



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 09:15 AM UTC

PDB ID : 8JFK / pdb_00008jfk
EMDB ID : EMD-36212
Title : PhK holoenzyme in inactive state, muscle isoform
Authors : Yang, X.K.; Xiao, J.Y.
Deposited on : 2023-05-18
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

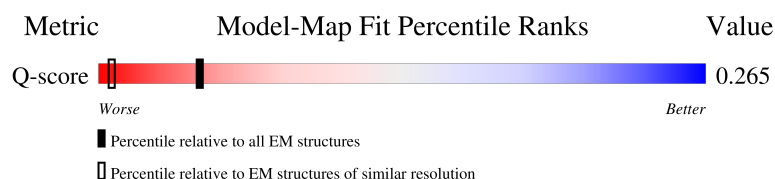
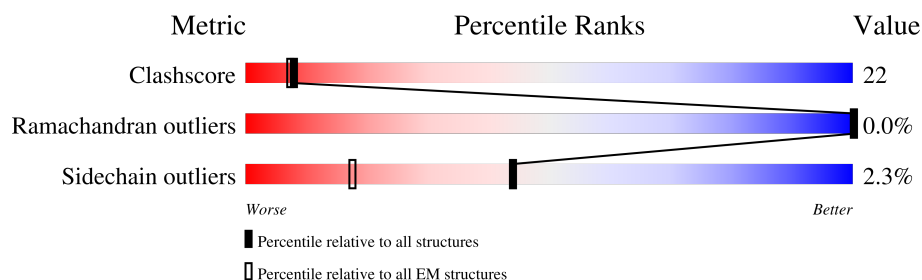
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.90 Å.

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



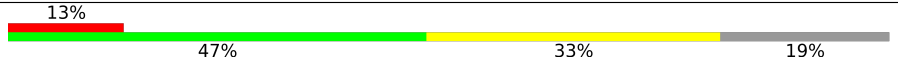
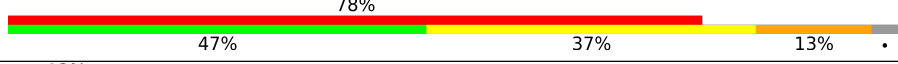
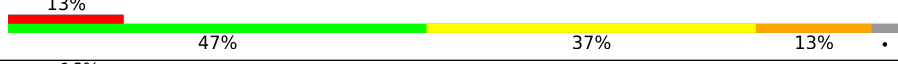
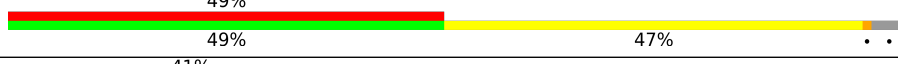
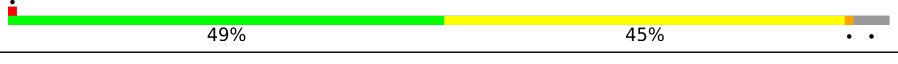
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13054 (2.40 - 3.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	1093	
1	F	1093	
1	J	1093	
1	N	1093	

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Mol	Chain	Length	Quality of chain
2	A	1223	
2	E	1223	
2	I	1223	
2	M	1223	
3	D	149	
3	H	149	
3	L	149	
3	P	149	
4	C	387	
4	G	387	
4	K	387	
4	O	387	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	FAR	A	1301	-	X	X	-
5	FAR	B	1101	-	-	X	-
5	FAR	E	1301	-	X	X	-
5	FAR	F	1101	-	-	X	-
5	FAR	I	1301	-	X	X	-
5	FAR	J	1101	-	-	X	-
5	FAR	M	1301	-	X	-	-
5	FAR	N	1101	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 81428 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 Phosphorylase b kinase regulatory subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	1033	Total	C	N	O	S	0	0
			8342	5338	1424	1543	37		
1	N	1033	Total	C	N	O	S	0	0
			8342	5338	1424	1543	37		
1	J	1033	Total	C	N	O	S	0	0
			8342	5338	1424	1543	37		
1	F	1033	Total	C	N	O	S	0	0
			8342	5338	1424	1543	37		

- Molecule 2 is a protein called Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	986	Total	C	N	O	S	0	0
			7801	4976	1319	1460	46		
2	A	986	Total	C	N	O	S	0	0
			7801	4976	1319	1460	46		
2	I	986	Total	C	N	O	S	0	0
			7801	4976	1319	1460	46		
2	E	986	Total	C	N	O	S	0	0
			7801	4976	1319	1460	46		

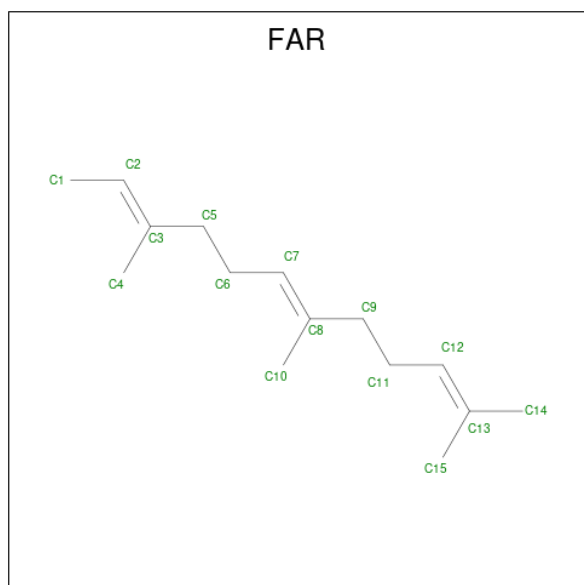
- Molecule 3 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	145	Total	C	N	O	S	0	0
			1143	701	184	249	9		
3	H	145	Total	C	N	O	S	0	0
			1143	701	184	249	9		
3	L	145	Total	C	N	O	S	0	0
			1143	701	184	249	9		
3	P	145	Total	C	N	O	S	0	0
			1143	701	184	249	9		

- Molecule 4 is a protein called Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	371	Total	C	N	O	S	0	0
			3041	1951	525	550	15		
4	G	371	Total	C	N	O	S	0	0
			3041	1951	525	550	15		
4	K	371	Total	C	N	O	S	0	0
			3041	1951	525	550	15		
4	O	371	Total	C	N	O	S	0	0
			3041	1951	525	550	15		

- Molecule 5 is FARNESYL (CCD ID: FAR) (formula: C₁₅H₂₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms		AltConf
5	B	1	Total	C	0
			15	15	
5	M	1	Total	C	0
			15	15	
5	A	1	Total	C	0
			15	15	
5	N	1	Total	C	0
			15	15	
5	J	1	Total	C	0
			15	15	
5	I	1	Total	C	0
			15	15	

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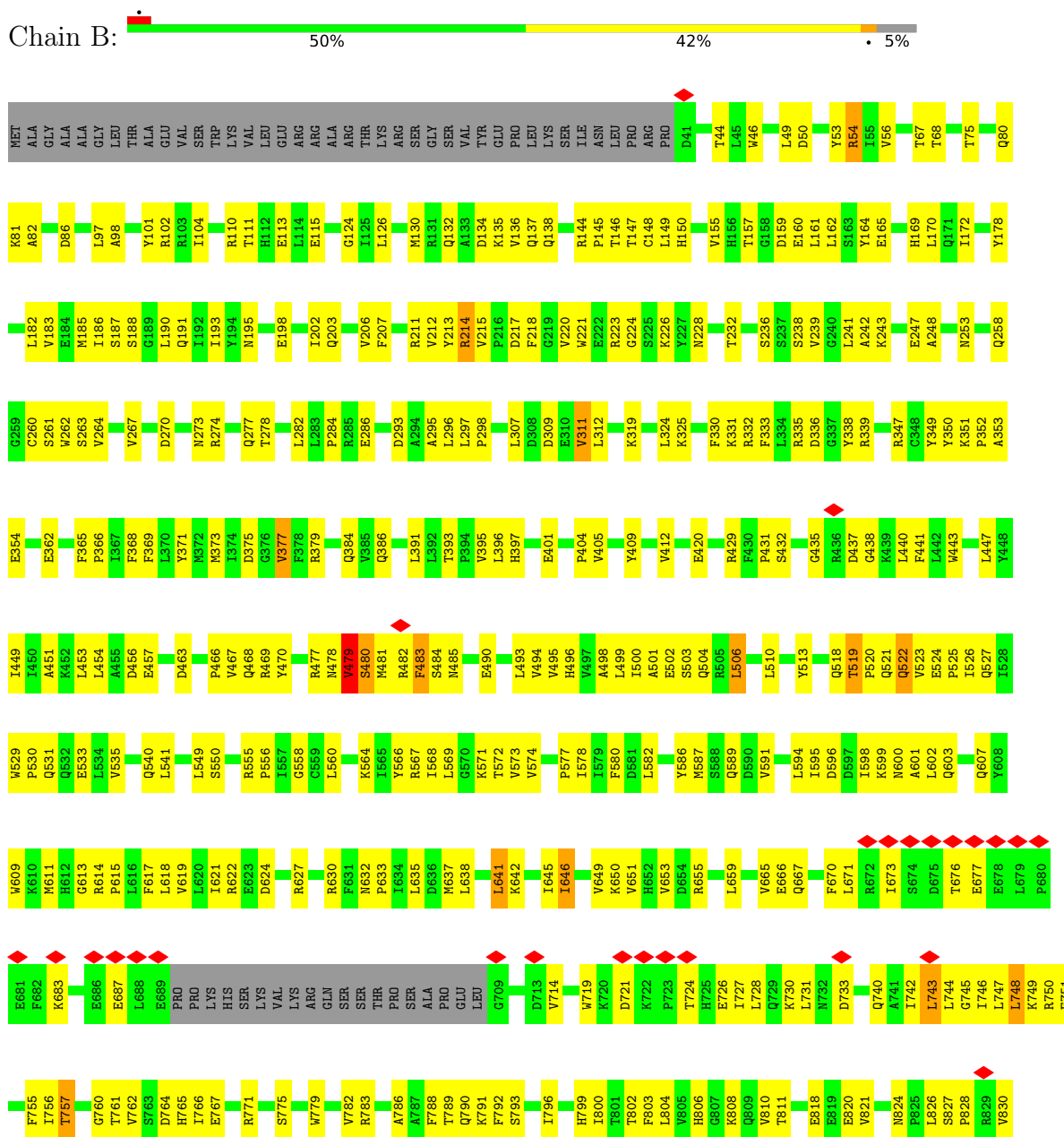
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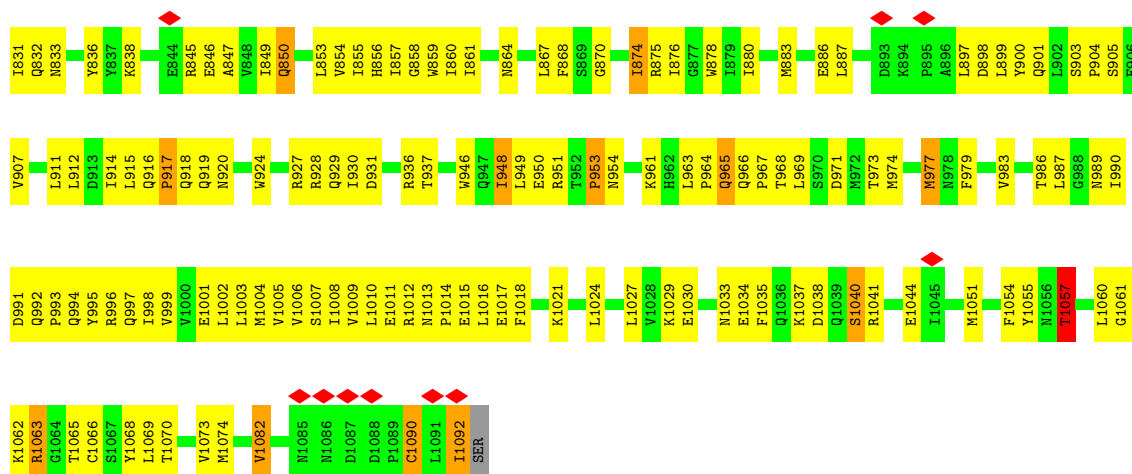
Mol	Chain	Residues	Atoms		AltConf
5	F	1	Total	C	0
			15	15	
5	E	1	Total	C	0
			15	15	

3 Residue-property plots

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

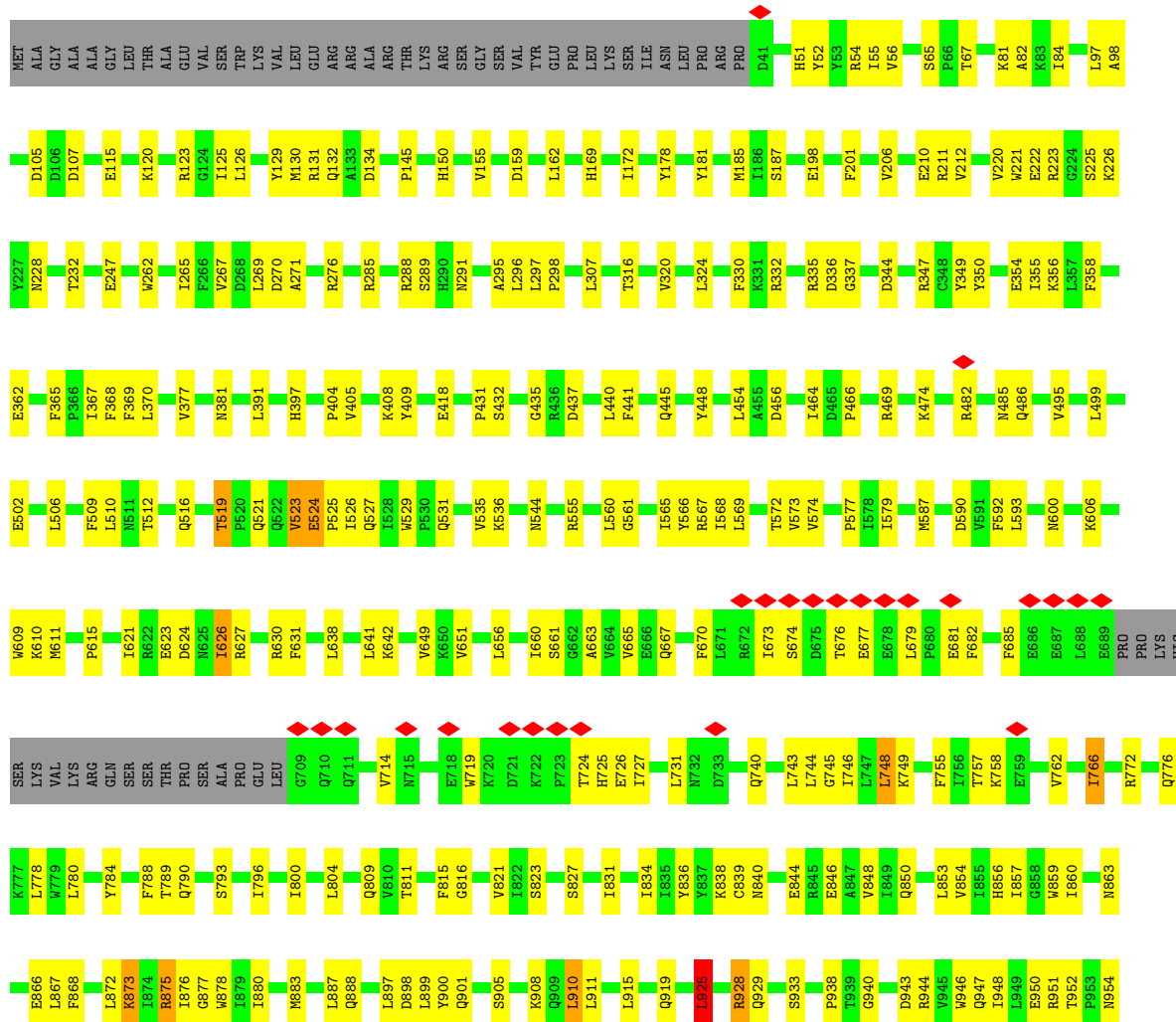
- Molecule 1: Phosphorylase b kinase regulatory subunit beta

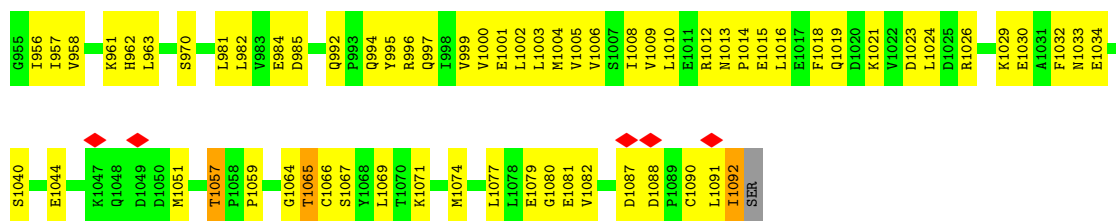




• Molecule 1: Phosphorylase b kinase regulatory subunit beta

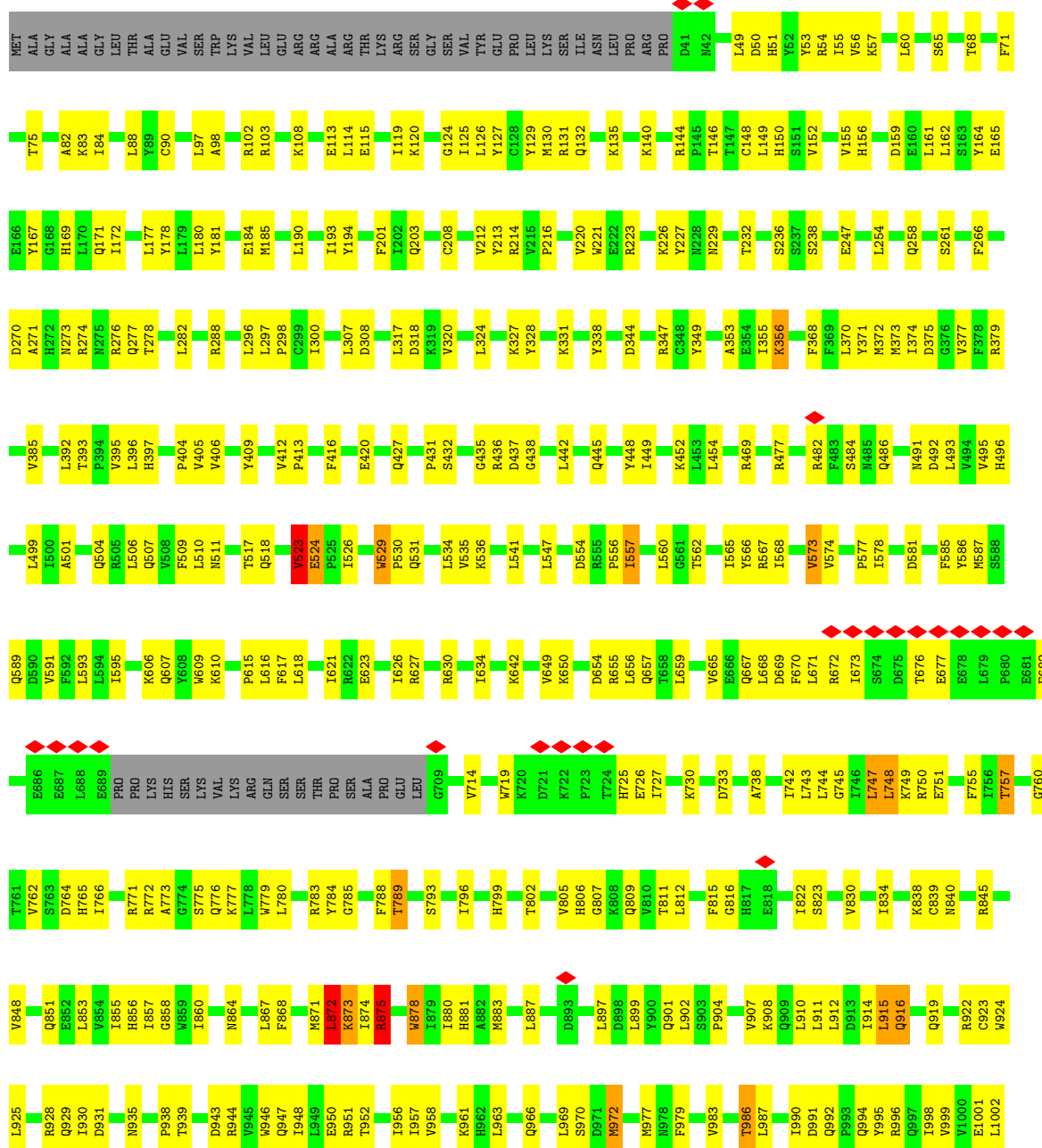
Chain N: 63% 30% 5%

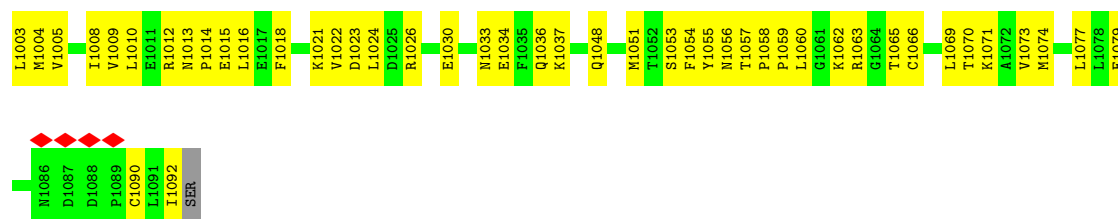




• Molecule 1: Phosphorylase b kinase regulatory subunit beta

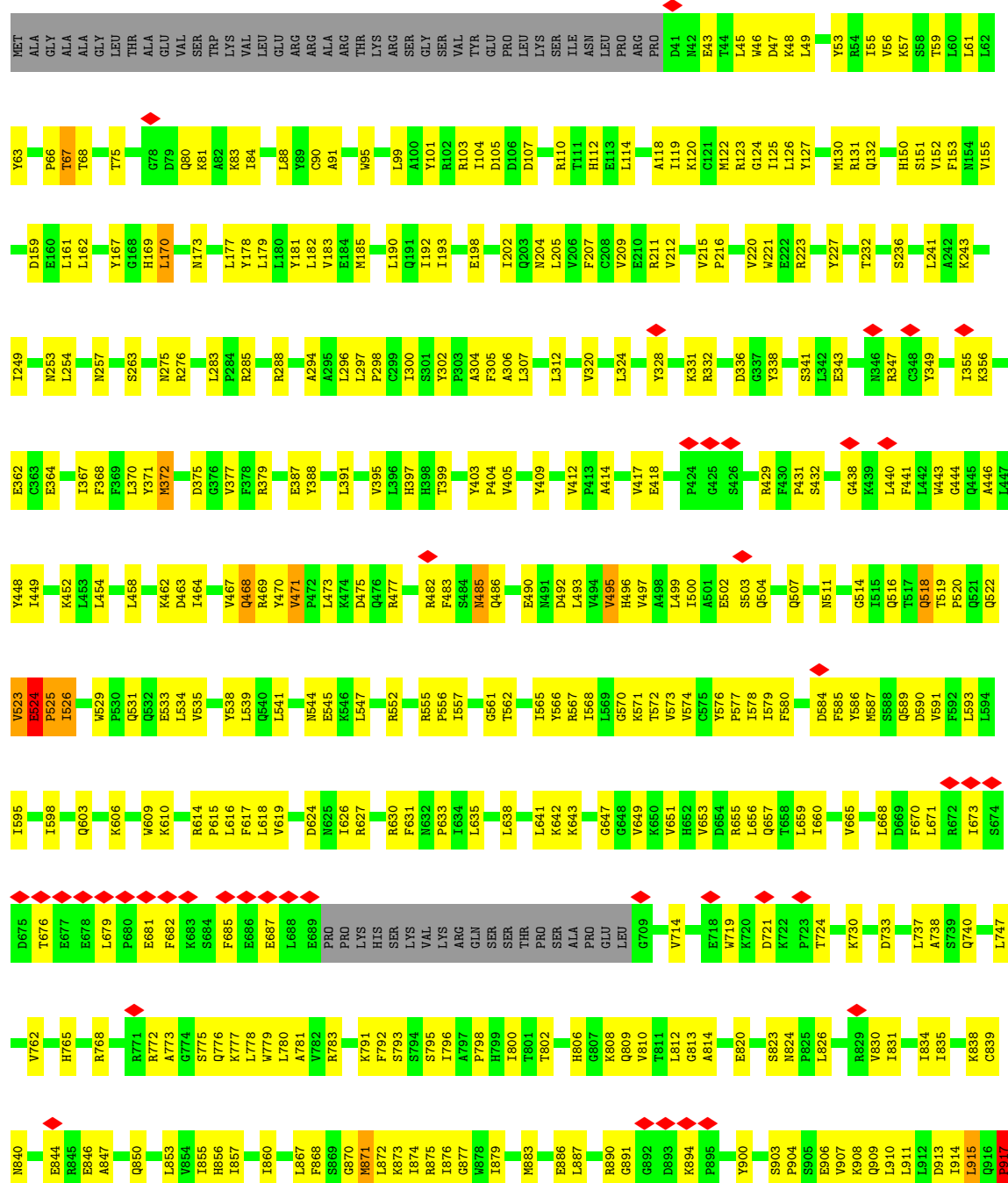
Chain J: 57% 36% 5%

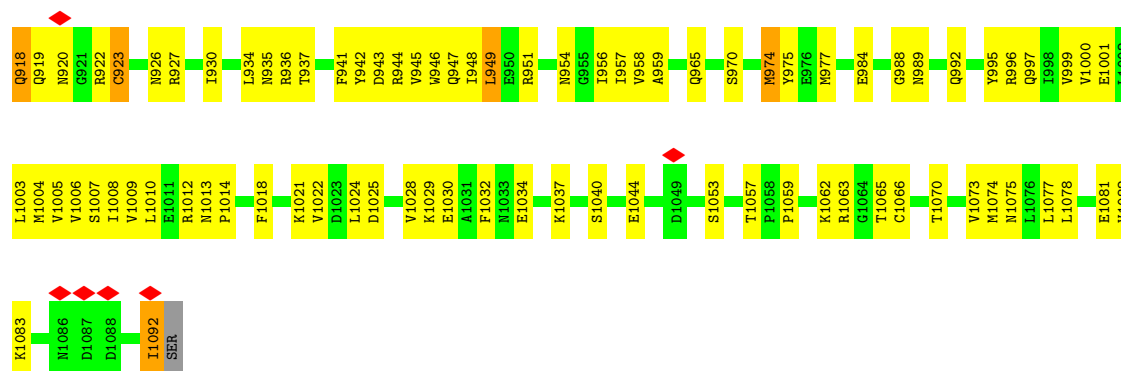




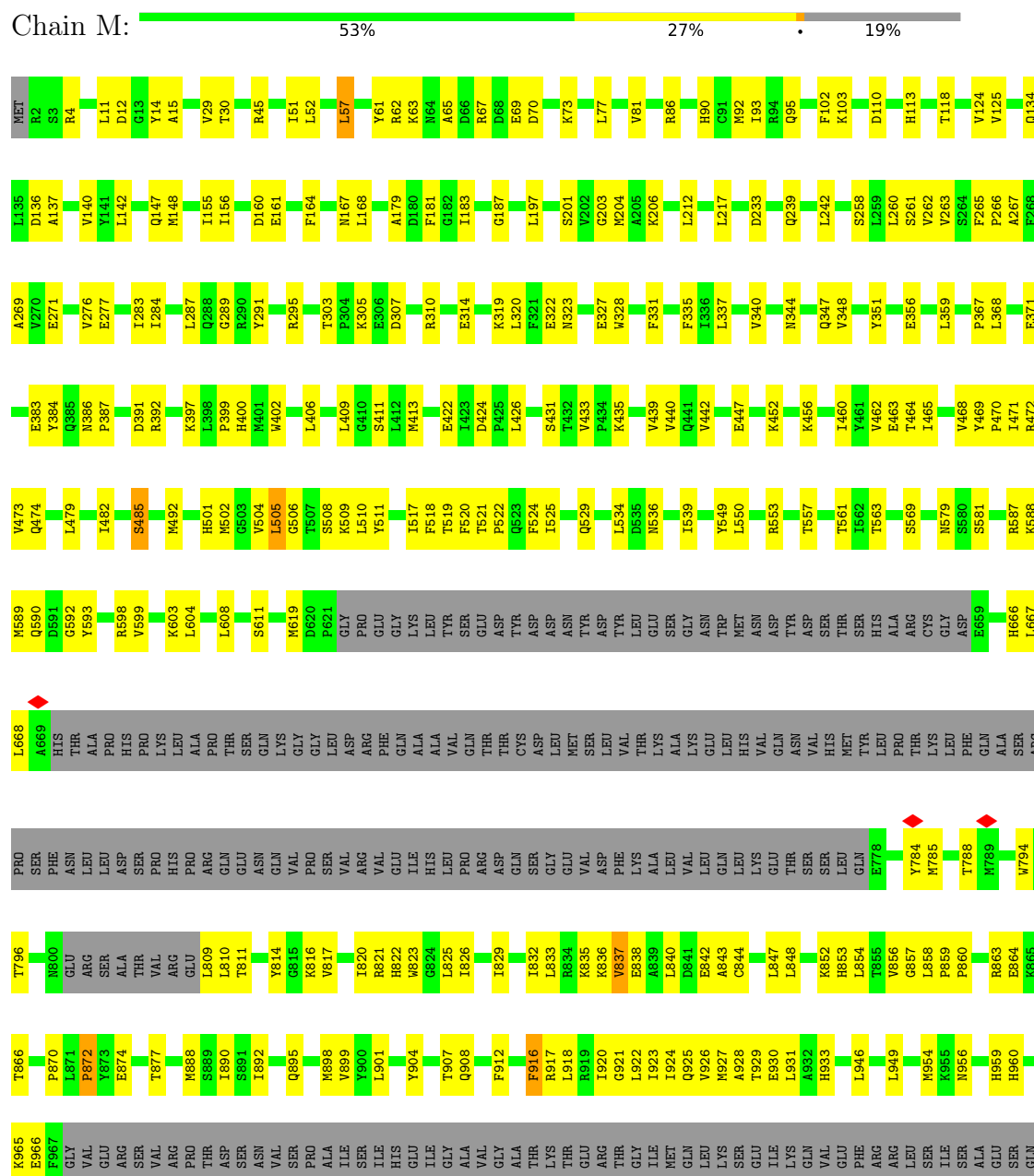
• Molecule 1: Phosphorylase b kinase regulatory subunit beta

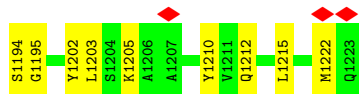
Chain F: 53% 40% 5%



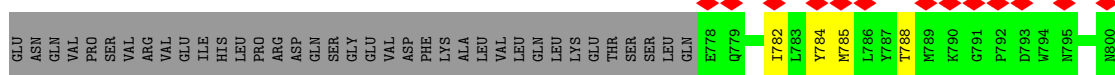
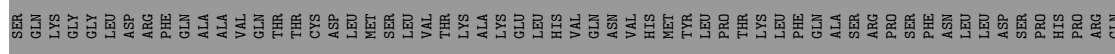
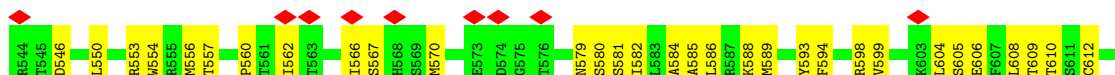
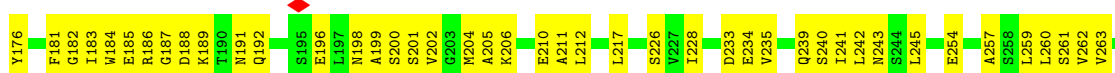
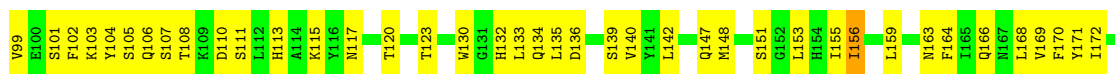
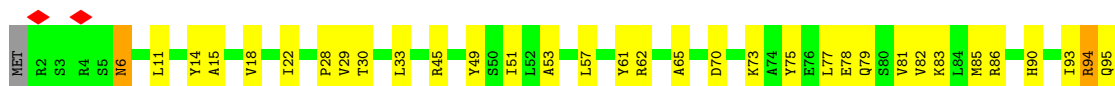


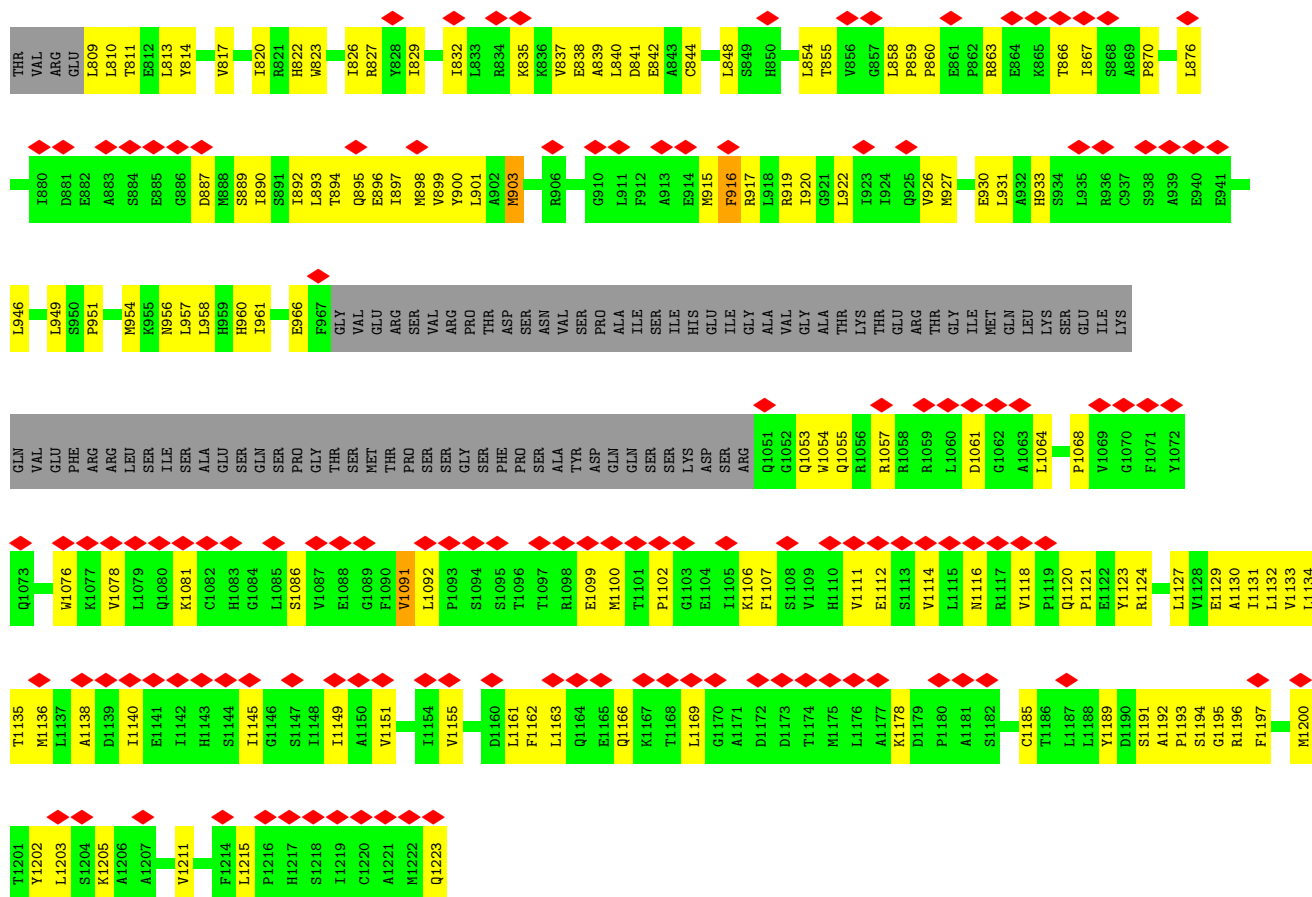
- Molecule 2: Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform



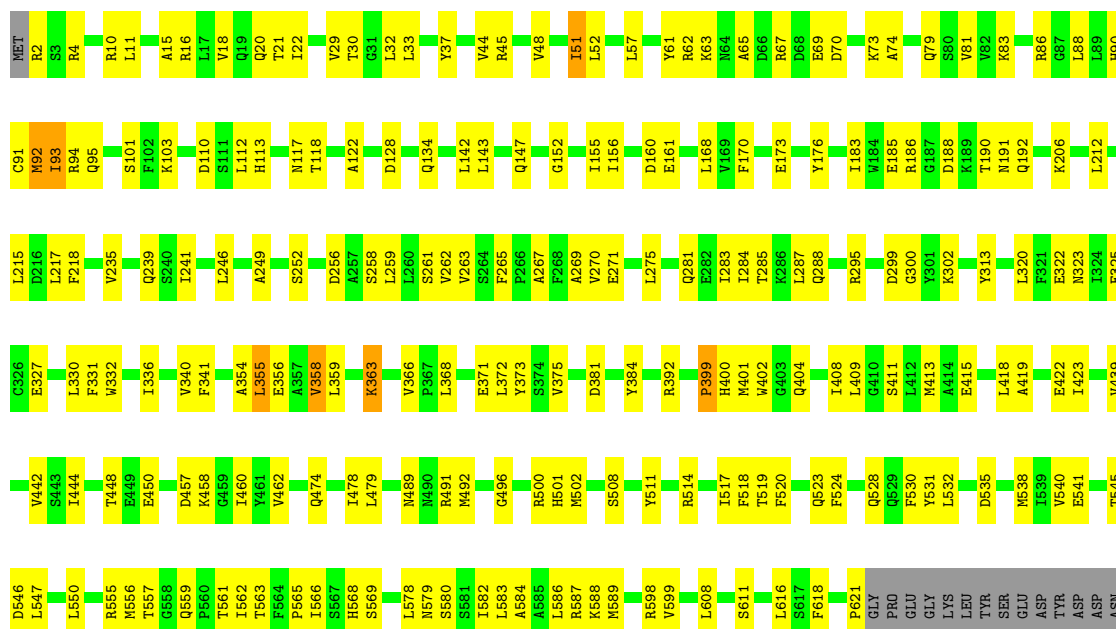


- Molecule 2: Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform

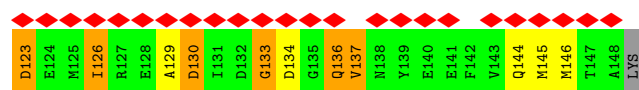




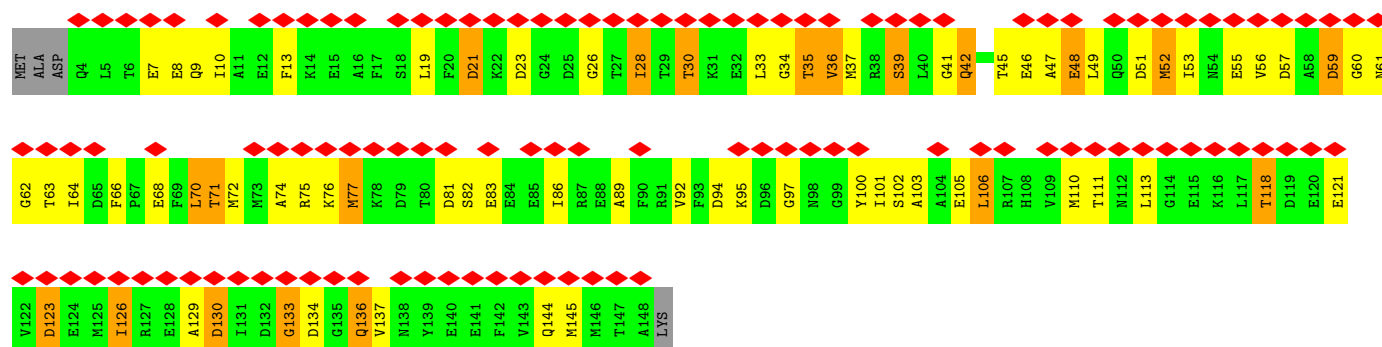
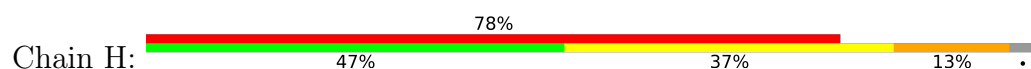
• Molecule 2: Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform



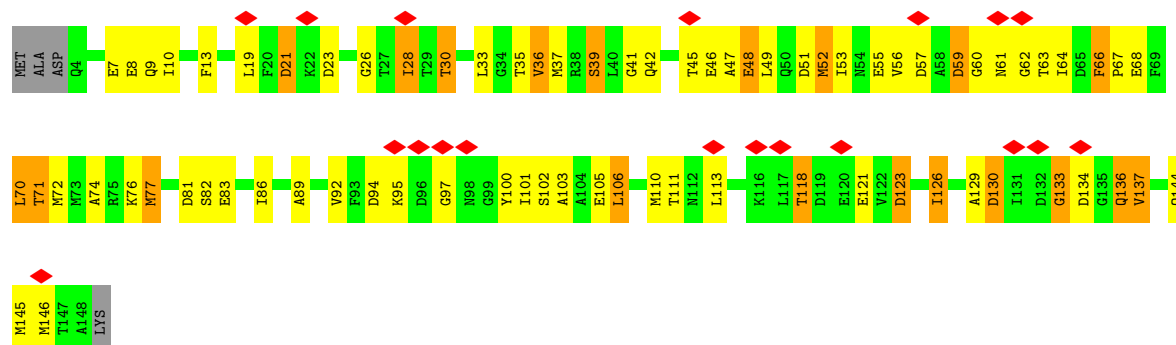




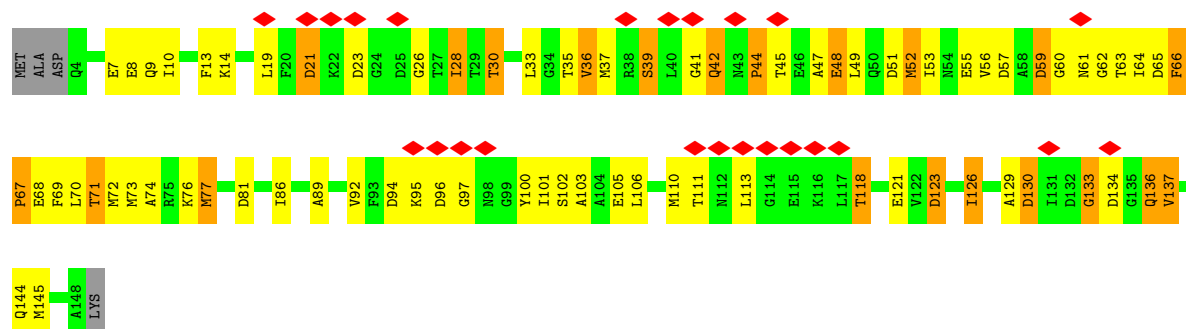
• Molecule 3: Calmodulin-1



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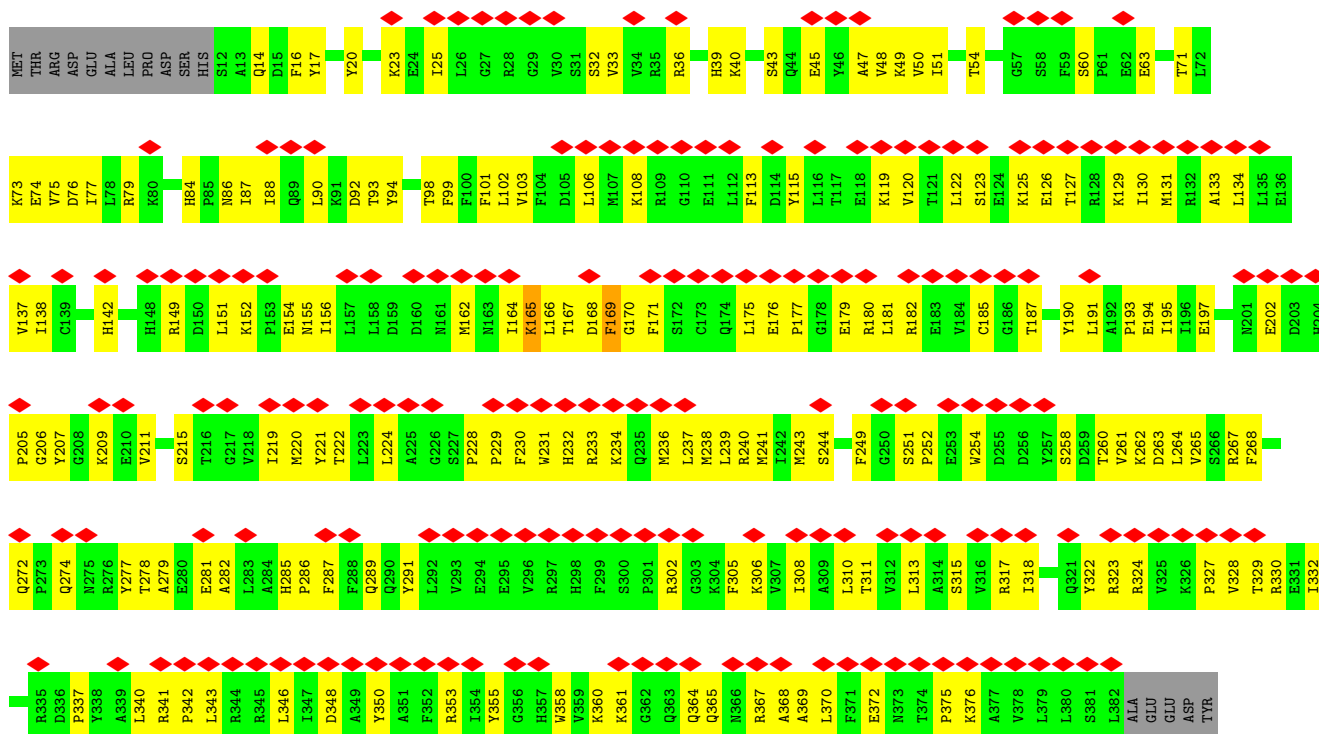


• Molecule 3: Calmodulin-1

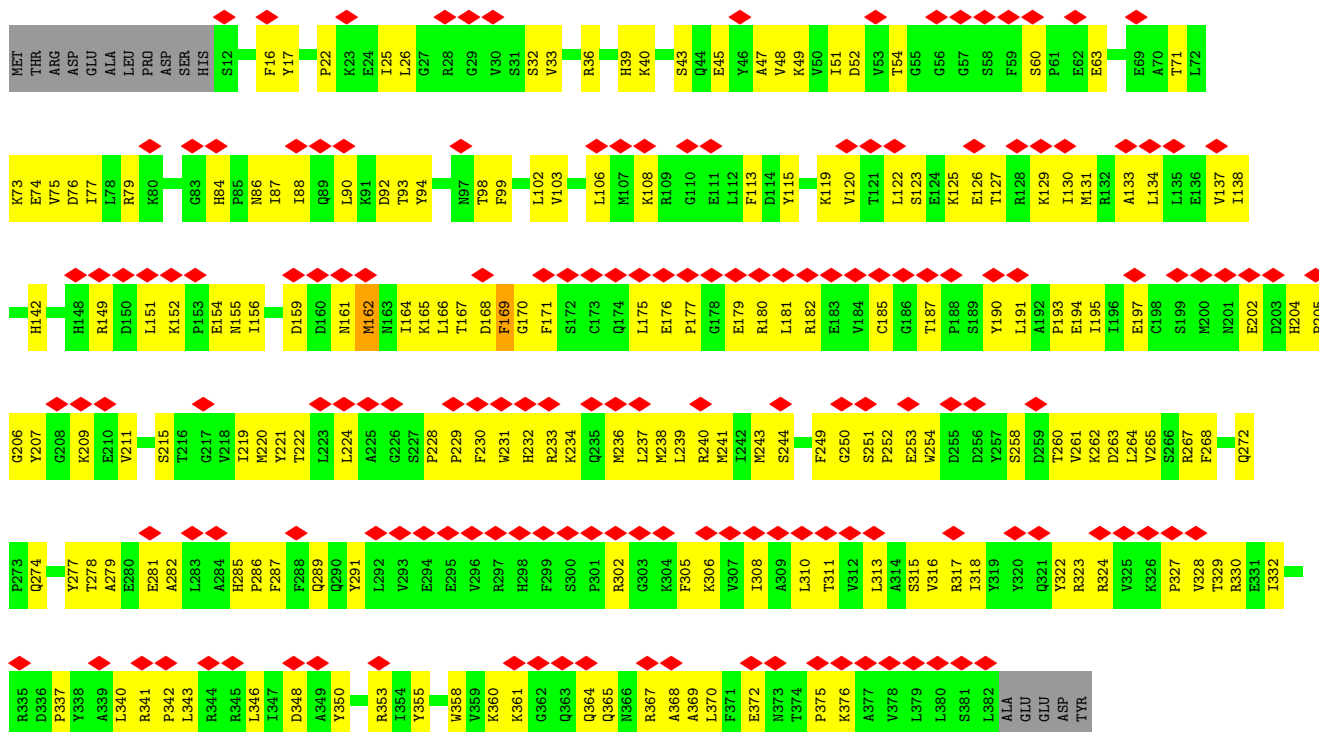
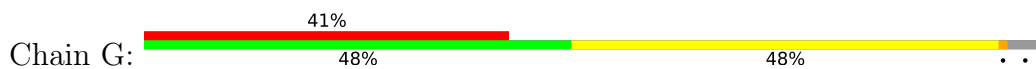


• Molecule 4: Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform

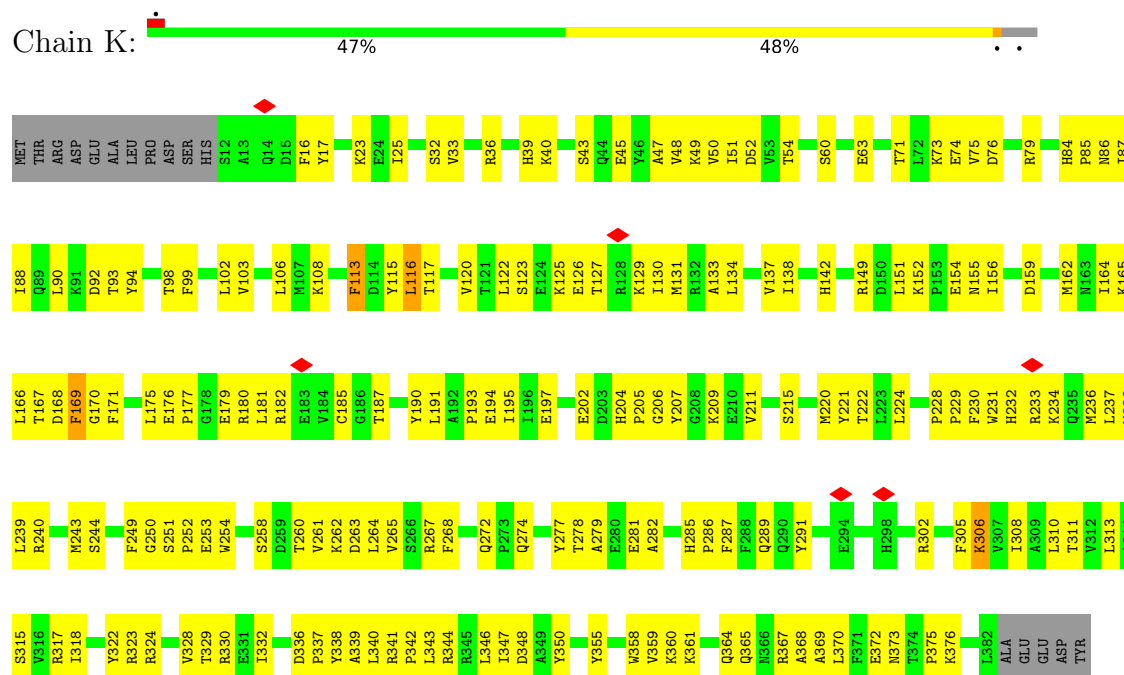




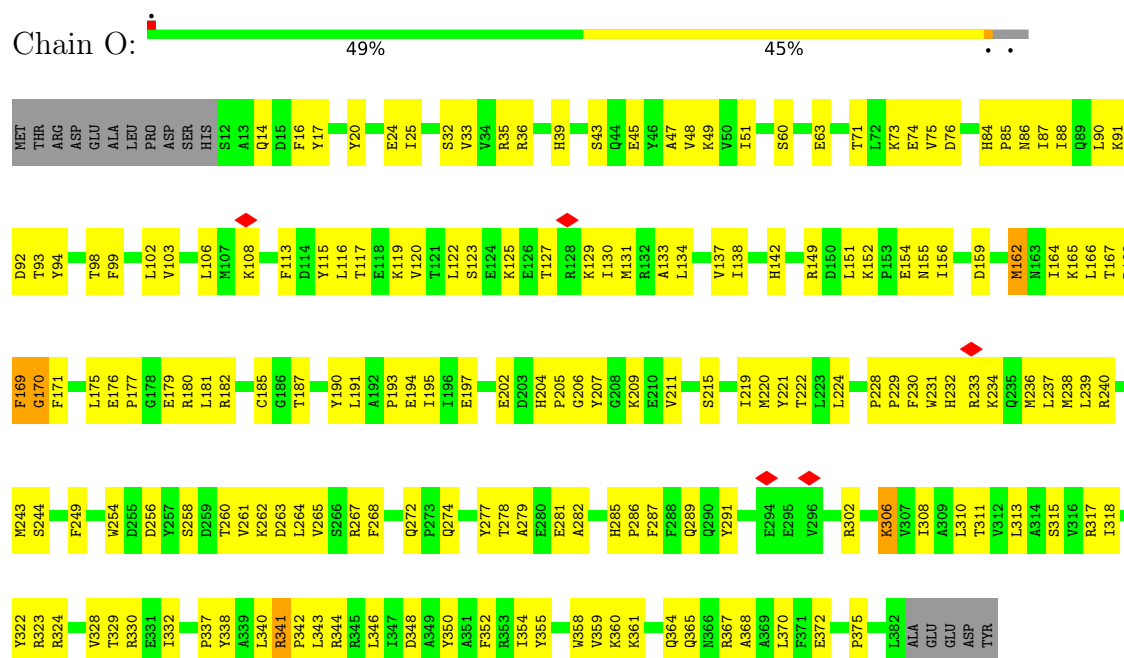
- Molecule 4: Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform



- Molecule 4: Phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform



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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	623973	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.085	Depositor
Minimum map value	-0.070	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.01	Depositor
Map size ($\text{\AA}$)	470.80002, 470.80002, 470.80002	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	B	0.52	11/8529 (0.1%)	0.74	33/11558 (0.3%)
1	F	0.34	2/8529 (0.0%)	0.57	16/11558 (0.1%)
1	J	0.38	4/8529 (0.0%)	0.56	14/11558 (0.1%)
1	N	0.32	3/8529 (0.0%)	0.47	5/11558 (0.0%)
2	A	0.19	0/7962	0.49	4/10785 (0.0%)
2	E	0.22	0/7962	0.46	1/10785 (0.0%)
2	I	0.24	2/7962 (0.0%)	0.49	10/10785 (0.1%)
2	M	0.20	0/7962	0.43	1/10785 (0.0%)
3	D	1.34	7/1155 (0.6%)	1.57	33/1551 (2.1%)
3	H	1.33	6/1155 (0.5%)	1.56	31/1551 (2.0%)
3	L	1.33	5/1155 (0.4%)	1.62	34/1551 (2.2%)
3	P	1.32	5/1155 (0.4%)	1.58	37/1551 (2.4%)
4	C	0.36	1/3112 (0.0%)	0.66	8/4209 (0.2%)
4	G	0.36	1/3112 (0.0%)	0.65	7/4209 (0.2%)
4	K	0.44	2/3112 (0.1%)	0.71	10/4209 (0.2%)
4	O	0.40	1/3112 (0.0%)	0.66	6/4209 (0.1%)
All	All	0.45	50/83032 (0.1%)	0.66	250/112412 (0.2%)

All (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	94	ARG	CA-C	-7.94	1.41	1.52
1	B	470	TYR	CA-C	-7.51	1.43	1.52
2	I	83	LYS	CA-C	-7.01	1.44	1.52
4	K	115	TYR	CA-C	-6.86	1.44	1.52
1	B	479	VAL	CA-C	-6.47	1.45	1.52
1	J	878	TRP	CA-C	-6.24	1.44	1.52
1	B	483	PHE	N-CA	-6.24	1.38	1.46
3	D	33	LEU	CA-C	-5.76	1.45	1.52
3	P	33	LEU	CA-C	-5.76	1.45	1.52
3	L	33	LEU	CA-C	-5.75	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	33	LEU	CA-C	-5.72	1.45	1.52
1	B	480	SER	CA-C	-5.66	1.45	1.52
1	N	925	LEU	CA-C	-5.64	1.45	1.52
1	B	467	VAL	CA-C	-5.61	1.46	1.52
1	J	873	LYS	CA-C	-5.59	1.45	1.52
1	B	484	SER	CA-C	-5.58	1.46	1.52
3	D	103	ALA	N-CA	-5.55	1.39	1.46
3	D	70	LEU	CA-C	-5.55	1.45	1.52
1	B	470	TYR	N-CA	-5.53	1.39	1.46
3	H	70	LEU	CA-C	-5.50	1.45	1.52
1	F	518	GLN	CA-C	-5.49	1.46	1.53
3	H	103	ALA	N-CA	-5.49	1.39	1.46
3	P	103	ALA	N-CA	-5.47	1.39	1.46
3	L	103	ALA	N-CA	-5.44	1.39	1.46
3	D	48	GLU	CA-C	-5.34	1.45	1.52
1	N	526	ILE	CA-C	-5.31	1.46	1.52
3	L	48	GLU	CA-C	-5.30	1.45	1.52
3	P	48	GLU	CA-C	-5.29	1.45	1.52
3	H	48	GLU	CA-C	-5.29	1.46	1.52
4	G	315	SER	CA-C	-5.29	1.46	1.52
3	H	39	SER	CA-C	-5.29	1.46	1.52
1	N	54	ARG	N-CA	-5.28	1.40	1.46
1	B	469	ARG	N-CA	-5.28	1.40	1.46
3	D	39	SER	CA-C	-5.25	1.46	1.52
3	L	39	SER	CA-C	-5.24	1.46	1.52
4	O	315	SER	CA-C	-5.18	1.46	1.52
4	K	315	SER	CA-C	-5.17	1.46	1.52
3	P	39	SER	CA-C	-5.17	1.46	1.52
1	B	1054	PHE	CA-C	-5.15	1.46	1.52
4	C	315	SER	CA-C	-5.14	1.46	1.52
1	B	463	ASP	CA-C	-5.14	1.46	1.52
1	J	523	VAL	CA-C	-5.11	1.46	1.52
1	F	312	LEU	CA-C	-5.11	1.46	1.52
3	L	89	ALA	CA-C	-5.10	1.46	1.52
3	H	59	ASP	CA-C	-5.08	1.46	1.52
3	D	59	ASP	CA-C	-5.06	1.46	1.52
3	D	89	ALA	CA-C	-5.04	1.46	1.52
1	J	875	ARG	CA-C	-5.02	1.46	1.52
1	B	467	VAL	N-CA	-5.01	1.40	1.46
3	P	89	ALA	CA-C	-5.01	1.46	1.52

All (250) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	59	ASP	N-CA-C	-14.38	86.79	108.79
3	L	41	GLY	N-CA-C	14.38	133.90	115.21
3	P	59	ASP	N-CA-C	-14.37	86.80	108.79
3	L	59	ASP	N-CA-C	-14.37	86.81	108.79
3	H	59	ASP	N-CA-C	-14.36	86.81	108.79
2	I	789	MET	N-CA-C	-13.83	96.47	113.20
3	D	41	GLY	N-CA-C	12.98	132.62	115.36
3	L	42	GLN	N-CA-C	-12.96	88.21	109.07
3	H	41	GLY	N-CA-C	12.15	131.44	115.40
1	B	483	PHE	N-CA-C	-11.94	90.37	109.59
1	J	523	VAL	N-CA-C	-11.26	85.92	109.34
1	B	467	VAL	N-CA-C	-11.00	94.25	109.21
1	B	948	ILE	N-CA-C	-10.76	101.44	111.45
1	B	481	MET	N-CA-C	-10.38	100.15	112.92
1	B	974	MET	N-CA-C	9.86	121.62	111.07
2	I	399	PRO	CA-N-CD	-9.84	97.73	111.50
3	P	103	ALA	N-CA-C	-9.56	100.86	111.28
3	D	103	ALA	N-CA-C	-9.54	100.88	111.28
3	H	103	ALA	N-CA-C	-9.52	100.90	111.28
3	L	103	ALA	N-CA-C	-9.52	100.91	111.28
2	E	367	PRO	CA-N-CD	-9.46	98.75	112.00
3	L	33	LEU	N-CA-C	-9.42	101.01	111.28
3	P	33	LEU	N-CA-C	-9.41	101.02	111.28
3	D	33	LEU	N-CA-C	-9.40	101.03	111.28
3	H	33	LEU	N-CA-C	-9.40	101.03	111.28
2	M	872	PRO	CA-N-CD	-9.35	98.91	112.00
1	N	524	GLU	N-CA-C	9.23	130.22	109.81
2	I	793	ASP	N-CA-C	-9.19	96.40	110.10
3	H	106	LEU	N-CA-C	-9.01	101.46	111.28
3	D	106	LEU	N-CA-C	-8.98	101.49	111.28
3	L	106	LEU	N-CA-C	-8.97	101.50	111.28
1	B	977	MET	N-CA-C	8.82	124.05	113.28
4	K	117	THR	N-CA-C	-8.79	101.78	111.36
1	B	521	GLN	N-CA-C	-8.78	101.79	111.36
1	N	524	GLU	CA-C-N	-8.58	110.09	119.19
1	N	524	GLU	C-N-CA	-8.58	110.09	119.19
3	P	67	PRO	N-CA-C	-8.55	101.64	113.53
2	I	791	GLY	N-CA-C	-8.49	95.03	112.34
1	B	965	GLN	N-CA-C	8.42	120.08	111.07
1	F	469	ARG	N-CA-C	-8.29	102.16	113.18
3	P	86	ILE	N-CA-C	-8.08	102.38	110.62
3	L	86	ILE	N-CA-C	-8.06	102.39	110.62
3	H	86	ILE	N-CA-C	-8.06	102.40	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	86	ILE	N-CA-C	-8.06	102.40	110.62
3	P	76	LYS	N-CA-C	-7.87	103.13	112.89
3	H	76	LYS	N-CA-C	-7.87	103.13	112.89
3	D	95	LYS	N-CA-C	-7.85	102.80	111.36
3	L	95	LYS	N-CA-C	-7.85	102.80	111.36
3	H	95	LYS	N-CA-C	-7.85	102.81	111.36
3	P	95	LYS	N-CA-C	-7.84	102.81	111.36
3	D	76	LYS	N-CA-C	-7.83	103.18	112.89
3	L	76	LYS	N-CA-C	-7.82	103.19	112.89
1	B	966	GLN	CA-C-N	-7.81	110.08	119.84
1	B	966	GLN	C-N-CA	-7.81	110.08	119.84
3	D	77	MET	N-CA-C	7.76	121.48	110.23
3	P	77	MET	N-CA-C	7.75	121.47	110.23
3	L	77	MET	N-CA-C	7.75	121.46	110.23
3	P	41	GLY	N-CA-C	7.74	126.99	115.08
3	H	77	MET	N-CA-C	7.73	121.43	110.23
3	H	74	ALA	N-CA-C	-7.60	99.78	110.50
4	K	169	PHE	CB-CA-C	-7.60	100.72	112.12
3	D	74	ALA	N-CA-C	-7.58	99.81	110.50
3	L	74	ALA	N-CA-C	-7.58	99.81	110.50
4	O	169	PHE	CB-CA-C	-7.58	100.75	112.12
3	P	74	ALA	N-CA-C	-7.57	99.83	110.50
4	C	169	PHE	CB-CA-C	-7.57	100.77	112.12
4	G	169	PHE	CB-CA-C	-7.57	100.77	112.12
1	F	468	GLN	CB-CA-C	7.57	121.88	109.70
1	B	520	PRO	N-CA-C	7.53	123.28	113.86
1	J	878	TRP	N-CA-C	-7.53	103.08	111.28
3	P	44	PRO	N-CD-CG	-7.42	92.07	103.20
1	B	484	SER	N-CA-C	-7.35	99.19	108.45
1	B	524	GLU	N-CA-C	7.29	125.91	109.81
3	L	111	THR	N-CA-C	-7.28	103.35	111.28
3	P	42	GLN	N-CA-C	-7.26	95.31	108.02
3	H	111	THR	N-CA-C	-7.26	103.37	111.28
3	D	111	THR	N-CA-C	-7.26	103.37	111.28
3	P	111	THR	N-CA-C	-7.25	103.38	111.28
1	B	525	PRO	N-CA-C	-7.21	103.51	113.53
3	H	92	VAL	N-CA-C	-7.21	103.27	110.62
4	C	79	ARG	N-CA-C	-7.20	104.13	113.12
3	P	92	VAL	N-CA-C	-7.20	103.28	110.62
3	L	92	VAL	N-CA-C	-7.17	103.31	110.62
3	D	92	VAL	N-CA-C	-7.17	103.31	110.62
1	J	524	GLU	CA-C-N	-7.01	111.27	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	524	GLU	C-N-CA	-7.01	111.27	119.05
3	H	26	GLY	N-CA-C	-6.96	105.71	115.32
3	D	26	GLY	N-CA-C	-6.96	105.72	115.32
3	L	26	GLY	N-CA-C	-6.96	105.72	115.32
3	P	26	GLY	N-CA-C	-6.94	105.75	115.32
1	F	526	ILE	N-CA-C	6.91	118.52	107.73
3	L	66	PHE	CA-C-N	-6.85	111.44	119.05
3	L	66	PHE	C-N-CA	-6.85	111.44	119.05
1	B	1057	THR	CA-C-N	-6.76	113.42	120.38
1	B	1057	THR	C-N-CA	-6.76	113.42	120.38
2	I	790	LYS	N-CA-C	-6.71	104.96	113.01
1	F	923	CYS	N-CA-C	-6.69	100.53	110.23
3	H	56	VAL	N-CA-C	6.68	117.47	110.72
3	D	56	VAL	N-CA-C	6.68	117.47	110.72
3	L	56	VAL	N-CA-C	6.67	117.46	110.72
1	B	917	PRO	CB-CA-C	-6.67	100.55	111.56
3	P	56	VAL	N-CA-C	6.65	117.43	110.72
3	P	66	PHE	CA-C-N	-6.64	111.68	119.05
3	P	66	PHE	C-N-CA	-6.64	111.68	119.05
1	B	953	PRO	CA-N-CD	-6.58	102.79	112.00
1	J	923	CYS	N-CA-C	-6.56	100.32	110.10
3	P	130	ASP	N-CA-C	6.53	119.17	108.52
1	F	524	GLU	CA-C-N	-6.53	111.80	119.05
1	F	524	GLU	C-N-CA	-6.53	111.80	119.05
3	D	130	ASP	N-CA-C	6.52	119.14	108.52
3	L	130	ASP	N-CA-C	6.52	119.14	108.52
4	C	341	ARG	N-CA-C	6.52	121.72	113.25
3	H	130	ASP	N-CA-C	6.51	119.13	108.52
1	B	404	PRO	CA-N-CD	-6.50	102.90	112.00
4	G	341	ARG	N-CA-C	6.46	121.64	113.25
1	F	468	GLN	N-CA-C	-6.42	101.19	110.24
3	D	123	ASP	N-CA-C	-6.41	104.30	111.28
3	P	7	GLU	N-CA-C	-6.39	103.59	111.33
1	F	917	PRO	N-CA-C	6.39	125.64	112.47
3	L	7	GLU	N-CA-C	-6.38	103.61	111.33
3	H	7	GLU	N-CA-C	-6.38	103.61	111.33
3	H	123	ASP	N-CA-C	-6.38	104.33	111.28
3	D	7	GLU	N-CA-C	-6.38	103.61	111.33
3	L	123	ASP	N-CA-C	-6.37	104.33	111.28
3	P	123	ASP	N-CA-C	-6.37	104.34	111.28
1	J	530	PRO	N-CA-C	-6.35	101.67	111.13
1	J	990	ILE	N-CA-C	6.32	112.97	106.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	468	GLN	N-CA-C	6.31	119.55	108.56
2	A	266	PRO	CA-N-CD	-6.30	102.67	111.50
3	D	134	ASP	N-CA-C	-6.26	98.33	108.41
3	L	134	ASP	N-CA-C	-6.25	98.34	108.41
3	H	134	ASP	N-CA-C	-6.25	98.36	108.41
3	P	134	ASP	N-CA-C	-6.25	98.36	108.41
1	B	470	TYR	CA-C-N	-6.24	117.91	123.33
1	B	470	TYR	C-N-CA	-6.24	117.91	123.33
1	J	524	GLU	N-CA-CB	6.22	121.44	110.37
1	J	529	TRP	CA-C-N	-6.19	114.39	120.52
1	J	529	TRP	C-N-CA	-6.19	114.39	120.52
1	F	523	VAL	N-CA-CB	-6.17	101.04	111.23
3	P	36	VAL	N-CA-C	6.17	116.92	110.62
3	D	36	VAL	N-CA-C	6.15	116.89	110.62
3	L	36	VAL	N-CA-C	6.14	116.88	110.62
3	D	42	GLN	N-CA-C	-6.12	95.40	107.69
3	H	36	VAL	N-CA-C	6.12	116.86	110.62
3	L	23	ASP	N-CA-C	-6.07	101.94	110.50
3	D	23	ASP	N-CA-C	-6.05	101.96	110.50
3	P	23	ASP	N-CA-C	-6.05	101.97	110.50
3	H	23	ASP	N-CA-C	-6.03	102.00	110.50
2	I	791	GLY	CA-C-N	-5.93	113.68	119.90
2	I	791	GLY	C-N-CA	-5.93	113.68	119.90
1	F	516	GLN	N-CA-C	5.91	118.93	108.24
3	P	35	THR	N-CA-C	-5.91	104.84	111.28
1	B	469	ARG	N-CA-C	-5.90	104.85	111.28
3	D	133	GLY	N-CA-C	-5.87	99.27	113.18
1	B	971	ASP	N-CA-C	5.86	117.67	111.28
3	D	35	THR	N-CA-C	-5.86	104.89	111.28
3	L	35	THR	N-CA-C	-5.86	104.89	111.28
3	H	35	THR	N-CA-C	-5.85	104.90	111.28
3	L	133	GLY	N-CA-C	-5.84	99.33	113.18
3	H	133	GLY	N-CA-C	-5.84	99.33	113.18
3	P	133	GLY	N-CA-C	-5.84	99.34	113.18
3	P	118	THR	N-CA-C	5.84	118.70	110.23
1	F	918	GLN	N-CA-C	-5.83	96.90	107.75
4	K	170	GLY	N-CA-C	-5.83	99.37	113.18
4	G	170	GLY	N-CA-C	-5.82	99.38	113.18
4	C	170	GLY	N-CA-C	-5.82	99.38	113.18
1	B	522	GLN	N-CA-C	5.82	117.30	111.07
1	B	523	VAL	N-CA-C	-5.82	99.99	106.21
4	O	170	GLY	N-CA-C	-5.81	99.41	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	118	THR	N-CA-C	5.79	118.63	110.23
3	H	118	THR	N-CA-C	5.79	118.63	110.23
3	L	118	THR	N-CA-C	5.79	118.62	110.23
4	O	341	ARG	N-CA-C	5.76	120.73	113.25
1	F	518	GLN	N-CA-C	-5.74	102.44	110.35
4	G	324	ARG	N-CA-C	5.73	117.53	111.28
4	C	324	ARG	N-CA-C	5.72	117.51	111.28
1	B	953	PRO	N-CD-CG	-5.71	94.63	103.20
4	O	324	ARG	N-CA-C	5.71	117.51	111.28
3	L	144	GLN	N-CA-C	-5.71	105.06	111.28
4	K	324	ARG	N-CA-C	5.71	117.50	111.28
3	P	144	GLN	N-CA-C	-5.70	105.06	111.28
3	H	144	GLN	N-CA-C	-5.70	105.07	111.28
3	D	144	GLN	N-CA-C	-5.69	105.08	111.28
2	A	903	MET	CA-CB-CG	5.68	125.46	114.10
4	K	113	PHE	N-CA-C	-5.67	105.01	111.14
1	F	525	PRO	N-CA-C	-5.64	105.69	113.53
1	B	477	ARG	N-CA-C	5.63	119.41	111.52
3	H	42	GLN	N-CA-C	-5.62	96.54	107.62
1	J	874	ILE	N-CA-C	-5.61	99.66	107.80
4	G	306	LYS	N-CA-C	-5.60	105.09	111.14
4	C	306	LYS	N-CA-C	-5.59	105.10	111.14
1	J	916	GLN	CA-C-N	-5.59	112.85	119.05
1	J	916	GLN	C-N-CA	-5.59	112.85	119.05
1	B	54	ARG	N-CA-C	-5.59	104.88	110.97
4	O	306	LYS	N-CA-C	-5.55	105.14	111.14
4	K	306	LYS	N-CA-C	-5.55	105.15	111.14
1	F	919	GLN	N-CA-C	-5.53	102.22	110.23
1	B	483	PHE	CB-CA-C	5.44	119.18	109.38
4	G	79	ARG	N-CA-C	-5.44	105.78	112.90
3	L	136	GLN	CA-C-N	-5.43	115.95	122.90
3	L	136	GLN	C-N-CA	-5.43	115.95	122.90
4	K	336	ASP	CA-C-N	-5.41	113.07	119.84
4	K	336	ASP	C-N-CA	-5.41	113.07	119.84
3	L	21	ASP	N-CA-C	5.38	117.08	108.41
3	P	21	ASP	N-CA-C	5.37	117.06	108.41
2	I	399	PRO	N-CD-CG	-5.36	97.37	103.80
3	D	21	ASP	N-CA-C	5.36	117.04	108.41
3	H	21	ASP	N-CA-C	5.36	117.04	108.41
1	J	875	ARG	N-CA-C	-5.33	99.82	108.52
2	I	37	TYR	N-CA-C	-5.32	105.39	111.14
1	B	1054	PHE	N-CA-C	-5.32	105.48	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	136	GLN	CA-C-N	-5.32	116.10	122.90
3	H	136	GLN	C-N-CA	-5.32	116.10	122.90
1	B	917	PRO	N-CA-C	5.30	123.40	112.47
3	D	30	THR	N-CA-C	-5.29	105.52	111.28
3	H	30	THR	N-CA-C	-5.28	105.52	111.28
3	P	30	THR	N-CA-C	-5.26	105.55	111.28
3	L	30	THR	N-CA-C	-5.26	105.55	111.28
3	L	97	GLY	N-CA-C	-5.25	107.74	115.30
4	O	323	ARG	N-CA-C	-5.24	105.57	111.28
4	G	323	ARG	N-CA-C	-5.24	105.57	111.28
3	D	136	GLN	CA-C-N	-5.23	116.20	122.90
3	D	136	GLN	C-N-CA	-5.23	116.20	122.90
3	P	97	GLY	N-CA-C	-5.23	107.77	115.30
3	P	136	GLN	CA-C-N	-5.23	116.20	122.90
3	P	136	GLN	C-N-CA	-5.23	116.20	122.90
3	D	97	GLY	N-CA-C	-5.23	107.77	115.30
4	K	323	ARG	N-CA-C	-5.23	105.58	111.28
1	N	525	PRO	N-CA-C	-5.22	106.73	113.57
3	H	97	GLY	N-CA-C	-5.22	107.79	115.30
4	C	323	ARG	N-CA-C	-5.20	105.61	111.28
1	B	311	VAL	N-CA-C	-5.19	105.43	110.42
3	D	89	ALA	N-CA-C	-5.19	105.62	111.28
1	N	928	ARG	N-CA-C	-5.18	106.79	113.01
1	F	312	LEU	N-CA-C	-5.16	105.74	111.36
2	A	327	GLU	CA-C-N	-5.16	113.79	121.83
2	A	327	GLU	C-N-CA	-5.16	113.79	121.83
3	P	89	ALA	N-CA-C	-5.15	105.67	111.28
3	H	89	ALA	N-CA-C	-5.15	105.67	111.28
3	L	89	ALA	N-CA-C	-5.15	105.67	111.28
1	F	920	ASN	N-CA-C	5.12	117.58	109.24
2	I	358	VAL	N-CA-C	-5.11	107.86	113.43
4	K	341	ARG	N-CA-C	5.06	120.98	109.81
3	P	137	VAL	N-CA-C	-5.02	100.66	107.99
3	P	72	MET	N-CA-C	5.02	116.83	111.36
3	P	96	ASP	N-CA-C	-5.02	105.81	111.28
3	L	137	VAL	N-CA-C	-5.01	100.67	107.99
3	D	96	ASP	N-CA-C	-5.01	105.82	111.28
3	D	137	VAL	N-CA-C	-5.01	100.67	107.99
4	C	165	LYS	CB-CG-CD	5.00	122.81	111.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	8342	0	8327	440	0
1	F	8342	0	8327	392	0
1	J	8342	0	8328	365	0
1	N	8342	0	8328	288	0
2	A	7801	0	7821	344	0
2	E	7801	0	7821	338	0
2	I	7801	0	7821	314	0
2	M	7801	0	7821	263	0
3	D	1143	0	1071	86	0
3	H	1143	0	1071	86	0
3	L	1143	0	1071	94	0
3	P	1143	0	1071	86	0
4	C	3041	0	3054	204	0
4	G	3041	0	3054	233	0
4	K	3041	0	3054	225	0
4	O	3041	0	3054	216	0
5	A	15	0	20	10	0
5	B	15	0	24	20	0
5	E	15	0	20	11	0
5	F	15	0	24	28	0
5	I	15	0	21	9	0
5	J	15	0	25	40	0
5	M	15	0	21	5	0
5	N	15	0	23	16	0
All	All	81428	0	81272	3627	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 22.

All (3627) 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:J:1060:LEU:HD21	5:F:1101:FAR:C4	1.33	1.51
1:J:1074:MET:CE	5:J:1101:FAR:H12	1.43	1.47
4:O:24:GLU:CD	4:O:36:ARG:HH21	1.20	1.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1074:MET:CE	5:J:1101:FAR:C12	1.96	1.42
4:G:26:LEU:HD21	4:G:36:ARG:CD	1.51	1.37
1:F:518:GLN:NE2	1:F:655:ARG:HB3	1.45	1.31
4:G:26:LEU:HD21	4:G:36:ARG:CG	1.62	1.28
4:O:24:GLU:CD	4:O:36:ARG:NH2	1.92	1.28
1:N:1090:CYS:SG	5:N:1101:FAR:C1	1.18	1.26
1:J:1060:LEU:CD2	5:F:1101:FAR:C4	2.12	1.25
3:D:37:MET:CE	3:D:49:LEU:CD2	2.13	1.25
3:H:37:MET:CE	3:H:49:LEU:CD2	2.14	1.24
3:L:37:MET:CE	3:L:49:LEU:CD2	2.14	1.24
3:P:37:MET:CE	3:P:49:LEU:CD2	2.14	1.24
1:J:1074:MET:HE2	5:J:1101:FAR:C15	1.68	1.23
3:L:100:TYR:HB3	3:L:136:GLN:CD	1.64	1.20
1:B:270:ASP:OD2	1:B:558:GLY:CA	1.91	1.18
1:J:1060:LEU:CD2	5:F:1101:FAR:H43	1.72	1.18
5:B:1101:FAR:H152	1:N:1074:MET:HE1	1.20	1.18
3:P:45:THR:HB	3:P:48:GLU:HG2	1.27	1.16
3:D:37:MET:HE1	3:D:49:LEU:HD23	1.27	1.16
1:B:1009:VAL:HG22	5:N:1101:FAR:H143	1.24	1.16
2:A:1138:ALA:HB2	5:A:1301:FAR:H152	1.27	1.14
2:I:1196:ARG:NH1	4:K:251:SER:O	1.81	1.13
3:P:37:MET:HE1	3:P:49:LEU:HD23	1.27	1.13
5:B:1101:FAR:H141	1:N:1009:VAL:CG2	1.77	1.13
1:J:1074:MET:HE2	5:J:1101:FAR:C13	1.79	1.12
1:J:1074:MET:HE1	5:J:1101:FAR:C12	1.75	1.12
5:J:1101:FAR:H151	1:F:1013:ASN:HD21	1.02	1.12
4:G:26:LEU:CD2	4:G:36:ARG:HD2	1.77	1.12
1:J:1074:MET:HE3	5:J:1101:FAR:H12	1.14	1.11
2:I:1129:GLU:CD	4:K:355:TYR:OH	1.93	1.11
1:J:1074:MET:HE2	5:J:1101:FAR:H153	1.28	1.11
3:H:37:MET:HE1	3:H:49:LEU:HD23	1.27	1.11
1:J:1090:CYS:CB	5:J:1101:FAR:H12A	1.80	1.10
2:I:1196:ARG:CZ	4:K:251:SER:O	1.98	1.10
4:G:26:LEU:CG	4:G:36:ARG:HG3	1.78	1.10
4:K:74:GLU:CD	4:K:169:PHE:O	1.94	1.10
4:O:313:LEU:O	4:O:317:ARG:HG3	1.48	1.10
4:C:74:GLU:CD	4:C:169:PHE:O	1.94	1.09
4:O:74:GLU:CD	4:O:169:PHE:O	1.94	1.09
1:J:1013:ASN:ND2	5:J:1101:FAR:H142	1.66	1.09
4:G:74:GLU:CD	4:G:169:PHE:O	1.94	1.09
1:J:1090:CYS:SG	5:J:1101:FAR:H12A	0.56	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:37:MET:HE1	3:L:49:LEU:HD23	1.27	1.08
2:A:1138:ALA:CB	5:A:1301:FAR:H152	1.82	1.08
1:J:1090:CYS:SG	5:J:1101:FAR:C1	1.13	1.08
2:E:1138:ALA:CB	5:E:1301:FAR:H152	1.84	1.07
2:E:1138:ALA:HB2	5:E:1301:FAR:H152	1.37	1.06
1:J:1013:ASN:HD21	5:J:1101:FAR:H142	1.07	1.06
4:O:113:PHE:O	4:O:367:ARG:NH2	1.87	1.06
1:J:531:GLN:NE2	1:J:578:ILE:HD13	1.68	1.06
3:L:102:SER:HB3	3:L:105:GLU:HG3	1.34	1.06
4:G:26:LEU:HD21	4:G:36:ARG:HD2	1.07	1.06
3:H:129:ALA:HB1	3:H:145:MET:CE	1.87	1.05
3:P:94:ASP:OD1	3:P:105:GLU:OE2	1.74	1.05
1:B:1070:THR:HG21	5:N:1101:FAR:H101	1.35	1.05
3:D:129:ALA:HB1	3:D:145:MET:CE	1.87	1.05
3:H:102:SER:HB3	3:H:105:GLU:HG3	1.34	1.05
3:L:129:ALA:HB1	3:L:145:MET:CE	1.87	1.05
3:P:129:ALA:HB1	3:P:145:MET:HE1	1.36	1.05
3:P:129:ALA:HB1	3:P:145:MET:CE	1.87	1.04
2:E:588:LYS:HE2	4:G:99:PHE:CZ	1.92	1.04
3:D:102:SER:HB3	3:D:105:GLU:HG3	1.34	1.04
3:D:129:ALA:HB1	3:D:145:MET:HE1	1.36	1.04
5:B:1101:FAR:H141	1:N:1009:VAL:HG22	1.05	1.03
4:K:116:LEU:HB3	4:K:367:ARG:HH12	1.22	1.03
1:B:270:ASP:OD2	1:B:558:GLY:HA3	1.57	1.03
1:J:1090:CYS:SG	5:J:1101:FAR:H13	1.63	1.03
2:E:1129:GLU:CD	4:G:355:TYR:OH	1.99	1.03
3:L:129:ALA:HB1	3:L:145:MET:HE1	1.36	1.02
1:N:1090:CYS:SG	5:N:1101:FAR:C2	2.48	1.01
3:D:37:MET:CE	3:D:49:LEU:HD21	1.87	1.01
3:P:37:MET:CE	3:P:49:LEU:HD21	1.87	1.01
3:H:37:MET:CE	3:H:49:LEU:HD21	1.87	1.01
3:P:129:ALA:CB	3:P:145:MET:HE1	1.91	1.01
3:L:37:MET:CE	3:L:49:LEU:HD21	1.87	1.00
4:K:207:TYR:CD1	4:K:211:VAL:HG21	1.96	1.00
4:C:207:TYR:CD1	4:C:211:VAL:HG21	1.96	1.00
4:K:74:GLU:OE1	4:K:169:PHE:O	1.79	1.00
3:P:37:MET:HE1	3:P:49:LEU:CD2	1.86	1.00
4:C:74:GLU:OE1	4:C:169:PHE:O	1.79	1.00
3:H:129:ALA:HB1	3:H:145:MET:HE1	1.36	1.00
4:O:74:GLU:OE1	4:O:169:PHE:O	1.79	1.00
5:B:1101:FAR:C14	1:N:1009:VAL:HG22	1.89	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:207:TYR:CD1	4:G:211:VAL:HG21	1.96	1.00
3:L:129:ALA:CB	3:L:145:MET:HE1	1.91	1.00
2:E:588:LYS:HE2	4:G:99:PHE:CE2	1.96	1.00
3:H:129:ALA:CB	3:H:145:MET:HE1	1.91	1.00
5:B:1101:FAR:H152	1:N:1074:MET:CE	1.91	0.99
4:O:36:ARG:HG2	4:O:106:LEU:HD11	1.43	0.99
3:D:129:ALA:CB	3:D:145:MET:HE1	1.91	0.99
4:G:26:LEU:CD2	4:G:36:ARG:CG	2.40	0.99
3:L:100:TYR:CB	3:L:136:GLN:CD	2.35	0.99
4:G:26:LEU:CD2	4:G:36:ARG:HG3	1.91	0.98
4:G:74:GLU:OE1	4:G:169:PHE:O	1.79	0.98
3:L:37:MET:HE1	3:L:49:LEU:CD2	1.86	0.98
1:J:1074:MET:HE2	5:J:1101:FAR:C12	1.84	0.98
3:H:37:MET:HE1	3:H:49:LEU:CD2	1.86	0.97
1:B:1009:VAL:HA	5:N:1101:FAR:C14	1.95	0.97
3:D:37:MET:HE3	3:D:49:LEU:HD21	1.46	0.97
4:O:117:THR:HA	4:O:367:ARG:HH12	1.25	0.97
1:F:518:GLN:HE22	1:F:655:ARG:CB	1.77	0.97
4:O:207:TYR:CD1	4:O:211:VAL:HG21	1.99	0.97
1:J:1090:CYS:SG	5:J:1101:FAR:C2	2.50	0.97
2:I:588:LYS:HZ1	4:K:52:ASP:CG	1.71	0.97
4:G:26:LEU:HG	4:G:36:ARG:HG3	1.47	0.97
2:A:1129:GLU:CD	4:C:355:TYR:OH	2.08	0.96
3:H:37:MET:HE3	3:H:49:LEU:HD21	1.46	0.96
1:F:518:GLN:NE2	1:F:655:ARG:CB	2.29	0.96
1:B:270:ASP:OD2	1:B:558:GLY:N	1.97	0.95
4:G:26:LEU:CD2	4:G:36:ARG:CD	2.38	0.95
3:L:37:MET:HE3	3:L:49:LEU:HD21	1.46	0.95
3:P:55:GLU:HG3	4:O:322:TYR:HD1	1.31	0.95
3:P:37:MET:HE3	3:P:49:LEU:HD21	1.46	0.94
3:P:102:SER:HB3	3:P:105:GLU:HG3	1.49	0.94
1:N:1090:CYS:HG	5:N:1101:FAR:C1	0.77	0.94
4:G:220:MET:HE1	4:G:268:PHE:HE2	1.32	0.94
2:I:1138:ALA:HB2	5:I:1301:FAR:H152	1.47	0.94
3:L:55:GLU:HG3	4:K:322:TYR:HD1	1.31	0.94
2:A:949:LEU:HB2	2:A:954:MET:HE1	1.48	0.94
4:O:220:MET:HE1	4:O:268:PHE:HE2	1.32	0.94
2:A:33:LEU:HD22	2:A:401:MET:HE1	1.50	0.94
5:J:1101:FAR:H151	1:F:1013:ASN:ND2	1.82	0.93
4:C:220:MET:HE1	4:C:268:PHE:HE2	1.32	0.93
4:K:220:MET:HE1	4:K:268:PHE:HE2	1.32	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:33:LEU:HD22	2:I:401:MET:HE1	1.46	0.93
2:I:1138:ALA:CB	5:I:1301:FAR:H152	1.99	0.93
2:E:588:LYS:CE	4:G:99:PHE:CE2	2.51	0.93
1:B:1082:VAL:HG11	5:B:1101:FAR:H101	1.49	0.92
2:E:1196:ARG:HD3	4:G:252:PRO:CD	1.98	0.92
3:D:55:GLU:CG	4:C:322:TYR:HD1	1.83	0.92
4:K:337:PRO:HB3	4:K:343:LEU:HD23	1.51	0.92
3:P:55:GLU:CG	4:O:322:TYR:HD1	1.82	0.92
3:D:55:GLU:HG3	4:C:322:TYR:HD1	1.33	0.92
3:H:55:GLU:CG	4:G:322:TYR:HD1	1.83	0.92
2:I:1196:ARG:NH2	4:K:252:PRO:HD3	1.85	0.92
3:H:55:GLU:HG3	4:G:322:TYR:HD1	1.31	0.92
1:B:1009:VAL:CG2	5:N:1101:FAR:H143	1.99	0.91
3:L:55:GLU:CG	4:K:322:TYR:HD1	1.83	0.91
1:J:531:GLN:CD	1:J:578:ILE:HD13	1.96	0.91
3:L:94:ASP:OD1	3:L:105:GLU:OE2	1.88	0.91
3:H:94:ASP:OD1	3:H:105:GLU:OE2	1.89	0.90
2:M:1138:ALA:HB2	5:M:1301:FAR:H152	1.52	0.90
5:J:1101:FAR:H2	1:F:1008:ILE:HG21	1.52	0.90
1:F:518:GLN:HE22	1:F:655:ARG:HB3	1.02	0.90
1:J:1012:ARG:NH2	5:F:1101:FAR:H142	1.87	0.90
3:D:94:ASP:OD1	3:D:105:GLU:OE2	1.89	0.89
1:J:1060:LEU:CD2	5:F:1101:FAR:C3	2.50	0.89
1:J:1013:ASN:HD21	5:J:1101:FAR:C14	1.86	0.88
1:B:853:LEU:HD12	1:B:876:ILE:HG23	1.53	0.87
1:J:1074:MET:CE	5:J:1101:FAR:C13	2.47	0.87
4:O:313:LEU:HD21	4:O:317:ARG:HH21	1.37	0.86
2:A:1196:ARG:HD3	4:C:252:PRO:CD	2.05	0.86
2:A:11:LEU:HB3	2:A:61:TYR:HE1	1.41	0.86
2:I:1129:GLU:CG	4:K:355:TYR:OH	2.22	0.85
2:I:356:GLU:HA	2:I:359:LEU:HD12	1.58	0.85
3:L:77:MET:SD	3:L:81:ASP:OD2	2.35	0.85
3:P:77:MET:SD	3:P:81:ASP:OD2	2.35	0.85
1:J:1090:CYS:SG	5:J:1101:FAR:H11	1.43	0.85
4:O:313:LEU:CD2	4:O:317:ARG:HH21	1.90	0.84
3:D:77:MET:SD	3:D:81:ASP:OD2	2.35	0.84
2:M:1138:ALA:CB	5:M:1301:FAR:H152	2.07	0.84
3:H:77:MET:SD	3:H:81:ASP:OD2	2.35	0.84
1:J:132:GLN:HE22	1:J:150:HIS:H	1.22	0.84
2:I:1196:ARG:HD3	4:K:373:ASN:O	1.76	0.84
1:J:1060:LEU:HD21	5:F:1101:FAR:H41	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:45:THR:HG22	3:P:47:ALA:H	1.41	0.83
4:O:352:PHE:HE2	4:O:367:ARG:HH11	1.25	0.83
2:I:1169:LEU:HD13	4:K:375:PRO:HG3	1.61	0.83
2:E:588:LYS:HA	4:G:98:THR:HG21	1.58	0.82
3:L:102:SER:HB3	3:L:105:GLU:CG	2.10	0.82
1:N:132:GLN:HE22	1:N:150:HIS:H	1.27	0.82
1:F:887:LEU:HD21	1:F:910:LEU:HD21	1.61	0.82
2:E:1092:LEU:HB2	2:E:1114:VAL:HG21	1.61	0.82
3:H:102:SER:HB3	3:H:105:GLU:CG	2.10	0.82
2:I:901:LEU:HD23	2:I:918:LEU:HD23	1.59	0.82
1:F:1082:VAL:HG11	5:F:1101:FAR:C10	2.09	0.82
1:J:1001:GLU:HB3	1:F:1092:ILE:HD12	1.62	0.81
5:J:1101:FAR:C15	1:F:1013:ASN:HD21	1.87	0.81
3:D:102:SER:HB3	3:D:105:GLU:CG	2.09	0.81
3:H:37:MET:HE2	3:H:49:LEU:CD2	2.09	0.81
1:F:773:ALA:HA	1:F:776:GLN:HE21	1.46	0.81
2:A:310:ARG:HD3	2:A:312:TYR:H	1.45	0.81
2:I:588:LYS:NZ	4:K:52:ASP:CG	2.38	0.81
1:F:45:LEU:HA	1:F:48:LYS:HD2	1.62	0.81
3:P:36:VAL:O	3:P:39:SER:OG	1.99	0.81
2:M:1172:ASP:H	2:M:1175:MET:HE3	1.45	0.80
3:D:37:MET:HE2	3:D:49:LEU:CD2	2.09	0.80
2:I:930:GLU:HG3	2:I:1056:ARG:HH21	1.47	0.80
2:I:1196:ARG:HH21	4:K:252:PRO:HD3	1.46	0.80
3:H:10:ILE:HD12	4:G:289:GLN:OE1	1.82	0.80
3:L:37:MET:HE2	3:L:49:LEU:CD2	2.09	0.80
4:O:117:THR:CA	4:O:367:ARG:HH12	1.94	0.80
2:A:1120:GLN:HE22	2:A:1123:TYR:HB3	1.47	0.80
2:E:480:SER:HA	2:E:502:MET:HE3	1.64	0.80
3:L:13:PHE:HD1	4:K:310:LEU:HD21	1.47	0.80
2:A:1053:GLN:OE1	4:C:233:ARG:NE	2.14	0.80
1:J:531:GLN:NE2	1:J:578:ILE:CD1	2.44	0.80
3:D:10:ILE:HD12	4:C:289:GLN:OE1	1.82	0.80
1:F:1034:GLU:HA	1:F:1037:LYS:HD2	1.63	0.79
4:K:359:VAL:HG21	4:K:367:ARG:HG2	1.64	0.79
3:P:37:MET:HE2	3:P:49:LEU:CD2	2.09	0.79
3:L:100:TYR:HB3	3:L:136:GLN:OE1	1.80	0.79
3:L:10:ILE:HD12	4:K:289:GLN:OE1	1.82	0.79
4:K:113:PHE:O	4:K:367:ARG:NH2	2.15	0.79
3:D:45:THR:HB	3:D:48:GLU:HG2	1.65	0.79
3:P:10:ILE:HD12	4:O:289:GLN:OE1	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:727:ILE:HG12	1:B:743:LEU:HD11	1.65	0.79
1:J:1009:VAL:HG22	5:F:1101:FAR:H152	1.65	0.79
2:I:444:ILE:HD13	2:I:586:LEU:HD12	1.64	0.79
2:I:588:LYS:NZ	4:K:52:ASP:OD1	2.16	0.79
1:J:1060:LEU:CD2	5:F:1101:FAR:H41	2.09	0.79
3:H:36:VAL:O	3:H:39:SER:OG	1.99	0.79
1:F:404:PRO:HB2	1:F:448:TYR:HE2	1.48	0.79
1:N:606:LYS:HD2	1:N:649:VAL:HG22	1.65	0.78
2:A:136:ASP:HB3	2:A:201:SER:HA	1.63	0.78
3:H:13:PHE:HD1	4:G:310:LEU:HD21	1.47	0.78
3:D:37:MET:HE1	3:D:49:LEU:CD2	1.86	0.78
2:E:400:HIS:HD2	2:E:403:GLY:H	1.31	0.78
3:D:36:VAL:O	3:D:39:SER:OG	1.99	0.78
5:J:1101:FAR:H152	1:F:1074:MET:CE	2.13	0.78
2:I:355:LEU:O	2:I:359:LEU:HG	1.84	0.78
3:H:10:ILE:CG2	4:G:289:GLN:OE1	2.31	0.78
3:P:10:ILE:CG2	4:O:289:GLN:OE1	2.31	0.78
2:M:844:CYS:HB2	2:M:898:MET:HE1	1.64	0.78
4:K:116:LEU:HB3	4:K:367:ARG:NH1	1.98	0.78
3:P:73:MET:HE1	4:O:317:ARG:HE	1.46	0.78
2:I:1076:TRP:HD1	2:I:1107:PHE:HE2	1.31	0.78
3:D:10:ILE:CG2	4:C:289:GLN:OE1	2.31	0.78
4:G:154:GLU:HG2	4:G:361:LYS:HG2	1.66	0.78
1:N:320:VAL:HA	1:N:324:LEU:HD12	1.66	0.78
1:F:922:ARG:HB2	1:F:927:ARG:HG3	1.66	0.78
3:P:45:THR:CB	3:P:48:GLU:HG2	2.11	0.78
4:K:154:GLU:HG2	4:K:361:LYS:HG2	1.66	0.77
1:B:1082:VAL:HG11	5:B:1101:FAR:C10	2.15	0.77
2:A:483:TYR:HB3	2:A:497:ARG:HD3	1.66	0.77
3:D:13:PHE:HD1	4:C:310:LEU:HD21	1.47	0.77
4:C:228:PRO:HD2	4:C:368:ALA:HB2	1.66	0.77
1:B:307:LEU:HD21	1:B:312:LEU:HB3	1.66	0.77
3:L:10:ILE:HG21	4:K:289:GLN:OE1	1.84	0.77
1:F:57:LYS:HA	1:F:61:LEU:HB2	1.67	0.77
3:L:10:ILE:CG2	4:K:289:GLN:OE1	2.31	0.77
3:P:10:ILE:HG21	4:O:289:GLN:OE1	1.84	0.77
2:M:907:THR:HG23	2:M:908:GLN:HG3	1.67	0.77
2:A:509:LYS:HB2	2:A:511:TYR:HE1	1.49	0.77
3:H:10:ILE:HG21	4:G:289:GLN:OE1	1.84	0.77
4:O:228:PRO:HD2	4:O:368:ALA:HB2	1.66	0.77
2:E:1053:GLN:OE1	4:G:233:ARG:NE	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:36:VAL:O	3:L:39:SER:OG	1.99	0.77
4:K:74:GLU:OE2	4:K:169:PHE:O	2.03	0.77
3:P:13:PHE:HD1	4:O:310:LEU:HD21	1.47	0.77
4:G:228:PRO:HD2	4:G:368:ALA:HB2	1.66	0.77
2:M:307:ASP:HB2	2:M:310:ARG:HD3	1.67	0.77
1:J:1090:CYS:HG	5:J:1101:FAR:H11	0.98	0.77
5:B:1101:FAR:C15	1:N:1074:MET:CE	2.62	0.77
1:J:943:ASP:O	1:J:947:GLN:NE2	2.18	0.76
1:J:1023:ASP:HB3	1:J:1026:ARG:HH12	1.50	0.76
2:E:176:TYR:HB2	2:E:241:ILE:HD12	1.67	0.76
1:B:779:TRP:NE1	1:B:904:PRO:HD3	2.00	0.76
3:P:68:GLU:HG3	4:O:125:LYS:HE2	1.66	0.76
4:O:220:MET:HE1	4:O:268:PHE:CE2	2.20	0.76
2:I:21:THR:HG21	2:I:404:GLN:HG2	1.66	0.76
3:D:10:ILE:HG21	4:C:289:GLN:OE1	1.84	0.76
1:J:951:ARG:NH1	1:J:1010:LEU:O	2.19	0.76
1:J:1060:LEU:HD21	5:F:1101:FAR:C3	2.12	0.76
4:O:313:LEU:HD21	4:O:317:ARG:NH2	2.00	0.76
1:B:67:THR:HG23	1:B:68:THR:HG23	1.67	0.76
2:A:479:LEU:HD12	2:A:482:ILE:HD11	1.68	0.76
1:F:1082:VAL:CG1	5:F:1101:FAR:H103	2.15	0.76
4:C:74:GLU:OE2	4:C:169:PHE:O	2.03	0.76
2:E:172:ILE:HD11	2:E:205:ALA:HA	1.67	0.76
4:C:154:GLU:HG2	4:C:361:LYS:HG2	1.66	0.76
4:K:220:MET:HE1	4:K:268:PHE:CE2	2.20	0.76
1:F:253:ASN:OD1	1:F:263:SER:OG	2.03	0.76
4:O:74:GLU:OE2	4:O:169:PHE:O	2.03	0.76
4:O:154:GLU:HG2	4:O:361:LYS:HG2	1.66	0.76
2:A:134:GLN:NE2	2:A:182:GLY:O	2.19	0.76
3:H:51:ASP:HB3	4:G:322:TYR:CE1	2.21	0.76
4:G:74:GLU:OE2	4:G:169:PHE:O	2.03	0.76
3:L:51:ASP:HB3	4:K:322:TYR:CE1	2.21	0.76
3:L:55:GLU:HG3	4:K:322:TYR:CD1	2.20	0.76
4:K:228:PRO:HD2	4:K:368:ALA:HB2	1.66	0.76
3:P:51:ASP:HB3	4:O:322:TYR:CE1	2.21	0.76
1:F:867:LEU:HG	1:F:915:LEU:HD13	1.66	0.75
3:D:10:ILE:HG21	4:C:289:GLN:CD	2.11	0.75
3:H:10:ILE:HG21	4:G:289:GLN:CD	2.11	0.75
3:L:100:TYR:CG	3:L:136:GLN:OE1	2.39	0.75
3:D:45:THR:HG22	3:D:47:ALA:H	1.50	0.75
2:I:356:GLU:HA	2:I:359:LEU:CD1	2.17	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1138:ALA:HB1	5:E:1301:FAR:H152	1.66	0.75
1:J:1060:LEU:HD21	5:F:1101:FAR:H43	0.76	0.75
1:B:1092:ILE:HB	1:N:938:PRO:HG3	1.68	0.75
3:P:10:ILE:HG21	4:O:289:GLN:CD	2.11	0.75
3:H:129:ALA:CB	3:H:145:MET:CE	2.59	0.75
2:E:588:LYS:HE3	4:G:98:THR:HG23	1.69	0.74
1:F:493:LEU:HD23	1:F:606:LYS:HA	1.66	0.74
4:O:149:ARG:NH2	4:O:185:CYS:SG	2.61	0.74
1:B:898:ASP:H	1:B:901:GLN:HE21	1.36	0.74
2:A:588:LYS:HA	4:C:98:THR:HG21	1.69	0.74
4:G:26:LEU:HD11	4:G:36:ARG:HG2	1.69	0.74
1:B:1070:THR:HG21	5:N:1101:FAR:C10	2.17	0.74
2:A:156:ILE:HG12	2:A:217:LEU:HB3	1.69	0.74
4:C:149:ARG:NH2	4:C:185:CYS:SG	2.61	0.74
1:B:1009:VAL:HA	5:N:1101:FAR:H143	1.68	0.74
2:A:29:VAL:HG13	2:A:30:THR:HG23	1.68	0.74
1:F:297:LEU:HD22	1:F:300:ILE:HD11	1.69	0.74
3:H:55:GLU:HG3	4:G:322:TYR:CD1	2.20	0.74
3:L:10:ILE:HG21	4:K:289:GLN:CD	2.11	0.74
1:B:1015:GLU:OE1	5:B:1101:FAR:H52	1.86	0.74
1:N:796:ILE:HG23	1:N:854:VAL:HG11	1.69	0.74
2:I:51:ILE:HG13	2:I:81:VAL:HG22	1.69	0.74
3:H:10:ILE:HG13	4:G:289:GLN:HE22	1.53	0.74
4:C:237:LEU:HA	4:C:240:ARG:HH21	1.53	0.74
4:K:237:LEU:HA	4:K:240:ARG:HH21	1.53	0.74
2:I:93:ILE:HD11	2:I:492:MET:HE1	1.70	0.73
2:I:859:PRO:HD3	2:I:925:GLN:HE22	1.52	0.73
4:K:149:ARG:NH2	4:K:185:CYS:SG	2.61	0.73
3:P:10:ILE:HG13	4:O:289:GLN:HE22	1.52	0.73
1:J:377:VAL:HG11	1:J:454:LEU:HB3	1.70	0.73
2:E:1196:ARG:HD3	4:G:252:PRO:HD3	1.69	0.73
4:K:23:LYS:HD2	4:K:36:ARG:HH12	1.53	0.73
3:P:57:ASP:HB3	4:O:125:LYS:HZ2	1.53	0.73
2:A:1196:ARG:HD3	4:C:252:PRO:HD3	1.70	0.73
4:G:149:ARG:NH2	4:G:185:CYS:SG	2.61	0.73
4:O:359:VAL:HG21	4:O:367:ARG:HG2	1.71	0.73
2:A:1092:LEU:HB2	2:A:1114:VAL:HG21	1.68	0.73
3:D:51:ASP:HB3	4:C:322:TYR:CE1	2.23	0.73
4:C:340:LEU:CD1	4:C:342:PRO:HD2	2.19	0.73
4:G:237:LEU:HA	4:G:240:ARG:HH21	1.53	0.73
1:B:1012:ARG:HH12	1:N:1014:PRO:HD2	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1129:GLU:CG	4:G:355:TYR:OH	2.37	0.73
3:D:129:ALA:CB	3:D:145:MET:CE	2.59	0.73
4:O:24:GLU:CG	4:O:36:ARG:NH2	2.52	0.73
4:C:340:LEU:HD12	4:C:342:PRO:HD2	1.71	0.73
1:B:1009:VAL:HG22	5:N:1101:FAR:C14	2.14	0.72
2:M:204:MET:HE1	2:M:266:PRO:HG2	1.70	0.72
2:M:1178:LYS:NZ	2:M:1185:CYS:SG	2.62	0.72
4:C:23:LYS:HD2	4:C:36:ARG:HH12	1.52	0.72
4:C:220:MET:HE1	4:C:268:PHE:CE2	2.20	0.72
3:L:45:THR:HB	3:L:48:GLU:HG2	1.70	0.72
4:K:340:LEU:CD1	4:K:342:PRO:HD2	2.19	0.72
4:O:237:LEU:HA	4:O:240:ARG:HH21	1.53	0.72
2:E:1191:SER:OG	4:G:376:LYS:NZ	2.22	0.72
3:L:10:ILE:HG13	4:K:289:GLN:HE22	1.53	0.72
3:P:55:GLU:HG3	4:O:322:TYR:CD1	2.19	0.72
4:O:340:LEU:HD12	4:O:342:PRO:HD2	1.71	0.72
2:A:502:MET:HE1	2:A:507:THR:HG23	1.71	0.72
4:G:340:LEU:CD1	4:G:342:PRO:HD2	2.19	0.72
2:I:160:ASP:HB3	2:I:492:MET:HE2	1.70	0.72
2:I:840:LEU:HD13	2:I:876:LEU:HD22	1.72	0.72
2:E:1138:ALA:HB2	5:E:1301:FAR:H12	1.72	0.72
2:A:211:ALA:HB2	2:A:428:ARG:HD2	1.71	0.72
3:D:10:ILE:HG13	4:C:289:GLN:HE22	1.52	0.72
4:G:220:MET:HE1	4:G:268:PHE:CE2	2.20	0.72
3:P:94:ASP:OD1	3:P:105:GLU:CD	2.33	0.72
2:M:833:LEU:HD22	2:M:835:LYS:HG3	1.72	0.72
2:I:926:VAL:HG21	2:I:1064:LEU:HD21	1.71	0.72
1:F:606:LYS:HD2	1:F:649:VAL:HG22	1.69	0.72
2:E:536:ASN:HB3	2:E:582:ILE:HD11	1.71	0.72
4:C:193:PRO:HB3	4:C:243:MET:HA	1.72	0.72
1:B:1060:LEU:HD22	1:N:1082:VAL:HG11	1.70	0.72
4:C:233:ARG:O	4:C:364:GLN:NE2	2.22	0.72
4:G:233:ARG:O	4:G:364:GLN:NE2	2.22	0.72
4:O:233:ARG:O	4:O:364:GLN:NE2	2.22	0.72
1:J:780:LEU:HD21	1:J:901:GLN:HG2	1.69	0.72
2:E:22:ILE:HG12	2:E:401:MET:HB3	1.72	0.72
4:G:340:LEU:HD12	4:G:342:PRO:HD2	1.71	0.72
1:J:1013:ASN:ND2	5:J:1101:FAR:H111	2.05	0.71
2:E:1078:VAL:HG21	2:E:1135:THR:HG22	1.71	0.71
4:K:116:LEU:HD21	4:K:122:LEU:HD23	1.71	0.71
4:O:193:PRO:HB3	4:O:243:MET:HA	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:340:LEU:CD1	4:O:342:PRO:HD2	2.19	0.71
1:F:103:ARG:NH1	1:F:458:LEU:O	2.23	0.71
3:H:42:GLN:HG3	3:H:42:GLN:O	1.91	0.71
4:G:193:PRO:HB3	4:G:243:MET:HA	1.72	0.71
1:B:602:LEU:HB3	1:B:649:VAL:HG11	1.73	0.71
2:A:1129:GLU:CG	4:C:355:TYR:OH	2.37	0.71
3:D:55:GLU:HG3	4:C:322:TYR:CD1	2.21	0.71
4:K:340:LEU:HD12	4:K:342:PRO:HD2	1.71	0.71
1:B:748:LEU:HB2	1:B:762:VAL:HG11	1.72	0.71
1:J:565:ILE:HG22	1:J:665:VAL:HG23	1.72	0.71
1:J:750:ARG:HG2	1:J:751:GLU:HG2	1.72	0.71
4:C:90:LEU:HD21	4:C:102:LEU:HD23	1.73	0.71
3:L:100:TYR:CB	3:L:136:GLN:OE1	2.38	0.71
2:M:860:PRO:HD2	2:M:863:ARG:HH12	1.54	0.71
3:H:45:THR:HB	3:H:48:GLU:HG2	1.71	0.71
3:L:45:THR:HG22	3:L:47:ALA:H	1.55	0.71
3:L:129:ALA:CB	3:L:145:MET:CE	2.59	0.71
3:P:73:MET:HE1	4:O:317:ARG:NE	2.05	0.71
1:B:132:GLN:HE22	1:B:150:HIS:H	1.39	0.71
2:A:242:LEU:HD11	2:A:270:VAL:HG22	1.71	0.71
1:F:91:ALA:HB1	1:F:118:ALA:HA	1.73	0.71
4:G:26:LEU:HD11	4:G:36:ARG:CG	2.20	0.71
4:G:90:LEU:HD21	4:G:102:LEU:HD23	1.73	0.71
2:M:263:VAL:HB	2:M:276:VAL:HG13	1.72	0.71
1:F:519:THR:HB	1:F:520:PRO:HD2	1.72	0.71
3:L:37:MET:CE	3:L:49:LEU:HD23	1.96	0.71
4:K:90:LEU:HD21	4:K:102:LEU:HD23	1.73	0.71
2:A:199:ALA:HB2	2:A:245:LEU:HD12	1.71	0.71
2:A:593:TYR:CD2	4:C:101:PHE:HE2	2.08	0.71
1:J:1051:MET:HE2	1:J:1051:MET:HA	1.73	0.71
1:F:772:ARG:NH1	1:F:775:SER:OG	2.24	0.71
3:L:118:THR:OG1	3:L:121:GLU:HB2	1.91	0.71
1:B:478:ASN:HB2	1:B:483:PHE:HB2	1.73	0.70
2:M:359:LEU:HD22	2:M:367:PRO:HB2	1.72	0.70
2:I:1215:LEU:O	4:K:330:ARG:NH2	2.23	0.70
1:B:789:THR:HB	1:B:791:LYS:NZ	2.06	0.70
2:A:536:ASN:HB3	2:A:582:ILE:HD11	1.72	0.70
1:F:526:ILE:HD11	1:F:660:ILE:HG21	1.73	0.70
2:E:1196:ARG:HD3	4:G:252:PRO:HD2	1.72	0.70
1:B:495:VAL:HG13	1:B:615:PRO:HG2	1.73	0.70
1:N:875:ARG:HB2	1:N:878:TRP:HB2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:584:ALA:HB1	4:G:54:THR:HG21	1.72	0.70
3:P:118:THR:OG1	3:P:121:GLU:HB2	1.91	0.70
1:B:927:ARG:HA	1:B:930:ILE:HG22	1.73	0.70
2:I:1197:PHE:CE2	4:K:375:PRO:HD3	2.27	0.70
2:E:439:VAL:HG13	2:E:598:ARG:HG3	1.73	0.70
2:E:1086:SER:HB2	2:E:1148:ILE:HD11	1.73	0.70
4:O:90:LEU:HD21	4:O:102:LEU:HD23	1.73	0.70
2:M:303:THR:HG22	2:M:305:LYS:H	1.56	0.70
2:A:1138:ALA:HB1	5:A:1301:FAR:H152	1.72	0.70
3:D:118:THR:OG1	3:D:121:GLU:HB2	1.91	0.70
3:P:102:SER:HB3	3:P:105:GLU:CG	2.20	0.70
2:M:598:ARG:HH22	4:O:14:GLN:HG2	1.56	0.70
1:F:567:ARG:HE	1:F:572:THR:HA	1.57	0.70
2:E:588:LYS:NZ	4:G:52:ASP:OD1	2.25	0.70
2:I:588:LYS:HA	4:K:98:THR:HG21	1.74	0.70
1:J:1016:LEU:HD13	1:J:1077:LEU:HD22	1.73	0.69
1:F:504:GLN:OE1	1:F:504:GLN:N	2.25	0.69
1:N:296:LEU:HD23	1:N:316:THR:HG22	1.74	0.69
1:N:482:ARG:HA	1:N:610:LYS:HG3	1.72	0.69
1:J:725:HIS:ND1	1:J:725:HIS:O	2.25	0.69
2:E:147:GLN:NE2	2:E:424:ASP:OD1	2.25	0.69
2:E:1129:GLU:OE2	4:G:355:TYR:OH	2.05	0.69
4:O:352:PHE:HE2	4:O:367:ARG:NH1	1.90	0.69
1:B:786:ALA:HA	1:B:791:LYS:HE3	1.75	0.69
1:B:1070:THR:CG2	5:N:1101:FAR:H101	2.20	0.69
3:H:118:THR:OG1	3:H:121:GLU:HB2	1.91	0.69
2:A:210:GLU:OE1	2:A:428:ARG:NH1	2.26	0.69
1:J:482:ARG:HA	1:J:610:LYS:HG3	1.74	0.69
1:J:834:ILE:HG22	1:J:838:LYS:HD3	1.74	0.69
1:J:883:MET:HE1	1:J:907:VAL:HG13	1.73	0.69
4:C:207:TYR:CD1	4:C:211:VAL:CG2	2.76	0.69
4:K:193:PRO:HB3	4:K:243:MET:HA	1.72	0.69
2:A:172:ILE:HD11	2:A:205:ALA:HA	1.73	0.69
1:F:574:VAL:HG21	1:F:656:LEU:HD21	1.74	0.69
2:I:1212:GLN:OE1	4:K:330:ARG:CZ	2.41	0.69
2:E:1153:LYS:HB3	2:E:1210:TYR:HE2	1.58	0.69
3:H:45:THR:HG22	3:H:47:ALA:H	1.56	0.69
4:O:117:THR:HA	4:O:367:ARG:NH1	2.04	0.69
1:B:811:THR:HG22	1:B:821:VAL:HG23	1.73	0.69
2:A:817:VAL:HA	2:A:820:ILE:HG12	1.73	0.69
1:F:1082:VAL:HG11	5:F:1101:FAR:H103	1.70	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:57:ASP:HB3	4:K:125:LYS:HZ2	1.56	0.69
1:B:498:ALA:HB3	1:B:618:LEU:HG	1.73	0.69
1:B:567:ARG:NH1	1:B:572:THR:OG1	2.26	0.69
1:F:212:VAL:HA	1:F:215:VAL:HG12	1.74	0.69
4:G:355:TYR:HB3	4:G:358:TRP:HD1	1.56	0.69
2:I:439:VAL:HG13	2:I:598:ARG:HB3	1.74	0.69
2:E:400:HIS:CD2	2:E:403:GLY:H	2.11	0.69
2:I:262:VAL:HG13	2:I:269:ALA:HB3	1.74	0.69
2:A:106:GLN:N	2:A:106:GLN:OE1	2.26	0.68
2:A:858:LEU:HD12	2:A:863:ARG:HE	1.58	0.68
1:F:297:LEU:HD12	1:F:371:TYR:HB3	1.74	0.68
1:F:954:ASN:HB3	1:F:1021:LYS:HG2	1.75	0.68
4:K:233:ARG:O	4:K:364:GLN:NE2	2.22	0.68
2:A:1120:GLN:NE2	2:A:1123:TYR:HB3	2.08	0.68
2:A:78:GLU:HB3	2:A:153:LEU:HD11	1.74	0.68
4:O:207:TYR:CD1	4:O:211:VAL:CG2	2.75	0.68
2:M:853:HIS:HB2	2:M:917:ARG:HG2	1.76	0.68
2:M:1167:LYS:HA	2:M:1167:LYS:HE3	1.76	0.68
1:J:796:ILE:HD13	1:J:851:GLN:HE22	1.57	0.68
4:K:346:LEU:HD22	4:K:350:TYR:HE1	1.59	0.68
3:D:57:ASP:HB3	4:C:125:LYS:HZ2	1.58	0.68
4:G:346:LEU:HD22	4:G:350:TYR:HE1	1.59	0.68
3:P:55:GLU:CG	4:O:322:TYR:CD1	2.73	0.68
1:B:1012:ARG:NH1	1:N:1013:ASN:HA	2.08	0.68
1:N:565:ILE:HD13	1:N:660:ILE:HG13	1.75	0.68
2:A:293:CYS:HG	2:A:332:TRP:CD1	2.11	0.68
1:J:606:LYS:HD2	1:J:649:VAL:HG22	1.75	0.68
1:F:566:TYR:HD2	1:F:668:LEU:HD21	1.59	0.68
4:O:131:MET:HA	4:O:134:LEU:HB3	1.75	0.68
1:N:951:ARG:NH1	1:N:1010:LEU:O	2.27	0.68
4:C:92:ASP:OD1	4:C:93:THR:N	2.27	0.68
4:C:131:MET:HA	4:C:134:LEU:HB3	1.75	0.68
4:K:75:VAL:O	4:K:79:ARG:HG3	1.93	0.68
2:A:1112:GLU:OE2	2:A:1124:ARG:NH2	2.23	0.68
3:D:42:GLN:HG3	3:D:42:GLN:O	1.93	0.68
4:G:131:MET:HA	4:G:134:LEU:HB3	1.76	0.68
1:N:512:THR:HB	2:I:559:GLN:HE21	1.59	0.67
1:N:859:TRP:O	1:N:863:ASN:ND2	2.27	0.67
1:J:839:CYS:SG	1:J:840:ASN:N	2.67	0.67
2:I:1212:GLN:OE1	4:K:330:ARG:NE	2.26	0.67
4:K:207:TYR:HD1	4:K:211:VAL:HG21	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:92:ASP:OD1	4:O:93:THR:N	2.27	0.67
1:B:150:HIS:HA	1:B:169:HIS:HB3	1.75	0.67
2:M:1092:LEU:HB2	2:M:1114:VAL:HG21	1.74	0.67
1:B:331:LYS:HD2	1:B:362:GLU:HB2	1.77	0.67
1:J:883:MET:HE3	1:J:899:LEU:HD11	1.75	0.67
3:H:55:GLU:CG	4:G:322:TYR:CD1	2.73	0.67
3:L:55:GLU:CG	4:K:322:TYR:CD1	2.73	0.67
2:A:536:ASN:HA	2:A:539:ILE:HD12	1.76	0.67
2:I:785:MET:HA	2:I:788:THR:HG22	1.76	0.67
2:E:86:ARG:HG3	2:E:90:HIS:CE1	2.29	0.67
2:E:320:LEU:O	2:E:384:TYR:OH	2.13	0.67
4:C:346:LEU:HD22	4:C:350:TYR:HE1	1.59	0.67
4:C:355:TYR:HB3	4:C:358:TRP:HD1	1.60	0.67
4:O:346:LEU:HD22	4:O:350:TYR:HE1	1.59	0.67
1:N:499:LEU:HD11	1:N:638:LEU:HD22	1.76	0.67
1:N:928:ARG:HH12	1:N:1065:THR:HG21	1.59	0.67
1:F:523:VAL:HG12	1:F:657:GLN:HE22	1.60	0.67
4:K:92:ASP:OD1	4:K:93:THR:N	2.27	0.67
5:J:1101:FAR:H152	1:F:1074:MET:HE3	1.75	0.67
1:F:643:LYS:O	1:F:643:LYS:NZ	2.23	0.67
5:E:1301:FAR:C4	4:G:330:ARG:HG3	2.24	0.67
4:O:117:THR:N	4:O:367:ARG:HH22	1.93	0.67
1:J:951:ARG:NH2	1:J:1016:LEU:O	2.27	0.67
1:J:995:TYR:O	1:J:999:VAL:HG23	1.95	0.67
2:E:206:LYS:HD2	2:E:239:GLN:HG2	1.77	0.67
2:I:249:ALA:CB	2:I:256:ASP:OD2	2.43	0.67
3:P:110:MET:HG2	4:O:308:ILE:HD13	1.77	0.67
4:G:92:ASP:OD1	4:G:93:THR:N	2.27	0.66
1:B:796:ILE:O	1:B:800:ILE:HD12	1.94	0.66
2:A:1215:LEU:O	4:C:330:ARG:NH2	2.28	0.66
1:J:509:PHE:HE2	1:J:626:ILE:HG21	1.59	0.66
4:G:207:TYR:HD1	4:G:211:VAL:HG21	1.58	0.66
3:P:129:ALA:CB	3:P:145:MET:CE	2.59	0.66
3:D:110:MET:HG2	4:C:308:ILE:HD13	1.77	0.66
4:C:207:TYR:HD1	4:C:211:VAL:HG21	1.58	0.66
4:G:26:LEU:CD1	4:G:36:ARG:HG3	2.26	0.66
1:J:956:ILE:HA	1:J:1022:VAL:HB	1.76	0.66
1:J:1066:CYS:SG	5:F:1101:FAR:H61	2.36	0.66
1:F:853:LEU:O	1:F:857:ILE:N	2.25	0.66
1:B:258:GLN:HG3	2:A:75:TYR:HB2	1.77	0.66
1:B:948:ILE:HD11	1:B:1007:SER:HA	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1212:GLN:HG3	4:G:330:ARG:HD3	1.77	0.66
1:B:818:GLU:OE1	1:B:818:GLU:N	2.21	0.66
1:B:859:TRP:HE3	1:B:860:ILE:HD13	1.61	0.66
1:B:1063:ARG:HH12	1:N:1079:GLU:HA	1.60	0.66
1:B:1070:THR:HA	1:B:1073:VAL:HG22	1.78	0.66
1:N:839:CYS:SG	1:N:840:ASN:ND2	2.68	0.66
1:F:56:VAL:HG22	1:F:449:ILE:HG13	1.76	0.66
4:K:207:TYR:CD1	4:K:211:VAL:CG2	2.76	0.66
2:M:817:VAL:HA	2:M:820:ILE:HG12	1.78	0.66
2:A:586:LEU:HA	2:A:589:MET:HE3	1.78	0.66
2:A:1078:VAL:HG21	2:A:1135:THR:HG22	1.77	0.66
1:N:727:ILE:HG12	1:N:743:LEU:HD11	1.78	0.66
1:J:130:MET:HB2	2:I:29:VAL:HG13	1.78	0.66
1:F:185:MET:HB3	1:F:190:LEU:HD12	1.76	0.66
1:F:820:GLU:OE1	1:F:820:GLU:N	2.27	0.66
2:I:458:LYS:HE2	2:I:458:LYS:HA	1.76	0.66
1:F:737:LEU:HD23	1:F:740:GLN:HE21	1.61	0.66
1:F:856:HIS:HA	1:F:908:LYS:HZ1	1.61	0.66
2:E:567:SER:HB2	2:E:570:MET:HE3	1.78	0.66
2:E:1215:LEU:O	4:G:330:ARG:NH2	2.28	0.66
1:J:589:GLN:O	1:J:777:LYS:NZ	2.29	0.66
2:E:166:GLN:HE21	2:E:486:LEU:HD22	1.61	0.66
4:K:220:MET:CE	4:K:268:PHE:HE2	2.09	0.66
2:A:606:GLU:N	2:A:606:GLU:OE2	2.29	0.65
1:J:1003:LEU:HD11	1:J:1024:LEU:HD13	1.78	0.65
3:H:110:MET:HG2	4:G:308:ILE:HD13	1.77	0.65
4:K:86:ASN:HA	4:K:165:LYS:HZ1	1.61	0.65
3:P:37:MET:CE	3:P:44:PRO:HG2	2.27	0.65
2:M:505:LEU:O	2:M:509:LYS:NZ	2.30	0.65
2:A:117:ASN:OD1	2:A:120:THR:N	2.29	0.65
3:L:110:MET:HG2	4:K:308:ILE:HD13	1.77	0.65
1:F:356:LYS:CD	1:F:970:SER:HB3	2.26	0.65
1:F:518:GLN:HE21	1:F:655:ARG:HB3	1.51	0.65
1:B:531:GLN:HG2	1:B:578:ILE:HG22	1.77	0.65
2:M:816:LYS:HD2	2:M:816:LYS:H	1.61	0.65
1:N:569:LEU:HD11	1:N:677:GLU:HA	1.78	0.65
2:E:40:LYS:NZ	2:E:117:ASN:OD1	2.29	0.65
3:H:57:ASP:HB3	4:G:125:LYS:HZ2	1.61	0.65
2:A:169:VAL:HA	2:A:172:ILE:HG22	1.79	0.65
1:N:772:ARG:HH12	1:N:776:GLN:HB2	1.61	0.65
1:J:75:THR:OG1	1:J:438:GLY:O	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:589:MET:HB3	2:I:599:VAL:HG11	1.78	0.65
2:E:168:LEU:O	2:E:172:ILE:HG22	1.96	0.65
2:E:892:ILE:HA	2:E:895:GLN:HE21	1.61	0.65
3:L:100:TYR:HB2	3:L:136:GLN:NE2	2.12	0.65
2:A:829:ILE:HD12	2:A:832:ILE:HD11	1.79	0.65
1:J:320:VAL:HG13	1:J:324:LEU:HD12	1.78	0.65
5:J:1101:FAR:H152	1:F:1074:MET:HE1	1.77	0.65
2:E:588:LYS:HE3	4:G:99:PHE:CE2	2.31	0.65
1:B:81:LYS:HZ1	1:B:162:LEU:HG	1.62	0.65
1:J:493:LEU:HD23	1:J:606:LYS:HA	1.78	0.65
2:E:828:TYR:HA	2:E:888:MET:HE1	1.79	0.65
1:B:50:ASP:O	1:B:54:ARG:HG3	1.97	0.65
2:M:29:VAL:HG11	1:N:131:ARG:HG3	1.77	0.65
2:E:419:ALA:HB3	2:E:422:GLU:HG3	1.79	0.65
4:K:131:MET:HA	4:K:134:LEU:HB3	1.79	0.65
4:O:36:ARG:HD2	4:O:106:LEU:HD21	1.77	0.65
1:B:607:GLN:NE2	1:B:607:GLN:O	2.30	0.64
2:A:892:ILE:HA	2:A:895:GLN:HE21	1.62	0.64
2:A:956:ASN:O	2:A:960:HIS:ND1	2.30	0.64
1:J:1053:SER:HA	1:J:1056:ASN:ND2	2.12	0.64
2:I:246:LEU:HD22	2:I:270:VAL:HG11	1.79	0.64
3:D:37:MET:HE2	3:D:49:LEU:HD22	1.79	0.64
4:G:207:TYR:CD1	4:G:211:VAL:CG2	2.76	0.64
4:G:220:MET:CE	4:G:268:PHE:HE2	2.09	0.64
3:L:100:TYR:CD1	3:L:136:GLN:OE1	2.50	0.64
1:B:1009:VAL:HA	5:N:1101:FAR:H141	1.77	0.64
2:A:202:VAL:HG11	2:A:241:ILE:HD11	1.79	0.64
3:L:100:TYR:HB3	3:L:136:GLN:CG	2.27	0.64
4:O:220:MET:CE	4:O:268:PHE:HE2	2.09	0.64
1:B:924:TRP:HA	1:B:927:ARG:HD3	1.78	0.64
2:M:368:LEU:HD12	2:M:399:PRO:HB3	1.79	0.64
2:M:956:ASN:O	2:M:960:HIS:ND1	2.30	0.64
2:A:567:SER:HB2	2:A:570:MET:HE2	1.79	0.64
1:F:1082:VAL:HB	5:F:1101:FAR:H62	1.79	0.64
2:E:1196:ARG:HH11	4:G:252:PRO:HD3	1.62	0.64
2:I:1077:LYS:O	2:I:1080:GLN:NE2	2.30	0.64
1:F:839:CYS:SG	1:F:840:ASN:N	2.70	0.64
1:F:1082:VAL:HG11	5:F:1101:FAR:H102	1.78	0.64
3:P:21:ASP:HB3	3:P:28:ILE:HD13	1.80	0.64
1:B:1001:GLU:HG2	1:N:1092:ILE:HD12	1.80	0.64
2:I:785:MET:N	2:I:785:MET:SD	2.70	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:860:ILE:HB	1:F:868:PHE:HE2	1.63	0.64
2:A:211:ALA:HB1	2:A:426:LEU:HD13	1.79	0.64
2:I:1054:TRP:NE1	4:K:369:ALA:O	2.29	0.64
1:F:356:LYS:HD3	1:F:970:SER:HB3	1.80	0.64
3:P:37:MET:HE2	3:P:49:LEU:HD22	1.80	0.64
2:M:340:VAL:HG11	2:M:413:MET:HE3	1.80	0.64
2:A:927:MET:HE2	2:A:957:LEU:HD23	1.80	0.64
1:B:347:ARG:NH1	1:B:349:TYR:O	2.30	0.64
1:B:569:LEU:HD21	1:B:677:GLU:HA	1.80	0.64
2:A:509:LYS:HB2	2:A:511:TYR:CE1	2.31	0.64
5:J:1101:FAR:C15	1:F:1013:ASN:ND2	2.54	0.64
2:E:439:VAL:H	2:E:559:GLN:HE22	1.46	0.64
2:E:858:LEU:HD12	2:E:863:ARG:HE	1.63	0.64
1:N:377:VAL:HG11	1:N:454:LEU:HB3	1.78	0.64
1:J:1060:LEU:HD22	5:F:1101:FAR:C3	2.28	0.64
1:F:820:GLU:OE2	1:F:838:LYS:NZ	2.31	0.64
2:E:57:LEU:HB3	2:E:77:LEU:HD13	1.79	0.64
4:G:86:ASN:HA	4:G:165:LYS:HZ1	1.62	0.64
3:L:21:ASP:HB3	3:L:28:ILE:HD13	1.80	0.64
4:O:86:ASN:HA	4:O:165:LYS:HZ1	1.61	0.64
1:F:631:PHE:HE1	1:F:635:LEU:HD22	1.63	0.63
2:E:1196:ARG:NH1	4:G:252:PRO:HD3	2.13	0.63
3:H:37:MET:HE2	3:H:49:LEU:HD22	1.79	0.63
4:C:240:ARG:O	4:C:244:SER:OG	2.11	0.63
1:B:779:TRP:HE1	1:B:904:PRO:HD3	1.62	0.63
1:F:876:ILE:H	1:F:876:ILE:HD12	1.62	0.63
2:E:515:LYS:N	2:E:515:LYS:HE2	2.14	0.63
2:E:1196:ARG:CZ	4:G:251:SER:O	2.47	0.63
1:B:193:ILE:O	2:A:75:TYR:OH	2.15	0.63
1:B:366:PRO:HB3	1:B:395:VAL:HG21	1.80	0.63
2:A:442:VAL:HG22	2:A:562:ILE:HB	1.79	0.63
2:A:1131:ILE:HA	2:A:1134:LEU:HD12	1.80	0.63
2:I:588:LYS:CE	4:K:52:ASP:OD2	2.46	0.63
2:I:788:THR:C	2:I:790:LYS:H	2.06	0.63
3:H:101:ILE:HB	3:H:137:VAL:H	1.63	0.63
3:P:101:ILE:HB	3:P:137:VAL:H	1.64	0.63
1:B:330:PHE:HB2	1:B:368:PHE:HB2	1.81	0.63
1:J:1090:CYS:HG	5:J:1101:FAR:C1	1.29	0.63
2:I:890:ILE:HD11	2:I:924:ILE:HG12	1.78	0.63
1:B:624:ASP:O	1:B:630:ARG:NH2	2.32	0.63
2:E:905:MET:HA	2:E:905:MET:HE3	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:258:SER:O	4:C:262:LYS:NZ	2.31	0.63
2:M:810:LEU:O	2:M:814:TYR:N	2.26	0.63
2:M:1094:SER:O	2:M:1097:THR:OG1	2.15	0.63
2:A:320:LEU:O	2:A:384:TYR:OH	2.15	0.63
1:N:840:ASN:ND2	1:N:850:GLN:OE1	2.31	0.63
1:N:853:LEU:O	1:N:857:ILE:HG13	1.99	0.63
1:J:1015:GLU:HG2	5:J:1101:FAR:H42	1.81	0.63
2:I:546:ASP:OD1	2:I:547:LEU:N	2.32	0.63
1:F:462:LYS:NZ	1:F:463:ASP:OD1	2.32	0.63
2:E:261:SER:HA	2:E:334:TYR:HE2	1.63	0.63
4:G:36:ARG:HG2	4:G:106:LEU:HD11	1.78	0.63
4:G:258:SER:O	4:G:262:LYS:NZ	2.31	0.63
1:B:223:ARG:HB3	1:B:228:ASN:HD21	1.64	0.63
2:E:239:GLN:HB2	2:E:553:ARG:HH21	1.63	0.63
2:E:513:ILE:HD11	2:E:619:MET:HB2	1.79	0.63
4:G:240:ARG:O	4:G:244:SER:OG	2.11	0.63
2:M:1161:LEU:HD21	2:M:1205:LYS:HD3	1.81	0.63
1:J:499:LEU:HB3	1:J:517:THR:HG22	1.81	0.63
1:J:745:GLY:HA3	1:J:788:PHE:HD2	1.63	0.63
2:I:90:HIS:HA	2:I:93:ILE:HG22	1.81	0.63
2:I:888:MET:SD	2:I:888:MET:N	2.64	0.63
1:F:285:ARG:NH2	1:F:288:ARG:O	2.31	0.63
2:E:559:GLN:H	2:E:611:SER:HA	1.64	0.63
2:E:593:TYR:HE2	4:G:16:PHE:HE2	1.47	0.63
1:B:98:ALA:HB1	1:B:115:GLU:HG3	1.80	0.62
2:M:140:VAL:HG23	2:M:204:MET:HE2	1.80	0.62
2:A:279:THR:O	2:A:283:ILE:HG13	1.98	0.62
1:F:331:LYS:HD2	1:F:362:GLU:HB2	1.81	0.62
2:E:492:MET:HE3	2:E:494:LEU:HD12	1.80	0.62
2:M:1157:ILE:O	2:M:1161:LEU:N	2.24	0.62
2:A:70:ASP:OD1	2:A:73:LYS:NZ	2.32	0.62
2:A:1192:ALA:HB3	4:C:372:GLU:HB2	1.80	0.62
4:K:258:SER:O	4:K:262:LYS:NZ	2.31	0.62
1:B:847:ALA:HA	1:B:850:GLN:NE2	2.14	0.62
1:B:887:LEU:HD22	1:B:897:LEU:HB2	1.81	0.62
2:M:29:VAL:HG22	1:N:130:MET:HB3	1.81	0.62
2:M:1155:VAL:HA	2:M:1203:LEU:HD21	1.80	0.62
2:I:1136:MET:HB3	4:K:350:TYR:CZ	2.34	0.62
3:D:55:GLU:CG	4:C:322:TYR:CD1	2.74	0.62
4:O:258:SER:O	4:O:262:LYS:NZ	2.31	0.62
2:E:356:GLU:HA	2:E:359:LEU:HD12	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:100:TYR:CB	3:L:136:GLN:NE2	2.62	0.62
3:P:45:THR:HG22	3:P:47:ALA:N	2.14	0.62
1:B:202:ILE:O	1:B:206:VAL:HG23	1.99	0.62
1:B:642:LYS:HA	1:B:653:VAL:HG21	1.82	0.62
2:A:11:LEU:HB3	2:A:61:TYR:CE1	2.31	0.62
2:A:593:TYR:HD2	4:C:101:PHE:CE2	2.16	0.62
2:A:1196:ARG:HD3	4:C:252:PRO:HD2	1.81	0.62
2:I:1196:ARG:HG2	4:K:373:ASN:HA	1.80	0.62
1:F:626:ILE:HG23	1:F:631:PHE:HD2	1.64	0.62
3:L:101:ILE:HB	3:L:137:VAL:H	1.63	0.62
1:F:46:TRP:HZ3	1:F:101:TYR:HE1	1.48	0.62
1:B:1013:ASN:OD1	1:N:1012:ARG:NH1	2.32	0.62
1:N:404:PRO:O	1:N:445:GLN:NE2	2.31	0.62
1:N:772:ARG:NH1	1:N:772:ARG:O	2.32	0.62
1:J:1071:LYS:NZ	1:F:1075:ASN:OD1	2.32	0.62
2:M:823:TRP:HA	2:M:826:ILE:HG22	1.81	0.62
2:A:1191:SER:OG	4:C:376:LYS:NZ	2.31	0.62
1:J:509:PHE:CE2	1:J:626:ILE:HG21	2.35	0.62
2:I:900:TYR:HE2	2:I:954:MET:HB3	1.65	0.62
1:F:999:VAL:HG13	1:F:1024:LEU:HD23	1.82	0.62
3:D:21:ASP:HB3	3:D:28:ILE:HD13	1.80	0.62
4:K:240:ARG:O	4:K:244:SER:OG	2.11	0.62
1:B:496:HIS:HB3	1:B:659:LEU:HD13	1.82	0.62
1:N:744:LEU:HB2	1:N:766:ILE:HG22	1.82	0.62
1:J:773:ALA:HA	1:J:776:GLN:NE2	2.15	0.62
2:I:1122:GLU:OE1	2:I:1122:GLU:N	2.29	0.62
2:I:1163:LEU:HD22	2:I:1176:LEU:HD13	1.81	0.62
1:F:831:ILE:HA	1:F:834:ILE:HD12	1.81	0.62
3:D:101:ILE:HB	3:D:137:VAL:H	1.64	0.62
4:O:24:GLU:OE1	4:O:36:ARG:NH2	2.32	0.62
4:O:117:THR:N	4:O:367:ARG:NH2	2.47	0.62
1:B:101:TYR:HB3	1:B:111:THR:HG22	1.81	0.62
2:M:479:LEU:HG	2:M:502:MET:HE3	1.80	0.62
1:J:523:VAL:HG11	1:J:656:LEU:HD23	1.82	0.62
2:I:1196:ARG:NH2	4:K:252:PRO:CD	2.60	0.62
1:F:586:TYR:OH	1:F:783:ARG:NH1	2.33	0.62
1:B:744:LEU:HD22	1:B:765:HIS:CE1	2.35	0.61
1:B:951:ARG:NH2	1:B:1016:LEU:O	2.33	0.61
2:M:45:ARG:NH2	2:M:134:GLN:OE1	2.33	0.61
1:N:335:ARG:NH2	1:N:970:SER:O	2.33	0.61
2:E:210:GLU:HG3	2:E:428:ARG:HH12	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:313:LEU:HG	4:O:317:ARG:NE	2.15	0.61
1:N:566:TYR:HB2	1:N:573:VAL:HG23	1.82	0.61
1:J:591:VAL:HG11	1:J:630:ARG:HB3	1.81	0.61
1:J:851:GLN:O	1:J:855:ILE:HG13	2.00	0.61
2:I:788:THR:C	2:I:790:LYS:N	2.56	0.61
2:I:1196:ARG:NH2	4:K:251:SER:O	2.33	0.61
2:E:579:ASN:OD1	2:E:580:SER:N	2.33	0.61
4:C:152:LYS:HZ3	4:C:190:TYR:HB2	1.65	0.61
3:L:37:MET:HE2	3:L:49:LEU:HD22	1.80	0.61
1:B:764:ASP:OD1	1:B:765:HIS:N	2.33	0.61
2:M:1169:LEU:HD13	4:O:375:PRO:HG3	1.82	0.61
2:A:1124:ARG:HA	2:A:1127:LEU:HD12	1.81	0.61
2:E:1192:ALA:HB3	4:G:372:GLU:HB2	1.83	0.61
3:L:66:PHE:HB3	4:K:291:TYR:HB2	1.81	0.61
2:M:431:SER:O	2:M:435:LYS:NZ	2.34	0.61
5:J:1101:FAR:H151	5:F:1101:FAR:H153	1.83	0.61
1:F:150:HIS:HA	1:F:169:HIS:HB3	1.81	0.61
2:E:369:LEU:N	2:E:404:GLN:OE1	2.30	0.61
3:H:21:ASP:HB3	3:H:28:ILE:HD13	1.80	0.61
4:O:152:LYS:HZ3	4:O:190:TYR:HB2	1.65	0.61
1:B:226:LYS:HD3	1:B:335:ARG:HB2	1.82	0.61
1:N:963:LEU:HD11	1:N:982:LEU:HG	1.83	0.61
1:J:213:TYR:HE2	1:J:274:ARG:HH11	1.49	0.61
5:J:1101:FAR:H141	1:F:1013:ASN:ND2	2.15	0.61
2:A:593:TYR:CD2	4:C:101:PHE:CE2	2.89	0.61
1:B:148:CYS:O	1:B:164:TYR:OH	2.18	0.61
1:B:954:ASN:HB2	1:B:1021:LYS:HG2	1.82	0.61
1:N:961:LYS:NZ	1:N:985:ASP:OD1	2.33	0.61
2:I:901:LEU:HD12	2:I:958:LEU:HD21	1.83	0.61
1:F:375:ASP:O	1:F:379:ARG:HG3	2.01	0.61
3:H:51:ASP:CB	4:G:322:TYR:CZ	2.84	0.61
2:M:239:GLN:HE22	2:M:271:GLU:HG3	1.66	0.61
2:I:588:LYS:NZ	4:K:52:ASP:OD2	2.33	0.61
1:F:776:GLN:HE22	1:F:778:LEU:HB2	1.64	0.61
4:K:131:MET:HE1	4:K:220:MET:HG3	1.82	0.61
3:P:51:ASP:CB	4:O:322:TYR:CZ	2.84	0.61
1:B:568:ILE:N	1:B:571:LYS:O	2.32	0.61
1:B:1002:LEU:HG	1:B:1024:LEU:HD12	1.83	0.61
1:F:467:VAL:O	1:F:468:GLN:C	2.43	0.61
1:F:879:ILE:O	1:F:883:MET:N	2.32	0.61
2:E:52:LEU:HB3	2:E:409:LEU:HD12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:958:LEU:HD12	2:E:961:ILE:HD11	1.83	0.61
2:A:262:VAL:HA	2:A:267:ALA:HB3	1.82	0.61
1:N:336:ASP:H	1:N:362:GLU:HG2	1.65	0.61
1:J:574:VAL:HB	1:J:618:LEU:HD11	1.83	0.61
2:I:538:MET:HE1	2:I:955:LYS:HD2	1.83	0.61
2:E:146:ALA:HB2	2:E:212:LEU:HD23	1.82	0.61
4:C:220:MET:CE	4:C:268:PHE:HE2	2.09	0.61
4:G:26:LEU:CG	4:G:36:ARG:CG	2.65	0.61
2:M:1149:ILE:HA	2:M:1210:TYR:HE2	1.66	0.60
1:J:796:ILE:HD13	1:J:851:GLN:NE2	2.15	0.60
2:E:1130:ALA:HB2	2:E:1203:LEU:HD22	1.82	0.60
1:B:270:ASP:OD2	1:B:558:GLY:C	2.44	0.60
2:M:561:THR:HG1	2:M:611:SER:HG	1.45	0.60
2:A:15:ALA:HB2	2:A:61:TYR:OH	2.02	0.60
2:A:101:SER:O	2:A:105:SER:OG	2.19	0.60
2:A:1196:ARG:CZ	4:C:251:SER:O	2.48	0.60
2:I:784:TYR:CE2	2:I:825:LEU:HD22	2.36	0.60
2:E:1096:THR:HB	2:E:1100:MET:HE2	1.82	0.60
2:M:197:LEU:HD13	2:M:870:PRO:HG2	1.82	0.60
2:M:1081:LYS:HB2	5:M:1301:FAR:H143	1.82	0.60
2:A:536:ASN:HD22	2:A:579:ASN:HD22	1.49	0.60
2:A:589:MET:HB3	2:A:599:VAL:HG11	1.83	0.60
1:N:276:ARG:HH12	1:N:482:ARG:HB2	1.66	0.60
1:J:98:ALA:HB2	1:J:114:LEU:HB2	1.83	0.60
3:L:51:ASP:CB	4:K:322:TYR:CZ	2.84	0.60
1:B:670:PHE:HA	1:B:673:ILE:HG12	1.83	0.60
1:B:916:GLN:OE1	1:B:917:PRO:HD2	2.01	0.60
1:B:1074:MET:HA	1:B:1074:MET:HE3	1.82	0.60
1:N:839:CYS:SG	1:N:840:ASN:N	2.73	0.60
1:N:1064:GLY:O	1:N:1067:SER:OG	2.18	0.60
2:I:1070:GLY:HA2	2:I:1073:GLN:HE21	1.66	0.60
1:F:91:ALA:HB3	1:F:122:MET:HE2	1.84	0.60
1:F:951:ARG:HH21	1:F:1010:LEU:HG	1.67	0.60
2:E:156:ILE:HG12	2:E:217:LEU:HG	1.83	0.60
2:E:787:TYR:HA	2:E:790:LYS:HG2	1.83	0.60
1:N:853:LEU:HD21	1:N:883:MET:HE1	1.83	0.60
2:A:1129:GLU:OE2	4:C:355:TYR:OH	2.14	0.60
1:N:285:ARG:NH2	1:N:288:ARG:O	2.35	0.60
1:N:1010:LEU:HD21	1:N:1018:PHE:HE1	1.65	0.60
1:B:503:SER:HA	1:B:687:GLU:HG2	1.84	0.60
1:B:745:GLY:HA3	1:B:788:PHE:HD2	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:1078:VAL:HG21	2:M:1135:THR:HG22	1.84	0.60
1:J:1033:ASN:O	1:J:1037:LYS:HG2	2.02	0.60
1:B:992:GLN:HG3	1:B:995:TYR:H	1.66	0.60
1:F:872:LEU:HD21	1:F:977:MET:HE2	1.83	0.60
4:G:152:LYS:HZ3	4:G:190:TYR:HB2	1.67	0.60
4:K:182:ARG:NH2	4:K:202:GLU:O	2.35	0.60
4:O:24:GLU:CG	4:O:36:ARG:HH21	2.08	0.60
4:O:182:ARG:NH2	4:O:202:GLU:O	2.35	0.60
1:N:592:PHE:HB2	1:N:905:SER:HB2	1.82	0.60
1:J:155:VAL:HG13	1:J:156:HIS:ND1	2.17	0.60
2:E:817:VAL:HA	2:E:820:ILE:HG12	1.83	0.60
1:B:221:TRP:CD2	1:B:332:ARG:HD2	2.37	0.59
2:M:57:LEU:HB3	2:M:77:LEU:HD13	1.84	0.59
1:J:1036:GLN:NE2	1:J:1048:GLN:OE1	2.35	0.59
5:J:1101:FAR:C2	1:F:1008:ILE:HG21	2.30	0.59
1:F:499:LEU:HD21	1:F:641:LEU:HD11	1.83	0.59
2:E:858:LEU:HB3	2:E:859:PRO:HD2	1.84	0.59
3:P:129:ALA:HA	4:O:302:ARG:HH12	1.67	0.59
2:M:147:GLN:HG2	2:M:426:LEU:HD12	1.84	0.59
1:N:527:GLN:HB2	1:N:573:VAL:HG12	1.84	0.59
3:D:129:ALA:HA	4:C:302:ARG:HH12	1.67	0.59
1:F:49:LEU:HD12	1:F:104:ILE:HD11	1.82	0.59
1:F:236:SER:HB2	1:F:296:LEU:HD21	1.83	0.59
2:A:181:PHE:HA	2:A:187:GLY:HA2	1.84	0.59
2:A:356:GLU:HA	2:A:359:LEU:HD12	1.84	0.59
2:A:916:PHE:HE1	2:A:1112:GLU:HG3	1.68	0.59
2:A:919:ARG:HD3	2:A:922:LEU:HD12	1.85	0.59
1:J:504:GLN:NE2	1:J:507:GLN:OE1	2.26	0.59
1:J:815:PHE:HD1	1:J:816:GLY:N	2.00	0.59
2:I:1129:GLU:OE2	4:K:355:TYR:OH	2.00	0.59
1:F:347:ARG:NH1	1:F:349:TYR:O	2.34	0.59
2:E:956:ASN:O	2:E:960:HIS:ND1	2.34	0.59
1:B:914:ILE:HA	1:B:930:ILE:HD11	1.85	0.59
2:M:1166:GLN:HB2	2:M:1176:LEU:HD11	1.83	0.59
2:I:206:LYS:HG3	2:I:235:VAL:HG13	1.83	0.59
2:I:1137:LEU:HB3	5:I:1301:FAR:H2	1.84	0.59
1:F:181:TYR:O	1:F:185:MET:HG2	2.03	0.59
2:M:51:ILE:HG13	2:M:81:VAL:HG22	1.84	0.59
2:M:536:ASN:HA	2:M:539:ILE:HG12	1.84	0.59
2:A:479:LEU:HD11	2:A:511:TYR:HE2	1.67	0.59
2:A:1196:ARG:NH1	4:C:252:PRO:HD3	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:810:VAL:HG22	1:F:874:ILE:HD11	1.84	0.59
4:C:182:ARG:NH2	4:C:202:GLU:O	2.35	0.59
1:B:499:LEU:HD21	1:B:653:VAL:HG13	1.85	0.59
1:B:830:VAL:HA	1:B:833:ASN:ND2	2.17	0.59
1:N:269:LEU:HD11	1:N:611:MET:HE2	1.85	0.59
1:F:747:LEU:HD22	1:F:762:VAL:HG21	1.83	0.59
4:C:329:THR:H	4:C:332:ILE:HD11	1.68	0.59
3:P:66:PHE:HB3	4:O:291:TYR:HB2	1.84	0.59
1:B:1029:LYS:HD3	1:B:1033:ASN:HD21	1.67	0.59
1:N:1023:ASP:OD2	1:N:1026:ARG:HB2	2.02	0.59
2:I:261:SER:HA	2:I:265:PHE:O	2.03	0.59
2:E:531:TYR:HE2	2:E:892:ILE:HD11	1.68	0.59
1:B:627:ARG:NH1	1:B:627:ARG:HB2	2.18	0.59
2:I:1061:ASP:OD1	2:I:1066:ARG:NE	2.35	0.59
4:O:329:THR:H	4:O:332:ILE:HD11	1.68	0.59
1:B:332:ARG:HG3	1:B:365:PHE:CE1	2.37	0.59
1:B:876:ILE:O	1:B:880:ILE:HD12	2.02	0.59
2:M:619:MET:HA	2:M:619:MET:HE3	1.84	0.59
1:N:587:MET:HB3	1:N:593:LEU:HD12	1.84	0.59
1:F:221:TRP:CE3	1:F:332:ARG:HD2	2.38	0.59
2:E:108:THR:HA	2:E:133:LEU:HD12	1.84	0.59
2:E:162:VAL:HG22	2:E:217:LEU:HD23	1.85	0.59
4:K:130:ILE:HG12	4:K:164:ILE:HD11	1.85	0.59
4:O:47:ALA:HB2	4:O:106:LEU:HD12	1.85	0.59
1:N:288:ARG:NH2	1:N:823:SER:O	2.36	0.58
1:J:1013:ASN:HD21	5:J:1101:FAR:H111	1.67	0.58
5:E:1301:FAR:H42	4:G:330:ARG:HA	1.84	0.58
3:H:129:ALA:HA	4:G:302:ARG:HH12	1.67	0.58
4:G:182:ARG:NH2	4:G:202:GLU:O	2.35	0.58
4:K:152:LYS:HZ3	4:K:190:TYR:HB2	1.67	0.58
4:O:221:TYR:HB3	4:O:229:PRO:HG3	1.85	0.58
1:B:1005:VAL:HG11	1:B:1069:LEU:HB3	1.85	0.58
1:N:929:GLN:NE2	1:N:994:GLN:OE1	2.36	0.58
1:F:95:TRP:CD1	1:F:190:LEU:HD11	2.38	0.58
1:F:671:LEU:O	1:F:676:THR:OG1	2.20	0.58
2:E:917:ARG:HH12	2:E:1112:GLU:HG2	1.69	0.58
3:L:129:ALA:HA	4:K:302:ARG:HH12	1.67	0.58
1:B:742:ILE:O	1:B:746:ILE:HG12	2.03	0.58
2:M:837:VAL:HG23	2:M:840:LEU:HD23	1.86	0.58
2:A:784:TYR:O	2:A:788:THR:OG1	2.18	0.58
2:A:958:LEU:HA	2:A:961:ILE:HD12	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:867:LEU:HD11	1:F:917:PRO:HD3	1.84	0.58
2:E:86:ARG:O	2:E:90:HIS:ND1	2.36	0.58
3:H:106:LEU:HD21	4:G:305:PHE:CD2	2.38	0.58
3:L:106:LEU:HD21	4:K:305:PHE:CD2	2.38	0.58
4:K:329:THR:H	4:K:332:ILE:HD11	1.68	0.58
1:J:1059:PRO:HA	1:J:1065:THR:HG22	1.85	0.58
2:I:863:ARG:HD2	2:I:885:GLU:HG2	1.86	0.58
1:F:496:HIS:HB3	1:F:659:LEU:HD22	1.84	0.58
1:F:518:GLN:NE2	1:F:655:ARG:CA	2.66	0.58
1:F:561:GLY:O	1:F:566:TYR:OH	2.22	0.58
2:E:199:ALA:N	2:E:249:ALA:O	2.32	0.58
4:C:221:TYR:HB3	4:C:229:PRO:HG3	1.85	0.58
4:K:221:TYR:HB3	4:K:229:PRO:HG3	1.85	0.58
1:B:351:LYS:HE3	1:B:353:ALA:HB3	1.86	0.58
1:N:98:ALA:HB1	1:N:115:GLU:HG3	1.84	0.58
1:J:744:LEU:HD22	1:J:765:HIS:ND1	2.17	0.58
2:I:92:MET:HG2	2:I:112:LEU:HD13	1.86	0.58
4:C:47:ALA:HB2	4:C:106:LEU:HD12	1.85	0.58
3:H:42:GLN:O	3:H:42:GLN:CG	2.51	0.58
4:G:329:THR:H	4:G:332:ILE:HD11	1.68	0.58
1:B:75:THR:OG1	1:B:438:GLY:O	2.15	0.58
1:B:135:LYS:HZ1	1:B:164:TYR:HE2	1.50	0.58
2:A:186:ARG:HH12	2:A:301:TYR:HA	1.69	0.58
2:A:1130:ALA:HB2	2:A:1203:LEU:HD22	1.85	0.58
2:A:1197:PHE:CE2	4:C:375:PRO:HD3	2.39	0.58
2:I:399:PRO:HD2	2:I:399:PRO:O	2.01	0.58
2:I:1195:GLY:HA3	4:K:372:GLU:H	1.69	0.58
1:F:1009:VAL:O	1:F:1013:ASN:HB2	2.04	0.58
4:O:240:ARG:O	4:O:244:SER:OG	2.11	0.58
1:J:144:ARG:HG2	1:J:146:THR:H	1.69	0.58
1:J:897:LEU:HD13	1:J:902:LEU:HD21	1.85	0.58
2:I:45:ARG:NH2	2:I:185:GLU:OE2	2.37	0.58
1:F:1066:CYS:O	1:F:1070:THR:HG22	2.03	0.58
4:G:130:ILE:HG12	4:G:164:ILE:HD11	1.85	0.58
1:B:1012:ARG:NH2	1:N:1015:GLU:OE1	2.37	0.58
2:A:104:TYR:OH	2:A:495:SER:OG	2.22	0.58
2:A:147:GLN:HG2	2:A:426:LEU:HD12	1.85	0.58
2:A:1131:ILE:O	2:A:1135:THR:HG23	2.03	0.58
1:N:1005:VAL:O	1:N:1009:VAL:HG23	2.03	0.58
1:J:589:GLN:HE21	1:J:771:ARG:HH12	1.51	0.58
1:J:757:THR:N	1:J:760:GLY:O	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:123:ARG:HG2	1:F:192:ILE:HG23	1.85	0.58
1:F:565:ILE:HG13	1:F:665:VAL:HA	1.85	0.58
4:C:130:ILE:HG12	4:C:164:ILE:HD11	1.85	0.58
1:B:791:LYS:H	1:B:791:LYS:HE2	1.68	0.58
1:N:867:LEU:HD11	1:N:915:LEU:HB3	1.86	0.58
2:E:400:HIS:O	2:E:404:GLN:HG2	2.04	0.58
3:D:106:LEU:HD21	4:C:305:PHE:CD2	2.38	0.58
4:C:23:LYS:HD2	4:C:36:ARG:NH1	2.17	0.58
1:B:377:VAL:HG11	1:B:454:LEU:HB3	1.85	0.58
1:B:1009:VAL:CA	5:N:1101:FAR:H143	2.34	0.58
2:M:1215:LEU:O	4:O:330:ARG:NH2	2.37	0.58
1:J:150:HIS:HA	1:J:169:HIS:HB3	1.86	0.58
2:I:10:ARG:NH2	2:I:415:GLU:OE1	2.30	0.58
2:E:810:LEU:HD12	2:E:829:ILE:HG23	1.86	0.58
2:M:86:ARG:NH1	2:M:161:GLU:OE2	2.36	0.57
1:N:600:ASN:OD1	1:N:859:TRP:NE1	2.37	0.57
1:J:370:LEU:HD22	1:J:448:TYR:HA	1.85	0.57
2:E:413:MET:HG2	2:E:418:LEU:HB3	1.85	0.57
4:G:221:TYR:HB3	4:G:229:PRO:HG3	1.85	0.57
4:K:23:LYS:HD2	4:K:36:ARG:NH1	2.18	0.57
2:M:785:MET:N	2:M:785:MET:SD	2.77	0.57
1:J:172:ILE:HG21	1:J:212:VAL:HG11	1.85	0.57
3:D:42:GLN:O	3:D:42:GLN:CG	2.52	0.57
4:O:130:ILE:HG12	4:O:164:ILE:HD11	1.85	0.57
2:A:319:LYS:HD3	2:A:1099:GLU:HA	1.85	0.57
2:A:427:ASN:OD1	2:A:429:ARG:NH1	2.37	0.57
2:I:511:TYR:O	2:I:518:PHE:N	2.32	0.57
1:F:853:LEU:O	1:F:857:ILE:HG12	2.03	0.57
3:D:10:ILE:HG13	4:C:289:GLN:NE2	2.19	0.57
1:B:762:VAL:HA	1:B:765:HIS:CE1	2.40	0.57
1:N:1002:LEU:O	1:N:1006:VAL:HG12	2.05	0.57
1:J:276:ARG:HH12	1:J:482:ARG:HB2	1.70	0.57
2:I:419:ALA:HB3	2:I:422:GLU:HG3	1.86	0.57
2:I:598:ARG:HG2	4:K:17:TYR:CZ	2.38	0.57
5:I:1301:FAR:C4	4:K:330:ARG:HG3	2.34	0.57
4:G:47:ALA:HB2	4:G:106:LEU:HD12	1.85	0.57
4:O:20:TYR:HE1	4:O:94:TYR:HH	1.52	0.57
4:O:313:LEU:O	4:O:317:ARG:CG	2.40	0.57
2:A:482:ILE:HD12	2:A:483:TYR:N	2.19	0.57
1:J:591:VAL:O	1:J:595:ILE:HD13	2.05	0.57
2:I:52:LEU:HB3	2:I:409:LEU:HD22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:152:LYS:NZ	4:C:187:THR:O	2.38	0.57
2:A:6:ASN:N	2:A:6:ASN:OD1	2.38	0.57
2:A:79:GLN:HA	2:A:82:VAL:HG12	1.86	0.57
1:F:514:GLY:O	1:F:642:LYS:NZ	2.36	0.57
1:F:857:ILE:HD13	1:F:911:LEU:HD21	1.86	0.57
1:F:930:ILE:O	1:F:934:LEU:HB3	2.05	0.57
2:E:291:TYR:OH	2:E:391:ASP:OD1	2.17	0.57
2:E:1197:PHE:CE2	4:G:375:PRO:HD3	2.40	0.57
4:K:232:HIS:HE1	4:K:234:LYS:HB3	1.68	0.57
1:B:130:MET:HG3	2:A:29:VAL:HG23	1.87	0.57
2:M:1093:PRO:O	2:M:1096:THR:OG1	2.23	0.57
1:J:266:PHE:HB2	1:J:541:LEU:HD21	1.87	0.57
2:E:330:LEU:HG	2:E:331:PHE:HD1	1.69	0.57
2:E:952:SER:O	2:E:956:ASN:ND2	2.37	0.57
2:E:1131:ILE:O	2:E:1135:THR:HG23	2.04	0.57
4:C:126:GLU:HA	4:C:129:LYS:HZ1	1.70	0.57
1:B:165:GLU:H	1:B:165:GLU:CD	2.12	0.57
1:N:624:ASP:O	1:N:630:ARG:NH2	2.38	0.57
1:N:743:LEU:HD13	1:N:746:ILE:HD11	1.85	0.57
1:J:772:ARG:O	1:J:775:SER:OG	2.23	0.57
2:I:858:LEU:HD13	2:I:925:GLN:HE21	1.70	0.57
3:H:10:ILE:HG13	4:G:289:GLN:NE2	2.19	0.57
1:B:336:ASP:H	1:B:362:GLU:HG2	1.70	0.57
1:F:377:VAL:HG11	1:F:454:LEU:HB3	1.85	0.57
2:E:260:LEU:HD12	2:E:283:ILE:HD13	1.87	0.57
1:B:137:GLN:HB2	1:B:549:LEU:HD13	1.86	0.57
2:I:63:LYS:NZ	2:I:422:GLU:OE2	2.37	0.57
2:E:539:ILE:HA	2:E:542:MET:HE2	1.86	0.57
2:E:584:ALA:HB1	4:G:54:THR:CG2	2.35	0.57
4:C:45:GLU:HB3	4:C:106:LEU:HD22	1.87	0.57
4:G:26:LEU:CD1	4:G:36:ARG:CG	2.82	0.57
4:G:152:LYS:NZ	4:G:187:THR:O	2.38	0.57
4:K:152:LYS:NZ	4:K:187:THR:O	2.38	0.57
3:P:51:ASP:HB3	4:O:322:TYR:CZ	2.40	0.57
1:B:144:ARG:HG3	1:B:145:PRO:HD2	1.87	0.56
1:B:567:ARG:HA	1:B:572:THR:HA	1.87	0.56
1:B:791:LYS:HE2	1:B:791:LYS:N	2.20	0.56
2:A:184:TRP:CE2	2:A:295:ARG:HD2	2.39	0.56
2:A:1054:TRP:NE1	4:C:369:ALA:O	2.35	0.56
1:N:418:GLU:OE1	1:N:418:GLU:N	2.35	0.56
1:N:509:PHE:CE2	1:N:631:PHE:HE2	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:18:VAL:HG22	2:I:408:ILE:HD13	1.86	0.56
2:I:561:THR:HG1	2:I:611:SER:HG	1.35	0.56
1:F:120:LYS:HG3	2:E:86:ARG:HH21	1.70	0.56
1:F:173:ASN:OD1	1:F:173:ASN:N	2.38	0.56
3:D:51:ASP:CB	4:C:322:TYR:CZ	2.88	0.56
3:D:57:ASP:HB3	3:D:59:ASP:O	2.05	0.56
4:K:359:VAL:HG21	4:K:367:ARG:CG	2.35	0.56
4:O:45:GLU:HB3	4:O:106:LEU:HD22	1.87	0.56
1:B:1066:CYS:O	1:B:1070:THR:HG22	2.06	0.56
2:A:18:VAL:HG22	2:A:408:ILE:HD13	1.86	0.56
1:F:123:ARG:NH2	1:F:198:GLU:OE2	2.38	0.56
1:F:507:GLN:HG2	1:F:519:THR:CG2	2.35	0.56
2:E:900:TYR:HA	2:E:903:MET:SD	2.45	0.56
4:K:47:ALA:HB2	4:K:106:LEU:HD12	1.85	0.56
4:O:24:GLU:HG3	4:O:36:ARG:NH2	2.20	0.56
1:B:397:HIS:HE1	1:B:431:PRO:HG3	1.70	0.56
1:B:494:VAL:HG23	1:F:105:ASP:HB3	1.88	0.56
2:M:456:LYS:HE2	2:M:456:LYS:HA	1.87	0.56
1:N:397:HIS:CE1	1:N:431:PRO:HG3	2.40	0.56
1:J:373:MET:HG2	1:J:385:VAL:HG13	1.86	0.56
1:J:379:ARG:HH11	1:J:379:ARG:HG3	1.71	0.56
1:J:535:VAL:HG22	1:J:557:ILE:HD12	1.87	0.56
2:I:21:THR:HG23	2:I:399:PRO:HG2	1.88	0.56
2:I:1057:ARG:HH11	4:K:358:TRP:HB3	1.70	0.56
1:F:243:LYS:HE2	1:F:276:ARG:HD3	1.88	0.56
2:E:588:LYS:HE3	4:G:98:THR:CG2	2.35	0.56
3:D:57:ASP:OD2	3:D:64:ILE:HA	2.05	0.56
4:C:84:HIS:CD2	4:C:86:ASN:H	2.24	0.56
4:G:84:HIS:CD2	4:G:86:ASN:H	2.24	0.56
4:K:156:ILE:HG23	4:K:164:ILE:HG23	1.87	0.56
4:K:272:GLN:OE1	4:K:274:GLN:N	2.39	0.56
4:K:285:HIS:CE1	4:K:287:PHE:HB2	2.41	0.56
4:O:156:ILE:HG23	4:O:164:ILE:HG23	1.88	0.56
1:J:531:GLN:OE1	1:J:578:ILE:HB	2.05	0.56
2:I:1160:ASP:OD1	2:I:1160:ASP:N	2.33	0.56
2:E:136:ASP:HB3	2:E:201:SER:HA	1.86	0.56
2:E:218:PHE:CE2	2:E:226:SER:HB3	2.41	0.56
3:H:57:ASP:HB3	3:H:59:ASP:O	2.05	0.56
3:L:52:MET:HG2	4:K:318:ILE:HG12	1.87	0.56
1:B:157:THR:HB	2:A:94:ARG:HH21	1.71	0.56
1:B:214:ARG:HH12	1:B:828:PRO:HD3	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:261:SER:HA	2:M:265:PHE:O	2.05	0.56
2:M:836:LYS:HE3	2:M:877:THR:HB	1.86	0.56
1:N:948:ILE:O	1:N:952:THR:HG23	2.05	0.56
1:J:856:HIS:O	1:J:860:ILE:HG13	2.05	0.56
2:E:927:MET:HB3	2:E:946:LEU:HD21	1.88	0.56
4:C:285:HIS:CE1	4:C:287:PHE:HB2	2.41	0.56
4:G:285:HIS:CE1	4:G:287:PHE:HB2	2.41	0.56
3:L:45:THR:HG22	3:L:46:GLU:N	2.19	0.56
4:K:45:GLU:HB3	4:K:106:LEU:HD22	1.87	0.56
4:O:272:GLN:OE1	4:O:274:GLN:N	2.39	0.56
1:B:990:ILE:HG12	1:B:996:ARG:HB2	1.88	0.56
1:N:297:LEU:HD23	1:N:320:VAL:HG11	1.88	0.56
1:N:876:ILE:O	1:N:880:ILE:HG23	2.06	0.56
2:E:509:LYS:HB2	2:E:511:TYR:HE1	1.70	0.56
2:E:1194:SER:OG	2:E:1195:GLY:N	2.39	0.56
4:G:277:TYR:CE1	4:G:281:GLU:HG3	2.41	0.56
3:P:57:ASP:OD2	3:P:64:ILE:HA	2.04	0.56
4:O:84:HIS:CD2	4:O:86:ASN:H	2.24	0.56
1:B:502:GLU:HB2	1:B:622:ARG:HH12	1.71	0.56
1:B:853:LEU:O	1:B:857:ILE:HG12	2.06	0.56
1:N:356:LYS:HD2	1:N:970:SER:HB3	1.88	0.56
3:D:102:SER:CB	3:D:105:GLU:HG3	2.23	0.56
4:C:277:TYR:CE1	4:C:281:GLU:HG3	2.41	0.56
1:B:533:GLU:OE2	1:B:683:LYS:N	2.39	0.56
2:A:159:LEU:O	2:A:163:ASN:ND2	2.39	0.56
2:A:418:LEU:HB3	2:A:423:ILE:HD11	1.87	0.56
2:A:810:LEU:HB3	2:A:829:ILE:HD11	1.88	0.56
2:A:1196:ARG:HH11	4:C:252:PRO:HD3	1.70	0.56
1:N:757:THR:HG22	1:N:758:LYS:H	1.71	0.56
1:J:148:CYS:O	1:J:164:TYR:OH	2.21	0.56
1:J:1013:ASN:HD21	5:J:1101:FAR:C11	2.19	0.56
1:F:737:LEU:HD23	1:F:740:GLN:NE2	2.20	0.56
4:G:142:HIS:NE2	4:G:209:LYS:O	2.39	0.56
3:L:51:ASP:HB3	4:K:322:TYR:CZ	2.40	0.56
4:K:277:TYR:CE1	4:K:281:GLU:HG3	2.41	0.56
4:O:152:LYS:NZ	4:O:187:THR:O	2.38	0.56
1:J:1023:ASP:HB3	1:J:1026:ARG:NH1	2.20	0.56
1:F:75:THR:OG1	1:F:438:GLY:O	2.23	0.56
1:F:909:GLN:NE2	1:F:913:ASP:OD1	2.39	0.56
3:H:51:ASP:HB3	4:G:322:TYR:CZ	2.40	0.56
4:G:272:GLN:OE1	4:G:274:GLN:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:337:PRO:HB3	4:O:343:LEU:HD23	1.88	0.56
2:M:472:ARG:NH1	2:M:472:ARG:HB2	2.21	0.56
2:M:966:GLU:OE1	2:M:1057:ARG:NH1	2.37	0.56
2:A:113:HIS:HA	2:A:132:HIS:HB3	1.88	0.56
1:F:507:GLN:HG2	1:F:519:THR:HG21	1.87	0.56
1:F:870:GLY:O	1:F:937:THR:OG1	2.19	0.56
2:E:68:ASP:OD1	2:E:68:ASP:N	2.35	0.56
2:E:1100:MET:HE3	2:E:1107:PHE:HA	1.88	0.56
4:G:45:GLU:HB3	4:G:106:LEU:HD22	1.87	0.56
3:L:57:ASP:HB3	3:L:59:ASP:O	2.05	0.56
1:B:373:MET:HE2	1:B:451:ALA:HB1	1.88	0.55
2:A:198:ASN:OD1	2:A:200:SER:N	2.40	0.55
5:A:1301:FAR:H43	4:C:330:ARG:HG3	1.88	0.55
1:J:1074:MET:CE	5:J:1101:FAR:H153	2.18	0.55
1:F:130:MET:C	1:F:132:GLN:N	2.64	0.55
4:C:142:HIS:NE2	4:C:209:LYS:O	2.39	0.55
4:C:272:GLN:OE1	4:C:274:GLN:N	2.39	0.55
3:H:45:THR:HG22	3:H:46:GLU:N	2.20	0.55
3:P:52:MET:HG2	4:O:318:ILE:HG12	1.87	0.55
3:P:57:ASP:HB3	3:P:59:ASP:O	2.05	0.55
4:O:277:TYR:CE1	4:O:281:GLU:HG3	2.41	0.55
4:O:285:HIS:CE1	4:O:287:PHE:HB2	2.41	0.55
1:B:187:SER:HB3	1:B:466:PRO:HB2	1.88	0.55
2:M:460:ILE:HG22	2:M:462:VAL:HG13	1.88	0.55
1:J:887:LEU:HD22	1:J:897:LEU:HB2	1.88	0.55
2:I:299:ASP:H	2:I:325:GLU:HG2	1.70	0.55
2:I:825:LEU:O	2:I:829:ILE:HG13	2.06	0.55
2:I:847:LEU:HB3	2:I:854:LEU:HD11	1.88	0.55
2:E:235:VAL:O	2:E:239:GLN:HG3	2.07	0.55
3:H:52:MET:HG2	4:G:318:ILE:HG12	1.87	0.55
3:L:10:ILE:HG13	4:K:289:GLN:NE2	2.19	0.55
1:B:582:LEU:HD22	1:B:589:GLN:HG2	1.87	0.55
1:J:523:VAL:HG12	1:J:526:ILE:HD12	1.87	0.55
1:J:944:ARG:HH22	1:J:1008:ILE:HD13	1.71	0.55
3:H:57:ASP:HB3	4:G:125:LYS:NZ	2.22	0.55
2:A:579:ASN:OD1	2:A:580:SER:N	2.39	0.55
1:J:131:ARG:NH2	1:J:159:ASP:OD1	2.37	0.55
1:J:809:GLN:HE22	1:J:811:THR:HG22	1.71	0.55
2:I:32:LEU:HD12	2:I:118:THR:HA	1.88	0.55
2:I:555:ARG:H	2:I:556:MET:HE3	1.72	0.55
2:I:616:LEU:HB3	2:I:618:PHE:CE1	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:193:ILE:HG13	1:F:254:LEU:HD13	1.88	0.55
2:E:277:GLU:O	2:E:281:GLN:NE2	2.36	0.55
4:G:113:PHE:HB2	4:G:154:GLU:HG3	1.88	0.55
1:B:496:HIS:CG	1:B:659:LEU:HD22	2.42	0.55
2:M:262:VAL:HA	2:M:267:ALA:HB3	1.88	0.55
2:A:426:LEU:HA	1:F:655:ARG:HH22	1.71	0.55
1:J:412:VAL:HG11	1:J:420:GLU:HG2	1.88	0.55
1:J:919:GLN:HB3	1:J:922:ARG:HD3	1.89	0.55
2:I:1122:GLU:H	2:I:1122:GLU:CD	2.11	0.55
1:F:66:PRO:HG3	2:E:492:MET:HG2	1.89	0.55
3:P:10:ILE:HG13	4:O:289:GLN:NE2	2.19	0.55
1:B:132:GLN:HB3	1:B:135:LYS:HD3	1.87	0.55
1:B:214:ARG:HH12	1:B:827:SER:HA	1.72	0.55
1:B:478:ASN:CB	1:B:483:PHE:HB2	2.35	0.55
1:B:779:TRP:HA	1:B:782:VAL:HG12	1.87	0.55
2:M:521:THR:HB	2:M:525:ILE:HD11	1.88	0.55
1:J:300:ILE:HG22	1:J:307:LEU:HB2	1.87	0.55
1:F:336:ASP:H	1:F:362:GLU:HG2	1.72	0.55
1:F:946:TRP:CD1	1:F:974:MET:HB2	2.42	0.55
1:F:948:ILE:HD11	1:F:1007:SER:HA	1.87	0.55
4:C:113:PHE:HB2	4:C:154:GLU:HG3	1.88	0.55
4:C:337:PRO:HB3	4:C:343:LEU:HD23	1.88	0.55
4:G:149:ARG:NH1	4:G:171:PHE:O	2.40	0.55
2:M:356:GLU:HA	2:M:359:LEU:HD12	1.89	0.55
2:M:1081:LYS:HE3	5:M:1301:FAR:H142	1.89	0.55
1:N:509:PHE:O	1:N:512:THR:OG1	2.24	0.55
1:J:270:ASP:O	1:J:274:ARG:HG3	2.07	0.55
1:F:1004:MET:O	1:F:1008:ILE:HG12	2.06	0.55
1:B:115:GLU:HG2	1:B:190:LEU:HD21	1.88	0.55
5:B:1101:FAR:C14	1:N:1009:VAL:CG2	2.66	0.55
2:M:86:ARG:HH22	1:N:120:LYS:HG3	1.72	0.55
1:N:951:ARG:NH2	1:N:1016:LEU:O	2.35	0.55
1:N:1071:LYS:NZ	1:N:1071:LYS:HB3	2.22	0.55
1:J:181:TYR:O	1:J:185:MET:HG3	2.06	0.55
1:J:672:ARG:HG3	1:J:677:GLU:HG2	1.89	0.55
2:I:142:LEU:HD22	2:I:212:LEU:HD11	1.89	0.55
2:I:327:GLU:OE2	2:I:392:ARG:NH2	2.40	0.55
1:F:922:ARG:HB3	1:F:926:ASN:HB2	1.88	0.55
3:D:10:ILE:CD1	4:C:289:GLN:OE1	2.54	0.55
4:G:156:ILE:HG23	4:G:164:ILE:HG23	1.88	0.55
4:K:84:HIS:CD2	4:K:86:ASN:H	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:527:GLN:HG3	1:B:571:LYS:HE2	1.89	0.55
1:B:991:ASP:N	1:B:991:ASP:OD1	2.37	0.55
2:M:536:ASN:HD22	2:M:579:ASN:HD22	1.55	0.55
2:A:226:SER:O	2:A:226:SER:OG	2.24	0.55
2:A:584:ALA:O	2:A:588:LYS:HG3	2.06	0.55
1:N:347:ARG:NH1	1:N:349:TYR:O	2.40	0.55
1:N:574:VAL:HG21	1:N:656:LEU:HD21	1.88	0.55
2:I:330:LEU:HD22	2:I:400:HIS:HE1	1.72	0.55
1:F:257:ASN:N	1:F:257:ASN:OD1	2.40	0.55
1:F:943:ASP:O	1:F:947:GLN:NE2	2.39	0.55
2:E:18:VAL:HG22	2:E:408:ILE:HD13	1.89	0.55
2:E:86:ARG:HG3	2:E:90:HIS:HE1	1.70	0.55
2:E:1054:TRP:HA	2:E:1057:ARG:HB2	1.89	0.55
4:C:149:ARG:NH1	4:C:171:PHE:O	2.40	0.55
1:B:198:GLU:OE2	2:A:83:LYS:NZ	2.26	0.55
1:J:51:HIS:O	1:J:55:ILE:HG13	2.07	0.55
1:J:958:VAL:N	1:J:961:LYS:O	2.28	0.55
1:J:1051:MET:HG3	1:J:1055:TYR:CE2	2.41	0.55
4:C:156:ILE:HG23	4:C:164:ILE:HG23	1.88	0.55
1:B:983:VAL:HG13	1:B:987:LEU:HD23	1.89	0.54
1:J:1008:ILE:HG23	5:F:1101:FAR:H143	1.89	0.54
1:F:211:ARG:HH12	1:F:555:ARG:NH1	2.05	0.54
1:F:499:LEU:HA	1:F:619:VAL:HG22	1.88	0.54
4:C:194:GLU:HA	4:C:197:GLU:HB3	1.89	0.54
2:A:85:MET:HE3	2:A:148:MET:SD	2.46	0.54
1:N:731:LEU:HB2	1:N:743:LEU:HG	1.87	0.54
2:I:517:ILE:HG21	2:I:608:LEU:HD21	1.89	0.54
2:I:924:ILE:HD12	2:I:925:GLN:HG3	1.89	0.54
1:F:584:ASP:OD1	1:F:585:PHE:N	2.39	0.54
2:E:884:SER:HA	2:E:890:ILE:HD11	1.89	0.54
3:D:57:ASP:HB3	4:C:125:LYS:NZ	2.22	0.54
4:O:142:HIS:NE2	4:O:209:LYS:O	2.39	0.54
4:O:149:ARG:NH1	4:O:171:PHE:O	2.40	0.54
1:N:958:VAL:HG12	1:N:1024:LEU:HB2	1.89	0.54
1:N:1026:ARG:O	1:N:1030:GLU:N	2.30	0.54
1:J:55:ILE:HD13	1:J:404:PRO:HD2	1.88	0.54
2:I:514:ARG:HD3	2:I:621:PRO:HD3	1.89	0.54
2:I:1172:ASP:HB3	2:I:1175:MET:HE1	1.89	0.54
3:D:52:MET:HG2	4:C:318:ILE:HG12	1.87	0.54
4:K:149:ARG:NH1	4:K:171:PHE:O	2.40	0.54
2:A:510:LEU:HD21	2:A:517:ILE:HG23	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1201:THR:HG22	4:K:347:ILE:HD13	1.90	0.54
1:B:789:THR:HB	1:B:791:LYS:HZ3	1.71	0.54
2:M:156:ILE:HG13	2:M:217:LEU:HD13	1.88	0.54
2:A:409:LEU:O	2:A:413:MET:HG3	2.08	0.54
1:N:1040:SER:HA	1:N:1044:GLU:HA	1.90	0.54
1:J:1018:PHE:HD2	1:J:1022:VAL:CG2	2.20	0.54
2:E:957:LEU:O	2:E:961:ILE:HG23	2.08	0.54
2:E:1138:ALA:HB2	5:E:1301:FAR:C12	2.37	0.54
4:G:194:GLU:HA	4:G:197:GLU:HB3	1.89	0.54
3:L:10:ILE:CD1	4:K:289:GLN:OE1	2.54	0.54
2:M:347:GLN:HG2	2:M:351:TYR:HE2	1.72	0.54
2:A:371:GLU:HG2	2:A:372:LEU:HD23	1.90	0.54
1:N:877:GLY:HA2	1:N:880:ILE:HG12	1.89	0.54
1:J:132:GLN:O	1:J:135:LYS:N	2.41	0.54
1:J:802:THR:O	1:J:806:HIS:ND1	2.40	0.54
2:I:598:ARG:HD3	4:K:17:TYR:CE1	2.42	0.54
4:C:86:ASN:HA	4:C:165:LYS:HZ1	1.71	0.54
4:O:263:ASP:O	4:O:267:ARG:HG2	2.08	0.54
2:A:619:MET:HE3	2:A:619:MET:HA	1.90	0.54
2:A:848:LEU:HD11	2:A:870:PRO:HG3	1.89	0.54
1:N:523:VAL:HG11	1:N:656:LEU:HD23	1.88	0.54
1:N:725:HIS:ND1	1:N:725:HIS:O	2.40	0.54
1:N:744:LEU:HD22	1:N:766:ILE:HA	1.90	0.54
1:F:568:ILE:HD13	1:F:573:VAL:HG21	1.90	0.54
2:E:55:TRP:HE1	2:E:153:LEU:HD13	1.72	0.54
4:K:142:HIS:NE2	4:K:209:LYS:O	2.39	0.54
5:B:1101:FAR:H143	1:N:1005:VAL:HG23	1.89	0.54
2:A:45:ARG:NH2	2:A:183:ILE:O	2.41	0.54
1:N:270:ASP:OD1	1:N:560:LEU:HB2	2.08	0.54
1:J:353:ALA:O	1:J:356:LYS:NZ	2.37	0.54
1:J:574:VAL:HG21	1:J:656:LEU:HD21	1.88	0.54
1:F:119:ILE:HD11	1:F:190:LEU:HB3	1.90	0.54
2:E:332:TRP:HB2	2:E:355:LEU:HD23	1.89	0.54
1:B:986:THR:HG22	1:B:987:LEU:HD22	1.90	0.54
2:A:1100:MET:SD	2:A:1106:LYS:HB2	2.48	0.54
2:I:1194:SER:OG	2:I:1195:GLY:N	2.41	0.54
2:E:184:TRP:CD2	2:E:295:ARG:HD2	2.43	0.54
2:E:208:ALA:O	2:E:212:LEU:HG	2.08	0.54
2:M:916:PHE:HE1	2:M:1112:GLU:HG3	1.73	0.54
2:M:1058:ARG:NH1	2:M:1189:TYR:O	2.40	0.54
2:A:584:ALA:HB1	4:C:54:THR:HG21	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:162:LEU:O	1:N:169:HIS:NE2	2.40	0.54
1:N:740:GLN:O	1:N:744:LEU:HG	2.07	0.54
1:J:308:ASP:OD2	1:J:482:ARG:HB3	2.07	0.54
1:J:727:ILE:HG12	1:J:743:LEU:HD11	1.89	0.54
2:I:173:GLU:OE1	2:I:500:ARG:NH1	2.39	0.54
1:F:518:GLN:HE22	1:F:655:ARG:CA	2.21	0.54
2:E:1076:TRP:CE2	2:E:1102:PRO:HD3	2.43	0.54
4:G:337:PRO:HB3	4:G:343:LEU:HD23	1.88	0.54
3:P:57:ASP:HB3	4:O:125:LYS:NZ	2.22	0.54
2:M:52:LEU:HB3	2:M:409:LEU:HD22	1.90	0.53
2:M:1129:GLU:HB3	4:O:354:ILE:HD13	1.89	0.53
2:A:166:GLN:HE21	2:A:486:LEU:HD11	1.73	0.53
2:A:332:TRP:HB2	2:A:355:LEU:HD23	1.89	0.53
2:A:1178:LYS:HA	2:A:1185:CYS:HA	1.91	0.53
1:N:134:ASP:OD1	1:N:134:ASP:N	2.40	0.53
1:J:213:TYR:CD2	1:J:274:ARG:HB2	2.42	0.53
1:J:356:LYS:HD3	1:J:970:SER:HB2	1.90	0.53
1:J:1060:LEU:HD23	5:F:1101:FAR:H41	1.88	0.53
1:J:1079:GLU:OE2	1:F:1063:ARG:NH1	2.41	0.53
2:I:95:GLN:HE22	2:I:113:HIS:CE1	2.26	0.53
2:I:320:LEU:O	2:I:384:TYR:OH	2.18	0.53
2:E:239:GLN:HA	2:E:242:LEU:HD12	1.88	0.53
3:H:68:GLU:HG3	4:G:125:LYS:HE2	1.90	0.53
3:L:57:ASP:HB3	4:K:125:LYS:NZ	2.22	0.53
4:K:113:PHE:HB2	4:K:154:GLU:HG3	1.90	0.53
1:J:297:LEU:HD21	1:J:372:MET:HG2	1.90	0.53
2:I:206:LYS:HE2	2:I:239:GLN:OE1	2.09	0.53
2:I:598:ARG:HD3	4:K:17:TYR:CD1	2.43	0.53
1:F:1070:THR:HA	1:F:1073:VAL:HG12	1.90	0.53
2:E:530:PHE:HD2	2:E:532:LEU:HG	1.72	0.53
4:C:138:ILE:HG23	4:C:142:HIS:CE1	2.44	0.53
3:H:102:SER:CB	3:H:105:GLU:HG3	2.23	0.53
4:K:75:VAL:HG12	4:K:79:ARG:HD2	1.89	0.53
1:B:951:ARG:HH12	1:B:1014:PRO:HA	1.74	0.53
2:A:426:LEU:HD23	1:F:655:ARG:HH12	1.72	0.53
1:J:1026:ARG:O	1:J:1030:GLU:HG3	2.09	0.53
1:F:748:LEU:HD23	1:F:749:LYS:HG3	1.91	0.53
1:F:762:VAL:HA	1:F:765:HIS:CD2	2.44	0.53
4:C:207:TYR:HD1	4:C:211:VAL:CG2	2.19	0.53
2:M:439:VAL:HG22	2:M:598:ARG:HB3	1.90	0.53
2:M:593:TYR:OH	4:O:35:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:857:ILE:HG23	1:N:868:PHE:CE2	2.43	0.53
2:I:933:HIS:HB2	2:I:1056:ARG:HH22	1.74	0.53
1:F:202:ILE:HD13	1:F:205:LEU:HD12	1.91	0.53
1:F:591:VAL:HG11	1:F:630:ARG:HB3	1.91	0.53
1:F:750:ARG:HB3	1:F:751:GLU:OE2	2.08	0.53
3:L:51:ASP:HB2	4:K:322:TYR:CZ	2.44	0.53
1:B:614:ARG:HE	2:E:221:LYS:HE2	1.74	0.53
1:B:1062:LYS:HA	1:N:1081:GLU:HA	1.91	0.53
2:A:893:LEU:HD21	2:A:946:LEU:HD13	1.90	0.53
2:A:927:MET:HE1	2:A:931:LEU:HD22	1.91	0.53
2:I:524:PHE:HE2	2:I:546:ASP:OD2	1.92	0.53
2:E:505:LEU:H	2:E:505:LEU:HD12	1.73	0.53
4:K:194:GLU:HA	4:K:197:GLU:HB3	1.89	0.53
4:O:86:ASN:HA	4:O:165:LYS:NZ	2.24	0.53
1:B:867:LEU:HD23	1:B:915:LEU:HD23	1.91	0.53
2:M:320:LEU:O	2:M:384:TYR:OH	2.23	0.53
2:M:433:VAL:O	2:M:435:LYS:HD2	2.07	0.53
2:M:587:ARG:HA	2:M:590:GLN:HG3	1.91	0.53
2:M:923:ILE:HA	2:M:926:VAL:HG22	1.90	0.53
1:J:950:GLU:HA	1:J:969:LEU:HD11	1.91	0.53
1:F:875:ARG:NH2	1:F:935:ASN:HD21	2.06	0.53
2:E:147:GLN:HE21	2:E:426:LEU:HD12	1.73	0.53
4:C:86:ASN:HA	4:C:165:LYS:NZ	2.24	0.53
4:G:263:ASP:O	4:G:267:ARG:HG2	2.08	0.53
3:L:53:ILE:HG21	3:L:62:GLY:C	2.34	0.53
3:L:102:SER:CB	3:L:105:GLU:HG3	2.23	0.53
4:K:267:ARG:HB3	4:K:277:TYR:HB2	1.91	0.53
1:B:160:GLU:OE1	1:B:160:GLU:N	2.26	0.53
1:B:577:PRO:HG2	1:B:617:PHE:CE1	2.43	0.53
1:B:1008:ILE:HD11	1:B:1012:ARG:HE	1.73	0.53
1:J:247:GLU:OE2	1:J:469:ARG:NH1	2.32	0.53
1:F:856:HIS:O	1:F:860:ILE:HG13	2.09	0.53
2:E:1138:ALA:HB2	5:E:1301:FAR:C15	2.25	0.53
4:K:263:ASP:O	4:K:267:ARG:HG2	2.08	0.53
4:O:194:GLU:HA	4:O:197:GLU:HB3	1.89	0.53
2:A:876:LEU:HD21	2:A:898:MET:HE1	1.90	0.53
1:J:82:ALA:HB2	1:J:155:VAL:HB	1.91	0.53
1:J:566:TYR:HB2	1:J:573:VAL:HG22	1.91	0.53
2:I:368:LEU:HG	2:I:399:PRO:HB3	1.91	0.53
2:I:411:SER:O	2:I:415:GLU:HG3	2.09	0.53
4:K:207:TYR:HD1	4:K:211:VAL:CG2	2.19	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:138:ILE:HG23	4:O:142:HIS:CE1	2.44	0.53
1:B:555:ARG:HD2	1:B:556:PRO:HD2	1.90	0.53
2:A:827:ARG:NH2	2:A:954:MET:SD	2.82	0.53
1:N:519:THR:HG23	1:N:521:GLN:H	1.74	0.53
1:J:165:GLU:H	1:J:165:GLU:CD	2.17	0.53
1:J:492:ASP:OD1	1:J:650:LYS:HD2	2.08	0.53
1:J:785:GLY:O	1:J:789:THR:OG1	2.17	0.53
1:J:946:TRP:O	1:J:950:GLU:HG3	2.08	0.53
1:F:151:SER:HB2	1:F:167:TYR:HE2	1.74	0.53
1:F:324:LEU:HD12	1:F:331:LYS:HB2	1.91	0.53
1:F:813:GLY:O	1:F:877:GLY:HA3	2.09	0.53
4:C:191:LEU:HD22	4:C:195:ILE:HG21	1.91	0.53
4:C:263:ASP:O	4:C:267:ARG:HG2	2.08	0.53
1:B:86:ASP:OD1	1:B:443:TRP:HB2	2.09	0.53
1:B:856:HIS:O	1:B:860:ILE:HG12	2.08	0.53
2:A:1068:PRO:HB3	4:C:353:ARG:O	2.08	0.53
1:J:162:LEU:O	1:J:169:HIS:NE2	2.40	0.53
1:J:278:THR:HG23	1:J:805:VAL:HG11	1.90	0.53
1:J:935:ASN:HA	1:J:996:ARG:HE	1.74	0.53
2:I:69:GLU:O	2:I:73:LYS:HG2	2.09	0.53
2:I:814:TYR:HB2	2:I:829:ILE:HG21	1.91	0.53
1:F:518:GLN:NE2	1:F:655:ARG:HA	2.24	0.53
1:F:520:PRO:CG	1:F:687:GLU:HB2	2.39	0.53
1:F:523:VAL:CG1	1:F:657:GLN:HE22	2.22	0.53
2:E:424:ASP:OD2	2:E:428:ARG:N	2.42	0.53
4:K:220:MET:CE	4:K:268:PHE:CE2	2.90	0.53
3:P:51:ASP:HB2	4:O:322:TYR:CZ	2.44	0.53
1:B:762:VAL:O	1:B:766:ILE:HG12	2.09	0.52
1:B:850:GLN:HB2	1:B:876:ILE:HG21	1.91	0.52
2:A:51:ILE:HD11	2:A:81:VAL:HA	1.91	0.52
2:A:135:LEU:O	2:A:139:SER:OG	2.14	0.52
2:A:259:LEU:O	2:A:263:VAL:HG22	2.09	0.52
2:A:1193:PRO:HD2	4:C:370:LEU:HA	1.91	0.52
1:N:1033:ASN:ND2	1:N:1034:GLU:OE1	2.42	0.52
2:I:810:LEU:O	2:I:814:TYR:N	2.31	0.52
2:I:1076:TRP:CD1	2:I:1107:PHE:HE2	2.19	0.52
3:P:53:ILE:HG21	3:P:62:GLY:C	2.34	0.52
4:O:191:LEU:HD22	4:O:195:ILE:HG21	1.91	0.52
1:B:456:ASP:O	1:B:457:GLU:CD	2.52	0.52
1:B:1012:ARG:NH1	1:N:1014:PRO:HD2	2.21	0.52
1:B:1013:ASN:HA	1:N:1012:ARG:NH1	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:593:TYR:CE2	4:C:101:PHE:HE2	2.28	0.52
2:I:1092:LEU:HB2	2:I:1114:VAL:HG21	1.90	0.52
4:G:138:ILE:HG23	4:G:142:HIS:CE1	2.44	0.52
2:M:4:ARG:NE	2:M:69:GLU:OE2	2.42	0.52
2:M:931:LEU:HD23	2:M:946:LEU:HD12	1.90	0.52
2:A:415:GLU:HB2	2:A:417:PHE:CE2	2.44	0.52
1:N:946:TRP:O	1:N:950:GLU:N	2.38	0.52
1:J:948:ILE:O	1:J:952:THR:HG23	2.08	0.52
1:J:1008:ILE:HG23	5:F:1101:FAR:C14	2.39	0.52
1:F:1082:VAL:HG12	5:F:1101:FAR:H103	1.90	0.52
4:C:267:ARG:HB3	4:C:277:TYR:HB2	1.91	0.52
4:K:138:ILE:HG23	4:K:142:HIS:CE1	2.44	0.52
3:P:45:THR:O	3:P:48:GLU:N	2.42	0.52
1:B:401:GLU:OE1	1:B:401:GLU:N	2.41	0.52
2:M:1153:LYS:HE2	2:M:1157:ILE:HD12	1.92	0.52
2:A:99:VAL:HG13	2:A:171:TYR:HD2	1.73	0.52
2:A:1138:ALA:HB2	5:A:1301:FAR:H12	1.90	0.52
2:A:1194:SER:OG	2:A:1195:GLY:N	2.43	0.52
1:N:367:ILE:HD12	1:N:441:PHE:CE2	2.44	0.52
1:N:408:LYS:HG2	1:N:409:TYR:HD2	1.74	0.52
1:N:623:GLU:OE1	1:N:623:GLU:N	2.30	0.52
1:N:766:ILE:HD11	1:N:789:THR:HB	1.92	0.52
1:N:928:ARG:HH21	1:N:1059:PRO:HD3	1.74	0.52
1:J:288:ARG:HD3	1:J:977:MET:HG2	1.91	0.52
1:J:857:ILE:HG23	1:J:868:PHE:CZ	2.45	0.52
3:D:53:ILE:HG21	3:D:62:GLY:C	2.34	0.52
4:O:352:PHE:CE2	4:O:367:ARG:NH1	2.75	0.52
1:B:82:ALA:HB2	1:B:155:VAL:HB	1.92	0.52
1:B:145:PRO:HG2	1:B:232:THR:HG21	1.90	0.52
1:B:223:ARG:HH21	1:B:339:ARG:HH12	1.57	0.52
1:B:236:SER:HB2	1:B:296:LEU:HD21	1.91	0.52
1:B:883:MET:HG3	1:B:914:ILE:HG12	1.90	0.52
2:M:920:ILE:HA	2:M:923:ILE:HD12	1.91	0.52
2:A:585:ALA:HA	2:A:588:LYS:NZ	2.25	0.52
2:A:662:ARG:HA	2:A:662:ARG:CZ	2.39	0.52
1:N:887:LEU:HD22	1:N:897:LEU:HB2	1.91	0.52
1:N:996:ARG:O	1:N:1000:VAL:HG23	2.09	0.52
1:J:90:CYS:SG	1:J:442:LEU:HB3	2.48	0.52
1:J:904:PRO:HA	1:J:907:VAL:HB	1.92	0.52
1:F:232:THR:O	1:F:824:ASN:ND2	2.41	0.52
1:F:356:LYS:HD2	1:F:970:SER:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:958:VAL:HG22	1:F:1024:LEU:HD22	1.92	0.52
1:F:992:GLN:HG3	1:F:995:TYR:H	1.75	0.52
2:E:837:VAL:HG12	2:E:839:ALA:H	1.74	0.52
3:D:45:THR:HG22	3:D:46:GLU:N	2.23	0.52
3:H:53:ILE:HG21	3:H:62:GLY:C	2.34	0.52
3:P:19:LEU:HB3	4:O:311:THR:HG21	1.92	0.52
2:M:295:ARG:HG2	2:M:331:PHE:CZ	2.45	0.52
1:J:1008:ILE:CG2	5:F:1101:FAR:H143	2.39	0.52
2:I:887:ASP:HB2	2:I:890:ILE:HG22	1.91	0.52
2:I:1137:LEU:HD23	5:I:1301:FAR:H51	1.92	0.52
1:F:1001:GLU:O	1:F:1005:VAL:N	2.38	0.52
2:E:589:MET:HB3	2:E:599:VAL:HG11	1.92	0.52
4:G:220:MET:CE	4:G:264:LEU:HD21	2.40	0.52
4:O:220:MET:CE	4:O:264:LEU:HD21	2.40	0.52
1:B:212:VAL:HG22	1:B:239:VAL:HG12	1.91	0.52
1:B:223:ARG:HH22	1:B:338:TYR:HA	1.73	0.52
1:B:273:ASN:O	1:B:277:GLN:HG3	2.08	0.52
1:B:351:LYS:HD2	1:B:352:PRO:N	2.25	0.52
1:B:875:ARG:HE	1:B:878:TRP:CG	2.28	0.52
2:M:1130:ALA:O	2:M:1133:VAL:HG22	2.09	0.52
2:A:95:GLN:HE22	2:A:113:HIS:CE1	2.27	0.52
2:A:206:LYS:NZ	2:A:269:ALA:O	2.41	0.52
2:A:299:ASP:HB3	2:A:325:GLU:CD	2.34	0.52
1:N:52:TYR:OH	1:N:456:ASP:OD2	2.18	0.52
1:F:88:LEU:HD21	1:F:178:TYR:HA	1.92	0.52
1:F:523:VAL:CB	1:F:657:GLN:HE22	2.22	0.52
2:E:176:TYR:OH	2:E:842:GLU:OE2	2.26	0.52
4:C:220:MET:CE	4:C:264:LEU:HD21	2.40	0.52
3:H:51:ASP:CB	4:G:322:TYR:CE1	2.92	0.52
4:G:86:ASN:HA	4:G:165:LYS:NZ	2.24	0.52
4:G:191:LEU:HD22	4:G:195:ILE:HG21	1.91	0.52
3:L:10:ILE:HG23	4:K:289:GLN:OE1	2.10	0.52
1:B:126:LEU:HD13	1:B:202:ILE:HD11	1.91	0.52
1:B:134:ASP:OD1	1:B:135:LYS:N	2.43	0.52
1:B:218:PHE:HA	1:B:224:GLY:HA2	1.92	0.52
1:B:624:ASP:HA	1:B:627:ARG:HH21	1.75	0.52
1:B:747:LEU:HD21	1:B:755:PHE:HD2	1.74	0.52
1:B:946:TRP:HA	1:B:979:PHE:HE2	1.74	0.52
2:M:784:TYR:O	2:M:788:THR:HG22	2.10	0.52
2:A:782:ILE:HA	2:A:785:MET:HE3	1.91	0.52
1:F:853:LEU:O	1:F:856:HIS:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:55:TRP:CG	2:E:148:MET:HE3	2.44	0.52
2:E:455:LEU:HD21	2:E:566:ILE:HG13	1.91	0.52
2:E:1120:GLN:CD	2:E:1123:TYR:HB3	2.35	0.52
4:C:240:ARG:HA	4:C:243:MET:HE2	1.92	0.52
3:L:19:LEU:HB3	4:K:311:THR:HG21	1.92	0.52
4:K:86:ASN:HA	4:K:165:LYS:NZ	2.24	0.52
4:K:240:ARG:HA	4:K:243:MET:HE2	1.92	0.52
3:P:14:LYS:HG3	3:P:66:PHE:CZ	2.44	0.52
3:P:66:PHE:O	3:P:67:PRO:C	2.51	0.52
1:B:630:ARG:O	1:B:633:PRO:HD2	2.10	0.52
2:M:164:PHE:HB2	2:M:492:MET:HE1	1.92	0.52
2:M:183:ILE:HD13	2:M:258:SER:HB2	1.91	0.52
2:M:1194:SER:OG	2:M:1195:GLY:N	2.42	0.52
2:A:1145:ILE:HD13	2:A:1149:ILE:HG12	1.90	0.52
1:N:957:ILE:HD13	1:N:962:HIS:HB2	1.91	0.52
1:N:1029:LYS:O	1:N:1032:PHE:HB3	2.09	0.52
2:I:474:GLN:HB3	2:I:478:ILE:HG21	1.92	0.52
1:F:670:PHE:HA	1:F:673:ILE:HG12	1.92	0.52
4:C:237:LEU:CA	4:C:240:ARG:HH21	2.23	0.52
4:G:133:ALA:O	4:G:137:VAL:N	2.39	0.52
2:I:2:ARG:NH1	2:I:2:ARG:HB2	2.25	0.52
2:I:86:ARG:NH1	2:I:161:GLU:OE2	2.43	0.52
2:I:784:TYR:O	2:I:788:THR:N	2.43	0.52
2:I:1133:VAL:O	2:I:1137:LEU:HD13	2.10	0.52
1:F:80:GLN:HB2	1:F:161:LEU:HD11	1.92	0.52
1:F:872:LEU:HB2	1:F:942:TYR:CE2	2.45	0.52
2:E:817:VAL:HG23	2:E:826:ILE:HG12	1.92	0.52
4:G:240:ARG:HA	4:G:243:MET:HE2	1.92	0.52
4:G:267:ARG:HB3	4:G:277:TYR:HB2	1.91	0.52
4:K:220:MET:CE	4:K:264:LEU:HD21	2.40	0.52
4:O:127:THR:O	4:O:131:MET:HG3	2.09	0.52
4:O:240:ARG:HA	4:O:243:MET:HE2	1.92	0.52
1:B:185:MET:HB3	1:B:190:LEU:HB2	1.92	0.51
1:B:332:ARG:NH2	1:B:336:ASP:OD1	2.43	0.51
1:B:519:THR:O	1:B:522:GLN:HB2	2.10	0.51
2:M:930:GLU:HG3	2:M:933:HIS:CE1	2.44	0.51
1:N:856:HIS:O	1:N:860:ILE:HG13	2.10	0.51
2:I:831:GLY:HA3	2:I:888:MET:HB2	1.91	0.51
1:F:294:ALA:HA	1:F:320:VAL:HG13	1.92	0.51
1:F:887:LEU:HA	1:F:890:ARG:HB2	1.92	0.51
1:F:1082:VAL:CB	5:F:1101:FAR:H62	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:191:LEU:HD22	4:K:195:ILE:HG21	1.91	0.51
4:O:313:LEU:HG	4:O:317:ARG:HE	1.74	0.51
1:B:286:GLU:HG3	1:B:293:ASP:HB3	1.92	0.51
2:M:863:ARG:NH1	2:M:863:ARG:HB3	2.26	0.51
2:M:1071:PHE:HD1	2:M:1132:LEU:HD21	1.74	0.51
2:A:519:THR:HG21	2:A:604:LEU:HD21	1.92	0.51
2:A:837:VAL:HG12	2:A:839:ALA:H	1.75	0.51
1:N:247:GLU:OE1	1:N:469:ARG:NH1	2.35	0.51
2:E:92:MET:HG2	2:E:112:LEU:HD13	1.91	0.51
2:E:295:ARG:HD3	2:E:328:TRP:CH2	2.46	0.51
4:C:220:MET:CE	4:C:268:PHE:CE2	2.90	0.51
3:H:10:ILE:CD1	4:G:289:GLN:OE1	2.54	0.51
1:B:110:ARG:O	1:B:113:GLU:HG2	2.09	0.51
1:B:443:TRP:HD1	1:B:447:LEU:HD23	1.74	0.51
2:M:447:GLU:HA	2:M:465:ILE:HG13	1.91	0.51
2:A:441:GLN:HE22	2:A:610:THR:HB	1.75	0.51
2:A:486:LEU:HD13	2:A:618:PHE:HD2	1.75	0.51
1:N:948:ILE:HG21	1:N:956:ILE:HD11	1.92	0.51
1:J:120:LYS:HG3	2:I:86:ARG:HH22	1.75	0.51
2:I:578:LEU:HD23	2:I:583:LEU:HD13	1.93	0.51
1:F:56:VAL:HG12	1:F:61:LEU:HG	1.92	0.51
1:F:580:PHE:CZ	1:F:598:ILE:HD11	2.45	0.51
3:H:51:ASP:HB2	4:G:322:TYR:CZ	2.44	0.51
1:B:566:TYR:CD1	1:B:666:GLU:HB3	2.45	0.51
1:B:1062:LYS:NZ	1:B:1063:ARG:HG2	2.25	0.51
2:M:924:ILE:HD12	2:M:924:ILE:H	1.75	0.51
2:A:491:ARG:H	2:A:491:ARG:NE	2.08	0.51
2:A:858:LEU:HB3	2:A:859:PRO:HD2	1.90	0.51
1:J:566:TYR:HD2	1:J:668:LEU:HD11	1.75	0.51
2:I:375:VAL:HA	2:I:392:ARG:HG2	1.92	0.51
2:E:277:GLU:O	2:E:281:GLN:HG2	2.10	0.51
2:E:368:LEU:HD22	2:E:399:PRO:HB3	1.92	0.51
4:O:232:HIS:HE1	4:O:234:LYS:HB2	1.74	0.51
1:B:53:TYR:HA	1:B:97:LEU:HD21	1.93	0.51
1:B:80:GLN:HB2	1:B:161:LEU:HD21	1.91	0.51
1:B:228:ASN:HB2	1:B:350:TYR:HB2	1.92	0.51
2:M:65:ALA:HA	2:M:70:ASP:OD1	2.11	0.51
2:M:822:HIS:CE1	2:M:825:LEU:HG	2.46	0.51
2:A:189:LYS:O	2:A:189:LYS:NZ	2.40	0.51
2:I:852:LYS:HB3	2:I:918:LEU:HD13	1.93	0.51
3:D:51:ASP:HB3	4:C:322:TYR:CZ	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:179:ALA:HB2	2:M:870:PRO:HD2	1.91	0.51
2:M:1193:PRO:HD2	4:O:370:LEU:HA	1.93	0.51
2:A:813:LEU:O	2:A:817:VAL:HG22	2.10	0.51
1:N:132:GLN:NE2	1:N:150:HIS:H	2.03	0.51
1:J:671:LEU:O	1:J:676:THR:OG1	2.26	0.51
1:J:853:LEU:O	1:J:857:ILE:HG13	2.11	0.51
2:I:541:GLU:O	2:I:545:THR:HG23	2.10	0.51
2:I:904:TYR:O	2:I:908:GLN:N	2.37	0.51
1:F:397:HIS:NE2	1:F:431:PRO:HG3	2.25	0.51
3:L:30:THR:O	3:L:49:LEU:HD13	2.11	0.51
4:O:267:ARG:HB3	4:O:277:TYR:HB2	1.91	0.51
2:M:511:TYR:O	2:M:518:PHE:N	2.38	0.51
2:M:833:LEU:O	2:M:833:LEU:HD23	2.11	0.51
2:M:1129:GLU:O	2:M:1133:VAL:HG13	2.11	0.51
1:N:516:GLN:HB2	2:I:557:THR:HG21	1.93	0.51
1:J:270:ASP:OD1	1:J:270:ASP:N	2.42	0.51
2:I:442:VAL:HG11	2:I:589:MET:HE1	1.93	0.51
2:I:949:LEU:HD23	2:I:953:ALA:HB1	1.93	0.51
1:F:49:LEU:O	1:F:53:TYR:N	2.43	0.51
2:E:51:ILE:HD13	2:E:84:LEU:HD22	1.92	0.51
2:E:238:CYS:O	2:E:242:LEU:HD12	2.11	0.51
2:E:398:LEU:HD12	2:E:399:PRO:HA	1.93	0.51
4:G:194:GLU:OE2	4:G:194:GLU:N	2.44	0.51
3:P:77:MET:HG3	4:O:317:ARG:NH1	2.26	0.51
4:O:113:PHE:HB2	4:O:154:GLU:HG3	1.93	0.51
1:B:132:GLN:O	1:B:135:LYS:N	2.44	0.51
1:B:449:ILE:O	1:B:453:LEU:HB2	2.10	0.51
1:B:609:TRP:NE1	1:B:613:GLY:O	2.43	0.51
1:B:1040:SER:HA	1:B:1044:GLU:HA	1.93	0.51
2:M:872:PRO:HD2	2:M:872:PRO:O	2.11	0.51
2:A:826:ILE:O	2:A:829:ILE:HG22	2.11	0.51
2:A:1053:GLN:OE1	4:C:233:ARG:CZ	2.59	0.51
1:N:568:ILE:HD12	1:N:573:VAL:HG21	1.92	0.51
1:N:883:MET:HE2	1:N:899:LEU:HD21	1.93	0.51
1:F:80:GLN:HA	1:F:155:VAL:HG12	1.91	0.51
1:F:738:ALA:HA	1:F:781:ALA:HB2	1.93	0.51
2:E:363:LYS:HE2	2:E:363:LYS:HA	1.93	0.51
2:E:1206:ALA:HA	2:E:1209:THR:HG22	1.93	0.51
3:H:30:THR:O	3:H:49:LEU:HD13	2.10	0.51
4:K:108:LYS:H	4:K:108:LYS:HD2	1.76	0.51
1:B:949:LEU:HD21	1:B:968:THR:OG1	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1069:LEU:O	1:B:1073:VAL:HG13	2.10	0.51
1:N:888:GLN:OE1	1:N:888:GLN:HA	2.10	0.51
1:N:1016:LEU:HD13	1:N:1082:VAL:HG23	1.92	0.51
2:I:858:LEU:HB2	2:I:863:ARG:HE	1.76	0.51
1:F:367:ILE:HG13	1:F:444:GLY:HA2	1.93	0.51
2:E:265:PHE:CD2	2:E:266:PRO:HD3	2.46	0.51
2:E:961:ILE:O	2:E:1066:ARG:NH2	2.43	0.51
4:O:36:ARG:CG	4:O:106:LEU:HD11	2.29	0.51
1:B:898:ASP:H	1:B:901:GLN:NE2	2.07	0.51
2:A:275:LEU:HD12	2:A:278:LEU:HD11	1.91	0.51
1:N:947:GLN:OE1	1:N:947:GLN:N	2.44	0.51
1:J:344:ASP:OD2	1:J:347:ARG:NH2	2.37	0.51
1:J:1012:ARG:HH21	5:F:1101:FAR:H142	1.73	0.51
2:I:11:LEU:O	2:I:15:ALA:N	2.37	0.51
2:I:1196:ARG:NH2	4:K:251:SER:C	2.69	0.51
1:F:83:LYS:HG2	1:F:152:VAL:HG12	1.93	0.51
2:E:200:SER:HA	2:E:262:VAL:HG21	1.93	0.51
3:H:19:LEU:HB3	4:G:311:THR:HG21	1.92	0.51
4:K:237:LEU:CA	4:K:240:ARG:HH21	2.23	0.51
3:P:10:ILE:CD1	4:O:289:GLN:OE1	2.54	0.51
3:P:30:THR:O	3:P:49:LEU:HD13	2.11	0.51
1:B:513:TYR:HA	2:E:610:THR:HG23	1.93	0.50
1:B:530:PRO:HD2	1:B:533:GLU:HG3	1.93	0.50
1:B:714:VAL:HG13	1:B:719:TRP:HD1	1.76	0.50
1:B:1008:ILE:O	1:B:1012:ARG:HB2	2.12	0.50
1:N:762:VAL:O	1:N:766:ILE:HG23	2.10	0.50
1:N:844:GLU:CD	1:N:844:GLU:H	2.19	0.50
1:N:1009:VAL:O	1:N:1013:ASN:ND2	2.44	0.50
1:F:288:ARG:NH2	1:F:823:SER:O	2.44	0.50
1:F:835:ILE:O	1:F:840:ASN:ND2	2.44	0.50
1:F:957:ILE:HD13	1:F:1021:LYS:HB3	1.93	0.50
1:F:974:MET:HE3	1:F:975:TYR:CE2	2.46	0.50
2:E:55:TRP:O	2:E:59:LEU:HD12	2.11	0.50
2:E:853:HIS:NE2	2:E:1105:ILE:HD12	2.27	0.50
4:G:142:HIS:CD2	4:G:209:LYS:HB2	2.46	0.50
3:P:51:ASP:CB	4:O:322:TYR:CE1	2.92	0.50
4:O:142:HIS:CD2	4:O:209:LYS:HB2	2.47	0.50
1:B:214:ARG:HH22	1:B:827:SER:HA	1.75	0.50
1:B:826:LEU:HB2	1:B:831:ILE:HD11	1.93	0.50
2:M:383:GLU:OE2	2:M:392:ARG:NH2	2.37	0.50
2:M:1076:TRP:CE2	2:M:1102:PRO:HD3	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:1212:GLN:HG3	4:O:330:ARG:HD3	1.93	0.50
2:A:106:GLN:HE21	2:A:500:ARG:HH12	1.58	0.50
2:A:508:SER:OG	2:A:550:LEU:HD11	2.12	0.50
1:N:474:LYS:HD3	1:N:474:LYS:N	2.26	0.50
1:J:777:LYS:HD2	1:J:779:TRP:CZ2	2.47	0.50
2:I:915:MET:SD	2:I:1064:LEU:HD12	2.51	0.50
2:I:1063:ALA:HB2	2:I:1121:PRO:HB3	1.94	0.50
2:I:1078:VAL:HG11	2:I:1135:THR:HG22	1.92	0.50
1:F:1000:VAL:O	1:F:1004:MET:HG2	2.11	0.50
3:D:19:LEU:HB3	4:C:311:THR:HG21	1.92	0.50
3:D:66:PHE:CB	4:C:291:TYR:HB2	2.41	0.50
4:G:195:ILE:HD11	4:G:211:VAL:HG22	1.94	0.50
4:O:133:ALA:O	4:O:137:VAL:N	2.39	0.50
4:O:340:LEU:HD13	4:O:342:PRO:HD2	1.92	0.50
1:B:193:ILE:HG23	1:B:198:GLU:HB2	1.93	0.50
1:B:1007:SER:O	1:B:1011:GLU:HG2	2.11	0.50
2:M:86:ARG:HD3	2:M:155:ILE:O	2.12	0.50
2:M:904:TYR:CZ	2:M:959:HIS:HB2	2.46	0.50
2:A:234:GLU:N	2:A:234:GLU:OE2	2.45	0.50
1:N:748:LEU:HD23	1:N:749:LYS:HG3	1.93	0.50
1:J:131:ARG:HG3	2:I:29:VAL:HG11	1.94	0.50
1:J:557:ILE:HG22	1:J:562:THR:HG23	1.93	0.50
1:J:609:TRP:CD1	1:J:615:PRO:HD3	2.46	0.50
2:I:790:LYS:HD3	2:I:793:ASP:HA	1.92	0.50
1:F:183:VAL:HG11	1:F:249:ILE:HA	1.93	0.50
2:E:379:ARG:HH11	2:E:379:ARG:HG3	1.76	0.50
3:L:94:ASP:OD1	3:L:105:GLU:CD	2.54	0.50
1:B:1009:VAL:CB	5:N:1101:FAR:H143	2.41	0.50
2:A:556:MET:HG2	2:A:557:THR:H	1.77	0.50
1:N:409:TYR:CE1	1:N:432:SER:HB2	2.46	0.50
1:N:509:PHE:HE2	1:N:631:PHE:HE2	1.58	0.50
2:I:16:ARG:HG3	2:I:16:ARG:HH11	1.76	0.50
2:I:530:PHE:HD2	2:I:532:LEU:HG	1.76	0.50
2:I:540:VAL:HG13	2:I:582:ILE:HG13	1.92	0.50
1:F:802:THR:O	1:F:806:HIS:ND1	2.44	0.50
2:E:209:LEU:HB3	2:E:230:VAL:HG11	1.93	0.50
2:E:1054:TRP:NE1	4:G:369:ALA:O	2.37	0.50
4:C:123:SER:O	4:C:127:THR:HG22	2.12	0.50
2:M:124:VAL:HG23	2:M:125:VAL:HG13	1.94	0.50
2:M:810:LEU:H	2:M:810:LEU:HD12	1.76	0.50
2:A:263:VAL:HB	2:A:276:VAL:HG13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:530:PHE:HD2	2:A:532:LEU:HG	1.75	0.50
1:J:1018:PHE:CE1	1:J:1077:LEU:HG	2.47	0.50
1:F:565:ILE:HG22	1:F:574:VAL:HG12	1.92	0.50
2:E:554:TRP:CE2	2:E:560:PRO:HD3	2.46	0.50
2:E:1169:LEU:HD13	4:G:375:PRO:HG3	1.94	0.50
3:D:30:THR:O	3:D:49:LEU:HD13	2.11	0.50
4:C:142:HIS:CD2	4:C:209:LYS:HB2	2.47	0.50
4:C:194:GLU:OE2	4:C:194:GLU:N	2.44	0.50
4:O:237:LEU:CA	4:O:240:ARG:HH21	2.23	0.50
1:B:531:GLN:O	1:B:535:VAL:HG23	2.12	0.50
1:B:912:LEU:HB3	1:B:916:GLN:HE21	1.77	0.50
2:A:430:PHE:O	2:A:435:LYS:NZ	2.43	0.50
2:A:528:GLN:O	2:A:835:LYS:NZ	2.43	0.50
2:I:206:LYS:NZ	2:I:206:LYS:HB3	2.27	0.50
2:I:568:HIS:C	2:I:568:HIS:HD1	2.19	0.50
1:F:332:ARG:NH2	1:F:336:ASP:OD1	2.44	0.50
1:F:795:SER:O	1:F:798:PRO:HD2	2.11	0.50
2:E:588:LYS:CE	4:G:99:PHE:CZ	2.80	0.50
2:E:588:LYS:HB2	2:E:594:PHE:HB2	1.92	0.50
2:E:1161:LEU:HD13	2:E:1205:LYS:HB3	1.94	0.50
3:D:10:ILE:HG23	4:C:289:GLN:OE1	2.10	0.50
3:H:10:ILE:HG23	4:G:289:GLN:OE1	2.10	0.50
4:G:123:SER:O	4:G:127:THR:HG22	2.12	0.50
4:K:195:ILE:HD11	4:K:211:VAL:HG22	1.94	0.50
1:B:325:LYS:HB2	1:B:330:PHE:CZ	2.47	0.50
1:B:502:GLU:HB2	1:B:622:ARG:NH1	2.27	0.50
2:M:506:GLY:O	2:M:511:TYR:OH	2.18	0.50
5:J:1101:FAR:H141	1:F:1013:ASN:CG	2.36	0.50
2:I:1200:MET:HG3	4:K:347:ILE:HG23	1.93	0.50
4:C:195:ILE:HD11	4:C:211:VAL:HG22	1.94	0.50
4:K:123:SER:O	4:K:127:THR:HG22	2.12	0.50
4:O:108:LYS:H	4:O:108:LYS:HD2	1.77	0.50
1:B:800:ILE:HG23	1:B:810:VAL:HG21	1.92	0.50
1:B:875:ARG:HB3	1:B:878:TRP:HB2	1.94	0.50
1:B:994:GLN:O	1:B:998:ILE:HG22	2.12	0.50
1:J:216:PRO:HB2	1:J:232:THR:HB	1.92	0.50
1:J:288:ARG:NH2	1:J:823:SER:O	2.44	0.50
2:I:44:VAL:HG13	2:I:88:LEU:HD22	1.94	0.50
2:I:176:TYR:HB2	2:I:241:ILE:HG13	1.94	0.50
2:E:102:PHE:HZ	2:E:178:THR:HG21	1.76	0.50
3:D:94:ASP:OD1	3:D:105:GLU:CD	2.54	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:100:TYR:HB3	3:H:136:GLN:HB3	1.94	0.50
4:O:220:MET:CE	4:O:268:PHE:CE2	2.90	0.50
2:M:1126:LEU:HA	2:M:1129:GLU:OE1	2.11	0.50
2:A:70:ASP:HA	2:A:73:LYS:NZ	2.27	0.50
2:A:283:ILE:HG23	2:A:287:LEU:HD12	1.93	0.50
2:A:484:SER:HA	2:A:497:ARG:HG2	1.94	0.50
1:N:641:LEU:HD23	1:N:651:VAL:HG21	1.94	0.50
1:J:1070:THR:HG21	5:F:1101:FAR:H12	1.94	0.50
1:F:131:ARG:NH2	1:F:159:ASP:OD1	2.44	0.50
1:F:300:ILE:HG22	1:F:307:LEU:HD23	1.93	0.50
2:E:4:ARG:NH1	2:E:12:ASP:OD2	2.45	0.50
2:E:531:TYR:CZ	2:E:827:ARG:HG2	2.47	0.50
2:E:593:TYR:OH	4:G:22:PRO:HG3	2.12	0.50
4:G:122:LEU:HD12	4:G:127:THR:HB	1.94	0.50
3:L:133:GLY:HA3	3:L:136:GLN:O	2.12	0.50
2:M:203:GLY:HA2	2:M:242:LEU:HD11	1.94	0.49
2:M:510:LEU:HD23	2:M:608:LEU:HD23	1.94	0.49
2:M:822:HIS:ND1	2:M:825:LEU:HG	2.26	0.49
2:A:1129:GLU:HB3	2:A:1200:MET:HE3	1.94	0.49
1:N:454:LEU:HD11	1:N:464:ILE:HD11	1.93	0.49
1:F:526:ILE:HG23	1:F:574:VAL:HG22	1.93	0.49
1:F:996:ARG:O	1:F:1000:VAL:HG13	2.12	0.49
2:E:1191:SER:HG	4:G:376:LYS:NZ	2.10	0.49
3:H:94:ASP:OD1	3:H:105:GLU:CD	2.54	0.49
4:G:220:MET:CE	4:G:268:PHE:CE2	2.90	0.49
4:K:171:PHE:CD1	4:K:185:CYS:HB3	2.47	0.49
1:B:223:ARG:HD2	1:B:228:ASN:ND2	2.27	0.49
2:A:1054:TRP:HA	2:A:1057:ARG:HB2	1.93	0.49
1:N:332:ARG:NH2	1:N:336:ASP:OD1	2.44	0.49
1:J:130:MET:HE2	1:J:547:LEU:HD21	1.92	0.49
2:I:4:ARG:NH1	2:I:70:ASP:OD1	2.44	0.49
2:I:22:ILE:HA	2:I:401:MET:HE3	1.94	0.49
1:F:526:ILE:CG2	1:F:574:VAL:HG22	2.41	0.49
1:F:886:GLU:CD	1:F:914:ILE:HG21	2.37	0.49
3:D:66:PHE:HB3	4:C:291:TYR:HB2	1.93	0.49
4:G:313:LEU:HA	4:G:316:VAL:HG22	1.94	0.49
4:O:171:PHE:CD1	4:O:185:CYS:HB3	2.47	0.49
1:B:144:ARG:HB3	1:B:147:THR:HG23	1.95	0.49
1:B:172:ILE:HB	1:B:238:SER:HB3	1.94	0.49
1:B:206:VAL:HG11	1:B:267:VAL:HG22	1.93	0.49
1:B:875:ARG:HH21	1:B:878:TRP:NE1	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:860:PRO:HG2	2:M:863:ARG:HH22	1.76	0.49
2:A:543:LEU:HG	2:A:594:PHE:HE2	1.77	0.49
2:A:814:TYR:HA	2:A:829:ILE:HG21	1.93	0.49
2:A:1112:GLU:O	2:A:1116:ASN:N	2.45	0.49
1:J:1034:GLU:CD	1:J:1071:LYS:HD2	2.36	0.49
2:I:822:HIS:ND1	2:I:825:LEU:HG	2.27	0.49
2:I:941:GLU:O	2:I:945:GLY:N	2.45	0.49
2:I:947:MET:N	2:I:947:MET:SD	2.85	0.49
2:I:1081:LYS:HB2	5:I:1301:FAR:H143	1.94	0.49
2:E:14:TYR:HB3	2:E:57:LEU:HD21	1.94	0.49
2:E:361:LYS:HD3	2:E:367:PRO:HD3	1.94	0.49
2:E:438:VAL:HG11	2:E:554:TRP:CD1	2.47	0.49
3:D:51:ASP:HB2	4:C:322:TYR:CZ	2.48	0.49
4:C:360:LYS:H	4:C:365:GLN:HB3	1.77	0.49
4:G:39:HIS:O	4:G:43:SER:N	2.41	0.49
4:K:142:HIS:CD2	4:K:209:LYS:HB2	2.47	0.49
4:K:337:PRO:HB3	4:K:343:LEU:CD2	2.34	0.49
4:O:16:PHE:HA	4:O:94:TYR:CE2	2.48	0.49
4:O:122:LEU:HD12	4:O:127:THR:HB	1.94	0.49
1:B:195:ASN:OD1	1:B:198:GLU:HG2	2.13	0.49
1:B:223:ARG:HB3	1:B:228:ASN:ND2	2.28	0.49
1:B:324:LEU:HD12	1:B:331:LYS:O	2.12	0.49
1:N:172:ILE:HG21	1:N:212:VAL:HG11	1.94	0.49
1:F:520:PRO:HG2	1:F:687:GLU:HB2	1.95	0.49
2:E:836:LYS:HD3	2:E:877:THR:HG21	1.94	0.49
2:E:958:LEU:O	2:E:961:ILE:HG12	2.13	0.49
4:C:222:THR:HG22	4:C:228:PRO:HA	1.95	0.49
1:B:211:ARG:O	1:B:215:VAL:HG23	2.13	0.49
1:B:757:THR:N	1:B:760:GLY:O	2.45	0.49
2:M:517:ILE:HG21	2:M:608:LEU:HD21	1.93	0.49
2:M:549:TYR:CE1	2:M:553:ARG:HD3	2.47	0.49
1:J:127:TYR:CE2	1:J:131:ARG:HD2	2.47	0.49
1:J:203:GLN:NE2	1:J:266:PHE:O	2.32	0.49
1:J:875:ARG:HB2	1:J:878:TRP:HB2	1.94	0.49
1:F:671:LEU:HD23	1:F:679:LEU:HD23	1.93	0.49
4:C:17:TYR:O	4:C:40:LYS:NZ	2.43	0.49
4:C:340:LEU:HD13	4:C:342:PRO:HD2	1.92	0.49
4:K:122:LEU:HD12	4:K:127:THR:HB	1.94	0.49
4:K:340:LEU:HD13	4:K:342:PRO:HD2	1.92	0.49
4:O:123:SER:O	4:O:127:THR:HG22	2.12	0.49
4:O:222:THR:HG22	4:O:228:PRO:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:CYS:SG	1:B:261:SER:N	2.84	0.49
1:B:443:TRP:CD1	1:B:447:LEU:HD23	2.48	0.49
1:B:786:ALA:HA	1:B:791:LYS:CE	2.41	0.49
1:B:1004:MET:O	1:B:1008:ILE:HG22	2.13	0.49
1:N:228:ASN:HB3	1:N:350:TYR:H	1.76	0.49
1:J:730:LYS:HD2	1:J:733:ASP:HB2	1.93	0.49
2:I:103:LYS:NZ	2:I:496:GLY:O	2.35	0.49
2:I:1191:SER:OG	4:K:376:LYS:NZ	2.43	0.49
1:F:850:GLN:HE22	1:F:876:ILE:HB	1.78	0.49
2:E:43:TRP:NE1	2:E:185:GLU:OE1	2.42	0.49
2:E:124:VAL:HG23	2:E:125:VAL:HG13	1.95	0.49
4:O:131:MET:HE1	4:O:220:MET:HG3	1.95	0.49
2:M:70:ASP:HA	2:M:73:LYS:HG2	1.95	0.49
2:M:916:PHE:CZ	2:M:917:ARG:HG3	2.48	0.49
2:M:1136:MET:HE2	2:M:1137:LEU:HG	1.94	0.49
1:N:951:ARG:NH1	1:N:1014:PRO:HA	2.28	0.49
1:N:992:GLN:HB2	1:N:995:TYR:HB2	1.94	0.49
2:I:92:MET:HE3	2:I:168:LEU:HD11	1.95	0.49
1:F:182:LEU:HD21	1:F:193:ILE:HD11	1.94	0.49
1:F:417:VAL:HG23	1:F:418:GLU:OE2	2.13	0.49
2:E:382:GLU:HG3	2:E:390:VAL:HG12	1.95	0.49
4:C:171:PHE:CD1	4:C:185:CYS:HB3	2.47	0.49
4:G:16:PHE:HA	4:G:94:TYR:CE2	2.48	0.49
4:G:171:PHE:CD1	4:G:185:CYS:HB3	2.47	0.49
4:K:16:PHE:HA	4:K:94:TYR:CE2	2.48	0.49
1:B:564:LYS:HG2	1:B:609:TRP:CH2	2.48	0.49
1:B:1001:GLU:HG2	1:N:1092:ILE:CD1	2.42	0.49
2:M:534:LEU:O	2:M:821:ARG:NH1	2.46	0.49
2:M:912:PHE:CD1	2:M:918:LEU:HD11	2.48	0.49
2:A:15:ALA:HA	2:A:57:LEU:HD21	1.94	0.49
2:A:900:TYR:OH	2:A:951:PRO:HB3	2.13	0.49
1:N:270:ASP:OD1	1:N:270:ASP:N	2.45	0.49
1:J:127:TYR:HE1	2:I:30:THR:HG22	1.77	0.49
1:J:236:SER:HB2	1:J:296:LEU:HD21	1.93	0.49
2:I:340:VAL:HG11	2:I:413:MET:HB3	1.94	0.49
2:I:837:VAL:HG12	2:I:839:ALA:H	1.77	0.49
1:F:1012:ARG:O	1:F:1014:PRO:HD3	2.13	0.49
2:E:135:LEU:HD13	2:E:175:ALA:HA	1.95	0.49
2:E:239:GLN:HB2	2:E:553:ARG:NH2	2.28	0.49
4:G:278:THR:HG22	4:G:281:GLU:CD	2.38	0.49
4:G:340:LEU:HD13	4:G:342:PRO:HD2	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:600:ASN:OD1	1:B:601:ALA:N	2.46	0.49
1:B:818:GLU:H	1:B:818:GLU:CD	2.13	0.49
1:B:965:GLN:HG2	1:B:969:LEU:HD12	1.95	0.49
2:M:93:ILE:HG23	1:N:67:THR:HG22	1.95	0.49
2:M:598:ARG:HD2	4:O:17:TYR:CG	2.47	0.49
2:M:859:PRO:HG2	2:M:860:PRO:HD3	1.93	0.49
2:M:1125:GLN:O	2:M:1129:GLU:HG3	2.12	0.49
2:A:887:ASP:O	2:A:890:ILE:HG12	2.13	0.49
1:N:667:GLN:OE1	1:N:667:GLN:HA	2.13	0.49
1:N:860:ILE:HG21	1:N:867:LEU:HD23	1.94	0.49
1:J:68:THR:O	1:J:124:GLY:HA3	2.13	0.49
1:J:88:LEU:HG	1:J:181:TYR:HD2	1.77	0.49
1:J:347:ARG:NH1	1:J:349:TYR:O	2.46	0.49
1:J:812:LEU:HD12	1:J:822:ILE:HD11	1.93	0.49
1:J:1065:THR:O	1:J:1069:LEU:HG	2.13	0.49
2:I:528:GLN:O	2:I:835:LYS:NZ	2.36	0.49
2:E:897:ILE:HD13	2:E:900:TYR:HD2	1.77	0.49
4:C:122:LEU:HD12	4:C:127:THR:HB	1.94	0.49
3:L:57:ASP:OD1	3:L:68:GLU:HG2	2.13	0.49
3:P:71:THR:HG23	4:O:258:SER:HB3	1.95	0.49
1:B:800:ILE:O	1:B:804:LEU:HG	2.13	0.49
1:B:828:PRO:O	1:B:832:GLN:HB2	2.13	0.49
2:M:922:LEU:H	2:M:922:LEU:HD12	1.77	0.49
2:A:542:MET:HE1	2:A:903:MET:HG2	1.93	0.49
2:A:837:VAL:HG11	2:A:899:VAL:HG21	1.93	0.49
1:J:261:SER:HB2	1:J:669:ASP:OD2	2.12	0.49
1:J:518:GLN:NE2	1:J:655:ARG:HD2	2.27	0.49
1:F:84:ILE:HD11	1:F:153:PHE:CE1	2.48	0.49
2:E:136:ASP:HA	2:E:139:SER:HB2	1.95	0.49
3:L:70:LEU:O	3:L:71:THR:C	2.56	0.49
4:K:222:THR:HG22	4:K:228:PRO:HA	1.95	0.49
1:B:1002:LEU:HD21	1:B:1027:LEU:HB2	1.94	0.48
2:M:283:ILE:HG23	2:M:287:LEU:HD12	1.95	0.48
2:A:504:VAL:HG21	2:A:546:ASP:HB3	1.93	0.48
1:J:213:TYR:HE2	1:J:274:ARG:NH1	2.08	0.48
2:I:598:ARG:HG2	4:K:17:TYR:CE1	2.48	0.48
2:I:848:LEU:HD23	2:I:854:LEU:HD13	1.95	0.48
2:I:858:LEU:O	2:I:864:GLU:HB2	2.13	0.48
1:F:243:LYS:N	1:F:275:ASN:HD21	2.11	0.48
2:E:55:TRP:CD2	2:E:148:MET:HE3	2.48	0.48
2:E:224:PRO:O	2:E:227:VAL:HG22	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:1193:PRO:HD2	4:G:370:LEU:HA	1.95	0.48
3:H:13:PHE:CD1	4:G:310:LEU:HD21	2.38	0.48
4:O:278:THR:HG22	4:O:281:GLU:CD	2.38	0.48
1:B:68:THR:O	1:B:124:GLY:HA3	2.12	0.48
1:B:307:LEU:HD23	1:B:309:ASP:H	1.78	0.48
1:B:1057:THR:HB	1:B:1065:THR:CG2	2.43	0.48
1:N:332:ARG:HD3	1:N:365:PHE:CZ	2.48	0.48
1:N:811:THR:HG22	1:N:821:VAL:HG12	1.95	0.48
1:J:126:LEU:HB2	1:J:178:TYR:OH	2.13	0.48
1:J:477:ARG:CZ	1:J:477:ARG:HB2	2.41	0.48
1:J:486:GLN:OE1	1:J:492:ASP:N	2.46	0.48
2:I:923:ILE:O	2:I:926:VAL:HG22	2.12	0.48
1:F:241:LEU:HD22	1:F:304:ALA:HB2	1.96	0.48
1:F:370:LEU:HD22	1:F:448:TYR:HA	1.94	0.48
1:F:524:GLU:HG3	1:F:525:PRO:HD3	1.95	0.48
1:F:857:ILE:HG23	1:F:868:PHE:CZ	2.48	0.48
2:E:497:ARG:NH2	2:E:500:ARG:HD2	2.29	0.48
3:D:106:LEU:HD21	4:C:305:PHE:HD2	1.78	0.48
3:H:77:MET:HG2	4:G:317:ARG:HH21	1.78	0.48
4:G:108:LYS:H	4:G:108:LYS:HD2	1.78	0.48
4:G:328:VAL:HA	4:G:332:ILE:HD11	1.95	0.48
4:O:328:VAL:HA	4:O:332:ILE:HD11	1.95	0.48
1:B:214:ARG:HH22	1:B:826:LEU:C	2.21	0.48
1:B:765:HIS:CE1	1:B:766:ILE:HG23	2.48	0.48
2:M:400:HIS:CE1	2:M:402:TRP:HB3	2.48	0.48
2:A:168:LEU:O	2:A:171:TYR:HB3	2.12	0.48
1:N:834:ILE:HA	1:N:838:LYS:NZ	2.28	0.48
2:I:448:THR:HG23	2:I:450:GLU:OE1	2.13	0.48
2:I:531:TYR:CZ	2:I:827:ARG:HG2	2.48	0.48
2:I:858:LEU:HB2	2:I:863:ARG:NE	2.29	0.48
2:I:858:LEU:HB3	2:I:859:PRO:HD2	1.96	0.48
1:F:538:TYR:HB3	1:F:552:ARG:HD3	1.96	0.48
1:F:868:PHE:HD1	1:F:871:MET:SD	2.35	0.48
4:C:278:THR:HG22	4:C:281:GLU:CD	2.38	0.48
3:H:106:LEU:HD21	4:G:305:PHE:HD2	1.78	0.48
3:L:51:ASP:CB	4:K:322:TYR:CE1	2.92	0.48
1:B:182:LEU:O	1:B:186:ILE:HG13	2.13	0.48
1:B:518:GLN:NE2	1:B:655:ARG:HA	2.29	0.48
2:A:275:LEU:O	2:A:279:THR:OG1	2.26	0.48
1:N:206:VAL:O	1:N:210:GLU:HG2	2.13	0.48
1:N:995:TYR:O	1:N:999:VAL:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:1066:CYS:HA	1:N:1069:LEU:HB2	1.95	0.48
1:F:486:GLN:HE22	1:F:492:ASP:C	2.21	0.48
1:F:571:LYS:N	1:F:571:LYS:HD2	2.28	0.48
1:F:945:VAL:HG11	1:F:1003:LEU:HD13	1.95	0.48
1:F:948:ILE:HD13	1:F:1010:LEU:HD22	1.95	0.48
2:E:927:MET:SD	2:E:957:LEU:HG	2.54	0.48
3:D:77:MET:HG2	4:C:317:ARG:HH21	1.78	0.48
4:C:16:PHE:HA	4:C:94:TYR:CE2	2.48	0.48
4:C:179:GLU:OE1	4:C:181:LEU:HD23	2.14	0.48
4:G:207:TYR:HD1	4:G:211:VAL:CG2	2.19	0.48
4:G:222:THR:HG22	4:G:228:PRO:HA	1.95	0.48
4:O:195:ILE:HD11	4:O:211:VAL:HG22	1.94	0.48
1:B:223:ARG:HD2	1:B:228:ASN:HD21	1.78	0.48
1:B:397:HIS:O	1:B:405:VAL:N	2.39	0.48
2:M:69:GLU:HB3	2:I:67:ARG:HH11	1.78	0.48
2:M:928:ALA:HA	2:M:946:LEU:HD11	1.96	0.48
2:A:811:THR:HA	2:A:814:TYR:HB3	1.96	0.48
2:A:822:HIS:O	2:A:826:ILE:HG13	2.14	0.48
1:N:123:ARG:NH2	1:N:198:GLU:OE2	2.47	0.48
1:N:131:ARG:NH1	1:N:159:ASP:OD1	2.46	0.48
1:J:88:LEU:HD13	1:J:125:ILE:HD13	1.96	0.48
1:J:413:PRO:HD2	1:J:416:PHE:HB2	1.95	0.48
1:J:1053:SER:HA	1:J:1056:ASN:HD22	1.76	0.48
2:I:332:TRP:CZ3	2:I:354:ALA:HB1	2.48	0.48
1:F:227:TYR:HA	1:F:355:ILE:HD11	1.95	0.48
1:F:497:VAL:HG12	1:F:617:PHE:HB3	1.94	0.48
1:F:1059:PRO:HA	1:F:1065:THR:OG1	2.12	0.48
2:E:61:TYR:HB3	2:E:74:ALA:HB2	1.95	0.48
2:E:183:ILE:HD11	2:E:402:TRP:HH2	1.78	0.48
2:E:361:LYS:HE2	2:E:361:LYS:N	2.29	0.48
4:G:179:GLU:OE1	4:G:181:LEU:HD23	2.14	0.48
4:G:237:LEU:CA	4:G:240:ARG:HH21	2.23	0.48
3:L:71:THR:HG23	4:K:258:SER:HB3	1.95	0.48
4:K:179:GLU:OE1	4:K:181:LEU:HD23	2.14	0.48
4:K:338:TYR:O	4:K:339:ALA:C	2.56	0.48
1:B:134:ASP:OD1	1:B:135:LYS:HG3	2.14	0.48
1:B:351:LYS:HD2	1:B:351:LYS:C	2.39	0.48
1:B:1030:GLU:HA	1:B:1033:ASN:ND2	2.28	0.48
2:M:69:GLU:HG3	2:M:70:ASP:N	2.28	0.48
2:M:452:LYS:HD3	2:M:464:THR:HG23	1.96	0.48
2:M:1120:GLN:H	2:M:1120:GLN:CD	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1130:ALA:O	2:A:1133:VAL:HG22	2.13	0.48
1:N:1065:THR:O	1:N:1069:LEU:HD23	2.14	0.48
2:I:15:ALA:HA	2:I:57:LEU:HD21	1.95	0.48
2:I:810:LEU:HD12	2:I:833:LEU:HD21	1.95	0.48
1:F:397:HIS:O	1:F:405:VAL:N	2.33	0.48
4:G:60:SER:OG	4:G:63:GLU:OE2	2.30	0.48
4:K:84:HIS:CD2	4:K:87:ILE:HG13	2.49	0.48
3:P:10:ILE:HG23	4:O:289:GLN:OE1	2.10	0.48
4:O:84:HIS:CD2	4:O:87:ILE:HG13	2.49	0.48
1:B:671:LEU:O	1:B:676:THR:OG1	2.24	0.48
1:B:860:ILE:O	1:B:864:ASN:N	2.36	0.48
2:M:277:GLU:OE1	2:M:277:GLU:HA	2.12	0.48
1:N:397:HIS:O	1:N:405:VAL:N	2.34	0.48
1:N:800:ILE:O	1:N:804:LEU:HD23	2.13	0.48
1:N:958:VAL:CG1	1:N:1024:LEU:HB2	2.43	0.48
1:J:258:GLN:OE1	2:I:62:ARG:NH1	2.43	0.48
1:J:506:LEU:HD13	1:J:623:GLU:HG3	1.96	0.48
1:J:587:MET:HE3	1:J:587:MET:HB2	1.69	0.48
2:I:65:ALA:HA	2:I:70:ASP:HB3	1.94	0.48
2:I:358:VAL:O	2:I:373:TYR:OH	2.23	0.48
1:F:1040:SER:HA	1:F:1044:GLU:HA	1.96	0.48
2:E:236:GLN:O	2:E:553:ARG:NH2	2.46	0.48
2:E:841:ASP:O	2:E:845:THR:HG22	2.14	0.48
3:D:13:PHE:CD1	4:C:310:LEU:HD21	2.38	0.48
3:D:68:GLU:HG3	4:C:125:LYS:HE2	1.95	0.48
3:D:71:THR:HG23	4:C:258:SER:HB3	1.95	0.48
4:G:84:HIS:CD2	4:G:87:ILE:HG13	2.49	0.48
4:K:278:THR:HG22	4:K:281:GLU:CD	2.38	0.48
2:M:1127:LEU:HG	2:M:1151:VAL:HG12	1.96	0.48
2:A:233:ASP:CG	2:A:503:GLY:H	2.20	0.48
2:A:426:LEU:HD23	1:F:655:ARG:NH1	2.29	0.48
2:A:823:TRP:N	2:A:823:TRP:CD1	2.81	0.48
2:A:930:GLU:HG3	2:A:933:HIS:CE1	2.48	0.48
1:N:502:GLU:HG3	1:N:685:PHE:CZ	2.49	0.48
1:N:944:ARG:HH22	1:N:1008:ILE:HD13	1.77	0.48
1:J:119:ILE:HG13	1:J:190:LEU:HD13	1.95	0.48
1:J:368:PHE:HA	1:J:371:TYR:HB2	1.96	0.48
1:J:951:ARG:HB2	1:J:1010:LEU:HD13	1.95	0.48
2:I:143:LEU:HD23	2:I:147:GLN:HG3	1.94	0.48
2:I:1055:GLN:HG3	2:I:1189:TYR:HB3	1.96	0.48
1:F:826:LEU:HD12	1:F:830:VAL:HG11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:140:VAL:HG23	2:E:204:MET:HE2	1.96	0.48
2:E:1107:PHE:O	2:E:1111:VAL:HG23	2.13	0.48
1:B:160:GLU:H	1:B:160:GLU:CD	2.16	0.48
1:B:587:MET:HG3	1:B:855:ILE:HG21	1.96	0.48
1:B:792:PHE:CE2	1:B:832:GLN:HA	2.48	0.48
1:B:1063:ARG:HD2	1:B:1068:TYR:CE1	2.49	0.48
2:A:482:ILE:HG21	2:A:664:LEU:HD12	1.96	0.48
2:A:1129:GLU:O	2:A:1133:VAL:HG13	2.14	0.48
1:J:799:HIS:CD2	1:J:858:GLY:HA3	2.49	0.48
2:I:322:GLU:OE2	2:I:323:ASN:CG	2.57	0.48
1:F:1074:MET:HE2	1:F:1074:MET:HA	1.95	0.48
2:E:452:LYS:HD3	2:E:464:THR:HG23	1.96	0.48
1:B:270:ASP:CG	1:B:558:GLY:HA3	2.32	0.48
1:B:951:ARG:NH1	1:B:1014:PRO:HA	2.28	0.48
2:A:295:ARG:HD3	2:A:328:TRP:CH2	2.48	0.48
2:A:413:MET:SD	2:A:423:ILE:HD13	2.54	0.48
2:A:926:VAL:HG11	2:A:1064:LEU:HD11	1.96	0.48
1:F:535:VAL:O	1:F:539:LEU:HD23	2.14	0.48
1:F:593:LEU:HA	1:F:593:LEU:HD23	1.61	0.48
1:F:641:LEU:HD13	1:F:653:VAL:HG21	1.96	0.48
1:F:812:LEU:HD23	1:F:876:ILE:HD13	1.96	0.48
1:F:875:ARG:HH21	1:F:935:ASN:HD21	1.61	0.48
2:E:579:ASN:ND2	2:E:581:SER:OG	2.47	0.48
4:K:133:ALA:O	4:K:137:VAL:N	2.39	0.48
1:N:951:ARG:HH12	1:N:1014:PRO:HA	1.79	0.47
1:J:129:TYR:HB3	1:J:201:PHE:CE2	2.48	0.47
1:J:296:LEU:O	1:J:300:ILE:HG13	2.14	0.47
1:J:784:TYR:OH	1:J:845:ARG:NH1	2.47	0.47
2:E:166:GLN:NE2	2:E:229:HIS:H	2.12	0.47
2:E:427:ASN:HB3	2:E:430:PHE:CD2	2.48	0.47
2:E:823:TRP:HB2	2:E:948:ASN:O	2.14	0.47
4:K:328:VAL:HA	4:K:332:ILE:HD11	1.95	0.47
4:O:179:GLU:OE1	4:O:181:LEU:HD23	2.14	0.47
1:B:494:VAL:HG22	1:B:650:LYS:HG2	1.96	0.47
1:B:820:GLU:N	1:B:820:GLU:OE2	2.47	0.47
2:M:295:ARG:HG2	2:M:331:PHE:HZ	1.79	0.47
2:M:1081:LYS:CB	5:M:1301:FAR:H143	2.43	0.47
2:A:53:ALA:HB1	2:A:408:ILE:HG21	1.95	0.47
1:J:529:TRP:CZ2	1:J:682:PHE:HB2	2.49	0.47
2:I:103:LYS:HD2	2:I:170:PHE:HB2	1.97	0.47
2:I:156:ILE:HD13	2:I:217:LEU:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:781:ASP:O	2:I:785:MET:HE2	2.14	0.47
4:C:93:THR:HG22	4:C:102:LEU:HG	1.96	0.47
4:C:108:LYS:H	4:C:108:LYS:HD2	1.78	0.47
1:B:297:LEU:HB3	1:B:298:PRO:HD3	1.95	0.47
1:B:868:PHE:CE1	1:B:915:LEU:HD11	2.49	0.47
5:B:1101:FAR:C15	1:N:1074:MET:HE1	2.11	0.47
2:M:347:GLN:HG2	2:M:351:TYR:CE2	2.48	0.47
2:M:426:LEU:HD23	1:J:655:ARG:NH2	2.30	0.47
2:A:855:THR:HG22	2:A:866:THR:HA	1.97	0.47
1:J:84:ILE:HD12	1:J:125:ILE:HG23	1.96	0.47
2:I:546:ASP:O	2:I:550:LEU:N	2.43	0.47
5:I:1301:FAR:H42	4:K:330:ARG:HA	1.96	0.47
1:F:936:ARG:HH11	1:F:936:ARG:HG3	1.79	0.47
3:D:51:ASP:CB	4:C:322:TYR:CE1	2.94	0.47
4:O:93:THR:HG22	4:O:102:LEU:HG	1.96	0.47
1:B:493:LEU:HD12	1:F:105:ASP:OD2	2.15	0.47
1:B:1063:ARG:HD2	1:B:1068:TYR:HE1	1.79	0.47
2:A:170:PHE:CE2	2:A:497:ARG:HB3	2.49	0.47
2:A:840:LEU:HD13	2:A:876:LEU:HD23	1.94	0.47
2:I:117:ASN:N	2:I:122:ALA:O	2.37	0.47
1:F:776:GLN:NE2	1:F:778:LEU:HB2	2.29	0.47
2:E:814:TYR:HB2	2:E:829:ILE:HG21	1.95	0.47
2:E:893:LEU:HB3	2:E:924:ILE:HD12	1.94	0.47
2:E:915:MET:HE2	2:E:1064:LEU:HD23	1.96	0.47
3:D:100:TYR:HB3	3:D:136:GLN:HB3	1.96	0.47
1:B:132:GLN:NE2	1:B:150:HIS:H	2.10	0.47
1:B:714:VAL:HG13	1:B:719:TRP:CD1	2.49	0.47
2:M:310:ARG:NH2	2:M:314:GLU:HG2	2.30	0.47
2:M:589:MET:HB3	2:M:599:VAL:HG11	1.95	0.47
2:M:817:VAL:HG21	2:M:829:ILE:HD12	1.97	0.47
2:A:1161:LEU:HD13	2:A:1205:LYS:HB3	1.95	0.47
1:J:167:TYR:OH	1:J:171:GLN:NE2	2.46	0.47
2:I:295:ARG:HG2	2:I:331:PHE:CZ	2.50	0.47
4:G:360:LYS:H	4:G:365:GLN:HB3	1.79	0.47
3:L:106:LEU:HD21	4:K:305:PHE:HD2	1.78	0.47
4:K:127:THR:O	4:K:131:MET:HG3	2.14	0.47
4:K:232:HIS:HB3	4:K:237:LEU:HD12	1.97	0.47
3:P:65:ASP:O	3:P:69:PHE:N	2.47	0.47
1:B:911:LEU:O	1:B:915:LEU:HB3	2.15	0.47
2:M:11:LEU:O	2:M:15:ALA:N	2.41	0.47
2:M:69:GLU:HB3	2:I:67:ARG:HD3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:322:GLU:HG2	2:M:323:ASN:HD22	1.79	0.47
1:N:523:VAL:HG11	1:N:656:LEU:HB3	1.95	0.47
2:I:215:LEU:HD23	2:I:217:LEU:HD23	1.97	0.47
1:F:173:ASN:HD21	1:F:220:VAL:HA	1.80	0.47
1:F:182:LEU:HD11	1:F:193:ILE:HD11	1.96	0.47
4:G:232:HIS:HB3	4:G:237:LEU:HD12	1.97	0.47
4:K:194:GLU:N	4:K:194:GLU:OE2	2.44	0.47
4:O:117:THR:OG1	4:O:367:ARG:NH2	2.48	0.47
1:B:510:LEU:HD11	1:B:621:ILE:HG21	1.96	0.47
1:B:624:ASP:HA	1:B:627:ARG:NH2	2.29	0.47
1:B:929:GLN:HE22	1:B:993:PRO:HG2	1.80	0.47
2:M:63:LYS:HE2	2:M:422:GLU:OE1	2.15	0.47
2:M:426:LEU:HA	1:J:655:ARG:HH22	1.80	0.47
2:A:293:CYS:HG	2:A:332:TRP:HD1	1.61	0.47
2:A:1145:ILE:HG21	2:A:1149:ILE:HD11	1.96	0.47
1:N:226:LYS:HE2	1:N:226:LYS:HB2	1.62	0.47
1:N:853:LEU:HD12	1:N:911:LEU:HD22	1.97	0.47
1:N:1051:MET:HE2	1:N:1051:MET:N	2.29	0.47
1:J:375:ASP:OD1	1:J:379:ARG:NH1	2.47	0.47
1:J:910:LEU:O	1:J:914:ILE:HG22	2.14	0.47
1:J:991:ASP:OD1	1:J:992:GLN:N	2.47	0.47
1:J:994:GLN:CD	1:J:994:GLN:N	2.73	0.47
2:I:263:VAL:HA	2:I:270:VAL:HG22	1.97	0.47
2:I:508:SER:OG	2:I:550:LEU:HD11	2.14	0.47
2:I:584:ALA:HB1	4:K:54:THR:HG21	1.95	0.47
2:I:598:ARG:HD2	2:I:598:ARG:HA	1.76	0.47
2:I:1112:GLU:OE2	2:I:1116:ASN:ND2	2.47	0.47
2:I:1167:LYS:HD2	2:I:1167:LYS:HA	1.63	0.47
1:F:579:ILE:HD11	1:F:617:PHE:HZ	1.80	0.47
1:F:873:LYS:NZ	1:F:875:ARG:HD3	2.30	0.47
2:E:233:ASP:HA	2:E:505:LEU:HD13	1.97	0.47
2:E:272:ASP:HB3	2:E:275:LEU:HG	1.97	0.47
2:E:330:LEU:HG	2:E:331:PHE:CD1	2.48	0.47
4:C:39:HIS:O	4:C:43:SER:N	2.41	0.47
4:C:328:VAL:HA	4:C:332:ILE:HD11	1.95	0.47
3:H:71:THR:HG23	4:G:258:SER:HB3	1.95	0.47
4:G:71:THR:O	4:G:75:VAL:HG23	2.15	0.47
4:G:93:THR:HG22	4:G:102:LEU:HG	1.96	0.47
3:L:52:MET:HE3	4:K:318:ILE:HD13	1.97	0.47
4:K:17:TYR:O	4:K:40:LYS:NZ	2.44	0.47
4:K:127:THR:HG21	4:K:224:LEU:HD21	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:180:ARG:HH12	4:K:205:PRO:HG2	1.80	0.47
4:O:115:TYR:CE1	4:O:119:LYS:HD2	2.50	0.47
4:O:127:THR:HG21	4:O:224:LEU:HD21	1.97	0.47
1:B:748:LEU:HD23	1:B:749:LYS:HG3	1.97	0.47
2:M:137:ALA:O	2:M:140:VAL:HG12	2.15	0.47
2:M:271:GLU:HB3	2:M:435:LYS:HZ3	1.80	0.47
2:M:1108:SER:O	2:M:1112:GLU:HB2	2.14	0.47
2:M:1167:LYS:HZ2	2:M:1176:LEU:HD12	1.80	0.47
2:A:479:LEU:HD11	2:A:511:TYR:CE2	2.49	0.47
2:A:506:GLY:O	2:A:511:TYR:OH	2.28	0.47
1:N:65:SER:HB2	1:N:155:VAL:HG22	1.97	0.47
1:J:194:TYR:CG	2:I:79:GLN:HB3	2.49	0.47
1:F:847:ALA:HA	1:F:850:GLN:HB3	1.97	0.47
1:F:873:LYS:HZ3	1:F:984:GLU:CD	2.18	0.47
2:E:547:LEU:HD12	2:E:594:PHE:CE2	2.50	0.47
3:H:68:GLU:HG3	4:G:125:LYS:CE	2.44	0.47
4:G:180:ARG:HH12	4:G:205:PRO:HG2	1.80	0.47
4:O:338:TYR:CE1	4:O:344:ARG:HG3	2.50	0.47
1:B:144:ARG:HG2	1:B:146:THR:H	1.80	0.47
1:B:412:VAL:HG21	1:B:420:GLU:HG2	1.95	0.47
1:B:602:LEU:HD12	1:B:646:ILE:HD11	1.97	0.47
1:B:793:SER:O	1:B:796:ILE:HG12	2.14	0.47
1:B:953:PRO:HD2	1:B:954:ASN:H	1.80	0.47
2:M:319:LYS:HD2	2:M:1098:ARG:HG3	1.97	0.47
2:A:280:LYS:HD3	2:A:338:ASP:OD2	2.14	0.47
2:A:469:TYR:CG	2:A:470:PRO:HA	2.50	0.47
1:J:670:PHE:HA	1:J:673:ILE:HG12	1.97	0.47
2:I:330:LEU:HD22	2:I:400:HIS:CE1	2.50	0.47
2:I:561:THR:OG1	2:I:611:SER:OG	2.14	0.47
2:I:1129:GLU:O	2:I:1133:VAL:HG13	2.15	0.47
2:I:1175:MET:H	2:I:1175:MET:HE3	1.79	0.47
2:I:1192:ALA:HB3	4:K:372:GLU:HB2	1.97	0.47
1:F:53:TYR:HB2	1:F:101:TYR:OH	2.15	0.47
1:F:126:LEU:HB2	1:F:178:TYR:OH	2.15	0.47
1:F:814:ALA:HB2	1:F:846:GLU:HG3	1.96	0.47
2:E:41:ASP:OD2	2:E:115:LYS:HB2	2.15	0.47
2:E:49:TYR:HB3	2:E:402:TRP:CD1	2.49	0.47
2:E:400:HIS:HD2	2:E:403:GLY:N	2.07	0.47
2:E:483:TYR:O	2:E:497:ARG:HB3	2.15	0.47
3:L:77:MET:HG2	4:K:317:ARG:HH21	1.78	0.47
4:K:51:ILE:HD12	4:K:51:ILE:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:24:GLU:OE2	4:O:36:ARG:NH2	2.20	0.47
1:B:262:TRP:CZ3	2:E:2:ARG:HG3	2.50	0.47
2:M:857:GLY:O	2:M:921:GLY:HA3	2.15	0.47
2:A:896:GLU:HG2	2:A:900:TYR:CZ	2.49	0.47
1:N:211:ARG:HG2	1:N:555:ARG:NH2	2.30	0.47
1:J:71:PHE:HB3	1:J:442:LEU:HD23	1.97	0.47
1:F:533:GLU:CD	1:F:682:PHE:HB3	2.40	0.47
1:F:591:VAL:O	1:F:595:ILE:N	2.48	0.47
2:E:335:PHE:HA	2:E:338:ASP:OD2	2.15	0.47
4:C:84:HIS:CD2	4:C:87:ILE:HG13	2.49	0.47
4:C:239:LEU:O	4:C:243:MET:HG3	2.15	0.47
3:H:133:GLY:HA3	3:H:136:GLN:O	2.14	0.47
4:G:166:LEU:HD12	4:G:167:THR:H	1.80	0.47
4:K:337:PRO:CB	4:K:343:LEU:HD23	2.36	0.47
4:O:232:HIS:HB3	4:O:237:LEU:HD12	1.97	0.47
1:B:113:GLU:OE2	2:A:159:LEU:HD21	2.15	0.46
1:B:262:TRP:HH2	2:A:73:LYS:HG2	1.80	0.46
2:M:1162:PHE:HD1	2:M:1202:TYR:CE2	2.33	0.46
1:N:1019:GLN:OE1	1:N:1080:GLY:HA2	2.14	0.46
1:J:484:SER:HB3	1:J:610:LYS:HD3	1.97	0.46
1:J:536:LYS:HE3	1:J:536:LYS:HB3	1.66	0.46
1:J:1018:PHE:HD2	1:J:1022:VAL:HG22	1.79	0.46
2:I:579:ASN:OD1	2:I:580:SER:N	2.48	0.46
1:F:485:ASN:OD1	1:F:485:ASN:N	2.46	0.46
2:E:281:GLN:HA	2:E:284:ILE:HD11	1.96	0.46
4:C:115:TYR:CE1	4:C:119:LYS:HD2	2.50	0.46
4:C:166:LEU:HD12	4:C:167:THR:H	1.80	0.46
4:G:51:ILE:N	4:G:51:ILE:HD12	2.30	0.46
4:G:152:LYS:H	4:G:152:LYS:HG2	1.42	0.46
4:G:313:LEU:O	4:G:317:ARG:HB2	2.15	0.46
3:L:13:PHE:CD1	4:K:310:LEU:HD21	2.38	0.46
3:L:52:MET:HE2	3:L:52:MET:HB3	1.69	0.46
4:K:360:LYS:H	4:K:365:GLN:HB3	1.79	0.46
1:B:594:LEU:O	1:B:598:ILE:HD13	2.14	0.46
1:B:1037:LYS:HA	1:B:1037:LYS:HE2	1.97	0.46
2:M:784:TYR:HE2	2:M:825:LEU:HD13	1.80	0.46
2:M:842:GLU:OE1	2:M:842:GLU:N	2.49	0.46
2:A:277:GLU:OE1	2:A:277:GLU:HA	2.15	0.46
5:A:1301:FAR:C4	4:C:330:ARG:HG3	2.45	0.46
1:N:330:PHE:HB2	1:N:368:PHE:HB2	1.96	0.46
1:N:356:LYS:HB2	1:N:356:LYS:HE3	1.55	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:623:GLU:H	1:N:623:GLU:CD	2.19	0.46
1:J:495:VAL:HG13	1:J:615:PRO:HG2	1.97	0.46
1:J:627:ARG:HE	1:J:627:ARG:HB3	1.57	0.46
2:I:363:LYS:HB2	2:I:366:VAL:HG22	1.98	0.46
2:I:1145:ILE:HD13	2:I:1149:ILE:HG12	1.95	0.46
1:F:372:MET:HG2	1:F:388:TYR:CE1	2.50	0.46
1:F:808:LYS:HE3	1:F:871:MET:O	2.16	0.46
3:H:57:ASP:OD2	3:H:64:ILE:HA	2.15	0.46
4:G:127:THR:HG21	4:G:224:LEU:HD21	1.97	0.46
4:K:39:HIS:O	4:K:43:SER:N	2.41	0.46
4:K:116:LEU:HA	4:K:116:LEU:HD22	1.34	0.46
1:B:1035:PHE:HA	1:B:1038:ASP:OD2	2.15	0.46
5:B:1101:FAR:H143	1:N:1005:VAL:CG2	2.45	0.46
2:M:402:TRP:CD1	2:M:406:LEU:HD11	2.50	0.46
2:M:529:GLN:OE1	2:M:838:GLU:N	2.48	0.46
2:M:949:LEU:H	2:M:949:LEU:HD12	1.80	0.46
2:A:240:SER:HB3	2:A:553:ARG:HH22	1.79	0.46
2:A:290:ARG:HE	2:A:389:THR:HA	1.80	0.46
1:N:187:SER:HB3	1:N:466:PRO:HB2	1.96	0.46
1:N:506:LEU:HD21	1:N:621:ILE:HG22	1.96	0.46
1:J:88:LEU:HD21	1:J:178:TYR:HA	1.98	0.46
1:J:568:ILE:HG13	1:J:668:LEU:HD13	1.97	0.46
1:J:714:VAL:HG13	1:J:719:TRP:HD1	1.80	0.46
1:J:744:LEU:HA	1:J:747:LEU:HB2	1.96	0.46
2:I:61:TYR:HB3	2:I:74:ALA:HB2	1.97	0.46
2:I:598:ARG:CD	4:K:17:TYR:CE1	2.99	0.46
2:I:1107:PHE:O	2:I:1107:PHE:HD1	1.98	0.46
1:F:362:GLU:O	1:F:429:ARG:NH1	2.43	0.46
2:E:184:TRP:CE2	2:E:295:ARG:HD2	2.51	0.46
2:E:932:ALA:HB2	2:E:942:ALA:HB2	1.97	0.46
3:D:68:GLU:HG3	4:C:125:LYS:CE	2.46	0.46
4:G:115:TYR:CE1	4:G:119:LYS:HD2	2.50	0.46
4:O:71:THR:O	4:O:75:VAL:HG23	2.15	0.46
4:O:249:PHE:HZ	4:O:265:VAL:HB	1.81	0.46
1:B:262:TRP:C	1:B:262:TRP:CD1	2.94	0.46
1:B:580:PHE:CZ	1:B:619:VAL:HA	2.51	0.46
1:B:845:ARG:HG3	1:B:900:TYR:CE1	2.50	0.46
2:M:12:ASP:OD1	2:M:61:TYR:OH	2.28	0.46
2:M:522:PRO:HB2	2:M:524:PHE:CE1	2.51	0.46
2:A:204:MET:HE1	2:A:261:SER:O	2.15	0.46
2:A:532:LEU:HD21	2:A:896:GLU:HG3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:485:ASN:OD1	1:N:485:ASN:N	2.47	0.46
1:J:132:GLN:NE2	1:J:150:HIS:H	2.02	0.46
1:J:193:ILE:HG13	1:J:254:LEU:HD13	1.96	0.46
1:J:958:VAL:HG22	1:J:1024:LEU:CD1	2.45	0.46
2:I:460:ILE:HG22	2:I:462:VAL:HG13	1.97	0.46
2:E:265:PHE:CD1	2:E:266:PRO:HA	2.51	0.46
2:E:280:LYS:O	2:E:284:ILE:HG13	2.15	0.46
2:E:284:ILE:HD12	2:E:285:THR:N	2.30	0.46
4:C:51:ILE:HD12	4:C:51:ILE:N	2.30	0.46
4:G:239:LEU:O	4:G:243:MET:HG3	2.15	0.46
3:L:45:THR:CG2	3:L:46:GLU:N	2.78	0.46
4:K:152:LYS:H	4:K:152:LYS:HG2	1.42	0.46
4:K:239:LEU:O	4:K:243:MET:HG3	2.15	0.46
1:B:1061:GLY:H	1:N:1082:VAL:HG12	1.81	0.46
2:M:463:GLU:HG3	2:M:603:LYS:HG2	1.97	0.46
2:M:858:LEU:O	2:M:864:GLU:HB2	2.16	0.46
2:M:925:GLN:O	2:M:929:THR:HG23	2.15	0.46
2:A:368:LEU:HB3	2:A:399:PRO:HB3	1.98	0.46
1:N:577:PRO:HB2	1:N:579:ILE:HG12	1.97	0.46
1:N:831:ILE:HA	1:N:834:ILE:HB	1.97	0.46
1:N:954:ASN:HB3	1:N:1021:LYS:HG2	1.98	0.46
1:J:113:GLU:HB2	2:I:218:PHE:HE2	1.80	0.46
1:J:271:ALA:HA	1:J:274:ARG:NH1	2.31	0.46
1:J:925:LEU:CD2	1:J:929:GLN:HE22	2.29	0.46
2:I:829:ILE:HA	2:I:832:ILE:HG12	1.98	0.46
2:I:859:PRO:HG2	2:I:860:PRO:HD3	1.98	0.46
1:F:503:SER:OG	1:F:504:GLN:OE1	2.28	0.46
2:E:472:ARG:NH1	2:E:667:LEU:O	2.49	0.46
2:E:510:LEU:HD22	2:E:519:THR:HG22	1.97	0.46
2:E:930:GLU:OE1	2:E:961:ILE:HG22	2.15	0.46
4:C:180:ARG:HH12	4:C:205:PRO:HG2	1.80	0.46
4:K:71:THR:O	4:K:75:VAL:HG23	2.15	0.46
4:O:39:HIS:O	4:O:43:SER:N	2.41	0.46
1:B:1035:PHE:HD1	1:B:1068:TYR:CE2	2.34	0.46
2:M:344:ASN:O	2:M:348:VAL:HG23	2.16	0.46
2:M:598:ARG:HD2	4:O:17:TYR:CD1	2.50	0.46
2:M:1153:LYS:C	2:M:1153:LYS:HD3	2.40	0.46
2:A:332:TRP:CB	2:A:355:LEU:HD23	2.45	0.46
2:A:445:LEU:O	2:A:566:ILE:N	2.40	0.46
2:A:557:THR:OG1	2:A:612:CYS:SG	2.72	0.46
1:J:115:GLU:OE2	1:J:190:LEU:HD21	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:519:THR:HB	2:I:563:THR:HG21	1.97	0.46
2:I:569:SER:O	2:I:821:ARG:NH1	2.43	0.46
2:I:787:TYR:O	2:I:790:LYS:HB2	2.15	0.46
1:F:441:PHE:CE1	1:F:443:TRP:HB3	2.50	0.46
1:F:765:HIS:O	1:F:768:ARG:HG2	2.15	0.46
1:F:867:LEU:HG	1:F:915:LEU:CD1	2.41	0.46
2:E:203:GLY:CA	2:E:242:LEU:HD21	2.46	0.46
2:E:332:TRP:CD1	2:E:351:TYR:HE2	2.34	0.46
4:C:88:ILE:HD12	4:C:88:ILE:O	2.16	0.46
4:C:232:HIS:HB3	4:C:237:LEU:HD12	1.97	0.46
3:H:36:VAL:C	3:H:39:SER:HG	2.09	0.46
3:L:57:ASP:OD2	3:L:64:ILE:HA	2.16	0.46
4:O:117:THR:H	4:O:367:ARG:HH22	1.63	0.46
4:O:313:LEU:CD2	4:O:317:ARG:NH2	2.66	0.46
2:M:90:HIS:HA	2:M:93:ILE:HG22	1.98	0.46
2:M:328:TRP:N	2:M:328:TRP:CD1	2.84	0.46
2:M:1111:VAL:O	2:M:1115:LEU:HD13	2.16	0.46
2:M:1153:LYS:NZ	2:M:1210:TYR:HB2	2.31	0.46
2:M:1173:ASP:N	2:M:1173:ASP:OD1	2.49	0.46
2:A:507:THR:HG21	2:A:522:PRO:HA	1.96	0.46
1:N:859:TRP:HE3	1:N:860:ILE:HG12	1.80	0.46
1:N:883:MET:HB3	1:N:910:LEU:HD12	1.98	0.46
1:N:1087:ASP:OD1	1:N:1088:ASP:N	2.45	0.46
1:J:748:LEU:HD23	1:J:749:LYS:HG3	1.96	0.46
1:J:764:ASP:OD1	1:J:765:HIS:N	2.49	0.46
1:J:925:LEU:HD12	1:J:1056:ASN:OD1	2.16	0.46
2:I:535:ASP:HB3	2:I:538:MET:HB2	1.96	0.46
1:F:894:LYS:HB2	1:F:894:LYS:HE3	1.77	0.46
1:F:903:SER:O	1:F:907:VAL:HG23	2.16	0.46
1:F:1006:VAL:HB	1:F:1073:VAL:HG21	1.98	0.46
2:E:1100:MET:HE1	2:E:1110:HIS:CG	2.51	0.46
3:D:52:MET:HE3	4:C:318:ILE:HD13	1.97	0.46
4:C:60:SER:OG	4:C:63:GLU:OE2	2.30	0.46
4:C:127:THR:HG21	4:C:224:LEU:HD21	1.97	0.46
3:H:51:ASP:CB	4:G:322:TYR:OH	2.64	0.46
3:H:106:LEU:O	3:H:110:MET:HG3	2.16	0.46
4:K:261:VAL:O	4:K:265:VAL:HG23	2.16	0.46
3:P:100:TYR:HB3	3:P:136:GLN:HB3	1.97	0.46
4:O:194:GLU:OE2	4:O:194:GLU:N	2.44	0.46
1:B:875:ARG:HE	1:B:878:TRP:CD1	2.34	0.46
2:M:588:LYS:HA	4:O:98:THR:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:1192:ALA:HB3	4:O:372:GLU:HB2	1.97	0.46
2:A:90:HIS:HA	2:A:93:ILE:HG22	1.98	0.46
2:A:102:PHE:HD2	2:A:171:TYR:CE2	2.34	0.46
1:N:84:ILE:HD12	1:N:125:ILE:HG12	1.97	0.46
1:N:510:LEU:HD21	1:N:626:ILE:HD11	1.97	0.46
1:N:943:ASP:N	1:N:943:ASP:OD1	2.48	0.46
1:J:998:ILE:HD12	1:J:1001:GLU:OE2	2.16	0.46
1:J:1005:VAL:O	1:J:1009:VAL:HG23	2.15	0.46
2:I:375:VAL:HG22	2:I:392:ARG:HD3	1.98	0.46
1:F:951:ARG:HE	1:F:1010:LEU:HD21	1.80	0.46
2:E:90:HIS:HA	2:E:93:ILE:HG22	1.97	0.46
2:E:141:TYR:CD1	2:E:141:TYR:C	2.94	0.46
2:E:146:ALA:HB2	2:E:212:LEU:CD2	2.45	0.46
2:E:176:TYR:HB3	2:E:238:CYS:SG	2.56	0.46
4:C:71:THR:O	4:C:75:VAL:HG23	2.15	0.46
4:C:127:THR:O	4:C:131:MET:HG3	2.16	0.46
4:K:338:TYR:HA	4:K:344:ARG:HB2	1.98	0.46
2:M:473:VAL:HA	2:M:519:THR:O	2.16	0.46
2:M:1129:GLU:HG2	4:O:355:TYR:OH	2.16	0.46
2:A:323:ASN:ND2	2:A:387:PRO:HB3	2.31	0.46
1:N:356:LYS:HG2	1:N:970:SER:O	2.16	0.46
1:N:834:ILE:HA	1:N:838:LYS:HZ2	1.80	0.46
1:J:50:ASP:OD2	1:J:54:ARG:NH2	2.49	0.46
1:J:53:TYR:HA	1:J:97:LEU:HD21	1.97	0.46
1:J:370:LEU:HD11	1:J:406:VAL:HG21	1.97	0.46
1:J:373:MET:HE1	1:J:392:LEU:HD22	1.97	0.46
1:F:800:ILE:HG23	1:F:810:VAL:HG11	1.98	0.46
4:G:346:LEU:O	4:G:350:TYR:HD1	1.99	0.46
3:L:51:ASP:CB	4:K:322:TYR:OH	2.64	0.46
4:K:166:LEU:HD12	4:K:167:THR:H	1.80	0.46
4:K:249:PHE:HZ	4:K:265:VAL:HB	1.81	0.46
4:O:60:SER:OG	4:O:63:GLU:OE2	2.30	0.46
4:O:166:LEU:HD12	4:O:167:THR:H	1.80	0.46
4:O:346:LEU:O	4:O:350:TYR:HD1	1.99	0.46
1:B:480:SER:C	1:B:482:ARG:H	2.21	0.46
1:B:747:LEU:HD23	1:B:751:GLU:HB2	1.98	0.46
1:B:806:HIS:ND1	1:B:861:ILE:HD11	2.31	0.46
2:M:1054:TRP:HA	2:M:1057:ARG:HB2	1.96	0.46
2:M:1153:LYS:HE3	2:M:1210:TYR:HD1	1.81	0.46
2:A:332:TRP:CZ3	2:A:354:ALA:HB1	2.51	0.46
2:A:608:LEU:HD23	2:A:609:THR:H	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1132:LEU:O	2:A:1135:THR:OG1	2.22	0.46
1:N:529:TRP:CZ2	1:N:682:PHE:HB2	2.51	0.46
1:N:565:ILE:HD12	1:N:663:ALA:HB3	1.99	0.46
1:J:853:LEU:HD21	1:J:911:LEU:HG	1.98	0.46
2:I:336:ILE:O	2:I:340:VAL:HG23	2.16	0.46
2:I:458:LYS:NZ	2:I:587:ARG:HH22	2.14	0.46
2:I:578:LEU:HD21	2:I:582:ILE:HG22	1.98	0.46
1:F:589:GLN:H	1:F:589:GLN:CD	2.24	0.46
2:E:100:GLU:HB2	2:E:494:LEU:HD23	1.97	0.46
2:E:1133:VAL:O	2:E:1136:MET:HG2	2.15	0.46
4:G:88:ILE:O	4:G:88:ILE:HD12	2.16	0.46
4:K:93:THR:HG22	4:K:102:LEU:HG	1.96	0.46
4:O:88:ILE:O	4:O:88:ILE:HD12	2.16	0.46
4:O:338:TYR:CD2	4:O:344:ARG:HD3	2.51	0.46
1:B:274:ARG:NH1	1:B:274:ARG:HB2	2.31	0.45
1:B:529:TRP:N	1:B:574:VAL:O	2.44	0.45
1:B:796:ILE:O	1:B:799:HIS:N	2.49	0.45
2:A:1086:SER:HA	2:A:1091:VAL:HA	1.99	0.45
1:N:661:SER:HB3	2:I:152:GLY:HA2	1.98	0.45
1:N:724:THR:HB	1:N:726:GLU:HG3	1.98	0.45
1:N:778:LEU:HD23	1:N:778:LEU:HA	1.79	0.45
1:N:1016:LEU:HB3	1:N:1077:LEU:HD22	1.98	0.45
2:I:847:LEU:HD23	2:I:905:MET:HE2	1.98	0.45
2:I:855:THR:HG22	2:I:866:THR:HA	1.97	0.45
2:E:51:ILE:HD12	2:E:81:VAL:HA	1.98	0.45
2:E:100:GLU:HA	2:E:103:LYS:HE2	1.96	0.45
2:E:662:ARG:NH1	2:E:663:TYR:HB2	2.30	0.45
3:L:129:ALA:HA	4:K:302:ARG:NH1	2.31	0.45
4:K:232:HIS:CE1	4:K:234:LYS:HB3	2.50	0.45
1:B:232:THR:O	1:B:824:ASN:ND2	2.48	0.45
2:M:136:ASP:HB3	2:M:201:SER:HA	1.97	0.45
2:A:513:ILE:HD11	2:A:616:LEU:HD12	1.99	0.45
2:A:535:ASP:O	2:A:539:ILE:HG13	2.16	0.45
2:A:900:TYR:HA	2:A:903:MET:SD	2.56	0.45
1:N:809:GLN:OE1	1:N:873:LYS:NZ	2.50	0.45
1:J:298:PRO:HG3	1:J:371:TYR:CZ	2.51	0.45
2:I:948:ASN:OD1	2:I:948:ASN:N	2.48	0.45
1:F:123:ARG:O	1:F:127:TYR:N	2.43	0.45
1:F:387:GLU:O	1:F:391:LEU:HG	2.16	0.45
2:E:1053:GLN:OE1	4:G:233:ARG:CZ	2.64	0.45
4:K:60:SER:OG	4:K:63:GLU:OE2	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:73:LYS:O	4:K:76:ASP:HB3	2.16	0.45
4:K:182:ARG:HH21	4:K:204:HIS:C	2.24	0.45
4:O:180:ARG:HH12	4:O:205:PRO:HG2	1.80	0.45
1:B:541:LEU:HD13	1:B:670:PHE:CD2	2.51	0.45
2:A:86:ARG:HD3	2:A:155:ILE:O	2.16	0.45
2:A:1107:PHE:O	2:A:1111:VAL:HG23	2.16	0.45
1:J:868:PHE:HA	1:J:871:MET:CE	2.46	0.45
2:I:479:LEU:HD21	2:I:502:MET:HE2	1.99	0.45
2:I:924:ILE:HD12	2:I:925:GLN:N	2.31	0.45
1:F:88:LEU:HD23	1:F:122:MET:HE1	1.97	0.45
1:F:475:ASP:HB3	1:F:483:PHE:CD1	2.52	0.45
3:D:106:LEU:O	3:D:110:MET:HG3	2.16	0.45
4:C:261:VAL:O	4:C:265:VAL:HG23	2.16	0.45
3:H:52:MET:HE3	4:G:318:ILE:HD13	1.97	0.45
4:K:166:LEU:HD12	4:K:167:THR:N	2.32	0.45
3:P:129:ALA:HA	4:O:302:ARG:NH1	2.31	0.45
4:O:239:LEU:O	4:O:243:MET:HG3	2.15	0.45
1:B:137:GLN:HE22	1:B:550:SER:HB3	1.80	0.45
1:B:270:ASP:OD1	1:B:560:LEU:HB2	2.16	0.45
1:B:961:LYS:HD3	1:B:989:ASN:ND2	2.32	0.45
2:M:206:LYS:NZ	2:M:269:ALA:O	2.48	0.45
2:A:490:ASN:HB2	2:A:491:ARG:NH1	2.32	0.45
2:A:554:TRP:CZ3	2:A:560:PRO:HB3	2.52	0.45
2:A:589:MET:HG2	2:A:599:VAL:HG21	1.98	0.45
1:N:1026:ARG:HG2	1:N:1026:ARG:HH11	1.81	0.45
1:J:726:GLU:OE2	1:J:726:GLU:N	2.32	0.45
1:J:755:PHE:O	1:J:762:VAL:N	2.48	0.45
1:F:500:ILE:HG13	1:F:618:LEU:HD23	1.98	0.45
1:F:777:LYS:HB2	1:F:779:TRP:NE1	2.31	0.45
2:E:307:ASP:OD2	2:E:310:ARG:HG3	2.17	0.45
2:E:930:GLU:HG3	2:E:933:HIS:CE1	2.51	0.45
4:G:32:SER:HB3	4:G:51:ILE:HG13	1.98	0.45
4:G:249:PHE:HZ	4:G:265:VAL:HB	1.81	0.45
4:K:180:ARG:HB3	4:K:206:GLY:C	2.42	0.45
3:P:51:ASP:CB	4:O:322:TYR:OH	2.64	0.45
4:O:166:LEU:HD12	4:O:167:THR:N	2.32	0.45
1:B:918:GLN:HG2	1:B:927:ARG:HH12	1.81	0.45
1:B:919:GLN:HB2	1:B:927:ARG:HG2	1.99	0.45
1:N:145:PRO:HG3	1:N:232:THR:HG21	1.98	0.45
1:N:355:ILE:H	1:N:355:ILE:HD12	1.80	0.45
1:J:83:LYS:HG2	1:J:152:VAL:HG12	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:152:VAL:HG22	1:J:169:HIS:HE1	1.81	0.45
1:F:519:THR:OG1	1:F:522:GLN:HG3	2.17	0.45
1:F:544:ASN:O	1:F:544:ASN:OD1	2.34	0.45
1:F:577:PRO:HG3	1:F:617:PHE:CE1	2.52	0.45
1:F:941:PHE:O	1:F:945:VAL:HG22	2.16	0.45
1:F:1006:VAL:O	1:F:1010:LEU:N	2.39	0.45
2:E:109:LYS:HA	2:E:109:LYS:HD3	1.64	0.45
2:E:186:ARG:HH12	2:E:301:TYR:HA	1.81	0.45
2:E:262:VAL:HA	2:E:267:ALA:HB3	1.97	0.45
2:E:1145:ILE:HD13	2:E:1149:ILE:HG12	1.97	0.45
2:E:1149:ILE:HG22	2:E:1154:ILE:HD11	1.98	0.45
4:G:73:LYS:O	4:G:76:ASP:HB3	2.16	0.45
4:G:261:VAL:O	4:G:265:VAL:HG23	2.16	0.45
3:P:52:MET:HE3	4:O:318:ILE:HD13	1.97	0.45
1:B:102:ARG:NH1	1:B:188:SER:O	2.47	0.45
1:B:365:PHE:CD2	1:B:409:TYR:HB3	2.52	0.45
1:B:409:TYR:CZ	1:B:432:SER:HB2	2.52	0.45
2:M:402:TRP:CD1	2:M:402:TRP:C	2.94	0.45
2:A:854:LEU:O	2:A:867:ILE:N	2.38	0.45
1:N:531:GLN:O	1:N:535:VAL:HG23	2.17	0.45
2:I:190:THR:OG1	2:I:192:GLN:HG3	2.17	0.45
2:I:1212:GLN:NE2	4:K:330:ARG:HD2	2.32	0.45
1:F:67:THR:HA	2:E:93:ILE:HG21	1.99	0.45
1:F:130:MET:C	1:F:132:GLN:H	2.24	0.45
1:F:162:LEU:O	1:F:169:HIS:NE2	2.48	0.45
1:F:1081:GLU:O	1:F:1083:LYS:NZ	2.44	0.45
2:E:415:GLU:HB2	2:E:417:PHE:CE2	2.52	0.45
4:C:133:ALA:O	4:C:137:VAL:N	2.39	0.45
3:H:118:THR:HG1	3:H:121:GLU:HB2	1.82	0.45
4:G:277:TYR:CE2	4:G:282:ALA:HA	2.52	0.45
4:K:165:LYS:HA	4:K:165:LYS:HE3	1.99	0.45
4:O:115:TYR:HE1	4:O:119:LYS:HD2	1.81	0.45
1:B:278:THR:HG22	1:B:282:LEU:HD12	1.97	0.45
2:M:30:THR:OG1	2:M:118:THR:O	2.27	0.45
1:J:864:ASN:HD21	1:J:867:LEU:HD22	1.80	0.45
2:I:920:ILE:HA	2:I:923:ILE:HB	1.98	0.45
2:I:1193:PRO:O	2:I:1200:MET:HG2	2.17	0.45
1:F:997:GLN:O	1:F:1001:GLU:HG3	2.17	0.45
2:E:784:TYR:CE2	2:E:825:LEU:HD22	2.52	0.45
2:E:841:ASP:HA	2:E:844:CYS:SG	2.56	0.45
2:E:901:LEU:HD22	2:E:912:PHE:CE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:346:LEU:O	4:C:350:TYR:HD1	1.99	0.45
4:G:126:GLU:HA	4:G:129:LYS:HZ1	1.81	0.45
3:L:106:LEU:O	3:L:110:MET:HG3	2.16	0.45
4:K:32:SER:HB3	4:K:51:ILE:HG13	1.98	0.45
4:O:51:ILE:N	4:O:51:ILE:HD12	2.30	0.45
4:O:232:HIS:CE1	4:O:234:LYS:HB2	2.50	0.45
1:B:226:LYS:HB2	1:B:226:LYS:HE3	1.73	0.45
1:B:641:LEU:HD22	1:B:651:VAL:HG21	1.99	0.45
1:B:833:ASN:HB2	1:B:838:LYS:NZ	2.31	0.45
2:A:130:TRP:HB3	2:A:132:HIS:CE1	2.52	0.45
2:A:291:TYR:O	2:A:329:PRO:HG3	2.16	0.45
1:N:107:ASP:OD1	1:N:107:ASP:N	2.49	0.45
1:N:670:PHE:HA	1:N:673:ILE:HG12	1.99	0.45
1:N:857:ILE:HG23	1:N:868:PHE:CZ	2.51	0.45
1:N:938:PRO:HG2	1:N:1004:MET:HG3	1.97	0.45
1:J:1021:LYS:HE3	1:J:1021:LYS:HB3	1.63	0.45
2:I:912:PHE:HE1	2:I:962:LEU:HD13	1.82	0.45
1:F:179:LEU:O	1:F:183:VAL:HG22	2.16	0.45
1:F:655:ARG:H	1:F:655:ARG:HG3	1.63	0.45
1:F:873:LYS:HZ1	1:F:875:ARG:HD3	1.82	0.45
2:E:186:ARG:NH1	2:E:313:TYR:OH	2.49	0.45
2:E:912:PHE:CZ	2:E:962:LEU:HD13	2.52	0.45
2:E:1120:GLN:OE1	2:E:1123:TYR:HB3	2.16	0.45
3:D:133:GLY:HA3	3:D:136:GLN:O	2.16	0.45
4:C:32:SER:HB3	4:C:51:ILE:HG13	1.98	0.45
4:C:73:LYS:O	4:C:76:ASP:HB3	2.16	0.45
4:C:166:LEU:HD12	4:C:167:THR:N	2.32	0.45
4:O:151:LEU:HB2	4:O:215:SER:HB3	1.99	0.45
1:B:990:ILE:HD12	1:B:990:ILE:O	2.16	0.45
1:B:1015:GLU:OE1	5:B:1101:FAR:H41	2.16	0.45
5:B:1101:FAR:H111	5:B:1101:FAR:H7	1.43	0.45
2:A:260:LEU:HD21	2:A:335:PHE:CD1	2.52	0.45
2:A:381:ASP:HA	2:A:384:TYR:HD2	1.82	0.45
2:A:579:ASN:OD1	2:A:581:SER:N	2.48	0.45
1:N:262:TRP:CE3	2:I:2:ARG:HA	2.52	0.45
1:J:589:GLN:NE2	1:J:771:ARG:HH12	2.14	0.45
2:I:262:VAL:HA	2:I:267:ALA:HB3	1.99	0.45
1:F:534:LEU:HD12	1:F:534:LEU:HA	1.82	0.45
1:F:1003:LEU:HD23	1:F:1003:LEU:HA	1.76	0.45
2:E:137:ALA:O	2:E:140:VAL:HG12	2.17	0.45
2:E:255:VAL:HG21	2:E:282:GLU:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:561:THR:OG1	2:E:611:SER:OG	2.31	0.45
4:O:73:LYS:O	4:O:76:ASP:HB3	2.16	0.45
4:O:261:VAL:O	4:O:265:VAL:HG23	2.16	0.45
4:O:277:TYR:CE2	4:O:282:ALA:HA	2.52	0.45
1:B:214:ARG:HH22	1:B:827:SER:CA	2.29	0.45
1:B:214:ARG:HH22	1:B:827:SER:N	2.15	0.45
1:B:589:GLN:NE2	1:B:771:ARG:HH12	2.15	0.45
2:M:95:GLN:HE22	2:M:113:HIS:CD2	2.35	0.45
2:M:529:GLN:OE1	2:M:838:GLU:HB2	2.16	0.45
1:N:172:ILE:HG21	1:N:212:VAL:HG21	1.99	0.45
1:N:181:TYR:O	1:N:185:MET:HG3	2.16	0.45
1:N:295:ALA:C	1:N:298:PRO:HD2	2.42	0.45
1:J:406:VAL:HG21	1:J:448:TYR:HB2	1.99	0.45
1:J:585:PHE:HD2	1:J:587:MET:HE2	1.81	0.45
2:I:340:VAL:HB	2:I:413:MET:HE2	1.99	0.45
2:E:329:PRO:HB3	2:E:358:VAL:HG21	1.99	0.45
2:E:441:GLN:O	2:E:561:THR:HA	2.17	0.45
3:H:19:LEU:HD12	3:H:113:LEU:HB3	1.98	0.45
4:K:88:ILE:HD12	4:K:88:ILE:O	2.16	0.45
4:K:151:LEU:HB2	4:K:215:SER:HB3	1.99	0.45
4:O:155:ASN:OD1	4:O:168:ASP:HB2	2.17	0.45
2:M:840:LEU:HA	2:M:843:ALA:HB3	1.97	0.44
2:M:1057:ARG:O	2:M:1061:ASP:HB2	2.16	0.44
2:M:1107:PHE:O	2:M:1111:VAL:HG23	2.18	0.44
2:A:108:THR:HG22	2:A:133:LEU:HD23	1.98	0.44
2:A:295:ARG:HD3	2:A:328:TRP:CZ3	2.52	0.44
2:A:844:CYS:HB3	2:A:898:MET:HE2	1.98	0.44
1:N:367:ILE:HD12	1:N:441:PHE:HE2	1.82	0.44
1:N:495:VAL:HG13	1:N:615:PRO:HG2	1.98	0.44
1:J:397:HIS:CE1	1:J:431:PRO:HG3	2.52	0.44
1:J:409:TYR:CZ	1:J:432:SER:HB3	2.52	0.44
1:J:523:VAL:HA	1:J:657:GLN:NE2	2.31	0.44
2:I:281:GLN:O	2:I:285:THR:HG22	2.17	0.44
2:I:371:GLU:HG2	2:I:372:LEU:HG	1.99	0.44
1:F:67:THR:HG23	1:F:68:THR:H	1.81	0.44
2:E:86:ARG:HH22	2:E:157:HIS:CD2	2.35	0.44
2:E:253:LYS:HD3	2:E:296:PHE:HB2	1.98	0.44
4:C:180:ARG:HB3	4:C:206:GLY:C	2.42	0.44
4:K:231:TRP:HA	4:K:238:MET:SD	2.57	0.44
1:B:157:THR:HB	2:A:94:ARG:NH2	2.32	0.44
1:B:803:PHE:CZ	1:B:857:ILE:HB	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1029:LYS:HD3	1:B:1033:ASN:ND2	2.30	0.44
2:M:103:LYS:NZ	2:M:167:ASN:OD1	2.35	0.44
2:M:920:ILE:O	2:M:923:ILE:HB	2.17	0.44
2:A:198:ASN:OD1	2:A:198:ASN:C	2.61	0.44
1:N:948:ILE:HD11	1:N:1006:VAL:HG13	1.99	0.44
1:N:1030:GLU:O	1:N:1034:GLU:HG2	2.18	0.44
1:J:452:LYS:HA	1:J:452:LYS:HD2	1.61	0.44
1:J:1004:MET:HE2	1:J:1004:MET:HB2	1.81	0.44
1:J:1051:MET:HG3	1:J:1055:TYR:CZ	2.52	0.44
5:J:1101:FAR:H62	5:J:1101:FAR:H43	1.68	0.44
2:I:381:ASP:HA	2:I:384:TYR:HD2	1.83	0.44
1:F:452:LYS:HD2	1:F:452:LYS:HA	1.61	0.44
1:F:526:ILE:HD13	1:F:656:LEU:HG	1.99	0.44
4:C:115:TYR:HE1	4:C:119:LYS:HD2	1.81	0.44
4:K:346:LEU:O	4:K:350:TYR:HD1	1.99	0.44
4:O:32:SER:HB3	4:O:51:ILE:HG13	1.98	0.44
4:O:165:LYS:HA	4:O:165:LYS:HE3	1.99	0.44
4:O:180:ARG:HB3	4:O:206:GLY:C	2.42	0.44
1:B:566:TYR:HD1	1:B:666:GLU:HB3	1.80	0.44
1:B:595:ILE:HG23	1:B:637:MET:HG3	1.99	0.44
1:B:650:LYS:HB2	1:B:650:LYS:HE3	1.49	0.44
1:B:919:GLN:HB2	1:B:927:ARG:HH11	1.81	0.44
1:B:1082:VAL:CG1	5:B:1101:FAR:C10	2.91	0.44
1:N:780:LEU:HG	1:N:784:TYR:HE2	1.82	0.44
1:N:1057:THR:HG23	1:N:1065:THR:HG23	1.99	0.44
2:I:142:LEU:HD11	2:I:168:LEU:HB3	1.98	0.44
2:I:341:PHE:CE2	2:I:413:MET:HE1	2.53	0.44
2:I:890:ILE:HD12	2:I:890:ILE:HA	1.76	0.44
2:I:943:THR:O	2:I:947:MET:HE2	2.17	0.44
2:I:1071:PHE:O	2:I:1075:VAL:HG23	2.17	0.44
1:F:341:SER:HB3	1:F:414:ALA:HB2	1.99	0.44
1:F:454:LEU:HD21	1:F:464:ILE:HG21	1.99	0.44
1:F:1003:LEU:HG	1:F:1024:LEU:HD21	2.00	0.44
2:E:204:MET:HE1	2:E:266:PRO:HG2	1.99	0.44
2:E:411:SER:O	2:E:415:GLU:HG2	2.17	0.44
2:E:919:ARG:HD3	2:E:922:LEU:HD12	2.00	0.44
2:E:1212:GLN:HG3	4:G:330:ARG:CD	2.46	0.44
3:D:19:LEU:HD12	3:D:113:LEU:HB3	1.98	0.44
4:C:155:ASN:OD1	4:C:168:ASP:HB2	2.17	0.44
4:C:249:PHE:HZ	4:C:265:VAL:HB	1.81	0.44
3:H:129:ALA:HA	4:G:302:ARG:NH1	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:127:THR:O	4:G:131:MET:HG3	2.17	0.44
3:P:10:ILE:HD11	4:O:286:PRO:HB3	1.99	0.44
3:P:19:LEU:HD12	3:P:113:LEU:HB3	1.98	0.44
1:B:212:VAL:HG11	1:B:242:ALA:CB	2.48	0.44
1:B:740:GLN:O	1:B:744:LEU:HD12	2.17	0.44
1:B:802:THR:O	1:B:806:HIS:ND1	2.49	0.44
1:B:854:VAL:HG12	1:B:876:ILE:HG12	2.00	0.44
1:B:880:ILE:HG23	1:B:899:LEU:HD13	1.99	0.44
1:B:931:ASP:OD1	1:B:997:GLN:HG3	2.17	0.44
2:M:1153:LYS:HE3	2:M:1210:TYR:CD1	2.53	0.44
2:A:22:ILE:HD13	2:A:401:MET:HE2	1.98	0.44
2:A:585:ALA:HA	2:A:588:LYS:HZ2	1.81	0.44
2:A:1163:LEU:HD11	2:A:1178:LYS:HE2	1.98	0.44
1:N:485:ASN:HB2	1:J:102:ARG:O	2.18	0.44
1:N:790:GLN:HA	1:N:836:TYR:CZ	2.52	0.44
1:N:809:GLN:NE2	1:N:981:LEU:HD11	2.32	0.44
1:F:496:HIS:HB2	1:F:616:LEU:HD12	2.00	0.44
2:E:14:TYR:OH	2:E:411:SER:HB3	2.17	0.44
4:C:176:GLU:HG2	4:C:177:PRO:HD2	1.99	0.44
4:G:176:GLU:HG2	4:G:177:PRO:HD2	1.99	0.44
4:G:231:TRP:HA	4:G:238:MET:SD	2.57	0.44
4:K:85:PRO:O	4:K:165:LYS:NZ	2.46	0.44
1:B:1034:GLU:HG3	1:B:1068:TYR:CD2	2.53	0.44
2:M:927:MET:HE1	2:M:954:MET:SD	2.58	0.44
2:M:1145:ILE:HD13	2:M:1149:ILE:HG12	1.99	0.44
2:A:142:LEU:HD11	2:A:168:LEU:HD22	1.98	0.44
1:N:853:LEU:HA	1:N:856:HIS:HB2	1.99	0.44
1:J:51:HIS:CE1	1:J:55:ILE:HD11	2.52	0.44
1:J:914:ILE:HG13	1:J:930:ILE:HG23	1.98	0.44
1:J:928:ARG:NH2	1:J:1065:THR:HG21	2.33	0.44
2:I:20:GLN:HE21	2:I:20:GLN:HB3	1.62	0.44
2:I:183:ILE:HD13	2:I:258:SER:HB2	1.99	0.44
2:I:241:ILE:HD11	2:I:845:THR:HG22	1.99	0.44
2:I:511:TYR:HD2	2:I:616:LEU:HD21	1.81	0.44
2:E:930:GLU:O	2:E:933:HIS:ND1	2.45	0.44
4:G:115:TYR:HE1	4:G:119:LYS:HD2	1.81	0.44
4:G:165:LYS:HA	4:G:165:LYS:HE3	1.99	0.44
3:L:10:ILE:HD11	4:K:286:PRO:HB3	1.99	0.44
3:L:19:LEU:HD12	3:L:113:LEU:HB3	1.98	0.44
4:K:155:ASN:OD1	4:K:168:ASP:HB2	2.17	0.44
1:B:258:GLN:OE1	1:B:258:GLN:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:ASP:OD1	1:B:309:ASP:C	2.61	0.44
1:B:369:PHE:CE2	1:B:391:LEU:HB3	2.53	0.44
2:M:310:ARG:HH21	2:M:314:GLU:HG2	1.83	0.44
2:A:82:VAL:HG23	2:A:155:ILE:HG12	2.00	0.44
2:A:189:LYS:HE2	2:A:296:PHE:CD2	2.53	0.44
2:A:212:LEU:HD21	2:A:228:ILE:HG12	1.98	0.44
2:A:1138:ALA:HB2	5:A:1301:FAR:C12	2.46	0.44
1:J:435:GLY:C	1:J:436:ARG:HG3	2.42	0.44
2:I:874:GLU:OE2	2:I:878:GLN:NE2	2.50	0.44
1:F:565:ILE:CG2	1:F:616:LEU:HD22	2.47	0.44
1:F:730:LYS:HA	1:F:733:ASP:HB2	2.00	0.44
1:F:867:LEU:HA	1:F:867:LEU:HD12	1.69	0.44
2:E:30:THR:HG23	2:E:32:LEU:HG	1.98	0.44
2:E:593:TYR:HE2	4:G:16:PHE:CE2	2.31	0.44
4:C:277:TYR:CE2	4:C:282:ALA:HA	2.52	0.44
4:G:155:ASN:OD1	4:G:168:ASP:HB2	2.17	0.44
4:G:180:ARG:HB3	4:G:206:GLY:C	2.42	0.44
3:L:66:PHE:O	3:L:67:PRO:C	2.57	0.44
4:K:33:VAL:O	4:K:50:VAL:N	2.39	0.44
4:K:176:GLU:HG2	4:K:177:PRO:HD2	1.99	0.44
3:P:10:ILE:HG21	4:O:289:GLN:NE2	2.33	0.44
4:O:262:LYS:N	4:O:262:LYS:HD3	2.33	0.44
1:B:46:TRP:CE3	1:B:104:ILE:HG21	2.53	0.44
1:B:170:LEU:O	1:B:217:ASP:HB2	2.18	0.44
1:B:220:VAL:HG23	1:B:221:TRP:CD2	2.53	0.44
1:B:1006:VAL:O	1:B:1010:LEU:HG	2.18	0.44
1:B:1082:VAL:CG1	5:B:1101:FAR:H101	2.34	0.44
2:M:284:ILE:HD11	2:M:351:TYR:OH	2.18	0.44
2:M:468:VAL:HG11	2:M:604:LEU:HD23	2.00	0.44
2:A:176:TYR:HE2	2:A:842:GLU:HG3	1.82	0.44
2:A:310:ARG:HD3	2:A:312:TYR:N	2.22	0.44
2:A:1211:VAL:HB	5:A:1301:FAR:H61	2.00	0.44
1:N:561:GLY:O	1:N:566:TYR:OH	2.25	0.44
1:N:963:LEU:HD12	1:N:963:LEU:HA	1.81	0.44
1:N:997:GLN:O	1:N:1001:GLU:N	2.34	0.44
1:J:152:VAL:HG22	1:J:169:HIS:CE1	2.53	0.44
2:I:511:TYR:CD2	2:I:616:LEU:HD21	2.53	0.44
2:I:854:LEU:O	2:I:867:ILE:N	2.50	0.44
1:F:80:GLN:O	1:F:155:VAL:N	2.46	0.44
1:F:471:VAL:HB	1:F:475:ASP:OD1	2.18	0.44
1:F:531:GLN:HG2	1:F:578:ILE:HG13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:915:LEU:HD13	1:F:915:LEU:O	2.18	0.44
2:E:504:VAL:HG22	2:E:550:LEU:HD13	1.98	0.44
4:C:180:ARG:HH22	4:C:205:PRO:HD2	1.83	0.44
3:H:10:ILE:HD11	4:G:286:PRO:HB3	1.99	0.44
1:B:441:PHE:CZ	1:B:443:TRP:HB3	2.53	0.44
2:M:15:ALA:HA	2:M:57:LEU:HD11	1.99	0.44
2:M:829:ILE:HA	2:M:832:ILE:HG12	1.99	0.44
2:A:784:TYR:HE1	2:A:829:ILE:HD13	1.83	0.44
1:N:600:ASN:ND2	1:N:863:ASN:OD1	2.51	0.44
1:N:627:ARG:HE	1:N:627:ARG:HB3	1.58	0.44
1:N:796:ILE:H	1:N:796:ILE:HD12	1.83	0.44
1:N:1013:ASN:OD1	5:N:1101:FAR:H153	2.17	0.44
1:J:793:SER:O	1:J:796:ILE:HD12	2.18	0.44
1:J:924:TRP:CD1	1:J:1058:PRO:HB3	2.53	0.44
2:I:1175:MET:H	2:I:1175:MET:CE	2.30	0.44
1:F:838:LYS:HE2	1:F:838:LYS:HB2	1.70	0.44
2:E:294:CYS:SG	2:E:325:GLU:HB2	2.57	0.44
4:G:151:LEU:HB2	4:G:215:SER:HB3	1.99	0.44
4:G:166:LEU:HD12	4:G:167:THR:N	2.32	0.44
1:B:75:THR:HG21	1:B:440:LEU:HB2	1.99	0.44
1:B:213:TYR:CE2	1:B:274:ARG:HD2	2.53	0.44
1:B:912:LEU:O	1:B:916:GLN:N	2.51	0.44
2:M:579:ASN:C	2:M:579:ASN:OD1	2.61	0.44
2:A:440:VAL:O	2:A:599:VAL:HA	2.17	0.44
1:N:105:ASP:HB2	1:J:486:GLN:HE21	1.83	0.44
1:J:324:LEU:HA	1:J:331:LYS:HE2	2.00	0.44
1:J:327:LYS:HB2	1:J:327:LYS:HE2	1.77	0.44
1:J:880:ILE:O	1:J:881:HIS:C	2.59	0.44
1:J:938:PRO:HG2	1:J:1004:MET:HE3	1.98	0.44
1:J:979:PHE:O	1:J:983:VAL:HG12	2.18	0.44
2:I:903:MET:HE3	2:I:955:LYS:HE3	1.98	0.44
2:I:1196:ARG:HG3	2:I:1197:PHE:CD2	2.53	0.44
1:F:223:ARG:HH22	1:F:338:TYR:HA	1.82	0.44
1:F:502:GLU:HG3	1:F:685:PHE:HZ	1.83	0.44
1:F:657:GLN:OE1	1:F:657:GLN:N	2.50	0.44
1:F:853:LEU:C	1:F:857:ILE:HG12	2.43	0.44
1:F:959:ALA:O	1:F:989:ASN:ND2	2.47	0.44
2:E:510:LEU:HD21	2:E:561:THR:HB	1.99	0.44
2:E:1118:VAL:HB	2:E:1120:GLN:NE2	2.33	0.44
4:G:154:GLU:HB3	4:G:361:LYS:HE3	2.00	0.44
4:K:277:TYR:CE2	4:K:282:ALA:HA	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:73:MET:SD	4:O:317:ARG:HD2	2.57	0.44
3:P:123:ASP:O	3:P:126:ILE:HG12	2.18	0.44
4:O:231:TRP:HA	4:O:238:MET:SD	2.57	0.44
4:O:360:LYS:H	4:O:365:GLN:HB3	1.83	0.44
1:B:846:GLU:O	1:B:849:ILE:HG22	2.18	0.43
2:A:199:ALA:HB2	2:A:245:LEU:CD1	2.45	0.43
1:N:1016:LEU:HD21	5:N:1101:FAR:H92	1.99	0.43
1:J:307:LEU:HD23	1:J:307:LEU:HA	1.72	0.43
1:J:416:PHE:HD2	1:J:427:GLN:HB3	1.81	0.43
1:J:506:LEU:HD12	1:J:506:LEU:HA	1.85	0.43
1:J:593:LEU:HD11	1:J:904:PRO:HB2	1.99	0.43
1:J:745:GLY:HA3	1:J:788:PHE:CD2	2.48	0.43
1:J:1003:LEU:HD11	1:J:1024:LEU:CD1	2.46	0.43
2:I:92:MET:HE2	2:I:92:MET:HB2	1.78	0.43
4:C:151:LEU:HB2	4:C:215:SER:HB3	1.99	0.43
4:C:154:GLU:HB3	4:C:361:LYS:HE3	2.00	0.43
4:C:285:HIS:CE1	4:C:287:PHE:H	2.36	0.43
4:C:367:ARG:H	4:C:367:ARG:HG2	1.48	0.43
3:H:45:THR:CG2	3:H:46:GLU:N	2.80	0.43
3:L:105:GLU:O	3:L:106:LEU:C	2.59	0.43
1:B:263:SER:O	1:B:263:SER:OG	2.37	0.43
1:B:586:TYR:OH	1:B:783:ARG:NE	2.49	0.43
1:B:600:ASN:HA	1:B:603:GLN:NE2	2.33	0.43
2:M:485:SER:O	2:M:485:SER:OG	2.35	0.43
2:M:1155:VAL:O	2:M:1159:ASN:N	2.46	0.43
2:A:28:PRO:O	2:A:83:LYS:NZ	2.28	0.43
2:A:501:HIS:HB2	2:A:838:GLU:OE1	2.17	0.43
1:N:344:ASP:OD1	1:N:344:ASP:C	2.62	0.43
1:N:369:PHE:CE2	1:N:391:LEU:HB3	2.53	0.43
1:N:567:ARG:NH2	1:N:665:VAL:HG21	2.32	0.43
1:N:815:PHE:CD1	1:N:816:GLY:N	2.86	0.43
1:J:57:LYS:HD3	1:J:113:GLU:OE1	2.18	0.43
1:J:132:GLN:HE21	1:J:149:LEU:HD23	1.83	0.43
1:J:911:LEU:HD22	1:J:915:LEU:HD23	2.00	0.43
1:J:994:GLN:CD	1:J:994:GLN:H	2.25	0.43
2:I:409:LEU:HD11	2:I:423:ILE:HD12	2.00	0.43
1:F:68:THR:O	1:F:124:GLY:HA3	2.17	0.43
1:F:90:CYS:HA	1:F:446:ALA:HB2	1.99	0.43
1:F:529:TRP:CZ2	1:F:682:PHE:HB2	2.53	0.43
1:F:793:SER:HB3	1:F:796:ILE:HG13	2.00	0.43
1:F:873:LYS:HD3	1:F:984:GLU:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1030:GLU:O	1:F:1034:GLU:HG3	2.18	0.43
2:E:170:PHE:HA	2:E:173:GLU:HB2	2.00	0.43
2:E:360:ILE:HG13	2:E:368:LEU:O	2.18	0.43
2:E:1196:ARG:NH1	4:G:251:SER:O	2.51	0.43
3:D:60:GLY:O	3:D:61:ASN:C	2.60	0.43
4:G:262:LYS:N	4:G:262:LYS:HD3	2.33	0.43
4:K:125:LYS:O	4:K:129:LYS:NZ	2.51	0.43
4:O:219:ILE:H	4:O:219:ILE:HG12	1.59	0.43
4:O:249:PHE:HB3	4:O:254:TRP:HB3	2.00	0.43
1:B:102:ARG:HB3	1:F:477:ARG:NH2	2.32	0.43
1:B:375:ASP:OD2	1:B:379:ARG:NH2	2.33	0.43
1:B:1063:ARG:HA	1:B:1063:ARG:HD3	1.57	0.43
2:M:69:GLU:O	2:M:73:LYS:HG2	2.18	0.43
2:M:954:MET:HE2	2:M:954:MET:HB2	1.75	0.43
2:A:440:VAL:HG22	2:A:560:PRO:HG2	2.00	0.43
2:A:479:LEU:HD12	2:A:479:LEU:HA	1.77	0.43
2:A:588:LYS:HZ3	2:A:588:LYS:HB2	1.82	0.43
1:N:223:ARG:HG2	1:N:228:ASN:OD1	2.18	0.43
1:N:1002:LEU:HA	1:N:1005:VAL:HG12	2.00	0.43
1:J:496:HIS:HB2	1:J:616:LEU:HA	1.99	0.43
1:F:777:LYS:HB2	1:F:779:TRP:HE1	1.84	0.43
1:F:1082:VAL:CG1	5:F:1101:FAR:C10	2.82	0.43
4:C:231:TRP:HA	4:C:238:MET:SD	2.57	0.43
4:K:154:GLU:HB3	4:K:361:LYS:HE3	2.00	0.43
3:P:118:THR:HG1	3:P:121:GLU:HB2	1.83	0.43
4:O:85:PRO:O	4:O:165:LYS:NZ	2.46	0.43
4:O:176:GLU:HG2	4:O:177:PRO:HD2	1.99	0.43
4:O:285:HIS:CE1	4:O:287:PHE:H	2.36	0.43
1:B:362:GLU:O	1:B:429:ARG:NH1	2.42	0.43
1:B:501:ALA:HB1	1:B:506:LEU:HB3	1.99	0.43
1:B:755:PHE:O	1:B:762:VAL:HG23	2.18	0.43
1:B:867:LEU:O	1:B:936:ARG:NH1	2.34	0.43
1:B:1003:LEU:HA	1:B:1006:VAL:HG22	2.01	0.43
1:B:1030:GLU:HA	1:B:1033:ASN:HD22	1.84	0.43
2:M:102:PHE:HB2	2:M:110:ASP:O	2.18	0.43
2:M:142:LEU:HD22	2:M:212:LEU:HD11	2.01	0.43
2:M:856:VAL:HG12	2:M:920:ILE:HB	1.99	0.43
2:M:965:LYS:HD2	2:M:965:LYS:C	2.43	0.43
2:A:111:SER:HB2	2:A:133:LEU:HD13	2.01	0.43
2:A:417:PHE:O	2:A:418:LEU:HD13	2.18	0.43
2:A:486:LEU:HB2	2:A:618:PHE:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:887:ASP:HB3	2:A:890:ILE:HG23	2.00	0.43
2:A:1136:MET:HB3	4:C:350:TYR:CZ	2.53	0.43
1:N:82:ALA:HB2	1:N:155:VAL:HB	1.99	0.43
1:N:642:LYS:NZ	1:N:642:LYS:HB3	2.32	0.43
1:N:714:VAL:HG13	1:N:719:TRP:HD1	1.81	0.43
1:N:929:GLN:O	1:N:933:SER:OG	2.24	0.43
1:J:501:ALA:HB1	1:J:506:LEU:HB3	2.00	0.43
1:J:911:LEU:O	1:J:915:LEU:HB2	2.18	0.43
1:J:912:LEU:O	1:J:916:GLN:NE2	2.48	0.43
2:I:186:ARG:HE	2:I:191:ASN:CG	2.26	0.43
2:I:186:ARG:NH1	2:I:295:ARG:HH22	2.16	0.43
1:F:368:PHE:HD1	1:F:371:TYR:HD2	1.66	0.43
1:F:556:PRO:HB3	1:F:578:ILE:HD12	2.00	0.43
1:F:603:GLN:NE2	1:F:647:GLY:O	2.36	0.43
1:F:714:VAL:HG13	1:F:719:TRP:CD1	2.53	0.43
1:F:1025:ASP:O	1:F:1029:LYS:HG2	2.18	0.43
2:E:13:GLY:O	2:E:16:ARG:HG2	2.18	0.43
2:E:281:GLN:HA	2:E:284:ILE:CD1	2.48	0.43
4:C:165:LYS:HA	4:C:165:LYS:HE3	1.99	0.43
4:C:249:PHE:HB3	4:C:254:TRP:HB3	2.00	0.43
3:L:10:ILE:HG21	4:K:289:GLN:NE2	2.33	0.43
4:K:180:ARG:HH22	4:K:205:PRO:HD2	1.83	0.43
4:O:116:LEU:HB3	4:O:367:ARG:NH2	2.33	0.43
1:B:191:GLN:CD	2:A:75:TYR:HE2	2.27	0.43
1:B:351:LYS:HD2	1:B:352:PRO:HD2	2.00	0.43
1:B:456:ASP:C	1:B:457:GLU:CD	2.86	0.43
1:B:627:ARG:HB2	1:B:627:ARG:HH11	1.82	0.43
1:B:728:LEU:O	1:B:731:LEU:HB3	2.19	0.43
1:B:792:PHE:CE1	1:B:796:ILE:HD11	2.53	0.43
2:A:605:SER:O	2:A:608:LEU:HD22	2.18	0.43
1:N:221:TRP:O	1:N:222:GLU:HG2	2.18	0.43
1:N:337:GLY:HA3	1:N:358:PHE:CE2	2.54	0.43
1:N:440:LEU:HD22	1:N:445:GLN:HG3	2.01	0.43
1:J:577:PRO:HG3	1:J:617:PHE:CE1	2.54	0.43
2:I:402:TRP:C	2:I:402:TRP:CD1	2.97	0.43
1:F:130:MET:HG2	1:F:547:LEU:HD11	2.01	0.43
1:F:204:ASN:HA	1:F:207:PHE:CD2	2.54	0.43
1:F:810:VAL:HA	1:F:874:ILE:HD12	2.00	0.43
1:F:872:LEU:HB2	1:F:942:TYR:HE2	1.84	0.43
1:F:1024:LEU:O	1:F:1028:VAL:N	2.47	0.43
2:E:1068:PRO:HB3	4:G:353:ARG:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:10:ILE:HG21	4:C:289:GLN:NE2	2.33	0.43
4:G:159:ASP:OD1	4:G:161:ASN:N	2.46	0.43
3:L:123:ASP:O	3:L:126:ILE:HG12	2.18	0.43
4:K:116:LEU:HD11	4:K:122:LEU:HB2	1.99	0.43
3:P:66:PHE:HA	3:P:69:PHE:CB	2.48	0.43
4:O:125:LYS:O	4:O:129:LYS:NZ	2.51	0.43
4:O:264:LEU:HB2	4:O:285:HIS:CD2	2.54	0.43
1:B:351:LYS:O	1:B:354:GLU:N	2.38	0.43
1:B:998:ILE:HA	1:B:1001:GLU:OE1	2.18	0.43
2:M:930:GLU:HG3	2:M:933:HIS:HE1	1.84	0.43
1:J:88:LEU:HD23	1:J:177:LEU:HD23	1.99	0.43
2:I:281:GLN:OE1	2:I:281:GLN:HA	2.17	0.43
2:I:822:HIS:O	2:I:826:ILE:HG13	2.19	0.43
2:I:840:LEU:HD21	2:I:877:THR:HG22	2.00	0.43
2:I:1145:ILE:HG21	2:I:1149:ILE:HD11	1.99	0.43
2:I:1196:ARG:HG3	2:I:1197:PHE:CE2	2.54	0.43
1:F:328:TYR:HA	1:F:395:VAL:HG11	2.00	0.43
1:F:609:TRP:NE1	1:F:615:PRO:HD3	2.34	0.43
1:F:887:LEU:O	1:F:891:GLY:N	2.39	0.43
2:E:32:LEU:HD12	2:E:118:THR:HA	2.01	0.43
2:E:93:ILE:HD12	2:E:164:PHE:CD1	2.53	0.43
3:D:123:ASP:O	3:D:126:ILE:HG12	2.18	0.43
4:C:125:LYS:O	4:C:129:LYS:NZ	2.51	0.43
4:G:125:LYS:O	4:G:129:LYS:NZ	2.51	0.43
4:G:180:ARG:HH22	4:G:205:PRO:HD2	1.83	0.43
3:L:118:THR:HG1	3:L:121:GLU:HB2	1.83	0.43
4:K:264:LEU:HB2	4:K:285:HIS:CD2	2.54	0.43
1:B:49:LEU:HB3	1:B:101:TYR:CE1	2.53	0.43
1:B:101:TYR:CE2	1:B:110:ARG:HD2	2.54	0.43
1:B:339:ARG:HH11	1:B:339:ARG:H	1.67	0.43
1:B:409:TYR:CE1	1:B:432:SER:HB2	2.53	0.43
1:B:449:ILE:HD13	1:B:449:ILE:HA	1.82	0.43
1:B:790:GLN:HA	1:B:836:TYR:CZ	2.53	0.43
1:B:870:GLY:O	1:B:937:THR:OG1	2.33	0.43
1:B:964:PRO:HB2	1:B:967:PRO:HD2	2.00	0.43
2:A:206:LYS:HD3	2:A:269:ALA:HB1	2.00	0.43
2:A:809:LEU:HD23	2:A:809:LEU:HA	1.85	0.43
2:A:1223:GLN:O	4:C:342:PRO:HB2	2.19	0.43
1:N:714:VAL:HG13	1:N:719:TRP:CD1	2.53	0.43
1:N:755:PHE:O	1:N:762:VAL:N	2.48	0.43
1:N:898:ASP:HB2	1:N:901:GLN:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:738:ALA:O	1:J:742:ILE:HG13	2.19	0.43
2:I:128:ASP:OD1	2:I:128:ASP:N	2.52	0.43
1:F:372:MET:HG2	1:F:388:TYR:CD1	2.53	0.43
1:F:496:HIS:CB	1:F:659:LEU:HD22	2.48	0.43
1:F:567:ARG:O	1:F:668:LEU:HB2	2.19	0.43
2:E:21:THR:HG22	2:E:22:ILE:HG13	2.01	0.43
2:E:1196:ARG:CD	4:G:252:PRO:HD2	2.44	0.43
4:C:262:LYS:HD3	4:C:262:LYS:N	2.33	0.43
4:G:241:MET:HE2	4:G:241:MET:HB3	1.87	0.43
4:G:264:LEU:HB2	4:G:285:HIS:CD2	2.54	0.43
4:G:285:HIS:CE1	4:G:287:PHE:H	2.36	0.43
1:B:368:PHE:HA	1:B:371:TYR:HB2	2.00	0.43
1:B:435:GLY:C	1:B:437:ASP:H	2.27	0.43
1:B:950:GLU:OE1	1:B:950:GLU:HA	2.18	0.43
1:B:1017:GLU:OE2	1:B:1018:PHE:N	2.51	0.43
2:M:472:ARG:HH21	2:M:668:LEU:HA	1.84	0.43
2:A:170:PHE:N	2:A:170:PHE:CD1	2.87	0.43
2:A:188:ASP:HA	2:A:196:GLU:CD	2.43	0.43
2:A:889:SER:O	2:A:892:ILE:HG13	2.18	0.43
1:N:745:GLY:HA3	1:N:788:PHE:CD2	2.54	0.43
1:N:1029:LYS:HB2	1:N:1029:LYS:HE2	1.66	0.43
1:J:1054:PHE:O	1:J:1057:THR:HG22	2.18	0.43
2:I:1138:ALA:HB1	5:I:1301:FAR:H152	1.94	0.43
1:F:112:HIS:ND1	2:E:218:PHE:HB3	2.34	0.43
1:F:298:PRO:HA	1:F:302:TYR:O	2.19	0.43
1:F:906:GLU:O	1:F:910:LEU:HB2	2.17	0.43
3:D:34:GLY:O	3:D:35:THR:C	2.61	0.43
3:D:37:MET:CE	3:D:49:LEU:HD23	1.96	0.43
3:H:34:GLY:O	3:H:35:THR:C	2.61	0.43
4:O:182:ARG:HH21	4:O:204:HIS:C	2.25	0.43
1:B:223:ARG:NH2	1:B:339:ARG:HH12	2.16	0.43
1:B:567:ARG:NH2	1:B:665:VAL:HG11	2.34	0.43
1:B:996:ARG:O	1:B:999:VAL:HG12	2.18	0.43
2:M:160:ASP:HB3	2:M:492:MET:SD	2.58	0.43
2:M:469:TYR:CD1	2:M:470:PRO:HA	2.54	0.43
2:M:557:THR:HA	1:J:511:ASN:OD1	2.18	0.43
2:M:1167:LYS:NZ	2:M:1176:LEU:HD12	2.34	0.43
2:A:310:ARG:HH11	2:A:312:TYR:HB2	1.84	0.43
1:N:210:GLU:OE1	1:N:267:VAL:HG13	2.18	0.43
1:N:307:LEU:HD23	1:N:307:LEU:HA	1.83	0.43
1:N:780:LEU:HD12	1:N:780:LEU:HA	1.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:227:TYR:HB2	1:J:229:ASN:OD1	2.18	0.43
2:I:284:ILE:HA	2:I:288:GLN:HB3	2.00	0.43
2:I:811:THR:O	2:I:815:GLY:N	2.52	0.43
1:F:495:VAL:HG13	1:F:651:VAL:HG12	2.00	0.43
2:E:326:CYS:SG	2:E:372:LEU:HD13	2.59	0.43
2:E:1129:GLU:O	2:E:1133:VAL:HG13	2.18	0.43
3:H:52:MET:HE2	3:H:52:MET:HB3	1.68	0.43
4:K:49:LYS:HG2	4:K:51:ILE:HD11	2.01	0.43
4:K:285:HIS:CE1	4:K:287:PHE:H	2.36	0.43
4:O:180:ARG:HH22	4:O:205:PRO:HD2	1.83	0.43
4:O:256:ASP:HB3	4:O:341:ARG:HH21	1.83	0.43
1:B:386:GLN:OE1	1:B:386:GLN:HA	2.19	0.43
1:B:540:GLN:N	1:B:540:GLN:CD	2.77	0.43
1:B:596:ASP:HA	1:B:599:LYS:HG3	2.00	0.43
1:B:744:LEU:HD23	1:B:747:LEU:HD13	2.01	0.43
2:M:472:ARG:HB2	2:M:472:ARG:HH11	1.83	0.43
2:A:139:SER:CB	2:A:204:MET:HB3	2.49	0.43
2:A:514:ARG:C	2:A:515:LYS:HG2	2.44	0.43
2:A:570:MET:N	2:A:570:MET:SD	2.92	0.43
2:A:662:ARG:HA	2:A:662:ARG:NH1	2.33	0.43
2:A:957:LEU:O	2:A:961:ILE:HG13	2.19	0.43
1:N:370:LEU:HD22	1:N:448:TYR:HA	2.01	0.43
1:N:1004:MET:O	1:N:1008:ILE:HG12	2.19	0.43
1:N:1032:PHE:C	1:N:1032:PHE:CD1	2.95	0.43
2:I:479:LEU:HD13	2:I:520:PHE:CE1	2.53	0.43
1:F:178:TYR:CZ	1:F:182:LEU:HD13	2.54	0.43
1:F:304:ALA:HB1	1:F:306:ALA:HB2	2.01	0.43
2:E:157:HIS:H	2:E:161:GLU:CD	2.26	0.43
2:E:822:HIS:CG	2:E:825:LEU:HG	2.54	0.43
2:E:1059:ARG:HA	2:E:1121:PRO:HB2	2.01	0.43
3:D:126:ILE:O	3:D:130:ASP:N	2.52	0.43
3:D:129:ALA:HA	4:C:302:ARG:NH1	2.31	0.43
4:C:33:VAL:O	4:C:50:VAL:N	2.39	0.43
4:G:49:LYS:HG2	4:G:51:ILE:HD11	2.01	0.43
3:P:52:MET:HB3	3:P:52:MET:HE2	1.68	0.43
1:B:766:ILE:HD12	1:B:789:THR:OG1	2.19	0.42
5:B:1101:FAR:H141	1:N:1009:VAL:HG23	1.87	0.42
2:M:63:LYS:O	1:J:567:ARG:HD2	2.19	0.42
2:M:1145:ILE:HG21	2:M:1149:ILE:HD11	2.01	0.42
2:A:62:ARG:HA	2:A:65:ALA:HB2	2.01	0.42
2:A:266:PRO:HD2	2:A:267:ALA:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:846:GLU:OE1	1:N:900:TYR:OH	2.28	0.42
1:J:129:TYR:HB3	1:J:201:PHE:CZ	2.54	0.42
1:J:491:ASN:HD21	1:J:607:GLN:HA	1.84	0.42
1:J:510:LEU:HD11	1:J:621:ILE:HG21	2.01	0.42
1:J:994:GLN:HB2	1:J:1055:TYR:CE2	2.53	0.42
2:I:300:GLY:O	2:I:313:TYR:OH	2.28	0.42
2:I:546:ASP:OD1	2:I:546:ASP:C	2.62	0.42
2:I:912:PHE:CE1	2:I:962:LEU:HD13	2.53	0.42
1:F:915:LEU:HD23	1:F:934:LEU:HD11	2.00	0.42
2:E:198:ASN:OD1	2:E:200:SER:OG	2.29	0.42
2:E:464:THR:O	2:E:468:VAL:HG23	2.19	0.42
2:E:535:ASP:HB2	2:E:951:PRO:HD2	2.01	0.42
2:E:561:THR:HG1	2:E:611:SER:HG	1.62	0.42
2:E:917:ARG:HD3	2:E:919:ARG:HG2	2.01	0.42
3:D:146:MET:HE2	3:D:146:MET:HB2	1.88	0.42
4:C:25:ILE:HD11	4:C:33:VAL:HG11	2.01	0.42
3:L:60:GLY:O	3:L:61:ASN:C	2.60	0.42
3:L:101:ILE:O	3:L:136:GLN:HA	2.19	0.42
4:O:25:ILE:HD11	4:O:33:VAL:HG11	2.01	0.42
4:O:63:GLU:H	4:O:63:GLU:HG3	1.67	0.42
4:O:154:GLU:HB3	4:O:361:LYS:HE3	2.00	0.42
1:B:207:PHE:HZ	1:B:541:LEU:HG	1.84	0.42
2:M:92:MET:HE2	2:M:168:LEU:HD11	2.01	0.42
2:M:442:VAL:HG11	2:M:589:MET:SD	2.58	0.42
2:M:472:ARG:NH2	2:M:668:LEU:HA	2.34	0.42
1:N:221:TRP:CE3	1:N:332:ARG:HD2	2.55	0.42
1:J:140:LYS:HG3	1:J:208:CYS:SG	2.59	0.42
1:J:223:ARG:HH22	1:J:338:TYR:HA	1.83	0.42
1:J:273:ASN:O	1:J:277:GLN:HG3	2.20	0.42
1:J:1062:LYS:HA	1:F:1081:GLU:HA	2.00	0.42
2:I:62:ARG:HA	2:I:62:ARG:HD3	1.85	0.42
1:F:368:PHE:HD1	1:F:368:PHE:HA	1.72	0.42
1:F:567:ARG:NH2	1:F:570:GLY:O	2.51	0.42
2:E:455:LEU:HB3	2:E:460:ILE:HG22	2.01	0.42
2:E:588:LYS:HE3	4:G:99:PHE:CD2	2.54	0.42
3:D:52:MET:HB3	3:D:52:MET:HE2	1.68	0.42
3:H:10:ILE:HG21	4:G:289:GLN:NE2	2.33	0.42
3:H:66:PHE:HB3	4:G:291:TYR:HB2	2.01	0.42
4:G:232:HIS:CE1	4:G:234:LYS:H	2.37	0.42
4:K:116:LEU:HD21	4:K:122:LEU:HB2	2.01	0.42
4:O:152:LYS:H	4:O:152:LYS:HG2	1.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:O:207:TYR:CE1	4:O:211:VAL:HG21	2.52	0.42
1:B:144:ARG:HB3	1:B:147:THR:CG2	2.49	0.42
1:B:295:ALA:O	1:B:298:PRO:HD2	2.18	0.42
1:B:504:GLN:OE1	1:B:519:THR:HG21	2.20	0.42
1:B:961:LYS:HD3	1:B:989:ASN:CG	2.44	0.42
2:M:291:TYR:OH	2:M:391:ASP:OD1	2.33	0.42
2:M:784:TYR:OH	2:M:817:VAL:HG11	2.19	0.42
2:A:257:ALA:O	2:A:260:LEU:HB2	2.19	0.42
2:A:579:ASN:OD1	2:A:579:ASN:C	2.62	0.42
1:N:51:HIS:O	1:N:55:ILE:HG13	2.19	0.42
1:N:1004:MET:HE3	1:N:1004:MET:HB3	1.83	0.42
1:N:1032:PHE:CE2	1:N:1051:MET:HE1	2.54	0.42
1:J:84:ILE:O	1:J:88:LEU:HB2	2.19	0.42
1:J:374:ILE:HG23	1:J:454:LEU:HD13	2.01	0.42
1:J:807:GLY:O	1:J:977:MET:HE1	2.19	0.42
1:J:880:ILE:HA	1:J:883:MET:HG3	2.01	0.42
2:I:283:ILE:HG23	2:I:287:LEU:HB2	2.01	0.42
2:I:1136:MET:O	2:I:1140:ILE:HG13	2.19	0.42
1:F:170:LEU:HD13	1:F:216:PRO:O	2.19	0.42
1:F:630:ARG:O	1:F:633:PRO:HD2	2.19	0.42
1:F:679:LEU:HD12	1:F:679:LEU:HA	1.93	0.42
1:F:1029:LYS:O	1:F:1032:PHE:N	2.53	0.42
2:E:102:PHE:CZ	2:E:178:THR:HG21	2.55	0.42
2:E:900:TYR:HD1	2:E:903:MET:HE1	1.85	0.42
2:E:1112:GLU:O	2:E:1116:ASN:N	2.52	0.42
4:G:249:PHE:HB3	4:G:254:TRP:HB3	2.00	0.42
4:G:367:ARG:H	4:G:367:ARG:HG2	1.48	0.42
4:O:120:VAL:HG21	4:O:348:ASP:O	2.20	0.42
1:B:324:LEU:HD11	1:B:333:PHE:HA	2.01	0.42
1:B:490:GLU:OE1	1:B:490:GLU:N	2.52	0.42
1:B:500:ILE:HG13	1:B:618:LEU:HD23	2.00	0.42
1:B:730:LYS:HD2	1:B:733:ASP:HB2	2.01	0.42
1:B:1002:LEU:O	1:B:1005:VAL:HG12	2.18	0.42
2:M:847:LEU:HB2	2:M:854:LEU:HD11	2.01	0.42
2:M:965:LYS:HD2	2:M:966:GLU:N	2.34	0.42
2:A:239:GLN:O	2:A:242:LEU:HB3	2.19	0.42
2:A:339:GLY:HA3	2:A:347:GLN:OE1	2.19	0.42
2:A:570:MET:HB3	2:A:582:ILE:HG13	2.00	0.42
2:A:919:ARG:NH1	2:A:1116:ASN:HD21	2.18	0.42
2:A:1132:LEU:HD23	2:A:1132:LEU:HA	1.91	0.42
1:J:65:SER:HB2	1:J:155:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:156:ILE:HG23	2:I:161:GLU:HB2	2.01	0.42
2:I:563:THR:O	2:I:565:PRO:HD3	2.19	0.42
2:I:816:LYS:HD2	2:I:817:VAL:N	2.35	0.42
1:F:590:ASP:HB2	1:F:779:TRP:CH2	2.54	0.42
1:F:820:GLU:OE2	1:F:839:CYS:HA	2.20	0.42
1:F:1018:PHE:CD1	1:F:1022:VAL:HG22	2.55	0.42
2:E:216:ASP:OD1	2:E:222:GLY:HA3	2.19	0.42
2:E:241:ILE:HG23	2:E:849:SER:OG	2.19	0.42
2:E:485:SER:HA	2:E:488:CYS:SG	2.59	0.42
2:E:855:THR:HG22	2:E:866:THR:HG22	2.01	0.42
3:D:10:ILE:HD11	4:C:286:PRO:HB3	1.99	0.42
4:C:49:LYS:HG2	4:C:51:ILE:HD11	2.01	0.42
4:C:264:LEU:HB2	4:C:285:HIS:CD2	2.54	0.42
3:H:126:ILE:O	3:H:130:ASP:N	2.52	0.42
4:G:25:ILE:HD11	4:G:33:VAL:HG11	2.01	0.42
4:K:63:GLU:H	4:K:63:GLU:HG3	1.67	0.42
4:O:48:VAL:HG22	4:O:103:VAL:HG22	2.01	0.42
4:O:236:MET:O	4:O:240:ARG:NE	2.53	0.42
1:B:796:ILE:HA	1:B:799:HIS:HB2	2.00	0.42
2:M:14:TYR:OH	2:M:411:SER:HB3	2.20	0.42
2:M:501:HIS:HB2	2:M:838:GLU:HB3	2.01	0.42
2:A:14:TYR:O	2:A:18:VAL:HG23	2.20	0.42
2:A:598:ARG:NH2	4:C:14:GLN:HG2	2.34	0.42
2:A:616:LEU:HB3	2:A:618:PHE:CE1	2.54	0.42
2:A:1151:VAL:O	2:A:1155:VAL:HG23	2.19	0.42
1:J:864:ASN:ND2	1:J:867:LEU:HD13	2.34	0.42
1:J:1071:LYS:HE2	1:J:1071:LYS:HB2	1.76	0.42
1:F:923:CYS:N	1:F:926:ASN:OD1	2.52	0.42
2:E:168:LEU:O	2:E:171:TYR:HB3	2.20	0.42
3:H:8:GLU:O	3:H:9:GLN:C	2.63	0.42
3:L:72:MET:HE2	3:L:72:MET:HB3	1.84	0.42
4:K:138:ILE:HG22	4:K:279:ALA:HB2	2.01	0.42
4:K:236:MET:O	4:K:240:ARG:NE	2.53	0.42
4:O:36:ARG:CD	4:O:106:LEU:HD21	2.49	0.42
4:O:138:ILE:HG22	4:O:279:ALA:HB2	2.01	0.42
1:B:214:ARG:HE	1:B:214:ARG:HB2	1.43	0.42
1:B:273:ASN:C	1:B:273:ASN:OD1	2.62	0.42
1:B:864:ASN:HB3	1:B:867:LEU:HD13	2.01	0.42
2:M:888:MET:O	2:M:892:ILE:HG12	2.20	0.42
2:A:841:ASP:HA	2:A:844:CYS:SG	2.60	0.42
2:A:1081:LYS:HB2	5:A:1301:FAR:H143	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1138:ALA:HB2	5:A:1301:FAR:C15	2.20	0.42
1:N:744:LEU:HD12	1:N:745:GLY:N	2.34	0.42
1:J:126:LEU:O	1:J:130:MET:HG3	2.20	0.42
1:J:586:TYR:OH	1:J:783:ARG:HG2	2.19	0.42
1:J:630:ARG:HD2	1:J:777:LYS:HE2	2.02	0.42
1:J:943:ASP:C	1:J:947:GLN:HE21	2.27	0.42
1:F:110:ARG:HH11	1:F:110:ARG:HG2	1.84	0.42
1:F:773:ALA:HA	1:F:776:GLN:NE2	2.25	0.42
2:E:32:LEU:HB3	2:E:47:ASN:OD1	2.19	0.42
2:E:536:ASN:HA	2:E:539:ILE:HD12	2.01	0.42
4:C:346:LEU:HD23	4:C:346:LEU:HA	1.89	0.42
4:G:138:ILE:HG22	4:G:279:ALA:HB2	2.01	0.42
4:G:236:MET:O	4:G:240:ARG:NE	2.53	0.42
3:L:126:ILE:O	3:L:130:ASP:N	2.52	0.42
4:K:25:ILE:HD11	4:K:33:VAL:HG11	2.01	0.42
4:K:232:HIS:CE1	4:K:234:LYS:H	2.37	0.42
4:K:262:LYS:HD3	4:K:262:LYS:N	2.33	0.42
3:P:133:GLY:HA3	3:P:136:GLN:O	2.20	0.42
4:O:49:LYS:HG2	4:O:51:ILE:HD11	2.01	0.42
4:O:346:LEU:HD23	4:O:346:LEU:HA	1.89	0.42
1:B:80:GLN:HA	1:B:155:VAL:HG12	2.01	0.42
1:B:365:PHE:CD1	1:B:365:PHE:N	2.87	0.42
1:B:602:LEU:HA	1:B:602:LEU:HD23	1.77	0.42
1:B:638:LEU:HD12	1:B:638:LEU:HA	1.88	0.42
1:B:857:ILE:O	1:B:861:ILE:HG22	2.20	0.42
1:B:903:SER:O	1:B:907:VAL:HG23	2.18	0.42
2:M:386:ASN:OD1	2:M:386:ASN:C	2.62	0.42
2:M:504:VAL:CG2	2:M:550:LEU:HG	2.50	0.42
2:A:134:GLN:HE22	2:A:185:GLU:HA	1.85	0.42
2:A:192:GLN:NE2	2:A:313:TYR:O	2.44	0.42
2:A:241:ILE:HD12	2:A:242:LEU:N	2.34	0.42
2:A:1223:GLN:HE22	4:C:327:PRO:HA	1.85	0.42
2:I:275:LEU:HD12	2:I:275:LEU:HA	1.89	0.42
2:I:457:ASP:OD1	2:I:457:ASP:C	2.62	0.42
1:F:541:LEU:HB2	1:F:670:PHE:CZ	2.54	0.42
1:F:1073:VAL:O	1:F:1077:LEU:HD23	2.18	0.42
2:E:19:GLN:OE1	2:E:19:GLN:HA	2.19	0.42
2:E:524:PHE:CD1	2:E:542:MET:HG3	2.55	0.42
2:E:945:GLY:O	2:E:949:LEU:HD12	2.20	0.42
3:D:57:ASP:OD2	3:D:63:THR:O	2.37	0.42
3:H:60:GLY:O	3:H:61:ASN:C	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:48:VAL:HG22	4:G:103:VAL:HG22	2.01	0.42
4:K:249:PHE:HB3	4:K:254:TRP:HB3	2.00	0.42
1:B:393:THR:HA	1:B:396:LEU:HD12	2.01	0.42
1:B:600:ASN:HA	1:B:603:GLN:HE21	1.84	0.42
1:B:1051:MET:HE2	1:B:1051:MET:HB3	1.95	0.42
2:A:784:TYR:CE1	2:A:829:ILE:HD13	2.54	0.42
1:N:661:SER:HB3	2:I:152:GLY:CA	2.49	0.42
1:J:161:LEU:HD23	1:J:161:LEU:HA	1.82	0.42
1:J:226:LYS:HB2	1:J:226:LYS:HE2	1.86	0.42
1:J:864:ASN:O	1:J:864:ASN:CG	2.62	0.42
1:J:883:MET:SD	1:J:911:LEU:HB2	2.60	0.42
2:I:267:ALA:HB1	2:I:269:ALA:HB2	2.02	0.42
2:I:848:LEU:CD2	2:I:854:LEU:HD13	2.50	0.42
1:F:75:THR:HG21	1:F:440:LEU:HB2	2.00	0.42
1:F:792:PHE:CE2	1:F:831:ILE:HG23	2.55	0.42
1:F:944:ARG:HB3	1:F:1007:SER:HB2	2.01	0.42
2:E:469:TYR:CG	2:E:470:PRO:HA	2.54	0.42
2:E:859:PRO:HG2	2:E:860:PRO:HD3	2.01	0.42
4:C:219:ILE:H	4:C:219:ILE:HG12	1.59	0.42
3:H:123:ASP:O	3:H:126:ILE:HG12	2.18	0.42
4:G:159:ASP:OD1	4:G:159:ASP:C	2.63	0.42
3:P:126:ILE:O	3:P:130:ASP:N	2.52	0.42
4:O:24:GLU:HG3	4:O:36:ARG:CZ	2.49	0.42
1:B:136:VAL:HG22	1:B:149:LEU:HD11	2.01	0.42
1:B:351:LYS:HD2	1:B:352:PRO:CD	2.50	0.42
1:B:485:ASN:O	1:F:103:ARG:HG3	2.19	0.42
5:B:1101:FAR:H151	1:N:1009:VAL:HG13	2.01	0.42
2:M:181:PHE:HA	2:M:187:GLY:HA2	2.02	0.42
2:M:260:LEU:HD11	2:M:335:PHE:CE2	2.54	0.42
2:M:265:PHE:CD2	2:M:337:LEU:HD13	2.55	0.42
2:M:468:VAL:HG12	2:M:471:ILE:O	2.20	0.42
2:M:508:SER:OG	2:M:550:LEU:HD11	2.20	0.42
2:M:592:GLY:HA2	2:M:599:VAL:O	2.20	0.42
2:M:784:TYR:O	2:M:788:THR:N	2.45	0.42
2:A:917:ARG:HH21	2:A:1112:GLU:HB3	1.83	0.42
1:N:859:TRP:CE3	1:N:860:ILE:HG12	2.55	0.42
1:N:859:TRP:CD2	1:N:908:LYS:HE2	2.55	0.42
1:N:925:LEU:O	1:N:929:GLN:HG3	2.20	0.42
1:J:925:LEU:HG	1:J:1055:TYR:HB3	2.02	0.42
1:J:961:LYS:HD2	1:J:986:THR:HA	2.02	0.42
1:J:966:GLN:OE1	1:J:966:GLN:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:972:MET:HE3	1:J:972:MET:HB3	1.92	0.42
2:I:1193:PRO:HD2	4:K:370:LEU:HA	2.02	0.42
1:F:53:TYR:CE1	1:F:110:ARG:HD3	2.55	0.42
1:F:81:LYS:HE3	1:F:81:LYS:HB3	1.82	0.42
1:F:379:ARG:HA	1:F:470:TYR:CZ	2.55	0.42
1:F:951:ARG:HE	1:F:1010:LEU:CD2	2.33	0.42
2:E:821:ARG:HA	2:E:826:ILE:HD11	2.01	0.42
2:E:1070:GLY:O	2:E:1074:LYS:N	2.53	0.42
2:E:1223:GLN:HE22	4:G:327:PRO:HA	1.85	0.42
3:D:45:THR:CG2	3:D:46:GLU:N	2.82	0.42
3:D:118:THR:OG1	3:D:121:GLU:CB	2.65	0.42
4:C:88:ILE:HG23	4:C:165:LYS:HB3	2.02	0.42
3:L:57:ASP:OD2	3:L:63:THR:O	2.37	0.42
1:B:203:GLN:CD	1:B:541:LEU:HD11	2.45	0.42
1:B:456:ASP:O	1:B:457:GLU:CG	2.68	0.42
1:B:948:ILE:HD13	1:B:948:ILE:HA	1.86	0.42
2:M:67:ARG:HB2	2:M:70:ASP:OD2	2.20	0.42
1:N:405:VAL:HG22	1:N:440:LEU:HD21	2.00	0.42
1:J:98:ALA:HB2	1:J:114:LEU:CB	2.48	0.42
1:J:317:LEU:O	1:J:318:ASP:C	2.62	0.42
1:J:370:LEU:HA	1:J:373:MET:HE3	2.01	0.42
1:J:1069:LEU:O	1:J:1073:VAL:HG23	2.20	0.42
1:F:55:ILE:O	1:F:59:THR:OG1	2.32	0.42
1:F:297:LEU:CD1	1:F:371:TYR:HB3	2.47	0.42
1:F:589:GLN:CD	1:F:589:GLN:N	2.78	0.42
2:E:444:ILE:HD13	2:E:586:LEU:HD22	2.02	0.42
2:E:1223:GLN:O	4:G:342:PRO:HB2	2.19	0.42
3:D:8:GLU:O	3:D:9:GLN:C	2.63	0.42
4:C:73:LYS:HE2	4:C:73:LYS:HB2	1.88	0.42
4:C:232:HIS:CE1	4:C:234:LYS:H	2.37	0.42
4:C:236:MET:O	4:C:240:ARG:NE	2.53	0.42
4:G:90:LEU:HD12	4:G:90:LEU:HA	1.95	0.42
3:P:102:SER:HB3	3:P:105:GLU:H	1.85	0.42
4:O:359:VAL:HG21	4:O:367:ARG:CG	2.46	0.42
1:B:228:ASN:HD22	1:B:228:ASN:HA	1.58	0.41
1:B:564:LYS:HB2	1:B:566:TYR:CE1	2.54	0.41
1:B:762:VAL:HA	1:B:765:HIS:NE2	2.35	0.41
1:B:1030:GLU:OE1	1:B:1030:GLU:C	2.63	0.41
2:M:289:GLY:N	2:M:327:GLU:OE2	2.52	0.41
2:M:811:THR:HA	2:M:814:TYR:HB3	2.02	0.41
2:A:166:GLN:NE2	2:A:486:LEU:HD21	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:254:GLU:OE2	2:A:254:GLU:N	2.48	0.41
1:N:81:LYS:HB3	1:N:81:LYS:HE2	1.69	0.41
1:N:210:GLU:OE2	1:N:271:ALA:HB3	2.20	0.41
1:J:108:LYS:HD2	1:J:108:LYS:HA	1.89	0.41
1:J:393:THR:HA	1:J:396:LEU:HD12	2.02	0.41
1:J:405:VAL:HA	1:J:445:GLN:NE2	2.34	0.41
1:J:449:ILE:HD13	1:J:449:ILE:HA	1.94	0.41
5:J:1101:FAR:H2	1:F:1008:ILE:CG2	2.38	0.41
2:I:134:GLN:NE2	2:I:185:GLU:HG3	2.35	0.41
2:I:489:ASN:HB3	2:I:492:MET:HB2	2.02	0.41
2:I:823:TRP:CD2	2:I:951:PRO:HD3	2.55	0.41
1:F:107:ASP:OD1	1:F:107:ASP:N	2.37	0.41
1:F:331:LYS:HG2	1:F:364:GLU:HG3	2.01	0.41
1:F:780:LEU:HD13	1:F:900:TYR:O	2.20	0.41
1:F:1006:VAL:HA	1:F:1009:VAL:HB	2.02	0.41
2:E:511:TYR:HD2	2:E:616:LEU:HD11	1.84	0.41
2:E:1079:LEU:O	2:E:1094:SER:OG	2.32	0.41
4:C:48:VAL:HG22	4:C:103:VAL:HG22	2.01	0.41
4:C:120:VAL:HG21	4:C:348:ASP:O	2.20	0.41
4:G:17:TYR:O	4:G:40:LYS:NZ	2.43	0.41
4:K:48:VAL:HG22	4:K:103:VAL:HG22	2.01	0.41
4:K:346:LEU:HD23	4:K:346:LEU:HA	1.89	0.41
3:P:102:SER:CB	3:P:105:GLU:HG3	2.34	0.41
1:B:56:VAL:HG21	1:B:97:LEU:HD22	2.01	0.41
1:B:221:TRP:HB3	1:B:332:ARG:NH1	2.36	0.41
1:B:1063:ARG:NH1	1:N:1079:GLU:HA	2.31	0.41
2:M:81:VAL:CG1	2:M:148:MET:HE2	2.51	0.41
2:M:1133:VAL:HA	2:M:1136:MET:HG2	2.01	0.41
2:M:1184:ILE:HG23	2:M:1188:LEU:HD23	2.01	0.41
2:A:1057:ARG:O	2:A:1061:ASP:HB2	2.20	0.41
2:A:1162:PHE:HD1	2:A:1202:TYR:CE2	2.38	0.41
1:N:228:ASN:O	1:N:349:TYR:HB2	2.20	0.41
1:N:435:GLY:C	1:N:437:ASP:H	2.29	0.41
1:J:88:LEU:HD21	1:J:178:TYR:CA	2.50	0.41
1:J:213:TYR:CE1	1:J:214:ARG:HG2	2.55	0.41
1:J:221:TRP:CZ2	1:J:368:PHE:HZ	2.38	0.41
1:J:328:TYR:HA	1:J:395:VAL:HG11	2.01	0.41
1:J:435:GLY:C	1:J:437:ASP:H	2.27	0.41
1:F:84:ILE:HG23	1:F:125:ILE:HD12	2.02	0.41
1:F:95:TRP:O	1:F:99:LEU:HD23	2.20	0.41
1:F:170:LEU:HD23	1:F:170:LEU:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:496:HIS:NE2	1:F:614:ARG:HG3	2.34	0.41
1:F:779:TRP:CE3	1:F:904:PRO:HD3	2.55	0.41
1:F:984:GLU:O	1:F:988:GLY:N	2.52	0.41
2:E:524:PHE:HZ	2:E:543:LEU:HD13	1.85	0.41
4:C:32:SER:HA	4:C:51:ILE:HA	2.02	0.41
4:C:138:ILE:HG22	4:C:279:ALA:HB2	2.00	0.41
4:G:88:ILE:HG23	4:G:165:LYS:HB3	2.02	0.41
4:G:229:PRO:HB2	4:G:230:PHE:CD1	2.55	0.41
4:K:229:PRO:HB2	4:K:230:PHE:CD1	2.55	0.41
4:O:232:HIS:CE1	4:O:234:LYS:H	2.38	0.41
1:B:655:ARG:H	1:B:655:ARG:HG3	1.69	0.41
1:B:928:ARG:NH1	1:B:1055:TYR:O	2.53	0.41
2:A:239:GLN:O	2:A:243:ASN:OD1	2.38	0.41
2:A:307:ASP:HA	2:A:308:PRO:HD3	1.93	0.41
2:A:892:ILE:HD12	2:A:893:LEU:HD12	2.02	0.41
2:A:897:ILE:O	2:A:901:LEU:HG	2.20	0.41
1:J:213:TYR:C	1:J:213:TYR:CD1	2.98	0.41
1:J:560:LEU:HD22	1:J:609:TRP:HE3	1.85	0.41
1:J:991:ASP:OD1	1:J:992:GLN:HG2	2.21	0.41
1:J:1001:GLU:HG2	1:F:1092:ILE:HB	2.01	0.41
1:F:772:ARG:HH11	1:F:776:GLN:HB3	1.85	0.41
1:F:792:PHE:HD1	1:F:793:SER:N	2.18	0.41
1:F:957:ILE:N	1:F:957:ILE:HD12	2.34	0.41
2:E:47:ASN:O	2:E:51:ILE:HG23	2.21	0.41
2:E:404:GLN:HE21	2:E:404:GLN:HB3	1.71	0.41
2:E:475:PRO:HA	2:E:521:THR:OG1	2.20	0.41
2:E:824:GLY:O	2:E:947:MET:HE1	2.20	0.41
3:H:55:GLU:HG2	4:G:322:TYR:CD1	2.54	0.41
4:G:182:ARG:HH21	4:G:204:HIS:C	2.28	0.41
4:G:236:MET:N	4:G:236:MET:SD	2.94	0.41
3:L:67:PRO:HA	3:L:70:LEU:HD23	2.03	0.41
3:L:82:SER:O	3:L:83:GLU:C	2.62	0.41
4:O:88:ILE:HG23	4:O:165:LYS:HB3	2.02	0.41
4:O:98:THR:HG23	4:O:99:PHE:CD2	2.55	0.41
1:B:243:LYS:NZ	1:B:247:GLU:OE2	2.52	0.41
1:B:746:ILE:O	1:B:750:ARG:HB2	2.20	0.41
1:B:995:TYR:HA	1:B:998:ILE:HG22	2.02	0.41
2:M:474:GLN:NE2	2:M:667:LEU:HD11	2.35	0.41
2:M:479:LEU:HD13	2:M:520:PHE:CE1	2.55	0.41
2:M:579:ASN:OD1	2:M:581:SER:N	2.51	0.41
2:M:1222:MET:N	2:M:1222:MET:SD	2.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1120:GLN:HA	2:A:1121:PRO:HD3	1.88	0.41
1:N:126:LEU:HB2	1:N:178:TYR:OH	2.20	0.41
1:N:206:VAL:HG21	1:N:265:ILE:HG21	2.02	0.41
1:N:486:GLN:HA	1:J:103:ARG:O	2.19	0.41
1:N:867:LEU:O	1:N:867:LEU:HD12	2.20	0.41
1:J:172:ILE:HB	1:J:238:SER:HB3	2.01	0.41
1:J:274:ARG:HA	1:J:277:GLN:HG3	2.01	0.41
1:J:534:LEU:HD23	1:J:557:ILE:HD13	2.02	0.41
1:J:642:LYS:NZ	1:J:642:LYS:HB3	2.35	0.41
1:J:654:ASP:HB3	1:J:659:LEU:HD13	2.03	0.41
1:J:1002:LEU:HD22	1:J:1069:LEU:HB3	2.02	0.41
2:I:566:ILE:HD12	2:I:578:LEU:HD11	2.02	0.41
1:F:307:LEU:HD13	1:F:307:LEU:HA	1.82	0.41
1:F:486:GLN:HB3	1:F:490:GLU:HB2	2.02	0.41
1:F:949:LEU:HD11	1:F:965:GLN:HA	2.01	0.41
2:E:26:GLN:HA	2:E:33:LEU:HD12	2.03	0.41
2:E:173:GLU:CD	2:E:497:ARG:HE	2.28	0.41
2:E:479:LEU:HB2	2:E:520:PHE:CD2	2.56	0.41
2:E:831:GLY:HA3	2:E:888:MET:HE2	2.02	0.41
2:E:1081:LYS:HB2	5:E:1301:FAR:H151	2.01	0.41
2:E:1184:ILE:HB	2:E:1189:TYR:CZ	2.54	0.41
4:C:236:MET:N	4:C:236:MET:SD	2.94	0.41
4:K:98:THR:HG23	4:K:99:PHE:CD2	2.55	0.41
3:P:57:ASP:OD2	3:P:63:THR:O	2.38	0.41
4:O:236:MET:N	4:O:236:MET:SD	2.94	0.41
1:B:724:THR:HB	1:B:726:GLU:HG3	2.01	0.41
1:B:833:ASN:HB2	1:B:838:LYS:HZ1	1.86	0.41
1:B:1074:MET:HG3	1:N:1074:MET:SD	2.61	0.41
2:A:106:GLN:NE2	2:A:500:ARG:HH12	2.18	0.41
2:A:894:THR:HA	2:A:920:ILE:HG21	2.03	0.41
1:N:536:LYS:HG2	1:N:682:PHE:HE2	1.86	0.41
1:N:1003:LEU:HD13	1:N:1003:LEU:HA	1.90	0.41
1:J:115:GLU:OE2	1:J:115:GLU:HA	2.21	0.41
1:J:853:LEU:HD12	1:J:880:ILE:HG12	2.03	0.41
1:J:1079:GLU:O	1:F:1062:LYS:HD3	2.19	0.41
2:I:48:VAL:O	2:I:51:ILE:HG22	2.20	0.41
2:I:51:ILE:HD12	2:I:51:ILE:HA	1.86	0.41
2:I:491:ARG:HE	2:I:491:ARG:HB3	1.70	0.41
2:I:1201:THR:HG23	4:K:347:ILE:HG21	2.01	0.41
1:F:399:THR:HG23	1:F:403:TYR:O	2.21	0.41
1:F:627:ARG:HE	1:F:627:ARG:HB3	1.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:638:LEU:O	1:F:642:LYS:HG3	2.20	0.41
3:D:105:GLU:O	3:D:106:LEU:C	2.59	0.41
3:H:57:ASP:OD2	3:H:63:THR:O	2.38	0.41
3:P:60:GLY:O	3:P:61:ASN:C	2.60	0.41
4:O:229:PRO:HB2	4:O:230:PHE:CD1	2.55	0.41
1:B:126:LEU:HB2	1:B:178:TYR:OH	2.20	0.41
2:A:164:PHE:HB2	2:A:492:MET:HE1	2.02	0.41
1:N:679:LEU:HD12	1:N:679:LEU:HA	1.87	0.41
2:I:1212:GLN:OE1	2:I:1212:GLN:HA	2.20	0.41
1:F:63:TYR:CD1	1:F:63:TYR:N	2.89	0.41
1:F:110:ARG:O	1:F:114:LEU:HG	2.21	0.41
2:E:847:LEU:HB3	2:E:854:LEU:HD21	2.03	0.41
4:C:98:THR:HG23	4:C:99:PHE:CD2	2.55	0.41
4:C:350:TYR:HA	4:C:353:ARG:HG2	2.03	0.41
4:K:120:VAL:HG21	4:K:348:ASP:O	2.20	0.41
4:O:32:SER:HA	4:O:51:ILE:HA	2.02	0.41
1:B:144:ARG:HG3	1:B:145:PRO:CD	2.49	0.41
1:B:1057:THR:HB	1:B:1065:THR:HG22	2.02	0.41
2:M:197:LEU:HB2	2:M:870:PRO:HG2	2.03	0.41
2:M:323:ASN:OD1	2:M:387:PRO:HB3	2.21	0.41
2:A:103:LYS:O	2:A:498:PRO:HG2	2.20	0.41
2:A:844:CYS:SG	2:A:876:LEU:HD22	2.60	0.41
2:A:1076:TRP:CE2	2:A:1102:PRO:HD3	2.55	0.41
1:N:609:TRP:CD1	1:N:615:PRO:HD3	2.55	0.41
1:J:621:ILE:HD12	1:J:634:ILE:HD11	2.02	0.41
1:J:830:VAL:O	1:J:834:ILE:HG23	2.20	0.41
1:J:872:LEU:HB3	1:J:873:LYS:H	1.72	0.41
1:J:958:VAL:HG11	1:J:987:LEU:HD23	2.03	0.41
2:I:413:MET:HG3	2:I:418:LEU:HB3	2.03	0.41
2:I:794:TRP:O	2:I:795:ASN:C	2.63	0.41
2:I:917:ARG:NH2	2:I:1112:GLU:HB3	2.36	0.41
1:F:409:TYR:CZ	1:F:432:SER:HB2	2.55	0.41
1:F:1082:VAL:HB	5:F:1101:FAR:C6	2.49	0.41
2:E:53:ALA:HB2	2:E:405:SER:HA	2.03	0.41
2:E:528:GLN:O	2:E:835:LYS:NZ	2.37	0.41
2:E:954:MET:N	2:E:954:MET:SD	2.94	0.41
2:E:1123:TYR:O	2:E:1127:LEU:HG	2.20	0.41
3:L:8:GLU:O	3:L:9:GLN:C	2.63	0.41
4:K:32:SER:HA	4:K:51:ILE:HA	2.02	0.41
3:P:70:LEU:O	3:P:71:THR:C	2.63	0.41
1:B:645:ILE:HD13	1:B:650:LYS:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:745:GLY:HA3	1:B:788:PHE:CD2	2.50	0.41
2:A:134:GLN:NE2	2:A:185:GLU:HA	2.35	0.41
2:A:328:TRP:CD1	2:A:372:LEU:HB3	2.56	0.41
2:A:423:ILE:H	2:A:423:ILE:HD12	1.86	0.41
2:A:557:THR:HG1	2:A:612:CYS:HG	1.65	0.41
1:N:944:ARG:NH2	1:N:1008:ILE:HD13	2.35	0.41
1:N:1059:PRO:O	1:N:1064:GLY:HA3	2.20	0.41
1:N:1077:LEU:HD23	1:N:1077:LEU:HA	1.78	0.41
1:J:856:HIS:HD2	1:J:908:LYS:HE3	1.85	0.41
2:I:186:ARG:HH12	2:I:295:ARG:HH22	1.69	0.41
2:I:239:GLN:NE2	2:I:271:GLU:H	2.19	0.41
2:I:1053:GLN:HE22	2:I:1057:ARG:HE	1.69	0.41
1:F:53:TYR:CZ	1:F:110:ARG:HD3	2.55	0.41
1:F:220:VAL:HG13	1:F:221:TRP:CD1	2.56	0.41
1:F:520:PRO:HG3	1:F:687:GLU:HB2	2.03	0.41
1:F:576:TYR:H	1:F:576:TYR:HD1	1.68	0.41
1:F:1074:MET:O	1:F:1078:LEU:HB2	2.21	0.41
4:C:229:PRO:HB2	4:C:230:PHE:CD1	2.55	0.41
4:G:63:GLU:H	4:G:63:GLU:HG3	1.67	0.41
1:B:159:ASP:OD1	1:B:159:ASP:C	2.64	0.41
1:B:309:ASP:OD1	1:B:311:VAL:N	2.54	0.41
1:B:339:ARG:HD3	1:B:339:ARG:HA	1.66	0.41
1:B:541:LEU:HD13	1:B:670:PHE:CE2	2.56	0.41
1:B:591:VAL:HG21	1:B:630:ARG:HB3	2.02	0.41
1:B:799:HIS:CD2	1:B:858:GLY:HA3	2.56	0.41
1:B:1041:ARG:H	1:B:1041:ARG:HG2	1.73	0.41
1:B:1090:CYS:SG	5:B:1101:FAR:H42	2.60	0.41
2:M:794:TRP:O	2:M:796:THR:HG23	2.21	0.41
2:M:832:ILE:HA	2:M:888:MET:SD	2.61	0.41
2:M:1159:ASN:ND2	2:M:1184:ILE:HA	2.35	0.41
2:A:102:PHE:HB2	2:A:110:ASP:O	2.21	0.41
2:A:336:ILE:O	2:A:340:VAL:HG23	2.21	0.41
2:A:484:SER:O	2:A:496:GLY:HA3	2.21	0.41
2:A:620:ASP:N	2:A:620:ASP:OD1	2.54	0.41
1:N:590:ASP:OD2	1:N:905:SER:N	2.54	0.41
1:N:1091:LEU:H	1:N:1091:LEU:HD22	1.85	0.41
1:J:180:LEU:O	1:J:184:GLU:HG2	2.20	0.41
1:J:392:LEU:HG	1:J:396:LEU:HG	2.03	0.41
1:J:951:ARG:HH12	1:J:1014:PRO:HA	1.85	0.41
1:J:998:ILE:HA	1:J:1001:GLU:OE2	2.21	0.41
1:J:1063:ARG:HA	1:J:1063:ARG:HD3	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:168:LEU:HD23	2:I:168:LEU:HA	1.89	0.41
2:I:188:ASP:OD2	2:I:252:SER:OG	2.39	0.41
2:I:295:ARG:HG2	2:I:331:PHE:HZ	1.85	0.41
2:I:302:LYS:HB2	2:I:372:LEU:HD21	2.02	0.41
2:I:837:VAL:HG11	2:I:899:VAL:HG21	2.03	0.41
2:I:898:MET:HE2	2:I:898:MET:HB3	1.94	0.41
1:F:567:ARG:HH21	1:F:572:THR:N	2.18	0.41
1:F:737:LEU:HA	1:F:740:GLN:NE2	2.36	0.41
1:F:989:ASN:OD1	1:F:989:ASN:N	2.37	0.41
2:E:91:CYS:HB3	2:E:116:TYR:CG	2.56	0.41
2:E:203:GLY:HA3	2:E:242:LEU:HD21	2.01	0.41
2:E:253:LYS:NZ	2:E:254:GLU:HG3	2.36	0.41
2:E:260:LEU:HD21	2:E:335:PHE:CE2	2.55	0.41
2:E:1162:PHE:O	2:E:1166:GLN:HG2	2.21	0.41
2:E:1211:VAL:HB	5:E:1301:FAR:H61	2.03	0.41
5:E:1301:FAR:H41	4:G:330:ARG:HG3	2.02	0.41
3:D:82:SER:O	3:D:83:GLU:C	2.62	0.41
3:H:75:ARG:HA	4:G:317:ARG:HH22	1.86	0.41
4:G:98:THR:HG23	4:G:99:PHE:CD2	2.55	0.41
4:K:75:VAL:HG12	4:K:79:ARG:CD	2.51	0.41
4:K:88:ILE:HG23	4:K:165:LYS:HB3	2.02	0.41
4:K:159:ASP:OD1	4:K:159:ASP:C	2.63	0.41
4:K:236:MET:N	4:K:236:MET:SD	2.94	0.41
1:B:183:VAL:HG21	1:B:248:ALA:HB1	2.01	0.41
1:B:284:PRO:HB2	1:B:319:LYS:HD3	2.03	0.41
1:B:375:ASP:OD1	1:B:384:GLN:NE2	2.54	0.41
1:B:627:ARG:NH2	1:B:630:ARG:HH22	2.19	0.41
1:B:853:LEU:HD23	1:B:883:MET:HE1	2.02	0.41
1:B:1012:ARG:HH12	1:N:1013:ASN:HA	1.81	0.41
2:M:233:ASP:OD1	2:M:505:LEU:HB2	2.21	0.41
2:M:440:VAL:O	2:M:599:VAL:HA	2.21	0.41
2:M:588:LYS:HE3	2:M:588:LYS:HB2	1.81	0.41
2:M:895:GLN:O	2:M:899:VAL:HG23	2.21	0.41
2:M:1159:ASN:ND2	2:M:1183:GLY:O	2.54	0.41
2:A:191:ASN:O	2:A:312:TYR:HD1	2.04	0.41
2:A:212:LEU:HD21	2:A:228:ILE:CD1	2.51	0.41
2:A:353:GLU:OE1	2:A:353:GLU:N	2.54	0.41
2:A:930:GLU:OE1	2:A:961:ILE:HG12	2.21	0.41
2:A:966:GLU:OE1	2:A:1057:ARG:NH1	2.53	0.41
1:N:482:ARG:O	1:N:482:ARG:HG2	2.20	0.41
1:N:901:GLN:HA	1:N:901:GLN:OE1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:317:LEU:HD12	1:J:317:LEU:HA	1.84	0.41
1:F:305:PHE:CE2	1:F:470:TYR:HB2	2.56	0.41
1:F:414:ALA:O	1:F:417:VAL:HG22	2.21	0.41
2:E:413:MET:O	2:E:414:ALA:C	2.64	0.41
2:E:588:LYS:CE	4:G:99:PHE:CD2	3.02	0.41
2:E:1057:ARG:NH2	4:G:358:TRP:HB3	2.36	0.41
4:C:20:TYR:HE1	4:C:94:TYR:HH	1.69	0.41
4:C:51:ILE:HD12	4:C:51:ILE:H	1.86	0.41
4:C:241:MET:HE2	4:C:241:MET:HB3	1.87	0.41
4:G:120:VAL:HG21	4:G:348:ASP:O	2.20	0.41
3:L:71:THR:HG23	4:K:258:SER:CB	2.51	0.41
4:K:84:HIS:NE2	4:K:137:VAL:HG22	2.36	0.41
4:O:159:ASP:C	4:O:159:ASP:OD1	2.63	0.41
2:M:295:ARG:HG3	2:M:328:TRP:NE1	2.36	0.40
2:M:371:GLU:OE1	2:M:397:LYS:HE2	2.21	0.40
2:M:482:ILE:HG23	2:M:619:MET:SD	2.61	0.40
2:A:260:LEU:HD11	2:A:335:PHE:CE1	2.56	0.40
2:A:514:ARG:HH12	2:A:664:LEU:HB3	1.85	0.40
1:N:56:VAL:HG21	1:N:97:LEU:HD22	2.03	0.40
1:J:56:VAL:HG22	1:J:60:LEU:HD21	2.02	0.40
2:I:249:ALA:HB3	2:I:256:ASP:OD2	2.19	0.40
2:I:256:ASP:HB2	2:I:259:LEU:HG	2.03	0.40
2:I:1196:ARG:CZ	4:K:252:PRO:CD	2.99	0.40
1:F:482:ARG:HA	1:F:610:LYS:HG3	2.02	0.40
1:F:791:LYS:HE3	1:F:791:LYS:HB2	1.76	0.40
2:E:169:VAL:HG22	2:E:212:LEU:HD12	2.03	0.40
2:E:460:ILE:HG23	2:E:462:VAL:HG13	2.03	0.40
2:E:858:LEU:O	2:E:864:GLU:HB2	2.21	0.40
4:C:221:TYR:CB	4:C:229:PRO:HG3	2.51	0.40
3:H:72:MET:HE2	3:H:72:MET:HB3	1.84	0.40
4:G:32:SER:HA	4:G:51:ILE:HA	2.02	0.40
4:G:350:TYR:HA	4:G:353:ARG:HG2	2.03	0.40
3:L:146:MET:HE2	3:L:146:MET:HB2	1.88	0.40
4:K:313:LEU:O	4:K:317:ARG:HB2	2.21	0.40
3:P:13:PHE:CD1	4:O:310:LEU:HD21	2.38	0.40
3:P:106:LEU:HD12	3:P:106:LEU:HA	1.95	0.40
4:O:20:TYR:OH	4:O:91:LYS:HD3	2.21	0.40
1:B:499:LEU:HA	1:B:619:VAL:HG12	2.02	0.40
1:B:767:GLU:O	1:B:771:ARG:HG2	2.21	0.40
2:M:604:LEU:HD12	2:M:604:LEU:HA	1.89	0.40
2:M:848:LEU:HD12	2:M:852:LYS:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:172:ILE:HD13	2:A:172:ILE:HG21	1.78	0.40
2:A:859:PRO:HG2	2:A:860:PRO:HD3	2.03	0.40
2:A:1136:MET:O	2:A:1140:ILE:HG13	2.21	0.40
2:A:1169:LEU:HD13	4:C:375:PRO:HG3	2.03	0.40
2:A:1196:ARG:NH2	4:C:251:SER:O	2.54	0.40
1:N:129:TYR:HB3	1:N:201:PHE:CE2	2.56	0.40
1:N:984:GLU:OE2	1:N:984:GLU:HA	2.20	0.40
1:J:88:LEU:HD21	1:J:178:TYR:N	2.36	0.40
1:J:783:ARG:NH2	1:J:902:LEU:O	2.53	0.40
1:J:1013:ASN:CG	5:J:1101:FAR:H111	2.44	0.40
2:I:101:SER:HB3	2:I:110:ASP:OD2	2.22	0.40
1:F:507:GLN:O	1:F:511:ASN:HB2	2.20	0.40
2:E:253:LYS:HE3	2:E:296:PHE:HB2	2.03	0.40
2:E:395:MET:HE3	2:E:395:MET:HB2	1.81	0.40
2:E:559:GLN:HB2	2:E:610:THR:O	2.21	0.40
2:E:620:ASP:HA	2:E:621:PRO:HD3	1.97	0.40
3:D:72:MET:HE2	3:D:72:MET:HB3	1.84	0.40
3:H:82:SER:O	3:H:83:GLU:C	2.62	0.40
3:H:118:THR:OG1	3:H:121:GLU:CB	2.65	0.40
4:G:73:LYS:O	4:G:77:ILE:HD12	2.22	0.40
4:G:219:ILE:H	4:G:219:ILE:HG12	1.59	0.40
4:K:250:GLY:O	4:K:253:GLU:HG3	2.22	0.40
1:B:98:ALA:CB	1:B:115:GLU:HG3	2.49	0.40
1:B:253:ASN:HD22	1:B:264:VAL:HG22	1.87	0.40
1:B:564:LYS:HG2	1:B:609:TRP:HH2	1.84	0.40
1:B:632:ASN:O	1:B:635:LEU:HG	2.21	0.40
2:M:62:ARG:HA	2:M:62:ARG:HD3	1.84	0.40
2:M:147:GLN:OE1	2:M:424:ASP:HA	2.21	0.40
2:M:1132:LEU:HA	2:M:1135:THR:HG23	2.03	0.40
2:A:49:TYR:CE2	2:A:140:VAL:HG21	2.56	0.40
2:A:823:TRP:HA	2:A:826:ILE:HB	2.03	0.40
1:N:381:ASN:C	1:N:381:ASN:OD1	2.64	0.40
2:I:86:ARG:HD3	2:I:155:ILE:O	2.21	0.40
2:I:531:TYR:OH	2:I:896:GLU:OE1	2.35	0.40
2:I:809:LEU:HD23	2:I:809:LEU:HA	1.90	0.40
2:I:1075:VAL:HA	2:I:1078:VAL:HG22	2.03	0.40
2:I:1211:VAL:HB	5:I:1301:FAR:H61	2.03	0.40
1:F:43:GLU:HB2	1:F:47:ASP:HB2	2.03	0.40
1:F:626:ILE:HG23	1:F:631:PHE:CD2	2.50	0.40
1:F:830:VAL:O	1:F:834:ILE:HG13	2.21	0.40
2:E:76:GLU:OE1	2:E:77:LEU:HG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:102:PHE:HB2	2:E:110:ASP:O	2.22	0.40
3:D:75:ARG:HA	4:C:317:ARG:HH22	1.86	0.40
4:C:84:HIS:NE2	4:C:137:VAL:HG22	2.36	0.40
4:C:329:THR:H	4:C:332:ILE:CD1	2.34	0.40
4:G:250:GLY:O	4:G:253:GLU:HG3	2.22	0.40
4:K:126:GLU:HA	4:K:129:LYS:NZ	2.36	0.40
4:K:220:MET:HE1	4:K:264:LEU:HD21	2.03	0.40
3:P:71:THR:HG23	4:O:258:SER:CB	2.51	0.40
4:O:74:GLU:OE2	4:O:170:GLY:HA2	2.22	0.40
1:B:49:LEU:HD23	1:B:101:TYR:CD1	2.57	0.40
1:B:130:MET:HG3	2:A:29:VAL:HA	2.02	0.40
1:B:479:VAL:HG12	1:B:611:MET:HE2	2.03	0.40
1:B:667:GLN:OE1	1:B:667:GLN:N	2.46	0.40
1:B:783:ARG:NH1	1:B:900:TYR:O	2.55	0.40
1:B:808:LYS:HB2	1:B:874:ILE:HD11	2.02	0.40
1:B:1008:ILE:HD11	1:B:1012:ARG:NE	2.36	0.40
2:M:809:LEU:HD23	2:M:809:LEU:HA	1.81	0.40
2:A:57:LEU:HB3	2:A:77:LEU:HD13	2.04	0.40
2:A:189:LYS:HE2	2:A:296:PHE:HD2	1.87	0.40
2:A:189:LYS:HD2	2:A:189:LYS:HA	1.91	0.40
1:N:347:ARG:HH22	1:N:354:GLU:CD	2.30	0.40
1:N:464:ILE:H	1:N:464:ILE:HG12	1.76	0.40
1:J:120:LYS:HG3	2:I:86:ARG:NH2	2.37	0.40
1:J:578:ILE:HD12	1:J:581:ASP:HB2	2.03	0.40
2:I:511:TYR:HB2	2:I:520:PHE:HE1	1.86	0.40
1:F:283:LEU:HD23	1:F:283:LEU:HA	1.86	0.40
1:F:948:ILE:HG22	1:F:956:ILE:HD11	2.03	0.40
1:F:1053:SER:O	1:F:1057:THR:OG1	2.40	0.40
2:E:246:LEU:HD22	2:E:259:LEU:HD13	2.04	0.40
4:C:73:LYS:O	4:C:77:ILE:HD12	2.22	0.40
4:C:313:LEU:O	4:C:317:ARG:HB2	2.22	0.40
4:G:115:TYR:HE2	4:G:162:MET:SD	2.45	0.40
3:P:8:GLU:O	3:P:9:GLN:C	2.63	0.40
4:O:115:TYR:HE2	4:O:162:MET:SD	2.45	0.40
4:O:220:MET:HE1	4:O:264:LEU:HD21	2.03	0.40
1:B:1002:LEU:HA	1:B:1005:VAL:HG12	2.03	0.40
2:M:852:LYS:HB3	2:M:918:LEU:HD23	2.02	0.40
2:A:136:ASP:HA	2:A:139:SER:HB2	2.03	0.40
2:A:584:ALA:HB1	4:C:54:THR:CG2	2.51	0.40
2:A:1055:GLN:HG3	2:A:1189:TYR:HB3	2.02	0.40
2:A:1162:PHE:O	2:A:1166:GLN:HG2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:291:ASN:OD1	1:N:291:ASN:N	2.52	0.40
1:N:940:GLY:O	1:N:944:ARG:HG2	2.21	0.40
1:J:49:LEU:HD23	1:J:49:LEU:HA	1.90	0.40
1:J:593:LEU:CD1	1:J:904:PRO:HB2	2.52	0.40
1:J:815:PHE:C	1:J:815:PHE:CD1	2.99	0.40
2:I:32:LEU:HD11	2:I:91:CYS:SG	2.61	0.40
1:F:545:GLU:CD	1:F:545:GLU:H	2.30	0.40
1:F:557:ILE:HG22	1:F:562:THR:HG23	2.04	0.40
1:F:587:MET:HE1	1:F:855:ILE:HB	2.03	0.40
1:F:765:HIS:HA	1:F:768:ARG:HG2	2.02	0.40
1:F:809:GLN:C	1:F:809:GLN:OE1	2.64	0.40
2:E:10:ARG:HG2	2:E:417:PHE:CZ	2.56	0.40
2:E:248:ARG:HD3	2:E:851:GLN:NE2	2.36	0.40
2:E:519:THR:HG21	2:E:604:LEU:HD21	2.03	0.40
4:G:126:GLU:HA	4:G:129:LYS:NZ	2.36	0.40
4:O:355:TYR:HB3	4:O:358:TRP:HD1	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	1029/1093 (94%)	997 (97%)	32 (3%)	0	100	100
1	F	1029/1093 (94%)	991 (96%)	37 (4%)	1 (0%)	48	77
1	J	1029/1093 (94%)	998 (97%)	30 (3%)	1 (0%)	48	77
1	N	1029/1093 (94%)	1002 (97%)	27 (3%)	0	100	100
2	A	976/1223 (80%)	955 (98%)	21 (2%)	0	100	100
2	E	976/1223 (80%)	957 (98%)	19 (2%)	0	100	100
2	I	976/1223 (80%)	956 (98%)	19 (2%)	1 (0%)	48	77

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	M	976/1223 (80%)	960 (98%)	16 (2%)	0	100	100
3	D	143/149 (96%)	140 (98%)	3 (2%)	0	100	100
3	H	143/149 (96%)	140 (98%)	3 (2%)	0	100	100
3	L	143/149 (96%)	141 (99%)	2 (1%)	0	100	100
3	P	143/149 (96%)	140 (98%)	3 (2%)	0	100	100
4	C	369/387 (95%)	360 (98%)	9 (2%)	0	100	100
4	G	369/387 (95%)	361 (98%)	8 (2%)	0	100	100
4	K	369/387 (95%)	359 (97%)	10 (3%)	0	100	100
4	O	369/387 (95%)	361 (98%)	8 (2%)	0	100	100
All	All	10068/11408 (88%)	9818 (98%)	247 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	872	LEU
2	I	795	ASN
1	F	917	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	924/975 (95%)	891 (96%)	33 (4%)	31	65
1	F	924/975 (95%)	900 (97%)	24 (3%)	40	73
1	J	924/975 (95%)	897 (97%)	27 (3%)	37	71
1	N	924/975 (95%)	897 (97%)	27 (3%)	37	71
2	A	857/1068 (80%)	842 (98%)	15 (2%)	51	80
2	E	857/1068 (80%)	845 (99%)	12 (1%)	59	85
2	I	857/1068 (80%)	840 (98%)	17 (2%)	48	78
2	M	857/1068 (80%)	843 (98%)	14 (2%)	55	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	124/127 (98%)	119 (96%)	5 (4%)	28	62
3	H	124/127 (98%)	119 (96%)	5 (4%)	28	62
3	L	124/127 (98%)	119 (96%)	5 (4%)	28	62
3	P	124/127 (98%)	119 (96%)	5 (4%)	28	62
4	C	335/349 (96%)	332 (99%)	3 (1%)	70	90
4	G	335/349 (96%)	332 (99%)	3 (1%)	70	90
4	K	335/349 (96%)	330 (98%)	5 (2%)	57	84
4	O	335/349 (96%)	331 (99%)	4 (1%)	63	86
All	All	8960/10076 (89%)	8756 (98%)	204 (2%)	44	76

All (204) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	44	THR
1	B	138	GLN
1	B	214	ARG
1	B	241	LEU
1	B	377	VAL
1	B	479	VAL
1	B	506	LEU
1	B	519	THR
1	B	526	ILE
1	B	573	VAL
1	B	641	LEU
1	B	646	ILE
1	B	721	ASP
1	B	743	LEU
1	B	748	LEU
1	B	756	ILE
1	B	757	THR
1	B	761	THR
1	B	775	SER
1	B	850	GLN
1	B	874	ILE
1	B	886	GLU
1	B	905	SER
1	B	920	ASN
1	B	963	LEU
1	B	973	THR

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Mol	Chain	Res	Type
1	B	977	MET
1	B	1040	SER
1	B	1057	THR
1	B	1063	ARG
1	B	1082	VAL
1	B	1090	CYS
1	B	1092	ILE
2	M	57	LEU
2	M	485	SER
2	M	505	LEU
2	M	563	THR
2	M	569	SER
2	M	666	HIS
2	M	837	VAL
2	M	866	THR
2	M	874	GLU
2	M	890	ILE
2	M	901	LEU
2	M	916	PHE
2	M	1115	LEU
2	M	1118	VAL
2	A	6	ASN
2	A	94	ARG
2	A	107	SER
2	A	115	LYS
2	A	123	THR
2	A	151	SER
2	A	156	ILE
2	A	235	VAL
2	A	363	LYS
2	A	433	VAL
2	A	538	MET
2	A	915	MET
2	A	916	PHE
2	A	1091	VAL
2	A	1118	VAL
1	N	220	VAL
1	N	225	SER
1	N	289	SER
1	N	519	THR
1	N	523	VAL
1	N	524	GLU

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Mol	Chain	Res	Type
1	N	544	ASN
1	N	572	THR
1	N	626	ILE
1	N	674	SER
1	N	676	THR
1	N	681	GLU
1	N	748	LEU
1	N	766	ILE
1	N	793	SER
1	N	827	SER
1	N	848	VAL
1	N	866	GLU
1	N	872	LEU
1	N	873	LYS
1	N	875	ARG
1	N	910	LEU
1	N	919	GLN
1	N	925	LEU
1	N	1057	THR
1	N	1065	THR
1	N	1092	ILE
1	J	220	VAL
1	J	282	LEU
1	J	355	ILE
1	J	356	LYS
1	J	523	VAL
1	J	524	GLU
1	J	554	ASP
1	J	556	PRO
1	J	557	ILE
1	J	573	VAL
1	J	667	GLN
1	J	747	LEU
1	J	748	LEU
1	J	757	THR
1	J	766	ILE
1	J	789	THR
1	J	848	VAL
1	J	872	LEU
1	J	875	ARG
1	J	915	LEU
1	J	931	ASP

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Mol	Chain	Res	Type
1	J	939	THR
1	J	957	ILE
1	J	963	LEU
1	J	972	MET
1	J	986	THR
1	J	1092	ILE
2	I	51	ILE
2	I	92	MET
2	I	93	ILE
2	I	355	LEU
2	I	363	LYS
2	I	501	HIS
2	I	523	GLN
2	I	562	ILE
2	I	788	THR
2	I	813	LEU
2	I	825	LEU
2	I	890	ILE
2	I	916	PHE
2	I	923	ILE
2	I	926	VAL
2	I	935	LEU
2	I	1160	ASP
1	F	67	THR
1	F	170	LEU
1	F	177	LEU
1	F	209	VAL
1	F	343	GLU
1	F	372	MET
1	F	412	VAL
1	F	471	VAL
1	F	473	LEU
1	F	485	ASN
1	F	495	VAL
1	F	524	GLU
1	F	624	ASP
1	F	681	GLU
1	F	721	ASP
1	F	724	THR
1	F	748	LEU
1	F	844	GLU
1	F	871	MET

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Mol	Chain	Res	Type
1	F	915	LEU
1	F	918	GLN
1	F	949	LEU
1	F	974	MET
1	F	1092	ILE
2	E	9	VAL
2	E	29	VAL
2	E	44	VAL
2	E	215	LEU
2	E	347	GLN
2	E	448	THR
2	E	460	ILE
2	E	561	THR
2	E	915	MET
2	E	1105	ILE
2	E	1118	VAL
2	E	1201	THR
3	D	28	ILE
3	D	52	MET
3	D	70	LEU
3	D	71	THR
3	D	126	ILE
4	C	162	MET
4	C	175	LEU
4	C	260	THR
3	H	28	ILE
3	H	52	MET
3	H	70	LEU
3	H	71	THR
3	H	126	ILE
4	G	162	MET
4	G	175	LEU
4	G	260	THR
3	L	28	ILE
3	L	52	MET
3	L	70	LEU
3	L	71	THR
3	L	126	ILE
4	K	116	LEU
4	K	162	MET
4	K	175	LEU
4	K	260	THR

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Mol	Chain	Res	Type
4	K	306	LYS
3	P	28	ILE
3	P	42	GLN
3	P	52	MET
3	P	71	THR
3	P	126	ILE
4	O	162	MET
4	O	175	LEU
4	O	260	THR
4	O	306	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (125) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	132	GLN
1	B	138	GLN
1	B	228	ASN
1	B	250	ASN
1	B	381	ASN
1	B	468	GLN
1	B	511	ASN
1	B	527	GLN
1	B	532	GLN
1	B	589	GLN
1	B	612	HIS
1	B	729	GLN
1	B	881	HIS
1	B	901	GLN
1	B	965	GLN
1	B	966	GLN
1	B	978	ASN
1	B	1048	GLN
1	B	1085	ASN
2	M	95	GLN
2	M	154	HIS
2	M	163	ASN
2	M	198	ASN
2	M	323	ASN
2	M	489	ASN
2	M	536	ASN
2	M	600	GLN
2	M	851	GLN

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Mol	Chain	Res	Type
2	M	959	HIS
2	M	1073	GLN
2	M	1159	ASN
2	M	1217	HIS
2	M	1223	GLN
2	A	79	GLN
2	A	95	GLN
2	A	132	HIS
2	A	163	ASN
2	A	166	GLN
2	A	385	GLN
2	A	441	GLN
2	A	536	ASN
2	A	568	HIS
2	A	800	ASN
2	A	895	GLN
2	A	1116	ASN
2	A	1217	HIS
2	A	1223	GLN
1	N	51	HIS
1	N	273	ASN
1	N	386	GLN
1	N	422	ASN
1	N	540	GLN
1	N	600	ASN
1	N	625	ASN
1	N	729	GLN
1	N	740	GLN
1	N	824	ASN
1	N	840	ASN
1	N	850	GLN
1	N	1085	ASN
1	J	112	HIS
1	J	171	GLN
1	J	250	ASN
1	J	389	GLN
1	J	427	GLN
1	J	491	ASN
1	J	518	GLN
1	J	667	GLN
1	J	711	GLN
1	J	729	GLN

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Mol	Chain	Res	Type
1	J	799	HIS
1	J	864	ASN
1	J	901	GLN
1	J	1013	ASN
1	J	1036	GLN
1	J	1056	ASN
2	I	95	GLN
2	I	134	GLN
2	I	154	HIS
2	I	163	ASN
2	I	198	ASN
2	I	385	GLN
2	I	400	HIS
2	I	474	GLN
2	I	489	ASN
2	I	559	GLN
2	I	800	ASN
2	I	851	GLN
2	I	878	GLN
2	I	925	GLN
2	I	1073	GLN
2	I	1110	HIS
2	I	1217	HIS
1	F	156	HIS
1	F	171	GLN
1	F	527	GLN
1	F	740	GLN
1	F	842	HIS
1	F	856	HIS
1	F	909	GLN
1	F	1013	ASN
1	F	1019	GLN
2	E	163	ASN
2	E	166	GLN
2	E	239	GLN
2	E	344	ASN
2	E	347	GLN
2	E	385	GLN
2	E	489	ASN
2	E	527	GLN
2	E	568	HIS
2	E	895	GLN

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Mol	Chain	Res	Type
2	E	1080	GLN
2	E	1223	GLN
3	D	9	GLN
4	C	86	ASN
4	C	246	ASN
3	H	9	GLN
4	G	86	ASN
4	G	246	ASN
3	L	9	GLN
4	K	86	ASN
3	P	9	GLN
3	P	42	GLN
4	O	86	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	FAR	N	1101	-	14,14,14	0.31	0	15,16,16	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FAR	A	1301	-	14,14,14	2.34	4 (28%)	15,16,16	9.72	10 (66%)
5	FAR	B	1101	1	14,14,14	0.62	0	15,16,16	2.63	8 (53%)
5	FAR	M	1301	-	14,14,14	2.44	4 (28%)	15,16,16	11.62	10 (66%)
5	FAR	I	1301	2	14,14,14	2.36	4 (28%)	15,16,16	9.69	10 (66%)
5	FAR	E	1301	-	14,14,14	2.33	4 (28%)	15,16,16	9.70	10 (66%)
5	FAR	F	1101	1	14,14,14	0.57	0	15,16,16	2.44	5 (33%)
5	FAR	J	1101	-	14,14,14	2.13	4 (28%)	15,16,16	10.98	8 (53%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FAR	N	1101	-	-	4/14/14/14	-
5	FAR	A	1301	-	-	5/14/14/14	-
5	FAR	B	1101	1	-	5/14/14/14	-
5	FAR	M	1301	-	-	5/14/14/14	-
5	FAR	I	1301	2	-	4/14/14/14	-
5	FAR	E	1301	-	-	4/14/14/14	-
5	FAR	F	1101	1	-	3/14/14/14	-
5	FAR	J	1101	-	-	4/14/14/14	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1301	FAR	C10-C8	4.72	1.62	1.50
5	I	1301	FAR	C10-C8	4.71	1.62	1.50
5	M	1301	FAR	C5-C3	4.69	1.61	1.51
5	E	1301	FAR	C10-C8	4.64	1.62	1.50
5	M	1301	FAR	C10-C8	4.55	1.61	1.50
5	J	1101	FAR	C5-C3	4.47	1.60	1.51
5	E	1301	FAR	C5-C3	4.40	1.60	1.51
5	I	1301	FAR	C5-C3	4.29	1.60	1.51
5	A	1301	FAR	C5-C3	4.22	1.60	1.51
5	M	1301	FAR	C9-C8	3.67	1.58	1.51
5	I	1301	FAR	C9-C8	3.56	1.58	1.51
5	A	1301	FAR	C9-C8	3.49	1.58	1.51
5	E	1301	FAR	C9-C8	3.45	1.58	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	J	1101	FAR	C9-C8	2.80	1.57	1.51
5	J	1101	FAR	C10-C8	2.68	1.57	1.50
5	J	1101	FAR	C6-C7	2.42	1.57	1.50
5	M	1301	FAR	C6-C7	2.30	1.57	1.50
5	I	1301	FAR	C6-C7	2.12	1.56	1.50
5	A	1301	FAR	C6-C7	2.11	1.56	1.50
5	E	1301	FAR	C6-C7	2.11	1.56	1.50

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	1101	FAR	C4-C3-C5	-26.54	69.16	115.23
5	M	1301	FAR	C4-C3-C5	-26.29	69.60	115.23
5	J	1101	FAR	C9-C8-C7	20.98	168.26	121.17
5	J	1101	FAR	C10-C8-C9	-17.67	84.56	115.23
5	A	1301	FAR	C4-C3-C5	-17.03	85.66	115.23
5	E	1301	FAR	C4-C3-C5	-16.68	86.28	115.23
5	I	1301	FAR	C4-C3-C5	-16.60	86.42	115.23
5	M	1301	FAR	C9-C8-C7	16.45	158.09	121.17
5	I	1301	FAR	C9-C8-C7	16.21	157.56	121.17
5	E	1301	FAR	C9-C8-C7	16.20	157.53	121.17
5	A	1301	FAR	C9-C8-C7	16.11	157.33	121.17
5	J	1101	FAR	C5-C3-C2	-15.63	85.76	120.36
5	M	1301	FAR	C5-C3-C2	-15.55	85.93	120.36
5	E	1301	FAR	C15-C13-C14	-15.07	79.90	114.59
5	A	1301	FAR	C15-C13-C14	-15.04	79.97	114.59
5	I	1301	FAR	C15-C13-C14	-14.93	80.23	114.59
5	M	1301	FAR	C15-C13-C14	-14.91	80.27	114.59
5	I	1301	FAR	C15-C13-C12	-14.10	80.34	122.66
5	A	1301	FAR	C15-C13-C12	-14.09	80.36	122.66
5	E	1301	FAR	C15-C13-C12	-14.05	80.51	122.66
5	M	1301	FAR	C15-C13-C12	-14.01	80.63	122.66
5	M	1301	FAR	C14-C13-C12	12.74	160.88	122.66
5	I	1301	FAR	C14-C13-C12	12.63	160.56	122.66
5	E	1301	FAR	C14-C13-C12	12.58	160.40	122.66
5	A	1301	FAR	C14-C13-C12	12.56	160.33	122.66
5	M	1301	FAR	C10-C8-C9	-12.25	93.97	115.23
5	E	1301	FAR	C10-C8-C9	-11.99	94.42	115.23
5	I	1301	FAR	C10-C8-C9	-11.92	94.53	115.23
5	A	1301	FAR	C10-C8-C9	-11.86	94.64	115.23
5	A	1301	FAR	C5-C3-C2	-7.29	104.22	120.36
5	I	1301	FAR	C5-C3-C2	-7.15	104.53	120.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	1301	FAR	C5-C3-C2	-7.09	104.66	120.36
5	E	1301	FAR	C1-C2-C3	-6.72	111.15	126.44
5	I	1301	FAR	C1-C2-C3	-6.71	111.15	126.44
5	M	1301	FAR	C1-C2-C3	-6.52	111.60	126.44
5	A	1301	FAR	C1-C2-C3	-6.48	111.69	126.44
5	J	1101	FAR	C10-C8-C7	-6.45	107.06	123.63
5	J	1101	FAR	C1-C2-C3	-6.35	111.97	126.44
5	I	1301	FAR	C10-C8-C7	-6.12	107.91	123.63
5	M	1301	FAR	C10-C8-C7	-6.11	107.94	123.63
5	A	1301	FAR	C10-C8-C7	-6.07	108.03	123.63
5	E	1301	FAR	C10-C8-C7	-6.06	108.05	123.63
5	B	1101	FAR	C1-C2-C3	-6.03	112.70	126.44
5	F	1101	FAR	C1-C2-C3	-4.81	115.48	126.44
5	F	1101	FAR	C4-C3-C5	4.75	123.47	115.23
5	B	1101	FAR	C15-C13-C14	4.00	123.80	114.59
5	F	1101	FAR	C6-C7-C8	-3.87	118.77	127.62
5	F	1101	FAR	C10-C8-C9	3.48	121.27	115.23
5	J	1101	FAR	C6-C7-C8	-3.47	119.68	127.62
5	E	1301	FAR	C11-C12-C13	-2.80	118.29	127.64
5	F	1101	FAR	C11-C12-C13	-2.77	118.40	127.64
5	B	1101	FAR	C5-C3-C2	2.76	126.47	120.36
5	I	1301	FAR	C11-C12-C13	-2.73	118.55	127.64
5	A	1301	FAR	C11-C12-C13	-2.71	118.61	127.64
5	B	1101	FAR	C9-C8-C7	-2.63	115.25	121.17
5	B	1101	FAR	C11-C9-C8	-2.61	104.55	113.19
5	M	1301	FAR	C11-C12-C13	-2.60	118.98	127.64
5	B	1101	FAR	C11-C12-C13	-2.55	119.15	127.64
5	B	1101	FAR	C6-C7-C8	2.54	133.45	127.62
5	B	1101	FAR	C10-C8-C7	2.53	130.12	123.63
5	J	1101	FAR	C11-C12-C13	-2.39	119.66	127.64

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1101	FAR	C5-C6-C7-C8
5	M	1301	FAR	C12-C11-C9-C8
5	M	1301	FAR	C9-C11-C12-C13
5	A	1301	FAR	C9-C11-C12-C13
5	I	1301	FAR	C9-C11-C12-C13
5	E	1301	FAR	C9-C11-C12-C13
5	F	1101	FAR	C4-C3-C5-C6

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Mol	Chain	Res	Type	Atoms
5	F	1101	FAR	C2-C3-C5-C6
5	M	1301	FAR	C3-C5-C6-C7
5	A	1301	FAR	C12-C11-C9-C8
5	I	1301	FAR	C12-C11-C9-C8
5	F	1101	FAR	C12-C11-C9-C8
5	B	1101	FAR	C3-C5-C6-C7
5	E	1301	FAR	C12-C11-C9-C8
5	N	1101	FAR	C3-C5-C6-C7
5	B	1101	FAR	C2-C3-C5-C6
5	J	1101	FAR	C10-C8-C9-C11
5	B	1101	FAR	C4-C3-C5-C6
5	J	1101	FAR	C7-C8-C9-C11
5	A	1301	FAR	C3-C5-C6-C7
5	J	1101	FAR	C12-C11-C9-C8
5	A	1301	FAR	C10-C8-C9-C11
5	N	1101	FAR	C10-C8-C9-C11
5	E	1301	FAR	C10-C8-C9-C11
5	N	1101	FAR	C7-C8-C9-C11
5	A	1301	FAR	C7-C8-C9-C11
5	E	1301	FAR	C7-C8-C9-C11
5	I	1301	FAR	C10-C8-C9-C11
5	B	1101	FAR	C12-C11-C9-C8
5	M	1301	FAR	C10-C8-C9-C11
5	I	1301	FAR	C7-C8-C9-C11
5	J	1101	FAR	C3-C5-C6-C7
5	M	1301	FAR	C7-C8-C9-C11
5	N	1101	FAR	C9-C11-C12-C13

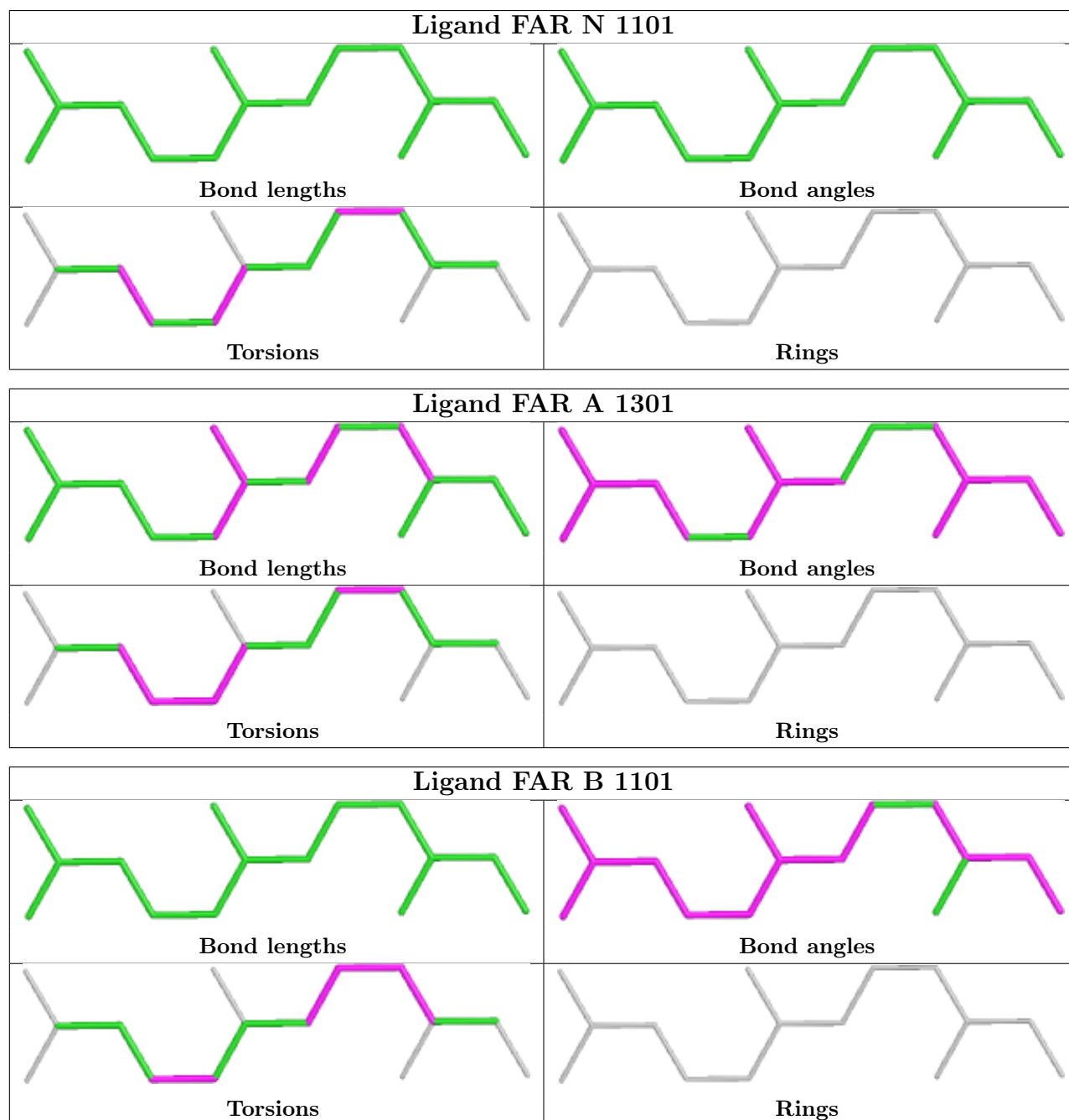
There are no ring outliers.

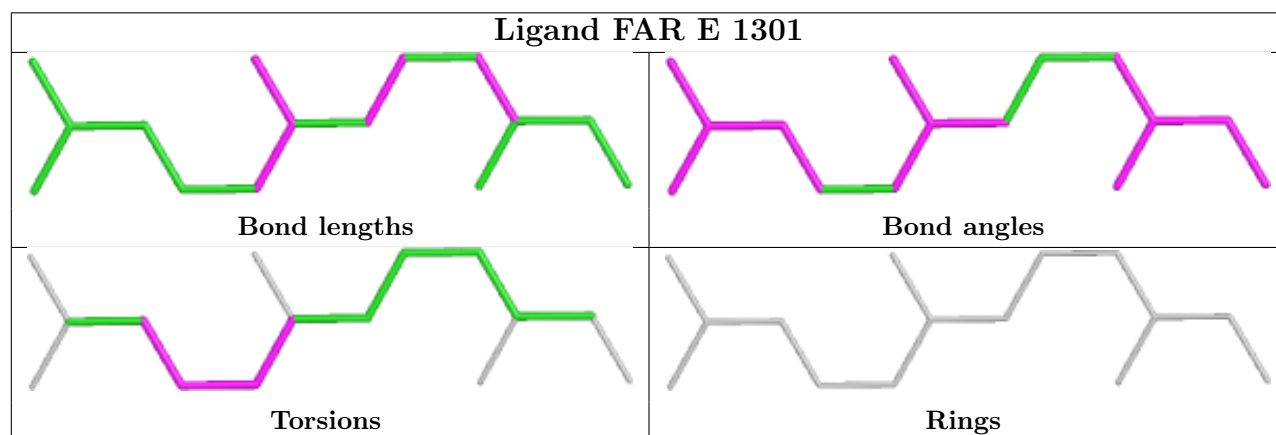
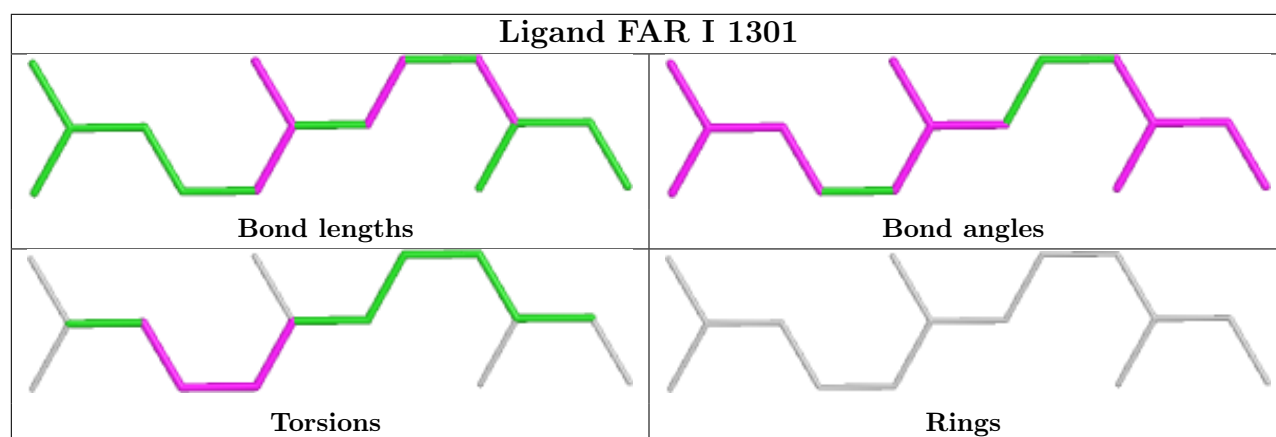
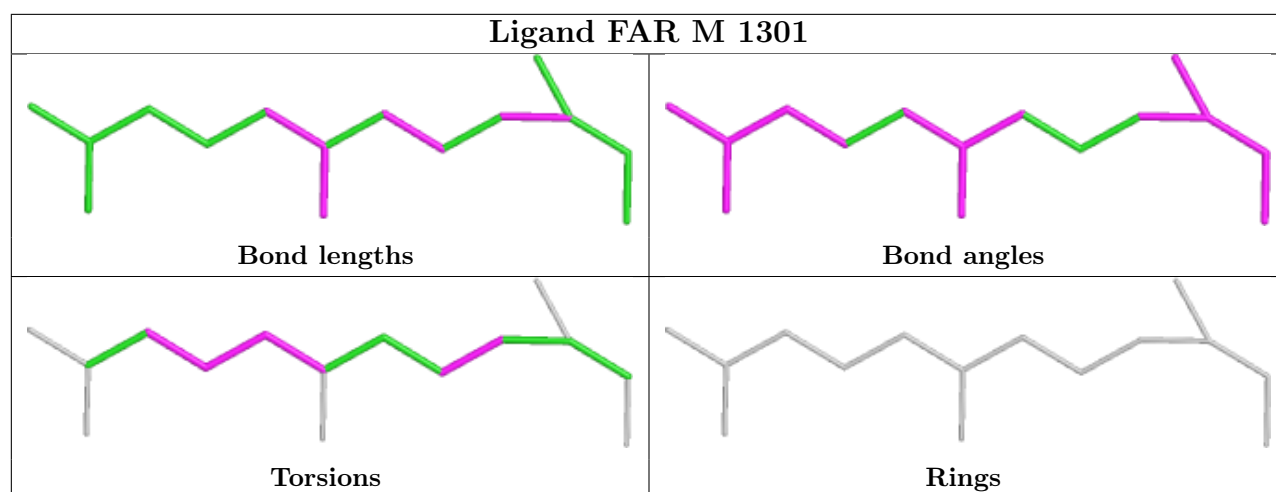
8 monomers are involved in 138 short contacts:

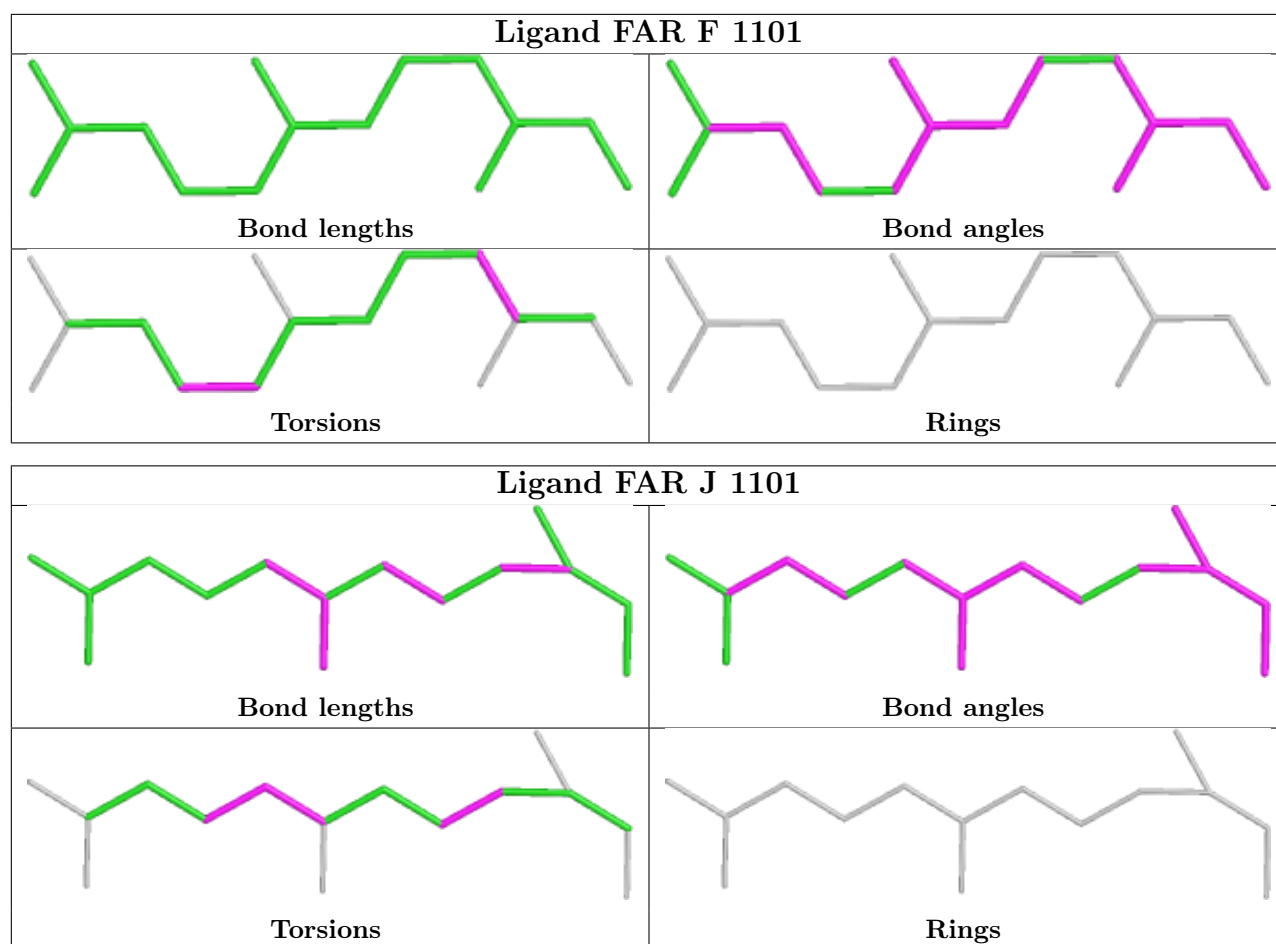
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	N	1101	FAR	16	0
5	A	1301	FAR	10	0
5	B	1101	FAR	20	0
5	M	1301	FAR	5	0
5	I	1301	FAR	9	0
5	E	1301	FAR	11	0
5	F	1101	FAR	28	0
5	J	1101	FAR	40	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

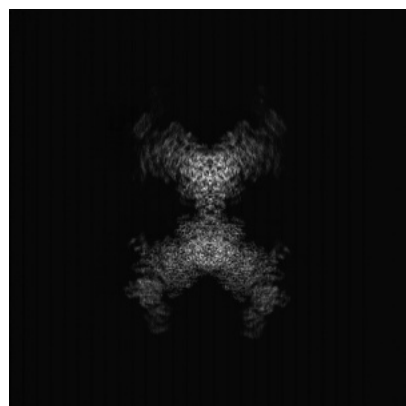
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36212. These allow visual inspection of the internal detail of the map and identification of artifacts.

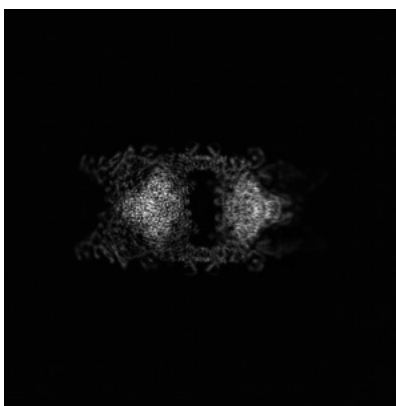
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

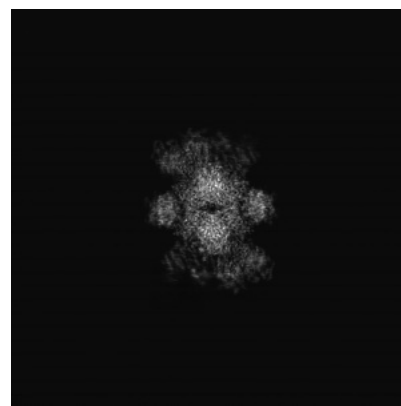
6.1.1 Primary map



X

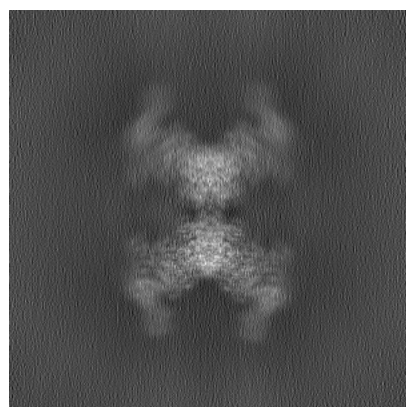


Y

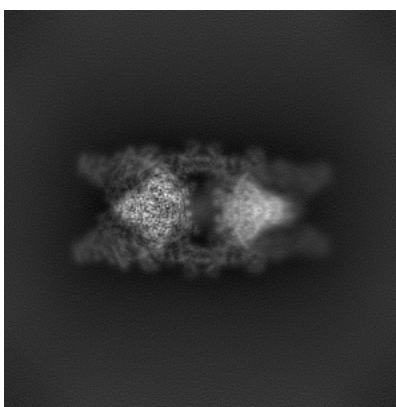


Z

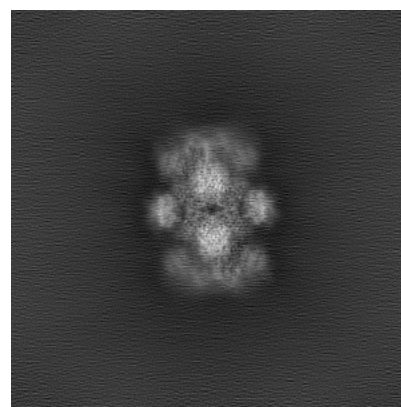
6.1.2 Raw map



X



Y



Z

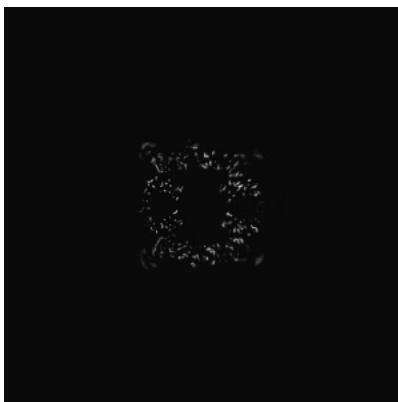
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

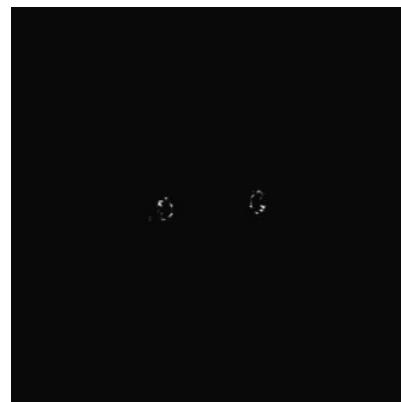
6.2.1 Primary map



X Index: 220

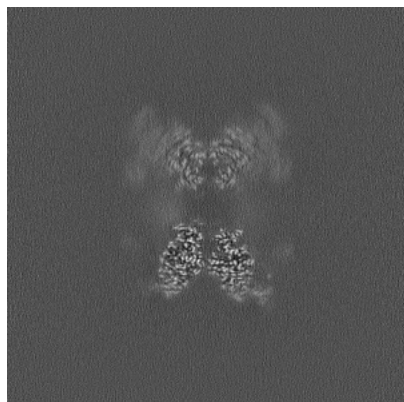


Y Index: 220

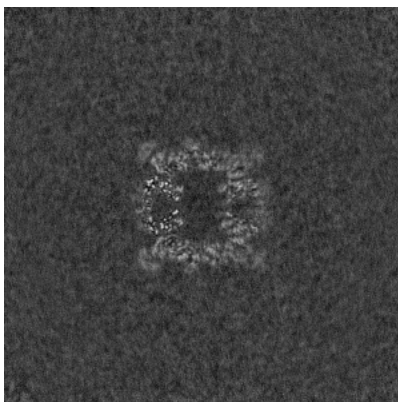


Z Index: 220

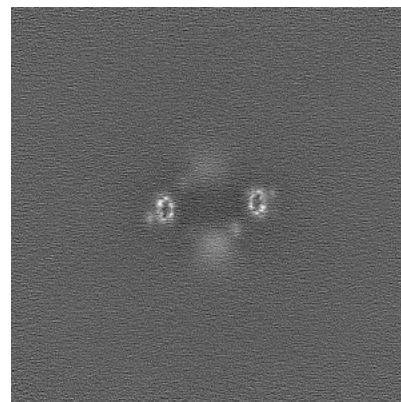
6.2.2 Raw map



X Index: 220



Y Index: 220

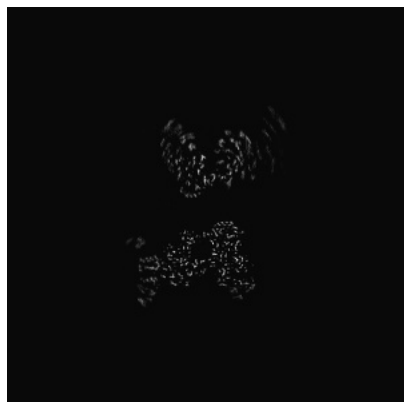


Z Index: 220

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: 228

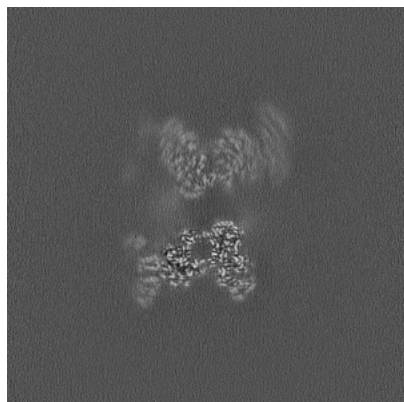


Y Index: 230

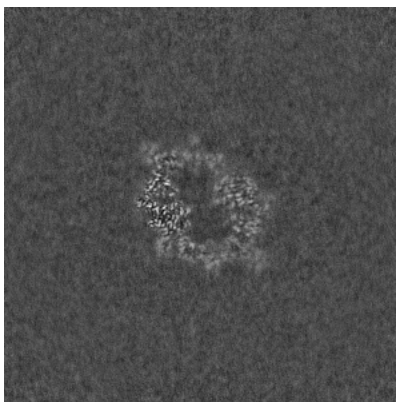


Z Index: 165

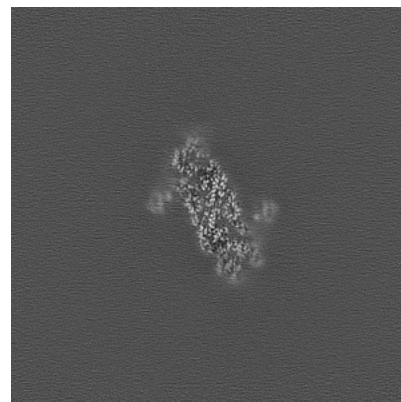
6.3.2 Raw map



X Index: 228



Y Index: 210

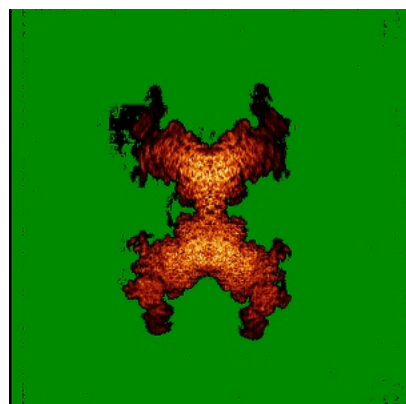


Z Index: 160

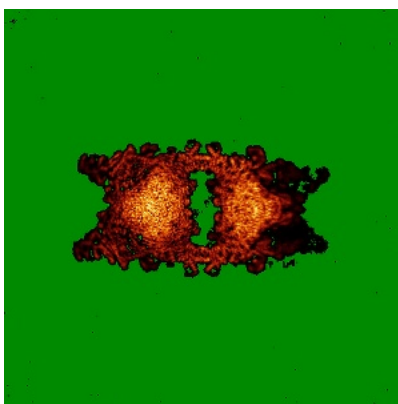
The images above show the largest variance slices of the map in three orthogonal directions.

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

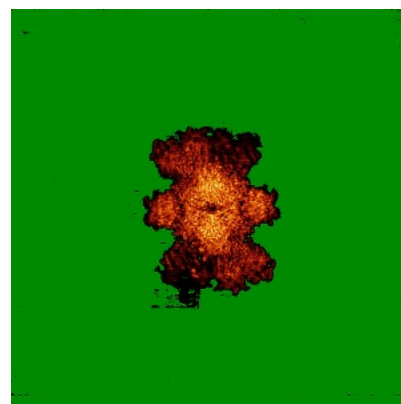
6.4.1 Primary map



X

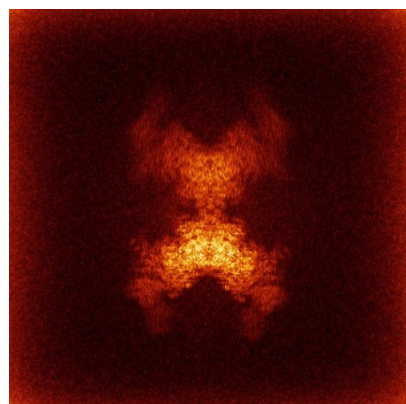


Y

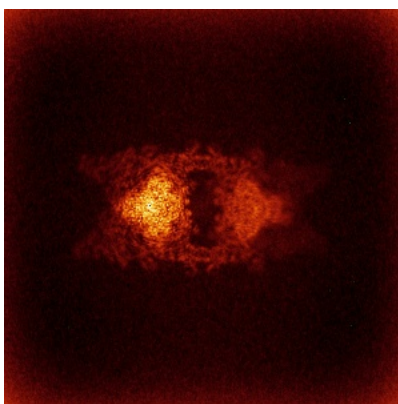


Z

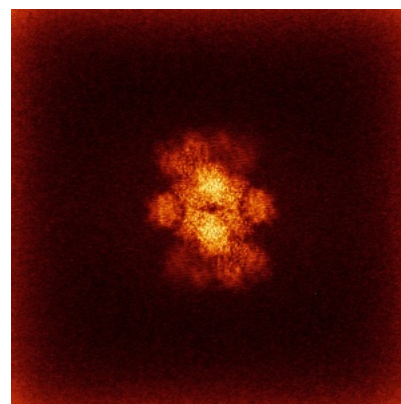
6.4.2 Raw map



X



Y

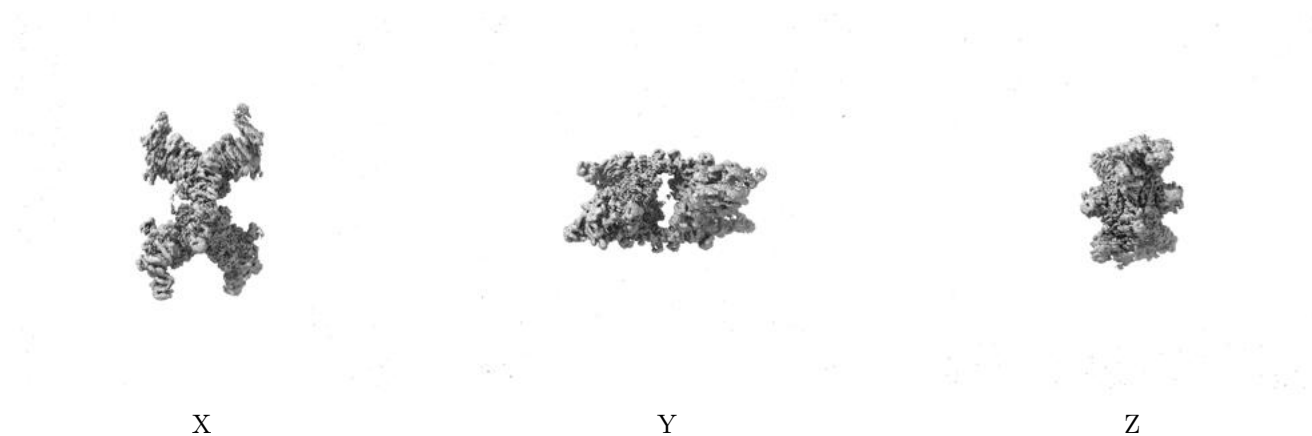


Z

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

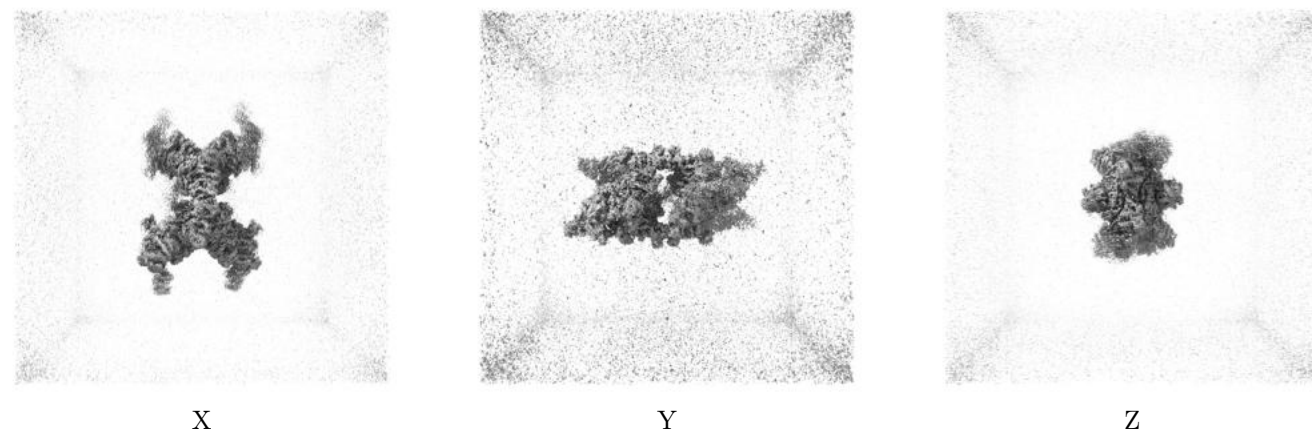
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

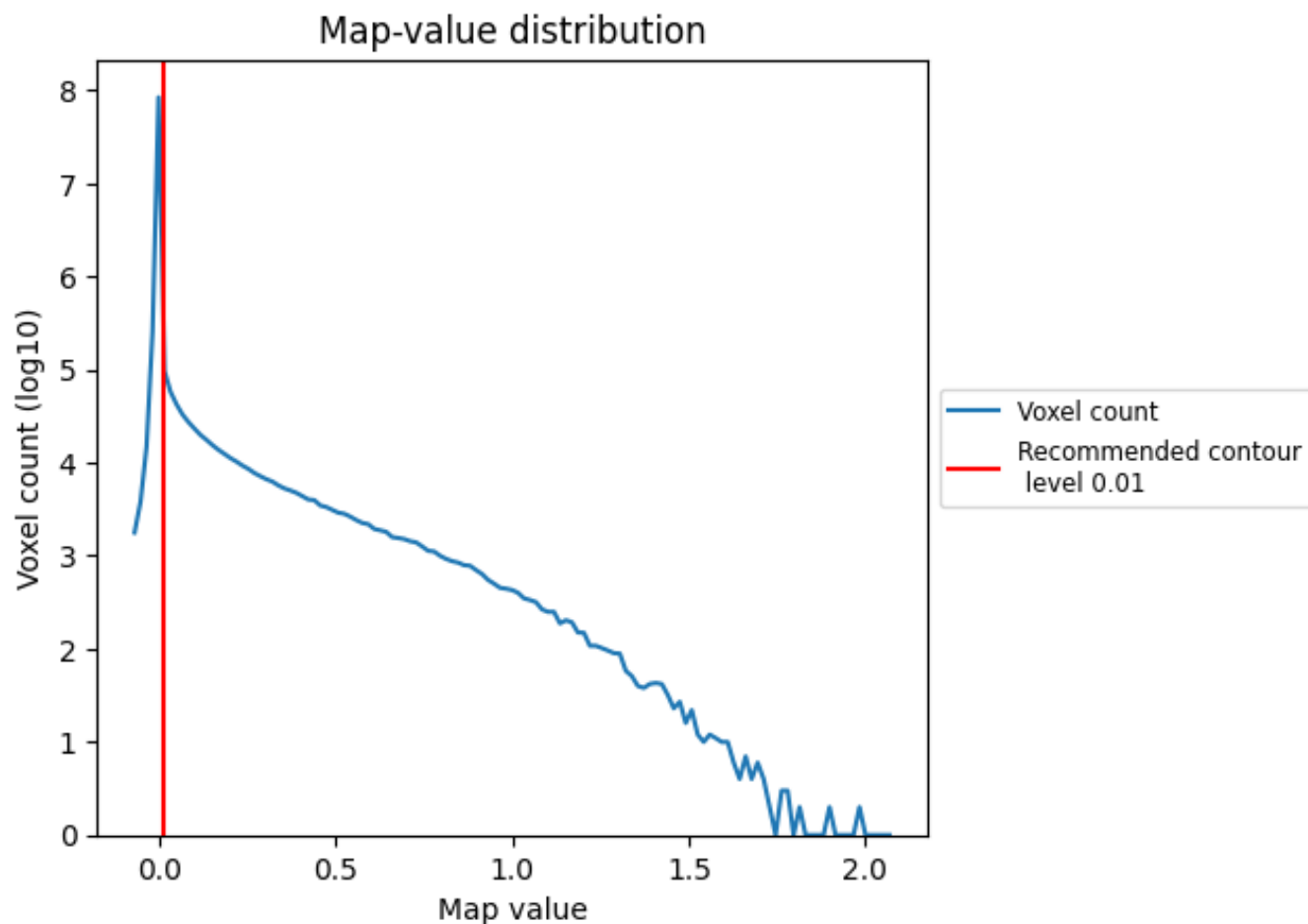
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

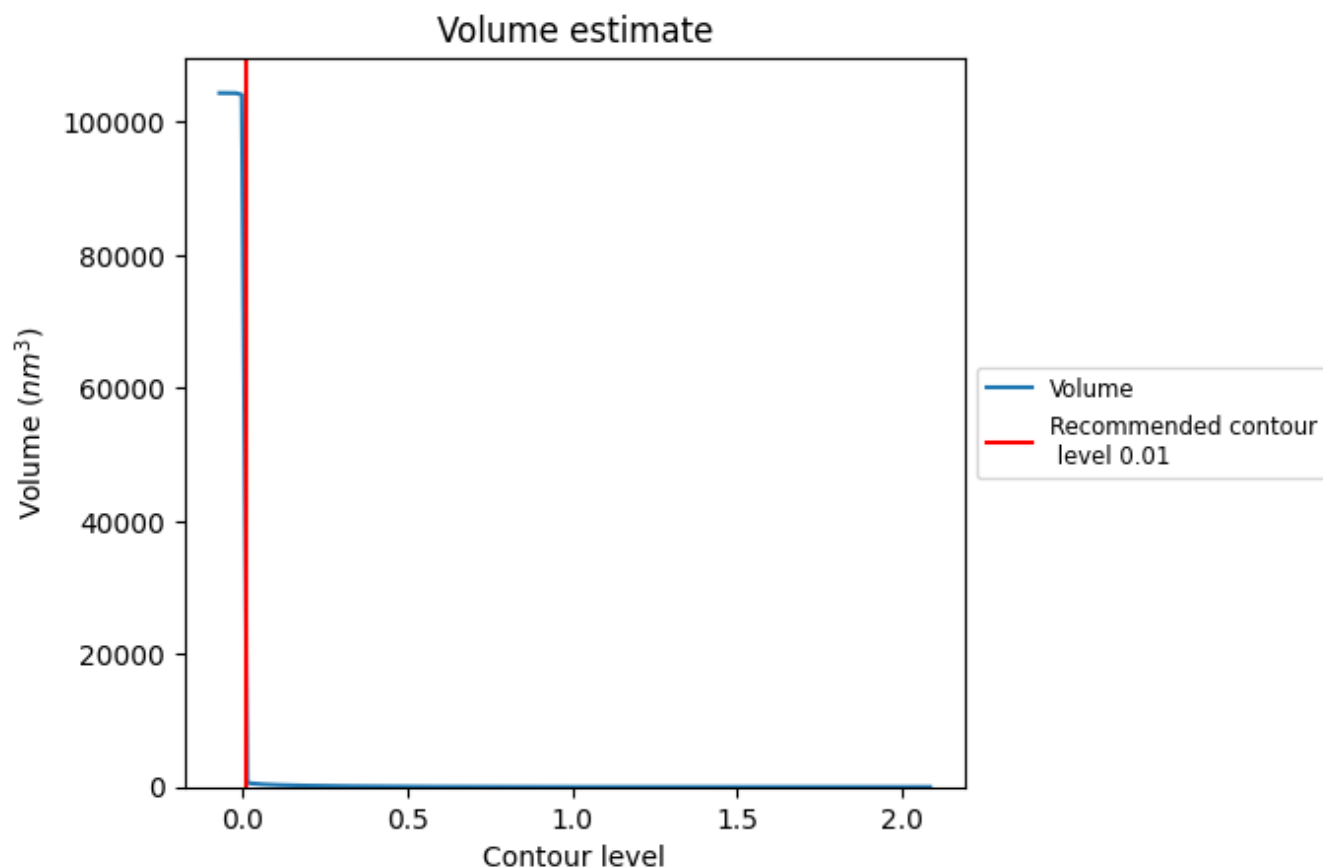
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

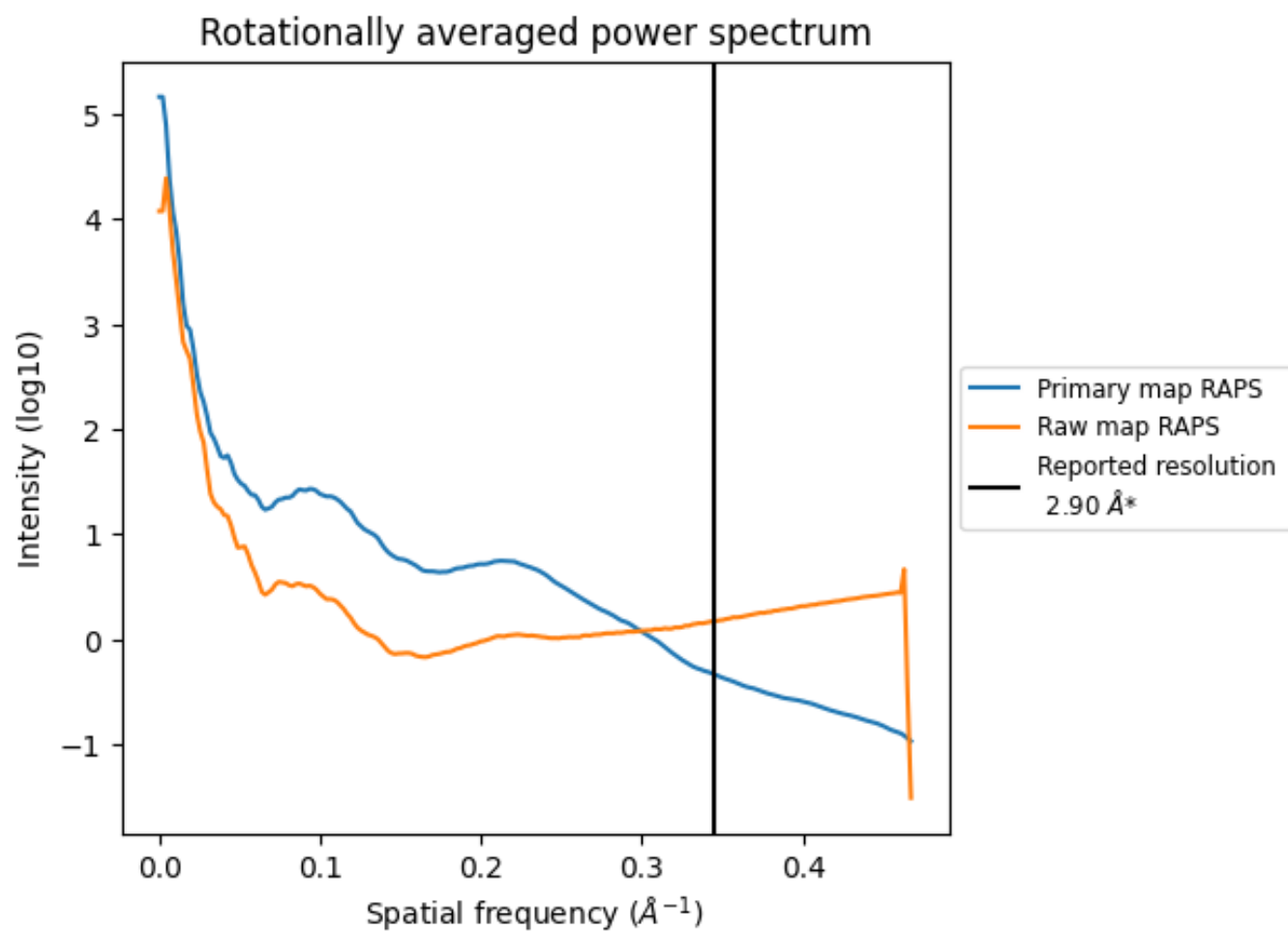
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 25680 nm^3 ; this corresponds to an approximate mass of 23197 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

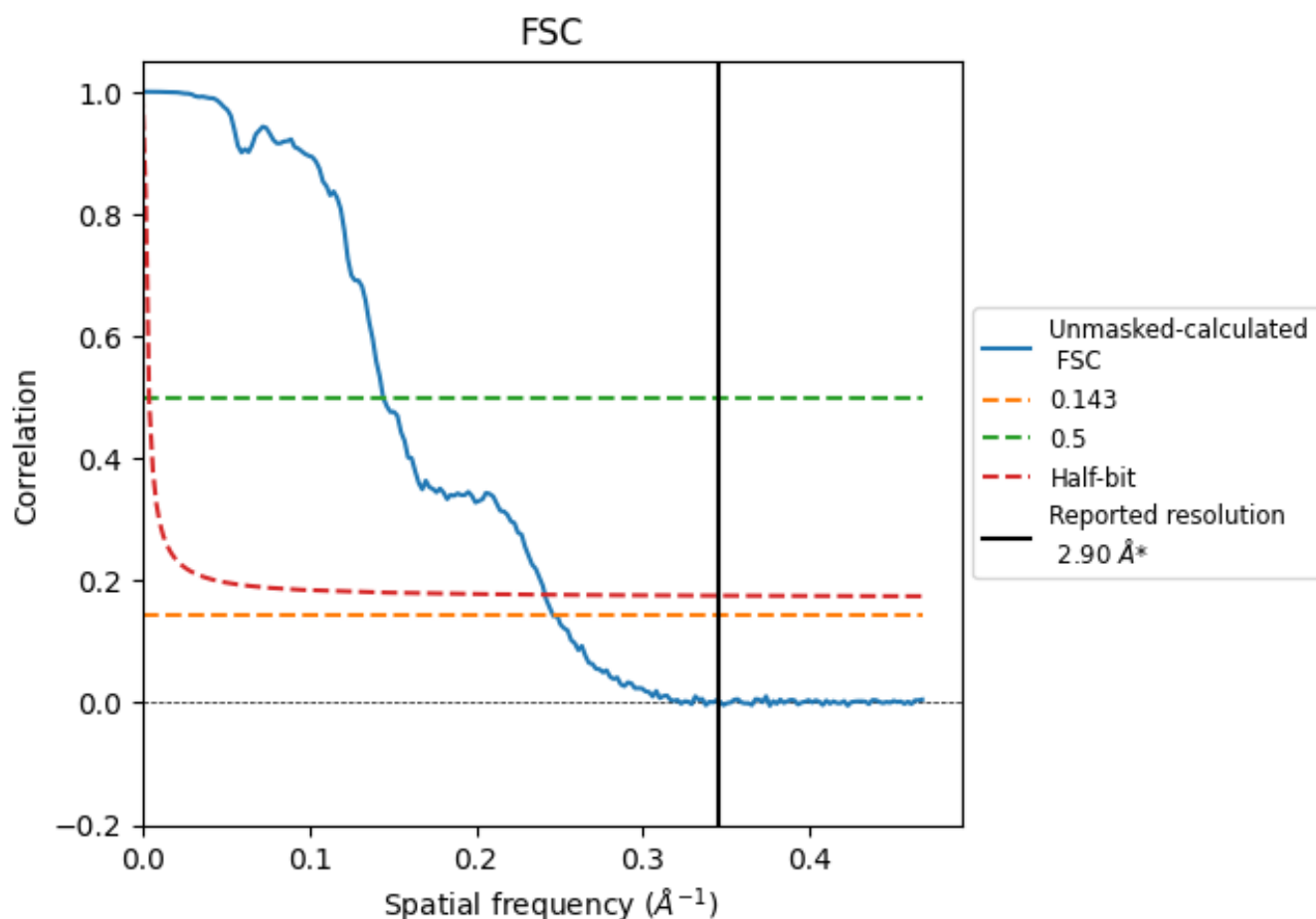


*Reported resolution corresponds to spatial frequency of $0.345 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.345 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

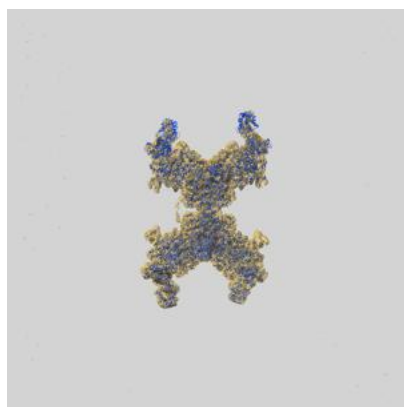
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.06	6.93	4.14

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.06 differs from the reported value 2.9 by more than 10 %

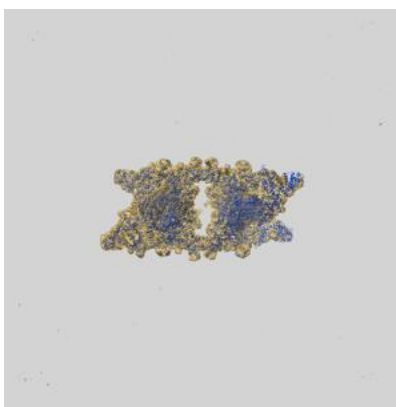
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-36212 and PDB model 8JFK. Per-residue inclusion information can be found in section [3](#) on page [7](#).

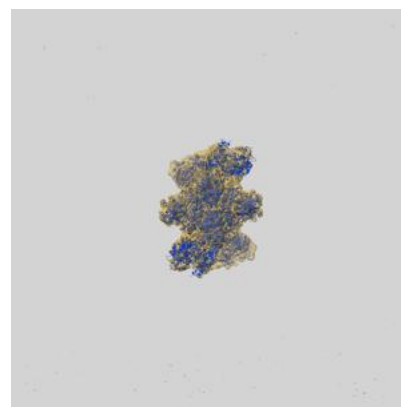
9.1 Map-model overlay [i](#)



X



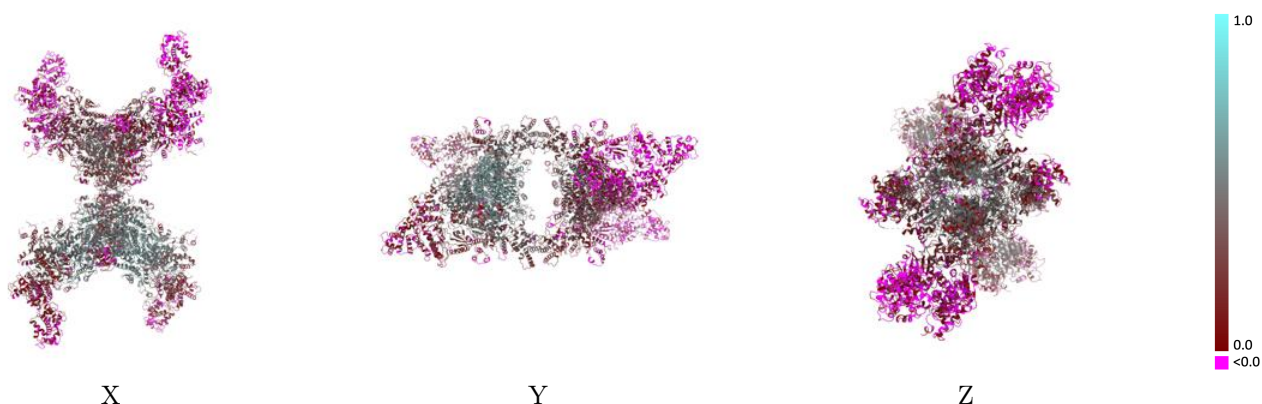
Y



Z

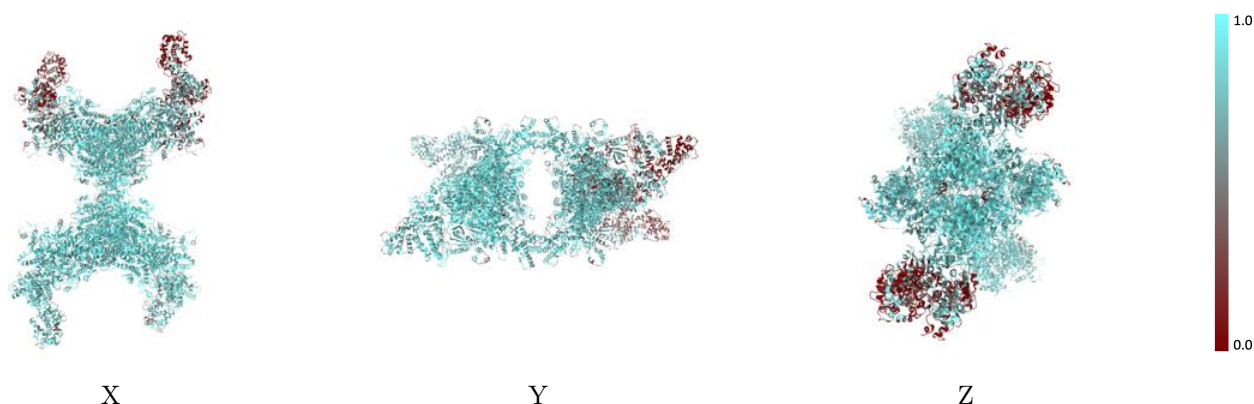
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



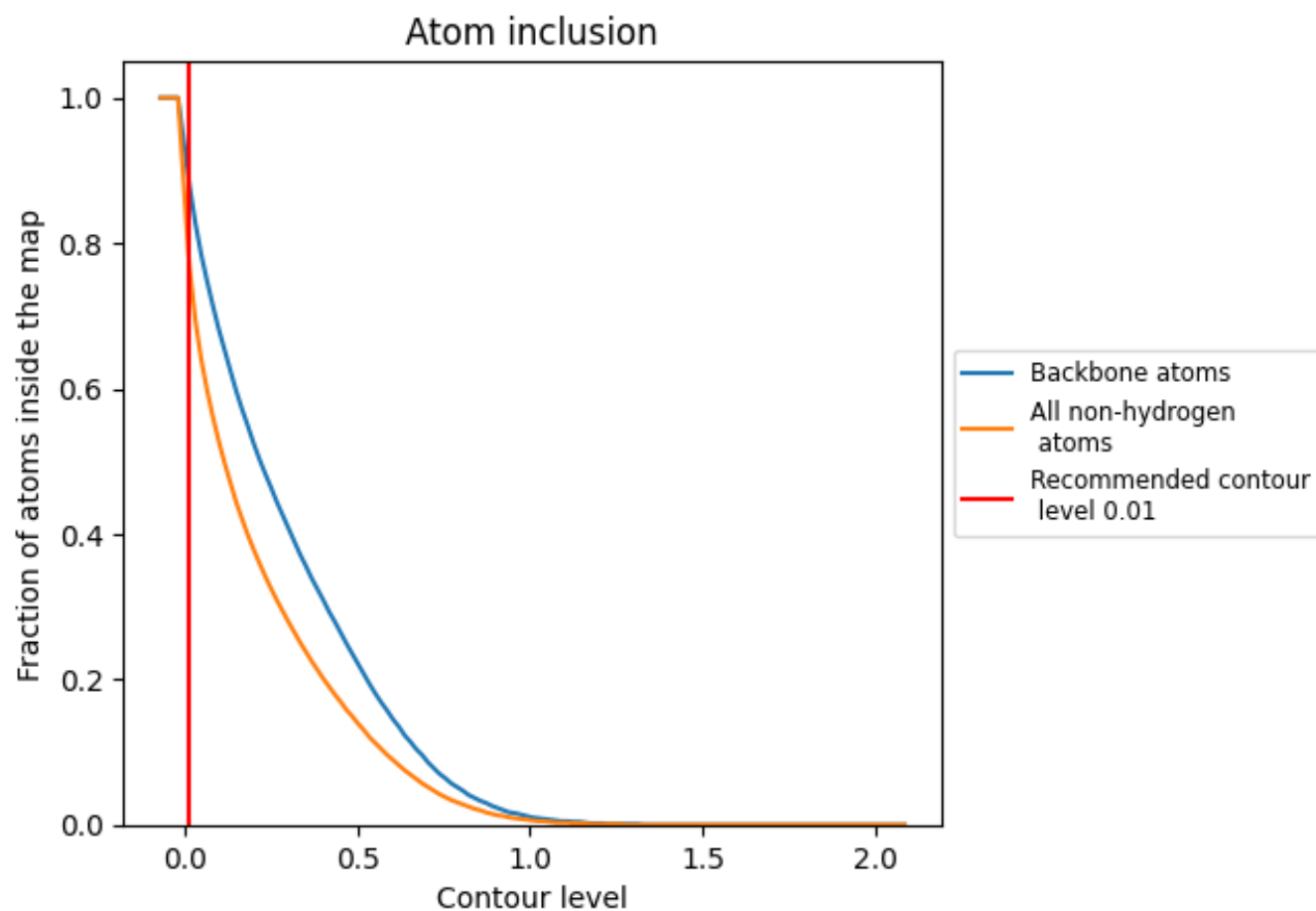
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7890	 0.2650
A	 0.7100	 0.1430
B	 0.8680	 0.2900
C	 0.4130	 0.0030
D	 0.1820	 -0.0250
E	 0.7120	 0.1180
F	 0.8360	 0.2560
G	 0.4740	 -0.0020
H	 0.2190	 -0.0270
I	 0.9150	 0.4190
J	 0.8930	 0.4170
K	 0.7900	 0.1690
L	 0.6790	 0.0570
M	 0.9180	 0.4300
N	 0.9120	 0.4490
O	 0.7910	 0.1810
P	 0.6640	 0.0510

