Full wwPDB EM Validation Report ⓘ

Feb 12, 2024 – 11:42 AM EST

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

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:

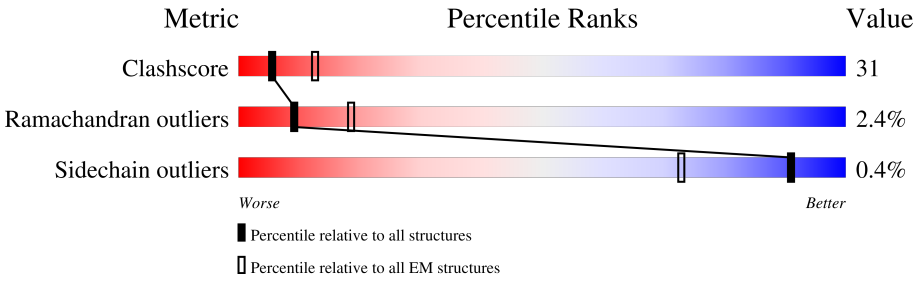
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance

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

The reported resolution of this entry is 7.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	41% 45% 44% • • 9%
1	B	747	28% 48% 40% • 10%
1	C	747	19% 46% 42% • 10%
1	D	747	34% 46% 43% • 10%
1	E	747	36% 44% 44% • 10%
1	F	747	37% 46% 40% • 12%
2	G	297	28% 56% 38% • •
2	H	297	23% 52% 42% • •

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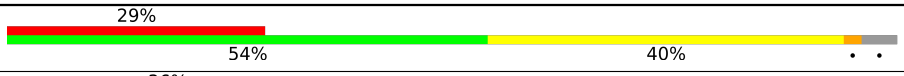
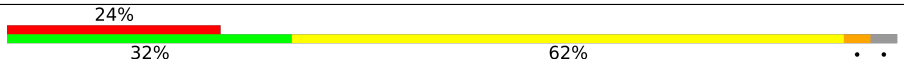
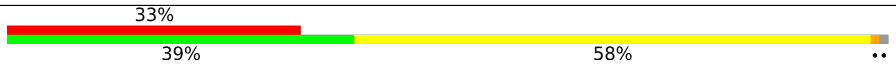
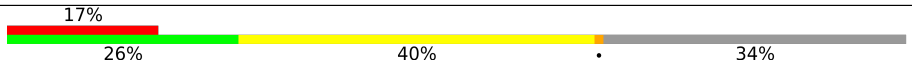
Mol	Chain	Length	Quality of chain
2	I	297	
2	J	297	
3	K	63	
4	L	67	
5	M	198	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 41095 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Vesicle-fusing ATPase.

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

There are 18 discrepancies between the modelled and reference sequences:

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

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

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

There are 8 discrepancies between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

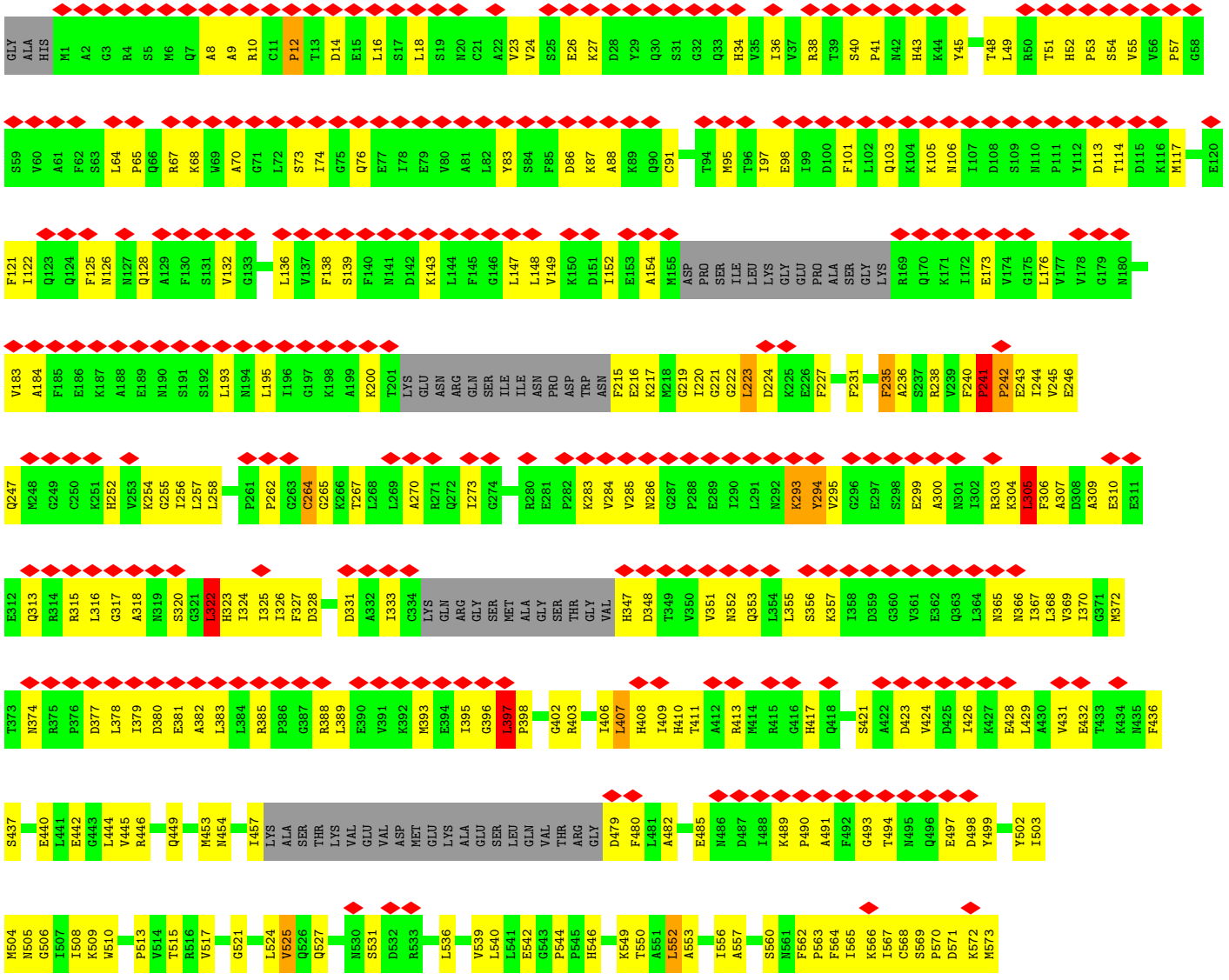
Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	131	Total	C	N	O	S	0	0
			1029	609	191	220	9		

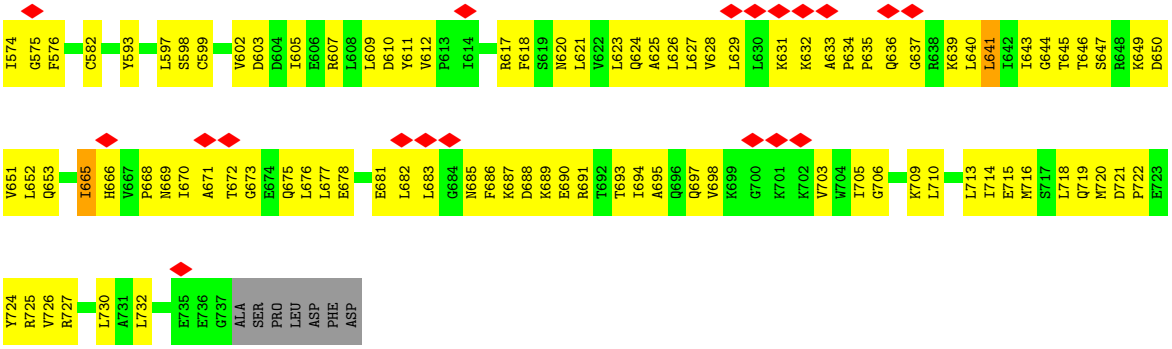
3 Residue-property plots (i)

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

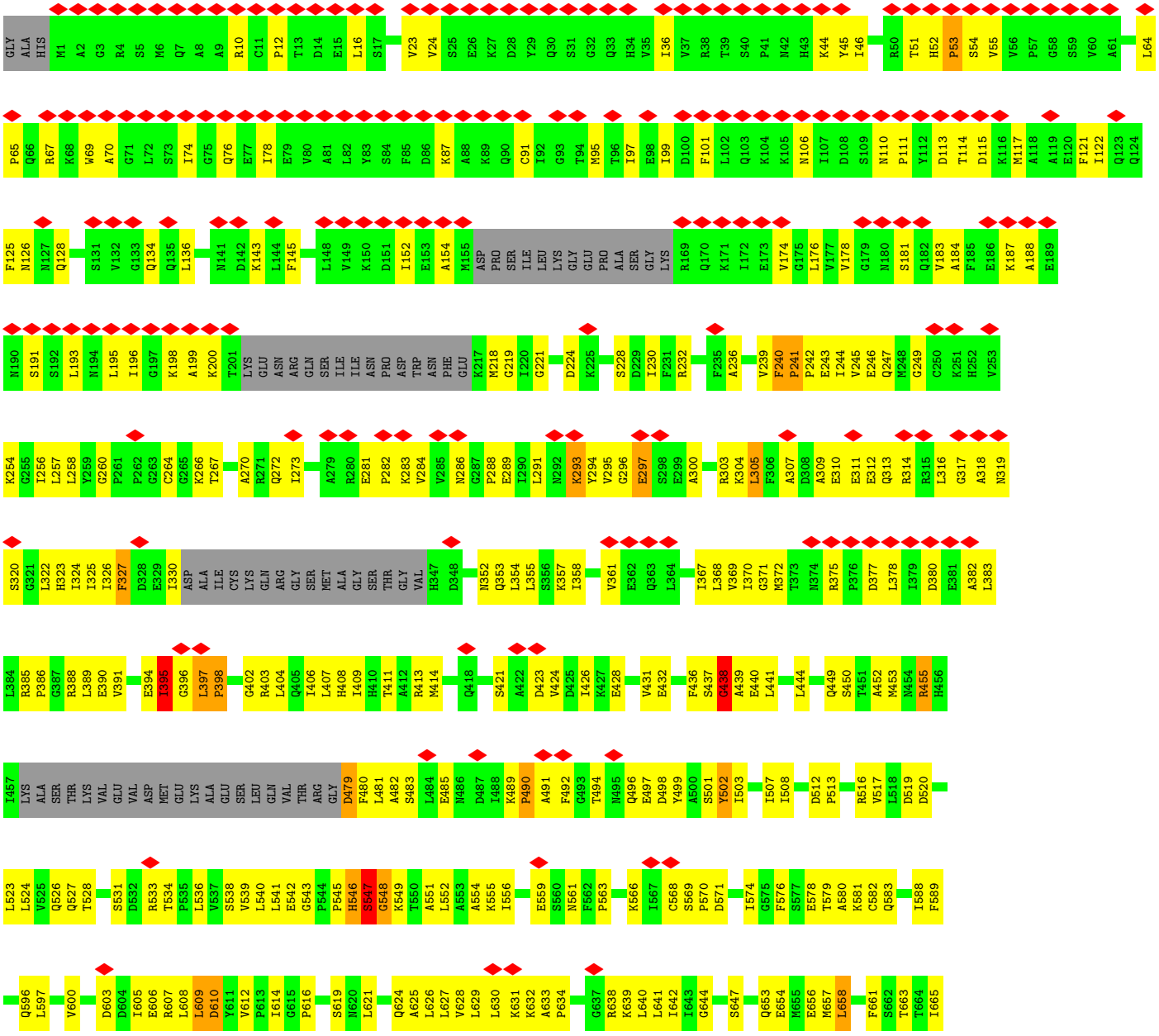
Chain A:

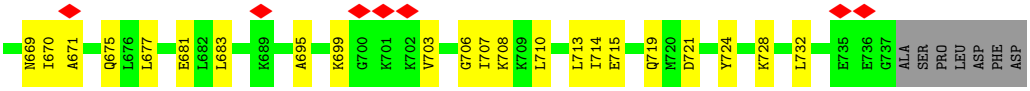




• Molecule 1: Vesicle-fusing ATPase

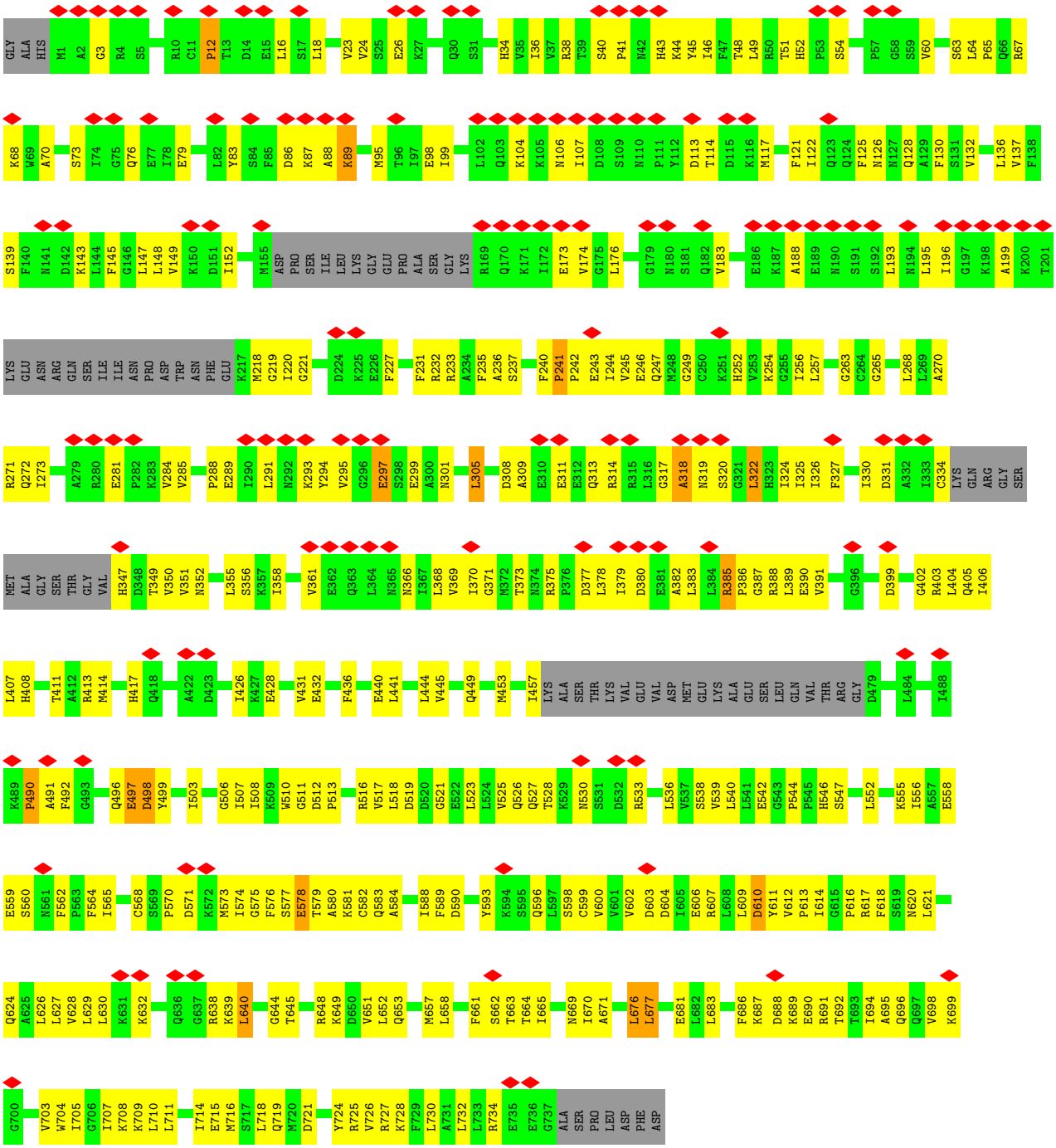
Chain B:





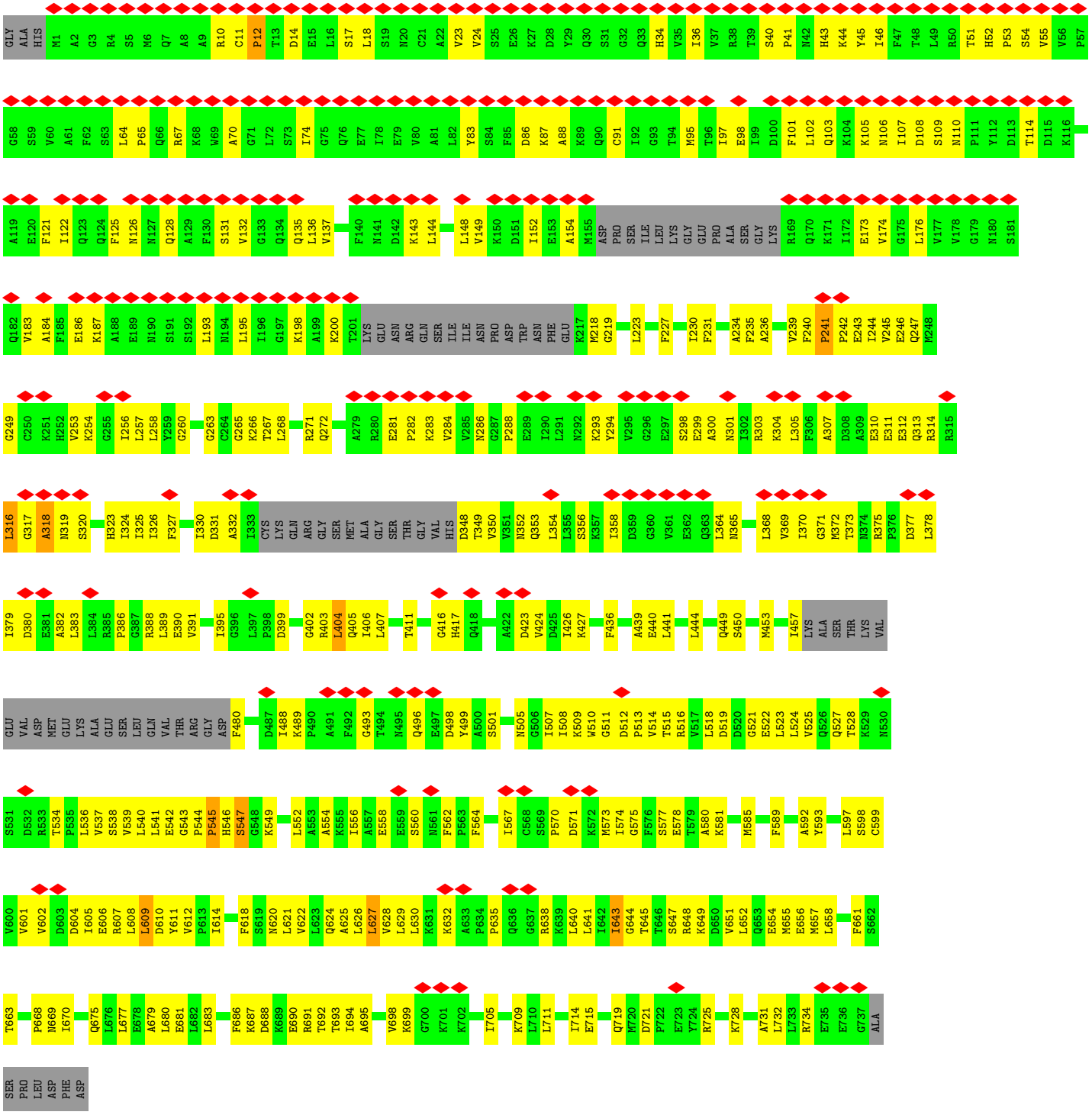
• Molecule 1: Vesicle-fusing ATPase

Chain C:



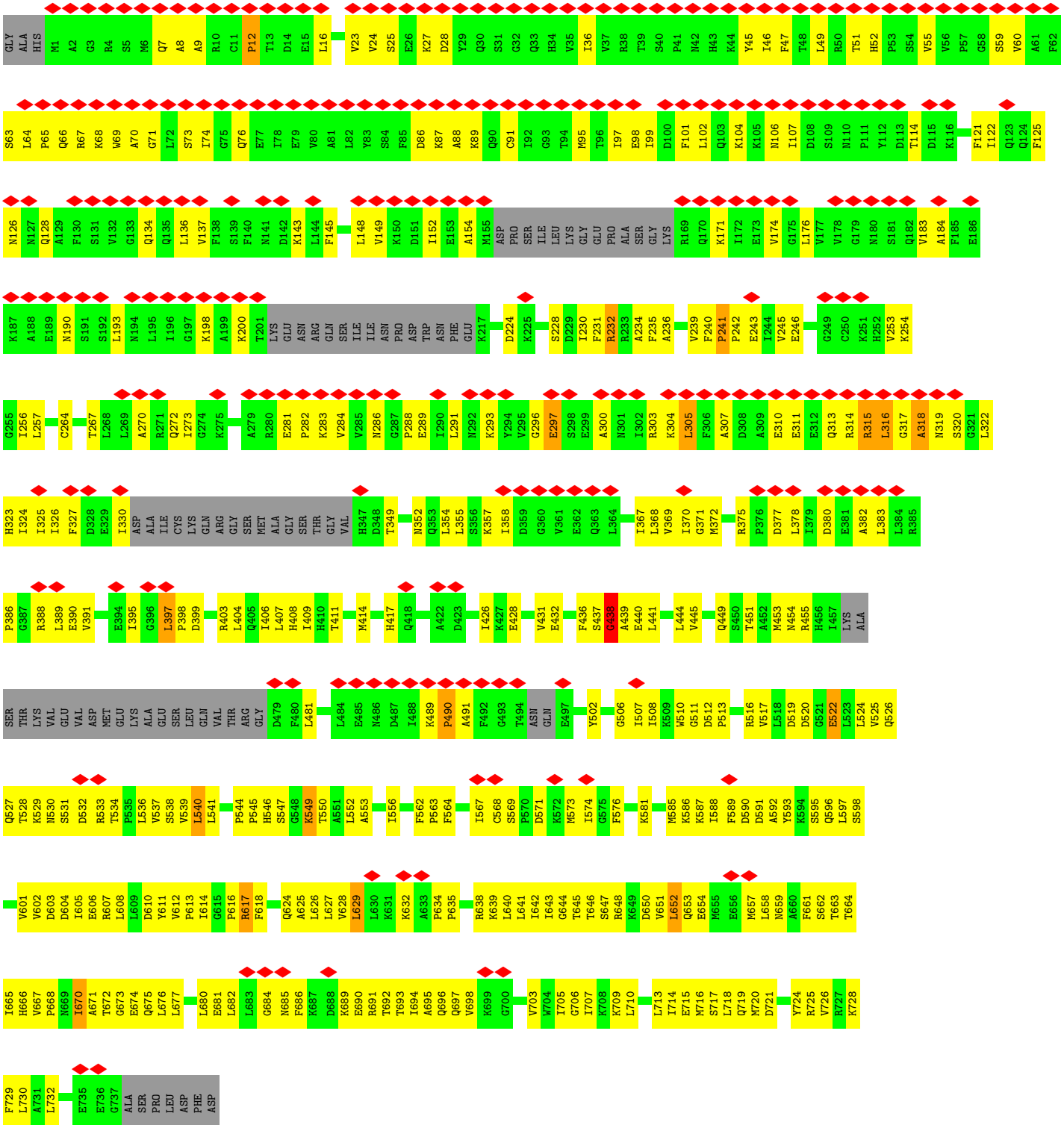
• Molecule 1: Vesicle-fusing ATPase

Chain D:



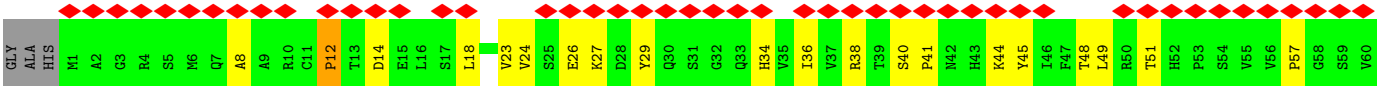
• Molecule 1: Vesicle-fusing ATPase

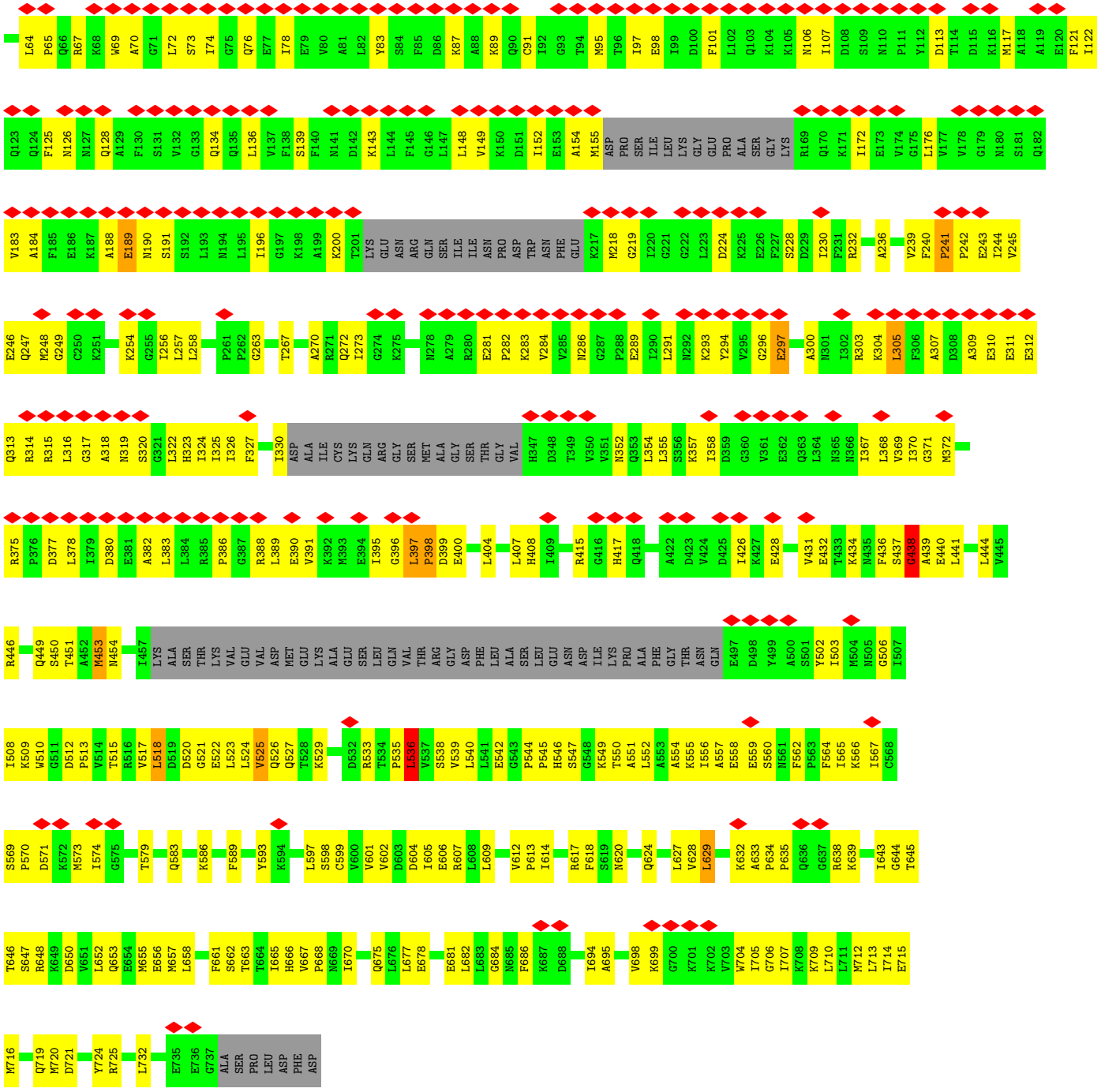
Chain E:



• Molecule 1: Vesicle-fusing ATPase

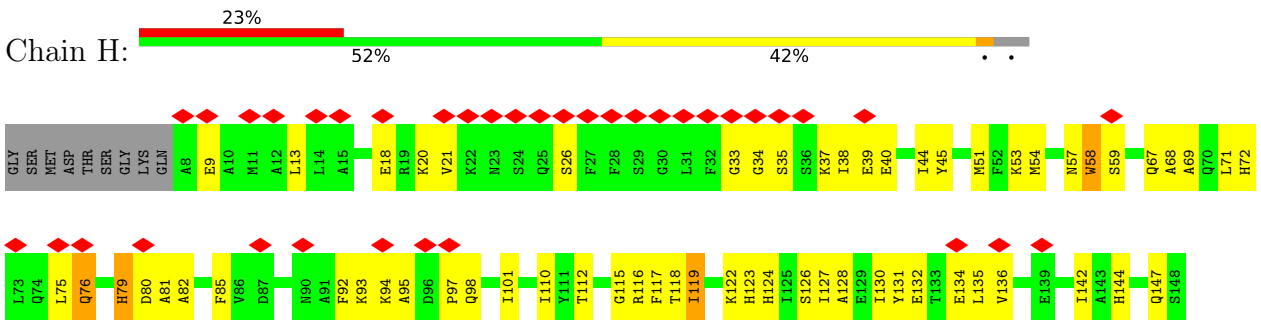
Chain F:

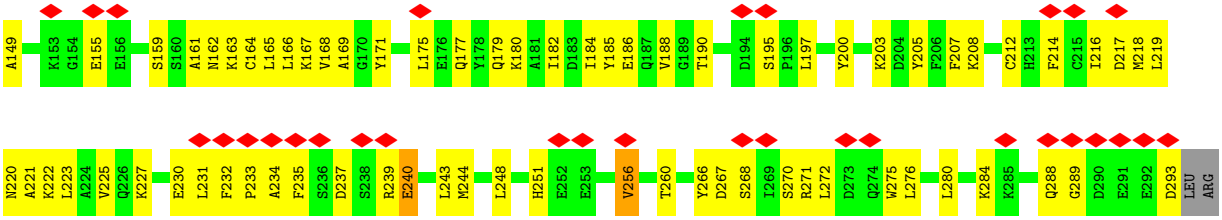




• Molecule 2: Alpha-soluble NSF attachment protein

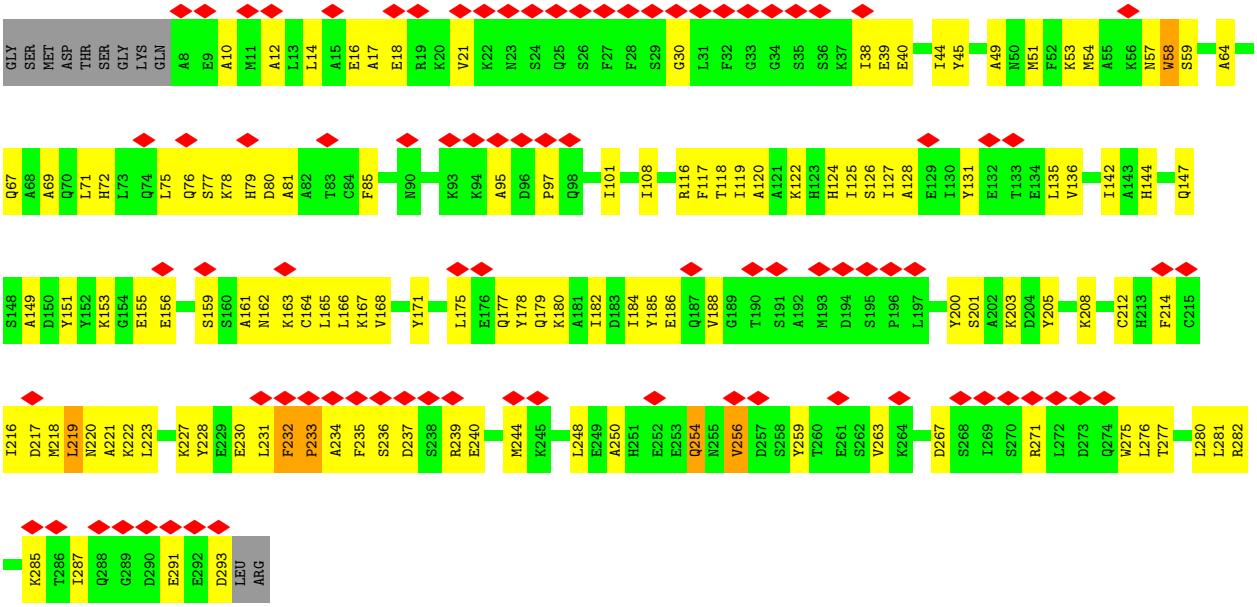
Chain H:





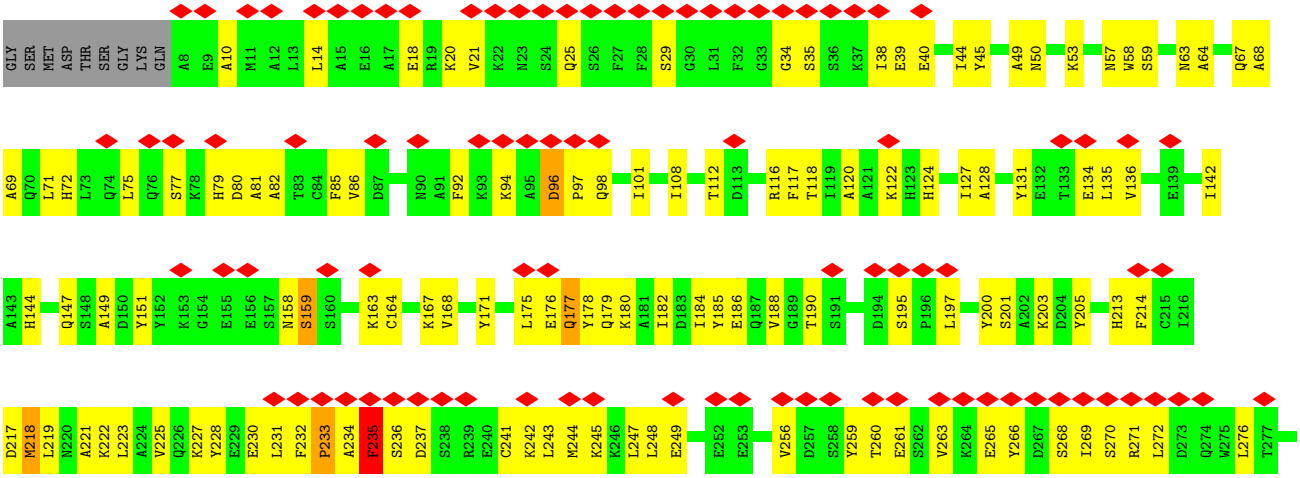
• Molecule 2: Alpha-soluble NSF attachment protein

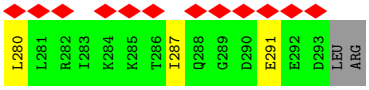
Chain I:



• Molecule 2: Alpha-soluble NSF attachment protein

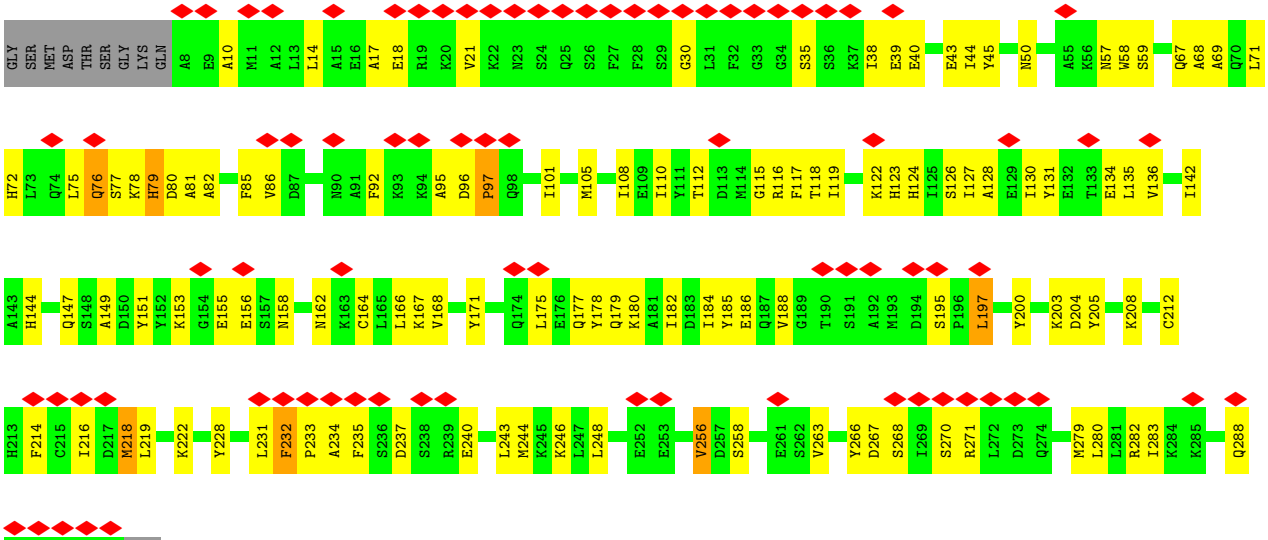
Chain J:





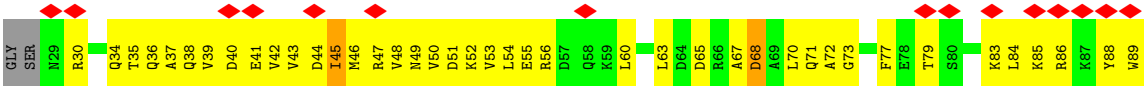
• Molecule 2: Alpha-soluble NSF attachment protein

Chain G:



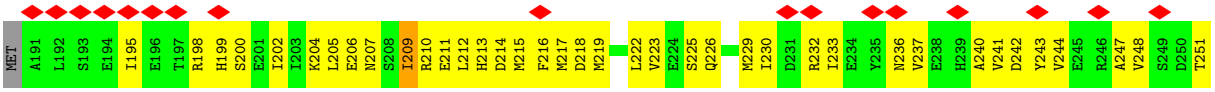
• Molecule 3: Vesicle-associated membrane protein 2

Chain K:



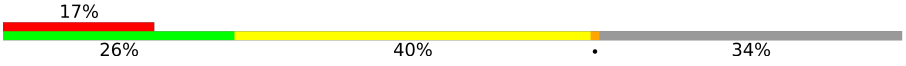
• Molecule 4: Syntaxin-1A

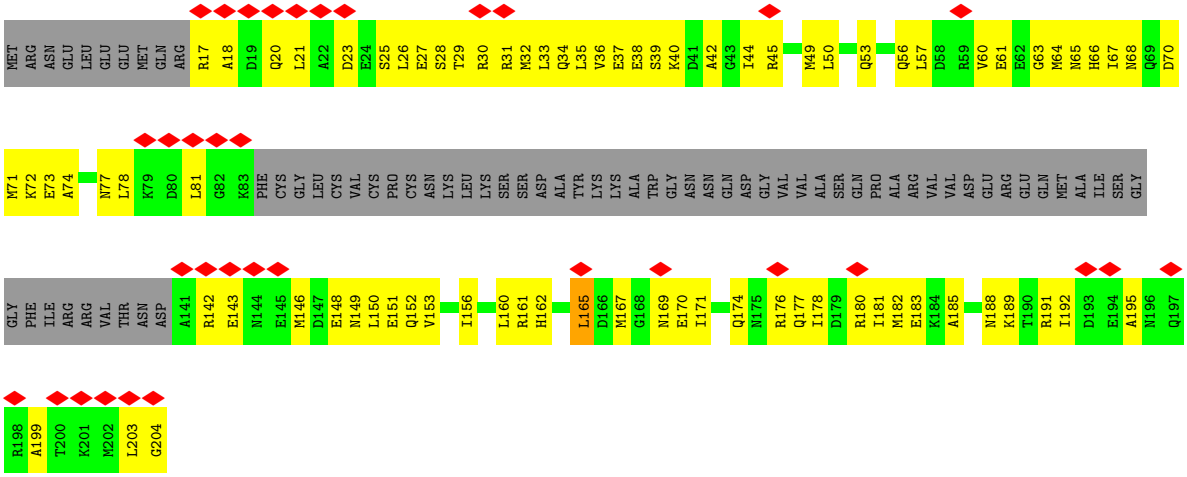
Chain L:



• Molecule 5: Synaptosomal-associated protein 25

Chain M:




MET ARG ASN GLU LEU GLU GLU MET GLN ARG R17 A18 D19 Q20 L21 A22 D23 E24 S25 L26 E27 S28 T29 R30 R31 M32 L33 Q34 L35 V36 E37 E38 S39 K40 D41 A42 G43 I44 R45 M49 L50 Q53 Q56 L57 D58 R59 V60 E61 E62 G63 M64 N65 H66 I67 N68 Q69 D70
M71 K72 E73 A74 N77 L78 K79 D80 L81 G82 K83 PHE CYS GLY LEU CYS VAL CYS PRO CYS ASN LYS LEU LYS SER SER ASP ALA TYR LYS LYS ALA TRP GLY ASN ASN GLN ASP GLY VAL VAL ALA SER GLN PRO ALA ARG VAL VAL ASP GLU ARG GLU GLN MET ALA ILE SER GLY
GLY PHE ILE ARG ARG VAL THR ASN ASP A141 R142 E143 N144 E145 M146 D147 E148 N149 L150 E151 Q152 V153 I156 L160 R161 H162 L165 D166 M167 G168 N169 E170 I171 Q174 N175 R176 Q177 I178 D179 R180 I181 M182 E183 K184 A185 N188 K189 T190 R191 I192 D193 E194 A195 N196 Q197
R198 A199 T200 K201 M202 L203 G204

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21489	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	44	Depositor
Minimum defocus (nm)	-1800	Depositor
Maximum defocus (nm)	-2800	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	11.321	Depositor
Minimum map value	-4.152	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5.0	Depositor
Map size (Å)	311.1936, 311.1936, 311.1936	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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	0.46	1/5120 (0.0%)	0.82	10/6930 (0.1%)
1	B	0.41	1/5091 (0.0%)	0.80	12/6887 (0.2%)
1	C	0.38	0/5104	0.72	5/6910 (0.1%)
1	D	0.43	0/5061	0.77	9/6854 (0.1%)
1	E	0.46	1/5095 (0.0%)	0.84	11/6890 (0.2%)
1	F	0.42	0/5007	0.78	10/6767 (0.1%)
2	G	0.33	0/2295	0.59	1/3086 (0.0%)
2	H	0.36	0/2295	0.63	1/3086 (0.0%)
2	I	0.33	0/2285	0.58	0/3074
2	J	0.34	0/2295	0.58	1/3086 (0.0%)
3	K	0.25	0/497	0.41	0/665
4	L	0.24	0/541	0.41	0/723
5	M	0.22	0/1029	0.45	0/1369
All	All	0.40	3/41715 (0.0%)	0.74	60/56327 (0.1%)

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

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	232	ARG	CB-CG	-6.33	1.35	1.52
1	B	547	SER	C-O	5.53	1.33	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	235	PHE	CB-CG	-5.23	1.42	1.51

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	316	LEU	CA-CB-CG	11.54	141.84	115.30
1	E	629	LEU	CB-CG-CD1	-9.86	94.24	111.00
1	F	518	LEU	CB-CG-CD1	-9.34	95.12	111.00
1	D	547	SER	C-N-CA	-8.76	103.92	122.30
1	F	629	LEU	CB-CG-CD1	-8.53	96.51	111.00
1	C	677	LEU	CB-CG-CD2	-8.30	96.88	111.00
2	G	197	LEU	CA-CB-CG	8.30	134.39	115.30
1	C	322	LEU	CA-CB-CG	7.96	133.62	115.30
1	A	397	LEU	CA-CB-CG	7.71	133.04	115.30
1	F	305	LEU	CA-CB-CG	7.56	132.69	115.30
1	B	305	LEU	CA-CB-CG	7.52	132.59	115.30
1	E	305	LEU	CA-CB-CG	7.30	132.09	115.30
1	E	316	LEU	CA-CB-CG	7.19	131.85	115.30
1	E	652	LEU	CB-CG-CD2	-7.11	98.91	111.00
1	B	479	ASP	N-CA-C	-7.09	91.86	111.00
1	A	322	LEU	CA-CB-CG	6.76	130.85	115.30
1	F	536	LEU	CA-CB-CG	6.63	130.55	115.30
1	F	518	LEU	CB-CG-CD2	6.60	122.22	111.00
1	A	305	LEU	CA-CB-CG	6.54	130.34	115.30
1	E	232	ARG	CB-CG-CD	-6.37	95.04	111.60
1	B	438	GLY	N-CA-C	6.27	128.78	113.10
1	B	708	LYS	CD-CE-NZ	6.23	126.03	111.70
1	A	641	LEU	CA-CB-CG	6.18	129.51	115.30
1	F	453	MET	CB-CG-SD	6.16	130.88	112.40
1	C	387	GLY	N-CA-C	-6.12	97.79	113.10
1	D	609	LEU	CA-CB-CG	6.10	129.32	115.30
1	F	536	LEU	CB-CG-CD2	-6.07	100.68	111.00
1	B	658	LEU	CB-CG-CD1	-6.02	100.77	111.00
1	B	548	GLY	N-CA-C	-6.00	98.11	113.10
1	B	543	GLY	N-CA-C	-5.99	98.12	113.10
1	B	395	ILE	CG1-CB-CG2	-5.79	98.67	111.40
1	A	525	VAL	CG1-CB-CG2	5.75	120.11	110.90
1	D	627	LEU	CB-CG-CD2	-5.72	101.28	111.00
1	E	438	GLY	N-CA-C	5.69	127.32	113.10
1	D	643	ILE	CB-CA-C	-5.68	100.24	111.60
2	H	119	ILE	CG1-CB-CG2	-5.66	98.95	111.40
1	F	629	LEU	CA-CB-CG	-5.65	102.30	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	617	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	B	455	ARG	CG-CD-NE	-5.61	100.03	111.80
1	D	316	LEU	CB-CA-C	-5.56	99.64	110.20
1	B	610	ASP	CB-CG-OD2	-5.55	113.31	118.30
1	B	455	ARG	NE-CZ-NH2	-5.49	117.56	120.30
1	E	522	GLU	CA-CB-CG	5.49	125.48	113.40
1	A	216	GLU	N-CA-C	-5.35	96.56	111.00
1	F	525	VAL	CG1-CB-CG2	5.35	119.45	110.90
1	E	397	LEU	CA-CB-CG	5.33	127.57	115.30
1	A	665	ILE	CG1-CB-CG2	-5.31	99.73	111.40
1	F	396	GLY	N-CA-C	5.30	126.35	113.10
1	A	236	ALA	N-CA-C	-5.28	96.73	111.00
1	D	404	LEU	CA-CB-CG	5.25	127.38	115.30
1	A	552	LEU	CA-CB-CG	5.25	127.38	115.30
1	C	385	ARG	CG-CD-NE	-5.24	100.80	111.80
1	E	670	ILE	CB-CA-C	-5.24	101.13	111.60
1	C	640	LEU	CA-CB-CG	5.17	127.18	115.30
1	D	416	GLY	N-CA-C	-5.16	100.21	113.10
1	E	540	LEU	CB-CG-CD1	-5.07	102.38	111.00
2	J	235	PHE	N-CA-CB	-5.07	101.47	110.60
1	A	407	LEU	CA-CB-CG	5.07	126.96	115.30
1	B	609	LEU	CA-CB-CG	-5.02	103.76	115.30
1	D	643	ILE	CG1-CB-CG2	-5.01	100.38	111.40

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	241	PRO	Peptide
1	B	438	GLY	Peptide
1	E	315	ARG	Mainchain
1	E	438	GLY	Peptide
1	F	438	GLY	Peptide
2	J	233	PRO	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5044	0	4963	347	0
1	B	5015	0	4953	300	0
1	C	5028	0	4939	343	0
1	D	4986	0	4905	341	0
1	E	5020	0	4974	390	0
1	F	4932	0	4914	335	0
2	G	2255	0	2199	126	0
2	H	2255	0	2199	138	0
2	I	2246	0	2185	109	0
2	J	2255	0	2199	132	0
3	K	494	0	488	80	0
4	L	536	0	527	73	0
5	M	1029	0	996	143	0
All	All	41095	0	40441	2529	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 31.

All (2529) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:518:LEU:HD23	1:F:555:LYS:HG2	1.21	1.10
2:H:219:LEU:HB2	2:H:222:LYS:HB3	1.34	1.08
2:I:201:SER:HA	3:K:47:ARG:HH12	1.11	1.08
1:E:593:TYR:O	1:E:638:ARG:NH1	1.90	1.04
1:B:264:CYS:HA	1:B:437:SER:HB2	1.38	1.04
1:B:240:PHE:HD2	1:B:244:ILE:HG21	1.22	1.03
3:K:43:VAL:HA	4:L:212:LEU:HD13	1.36	1.03
2:J:201:SER:HG	2:J:205:TYR:HE1	1.05	1.02
1:C:507:ILE:CD1	1:C:555:LYS:HG2	1.87	1.02
1:B:258:LEU:HB3	1:B:395:ILE:HD11	1.37	1.01
1:E:528:THR:HG21	1:E:641:LEU:HD23	1.41	0.99
5:M:203:LEU:HD23	5:M:204:GLY:H	1.25	0.99
1:A:424:VAL:HG13	1:A:482:ALA:HB2	1.44	0.99
1:A:685:ASN:OD1	1:F:533:ARG:NH1	1.97	0.98
3:K:53:VAL:HG22	4:L:226:GLN:HE22	1.26	0.98
1:C:327:PHE:HB3	1:C:330:ILE:HD11	1.42	0.98
1:C:257:LEU:HB2	1:C:389:LEU:HD13	1.44	0.97
2:J:159:SER:HB2	5:M:169:ASN:HB3	1.46	0.97
1:E:596:GLN:HA	1:E:638:ARG:HG2	1.46	0.97
1:C:507:ILE:HD11	1:C:555:LYS:HB2	1.42	0.96
1:E:540:LEU:HD11	1:E:646:THR:HG22	1.45	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:715:GLU:HG3	1:F:527:GLN:HE21	1.30	0.96
2:G:219:LEU:HB2	2:G:222:LYS:HB3	1.47	0.95
1:A:331:ASP:HA	1:A:379:ILE:HD11	1.46	0.95
1:E:232:ARG:HH22	1:F:451:THR:HA	1.28	0.95
1:D:628:VAL:HG11	1:E:574:ILE:HG21	1.49	0.95
1:C:507:ILE:CD1	1:C:555:LYS:CG	2.45	0.94
1:E:232:ARG:HE	1:F:454:ASN:HB2	1.29	0.94
1:E:528:THR:HG22	1:E:537:VAL:HG21	1.50	0.94
3:K:83:LYS:HD3	5:M:203:LEU:HD11	1.49	0.94
1:D:509:LYS:HG2	1:D:515:THR:HG23	1.47	0.93
1:C:618:PHE:HE2	1:D:614:ILE:HD11	1.31	0.92
1:D:406:ILE:HG22	1:D:441:LEU:HD22	1.48	0.92
1:F:521:GLY:HA2	1:F:524:LEU:HD12	1.49	0.92
1:A:569:SER:OG	1:A:571:ASP:OD1	1.86	0.92
1:D:256:ILE:HG13	1:D:370:ILE:HG22	1.51	0.92
1:A:264:CYS:SG	1:A:265:GLY:N	2.41	0.91
1:C:240:PHE:HD2	1:C:244:ILE:HG21	1.34	0.91
3:K:36:GLN:HA	4:L:205:LEU:HD13	1.52	0.91
2:J:201:SER:HB2	5:M:165:LEU:HD11	1.53	0.91
1:A:497:GLU:O	1:A:499:TYR:N	2.04	0.91
1:C:490:PRO:HA	1:C:491:ALA:HB3	1.52	0.91
2:G:72:HIS:CE1	2:G:80:ASP:HB2	2.07	0.90
1:B:327:PHE:HB2	1:B:330:ILE:HG22	1.54	0.89
1:D:240:PHE:HD2	1:D:244:ILE:HG21	1.37	0.89
2:J:219:LEU:HB2	2:J:222:LYS:HB3	1.54	0.89
1:A:295:VAL:HB	1:B:294:TYR:HB2	1.55	0.89
5:M:73:GLU:HG3	5:M:77:ASN:HD21	1.36	0.88
2:G:218:MET:HG2	2:G:219:LEU:H	1.36	0.88
2:H:218:MET:HG2	2:H:219:LEU:H	1.35	0.88
1:B:266:LYS:HG2	1:B:395:ILE:HG12	1.52	0.87
1:A:542:GLU:HG2	1:A:649:LYS:HD2	1.56	0.87
1:A:502:TYR:HE2	1:A:567:ILE:HG21	1.40	0.87
1:A:562:PHE:CD2	1:A:597:LEU:HD21	2.09	0.86
1:F:327:PHE:HB2	1:F:330:ILE:HG22	1.55	0.86
1:B:566:LYS:HD2	1:B:588:ILE:HG23	1.57	0.86
1:E:625:ALA:HA	1:F:574:ILE:HD11	1.55	0.86
1:C:507:ILE:HD11	1:C:555:LYS:CB	2.03	0.86
1:D:313:GLN:HE22	1:D:364:LEU:HA	1.40	0.86
1:C:497:GLU:O	1:C:499:TYR:N	2.07	0.86
1:E:256:ILE:HG13	1:E:370:ILE:HG22	1.56	0.86
1:E:327:PHE:HB2	1:E:330:ILE:HG22	1.55	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:545:PRO:HA	1:F:547:SER:H	1.39	0.86
1:A:421:SER:HB3	1:A:424:VAL:HG23	1.56	0.86
1:D:606:GLU:HA	1:D:609:LEU:HG	1.57	0.85
1:F:538:SER:HB3	1:F:662:SER:H	1.40	0.85
5:M:40:LYS:HD3	5:M:156:ILE:HG23	1.58	0.85
1:C:386:PRO:HA	1:C:390:GLU:HA	1.57	0.85
3:K:43:VAL:HG22	4:L:212:LEU:HB2	1.59	0.85
1:E:64:LEU:HA	1:E:67:ARG:HE	1.39	0.84
1:F:538:SER:HG	1:F:661:PHE:HD1	1.23	0.84
2:G:38:ILE:HD11	2:G:71:LEU:HB3	1.57	0.84
1:F:539:VAL:HB	1:F:643:ILE:HG12	1.60	0.84
1:A:305:LEU:HD23	1:A:325:ILE:HG21	1.58	0.84
1:E:232:ARG:HH22	1:F:451:THR:CA	1.89	0.84
1:E:490:PRO:HA	1:E:491:ALA:HB3	1.59	0.84
1:E:618:PHE:HZ	1:F:612:VAL:HG11	1.39	0.83
1:D:510:TRP:CD2	1:D:670:ILE:HG22	2.14	0.83
1:F:525:VAL:HG13	1:F:562:PHE:CE1	2.12	0.83
1:F:555:LYS:NZ	1:F:559:GLU:OE2	2.11	0.83
1:A:705:ILE:HD13	1:A:710:LEU:HD12	1.60	0.83
1:E:720:MET:HG3	1:E:728:LYS:HE3	1.60	0.83
1:B:64:LEU:HB2	2:H:293:ASP:O	1.78	0.83
1:B:256:ILE:HG13	1:B:370:ILE:HG22	1.59	0.83
1:D:510:TRP:HE3	1:D:675:GLN:HG2	1.44	0.83
1:C:687:LYS:N	1:C:690:GLU:OE2	2.11	0.83
1:E:585:MET:HG3	1:E:589:PHE:CZ	2.13	0.83
1:E:527:GLN:O	1:E:531:SER:OG	1.95	0.83
1:F:256:ILE:HG13	1:F:370:ILE:HG22	1.58	0.83
2:J:200:TYR:OH	3:K:41:GLU:O	1.96	0.83
2:I:201:SER:CA	3:K:47:ARG:HH12	1.91	0.82
1:C:256:ILE:HG13	1:C:370:ILE:HG22	1.58	0.82
2:J:271:ARG:NH2	2:G:234:ALA:HB2	1.94	0.82
1:A:686:PHE:HE2	1:A:714:ILE:HG12	1.43	0.82
2:I:38:ILE:HG23	2:I:75:LEU:HD12	1.61	0.82
1:A:624:GLN:HG3	1:B:610:ASP:OD2	1.80	0.82
1:F:544:PRO:O	1:F:547:SER:OG	1.96	0.82
2:J:235:PHE:HB3	3:K:38:GLN:HG2	1.62	0.82
2:G:232:PHE:HB2	2:G:233:PRO:HD3	1.59	0.82
1:B:490:PRO:HA	1:B:491:ALA:HB3	1.62	0.82
2:J:228:TYR:OH	2:J:237:ASP:OD1	1.98	0.81
1:A:428:GLU:HG2	1:A:479:ASP:HA	1.62	0.81
1:B:111:PRO:HB2	1:B:196:ILE:HD13	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:232:ARG:NE	1:F:454:ASN:HB2	1.95	0.81
1:C:627:LEU:HD12	1:D:607:ARG:HH12	1.46	0.81
1:F:536:LEU:HD11	1:F:634:PRO:HD3	1.61	0.81
1:D:518:LEU:HD21	1:D:552:LEU:HD22	1.63	0.81
2:I:201:SER:HA	3:K:47:ARG:NH1	1.95	0.81
2:J:218:MET:HG2	2:J:219:LEU:H	1.44	0.81
1:A:285:VAL:HG13	1:A:326:ILE:HD11	1.63	0.80
1:F:386:PRO:HA	1:F:390:GLU:HA	1.63	0.80
1:A:713:LEU:HD21	1:A:732:LEU:HB3	1.63	0.80
3:K:48:VAL:HG12	3:K:52:LYS:HE3	1.61	0.80
1:A:557:ALA:O	1:A:560:SER:OG	1.99	0.80
1:E:549:LYS:HA	1:E:552:LEU:HD12	1.62	0.80
1:C:676:LEU:HD12	1:C:705:ILE:HG21	1.64	0.80
1:F:538:SER:H	1:F:662:SER:HB3	1.45	0.80
2:J:235:PHE:HE2	3:K:37:ALA:HB3	1.42	0.80
1:C:313:GLN:O	1:C:317:GLY:N	2.15	0.80
1:E:586:LYS:NZ	1:F:574:ILE:O	2.14	0.80
1:E:589:PHE:CZ	1:E:629:LEU:HD11	2.16	0.80
1:C:618:PHE:CE2	1:D:614:ILE:HD11	2.16	0.79
1:D:626:LEU:HB3	1:D:657:MET:HE3	1.65	0.79
1:E:386:PRO:HA	1:E:390:GLU:HA	1.63	0.79
1:B:526:GLN:HE21	1:C:719:GLN:HB3	1.47	0.79
1:C:98:GLU:HB3	1:C:148:LEU:HB3	1.65	0.79
1:C:407:LEU:HD11	1:C:426:ILE:HG23	1.64	0.79
1:E:190:ASN:HD21	1:E:316:LEU:HG	1.49	0.78
1:E:563:PRO:HG2	1:E:595:SER:OG	1.83	0.78
1:A:562:PHE:HD2	1:A:597:LEU:HD21	1.46	0.78
2:J:235:PHE:CB	3:K:38:GLN:HG2	2.12	0.78
1:A:490:PRO:HA	1:A:491:ALA:HB3	1.65	0.78
1:E:686:PHE:HE1	1:E:714:ILE:HG23	1.49	0.78
1:E:526:GLN:NE2	1:F:719:GLN:O	2.17	0.78
1:D:654:GLU:HB3	1:E:614:ILE:HD11	1.66	0.78
1:E:587:LYS:O	1:E:587:LYS:NZ	2.15	0.78
1:E:510:TRP:HE1	1:E:707:ILE:HD11	1.48	0.78
1:B:111:PRO:HD3	1:B:316:LEU:HG	1.66	0.78
2:J:201:SER:HB2	5:M:165:LEU:CD1	2.14	0.78
1:D:353:GLN:HE22	1:E:288:PRO:HG2	1.47	0.78
1:A:502:TYR:CE2	1:A:567:ILE:HG21	2.19	0.77
1:B:386:PRO:HA	1:B:390:GLU:HA	1.64	0.77
1:C:652:LEU:HD22	1:C:657:MET:HG2	1.66	0.77
1:A:67:ARG:HD2	2:H:218:MET:HG3	1.64	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:525:VAL:HG13	1:A:562:PHE:CZ	2.20	0.77
3:K:39:VAL:HG11	4:L:209:ILE:HD13	1.66	0.77
2:H:289:GLY:O	2:H:293:ASP:HB2	1.84	0.77
1:C:690:GLU:HB2	1:C:726:VAL:HG21	1.66	0.77
1:F:407:LEU:HD11	1:F:426:ILE:HG23	1.66	0.77
1:D:240:PHE:CD2	1:D:244:ILE:HG21	2.19	0.77
1:E:234:ALA:HA	1:F:446:ARG:NH2	1.99	0.77
1:B:589:PHE:HE1	1:B:600:VAL:HG11	1.49	0.77
1:C:540:LEU:HB3	1:C:664:THR:HG22	1.64	0.77
1:C:691:ARG:HA	1:C:694:ILE:HD12	1.67	0.77
1:A:48:THR:HG21	1:A:128:GLN:HG2	1.66	0.77
1:E:653:GLN:HA	1:E:658:LEU:HB2	1.66	0.76
1:B:540:LEU:HD23	1:B:661:PHE:CD1	2.21	0.76
1:C:544:PRO:O	1:C:547:SER:OG	2.01	0.76
1:B:10:ARG:HE	2:H:293:ASP:CG	1.89	0.76
1:B:581:LYS:NZ	1:B:608:LEU:O	2.18	0.76
1:C:40:SER:HB2	1:C:41:PRO:HD2	1.65	0.76
1:A:549:LYS:NZ	1:A:647:SER:OG	2.16	0.76
1:C:496:GLN:O	1:C:498:ASP:N	2.18	0.76
1:C:507:ILE:HD12	1:C:555:LYS:CD	2.16	0.76
1:E:407:LEU:HD11	1:E:426:ILE:HG23	1.66	0.76
1:F:240:PHE:CD2	1:F:244:ILE:HG21	2.20	0.76
1:F:570:PRO:HG2	1:F:604:ASP:HB2	1.68	0.76
5:M:61:GLU:HG2	5:M:65:ASN:HD21	1.50	0.76
1:E:585:MET:HA	1:E:588:ILE:HD12	1.68	0.75
1:F:564:PHE:O	1:F:598:SER:OG	2.04	0.75
1:F:569:SER:OG	1:F:571:ASP:OD2	2.04	0.75
1:A:453:MET:O	1:F:232:ARG:NH2	2.19	0.75
1:D:310:GLU:O	1:D:313:GLN:HG2	1.86	0.75
1:E:311:GLU:OE1	1:E:314:ARG:NE	2.19	0.75
2:G:72:HIS:HE1	2:G:80:ASP:HB2	1.51	0.75
2:G:21:VAL:HG21	2:G:71:LEU:HD22	1.68	0.75
1:D:728:LYS:HE3	1:D:732:LEU:HD11	1.67	0.75
1:B:240:PHE:CD2	1:B:244:ILE:HG21	2.15	0.75
1:E:313:GLN:O	1:E:317:GLY:N	2.20	0.75
4:L:209:ILE:HG21	5:M:32:MET:HG3	1.69	0.75
1:A:677:LEU:HD21	1:A:695:ALA:HA	1.68	0.74
1:A:397:LEU:HB3	1:A:398:PRO:CD	2.17	0.74
1:C:507:ILE:HD12	1:C:555:LYS:HG2	1.69	0.74
1:F:12:PRO:HG2	1:F:23:VAL:HG11	1.69	0.74
1:E:300:ALA:O	1:E:304:LYS:HG2	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:553:ALA:HA	1:A:556:ILE:HD12	1.68	0.74
1:A:262:PRO:HG2	1:A:374:ASN:OD1	1.87	0.74
1:E:349:THR:HA	1:E:352:ASN:HD22	1.52	0.74
1:C:578:GLU:HB3	1:C:621:LEU:HB3	1.67	0.74
5:M:31:ARG:O	5:M:35:LEU:HG	1.88	0.74
1:B:524:LEU:HD21	1:B:663:THR:HG21	1.69	0.74
1:C:630:LEU:HD11	1:C:661:PHE:CE1	2.23	0.74
1:C:724:TYR:HD2	1:C:727:ARG:HH21	1.35	0.74
1:E:686:PHE:HB3	1:E:690:GLU:HB2	1.69	0.74
2:G:228:TYR:OH	2:G:237:ASP:OD1	2.05	0.74
1:F:397:LEU:HD22	1:F:398:PRO:HD3	1.69	0.73
1:A:352:ASN:HB3	1:B:288:PRO:HB2	1.68	0.73
1:D:301:ASN:HA	1:D:304:LYS:HD3	1.70	0.73
1:C:318:ALA:O	1:C:319:ASN:ND2	2.21	0.73
1:C:513:PRO:O	1:C:516:ARG:HG2	1.88	0.73
1:B:300:ALA:O	1:B:304:LYS:HG2	1.88	0.73
1:E:106:ASN:HB3	1:E:143:LYS:NZ	2.03	0.73
1:B:621:LEU:HD11	1:C:575:GLY:HA2	1.70	0.73
1:A:67:ARG:NH1	2:H:217:ASP:O	2.20	0.73
1:F:73:SER:O	1:F:76:GLN:HG2	1.89	0.73
1:D:399:ASP:O	1:D:403:ARG:N	2.22	0.73
1:F:536:LEU:HD21	1:F:632:LYS:O	1.89	0.73
1:F:634:PRO:HB2	1:F:638:ARG:HG3	1.68	0.73
1:E:670:ILE:HG22	1:E:672:THR:H	1.54	0.72
1:F:300:ALA:O	1:F:304:LYS:HG2	1.87	0.72
1:D:46:ILE:HD12	1:D:174:VAL:HG21	1.71	0.72
1:E:553:ALA:HA	1:E:556:ILE:HD12	1.72	0.72
1:B:187:LYS:HB2	1:B:191:SER:HB3	1.70	0.72
1:B:533:ARG:HG3	1:B:534:THR:H	1.54	0.72
1:E:538:SER:OG	1:E:661:PHE:HA	1.90	0.72
2:H:94:LYS:HE3	2:I:153:LYS:HG3	1.70	0.72
1:B:407:LEU:HD11	1:B:426:ILE:HG23	1.71	0.72
1:B:563:PRO:HD2	1:B:597:LEU:HB2	1.69	0.72
1:C:236:ALA:HB1	1:D:453:MET:HB3	1.72	0.72
1:C:596:GLN:HA	1:C:638:ARG:HD3	1.72	0.72
1:A:10:ARG:HB2	2:H:217:ASP:OD2	1.90	0.72
1:E:236:ALA:HB1	1:F:453:MET:HG3	1.72	0.72
1:D:98:GLU:HB3	1:D:148:LEU:HB3	1.72	0.71
1:D:544:PRO:O	1:D:547:SER:HB3	1.90	0.71
1:B:496:GLN:O	1:B:498:ASP:N	2.22	0.71
1:D:513:PRO:HA	1:D:516:ARG:HG2	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:HIS:ND1	1:F:246:GLU:O	2.23	0.71
1:A:602:VAL:HG12	1:A:605:ILE:HG12	1.73	0.71
1:E:303:ARG:HG3	1:E:357:LYS:HE2	1.72	0.71
1:E:190:ASN:OD1	1:E:315:ARG:C	2.29	0.71
1:C:507:ILE:HD11	1:C:555:LYS:CG	2.17	0.71
1:F:517:VAL:HG13	1:F:665:ILE:HG21	1.72	0.71
5:M:36:VAL:HG21	5:M:153:VAL:HG13	1.72	0.71
1:A:258:LEU:HA	1:A:393:MET:O	1.90	0.71
1:F:311:GLU:OE1	1:F:314:ARG:NE	2.24	0.71
1:A:309:ALA:HB1	1:A:367:ILE:HG21	1.73	0.71
1:B:538:SER:HB3	1:B:661:PHE:HD2	1.55	0.71
1:E:9:ALA:HA	1:E:74:ILE:HG23	1.72	0.71
1:E:680:LEU:HD13	1:E:694:ILE:HD13	1.70	0.71
1:D:310:GLU:O	1:D:313:GLN:CG	2.39	0.71
1:D:605:ILE:HD11	1:D:644:GLY:HA3	1.72	0.71
2:H:93:LYS:NZ	2:I:156:GLU:OE2	2.21	0.71
1:D:711:LEU:HA	1:D:714:ILE:HD12	1.72	0.71
1:B:627:LEU:HD21	1:B:657:MET:HG3	1.73	0.70
1:B:361:VAL:O	1:C:271:ARG:HD2	1.91	0.70
1:C:564:PHE:O	1:C:598:SER:OG	2.07	0.70
1:B:624:GLN:NE2	1:C:610:ASP:O	2.24	0.70
1:C:611:TYR:CE1	1:C:616:PRO:HB2	2.26	0.70
3:K:39:VAL:O	3:K:43:VAL:HG23	1.91	0.70
1:A:423:ASP:HB3	1:A:480:PHE:CB	2.22	0.70
1:C:236:ALA:HB1	1:D:453:MET:CB	2.21	0.70
1:E:527:GLN:HE22	1:F:716:MET:HG2	1.57	0.70
1:D:620:ASN:O	1:D:624:GLN:HG2	1.91	0.70
1:E:190:ASN:OD1	1:E:315:ARG:O	2.09	0.70
1:E:513:PRO:HA	1:E:516:ARG:HG2	1.74	0.70
2:I:51:MET:HA	2:I:54:MET:HG2	1.74	0.70
1:A:562:PHE:HD2	1:A:597:LEU:CD2	2.05	0.70
1:E:589:PHE:CD2	1:E:629:LEU:HD21	2.26	0.70
1:D:10:ARG:NH2	2:I:293:ASP:OD1	2.24	0.70
2:J:213:HIS:HE1	2:J:221:ALA:HB2	1.55	0.70
1:A:503:ILE:O	1:A:505:ASN:N	2.25	0.70
1:E:190:ASN:HD21	1:E:316:LEU:CG	2.03	0.70
1:E:232:ARG:HH21	1:F:454:ASN:HB3	1.56	0.70
1:F:713:LEU:HD22	1:F:732:LEU:HB3	1.74	0.70
2:J:235:PHE:HD1	3:K:34:GLN:NE2	1.89	0.70
1:A:125:PHE:HA	1:A:128:GLN:NE2	2.06	0.70
1:A:353:GLN:HE21	1:A:357:LYS:HG2	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:PHE:CD2	1:C:244:ILE:HG21	2.24	0.70
1:F:535:PRO:HA	1:F:639:LYS:HG2	1.74	0.70
1:F:125:PHE:HA	1:F:128:GLN:NE2	2.06	0.69
5:M:152:GLN:O	5:M:156:ILE:HG13	1.91	0.69
1:C:125:PHE:HA	1:C:128:GLN:NE2	2.07	0.69
1:D:353:GLN:HE22	1:E:288:PRO:CG	2.04	0.69
1:F:606:GLU:OE1	1:F:606:GLU:N	2.22	0.69
2:J:235:PHE:CE2	3:K:37:ALA:HB3	2.25	0.69
1:A:231:PHE:CD1	1:A:235:PHE:HE2	2.10	0.69
1:C:718:LEU:O	1:C:725:ARG:NH1	2.26	0.69
1:E:606:GLU:OE2	1:E:646:THR:OG1	2.09	0.69
1:E:234:ALA:HA	1:F:446:ARG:HH21	1.57	0.69
1:F:721:ASP:HB2	1:F:724:TYR:HD1	1.57	0.69
1:C:331:ASP:HA	1:C:379:ILE:HD11	1.75	0.69
1:E:232:ARG:NH2	1:F:450:SER:O	2.25	0.69
1:F:545:PRO:HA	1:F:547:SER:N	2.05	0.69
1:B:125:PHE:HA	1:B:128:GLN:NE2	2.08	0.69
1:C:247:GLN:HA	1:D:417:HIS:CD2	2.26	0.69
1:D:230:ILE:HD11	1:D:256:ILE:HD13	1.73	0.69
1:D:245:VAL:O	1:D:249:GLY:N	2.26	0.69
1:D:386:PRO:HA	1:D:390:GLU:HA	1.74	0.69
1:E:592:ALA:HB1	1:E:640:LEU:HD22	1.73	0.69
1:F:670:ILE:HG23	1:F:675:GLN:HB2	1.74	0.69
4:L:205:LEU:O	4:L:209:ILE:HG12	1.93	0.69
2:I:116:ARG:NH2	5:M:183:GLU:OE1	2.25	0.69
1:B:538:SER:HB3	1:B:661:PHE:CD2	2.28	0.69
1:E:604:ASP:HB3	1:E:607:ARG:HB3	1.74	0.69
1:B:303:ARG:HG3	1:B:357:LYS:HE2	1.74	0.68
1:B:489:LYS:O	1:B:491:ALA:HB3	1.94	0.68
1:C:507:ILE:HD12	1:C:555:LYS:CG	2.20	0.68
1:F:589:PHE:HD2	1:F:629:LEU:HD13	1.57	0.68
1:D:125:PHE:HA	1:D:128:GLN:NE2	2.07	0.68
1:F:303:ARG:HG3	1:F:357:LYS:HE2	1.74	0.68
1:E:640:LEU:HD12	1:E:641:LEU:N	2.09	0.68
1:A:564:PHE:CE1	1:A:566:LYS:HB2	2.28	0.68
1:C:358:ILE:CB	1:C:388:ARG:HG3	2.23	0.68
1:D:539:VAL:HG23	1:D:663:THR:HG23	1.75	0.68
2:I:228:TYR:OH	2:I:237:ASP:OD1	2.09	0.68
1:F:358:ILE:HD12	1:F:388:ARG:HB3	1.75	0.68
5:M:73:GLU:HG3	5:M:77:ASN:ND2	2.09	0.68
1:A:351:VAL:O	1:A:355:LEU:HG	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:521:GLY:O	1:A:525:VAL:HG23	1.94	0.68
1:D:543:GLY:H	1:D:549:LYS:HD3	1.59	0.68
1:E:685:ASN:HB3	1:E:718:LEU:HD11	1.74	0.68
1:B:311:GLU:OE1	1:B:314:ARG:NE	2.26	0.68
1:C:533:ARG:O	1:D:505:ASN:ND2	2.27	0.68
1:E:358:ILE:HD12	1:E:388:ARG:HB3	1.75	0.68
1:F:550:THR:HA	1:F:645:THR:HG21	1.76	0.68
3:K:42:VAL:HG13	3:K:45:ILE:HD11	1.76	0.68
1:C:649:LYS:HE2	1:C:658:LEU:HD13	1.75	0.68
2:J:50:ASN:HD21	2:G:115:GLY:CA	2.05	0.67
1:D:527:GLN:NE2	1:E:715:GLU:O	2.27	0.67
1:E:246:GLU:HG3	1:F:417:HIS:HE1	1.59	0.67
1:A:326:ILE:HG22	1:A:370:ILE:HG12	1.74	0.67
5:M:170:GLU:HG3	5:M:174:GLN:NE2	2.09	0.67
1:A:612:VAL:HG11	1:F:618:PHE:HZ	1.59	0.67
1:E:510:TRP:CZ3	1:E:670:ILE:HG13	2.29	0.67
3:K:34:GLN:O	3:K:38:GLN:HG3	1.94	0.67
1:C:64:LEU:HB3	1:C:65:PRO:HD3	1.75	0.67
1:B:358:ILE:HD12	1:B:388:ARG:HB3	1.76	0.67
1:A:683:LEU:HB3	1:A:685:ASN:ND2	2.09	0.67
1:E:525:VAL:O	1:E:528:THR:OG1	2.11	0.67
1:D:407:LEU:HG	1:D:441:LEU:HD11	1.76	0.67
1:F:518:LEU:H	1:F:518:LEU:HD12	1.59	0.67
1:A:247:GLN:O	1:B:413:ARG:NH1	2.28	0.67
1:B:240:PHE:CE1	1:C:457:ILE:HD11	2.29	0.67
2:H:35:SER:HB3	2:H:75:LEU:HD12	1.76	0.67
1:A:720:MET:O	1:A:725:ARG:NE	2.24	0.67
1:E:232:ARG:HH21	1:F:454:ASN:H	1.41	0.67
1:B:224:ASP:O	1:B:228:SER:HB2	1.95	0.66
1:C:542:GLU:CB	1:C:649:LYS:HD3	2.25	0.66
1:E:398:PRO:HG3	1:E:436:PHE:O	1.94	0.66
1:E:540:LEU:HD11	1:E:646:THR:CG2	2.21	0.66
1:A:563:PRO:HD2	1:A:597:LEU:HD22	1.77	0.66
1:F:538:SER:O	1:F:663:THR:HG22	1.95	0.66
5:M:27:GLU:O	5:M:31:ARG:HG3	1.96	0.66
1:E:232:ARG:NH2	1:F:451:THR:HA	2.07	0.66
1:E:602:VAL:O	1:E:644:GLY:HA2	1.95	0.66
1:A:653:GLN:NE2	1:A:653:GLN:O	2.29	0.66
1:E:534:THR:HG23	1:F:715:GLU:HG3	1.77	0.66
1:F:518:LEU:CD2	1:F:555:LYS:HG2	2.13	0.66
1:F:695:ALA:HB1	1:F:699:LYS:HE3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:149:ALA:HB2	2:G:164:CYS:HB2	1.76	0.66
1:B:713:LEU:HD22	1:B:732:LEU:HB3	1.76	0.66
1:A:671:ALA:HA	1:A:703:VAL:O	1.96	0.66
1:B:528:THR:O	1:B:639:LYS:HD2	1.96	0.66
1:D:627:LEU:HD21	1:D:657:MET:HG3	1.77	0.66
1:E:253:VAL:H	1:F:446:ARG:HH12	1.41	0.66
1:D:319:ASN:HB3	1:D:320:SER:HB2	1.78	0.66
4:L:198:ARG:O	4:L:202:ILE:HG13	1.95	0.66
1:E:625:ALA:O	1:E:629:LEU:HG	1.95	0.66
1:F:224:ASP:O	1:F:228:SER:HB2	1.96	0.66
2:H:230:GLU:HG3	2:H:237:ASP:HB3	1.78	0.66
4:L:212:LEU:HA	4:L:215:MET:HE2	1.77	0.66
4:L:255:VAL:HG11	5:M:77:ASN:HB3	1.78	0.66
1:B:67:ARG:NH1	1:B:74:ILE:HD11	2.11	0.66
1:C:533:ARG:HB2	1:D:715:GLU:OE1	1.96	0.66
1:E:544:PRO:O	1:E:547:SER:HB3	1.96	0.66
2:H:72:HIS:HE1	2:H:80:ASP:HB2	1.61	0.66
1:A:687:LYS:N	1:A:690:GLU:OE1	2.27	0.66
1:B:245:VAL:O	1:B:249:GLY:N	2.28	0.66
1:E:603:ASP:OD2	1:E:645:THR:OG1	2.10	0.66
2:G:197:LEU:HD23	5:M:162:HIS:NE2	2.10	0.66
1:E:547:SER:OG	1:E:549:LYS:HD3	1.96	0.65
1:D:510:TRP:CE3	1:D:670:ILE:HG22	2.31	0.65
5:M:26:LEU:HD13	5:M:146:MET:HG3	1.77	0.65
1:A:550:THR:HA	1:A:645:THR:HG21	1.76	0.65
1:B:424:VAL:N	1:B:479:ASP:N	2.44	0.65
1:D:573:MET:SD	1:D:581:LYS:HD3	2.36	0.65
2:H:57:ASN:O	2:H:59:SER:N	2.29	0.65
2:G:112:THR:HG23	2:G:117:PHE:HE1	1.61	0.65
1:B:589:PHE:CE1	1:B:600:VAL:HG11	2.30	0.65
1:D:358:ILE:HD12	1:D:388:ARG:HB3	1.78	0.65
1:D:234:ALA:HA	1:D:253:VAL:HG11	1.79	0.65
1:E:640:LEU:HD12	1:E:641:LEU:H	1.61	0.65
2:G:175:LEU:HD23	2:G:177:GLN:HE21	1.61	0.65
1:A:356:SER:CB	1:B:288:PRO:HD3	2.27	0.65
1:A:686:PHE:CE2	1:A:714:ILE:HG12	2.31	0.65
1:E:232:ARG:HH21	1:F:454:ASN:CB	2.09	0.65
1:A:620:ASN:ND2	1:B:610:ASP:OD1	2.30	0.65
1:B:501:SER:O	1:B:503:ILE:N	2.29	0.65
1:F:565:ILE:HG23	1:F:599:CYS:HB3	1.77	0.65
2:G:235:PHE:CD1	5:M:152:GLN:HG2	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:449:GLN:O	1:B:453:MET:HG2	1.97	0.65
1:E:125:PHE:HA	1:E:128:GLN:NE2	2.11	0.65
1:A:64:LEU:HB3	1:A:65:PRO:HD3	1.77	0.64
1:A:527:GLN:HB2	1:B:719:GLN:HG3	1.78	0.64
1:A:670:ILE:HG23	1:A:675:GLN:HB2	1.79	0.64
1:C:711:LEU:HA	1:C:714:ILE:HD12	1.79	0.64
1:F:240:PHE:HD2	1:F:244:ILE:HG21	1.58	0.64
1:D:286:ASN:HB2	1:D:327:PHE:HD1	1.62	0.64
1:E:536:LEU:HD12	1:E:640:LEU:O	1.97	0.64
1:F:245:VAL:O	1:F:249:GLY:N	2.29	0.64
1:C:711:LEU:O	1:C:715:GLU:HG2	1.97	0.64
1:F:513:PRO:O	1:F:517:VAL:HG23	1.97	0.64
2:H:200:TYR:CE2	5:M:38:GLU:HG3	2.32	0.64
2:G:158:ASN:OD1	2:G:162:ASN:ND2	2.30	0.64
1:F:73:SER:HA	2:G:218:MET:SD	2.38	0.64
1:F:307:ALA:O	1:F:311:GLU:HG2	1.97	0.64
1:A:408:HIS:HA	1:A:426:ILE:HD12	1.80	0.64
1:B:496:GLN:O	1:B:499:TYR:N	2.25	0.64
1:E:652:LEU:CD2	1:E:657:MET:HB3	2.28	0.64
1:D:546:HIS:ND1	1:D:709:LYS:HD3	2.11	0.64
2:J:39:GLU:HB2	2:J:75:LEU:HD13	1.78	0.64
1:F:544:PRO:HD2	1:F:547:SER:OG	1.96	0.64
2:I:232:PHE:HB2	2:I:233:PRO:HD3	1.80	0.64
5:M:188:ASN:O	5:M:192:ILE:HG13	1.98	0.64
1:D:534:THR:OG1	1:E:715:GLU:HG2	1.98	0.64
1:D:695:ALA:HB1	1:D:699:LYS:HE3	1.79	0.64
3:K:56:ARG:HD2	5:M:171:ILE:HG23	1.80	0.64
1:D:284:VAL:HG23	1:D:324:ILE:O	1.97	0.64
2:J:128:ALA:HB2	2:J:144:HIS:HB2	1.79	0.64
3:K:63:LEU:HD22	5:M:178:ILE:HG23	1.79	0.63
1:A:256:ILE:HG13	1:A:370:ILE:HG22	1.79	0.63
1:A:453:MET:C	1:F:232:ARG:HH22	2.01	0.63
1:C:375:ARG:HH12	1:C:378:LEU:HG	1.64	0.63
1:D:64:LEU:HA	1:D:67:ARG:HE	1.63	0.63
1:E:89:LYS:HB3	1:E:89:LYS:HZ3	1.63	0.63
2:H:101:ILE:HG21	2:H:135:LEU:HD11	1.80	0.63
1:B:295:VAL:O	1:C:294:TYR:HB2	1.99	0.63
1:D:256:ILE:CG1	1:D:370:ILE:HG22	2.27	0.63
1:D:404:LEU:HA	1:D:407:LEU:HD12	1.79	0.63
2:I:38:ILE:HD11	2:I:71:LEU:HB3	1.79	0.63
1:F:612:VAL:HG12	1:F:617:ARG:HB2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:216:ILE:HG12	2:H:220:ASN:HB2	1.80	0.63
2:J:72:HIS:CE1	2:J:80:ASP:HB2	2.34	0.63
1:A:710:LEU:O	1:A:714:ILE:HG13	1.98	0.63
1:B:307:ALA:O	1:B:311:GLU:HG2	1.98	0.63
1:E:232:ARG:NH2	1:F:454:ASN:HB3	2.13	0.63
1:E:307:ALA:O	1:E:311:GLU:HG2	1.97	0.63
1:F:570:PRO:HA	1:F:573:MET:HE2	1.79	0.63
5:M:167:MET:O	5:M:171:ILE:HG13	1.99	0.63
5:M:176:ARG:O	5:M:176:ARG:HD3	1.99	0.63
1:B:397:LEU:HB3	1:B:398:PRO:CD	2.29	0.63
1:B:526:GLN:NE2	1:C:719:GLN:HB3	2.11	0.63
1:D:105:LYS:NZ	2:I:291:GLU:HB3	2.13	0.63
1:E:63:SER:O	1:E:67:ARG:HG3	1.99	0.63
1:E:437:SER:O	1:E:440:GLU:HB2	1.98	0.63
1:E:674:GLU:HA	1:E:677:LEU:HD12	1.81	0.63
2:H:231:LEU:HD13	2:G:271:ARG:HG2	1.80	0.63
2:J:57:ASN:O	2:J:59:SER:N	2.32	0.63
2:G:69:ALA:HB1	2:G:85:PHE:CE1	2.33	0.63
1:B:503:ILE:HG12	1:B:551:ALA:HA	1.80	0.63
1:F:635:PRO:O	1:F:638:ARG:HG2	1.98	0.63
4:L:229:MET:HG2	4:L:232:ARG:HH22	1.63	0.63
5:M:34:GLN:HA	5:M:37:GLU:HB2	1.81	0.63
1:A:313:GLN:NE2	1:A:365:ASN:O	2.30	0.63
1:A:449:GLN:NE2	1:F:248:MET:O	2.31	0.63
1:B:64:LEU:HB3	1:B:65:PRO:HD3	1.80	0.63
1:B:548:GLY:O	1:B:552:LEU:HD23	1.99	0.63
1:E:670:ILE:H	1:E:670:ILE:HD12	1.64	0.63
1:B:101:PHE:CZ	1:B:193:LEU:HD13	2.34	0.62
1:B:295:VAL:C	1:C:294:TYR:HB2	2.19	0.62
1:B:380:ASP:OD1	1:B:382:ALA:N	2.32	0.62
1:F:64:LEU:HB3	1:F:65:PRO:HD3	1.79	0.62
2:H:232:PHE:HB2	2:H:233:PRO:HD3	1.80	0.62
2:J:235:PHE:CD1	3:K:34:GLN:NE2	2.67	0.62
1:D:256:ILE:HG22	1:D:391:VAL:HG12	1.80	0.62
1:E:581:LYS:NZ	1:E:610:ASP:OD1	2.31	0.62
1:B:326:ILE:HG22	1:B:370:ILE:HG13	1.82	0.62
1:B:394:GLU:O	1:B:396:GLY:N	2.32	0.62
1:C:624:GLN:NE2	1:D:610:ASP:HB2	2.14	0.62
1:C:728:LYS:O	1:C:732:LEU:HG	1.99	0.62
1:E:686:PHE:CE1	1:E:714:ILE:HG23	2.34	0.62
2:G:38:ILE:HG23	2:G:75:LEU:HD12	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:ILE:HD12	1:B:174:VAL:HG21	1.80	0.62
1:D:521:GLY:O	1:D:525:VAL:HG23	1.98	0.62
1:F:326:ILE:HG22	1:F:370:ILE:HG13	1.81	0.62
1:F:404:LEU:O	1:F:408:HIS:HB2	1.99	0.62
1:D:604:ASP:HB3	1:D:607:ARG:CB	2.29	0.62
1:E:380:ASP:OD1	1:E:382:ALA:N	2.33	0.62
1:E:706:GLY:O	1:E:710:LEU:N	2.24	0.62
1:C:383:LEU:O	1:C:389:LEU:HB2	1.98	0.62
1:D:12:PRO:HG2	1:D:23:VAL:HG11	1.81	0.62
1:D:648:ARG:HG3	1:D:651:VAL:HG23	1.82	0.62
1:F:549:LYS:HE2	1:F:645:THR:HB	1.80	0.62
2:H:115:GLY:HA2	2:G:50:ASN:HD21	1.64	0.62
2:J:269:ILE:HA	5:M:151:GLU:OE1	1.99	0.62
1:A:607:ARG:HD3	1:F:624:GLN:NE2	2.13	0.62
1:C:624:GLN:O	1:C:628:VAL:HG23	1.99	0.62
1:D:267:THR:HA	1:D:372:MET:SD	2.40	0.62
1:D:312:GLU:CG	1:D:313:GLN:H	2.12	0.62
1:D:651:VAL:O	1:D:655:MET:HG2	1.99	0.62
2:J:159:SER:CB	5:M:169:ASN:HB3	2.25	0.62
1:C:490:PRO:HB2	1:C:492:PHE:N	2.15	0.62
1:C:546:HIS:HA	1:C:708:LYS:HD3	1.82	0.62
1:E:349:THR:HG21	1:F:294:TYR:HE1	1.63	0.62
1:F:27:LYS:HD2	1:F:57:PRO:HG3	1.81	0.62
1:F:570:PRO:HG2	1:F:604:ASP:CB	2.29	0.62
1:A:12:PRO:HG2	1:A:23:VAL:HG11	1.80	0.62
1:A:617:ARG:HH11	1:A:617:ARG:HG3	1.63	0.62
1:C:311:GLU:HA	1:C:314:ARG:HG2	1.81	0.62
1:D:240:PHE:HB3	1:D:244:ILE:HD13	1.80	0.62
1:D:527:GLN:HE22	1:E:715:GLU:C	2.03	0.62
1:D:652:LEU:HB3	1:D:658:LEU:HB2	1.82	0.62
2:G:128:ALA:HB2	2:G:144:HIS:HB2	1.80	0.62
2:G:218:MET:HG2	2:G:219:LEU:N	2.11	0.62
5:M:74:ALA:O	5:M:78:LEU:HG	2.00	0.62
1:C:285:VAL:HG13	1:C:326:ILE:HD11	1.80	0.61
1:E:624:GLN:HA	1:E:624:GLN:OE1	2.00	0.61
2:H:93:LYS:HE2	2:H:130:ILE:HD11	1.82	0.61
5:M:25:SER:O	5:M:29:THR:HG23	1.98	0.61
1:D:512:ASP:O	1:D:515:THR:OG1	2.15	0.61
1:D:528:THR:OG1	1:D:641:LEU:HD12	2.00	0.61
1:D:545:PRO:HD3	1:D:647:SER:OG	2.00	0.61
1:E:64:LEU:HB3	1:E:65:PRO:HD3	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:652:LEU:HD23	1:E:657:MET:HB3	1.82	0.61
1:F:524:LEU:HD13	1:F:539:VAL:HG22	1.82	0.61
2:J:35:SER:HB3	2:J:75:LEU:HD12	1.81	0.61
5:M:203:LEU:CD2	5:M:204:GLY:H	2.06	0.61
1:D:36:ILE:HD11	1:D:44:LYS:HB3	1.82	0.61
1:A:9:ALA:HA	1:A:74:ILE:HG23	1.81	0.61
1:C:334:CYS:HA	1:C:351:VAL:HG22	1.82	0.61
1:C:407:LEU:CD1	1:C:426:ILE:HG23	2.30	0.61
1:D:236:ALA:HB1	1:E:453:MET:HG3	1.82	0.61
1:E:349:THR:HG21	1:F:294:TYR:CE1	2.35	0.61
2:H:218:MET:HG2	2:H:219:LEU:N	2.13	0.61
4:L:216:PHE:HB3	5:M:39:SER:HB2	1.82	0.61
5:M:174:GLN:O	5:M:178:ILE:HG13	2.01	0.61
5:M:177:GLN:HG3	5:M:180:ARG:HH21	1.65	0.61
1:B:383:LEU:O	1:B:389:LEU:HB2	2.01	0.61
1:C:511:GLY:HA3	1:C:513:PRO:HD2	1.82	0.61
1:C:590:ASP:HA	1:C:593:TYR:CD2	2.35	0.61
1:E:326:ILE:HG22	1:E:370:ILE:HG13	1.81	0.61
1:E:404:LEU:O	1:E:408:HIS:HB2	2.00	0.61
1:F:562:PHE:CD1	1:F:599:CYS:HB2	2.36	0.61
2:G:80:ASP:OD1	4:L:243:TYR:CE1	2.52	0.61
1:A:598:SER:OG	1:A:640:LEU:HD12	2.00	0.61
1:E:672:THR:OG1	1:E:675:GLN:HB2	2.00	0.61
1:F:650:ASP:O	1:F:653:GLN:HG3	2.01	0.61
1:A:231:PHE:CE1	1:A:235:PHE:HE2	2.19	0.61
1:B:625:ALA:O	1:B:629:LEU:HG	2.01	0.61
1:C:12:PRO:HG2	1:C:23:VAL:HG11	1.82	0.61
1:C:254:LYS:O	1:C:368:LEU:HA	2.01	0.61
1:D:239:VAL:HG13	1:D:240:PHE:CD1	2.36	0.61
1:D:606:GLU:O	1:D:610:ASP:N	2.34	0.61
1:D:632:LYS:NZ	1:E:571:ASP:HB3	2.16	0.61
1:E:710:LEU:O	1:E:714:ILE:HG13	2.00	0.61
1:F:258:LEU:HB3	1:F:395:ILE:HD11	1.82	0.61
1:B:670:ILE:HG23	1:B:675:GLN:HB2	1.83	0.61
1:C:579:THR:O	1:C:583:GLN:HG2	2.00	0.61
1:D:554:ALA:O	1:D:558:GLU:HG2	2.01	0.61
1:E:224:ASP:O	1:E:228:SER:HB2	2.01	0.61
1:E:407:LEU:CD1	1:E:426:ILE:HG23	2.31	0.61
1:F:612:VAL:CG1	1:F:617:ARG:HB2	2.31	0.61
1:D:348:ASP:O	1:D:352:ASN:ND2	2.34	0.60
1:E:513:PRO:O	1:E:517:VAL:HG23	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:552:LEU:HD11	1:E:667:VAL:HG11	1.82	0.60
3:K:84:LEU:HD21	5:M:199:ALA:HB1	1.83	0.60
1:B:95:MET:HG3	1:B:152:ILE:HG12	1.82	0.60
1:B:437:SER:O	1:B:440:GLU:HB2	2.01	0.60
1:C:404:LEU:O	1:C:408:HIS:HB2	2.01	0.60
1:E:64:LEU:O	1:E:68:LYS:HG3	2.01	0.60
2:H:231:LEU:HD13	2:G:271:ARG:HE	1.65	0.60
1:A:610:ASP:HA	1:F:624:GLN:NE2	2.16	0.60
1:D:599:CYS:SG	1:D:641:LEU:HD22	2.42	0.60
3:K:83:LYS:HG2	3:K:86:ARG:HH22	1.64	0.60
1:A:678:GLU:O	1:A:682:LEU:HD12	2.01	0.60
1:F:380:ASP:OD1	1:F:382:ALA:N	2.32	0.60
2:H:115:GLY:HA2	2:G:50:ASN:ND2	2.17	0.60
2:H:142:ILE:HG23	2:H:168:VAL:HG13	1.83	0.60
1:C:73:SER:O	1:C:76:GLN:HG2	2.00	0.60
1:D:436:PHE:HE2	1:D:444:LEU:HD12	1.66	0.60
1:E:264:CYS:SG	1:E:395:ILE:HG21	2.41	0.60
1:F:521:GLY:O	1:F:525:VAL:HG23	2.01	0.60
1:F:525:VAL:HG13	1:F:562:PHE:HE1	1.62	0.60
2:G:234:ALA:HB3	2:G:237:ASP:HB2	1.84	0.60
1:B:404:LEU:O	1:B:408:HIS:HB2	2.02	0.60
1:D:585:MET:O	1:D:589:PHE:HD2	1.84	0.60
1:A:413:ARG:NH1	1:F:249:GLY:O	2.27	0.60
1:E:383:LEU:O	1:E:389:LEU:HB2	2.02	0.60
1:F:655:MET:O	1:F:656:GLU:HG2	2.01	0.60
1:A:582:CYS:SG	1:A:621:LEU:HG	2.42	0.60
1:A:597:LEU:C	1:A:597:LEU:HD23	2.22	0.60
1:D:256:ILE:O	1:D:370:ILE:HA	2.01	0.60
1:D:527:GLN:NE2	1:E:716:MET:HA	2.16	0.60
1:D:547:SER:OG	1:D:549:LYS:HG3	2.02	0.60
1:E:705:ILE:HD13	1:E:710:LEU:HD13	1.84	0.60
1:F:407:LEU:CD1	1:F:426:ILE:HG23	2.32	0.60
2:I:128:ALA:HB2	2:I:144:HIS:HB2	1.84	0.60
3:K:79:THR:HG22	3:K:83:LYS:HE3	1.84	0.60
5:M:203:LEU:HD23	5:M:204:GLY:N	2.07	0.60
1:A:508:ILE:HB	1:A:682:LEU:HD22	1.83	0.60
1:C:695:ALA:HB1	1:C:699:LYS:HE3	1.83	0.60
1:D:64:LEU:HB3	1:D:65:PRO:HD3	1.82	0.60
1:D:513:PRO:HB3	1:D:516:ARG:HE	1.66	0.60
1:E:289:GLU:O	1:E:291:LEU:N	2.24	0.60
2:H:128:ALA:HB2	2:H:144:HIS:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:270:ALA:O	1:A:273:ILE:HG22	2.02	0.60
1:B:36:ILE:HD11	1:B:44:LYS:HB3	1.84	0.60
1:B:533:ARG:HG3	1:B:534:THR:HG23	1.84	0.60
1:D:513:PRO:O	1:D:516:ARG:HG2	2.02	0.60
1:E:671:ALA:HA	1:E:703:VAL:O	2.02	0.60
1:A:628:VAL:HG11	1:B:571:ASP:HA	1.83	0.59
1:A:687:LYS:HB2	1:A:690:GLU:HG3	1.83	0.59
1:B:240:PHE:HB3	1:B:244:ILE:HB	1.84	0.59
1:C:383:LEU:HD22	1:C:388:ARG:HD2	1.84	0.59
2:I:57:ASN:O	2:I:59:SER:N	2.35	0.59
1:B:407:LEU:CD1	1:B:426:ILE:HG23	2.31	0.59
2:I:21:VAL:HG21	2:I:71:LEU:HD22	1.82	0.59
2:I:101:ILE:HG21	2:I:135:LEU:HD11	1.84	0.59
2:I:287:ILE:O	2:I:291:GLU:HG3	2.02	0.59
2:J:233:PRO:HA	2:J:235:PHE:CE1	2.37	0.59
1:A:627:LEU:HD13	1:B:607:ARG:HH12	1.66	0.59
1:A:676:LEU:CD1	1:A:710:LEU:HD11	2.33	0.59
1:B:284:VAL:HG23	1:B:324:ILE:O	2.02	0.59
1:E:284:VAL:HG23	1:E:324:ILE:O	2.02	0.59
3:K:56:ARG:HH11	5:M:171:ILE:HG23	1.67	0.59
1:C:507:ILE:HD13	1:C:555:LYS:HG2	1.77	0.59
1:C:606:GLU:HG2	1:C:607:ARG:N	2.18	0.59
1:D:618:PHE:CE2	1:E:614:ILE:HD12	2.37	0.59
1:E:532:ASP:OD2	1:E:533:ARG:N	2.35	0.59
5:M:40:LYS:O	5:M:44:ILE:HG13	2.03	0.59
1:A:694:ILE:O	1:A:698:VAL:HG13	2.02	0.59
1:B:540:LEU:HA	1:B:644:GLY:O	2.02	0.59
1:B:589:PHE:HE2	1:B:629:LEU:HB3	1.67	0.59
1:C:540:LEU:HB2	1:C:661:PHE:CD2	2.37	0.59
1:C:542:GLU:HB3	1:C:649:LYS:HD3	1.82	0.59
2:I:69:ALA:HB1	2:I:85:PHE:CE1	2.36	0.59
5:M:17:ARG:O	5:M:21:LEU:HG	2.02	0.59
1:B:121:PHE:CD2	1:B:183:VAL:HG21	2.37	0.59
1:D:18:LEU:HA	1:D:137:VAL:CG2	2.32	0.59
1:D:310:GLU:O	1:D:313:GLN:NE2	2.36	0.59
1:E:713:LEU:HD22	1:E:732:LEU:HD13	1.85	0.59
1:F:236:ALA:HA	1:F:239:VAL:HG12	1.83	0.59
2:H:200:TYR:CE2	5:M:42:ALA:HB2	2.38	0.59
2:H:235:PHE:CD2	5:M:31:ARG:HA	2.37	0.59
1:C:540:LEU:HD12	1:C:644:GLY:O	2.02	0.59
1:F:437:SER:O	1:F:440:GLU:HB2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:18:GLU:HA	2:H:21:VAL:HG12	1.85	0.59
2:H:289:GLY:O	2:H:293:ASP:CB	2.51	0.59
1:A:449:GLN:O	1:A:453:MET:HG2	2.03	0.59
1:E:502:TYR:OH	1:E:569:SER:OG	2.19	0.59
1:E:510:TRP:NE1	1:E:707:ILE:HD11	2.18	0.59
1:E:586:LYS:HA	1:E:589:PHE:CD2	2.37	0.59
4:L:199:HIS:CE1	5:M:21:LEU:HD22	2.38	0.59
1:B:571:ASP:OD2	1:B:571:ASP:N	2.35	0.59
1:D:312:GLU:HG2	1:D:313:GLN:H	1.68	0.59
2:G:101:ILE:HG21	2:G:135:LEU:HD11	1.85	0.59
1:B:67:ARG:NH2	2:H:293:ASP:O	2.36	0.59
1:B:421:SER:HG	1:B:479:ASP:N	2.01	0.59
1:C:577:SER:O	1:C:580:ALA:N	2.34	0.59
1:D:383:LEU:O	1:D:389:LEU:HB2	2.03	0.59
1:F:589:PHE:CD2	1:F:629:LEU:HD22	2.37	0.59
1:A:238:ARG:HA	1:A:252:HIS:CE1	2.37	0.58
1:A:307:ALA:O	1:A:310:GLU:HG3	2.02	0.58
1:A:397:LEU:HB3	1:A:398:PRO:HD3	1.84	0.58
1:A:716:MET:HG2	1:A:732:LEU:HD11	1.85	0.58
1:E:190:ASN:ND2	1:E:316:LEU:HA	2.18	0.58
1:E:506:GLY:O	1:E:508:ILE:N	2.36	0.58
5:M:148:GLU:O	5:M:152:GLN:HG3	2.03	0.58
1:A:411:THR:OG1	1:A:426:ILE:HD11	2.03	0.58
1:A:503:ILE:HG23	1:A:506:GLY:HA2	1.83	0.58
1:C:527:GLN:HB2	1:D:719:GLN:HG3	1.85	0.58
1:D:11:CYS:SG	1:D:17:SER:HB2	2.43	0.58
1:F:383:LEU:O	1:F:389:LEU:HB2	2.02	0.58
2:G:235:PHE:CZ	5:M:151:GLU:HG2	2.38	0.58
2:H:218:MET:CG	2:H:219:LEU:H	2.06	0.58
2:J:167:LYS:HE2	2:J:171:TYR:HE2	1.67	0.58
1:A:382:ALA:O	1:A:385:ARG:HG2	2.02	0.58
1:B:596:GLN:HA	1:B:638:ARG:HG2	1.86	0.58
1:D:527:GLN:HE21	1:E:715:GLU:HG3	1.68	0.58
5:M:49:MET:HG2	5:M:53:GLN:HE21	1.68	0.58
1:B:578:GLU:HG3	1:B:619:SER:HB2	1.85	0.58
1:C:377:ASP:OD2	1:C:377:ASP:N	2.36	0.58
1:E:310:GLU:OE2	1:E:357:LYS:NZ	2.36	0.58
2:J:18:GLU:HA	2:J:21:VAL:HG12	1.85	0.58
3:K:35:THR:HA	3:K:38:GLN:OE1	2.03	0.58
5:M:34:GLN:O	5:M:38:GLU:N	2.35	0.58
5:M:191:ARG:HH11	5:M:191:ARG:HG3	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:605:ILE:HD11	1:B:644:GLY:HA3	1.85	0.58
1:E:628:VAL:O	1:E:632:LYS:N	2.35	0.58
2:H:231:LEU:HD13	2:G:271:ARG:NE	2.18	0.58
1:C:621:LEU:HD11	1:D:575:GLY:HA2	1.85	0.58
1:D:312:GLU:OE1	1:D:323:HIS:ND1	2.33	0.58
1:E:289:GLU:C	1:E:291:LEU:H	2.05	0.58
1:E:587:LYS:HZ3	1:E:587:LYS:C	2.06	0.58
2:G:218:MET:CG	2:G:219:LEU:H	2.05	0.58
1:A:353:GLN:HA	1:B:288:PRO:CG	2.34	0.58
1:B:236:ALA:HA	1:B:239:VAL:HG12	1.86	0.58
1:B:631:LYS:NZ	1:C:604:ASP:OD2	2.36	0.58
1:D:242:PRO:HD2	1:D:243:GLU:H	1.69	0.58
1:F:284:VAL:HG23	1:F:324:ILE:O	2.03	0.58
2:H:21:VAL:HG21	2:H:71:LEU:HD22	1.84	0.58
2:I:108:ILE:HD12	2:I:127:ILE:HD12	1.85	0.58
1:A:257:LEU:HG	1:A:389:LEU:HD12	1.86	0.58
1:C:289:GLU:O	1:C:291:LEU:N	2.31	0.58
1:E:296:GLY:H	1:E:297:GLU:CB	2.17	0.58
1:B:64:LEU:HA	1:B:67:ARG:HE	1.69	0.58
1:C:490:PRO:HA	1:C:491:ALA:CB	2.28	0.58
1:D:313:GLN:O	1:D:317:GLY:N	2.36	0.58
1:E:270:ALA:O	1:E:273:ILE:HG22	2.04	0.58
1:F:566:LYS:HD2	1:F:567:ILE:N	2.19	0.58
1:F:715:GLU:O	1:F:719:GLN:HG2	2.04	0.58
1:A:18:LEU:HD13	1:A:139:SER:HB2	1.84	0.57
1:A:428:GLU:HG2	1:A:479:ASP:CA	2.31	0.57
1:A:571:ASP:HA	1:A:574:ILE:HG23	1.86	0.57
1:A:726:VAL:O	1:A:730:LEU:HG	2.04	0.57
1:C:507:ILE:CD1	1:C:555:LYS:CD	2.79	0.57
1:D:18:LEU:HA	1:D:137:VAL:HG23	1.85	0.57
1:D:687:LYS:O	1:D:691:ARG:HG3	2.05	0.57
2:H:94:LYS:CE	2:I:153:LYS:HG3	2.34	0.57
5:M:170:GLU:HG3	5:M:174:GLN:HE21	1.68	0.57
1:A:549:LYS:HE3	1:A:646:THR:C	2.24	0.57
1:B:423:ASP:HB2	1:B:479:ASP:N	2.19	0.57
1:B:695:ALA:HB1	1:B:699:LYS:HE3	1.85	0.57
1:C:614:ILE:C	1:C:616:PRO:HA	2.24	0.57
1:C:658:LEU:HD11	1:C:664:THR:HG21	1.86	0.57
1:E:171:LYS:HB3	1:E:171:LYS:NZ	2.20	0.57
1:F:106:ASN:HB3	1:F:143:LYS:NZ	2.18	0.57
1:F:604:ASP:HB3	1:F:607:ARG:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:201:SER:OG	2:J:205:TYR:HE1	1.81	0.57
4:L:218:ASP:O	4:L:222:LEU:HG	2.03	0.57
1:C:510:TRP:CE3	1:C:670:ILE:HG12	2.39	0.57
1:C:688:ASP:OD1	1:C:691:ARG:NH2	2.26	0.57
1:F:606:GLU:OE2	1:F:647:SER:HB2	2.04	0.57
2:H:271:ARG:HH22	2:I:231:LEU:HB2	1.69	0.57
2:I:235:PHE:CB	4:L:207:ASN:HB3	2.35	0.57
2:G:235:PHE:CD2	5:M:152:GLN:HA	2.40	0.57
1:A:299:GLU:HG2	1:A:353:GLN:HG2	1.86	0.57
1:A:536:LEU:HD23	1:A:633:ALA:HA	1.86	0.57
1:A:542:GLU:OE2	1:A:666:HIS:NE2	2.37	0.57
1:C:256:ILE:HG22	1:C:391:VAL:HG11	1.84	0.57
1:D:380:ASP:OD1	1:D:382:ALA:N	2.36	0.57
1:E:267:THR:HA	1:E:372:MET:SD	2.44	0.57
1:E:697:GLN:HG3	1:E:730:LEU:HD11	1.84	0.57
2:H:149:ALA:HB2	2:H:164:CYS:HB2	1.86	0.57
1:A:445:VAL:O	1:A:449:GLN:HG2	2.04	0.57
1:B:289:GLU:O	1:B:291:LEU:N	2.28	0.57
1:E:721:ASP:O	1:E:725:ARG:HG3	2.05	0.57
1:A:560:SER:HB2	1:A:562:PHE:CE1	2.40	0.57
1:A:678:GLU:O	1:A:681:GLU:HG2	2.04	0.57
1:B:589:PHE:CE2	1:B:629:LEU:HB3	2.39	0.57
1:D:604:ASP:HB3	1:D:607:ARG:HB3	1.86	0.57
1:E:550:THR:HA	1:E:645:THR:HG21	1.85	0.57
1:D:223:LEU:HD12	1:D:395:ILE:HG23	1.87	0.57
1:D:404:LEU:HD11	1:D:427:LYS:HE3	1.85	0.57
1:D:528:THR:OG1	1:D:537:VAL:HG21	2.05	0.57
1:D:628:VAL:HG13	1:E:571:ASP:OD1	2.02	0.57
1:F:242:PRO:HD2	1:F:243:GLU:H	1.69	0.57
1:F:653:GLN:HB3	1:F:658:LEU:HD23	1.86	0.57
2:H:116:ARG:NH2	3:K:68:ASP:HB3	2.20	0.57
2:G:256:VAL:HG11	2:G:288:GLN:HG2	1.87	0.57
4:L:199:HIS:CD2	5:M:21:LEU:HD13	2.39	0.57
1:A:352:ASN:HA	1:A:355:LEU:HD12	1.87	0.57
1:B:110:ASN:HB3	1:B:111:PRO:HD2	1.85	0.57
1:C:540:LEU:HD23	1:C:649:LYS:HE3	1.86	0.57
1:D:625:ALA:O	1:D:629:LEU:HG	2.04	0.57
1:E:27:LYS:N	1:E:27:LYS:HD2	2.20	0.57
1:A:267:THR:OG1	1:A:328:ASP:OD2	2.23	0.57
1:B:542:GLU:HG3	1:B:542:GLU:O	2.05	0.57
1:C:436:PHE:HB3	1:C:440:GLU:OE1	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:677:LEU:HD11	1:C:698:VAL:HG21	1.87	0.57
1:E:397:LEU:HD22	1:E:398:PRO:HD2	1.86	0.57
1:E:673:GLY:HA3	1:E:698:VAL:HB	1.87	0.57
1:F:296:GLY:H	1:F:297:GLU:CB	2.17	0.57
1:F:562:PHE:HE2	1:F:597:LEU:HD12	1.69	0.57
2:J:96:ASP:H	2:J:97:PRO:HD2	1.70	0.57
2:J:231:LEU:O	2:J:234:ALA:N	2.19	0.57
1:A:489:LYS:N	1:A:490:PRO:HD2	2.19	0.56
1:B:296:GLY:H	1:B:297:GLU:CB	2.18	0.56
1:E:190:ASN:ND2	1:E:316:LEU:HG	2.17	0.56
1:F:562:PHE:HB2	1:F:565:ILE:HG12	1.86	0.56
1:A:295:VAL:HB	1:B:294:TYR:CB	2.34	0.56
1:A:513:PRO:O	1:A:517:VAL:HG23	2.05	0.56
1:A:568:CYS:O	1:A:603:ASP:HB3	2.04	0.56
1:B:404:LEU:HG	1:B:426:ILE:HG22	1.87	0.56
1:B:654:GLU:O	1:C:613:PRO:HG3	2.04	0.56
1:D:300:ALA:O	1:D:303:ARG:HB3	2.05	0.56
1:D:686:PHE:HB2	1:D:691:ARG:HG2	1.87	0.56
1:A:544:PRO:HB2	1:A:669:ASN:ND2	2.21	0.56
1:A:565:ILE:HG13	1:A:599:CYS:HB3	1.88	0.56
1:A:690:GLU:O	1:A:694:ILE:HG13	2.04	0.56
1:B:559:GLU:O	1:B:561:ASN:ND2	2.38	0.56
1:C:375:ARG:NH2	1:C:377:ASP:OD1	2.38	0.56
1:C:555:LYS:HA	1:C:558:GLU:OE1	2.05	0.56
1:D:312:GLU:CG	1:D:313:GLN:N	2.67	0.56
1:D:313:GLN:HG3	1:D:314:ARG:N	2.20	0.56
1:D:493:GLY:HA2	1:D:496:GLN:CB	2.36	0.56
1:D:656:GLU:OE1	1:E:613:PRO:HB3	2.05	0.56
1:E:693:THR:O	1:E:697:GLN:NE2	2.20	0.56
1:F:632:LYS:HD2	1:F:633:ALA:H	1.71	0.56
3:K:63:LEU:HD13	5:M:182:MET:HG2	1.87	0.56
4:L:199:HIS:CG	5:M:21:LEU:HD13	2.40	0.56
2:H:230:GLU:HG2	2:H:231:LEU:N	2.20	0.56
1:D:284:VAL:HB	1:D:325:ILE:HA	1.87	0.56
1:E:598:SER:OG	1:E:639:LYS:O	2.20	0.56
2:J:266:TYR:CZ	2:J:270:SER:HB2	2.40	0.56
4:L:202:ILE:O	4:L:205:LEU:HB3	2.05	0.56
1:A:64:LEU:HA	1:A:67:ARG:HE	1.71	0.56
1:A:539:VAL:HG13	1:A:643:ILE:HA	1.87	0.56
1:C:694:ILE:O	1:C:698:VAL:HG22	2.05	0.56
1:D:299:GLU:OE1	1:D:350:VAL:HG13	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:352:ASN:HA	1:E:355:LEU:HD12	1.87	0.56
1:F:542:GLU:HB2	1:F:666:HIS:HA	1.87	0.56
2:J:53:LYS:HE3	2:G:117:PHE:CE2	2.40	0.56
1:B:242:PRO:HD2	1:B:243:GLU:H	1.71	0.56
1:B:327:PHE:HB2	1:B:330:ILE:CG2	2.33	0.56
1:B:545:PRO:O	1:B:546:HIS:HB2	2.05	0.56
1:C:245:VAL:O	1:C:249:GLY:N	2.36	0.56
1:C:503:ILE:HG22	1:C:506:GLY:HA2	1.86	0.56
1:E:98:GLU:HB3	1:E:148:LEU:HB3	1.87	0.56
1:E:502:TYR:CZ	1:E:567:ILE:HG21	2.40	0.56
1:E:648:ARG:NE	1:E:650:ASP:OD1	2.32	0.56
1:A:73:SER:O	1:A:76:GLN:HG2	2.06	0.56
1:A:223:LEU:CD1	1:A:227:PHE:HB2	2.36	0.56
1:C:330:ILE:HG22	1:C:379:ILE:CD1	2.36	0.56
1:C:653:GLN:HG3	1:C:658:LEU:HD23	1.86	0.56
1:D:40:SER:OG	1:D:41:PRO:HD2	2.06	0.56
1:E:490:PRO:HA	1:E:491:ALA:CB	2.33	0.56
1:F:267:THR:HA	1:F:372:MET:SD	2.45	0.56
2:H:256:VAL:HG21	2:H:288:GLN:HG3	1.88	0.56
2:I:200:TYR:CE2	4:L:211:GLU:HG3	2.41	0.56
5:M:26:LEU:HD22	5:M:146:MET:HE3	1.88	0.56
1:A:525:VAL:HG13	1:A:562:PHE:CE1	2.40	0.56
1:A:540:LEU:HD11	1:A:646:THR:HG22	1.86	0.56
1:C:375:ARG:NH1	1:C:378:LEU:HG	2.20	0.56
2:H:179:GLN:HB3	2:H:214:PHE:HB3	1.88	0.56
2:H:271:ARG:HH22	2:I:231:LEU:CB	2.17	0.56
2:I:127:ILE:HG23	2:I:131:TYR:CE1	2.41	0.56
1:C:40:SER:OG	1:C:43:HIS:HB2	2.05	0.56
1:D:627:LEU:HD13	1:E:607:ARG:HH12	1.70	0.56
1:F:270:ALA:O	1:F:273:ILE:HG22	2.06	0.56
1:F:559:GLU:HA	1:F:559:GLU:OE1	2.06	0.56
1:F:602:VAL:N	1:F:643:ILE:O	2.23	0.56
2:I:67:GLN:O	2:I:71:LEU:HG	2.06	0.56
2:J:69:ALA:HB1	2:J:85:PHE:CE1	2.41	0.56
5:M:42:ALA:HA	5:M:45:ARG:CZ	2.36	0.56
1:A:536:LEU:HD23	1:A:634:PRO:HD3	1.88	0.55
1:B:10:ARG:NE	2:H:293:ASP:OD2	2.34	0.55
1:C:688:ASP:O	1:C:692:THR:HG23	2.07	0.55
1:E:354:LEU:O	1:E:358:ILE:HG12	2.06	0.55
1:E:681:GLU:HA	1:E:691:ARG:HE	1.71	0.55
2:J:218:MET:CG	2:J:219:LEU:H	2.14	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:ARG:HD2	2:H:218:MET:CG	2.35	0.55
1:B:398:PRO:HG3	1:B:436:PHE:O	2.06	0.55
1:C:106:ASN:HB3	1:C:143:LYS:NZ	2.21	0.55
1:E:528:THR:HG21	1:E:641:LEU:CD2	2.27	0.55
1:E:705:ILE:HG13	1:E:709:LYS:HG3	1.88	0.55
2:J:243:LEU:HD22	2:J:266:TYR:CG	2.41	0.55
2:G:57:ASN:O	2:G:59:SER:N	2.39	0.55
4:L:233:ILE:O	4:L:237:VAL:HG23	2.06	0.55
5:M:50:LEU:HD12	5:M:167:MET:HG2	1.88	0.55
1:A:549:LYS:HG3	1:A:550:THR:N	2.21	0.55
1:A:709:LYS:HE2	1:A:709:LYS:HA	1.89	0.55
1:B:198:LYS:N	1:B:198:LYS:HD2	2.21	0.55
1:E:242:PRO:HD2	1:E:243:GLU:H	1.70	0.55
1:E:573:MET:SD	1:E:581:LYS:HG2	2.46	0.55
1:F:69:TRP:NE1	1:F:134:GLN:HA	2.21	0.55
1:A:531:SER:O	1:A:639:LYS:HE2	2.07	0.55
1:B:270:ALA:O	1:B:273:ILE:HG22	2.06	0.55
1:E:232:ARG:NH2	1:F:454:ASN:H	2.03	0.55
1:F:554:ALA:O	1:F:558:GLU:HG3	2.06	0.55
2:H:119:ILE:HD13	3:K:65:ASP:OD1	2.06	0.55
5:M:56:GLN:O	5:M:60:VAL:HG23	2.05	0.55
1:A:383:LEU:O	1:A:389:LEU:HB2	2.07	0.55
1:A:724:TYR:HD1	1:A:727:ARG:HH12	1.54	0.55
1:C:128:GLN:O	1:C:176:LEU:HD12	2.07	0.55
1:F:91:CYS:O	1:F:154:ALA:HA	2.07	0.55
2:J:175:LEU:HD23	2:J:177:GLN:HE21	1.70	0.55
2:J:182:ILE:O	2:J:186:GLU:HG2	2.07	0.55
1:A:355:LEU:HB3	1:A:388:ARG:NH1	2.21	0.55
1:B:289:GLU:C	1:B:291:LEU:H	2.09	0.55
1:C:95:MET:HG3	1:C:152:ILE:HG12	1.87	0.55
1:C:256:ILE:HA	1:C:391:VAL:HG13	1.87	0.55
1:C:507:ILE:HD12	1:C:555:LYS:HD3	1.89	0.55
1:D:510:TRP:CE3	1:D:675:GLN:HG2	2.34	0.55
2:I:175:LEU:HD23	2:I:177:GLN:HE21	1.72	0.55
3:K:70:LEU:HD13	5:M:185:ALA:O	2.07	0.55
1:B:354:LEU:O	1:B:358:ILE:HG12	2.05	0.55
1:B:552:LEU:O	1:B:556:ILE:HG13	2.07	0.55
1:C:327:PHE:CB	1:C:330:ILE:HD11	2.28	0.55
1:F:354:LEU:O	1:F:358:ILE:HG12	2.07	0.55
2:H:72:HIS:CE1	2:H:80:ASP:HB2	2.42	0.55
4:L:211:GLU:HA	4:L:214:ASP:OD2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:688:ASP:OD1	1:A:689:LYS:N	2.40	0.55
1:A:705:ILE:HD13	1:A:710:LEU:CD1	2.34	0.55
1:C:284:VAL:HG11	1:C:305:LEU:HD11	1.88	0.55
1:D:681:GLU:HG2	1:D:691:ARG:NH1	2.21	0.55
2:H:182:ILE:O	2:H:186:GLU:HG2	2.06	0.55
4:L:213:HIS:CD2	5:M:35:LEU:HB3	2.42	0.55
1:A:40:SER:OG	1:A:41:PRO:HD2	2.07	0.55
1:A:485:GLU:O	1:A:489:LYS:CB	2.54	0.55
1:E:449:GLN:O	1:E:453:MET:HG2	2.05	0.55
1:E:604:ASP:O	1:E:608:LEU:N	2.38	0.55
3:K:37:ALA:HA	3:K:40:ASP:OD2	2.06	0.55
1:A:286:ASN:HB2	1:A:327:PHE:CB	2.37	0.55
1:B:421:SER:HB3	1:B:424:VAL:HG23	1.87	0.55
1:D:40:SER:HB3	1:D:43:HIS:HB2	1.88	0.55
1:F:617:ARG:HH11	1:F:617:ARG:HG3	1.72	0.55
2:J:101:ILE:HG21	2:J:135:LEU:HD11	1.89	0.55
5:M:26:LEU:HB2	5:M:146:MET:HE2	1.88	0.55
5:M:149:ASN:O	5:M:153:VAL:HG23	2.07	0.55
1:A:406:ILE:O	1:A:409:ILE:HG22	2.06	0.54
1:A:562:PHE:CD2	1:A:597:LEU:CD2	2.83	0.54
1:B:267:THR:HA	1:B:372:MET:SD	2.47	0.54
3:K:52:LYS:HB2	3:K:52:LYS:NZ	2.23	0.54
1:A:293:LYS:O	1:A:294:TYR:CG	2.60	0.54
1:A:315:ARG:HG2	1:A:316:LEU:CD1	2.37	0.54
1:A:398:PRO:HG3	1:A:437:SER:HA	1.90	0.54
1:D:690:GLU:O	1:D:693:THR:OG1	2.21	0.54
1:F:538:SER:OG	1:F:661:PHE:HD1	1.88	0.54
4:L:202:ILE:CG2	5:M:25:SER:HB3	2.37	0.54
1:A:563:PRO:HG2	1:A:597:LEU:O	2.06	0.54
1:B:570:PRO:HG3	1:B:608:LEU:HD23	1.88	0.54
1:C:355:LEU:O	1:C:388:ARG:NH2	2.34	0.54
1:C:577:SER:O	1:C:579:THR:N	2.40	0.54
1:D:423:ASP:HB2	1:D:480:PHE:CB	2.37	0.54
1:D:686:PHE:CE1	1:D:714:ILE:HG23	2.42	0.54
1:E:508:ILE:HB	1:E:682:LEU:HD13	1.89	0.54
1:F:89:LYS:O	1:F:172:ILE:HG21	2.07	0.54
1:F:721:ASP:HB2	1:F:724:TYR:CD1	2.41	0.54
2:I:231:LEU:O	2:I:234:ALA:N	2.40	0.54
1:A:625:ALA:O	1:A:629:LEU:HG	2.08	0.54
1:A:677:LEU:HG	1:A:695:ALA:HB2	1.88	0.54
1:B:64:LEU:HB2	2:H:293:ASP:C	2.28	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:570:PRO:HD3	1:B:603:ASP:HB3	1.90	0.54
1:B:571:ASP:O	1:B:574:ILE:HG13	2.08	0.54
1:D:651:VAL:HG13	1:D:655:MET:HE3	1.88	0.54
2:J:243:LEU:HD13	2:J:266:TYR:HB2	1.88	0.54
5:M:78:LEU:CD1	5:M:195:ALA:HB1	2.37	0.54
1:A:457:ILE:HG13	1:F:240:PHE:HE1	1.73	0.54
1:A:570:PRO:HD3	1:A:603:ASP:OD2	2.08	0.54
1:B:527:GLN:NE2	1:C:716:MET:SD	2.69	0.54
1:C:281:GLU:CB	1:C:324:ILE:HD13	2.38	0.54
1:D:353:GLN:NE2	1:E:288:PRO:HG2	2.21	0.54
1:C:570:PRO:HG2	1:C:604:ASP:HB2	1.90	0.54
1:C:589:PHE:CD2	1:C:629:LEU:HD13	2.42	0.54
1:D:657:MET:HG2	1:D:661:PHE:CE2	2.42	0.54
1:E:590:ASP:O	1:E:593:TYR:HB2	2.08	0.54
1:F:686:PHE:HE1	1:F:714:ILE:HG23	1.73	0.54
2:J:112:THR:HG23	2:J:117:PHE:HE1	1.73	0.54
1:A:565:ILE:HA	1:A:599:CYS:O	2.08	0.54
1:A:672:THR:OG1	1:A:675:GLN:OE1	2.14	0.54
1:A:686:PHE:CE2	1:A:714:ILE:HG23	2.43	0.54
1:E:8:ALA:HB3	1:E:73:SER:O	2.08	0.54
2:H:124:HIS:HE1	2:H:147:GLN:HB3	1.73	0.54
2:I:124:HIS:HE1	2:I:147:GLN:HB3	1.72	0.54
2:G:142:ILE:HG23	2:G:168:VAL:HG13	1.89	0.54
1:A:286:ASN:HB2	1:A:327:PHE:HB3	1.90	0.54
1:C:388:ARG:NH1	1:C:388:ARG:HB2	2.23	0.54
1:C:690:GLU:CB	1:C:726:VAL:HG21	2.36	0.54
1:D:356:SER:HB2	1:E:288:PRO:HG3	1.90	0.54
1:E:516:ARG:O	1:E:519:ASP:OD1	2.25	0.54
5:M:156:ILE:HG22	5:M:160:LEU:HG	1.89	0.54
1:A:407:LEU:HD12	1:A:426:ILE:HG23	1.90	0.54
1:A:610:ASP:OD1	1:F:624:GLN:HG3	2.06	0.54
1:C:34:HIS:HB2	1:C:83:TYR:O	2.08	0.54
1:C:63:SER:O	1:C:67:ARG:HG3	2.08	0.54
1:C:399:ASP:O	1:C:402:GLY:N	2.41	0.54
1:D:260:GLY:N	1:D:266:LYS:HD3	2.23	0.54
1:E:236:ALA:O	1:E:239:VAL:HG12	2.08	0.54
1:F:40:SER:HB2	1:F:41:PRO:HD2	1.90	0.54
4:L:229:MET:O	4:L:233:ILE:HG13	2.08	0.54
1:B:539:VAL:HG21	1:B:665:ILE:HD12	1.88	0.53
1:C:46:ILE:HD12	1:C:174:VAL:HG21	1.89	0.53
1:F:113:ASP:O	1:F:117:MET:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:61:GLU:HG2	5:M:65:ASN:ND2	2.19	0.53
1:A:122:ILE:O	1:A:126:ASN:HB3	2.08	0.53
1:B:452:ALA:HA	1:B:455:ARG:NH2	2.23	0.53
1:C:242:PRO:HD2	1:C:243:GLU:H	1.73	0.53
1:E:149:VAL:HG11	1:E:152:ILE:HD11	1.89	0.53
1:E:585:MET:HG3	1:E:589:PHE:HZ	1.70	0.53
1:F:522:GLU:OE2	1:F:526:GLN:HG2	2.09	0.53
1:F:535:PRO:HB2	1:F:536:LEU:HD13	1.90	0.53
2:J:179:GLN:HB3	2:J:214:PHE:CG	2.43	0.53
2:J:201:SER:HA	5:M:161:ARG:HD2	1.90	0.53
5:M:29:THR:HB	5:M:150:LEU:HD21	1.89	0.53
5:M:143:GLU:HA	5:M:146:MET:HB3	1.89	0.53
1:A:521:GLY:HA2	1:A:524:LEU:HD12	1.89	0.53
1:C:347:HIS:O	1:C:350:VAL:HG22	2.08	0.53
1:D:593:TYR:O	1:D:638:ARG:HG2	2.08	0.53
2:H:20:LYS:HE2	2:H:37:LYS:HA	1.89	0.53
1:C:612:VAL:HG12	1:C:617:ARG:HB3	1.90	0.53
1:E:313:GLN:HE21	1:E:317:GLY:HA3	1.72	0.53
1:F:555:LYS:HE2	1:F:555:LYS:HA	1.90	0.53
2:J:218:MET:HG2	2:J:219:LEU:N	2.19	0.53
1:B:101:PHE:HZ	1:B:193:LEU:HD13	1.72	0.53
1:C:536:LEU:HD12	1:C:640:LEU:HB3	1.89	0.53
2:H:95:ALA:HB1	2:H:97:PRO:HD2	1.91	0.53
2:I:120:ALA:O	2:I:124:HIS:HB2	2.08	0.53
1:F:26:GLU:HG2	1:F:51:THR:HB	1.91	0.53
1:F:184:ALA:HB1	1:F:200:LYS:O	2.09	0.53
1:F:503:ILE:HG22	1:F:506:GLY:H	1.73	0.53
1:F:710:LEU:O	1:F:714:ILE:HG13	2.09	0.53
2:I:232:PHE:C	2:I:234:ALA:H	2.12	0.53
3:K:68:ASP:O	3:K:71:GLN:HG3	2.09	0.53
1:B:184:ALA:HB1	1:B:200:LYS:O	2.07	0.53
1:B:576:PHE:HB2	1:B:581:LYS:HG3	1.90	0.53
1:D:136:LEU:HD23	1:D:136:LEU:H	1.73	0.53
1:D:510:TRP:HB3	1:D:679:ALA:HB2	1.90	0.53
1:D:731:ALA:HA	1:D:734:ARG:NH1	2.23	0.53
1:F:525:VAL:HG11	1:F:560:SER:CB	2.38	0.53
2:I:179:GLN:O	2:I:182:ILE:HG12	2.08	0.53
2:I:254:GLN:HB2	2:I:291:GLU:HG2	1.89	0.53
5:M:67:ILE:O	5:M:71:MET:HG2	2.08	0.53
1:B:546:HIS:O	1:B:549:LYS:HE3	2.09	0.53
1:B:569:SER:HA	1:B:603:ASP:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:14:ASP:O	1:D:18:LEU:HG	2.08	0.53
1:D:263:GLY:O	1:D:439:ALA:N	2.38	0.53
1:D:522:GLU:OE2	1:D:556:ILE:HA	2.08	0.53
1:D:686:PHE:HB3	1:D:690:GLU:HG3	1.91	0.53
1:E:664:THR:C	1:E:665:ILE:HD13	2.29	0.53
1:F:525:VAL:HG11	1:F:560:SER:HB2	1.91	0.53
1:A:300:ALA:HA	1:A:303:ARG:HG2	1.91	0.53
1:A:306:PHE:CD1	1:A:357:LYS:HB3	2.44	0.53
1:A:347:HIS:N	1:A:348:ASP:HA	2.23	0.53
1:A:421:SER:HB3	1:A:424:VAL:CG2	2.33	0.53
1:B:310:GLU:OE2	1:B:357:LYS:NZ	2.41	0.53
1:C:38:ARG:HB3	1:C:79:GLU:HB2	1.91	0.53
1:E:89:LYS:HB3	1:E:89:LYS:NZ	2.23	0.53
1:E:307:ALA:HA	1:E:310:GLU:HG2	1.91	0.53
1:F:34:HIS:HB2	1:F:83:TYR:O	2.08	0.53
5:M:33:LEU:HA	5:M:153:VAL:HG22	1.90	0.53
1:A:255:GLY:HA3	1:A:389:LEU:HD13	1.90	0.53
1:C:606:GLU:HB2	1:C:648:ARG:HD2	1.90	0.53
1:D:101:PHE:CD2	1:D:107:ILE:HA	2.44	0.53
1:D:303:ARG:HD3	1:D:353:GLN:CD	2.28	0.53
1:F:605:ILE:HD11	1:F:644:GLY:HA3	1.89	0.53
1:A:550:THR:HG23	1:A:603:ASP:OD1	2.08	0.52
1:D:67:ARG:NH1	1:D:74:ILE:HD11	2.24	0.52
1:D:528:THR:HG22	1:D:597:LEU:HD11	1.90	0.52
1:F:635:PRO:HD2	1:F:638:ARG:HD2	1.90	0.52
2:I:219:LEU:HA	2:I:222:LYS:HB3	1.91	0.52
2:G:179:GLN:O	2:G:182:ILE:HG12	2.09	0.52
1:D:527:GLN:HE22	1:E:716:MET:HA	1.73	0.52
1:D:680:LEU:HB2	1:D:691:ARG:HH21	1.73	0.52
1:E:540:LEU:HD12	1:E:541:LEU:N	2.24	0.52
1:F:517:VAL:HG13	1:F:665:ILE:CG2	2.38	0.52
1:F:612:VAL:HG13	1:F:614:ILE:O	2.10	0.52
2:H:235:PHE:HB3	5:M:31:ARG:HB3	1.91	0.52
2:J:225:VAL:HG23	2:J:241:CYS:HB2	1.91	0.52
3:K:73:GLY:HA3	5:M:189:LYS:HE2	1.91	0.52
1:A:68:LYS:HD2	2:H:219:LEU:CD2	2.39	0.52
1:A:437:SER:OG	1:A:440:GLU:HG2	2.09	0.52
1:D:604:ASP:HB3	1:D:607:ARG:HB2	1.91	0.52
4:L:210:ARG:HG2	4:L:210:ARG:HH11	1.75	0.52
5:M:177:GLN:O	5:M:181:ILE:HG13	2.09	0.52
1:A:611:TYR:CE2	1:A:651:VAL:HG11	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:402:GLY:O	1:B:406:ILE:HD12	2.10	0.52
1:B:656:GLU:OE1	1:C:648:ARG:NH2	2.42	0.52
1:C:308:ASP:OD1	1:C:309:ALA:N	2.42	0.52
1:F:720:MET:HB3	1:F:724:TYR:HB2	1.90	0.52
2:H:127:ILE:HG23	2:H:131:TYR:CE1	2.44	0.52
1:C:45:TYR:CE2	1:C:70:ALA:HA	2.44	0.52
1:C:677:LEU:HD21	1:C:695:ALA:CB	2.40	0.52
1:F:315:ARG:HG3	1:F:316:LEU:HD12	1.90	0.52
1:F:515:THR:HA	1:F:518:LEU:CD1	2.39	0.52
2:H:69:ALA:HB1	2:H:85:PHE:CE1	2.44	0.52
2:I:39:GLU:HB2	2:I:75:LEU:CD1	2.39	0.52
2:I:149:ALA:HB2	2:I:164:CYS:HB2	1.92	0.52
2:I:159:SER:OG	3:K:55:GLU:HG2	2.09	0.52
2:J:127:ILE:HG23	2:J:131:TYR:CE1	2.43	0.52
5:M:68:ASN:O	5:M:72:LYS:HG3	2.10	0.52
1:F:310:GLU:OE2	1:F:357:LYS:NZ	2.42	0.52
2:G:267:ASP:CG	2:G:271:ARG:HH11	2.13	0.52
3:K:83:LYS:HB3	5:M:203:LEU:HD21	1.92	0.52
1:B:503:ILE:HD11	1:B:554:ALA:HB3	1.90	0.52
1:E:128:GLN:O	1:E:176:LEU:HD12	2.10	0.52
1:E:696:GLN:HB3	1:E:697:GLN:NE2	2.25	0.52
2:H:126:SER:O	2:H:130:ILE:HG13	2.09	0.52
2:G:127:ILE:HG23	2:G:131:TYR:CE1	2.44	0.52
1:A:64:LEU:O	1:A:68:LYS:HG2	2.10	0.52
1:A:454:ASN:HA	1:F:232:ARG:CZ	2.39	0.52
1:B:728:LYS:HE3	1:B:732:LEU:HD21	1.90	0.52
1:C:227:PHE:O	1:C:231:PHE:HB2	2.09	0.52
1:C:231:PHE:O	1:C:235:PHE:HB2	2.10	0.52
1:D:136:LEU:HD23	1:D:136:LEU:N	2.25	0.52
1:D:326:ILE:HG22	1:D:370:ILE:HG13	1.92	0.52
1:E:536:LEU:HD22	1:E:634:PRO:HD3	1.92	0.52
2:H:244:MET:O	2:H:248:LEU:HG	2.10	0.52
2:G:40:GLU:O	2:G:44:ILE:HG12	2.09	0.52
2:G:243:LEU:HD13	2:G:266:TYR:HB2	1.92	0.52
4:L:216:PHE:CE2	5:M:160:LEU:HD22	2.45	0.52
5:M:26:LEU:O	5:M:30:ARG:HG3	2.10	0.52
1:A:73:SER:HA	2:H:218:MET:SD	2.49	0.52
1:A:223:LEU:HD12	1:A:227:PHE:HB2	1.91	0.52
1:A:356:SER:HB2	1:B:288:PRO:HD3	1.91	0.52
1:B:533:ARG:HG3	1:B:534:THR:N	2.23	0.52
1:C:596:GLN:HA	1:C:638:ARG:CD	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:611:TYR:HE1	1:C:616:PRO:HB2	1.75	0.52
1:C:686:PHE:CE1	1:C:714:ILE:HG23	2.45	0.52
1:D:187:LYS:NZ	1:D:316:LEU:HD11	2.25	0.52
1:E:612:VAL:HG11	1:E:617:ARG:HH21	1.74	0.52
1:B:122:ILE:O	1:B:126:ASN:HB3	2.09	0.52
1:D:512:ASP:N	1:D:513:PRO:CD	2.73	0.52
2:H:179:GLN:O	2:H:182:ILE:HG12	2.10	0.52
1:A:136:LEU:N	1:A:136:LEU:HD23	2.25	0.51
1:A:227:PHE:CE1	1:A:273:ILE:HD13	2.45	0.51
1:A:258:LEU:O	1:A:372:MET:HA	2.09	0.51
1:D:18:LEU:HD13	1:D:144:LEU:HD21	1.90	0.51
1:D:24:VAL:O	1:D:51:THR:HA	2.10	0.51
1:D:184:ALA:HB1	1:D:200:LYS:O	2.10	0.51
1:E:618:PHE:CZ	1:F:612:VAL:HG11	2.31	0.51
2:G:244:MET:O	2:G:248:LEU:HG	2.10	0.51
1:C:64:LEU:O	1:C:68:LYS:HG3	2.10	0.51
1:C:285:VAL:HA	1:C:326:ILE:HG13	1.92	0.51
1:D:539:VAL:HG23	1:D:663:THR:CG2	2.41	0.51
1:E:45:TYR:CE2	1:E:70:ALA:HA	2.45	0.51
2:I:40:GLU:O	2:I:44:ILE:HG12	2.11	0.51
2:J:149:ALA:HB2	2:J:164:CYS:HB2	1.91	0.51
2:G:78:LYS:HB3	2:G:110:ILE:HG23	1.92	0.51
3:K:49:ASN:HB3	4:L:219:MET:CE	2.39	0.51
3:K:84:LEU:HD13	5:M:78:LEU:HD22	1.91	0.51
1:A:489:LYS:H	1:A:490:PRO:HD2	1.75	0.51
1:B:626:LEU:O	1:B:630:LEU:HG	2.10	0.51
1:C:616:PRO:HG2	1:D:614:ILE:HD13	1.92	0.51
1:D:657:MET:HG2	1:D:661:PHE:HE2	1.75	0.51
1:E:106:ASN:HB3	1:E:143:LYS:HZ1	1.73	0.51
1:F:327:PHE:HB2	1:F:330:ILE:CG2	2.33	0.51
3:K:88:TYR:HB2	5:M:81:LEU:HD11	1.91	0.51
5:M:156:ILE:O	5:M:160:LEU:HG	2.09	0.51
1:C:399:ASP:O	1:C:403:ARG:N	2.39	0.51
1:C:612:VAL:CG1	1:C:617:ARG:HB3	2.40	0.51
1:C:686:PHE:HE1	1:C:714:ILE:HG23	1.75	0.51
1:D:528:THR:CB	1:D:641:LEU:HD12	2.40	0.51
1:E:136:LEU:N	1:E:136:LEU:HD23	2.25	0.51
1:E:627:LEU:HG	1:E:657:MET:HE1	1.92	0.51
1:E:666:HIS:CD2	1:E:668:PRO:HD3	2.45	0.51
3:K:83:LYS:CD	5:M:203:LEU:HD11	2.33	0.51
1:A:184:ALA:HB1	1:A:200:LYS:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:607:ARG:NH1	1:F:624:GLN:OE1	2.44	0.51
1:C:121:PHE:CD2	1:C:183:VAL:HG21	2.46	0.51
1:C:270:ALA:O	1:C:273:ILE:HG22	2.10	0.51
1:C:521:GLY:HA3	1:C:556:ILE:HD13	1.91	0.51
1:C:728:LYS:HE3	1:C:732:LEU:HD21	1.91	0.51
1:D:254:LYS:O	1:D:368:LEU:HA	2.11	0.51
1:D:325:ILE:O	1:D:369:VAL:HA	2.10	0.51
1:E:540:LEU:HD12	1:E:541:LEU:H	1.76	0.51
2:H:235:PHE:CD1	5:M:31:ARG:HG2	2.45	0.51
2:J:50:ASN:HD21	2:G:115:GLY:HA2	1.75	0.51
1:A:106:ASN:HB3	1:A:143:LYS:NZ	2.24	0.51
1:B:236:ALA:O	1:B:239:VAL:HG12	2.10	0.51
1:B:249:GLY:HA3	1:C:414:MET:CE	2.40	0.51
1:B:327:PHE:CZ	1:B:369:VAL:HG21	2.46	0.51
1:B:395:ILE:H	1:B:395:ILE:HD12	1.75	0.51
1:E:121:PHE:HD2	1:E:183:VAL:HG21	1.75	0.51
1:E:510:TRP:CE3	1:E:511:GLY:HA3	2.45	0.51
1:E:674:GLU:O	1:E:677:LEU:HB2	2.11	0.51
1:F:122:ILE:O	1:F:126:ASN:HB3	2.10	0.51
2:I:208:LYS:HG2	2:I:275:TRP:CZ3	2.45	0.51
2:G:267:ASP:OD2	2:G:271:ARG:NH1	2.42	0.51
1:C:411:THR:O	1:C:414:MET:HB2	2.10	0.51
1:E:327:PHE:CZ	1:E:369:VAL:HG21	2.46	0.51
2:J:233:PRO:HA	2:J:235:PHE:CZ	2.45	0.51
4:L:225:SER:O	4:L:229:MET:HE2	2.10	0.51
1:B:397:LEU:HD11	1:B:638:ARG:HH21	1.76	0.51
1:E:545:PRO:O	1:E:546:HIS:HB2	2.10	0.51
1:A:222:GLY:O	1:A:224:ASP:N	2.44	0.51
1:B:313:GLN:O	1:B:317:GLY:N	2.43	0.51
1:C:322:LEU:HD12	1:C:324:ILE:HD11	1.93	0.51
1:C:356:SER:HB3	1:D:288:PRO:HG3	1.92	0.51
1:C:689:LYS:O	1:C:692:THR:OG1	2.19	0.51
1:D:524:LEU:HD13	1:D:663:THR:HG21	1.93	0.51
1:D:602:VAL:O	1:D:644:GLY:HA2	2.11	0.51
2:I:119:ILE:HD12	2:I:122:LYS:HB2	1.93	0.51
2:G:21:VAL:HG23	2:G:38:ILE:HD13	1.92	0.51
1:A:270:ALA:HA	1:A:273:ILE:HG22	1.92	0.51
1:C:136:LEU:N	1:C:136:LEU:HD23	2.26	0.51
1:C:691:ARG:HH11	1:C:691:ARG:HB2	1.77	0.51
1:D:330:ILE:HD12	1:D:331:ASP:N	2.25	0.51
1:D:508:ILE:HG12	1:D:683:LEU:HD21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:560:SER:HB2	1:D:562:PHE:CD1	2.45	0.51
1:E:652:LEU:HD22	1:E:658:LEU:HD13	1.91	0.51
1:E:666:HIS:HD2	1:E:668:PRO:HD3	1.76	0.51
1:F:512:ASP:OD1	1:F:513:PRO:HD3	2.10	0.51
1:F:542:GLU:O	1:F:666:HIS:ND1	2.44	0.51
1:F:609:LEU:HD13	1:F:655:MET:CE	2.41	0.51
1:F:658:LEU:HA	1:F:661:PHE:HD2	1.76	0.51
2:I:39:GLU:HB2	2:I:75:LEU:HD11	1.92	0.51
1:A:489:LYS:N	1:A:490:PRO:CD	2.74	0.50
1:C:542:GLU:HB2	1:C:649:LYS:HD3	1.93	0.50
1:D:108:ASP:OD2	1:D:143:LYS:HE2	2.10	0.50
1:D:257:LEU:HG	1:D:371:GLY:O	2.11	0.50
1:D:313:GLN:OE1	1:D:365:ASN:O	2.29	0.50
1:D:589:PHE:CE2	1:D:629:LEU:HD13	2.46	0.50
1:D:677:LEU:O	1:D:691:ARG:NH2	2.44	0.50
1:E:24:VAL:O	1:E:51:THR:HA	2.11	0.50
1:F:136:LEU:N	1:F:136:LEU:HD23	2.26	0.50
1:A:16:LEU:HD11	1:A:52:HIS:HD2	1.75	0.50
1:A:300:ALA:O	1:A:304:LYS:HG3	2.10	0.50
1:C:121:PHE:HD2	1:C:183:VAL:HG21	1.76	0.50
1:C:560:SER:HB2	1:C:562:PHE:CE1	2.46	0.50
1:C:688:ASP:HA	1:C:691:ARG:NH1	2.26	0.50
1:D:128:GLN:O	1:D:176:LEU:HD12	2.12	0.50
1:D:511:GLY:HA3	1:D:675:GLN:HE21	1.76	0.50
1:E:327:PHE:HB2	1:E:330:ILE:CG2	2.33	0.50
2:H:185:TYR:HA	2:H:188:VAL:HG12	1.93	0.50
2:G:235:PHE:CG	5:M:152:GLN:HG2	2.46	0.50
3:K:39:VAL:HG21	4:L:209:ILE:CD1	2.39	0.50
1:A:242:PRO:HD2	1:A:243:GLU:CD	2.32	0.50
1:C:611:TYR:CZ	1:C:651:VAL:HG11	2.46	0.50
1:C:614:ILE:O	1:C:616:PRO:HA	2.11	0.50
1:D:356:SER:OG	1:E:288:PRO:HB3	2.12	0.50
1:D:686:PHE:HE1	1:D:714:ILE:HG23	1.76	0.50
1:E:232:ARG:CZ	1:F:450:SER:O	2.58	0.50
2:J:40:GLU:O	2:J:44:ILE:HG12	2.11	0.50
5:M:64:MET:HE3	5:M:181:ILE:O	2.11	0.50
1:A:326:ILE:HG22	1:A:370:ILE:CG1	2.40	0.50
1:C:576:PHE:HB2	1:C:581:LYS:HE3	1.94	0.50
1:D:540:LEU:HD12	1:D:661:PHE:CE1	2.46	0.50
1:E:549:LYS:HG2	1:E:550:THR:N	2.26	0.50
1:E:563:PRO:HD2	1:E:597:LEU:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:116:ARG:HH22	5:M:183:GLU:HA	1.75	0.50
3:K:68:ASP:OD2	4:L:236:ASN:ND2	2.45	0.50
1:A:18:LEU:HD13	1:A:139:SER:CB	2.41	0.50
1:B:576:PHE:HB3	1:B:580:ALA:HB3	1.92	0.50
1:C:404:LEU:HG	1:C:426:ILE:HG22	1.94	0.50
1:C:730:LEU:O	1:C:734:ARG:HG3	2.12	0.50
1:D:198:LYS:O	1:D:198:LYS:HD3	2.12	0.50
1:D:298:SER:O	1:D:301:ASN:HB3	2.11	0.50
1:D:593:TYR:OH	1:D:632:LYS:HD2	2.12	0.50
1:E:232:ARG:NH2	1:F:454:ASN:CB	2.74	0.50
1:F:289:GLU:O	1:F:291:LEU:N	2.33	0.50
1:F:327:PHE:CZ	1:F:369:VAL:HG21	2.46	0.50
2:I:18:GLU:HA	2:I:21:VAL:HG12	1.93	0.50
2:J:72:HIS:CE1	2:J:77:SER:HB2	2.46	0.50
2:J:223:LEU:O	2:J:227:LYS:HG3	2.11	0.50
1:C:703:VAL:O	1:C:704:TRP:HD1	1.95	0.50
1:D:375:ARG:NH2	1:D:377:ASP:OD2	2.42	0.50
1:E:232:ARG:HH21	1:F:454:ASN:N	2.07	0.50
1:E:596:GLN:O	1:E:638:ARG:HA	2.12	0.50
1:F:188:ALA:O	1:F:191:SER:HB2	2.12	0.50
1:F:529:LYS:HG3	1:F:597:LEU:HD11	1.93	0.50
2:I:72:HIS:CE1	2:I:80:ASP:HB2	2.47	0.50
2:J:53:LYS:HE3	2:G:117:PHE:CD2	2.47	0.50
2:G:118:THR:O	2:G:122:LYS:HG2	2.12	0.50
2:G:243:LEU:HD22	2:G:266:TYR:CD2	2.47	0.50
5:M:36:VAL:HG23	5:M:156:ILE:HD12	1.94	0.50
1:A:612:VAL:HG12	1:A:617:ARG:HB2	1.93	0.50
1:B:23:VAL:HG12	1:B:55:VAL:HG21	1.93	0.50
1:B:428:GLU:O	1:B:432:GLU:HG2	2.12	0.50
1:C:428:GLU:O	1:C:432:GLU:HG2	2.12	0.50
1:C:445:VAL:HG12	1:C:449:GLN:HE22	1.76	0.50
1:C:568:CYS:HB2	1:C:602:VAL:HA	1.93	0.50
1:C:721:ASP:O	1:C:725:ARG:HG3	2.11	0.50
1:E:256:ILE:O	1:E:370:ILE:HA	2.12	0.50
1:E:538:SER:OG	1:E:662:SER:N	2.40	0.50
2:H:79:HIS:CE1	3:K:72:ALA:HB1	2.46	0.50
2:I:244:MET:O	2:I:248:LEU:HG	2.12	0.50
2:G:180:LYS:O	2:G:184:ILE:HG13	2.12	0.50
3:K:56:ARG:HD2	5:M:171:ILE:HG12	1.94	0.50
4:L:209:ILE:HG21	5:M:32:MET:CG	2.40	0.50
1:A:128:GLN:O	1:A:176:LEU:HD12	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:VAL:HG11	1:A:152:ILE:HD11	1.94	0.50
1:C:618:PHE:HE1	1:C:620:ASN:OD1	1.94	0.50
1:D:91:CYS:O	1:D:154:ALA:HA	2.11	0.50
1:D:402:GLY:HA2	1:D:405:GLN:OE1	2.12	0.50
2:I:53:LYS:HE3	2:J:117:PHE:CE2	2.46	0.50
1:A:14:ASP:O	1:A:18:LEU:HG	2.12	0.50
1:A:353:GLN:HA	1:B:288:PRO:HG3	1.94	0.50
1:B:106:ASN:HB3	1:B:143:LYS:NZ	2.26	0.50
1:B:395:ILE:HD12	1:B:395:ILE:N	2.27	0.50
1:B:490:PRO:HA	1:B:491:ALA:CB	2.31	0.50
1:C:507:ILE:CD1	1:C:555:LYS:HD3	2.42	0.50
1:C:525:VAL:HG13	1:C:562:PHE:CZ	2.47	0.50
1:D:331:ASP:HA	1:D:379:ILE:HD11	1.92	0.50
1:D:539:VAL:HG13	1:D:643:ILE:HG13	1.93	0.50
1:E:47:PHE:HE2	1:E:66:GLN:HB3	1.76	0.50
1:F:303:ARG:CG	1:F:357:LYS:HE2	2.40	0.50
2:H:266:TYR:CZ	2:H:270:SER:HB2	2.47	0.50
2:I:179:GLN:HB3	2:I:214:PHE:HB3	1.93	0.50
3:K:70:LEU:HD22	5:M:185:ALA:HA	1.94	0.50
1:A:454:ASN:HA	1:F:232:ARG:NH2	2.27	0.49
1:A:598:SER:O	1:A:640:LEU:HA	2.11	0.49
1:B:516:ARG:O	1:B:519:ASP:OD1	2.29	0.49
1:E:428:GLU:O	1:E:432:GLU:HG2	2.12	0.49
1:F:428:GLU:O	1:F:432:GLU:HG2	2.12	0.49
2:H:233:PRO:CG	2:G:268:SER:HA	2.42	0.49
2:G:67:GLN:O	2:G:71:LEU:HG	2.11	0.49
4:L:223:VAL:O	5:M:49:MET:HE3	2.12	0.49
1:B:256:ILE:O	1:B:370:ILE:HA	2.12	0.49
1:C:361:VAL:HA	1:D:267:THR:CG2	2.43	0.49
1:C:677:LEU:HD11	1:C:698:VAL:CG2	2.41	0.49
1:D:95:MET:HG3	1:D:152:ILE:HG12	1.94	0.49
1:D:628:VAL:O	1:D:632:LYS:N	2.45	0.49
1:E:236:ALA:HA	1:E:239:VAL:HG12	1.94	0.49
1:E:524:LEU:HD11	1:E:663:THR:HG21	1.93	0.49
1:F:450:SER:O	1:F:453:MET:HB2	2.12	0.49
2:I:167:LYS:HE2	2:I:171:TYR:HE2	1.77	0.49
1:B:45:TYR:CE2	1:B:70:ALA:HA	2.46	0.49
1:C:533:ARG:HD2	1:D:505:ASN:OD1	2.12	0.49
1:D:609:LEU:CD1	1:D:611:TYR:HB2	2.42	0.49
2:J:118:THR:O	2:J:122:LYS:HG2	2.13	0.49
3:K:88:TYR:CB	5:M:81:LEU:HD11	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:687:LYS:NZ	1:A:722:PRO:HB3	2.27	0.49
1:B:136:LEU:N	1:B:136:LEU:HD23	2.26	0.49
1:C:149:VAL:HG11	1:C:152:ILE:HD11	1.93	0.49
1:C:256:ILE:O	1:C:370:ILE:HA	2.13	0.49
1:D:105:LYS:HZ3	2:I:291:GLU:HB3	1.75	0.49
1:D:694:ILE:O	1:D:698:VAL:HG22	2.12	0.49
2:I:95:ALA:HB1	2:I:97:PRO:HD2	1.93	0.49
2:J:142:ILE:HG23	2:J:168:VAL:HG13	1.94	0.49
2:J:233:PRO:O	2:J:235:PHE:CE2	2.66	0.49
1:A:540:LEU:HD12	1:A:644:GLY:O	2.12	0.49
1:B:499:TYR:HA	1:B:502:TYR:CE2	2.48	0.49
1:B:578:GLU:CG	1:B:619:SER:HB2	2.42	0.49
1:C:589:PHE:CE1	1:C:600:VAL:HG11	2.46	0.49
1:F:311:GLU:O	1:F:314:ARG:HG2	2.13	0.49
5:M:34:GLN:O	5:M:37:GLU:HB2	2.13	0.49
1:A:610:ASP:OD1	1:F:620:ASN:ND2	2.45	0.49
1:B:113:ASP:OD1	1:B:115:ASP:HB2	2.12	0.49
1:B:303:ARG:CG	1:B:357:LYS:HE2	2.41	0.49
1:B:406:ILE:HB	1:B:441:LEU:HD13	1.94	0.49
1:B:479:ASP:O	1:B:482:ALA:N	2.45	0.49
1:C:593:TYR:CE2	1:C:632:LYS:NZ	2.80	0.49
1:D:312:GLU:HG3	1:D:313:GLN:N	2.28	0.49
1:E:303:ARG:CG	1:E:357:LYS:HE2	2.39	0.49
1:F:536:LEU:HD11	1:F:633:ALA:HA	1.94	0.49
2:H:94:LYS:HG3	2:H:94:LYS:O	2.12	0.49
1:A:113:ASP:O	1:A:117:MET:HG3	2.11	0.49
1:A:571:ASP:OD1	1:A:572:LYS:N	2.46	0.49
1:B:606:GLU:OE1	1:B:606:GLU:N	2.45	0.49
1:B:710:LEU:O	1:B:714:ILE:HG13	2.13	0.49
1:C:311:GLU:O	1:C:314:ARG:HG2	2.13	0.49
1:E:101:PHE:HE1	1:E:193:LEU:HB2	1.78	0.49
1:E:540:LEU:HD12	1:E:644:GLY:O	2.12	0.49
1:E:562:PHE:CD1	1:E:597:LEU:HG	2.48	0.49
2:H:98:GLN:H	2:H:98:GLN:CD	2.15	0.49
2:G:18:GLU:HA	2:G:21:VAL:HG12	1.95	0.49
2:G:182:ILE:O	2:G:186:GLU:HG2	2.13	0.49
3:K:44:ASP:O	3:K:47:ARG:HB3	2.13	0.49
4:L:247:ALA:O	4:L:251:THR:HG23	2.13	0.49
1:A:231:PHE:CE2	1:A:235:PHE:HD2	2.31	0.49
1:A:283:LYS:HA	1:A:324:ILE:O	2.13	0.49
1:A:313:GLN:OE1	1:A:317:GLY:HA2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:517:VAL:HG13	1:A:665:ILE:HG21	1.94	0.49
1:A:617:ARG:HG3	1:A:617:ARG:NH1	2.28	0.49
1:B:95:MET:CE	1:B:97:ILE:HD11	2.43	0.49
1:B:653:GLN:OE1	1:B:658:LEU:HD22	2.12	0.49
1:C:512:ASP:N	1:C:513:PRO:CD	2.76	0.49
1:B:121:PHE:HD2	1:B:183:VAL:HG21	1.77	0.49
1:D:114:THR:HG21	1:D:200:LYS:HG2	1.95	0.49
1:E:64:LEU:HB2	1:E:67:ARG:HH21	1.77	0.49
1:E:232:ARG:HH22	1:F:451:THR:C	2.16	0.49
1:F:236:ALA:O	1:F:239:VAL:HG12	2.12	0.49
2:H:162:ASN:O	2:H:166:LEU:HG	2.13	0.49
2:J:94:LYS:HE3	2:G:153:LYS:HG3	1.94	0.49
2:J:116:ARG:HH22	5:M:65:ASN:CG	2.16	0.49
2:J:266:TYR:C	2:J:268:SER:H	2.15	0.49
2:G:175:LEU:HD23	2:G:177:GLN:NE2	2.26	0.49
3:K:70:LEU:HA	5:M:189:LYS:HD3	1.94	0.49
1:A:67:ARG:CD	2:H:218:MET:HG3	2.38	0.49
1:A:95:MET:HG3	1:A:152:ILE:HG12	1.95	0.49
1:A:636:GLN:HA	1:A:637:GLY:HA2	1.49	0.49
1:B:128:GLN:O	1:B:176:LEU:HD12	2.13	0.49
1:B:193:LEU:HG	1:B:195:LEU:HG	1.94	0.49
1:D:511:GLY:CA	1:D:675:GLN:HE21	2.26	0.49
1:E:46:ILE:HD12	1:E:174:VAL:HG21	1.93	0.49
1:B:523:LEU:HA	1:B:526:GLN:HG2	1.95	0.48
1:C:16:LEU:HD11	1:C:52:HIS:HD2	1.78	0.48
1:D:86:ASP:C	1:D:88:ALA:H	2.16	0.48
1:D:681:GLU:HG2	1:D:691:ARG:CZ	2.42	0.48
1:E:254:LYS:O	1:E:368:LEU:HA	2.13	0.48
1:E:684:GLY:HA2	1:E:691:ARG:HH21	1.78	0.48
2:J:287:ILE:O	2:J:291:GLU:HG3	2.13	0.48
2:G:72:HIS:HE1	2:G:80:ASP:CB	2.23	0.48
1:B:258:LEU:HB3	1:B:395:ILE:CD1	2.27	0.48
1:C:18:LEU:HD13	1:C:139:SER:OG	2.12	0.48
1:E:95:MET:HG3	1:E:152:ILE:HG12	1.94	0.48
1:E:281:GLU:N	1:E:282:PRO:HA	2.28	0.48
1:E:411:THR:O	1:E:414:MET:HB2	2.13	0.48
1:F:395:ILE:HD12	1:F:395:ILE:N	2.29	0.48
2:G:101:ILE:HD13	2:G:135:LEU:HD11	1.95	0.48
2:G:218:MET:CG	2:G:219:LEU:N	2.75	0.48
1:A:45:TYR:CE2	1:A:70:ALA:HA	2.49	0.48
1:C:299:GLU:OE2	1:C:349:THR:OG1	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:330:ILE:HB	1:C:373:THR:HB	1.94	0.48
1:C:584:ALA:O	1:C:588:ILE:HG13	2.12	0.48
1:D:552:LEU:O	1:D:556:ILE:HG13	2.12	0.48
1:D:592:ALA:HB1	1:D:640:LEU:HD13	1.93	0.48
1:D:670:ILE:HD11	1:D:705:ILE:HG23	1.95	0.48
1:E:670:ILE:HG22	1:E:672:THR:N	2.25	0.48
1:E:689:LYS:O	1:E:692:THR:OG1	2.26	0.48
1:F:313:GLN:O	1:F:317:GLY:N	2.46	0.48
1:F:319:ASN:HB3	1:F:320:SER:HB2	1.95	0.48
2:H:72:HIS:O	2:H:75:LEU:HB3	2.13	0.48
2:H:180:LYS:O	2:H:184:ILE:HG13	2.13	0.48
2:J:67:GLN:O	2:J:71:LEU:HG	2.13	0.48
4:L:198:ARG:HG2	4:L:202:ILE:HD11	1.95	0.48
5:M:33:LEU:HD12	5:M:149:ASN:CB	2.44	0.48
1:A:627:LEU:O	1:A:631:LYS:NZ	2.46	0.48
1:B:193:LEU:HD21	1:B:195:LEU:HD21	1.95	0.48
1:B:281:GLU:N	1:B:282:PRO:HA	2.28	0.48
1:C:681:GLU:HG3	1:C:691:ARG:HD2	1.96	0.48
1:E:16:LEU:HD11	1:E:52:HIS:HD2	1.79	0.48
1:E:243:GLU:O	1:E:246:GLU:HG2	2.13	0.48
1:E:404:LEU:HG	1:E:426:ILE:HG22	1.94	0.48
1:F:36:ILE:HD11	1:F:44:LYS:HD2	1.95	0.48
2:H:207:PHE:HB2	2:H:240:GLU:HG2	1.96	0.48
1:C:89:LYS:O	1:C:89:LYS:HG2	2.12	0.48
1:C:325:ILE:HG13	1:C:369:VAL:HG23	1.95	0.48
1:C:386:PRO:HD2	1:D:440:GLU:OE1	2.13	0.48
1:D:326:ILE:HG22	1:D:370:ILE:CG1	2.44	0.48
1:E:526:GLN:HA	1:E:529:LYS:HG2	1.95	0.48
2:I:178:TYR:OH	2:I:282:ARG:HG2	2.14	0.48
2:J:49:ALA:HB2	2:J:64:ALA:HB3	1.95	0.48
2:J:271:ARG:HD2	2:G:231:LEU:HD12	1.96	0.48
2:G:59:SER:OG	2:G:97:PRO:HD3	2.13	0.48
3:K:51:ASP:O	3:K:55:GLU:HG3	2.14	0.48
1:A:193:LEU:HD21	1:A:195:LEU:HD21	1.96	0.48
1:A:353:GLN:HA	1:B:288:PRO:HG2	1.95	0.48
1:B:609:LEU:HD23	1:B:609:LEU:HA	1.67	0.48
1:C:540:LEU:HD22	1:C:661:PHE:CD2	2.49	0.48
1:C:609:LEU:O	1:C:610:ASP:HB2	2.13	0.48
1:D:257:LEU:HB2	1:D:389:LEU:HD13	1.95	0.48
1:F:230:ILE:HD11	1:F:391:VAL:HG11	1.95	0.48
1:F:256:ILE:O	1:F:370:ILE:HA	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:ALA:HB3	1:A:73:SER:O	2.13	0.48
1:A:240:PHE:HE2	1:B:453:MET:SD	2.37	0.48
1:C:613:PRO:HD3	1:C:648:ARG:NH2	2.29	0.48
1:D:286:ASN:HB2	1:D:327:PHE:CD1	2.46	0.48
1:D:581:LYS:O	1:D:585:MET:HG2	2.13	0.48
1:D:635:PRO:O	1:D:638:ARG:HB2	2.14	0.48
1:E:658:LEU:HD12	1:E:658:LEU:HA	1.64	0.48
1:F:635:PRO:HB2	1:F:638:ARG:NH1	2.29	0.48
2:I:38:ILE:CD1	2:I:71:LEU:HB3	2.43	0.48
2:J:235:PHE:CG	3:K:38:GLN:HG2	2.48	0.48
3:K:39:VAL:HA	3:K:42:VAL:HG23	1.96	0.48
5:M:53:GLN:HA	5:M:56:GLN:HG2	1.96	0.48
1:A:407:LEU:CD1	1:A:426:ILE:HG23	2.44	0.48
1:C:380:ASP:OD1	1:C:382:ALA:N	2.43	0.48
1:D:536:LEU:HD21	1:D:630:LEU:O	2.14	0.48
1:E:184:ALA:HB1	1:E:200:LYS:O	2.14	0.48
1:E:440:GLU:O	1:E:444:LEU:HG	2.14	0.48
1:F:601:VAL:HG22	1:F:643:ILE:HD12	1.95	0.48
2:H:233:PRO:HB3	2:G:268:SER:O	2.14	0.48
3:K:83:LYS:HG2	3:K:86:ARG:NH2	2.29	0.48
1:A:562:PHE:CE1	1:A:641:LEU:HD21	2.49	0.48
1:B:589:PHE:HD2	1:B:629:LEU:HD22	1.78	0.48
1:C:64:LEU:HG	1:C:68:LYS:HD2	1.96	0.48
1:C:322:LEU:HD22	1:C:366:ASN:O	2.14	0.48
1:C:538:SER:OG	1:C:662:SER:N	2.40	0.48
1:D:564:PHE:HB3	1:D:598:SER:HB3	1.95	0.48
1:E:314:ARG:HG3	1:E:315:ARG:N	2.29	0.48
1:E:653:GLN:OE1	1:E:658:LEU:HD23	2.13	0.48
1:F:113:ASP:HA	1:F:196:ILE:HG13	1.96	0.48
1:F:517:VAL:HG21	1:F:667:VAL:HG22	1.95	0.48
2:H:81:ALA:O	2:H:85:PHE:HD1	1.97	0.48
2:J:185:TYR:HA	2:J:188:VAL:HG12	1.96	0.48
1:D:721:ASP:O	1:D:725:ARG:HG3	2.13	0.48
1:E:445:VAL:O	1:E:449:GLN:HG2	2.14	0.48
1:F:286:ASN:OD1	1:F:327:PHE:HD1	1.97	0.48
2:H:40:GLU:O	2:H:44:ILE:HG12	2.14	0.48
2:J:276:LEU:O	2:J:280:LEU:HG	2.14	0.48
2:G:79:HIS:CG	4:L:242:ASP:OD2	2.67	0.48
5:M:191:ARG:HG3	5:M:191:ARG:NH1	2.29	0.48
1:A:388:ARG:O	1:A:389:LEU:HD22	2.14	0.47
1:B:640:LEU:CD2	1:B:642:ILE:HG13	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:527:GLN:HA	1:F:719:GLN:CD	2.34	0.47
1:F:14:ASP:O	1:F:18:LEU:HG	2.13	0.47
1:F:236:ALA:HA	1:F:239:VAL:CG1	2.44	0.47
1:F:327:PHE:CE2	1:F:369:VAL:HG21	2.49	0.47
1:F:428:GLU:O	1:F:431:VAL:HG12	2.14	0.47
1:F:436:PHE:HB3	1:F:440:GLU:CB	2.44	0.47
2:J:222:LYS:HA	2:J:225:VAL:HG12	1.96	0.47
1:A:673:GLY:O	1:A:677:LEU:HD22	2.12	0.47
1:A:719:GLN:HG2	1:F:523:LEU:HG	1.96	0.47
1:C:618:PHE:HZ	1:D:612:VAL:HG11	1.79	0.47
1:D:242:PRO:HD2	1:D:243:GLU:N	2.28	0.47
1:D:281:GLU:N	1:D:282:PRO:HA	2.30	0.47
1:E:257:LEU:HG	1:E:371:GLY:O	2.14	0.47
1:E:436:PHE:HB3	1:E:440:GLU:CB	2.44	0.47
1:F:653:GLN:HA	1:F:658:LEU:HB3	1.95	0.47
2:I:17:ALA:O	2:I:21:VAL:HG12	2.13	0.47
2:I:281:LEU:O	2:I:285:LYS:HG3	2.14	0.47
1:A:331:ASP:CA	1:A:379:ILE:HD11	2.32	0.47
1:B:76:GLN:HE21	1:B:78:ILE:CG2	2.26	0.47
1:B:257:LEU:HB2	1:B:389:LEU:HD13	1.95	0.47
1:C:331:ASP:HA	1:C:379:ILE:CD1	2.41	0.47
1:C:355:LEU:HA	1:C:388:ARG:NE	2.30	0.47
1:D:407:LEU:O	1:D:411:THR:HG23	2.14	0.47
1:F:557:ALA:HB2	1:F:601:VAL:HG21	1.97	0.47
2:J:268:SER:HA	2:G:233:PRO:HB2	1.97	0.47
1:B:436:PHE:CD2	1:B:444:LEU:HD11	2.49	0.47
1:C:36:ILE:O	1:C:36:ILE:HG23	2.15	0.47
1:D:149:VAL:HG11	1:D:152:ILE:HD11	1.95	0.47
1:E:23:VAL:HG12	1:E:55:VAL:CG2	2.44	0.47
1:E:428:GLU:O	1:E:431:VAL:HG12	2.14	0.47
1:F:307:ALA:HA	1:F:310:GLU:HG2	1.96	0.47
1:A:242:PRO:O	1:A:246:GLU:OE1	2.33	0.47
1:A:411:THR:HG21	1:A:426:ILE:HD11	1.96	0.47
1:A:609:LEU:O	1:A:610:ASP:HB3	2.13	0.47
1:B:307:ALA:HA	1:B:310:GLU:HG2	1.96	0.47
1:B:436:PHE:N	1:B:436:PHE:CD1	2.82	0.47
1:B:479:ASP:O	1:B:480:PHE:C	2.51	0.47
1:C:193:LEU:HD21	1:C:195:LEU:HD21	1.96	0.47
1:D:284:VAL:HG21	1:D:325:ILE:HG22	1.95	0.47
1:E:573:MET:O	1:E:576:PHE:HB2	2.15	0.47
1:F:87:LYS:HA	1:F:91:CYS:SG	2.55	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:163:LYS:O	2:J:167:LYS:HG2	2.15	0.47
2:J:186:GLU:O	2:J:190:THR:HG23	2.14	0.47
1:C:582:CYS:SG	1:C:621:LEU:HG	2.55	0.47
1:D:318:ALA:O	1:D:319:ASN:ND2	2.47	0.47
1:D:567:ILE:HG23	1:D:601:VAL:HB	1.96	0.47
1:F:149:VAL:HG11	1:F:152:ILE:HD11	1.95	0.47
1:F:281:GLU:N	1:F:282:PRO:HA	2.29	0.47
2:I:188:VAL:HG13	2:I:205:TYR:HD2	1.80	0.47
2:J:45:TYR:HB2	2:J:68:ALA:HB2	1.96	0.47
2:J:124:HIS:HE1	2:J:147:GLN:HB3	1.79	0.47
2:J:219:LEU:HD12	2:J:223:LEU:HB2	1.97	0.47
1:A:23:VAL:HG12	1:A:55:VAL:HG21	1.95	0.47
1:A:34:HIS:HB2	1:A:83:TYR:O	2.14	0.47
1:A:98:GLU:HB3	1:A:148:LEU:HB3	1.97	0.47
1:A:240:PHE:CE2	1:B:453:MET:SD	3.08	0.47
1:A:429:LEU:HG	1:A:482:ALA:HB1	1.96	0.47
1:A:650:ASP:OD1	1:A:650:ASP:N	2.46	0.47
1:A:683:LEU:HB3	1:A:685:ASN:HD22	1.76	0.47
1:B:295:VAL:HB	1:C:294:TYR:CG	2.50	0.47
1:B:428:GLU:O	1:B:431:VAL:HG12	2.14	0.47
1:C:122:ILE:O	1:C:126:ASN:HB3	2.14	0.47
1:C:510:TRP:CZ3	1:C:670:ILE:HG12	2.50	0.47
1:D:122:ILE:O	1:D:126:ASN:HB3	2.14	0.47
1:D:246:GLU:HG2	1:D:247:GLN:N	2.29	0.47
1:D:570:PRO:HA	1:D:573:MET:HB3	1.97	0.47
1:D:609:LEU:O	1:D:610:ASP:OD1	2.32	0.47
1:D:652:LEU:HD13	1:D:657:MET:HB3	1.95	0.47
1:D:688:ASP:O	1:D:692:THR:HG23	2.14	0.47
1:E:23:VAL:HG12	1:E:55:VAL:HG21	1.95	0.47
1:E:67:ARG:HB3	2:J:217:ASP:OD2	2.14	0.47
1:E:241:PRO:HA	1:E:242:PRO:HA	1.54	0.47
1:F:64:LEU:HA	1:F:67:ARG:HE	1.79	0.47
1:F:404:LEU:HG	1:F:426:ILE:HG22	1.96	0.47
1:F:415:ARG:O	1:F:417:HIS:O	2.33	0.47
1:F:508:ILE:C	1:F:509:LYS:HD3	2.34	0.47
2:H:243:LEU:HD22	2:H:266:TYR:CG	2.50	0.47
2:I:58:TRP:HB3	2:I:95:ALA:HB2	1.96	0.47
2:J:92:PHE:HB3	2:J:98:GLN:O	2.15	0.47
4:L:237:VAL:HG11	5:M:60:VAL:HG13	1.96	0.47
4:L:240:ALA:O	4:L:244:VAL:HG23	2.14	0.47
1:A:247:GLN:C	1:B:413:ARG:HH12	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246:GLU:HG3	1:C:417:HIS:CE1	2.50	0.47
1:B:272:GLN:OE1	1:B:272:GLN:HA	2.15	0.47
1:C:106:ASN:HB3	1:C:143:LYS:HZ1	1.80	0.47
1:C:407:LEU:O	1:C:411:THR:OG1	2.27	0.47
1:C:539:VAL:HG23	1:C:663:THR:HG23	1.95	0.47
1:D:519:ASP:O	1:D:523:LEU:HG	2.15	0.47
1:E:318:ALA:O	1:E:319:ASN:ND2	2.48	0.47
1:F:188:ALA:O	1:F:189:GLU:C	2.53	0.47
1:F:257:LEU:HG	1:F:371:GLY:O	2.14	0.47
1:F:570:PRO:CG	1:F:604:ASP:HB2	2.41	0.47
2:J:21:VAL:HG21	2:J:71:LEU:HD22	1.96	0.47
2:G:81:ALA:O	2:G:85:PHE:HD1	1.98	0.47
2:G:267:ASP:OD1	2:G:271:ARG:NH1	2.48	0.47
1:B:247:GLN:O	1:C:414:MET:SD	2.73	0.47
1:B:327:PHE:CE2	1:B:369:VAL:HG21	2.50	0.47
1:B:568:CYS:SG	1:B:588:ILE:HD12	2.55	0.47
1:B:614:ILE:O	1:B:616:PRO:HA	2.15	0.47
1:B:627:LEU:CD2	1:B:657:MET:HG3	2.42	0.47
1:C:233:ARG:CZ	1:C:233:ARG:HB2	2.44	0.47
1:C:499:TYR:HB3	1:C:558:GLU:OE2	2.15	0.47
1:D:527:GLN:HA	1:E:719:GLN:HG3	1.97	0.47
1:E:627:LEU:HG	1:E:657:MET:CE	2.45	0.47
1:F:613:PRO:HD3	1:F:648:ARG:HH12	1.80	0.47
2:I:200:TYR:H	2:I:200:TYR:HD1	1.63	0.47
2:I:228:TYR:CE2	2:I:230:GLU:HB2	2.49	0.47
1:C:511:GLY:CA	1:C:513:PRO:HD2	2.45	0.47
1:C:632:LYS:HG3	1:D:571:ASP:CG	2.36	0.47
1:D:407:LEU:HA	1:D:441:LEU:HD21	1.96	0.47
1:E:436:PHE:N	1:E:436:PHE:CD1	2.83	0.47
1:E:612:VAL:HG22	1:E:613:PRO:HD2	1.97	0.47
1:E:627:LEU:HD13	1:F:607:ARG:NE	2.30	0.47
2:H:39:GLU:HB2	2:H:75:LEU:HD13	1.97	0.47
5:M:23:ASP:O	5:M:27:GLU:N	2.44	0.47
1:A:24:VAL:O	1:A:51:THR:HA	2.16	0.46
1:A:36:ILE:HG23	1:A:36:ILE:O	2.15	0.46
1:A:517:VAL:HG13	1:A:665:ILE:CG2	2.45	0.46
1:A:690:GLU:HB3	1:A:726:VAL:HG22	1.97	0.46
1:B:319:ASN:HB3	1:B:320:SER:HB2	1.97	0.46
1:B:353:GLN:HA	1:C:288:PRO:HG3	1.97	0.46
1:C:513:PRO:HA	1:C:516:ARG:HG2	1.97	0.46
1:E:106:ASN:HB3	1:E:143:LYS:HZ2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:628:VAL:HB	1:F:574:ILE:CD1	2.44	0.46
2:H:195:SER:C	2:H:197:LEU:H	2.18	0.46
2:H:219:LEU:HD12	2:H:223:LEU:HB2	1.97	0.46
2:J:244:MET:O	2:J:248:LEU:HG	2.14	0.46
1:A:611:TYR:HD1	1:A:618:PHE:HB3	1.81	0.46
1:C:240:PHE:HB3	1:C:244:ILE:HB	1.97	0.46
1:C:428:GLU:O	1:C:431:VAL:HG12	2.14	0.46
1:E:122:ILE:O	1:E:126:ASN:HB3	2.14	0.46
2:H:186:GLU:O	2:H:190:THR:HG23	2.15	0.46
2:H:243:LEU:HD22	2:H:266:TYR:CD2	2.51	0.46
2:J:112:THR:HG23	2:J:117:PHE:CE1	2.50	0.46
2:J:179:GLN:O	2:J:182:ILE:HG12	2.15	0.46
2:G:108:ILE:HD12	2:G:127:ILE:HD12	1.96	0.46
2:G:219:LEU:HB2	2:G:222:LYS:CB	2.33	0.46
1:A:428:GLU:O	1:A:431:VAL:HG12	2.15	0.46
1:A:593:TYR:HB3	1:A:635:PRO:HD3	1.97	0.46
1:B:230:ILE:HD11	1:B:391:VAL:HG11	1.97	0.46
1:B:311:GLU:O	1:B:314:ARG:HG2	2.15	0.46
1:B:385:ARG:NH1	1:C:263:GLY:HA2	2.29	0.46
1:C:16:LEU:HD11	1:C:52:HIS:CD2	2.51	0.46
1:C:385:ARG:NH2	1:D:263:GLY:HA3	2.30	0.46
1:C:555:LYS:O	1:C:559:GLU:HG2	2.15	0.46
1:C:573:MET:HB3	1:C:576:PHE:CD2	2.49	0.46
1:D:36:ILE:HG23	1:D:36:ILE:O	2.15	0.46
1:D:627:LEU:CD2	1:D:657:MET:HG3	2.44	0.46
1:E:73:SER:HB2	1:E:76:GLN:HG2	1.96	0.46
1:F:189:GLU:O	1:F:190:ASN:HB2	2.15	0.46
2:H:45:TYR:HB2	2:H:68:ALA:HB2	1.96	0.46
2:I:21:VAL:HG23	2:I:38:ILE:CD1	2.44	0.46
2:J:45:TYR:HE2	2:J:71:LEU:HD11	1.79	0.46
2:G:246:LYS:HZ1	2:G:258:SER:HB3	1.80	0.46
3:K:79:THR:O	3:K:83:LYS:HG3	2.15	0.46
4:L:216:PHE:HE2	5:M:160:LEU:HD22	1.81	0.46
1:A:121:PHE:HD2	1:A:183:VAL:HG21	1.81	0.46
1:A:493:GLY:HA2	1:A:494:THR:CB	2.45	0.46
1:B:236:ALA:HA	1:B:239:VAL:CG1	2.45	0.46
1:B:540:LEU:HD12	1:B:540:LEU:O	2.16	0.46
1:C:511:GLY:C	1:C:513:PRO:HD2	2.35	0.46
1:C:612:VAL:CG2	1:C:613:PRO:HD2	2.46	0.46
1:C:657:MET:HE3	1:C:661:PHE:CZ	2.51	0.46
1:D:436:PHE:CE2	1:D:444:LEU:HD12	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:73:SER:HB2	1:E:76:GLN:CG	2.46	0.46
1:E:246:GLU:CG	1:F:417:HIS:HE1	2.27	0.46
1:E:327:PHE:CE2	1:E:369:VAL:HG21	2.50	0.46
1:F:272:GLN:OE1	1:F:272:GLN:HA	2.15	0.46
2:H:276:LEU:O	2:H:280:LEU:HG	2.16	0.46
2:G:167:LYS:HE2	2:G:171:TYR:HE2	1.80	0.46
3:K:46:MET:CE	4:L:216:PHE:HA	2.45	0.46
1:B:99:ILE:HD11	1:B:145:PHE:CD2	2.50	0.46
1:C:48:THR:HG21	1:C:128:GLN:HG2	1.97	0.46
1:C:86:ASP:C	1:C:88:ALA:H	2.18	0.46
1:C:326:ILE:HB	1:C:370:ILE:HD11	1.96	0.46
1:D:18:LEU:HD23	1:D:137:VAL:HG21	1.98	0.46
1:E:272:GLN:OE1	1:E:272:GLN:HA	2.15	0.46
1:E:677:LEU:HD11	1:E:695:ALA:HA	1.96	0.46
1:E:721:ASP:HB2	1:E:724:TYR:CD2	2.51	0.46
1:F:552:LEU:O	1:F:556:ILE:HG13	2.15	0.46
3:K:39:VAL:HG21	4:L:209:ILE:HD11	1.97	0.46
3:K:56:ARG:HD2	5:M:171:ILE:CG2	2.45	0.46
1:D:589:PHE:CD2	1:D:629:LEU:HD13	2.50	0.46
1:E:36:ILE:HG23	1:E:36:ILE:O	2.16	0.46
1:E:198:LYS:HG2	1:E:198:LYS:O	2.16	0.46
1:F:106:ASN:HB3	1:F:143:LYS:HZ1	1.81	0.46
1:F:128:GLN:O	1:F:176:LEU:HD12	2.15	0.46
1:F:325:ILE:HG13	1:F:369:VAL:HB	1.98	0.46
2:H:200:TYR:CZ	5:M:42:ALA:HB2	2.51	0.46
2:J:263:VAL:HG23	2:J:280:LEU:HD13	1.97	0.46
4:L:199:HIS:ND1	5:M:21:LEU:HB3	2.31	0.46
5:M:32:MET:HA	5:M:35:LEU:HD12	1.97	0.46
5:M:42:ALA:HA	5:M:45:ARG:NH2	2.31	0.46
5:M:57:LEU:HD12	5:M:174:GLN:OE1	2.16	0.46
1:A:315:ARG:O	1:A:316:LEU:HD12	2.15	0.46
1:C:536:LEU:CD1	1:C:640:LEU:HB3	2.45	0.46
1:C:690:GLU:HB2	1:C:726:VAL:CG2	2.42	0.46
1:D:132:VAL:HG23	1:D:173:GLU:HA	1.97	0.46
1:D:524:LEU:O	1:D:527:GLN:HB3	2.15	0.46
1:E:232:ARG:HE	1:F:454:ASN:CB	2.15	0.46
1:E:240:PHE:HA	1:E:241:PRO:HD3	1.69	0.46
1:E:314:ARG:CG	1:E:315:ARG:N	2.78	0.46
1:E:527:GLN:HG3	1:F:719:GLN:HG3	1.98	0.46
1:E:527:GLN:NE2	1:F:716:MET:HG2	2.27	0.46
1:E:628:VAL:HB	1:F:574:ILE:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:246:GLU:HG2	1:F:247:GLN:N	2.31	0.46
1:F:579:THR:O	1:F:583:GLN:HG2	2.15	0.46
2:H:219:LEU:CD1	2:H:223:LEU:HB2	2.45	0.46
2:I:230:GLU:HG2	2:I:231:LEU:N	2.31	0.46
2:J:147:GLN:HG2	2:J:151:TYR:CE2	2.51	0.46
3:K:43:VAL:HA	4:L:212:LEU:CD1	2.25	0.46
1:A:215:PHE:N	1:A:231:PHE:CE2	2.84	0.46
1:B:352:ASN:HA	1:B:355:LEU:HD12	1.98	0.46
1:B:536:LEU:HD12	1:B:640:LEU:O	2.16	0.46
1:C:236:ALA:HB1	1:D:453:MET:HB2	1.98	0.46
1:D:268:LEU:HA	1:D:271:ARG:HD2	1.97	0.46
1:F:352:ASN:HA	1:F:355:LEU:HD12	1.98	0.46
1:F:540:LEU:O	1:F:665:ILE:HB	2.16	0.46
1:F:686:PHE:CE1	1:F:714:ILE:HG23	2.50	0.46
2:H:51:MET:O	2:H:54:MET:HB3	2.16	0.46
4:L:219:MET:O	4:L:223:VAL:HG23	2.16	0.46
1:A:64:LEU:HA	1:A:67:ARG:HH21	1.81	0.46
1:A:103:GLN:C	1:A:105:LYS:H	2.19	0.46
1:B:91:CYS:O	1:B:154:ALA:HA	2.16	0.46
1:B:240:PHE:HA	1:B:241:PRO:HD3	1.73	0.46
1:B:539:VAL:HA	1:B:663:THR:O	2.16	0.46
1:D:571:ASP:O	1:D:574:ILE:HG13	2.15	0.46
1:D:578:GLU:OE1	1:D:621:LEU:HD13	2.15	0.46
1:D:711:LEU:O	1:D:715:GLU:HG2	2.15	0.46
1:E:595:SER:HB3	1:E:598:SER:HB3	1.96	0.46
1:E:654:GLU:CD	1:F:614:ILE:HD11	2.36	0.46
1:F:8:ALA:HB3	1:F:73:SER:O	2.16	0.46
1:F:241:PRO:HA	1:F:242:PRO:HA	1.60	0.46
1:F:436:PHE:N	1:F:436:PHE:CD1	2.83	0.46
2:H:256:VAL:HG21	2:H:288:GLN:CG	2.44	0.46
2:I:185:TYR:HA	2:I:188:VAL:HG12	1.97	0.46
2:J:72:HIS:O	2:J:75:LEU:HB3	2.16	0.46
2:J:80:ASP:OD1	5:M:66:HIS:CD2	2.69	0.46
2:G:162:ASN:OD1	2:G:188:VAL:HG23	2.16	0.46
4:L:236:ASN:O	4:L:240:ALA:HB2	2.16	0.46
1:A:322:LEU:HD12	1:A:323:HIS:H	1.81	0.46
1:A:410:HIS:NE2	1:A:442:GLU:HG2	2.31	0.46
1:C:705:ILE:HD11	1:C:710:LEU:HA	1.97	0.46
1:D:218:MET:HA	1:D:219:GLY:HA2	1.72	0.46
1:E:24:VAL:HG11	1:E:49:LEU:HD22	1.96	0.46
1:E:611:TYR:CE1	1:E:616:PRO:HB2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:121:PHE:HD2	1:F:183:VAL:HG21	1.81	0.46
2:G:10:ALA:O	2:G:14:LEU:HG	2.16	0.46
2:G:45:TYR:HB2	2:G:68:ALA:HB2	1.97	0.46
1:A:240:PHE:HA	1:A:241:PRO:HD3	1.81	0.45
1:A:542:GLU:OE2	1:A:666:HIS:CD2	2.68	0.45
1:C:104:LYS:HA	1:C:107:ILE:HG13	1.98	0.45
1:D:40:SER:HB3	1:D:43:HIS:CG	2.50	0.45
1:D:135:GLN:HG2	1:D:148:LEU:HD13	1.97	0.45
1:E:104:LYS:HA	1:E:107:ILE:HD11	1.97	0.45
1:F:95:MET:HG3	1:F:152:ILE:HG12	1.97	0.45
2:H:233:PRO:HB3	2:G:268:SER:HA	1.98	0.45
2:J:266:TYR:HD2	2:J:272:LEU:HD21	1.80	0.45
3:K:54:LEU:HD21	4:L:222:LEU:HD22	1.98	0.45
1:A:356:SER:OG	1:B:288:PRO:HD3	2.16	0.45
1:B:254:LYS:O	1:B:368:LEU:HA	2.16	0.45
1:C:349:THR:O	1:C:352:ASN:HB3	2.15	0.45
1:C:507:ILE:HD12	1:C:555:LYS:HE2	1.98	0.45
1:D:542:GLU:OE2	1:D:649:LYS:HD2	2.16	0.45
1:D:669:ASN:OD1	1:D:669:ASN:N	2.44	0.45
1:E:286:ASN:OD1	1:E:327:PHE:HD1	1.99	0.45
1:E:714:ILE:O	1:E:718:LEU:HG	2.15	0.45
2:I:142:ILE:HG23	2:I:168:VAL:HG13	1.99	0.45
1:B:669:ASN:CG	1:B:706:GLY:HA2	2.36	0.45
1:D:303:ARG:HD2	1:D:353:GLN:NE2	2.32	0.45
1:E:438:GLY:O	1:E:441:LEU:N	2.39	0.45
2:H:38:ILE:HD11	2:H:71:LEU:HB3	1.98	0.45
3:K:85:LYS:O	3:K:89:TRP:HB3	2.15	0.45
5:M:17:ARG:CB	5:M:20:GLN:HB3	2.46	0.45
1:A:721:ASP:O	1:A:725:ARG:HG3	2.17	0.45
1:B:528:THR:HG21	1:B:641:LEU:HD13	1.98	0.45
1:B:531:SER:HA	1:B:639:LYS:HD3	1.98	0.45
1:C:221:GLY:HA3	1:C:406:ILE:HG13	1.97	0.45
1:C:671:ALA:HA	1:C:703:VAL:O	2.17	0.45
1:E:399:ASP:O	1:E:403:ARG:N	2.42	0.45
1:E:519:ASP:O	1:E:522:GLU:HB2	2.17	0.45
1:E:593:TYR:CD2	1:E:635:PRO:HD3	2.50	0.45
2:J:243:LEU:O	2:J:247:LEU:HG	2.17	0.45
1:B:307:ALA:O	1:B:310:GLU:HG2	2.17	0.45
1:D:193:LEU:HD21	1:D:195:LEU:HD21	1.97	0.45
1:E:246:GLU:HG3	1:F:417:HIS:CE1	2.46	0.45
1:F:307:ALA:O	1:F:310:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:602:VAL:O	1:F:644:GLY:HA2	2.17	0.45
2:I:223:LEU:O	2:I:227:LYS:HG3	2.16	0.45
5:M:36:VAL:O	5:M:40:LYS:HB2	2.16	0.45
1:A:27:LYS:HD2	1:A:57:PRO:HG2	1.99	0.45
1:A:242:PRO:HD2	1:A:243:GLU:OE1	2.17	0.45
1:A:402:GLY:O	1:A:406:ILE:HD12	2.15	0.45
1:A:546:HIS:CE1	1:A:709:LYS:HE3	2.52	0.45
1:A:575:GLY:HA3	1:F:586:LYS:CE	2.45	0.45
1:C:143:LYS:HB3	1:C:145:PHE:HE1	1.81	0.45
1:C:327:PHE:HB3	1:C:330:ILE:CD1	2.31	0.45
1:C:707:ILE:O	1:C:711:LEU:HG	2.16	0.45
1:D:109:SER:O	1:D:110:ASN:C	2.54	0.45
1:D:424:VAL:HG22	1:D:480:PHE:N	2.32	0.45
1:E:16:LEU:HD11	1:E:52:HIS:CD2	2.52	0.45
1:E:143:LYS:HB3	1:E:145:PHE:HE1	1.81	0.45
1:E:289:GLU:C	1:E:291:LEU:N	2.69	0.45
1:E:325:ILE:HG13	1:E:369:VAL:HB	1.98	0.45
2:H:53:LYS:HE3	2:I:117:PHE:CE2	2.52	0.45
2:H:200:TYR:HD2	4:L:217:MET:SD	2.40	0.45
2:I:125:ILE:HD12	2:I:126:SER:N	2.32	0.45
2:G:204:ASP:OD2	2:G:208:LYS:HE2	2.17	0.45
4:L:223:VAL:HG12	5:M:49:MET:CE	2.46	0.45
5:M:33:LEU:HD12	5:M:149:ASN:HB3	1.99	0.45
1:A:421:SER:CB	1:A:424:VAL:HG23	2.39	0.45
1:A:446:ARG:HA	1:A:449:GLN:HG3	1.98	0.45
1:B:36:ILE:HG23	1:B:36:ILE:O	2.16	0.45
1:B:507:ILE:CG1	1:B:555:LYS:HD3	2.47	0.45
1:B:508:ILE:HD13	1:B:683:LEU:HD21	1.99	0.45
1:B:531:SER:CB	1:B:639:LYS:HD3	2.47	0.45
1:C:388:ARG:O	1:C:389:LEU:HD23	2.17	0.45
1:C:677:LEU:O	1:C:681:GLU:OE1	2.35	0.45
1:E:397:LEU:HD13	1:E:398:PRO:HD2	1.99	0.45
2:I:182:ILE:O	2:I:186:GLU:HG2	2.17	0.45
2:I:182:ILE:CG2	2:I:212:CYS:HB2	2.47	0.45
2:I:216:ILE:HG12	2:I:217:ASP:N	2.31	0.45
2:I:276:LEU:O	2:I:280:LEU:HG	2.17	0.45
2:J:50:ASN:HD21	2:G:115:GLY:HA3	1.82	0.45
2:J:134:GLU:O	2:J:136:VAL:HG23	2.17	0.45
2:J:175:LEU:HD23	2:J:177:GLN:NE2	2.32	0.45
2:J:231:LEU:O	2:J:232:PHE:C	2.55	0.45
5:M:50:LEU:HD13	5:M:167:MET:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:GLY:O	1:A:220:ILE:HG13	2.16	0.45
1:A:403:ARG:O	1:A:407:LEU:HG	2.16	0.45
1:B:249:GLY:HA3	1:C:414:MET:HE1	1.98	0.45
1:C:441:LEU:O	1:C:444:LEU:HG	2.17	0.45
1:D:286:ASN:CB	1:D:327:PHE:HD1	2.29	0.45
1:D:406:ILE:CG2	1:D:441:LEU:HD22	2.34	0.45
1:E:64:LEU:CA	1:E:67:ARG:HE	2.20	0.45
1:F:242:PRO:CD	1:F:243:GLU:H	2.30	0.45
1:F:694:ILE:O	1:F:698:VAL:HG22	2.17	0.45
2:I:118:THR:O	2:I:122:LYS:HG2	2.16	0.45
2:I:214:PHE:HD1	2:I:214:PHE:H	1.62	0.45
2:J:176:GLU:O	2:J:178:TYR:N	2.49	0.45
2:G:263:VAL:O	2:G:267:ASP:HB2	2.16	0.45
1:A:607:ARG:NH2	1:F:627:LEU:HD22	2.31	0.45
1:B:246:GLU:HB2	1:C:413:ARG:HH22	1.80	0.45
1:C:324:ILE:HD12	1:C:324:ILE:N	2.32	0.45
1:D:223:LEU:HD23	1:D:223:LEU:O	2.17	0.45
1:E:612:VAL:CG2	1:E:613:PRO:HD2	2.47	0.45
1:E:641:LEU:HD12	1:E:641:LEU:O	2.16	0.45
2:I:219:LEU:O	2:I:221:ALA:N	2.46	0.45
1:A:355:LEU:HD22	1:A:388:ARG:NH1	2.32	0.45
1:A:357:LYS:HA	1:A:357:LYS:HE3	1.97	0.45
1:B:284:VAL:O	1:B:326:ILE:HG12	2.17	0.45
1:C:24:VAL:HG11	1:C:49:LEU:HD22	1.99	0.45
1:C:330:ILE:HA	1:C:330:ILE:HD13	1.60	0.45
1:D:453:MET:O	1:D:457:ILE:HG13	2.17	0.45
1:D:626:LEU:HD23	1:D:626:LEU:HA	1.72	0.45
1:D:626:LEU:O	1:D:630:LEU:HG	2.17	0.45
1:E:25:SER:HB3	1:E:28:ASP:OD2	2.17	0.45
1:E:114:THR:HG21	1:E:200:LYS:HG2	1.99	0.45
1:E:319:ASN:HB3	1:E:320:SER:HB2	1.99	0.45
1:E:527:GLN:HA	1:F:719:GLN:HG3	1.99	0.45
1:E:605:ILE:HA	1:E:608:LEU:HB3	1.99	0.45
1:F:525:VAL:CG1	1:F:560:SER:HB2	2.46	0.45
2:G:82:ALA:O	2:G:86:VAL:HG23	2.17	0.45
2:G:101:ILE:HB	2:G:131:TYR:CZ	2.51	0.45
2:G:243:LEU:HD22	2:G:266:TYR:CG	2.52	0.45
3:K:43:VAL:HG22	4:L:212:LEU:HD22	1.98	0.45
3:K:51:ASP:OD2	3:K:55:GLU:OE2	2.35	0.45
4:L:216:PHE:CB	5:M:39:SER:HB2	2.45	0.45
5:M:142:ARG:HG2	5:M:143:GLU:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:523:LEU:O	1:B:526:GLN:HG2	2.16	0.44
1:C:677:LEU:CD1	1:C:698:VAL:HG21	2.47	0.44
1:C:715:GLU:OE1	1:C:715:GLU:HA	2.16	0.44
1:D:105:LYS:HZ1	2:I:291:GLU:CB	2.29	0.44
1:D:300:ALA:O	1:D:304:LYS:HG3	2.17	0.44
1:D:510:TRP:HZ2	1:D:668:PRO:O	2.00	0.44
1:E:596:GLN:HA	1:E:638:ARG:CG	2.32	0.44
1:E:696:GLN:OE1	1:E:696:GLN:HA	2.17	0.44
2:J:21:VAL:HG23	2:J:38:ILE:HD12	2.00	0.44
2:G:185:TYR:HA	2:G:188:VAL:HG12	1.98	0.44
5:M:33:LEU:HA	5:M:153:VAL:CG2	2.47	0.44
1:B:424:VAL:H	1:B:479:ASP:N	2.15	0.44
1:B:626:LEU:HD23	1:B:626:LEU:HA	1.52	0.44
1:C:562:PHE:O	1:C:565:ILE:HD11	2.16	0.44
1:D:564:PHE:HD2	1:D:598:SER:HB2	1.83	0.44
1:E:596:GLN:CA	1:E:638:ARG:HG2	2.31	0.44
1:E:717:SER:OG	1:E:729:PHE:HB2	2.17	0.44
1:F:36:ILE:HG23	1:F:36:ILE:O	2.16	0.44
1:F:375:ARG:NH2	1:F:377:ASP:OD2	2.50	0.44
1:F:552:LEU:HD12	1:F:667:VAL:HG21	1.98	0.44
1:F:707:ILE:O	1:F:710:LEU:HB3	2.17	0.44
2:H:237:ASP:C	2:H:239:ARG:H	2.20	0.44
2:J:180:LYS:O	2:J:184:ILE:HG13	2.18	0.44
2:G:40:GLU:O	2:G:43:GLU:HG3	2.17	0.44
2:G:72:HIS:NE2	2:G:77:SER:HB2	2.32	0.44
1:A:106:ASN:HB3	1:A:143:LYS:HZ1	1.83	0.44
1:B:114:THR:OG1	1:B:199:ALA:HB3	2.17	0.44
1:B:260:GLY:CA	1:B:395:ILE:HB	2.48	0.44
1:B:523:LEU:HD22	1:B:526:GLN:NE2	2.32	0.44
1:C:113:ASP:O	1:C:117:MET:HG3	2.17	0.44
1:C:114:THR:OG1	1:C:199:ALA:HB3	2.17	0.44
1:C:540:LEU:HD22	1:C:661:PHE:CE2	2.53	0.44
1:D:304:LYS:HA	1:D:307:ALA:HB3	1.99	0.44
1:E:510:TRP:CE3	1:E:670:ILE:HG13	2.51	0.44
1:F:284:VAL:O	1:F:326:ILE:HG12	2.17	0.44
2:H:95:ALA:CB	2:H:97:PRO:HD2	2.47	0.44
2:H:161:ALA:O	2:H:165:LEU:HG	2.17	0.44
2:H:203:LYS:HB3	2:H:240:GLU:HG3	1.99	0.44
2:G:17:ALA:O	2:G:21:VAL:HG12	2.16	0.44
4:L:223:VAL:HG12	5:M:49:MET:HE3	2.00	0.44
1:B:325:ILE:HG13	1:B:369:VAL:HB	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:295:VAL:O	1:D:294:TYR:HB2	2.17	0.44
1:C:518:LEU:HD23	1:C:518:LEU:HA	1.84	0.44
1:D:18:LEU:HD13	1:D:144:LEU:CD2	2.48	0.44
1:D:510:TRP:NE1	1:D:514:VAL:HG21	2.33	0.44
1:E:27:LYS:HD2	1:E:27:LYS:H	1.82	0.44
1:E:697:GLN:HG3	1:E:730:LEU:CD1	2.45	0.44
1:F:95:MET:CE	1:F:97:ILE:HD11	2.47	0.44
1:F:242:PRO:HD2	1:F:243:GLU:N	2.33	0.44
1:F:449:GLN:O	1:F:453:MET:HG2	2.18	0.44
2:J:38:ILE:HD11	2:J:71:LEU:HB3	1.98	0.44
2:G:266:TYR:C	2:G:268:SER:H	2.21	0.44
4:L:211:GLU:O	4:L:214:ASP:HB2	2.18	0.44
1:A:101:PHE:CE1	1:A:193:LEU:HD13	2.53	0.44
1:A:132:VAL:HG23	1:A:173:GLU:O	2.18	0.44
1:A:295:VAL:HG12	1:B:293:LYS:N	2.32	0.44
1:B:95:MET:HE2	1:B:97:ILE:HD11	2.00	0.44
1:B:258:LEU:CB	1:B:395:ILE:HD11	2.27	0.44
1:B:628:VAL:HG13	1:C:571:ASP:OD1	2.16	0.44
1:C:721:ASP:HB2	1:C:724:TYR:CD1	2.52	0.44
1:E:69:TRP:CE2	1:E:134:GLN:HA	2.52	0.44
1:E:91:CYS:O	1:E:154:ALA:HA	2.17	0.44
1:E:520:ASP:OD2	1:E:665:ILE:HD12	2.18	0.44
1:E:585:MET:HG3	1:E:589:PHE:CE2	2.51	0.44
1:E:676:LEU:O	1:E:680:LEU:HG	2.17	0.44
1:E:726:VAL:O	1:E:730:LEU:HG	2.17	0.44
1:F:218:MET:HA	1:F:219:GLY:HA2	1.78	0.44
1:F:399:ASP:N	1:F:399:ASP:OD1	2.49	0.44
2:H:164:CYS:O	2:H:168:VAL:HG23	2.17	0.44
2:J:108:ILE:HD12	2:J:127:ILE:HD12	1.99	0.44
2:J:245:LYS:O	2:J:249:GLU:HG3	2.16	0.44
3:K:43:VAL:CG2	4:L:212:LEU:HD22	2.48	0.44
5:M:63:GLY:O	5:M:67:ILE:HG13	2.16	0.44
1:A:380:ASP:OD1	1:A:381:GLU:N	2.51	0.44
1:A:624:GLN:OE1	1:A:624:GLN:HA	2.17	0.44
1:B:507:ILE:HG13	1:B:555:LYS:HD3	1.98	0.44
1:B:513:PRO:O	1:B:517:VAL:HG23	2.17	0.44
1:D:95:MET:CE	1:D:97:ILE:HD11	2.48	0.44
1:D:564:PHE:HB3	1:D:598:SER:CB	2.47	0.44
1:D:670:ILE:HG12	1:D:705:ILE:O	2.18	0.44
1:D:686:PHE:HB2	1:D:691:ARG:CG	2.47	0.44
1:E:8:ALA:HA	1:E:60:VAL:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:589:PHE:CE2	1:E:629:LEU:HD21	2.52	0.44
1:F:45:TYR:CE2	1:F:70:ALA:HA	2.53	0.44
4:L:200:SER:O	4:L:204:LYS:HG3	2.17	0.44
4:L:206:GLU:O	4:L:209:ILE:HB	2.18	0.44
1:A:95:MET:CE	1:A:97:ILE:HD11	2.47	0.44
1:A:315:ARG:C	1:A:316:LEU:HD12	2.38	0.44
1:B:246:GLU:O	1:C:414:MET:HE1	2.17	0.44
1:B:297:GLU:O	1:B:300:ALA:HB3	2.18	0.44
1:B:541:LEU:HA	1:B:665:ILE:O	2.18	0.44
1:B:576:PHE:HB2	1:B:581:LYS:CG	2.48	0.44
1:C:24:VAL:O	1:C:51:THR:HA	2.18	0.44
1:D:23:VAL:HG12	1:D:55:VAL:CG2	2.48	0.44
1:D:268:LEU:HA	1:D:271:ARG:CD	2.48	0.44
1:E:24:VAL:CG1	1:E:49:LEU:HD22	2.48	0.44
2:J:120:ALA:O	2:J:124:HIS:HB2	2.18	0.44
3:K:77:PHE:HB2	5:M:192:ILE:CG2	2.47	0.44
4:L:209:ILE:HG13	5:M:32:MET:CE	2.46	0.44
1:A:121:PHE:CD2	1:A:183:VAL:HG21	2.52	0.44
1:A:573:MET:HA	1:A:576:PHE:CD2	2.53	0.44
1:B:450:SER:O	1:B:453:MET:HB2	2.16	0.44
1:B:669:ASN:OD1	1:B:706:GLY:HA2	2.17	0.44
1:C:237:SER:OG	1:C:252:HIS:ND1	2.49	0.44
1:E:95:MET:CE	1:E:97:ILE:HD11	2.48	0.44
1:E:102:LEU:HD22	1:E:137:VAL:HG12	2.00	0.44
1:E:190:ASN:HD21	1:E:316:LEU:CB	2.30	0.44
2:J:20:LYS:NZ	2:J:40:GLU:HG2	2.33	0.44
2:G:182:ILE:CG2	2:G:212:CYS:HB2	2.47	0.44
2:G:182:ILE:HG22	2:G:212:CYS:HB2	1.99	0.44
2:G:263:VAL:HG23	2:G:280:LEU:HD13	2.00	0.44
5:M:29:THR:O	5:M:32:MET:HB3	2.17	0.44
5:M:142:ARG:HG2	5:M:143:GLU:H	1.82	0.44
1:B:260:GLY:HA3	1:B:266:LYS:HD3	2.00	0.44
1:B:582:CYS:SG	1:C:574:ILE:HG22	2.58	0.44
1:C:590:ASP:HA	1:C:593:TYR:HD2	1.81	0.44
1:C:603:ASP:HA	1:C:645:THR:OG1	2.18	0.44
1:C:613:PRO:HD3	1:C:648:ARG:HH22	1.83	0.44
1:C:686:PHE:HB3	1:C:690:GLU:OE2	2.18	0.44
1:D:231:PHE:HA	1:D:235:PHE:CD2	2.52	0.44
1:D:651:VAL:CG1	1:D:655:MET:HE3	2.47	0.44
1:F:48:THR:HG22	1:F:49:LEU:N	2.33	0.44
1:F:562:PHE:CE2	1:F:597:LEU:HD12	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:134:GLU:O	2:H:136:VAL:HG23	2.18	0.44
2:H:223:LEU:O	2:H:227:LYS:HG3	2.18	0.44
2:H:256:VAL:HG11	2:H:288:GLN:HG2	2.00	0.44
2:I:45:TYR:HE2	2:I:71:LEU:HD11	1.83	0.44
2:J:243:LEU:HD22	2:J:266:TYR:CD2	2.53	0.44
1:A:240:PHE:HB3	1:A:244:ILE:HD11	1.99	0.43
1:A:575:GLY:HA3	1:F:586:LYS:HZ1	1.83	0.43
1:A:632:LYS:HE3	1:A:633:ALA:O	2.18	0.43
1:C:132:VAL:HG23	1:C:173:GLU:O	2.18	0.43
1:D:121:PHE:HD2	1:D:183:VAL:HG21	1.83	0.43
1:D:303:ARG:HD3	1:D:353:GLN:CG	2.48	0.43
1:E:12:PRO:HG2	1:E:23:VAL:HG11	1.98	0.43
2:H:92:PHE:HB3	2:H:98:GLN:O	2.17	0.43
2:H:119:ILE:HD11	2:H:123:HIS:CE1	2.53	0.43
2:H:182:ILE:CG2	2:H:212:CYS:HB2	2.48	0.43
2:I:81:ALA:O	2:I:85:PHE:HD1	2.01	0.43
2:G:119:ILE:HD11	2:G:123:HIS:HE1	1.82	0.43
1:A:300:ALA:O	1:A:303:ARG:HG2	2.19	0.43
1:C:507:ILE:HD12	1:C:555:LYS:CE	2.47	0.43
1:D:103:GLN:C	1:D:105:LYS:H	2.20	0.43
1:D:310:GLU:O	1:D:313:GLN:CD	2.55	0.43
1:D:354:LEU:HD23	1:D:354:LEU:HA	1.77	0.43
1:E:7:GLN:O	1:E:59:SER:HB2	2.18	0.43
1:E:512:ASP:N	1:E:513:PRO:CD	2.81	0.43
1:E:713:LEU:CD2	1:E:732:LEU:HD13	2.47	0.43
1:F:589:PHE:O	1:F:593:TYR:CD1	2.71	0.43
1:F:657:MET:SD	1:F:661:PHE:CE2	3.10	0.43
1:F:712:MET:O	1:F:716:MET:HG3	2.18	0.43
2:I:182:ILE:HG22	2:I:212:CYS:HB2	2.01	0.43
2:G:124:HIS:HE1	2:G:147:GLN:HB3	1.83	0.43
2:G:179:GLN:HG3	2:G:180:LYS:N	2.33	0.43
2:G:195:SER:C	2:G:197:LEU:H	2.21	0.43
1:A:262:PRO:CG	1:A:374:ASN:OD1	2.64	0.43
1:B:69:TRP:NE1	1:B:134:GLN:HA	2.33	0.43
1:B:221:GLY:HA3	1:B:406:ILE:HD12	1.99	0.43
1:B:241:PRO:HA	1:B:242:PRO:HA	1.55	0.43
1:B:677:LEU:O	1:B:681:GLU:HG3	2.18	0.43
1:C:402:GLY:O	1:C:406:ILE:HD12	2.18	0.43
1:C:688:ASP:HA	1:C:691:ARG:CZ	2.48	0.43
1:D:632:LYS:HZ3	1:E:571:ASP:HB3	1.82	0.43
1:E:375:ARG:NH2	1:E:377:ASP:OD2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:118:THR:O	2:H:122:LYS:HG2	2.18	0.43
2:H:188:VAL:HG13	2:H:205:TYR:HD2	1.83	0.43
2:H:222:LYS:HA	2:H:225:VAL:HG12	2.00	0.43
2:G:112:THR:HG23	2:G:117:PHE:CE1	2.47	0.43
3:K:50:VAL:O	3:K:53:VAL:HG12	2.19	0.43
1:A:67:ARG:HD2	2:H:218:MET:SD	2.58	0.43
1:A:68:LYS:HD2	2:H:219:LEU:HD23	2.00	0.43
1:A:242:PRO:HD2	1:A:243:GLU:H	1.82	0.43
1:A:258:LEU:O	1:A:258:LEU:HD12	2.18	0.43
1:A:395:ILE:HD12	1:A:395:ILE:N	2.32	0.43
1:A:395:ILE:HG22	1:A:396:GLY:N	2.33	0.43
1:A:502:TYR:N	1:A:502:TYR:HD1	2.17	0.43
1:B:440:GLU:O	1:B:444:LEU:HG	2.18	0.43
1:D:241:PRO:HA	1:D:242:PRO:HA	1.68	0.43
1:E:231:PHE:O	1:E:235:PHE:CD2	2.71	0.43
1:F:74:ILE:HB	2:G:216:ILE:CD1	2.48	0.43
1:F:101:PHE:CD2	1:F:107:ILE:HA	2.53	0.43
2:H:203:LYS:NZ	2:H:239:ARG:HH21	2.15	0.43
2:H:230:GLU:HG2	2:H:231:LEU:H	1.83	0.43
2:I:162:ASN:O	2:I:166:LEU:HG	2.18	0.43
2:J:203:LYS:HE3	2:J:203:LYS:HB2	1.85	0.43
1:A:457:ILE:HD12	1:F:232:ARG:HH21	1.83	0.43
1:A:510:TRP:CE3	1:A:675:GLN:HG2	2.54	0.43
1:A:718:LEU:O	1:A:725:ARG:NE	2.51	0.43
1:B:455:ARG:NH2	1:B:481:LEU:CB	2.81	0.43
1:D:34:HIS:HB2	1:D:83:TYR:O	2.18	0.43
1:D:498:ASP:O	1:D:501:SER:HB3	2.19	0.43
1:D:632:LYS:HZ1	1:E:571:ASP:HB3	1.82	0.43
1:F:72:LEU:O	2:G:218:MET:SD	2.77	0.43
2:J:167:LYS:HE2	2:J:171:TYR:CE2	2.49	0.43
2:J:230:GLU:HG2	2:J:231:LEU:N	2.34	0.43
2:J:235:PHE:HD1	3:K:34:GLN:HE21	1.62	0.43
4:L:209:ILE:CG2	5:M:32:MET:HG3	2.45	0.43
1:A:256:ILE:CG1	1:A:370:ILE:HG22	2.47	0.43
1:A:612:VAL:CG1	1:A:617:ARG:HB2	2.49	0.43
1:A:646:THR:HG21	1:A:652:LEU:HD22	1.99	0.43
1:B:549:LYS:NZ	1:B:647:SER:HA	2.34	0.43
1:B:715:GLU:O	1:B:719:GLN:HG2	2.18	0.43
1:C:241:PRO:HA	1:C:242:PRO:HA	1.66	0.43
1:C:265:GLY:O	1:C:268:LEU:HG	2.18	0.43
1:D:102:LEU:HD22	1:D:137:VAL:CG1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:331:ASP:CA	1:D:379:ILE:HD11	2.48	0.43
1:E:531:SER:HB3	1:E:534:THR:O	2.18	0.43
1:E:676:LEU:HD22	1:E:703:VAL:HG11	2.01	0.43
1:E:732:LEU:HA	1:E:732:LEU:HD23	1.73	0.43
1:F:555:LYS:HD3	1:F:559:GLU:HG2	2.00	0.43
1:F:629:LEU:O	1:F:632:LYS:HB3	2.18	0.43
2:H:130:ILE:C	2:H:132:GLU:H	2.21	0.43
2:H:231:LEU:HD13	2:G:271:ARG:CG	2.48	0.43
2:J:21:VAL:HG23	2:J:38:ILE:CD1	2.48	0.43
4:L:210:ARG:HG2	4:L:210:ARG:NH1	2.32	0.43
5:M:49:MET:O	5:M:53:GLN:HG3	2.19	0.43
1:A:377:ASP:OD2	1:A:378:LEU:HD23	2.19	0.43
1:A:436:PHE:CD2	1:A:444:LEU:HD11	2.54	0.43
1:A:457:ILE:HD12	1:F:232:ARG:NH2	2.33	0.43
1:A:564:PHE:CZ	1:A:566:LYS:HB2	2.53	0.43
1:C:508:ILE:HD13	1:C:683:LEU:HD21	2.01	0.43
1:C:526:GLN:OE1	1:C:530:ASN:ND2	2.52	0.43
1:C:544:PRO:HG2	1:C:669:ASN:CG	2.39	0.43
1:D:655:MET:O	1:D:656:GLU:HB2	2.18	0.43
1:E:684:GLY:HA2	1:E:691:ARG:NH2	2.33	0.43
1:F:597:LEU:HA	1:F:639:LYS:O	2.18	0.43
2:H:82:ALA:HB2	2:H:110:ILE:HG21	2.00	0.43
2:J:197:LEU:CD2	3:K:48:VAL:HG11	2.48	0.43
2:G:96:ASP:N	2:G:97:PRO:HD2	2.34	0.43
3:K:46:MET:O	3:K:50:VAL:HG23	2.19	0.43
4:L:248:VAL:HB	5:M:70:ASP:HB3	1.99	0.43
1:A:114:THR:HG21	1:A:200:LYS:HG2	2.00	0.43
1:A:713:LEU:CD2	1:A:732:LEU:HB3	2.40	0.43
1:B:388:ARG:O	1:B:389:LEU:HD23	2.19	0.43
1:B:485:GLU:O	1:B:489:LYS:CB	2.67	0.43
1:B:541:LEU:HD12	1:B:541:LEU:O	2.19	0.43
1:B:547:SER:HA	1:B:707:ILE:HG22	2.00	0.43
1:C:12:PRO:HB3	1:C:54:SER:OG	2.18	0.43
1:C:709:LYS:HA	1:C:709:LYS:HD2	1.84	0.43
1:D:105:LYS:O	1:D:106:ASN:ND2	2.51	0.43
1:E:242:PRO:CD	1:E:243:GLU:H	2.32	0.43
1:E:530:ASN:O	1:E:639:LYS:HE3	2.19	0.43
1:E:625:ALA:HA	1:F:574:ILE:CD1	2.39	0.43
1:F:76:GLN:HE21	1:F:78:ILE:CG2	2.32	0.43
1:F:91:CYS:HB3	1:F:155:MET:CE	2.49	0.43
1:F:571:ASP:HA	1:F:574:ILE:HB	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:677:LEU:O	1:F:681:GLU:HG3	2.18	0.43
2:I:72:HIS:ND1	2:I:81:ALA:HB2	2.34	0.43
2:J:10:ALA:O	2:J:14:LEU:HG	2.19	0.43
2:J:101:ILE:HB	2:J:131:TYR:OH	2.18	0.43
2:G:45:TYR:HE2	2:G:71:LEU:HD11	1.83	0.43
2:G:147:GLN:HG2	2:G:151:TYR:CE2	2.53	0.43
4:L:248:VAL:O	4:L:252:LYS:HG3	2.18	0.43
1:A:247:GLN:CA	1:B:413:ARG:HH12	2.32	0.43
1:B:218:MET:HA	1:B:219:GLY:HA2	1.70	0.43
1:B:549:LYS:HZ3	1:B:647:SER:HA	1.84	0.43
1:C:24:VAL:HG12	1:C:60:VAL:HG13	1.99	0.43
1:D:227:PHE:O	1:D:230:ILE:HG22	2.18	0.43
1:D:247:GLN:O	1:E:414:MET:SD	2.77	0.43
1:D:327:PHE:HB2	1:D:330:ILE:CG2	2.48	0.43
1:F:24:VAL:HG21	1:F:29:TYR:HB2	2.00	0.43
1:F:106:ASN:HB3	1:F:143:LYS:HZ2	1.83	0.43
1:F:254:LYS:O	1:F:368:LEU:HA	2.18	0.43
1:F:263:GLY:HA3	1:F:437:SER:HB2	2.01	0.43
1:F:408:HIS:O	1:F:408:HIS:ND1	2.45	0.43
1:F:524:LEU:HD13	1:F:539:VAL:CG2	2.49	0.43
1:F:560:SER:HB2	1:F:562:PHE:CD1	2.54	0.43
2:H:231:LEU:HB2	2:H:234:ALA:CB	2.49	0.43
2:I:12:ALA:O	2:I:16:GLU:HG3	2.19	0.43
2:I:147:GLN:HG2	2:I:151:TYR:CE2	2.53	0.43
2:I:200:TYR:O	2:I:203:LYS:NZ	2.45	0.43
2:J:21:VAL:HG13	2:J:21:VAL:O	2.19	0.43
2:J:63:ASN:O	2:J:67:GLN:HG3	2.19	0.43
2:G:35:SER:HA	2:G:38:ILE:HG22	2.01	0.43
2:G:179:GLN:HB3	2:G:214:PHE:HB3	2.00	0.43
1:A:231:PHE:CE1	1:A:235:PHE:CE2	3.04	0.43
1:A:313:GLN:NE2	1:A:365:ASN:OD1	2.52	0.43
1:B:288:PRO:HG2	1:B:289:GLU:H	1.83	0.43
1:B:375:ARG:NH2	1:B:377:ASP:OD2	2.51	0.43
1:B:492:PHE:C	1:B:494:THR:H	2.19	0.43
1:D:105:LYS:HZ1	2:I:291:GLU:HB3	1.84	0.43
1:D:406:ILE:HD12	1:D:406:ILE:HG23	1.70	0.43
1:E:586:LYS:O	1:E:589:PHE:HB2	2.19	0.43
2:H:67:GLN:O	2:H:71:LEU:HG	2.19	0.43
2:H:169:ALA:HB2	2:H:184:ILE:HB	2.01	0.43
2:I:45:TYR:CE2	2:I:71:LEU:HD11	2.54	0.43
2:I:167:LYS:HE2	2:I:171:TYR:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:263:VAL:HG21	2:I:280:LEU:HD13	2.01	0.43
2:J:271:ARG:CZ	2:G:234:ALA:HB2	2.48	0.43
2:G:167:LYS:HE2	2:G:171:TYR:CE2	2.54	0.43
3:K:48:VAL:HG12	3:K:52:LYS:CE	2.40	0.43
3:K:48:VAL:O	3:K:52:LYS:HG3	2.18	0.43
4:L:225:SER:C	4:L:229:MET:HE2	2.39	0.43
1:B:286:ASN:OD1	1:B:327:PHE:HD1	2.02	0.42
1:C:620:ASN:O	1:C:624:GLN:HG2	2.20	0.42
1:E:67:ARG:HH11	1:E:74:ILE:HD11	1.84	0.42
1:E:242:PRO:HD2	1:E:243:GLU:N	2.34	0.42
1:E:564:PHE:HB3	1:E:595:SER:HB2	2.01	0.42
1:E:587:LYS:HZ1	1:E:591:ASP:CG	2.22	0.42
1:F:518:LEU:HD23	1:F:555:LYS:CG	2.16	0.42
2:I:17:ALA:HB2	2:I:44:ILE:HG21	2.01	0.42
2:I:161:ALA:O	2:I:165:LEU:HG	2.18	0.42
2:J:269:ILE:HG22	5:M:151:GLU:OE1	2.19	0.42
2:G:95:ALA:HB1	2:G:97:PRO:HD2	2.00	0.42
5:M:167:MET:HA	5:M:170:GLU:HB3	2.00	0.42
1:A:12:PRO:HB3	1:A:54:SER:OG	2.19	0.42
1:A:407:LEU:O	1:A:411:THR:HG23	2.19	0.42
1:A:453:MET:HA	1:F:240:PHE:CE2	2.54	0.42
1:B:671:ALA:HA	1:B:703:VAL:O	2.19	0.42
1:D:236:ALA:HA	1:D:239:VAL:HG12	2.00	0.42
1:D:690:GLU:O	1:D:694:ILE:HG13	2.19	0.42
1:E:73:SER:O	1:E:76:GLN:HG2	2.19	0.42
1:E:297:GLU:O	1:E:300:ALA:HB3	2.19	0.42
1:E:608:LEU:HD23	1:E:626:LEU:HD11	2.01	0.42
1:F:440:GLU:O	1:F:444:LEU:HG	2.18	0.42
2:H:58:TRP:HB3	2:H:95:ALA:HB2	2.00	0.42
2:H:218:MET:CG	2:H:219:LEU:N	2.77	0.42
2:I:17:ALA:HB2	2:I:44:ILE:CG2	2.50	0.42
2:I:267:ASP:OD2	2:I:271:ARG:NH2	2.52	0.42
2:G:266:TYR:CZ	2:G:270:SER:HB2	2.55	0.42
1:A:73:SER:HB2	1:A:76:GLN:OE1	2.18	0.42
1:A:235:PHE:N	1:A:235:PHE:CD1	2.81	0.42
1:B:612:VAL:HG13	1:B:614:ILE:O	2.19	0.42
1:C:533:ARG:C	1:D:505:ASN:HD21	2.22	0.42
1:D:131:SER:HA	1:D:173:GLU:O	2.20	0.42
1:D:518:LEU:HA	1:D:518:LEU:HD23	1.86	0.42
1:E:86:ASP:C	1:E:88:ALA:H	2.21	0.42
1:E:705:ILE:CD1	1:E:713:LEU:HD12	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:436:PHE:CD2	1:F:444:LEU:HD11	2.55	0.42
1:F:503:ILE:HD11	1:F:554:ALA:HB3	2.02	0.42
1:F:721:ASP:O	1:F:725:ARG:HG3	2.20	0.42
2:H:75:LEU:O	2:H:76:GLN:HB2	2.19	0.42
2:G:134:GLU:O	2:G:136:VAL:HG23	2.19	0.42
3:K:60:LEU:HD23	5:M:178:ILE:HD13	2.01	0.42
3:K:67:ALA:HB1	4:L:237:VAL:HG22	2.01	0.42
3:K:77:PHE:HB2	5:M:192:ILE:HG23	2.02	0.42
1:A:611:TYR:HA	1:A:618:PHE:HB3	2.00	0.42
1:B:24:VAL:O	1:B:51:THR:HA	2.19	0.42
1:B:436:PHE:CE2	1:B:444:LEU:HD11	2.54	0.42
1:C:386:PRO:HA	1:C:390:GLU:CA	2.39	0.42
1:C:490:PRO:HB2	1:C:492:PHE:H	1.83	0.42
1:C:517:VAL:HG13	1:C:665:ILE:HG21	2.02	0.42
1:C:629:LEU:HD23	1:C:629:LEU:HA	1.74	0.42
1:C:691:ARG:HB2	1:C:691:ARG:NH1	2.35	0.42
1:D:52:HIS:C	1:D:54:SER:H	2.23	0.42
1:D:388:ARG:O	1:D:389:LEU:HD23	2.19	0.42
1:D:510:TRP:CB	1:D:679:ALA:HB2	2.50	0.42
1:D:543:GLY:N	1:D:549:LYS:HD3	2.30	0.42
1:E:388:ARG:O	1:E:389:LEU:HD23	2.20	0.42
1:E:691:ARG:HA	1:E:694:ILE:HD12	2.01	0.42
1:F:618:PHE:HE1	1:F:620:ASN:HA	1.85	0.42
1:F:653:GLN:CB	1:F:658:LEU:HD23	2.49	0.42
2:H:179:GLN:HB3	2:H:214:PHE:CB	2.50	0.42
2:J:188:VAL:HG13	2:J:205:TYR:CD2	2.55	0.42
2:J:200:TYR:O	2:J:203:LYS:HG3	2.19	0.42
2:J:260:THR:HA	2:J:263:VAL:HG12	2.01	0.42
2:G:166:LEU:HD21	2:G:205:TYR:CE2	2.54	0.42
2:G:232:PHE:CB	2:G:233:PRO:HD3	2.40	0.42
2:G:235:PHE:CG	5:M:152:GLN:HA	2.53	0.42
1:A:231:PHE:CE2	1:A:235:PHE:CD2	3.08	0.42
1:A:322:LEU:HD13	1:A:366:ASN:O	2.20	0.42
1:A:502:TYR:N	1:A:502:TYR:CD1	2.86	0.42
1:A:687:LYS:HZ3	1:A:722:PRO:HB3	1.82	0.42
1:B:23:VAL:HG12	1:B:55:VAL:CG2	2.50	0.42
1:B:232:ARG:O	1:B:236:ALA:HB3	2.19	0.42
1:C:220:ILE:HD11	1:C:272:GLN:HG3	2.01	0.42
1:C:318:ALA:C	1:C:319:ASN:HD22	2.21	0.42
1:C:499:TYR:OH	1:C:565:ILE:HB	2.20	0.42
1:C:519:ASP:O	1:C:523:LEU:HG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:560:SER:HB2	1:C:562:PHE:CZ	2.54	0.42
1:D:331:ASP:O	1:D:332:ALA:HB3	2.19	0.42
1:D:407:LEU:HB2	1:D:426:ILE:HG23	2.02	0.42
1:D:538:SER:OG	1:D:661:PHE:HA	2.19	0.42
1:E:245:VAL:HG13	1:E:246:GLU:N	2.34	0.42
1:F:38:ARG:HG2	1:F:38:ARG:HH11	1.84	0.42
2:H:101:ILE:HB	2:H:131:TYR:OH	2.20	0.42
2:H:163:LYS:O	2:H:167:LYS:HG2	2.19	0.42
2:I:277:THR:O	2:I:281:LEU:HD13	2.20	0.42
2:J:184:ILE:O	2:J:188:VAL:HG12	2.20	0.42
1:A:220:ILE:HG22	1:A:221:GLY:N	2.34	0.42
1:B:64:LEU:HA	1:B:67:ARG:HH21	1.84	0.42
1:B:242:PRO:HD2	1:B:243:GLU:N	2.34	0.42
1:D:499:TYR:CD1	1:D:499:TYR:N	2.86	0.42
1:D:549:LYS:HB3	1:D:645:THR:HB	2.01	0.42
1:E:122:ILE:HD11	1:E:183:VAL:CG2	2.50	0.42
1:E:406:ILE:O	1:E:409:ILE:HG22	2.19	0.42
1:E:648:ARG:NE	1:E:651:VAL:HG13	2.33	0.42
1:F:388:ARG:O	1:F:389:LEU:HD23	2.20	0.42
1:F:524:LEU:HD11	1:F:665:ILE:HD11	2.01	0.42
2:H:118:THR:HG22	2:H:155:GLU:HG3	2.00	0.42
2:H:266:TYR:HD2	2:H:272:LEU:HD21	1.85	0.42
2:I:118:THR:HG22	2:I:155:GLU:HG3	2.02	0.42
5:M:28:SER:O	5:M:32:MET:N	2.53	0.42
1:A:86:ASP:C	1:A:88:ALA:H	2.22	0.42
1:A:315:ARG:HG2	1:A:316:LEU:HD12	2.00	0.42
1:A:552:LEU:HD22	1:A:556:ILE:HD11	2.00	0.42
1:C:576:PHE:HB3	1:C:580:ALA:HB3	2.01	0.42
1:D:240:PHE:HA	1:D:241:PRO:HD3	1.89	0.42
1:D:709:LYS:HA	1:D:709:LYS:HD2	1.85	0.42
1:E:313:GLN:HE21	1:E:317:GLY:CA	2.32	0.42
1:E:643:ILE:N	1:E:643:ILE:HD12	2.35	0.42
1:F:589:PHE:N	1:F:589:PHE:CD1	2.84	0.42
1:F:632:LYS:NZ	1:F:633:ALA:O	2.36	0.42
2:H:219:LEU:HD12	2:H:219:LEU:O	2.19	0.42
2:I:49:ALA:HB2	2:I:64:ALA:HB3	2.02	0.42
2:I:216:ILE:HG12	2:I:217:ASP:H	1.85	0.42
5:M:49:MET:HG2	5:M:53:GLN:NE2	2.33	0.42
1:A:676:LEU:HD12	1:A:710:LEU:HD11	2.01	0.42
1:A:706:GLY:O	1:A:710:LEU:N	2.53	0.42
1:B:546:HIS:O	1:B:547:SER:OG	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:24:VAL:CG1	1:C:49:LEU:HD22	2.49	0.42
1:C:26:GLU:HG2	1:C:51:THR:HB	2.01	0.42
1:C:521:GLY:O	1:C:525:VAL:HG23	2.20	0.42
1:D:186:GLU:HG3	1:D:186:GLU:O	2.19	0.42
1:D:268:LEU:O	1:D:271:ARG:HG2	2.19	0.42
1:D:670:ILE:HD13	1:D:670:ILE:HG21	1.75	0.42
1:E:284:VAL:O	1:E:326:ILE:HG12	2.19	0.42
1:E:307:ALA:O	1:E:310:GLU:HG2	2.20	0.42
1:E:377:ASP:OD1	1:E:378:LEU:N	2.53	0.42
1:E:714:ILE:HG12	1:E:729:PHE:HE1	1.84	0.42
1:F:12:PRO:HD2	1:F:23:VAL:HG21	2.01	0.42
1:F:74:ILE:HB	2:G:216:ILE:HD11	2.01	0.42
2:H:45:TYR:HE2	2:H:71:LEU:HD11	1.84	0.42
2:I:163:LYS:O	2:I:167:LYS:HG2	2.20	0.42
2:J:25:GLN:N	2:J:29:SER:HB2	2.35	0.42
2:J:81:ALA:O	2:J:85:PHE:HD1	2.02	0.42
2:J:203:LYS:HD3	2:J:236:SER:HB3	2.02	0.42
2:J:265:GLU:O	2:J:268:SER:HB2	2.20	0.42
5:M:23:ASP:O	5:M:27:GLU:HB2	2.20	0.42
1:A:16:LEU:HD11	1:A:52:HIS:CD2	2.54	0.42
1:A:38:ARG:HG2	1:A:38:ARG:HH11	1.85	0.42
1:A:247:GLN:HA	1:B:413:ARG:HH12	1.85	0.42
1:A:542:GLU:HA	1:A:646:THR:O	2.19	0.42
1:B:579:THR:O	1:B:583:GLN:HG2	2.20	0.42
1:D:545:PRO:CD	1:D:647:SER:OG	2.68	0.42
1:D:627:LEU:HA	1:D:627:LEU:HD23	1.65	0.42
1:E:534:THR:HG21	1:F:712:MET:HA	2.01	0.42
1:F:289:GLU:C	1:F:291:LEU:H	2.16	0.42
1:F:545:PRO:HB3	1:F:546:HIS:HA	2.01	0.42
2:I:95:ALA:CB	2:I:97:PRO:HD2	2.50	0.42
1:A:240:PHE:CG	1:A:244:ILE:HD11	2.55	0.42
1:B:452:ALA:HA	1:B:455:ARG:CZ	2.50	0.42
1:B:520:ASP:OD2	1:B:665:ILE:HG12	2.20	0.42
1:C:284:VAL:HB	1:C:325:ILE:HA	2.01	0.42
1:C:508:ILE:HD11	1:C:707:ILE:HD11	2.02	0.42
1:C:562:PHE:HD2	1:C:599:CYS:CB	2.33	0.42
1:D:573:MET:SD	1:D:608:LEU:HD22	2.59	0.42
1:E:545:PRO:HG3	1:E:647:SER:OG	2.20	0.42
1:E:568:CYS:HB3	1:E:601:VAL:O	2.20	0.42
2:I:250:ALA:HB1	2:I:259:TYR:HB2	2.02	0.42
2:G:75:LEU:O	2:G:76:GLN:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:92:PHE:HD1	2:G:97:PRO:HG2	1.84	0.42
2:G:164:CYS:O	2:G:168:VAL:HG23	2.20	0.42
4:L:195:ILE:HG21	5:M:18:ALA:HB1	2.02	0.42
1:B:295:VAL:HB	1:C:294:TYR:CB	2.50	0.41
1:B:539:VAL:CG2	1:B:665:ILE:HD12	2.50	0.41
1:C:218:MET:HA	1:C:219:GLY:HA2	1.76	0.41
1:E:670:ILE:HG21	1:E:675:GLN:HB3	2.02	0.41
1:F:438:GLY:O	1:F:441:LEU:N	2.45	0.41
2:H:208:LYS:HG2	2:H:275:TRP:CZ3	2.55	0.41
2:J:82:ALA:O	2:J:86:VAL:HG23	2.20	0.41
2:J:117:PHE:HA	2:J:120:ALA:HB3	2.01	0.41
2:J:247:LEU:HD22	2:J:259:TYR:CE1	2.55	0.41
4:L:241:VAL:HG21	5:M:63:GLY:HA3	2.01	0.41
5:M:36:VAL:HA	5:M:39:SER:OG	2.20	0.41
1:A:10:ARG:HD2	2:H:217:ASP:HB2	2.02	0.41
1:A:97:ILE:HG21	1:A:147:LEU:HD22	2.03	0.41
1:A:220:ILE:HD11	1:A:227:PHE:CZ	2.54	0.41
1:A:235:PHE:HD1	1:A:235:PHE:HA	1.58	0.41
1:A:509:LYS:HG2	1:A:515:THR:OG1	2.20	0.41
1:A:686:PHE:O	1:A:691:ARG:NH2	2.52	0.41
1:B:377:ASP:OD1	1:B:378:LEU:N	2.53	0.41
1:C:113:ASP:HA	1:C:196:ILE:HG13	2.01	0.41
1:C:624:GLN:OE1	1:C:624:GLN:HA	2.20	0.41
1:D:122:ILE:HD11	1:D:183:VAL:CG2	2.50	0.41
1:D:349:THR:HA	1:D:352:ASN:HD22	1.84	0.41
1:D:377:ASP:OD1	1:D:378:LEU:N	2.53	0.41
1:D:570:PRO:O	1:D:573:MET:HB3	2.20	0.41
1:E:99:ILE:HD11	1:E:145:PHE:CD2	2.55	0.41
1:E:190:ASN:HB2	1:E:315:ARG:HH12	1.85	0.41
1:F:18:LEU:HD13	1:F:139:SER:OG	2.21	0.41
1:F:377:ASP:OD1	1:F:378:LEU:N	2.53	0.41
1:F:400:GLU:OE2	1:F:434:LYS:HA	2.21	0.41
1:F:542:GLU:N	1:F:665:ILE:O	2.52	0.41
1:F:549:LYS:HE3	1:F:646:THR:C	2.40	0.41
2:I:236:SER:HA	2:I:239:ARG:NH1	2.35	0.41
2:J:195:SER:C	2:J:197:LEU:H	2.23	0.41
3:K:35:THR:O	3:K:35:THR:HG22	2.20	0.41
4:L:202:ILE:HG22	5:M:25:SER:HB3	2.01	0.41
5:M:36:VAL:CG2	5:M:156:ILE:HD12	2.51	0.41
1:B:536:LEU:HD22	1:B:632:LYS:O	2.19	0.41
1:C:125:PHE:CD2	1:C:130:PHE:HZ	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:232:ARG:O	1:C:236:ALA:HB3	2.21	0.41
1:C:233:ARG:HA	1:D:450:SER:HB2	2.02	0.41
1:D:541:LEU:HD12	1:D:541:LEU:O	2.21	0.41
1:E:242:PRO:O	1:E:245:VAL:HG12	2.20	0.41
1:E:539:VAL:HG13	1:E:643:ILE:HA	2.02	0.41
1:E:670:ILE:CG2	1:E:672:THR:H	2.29	0.41
1:F:263:GLY:HA3	1:F:437:SER:CB	2.50	0.41
1:F:324:ILE:HG12	1:F:368:LEU:HD11	2.03	0.41
1:F:624:GLN:O	1:F:628:VAL:HG23	2.21	0.41
2:H:21:VAL:HG23	2:H:38:ILE:CD1	2.50	0.41
2:H:256:VAL:O	2:H:256:VAL:HG22	2.19	0.41
2:I:219:LEU:O	2:I:220:ASN:HB3	2.21	0.41
2:J:271:ARG:NH2	2:G:231:LEU:HB2	2.35	0.41
3:K:54:LEU:HD21	4:L:222:LEU:HD13	2.02	0.41
1:A:24:VAL:HG11	1:A:49:LEU:HD22	2.02	0.41
1:A:138:PHE:HB2	1:A:147:LEU:HD11	2.01	0.41
1:A:254:LYS:O	1:A:368:LEU:HA	2.20	0.41
1:B:479:ASP:C	1:B:483:SER:H	2.23	0.41
1:C:67:ARG:CZ	2:I:217:ASP:OD1	2.69	0.41
1:C:538:SER:O	1:C:662:SER:OG	2.27	0.41
1:D:256:ILE:HG22	1:D:391:VAL:CG1	2.48	0.41
1:D:331:ASP:HA	1:D:379:ILE:CD1	2.51	0.41
2:I:203:LYS:HD2	2:I:237:ASP:HA	2.03	0.41
2:J:188:VAL:HG13	2:J:205:TYR:HD2	1.86	0.41
2:J:232:PHE:CZ	2:J:242:LYS:HD3	2.55	0.41
2:G:39:GLU:HB2	2:G:75:LEU:HD11	2.01	0.41
5:M:33:LEU:HD23	5:M:33:LEU:C	2.40	0.41
1:A:242:PRO:O	1:A:245:VAL:HG12	2.20	0.41
1:A:510:TRP:CE3	1:A:675:GLN:HB3	2.56	0.41
1:B:52:HIS:C	1:B:54:SER:H	2.23	0.41
1:B:69:TRP:CE2	1:B:134:GLN:HA	2.56	0.41
1:C:38:ARG:HH11	1:C:38:ARG:HG2	1.85	0.41
1:C:436:PHE:N	1:C:436:PHE:CD1	2.84	0.41
1:C:528:THR:O	1:C:639:LYS:HD3	2.20	0.41
1:D:11:CYS:HA	1:D:12:PRO:HD3	1.92	0.41
1:D:45:TYR:CE2	1:D:70:ALA:HA	2.56	0.41
1:D:272:GLN:OE1	1:D:272:GLN:HA	2.21	0.41
1:E:230:ILE:HD11	1:E:391:VAL:HG11	2.02	0.41
1:E:586:LYS:NZ	1:F:574:ILE:HG23	2.35	0.41
1:F:101:PHE:HD1	1:F:101:PHE:H	1.67	0.41
1:F:520:ASP:O	1:F:524:LEU:HG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:9:GLU:O	2:H:13:LEU:HG	2.20	0.41
2:G:116:ARG:HB3	2:G:119:ILE:HG22	2.02	0.41
2:G:118:THR:HG22	2:G:155:GLU:HG3	2.03	0.41
1:A:693:THR:O	1:A:697:GLN:OE1	2.38	0.41
1:B:143:LYS:HB3	1:B:145:PHE:HE1	1.84	0.41
1:B:414:MET:HE2	1:B:414:MET:HA	2.03	0.41
1:B:512:ASP:N	1:B:513:PRO:CD	2.83	0.41
1:B:631:LYS:HB2	1:B:631:LYS:HE3	1.67	0.41
1:C:320:SER:O	1:C:320:SER:OG	2.31	0.41
1:C:552:LEU:HD23	1:C:552:LEU:HA	1.78	0.41
1:D:247:GLN:HA	1:E:417:HIS:ND1	2.35	0.41
1:D:604:ASP:O	1:D:607:ARG:N	2.54	0.41
1:D:627:LEU:CD1	1:E:607:ARG:HH12	2.32	0.41
1:E:441:LEU:O	1:E:445:VAL:HG23	2.21	0.41
1:E:721:ASP:HB2	1:E:724:TYR:HD2	1.85	0.41
1:F:323:HIS:HB2	1:F:367:ILE:HG22	2.01	0.41
1:F:670:ILE:O	1:F:704:TRP:HA	2.20	0.41
2:I:164:CYS:O	2:I:168:VAL:HG23	2.20	0.41
2:I:180:LYS:O	2:I:184:ILE:HG13	2.20	0.41
2:J:219:LEU:O	2:J:223:LEU:N	2.52	0.41
2:G:179:GLN:HG3	2:G:180:LYS:H	1.85	0.41
3:K:84:LEU:HD21	5:M:199:ALA:CB	2.50	0.41
1:A:241:PRO:HA	1:A:242:PRO:HA	1.62	0.41
1:B:143:LYS:HB3	1:B:145:PHE:CE1	2.56	0.41
1:B:407:LEU:O	1:B:411:THR:OG1	2.27	0.41
1:C:272:GLN:OE1	1:C:272:GLN:HA	2.20	0.41
1:C:297:GLU:O	1:C:301:ASN:N	2.32	0.41
1:C:414:MET:HE2	1:C:414:MET:HA	2.02	0.41
1:C:604:ASP:HB3	1:C:607:ARG:HB3	2.02	0.41
1:C:626:LEU:HA	1:C:626:LEU:HD23	1.87	0.41
1:D:258:LEU:HB2	1:D:395:ILE:HD11	2.02	0.41
1:D:265:GLY:O	1:D:268:LEU:HG	2.20	0.41
1:D:509:LYS:HE2	1:D:515:THR:HG22	2.03	0.41
1:E:562:PHE:HE2	1:E:641:LEU:CD2	2.34	0.41
1:E:640:LEU:HG	1:E:642:ILE:CD1	2.50	0.41
1:E:659:ASN:HD21	1:F:545:PRO:HB2	1.86	0.41
1:E:709:LYS:O	1:E:709:LYS:HD3	2.20	0.41
1:F:510:TRP:HZ3	1:F:675:GLN:NE2	2.18	0.41
1:F:709:LYS:HG3	1:F:713:LEU:HG	2.02	0.41
2:H:112:THR:HG23	2:H:117:PHE:CE1	2.56	0.41
2:H:175:LEU:HD23	2:H:177:GLN:HE21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:217:ASP:OD1	2:H:217:ASP:N	2.50	0.41
3:K:52:LYS:NZ	3:K:52:LYS:CB	2.84	0.41
1:A:215:PHE:N	1:A:231:PHE:CZ	2.89	0.41
1:A:673:GLY:O	1:A:676:LEU:HB3	2.21	0.41
1:B:257:LEU:HG	1:B:371:GLY:O	2.21	0.41
1:C:240:PHE:HA	1:C:241:PRO:HD3	1.94	0.41
1:C:649:LYS:HE2	1:C:658:LEU:CD1	2.45	0.41
1:D:198:LYS:HD3	1:D:198:LYS:C	2.41	0.41
1:D:527:GLN:HE22	1:E:716:MET:CA	2.33	0.41
1:D:562:PHE:CD2	1:D:597:LEU:HG	2.55	0.41
1:E:395:ILE:H	1:E:395:ILE:HD12	1.86	0.41
1:E:451:THR:O	1:E:454:ASN:HB3	2.21	0.41
2:I:124:HIS:CE1	2:I:147:GLN:HB3	2.55	0.41
2:G:95:ALA:CB	2:G:97:PRO:HD2	2.51	0.41
2:G:200:TYR:O	2:G:203:LYS:HE2	2.21	0.41
4:L:237:VAL:O	4:L:241:VAL:HG23	2.21	0.41
1:A:26:GLU:HG2	1:A:51:THR:HB	2.03	0.41
1:A:27:LYS:HD2	1:A:57:PRO:CG	2.51	0.41
1:A:40:SER:HB3	1:A:43:HIS:ND1	2.36	0.41
1:A:91:CYS:O	1:A:154:ALA:HA	2.21	0.41
1:A:457:ILE:HB	1:F:232:ARG:HH21	1.86	0.41
1:B:16:LEU:HD11	1:B:52:HIS:HD2	1.86	0.41
1:B:406:ILE:O	1:B:409:ILE:HG22	2.20	0.41
1:C:257:LEU:HG	1:C:371:GLY:O	2.21	0.41
1:C:653:GLN:HA	1:C:658:LEU:HB3	2.02	0.41
1:D:40:SER:HB3	1:D:43:HIS:CB	2.51	0.41
1:D:330:ILE:CD1	1:D:373:THR:HB	2.50	0.41
1:D:449:GLN:O	1:D:453:MET:HG2	2.21	0.41
1:D:560:SER:HB2	1:D:562:PHE:CE1	2.55	0.41
1:D:608:LEU:O	1:D:622:VAL:HG11	2.20	0.41
1:E:455:ARG:HH21	1:E:481:LEU:H	1.69	0.41
1:E:598:SER:O	1:E:640:LEU:HA	2.21	0.41
1:E:604:ASP:HB3	1:E:607:ARG:CB	2.49	0.41
1:F:98:GLU:HB3	1:F:148:LEU:HB3	2.02	0.41
1:F:121:PHE:CD2	1:F:183:VAL:HG21	2.56	0.41
1:F:230:ILE:HD13	1:F:391:VAL:HG21	2.03	0.41
1:F:503:ILE:HD11	1:F:551:ALA:HA	2.02	0.41
1:F:658:LEU:HD12	1:F:658:LEU:O	2.20	0.41
1:F:705:ILE:HG12	1:F:706:GLY:O	2.20	0.41
1:F:709:LYS:HB2	1:F:709:LYS:HE2	1.82	0.41
2:H:167:LYS:HE2	2:H:171:TYR:HE2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:260:THR:HG21	2:H:284:LYS:HE3	2.02	0.41
2:J:213:HIS:CE1	2:J:221:ALA:HB2	2.44	0.41
2:G:178:TYR:OH	2:G:282:ARG:HG2	2.20	0.41
3:K:39:VAL:CG1	4:L:209:ILE:HD13	2.46	0.41
5:M:174:GLN:O	5:M:177:GLN:HB3	2.21	0.41
1:A:243:GLU:O	1:A:246:GLU:HG2	2.21	0.41
1:B:178:VAL:HG22	1:B:181:SER:OG	2.20	0.41
1:B:633:ALA:HA	1:B:634:PRO:HD3	1.94	0.41
1:C:379:ILE:HD13	1:C:379:ILE:HA	1.74	0.41
1:C:402:GLY:O	1:C:405:GLN:HB2	2.22	0.41
1:C:696:GLN:NE2	1:C:696:GLN:O	2.54	0.41
1:D:507:ILE:HG21	1:D:509:LYS:NZ	2.36	0.41
1:D:577:SER:O	1:D:580:ALA:N	2.54	0.41
1:D:609:LEU:HD12	1:D:611:TYR:H	1.86	0.41
1:E:553:ALA:HB1	1:E:643:ILE:HG21	2.03	0.41
1:F:257:LEU:HB2	1:F:389:LEU:HD13	2.03	0.41
1:F:297:GLU:O	1:F:300:ALA:HB3	2.21	0.41
1:F:309:ALA:HA	1:F:312:GLU:OE1	2.21	0.41
2:I:236:SER:HA	2:I:239:ARG:HH12	1.86	0.41
2:G:101:ILE:O	2:G:105:MET:HG3	2.20	0.41
4:L:226:GLN:O	4:L:230:ILE:HG13	2.20	0.41
1:A:352:ASN:CB	1:B:288:PRO:HB2	2.44	0.40
1:A:429:LEU:CD2	1:A:482:ALA:HB1	2.51	0.40
1:A:623:LEU:O	1:A:626:LEU:HB3	2.22	0.40
1:B:67:ARG:HH12	1:B:74:ILE:HD11	1.84	0.40
1:B:309:ALA:HA	1:B:312:GLU:OE1	2.22	0.40
1:C:449:GLN:O	1:C:453:MET:HG2	2.21	0.40
1:E:190:ASN:HB2	1:E:315:ARG:NH1	2.36	0.40
1:E:323:HIS:HB2	1:E:367:ILE:HG22	2.03	0.40
1:E:324:ILE:HG12	1:E:368:LEU:HD11	2.03	0.40
2:H:221:ALA:O	2:H:225:VAL:N	2.53	0.40
2:G:279:MET:O	2:G:283:ILE:HG13	2.21	0.40
5:M:165:LEU:O	5:M:169:ASN:ND2	2.48	0.40
1:A:428:GLU:O	1:A:432:GLU:HG2	2.21	0.40
1:C:331:ASP:CA	1:C:379:ILE:HD11	2.46	0.40
1:E:414:MET:HA	1:E:414:MET:HE2	2.02	0.40
1:F:437:SER:OG	1:F:440:GLU:HG2	2.20	0.40
2:H:116:ARG:HG3	2:H:116:ARG:NH1	2.37	0.40
4:L:223:VAL:C	5:M:49:MET:HE3	2.42	0.40
1:A:231:PHE:CD2	1:A:235:PHE:HD2	2.38	0.40
1:A:255:GLY:HA2	1:A:369:VAL:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:ASP:O	1:B:117:MET:HG3	2.21	0.40
1:B:721:ASP:HB2	1:B:724:TYR:CD1	2.57	0.40
1:C:36:ILE:HD11	1:C:44:LYS:HB3	2.03	0.40
1:C:65:PRO:HG2	1:C:137:VAL:HG13	2.03	0.40
1:C:98:GLU:HG2	1:C:188:ALA:HB2	2.04	0.40
1:C:98:GLU:O	1:C:147:LEU:HA	2.21	0.40
1:C:630:LEU:HD23	1:C:630:LEU:HA	1.94	0.40
1:E:236:ALA:HA	1:E:239:VAL:CG1	2.50	0.40
1:E:618:PHE:CD1	1:E:618:PHE:C	2.95	0.40
1:F:502:TYR:HD2	1:F:503:ILE:HG13	1.86	0.40
1:F:678:GLU:O	1:F:682:LEU:HG	2.22	0.40
2:H:266:TYR:C	2:H:268:SER:H	2.25	0.40
2:I:10:ALA:O	2:I:14:LEU:HG	2.20	0.40
2:J:235:PHE:CG	3:K:38:GLN:CG	3.04	0.40
2:G:17:ALA:HB2	2:G:44:ILE:HG21	2.04	0.40
3:K:53:VAL:HB	4:L:219:MET:HE1	2.02	0.40
4:L:209:ILE:HG21	5:M:32:MET:HE2	2.03	0.40
1:A:284:VAL:O	1:A:326:ILE:HG13	2.21	0.40
1:A:624:GLN:HG3	1:B:610:ASP:CG	2.39	0.40
1:B:52:HIS:HA	1:B:53:PRO:HD3	1.91	0.40
1:B:221:GLY:HA3	1:B:406:ILE:CD1	2.52	0.40
1:B:323:HIS:HB2	1:B:367:ILE:HG22	2.02	0.40
1:B:403:ARG:O	1:B:407:LEU:HG	2.22	0.40
1:C:99:ILE:HD11	1:C:145:PHE:CD2	2.57	0.40
1:D:18:LEU:HD21	1:D:144:LEU:HD13	2.02	0.40
1:E:242:PRO:CD	1:E:243:GLU:N	2.85	0.40
1:E:641:LEU:CD1	1:E:643:ILE:HD11	2.51	0.40
1:F:242:PRO:CD	1:F:243:GLU:N	2.84	0.40
1:F:652:LEU:O	1:F:655:MET:HB2	2.22	0.40
2:I:256:VAL:HG22	2:I:256:VAL:O	2.21	0.40
2:J:45:TYR:CE2	2:J:71:LEU:HD11	2.56	0.40
2:J:59:SER:OG	2:J:97:PRO:HD3	2.21	0.40
2:G:126:SER:O	2:G:130:ILE:HG13	2.22	0.40
1:A:215:PHE:C	1:A:217:LYS:N	2.75	0.40
1:A:694:ILE:HA	1:A:697:GLN:OE1	2.22	0.40
1:C:246:GLU:HG2	1:C:247:GLN:N	2.37	0.40
1:D:379:ILE:HD13	1:D:379:ILE:HA	1.74	0.40
1:E:64:LEU:HA	1:E:67:ARG:NE	2.21	0.40
1:E:190:ASN:ND2	1:E:316:LEU:CA	2.85	0.40
1:E:253:VAL:H	1:F:446:ARG:NH1	2.15	0.40
1:E:257:LEU:HB2	1:E:389:LEU:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:544:PRO:O	1:E:547:SER:CB	2.68	0.40
1:E:686:PHE:O	1:E:691:ARG:NH1	2.54	0.40
2:H:216:ILE:HG21	2:H:220:ASN:HB3	2.03	0.40
2:I:175:LEU:HD23	2:I:177:GLN:NE2	2.37	0.40
2:I:232:PHE:O	2:I:234:ALA:N	2.54	0.40
2:J:261:GLU:O	2:J:265:GLU:HG3	2.21	0.40
4:L:209:ILE:HG22	4:L:210:ARG:N	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	668/747 (89%)	613 (92%)	39 (6%)	16 (2%)	6 33
1	B	662/747 (89%)	589 (89%)	54 (8%)	19 (3%)	4 29
1	C	666/747 (89%)	616 (92%)	37 (6%)	13 (2%)	7 38
1	D	663/747 (89%)	601 (91%)	52 (8%)	10 (2%)	10 46
1	E	658/747 (88%)	603 (92%)	42 (6%)	13 (2%)	7 38
1	F	644/747 (86%)	585 (91%)	46 (7%)	13 (2%)	7 38
2	G	284/297 (96%)	227 (80%)	47 (16%)	10 (4%)	3 25
2	H	284/297 (96%)	230 (81%)	44 (16%)	10 (4%)	3 25
2	I	284/297 (96%)	229 (81%)	41 (14%)	14 (5%)	2 20
2	J	284/297 (96%)	229 (81%)	45 (16%)	10 (4%)	3 25
3	K	59/63 (94%)	56 (95%)	2 (3%)	1 (2%)	9 42
4	L	64/67 (96%)	58 (91%)	5 (8%)	1 (2%)	9 44
5	M	127/198 (64%)	119 (94%)	7 (6%)	1 (1%)	19 60
All	All	5347/5998 (89%)	4755 (89%)	461 (9%)	131 (2%)	9 33

All (131) 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	320	SER
1	A	333	ILE
1	A	498	ASP
1	A	504	MET
1	B	283	LYS
1	B	297	GLU
1	B	318	ALA
1	B	395	ILE
1	B	439	ALA
1	B	497	GLU
1	B	502	TYR
1	C	297	GLU
1	C	318	ALA
1	C	497	GLU
1	C	498	ASP
1	C	578	GLU
1	D	283	LYS
1	D	318	ALA
1	D	489	LYS
1	E	283	LYS
1	E	297	GLU
1	E	318	ALA
1	E	439	ALA
1	E	489	LYS
1	F	12	PRO
1	F	283	LYS
1	F	297	GLU
1	F	318	ALA
1	F	439	ALA
2	H	58	TRP
2	H	76	GLN
2	I	58	TRP
2	I	77	SER
2	I	219	LEU
2	J	58	TRP
2	J	218	MET
2	J	235	PHE
2	G	58	TRP

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Mol	Chain	Res	Type
1	A	397	LEU
1	B	12	PRO
1	B	188	ALA
1	C	12	PRO
1	C	89	LYS
1	C	293	LYS
1	C	610	ASP
1	D	12	PRO
1	E	507	ILE
1	F	189	GLU
2	H	33	GLY
2	H	79	HIS
2	I	136	VAL
2	I	218	MET
2	I	254	GLN
2	I	256	VAL
2	G	76	GLN
3	K	30	ARG
4	L	209	ILE
1	A	12	PRO
1	A	241	PRO
1	A	264	CYS
1	B	241	PRO
1	B	293	LYS
1	B	546	HIS
1	C	87	LYS
1	C	241	PRO
1	D	87	LYS
1	D	293	LYS
1	E	87	LYS
1	E	241	PRO
1	E	293	LYS
1	F	241	PRO
1	F	293	LYS
2	H	159	SER
2	H	240	GLU
2	H	256	VAL
2	I	78	LYS
2	J	158	ASN
2	J	159	SER
2	G	79	HIS
2	G	156	GLU

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

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Mol	Chain	Res	Type
1	E	12	PRO
2	H	34	GLY
1	A	53	PRO
2	J	34	GLY
1	C	3	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	514/638 (81%)	512 (100%)	2 (0%)	91 94
1	B	514/638 (81%)	510 (99%)	4 (1%)	81 89
1	C	513/638 (80%)	511 (100%)	2 (0%)	91 94
1	D	509/638 (80%)	507 (100%)	2 (0%)	91 94
1	E	518/638 (81%)	515 (99%)	3 (1%)	86 92
1	F	513/638 (80%)	510 (99%)	3 (1%)	86 92
2	G	235/244 (96%)	235 (100%)	0	100 100
2	H	235/244 (96%)	234 (100%)	1 (0%)	91 94
2	I	233/244 (96%)	233 (100%)	0	100 100
2	J	235/244 (96%)	235 (100%)	0	100 100
3	K	52/54 (96%)	50 (96%)	2 (4%)	33 57
4	L	60/61 (98%)	60 (100%)	0	100 100
5	M	111/171 (65%)	111 (100%)	0	100 100
All	All	4242/5090 (83%)	4223 (100%)	19 (0%)	91 94

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	305	LEU
1	A	322	LEU
1	B	240	PHE

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Mol	Chain	Res	Type
1	B	305	LEU
1	B	322	LEU
1	B	327	PHE
1	C	305	LEU
1	C	676	LEU
1	D	305	LEU
1	D	311	GLU
1	E	305	LEU
1	E	322	LEU
1	E	549	LYS
1	F	305	LEU
1	F	322	LEU
1	F	536	LEU
2	H	251	HIS
3	K	45	ILE
3	K	68	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	353	GLN
1	B	128	GLN
1	B	526	GLN
1	B	561	ASN
1	B	624	GLN
1	C	319	ASN
1	D	20	ASN
1	D	313	GLN
1	D	319	ASN
1	D	352	ASN
1	D	353	GLN
1	D	527	GLN
1	D	675	GLN
1	E	170	GLN
1	E	313	GLN
1	E	319	ASN
1	E	352	ASN
1	E	527	GLN
1	E	659	ASN
1	E	666	HIS
1	F	456	HIS
1	F	527	GLN

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Mol	Chain	Res	Type
2	H	72	HIS
2	H	124	HIS
2	H	147	GLN
2	H	162	ASN
2	J	50	ASN
2	J	124	HIS
2	J	147	GLN
2	J	213	HIS
2	G	50	ASN
2	G	72	HIS
3	K	34	GLN
4	L	199	HIS
4	L	213	HIS
4	L	226	GLN
5	M	53	GLN
5	M	65	ASN
5	M	77	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

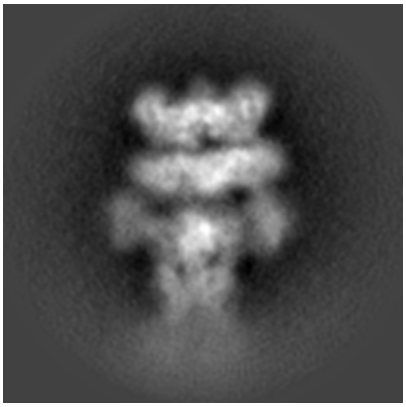
6 Map visualisation

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

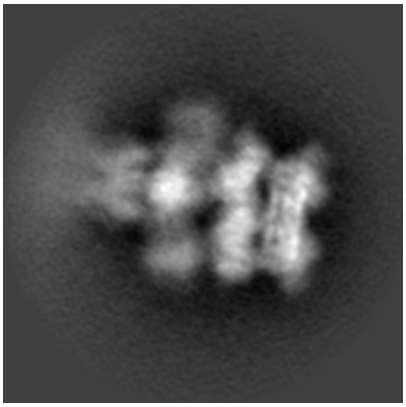
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

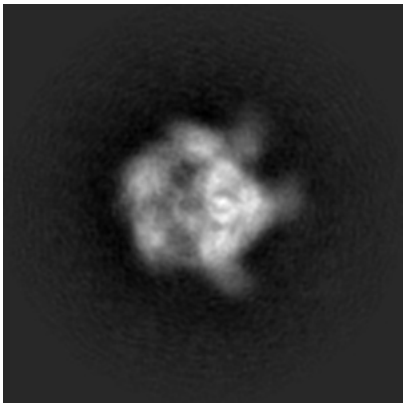
6.1.1 Primary map



X



Y

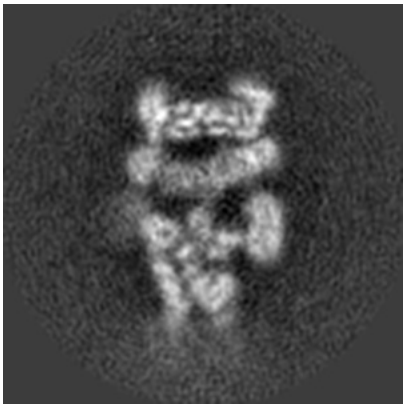


Z

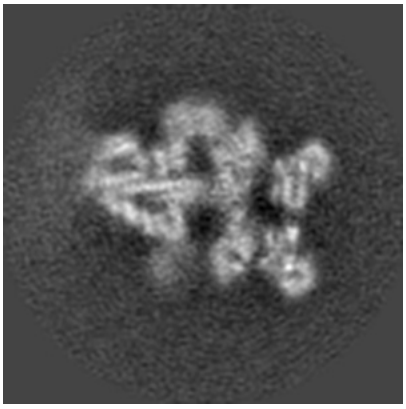
The images above show the map projected in three orthogonal directions.

6.2 Central slices

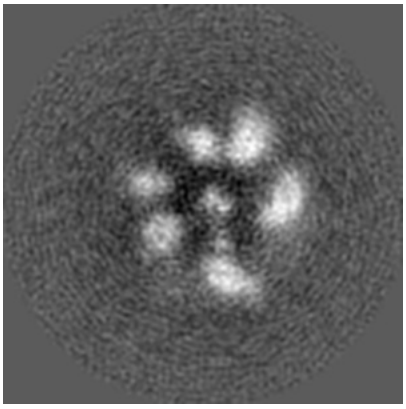
6.2.1 Primary map



X Index: 64



Y Index: 64



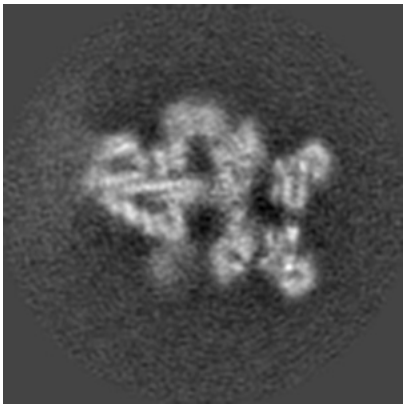
Z Index: 64

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

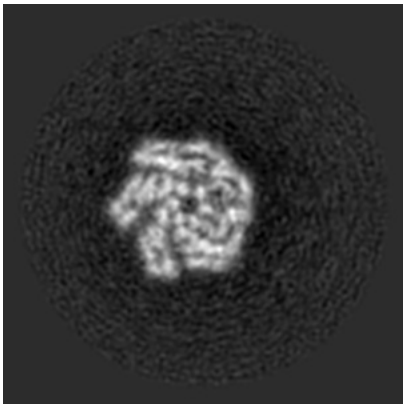
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 70



Y Index: 64

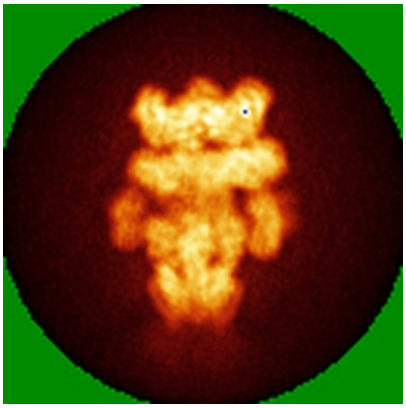


Z Index: 93

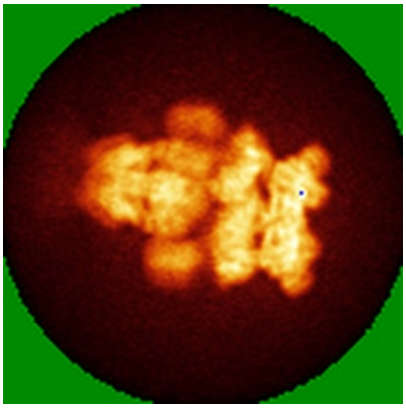
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

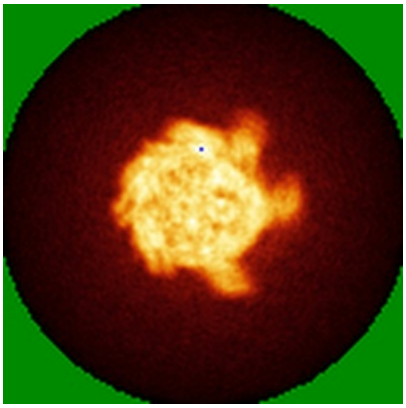
6.4.1 Primary map



X



Y

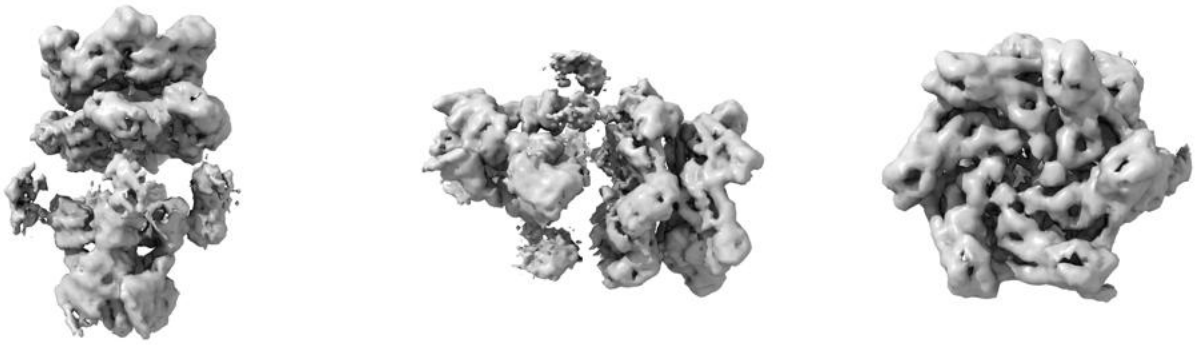


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

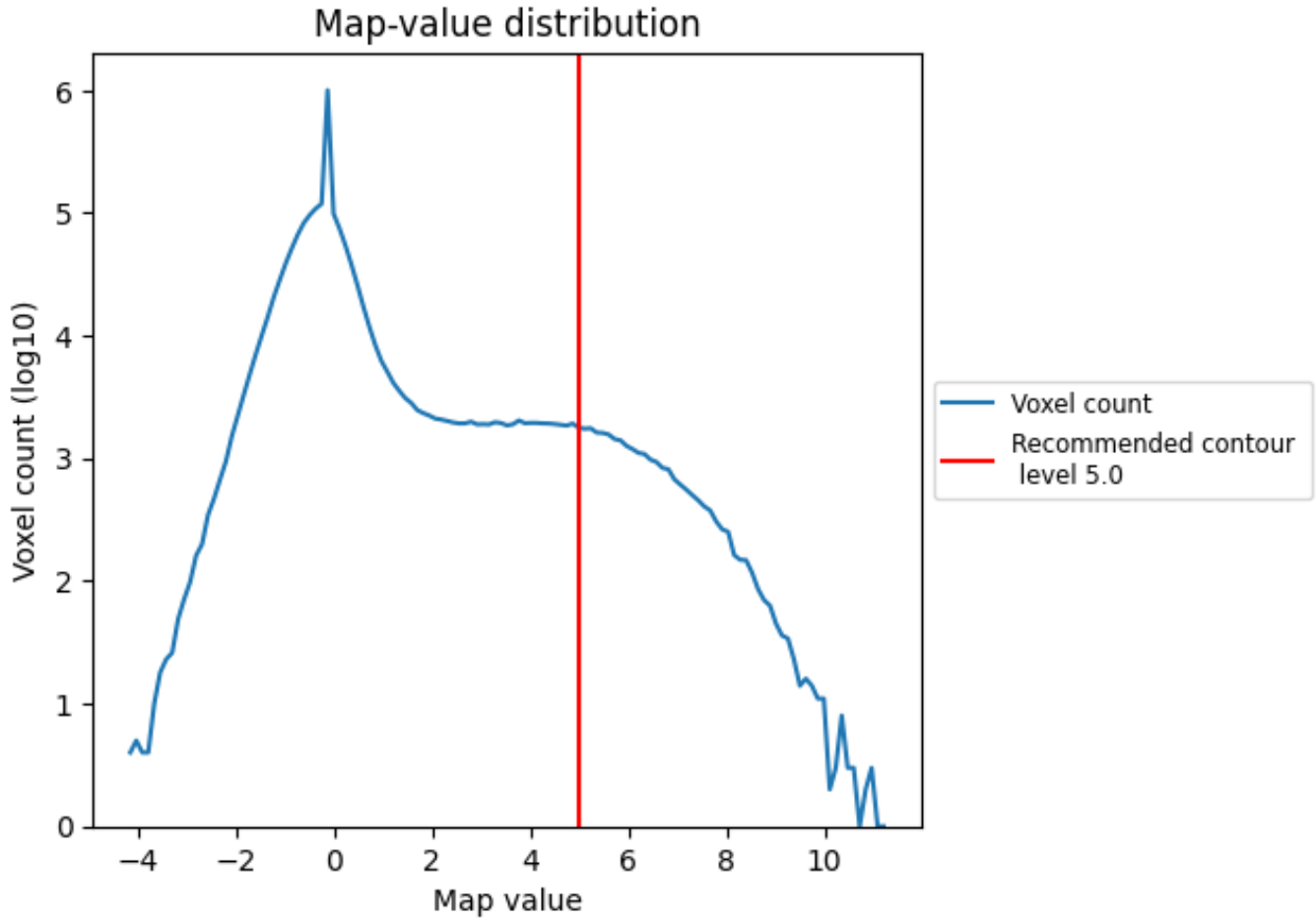
6.6 Mask visualisation (i)

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

7 Map analysis

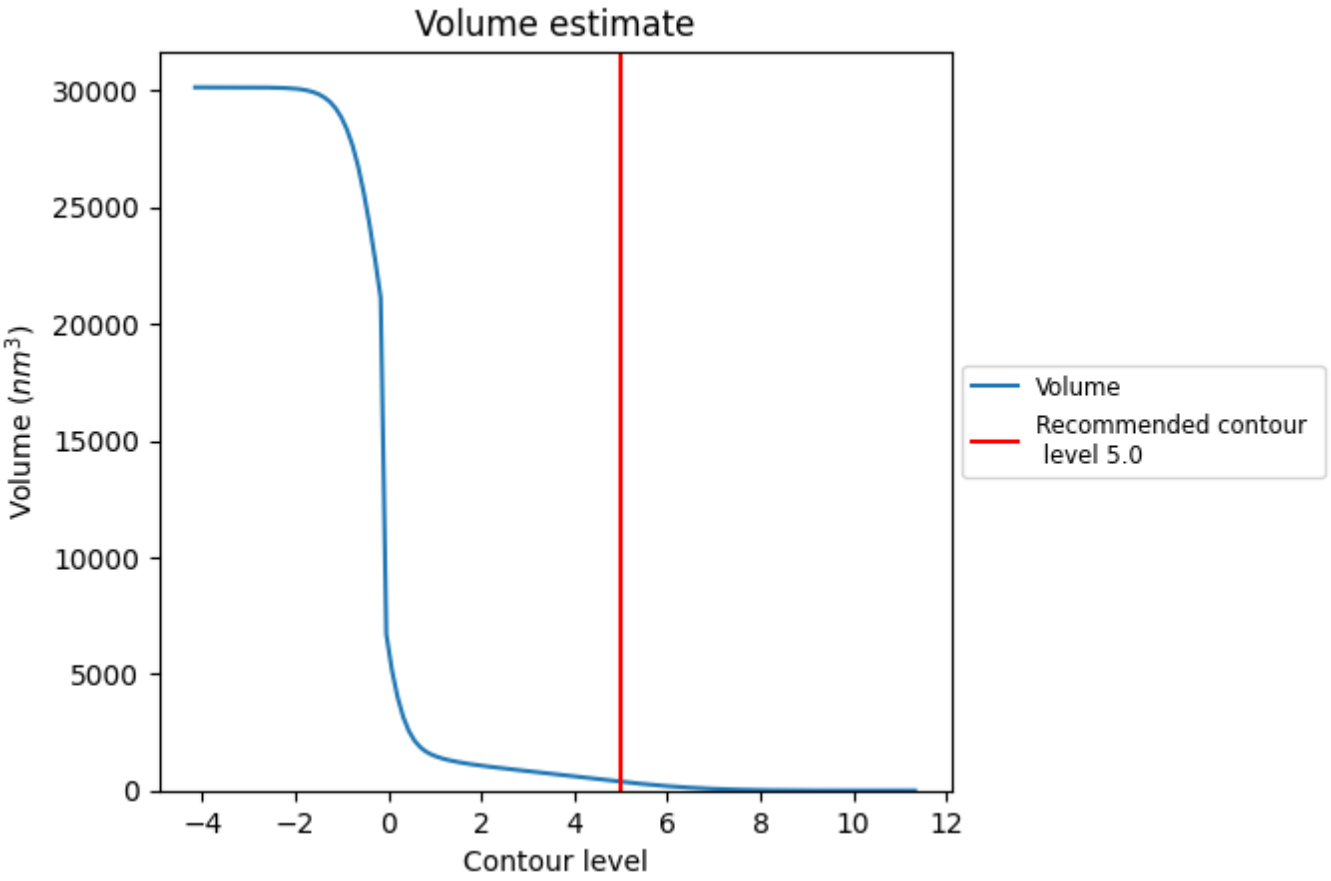
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

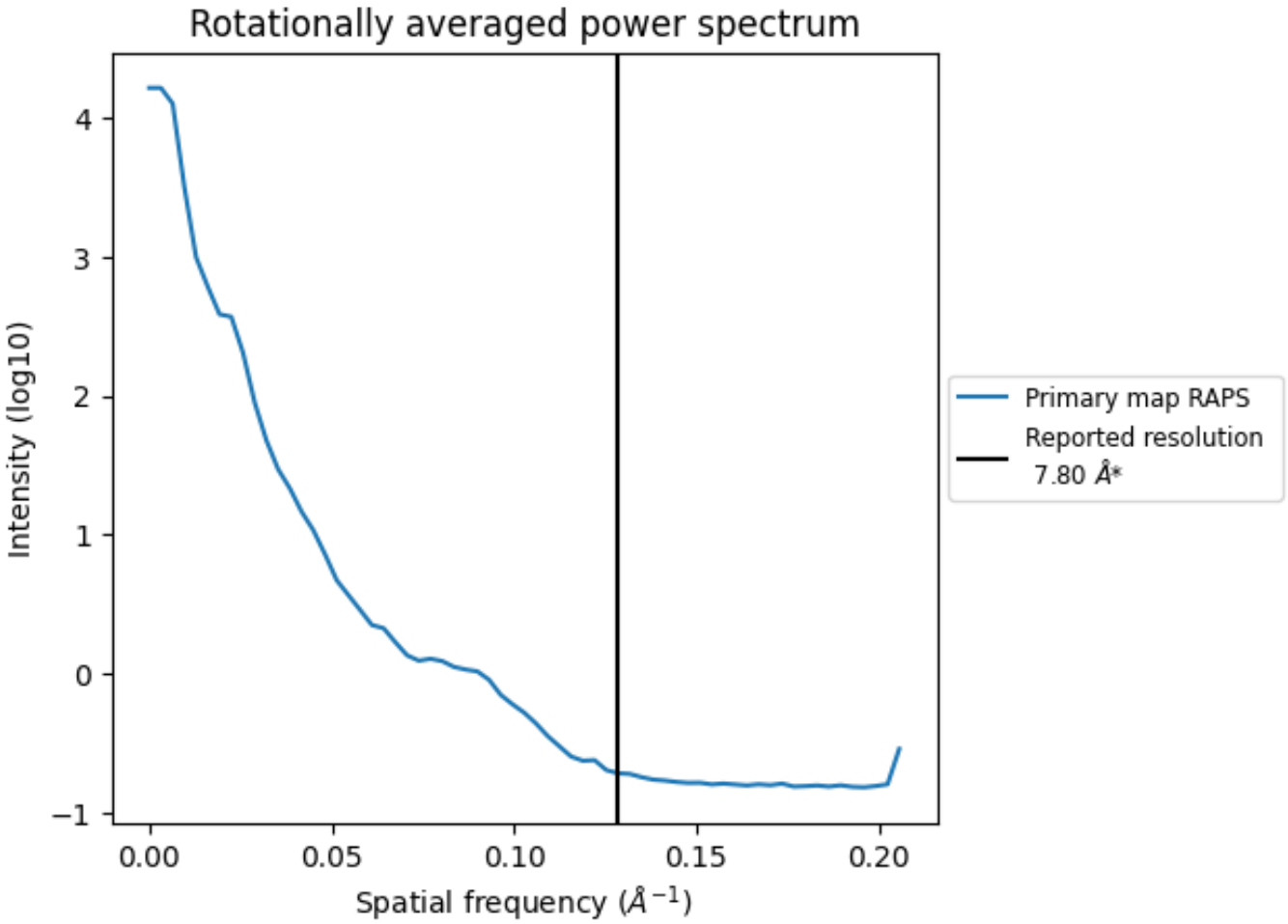
7.2 Volume estimate (i)



The volume at the recommended contour level is 379 nm^3; this corresponds to an approximate mass of 342 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.128 $Å^{-1}$

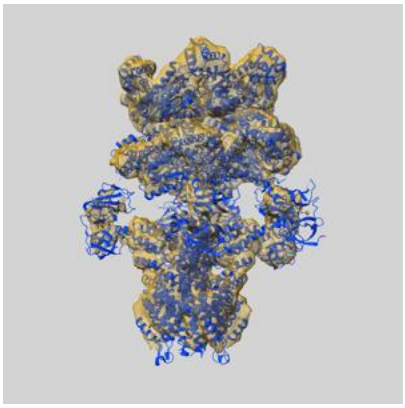
8 Fourier-Shell correlation

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

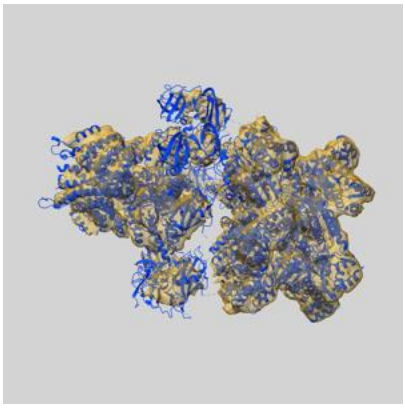
9 Map-model fit

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

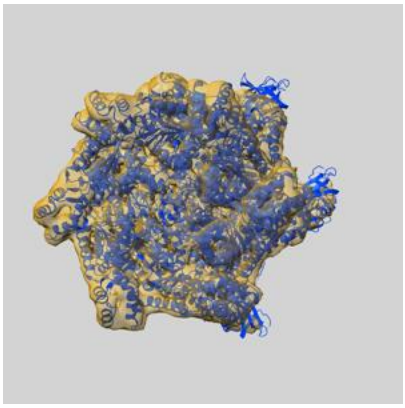
9.1 Map-model overlay



X



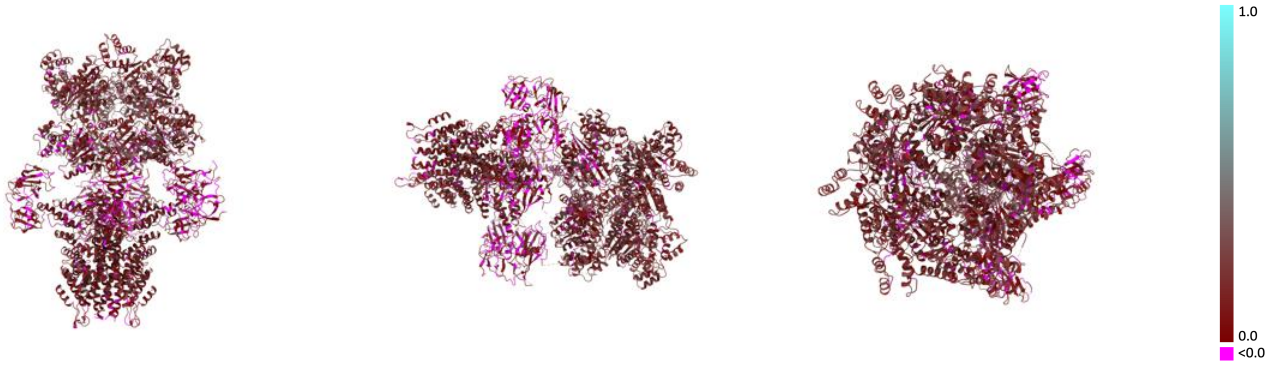
Y



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.

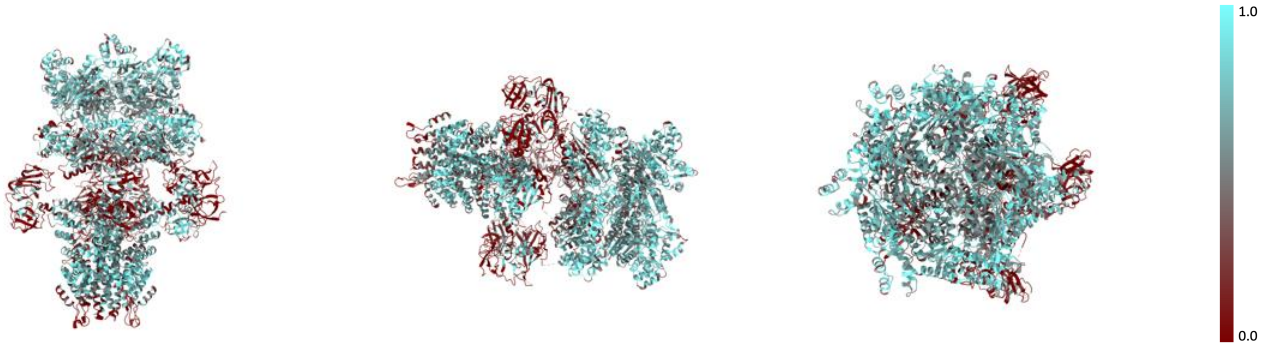
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

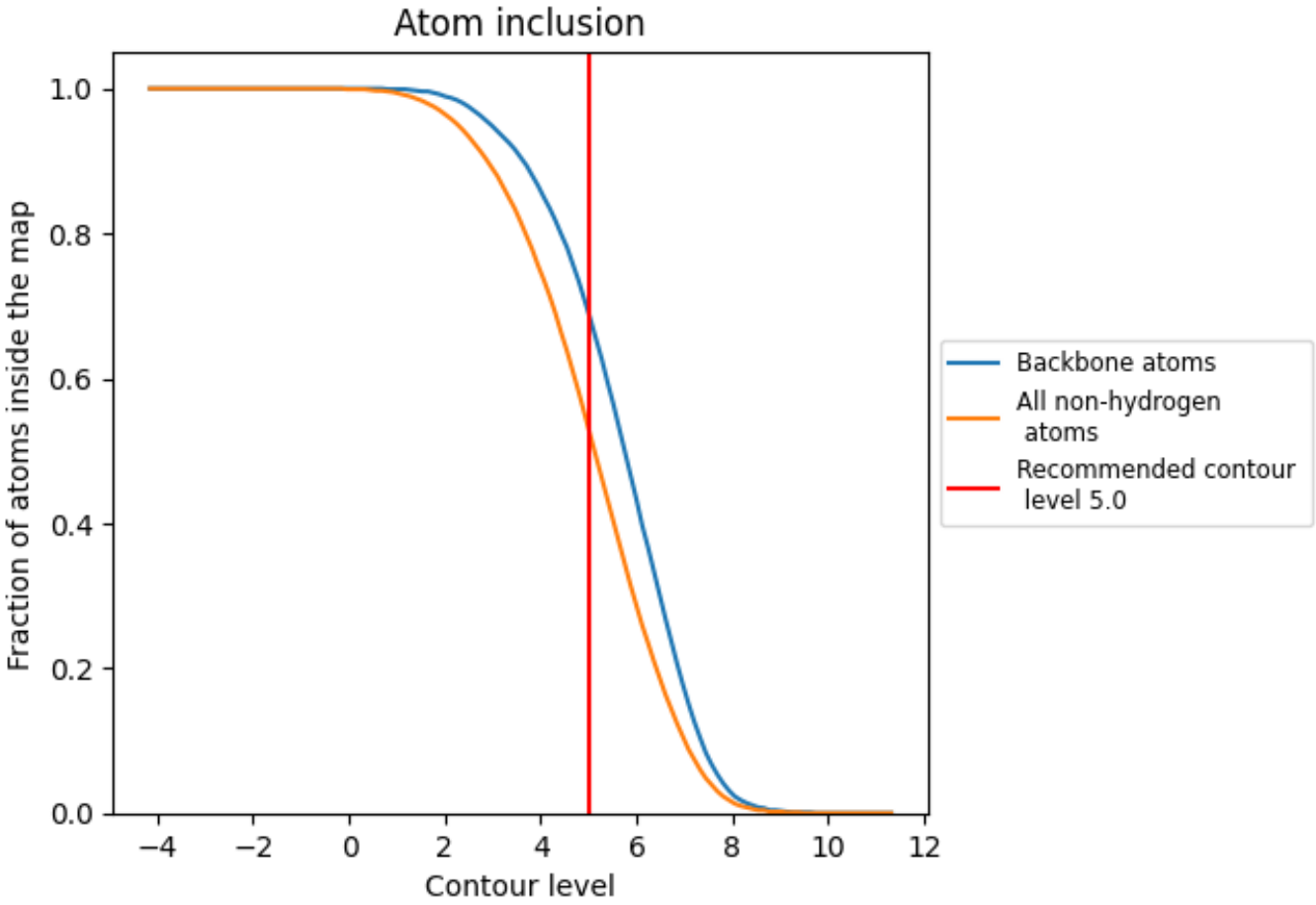
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (5.0).

9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 53% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (5.0) and Q-score for the entire model and for each chain.

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