HD11	1:A:646:THR:HG22	1.82	0.62
1:D:657:MET:HG2	1:D:661:PHE:HE2	1.65	0.62
1:E:224:ASP:O	1:E:228:SER:HB2	2.00	0.62
1:F:354:LEU:O	1:F:358:ILE:HG12	2.00	0.62
1:B:407:LEU:CD1	1:B:426:ILE:HG23	2.30	0.62
1:E:303:ARG:HG3	1:E:357:LYS:HE2	1.80	0.62
2:G:104:LEU:HB3	2:G:127:ILE:HD12	1.80	0.62
3:K:48:VAL:HG12	3:K:52:LYS:HZ1	1.63	0.62
1:E:404:LEU:O	1:E:408:HIS:HB2	2.00	0.62
1:F:64:LEU:HB3	1:F:65:PRO:HD3	1.81	0.62
1:F:513:PRO:O	1:F:517:VAL:HG23	1.99	0.62
2:G:231:LEU:HD22	2:J:271:ARG:HH11	1.63	0.62
2:I:128:ALA:HB2	2:I:144:HIS:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:674:GLU:HA	1:E:677:LEU:HD12	1.82	0.62
2:G:267:ASP:O	2:H:233:PRO:HG2	1.99	0.62
1:C:289:GLU:O	1:C:291:LEU:N	2.27	0.61
1:E:358:ILE:HD12	1:E:388:ARG:HB3	1.81	0.61
2:I:47:ARG:O	2:I:50:ASN:HB3	2.00	0.61
1:B:651:VAL:HG12	1:B:655:MET:HE3	1.82	0.61
1:E:652:LEU:CD2	1:E:657:MET:HB3	2.30	0.61
1:D:521:GLY:O	1:D:525:VAL:HG23	2.00	0.61
1:E:693:THR:O	1:E:697:GLN:NE2	2.18	0.61
1:F:535:PRO:HB2	1:F:536:LEU:HD13	1.83	0.61
2:J:112:THR:HG23	2:J:117:PHE:HE1	1.64	0.61
1:A:490:PRO:HA	1:A:491:ALA:CB	2.19	0.61
1:A:624:GLN:HG3	1:B:610:ASP:CB	2.29	0.61
1:B:542:GLU:HB3	1:B:649:LYS:HG3	1.82	0.61
1:C:64:LEU:HB3	1:C:65:PRO:HD3	1.82	0.61
5:M:179:ASP:HA	5:M:182:MET:HE3	1.82	0.61
1:A:527:GLN:HB2	1:B:719:GLN:HG3	1.82	0.61
1:B:437:SER:O	1:B:440:GLU:HB2	1.99	0.61
1:D:604:ASP:HB3	1:D:607:ARG:CB	2.31	0.61
1:F:529:LYS:HG3	1:F:597:LEU:HD11	1.81	0.61
1:C:295:VAL:O	1:D:294:TYR:HB2	2.00	0.61
1:D:527:GLN:NE2	1:E:716:MET:HA	2.15	0.61
1:E:623:LEU:HD23	1:E:624:GLN:NE2	2.16	0.61
1:E:710:LEU:O	1:E:714:ILE:HG13	2.01	0.61
1:B:728:LYS:HE3	1:B:732:LEU:HD21	1.83	0.61
1:B:499:TYR:HA	1:B:502:TYR:CD2	2.36	0.61
1:C:511:GLY:HA3	1:C:513:PRO:HD2	1.82	0.61
1:C:540:LEU:HD23	1:C:649:LYS:HE3	1.83	0.61
1:E:245:VAL:O	1:E:249:GLY:N	2.33	0.61
2:J:142:ILE:HG23	2:J:168:VAL:HG13	1.83	0.61
3:K:43:VAL:HG13	4:L:215:MET:HE1	1.82	0.61
1:F:562:PHE:HE2	1:F:597:LEU:HD12	1.65	0.61
2:J:200:TYR:HB3	5:M:40:LYS:NZ	2.15	0.61
1:A:299:GLU:HG2	1:A:353:GLN:HG2	1.82	0.61
1:C:536:LEU:HD12	1:C:640:LEU:HB3	1.83	0.61
1:D:46:ILE:HD12	1:D:174:VAL:HG11	1.82	0.61
1:D:728:LYS:HE3	1:D:732:LEU:HD11	1.82	0.61
3:K:63:LEU:HD13	5:M:182:MET:HA	1.81	0.61
3:K:87:LYS:HE3	5:M:204:GLY:HA2	1.82	0.61
1:D:234:ALA:HA	1:D:253:VAL:HG11	1.83	0.60
2:H:120:ALA:O	2:H:124:HIS:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ARG:HA	1:A:252:HIS:CE1	2.36	0.60
1:A:625:ALA:O	1:A:629:LEU:HG	2.00	0.60
1:A:671:ALA:HA	1:A:703:VAL:O	2.01	0.60
1:D:300:ALA:O	1:D:303:ARG:HB3	2.01	0.60
1:D:513:PRO:O	1:D:516:ARG:HG2	2.01	0.60
1:D:534:THR:OG1	1:E:715:GLU:HG2	2.01	0.60
2:J:96:ASP:OD1	2:J:97:PRO:HD3	2.01	0.60
1:A:91:CYS:HB3	1:A:155:MET:HE2	1.83	0.60
1:B:538:SER:HB3	1:B:661:PHE:HD2	1.66	0.60
1:D:64:LEU:HD21	2:J:290:ASP:OD1	2.00	0.60
1:F:538:SER:O	1:F:663:THR:HG22	2.01	0.60
2:G:195:SER:C	2:G:197:LEU:H	2.08	0.60
1:A:104:LYS:NZ	1:A:104:LYS:HB3	2.16	0.60
1:A:715:GLU:HG3	1:F:527:GLN:HE21	1.66	0.60
1:B:589:PHE:HE2	1:B:629:LEU:HB3	1.65	0.60
1:D:116:LYS:NZ	1:D:116:LYS:HB3	2.16	0.60
1:D:383:LEU:O	1:D:389:LEU:HB2	2.00	0.60
1:F:18:LEU:HD13	1:F:139:SER:OG	2.00	0.60
1:F:95:MET:HG3	1:F:152:ILE:HG12	1.82	0.60
1:F:411:THR:O	1:F:414:MET:HB2	2.02	0.60
2:J:160:SER:OG	5:M:52:GLU:OE2	2.18	0.60
1:C:399:ASP:O	1:C:403:ARG:N	2.30	0.60
2:H:207:PHE:HB2	2:H:240:GLU:HG2	1.82	0.60
1:B:385:ARG:HH21	1:B:388:ARG:CZ	2.15	0.60
1:B:404:LEU:O	1:B:408:HIS:HB2	2.01	0.60
1:B:548:GLY:O	1:B:552:LEU:HB2	2.01	0.60
1:B:621:LEU:HD11	1:C:575:GLY:HA2	1.82	0.60
1:D:256:ILE:HG22	1:D:391:VAL:HG12	1.83	0.60
1:E:397:LEU:HD13	1:E:398:PRO:HD2	1.83	0.60
1:E:640:LEU:HD12	1:E:641:LEU:N	2.17	0.60
1:F:521:GLY:O	1:F:525:VAL:HG23	2.02	0.60
1:F:650:ASP:O	1:F:653:GLN:HG3	2.02	0.60
1:A:355:LEU:HB3	1:A:388:ARG:NH1	2.17	0.60
1:C:579:THR:O	1:C:583:GLN:HG2	2.02	0.60
1:C:589:PHE:CD2	1:C:629:LEU:HD13	2.37	0.60
1:D:436:PHE:CE2	1:D:444:LEU:HD12	2.37	0.60
1:D:546:HIS:ND1	1:D:709:LYS:HD3	2.17	0.60
1:E:399:ASP:O	1:E:403:ARG:N	2.32	0.60
2:H:149:ALA:HB2	2:H:164:CYS:HB2	1.82	0.60
1:B:284:VAL:HG23	1:B:324:ILE:O	2.02	0.60
1:B:576:PHE:HB3	1:B:580:ALA:HB3	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:236:ALA:HB1	1:E:453:MET:HG3	1.83	0.60
1:E:95:MET:HG3	1:E:152:ILE:HG12	1.83	0.60
1:F:307:ALA:O	1:F:311:GLU:HG2	2.01	0.60
1:A:687:LYS:N	1:A:690:GLU:OE1	2.33	0.60
4:L:207:ASN:HA	4:L:210:ARG:HB2	1.83	0.60
1:A:270:ALA:O	1:A:273:ILE:HG22	2.02	0.60
1:D:528:THR:OG1	1:D:641:LEU:HD12	2.02	0.60
1:E:399:ASP:HB2	1:E:402:GLY:H	1.67	0.60
2:I:53:LYS:HE3	2:J:117:PHE:CE2	2.36	0.60
2:J:256:VAL:HG11	2:J:288:GLN:HG2	1.84	0.60
1:A:102:LEU:HD23	1:A:144:LEU:HB3	1.84	0.59
1:C:613:PRO:HD3	1:C:648:ARG:HH22	1.66	0.59
1:D:239:VAL:HG13	1:D:240:PHE:CD1	2.37	0.59
1:D:648:ARG:HG3	1:D:651:VAL:HG23	1.84	0.59
1:E:106:ASN:HB3	1:E:143:LYS:HZ1	1.65	0.59
5:M:81:LEU:HD23	5:M:202:MET:SD	2.42	0.59
1:A:670:ILE:HG23	1:A:675:GLN:HB2	1.84	0.59
1:D:249:GLY:HA3	1:E:413:ARG:NH1	2.17	0.59
1:E:532:ASP:OD2	1:E:533:ARG:N	2.34	0.59
1:F:194:ASN:HD21	1:F:312:GLU:HG2	1.65	0.59
2:G:200:TYR:CE2	5:M:38:GLU:HG2	2.38	0.59
1:B:65:PRO:HG2	1:B:137:VAL:HG13	1.84	0.59
1:D:12:PRO:HB3	1:D:54:SER:OG	2.03	0.59
1:A:720:MET:HG3	1:A:728:LYS:HD2	1.85	0.59
1:D:625:ALA:O	1:D:629:LEU:HG	2.02	0.59
1:F:428:GLU:O	1:F:432:GLU:HG2	2.02	0.59
1:E:67:ARG:NH1	2:G:217:ASP:OD2	2.36	0.59
1:E:196:ILE:HD13	1:E:196:ILE:N	2.16	0.59
1:E:507:ILE:CD1	1:E:555:LYS:HB2	2.32	0.59
1:E:623:LEU:HD23	1:E:624:GLN:HE22	1.67	0.59
1:B:171:LYS:HB2	1:B:171:LYS:NZ	2.17	0.59
1:B:570:PRO:HD3	1:B:603:ASP:HB3	1.83	0.59
1:D:404:LEU:HD11	1:D:427:LYS:HE3	1.84	0.59
1:D:407:LEU:HG	1:D:441:LEU:HD11	1.85	0.59
1:D:628:VAL:HG11	1:E:574:ILE:HG21	1.84	0.59
1:E:589:PHE:CD2	1:E:629:LEU:HD21	2.37	0.59
1:E:705:ILE:HD12	1:E:713:LEU:HD12	1.84	0.59
2:G:271:ARG:NH2	2:H:231:LEU:HB2	2.18	0.59
2:J:230:GLU:HG2	2:J:231:LEU:N	2.18	0.59
3:K:43:VAL:HG22	4:L:212:LEU:HB2	1.84	0.59
1:D:268:LEU:HA	1:D:271:ARG:HD2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:114:THR:HG21	1:F:200:LYS:HG2	1.85	0.59
2:G:155:GLU:C	2:G:157:SER:H	2.11	0.59
1:A:598:SER:OG	1:A:640:LEU:HD12	2.02	0.59
1:B:95:MET:HE3	1:B:97:ILE:HD11	1.84	0.59
1:C:334:CYS:HA	1:C:351:VAL:HG22	1.85	0.59
1:C:711:LEU:HA	1:C:714:ILE:HD12	1.85	0.59
2:I:188:VAL:HG13	2:I:205:TYR:HD2	1.68	0.59
2:J:69:ALA:HB1	2:J:85:PHE:CE1	2.38	0.59
4:L:237:VAL:HG11	5:M:60:VAL:HA	1.84	0.59
1:C:407:LEU:CD1	1:C:426:ILE:HG23	2.27	0.59
1:F:380:ASP:OD1	1:F:382:ALA:N	2.36	0.59
2:G:268:SER:O	2:H:233:PRO:HB3	2.02	0.59
5:M:42:ALA:HA	5:M:45:ARG:HD3	1.84	0.59
5:M:170:GLU:HG3	5:M:174:GLN:HE21	1.67	0.59
1:A:40:SER:HB2	1:A:41:PRO:HD2	1.85	0.59
1:A:536:LEU:HD23	1:A:634:PRO:HD3	1.85	0.59
1:C:624:GLN:O	1:C:628:VAL:HG23	2.03	0.59
2:G:115:GLY:HA3	2:J:50:ASN:HD21	1.66	0.59
2:H:271:ARG:NH1	2:I:234:ALA:HB2	2.11	0.59
1:B:570:PRO:HG3	1:B:608:LEU:HD23	1.84	0.58
1:C:542:GLU:CB	1:C:649:LYS:HD3	2.33	0.58
1:E:536:LEU:HD22	1:E:634:PRO:HD3	1.85	0.58
2:H:116:ARG:NH1	5:M:186:ASP:OD2	2.36	0.58
2:H:235:PHE:CE1	4:L:204:LYS:HA	2.37	0.58
2:I:80:ASP:OD1	5:M:66:HIS:CD2	2.56	0.58
1:A:686:PHE:CE2	1:A:714:ILE:HG12	2.32	0.58
1:E:659:ASN:HD21	1:F:545:PRO:HB2	1.68	0.58
1:F:570:PRO:HA	1:F:573:MET:HE2	1.84	0.58
2:H:230:GLU:HG2	2:H:231:LEU:N	2.18	0.58
5:M:153:VAL:O	5:M:157:ILE:HD13	2.02	0.58
1:A:257:LEU:HG	1:A:389:LEU:HD12	1.84	0.58
1:A:322:LEU:HD12	1:A:323:HIS:H	1.68	0.58
1:B:74:ILE:H	2:I:218:MET:HE3	1.67	0.58
1:B:540:LEU:HA	1:B:644:GLY:O	2.03	0.58
1:C:578:GLU:HB3	1:C:621:LEU:HB3	1.83	0.58
1:F:358:ILE:HD12	1:F:388:ARG:HB3	1.84	0.58
1:B:313:GLN:O	1:B:317:GLY:N	2.37	0.58
1:B:404:LEU:HG	1:B:426:ILE:HG22	1.85	0.58
1:E:36:ILE:HD11	1:E:44:LYS:HB3	1.85	0.58
1:F:121:PHE:CD2	1:F:183:VAL:HG21	2.38	0.58
1:F:284:VAL:HG23	1:F:324:ILE:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:203:LYS:HB3	2:I:240:GLU:HG3	1.84	0.58
4:L:206:GLU:HA	5:M:32:MET:HG2	1.84	0.58
4:L:207:ASN:HA	4:L:210:ARG:HD3	1.84	0.58
5:M:31:ARG:O	5:M:35:LEU:HG	2.04	0.58
1:A:657:MET:HE3	1:A:661:PHE:HE1	1.69	0.58
1:C:540:LEU:HD12	1:C:644:GLY:O	2.04	0.58
1:D:654:GLU:HB3	1:E:614:ILE:HD11	1.83	0.58
1:D:686:PHE:HB3	1:D:690:GLU:HG3	1.83	0.58
2:G:124:HIS:HE1	2:G:147:GLN:HB3	1.68	0.58
1:A:563:PRO:HD2	1:A:597:LEU:CD2	2.33	0.58
2:H:17:ALA:O	2:H:21:VAL:HG12	2.03	0.58
3:K:45:ILE:CD1	5:M:161:ARG:HG3	2.34	0.58
1:C:606:GLU:HG2	1:C:607:ARG:N	2.18	0.58
1:E:604:ASP:O	1:E:608:LEU:N	2.37	0.58
1:E:664:THR:C	1:E:665:ILE:HD13	2.28	0.58
1:C:404:LEU:O	1:C:408:HIS:HB2	2.04	0.58
1:C:653:GLN:HG3	1:C:658:LEU:HD23	1.84	0.58
1:E:270:ALA:O	1:E:273:ILE:HG22	2.04	0.58
1:E:513:PRO:O	1:E:517:VAL:HG23	2.03	0.58
2:H:21:VAL:HG21	2:H:71:LEU:HD22	1.85	0.58
1:C:281:GLU:CB	1:C:324:ILE:HD13	2.34	0.58
1:C:555:LYS:HA	1:C:558:GLU:OE1	2.03	0.58
1:E:596:GLN:CA	1:E:638:ARG:HG2	2.31	0.58
4:L:229:MET:O	4:L:233:ILE:HG13	2.04	0.58
1:A:315:ARG:HG2	1:A:316:LEU:CD1	2.33	0.58
1:C:233:ARG:HA	1:D:450:SER:HB2	1.86	0.58
1:D:256:ILE:O	1:D:370:ILE:HA	2.04	0.58
1:D:284:VAL:HG23	1:D:324:ILE:O	2.04	0.58
1:F:256:ILE:O	1:F:370:ILE:HA	2.03	0.58
1:F:436:PHE:HB3	1:F:440:GLU:CB	2.34	0.58
1:B:686:PHE:HB3	1:B:690:GLU:HB2	1.85	0.57
2:I:235:PHE:CD2	3:K:37:ALA:HB3	2.39	0.57
1:A:503:ILE:O	1:A:505:ASN:N	2.36	0.57
1:E:671:ALA:HA	1:E:703:VAL:O	2.04	0.57
2:J:75:LEU:HD23	2:J:76:GLN:HG2	1.85	0.57
5:M:199:ALA:HA	5:M:202:MET:HE2	1.86	0.57
1:A:542:GLU:OE2	1:A:666:HIS:NE2	2.37	0.57
1:F:670:ILE:HG23	1:F:675:GLN:HB2	1.85	0.57
2:I:149:ALA:HB2	2:I:164:CYS:HB2	1.86	0.57
1:B:236:ALA:HA	1:B:239:VAL:HG12	1.87	0.57
1:B:296:GLY:H	1:B:297:GLU:CB	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:570:PRO:HG2	1:F:604:ASP:CB	2.32	0.57
2:H:119:ILE:HD11	2:H:123:HIS:ND1	2.19	0.57
2:I:244:MET:O	2:I:248:LEU:HG	2.05	0.57
1:A:726:VAL:O	1:A:730:LEU:HG	2.04	0.57
1:D:286:ASN:HB2	1:D:327:PHE:HD1	1.68	0.57
5:M:164:ALA:HA	5:M:167:MET:HE3	1.86	0.57
1:A:457:ILE:HG13	1:F:240:PHE:CE1	2.40	0.57
1:C:132:VAL:HG23	1:C:173:GLU:O	2.04	0.57
1:C:688:ASP:O	1:C:692:THR:HG23	2.04	0.57
1:D:404:LEU:HA	1:D:407:LEU:HD12	1.86	0.57
1:E:26:GLU:HG2	1:E:51:THR:HB	1.86	0.57
1:F:236:ALA:HA	1:F:239:VAL:HG12	1.87	0.57
2:G:69:ALA:HB1	2:G:85:PHE:CE1	2.39	0.57
2:H:235:PHE:CD1	4:L:204:LYS:HG3	2.39	0.57
2:J:101:ILE:HG21	2:J:135:LEU:HD11	1.87	0.57
1:B:428:GLU:O	1:B:432:GLU:HG2	2.05	0.57
1:C:14:ASP:O	1:C:18:LEU:HG	2.04	0.57
1:C:194:ASN:ND2	1:C:316:LEU:HG	2.20	0.57
1:C:330:ILE:HG22	1:C:379:ILE:CD1	2.34	0.57
1:E:113:ASP:O	1:E:117:MET:HG3	2.05	0.57
1:E:618:PHE:CZ	1:F:612:VAL:HG11	2.37	0.57
1:A:397:LEU:CB	1:A:398:PRO:HD3	2.34	0.57
1:B:625:ALA:O	1:B:629:LEU:HG	2.05	0.57
1:F:515:THR:HA	1:F:518:LEU:CD1	2.35	0.57
1:F:721:ASP:HB2	1:F:724:TYR:CD1	2.38	0.57
5:M:44:ILE:O	5:M:48:VAL:HG23	2.04	0.57
5:M:190:THR:O	5:M:194:GLU:HG3	2.04	0.57
1:A:724:TYR:HD1	1:A:727:ARG:HH12	1.51	0.57
1:E:296:GLY:H	1:E:297:GLU:CB	2.17	0.57
3:K:56:ARG:HH12	4:L:226:GLN:HE21	1.53	0.57
1:B:20:ASN:HD22	1:B:66:GLN:NE2	2.03	0.57
1:B:113:ASP:O	1:B:117:MET:HG3	2.04	0.57
1:C:67:ARG:NH1	1:C:74:ILE:HD11	2.20	0.57
1:D:585:MET:O	1:D:589:PHE:HD2	1.88	0.57
1:E:289:GLU:O	1:E:291:LEU:N	2.28	0.57
1:F:11:CYS:SG	1:F:17:SER:HB2	2.45	0.57
1:F:566:LYS:HD2	1:F:567:ILE:N	2.20	0.57
2:G:210:ALA:HB3	2:G:244:MET:HE3	1.86	0.57
1:C:353:GLN:HA	1:D:288:PRO:HG3	1.87	0.56
1:D:312:GLU:CD	1:D:323:HIS:ND1	2.63	0.56
1:D:510:TRP:HB3	1:D:679:ALA:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:640:LEU:HD12	1:E:641:LEU:H	1.70	0.56
2:J:159:SER:OG	5:M:48:VAL:O	2.15	0.56
2:J:210:ALA:HB3	2:J:244:MET:HE3	1.87	0.56
5:M:49:MET:HB3	5:M:53:GLN:NE2	2.19	0.56
1:A:64:LEU:HA	1:A:67:ARG:HE	1.70	0.56
1:A:67:ARG:NH1	1:A:74:ILE:HD11	2.20	0.56
1:E:525:VAL:O	1:E:528:THR:OG1	2.14	0.56
2:I:38:ILE:HD11	2:I:71:LEU:HB3	1.87	0.56
2:J:18:GLU:HA	2:J:21:VAL:HG12	1.87	0.56
3:K:45:ILE:HG21	5:M:164:ALA:HB1	1.87	0.56
1:A:544:PRO:HB2	1:A:669:ASN:ND2	2.20	0.56
1:A:550:THR:HG23	1:A:645:THR:OG1	2.04	0.56
1:B:67:ARG:NH1	1:B:67:ARG:HB2	2.20	0.56
1:B:571:ASP:OD2	1:B:571:ASP:N	2.35	0.56
1:B:662:SER:HB3	1:C:712:MET:HE3	1.86	0.56
1:C:98:GLU:HB3	1:C:148:LEU:HB3	1.85	0.56
1:C:231:PHE:O	1:C:235:PHE:HB2	2.05	0.56
1:D:618:PHE:HE1	1:E:612:VAL:HG21	1.69	0.56
1:E:383:LEU:O	1:E:389:LEU:HB2	2.06	0.56
1:F:536:LEU:HD21	1:F:632:LYS:O	2.05	0.56
2:G:119:ILE:HD12	2:G:122:LYS:HB2	1.85	0.56
2:H:142:ILE:HG23	2:H:168:VAL:HG13	1.86	0.56
2:I:254:GLN:HB2	2:I:291:GLU:HG2	1.87	0.56
3:K:46:MET:HB3	4:L:215:MET:SD	2.46	0.56
5:M:177:GLN:HG3	5:M:180:ARG:NH2	2.20	0.56
1:B:559:GLU:O	1:B:561:ASN:ND2	2.37	0.56
1:B:589:PHE:CE2	1:B:629:LEU:HB3	2.40	0.56
1:F:270:ALA:O	1:F:273:ILE:HG22	2.05	0.56
1:F:686:PHE:HE1	1:F:714:ILE:HG23	1.71	0.56
4:L:232:ARG:O	4:L:236:ASN:ND2	2.36	0.56
1:A:563:PRO:HD2	1:A:597:LEU:HD22	1.88	0.56
1:C:490:PRO:HB2	1:C:492:PHE:N	2.19	0.56
1:D:652:LEU:HB3	1:D:658:LEU:HB2	1.87	0.56
1:E:502:TYR:CZ	1:E:567:ILE:HG21	2.41	0.56
3:K:48:VAL:HG12	3:K:52:LYS:NZ	2.20	0.56
1:A:231:PHE:CD1	1:A:235:PHE:HE2	2.22	0.56
1:A:694:ILE:O	1:A:698:VAL:HG13	2.04	0.56
1:C:577:SER:O	1:C:580:ALA:N	2.33	0.56
1:E:428:GLU:O	1:E:432:GLU:HG2	2.05	0.56
2:G:21:VAL:HG21	2:G:71:LEU:HD22	1.86	0.56
5:M:177:GLN:HA	5:M:180:ARG:HH12	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:654:GLU:O	1:C:613:PRO:HG3	2.06	0.56
1:E:585:MET:HG3	1:E:589:PHE:HZ	1.65	0.56
1:E:721:ASP:O	1:E:725:ARG:HG3	2.06	0.56
2:J:127:ILE:HG23	2:J:131:TYR:CE1	2.41	0.56
1:B:383:LEU:O	1:B:389:LEU:HB2	2.06	0.56
1:C:312:GLU:O	1:C:316:LEU:HD13	2.06	0.56
1:C:584:ALA:O	1:C:588:ILE:HG13	2.06	0.56
1:C:613:PRO:HD3	1:C:648:ARG:NH2	2.20	0.56
1:D:45:TYR:CE2	1:D:70:ALA:HA	2.41	0.56
1:D:353:GLN:HE22	1:E:288:PRO:CG	2.19	0.56
1:D:524:LEU:O	1:D:527:GLN:HB3	2.06	0.56
1:D:604:ASP:HB3	1:D:607:ARG:HB3	1.87	0.56
1:E:132:VAL:HG23	1:E:173:GLU:O	2.06	0.56
2:G:112:THR:HG23	2:G:117:PHE:HE1	1.70	0.56
4:L:218:ASP:O	4:L:222:LEU:HG	2.06	0.56
1:D:527:GLN:HE22	1:E:716:MET:HA	1.71	0.56
1:E:670:ILE:H	1:E:670:ILE:HD12	1.71	0.56
1:E:672:THR:OG1	1:E:675:GLN:HB2	2.05	0.56
1:F:713:LEU:HD22	1:F:732:LEU:HB3	1.87	0.56
3:K:56:ARG:NH1	4:L:226:GLN:NE2	2.54	0.56
5:M:46:THR:HA	5:M:49:MET:HE3	1.88	0.56
1:C:67:ARG:HH12	1:C:74:ILE:HD11	1.70	0.56
1:C:544:PRO:HG2	1:C:669:ASN:CG	2.31	0.56
2:J:188:VAL:HG13	2:J:205:TYR:HD2	1.71	0.56
3:K:56:ARG:NH1	4:L:226:GLN:HE21	2.03	0.56
1:A:46:ILE:HD12	1:A:174:VAL:HG11	1.87	0.55
1:B:240:PHE:HB3	1:B:244:ILE:HB	1.88	0.55
1:D:284:VAL:HG21	1:D:325:ILE:HG22	1.88	0.55
1:D:353:GLN:HE22	1:E:288:PRO:HG2	1.71	0.55
1:B:423:ASP:C	1:B:479:ASP:N	2.64	0.55
1:D:104:LYS:HD3	2:J:257:ASP:OD2	2.06	0.55
1:D:512:ASP:O	1:D:515:THR:OG1	2.20	0.55
1:E:311:GLU:O	1:E:314:ARG:HG2	2.07	0.55
1:A:457:ILE:HG13	1:F:240:PHE:HE1	1.72	0.55
1:C:239:VAL:HG11	1:D:457:ILE:HD11	1.87	0.55
1:C:428:GLU:O	1:C:432:GLU:HG2	2.07	0.55
1:C:596:GLN:HA	1:C:638:ARG:CD	2.36	0.55
1:F:538:SER:H	1:F:662:SER:HB3	1.70	0.55
1:F:715:GLU:O	1:F:719:GLN:HG2	2.07	0.55
2:I:228:TYR:OH	2:I:237:ASP:OD1	2.22	0.55
1:E:689:LYS:O	1:E:692:THR:OG1	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:63:SER:O	1:F:67:ARG:HG3	2.06	0.55
2:J:235:PHE:HE2	5:M:155:GLY:HA3	1.72	0.55
1:B:536:LEU:HD22	1:B:632:LYS:O	2.06	0.55
1:D:135:GLN:HG2	1:D:148:LEU:HD13	1.89	0.55
1:D:543:GLY:O	1:D:647:SER:HA	2.06	0.55
1:D:554:ALA:O	1:D:558:GLU:HG2	2.07	0.55
1:E:380:ASP:OD1	1:E:382:ALA:N	2.36	0.55
1:E:528:THR:HG21	1:E:641:LEU:CD2	2.34	0.55
1:F:242:PRO:HD2	1:F:243:GLU:H	1.72	0.55
1:F:314:ARG:HG3	1:F:315:ARG:N	2.22	0.55
1:A:286:ASN:HB2	1:A:327:PHE:HB3	1.88	0.55
1:A:449:GLN:O	1:A:453:MET:HG2	2.06	0.55
1:D:547:SER:HG	1:D:549:LYS:HG3	1.69	0.55
1:E:91:CYS:O	1:E:154:ALA:HA	2.07	0.55
1:F:617:ARG:HH11	1:F:617:ARG:HG3	1.72	0.55
2:G:119:ILE:HD11	2:G:123:HIS:CE1	2.42	0.55
4:L:229:MET:HG3	4:L:232:ARG:NH2	2.21	0.55
4:L:236:ASN:H	4:L:236:ASN:HD22	1.53	0.55
1:B:132:VAL:HG23	1:B:173:GLU:O	2.07	0.55
1:B:569:SER:HA	1:B:603:ASP:HB3	1.88	0.55
1:C:91:CYS:O	1:C:154:ALA:HA	2.06	0.55
1:E:705:ILE:CD1	1:E:713:LEU:HD12	2.37	0.55
2:H:188:VAL:HG13	2:H:205:TYR:HD2	1.71	0.55
2:H:219:LEU:HD12	2:H:223:LEU:HB2	1.88	0.55
1:A:122:ILE:O	1:A:126:ASN:HB3	2.07	0.55
1:A:485:GLU:O	1:A:489:LYS:CB	2.54	0.55
1:B:385:ARG:NH1	1:C:263:GLY:HA2	2.22	0.55
1:C:12:PRO:HG2	1:C:23:VAL:HG11	1.89	0.55
1:D:592:ALA:HB1	1:D:640:LEU:HD13	1.88	0.55
1:F:67:ARG:NH1	1:F:74:ILE:HD11	2.22	0.55
1:B:124:GLN:HE21	1:B:125:PHE:HE1	1.53	0.55
1:C:511:GLY:C	1:C:513:PRO:HD2	2.32	0.55
1:C:577:SER:O	1:C:579:THR:N	2.40	0.55
1:E:121:PHE:CD2	1:E:183:VAL:HG21	2.42	0.55
1:F:102:LEU:H	1:F:145:PHE:HA	1.72	0.55
5:M:45:ARG:O	5:M:49:MET:HG3	2.07	0.55
1:C:308:ASP:OD1	1:C:309:ALA:N	2.40	0.55
1:C:721:ASP:O	1:C:725:ARG:HG3	2.07	0.55
1:D:731:ALA:HA	1:D:734:ARG:NH1	2.21	0.55
1:A:128:GLN:O	1:A:176:LEU:HD12	2.07	0.54
1:B:614:ILE:O	1:B:616:PRO:HA	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:380:ASP:OD1	1:D:382:ALA:N	2.40	0.54
1:F:284:VAL:O	1:F:326:ILE:HG12	2.06	0.54
1:A:406:ILE:O	1:A:409:ILE:HG22	2.08	0.54
1:D:303:ARG:HD3	1:D:353:GLN:CG	2.38	0.54
1:E:40:SER:OG	1:E:41:PRO:HD2	2.07	0.54
2:G:212:CYS:SG	2:G:279:MET:HE1	2.47	0.54
1:D:686:PHE:HB2	1:D:691:ARG:HG2	1.89	0.54
1:F:267:THR:HA	1:F:372:MET:SD	2.47	0.54
1:F:296:GLY:H	1:F:297:GLU:CB	2.20	0.54
1:F:606:GLU:OE2	1:F:647:SER:HB2	2.07	0.54
1:F:612:VAL:CG1	1:F:617:ARG:HB2	2.37	0.54
2:G:102:ASN:HA	2:G:105:MET:HE3	1.89	0.54
2:G:243:LEU:HD22	2:G:266:TYR:CG	2.42	0.54
2:I:177:GLN:HB3	2:I:180:LYS:HB2	1.89	0.54
2:I:243:LEU:HD22	2:I:266:TYR:CD2	2.42	0.54
2:J:72:HIS:CE1	2:J:80:ASP:HB2	2.40	0.54
3:K:64:ASP:O	3:K:68:ASP:HB2	2.07	0.54
1:A:300:ALA:O	1:A:304:LYS:HG3	2.08	0.54
1:A:683:LEU:HB3	1:A:685:ASN:HD22	1.72	0.54
1:B:436:PHE:HB3	1:B:440:GLU:CB	2.37	0.54
1:B:695:ALA:HB1	1:B:699:LYS:HE3	1.89	0.54
1:C:686:PHE:HE1	1:C:714:ILE:HG23	1.72	0.54
1:E:596:GLN:HA	1:E:638:ARG:CG	2.34	0.54
2:H:210:ALA:HB3	2:H:244:MET:HE3	1.89	0.54
1:A:313:GLN:OE1	1:A:317:GLY:HA2	2.08	0.54
1:A:493:GLY:HA2	1:A:494:THR:CB	2.37	0.54
1:C:691:ARG:HH11	1:C:691:ARG:HB2	1.72	0.54
1:A:315:ARG:HG2	1:A:316:LEU:HD13	1.90	0.54
1:D:312:GLU:HG2	1:D:313:GLN:H	1.72	0.54
1:F:437:SER:O	1:F:440:GLU:HB2	2.07	0.54
2:G:115:GLY:HA3	2:J:50:ASN:ND2	2.22	0.54
2:I:72:HIS:CE1	2:I:80:ASP:HB2	2.42	0.54
1:A:121:PHE:HD2	1:A:183:VAL:HG21	1.73	0.54
1:A:306:PHE:CD1	1:A:357:LYS:HB3	2.43	0.54
1:B:1:MET:HG2	1:B:82:LEU:HB2	1.90	0.54
1:C:540:LEU:HB2	1:C:661:PHE:CD2	2.42	0.54
1:A:690:GLU:O	1:A:694:ILE:HG13	2.07	0.54
1:B:354:LEU:O	1:B:358:ILE:HG12	2.08	0.54
1:C:256:ILE:HA	1:C:391:VAL:HG13	1.90	0.54
1:E:354:LEU:O	1:E:358:ILE:HG12	2.08	0.54
1:E:620:ASN:ND2	1:F:617:ARG:HB3	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:128:GLN:O	1:F:176:LEU:HD12	2.08	0.54
1:A:690:GLU:HB3	1:A:726:VAL:HG22	1.89	0.54
1:F:383:LEU:O	1:F:389:LEU:HB2	2.08	0.54
2:G:49:ALA:HB2	2:G:64:ALA:HB3	1.89	0.54
2:G:235:PHE:HB3	5:M:31:ARG:HG2	1.90	0.54
2:G:246:LYS:HZ1	2:G:258:SER:HB3	1.73	0.54
2:H:92:PHE:HD1	2:H:97:PRO:HG2	1.73	0.54
1:A:536:LEU:HD23	1:A:633:ALA:HA	1.89	0.54
1:B:270:ALA:O	1:B:273:ILE:HG22	2.08	0.54
1:B:327:PHE:HB2	1:B:330:ILE:CG2	2.38	0.54
1:D:599:CYS:SG	1:D:641:LEU:HD22	2.48	0.54
1:E:654:GLU:CG	1:F:614:ILE:HD11	2.37	0.54
2:G:101:ILE:HG13	2:G:102:ASN:N	2.23	0.54
2:H:195:SER:C	2:H:197:LEU:H	2.15	0.54
2:J:167:LYS:HE2	2:J:171:TYR:HE2	1.73	0.54
3:K:45:ILE:HD13	5:M:161:ARG:HG3	1.89	0.54
5:M:40:LYS:HG3	5:M:163:MET:CE	2.32	0.54
1:A:293:LYS:O	1:A:294:TYR:CG	2.61	0.53
1:C:86:ASP:C	1:C:88:ALA:H	2.15	0.53
1:C:614:ILE:O	1:C:616:PRO:HA	2.07	0.53
1:C:694:ILE:O	1:C:698:VAL:HG22	2.08	0.53
1:D:533:ARG:HD2	1:E:505:ASN:HD22	1.73	0.53
1:D:568:CYS:N	1:D:601:VAL:O	2.21	0.53
1:E:244:ILE:CG2	1:F:453:MET:HE1	2.38	0.53
1:E:552:LEU:HD11	1:E:667:VAL:HG11	1.90	0.53
5:M:152:GLN:O	5:M:156:ILE:HG13	2.08	0.53
1:B:149:VAL:HG11	1:B:152:ILE:HD11	1.90	0.53
1:B:310:GLU:OE2	1:B:357:LYS:NZ	2.41	0.53
1:C:510:TRP:CZ3	1:C:670:ILE:HG12	2.43	0.53
1:C:606:GLU:HB2	1:C:648:ARG:HD2	1.90	0.53
1:C:689:LYS:O	1:C:692:THR:OG1	2.17	0.53
1:F:712:MET:O	1:F:716:MET:HG3	2.07	0.53
2:I:276:LEU:O	2:I:280:LEU:HG	2.08	0.53
2:J:38:ILE:HD11	2:J:71:LEU:HB3	1.90	0.53
2:J:235:PHE:CE2	5:M:155:GLY:HA3	2.42	0.53
1:B:533:ARG:HH22	1:C:683:LEU:HD22	1.72	0.53
1:E:713:LEU:HD22	1:E:732:LEU:HD13	1.90	0.53
1:F:615:GLY:HA3	1:F:616:PRO:C	2.33	0.53
3:K:42:VAL:HA	3:K:45:ILE:HD12	1.89	0.53
1:B:22:ALA:HB3	1:B:49:LEU:HD23	1.89	0.53
1:B:46:ILE:HD12	1:B:174:VAL:HG21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:LYS:C	1:B:89:LYS:H	2.17	0.53
1:B:649:LYS:HE3	1:B:658:LEU:CD1	2.31	0.53
1:C:708:LYS:HA	1:C:711:LEU:HG	1.90	0.53
1:F:560:SER:HB2	1:F:562:PHE:CD1	2.44	0.53
2:G:119:ILE:HD13	3:K:65:ASP:OD1	2.08	0.53
2:J:179:GLN:O	2:J:182:ILE:HG12	2.09	0.53
4:L:198:ARG:O	4:L:202:ILE:HG13	2.09	0.53
1:A:136:LEU:N	1:A:136:LEU:HD23	2.22	0.53
1:A:509:LYS:HG2	1:A:515:THR:OG1	2.09	0.53
1:B:40:SER:HB2	1:B:43:HIS:ND1	2.23	0.53
1:D:43:HIS:HB3	1:D:45:TYR:HE1	1.73	0.53
1:E:549:LYS:HG3	1:E:550:THR:N	2.24	0.53
1:E:592:ALA:HB1	1:E:640:LEU:HD22	1.90	0.53
2:I:216:ILE:HD11	2:I:218:MET:HB2	1.90	0.53
1:A:104:LYS:C	1:A:106:ASN:H	2.17	0.53
1:A:307:ALA:O	1:A:310:GLU:HG3	2.08	0.53
1:C:256:ILE:HG22	1:C:391:VAL:HG11	1.88	0.53
1:C:533:ARG:O	1:D:505:ASN:ND2	2.41	0.53
1:C:547:SER:HB2	1:C:549:LYS:HG3	1.89	0.53
1:D:512:ASP:N	1:D:513:PRO:CD	2.72	0.53
1:E:240:PHE:HD2	1:E:244:ILE:CG2	2.19	0.53
1:E:705:ILE:HG13	1:E:709:LYS:HG3	1.90	0.53
2:H:128:ALA:HB2	2:H:144:HIS:HB2	1.90	0.53
2:I:185:TYR:HA	2:I:188:VAL:HG12	1.90	0.53
2:J:182:ILE:O	2:J:186:GLU:HG2	2.08	0.53
1:A:428:GLU:O	1:A:432:GLU:HG2	2.08	0.53
1:A:687:LYS:HB2	1:A:690:GLU:HG3	1.91	0.53
1:B:571:ASP:O	1:B:574:ILE:HG13	2.09	0.53
1:C:542:GLU:HB3	1:C:649:LYS:HD3	1.89	0.53
1:D:540:LEU:HD12	1:D:661:PHE:CE1	2.44	0.53
1:E:247:GLN:HA	1:F:417:HIS:ND1	2.24	0.53
1:E:407:LEU:CD1	1:E:426:ILE:HG23	2.35	0.53
1:F:86:ASP:C	1:F:88:ALA:H	2.17	0.53
1:F:526:GLN:O	1:F:530:ASN:HB2	2.08	0.53
2:J:195:SER:C	2:J:197:LEU:H	2.17	0.53
1:A:352:ASN:HA	1:A:355:LEU:HD12	1.91	0.53
1:A:513:PRO:O	1:A:517:VAL:HG23	2.08	0.53
1:C:510:TRP:CE3	1:C:670:ILE:HG12	2.43	0.53
1:D:312:GLU:CG	1:D:313:GLN:H	2.22	0.53
2:G:101:ILE:HD13	2:G:135:LEU:HD11	1.90	0.53
2:H:108:ILE:HD12	2:H:127:ILE:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:244:MET:O	2:H:248:LEU:HG	2.09	0.53
2:I:92:PHE:HB3	2:I:98:GLN:O	2.08	0.53
3:K:41:GLU:O	3:K:45:ILE:HG13	2.09	0.53
5:M:167:MET:O	5:M:171:ILE:HG13	2.09	0.53
1:B:406:ILE:HB	1:B:441:LEU:HD13	1.91	0.53
1:C:311:GLU:HA	1:C:314:ARG:HG2	1.89	0.53
1:D:313:GLN:O	1:D:317:GLY:N	2.41	0.53
1:A:315:ARG:C	1:A:316:LEU:HD12	2.34	0.53
1:A:564:PHE:HE1	1:A:566:LYS:HB2	1.72	0.53
1:B:627:LEU:CD2	1:B:657:MET:HG3	2.39	0.53
1:C:227:PHE:O	1:C:231:PHE:HB2	2.09	0.53
1:D:67:ARG:NH1	1:D:74:ILE:HD11	2.23	0.53
1:D:326:ILE:HG22	1:D:370:ILE:CG1	2.39	0.53
1:D:407:LEU:O	1:D:411:THR:HG23	2.09	0.53
1:E:573:MET:O	1:E:576:PHE:HB2	2.09	0.53
2:G:200:TYR:C	4:L:217:MET:HE1	2.34	0.53
5:M:174:GLN:O	5:M:178:ILE:HG13	2.09	0.53
1:C:525:VAL:HG13	1:C:562:PHE:CZ	2.44	0.52
1:D:136:LEU:N	1:D:136:LEU:HD23	2.24	0.52
1:E:696:GLN:HB3	1:E:697:GLN:NE2	2.24	0.52
1:F:64:LEU:HA	1:F:67:ARG:HD2	1.91	0.52
1:F:407:LEU:CD1	1:F:426:ILE:HG23	2.39	0.52
2:G:18:GLU:HA	2:G:21:VAL:HG12	1.90	0.52
2:G:57:ASN:O	2:G:59:SER:N	2.42	0.52
1:A:256:ILE:HG13	1:A:370:ILE:HG22	1.90	0.52
1:A:614:ILE:HD12	1:F:654:GLU:HG2	1.91	0.52
1:F:149:VAL:HG11	1:F:152:ILE:HD11	1.91	0.52
2:G:231:LEU:HD13	2:J:271:ARG:HB3	1.91	0.52
2:I:98:GLN:CD	2:I:98:GLN:H	2.17	0.52
2:J:182:ILE:HG22	2:J:212:CYS:HB2	1.92	0.52
1:A:95:MET:HG3	1:A:152:ILE:HG12	1.90	0.52
1:A:106:ASN:HB3	1:A:143:LYS:NZ	2.24	0.52
1:A:236:ALA:HB1	1:B:453:MET:CB	2.40	0.52
1:D:298:SER:O	1:D:301:ASN:HB3	2.10	0.52
1:F:517:VAL:HG21	1:F:667:VAL:HG22	1.92	0.52
2:I:18:GLU:HA	2:I:21:VAL:HG12	1.90	0.52
2:I:116:ARG:HH11	2:I:116:ARG:HG3	1.72	0.52
2:I:203:LYS:HE2	5:M:161:ARG:NH1	2.22	0.52
3:K:53:VAL:HG23	4:L:226:GLN:HE22	1.73	0.52
1:A:678:GLU:O	1:A:681:GLU:HG2	2.09	0.52
1:B:267:THR:HA	1:B:372:MET:SD	2.49	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:527:GLN:NE2	1:E:715:GLU:C	2.66	0.52
1:E:674:GLU:O	1:E:677:LEU:HB2	2.09	0.52
1:F:310:GLU:OE2	1:F:357:LYS:NZ	2.38	0.52
1:F:707:ILE:O	1:F:710:LEU:HB3	2.10	0.52
2:I:219:LEU:H	2:I:219:LEU:HD23	1.74	0.52
2:J:92:PHE:HA	2:J:95:ALA:HB3	1.90	0.52
4:L:207:ASN:O	4:L:210:ARG:HB2	2.09	0.52
1:A:184:ALA:HB1	1:A:200:LYS:O	2.09	0.52
1:A:454:ASN:HA	1:F:232:ARG:NH2	2.25	0.52
1:B:533:ARG:HD2	1:C:711:LEU:HD13	1.92	0.52
1:C:46:ILE:HD12	1:C:174:VAL:HG21	1.92	0.52
1:D:543:GLY:N	1:D:549:LYS:HD3	2.22	0.52
1:D:681:GLU:HG2	1:D:691:ARG:NH1	2.25	0.52
1:D:690:GLU:O	1:D:693:THR:OG1	2.24	0.52
1:F:538:SER:OG	1:F:661:PHE:HD1	1.91	0.52
2:H:80:ASP:OD2	5:M:191:ARG:NH2	2.42	0.52
5:M:198:ARG:O	5:M:202:MET:HE2	2.09	0.52
1:A:300:ALA:HA	1:A:303:ARG:HG2	1.90	0.52
1:A:611:TYR:CE2	1:A:651:VAL:HG11	2.45	0.52
1:A:677:LEU:HG	1:A:695:ALA:HB2	1.90	0.52
1:A:686:PHE:O	1:A:691:ARG:NH2	2.43	0.52
1:C:686:PHE:CE1	1:C:714:ILE:HG23	2.44	0.52
1:C:690:GLU:CB	1:C:726:VAL:HG21	2.40	0.52
1:E:136:LEU:N	1:E:136:LEU:HD23	2.25	0.52
1:E:653:GLN:OE1	1:E:658:LEU:HD23	2.09	0.52
2:G:101:ILE:HG21	2:G:135:LEU:HD11	1.92	0.52
3:K:82:ALA:HB1	3:K:86:ARG:HH12	1.75	0.52
1:A:531:SER:O	1:A:639:LYS:HE2	2.10	0.52
1:C:20:ASN:ND2	1:C:66:GLN:HE21	2.08	0.52
1:E:128:GLN:O	1:E:176:LEU:HD12	2.10	0.52
1:F:309:ALA:HA	1:F:312:GLU:OE1	2.10	0.52
1:F:503:ILE:HG22	1:F:506:GLY:H	1.73	0.52
2:H:124:HIS:HE1	2:H:147:GLN:HB3	1.75	0.52
4:L:233:ILE:O	4:L:237:VAL:HG23	2.10	0.52
1:B:26:GLU:HG2	1:B:51:THR:HB	1.92	0.52
1:E:516:ARG:O	1:E:519:ASP:OD1	2.27	0.52
3:K:59:LYS:HD3	5:M:178:ILE:HB	1.91	0.52
1:B:128:GLN:O	1:B:176:LEU:HD12	2.10	0.52
1:C:658:LEU:HD11	1:C:664:THR:HG21	1.90	0.52
1:D:721:ASP:O	1:D:725:ARG:HG3	2.09	0.52
1:E:289:GLU:C	1:E:291:LEU:H	2.14	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:508:ILE:C	1:F:509:LYS:HD3	2.34	0.52
2:G:197:LEU:HD22	5:M:45:ARG:CZ	2.40	0.52
2:H:69:ALA:HB1	2:H:85:PHE:CE1	2.45	0.52
2:I:216:ILE:HG13	2:I:218:MET:H	1.75	0.52
2:J:108:ILE:HD12	2:J:127:ILE:HD12	1.91	0.52
5:M:149:ASN:O	5:M:153:VAL:HG23	2.09	0.52
1:A:650:ASP:OD1	1:A:650:ASP:N	2.43	0.51
1:C:247:GLN:HA	1:D:417:HIS:CD2	2.45	0.51
1:C:331:ASP:HA	1:C:379:ILE:CD1	2.41	0.51
1:D:18:LEU:HA	1:D:137:VAL:HG23	1.91	0.51
1:D:593:TYR:OH	1:D:632:LYS:HD2	2.10	0.51
1:F:307:ALA:HA	1:F:310:GLU:HG2	1.92	0.51
1:F:589:PHE:CD2	1:F:629:LEU:HD22	2.45	0.51
1:F:608:LEU:HD12	1:F:609:LEU:N	2.24	0.51
2:I:49:ALA:HB2	2:I:64:ALA:HB3	1.91	0.51
2:J:219:LEU:HD12	2:J:223:LEU:HB2	1.92	0.51
2:G:231:LEU:HB2	2:G:234:ALA:CB	2.40	0.51
2:H:40:GLU:O	2:H:44:ILE:HG12	2.10	0.51
2:I:182:ILE:O	2:I:186:GLU:HG2	2.11	0.51
4:L:202:ILE:CD1	5:M:25:SER:HB3	2.40	0.51
1:A:101:PHE:HE1	1:A:193:LEU:HB2	1.75	0.51
1:C:560:SER:HB2	1:C:562:PHE:CE1	2.45	0.51
1:E:327:PHE:HB2	1:E:330:ILE:CG2	2.39	0.51
2:H:38:ILE:CD1	2:H:71:LEU:HB3	2.38	0.51
2:H:118:THR:O	2:H:122:LYS:HG2	2.09	0.51
2:H:159:SER:OG	3:K:54:LEU:HB3	2.10	0.51
1:C:24:VAL:O	1:C:51:THR:HA	2.11	0.51
1:D:95:MET:HG3	1:D:152:ILE:HG12	1.93	0.51
1:D:143:LYS:HB3	1:D:145:PHE:HE1	1.74	0.51
1:D:258:LEU:HB2	1:D:395:ILE:HD11	1.91	0.51
1:E:236:ALA:O	1:E:239:VAL:HG12	2.09	0.51
1:F:236:ALA:O	1:F:239:VAL:HG12	2.11	0.51
1:F:327:PHE:CZ	1:F:369:VAL:HG21	2.46	0.51
2:H:167:LYS:HE2	2:H:171:TYR:HE2	1.74	0.51
1:A:231:PHE:CE1	1:A:235:PHE:HE2	2.28	0.51
1:A:676:LEU:CD1	1:A:710:LEU:HD11	2.40	0.51
1:C:383:LEU:HD22	1:C:388:ARG:HD2	1.93	0.51
1:D:509:LYS:HE2	1:D:515:THR:HG22	1.92	0.51
1:D:609:LEU:CD1	1:D:611:TYR:HB2	2.41	0.51
2:G:167:LYS:HE2	2:G:171:TYR:HE2	1.75	0.51
2:H:57:ASN:O	2:H:59:SER:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:72:HIS:CE1	2:H:80:ASP:HB2	2.42	0.51
3:K:36:GLN:HA	4:L:205:LEU:HD13	1.92	0.51
5:M:46:THR:O	5:M:50:LEU:HG	2.09	0.51
1:D:527:GLN:NE2	1:E:715:GLU:HG3	2.24	0.51
1:E:284:VAL:O	1:E:326:ILE:HG12	2.09	0.51
1:F:101:PHE:CB	1:F:107:ILE:HG12	2.40	0.51
2:G:266:TYR:C	2:G:268:SER:H	2.19	0.51
2:I:142:ILE:HG23	2:I:168:VAL:HG13	1.93	0.51
2:I:219:LEU:HB2	2:I:222:LYS:CB	2.40	0.51
1:B:136:LEU:N	1:B:136:LEU:HD23	2.26	0.51
1:C:101:PHE:CD2	1:C:107:ILE:HA	2.46	0.51
1:C:728:LYS:HE3	1:C:732:LEU:HD21	1.93	0.51
1:D:657:MET:HE2	1:D:661:PHE:CZ	2.45	0.51
2:J:244:MET:O	2:J:248:LEU:HG	2.10	0.51
3:K:77:PHE:CE2	4:L:247:ALA:HB1	2.46	0.51
5:M:25:SER:O	5:M:29:THR:HG23	2.11	0.51
5:M:28:SER:HA	5:M:31:ARG:CZ	2.41	0.51
1:D:407:LEU:HB2	1:D:426:ILE:HG23	1.92	0.51
1:D:604:ASP:HB3	1:D:607:ARG:HB2	1.92	0.51
2:H:67:GLN:O	2:H:71:LEU:HG	2.11	0.51
2:H:127:ILE:HG23	2:H:131:TYR:CE1	2.46	0.51
1:A:222:GLY:O	1:A:224:ASP:N	2.43	0.51
1:A:246:GLU:O	1:B:413:ARG:NH1	2.41	0.51
1:C:45:TYR:CE2	1:C:70:ALA:HA	2.45	0.51
1:D:98:GLU:HB3	1:D:148:LEU:HB3	1.93	0.51
1:E:503:ILE:HG12	1:E:507:ILE:HD11	1.93	0.51
1:F:222:GLY:HA3	1:F:399:ASP:OD2	2.11	0.51
1:F:524:LEU:HD13	1:F:539:VAL:HG22	1.91	0.51
2:G:53:LYS:HE3	2:H:117:PHE:CE2	2.46	0.51
2:G:235:PHE:CB	5:M:31:ARG:HG2	2.41	0.51
2:I:124:HIS:CE1	2:I:147:GLN:HB3	2.42	0.51
1:B:578:GLU:HG3	1:B:619:SER:HB2	1.93	0.51
1:C:611:TYR:CZ	1:C:651:VAL:HG11	2.45	0.51
1:E:263:GLY:O	1:E:439:ALA:HB3	2.11	0.51
1:E:352:ASN:HA	1:E:355:LEU:HD12	1.93	0.51
1:E:436:PHE:HB3	1:E:440:GLU:CB	2.41	0.51
2:G:78:LYS:HB3	2:G:110:ILE:HG23	1.92	0.51
2:G:179:GLN:O	2:G:182:ILE:HG12	2.11	0.51
2:J:188:VAL:HG13	2:J:205:TYR:CD2	2.46	0.51
3:K:53:VAL:CG2	4:L:226:GLN:HE22	2.24	0.51
5:M:17:ARG:O	5:M:21:LEU:HG	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:SER:CB	1:B:288:PRO:HD3	2.40	0.50
1:A:628:VAL:CG1	1:B:571:ASP:HA	2.41	0.50
1:A:709:LYS:HE2	1:A:709:LYS:HA	1.93	0.50
1:C:233:ARG:CZ	1:C:233:ARG:HB2	2.41	0.50
1:C:386:PRO:HA	1:C:390:GLU:CA	2.35	0.50
1:E:184:ALA:HB1	1:E:200:LYS:O	2.10	0.50
1:E:260:GLY:HA3	1:E:266:LYS:HD3	1.93	0.50
1:E:310:GLU:OE2	1:E:357:LYS:NZ	2.44	0.50
1:F:522:GLU:OE2	1:F:526:GLN:HG2	2.10	0.50
4:L:226:GLN:HA	4:L:229:MET:CE	2.40	0.50
5:M:200:THR:HG22	5:M:200:THR:O	2.12	0.50
1:B:540:LEU:HD11	1:B:649:LYS:HZ2	1.75	0.50
1:C:730:LEU:O	1:C:734:ARG:HG3	2.11	0.50
1:D:190:ASN:HB3	1:D:316:LEU:HG	1.93	0.50
1:F:258:LEU:CB	1:F:395:ILE:HD11	2.41	0.50
2:I:230:GLU:HG3	2:I:237:ASP:CB	2.40	0.50
2:J:212:CYS:SG	2:J:279:MET:HE1	2.51	0.50
1:A:673:GLY:O	1:A:677:LEU:HD22	2.10	0.50
1:A:721:ASP:O	1:A:725:ARG:HG3	2.12	0.50
1:D:687:LYS:O	1:D:691:ARG:HG3	2.11	0.50
1:E:620:ASN:HD21	1:F:617:ARG:HB3	1.77	0.50
1:E:624:GLN:CD	1:F:610:ASP:OD1	2.53	0.50
2:G:117:PHE:CD2	2:J:53:LYS:HE3	2.46	0.50
2:G:188:VAL:HG13	2:G:205:TYR:CD2	2.44	0.50
4:L:240:ALA:O	4:L:244:VAL:HG23	2.12	0.50
1:B:264:CYS:HA	1:B:437:SER:HB2	1.93	0.50
1:B:686:PHE:HE1	1:B:714:ILE:HG23	1.76	0.50
1:D:11:CYS:SG	1:D:17:SER:HB2	2.51	0.50
1:D:91:CYS:SG	1:D:155:MET:HE2	2.52	0.50
1:D:233:ARG:HA	1:E:450:SER:HB2	1.94	0.50
1:D:611:TYR:CE2	1:D:613:PRO:HA	2.47	0.50
1:E:73:SER:O	1:E:76:GLN:HG2	2.11	0.50
1:E:242:PRO:HD2	1:E:243:GLU:H	1.76	0.50
1:E:581:LYS:NZ	1:E:610:ASP:OD1	2.41	0.50
1:F:632:LYS:HD2	1:F:633:ALA:H	1.76	0.50
2:G:104:LEU:HB3	2:G:127:ILE:CD1	2.41	0.50
4:L:226:GLN:HA	4:L:229:MET:HE2	1.93	0.50
1:A:610:ASP:HA	1:F:624:GLN:NE2	2.27	0.50
1:B:542:GLU:OE1	1:B:649:LYS:HD3	2.12	0.50
1:B:552:LEU:O	1:B:556:ILE:HG13	2.11	0.50
1:C:236:ALA:HB1	1:D:453:MET:CB	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:445:VAL:HG12	1:C:449:GLN:HE22	1.77	0.50
1:D:268:LEU:HA	1:D:271:ARG:CD	2.42	0.50
1:D:713:LEU:HD21	1:D:732:LEU:HB3	1.93	0.50
1:E:281:GLU:N	1:E:282:PRO:HA	2.27	0.50
1:F:605:ILE:HD11	1:F:644:GLY:HA3	1.93	0.50
2:G:200:TYR:HB3	4:L:217:MET:CE	2.38	0.50
2:H:277:THR:O	2:H:281:LEU:HB2	2.12	0.50
2:I:79:HIS:CD2	5:M:69:GLN:HG3	2.47	0.50
3:K:39:VAL:CG1	4:L:209:ILE:HG12	2.41	0.50
4:L:219:MET:O	4:L:223:VAL:HG23	2.11	0.50
1:A:688:ASP:OD1	1:A:689:LYS:N	2.44	0.50
1:B:20:ASN:ND2	1:B:66:GLN:HE21	2.09	0.50
1:B:531:SER:CB	1:B:639:LYS:HD3	2.40	0.50
1:B:589:PHE:CE1	1:B:600:VAL:HG11	2.47	0.50
1:C:688:ASP:OD1	1:C:691:ARG:NH2	2.31	0.50
1:D:303:ARG:HD3	1:D:353:GLN:CD	2.37	0.50
1:D:312:GLU:CG	1:D:313:GLN:N	2.74	0.50
1:D:573:MET:CE	1:D:585:MET:HE3	2.42	0.50
1:E:666:HIS:CD2	1:E:668:PRO:HD3	2.46	0.50
1:F:256:ILE:CG1	1:F:370:ILE:HG22	2.35	0.50
1:F:512:ASP:OD1	1:F:513:PRO:HD3	2.12	0.50
1:F:609:LEU:HD21	1:F:623:LEU:HD13	1.93	0.50
2:H:75:LEU:O	2:H:76:GLN:HB3	2.12	0.50
2:I:178:TYR:OH	2:I:282:ARG:HG2	2.12	0.50
2:J:235:PHE:CG	5:M:152:GLN:HA	2.46	0.50
1:A:428:GLU:O	1:A:431:VAL:HG12	2.11	0.50
1:A:611:TYR:HA	1:A:618:PHE:HB3	1.94	0.50
1:B:309:ALA:HB1	1:B:367:ILE:HG21	1.94	0.50
1:D:24:VAL:O	1:D:51:THR:HA	2.12	0.50
1:D:567:ILE:HG23	1:D:601:VAL:HB	1.94	0.50
1:D:589:PHE:CE2	1:D:629:LEU:HD13	2.47	0.50
1:E:236:ALA:HA	1:E:239:VAL:HG12	1.94	0.50
2:I:195:SER:C	2:I:197:LEU:H	2.19	0.50
1:A:198:LYS:HB2	1:A:198:LYS:NZ	2.26	0.50
1:A:227:PHE:CE1	1:A:273:ILE:HD13	2.46	0.50
1:A:502:TYR:O	1:A:551:ALA:HB1	2.11	0.50
1:B:352:ASN:HA	1:B:355:LEU:HD12	1.93	0.50
1:C:91:CYS:HB3	1:C:155:MET:HE2	1.94	0.50
1:C:136:LEU:N	1:C:136:LEU:HD23	2.26	0.50
1:F:559:GLU:HA	1:F:559:GLU:OE1	2.11	0.50
2:G:233:PRO:HB2	2:J:271:ARG:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:184:ILE:O	2:J:188:VAL:HG12	2.12	0.50
3:K:32:LEU:HD11	4:L:202:ILE:HG12	1.94	0.50
1:A:103:GLN:O	1:A:107:ILE:HG13	2.11	0.50
1:A:286:ASN:HB2	1:A:327:PHE:CB	2.41	0.50
1:A:315:ARG:O	1:A:316:LEU:HD12	2.12	0.50
1:A:509:LYS:HE3	1:A:514:VAL:HG12	1.94	0.50
1:A:597:LEU:C	1:A:597:LEU:HD23	2.36	0.50
1:B:98:GLU:HB3	1:B:148:LEU:HB3	1.93	0.50
1:C:388:ARG:NH1	1:C:388:ARG:HB2	2.27	0.50
1:C:569:SER:HB3	1:C:572:LYS:HG2	1.94	0.50
1:D:560:SER:HB2	1:D:562:PHE:CD1	2.46	0.50
1:F:18:LEU:HA	1:F:137:VAL:HG23	1.93	0.50
1:F:136:LEU:N	1:F:136:LEU:HD23	2.26	0.50
1:F:710:LEU:O	1:F:714:ILE:HG13	2.12	0.50
5:M:75:GLU:O	5:M:79:LYS:HG2	2.12	0.50
1:A:242:PRO:HD2	1:A:243:GLU:OE1	2.11	0.49
1:A:283:LYS:HA	1:A:324:ILE:O	2.12	0.49
1:A:596:GLN:HA	1:A:638:ARG:HD3	1.94	0.49
1:E:428:GLU:O	1:E:431:VAL:HG12	2.12	0.49
1:E:506:GLY:O	1:E:508:ILE:N	2.45	0.49
1:E:673:GLY:HA3	1:E:698:VAL:HB	1.93	0.49
2:G:185:TYR:HA	2:G:188:VAL:HG12	1.94	0.49
1:A:575:GLY:HA3	1:F:586:LYS:CE	2.43	0.49
1:B:265:GLY:O	1:B:268:LEU:HG	2.11	0.49
1:B:631:LYS:NZ	1:C:604:ASP:OD2	2.45	0.49
1:C:349:THR:O	1:C:352:ASN:HB3	2.12	0.49
1:C:688:ASP:HA	1:C:691:ARG:NH1	2.27	0.49
1:D:149:VAL:HG11	1:D:152:ILE:HD11	1.93	0.49
1:D:690:GLU:O	1:D:694:ILE:HG13	2.12	0.49
1:F:720:MET:HB3	1:F:724:TYR:HB2	1.94	0.49
2:H:256:VAL:HG21	2:H:288:GLN:HG3	1.94	0.49
2:J:216:ILE:HG13	2:J:218:MET:H	1.76	0.49
1:A:114:THR:HG21	1:A:200:LYS:HG2	1.95	0.49
1:A:247:GLN:O	1:B:413:ARG:NH1	2.46	0.49
1:A:611:TYR:CE1	1:A:616:PRO:HB2	2.46	0.49
1:B:315:ARG:HG3	1:B:316:LEU:HD12	1.94	0.49
1:C:242:PRO:HD2	1:C:243:GLU:H	1.77	0.49
1:D:564:PHE:HB3	1:D:598:SER:CB	2.42	0.49
1:D:628:VAL:HG11	1:E:574:ILE:CG2	2.42	0.49
1:E:267:THR:HA	1:E:372:MET:SD	2.52	0.49
2:G:149:ALA:HB2	2:G:164:CYS:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:159:SER:HB3	3:K:58:GLN:OE1	2.11	0.49
1:A:153:GLU:OE1	1:A:169:ARG:HD3	2.13	0.49
1:A:540:LEU:HD12	1:A:644:GLY:O	2.13	0.49
1:A:624:GLN:OE1	1:A:624:GLN:HA	2.13	0.49
1:B:289:GLU:C	1:B:291:LEU:N	2.71	0.49
1:B:380:ASP:OD1	1:B:382:ALA:N	2.41	0.49
1:B:549:LYS:NZ	1:B:647:SER:HA	2.26	0.49
1:C:95:MET:HG3	1:C:152:ILE:HG12	1.94	0.49
1:C:657:MET:HE3	1:C:661:PHE:CZ	2.47	0.49
1:D:527:GLN:HA	1:E:719:GLN:HG3	1.94	0.49
1:D:528:THR:CB	1:D:641:LEU:HD12	2.42	0.49
1:F:184:ALA:HB1	1:F:200:LYS:O	2.12	0.49
1:F:257:LEU:HB2	1:F:389:LEU:HD13	1.95	0.49
2:G:243:LEU:HD22	2:G:266:TYR:CD2	2.48	0.49
2:H:260:THR:HG21	2:H:284:LYS:HE3	1.93	0.49
2:J:128:ALA:HB2	2:J:144:HIS:HB2	1.93	0.49
1:A:397:LEU:CB	1:A:398:PRO:CD	2.90	0.49
1:A:652:LEU:HA	1:A:655:MET:SD	2.52	0.49
1:A:719:GLN:HG2	1:F:523:LEU:HD21	1.92	0.49
1:F:98:GLU:HB3	1:F:148:LEU:HB3	1.94	0.49
1:F:113:ASP:O	1:F:117:MET:HG3	2.13	0.49
2:G:123:HIS:O	2:G:127:ILE:HG12	2.12	0.49
3:K:55:GLU:HB3	3:K:59:LYS:NZ	2.28	0.49
1:A:69:TRP:NE1	1:A:134:GLN:HA	2.27	0.49
1:B:353:GLN:OE1	1:C:288:PRO:HG2	2.13	0.49
1:B:414:MET:HE2	1:B:414:MET:HA	1.94	0.49
1:B:533:ARG:HG3	1:B:534:THR:N	2.25	0.49
1:E:397:LEU:HD22	1:E:398:PRO:HD2	1.95	0.49
1:F:261:PRO:O	1:F:264:CYS:HB2	2.11	0.49
1:C:315:ARG:HB2	1:C:316:LEU:HD12	1.95	0.49
1:D:116:LYS:HB3	1:D:116:LYS:HZ3	1.77	0.49
1:E:586:LYS:NZ	1:F:575:GLY:HA3	2.28	0.49
1:F:326:ILE:HG22	1:F:370:ILE:CG1	2.41	0.49
1:F:686:PHE:CE1	1:F:714:ILE:HG23	2.48	0.49
2:G:239:ARG:HH11	4:L:210:ARG:HH12	1.59	0.49
2:H:45:TYR:HB2	2:H:68:ALA:HB2	1.94	0.49
2:H:147:GLN:HG2	2:H:151:TYR:CE2	2.47	0.49
2:I:21:VAL:HG21	2:I:71:LEU:HD22	1.94	0.49
1:B:236:ALA:O	1:B:239:VAL:HG12	2.13	0.49
1:B:606:GLU:OE1	1:B:606:GLU:N	2.45	0.49
1:C:128:GLN:O	1:C:176:LEU:HD12	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:533:ARG:HB2	1:D:715:GLU:OE1	2.13	0.49
1:D:257:LEU:HB2	1:D:389:LEU:HD13	1.95	0.49
1:D:536:LEU:HD21	1:D:630:LEU:O	2.12	0.49
1:E:244:ILE:HG21	1:F:453:MET:HE1	1.94	0.49
1:E:598:SER:O	1:E:640:LEU:HA	2.13	0.49
2:G:182:ILE:CG2	2:G:212:CYS:HB2	2.42	0.49
2:G:244:MET:O	2:G:248:LEU:HG	2.13	0.49
2:J:47:ARG:O	2:J:50:ASN:HB3	2.13	0.49
1:A:247:GLN:O	1:B:414:MET:CE	2.60	0.49
1:A:531:SER:OG	1:B:715:GLU:OE1	2.30	0.49
1:C:624:GLN:CD	1:D:610:ASP:HB2	2.36	0.49
1:D:627:LEU:CD2	1:D:657:MET:HG3	2.42	0.49
1:D:688:ASP:O	1:D:692:THR:HG23	2.12	0.49
1:E:569:SER:HB2	1:E:572:LYS:HG2	1.95	0.49
1:F:38:ARG:HG2	1:F:38:ARG:HH11	1.78	0.49
1:F:324:ILE:HG12	1:F:368:LEU:HD11	1.94	0.49
1:F:436:PHE:HB3	1:F:440:GLU:HB2	1.95	0.49
1:A:398:PRO:HG3	1:A:436:PHE:C	2.38	0.49
1:A:503:ILE:HG22	1:A:506:GLY:H	1.78	0.49
1:C:512:ASP:N	1:C:513:PRO:CD	2.76	0.49
1:C:586:LYS:NZ	1:D:574:ILE:O	2.40	0.49
1:D:242:PRO:HD2	1:D:243:GLU:H	1.78	0.49
1:D:552:LEU:O	1:D:556:ILE:HG13	2.13	0.49
1:F:653:GLN:HA	1:F:658:LEU:HB3	1.94	0.49
2:I:210:ALA:HB3	2:I:244:MET:HE3	1.94	0.49
2:I:212:CYS:SG	2:I:279:MET:HE1	2.53	0.49
2:J:112:THR:HG23	2:J:117:PHE:CE1	2.45	0.49
5:M:41:ASP:O	5:M:45:ARG:HD3	2.13	0.49
1:A:231:PHE:CD2	1:A:235:PHE:HD2	2.31	0.48
1:A:457:ILE:HD12	1:F:232:ARG:NH2	2.28	0.48
1:A:598:SER:O	1:A:640:LEU:HA	2.13	0.48
1:C:95:MET:HE3	1:C:97:ILE:HD11	1.95	0.48
1:C:231:PHE:CE1	1:C:235:PHE:HD2	2.30	0.48
1:C:284:VAL:HB	1:C:325:ILE:HA	1.95	0.48
1:D:686:PHE:HB2	1:D:691:ARG:CG	2.43	0.48
1:E:697:GLN:HG3	1:E:730:LEU:CD1	2.43	0.48
2:H:164:CYS:O	2:H:168:VAL:HG23	2.13	0.48
2:H:177:GLN:OE1	2:H:180:LYS:HD3	2.13	0.48
2:I:50:ASN:HD21	2:J:115:GLY:CA	2.25	0.48
2:I:118:THR:O	2:I:122:LYS:HG2	2.13	0.48
2:I:167:LYS:HE2	2:I:171:TYR:HE2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:LEU:O	1:A:389:LEU:HB2	2.13	0.48
1:B:440:GLU:O	1:B:444:LEU:HG	2.13	0.48
1:B:533:ARG:HG3	1:B:534:THR:HG23	1.95	0.48
1:D:602:VAL:O	1:D:644:GLY:HA2	2.13	0.48
1:F:236:ALA:HA	1:F:239:VAL:CG1	2.43	0.48
2:G:266:TYR:CZ	2:G:270:SER:HB2	2.48	0.48
2:I:246:LYS:HZ3	2:I:258:SER:HB3	1.78	0.48
5:M:142:ARG:O	5:M:146:MET:HB2	2.12	0.48
1:A:16:LEU:HD11	1:A:52:HIS:HD2	1.78	0.48
1:A:322:LEU:HD12	1:A:323:HIS:N	2.28	0.48
1:A:612:VAL:HG11	1:F:618:PHE:HZ	1.78	0.48
1:B:23:VAL:HG12	1:B:55:VAL:CG2	2.43	0.48
1:B:45:TYR:CE2	1:B:70:ALA:HA	2.49	0.48
1:C:122:ILE:O	1:C:126:ASN:HB3	2.12	0.48
1:D:652:LEU:HD13	1:D:657:MET:HB3	1.94	0.48
1:D:681:GLU:HG2	1:D:691:ARG:CZ	2.43	0.48
1:E:705:ILE:HD13	1:E:710:LEU:HD13	1.95	0.48
1:A:196:ILE:HD12	1:A:316:LEU:HD22	1.96	0.48
1:A:403:ARG:O	1:A:407:LEU:HG	2.13	0.48
1:B:43:HIS:HB3	1:B:45:TYR:HE1	1.79	0.48
1:B:284:VAL:O	1:B:326:ILE:HG12	2.13	0.48
1:C:322:LEU:HD12	1:C:324:ILE:HD11	1.94	0.48
1:D:564:PHE:HB3	1:D:598:SER:HB3	1.95	0.48
1:D:606:GLU:O	1:D:610:ASP:N	2.46	0.48
1:E:307:ALA:HA	1:E:310:GLU:HG2	1.95	0.48
2:G:118:THR:O	2:G:122:LYS:HG2	2.12	0.48
2:I:69:ALA:HB1	2:I:85:PHE:CE1	2.48	0.48
3:K:35:THR:O	3:K:39:VAL:HG23	2.13	0.48
5:M:163:MET:O	5:M:167:MET:HG2	2.13	0.48
1:B:67:ARG:HH11	1:B:67:ARG:HB2	1.79	0.48
1:C:656:GLU:OE2	1:D:648:ARG:NH1	2.46	0.48
1:E:63:SER:C	1:E:67:ARG:HE	2.22	0.48
1:F:539:VAL:CB	1:F:643:ILE:HG12	2.39	0.48
2:H:256:VAL:HG21	2:H:288:GLN:CG	2.43	0.48
4:L:237:VAL:CG2	5:M:60:VAL:HG13	2.43	0.48
1:A:411:THR:HG21	1:A:426:ILE:HD11	1.95	0.48
1:A:436:PHE:HA	1:A:440:GLU:OE2	2.14	0.48
1:B:36:ILE:HG23	1:B:36:ILE:O	2.13	0.48
1:B:64:LEU:O	1:B:68:LYS:HG3	2.14	0.48
1:B:256:ILE:O	1:B:370:ILE:HA	2.14	0.48
1:B:528:THR:HG21	1:B:641:LEU:HD13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:LEU:HB2	1:C:67:ARG:HH21	1.79	0.48
1:C:611:TYR:HE1	1:C:616:PRO:HB2	1.78	0.48
1:D:402:GLY:HA2	1:D:405:GLN:OE1	2.14	0.48
1:D:655:MET:O	1:D:656:GLU:HB2	2.13	0.48
1:E:726:VAL:O	1:E:730:LEU:HG	2.14	0.48
2:G:246:LYS:NZ	2:G:258:SER:HB3	2.29	0.48
2:H:160:SER:OG	3:K:58:GLN:NE2	2.41	0.48
3:K:85:LYS:HG3	3:K:89:TRP:HE3	1.79	0.48
1:B:259:TYR:C	1:B:395:ILE:HD13	2.38	0.48
1:C:612:VAL:CG2	1:C:613:PRO:HD2	2.44	0.48
1:D:582:CYS:O	1:D:586:LYS:HG3	2.14	0.48
1:F:281:GLU:N	1:F:282:PRO:HA	2.29	0.48
1:F:542:GLU:O	1:F:666:HIS:ND1	2.46	0.48
1:F:658:LEU:HA	1:F:661:PHE:HD2	1.79	0.48
2:G:231:LEU:HD22	2:J:271:ARG:NH1	2.29	0.48
2:I:81:ALA:O	2:I:85:PHE:HD1	1.95	0.48
1:A:423:ASP:O	1:A:479:ASP:N	2.46	0.48
1:A:715:GLU:HG3	1:F:527:GLN:NE2	2.27	0.48
1:B:610:ASP:CG	1:B:610:ASP:O	2.56	0.48
1:D:542:GLU:OE2	1:D:649:LYS:HD2	2.14	0.48
1:E:248:MET:HA	1:F:449:GLN:OE1	2.13	0.48
1:F:653:GLN:HB3	1:F:658:LEU:HD23	1.96	0.48
2:G:17:ALA:O	2:G:21:VAL:HG12	2.14	0.48
2:G:101:ILE:HG13	2:G:102:ASN:H	1.79	0.48
2:G:239:ARG:HH11	4:L:210:ARG:NH1	2.10	0.48
2:J:200:TYR:O	2:J:203:LYS:HE2	2.13	0.48
1:B:67:ARG:HH11	1:B:67:ARG:CB	2.27	0.48
1:B:67:ARG:HB3	2:I:218:MET:SD	2.53	0.48
1:B:545:PRO:O	1:B:546:HIS:HB2	2.13	0.48
1:C:122:ILE:HD11	1:C:183:VAL:HG23	1.96	0.48
1:C:576:PHE:HB3	1:C:580:ALA:HB3	1.96	0.48
1:D:358:ILE:CD1	1:D:388:ARG:HB3	2.42	0.48
1:D:530:ASN:ND2	1:E:719:GLN:OE1	2.40	0.48
1:D:609:LEU:HD12	1:D:611:TYR:H	1.77	0.48
1:E:538:SER:HG	1:E:661:PHE:HA	1.79	0.48
1:E:721:ASP:HB2	1:E:724:TYR:CD2	2.48	0.48
2:H:281:LEU:O	2:H:285:LYS:HG3	2.14	0.48
2:I:138:VAL:O	2:I:142:ILE:HG13	2.14	0.48
1:A:97:ILE:HG21	1:A:147:LEU:HD22	1.94	0.48
1:B:74:ILE:HG13	2:I:218:MET:CE	2.44	0.48
1:B:232:ARG:O	1:B:236:ALA:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:436:PHE:CD1	1:C:436:PHE:N	2.82	0.48
1:C:590:ASP:HA	1:C:593:TYR:HD2	1.77	0.48
1:D:184:ALA:HB1	1:D:200:LYS:O	2.14	0.48
1:F:407:LEU:O	1:F:411:THR:OG1	2.27	0.48
2:J:232:PHE:O	2:J:234:ALA:N	2.47	0.48
1:A:104:LYS:HA	1:A:107:ILE:HG13	1.94	0.47
1:A:113:ASP:OD2	1:A:316:LEU:HD11	2.14	0.47
1:A:258:LEU:HD12	1:A:258:LEU:O	2.13	0.47
1:A:445:VAL:O	1:A:449:GLN:HG2	2.14	0.47
1:A:453:MET:C	1:F:232:ARG:HH22	2.22	0.47
1:B:541:LEU:HA	1:B:665:ILE:O	2.14	0.47
1:B:593:TYR:O	1:B:638:ARG:NE	2.46	0.47
1:C:265:GLY:O	1:C:268:LEU:HG	2.14	0.47
1:D:499:TYR:N	1:D:499:TYR:CD1	2.80	0.47
1:D:635:PRO:O	1:D:638:ARG:HB2	2.14	0.47
1:F:286:ASN:OD1	1:F:327:PHE:HD1	1.97	0.47
1:F:440:GLU:O	1:F:444:LEU:HG	2.14	0.47
1:F:635:PRO:HB2	1:F:638:ARG:NH1	2.29	0.47
2:G:266:TYR:C	2:G:268:SER:N	2.72	0.47
2:I:287:ILE:O	2:I:291:GLU:HG3	2.13	0.47
2:J:223:LEU:O	2:J:227:LYS:HG3	2.14	0.47
1:B:516:ARG:O	1:B:519:ASP:OD1	2.32	0.47
1:B:576:PHE:HB2	1:B:581:LYS:HG3	1.96	0.47
1:C:237:SER:OG	1:C:252:HIS:ND1	2.41	0.47
1:C:270:ALA:O	1:C:273:ILE:HG22	2.15	0.47
1:C:513:PRO:HA	1:C:516:ARG:HG2	1.95	0.47
1:D:578:GLU:OE1	1:D:621:LEU:HD13	2.15	0.47
1:E:64:LEU:N	1:E:67:ARG:NH2	2.59	0.47
1:E:404:LEU:HG	1:E:426:ILE:HG22	1.96	0.47
1:F:34:HIS:HB2	1:F:83:TYR:O	2.14	0.47
1:F:655:MET:O	1:F:656:GLU:CG	2.62	0.47
2:I:147:GLN:HG2	2:I:151:TYR:CE2	2.48	0.47
2:J:40:GLU:O	2:J:44:ILE:HG12	2.14	0.47
2:J:243:LEU:HD13	2:J:266:TYR:HB2	1.95	0.47
1:A:34:HIS:HB2	1:A:83:TYR:O	2.14	0.47
1:A:231:PHE:CE2	1:A:235:PHE:HD2	2.33	0.47
1:A:347:HIS:N	1:A:348:ASP:HA	2.29	0.47
1:A:489:LYS:N	1:A:490:PRO:HD2	2.29	0.47
1:B:103:GLN:C	1:B:105:LYS:H	2.22	0.47
1:C:135:GLN:HG2	1:C:148:LEU:HD13	1.97	0.47
1:C:609:LEU:O	1:C:610:ASP:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:593:TYR:HB3	1:D:635:PRO:HD3	1.96	0.47
1:D:669:ASN:OD1	1:D:669:ASN:N	2.47	0.47
1:F:396:GLY:O	1:F:397:LEU:HG	2.14	0.47
2:G:21:VAL:HG23	2:G:38:ILE:HD13	1.95	0.47
2:H:232:PHE:HB2	2:H:233:PRO:HD3	1.96	0.47
5:M:36:VAL:HG23	5:M:37:GLU:N	2.29	0.47
1:A:100:ASP:O	1:A:146:GLY:N	2.48	0.47
1:D:101:PHE:CD2	1:D:107:ILE:HA	2.48	0.47
1:F:557:ALA:HB2	1:F:601:VAL:HG21	1.96	0.47
2:G:195:SER:C	2:G:197:LEU:N	2.72	0.47
2:J:188:VAL:HG22	2:J:205:TYR:HE2	1.79	0.47
1:A:64:LEU:O	1:A:68:LYS:HG3	2.15	0.47
1:A:91:CYS:O	1:A:154:ALA:HA	2.14	0.47
1:A:388:ARG:O	1:A:389:LEU:HD22	2.15	0.47
1:B:451:THR:HG22	1:B:455:ARG:HH21	1.79	0.47
1:C:618:PHE:HE1	1:C:620:ASN:OD1	1.97	0.47
1:D:265:GLY:O	1:D:268:LEU:HG	2.14	0.47
1:E:549:LYS:HD2	1:E:645:THR:HB	1.96	0.47
2:G:117:PHE:HD2	2:J:53:LYS:HE3	1.79	0.47
2:H:80:ASP:OD2	5:M:191:ARG:NH1	2.48	0.47
3:K:30:ARG:O	3:K:34:GLN:HB2	2.14	0.47
3:K:59:LYS:HE2	5:M:175:ASN:HB3	1.95	0.47
1:A:424:VAL:HG22	1:A:479:ASP:O	2.15	0.47
1:A:627:LEU:O	1:A:631:LYS:NZ	2.47	0.47
1:C:232:ARG:O	1:C:236:ALA:HB3	2.14	0.47
1:D:268:LEU:O	1:D:271:ARG:HG2	2.14	0.47
1:D:528:THR:HG22	1:D:597:LEU:HD11	1.95	0.47
1:D:690:GLU:HB2	1:D:726:VAL:CG2	2.44	0.47
1:E:303:ARG:CG	1:E:357:LYS:HE2	2.44	0.47
1:F:569:SER:O	1:F:572:LYS:HB2	2.14	0.47
2:G:276:LEU:O	2:G:280:LEU:HG	2.14	0.47
2:J:124:HIS:HE1	2:J:147:GLN:HB3	1.80	0.47
1:A:326:ILE:HG22	1:A:370:ILE:CG1	2.43	0.47
1:A:571:ASP:HA	1:A:574:ILE:HG23	1.95	0.47
1:A:617:ARG:HG3	1:A:617:ARG:NH1	2.29	0.47
1:B:523:LEU:HA	1:B:526:GLN:HG2	1.95	0.47
1:B:640:LEU:CD2	1:B:642:ILE:HG13	2.45	0.47
1:C:240:PHE:HZ	1:D:456:HIS:HB3	1.80	0.47
1:C:284:VAL:HG11	1:C:305:LEU:HD11	1.96	0.47
1:C:399:ASP:O	1:C:402:GLY:N	2.48	0.47
1:C:510:TRP:O	1:C:675:GLN:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:231:PHE:CD1	1:D:235:PHE:HD2	2.32	0.47
1:E:272:GLN:OE1	1:E:272:GLN:HA	2.15	0.47
1:E:406:ILE:HB	1:E:441:LEU:HD13	1.96	0.47
1:E:550:THR:HG23	1:E:603:ASP:OD1	2.14	0.47
1:E:633:ALA:HA	1:E:634:PRO:HD3	1.81	0.47
2:G:235:PHE:HB3	5:M:31:ARG:CG	2.45	0.47
2:H:243:LEU:HD22	2:H:266:TYR:CD2	2.49	0.47
2:I:72:HIS:HE1	2:I:80:ASP:HB2	1.80	0.47
2:I:102:ASN:HA	2:I:105:MET:HE3	1.96	0.47
2:J:203:LYS:NZ	2:J:236:SER:HB3	2.29	0.47
2:J:266:TYR:C	2:J:268:SER:H	2.21	0.47
2:J:281:LEU:O	2:J:285:LYS:HG3	2.15	0.47
3:K:70:LEU:CD1	5:M:192:ILE:HD12	2.43	0.47
4:L:248:VAL:O	4:L:252:LYS:HG3	2.15	0.47
1:A:215:PHE:N	1:A:231:PHE:CZ	2.83	0.47
1:B:85:PHE:HE2	1:B:174:VAL:HG22	1.79	0.47
1:B:499:TYR:HA	1:B:502:TYR:CE2	2.50	0.47
1:C:285:VAL:HA	1:C:326:ILE:HG13	1.97	0.47
1:C:353:GLN:HA	1:D:288:PRO:CG	2.44	0.47
1:C:511:GLY:CA	1:C:513:PRO:HD2	2.45	0.47
1:D:330:ILE:HD12	1:D:331:ASP:N	2.30	0.47
1:D:546:HIS:HB3	1:D:708:LYS:HB3	1.97	0.47
1:D:608:LEU:O	1:D:622:VAL:HG11	2.15	0.47
1:D:609:LEU:O	1:D:610:ASP:OD1	2.33	0.47
1:F:121:PHE:HD2	1:F:183:VAL:HG21	1.79	0.47
1:F:450:SER:O	1:F:453:MET:HB2	2.15	0.47
2:H:51:MET:O	2:H:54:MET:HB3	2.15	0.47
2:I:203:LYS:CE	5:M:161:ARG:HH12	2.21	0.47
1:B:388:ARG:O	1:B:389:LEU:HD23	2.15	0.47
1:E:172:ILE:HD12	1:E:174:VAL:O	2.15	0.47
1:E:563:PRO:HD2	1:E:597:LEU:O	2.15	0.47
1:F:428:GLU:O	1:F:431:VAL:HG12	2.15	0.47
2:I:116:ARG:NH1	5:M:65:ASN:ND2	2.63	0.47
4:L:237:VAL:HG21	5:M:60:VAL:HG22	1.96	0.47
5:M:156:ILE:O	5:M:160:LEU:HG	2.15	0.47
1:A:299:GLU:OE1	1:A:303:ARG:NH2	2.44	0.47
1:B:428:GLU:O	1:B:431:VAL:HG12	2.15	0.47
1:C:582:CYS:SG	1:C:621:LEU:HG	2.55	0.47
1:D:18:LEU:HA	1:D:137:VAL:CG2	2.44	0.47
1:D:581:LYS:O	1:D:585:MET:HG2	2.15	0.47
1:D:586:LYS:HG2	1:E:574:ILE:CD1	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:694:ILE:O	1:D:698:VAL:HG22	2.15	0.47
1:E:717:SER:OG	1:E:729:PHE:HB2	2.15	0.47
1:F:289:GLU:C	1:F:291:LEU:H	2.21	0.47
1:F:597:LEU:HA	1:F:639:LYS:O	2.15	0.47
2:H:63:ASN:O	2:H:67:GLN:HG3	2.14	0.47
2:I:75:LEU:O	2:I:76:GLN:HB2	2.15	0.47
5:M:178:ILE:HG22	5:M:182:MET:HE2	1.97	0.47
1:B:104:LYS:HA	1:B:107:ILE:HG13	1.96	0.46
1:B:319:ASN:HB3	1:B:320:SER:HB2	1.97	0.46
1:B:503:ILE:HD11	1:B:554:ALA:HB3	1.96	0.46
1:B:533:ARG:HD2	1:C:711:LEU:CD1	2.45	0.46
1:B:605:ILE:HD11	1:B:644:GLY:HA3	1.96	0.46
1:C:453:MET:O	1:C:457:ILE:HD12	2.14	0.46
1:C:555:LYS:O	1:C:559:GLU:HG2	2.15	0.46
1:C:593:TYR:CE2	1:C:632:LYS:NZ	2.83	0.46
1:D:627:LEU:CD1	1:E:607:ARG:HH12	2.28	0.46
1:F:46:ILE:HD12	1:F:174:VAL:HG21	1.97	0.46
2:G:124:HIS:HA	2:G:127:ILE:HG12	1.97	0.46
2:G:263:VAL:HG23	2:G:280:LEU:HD13	1.96	0.46
2:J:49:ALA:HB2	2:J:64:ALA:HB3	1.97	0.46
2:J:98:GLN:H	2:J:98:GLN:CD	2.23	0.46
1:A:45:TYR:CE2	1:A:70:ALA:HA	2.50	0.46
1:A:169:ARG:HH11	1:A:169:ARG:HG2	1.80	0.46
1:A:299:GLU:HG3	1:B:289:GLU:CB	2.45	0.46
1:A:407:LEU:O	1:A:411:THR:HG23	2.15	0.46
1:B:74:ILE:H	2:I:218:MET:CE	2.28	0.46
1:D:267:THR:HA	1:D:372:MET:SD	2.55	0.46
1:E:246:GLU:HG2	1:E:247:GLN:N	2.30	0.46
1:E:527:GLN:HA	1:F:719:GLN:CD	2.40	0.46
2:G:96:ASP:N	2:G:97:PRO:HD2	2.31	0.46
2:H:81:ALA:O	2:H:85:PHE:HD1	1.97	0.46
2:H:216:ILE:HG12	2:H:220:ASN:HB2	1.97	0.46
2:H:232:PHE:N	2:H:233:PRO:CD	2.78	0.46
2:J:182:ILE:CG2	2:J:212:CYS:HB2	2.45	0.46
5:M:74:ALA:O	5:M:78:LEU:HG	2.15	0.46
1:A:101:PHE:CE1	1:A:193:LEU:HD13	2.50	0.46
1:A:240:PHE:HD2	1:B:453:MET:SD	2.38	0.46
1:A:686:PHE:CE2	1:A:714:ILE:HG23	2.50	0.46
1:B:242:PRO:HD2	1:B:243:GLU:H	1.79	0.46
1:B:327:PHE:CE2	1:B:369:VAL:HG21	2.50	0.46
1:B:579:THR:O	1:B:583:GLN:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:677:LEU:O	1:B:681:GLU:HG3	2.15	0.46
1:E:241:PRO:HA	1:E:242:PRO:HA	1.62	0.46
2:H:162:ASN:O	2:H:166:LEU:HG	2.15	0.46
2:H:213:HIS:CE1	2:H:221:ALA:HB2	2.30	0.46
2:I:271:ARG:HA	2:I:271:ARG:HD3	1.75	0.46
3:K:39:VAL:HA	5:M:157:ILE:HG21	1.97	0.46
3:K:77:PHE:CZ	5:M:195:ALA:HB1	2.50	0.46
1:A:607:ARG:HD3	1:F:624:GLN:NE2	2.29	0.46
1:C:52:HIS:C	1:C:54:SER:H	2.24	0.46
1:C:194:ASN:ND2	1:C:316:LEU:CG	2.79	0.46
1:C:681:GLU:HG3	1:C:691:ARG:HD2	1.98	0.46
1:D:153:GLU:OE1	1:D:169:ARG:HD3	2.15	0.46
1:D:223:LEU:HD12	1:D:395:ILE:HG23	1.96	0.46
1:E:240:PHE:HE1	1:F:457:ILE:CD1	2.26	0.46
2:I:166:LEU:HD21	2:I:205:TYR:CE2	2.50	0.46
2:J:95:ALA:HB1	2:J:97:PRO:HD2	1.97	0.46
1:A:223:LEU:CD1	1:A:227:PHE:HB2	2.46	0.46
1:A:255:GLY:C	1:A:389:LEU:HD13	2.40	0.46
1:A:509:LYS:NZ	1:A:518:LEU:HD11	2.31	0.46
1:B:320:SER:O	1:B:320:SER:OG	2.32	0.46
1:C:299:GLU:OE2	1:C:349:THR:OG1	2.22	0.46
1:C:318:ALA:C	1:C:319:ASN:HD22	2.23	0.46
1:E:319:ASN:HB3	1:E:320:SER:HB2	1.96	0.46
1:E:398:PRO:HG2	1:E:434:LYS:O	2.15	0.46
1:F:549:LYS:HE3	1:F:646:THR:C	2.40	0.46
2:I:46:ALA:O	2:I:50:ASN:HB2	2.14	0.46
2:I:67:GLN:O	2:I:71:LEU:HG	2.15	0.46
2:I:126:SER:O	2:I:130:ILE:HG13	2.16	0.46
1:A:99:ILE:HB	1:A:185:PHE:HD2	1.79	0.46
1:A:261:PRO:HD2	1:A:395:ILE:O	2.15	0.46
1:A:582:CYS:SG	1:A:621:LEU:HG	2.56	0.46
1:B:596:GLN:HA	1:B:638:ARG:HG2	1.97	0.46
1:B:612:VAL:HG13	1:B:614:ILE:O	2.16	0.46
1:C:652:LEU:HD22	1:C:657:MET:HG2	1.97	0.46
1:D:113:ASP:HA	1:D:196:ILE:HG13	1.98	0.46
1:D:121:PHE:CD2	1:D:183:VAL:HG21	2.50	0.46
1:D:264:CYS:HA	1:D:437:SER:HB3	1.96	0.46
1:E:36:ILE:HG23	1:E:36:ILE:O	2.15	0.46
1:E:327:PHE:CZ	1:E:369:VAL:HG21	2.50	0.46
1:F:241:PRO:HA	1:F:242:PRO:HA	1.67	0.46
1:F:606:GLU:H	1:F:606:GLU:CD	2.20	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:260:THR:HA	2:G:263:VAL:HG12	1.97	0.46
1:A:149:VAL:HG11	1:A:152:ILE:HD11	1.98	0.46
1:B:250:CYS:HB2	1:C:449:GLN:CD	2.41	0.46
1:B:669:ASN:CG	1:B:706:GLY:HA2	2.41	0.46
1:C:566:LYS:HD2	1:C:567:ILE:H	1.80	0.46
1:F:577:SER:O	1:F:581:LYS:HG3	2.16	0.46
2:I:101:ILE:HB	2:I:131:TYR:OH	2.16	0.46
1:B:121:PHE:CD2	1:B:183:VAL:HG21	2.51	0.46
1:B:397:LEU:HD11	1:B:638:ARG:NH2	2.30	0.46
1:C:143:LYS:HB3	1:C:145:PHE:HE1	1.81	0.46
1:C:325:ILE:HG13	1:C:369:VAL:HG23	1.97	0.46
1:D:136:LEU:HD23	1:D:136:LEU:H	1.80	0.46
1:D:731:ALA:HA	1:D:734:ARG:HH12	1.81	0.46
1:E:56:VAL:HG13	1:E:57:PRO:HD2	1.98	0.46
1:E:436:PHE:N	1:E:436:PHE:CD1	2.83	0.46
1:E:519:ASP:O	1:E:522:GLU:HB2	2.16	0.46
1:E:714:ILE:O	1:E:718:LEU:HG	2.16	0.46
1:F:542:GLU:N	1:F:665:ILE:O	2.48	0.46
2:G:232:PHE:HB2	2:G:233:PRO:HD3	1.98	0.46
2:G:260:THR:HG21	2:G:284:LYS:HE3	1.96	0.46
2:H:184:ILE:O	2:H:188:VAL:HG12	2.14	0.46
2:H:266:TYR:C	2:H:268:SER:H	2.24	0.46
2:I:179:GLN:HA	2:I:182:ILE:HG12	1.98	0.46
2:J:118:THR:O	2:J:122:LYS:HG2	2.16	0.46
4:L:192:LEU:N	4:L:192:LEU:HD22	2.31	0.46
4:L:247:ALA:O	4:L:251:THR:HG23	2.16	0.46
1:A:23:VAL:HG12	1:A:55:VAL:HG21	1.98	0.46
1:B:327:PHE:CZ	1:B:369:VAL:HG21	2.50	0.46
1:B:593:TYR:OH	1:B:632:LYS:HG2	2.16	0.46
1:B:721:ASP:HB2	1:B:724:TYR:CD1	2.51	0.46
1:D:510:TRP:CE3	1:D:675:GLN:HG2	2.37	0.46
1:E:524:LEU:HD11	1:E:663:THR:HG21	1.98	0.46
1:E:549:LYS:O	1:E:552:LEU:HB2	2.15	0.46
1:E:618:PHE:C	1:E:618:PHE:CD1	2.93	0.46
1:E:648:ARG:NE	1:E:651:VAL:HG13	2.31	0.46
1:F:254:LYS:O	1:F:368:LEU:HA	2.16	0.46
2:G:208:LYS:HG2	2:G:275:TRP:CZ3	2.51	0.46
2:I:40:GLU:O	2:I:44:ILE:HG12	2.16	0.46
2:I:127:ILE:HG23	2:I:131:TYR:CE1	2.51	0.46
2:I:200:TYR:HD1	2:I:200:TYR:H	1.62	0.46
2:J:118:THR:HB	5:M:59:ARG:HH12	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:609:LEU:O	1:A:610:ASP:HB3	2.16	0.46
1:C:560:SER:HB2	1:C:562:PHE:CZ	2.51	0.46
1:C:677:LEU:HD21	1:C:695:ALA:CB	2.46	0.46
1:D:121:PHE:HD2	1:D:183:VAL:HG21	1.81	0.46
1:D:528:THR:HG21	1:D:641:LEU:HD12	1.98	0.46
1:D:545:PRO:O	1:D:546:HIS:HB2	2.16	0.46
1:E:696:GLN:OE1	1:E:696:GLN:HA	2.15	0.46
1:F:502:TYR:CD2	1:F:503:ILE:HG13	2.51	0.46
2:G:45:TYR:HE2	2:G:71:LEU:HD11	1.81	0.46
2:G:213:HIS:HE1	2:G:221:ALA:HB2	1.81	0.46
2:J:180:LYS:O	2:J:184:ILE:HG13	2.16	0.46
2:J:186:GLU:O	2:J:190:THR:HG23	2.16	0.46
1:C:322:LEU:HD22	1:C:366:ASN:O	2.17	0.45
1:D:128:GLN:O	1:D:176:LEU:HD12	2.15	0.45
1:D:577:SER:O	1:D:580:ALA:N	2.49	0.45
1:D:616:PRO:HG2	1:E:614:ILE:HG21	1.98	0.45
1:E:125:PHE:HA	1:E:128:GLN:HE22	1.81	0.45
1:E:325:ILE:O	1:E:369:VAL:HG23	2.15	0.45
1:F:323:HIS:HB2	1:F:367:ILE:HG22	1.98	0.45
2:H:138:VAL:O	2:H:142:ILE:HG13	2.16	0.45
2:I:80:ASP:OD1	5:M:66:HIS:HD2	1.98	0.45
3:K:51:ASP:O	3:K:55:GLU:HG3	2.15	0.45
1:A:36:ILE:HG23	1:A:36:ILE:O	2.17	0.45
1:B:122:ILE:O	1:B:126:ASN:HB3	2.15	0.45
1:C:69:TRP:CE2	1:C:134:GLN:HA	2.51	0.45
1:C:231:PHE:CE1	1:C:235:PHE:CD2	3.04	0.45
1:C:428:GLU:O	1:C:431:VAL:HG12	2.16	0.45
1:C:540:LEU:HD22	1:C:661:PHE:CE2	2.51	0.45
1:D:508:ILE:HG12	1:D:683:LEU:HD21	1.97	0.45
1:E:121:PHE:CE2	1:E:183:VAL:HG21	2.52	0.45
1:E:307:ALA:O	1:E:310:GLU:HG2	2.16	0.45
1:F:388:ARG:O	1:F:389:LEU:HD23	2.15	0.45
1:F:400:GLU:OE2	1:F:434:LYS:HA	2.15	0.45
2:H:203:LYS:HE3	2:H:203:LYS:HB2	1.74	0.45
1:A:241:PRO:HA	1:A:242:PRO:HA	1.52	0.45
1:A:258:LEU:O	1:A:372:MET:HA	2.16	0.45
1:C:508:ILE:HD13	1:C:683:LEU:HD21	1.98	0.45
1:E:16:LEU:HD11	1:E:52:HIS:HD2	1.82	0.45
1:F:319:ASN:HB3	1:F:320:SER:HB2	1.99	0.45
1:F:377:ASP:OD1	1:F:378:LEU:N	2.49	0.45
1:F:579:THR:O	1:F:583:GLN:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:10:ALA:HB1	2:H:52:PHE:CZ	2.50	0.45
2:H:53:LYS:HE3	2:I:117:PHE:CE2	2.51	0.45
2:I:45:TYR:HE2	2:I:71:LEU:HD11	1.81	0.45
2:I:223:LEU:O	2:I:227:LYS:HG3	2.17	0.45
2:I:243:LEU:HD22	2:I:266:TYR:CG	2.50	0.45
3:K:46:MET:HE2	3:K:46:MET:HA	1.97	0.45
3:K:48:VAL:O	3:K:52:LYS:HG3	2.16	0.45
1:A:36:ILE:HD11	1:A:44:LYS:HB3	1.97	0.45
1:A:121:PHE:CD2	1:A:183:VAL:HG21	2.51	0.45
1:A:611:TYR:HD1	1:A:618:PHE:HB3	1.81	0.45
1:A:687:LYS:HZ2	1:A:722:PRO:HB3	1.81	0.45
1:B:24:VAL:C	1:B:55:VAL:HG11	2.41	0.45
1:B:452:ALA:HA	1:B:455:ARG:NH2	2.32	0.45
1:D:246:GLU:HG2	1:D:247:GLN:N	2.32	0.45
1:D:281:GLU:N	1:D:282:PRO:HA	2.31	0.45
1:D:377:ASP:OD1	1:D:378:LEU:N	2.50	0.45
1:D:618:PHE:CE2	1:E:614:ILE:HD12	2.52	0.45
1:E:573:MET:SD	1:E:581:LYS:HG2	2.55	0.45
2:G:176:GLU:O	2:G:178:TYR:N	2.49	0.45
2:I:200:TYR:CB	5:M:161:ARG:HD2	2.32	0.45
5:M:161:ARG:HG2	5:M:165:LEU:HG	1.98	0.45
1:B:4:ARG:HD3	1:B:29:TYR:OH	2.17	0.45
1:B:589:PHE:CD2	1:B:629:LEU:HD13	2.51	0.45
1:C:703:VAL:O	1:C:704:TRP:HD1	2.00	0.45
1:E:327:PHE:CE2	1:E:369:VAL:HG21	2.52	0.45
1:E:531:SER:HB3	1:E:534:THR:O	2.16	0.45
1:E:534:THR:HG23	1:F:715:GLU:HG3	1.97	0.45
1:E:666:HIS:HD2	1:E:668:PRO:HD3	1.81	0.45
1:F:309:ALA:HB1	1:F:367:ILE:HG21	1.98	0.45
1:F:327:PHE:CE2	1:F:369:VAL:HG21	2.51	0.45
1:F:502:TYR:CE2	1:F:554:ALA:HB2	2.50	0.45
1:F:686:PHE:HB3	1:F:690:GLU:HB2	1.99	0.45
2:G:10:ALA:O	2:G:14:LEU:HG	2.17	0.45
2:G:75:LEU:O	2:G:76:GLN:HB3	2.17	0.45
2:I:184:ILE:O	2:I:188:VAL:HG12	2.17	0.45
3:K:52:LYS:HE2	5:M:168:GLY:CA	2.46	0.45
1:A:358:ILE:HD12	1:A:359:ASP:H	1.81	0.45
1:A:502:TYR:N	1:A:502:TYR:CD1	2.84	0.45
1:B:241:PRO:HA	1:B:242:PRO:HA	1.61	0.45
1:C:378:LEU:HD23	1:C:378:LEU:HA	1.85	0.45
1:C:691:ARG:HB2	1:C:691:ARG:NH1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:624:GLN:OE1	1:D:624:GLN:HA	2.16	0.45
1:E:586:LYS:O	1:E:589:PHE:HB2	2.17	0.45
1:E:587:LYS:HZ1	1:E:591:ASP:CG	2.24	0.45
2:G:222:LYS:HA	2:G:225:VAL:HG12	1.98	0.45
2:I:119:ILE:HD11	2:I:123:HIS:HE1	1.82	0.45
4:L:214:ASP:O	4:L:217:MET:HB2	2.17	0.45
1:A:327:PHE:CE1	1:A:330:ILE:HG22	2.52	0.45
1:B:281:GLU:N	1:B:282:PRO:HA	2.31	0.45
1:B:485:GLU:O	1:B:490:PRO:HD3	2.17	0.45
1:B:540:LEU:HD11	1:B:649:LYS:HZ1	1.81	0.45
1:B:612:VAL:HG12	1:B:617:ARG:O	2.16	0.45
1:C:333:ILE:O	1:C:351:VAL:HG22	2.17	0.45
1:D:564:PHE:HD2	1:D:598:SER:HB2	1.81	0.45
1:E:24:VAL:HG21	1:E:29:TYR:HB2	1.98	0.45
1:E:286:ASN:OD1	1:E:327:PHE:HD1	2.00	0.45
1:E:655:MET:C	1:E:656:GLU:HG3	2.41	0.45
1:F:36:ILE:HG23	1:F:36:ILE:O	2.17	0.45
2:G:114:MET:O	2:J:50:ASN:ND2	2.41	0.45
2:H:255:ASN:OD1	2:H:258:SER:N	2.46	0.45
1:A:52:HIS:C	1:A:54:SER:H	2.25	0.45
1:A:331:ASP:CA	1:A:379:ILE:HD11	2.38	0.45
1:A:355:LEU:HD22	1:A:388:ARG:NH1	2.32	0.45
1:A:566:LYS:HD3	1:A:566:LYS:HA	1.63	0.45
1:B:423:ASP:HB3	1:B:479:ASP:N	2.31	0.45
1:C:36:ILE:O	1:C:36:ILE:HG23	2.16	0.45
1:C:241:PRO:HA	1:C:242:PRO:HA	1.64	0.45
1:E:611:TYR:CE1	1:E:616:PRO:HB2	2.52	0.45
1:F:23:VAL:HG12	1:F:55:VAL:CG2	2.46	0.45
1:F:99:ILE:HG23	1:F:193:LEU:HD23	1.99	0.45
1:F:136:LEU:HD23	1:F:136:LEU:H	1.82	0.45
1:F:552:LEU:HD12	1:F:667:VAL:HG21	1.98	0.45
2:G:254:GLN:HB2	2:G:291:GLU:HG2	1.98	0.45
2:H:167:LYS:HE2	2:H:171:TYR:CE2	2.52	0.45
1:A:215:PHE:N	1:A:231:PHE:CE2	2.85	0.45
1:C:331:ASP:CA	1:C:379:ILE:HD11	2.45	0.45
1:C:528:THR:O	1:C:639:LYS:HD3	2.16	0.45
1:C:612:VAL:CG1	1:C:617:ARG:HB3	2.47	0.45
1:D:486:ASN:O	1:D:490:PRO:HD3	2.17	0.45
1:F:24:VAL:HG12	1:F:60:VAL:HG13	1.98	0.45
1:F:588:ILE:O	1:F:591:ASP:HB2	2.17	0.45
2:G:142:ILE:HG23	2:G:168:VAL:HG13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:162:ASN:O	2:I:166:LEU:HG	2.17	0.45
2:J:203:LYS:HZ2	2:J:236:SER:C	2.25	0.45
2:J:263:VAL:O	2:J:267:ASP:HB2	2.17	0.45
1:A:255:GLY:HA3	1:A:389:LEU:HD13	1.99	0.45
1:A:571:ASP:OD1	1:A:572:LYS:N	2.49	0.45
1:B:268:LEU:HD12	1:B:269:LEU:N	2.32	0.45
1:C:401:LYS:O	1:C:404:LEU:HB3	2.16	0.45
1:C:576:PHE:HB2	1:C:581:LYS:HG2	1.98	0.45
1:C:705:ILE:HD11	1:C:710:LEU:HA	1.98	0.45
1:D:388:ARG:O	1:D:389:LEU:HD23	2.17	0.45
1:F:40:SER:C	1:F:42:ASN:H	2.25	0.45
1:F:322:LEU:HD12	1:F:323:HIS:N	2.32	0.45
2:G:126:SER:O	2:G:130:ILE:HG13	2.17	0.45
2:H:54:MET:C	2:H:56:LYS:H	2.25	0.45
2:J:10:ALA:N	2:J:51:MET:SD	2.90	0.45
2:J:57:ASN:O	2:J:59:SER:N	2.48	0.45
2:J:81:ALA:O	2:J:85:PHE:HD1	1.99	0.45
2:J:147:GLN:HG2	2:J:151:TYR:CE2	2.52	0.45
4:L:205:LEU:O	4:L:209:ILE:HG13	2.17	0.45
1:A:124:GLN:NE2	1:A:125:PHE:CE1	2.82	0.44
1:B:20:ASN:ND2	1:B:66:GLN:NE2	2.64	0.44
1:B:626:LEU:O	1:B:630:LEU:HG	2.17	0.44
1:C:114:THR:CB	1:C:199:ALA:HB3	2.47	0.44
1:C:311:GLU:O	1:C:314:ARG:HG2	2.18	0.44
1:C:325:ILE:O	1:C:369:VAL:HA	2.17	0.44
1:C:604:ASP:N	1:C:645:THR:OG1	2.44	0.44
1:C:611:TYR:HE2	1:C:648:ARG:NH1	2.14	0.44
1:D:132:VAL:HG23	1:D:173:GLU:O	2.17	0.44
1:D:286:ASN:CB	1:D:327:PHE:HD1	2.30	0.44
1:E:65:PRO:HG2	1:E:137:VAL:HG13	1.99	0.44
1:E:236:ALA:HB1	1:F:453:MET:HB3	1.98	0.44
1:E:587:LYS:HZ3	1:E:587:LYS:C	2.15	0.44
1:F:677:LEU:O	1:F:681:GLU:HG3	2.17	0.44
2:G:67:GLN:O	2:G:71:LEU:HG	2.17	0.44
2:G:120:ALA:O	2:G:124:HIS:HB2	2.17	0.44
2:G:124:HIS:CE1	2:G:147:GLN:HB3	2.50	0.44
2:G:182:ILE:O	2:G:186:GLU:HG2	2.17	0.44
3:K:52:LYS:HE2	5:M:168:GLY:HA2	1.99	0.44
4:L:206:GLU:O	4:L:209:ILE:HB	2.17	0.44
1:A:240:PHE:CE1	1:B:457:ILE:HD11	2.52	0.44
1:A:407:LEU:CD1	1:A:426:ILE:HG23	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:687:LYS:NZ	1:A:722:PRO:HB3	2.32	0.44
1:B:24:VAL:O	1:B:51:THR:HA	2.17	0.44
1:B:101:PHE:CE1	1:B:193:LEU:HD13	2.52	0.44
1:B:272:GLN:OE1	1:B:272:GLN:HA	2.16	0.44
1:E:23:VAL:HG12	1:E:55:VAL:HG21	1.98	0.44
1:E:628:VAL:O	1:E:632:LYS:N	2.48	0.44
1:F:604:ASP:HB3	1:F:607:ARG:HB2	2.00	0.44
2:H:118:THR:HG21	3:K:66:ARG:NH2	2.32	0.44
2:I:54:MET:HE3	2:I:54:MET:O	2.17	0.44
1:A:270:ALA:HA	1:A:273:ILE:HG22	1.99	0.44
1:A:563:PRO:HG2	1:A:597:LEU:O	2.17	0.44
1:A:612:VAL:HG12	1:A:617:ARG:HB2	1.99	0.44
1:A:646:THR:HG21	1:A:652:LEU:HD22	2.00	0.44
1:B:297:GLU:O	1:B:300:ALA:HB3	2.17	0.44
1:B:414:MET:HE2	1:B:414:MET:N	2.33	0.44
1:C:499:TYR:HB3	1:C:558:GLU:OE2	2.17	0.44
1:C:526:GLN:OE1	1:C:530:ASN:ND2	2.50	0.44
1:E:585:MET:HE2	1:E:626:LEU:HD21	1.99	0.44
2:H:212:CYS:SG	2:H:279:MET:HE1	2.58	0.44
2:I:149:ALA:HB2	2:I:164:CYS:CB	2.47	0.44
1:A:67:ARG:HH12	1:A:74:ILE:HD11	1.81	0.44
1:B:377:ASP:OD1	1:B:378:LEU:N	2.50	0.44
1:B:609:LEU:HD23	1:B:622:VAL:HB	1.99	0.44
1:C:347:HIS:O	1:C:350:VAL:HG22	2.17	0.44
1:C:499:TYR:OH	1:C:565:ILE:HB	2.17	0.44
1:C:519:ASP:O	1:C:523:LEU:HG	2.16	0.44
1:C:671:ALA:HA	1:C:703:VAL:O	2.17	0.44
1:D:685:ASN:HB3	1:D:718:LEU:HD11	1.99	0.44
1:E:190:ASN:OD1	1:E:315:ARG:HA	2.18	0.44
1:E:510:TRP:CE3	1:E:511:GLY:HA3	2.52	0.44
1:E:713:LEU:CD2	1:E:732:LEU:HD13	2.47	0.44
2:G:40:GLU:O	2:G:44:ILE:HG12	2.17	0.44
2:G:271:ARG:HH21	2:H:231:LEU:HB2	1.82	0.44
2:H:179:GLN:O	2:H:182:ILE:HG12	2.17	0.44
2:I:53:LYS:HE3	2:J:117:PHE:CD2	2.51	0.44
2:I:95:ALA:HB1	2:I:97:PRO:HD2	1.99	0.44
1:B:626:LEU:HD23	1:B:626:LEU:HA	1.66	0.44
1:B:686:PHE:CE1	1:B:714:ILE:HG23	2.53	0.44
1:C:677:LEU:O	1:C:681:GLU:OE1	2.35	0.44
1:D:122:ILE:O	1:D:126:ASN:HB3	2.17	0.44
1:D:656:GLU:OE1	1:E:613:PRO:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:715:GLU:O	1:D:719:GLN:HG2	2.18	0.44
1:E:248:MET:C	1:F:414:MET:HE1	2.43	0.44
2:H:134:GLU:O	2:H:136:VAL:HG23	2.18	0.44
2:I:218:MET:HB3	2:I:219:LEU:H	1.51	0.44
2:J:32:PHE:HD1	2:J:32:PHE:H	1.66	0.44
1:A:576:PHE:HB3	1:A:580:ALA:HB3	1.99	0.44
1:B:236:ALA:HA	1:B:239:VAL:CG1	2.48	0.44
1:B:524:LEU:HD21	1:B:663:THR:HG21	1.98	0.44
1:C:604:ASP:H	1:C:645:THR:HG1	1.61	0.44
1:D:99:ILE:HD11	1:D:145:PHE:CD2	2.52	0.44
1:E:218:MET:HA	1:E:219:GLY:HA2	1.81	0.44
1:E:264:CYS:HA	1:E:437:SER:HB2	1.98	0.44
1:E:313:GLN:O	1:E:317:GLY:N	2.50	0.44
1:E:684:GLY:HA2	1:E:691:ARG:NH2	2.33	0.44
1:F:24:VAL:O	1:F:51:THR:HA	2.18	0.44
1:F:86:ASP:OD2	1:F:88:ALA:HB3	2.17	0.44
1:F:272:GLN:OE1	1:F:272:GLN:HA	2.18	0.44
1:F:605:ILE:O	1:F:608:LEU:HG	2.17	0.44
2:H:122:LYS:HD2	2:H:152:TYR:OH	2.18	0.44
2:H:188:VAL:HG13	2:H:205:TYR:CD2	2.52	0.44
2:H:213:HIS:C	2:H:215:CYS:H	2.25	0.44
2:J:173:ALA:HB3	2:J:275:TRP:HE1	1.82	0.44
4:L:226:GLN:HE21	4:L:226:GLN:HB2	1.56	0.44
1:A:240:PHE:CD2	1:B:453:MET:SD	3.11	0.44
1:B:254:LYS:O	1:B:368:LEU:HA	2.18	0.44
1:B:286:ASN:OD1	1:B:327:PHE:HD1	2.01	0.44
1:B:541:LEU:HD12	1:B:541:LEU:O	2.17	0.44
1:B:627:LEU:HB3	1:C:607:ARG:CZ	2.47	0.44
1:C:441:LEU:HD23	1:C:441:LEU:HA	1.83	0.44
1:C:638:ARG:HH11	1:C:638:ARG:HG3	1.82	0.44
1:D:18:LEU:HD23	1:D:137:VAL:HG21	2.00	0.44
1:D:223:LEU:HD23	1:D:223:LEU:O	2.18	0.44
1:E:74:ILE:H	2:G:218:MET:HE1	1.83	0.44
1:E:265:GLY:O	1:E:268:LEU:HG	2.18	0.44
1:F:23:VAL:HG12	1:F:55:VAL:HG21	2.00	0.44
1:F:45:TYR:CE2	1:F:70:ALA:HA	2.52	0.44
1:F:69:TRP:NE1	1:F:134:GLN:HA	2.33	0.44
1:F:352:ASN:HA	1:F:355:LEU:HD12	1.99	0.44
1:F:658:LEU:HD12	1:F:658:LEU:O	2.17	0.44
2:H:291:GLU:C	2:H:293:ASP:N	2.75	0.44
2:J:66:CYS:SG	2:J:92:PHE:HE2	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:PRO:HD2	1:A:243:GLU:H	1.81	0.44
1:B:180:ASN:O	1:B:180:ASN:ND2	2.42	0.44
1:C:611:TYR:HE2	1:C:648:ARG:CZ	2.30	0.44
1:C:618:PHE:CZ	1:D:612:VAL:HG11	2.47	0.44
1:D:22:ALA:HB3	1:D:49:LEU:HD23	2.00	0.44
1:D:331:ASP:HA	1:D:379:ILE:HD11	2.00	0.44
1:D:331:ASP:O	1:D:332:ALA:HB3	2.18	0.44
1:E:320:SER:O	1:E:320:SER:OG	2.33	0.44
1:E:590:ASP:O	1:E:593:TYR:HB2	2.18	0.44
2:J:185:TYR:CZ	2:J:208:LYS:HD3	2.53	0.44
2:J:185:TYR:HA	2:J:188:VAL:HG12	2.00	0.44
4:L:205:LEU:HG	5:M:32:MET:SD	2.57	0.44
1:A:64:LEU:HA	1:A:67:ARG:HH21	1.82	0.44
1:A:113:ASP:OD1	1:A:115:ASP:HB2	2.17	0.44
1:A:677:LEU:HD13	1:A:677:LEU:HA	1.79	0.44
1:A:685:ASN:OD1	1:F:533:ARG:CZ	2.66	0.44
1:B:24:VAL:HG12	1:B:60:VAL:HG13	2.00	0.44
1:C:632:LYS:HG3	1:D:571:ASP:CG	2.43	0.44
1:E:23:VAL:HG12	1:E:55:VAL:CG2	2.48	0.44
1:F:48:THR:HG21	1:F:128:GLN:HG2	2.00	0.44
2:H:119:ILE:HD11	2:H:123:HIS:CE1	2.53	0.44
2:H:223:LEU:O	2:H:227:LYS:HG3	2.18	0.44
2:I:63:ASN:O	2:I:67:GLN:HG3	2.18	0.44
2:I:108:ILE:HD12	2:I:127:ILE:HD12	1.99	0.44
2:I:281:LEU:O	2:I:285:LYS:HG3	2.17	0.44
2:J:243:LEU:O	2:J:247:LEU:HG	2.18	0.44
2:J:256:VAL:HG21	2:J:288:GLN:HG3	1.99	0.44
1:B:250:CYS:SG	1:C:446:ARG:HA	2.58	0.43
1:B:536:LEU:HD12	1:B:640:LEU:O	2.18	0.43
1:C:18:LEU:HD23	1:C:137:VAL:HG21	2.00	0.43
1:D:257:LEU:HG	1:D:371:GLY:O	2.17	0.43
1:D:498:ASP:O	1:D:501:SER:HB3	2.18	0.43
1:D:651:VAL:HG13	1:D:655:MET:HE3	2.00	0.43
1:E:69:TRP:CE2	1:E:134:GLN:HA	2.53	0.43
1:E:507:ILE:HD12	1:E:555:LYS:HB2	1.98	0.43
2:G:218:MET:HG3	2:G:219:LEU:N	2.32	0.43
1:A:614:ILE:O	1:A:614:ILE:HG23	2.18	0.43
1:B:48:THR:HG21	1:B:128:GLN:HG2	2.00	0.43
1:B:64:LEU:HA	1:B:67:ARG:CZ	2.48	0.43
1:B:172:ILE:HD12	1:B:174:VAL:O	2.18	0.43
1:B:318:ALA:O	1:B:319:ASN:ND2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:PHE:HB3	1:C:244:ILE:HB	2.00	0.43
1:D:73:SER:O	1:D:76:GLN:HG2	2.18	0.43
1:D:256:ILE:HG22	1:D:391:VAL:CG1	2.48	0.43
1:D:263:GLY:O	1:D:439:ALA:N	2.51	0.43
1:E:406:ILE:O	1:E:409:ILE:HG22	2.18	0.43
1:E:596:GLN:O	1:E:638:ARG:HA	2.17	0.43
1:F:86:ASP:C	1:F:88:ALA:N	2.76	0.43
1:F:436:PHE:HD2	1:F:444:LEU:HD11	1.83	0.43
1:F:648:ARG:O	1:F:652:LEU:HD23	2.18	0.43
2:G:112:THR:HG23	2:G:117:PHE:CE1	2.50	0.43
2:J:119:ILE:O	2:J:122:LYS:HB2	2.18	0.43
1:A:673:GLY:O	1:A:676:LEU:HB3	2.18	0.43
1:C:24:VAL:HG11	1:C:49:LEU:HD22	2.00	0.43
1:D:694:ILE:HG12	1:D:726:VAL:HG13	2.00	0.43
1:E:190:ASN:OD1	1:E:315:ARG:CB	2.66	0.43
1:E:673:GLY:O	1:E:676:LEU:HB3	2.18	0.43
1:E:713:LEU:HA	1:E:713:LEU:HD23	1.82	0.43
1:F:36:ILE:HG13	1:F:45:TYR:O	2.18	0.43
1:F:516:ARG:HB3	1:F:516:ARG:NH1	2.34	0.43
2:G:35:SER:HA	2:G:38:ILE:HG22	2.01	0.43
2:G:122:LYS:HA	2:G:152:TYR:OH	2.18	0.43
2:G:154:GLY:HA2	2:J:94:LYS:HD3	1.99	0.43
2:H:21:VAL:HG23	2:H:38:ILE:HD13	2.01	0.43
2:H:243:LEU:HD13	2:H:266:TYR:HB2	1.99	0.43
4:L:237:VAL:O	4:L:241:VAL:HG23	2.17	0.43
1:A:122:ILE:HD11	1:A:183:VAL:HG23	2.01	0.43
1:A:573:MET:HA	1:A:576:PHE:CD2	2.53	0.43
1:A:624:GLN:NE2	1:B:610:ASP:HA	2.33	0.43
1:B:578:GLU:CG	1:B:619:SER:HB2	2.47	0.43
1:C:34:HIS:HB2	1:C:83:TYR:O	2.19	0.43
1:C:193:LEU:HD21	1:C:195:LEU:HD21	2.01	0.43
1:C:490:PRO:HA	1:C:491:ALA:CB	2.36	0.43
1:C:696:GLN:O	1:C:696:GLN:NE2	2.51	0.43
1:E:48:THR:HG22	1:E:49:LEU:N	2.32	0.43
1:E:449:GLN:O	1:E:453:MET:HG2	2.18	0.43
1:E:669:ASN:CG	1:E:706:GLY:HA2	2.44	0.43
1:F:18:LEU:HA	1:F:137:VAL:CG2	2.48	0.43
2:G:134:GLU:O	2:G:136:VAL:HG23	2.18	0.43
2:H:161:ALA:O	2:H:165:LEU:HG	2.18	0.43
2:H:237:ASP:C	2:H:239:ARG:H	2.26	0.43
2:J:167:LYS:HE2	2:J:171:TYR:CE2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:GLU:HB3	1:A:148:LEU:HB3	2.00	0.43
1:B:91:CYS:O	1:B:154:ALA:HA	2.19	0.43
1:B:406:ILE:O	1:B:409:ILE:HG22	2.19	0.43
1:B:542:GLU:CD	1:B:649:LYS:HD3	2.44	0.43
1:C:573:MET:HB3	1:C:576:PHE:CD2	2.53	0.43
1:D:86:ASP:C	1:D:88:ALA:H	2.26	0.43
1:D:258:LEU:HD11	1:D:372:MET:HG2	1.99	0.43
1:D:571:ASP:O	1:D:574:ILE:HG13	2.19	0.43
1:E:141:ASN:O	1:E:142:ASP:C	2.61	0.43
1:E:590:ASP:OD2	1:E:594:LYS:NZ	2.50	0.43
1:F:397:LEU:HB3	1:F:398:PRO:HD3	1.99	0.43
1:F:562:PHE:HB2	1:F:565:ILE:HG12	1.99	0.43
2:G:255:ASN:C	2:G:257:ASP:H	2.27	0.43
2:H:45:TYR:HE2	2:H:71:LEU:HD11	1.83	0.43
2:J:126:SER:O	2:J:130:ILE:HG13	2.18	0.43
2:J:287:ILE:O	2:J:290:ASP:HB3	2.19	0.43
1:A:377:ASP:OD2	1:A:378:LEU:HD23	2.17	0.43
1:B:24:VAL:HG11	1:B:49:LEU:HD22	2.00	0.43
1:B:507:ILE:CG1	1:B:555:LYS:HD3	2.48	0.43
1:B:523:LEU:HD22	1:B:526:GLN:NE2	2.33	0.43
1:B:533:ARG:CG	1:B:534:THR:H	2.24	0.43
1:B:662:SER:CB	1:C:712:MET:HE3	2.49	0.43
1:C:289:GLU:C	1:C:291:LEU:H	2.21	0.43
1:C:326:ILE:HB	1:C:370:ILE:HD11	2.00	0.43
1:C:330:ILE:HD13	1:C:330:ILE:HA	1.71	0.43
1:C:355:LEU:HG	1:C:388:ARG:CZ	2.47	0.43
1:D:221:GLY:HA3	1:D:406:ILE:HD13	2.00	0.43
1:E:63:SER:C	1:E:67:ARG:HH21	2.27	0.43
1:E:721:ASP:HB2	1:E:724:TYR:HD2	1.84	0.43
2:H:282:ARG:O	2:H:286:THR:HG23	2.19	0.43
2:J:118:THR:HB	5:M:59:ARG:NH1	2.34	0.43
3:K:34:GLN:O	3:K:38:GLN:HG3	2.19	0.43
4:L:210:ARG:HG3	4:L:210:ARG:HH11	1.84	0.43
1:A:50:ARG:HH11	1:A:50:ARG:HG2	1.82	0.43
1:B:423:ASP:O	1:B:479:ASP:N	2.52	0.43
1:B:540:LEU:HD12	1:B:540:LEU:O	2.19	0.43
1:C:552:LEU:HD23	1:C:552:LEU:HA	1.75	0.43
1:C:721:ASP:HB2	1:C:724:TYR:CD1	2.53	0.43
1:D:589:PHE:CD2	1:D:629:LEU:HD13	2.52	0.43
1:E:534:THR:HG21	1:F:712:MET:HA	2.01	0.43
2:I:98:GLN:C	2:I:100:ALA:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:282:ARG:O	2:J:286:THR:HG23	2.19	0.43
1:A:503:ILE:CG2	1:A:506:GLY:H	2.31	0.43
1:B:546:HIS:HD2	1:B:708:LYS:HD2	1.83	0.43
1:C:542:GLU:HG2	1:C:666:HIS:HA	2.00	0.43
1:D:218:MET:HA	1:D:219:GLY:HA2	1.76	0.43
1:D:728:LYS:O	1:D:732:LEU:HG	2.19	0.43
1:E:106:ASN:HB3	1:E:143:LYS:HZ2	1.84	0.43
1:E:377:ASP:OD1	1:E:378:LEU:N	2.51	0.43
1:F:436:PHE:CD2	1:F:444:LEU:HD11	2.54	0.43
1:F:503:ILE:HG22	1:F:503:ILE:O	2.19	0.43
1:F:510:TRP:HZ3	1:F:675:GLN:NE2	2.17	0.43
2:G:184:ILE:O	2:G:188:VAL:HG12	2.18	0.43
2:G:203:LYS:HB2	2:G:203:LYS:HE3	1.75	0.43
2:H:178:TYR:OH	2:H:282:ARG:HG2	2.19	0.43
2:H:208:LYS:HG2	2:H:275:TRP:CZ3	2.54	0.43
2:J:98:GLN:C	2:J:100:ALA:H	2.27	0.43
2:J:100:ALA:O	2:J:104:LEU:HG	2.19	0.43
2:J:134:GLU:O	2:J:136:VAL:HG23	2.19	0.43
3:K:48:VAL:CG1	3:K:52:LYS:HZ1	2.29	0.43
3:K:53:VAL:HG13	3:K:54:LEU:HD22	2.01	0.43
1:A:231:PHE:CD2	1:A:235:PHE:CD2	3.07	0.43
1:A:507:ILE:HD12	1:A:555:LYS:HG2	1.99	0.43
1:D:73:SER:H	1:D:76:GLN:CD	2.27	0.43
1:E:512:ASP:N	1:E:513:PRO:CD	2.82	0.43
1:E:524:LEU:O	1:E:528:THR:HG23	2.18	0.43
1:E:562:PHE:HE2	1:E:641:LEU:CD2	2.31	0.43
2:G:99:GLU:O	2:G:100:ALA:C	2.62	0.43
3:K:77:PHE:CD2	4:L:247:ALA:HB1	2.54	0.43
1:A:87:LYS:HA	1:A:91:CYS:SG	2.58	0.43
1:A:411:THR:OG1	1:A:426:ILE:HD11	2.18	0.43
1:A:636:GLN:HA	1:A:637:GLY:HA2	1.52	0.43
1:C:20:ASN:HD22	1:C:66:GLN:NE2	2.17	0.43
1:C:114:THR:HB	1:C:199:ALA:HB3	2.01	0.43
1:C:327:PHE:O	1:C:371:GLY:HA2	2.18	0.43
1:C:540:LEU:HD22	1:C:661:PHE:CD2	2.54	0.43
1:C:624:GLN:OE1	1:C:624:GLN:HA	2.18	0.43
1:C:715:GLU:OE1	1:C:715:GLU:HA	2.19	0.43
1:E:24:VAL:HG12	1:E:60:VAL:HG13	2.00	0.43
1:E:45:TYR:CE2	1:E:70:ALA:HA	2.54	0.43
1:F:303:ARG:CG	1:F:357:LYS:HE2	2.44	0.43
2:G:54:MET:HE1	2:H:112:THR:CG2	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:263:VAL:O	2:H:267:ASP:HB2	2.19	0.43
2:I:200:TYR:CE2	3:K:41:GLU:HG3	2.54	0.43
2:I:207:PHE:HB2	2:I:240:GLU:HG2	1.99	0.43
2:I:208:LYS:HG2	2:I:275:TRP:CZ3	2.54	0.43
2:J:227:LYS:HB3	2:J:227:LYS:NZ	2.34	0.43
2:J:231:LEU:C	2:J:233:PRO:HD2	2.43	0.43
1:A:456:HIS:HB2	1:F:240:PHE:CE2	2.53	0.42
1:A:483:SER:C	1:A:486:ASN:H	2.26	0.42
1:A:543:GLY:N	1:A:549:LYS:HD3	2.34	0.42
1:B:502:TYR:CE2	1:B:567:ILE:HD13	2.54	0.42
1:B:655:MET:C	1:B:656:GLU:HG3	2.44	0.42
1:C:114:THR:OG1	1:C:199:ALA:HB3	2.19	0.42
1:D:272:GLN:OE1	1:D:272:GLN:HA	2.18	0.42
1:D:538:SER:OG	1:D:661:PHE:HA	2.19	0.42
1:D:573:MET:SD	1:D:608:LEU:HD22	2.59	0.42
1:E:289:GLU:C	1:E:291:LEU:N	2.75	0.42
1:F:102:LEU:HD23	1:F:144:LEU:HB3	1.99	0.42
1:F:262:PRO:HB3	1:F:374:ASN:OD1	2.18	0.42
1:F:721:ASP:O	1:F:725:ARG:HG3	2.18	0.42
2:H:235:PHE:CD1	4:L:204:LYS:HA	2.54	0.42
2:H:260:THR:HA	2:H:263:VAL:HG12	2.00	0.42
4:L:213:HIS:O	4:L:217:MET:HG2	2.19	0.42
5:M:177:GLN:HG3	5:M:180:ARG:HH22	1.83	0.42
1:A:235:PHE:N	1:A:235:PHE:CD1	2.86	0.42
1:A:607:ARG:CZ	1:F:627:LEU:HD22	2.48	0.42
1:B:325:ILE:HG13	1:B:369:VAL:HB	2.01	0.42
1:B:414:MET:HE2	1:B:414:MET:CA	2.49	0.42
1:C:320:SER:O	1:C:320:SER:OG	2.32	0.42
1:C:538:SER:O	1:C:662:SER:OG	2.35	0.42
1:C:542:GLU:HB2	1:C:649:LYS:HD3	2.01	0.42
1:C:709:LYS:HA	1:C:709:LYS:HD2	1.83	0.42
1:D:539:VAL:HG13	1:D:643:ILE:HG13	2.01	0.42
1:E:230:ILE:HD11	1:E:391:VAL:HG11	2.00	0.42
1:E:571:ASP:O	1:E:574:ILE:HG13	2.19	0.42
1:E:701:LYS:HE3	1:E:734:ARG:HH22	1.84	0.42
1:F:104:LYS:C	1:F:106:ASN:H	2.26	0.42
1:F:441:LEU:O	1:F:445:VAL:HG23	2.19	0.42
1:F:602:VAL:O	1:F:644:GLY:HA2	2.19	0.42
2:G:287:ILE:O	2:G:291:GLU:HG3	2.19	0.42
2:H:192:ALA:O	2:H:198:LEU:HB2	2.19	0.42
2:H:256:VAL:O	2:H:256:VAL:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:92:PHE:HD1	2:I:97:PRO:HG2	1.83	0.42
2:J:130:ILE:O	2:J:134:GLU:HB2	2.19	0.42
2:J:201:SER:OG	2:J:205:TYR:HE1	2.01	0.42
2:J:225:VAL:HG23	2:J:241:CYS:HB2	2.00	0.42
3:K:45:ILE:CG2	5:M:164:ALA:HB1	2.49	0.42
5:M:161:ARG:HA	5:M:164:ALA:HB3	2.00	0.42
5:M:176:ARG:HG2	5:M:176:ARG:HH11	1.83	0.42
1:C:404:LEU:HG	1:C:426:ILE:HG22	2.01	0.42
1:C:452:ALA:O	1:C:456:HIS:ND1	2.52	0.42
1:C:511:GLY:HA3	1:C:675:GLN:HE21	1.83	0.42
1:F:314:ARG:CG	1:F:315:ARG:N	2.82	0.42
2:I:106:ARG:O	2:I:109:GLU:HB3	2.19	0.42
1:A:299:GLU:HG2	1:A:353:GLN:CG	2.48	0.42
1:A:357:LYS:HA	1:A:357:LYS:HE3	2.00	0.42
1:A:502:TYR:N	1:A:502:TYR:HD1	2.15	0.42
1:B:91:CYS:HB3	1:B:155:MET:HE2	2.01	0.42
1:B:513:PRO:O	1:B:517:VAL:HG23	2.19	0.42
1:C:18:LEU:HD23	1:C:137:VAL:CG2	2.48	0.42
1:D:227:PHE:O	1:D:230:ILE:HG22	2.18	0.42
1:D:268:LEU:HD12	1:D:269:LEU:N	2.33	0.42
1:D:271:ARG:HG2	1:D:272:GLN:N	2.35	0.42
1:D:657:MET:HE2	1:D:661:PHE:HZ	1.84	0.42
1:E:324:ILE:HG12	1:E:368:LEU:HD11	2.02	0.42
1:E:677:LEU:HD11	1:E:695:ALA:HA	2.00	0.42
1:F:18:LEU:HD23	1:F:137:VAL:HG21	2.01	0.42
2:I:95:ALA:CB	2:I:97:PRO:HD2	2.49	0.42
2:J:46:ALA:O	2:J:50:ASN:HB2	2.19	0.42
1:A:299:GLU:CD	1:A:303:ARG:HH21	2.27	0.42
1:B:23:VAL:HG12	1:B:55:VAL:HG21	2.02	0.42
1:B:64:LEU:HA	1:B:67:ARG:NH2	2.35	0.42
1:B:264:CYS:SG	1:B:395:ILE:HG21	2.59	0.42
1:D:36:ILE:HG23	1:D:36:ILE:O	2.20	0.42
1:D:618:PHE:CE1	1:E:612:VAL:HG21	2.53	0.42
2:G:185:TYR:HB2	2:G:209:ALA:HB2	2.02	0.42
2:I:10:ALA:O	2:I:14:LEU:HG	2.19	0.42
2:J:267:ASP:OD1	2:J:271:ARG:HD3	2.20	0.42
5:M:25:SER:O	5:M:28:SER:HB3	2.20	0.42
5:M:198:ARG:HH11	5:M:198:ARG:HG3	1.85	0.42
1:A:285:VAL:HG13	1:A:326:ILE:CD1	2.46	0.42
1:B:246:GLU:HG2	1:B:247:GLN:N	2.34	0.42
1:C:611:TYR:CE2	1:C:648:ARG:CZ	3.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:510:TRP:CB	1:D:679:ALA:HB2	2.49	0.42
1:E:298:SER:O	1:E:301:ASN:HB2	2.20	0.42
1:F:270:ALA:HA	1:F:273:ILE:HG22	2.02	0.42
1:F:401:LYS:O	1:F:404:LEU:HB3	2.20	0.42
1:F:697:GLN:HG3	1:F:730:LEU:HD11	2.02	0.42
1:F:728:LYS:O	1:F:732:LEU:HG	2.20	0.42
2:G:38:ILE:CD1	2:G:71:LEU:HB3	2.41	0.42
5:M:40:LYS:O	5:M:44:ILE:HG13	2.20	0.42
1:B:307:ALA:HA	1:B:310:GLU:HG2	2.01	0.42
1:B:311:GLU:O	1:B:314:ARG:HG2	2.19	0.42
1:B:576:PHE:HB2	1:B:581:LYS:CG	2.49	0.42
1:B:690:GLU:O	1:B:694:ILE:HG13	2.20	0.42
1:C:677:LEU:HD11	1:C:698:VAL:CG2	2.50	0.42
1:D:263:GLY:C	1:D:437:SER:HB3	2.45	0.42
1:E:397:LEU:HD13	1:E:398:PRO:CD	2.48	0.42
1:E:438:GLY:O	1:E:441:LEU:N	2.42	0.42
1:E:585:MET:HE3	1:E:589:PHE:CZ	2.55	0.42
1:F:242:PRO:HD2	1:F:243:GLU:N	2.35	0.42
1:F:629:LEU:C	1:F:629:LEU:HD23	2.44	0.42
2:G:119:ILE:HD11	2:G:123:HIS:HE1	1.82	0.42
2:H:78:LYS:HB3	2:H:110:ILE:HG23	2.01	0.42
2:J:58:TRP:HB3	2:J:95:ALA:HB2	2.02	0.42
1:A:624:GLN:HG3	1:B:610:ASP:OD2	2.19	0.42
1:B:309:ALA:HA	1:B:312:GLU:OE1	2.19	0.42
1:C:536:LEU:CD1	1:C:640:LEU:HB3	2.49	0.42
1:D:231:PHE:CD1	1:D:235:PHE:CD2	3.07	0.42
1:F:436:PHE:N	1:F:436:PHE:CD1	2.85	0.42
2:H:117:PHE:HA	2:H:120:ALA:HB3	2.00	0.42
2:H:119:ILE:HD11	2:H:123:HIS:HD1	1.84	0.42
2:I:182:ILE:CG2	2:I:212:CYS:HB2	2.49	0.42
2:J:172:ALA:O	2:J:177:GLN:HB2	2.19	0.42
2:J:203:LYS:HE3	2:J:203:LYS:HB2	1.80	0.42
2:J:230:GLU:HG3	2:J:237:ASP:CB	2.49	0.42
5:M:29:THR:HA	5:M:32:MET:CE	2.40	0.42
1:A:242:PRO:O	1:A:245:VAL:HG12	2.19	0.42
1:A:549:LYS:CE	1:A:646:THR:C	2.89	0.42
1:A:632:LYS:HE3	1:A:633:ALA:O	2.20	0.42
1:A:705:ILE:HD13	1:A:710:LEU:CD1	2.42	0.42
1:B:219:GLY:C	1:B:220:ILE:HD12	2.45	0.42
1:B:712:MET:O	1:B:716:MET:HG3	2.20	0.42
1:D:308:ASP:O	1:D:311:GLU:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:268:LEU:HD12	1:E:269:LEU:N	2.35	0.42
1:E:568:CYS:HB3	1:E:601:VAL:O	2.19	0.42
1:F:709:LYS:O	1:F:713:LEU:HG	2.19	0.42
2:G:92:PHE:CG	2:G:99:GLU:HB2	2.54	0.42
2:G:175:LEU:HD23	2:G:177:GLN:NE2	2.33	0.42
2:I:261:GLU:O	2:I:264:LYS:HB3	2.20	0.42
1:A:220:ILE:HG22	1:A:221:GLY:N	2.35	0.42
1:A:423:ASP:C	1:A:479:ASP:N	2.78	0.42
1:C:138:PHE:HB2	1:C:147:LEU:HD11	2.01	0.42
1:C:539:VAL:HG23	1:C:663:THR:HG23	2.02	0.42
1:C:676:LEU:HD12	1:C:705:ILE:CG2	2.46	0.42
1:D:527:GLN:CD	1:E:716:MET:HA	2.45	0.42
1:D:569:SER:HA	1:D:570:PRO:HD3	1.89	0.42
1:D:618:PHE:O	1:E:617:ARG:NH2	2.52	0.42
1:D:705:ILE:CD1	1:D:713:LEU:HD12	2.50	0.42
1:D:720:MET:HB3	1:D:724:TYR:CE1	2.55	0.42
1:F:502:TYR:HD2	1:F:503:ILE:HG13	1.85	0.42
1:F:596:GLN:O	1:F:638:ARG:HA	2.20	0.42
2:H:182:ILE:HG22	2:H:209:ALA:HA	2.02	0.42
2:J:232:PHE:C	2:J:234:ALA:N	2.70	0.42
3:K:63:LEU:HB2	5:M:182:MET:HG2	2.01	0.42
3:K:77:PHE:CZ	5:M:78:LEU:HD11	2.55	0.42
1:A:27:LYS:HD2	1:A:57:PRO:HG3	2.01	0.41
1:A:243:GLU:O	1:A:246:GLU:HG2	2.19	0.41
1:A:720:MET:HG3	1:A:728:LYS:CD	2.50	0.41
1:B:707:ILE:O	1:B:711:LEU:HG	2.20	0.41
1:C:313:GLN:NE2	1:C:365:ASN:O	2.51	0.41
1:C:528:THR:OG1	1:C:537:VAL:HG21	2.20	0.41
1:C:640:LEU:HG	1:C:642:ILE:HG13	2.02	0.41
1:E:11:CYS:HA	1:E:12:PRO:HD3	1.95	0.41
2:G:95:ALA:HB1	2:G:97:PRO:HD2	2.02	0.41
2:H:200:TYR:O	2:H:203:LYS:HE2	2.19	0.41
2:I:200:TYR:CD1	2:I:200:TYR:N	2.88	0.41
1:A:223:LEU:HD12	1:A:227:PHE:HB2	2.02	0.41
1:A:713:LEU:CD2	1:A:732:LEU:HB3	2.44	0.41
1:B:40:SER:C	1:B:42:ASN:H	2.28	0.41
1:B:436:PHE:N	1:B:436:PHE:CD1	2.86	0.41
1:C:219:GLY:C	1:C:220:ILE:HD12	2.46	0.41
1:D:103:GLN:OE1	1:D:106:ASN:ND2	2.53	0.41
1:D:510:TRP:NE1	1:D:514:VAL:HG21	2.35	0.41
1:E:219:GLY:C	1:E:220:ILE:HD12	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:525:VAL:O	1:E:529:LYS:HG2	2.21	0.41
1:F:268:LEU:HD12	1:F:269:LEU:N	2.35	0.41
2:G:79:HIS:CE1	2:G:114:MET:HE3	2.54	0.41
2:G:81:ALA:O	2:G:85:PHE:HD1	2.03	0.41
2:I:243:LEU:HD13	2:I:266:TYR:HB2	2.03	0.41
2:J:203:LYS:HG2	2:J:228:TYR:OH	2.20	0.41
1:A:69:TRP:CE2	1:A:134:GLN:HA	2.55	0.41
1:A:240:PHE:HD1	1:A:240:PHE:HA	1.72	0.41
1:A:565:ILE:HA	1:A:599:CYS:O	2.19	0.41
1:A:607:ARG:HD3	1:A:607:ARG:HA	1.85	0.41
1:A:693:THR:O	1:A:697:GLN:OE1	2.37	0.41
1:A:694:ILE:HA	1:A:697:GLN:OE1	2.20	0.41
1:B:326:ILE:HG22	1:B:370:ILE:CG1	2.47	0.41
1:B:648:ARG:HG3	1:B:651:VAL:CG2	2.50	0.41
1:C:414:MET:HE2	1:C:414:MET:HA	2.02	0.41
1:C:438:GLY:O	1:C:441:LEU:HB2	2.20	0.41
1:E:513:PRO:O	1:E:516:ARG:HG2	2.20	0.41
1:F:64:LEU:HD21	2:G:292:GLU:HB3	2.03	0.41
1:F:243:GLU:O	1:F:246:GLU:HG2	2.21	0.41
1:F:445:VAL:O	1:F:449:GLN:HG2	2.20	0.41
2:G:205:TYR:H	2:G:205:TYR:HD1	1.68	0.41
2:J:75:LEU:O	2:J:76:GLN:HB3	2.20	0.41
2:J:208:LYS:HG2	2:J:275:TRP:CZ3	2.56	0.41
2:J:231:LEU:O	2:J:234:ALA:N	2.53	0.41
1:A:300:ALA:O	1:A:303:ARG:HG2	2.20	0.41
1:A:552:LEU:HD22	1:A:556:ILE:HD11	2.01	0.41
1:A:676:LEU:HD12	1:A:710:LEU:HD11	2.01	0.41
1:B:62:PHE:HB2	1:B:67:ARG:CG	2.49	0.41
1:B:99:ILE:HD11	1:B:145:PHE:CD2	2.55	0.41
1:B:218:MET:HA	1:B:219:GLY:HA2	1.80	0.41
1:B:260:GLY:HA3	1:B:266:LYS:HD3	2.02	0.41
1:B:584:ALA:O	1:B:588:ILE:HG13	2.19	0.41
1:C:408:HIS:HD1	1:C:412:ALA:HB2	1.86	0.41
1:D:437:SER:O	1:D:440:GLU:HB3	2.19	0.41
1:E:98:GLU:HB3	1:E:148:LEU:HB3	2.01	0.41
1:E:526:GLN:HA	1:E:529:LYS:HG2	2.02	0.41
1:F:705:ILE:HG12	1:F:706:GLY:O	2.19	0.41
2:G:163:LYS:O	2:G:167:LYS:HG2	2.21	0.41
2:H:182:ILE:CG2	2:H:212:CYS:HB2	2.51	0.41
2:I:116:ARG:CZ	5:M:65:ASN:ND2	2.83	0.41
2:I:197:LEU:HD22	3:K:48:VAL:HG11	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:LYS:HA	1:A:107:ILE:CG1	2.50	0.41
1:B:230:ILE:HD11	1:B:391:VAL:HG11	2.01	0.41
1:B:263:GLY:O	1:B:439:ALA:HB3	2.20	0.41
1:B:508:ILE:HD13	1:B:683:LEU:HD21	2.02	0.41
1:B:533:ARG:NH1	1:C:711:LEU:HD13	2.35	0.41
1:B:609:LEU:HD23	1:B:609:LEU:HA	1.67	0.41
1:B:694:ILE:HD13	1:B:729:PHE:CD2	2.56	0.41
1:D:23:VAL:HG12	1:D:55:VAL:HG21	2.02	0.41
1:D:138:PHE:HB2	1:D:147:LEU:HD11	2.03	0.41
1:D:188:ALA:O	1:D:189:GLU:C	2.63	0.41
1:E:605:ILE:HA	1:E:608:LEU:HB3	2.03	0.41
1:E:676:LEU:HD12	1:E:710:LEU:HD21	2.02	0.41
1:F:64:LEU:CD2	2:G:292:GLU:HB3	2.50	0.41
1:F:347:HIS:O	1:F:350:VAL:HG22	2.21	0.41
2:G:117:PHE:HA	2:G:120:ALA:HB3	2.01	0.41
2:G:271:ARG:HH11	2:G:271:ARG:HG2	1.86	0.41
2:I:275:TRP:CE3	2:I:276:LEU:HD23	2.54	0.41
2:J:149:ALA:HB2	2:J:164:CYS:CB	2.49	0.41
2:J:270:SER:HA	5:M:34:GLN:NE2	2.35	0.41
1:A:262:PRO:CG	1:A:374:ASN:OD1	2.65	0.41
1:A:313:GLN:NE2	1:A:365:ASN:OD1	2.54	0.41
1:B:138:PHE:HB2	1:B:147:LEU:HD11	2.01	0.41
1:C:36:ILE:HD11	1:C:44:LYS:HB3	2.03	0.41
1:C:184:ALA:HB1	1:C:200:LYS:O	2.19	0.41
1:C:218:MET:HA	1:C:219:GLY:HA2	1.83	0.41
1:C:707:ILE:O	1:C:711:LEU:HG	2.21	0.41
1:D:284:VAL:HB	1:D:325:ILE:HA	2.02	0.41
1:D:626:LEU:HD23	1:D:626:LEU:HA	1.81	0.41
1:D:670:ILE:HD11	1:D:705:ILE:HG23	2.01	0.41
1:E:522:GLU:CD	1:E:559:GLU:OE1	2.64	0.41
1:E:614:ILE:C	1:E:616:PRO:HA	2.45	0.41
1:E:652:LEU:HD21	1:E:661:PHE:HE1	1.85	0.41
1:F:609:LEU:HD23	1:F:609:LEU:HA	1.61	0.41
2:G:45:TYR:CE2	2:G:71:LEU:HD11	2.55	0.41
2:G:161:ALA:O	2:G:165:LEU:HG	2.20	0.41
1:A:517:VAL:HG13	1:A:665:ILE:HG21	2.02	0.41
1:B:24:VAL:CG1	1:B:49:LEU:HD22	2.51	0.41
1:B:325:ILE:O	1:B:369:VAL:HG23	2.21	0.41
1:B:648:ARG:HG3	1:B:651:VAL:HG23	2.03	0.41
1:C:64:LEU:CB	1:C:67:ARG:HH21	2.33	0.41
1:C:375:ARG:NH1	1:C:378:LEU:HG	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:517:VAL:HG13	1:C:665:ILE:HG21	2.02	0.41
1:D:92:ILE:HG13	1:D:176:LEU:N	2.35	0.41
1:D:562:PHE:CZ	1:D:597:LEU:HD21	2.56	0.41
1:F:578:GLU:OE2	1:F:619:SER:HB3	2.21	0.41
2:G:47:ARG:O	2:G:50:ASN:HB3	2.20	0.41
2:G:101:ILE:HB	2:G:131:TYR:OH	2.20	0.41
2:H:182:ILE:O	2:H:186:GLU:HG2	2.20	0.41
2:H:237:ASP:C	2:H:239:ARG:N	2.77	0.41
2:I:164:CYS:O	2:I:168:VAL:HG23	2.20	0.41
2:I:188:VAL:HG13	2:I:205:TYR:CD2	2.53	0.41
1:A:235:PHE:HD1	1:A:235:PHE:HA	1.64	0.41
1:B:86:ASP:O	1:B:87:LYS:C	2.63	0.41
1:C:324:ILE:HD12	1:C:324:ILE:N	2.35	0.41
1:D:103:GLN:NE2	2:J:292:GLU:OE2	2.54	0.41
1:E:40:SER:OG	1:E:41:PRO:CD	2.69	0.41
1:E:240:PHE:HA	1:E:241:PRO:HD3	1.91	0.41
1:E:550:THR:CG2	1:E:603:ASP:OD1	2.69	0.41
1:E:585:MET:HE2	1:E:626:LEU:CD2	2.51	0.41
2:H:98:GLN:C	2:H:100:ALA:H	2.29	0.41
5:M:198:ARG:O	5:M:198:ARG:HG2	2.20	0.41
1:A:102:LEU:HB2	1:A:145:PHE:O	2.20	0.41
1:A:231:PHE:CE2	1:A:235:PHE:CD2	3.09	0.41
1:A:240:PHE:HA	1:A:241:PRO:HD3	1.80	0.41
1:A:407:LEU:HD12	1:A:426:ILE:HG23	2.03	0.41
1:A:654:GLU:HG2	1:B:614:ILE:HG13	2.03	0.41
1:B:142:ASP:OD1	1:B:142:ASP:O	2.38	0.41
1:B:324:ILE:HG12	1:B:368:LEU:HD11	2.03	0.41
1:B:397:LEU:HD13	1:B:596:GLN:HG3	2.02	0.41
1:B:488:ILE:O	1:B:490:PRO:N	2.54	0.41
1:B:539:VAL:CG2	1:B:665:ILE:HD12	2.51	0.41
1:B:542:GLU:HG3	1:B:666:HIS:CE1	2.56	0.41
1:D:52:HIS:HA	1:D:53:PRO:HD3	1.92	0.41
1:D:240:PHE:HA	1:D:241:PRO:HD3	1.94	0.41
1:D:513:PRO:CA	1:D:516:ARG:HG2	2.48	0.41
1:D:544:PRO:O	1:D:545:PRO:C	2.64	0.41
1:D:670:ILE:HD11	1:D:705:ILE:CG2	2.51	0.41
1:E:69:TRP:NE1	1:E:134:GLN:HA	2.36	0.41
1:E:399:ASP:OD1	1:E:399:ASP:N	2.54	0.41
1:E:445:VAL:O	1:E:449:GLN:HG2	2.21	0.41
1:E:652:LEU:HD22	1:E:658:LEU:HD13	2.01	0.41
2:G:95:ALA:CB	2:G:97:PRO:HD2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:200:TYR:CZ	5:M:38:GLU:HG2	2.55	0.41
2:G:256:VAL:HG22	2:G:256:VAL:O	2.21	0.41
2:I:155:GLU:HB3	5:M:176:ARG:NH2	2.35	0.41
2:I:161:ALA:O	2:I:165:LEU:HG	2.21	0.41
2:J:179:GLN:HB3	2:J:214:PHE:HB3	2.03	0.41
2:J:211:LEU:HG	2:J:244:MET:HE1	2.03	0.41
2:J:256:VAL:HG22	2:J:256:VAL:O	2.21	0.41
2:J:266:TYR:C	2:J:268:SER:N	2.79	0.41
5:M:148:GLU:O	5:M:152:GLN:HG3	2.21	0.41
1:A:436:PHE:CD2	1:A:444:LEU:HD11	2.55	0.41
1:B:503:ILE:HG22	1:B:506:GLY:H	1.86	0.41
1:C:525:VAL:HG22	1:C:641:LEU:CD2	2.51	0.41
1:D:330:ILE:CD1	1:D:373:THR:HB	2.52	0.41
1:D:541:LEU:HD12	1:D:541:LEU:O	2.20	0.41
1:D:670:ILE:HG12	1:D:705:ILE:O	2.20	0.41
1:D:671:ALA:HA	1:D:703:VAL:O	2.21	0.41
1:D:710:LEU:HG	1:D:714:ILE:HD11	2.03	0.41
1:E:502:TYR:OH	1:E:569:SER:OG	2.39	0.41
1:E:538:SER:OG	1:E:662:SER:N	2.44	0.41
1:F:300:ALA:C	1:F:304:LYS:HG2	2.46	0.41
1:F:525:VAL:HG11	1:F:560:SER:HA	2.03	0.41
2:G:39:GLU:HB2	2:G:75:LEU:HD11	2.03	0.41
2:G:203:LYS:HZ1	2:G:239:ARG:NH2	2.18	0.41
2:H:53:LYS:HE3	2:I:117:PHE:CD2	2.56	0.41
2:J:117:PHE:HA	2:J:120:ALA:HB3	2.03	0.41
2:J:176:GLU:O	2:J:178:TYR:N	2.51	0.41
1:A:402:GLY:O	1:A:406:ILE:HD12	2.20	0.40
1:B:313:GLN:O	1:B:317:GLY:CA	2.70	0.40
1:B:510:TRP:HH2	1:B:668:PRO:O	2.04	0.40
1:B:633:ALA:HA	1:B:634:PRO:HD3	1.89	0.40
1:C:507:ILE:HD11	1:C:551:ALA:HB1	2.03	0.40
1:D:11:CYS:HA	1:D:12:PRO:HD3	1.94	0.40
1:D:52:HIS:C	1:D:54:SER:H	2.29	0.40
1:D:406:ILE:HG23	1:D:410:HIS:CE1	2.55	0.40
1:D:540:LEU:HB2	1:D:661:PHE:CD1	2.56	0.40
1:D:608:LEU:C	1:D:622:VAL:HG11	2.46	0.40
1:E:97:ILE:HG21	1:E:147:LEU:HB3	2.03	0.40
1:E:149:VAL:HG11	1:E:152:ILE:HD11	2.02	0.40
1:E:236:ALA:HA	1:E:239:VAL:CG1	2.51	0.40
1:E:295:VAL:HG23	1:E:296:GLY:N	2.36	0.40
1:F:73:SER:O	1:F:76:GLN:HG2	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:122:ILE:O	1:F:126:ASN:HB3	2.20	0.40
1:F:613:PRO:HD3	1:F:648:ARG:NH1	2.27	0.40
2:G:82:ALA:O	2:G:86:VAL:HG23	2.21	0.40
2:H:205:TYR:H	2:H:205:TYR:HD1	1.69	0.40
2:I:201:SER:HB2	2:I:205:TYR:HE1	1.86	0.40
1:A:395:ILE:HD12	1:A:395:ILE:N	2.36	0.40
1:A:437:SER:O	1:A:440:GLU:HG2	2.22	0.40
1:A:624:GLN:O	1:A:625:ALA:C	2.64	0.40
1:B:240:PHE:HA	1:B:241:PRO:HD3	1.87	0.40
1:B:512:ASP:N	1:B:513:PRO:CD	2.84	0.40
1:B:649:LYS:NZ	1:B:664:THR:HG21	2.37	0.40
1:C:577:SER:O	1:C:578:GLU:C	2.65	0.40
1:D:397:LEU:HD22	1:D:435:ASN:O	2.22	0.40
1:D:529:LYS:HD3	1:D:597:LEU:CD2	2.52	0.40
1:E:196:ILE:N	1:E:196:ILE:CD1	2.83	0.40
1:E:440:GLU:O	1:E:444:LEU:HG	2.21	0.40
1:E:670:ILE:HG22	1:E:672:THR:N	2.30	0.40
1:E:684:GLY:HA2	1:E:691:ARG:HH21	1.86	0.40
1:E:721:ASP:O	1:E:724:TYR:HB2	2.22	0.40
1:F:246:GLU:HG2	1:F:247:GLN:N	2.36	0.40
1:F:635:PRO:HD2	1:F:638:ARG:HD2	2.02	0.40
2:I:45:TYR:HB2	2:I:68:ALA:HB2	2.03	0.40
2:I:180:LYS:O	2:I:184:ILE:HG13	2.22	0.40
2:J:231:LEU:O	2:J:232:PHE:C	2.64	0.40
5:M:47:LEU:HD23	5:M:50:LEU:HD12	2.02	0.40
1:A:497:GLU:O	1:A:498:ASP:C	2.65	0.40
1:B:189:GLU:O	1:B:190:ASN:C	2.64	0.40
1:B:544:PRO:HG3	1:B:669:ASN:H	1.86	0.40
1:B:589:PHE:CE2	1:B:629:LEU:HD13	2.57	0.40
1:B:632:LYS:HE3	1:B:633:ALA:O	2.21	0.40
1:B:710:LEU:O	1:B:714:ILE:HG13	2.21	0.40
1:C:153:GLU:OE1	1:C:169:ARG:HD3	2.21	0.40
1:C:258:LEU:HD12	1:C:258:LEU:O	2.21	0.40
1:C:603:ASP:HA	1:C:645:THR:OG1	2.21	0.40
1:C:687:LYS:HB2	1:C:690:GLU:OE1	2.21	0.40
1:C:709:LYS:HE2	1:C:713:LEU:HD21	2.04	0.40
1:D:186:GLU:O	1:D:186:GLU:HG3	2.22	0.40
1:D:198:LYS:HG2	1:D:243:GLU:OE2	2.22	0.40
1:D:300:ALA:O	1:D:304:LYS:HG3	2.21	0.40
1:E:254:LYS:O	1:E:368:LEU:HA	2.21	0.40
1:F:52:HIS:C	1:F:54:SER:H	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:257:LEU:HG	1:F:371:GLY:O	2.20	0.40
1:F:612:VAL:HG13	1:F:614:ILE:O	2.21	0.40
1:F:686:PHE:HB2	1:F:691:ARG:HG3	2.03	0.40
3:K:74:ALA:HA	5:M:192:ILE:HG21	2.02	0.40
1:A:256:ILE:CG1	1:A:370:ILE:HG22	2.51	0.40
1:A:295:VAL:HG12	1:B:293:LYS:N	2.36	0.40
1:A:375:ARG:HA	1:A:376:PRO:HD2	1.97	0.40
1:A:408:HIS:HA	1:A:426:ILE:HD12	2.04	0.40
1:A:426:ILE:HG23	1:A:426:ILE:HD12	1.71	0.40
1:B:323:HIS:HB2	1:B:367:ILE:HG22	2.03	0.40
1:B:533:ARG:HD3	1:C:505:ASN:ND2	2.36	0.40
1:B:546:HIS:C	1:B:547:SER:HG	2.18	0.40
1:B:720:MET:HB3	1:B:724:TYR:HB2	2.04	0.40
1:C:64:LEU:O	1:C:68:LYS:HG3	2.21	0.40
1:C:254:LYS:O	1:C:368:LEU:HA	2.22	0.40
1:C:411:THR:O	1:C:414:MET:HB2	2.22	0.40
1:C:629:LEU:HA	1:C:629:LEU:HD23	1.74	0.40
1:D:356:SER:OG	1:E:288:PRO:HB3	2.22	0.40
1:D:570:PRO:O	1:D:573:MET:HB3	2.22	0.40
1:D:627:LEU:HA	1:D:627:LEU:HD23	1.71	0.40
1:D:694:ILE:HD13	1:D:729:PHE:CD2	2.55	0.40
1:E:99:ILE:HA	1:E:146:GLY:O	2.21	0.40
1:E:587:LYS:NZ	1:E:591:ASP:CG	2.79	0.40
1:F:101:PHE:HB2	1:F:107:ILE:HG12	2.03	0.40
1:F:678:GLU:O	1:F:682:LEU:HG	2.21	0.40
2:G:98:GLN:O	2:G:99:GLU:C	2.64	0.40
2:H:243:LEU:O	2:H:247:LEU:HG	2.21	0.40
2:I:79:HIS:HD2	5:M:69:GLN:HG3	1.85	0.40
2:J:45:TYR:HE2	2:J:71:LEU:HD11	1.86	0.40
5:M:177:GLN:O	5:M:181:ILE:HG13	2.22	0.40
1:A:263:GLY:O	1:A:437:SER:HB3	2.21	0.40
1:A:526:GLN:O	1:A:530:ASN:HB2	2.20	0.40
1:A:612:VAL:N	1:A:617:ARG:O	2.46	0.40
1:B:100:ASP:O	1:B:146:GLY:N	2.55	0.40
1:B:399:ASP:CB	1:B:402:GLY:H	2.34	0.40
1:B:721:ASP:C	1:B:723:GLU:H	2.29	0.40
1:C:180:ASN:HD22	1:C:180:ASN:C	2.26	0.40
1:C:284:VAL:HG23	1:C:324:ILE:O	2.21	0.40
1:C:407:LEU:C	1:C:407:LEU:HD12	2.47	0.40
1:C:626:LEU:HA	1:C:626:LEU:HD23	1.86	0.40
1:D:258:LEU:CD1	1:D:372:MET:HG2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:278:ASN:O	1:D:279:ALA:C	2.64	0.40
1:D:527:GLN:HE22	1:E:716:MET:CA	2.33	0.40
1:D:549:LYS:HB3	1:D:645:THR:HB	2.03	0.40
1:D:687:LYS:O	1:D:690:GLU:HG2	2.22	0.40
1:E:326:ILE:HG22	1:E:370:ILE:CG1	2.49	0.40
1:E:643:ILE:HD12	1:E:643:ILE:N	2.36	0.40
2:G:282:ARG:O	2:G:286:THR:HG23	2.21	0.40
2:I:186:GLU:O	2:I:190:THR:HG23	2.22	0.40
5:M:67:ILE:O	5:M:71:MET:HG2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	668/747 (89%)	610 (91%)	43 (6%)	15 (2%)	5	29
1	B	662/747 (89%)	592 (89%)	55 (8%)	15 (2%)	5	28
1	C	666/747 (89%)	616 (92%)	37 (6%)	13 (2%)	6	31
1	D	663/747 (89%)	607 (92%)	44 (7%)	12 (2%)	6	34
1	E	658/747 (88%)	604 (92%)	43 (6%)	11 (2%)	7	36
1	F	644/747 (86%)	583 (90%)	43 (7%)	18 (3%)	4	24
2	G	284/297 (96%)	238 (84%)	34 (12%)	12 (4%)	2	17
2	H	284/297 (96%)	232 (82%)	44 (16%)	8 (3%)	4	24
2	I	284/297 (96%)	233 (82%)	44 (16%)	7 (2%)	4	26
2	J	284/297 (96%)	234 (82%)	41 (14%)	9 (3%)	3	21
3	K	59/63 (94%)	55 (93%)	2 (3%)	2 (3%)	3	21
4	L	64/67 (96%)	60 (94%)	3 (5%)	1 (2%)	7	38
5	M	127/188 (68%)	125 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	5347/5988 (89%)	4789 (90%)	435 (8%)	123 (2%)	7	28

All (123) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	LEU
1	A	293	LYS
1	A	294	TYR
1	A	318	ALA
1	A	333	ILE
1	A	397	LEU
1	A	498	ASP
1	B	283	LYS
1	B	297	GLU
1	B	318	ALA
1	B	439	ALA
1	B	489	LYS
1	C	190	ASN
1	C	297	GLU
1	C	318	ALA
1	C	497	GLU
1	C	498	ASP
1	C	578	GLU
1	D	12	PRO
1	D	283	LYS
1	D	318	ALA
1	D	489	LYS
1	E	12	PRO
1	E	283	LYS
1	E	297	GLU
1	E	318	ALA
1	E	439	ALA
1	E	489	LYS
1	F	283	LYS
1	F	297	GLU
1	F	318	ALA
1	F	397	LEU
1	F	439	ALA
2	G	58	TRP
2	G	76	GLN
2	G	100	ALA
2	H	79	HIS

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Mol	Chain	Res	Type
2	I	58	TRP
2	I	76	GLN
2	J	76	GLN
1	A	88	ALA
1	B	12	PRO
1	B	89	LYS
1	B	502	TYR
1	C	293	LYS
1	C	610	ASP
1	F	12	PRO
1	F	89	LYS
1	F	102	LEU
1	F	193	LEU
2	G	79	HIS
2	G	157	SER
2	G	176	GLU
2	G	177	GLN
2	G	240	GLU
2	H	58	TRP
2	H	76	GLN
2	I	176	GLU
2	J	33	GLY
2	J	58	TRP
2	J	79	HIS
3	K	36	GLN
1	A	105	LYS
1	A	241	PRO
1	A	242	PRO
1	A	264	CYS
1	B	87	LYS
1	B	241	PRO
1	B	293	LYS
1	C	87	LYS
1	C	241	PRO
1	D	293	LYS
1	E	241	PRO
1	E	293	LYS
1	E	507	ILE
1	F	241	PRO
1	F	293	LYS
2	H	254	GLN
2	I	177	GLN

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Mol	Chain	Res	Type
2	J	240	GLU
3	K	61	SER
1	B	88	ALA
1	B	546	HIS
1	C	12	PRO
1	D	13	THR
1	D	87	LYS
1	D	189	GLU
2	G	26	SER
2	G	99	GLU
2	H	196	PRO
2	H	240	GLU
2	H	267	ASP
2	I	79	HIS
2	I	240	GLU
1	A	398	PRO
1	A	668	PRO
1	C	53	PRO
1	D	241	PRO
1	E	438	GLY
2	G	235	PHE
2	I	256	VAL
2	J	21	VAL
2	J	97	PRO
2	J	256	VAL
4	L	237	VAL
1	A	53	PRO
1	B	438	GLY
1	B	490	PRO
1	D	53	PRO
1	E	490	PRO
1	F	87	LYS
1	F	438	GLY
1	F	668	PRO
2	G	256	VAL
1	D	488	ILE
1	D	545	PRO
1	F	684	GLY
1	F	53	PRO
2	J	233	PRO
1	C	490	PRO
1	F	398	PRO

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Mol	Chain	Res	Type
1	F	544	PRO
2	H	233	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	515/638 (81%)	483 (94%)	32 (6%)	16	38
1	B	521/638 (82%)	504 (97%)	17 (3%)	33	55
1	C	516/638 (81%)	491 (95%)	25 (5%)	23	44
1	D	511/638 (80%)	491 (96%)	20 (4%)	28	49
1	E	516/638 (81%)	494 (96%)	22 (4%)	26	47
1	F	512/638 (80%)	493 (96%)	19 (4%)	30	51
2	G	235/244 (96%)	235 (100%)	0	100	100
2	H	235/244 (96%)	234 (100%)	1 (0%)	84	84
2	I	234/244 (96%)	234 (100%)	0	100	100
2	J	235/244 (96%)	234 (100%)	1 (0%)	84	84
3	K	52/54 (96%)	52 (100%)	0	100	100
4	L	60/61 (98%)	58 (97%)	2 (3%)	33	55
5	M	113/161 (70%)	113 (100%)	0	100	100
All	All	4255/5080 (84%)	4116 (97%)	139 (3%)	34	55

All (139) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	LYS
1	A	198	LYS
1	A	246	GLU
1	A	253	VAL
1	A	284	VAL
1	A	305	LEU

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Mol	Chain	Res	Type
1	A	322	LEU
1	A	326	ILE
1	A	358	ILE
1	A	367	ILE
1	A	375	ARG
1	A	409	ILE
1	A	445	VAL
1	A	449	GLN
1	A	504	MET
1	A	530	ASN
1	A	537	VAL
1	A	539	VAL
1	A	550	THR
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	A	710	LEU
1	B	42	ASN
1	B	180	ASN
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	389	LEU
1	B	411	THR
1	B	567	ILE
1	B	610	ASP
1	B	623	LEU
1	B	626	LEU

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Mol	Chain	Res	Type
1	B	651	VAL
1	C	180	ASN
1	C	246	GLU
1	C	268	LEU
1	C	273	ILE
1	C	305	LEU
1	C	312	GLU
1	C	316	LEU
1	C	322	LEU
1	C	324	ILE
1	C	326	ILE
1	C	367	ILE
1	C	411	THR
1	C	537	VAL
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	105	LYS
1	D	189	GLU
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	389	LEU
1	D	407	LEU
1	D	419	LEU
1	D	424	VAL
1	D	601	VAL
1	D	602	VAL
1	D	645	THR
1	D	663	THR

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Mol	Chain	Res	Type
1	D	666	HIS
1	D	681	GLU
1	D	713	LEU
1	D	716	MET
1	E	196	ILE
1	E	246	GLU
1	E	284	VAL
1	E	285	VAL
1	E	305	LEU
1	E	322	LEU
1	E	325	ILE
1	E	330	ILE
1	E	351	VAL
1	E	381	GLU
1	E	389	LEU
1	E	397	LEU
1	E	411	THR
1	E	457	ILE
1	E	508	ILE
1	E	522	GLU
1	E	537	VAL
1	E	586	LYS
1	E	602	VAL
1	E	626	LEU
1	E	658	LEU
1	E	689	LYS
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	411	THR
1	F	457	ILE
1	F	519	ASP
1	F	524	LEU
1	F	536	LEU
1	F	537	VAL

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Mol	Chain	Res	Type
1	F	578	GLU
1	F	606	GLU
1	F	651	VAL
2	H	281	LEU
2	J	199	LYS
4	L	210	ARG
4	L	226	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (79) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	33	GLN
1	A	103	GLN
1	A	272	GLN
1	A	353	GLN
1	A	418	GLN
1	A	526	GLN
1	A	527	GLN
1	A	530	ASN
1	A	583	GLN
1	A	719	GLN
1	B	20	ASN
1	B	33	GLN
1	B	42	ASN
1	B	319	ASN
1	B	405	GLN
1	B	418	GLN
1	B	456	HIS
1	B	526	GLN
1	B	530	ASN
1	B	546	HIS
1	C	20	ASN
1	C	194	ASN
1	C	319	ASN
1	C	405	GLN
1	C	418	GLN
1	C	675	GLN
1	D	42	ASN
1	D	90	GLN
1	D	106	ASN
1	D	110	ASN

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Mol	Chain	Res	Type
1	D	141	ASN
1	D	286	ASN
1	D	353	GLN
1	D	454	ASN
1	D	526	GLN
1	D	527	GLN
1	D	596	GLN
1	D	675	GLN
1	E	20	ASN
1	E	43	HIS
1	E	134	GLN
1	E	141	ASN
1	E	405	GLN
1	E	418	GLN
1	E	505	ASN
1	E	527	GLN
1	E	620	ASN
1	E	624	GLN
1	E	659	ASN
1	F	194	ASN
1	F	319	ASN
1	F	405	GLN
1	F	418	GLN
1	F	527	GLN
1	F	675	GLN
2	G	67	GLN
2	G	72	HIS
2	G	162	ASN
2	G	177	GLN
2	G	179	GLN
2	H	72	HIS
2	H	179	GLN
2	H	187	GLN
2	H	213	HIS
2	H	226	GLN
2	I	50	ASN
2	I	79	HIS
2	I	123	HIS
2	I	177	GLN
2	I	187	GLN
2	I	226	GLN
2	J	57	ASN

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Mol	Chain	Res	Type
2	J	72	HIS
2	J	187	GLN
2	J	251	HIS
4	L	207	ASN
4	L	226	GLN
5	M	69	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [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.

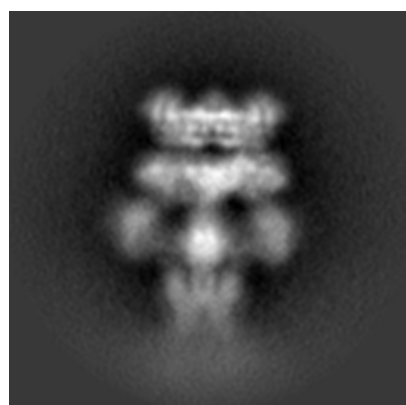
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6206. These allow visual inspection of the internal detail of the map and identification of artifacts.

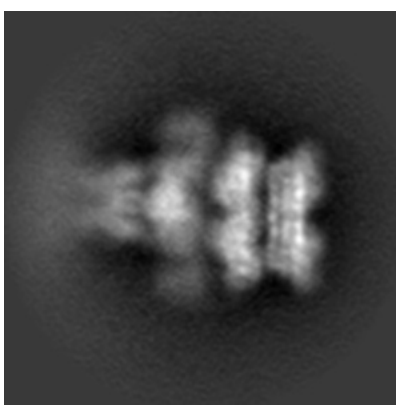
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

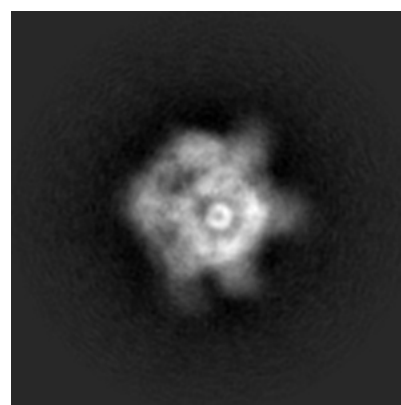
6.1.1 Primary map



X



Y



Z

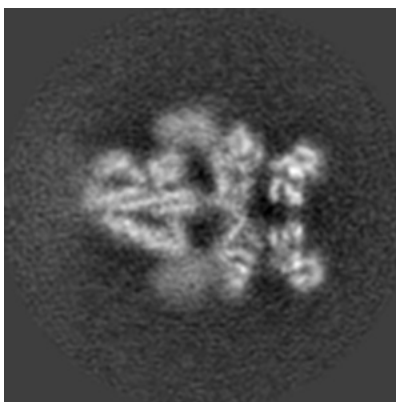
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

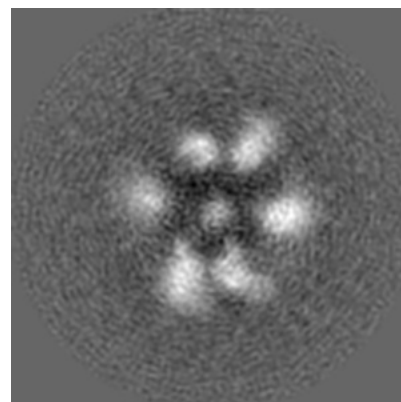
6.2.1 Primary map



X Index: 64



Y Index: 64



Z Index: 64

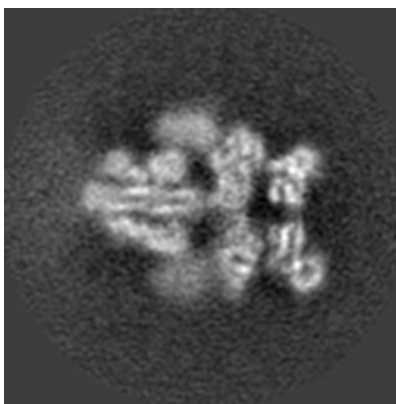
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

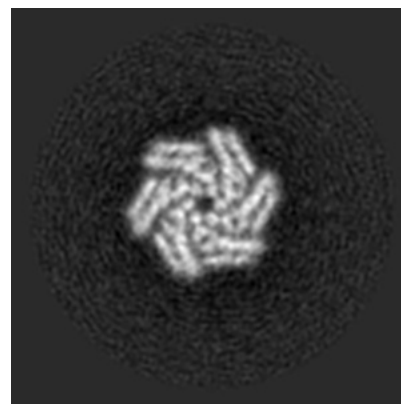
6.3.1 Primary map



X Index: 68



Y Index: 63



Z Index: 94

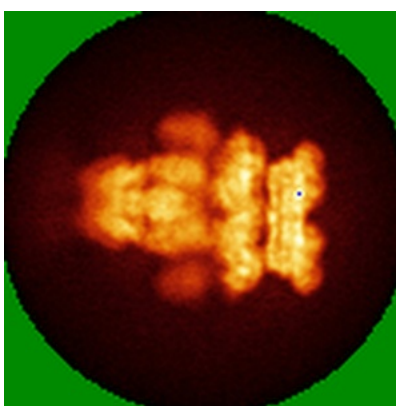
The images above show the largest variance slices of the map in three orthogonal directions.

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

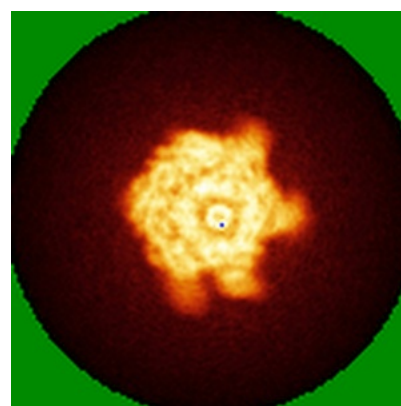
6.4.1 Primary map



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

This section was not generated.

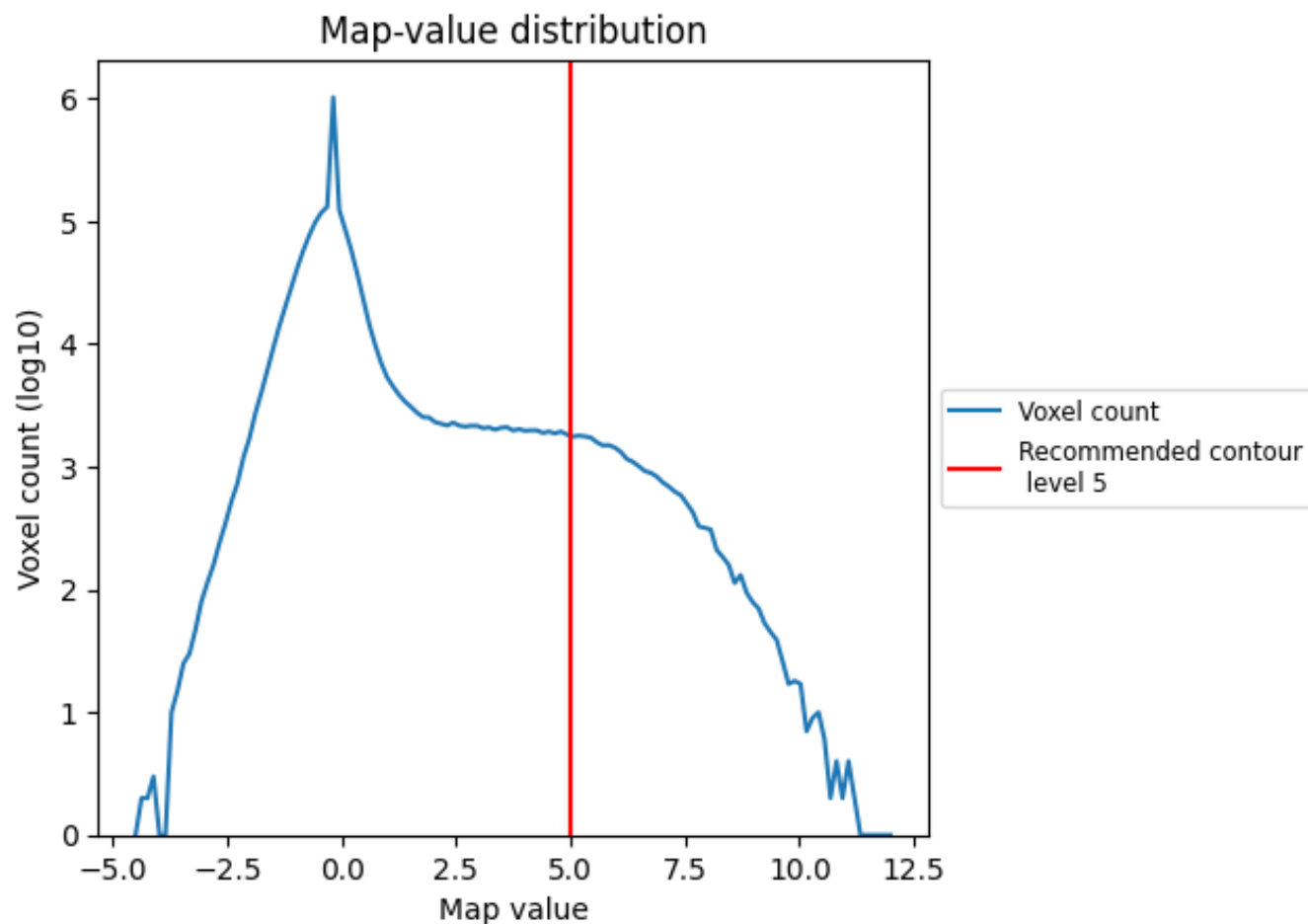
6.6 Mask visualisation

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

7 Map analysis [i](#)

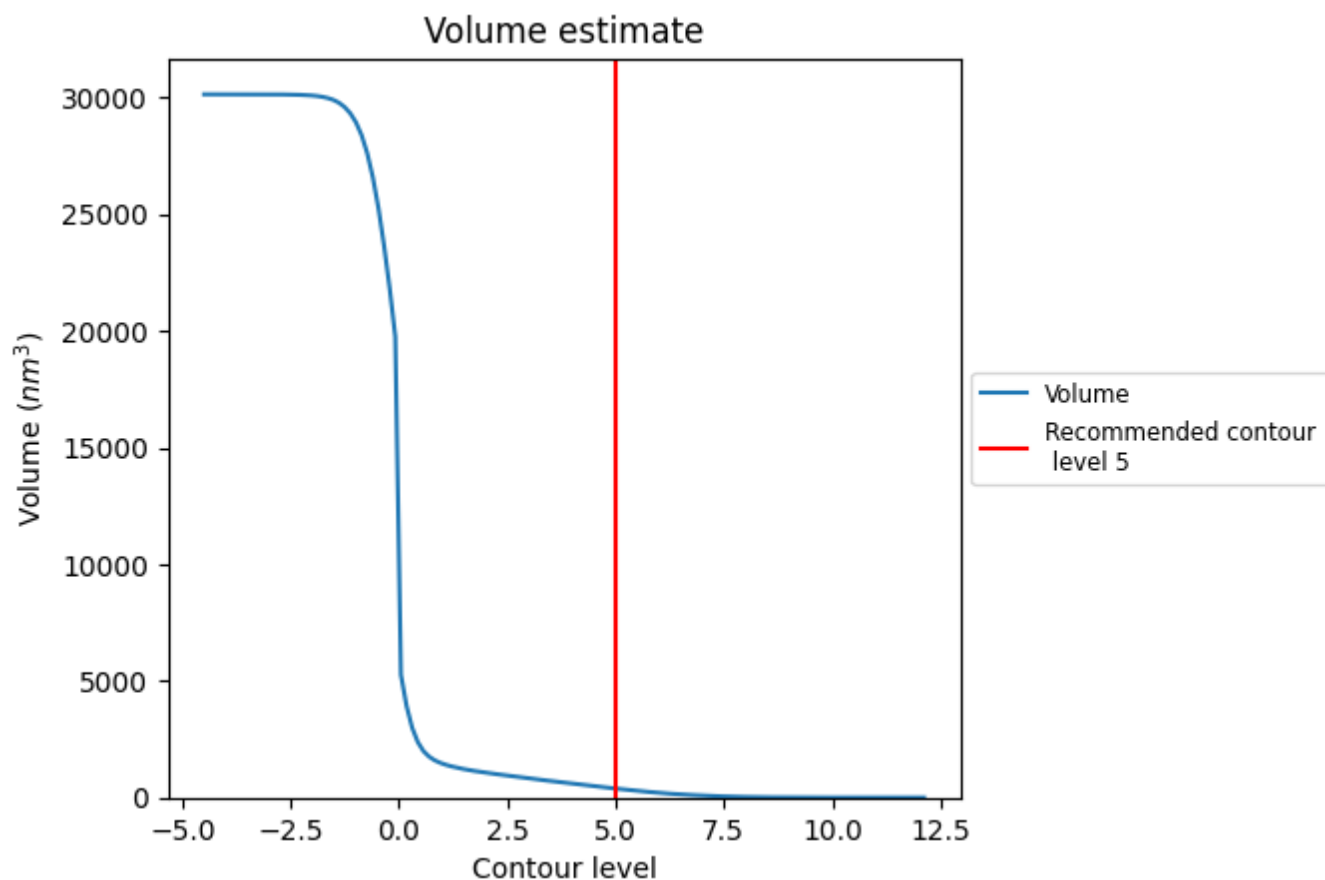
This section contains the results of statistical analysis of the map.

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.

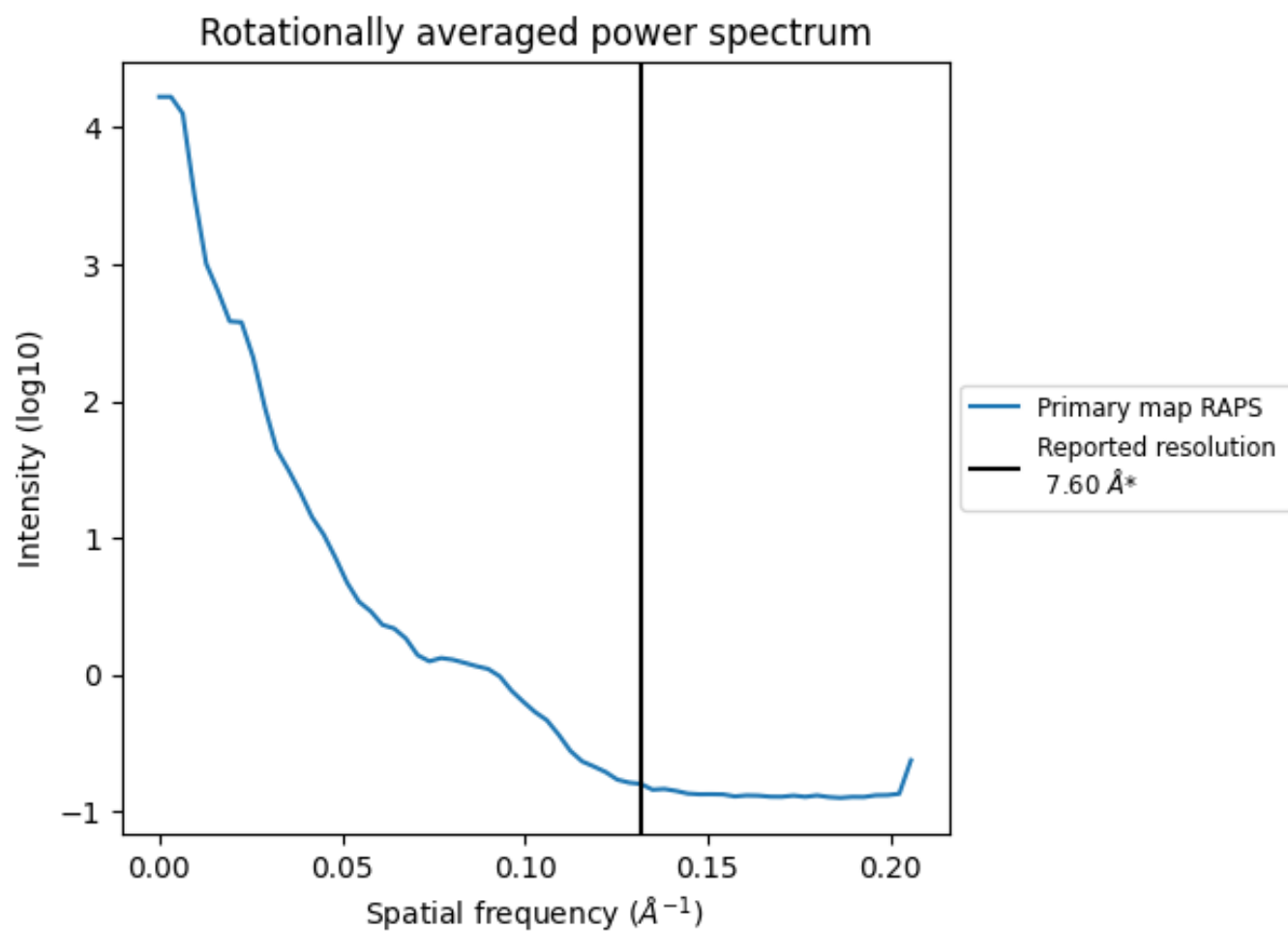
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 386 nm³; this corresponds to an approximate mass of 349 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 0.132 Å⁻¹

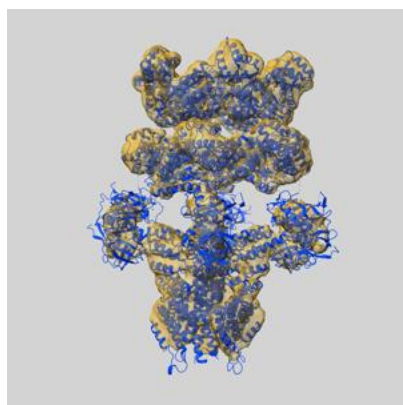
8 Fourier-Shell correlation

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

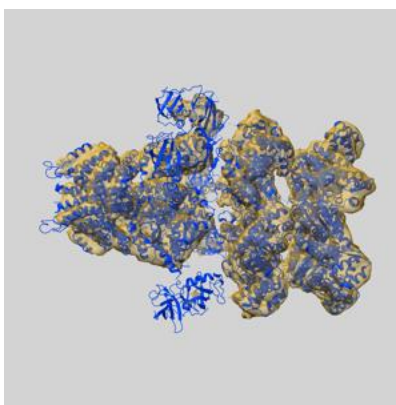
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6206 and PDB model 3J96. Per-residue inclusion information can be found in section [3](#) on page [7](#).

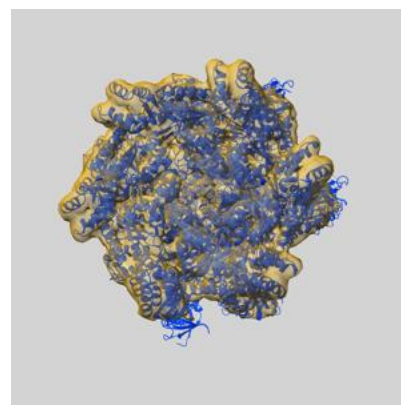
9.1 Map-model overlay [i](#)



X



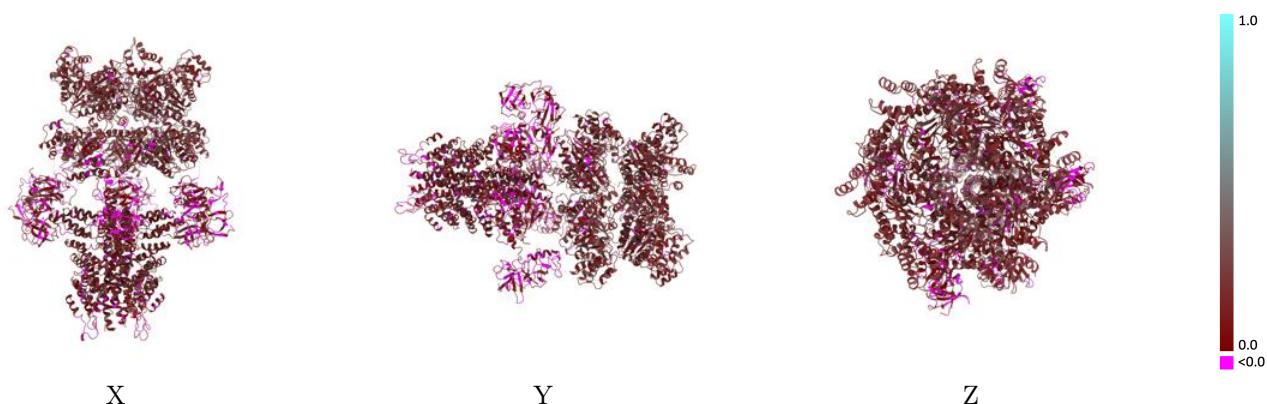
Y



Z

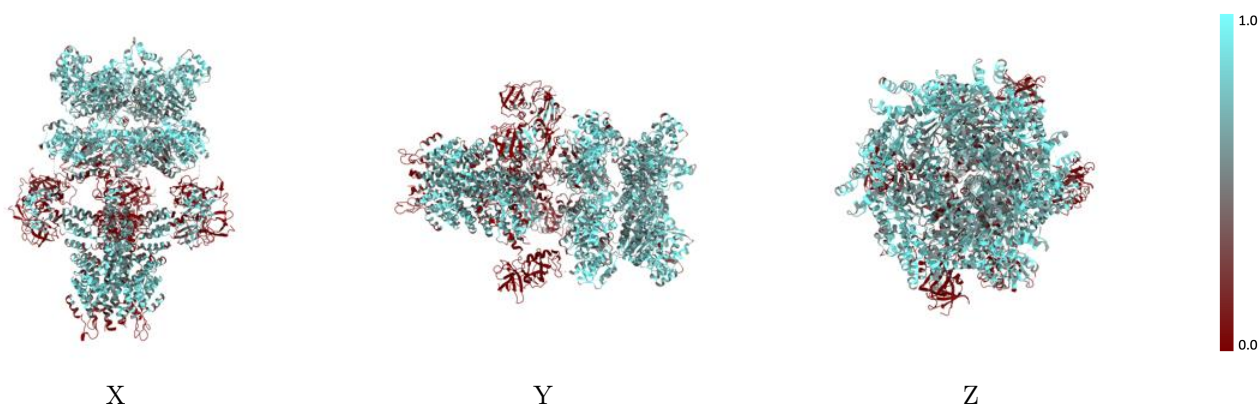
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



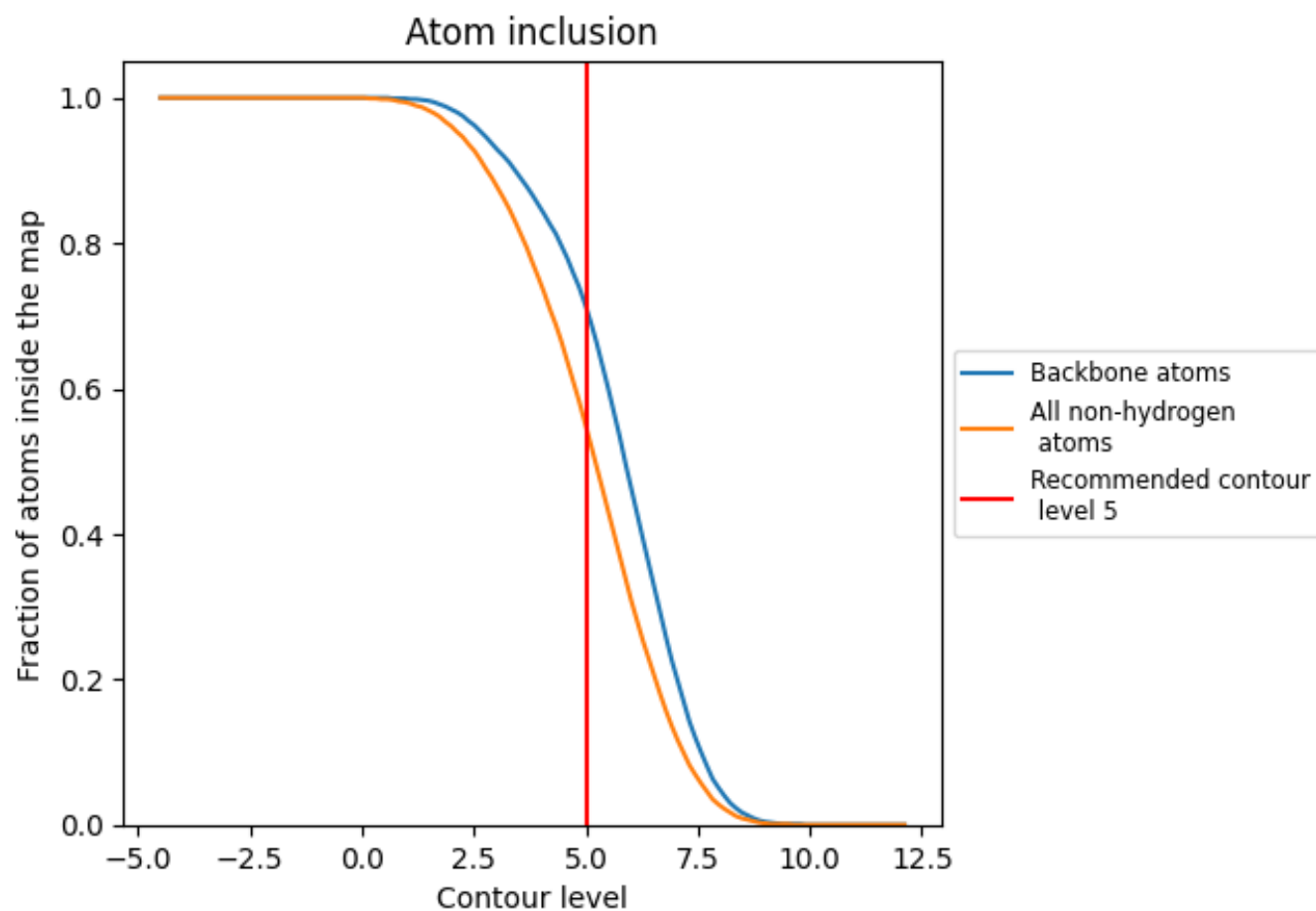
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 55% 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	 0.5490	 0.1400
A	 0.4770	 0.1340
B	 0.6420	 0.1580
C	 0.5610	 0.1520
D	 0.5380	 0.1420
E	 0.5540	 0.1530
F	 0.4770	 0.1300
G	 0.5890	 0.1370
H	 0.5810	 0.1250
I	 0.5710	 0.1260
J	 0.5540	 0.1200
K	 0.5320	 0.1260
L	 0.5460	 0.1200
M	 0.5510	 0.1390

