Full wwPDB EM Validation Report ⓘ

Jun 9, 2025 – 08:47 PM JST

PDB ID	:	7EY6 / pdb_00007ey6
EMDB ID	:	EMD-31321
Title	:	The portal protein (GP8) of bacteriophage T7
Authors	:	Liu, H.R.; Chen, W.Y.
Deposited on	:	2021-05-30
Resolution	:	4.30 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:

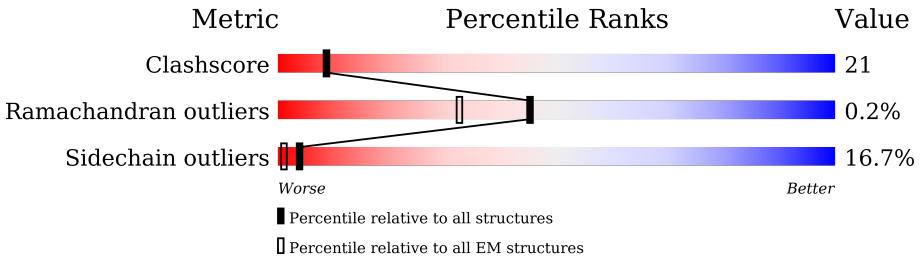
EMDB validation analysis	:	0.0.1.dev118
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	A	536	22% 48% 32% 7% • 12%
1	B	536	18% 48% 33% 7% • 12%
1	C	536	22% 48% 32% 6% • 12%
1	D	536	18% 48% 32% 7% • 12%
1	E	536	22% 48% 33% 6% • 12%
1	F	536	18% 48% 33% 6% • 12%
1	G	536	22% 47% 34% 6% • 12%
1	H	536	18% 47% 33% 6% • 12%

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Mol	Chain	Length	Quality of chain
1	I	536	22% 47% 34% 6% • 12%
1	J	536	18% 46% 35% 6% • 12%
1	K	536	22% 48% 33% 6% • 12%
1	L	536	18% 49% 32% 6% • 12%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 44028 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 Portal protein.

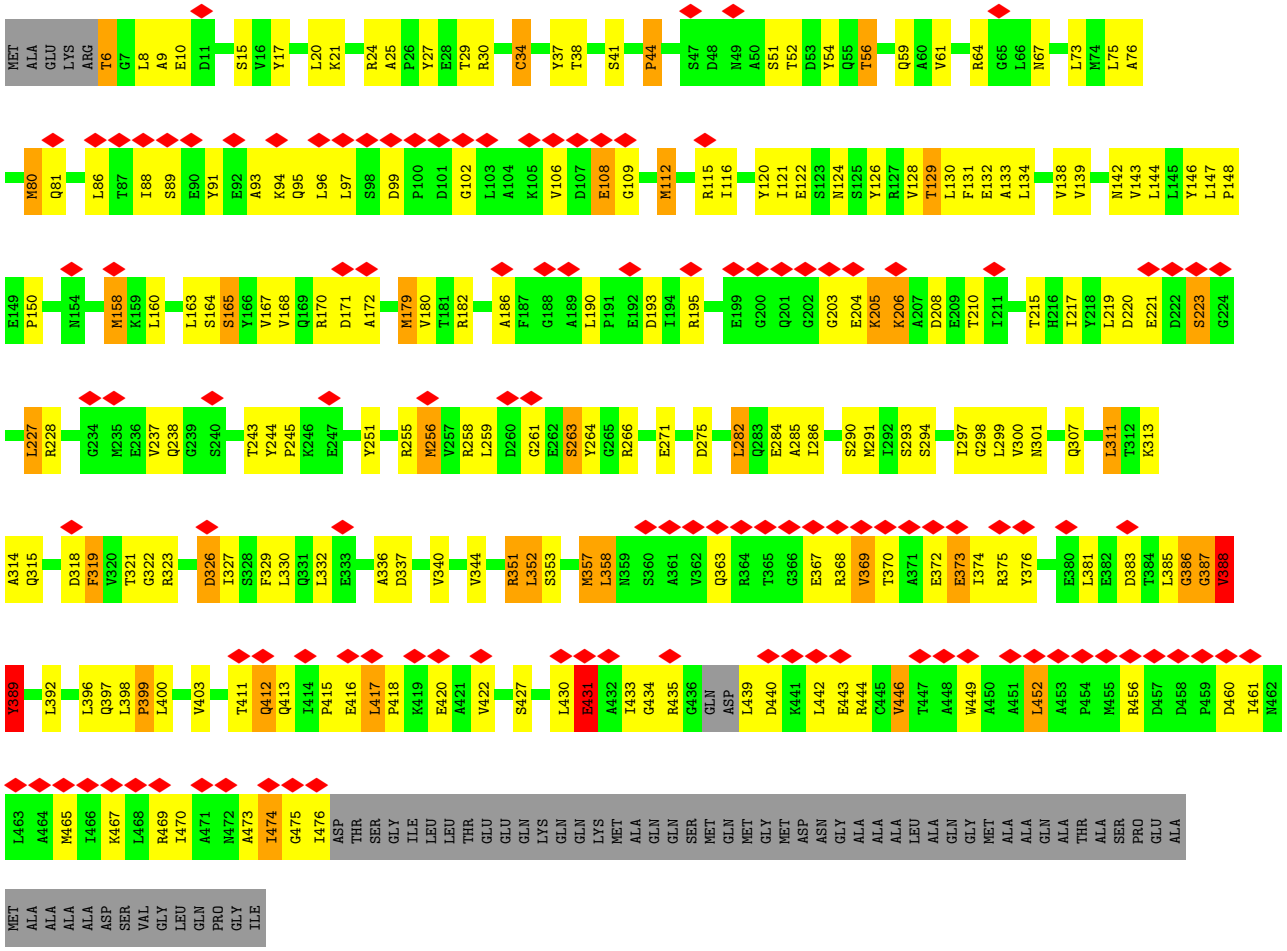
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	B	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	C	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	D	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	E	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	F	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	G	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	H	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	I	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	J	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	K	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		
1	L	469	Total	C	N	O	S	0	0
			3669	2313	619	720	17		

3 Residue-property plots (i)

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

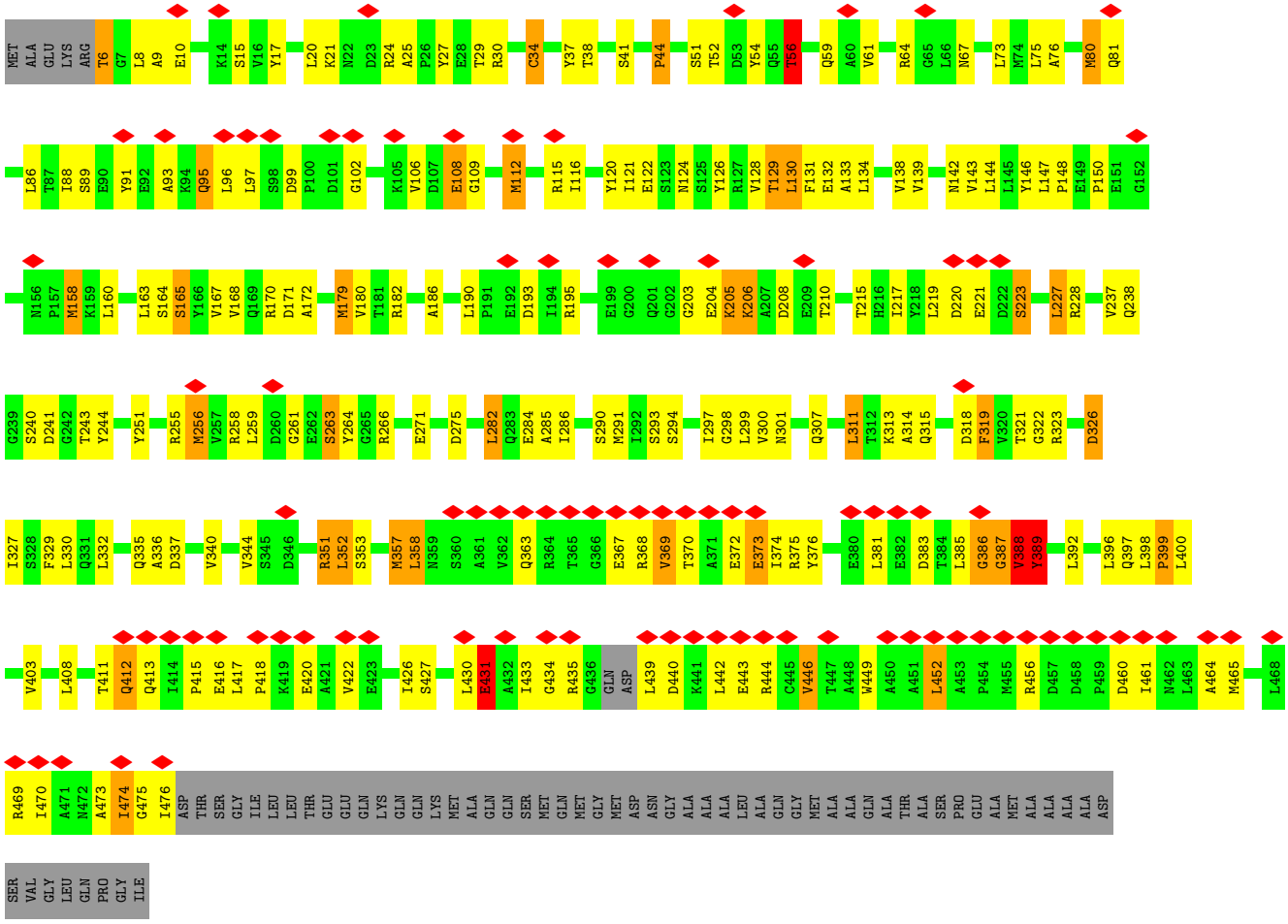
• Molecule 1: Portal protein

Chain A:



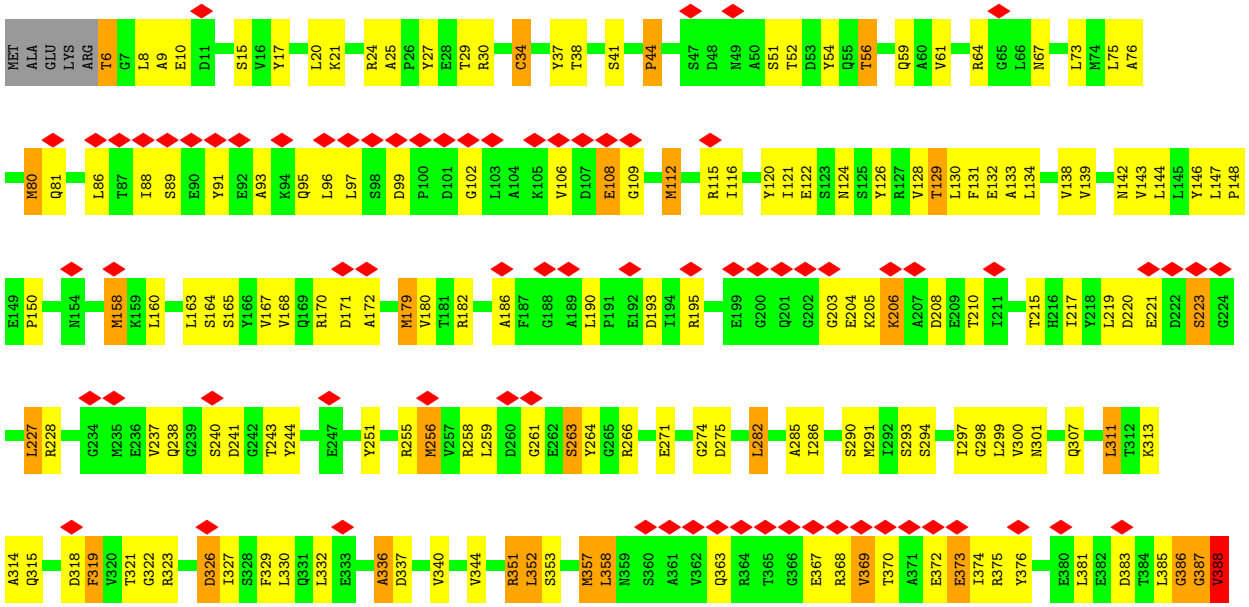
• Molecule 1: Portal protein

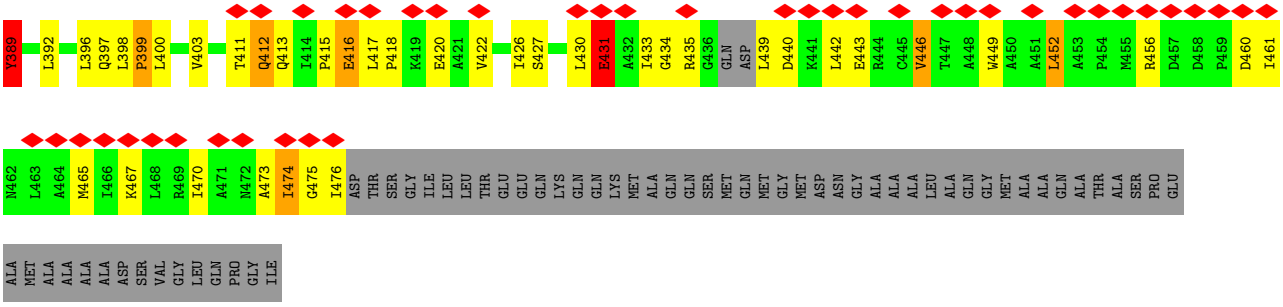
Chain B:



• Molecule 1: Portal protein

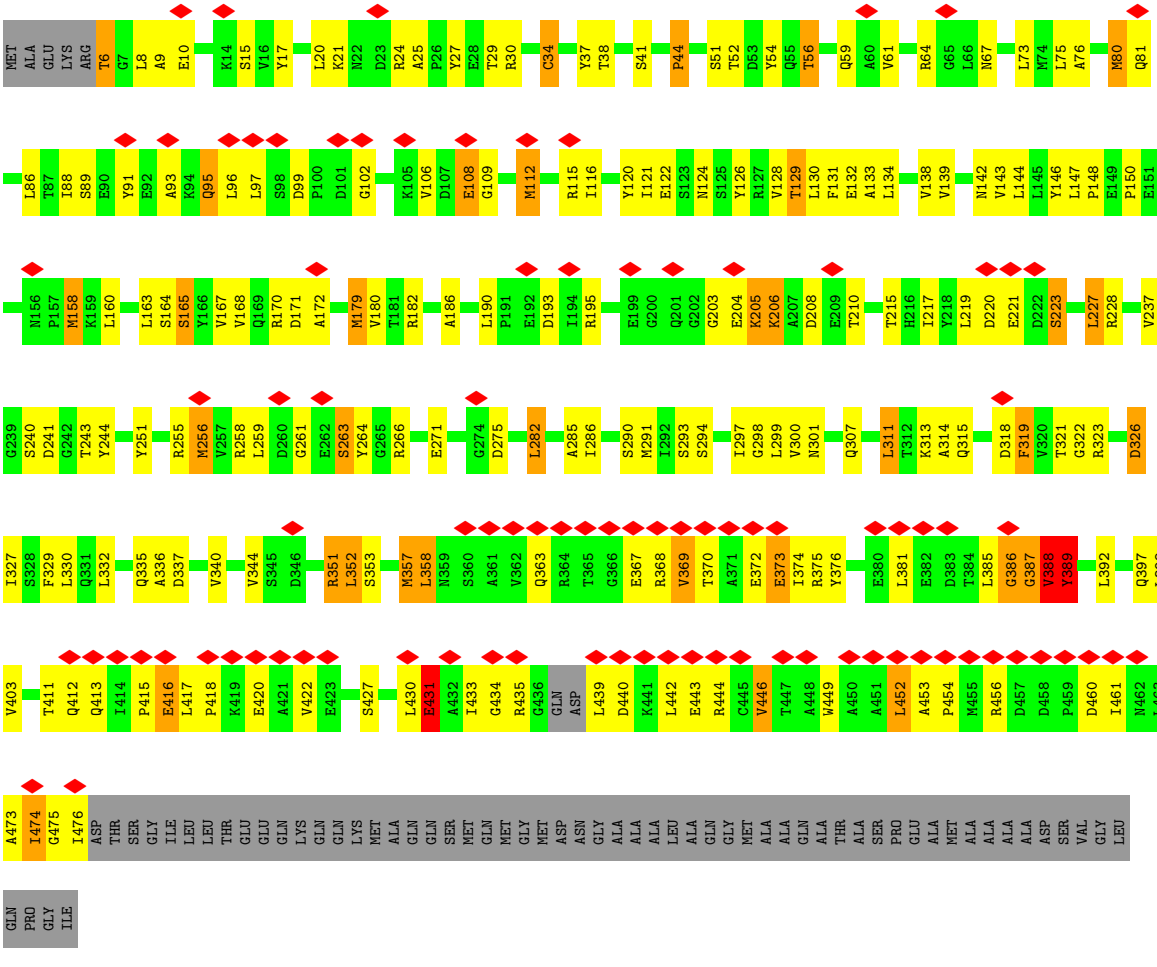
Chain C:





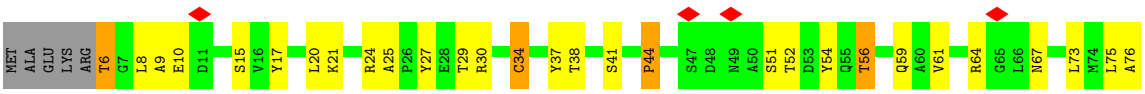
• Molecule 1: Portal protein

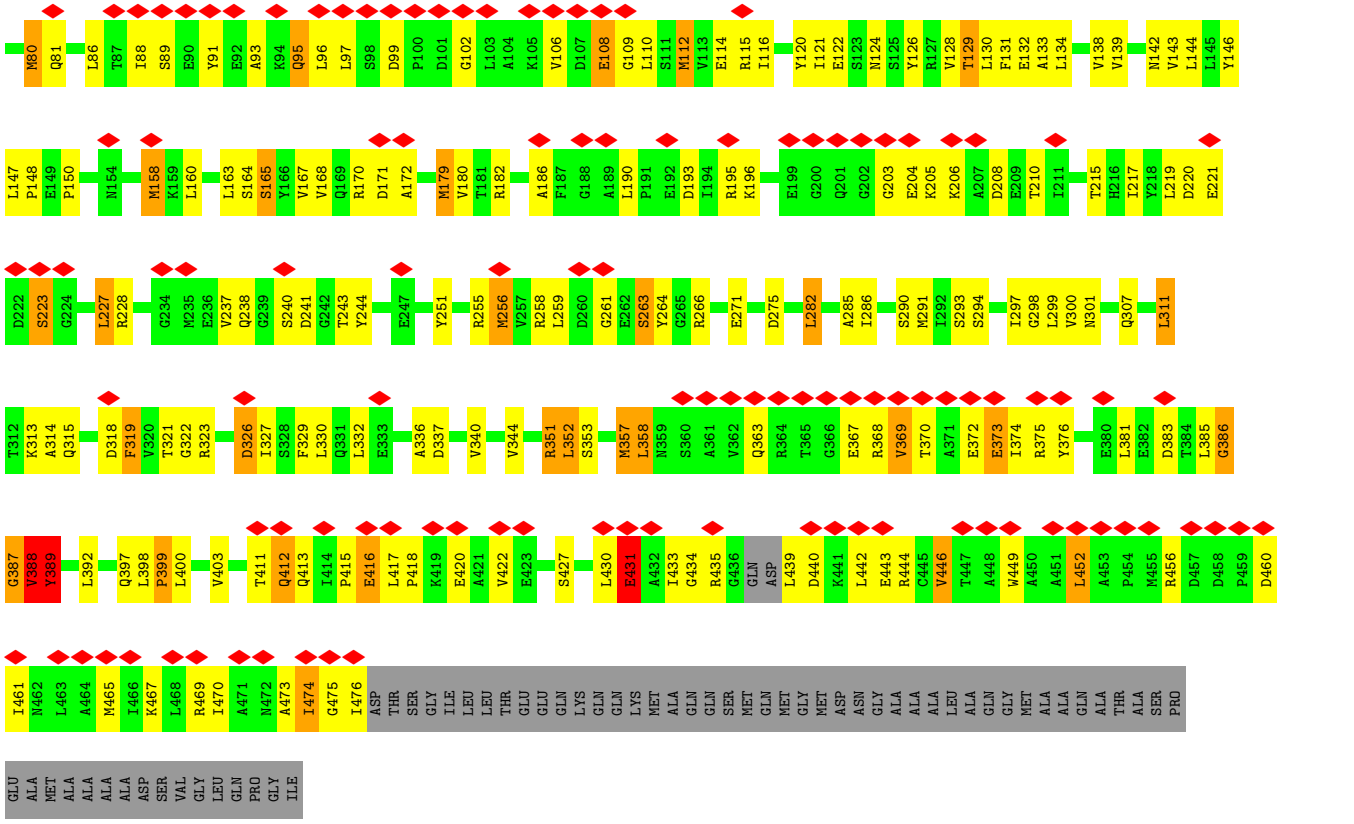
Chain D:



• Molecule 1: Portal protein

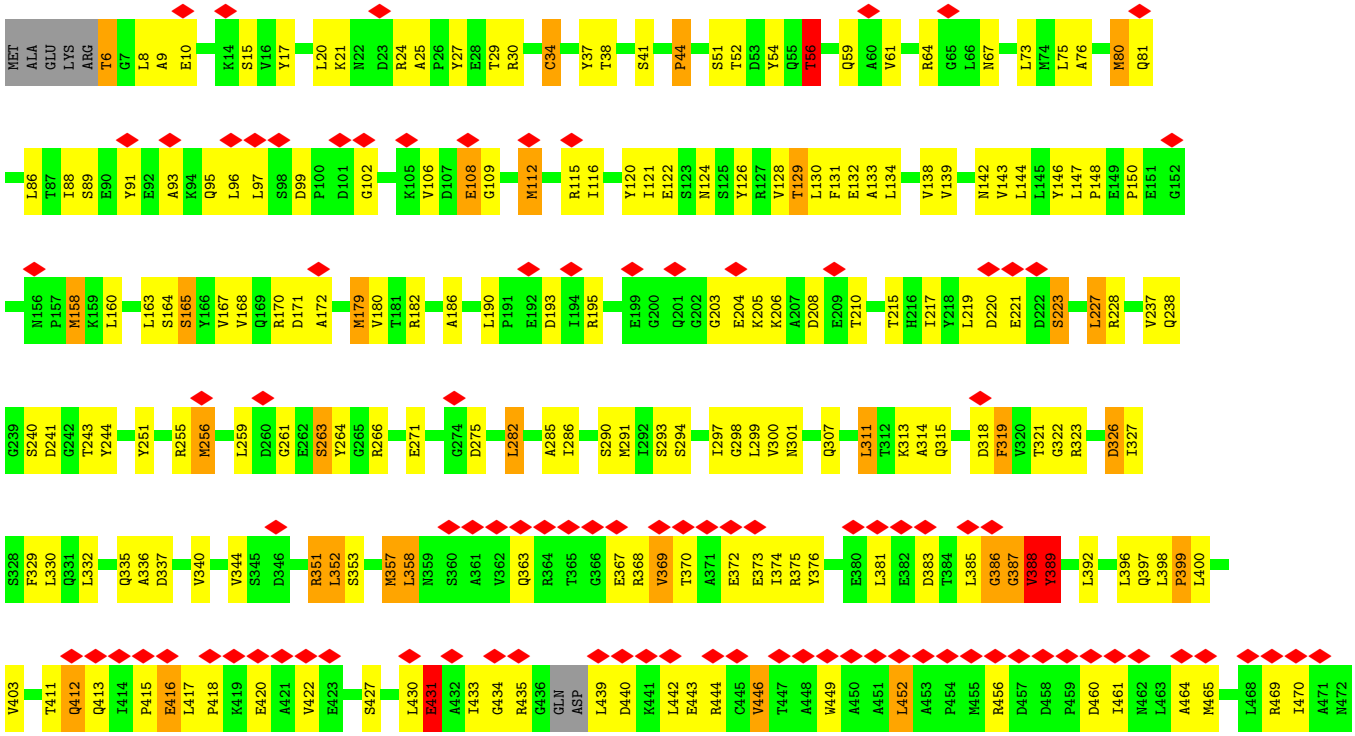
Chain E:

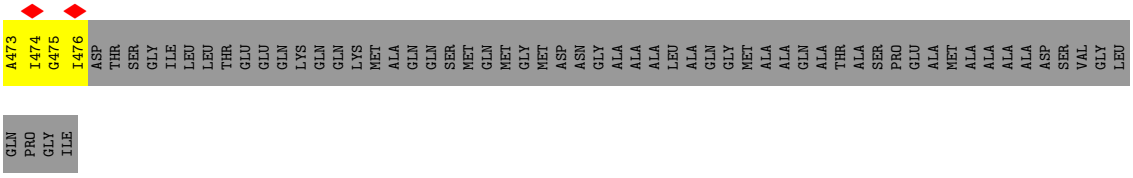




• Molecule 1: Portal protein

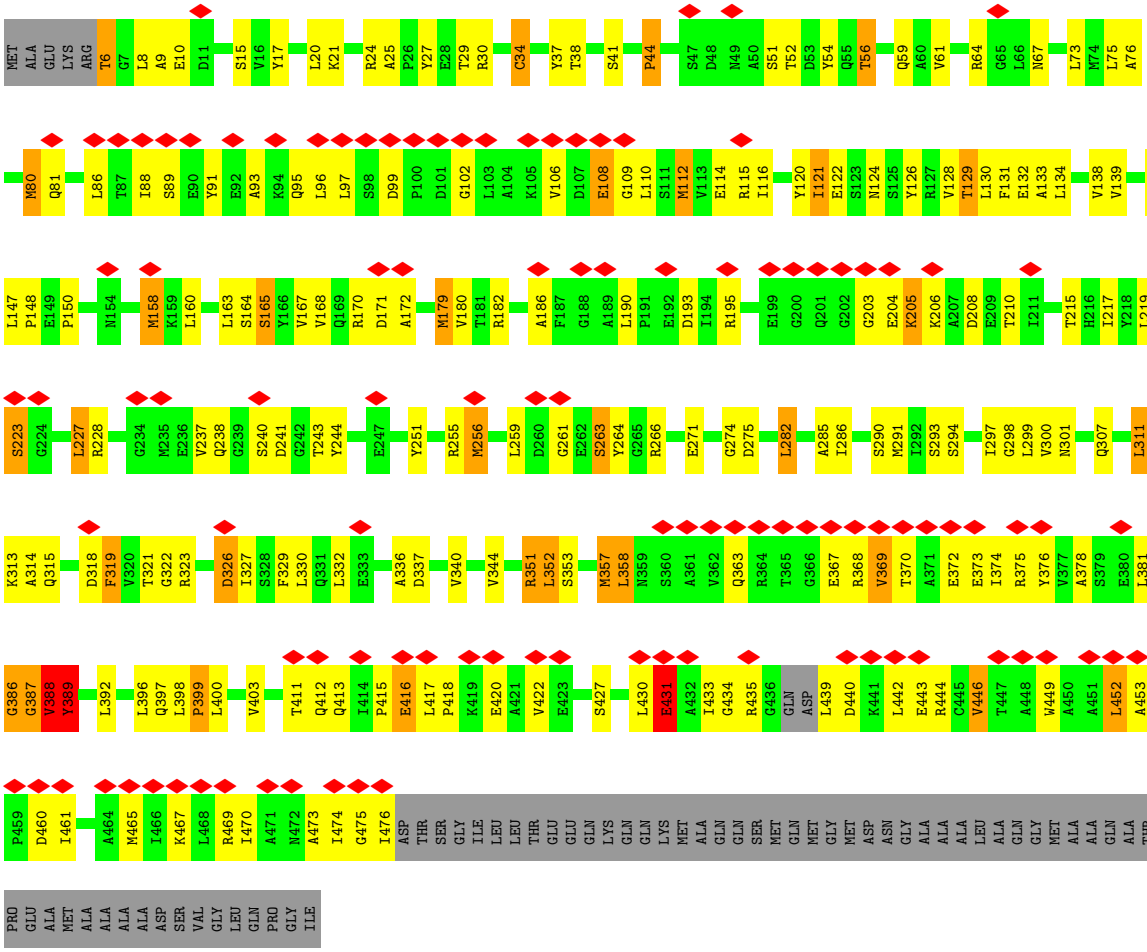
Chain F:





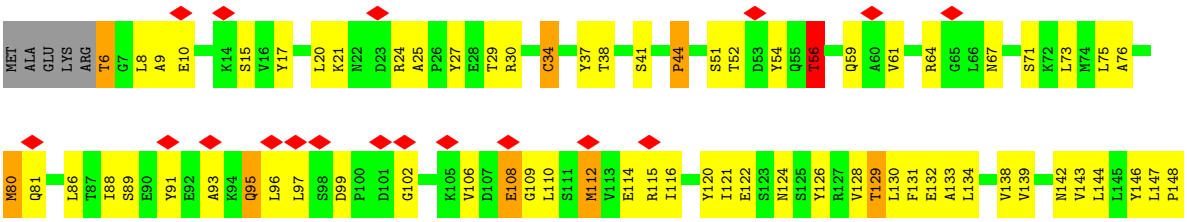
• Molecule 1: Portal protein

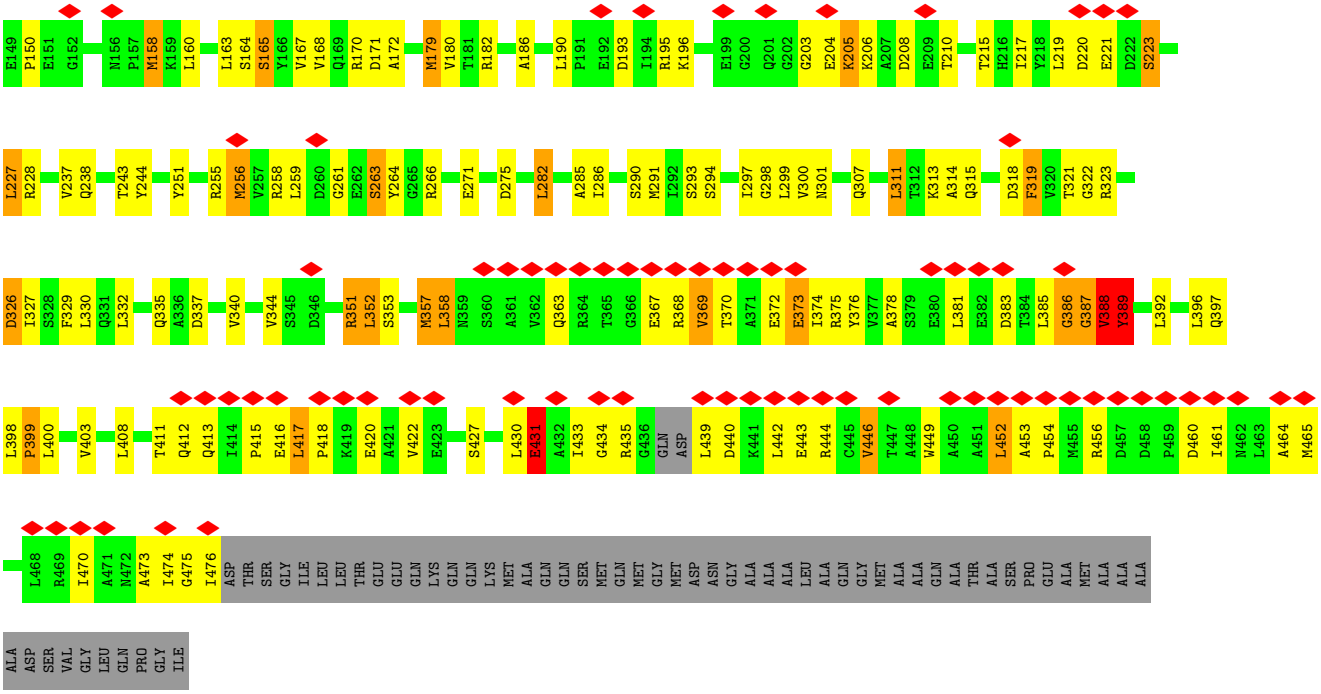
Chain G:



• Molecule 1: Portal protein

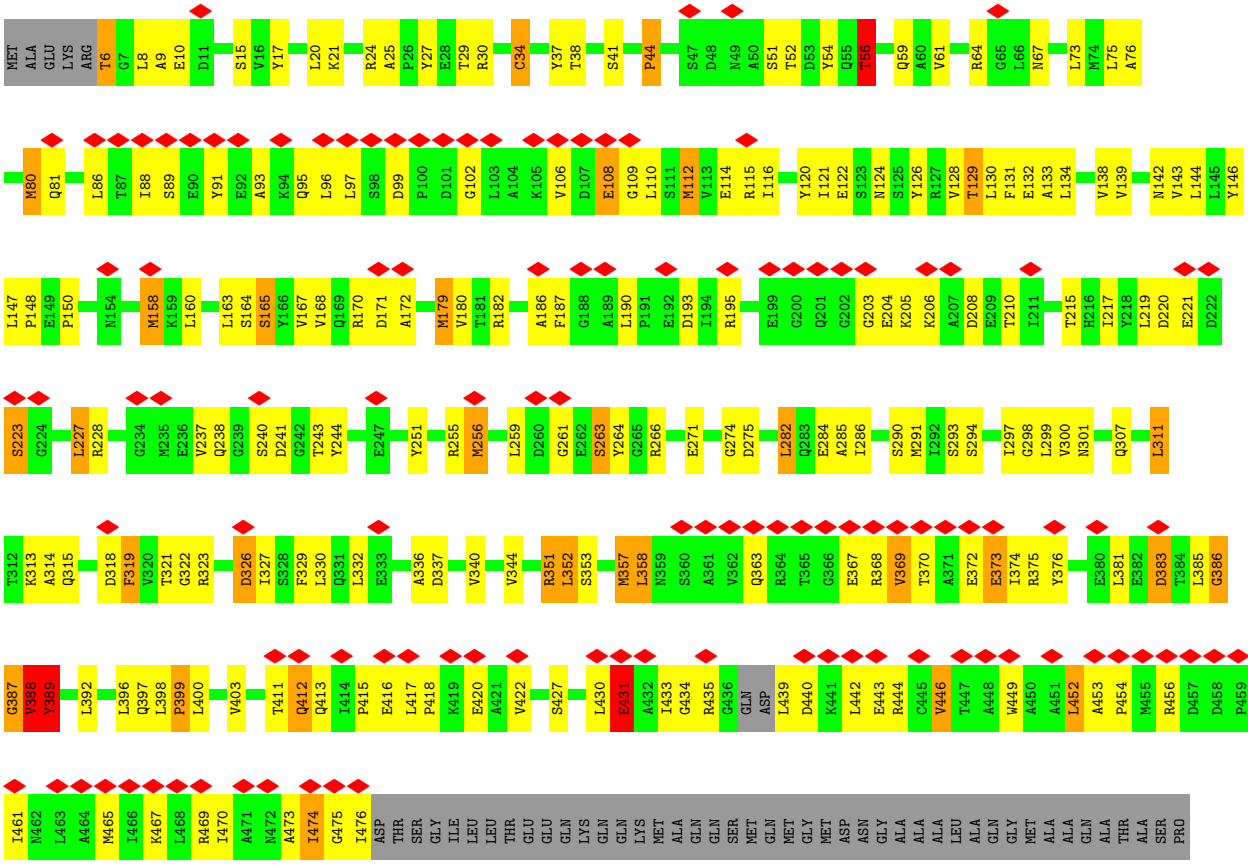
Chain H:





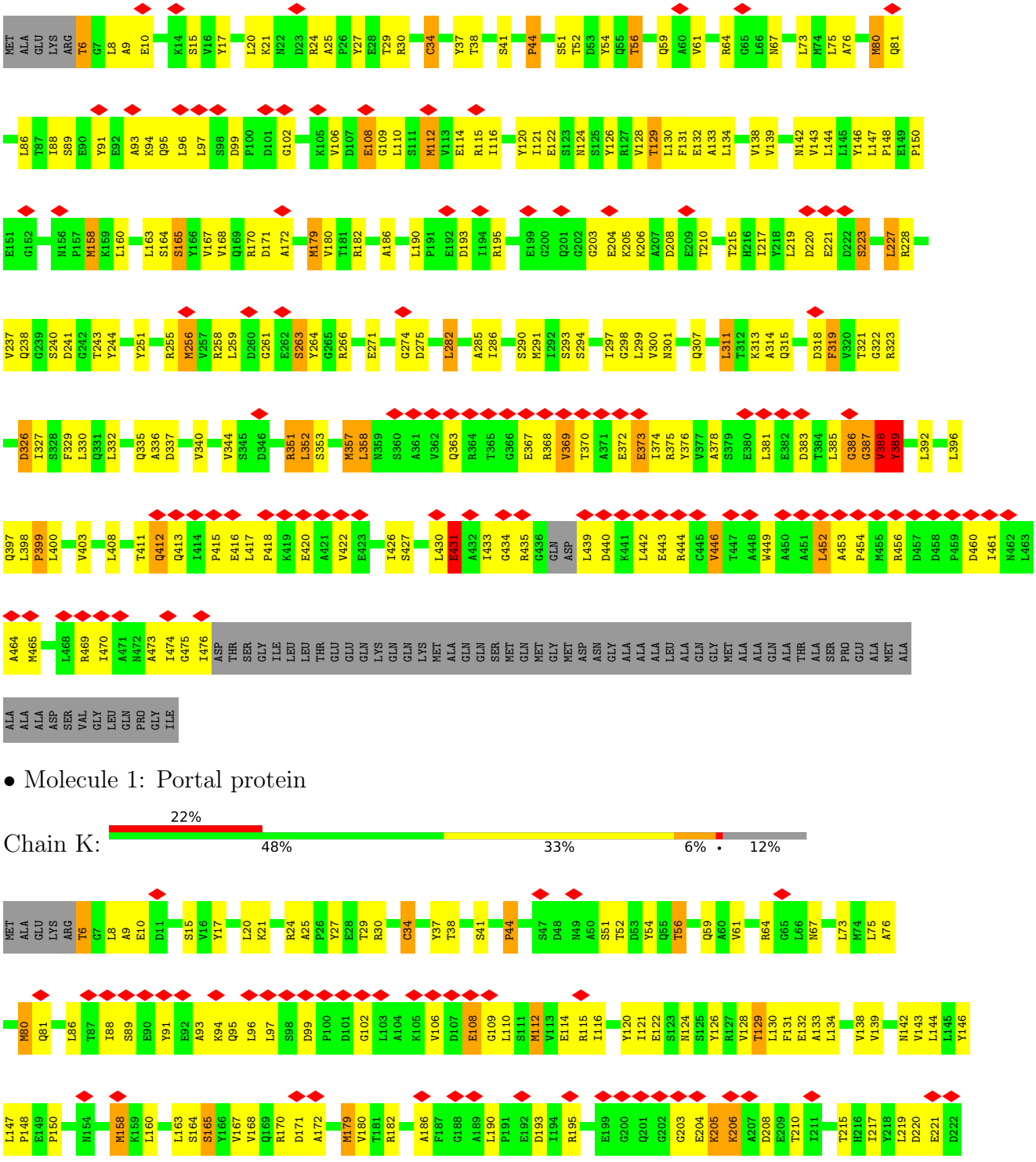
• Molecule 1: Portal protein

Chain I:



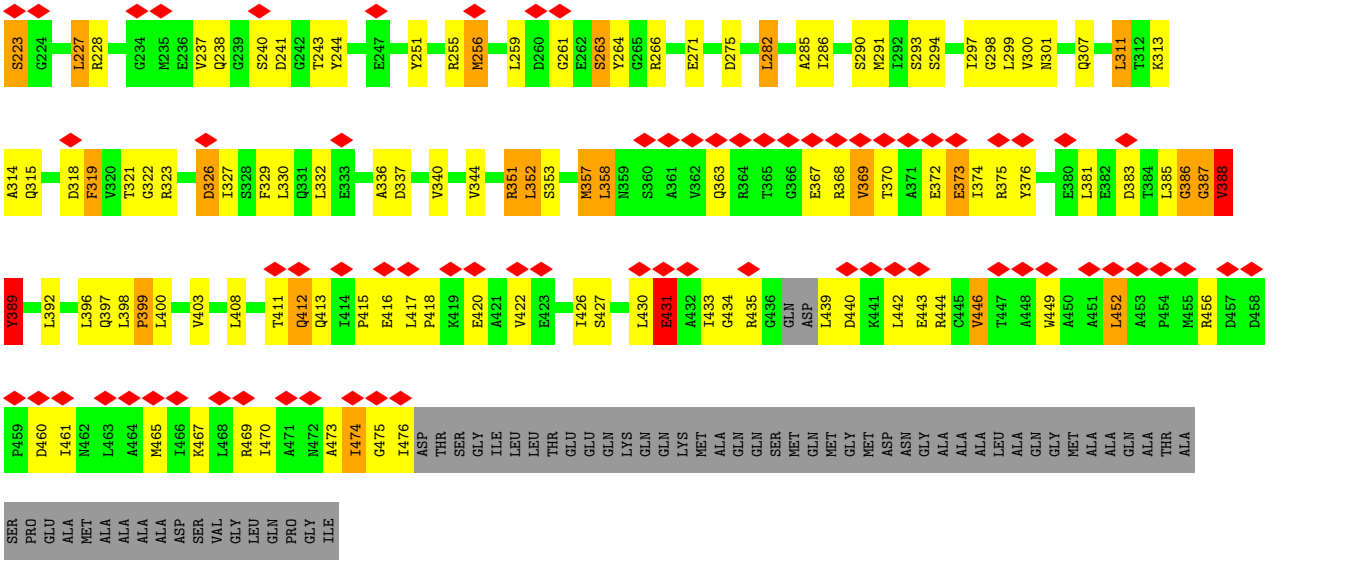
• Molecule 1: Portal protein

Chain J:



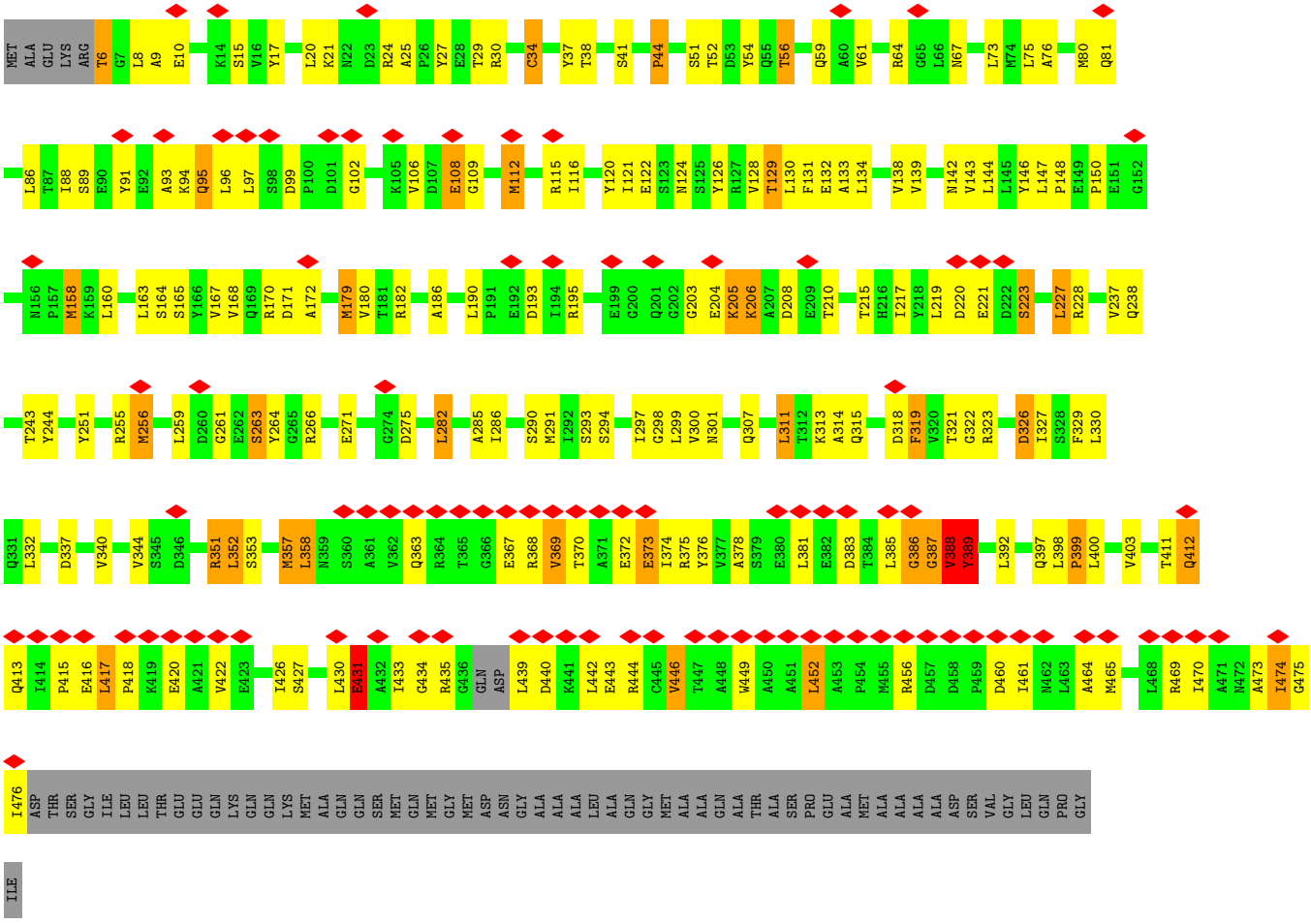
• Molecule 1: Portal protein

Chain K:



• Molecule 1: Portal protein

Chain L:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	59985	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	43.195	Depositor
Minimum map value	-27.980	Depositor
Average map value	0.013	Depositor
Map value standard deviation	2.048	Depositor
Recommended contour level	8	Depositor
Map size (Å)	508.0, 508.0, 508.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.27, 1.27, 1.27	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.69	0/3728	1.08	37/5049 (0.7%)
1	B	0.68	0/3728	1.08	37/5049 (0.7%)
1	C	0.68	0/3728	1.08	35/5049 (0.7%)
1	D	0.68	0/3728	1.08	35/5049 (0.7%)
1	E	0.68	0/3728	1.08	34/5049 (0.7%)
1	F	0.68	0/3728	1.08	35/5049 (0.7%)
1	G	0.68	0/3728	1.08	35/5049 (0.7%)
1	H	0.68	0/3728	1.08	35/5049 (0.7%)
1	I	0.68	0/3728	1.08	35/5049 (0.7%)
1	J	0.68	0/3728	1.08	35/5049 (0.7%)
1	K	0.68	0/3728	1.08	35/5049 (0.7%)
1	L	0.68	0/3728	1.08	34/5049 (0.7%)
All	All	0.68	0/44736	1.08	422/60588 (0.7%)

There are no bond length outliers.

All (422) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	208	ASP	N-CA-C	11.72	124.14	111.36
1	A	208	ASP	N-CA-C	11.72	124.13	111.36
1	B	208	ASP	N-CA-C	11.71	124.13	111.36
1	E	208	ASP	N-CA-C	11.69	124.11	111.36
1	J	208	ASP	N-CA-C	11.69	124.10	111.36
1	F	208	ASP	N-CA-C	11.68	124.09	111.36
1	K	208	ASP	N-CA-C	11.67	124.08	111.36
1	H	208	ASP	N-CA-C	11.66	124.07	111.36
1	L	208	ASP	N-CA-C	11.66	124.07	111.36
1	G	208	ASP	N-CA-C	11.66	124.07	111.36
1	C	208	ASP	N-CA-C	11.65	124.06	111.36
1	I	208	ASP	N-CA-C	11.63	124.04	111.36
1	I	386	GLY	N-CA-C	-9.64	97.45	110.56
1	F	386	GLY	N-CA-C	-9.63	97.47	110.56
1	G	386	GLY	N-CA-C	-9.62	97.48	110.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	386	GLY	N-CA-C	-9.61	97.49	110.56
1	B	386	GLY	N-CA-C	-9.61	97.49	110.56
1	J	386	GLY	N-CA-C	-9.61	97.49	110.56
1	L	386	GLY	N-CA-C	-9.60	97.50	110.56
1	K	386	GLY	N-CA-C	-9.60	97.51	110.56
1	D	386	GLY	N-CA-C	-9.58	97.53	110.56
1	E	386	GLY	N-CA-C	-9.58	97.53	110.56
1	A	386	GLY	N-CA-C	-9.58	97.53	110.56
1	C	386	GLY	N-CA-C	-9.57	97.54	110.56
1	C	9	ALA	N-CA-C	-9.43	101.00	111.28
1	A	9	ALA	N-CA-C	-9.42	101.01	111.28
1	F	9	ALA	N-CA-C	-9.41	101.02	111.28
1	L	9	ALA	N-CA-C	-9.41	101.03	111.28
1	E	9	ALA	N-CA-C	-9.39	101.04	111.28
1	K	9	ALA	N-CA-C	-9.39	101.04	111.28
1	I	9	ALA	N-CA-C	-9.39	101.04	111.28
1	G	9	ALA	N-CA-C	-9.38	101.05	111.28
1	J	9	ALA	N-CA-C	-9.38	101.05	111.28
1	D	9	ALA	N-CA-C	-9.38	101.06	111.28
1	H	9	ALA	N-CA-C	-9.37	101.06	111.28
1	B	9	ALA	N-CA-C	-9.37	101.07	111.28
1	K	465	MET	N-CA-C	8.28	120.38	111.36
1	E	465	MET	N-CA-C	8.27	120.37	111.36
1	A	465	MET	N-CA-C	8.26	120.37	111.36
1	B	465	MET	N-CA-C	8.26	120.36	111.36
1	D	465	MET	N-CA-C	8.26	120.36	111.36
1	H	465	MET	N-CA-C	8.26	120.36	111.36
1	I	465	MET	N-CA-C	8.26	120.36	111.36
1	F	465	MET	N-CA-C	8.24	120.35	111.36
1	L	465	MET	N-CA-C	8.24	120.34	111.36
1	J	465	MET	N-CA-C	8.24	120.34	111.36
1	C	465	MET	N-CA-C	8.23	120.34	111.36
1	G	465	MET	N-CA-C	8.21	120.30	111.36
1	B	91	TYR	N-CA-C	-8.13	100.09	113.50
1	F	91	TYR	N-CA-C	-8.12	100.10	113.50
1	D	91	TYR	N-CA-C	-8.12	100.10	113.50
1	K	91	TYR	N-CA-C	-8.12	100.11	113.50
1	L	91	TYR	N-CA-C	-8.12	100.11	113.50
1	J	91	TYR	N-CA-C	-8.11	100.11	113.50
1	A	91	TYR	N-CA-C	-8.11	100.11	113.50
1	G	91	TYR	N-CA-C	-8.11	100.12	113.50
1	H	91	TYR	N-CA-C	-8.11	100.12	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	91	TYR	N-CA-C	-8.11	100.12	113.50
1	C	91	TYR	N-CA-C	-8.10	100.13	113.50
1	E	91	TYR	N-CA-C	-8.10	100.14	113.50
1	C	315	GLN	N-CA-C	-7.81	100.45	110.53
1	K	315	GLN	N-CA-C	-7.81	100.46	110.53
1	D	315	GLN	N-CA-C	-7.79	100.49	110.53
1	E	315	GLN	N-CA-C	-7.79	100.49	110.53
1	G	315	GLN	N-CA-C	-7.79	100.49	110.53
1	A	315	GLN	N-CA-C	-7.78	100.50	110.53
1	F	315	GLN	N-CA-C	-7.78	100.50	110.53
1	L	315	GLN	N-CA-C	-7.78	100.50	110.53
1	I	315	GLN	N-CA-C	-7.77	100.50	110.53
1	H	315	GLN	N-CA-C	-7.77	100.51	110.53
1	B	315	GLN	N-CA-C	-7.77	100.51	110.53
1	J	315	GLN	N-CA-C	-7.77	100.51	110.53
1	K	10	GLU	CB-CA-C	-7.10	108.39	116.63
1	L	10	GLU	CB-CA-C	-7.10	108.40	116.63
1	G	10	GLU	CB-CA-C	-7.09	108.41	116.63
1	J	387	GLY	N-CA-C	-7.08	104.12	115.66
1	C	10	GLU	CB-CA-C	-7.08	108.42	116.63
1	F	10	GLU	CB-CA-C	-7.07	108.42	116.63
1	H	10	GLU	CB-CA-C	-7.07	108.43	116.63
1	J	10	GLU	CB-CA-C	-7.07	108.43	116.63
1	A	10	GLU	CB-CA-C	-7.06	108.44	116.63
1	I	10	GLU	CB-CA-C	-7.06	108.44	116.63
1	L	387	GLY	N-CA-C	-7.06	104.15	115.66
1	E	10	GLU	CB-CA-C	-7.05	108.45	116.63
1	K	387	GLY	N-CA-C	-7.05	104.17	115.66
1	I	387	GLY	N-CA-C	-7.05	104.17	115.66
1	B	10	GLU	CB-CA-C	-7.05	108.46	116.63
1	D	10	GLU	CB-CA-C	-7.04	108.46	116.63
1	D	387	GLY	N-CA-C	-7.04	104.18	115.66
1	A	112	MET	N-CA-C	-6.89	103.70	111.07
1	C	112	MET	N-CA-C	-6.89	103.70	111.07
1	F	112	MET	N-CA-C	-6.89	103.70	111.07
1	B	112	MET	N-CA-C	-6.87	103.72	111.07
1	H	112	MET	N-CA-C	-6.87	103.72	111.07
1	I	112	MET	N-CA-C	-6.87	103.72	111.07
1	E	112	MET	N-CA-C	-6.87	103.72	111.07
1	K	112	MET	N-CA-C	-6.87	103.72	111.07
1	D	112	MET	N-CA-C	-6.86	103.73	111.07
1	G	112	MET	N-CA-C	-6.86	103.73	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	J	112	MET	N-CA-C	-6.86	103.73	111.07
1	L	112	MET	N-CA-C	-6.83	103.76	111.07
1	J	99	ASP	CA-C-N	-6.74	112.84	119.64
1	J	99	ASP	C-N-CA	-6.74	112.84	119.64
1	G	99	ASP	CA-C-N	-6.73	112.84	119.64
1	G	99	ASP	C-N-CA	-6.73	112.84	119.64
1	I	99	ASP	CA-C-N	-6.72	112.85	119.64
1	I	99	ASP	C-N-CA	-6.72	112.85	119.64
1	B	99	ASP	CA-C-N	-6.71	112.86	119.64
1	B	99	ASP	C-N-CA	-6.71	112.86	119.64
1	E	99	ASP	CA-C-N	-6.71	112.86	119.64
1	E	99	ASP	C-N-CA	-6.71	112.86	119.64
1	G	387	GLY	N-CA-C	-6.71	104.13	115.34
1	E	387	GLY	N-CA-C	-6.71	104.14	115.34
1	C	387	GLY	N-CA-C	-6.71	104.14	115.34
1	K	99	ASP	CA-C-N	-6.71	112.87	119.64
1	K	99	ASP	C-N-CA	-6.71	112.87	119.64
1	H	387	GLY	N-CA-C	-6.70	104.14	115.34
1	H	99	ASP	CA-C-N	-6.70	112.87	119.64
1	H	99	ASP	C-N-CA	-6.70	112.87	119.64
1	F	99	ASP	CA-C-N	-6.69	112.89	119.64
1	F	99	ASP	C-N-CA	-6.69	112.89	119.64
1	F	387	GLY	N-CA-C	-6.69	104.17	115.34
1	A	387	GLY	N-CA-C	-6.68	104.18	115.34
1	L	99	ASP	CA-C-N	-6.68	112.89	119.64
1	L	99	ASP	C-N-CA	-6.68	112.89	119.64
1	C	99	ASP	CA-C-N	-6.67	112.90	119.64
1	C	99	ASP	C-N-CA	-6.67	112.90	119.64
1	A	99	ASP	CA-C-N	-6.67	112.90	119.64
1	A	99	ASP	C-N-CA	-6.67	112.90	119.64
1	B	387	GLY	N-CA-C	-6.67	104.20	115.34
1	D	99	ASP	CA-C-N	-6.66	112.91	119.64
1	D	99	ASP	C-N-CA	-6.66	112.91	119.64
1	G	204	GLU	N-CA-C	-6.66	100.17	110.10
1	E	204	GLU	N-CA-C	-6.65	100.19	110.10
1	B	204	GLU	N-CA-C	-6.64	100.20	110.10
1	D	204	GLU	N-CA-C	-6.64	100.21	110.10
1	F	204	GLU	N-CA-C	-6.63	100.21	110.10
1	K	204	GLU	N-CA-C	-6.63	100.22	110.10
1	H	204	GLU	N-CA-C	-6.62	100.23	110.10
1	C	204	GLU	N-CA-C	-6.62	100.24	110.10
1	I	204	GLU	N-CA-C	-6.62	100.24	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	J	204	GLU	N-CA-C	-6.62	100.24	110.10
1	L	204	GLU	N-CA-C	-6.62	100.24	110.10
1	A	204	GLU	N-CA-C	-6.61	100.25	110.10
1	H	358	LEU	N-CA-C	-6.59	98.23	109.24
1	B	358	LEU	N-CA-C	-6.58	98.25	109.24
1	C	358	LEU	N-CA-C	-6.57	98.27	109.24
1	G	358	LEU	N-CA-C	-6.56	98.28	109.24
1	D	358	LEU	N-CA-C	-6.56	98.29	109.24
1	L	358	LEU	N-CA-C	-6.56	98.28	109.24
1	E	358	LEU	N-CA-C	-6.55	98.30	109.24
1	F	358	LEU	N-CA-C	-6.55	98.30	109.24
1	K	358	LEU	N-CA-C	-6.55	98.31	109.24
1	I	358	LEU	N-CA-C	-6.55	98.31	109.24
1	A	358	LEU	N-CA-C	-6.54	98.31	109.24
1	J	358	LEU	N-CA-C	-6.54	98.31	109.24
1	L	56	THR	CA-C-N	-6.48	113.61	120.03
1	L	56	THR	C-N-CA	-6.48	113.61	120.03
1	A	56	THR	CA-C-N	-6.47	113.62	120.03
1	A	56	THR	C-N-CA	-6.47	113.62	120.03
1	G	56	THR	CA-C-N	-6.47	113.62	120.03
1	G	56	THR	C-N-CA	-6.47	113.62	120.03
1	B	56	THR	CA-C-N	-6.46	113.63	120.03
1	B	56	THR	C-N-CA	-6.46	113.63	120.03
1	D	56	THR	CA-C-N	-6.46	113.64	120.03
1	D	56	THR	C-N-CA	-6.46	113.64	120.03
1	C	56	THR	CA-C-N	-6.46	113.64	120.03
1	C	56	THR	C-N-CA	-6.46	113.64	120.03
1	J	56	THR	CA-C-N	-6.45	113.64	120.03
1	J	56	THR	C-N-CA	-6.45	113.64	120.03
1	K	56	THR	CA-C-N	-6.44	113.66	120.03
1	K	56	THR	C-N-CA	-6.44	113.66	120.03
1	H	56	THR	CA-C-N	-6.44	113.66	120.03
1	H	56	THR	C-N-CA	-6.44	113.66	120.03
1	I	56	THR	CA-C-N	-6.42	113.68	120.03
1	I	56	THR	C-N-CA	-6.42	113.68	120.03
1	E	56	THR	CA-C-N	-6.40	113.69	120.03
1	E	56	THR	C-N-CA	-6.40	113.69	120.03
1	F	56	THR	CA-C-N	-6.40	113.70	120.03
1	F	56	THR	C-N-CA	-6.40	113.70	120.03
1	B	10	GLU	N-CA-C	6.30	118.72	108.08
1	C	10	GLU	N-CA-C	6.29	118.71	108.08
1	I	10	GLU	N-CA-C	6.29	118.71	108.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	10	GLU	N-CA-C	6.28	118.69	108.08
1	K	10	GLU	N-CA-C	6.28	118.69	108.08
1	F	10	GLU	N-CA-C	6.27	118.68	108.08
1	D	10	GLU	N-CA-C	6.27	118.68	108.08
1	G	10	GLU	N-CA-C	6.27	118.68	108.08
1	H	10	GLU	N-CA-C	6.27	118.68	108.08
1	J	10	GLU	N-CA-C	6.27	118.68	108.08
1	A	10	GLU	N-CA-C	6.26	118.66	108.08
1	L	10	GLU	N-CA-C	6.26	118.65	108.08
1	K	431	GLU	N-CA-C	-6.24	104.53	111.71
1	A	431	GLU	N-CA-C	-6.23	104.55	111.71
1	D	431	GLU	N-CA-C	-6.23	104.55	111.71
1	G	431	GLU	N-CA-C	-6.22	104.55	111.71
1	J	431	GLU	N-CA-C	-6.22	104.56	111.71
1	E	431	GLU	N-CA-C	-6.21	104.56	111.71
1	L	431	GLU	N-CA-C	-6.20	104.58	111.71
1	B	431	GLU	N-CA-C	-6.20	104.58	111.71
1	H	431	GLU	N-CA-C	-6.19	104.59	111.71
1	C	431	GLU	N-CA-C	-6.19	104.60	111.71
1	F	431	GLU	N-CA-C	-6.19	104.60	111.71
1	B	44	PRO	N-CA-C	6.18	122.03	111.03
1	I	431	GLU	N-CA-C	-6.18	104.60	111.71
1	I	44	PRO	N-CA-C	6.17	122.01	111.03
1	J	44	PRO	N-CA-C	6.16	122.00	111.03
1	H	44	PRO	N-CA-C	6.16	122.00	111.03
1	C	44	PRO	N-CA-C	6.16	121.99	111.03
1	D	44	PRO	N-CA-C	6.15	121.98	111.03
1	G	400	LEU	N-CA-C	-6.15	104.58	111.28
1	L	44	PRO	N-CA-C	6.15	121.97	111.03
1	K	44	PRO	N-CA-C	6.14	121.97	111.03
1	E	44	PRO	N-CA-C	6.14	121.96	111.03
1	G	44	PRO	N-CA-C	6.14	121.96	111.03
1	F	44	PRO	N-CA-C	6.13	121.95	111.03
1	A	44	PRO	N-CA-C	6.13	121.94	111.03
1	H	400	LEU	N-CA-C	-6.11	104.62	111.28
1	I	400	LEU	N-CA-C	-6.10	104.63	111.28
1	F	400	LEU	N-CA-C	-6.10	104.63	111.28
1	E	400	LEU	N-CA-C	-6.10	104.63	111.28
1	K	400	LEU	N-CA-C	-6.10	104.63	111.28
1	B	400	LEU	N-CA-C	-6.09	104.64	111.28
1	L	400	LEU	N-CA-C	-6.08	104.65	111.28
1	C	400	LEU	N-CA-C	-6.08	104.65	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	400	LEU	N-CA-C	-6.08	104.65	111.28
1	J	400	LEU	N-CA-C	-6.08	104.65	111.28
1	F	37	TYR	N-CA-C	6.07	117.98	111.36
1	A	400	LEU	N-CA-C	-6.06	104.68	111.28
1	B	37	TYR	N-CA-C	6.04	117.95	111.36
1	H	37	TYR	N-CA-C	6.04	117.95	111.36
1	C	37	TYR	N-CA-C	6.04	117.94	111.36
1	G	37	TYR	N-CA-C	6.03	117.94	111.36
1	K	37	TYR	N-CA-C	6.03	117.94	111.36
1	E	37	TYR	N-CA-C	6.02	117.92	111.36
1	A	37	TYR	N-CA-C	6.02	117.92	111.36
1	I	37	TYR	N-CA-C	6.01	117.92	111.36
1	J	37	TYR	N-CA-C	6.01	117.91	111.36
1	F	373	GLU	N-CA-C	-5.99	104.55	112.34
1	D	37	TYR	N-CA-C	5.99	117.89	111.36
1	I	373	GLU	N-CA-C	-5.99	104.55	112.34
1	L	37	TYR	N-CA-C	5.98	117.88	111.36
1	K	373	GLU	N-CA-C	-5.98	104.56	112.34
1	D	373	GLU	N-CA-C	-5.97	104.58	112.34
1	C	373	GLU	N-CA-C	-5.96	104.59	112.34
1	J	373	GLU	N-CA-C	-5.96	104.59	112.34
1	A	373	GLU	N-CA-C	-5.96	104.60	112.34
1	G	373	GLU	N-CA-C	-5.95	104.60	112.34
1	B	373	GLU	N-CA-C	-5.95	104.61	112.34
1	H	373	GLU	N-CA-C	-5.95	104.60	112.34
1	L	373	GLU	N-CA-C	-5.95	104.61	112.34
1	E	373	GLU	N-CA-C	-5.94	104.62	112.34
1	C	102	GLY	N-CA-C	-5.67	105.92	112.73
1	L	102	GLY	N-CA-C	-5.63	105.98	112.73
1	J	102	GLY	N-CA-C	-5.62	105.98	112.73
1	K	102	GLY	N-CA-C	-5.62	105.99	112.73
1	A	102	GLY	N-CA-C	-5.61	105.99	112.73
1	G	102	GLY	N-CA-C	-5.61	105.99	112.73
1	I	102	GLY	N-CA-C	-5.61	105.99	112.73
1	B	102	GLY	N-CA-C	-5.60	106.01	112.73
1	H	102	GLY	N-CA-C	-5.60	106.01	112.73
1	D	102	GLY	N-CA-C	-5.59	106.02	112.73
1	F	102	GLY	N-CA-C	-5.57	106.04	112.73
1	E	102	GLY	N-CA-C	-5.57	106.05	112.73
1	A	326	ASP	N-CA-C	5.46	117.23	111.28
1	G	51	SER	N-CA-C	5.46	119.43	112.34
1	K	51	SER	N-CA-C	5.44	119.41	112.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	326	ASP	N-CA-C	5.44	117.21	111.28
1	E	326	ASP	N-CA-C	5.43	117.20	111.28
1	F	326	ASP	N-CA-C	5.43	117.20	111.28
1	D	51	SER	N-CA-C	5.43	119.40	112.34
1	J	51	SER	N-CA-C	5.43	119.39	112.34
1	B	326	ASP	N-CA-C	5.42	117.19	111.28
1	C	326	ASP	N-CA-C	5.42	117.19	111.28
1	E	51	SER	N-CA-C	5.42	119.39	112.34
1	G	326	ASP	N-CA-C	5.42	117.19	111.28
1	J	326	ASP	N-CA-C	5.42	117.19	111.28
1	F	51	SER	N-CA-C	5.41	119.38	112.34
1	H	326	ASP	N-CA-C	5.41	117.18	111.28
1	D	326	ASP	N-CA-C	5.41	117.17	111.28
1	L	326	ASP	N-CA-C	5.41	117.17	111.28
1	B	51	SER	N-CA-C	5.40	119.37	112.34
1	C	51	SER	N-CA-C	5.40	119.36	112.34
1	A	51	SER	N-CA-C	5.39	119.35	112.34
1	H	51	SER	N-CA-C	5.39	119.35	112.34
1	L	51	SER	N-CA-C	5.39	119.35	112.34
1	I	51	SER	N-CA-C	5.38	119.33	112.34
1	K	326	ASP	N-CA-C	5.38	117.14	111.28
1	J	34	CYS	N-CA-C	-5.37	105.42	111.28
1	H	34	CYS	N-CA-C	-5.37	105.43	111.28
1	G	34	CYS	N-CA-C	-5.36	105.43	111.28
1	C	34	CYS	N-CA-C	-5.36	105.44	111.28
1	B	34	CYS	N-CA-C	-5.35	105.45	111.28
1	K	34	CYS	N-CA-C	-5.35	105.45	111.28
1	A	34	CYS	N-CA-C	-5.35	105.45	111.28
1	I	34	CYS	N-CA-C	-5.35	105.45	111.28
1	L	34	CYS	N-CA-C	-5.33	105.47	111.28
1	E	388	VAL	CA-C-N	-5.33	113.14	120.28
1	E	388	VAL	C-N-CA	-5.33	113.14	120.28
1	K	388	VAL	CA-C-N	-5.33	113.14	120.28
1	K	388	VAL	C-N-CA	-5.33	113.14	120.28
1	A	388	VAL	CA-C-N	-5.32	113.15	120.28
1	A	388	VAL	C-N-CA	-5.32	113.15	120.28
1	F	34	CYS	N-CA-C	-5.32	105.48	111.28
1	E	34	CYS	N-CA-C	-5.31	105.49	111.28
1	C	388	VAL	CA-C-N	-5.31	113.16	120.28
1	C	388	VAL	C-N-CA	-5.31	113.16	120.28
1	H	388	VAL	CA-C-N	-5.29	113.19	120.28
1	H	388	VAL	C-N-CA	-5.29	113.19	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	388	VAL	CA-C-N	-5.29	113.19	120.28
1	D	388	VAL	C-N-CA	-5.29	113.19	120.28
1	J	388	VAL	CA-C-N	-5.29	113.19	120.28
1	J	388	VAL	C-N-CA	-5.29	113.19	120.28
1	L	388	VAL	CA-C-N	-5.29	113.20	120.28
1	L	388	VAL	C-N-CA	-5.29	113.20	120.28
1	D	34	CYS	N-CA-C	-5.28	105.53	111.28
1	F	388	VAL	CA-C-N	-5.27	113.22	120.28
1	F	388	VAL	C-N-CA	-5.27	113.22	120.28
1	G	388	VAL	CA-C-N	-5.26	113.23	120.28
1	G	388	VAL	C-N-CA	-5.26	113.23	120.28
1	B	388	VAL	CA-C-N	-5.26	113.23	120.28
1	B	388	VAL	C-N-CA	-5.26	113.23	120.28
1	I	388	VAL	CA-C-N	-5.25	113.24	120.28
1	I	388	VAL	C-N-CA	-5.25	113.24	120.28
1	B	319	PHE	N-CA-C	5.24	117.64	108.52
1	E	319	PHE	N-CA-C	5.24	117.64	108.52
1	A	319	PHE	N-CA-C	5.24	117.64	108.52
1	H	319	PHE	N-CA-C	5.23	117.63	108.52
1	L	319	PHE	N-CA-C	5.23	117.62	108.52
1	J	319	PHE	N-CA-C	5.23	117.62	108.52
1	G	319	PHE	N-CA-C	5.22	117.61	108.52
1	D	319	PHE	N-CA-C	5.22	117.60	108.52
1	F	319	PHE	N-CA-C	5.22	117.60	108.52
1	C	319	PHE	N-CA-C	5.21	117.59	108.52
1	I	319	PHE	N-CA-C	5.21	117.59	108.52
1	D	81	GLN	N-CA-C	5.21	116.64	111.07
1	K	319	PHE	N-CA-C	5.21	117.58	108.52
1	F	120	TYR	N-CA-C	-5.18	105.75	111.71
1	B	120	TYR	N-CA-C	-5.18	105.75	111.71
1	H	120	TYR	N-CA-C	-5.18	105.75	111.71
1	G	89	SER	N-CA-C	5.18	116.94	109.07
1	K	120	TYR	N-CA-C	-5.18	105.76	111.71
1	A	120	TYR	N-CA-C	-5.17	105.76	111.71
1	L	81	GLN	N-CA-C	5.17	116.60	111.07
1	D	89	SER	N-CA-C	5.17	116.92	109.07
1	B	81	GLN	N-CA-C	5.16	116.59	111.07
1	F	81	GLN	N-CA-C	5.16	116.59	111.07
1	A	81	GLN	N-CA-C	5.16	116.59	111.07
1	A	89	SER	N-CA-C	5.16	116.92	109.07
1	C	120	TYR	N-CA-C	-5.16	105.78	111.71
1	E	81	GLN	N-CA-C	5.16	116.59	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	89	SER	N-CA-C	5.16	116.92	109.07
1	I	120	TYR	N-CA-C	-5.16	105.78	111.71
1	L	120	TYR	N-CA-C	-5.16	105.78	111.71
1	C	81	GLN	N-CA-C	5.16	116.59	111.07
1	E	120	TYR	N-CA-C	-5.16	105.78	111.71
1	L	89	SER	N-CA-C	5.16	116.91	109.07
1	I	89	SER	N-CA-C	5.15	116.90	109.07
1	J	89	SER	N-CA-C	5.15	116.90	109.07
1	K	81	GLN	N-CA-C	5.15	116.58	111.07
1	K	89	SER	N-CA-C	5.15	116.89	109.07
1	G	120	TYR	N-CA-C	-5.14	105.79	111.71
1	H	81	GLN	N-CA-C	5.14	116.58	111.07
1	H	89	SER	N-CA-C	5.14	116.89	109.07
1	D	120	TYR	N-CA-C	-5.14	105.80	111.71
1	C	89	SER	N-CA-C	5.14	116.88	109.07
1	J	120	TYR	N-CA-C	-5.14	105.80	111.71
1	J	81	GLN	N-CA-C	5.13	116.56	111.07
1	J	389	TYR	N-CA-C	-5.13	105.69	111.28
1	G	81	GLN	N-CA-C	5.13	116.56	111.07
1	D	389	TYR	N-CA-C	-5.13	105.69	111.28
1	I	81	GLN	N-CA-C	5.13	116.56	111.07
1	E	89	SER	N-CA-C	5.12	116.86	109.07
1	B	89	SER	N-CA-C	5.12	116.86	109.07
1	I	389	TYR	N-CA-C	-5.12	105.70	111.28
1	B	389	TYR	N-CA-C	-5.12	105.70	111.28
1	L	389	TYR	N-CA-C	-5.10	105.72	111.28
1	F	389	TYR	N-CA-C	-5.10	105.72	111.28
1	C	389	TYR	N-CA-C	-5.10	105.72	111.28
1	H	389	TYR	N-CA-C	-5.10	105.72	111.28
1	G	389	TYR	N-CA-C	-5.09	105.73	111.28
1	A	389	TYR	N-CA-C	-5.08	105.74	111.28
1	J	336	ALA	N-CA-C	-5.08	105.74	111.28
1	K	389	TYR	N-CA-C	-5.08	105.75	111.28
1	A	383	ASP	N-CA-C	5.07	116.50	111.07
1	J	383	ASP	N-CA-C	5.07	116.50	111.07
1	I	383	ASP	N-CA-C	5.07	116.50	111.07
1	F	383	ASP	N-CA-C	5.07	116.49	111.07
1	I	80	MET	N-CA-C	5.06	116.49	111.07
1	G	383	ASP	N-CA-C	5.06	116.48	111.07
1	H	383	ASP	N-CA-C	5.06	116.48	111.07
1	E	389	TYR	N-CA-C	-5.05	105.77	111.28
1	A	336	ALA	N-CA-C	-5.05	105.78	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	205	LYS	N-CA-C	5.05	117.35	109.52
1	D	336	ALA	N-CA-C	-5.05	105.78	111.28
1	E	383	ASP	N-CA-C	5.05	116.47	111.07
1	F	80	MET	N-CA-C	5.05	116.47	111.07
1	D	80	MET	N-CA-C	5.04	116.47	111.07
1	J	80	MET	N-CA-C	5.04	116.47	111.07
1	K	383	ASP	N-CA-C	5.04	116.47	111.07
1	C	383	ASP	N-CA-C	5.04	116.47	111.07
1	C	80	MET	N-CA-C	5.04	116.46	111.07
1	D	205	LYS	N-CA-C	5.04	117.33	109.52
1	L	383	ASP	N-CA-C	5.04	116.46	111.07
1	K	205	LYS	N-CA-C	5.03	117.32	109.52
1	A	80	MET	N-CA-C	5.03	116.45	111.07
1	G	80	MET	N-CA-C	5.03	116.45	111.07
1	B	284	GLU	N-CA-C	-5.03	105.80	111.28
1	G	205	LYS	N-CA-C	5.03	117.31	109.52
1	H	80	MET	N-CA-C	5.02	116.45	111.07
1	K	80	MET	N-CA-C	5.02	116.44	111.07
1	B	80	MET	N-CA-C	5.02	116.44	111.07
1	B	383	ASP	N-CA-C	5.02	116.44	111.07
1	B	205	LYS	N-CA-C	5.02	117.29	109.52
1	I	284	GLU	N-CA-C	-5.02	105.81	111.28
1	A	284	GLU	N-CA-C	-5.01	105.81	111.28
1	C	336	ALA	N-CA-C	-5.01	105.82	111.28
1	B	336	ALA	N-CA-C	-5.01	105.82	111.28
1	A	205	LYS	N-CA-C	5.01	117.28	109.52
1	F	336	ALA	N-CA-C	-5.01	105.82	111.28
1	E	80	MET	N-CA-C	5.00	116.42	111.07
1	L	205	LYS	N-CA-C	5.00	117.28	109.52

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3669	0	3672	219	0
1	B	3669	0	3672	221	0
1	C	3669	0	3672	217	0
1	D	3669	0	3672	223	0
1	E	3669	0	3672	221	0
1	F	3669	0	3672	221	0
1	G	3669	0	3672	220	0
1	H	3669	0	3672	219	0
1	I	3669	0	3672	224	0
1	J	3669	0	3672	223	0
1	K	3669	0	3672	215	0
1	L	3669	0	3672	216	0
All	All	44028	0	44064	1829	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

All (1829) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:131:PHE:HE2	1:G:387:GLY:HA3	1.12	1.14
1:D:126:TYR:CG	1:D:158:MET:SD	2.42	1.13
1:E:126:TYR:CG	1:E:158:MET:SD	2.42	1.13
1:G:126:TYR:CG	1:G:158:MET:SD	2.42	1.13
1:H:126:TYR:CG	1:H:158:MET:SD	2.42	1.13
1:J:126:TYR:CG	1:J:158:MET:SD	2.42	1.13
1:B:126:TYR:CG	1:B:158:MET:SD	2.42	1.13
1:I:126:TYR:CG	1:I:158:MET:SD	2.42	1.13
1:A:126:TYR:CG	1:A:158:MET:SD	2.42	1.13
1:C:126:TYR:CG	1:C:158:MET:SD	2.42	1.13
1:F:126:TYR:CG	1:F:158:MET:SD	2.42	1.13
1:L:126:TYR:CD1	1:L:158:MET:SD	2.42	1.13
1:C:126:TYR:CD1	1:C:158:MET:SD	2.42	1.12
1:I:126:TYR:CD1	1:I:158:MET:SD	2.42	1.12
1:K:126:TYR:CG	1:K:158:MET:SD	2.42	1.12
1:H:126:TYR:CD1	1:H:158:MET:SD	2.42	1.12
1:J:126:TYR:CD1	1:J:158:MET:SD	2.42	1.12
1:K:126:TYR:CD1	1:K:158:MET:SD	2.42	1.12
1:A:126:TYR:CD1	1:A:158:MET:SD	2.42	1.12
1:D:126:TYR:CD1	1:D:158:MET:SD	2.42	1.12
1:E:126:TYR:CD1	1:E:158:MET:SD	2.42	1.12
1:G:126:TYR:CD1	1:G:158:MET:SD	2.42	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:TYR:CD1	1:B:158:MET:SD	2.42	1.11
1:L:126:TYR:CG	1:L:158:MET:SD	2.42	1.11
1:F:126:TYR:CD1	1:F:158:MET:SD	2.43	1.11
1:B:131:PHE:HE2	1:C:387:GLY:HA3	1.12	1.09
1:D:131:PHE:HE2	1:E:387:GLY:HA3	1.16	1.09
1:H:131:PHE:HE2	1:I:387:GLY:HA3	1.13	1.08
1:J:131:PHE:HE2	1:K:387:GLY:HA3	1.15	1.07
1:A:387:GLY:HA3	1:L:131:PHE:HE2	1.16	1.05
1:K:131:PHE:HE2	1:L:387:GLY:HA3	1.21	1.03
1:C:131:PHE:HE2	1:D:387:GLY:HA3	1.23	1.03
1:B:131:PHE:CE2	1:C:387:GLY:HA3	1.94	1.02
1:A:291:MET:HG2	1:B:282:LEU:CD1	1.90	1.02
1:G:131:PHE:HE2	1:H:387:GLY:HA3	1.25	1.02
1:C:291:MET:HG2	1:D:282:LEU:CD1	1.90	1.01
1:H:131:PHE:CE2	1:I:387:GLY:HA3	1.95	1.01
1:I:291:MET:HG2	1:J:282:LEU:CD1	1.91	1.01
1:E:131:PHE:HE2	1:F:387:GLY:HA3	1.23	1.00
1:F:131:PHE:CE2	1:G:387:GLY:HA3	1.94	1.00
1:J:131:PHE:CE2	1:K:387:GLY:HA3	1.96	1.00
1:A:131:PHE:HE2	1:B:387:GLY:HA3	1.24	1.00
1:A:387:GLY:HA3	1:L:131:PHE:CE2	1.97	1.00
1:G:291:MET:HG2	1:H:282:LEU:CD1	1.90	1.00
1:E:291:MET:HG2	1:F:282:LEU:CD1	1.92	0.99
1:K:291:MET:HG2	1:L:282:LEU:CD1	1.91	0.99
1:I:80:MET:HE1	1:J:431:GLU:CD	1.86	0.99
1:C:80:MET:HE1	1:D:431:GLU:CD	1.88	0.98
1:I:131:PHE:HE2	1:J:387:GLY:HA3	1.23	0.98
1:F:413:GLN:HB2	1:G:93:ALA:CB	1.94	0.98
1:D:131:PHE:CE2	1:E:387:GLY:HA3	1.97	0.98
1:D:291:MET:HG2	1:E:282:LEU:CD1	1.94	0.98
1:J:291:MET:HG2	1:K:282:LEU:CD1	1.92	0.98
1:B:413:GLN:HB2	1:C:93:ALA:CB	1.95	0.97
1:G:80:MET:HE1	1:H:431:GLU:CD	1.89	0.97
1:B:413:GLN:HB2	1:C:93:ALA:HB3	1.43	0.97
1:F:413:GLN:HB2	1:G:93:ALA:HB3	1.43	0.97
1:I:439:LEU:HB2	1:J:473:ALA:CB	1.95	0.97
1:A:80:MET:HE1	1:B:431:GLU:CD	1.90	0.96
1:H:413:GLN:HB2	1:I:93:ALA:HB3	1.44	0.96
1:F:291:MET:HG2	1:G:282:LEU:CD1	1.94	0.96
1:J:413:GLN:HB2	1:K:93:ALA:HB3	1.47	0.96
1:B:291:MET:HG2	1:C:282:LEU:CD1	1.96	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:80:MET:HE1	1:F:431:GLU:CD	1.90	0.96
1:H:291:MET:HG2	1:I:282:LEU:CD1	1.95	0.95
1:H:413:GLN:HB2	1:I:93:ALA:CB	1.96	0.95
1:A:282:LEU:CD1	1:L:291:MET:HG2	1.95	0.95
1:A:93:ALA:HB3	1:L:413:GLN:HB2	1.47	0.95
1:K:291:MET:HG2	1:L:282:LEU:HD11	1.49	0.95
1:K:131:PHE:CE2	1:L:387:GLY:HA3	2.02	0.95
1:K:80:MET:HE1	1:L:431:GLU:CD	1.91	0.94
1:I:291:MET:HG2	1:J:282:LEU:HD11	1.50	0.94
1:J:413:GLN:HB2	1:K:93:ALA:CB	1.96	0.94
1:D:413:GLN:HB2	1:E:93:ALA:HB3	1.48	0.94
1:I:131:PHE:CE2	1:J:387:GLY:HA3	2.04	0.93
1:I:439:LEU:HB2	1:J:473:ALA:HB1	1.50	0.93
1:A:291:MET:HG2	1:B:282:LEU:HD11	1.49	0.93
1:D:80:MET:HE1	1:E:431:GLU:CD	1.94	0.93
1:G:291:MET:HG2	1:H:282:LEU:HD11	1.50	0.93
1:D:413:GLN:HB2	1:E:93:ALA:CB	1.99	0.93
1:E:131:PHE:CE2	1:F:387:GLY:HA3	2.03	0.92
1:H:80:MET:HE1	1:I:431:GLU:CD	1.94	0.92
1:A:93:ALA:CB	1:L:413:GLN:HB2	1.99	0.92
1:A:431:GLU:CD	1:L:80:MET:HE1	1.93	0.92
1:G:439:LEU:HB2	1:H:473:ALA:CB	2.00	0.92
1:D:439:LEU:HB2	1:E:473:ALA:CB	1.99	0.92
1:F:291:MET:HG2	1:G:282:LEU:HD11	1.51	0.92
1:A:131:PHE:CE2	1:B:387:GLY:HA3	2.05	0.91
1:C:323:ARG:HG3	1:D:301:ASN:ND2	1.86	0.91
1:A:473:ALA:CB	1:L:439:LEU:HB2	1.99	0.91
1:C:131:PHE:CE2	1:D:387:GLY:HA3	2.04	0.91
1:B:80:MET:HE1	1:C:431:GLU:CD	1.94	0.91
1:J:323:ARG:HG3	1:K:301:ASN:ND2	1.86	0.91
1:C:439:LEU:HB2	1:D:473:ALA:CB	1.98	0.91
1:C:291:MET:HG2	1:D:282:LEU:HD11	1.48	0.91
1:E:439:LEU:HB2	1:F:473:ALA:CB	1.99	0.91
1:G:131:PHE:CE2	1:H:387:GLY:HA3	2.06	0.91
1:G:323:ARG:HG3	1:H:301:ASN:ND2	1.86	0.90
1:E:291:MET:HG2	1:F:282:LEU:HD11	1.50	0.90
1:J:291:MET:HG2	1:K:282:LEU:HD11	1.50	0.90
1:A:282:LEU:HD11	1:L:291:MET:HG2	1.52	0.90
1:C:439:LEU:HB2	1:D:473:ALA:HB1	1.53	0.90
1:A:323:ARG:HG3	1:B:301:ASN:ND2	1.86	0.90
1:H:439:LEU:HB2	1:I:473:ALA:HB1	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:439:LEU:HB2	1:E:473:ALA:HB1	1.51	0.89
1:J:439:LEU:HB2	1:K:473:ALA:CB	2.02	0.89
1:A:439:LEU:HB2	1:B:473:ALA:CB	2.01	0.89
1:D:291:MET:HG2	1:E:282:LEU:HD11	1.52	0.89
1:F:323:ARG:HG3	1:G:301:ASN:ND2	1.86	0.89
1:K:439:LEU:HB2	1:L:473:ALA:CB	2.03	0.89
1:A:473:ALA:HB1	1:L:439:LEU:HB2	1.51	0.89
1:J:80:MET:HE1	1:K:431:GLU:CD	1.96	0.89
1:H:439:LEU:HB2	1:I:473:ALA:CB	2.03	0.89
1:I:323:ARG:HG3	1:J:301:ASN:ND2	1.87	0.89
1:K:323:ARG:HG3	1:L:301:ASN:ND2	1.87	0.89
1:F:80:MET:HE1	1:G:431:GLU:CD	1.96	0.89
1:E:413:GLN:HB2	1:F:93:ALA:HB3	1.55	0.88
1:H:291:MET:HG2	1:I:282:LEU:HD11	1.52	0.88
1:D:323:ARG:HG3	1:E:301:ASN:ND2	1.87	0.88
1:B:323:ARG:HG3	1:C:301:ASN:ND2	1.88	0.88
1:J:439:LEU:HB2	1:K:473:ALA:HB1	1.55	0.88
1:A:301:ASN:ND2	1:L:323:ARG:HG3	1.89	0.88
1:B:439:LEU:HB2	1:C:473:ALA:HB1	1.54	0.87
1:K:413:GLN:HB2	1:L:93:ALA:HB3	1.54	0.87
1:B:439:LEU:HB2	1:C:473:ALA:CB	2.04	0.87
1:G:439:LEU:HB2	1:H:473:ALA:HB1	1.55	0.87
1:E:439:LEU:HB2	1:F:473:ALA:HB1	1.54	0.87
1:F:439:LEU:HB2	1:G:473:ALA:CB	2.05	0.87
1:E:323:ARG:HG3	1:F:301:ASN:ND2	1.90	0.87
1:B:291:MET:HG2	1:C:282:LEU:HD11	1.53	0.87
1:H:323:ARG:HG3	1:I:301:ASN:ND2	1.88	0.86
1:A:439:LEU:HB2	1:B:473:ALA:HB1	1.56	0.86
1:K:439:LEU:HB2	1:L:473:ALA:HB1	1.56	0.86
1:F:439:LEU:HB2	1:G:473:ALA:HB1	1.55	0.86
1:C:413:GLN:HB2	1:D:93:ALA:HB3	1.57	0.85
1:I:413:GLN:HB2	1:J:93:ALA:HB3	1.57	0.84
1:A:413:GLN:HB2	1:B:93:ALA:HB3	1.57	0.84
1:K:413:GLN:HB2	1:L:93:ALA:CB	2.07	0.84
1:F:293:SER:OG	1:G:337:ASP:HB3	1.78	0.84
1:I:80:MET:HE1	1:J:431:GLU:OE1	1.78	0.83
1:J:293:SER:OG	1:K:337:ASP:HB3	1.77	0.83
1:H:80:MET:HE1	1:I:431:GLU:OE1	1.78	0.83
1:E:413:GLN:HB2	1:F:93:ALA:CB	2.09	0.83
1:G:413:GLN:HB2	1:H:93:ALA:HB3	1.58	0.83
1:H:293:SER:OG	1:I:337:ASP:HB3	1.79	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:MET:HE1	1:D:431:GLU:OE1	1.79	0.83
1:D:293:SER:OG	1:E:337:ASP:HB3	1.79	0.82
1:B:80:MET:HE1	1:C:431:GLU:OE1	1.78	0.82
1:A:413:GLN:HB2	1:B:93:ALA:CB	2.10	0.82
1:K:80:MET:HE1	1:L:431:GLU:OE1	1.80	0.81
1:F:367:GLU:HG2	1:G:376:TYR:HE1	1.45	0.81
1:H:367:GLU:HG2	1:I:376:TYR:HE1	1.45	0.81
1:E:80:MET:HE1	1:F:431:GLU:OE1	1.81	0.81
1:F:80:MET:HE1	1:G:431:GLU:OE1	1.79	0.81
1:B:293:SER:OG	1:C:337:ASP:HB3	1.79	0.81
1:G:413:GLN:HB2	1:H:93:ALA:CB	2.11	0.81
1:A:431:GLU:OE1	1:L:80:MET:HE1	1.79	0.81
1:C:413:GLN:HB2	1:D:93:ALA:CB	2.11	0.81
1:D:442:LEU:HB3	1:E:470:ILE:HD11	1.63	0.81
1:B:367:GLU:HG2	1:C:376:TYR:HE1	1.44	0.80
1:A:293:SER:OG	1:B:337:ASP:HB3	1.81	0.80
1:D:80:MET:HE1	1:E:431:GLU:OE1	1.80	0.80
1:G:80:MET:HE1	1:H:431:GLU:OE1	1.82	0.80
1:J:80:MET:HE1	1:K:431:GLU:OE1	1.82	0.80
1:A:80:MET:HE1	1:B:431:GLU:OE1	1.81	0.80
1:A:337:ASP:HB3	1:L:293:SER:OG	1.80	0.80
1:J:367:GLU:HG2	1:K:376:TYR:HE1	1.45	0.80
1:K:293:SER:OG	1:L:337:ASP:HB3	1.81	0.80
1:C:293:SER:OG	1:D:337:ASP:HB3	1.81	0.79
1:D:367:GLU:HG2	1:E:376:TYR:HE1	1.45	0.79
1:J:442:LEU:HB3	1:K:470:ILE:HD11	1.65	0.79
1:I:293:SER:OG	1:J:337:ASP:HB3	1.82	0.79
1:A:97:LEU:HD22	1:L:112:MET:HE2	1.64	0.79
1:A:376:TYR:HE1	1:L:367:GLU:HG2	1.46	0.79
1:A:470:ILE:HD11	1:L:442:LEU:HB3	1.65	0.78
1:H:112:MET:HE2	1:I:97:LEU:HD22	1.65	0.78
1:D:112:MET:HE2	1:E:97:LEU:HD22	1.64	0.78
1:I:413:GLN:HB2	1:J:93:ALA:CB	2.13	0.78
1:I:439:LEU:HD12	1:J:473:ALA:HB3	1.64	0.77
1:G:293:SER:OG	1:H:337:ASP:HB3	1.81	0.77
1:F:59:GLN:HA	1:G:351:ARG:HH22	1.50	0.77
1:F:112:MET:HE2	1:G:97:LEU:HD22	1.66	0.77
1:J:112:MET:HE2	1:K:97:LEU:HD22	1.65	0.77
1:C:439:LEU:HD12	1:D:473:ALA:HB3	1.66	0.77
1:E:293:SER:OG	1:F:337:ASP:HB3	1.83	0.77
1:B:112:MET:HE2	1:C:97:LEU:HD22	1.65	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:59:GLN:HA	1:K:351:ARG:HH22	1.48	0.76
1:G:323:ARG:HG3	1:H:301:ASN:HD21	1.51	0.76
1:I:467:LYS:HB2	1:J:460:ASP:OD2	1.84	0.76
1:D:59:GLN:HA	1:E:351:ARG:HH22	1.50	0.76
1:A:323:ARG:HG3	1:B:301:ASN:HD21	1.51	0.75
1:A:291:MET:HG2	1:B:282:LEU:HD13	1.69	0.75
1:H:59:GLN:HA	1:I:351:ARG:HH22	1.51	0.75
1:A:351:ARG:HH22	1:L:59:GLN:HA	1.51	0.75
1:B:442:LEU:HB3	1:C:470:ILE:HD11	1.69	0.75
1:B:59:GLN:HA	1:C:351:ARG:HH22	1.51	0.75
1:C:323:ARG:HG3	1:D:301:ASN:HD21	1.50	0.75
1:G:439:LEU:HD12	1:H:473:ALA:HB3	1.68	0.74
1:G:291:MET:HG2	1:H:282:LEU:HD13	1.67	0.74
1:E:439:LEU:HD12	1:F:473:ALA:HB3	1.70	0.74
1:C:467:LYS:HB2	1:D:460:ASP:OD2	1.86	0.74
1:I:291:MET:HG2	1:J:282:LEU:HD13	1.69	0.74
1:H:442:LEU:HB3	1:I:470:ILE:HD11	1.69	0.73
1:A:439:LEU:HD12	1:B:473:ALA:HB3	1.69	0.73
1:I:439:LEU:HD12	1:J:473:ALA:CB	2.17	0.73
1:K:323:ARG:HG3	1:L:301:ASN:HD21	1.53	0.73
1:C:439:LEU:HD12	1:D:473:ALA:CB	2.18	0.73
1:F:442:LEU:HB3	1:G:470:ILE:HD11	1.69	0.73
1:I:323:ARG:HG3	1:J:301:ASN:HD21	1.52	0.73
1:K:186:ALA:HB2	1:L:171:ASP:HB3	1.71	0.73
1:G:467:LYS:HB2	1:H:460:ASP:OD2	1.89	0.72
1:E:186:ALA:HB2	1:F:171:ASP:HB3	1.72	0.72
1:A:467:LYS:HB2	1:B:460:ASP:OD2	1.90	0.71
1:C:291:MET:HG2	1:D:282:LEU:HD13	1.69	0.71
1:K:439:LEU:HD12	1:L:473:ALA:HB3	1.71	0.71
1:A:186:ALA:HB2	1:B:171:ASP:HB3	1.72	0.71
1:B:398:LEU:HB3	1:B:399:PRO:HD3	1.73	0.71
1:A:398:LEU:HB3	1:A:399:PRO:HD3	1.73	0.71
1:C:398:LEU:HB3	1:C:399:PRO:HD3	1.73	0.71
1:C:59:GLN:HA	1:D:351:ARG:HH22	1.56	0.71
1:D:6:THR:O	1:D:6:THR:OG1	2.09	0.71
1:G:186:ALA:HB2	1:H:171:ASP:HB3	1.73	0.71
1:H:398:LEU:HB3	1:H:399:PRO:HD3	1.73	0.71
1:K:291:MET:HG2	1:L:282:LEU:HD13	1.71	0.71
1:E:291:MET:HG2	1:F:282:LEU:HD13	1.71	0.70
1:G:439:LEU:HD12	1:H:473:ALA:CB	2.20	0.70
1:L:398:LEU:HB3	1:L:399:PRO:HD3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:186:ALA:HB2	1:D:171:ASP:HB3	1.73	0.70
1:D:398:LEU:HB3	1:D:399:PRO:HD3	1.73	0.70
1:E:323:ARG:HG3	1:F:301:ASN:HD21	1.55	0.70
1:I:398:LEU:HB3	1:I:399:PRO:HD3	1.73	0.70
1:E:467:LYS:HB2	1:F:460:ASP:OD2	1.91	0.70
1:E:398:LEU:HB3	1:E:399:PRO:HD3	1.73	0.70
1:G:290:SER:CB	1:H:344:VAL:HG11	2.22	0.70
1:K:59:GLN:HA	1:L:351:ARG:HH22	1.55	0.70
1:G:398:LEU:HB3	1:G:399:PRO:HD3	1.73	0.70
1:C:109:GLY:HA2	1:C:112:MET:SD	2.32	0.70
1:B:109:GLY:HA2	1:B:112:MET:SD	2.32	0.69
1:H:109:GLY:HA2	1:H:112:MET:SD	2.32	0.69
1:J:398:LEU:HB3	1:J:399:PRO:HD3	1.73	0.69
1:L:109:GLY:HA2	1:L:112:MET:SD	2.32	0.69
1:A:439:LEU:HD12	1:B:473:ALA:CB	2.21	0.69
1:I:112:MET:HE2	1:J:97:LEU:HD22	1.73	0.69
1:I:439:LEU:HB2	1:J:473:ALA:HB2	1.74	0.69
1:A:109:GLY:HA2	1:A:112:MET:SD	2.32	0.69
1:D:109:GLY:HA2	1:D:112:MET:SD	2.32	0.69
1:E:59:GLN:HA	1:F:351:ARG:HH22	1.56	0.69
1:F:109:GLY:HA2	1:F:112:MET:SD	2.32	0.69
1:F:398:LEU:HB3	1:F:399:PRO:HD3	1.73	0.69
1:A:59:GLN:HA	1:B:351:ARG:HH22	1.56	0.69
1:B:126:TYR:CD2	1:B:158:MET:SD	2.86	0.69
1:E:112:MET:HE2	1:F:97:LEU:HD22	1.73	0.69
1:I:109:GLY:HA2	1:I:112:MET:SD	2.32	0.69
1:I:186:ALA:HB2	1:J:171:ASP:HB3	1.74	0.69
1:A:126:TYR:CD2	1:A:158:MET:SD	2.86	0.69
1:K:398:LEU:HB3	1:K:399:PRO:HD3	1.73	0.69
1:A:73:LEU:HD23	1:A:134:LEU:HD21	1.75	0.69
1:E:109:GLY:HA2	1:E:112:MET:SD	2.32	0.69
1:H:6:THR:O	1:H:6:THR:OG1	2.09	0.69
1:I:6:THR:O	1:I:6:THR:OG1	2.09	0.69
1:K:109:GLY:HA2	1:K:112:MET:SD	2.32	0.69
1:K:467:LYS:HB2	1:L:460:ASP:OD2	1.93	0.69
1:L:73:LEU:HD23	1:L:134:LEU:HD21	1.75	0.69
1:L:126:TYR:CD2	1:L:158:MET:SD	2.86	0.69
1:C:126:TYR:CD2	1:C:158:MET:SD	2.86	0.69
1:B:6:THR:O	1:B:6:THR:OG1	2.09	0.69
1:B:73:LEU:HD23	1:B:134:LEU:HD21	1.75	0.69
1:G:6:THR:O	1:G:6:THR:OG1	2.09	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:73:LEU:HD23	1:C:134:LEU:HD21	1.75	0.68
1:E:73:LEU:HD23	1:E:134:LEU:HD21	1.75	0.68
1:D:73:LEU:HD23	1:D:134:LEU:HD21	1.75	0.68
1:F:186:ALA:HB2	1:G:171:ASP:HB3	1.75	0.68
1:G:59:GLN:HA	1:H:351:ARG:HH22	1.57	0.68
1:G:109:GLY:HA2	1:G:112:MET:SD	2.32	0.68
1:J:6:THR:O	1:J:6:THR:OG1	2.09	0.68
1:K:73:LEU:HD23	1:K:134:LEU:HD21	1.75	0.68
1:K:126:TYR:CD2	1:K:158:MET:SD	2.86	0.68
1:C:290:SER:CB	1:D:344:VAL:HG11	2.23	0.68
1:D:126:TYR:CD2	1:D:158:MET:SD	2.86	0.68
1:I:59:GLN:HA	1:J:351:ARG:HH22	1.58	0.68
1:J:73:LEU:HD23	1:J:134:LEU:HD21	1.75	0.68
1:J:186:ALA:HB2	1:K:171:ASP:HB3	1.76	0.68
1:E:439:LEU:HD12	1:F:473:ALA:CB	2.23	0.68
1:F:73:LEU:HD23	1:F:134:LEU:HD21	1.75	0.68
1:I:73:LEU:HD23	1:I:134:LEU:HD21	1.75	0.68
1:I:126:TYR:CD2	1:I:158:MET:SD	2.86	0.68
1:E:126:TYR:CD2	1:E:158:MET:SD	2.86	0.68
1:G:73:LEU:HD23	1:G:134:LEU:HD21	1.75	0.68
1:H:73:LEU:HD23	1:H:134:LEU:HD21	1.75	0.68
1:I:290:SER:CB	1:J:344:VAL:HG11	2.24	0.68
1:J:109:GLY:HA2	1:J:112:MET:SD	2.32	0.68
1:J:126:TYR:CD2	1:J:158:MET:SD	2.86	0.68
1:I:126:TYR:CE1	1:I:158:MET:SD	2.87	0.68
1:K:439:LEU:HD12	1:L:473:ALA:CB	2.23	0.68
1:H:126:TYR:CD2	1:H:158:MET:SD	2.86	0.68
1:H:126:TYR:CE1	1:H:158:MET:SD	2.87	0.67
1:H:186:ALA:HB2	1:I:171:ASP:HB3	1.76	0.67
1:K:6:THR:O	1:K:6:THR:OG1	2.09	0.67
1:A:290:SER:CB	1:B:344:VAL:HG11	2.23	0.67
1:E:290:SER:CB	1:F:344:VAL:HG11	2.24	0.67
1:G:126:TYR:CD2	1:G:158:MET:SD	2.86	0.67
1:D:291:MET:HG2	1:E:282:LEU:HD13	1.74	0.67
1:J:126:TYR:CE1	1:J:158:MET:SD	2.88	0.67
1:C:291:MET:CG	1:D:282:LEU:HD11	2.24	0.67
1:A:282:LEU:HD13	1:L:291:MET:HG2	1.76	0.67
1:G:126:TYR:CE1	1:G:158:MET:SD	2.88	0.67
1:F:6:THR:O	1:F:6:THR:OG1	2.09	0.67
1:B:126:TYR:CE1	1:B:158:MET:SD	2.87	0.67
1:B:186:ALA:HB2	1:C:171:ASP:HB3	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:126:TYR:CD2	1:F:158:MET:SD	2.86	0.67
1:K:126:TYR:CE1	1:K:158:MET:SD	2.88	0.67
1:A:171:ASP:HB3	1:L:186:ALA:HB2	1.77	0.67
1:G:439:LEU:HB2	1:H:473:ALA:HB2	1.77	0.67
1:G:327:ILE:HD12	1:H:330:LEU:CD1	2.25	0.67
1:A:126:TYR:CE1	1:A:158:MET:SD	2.88	0.66
1:E:20:LEU:HB2	1:E:167:VAL:HG21	1.78	0.66
1:H:20:LEU:HB2	1:H:167:VAL:HG21	1.78	0.66
1:K:112:MET:HE2	1:L:97:LEU:HD22	1.76	0.66
1:K:291:MET:CG	1:L:282:LEU:HD11	2.25	0.66
1:C:126:TYR:CE1	1:C:158:MET:SD	2.87	0.66
1:L:126:TYR:CE1	1:L:158:MET:SD	2.87	0.66
1:F:20:LEU:HB2	1:F:167:VAL:HG21	1.78	0.66
1:I:20:LEU:HB2	1:I:167:VAL:HG21	1.78	0.66
1:B:20:LEU:HB2	1:B:167:VAL:HG21	1.78	0.66
1:D:20:LEU:HB2	1:D:167:VAL:HG21	1.78	0.66
1:G:20:LEU:HB2	1:G:167:VAL:HG21	1.78	0.66
1:J:20:LEU:HB2	1:J:167:VAL:HG21	1.77	0.66
1:A:20:LEU:HB2	1:A:167:VAL:HG21	1.78	0.66
1:C:20:LEU:HB2	1:C:167:VAL:HG21	1.78	0.66
1:C:112:MET:HE2	1:D:97:LEU:HD22	1.76	0.66
1:F:126:TYR:CE1	1:F:158:MET:SD	2.88	0.66
1:G:329:PHE:CE2	1:H:332:LEU:CD2	2.79	0.66
1:L:6:THR:O	1:L:6:THR:OG1	2.09	0.66
1:D:126:TYR:CE1	1:D:158:MET:SD	2.88	0.66
1:E:126:TYR:CE1	1:E:158:MET:SD	2.88	0.66
1:J:291:MET:HG2	1:K:282:LEU:HD13	1.73	0.66
1:L:20:LEU:HB2	1:L:167:VAL:HG21	1.78	0.66
1:D:186:ALA:HB2	1:E:171:ASP:HB3	1.78	0.66
1:K:20:LEU:HB2	1:K:167:VAL:HG21	1.78	0.66
1:E:6:THR:OG1	1:E:6:THR:O	2.09	0.65
1:A:327:ILE:HD12	1:B:330:LEU:CD1	2.27	0.65
1:C:439:LEU:HB2	1:D:473:ALA:HB2	1.76	0.65
1:F:367:GLU:HG2	1:G:376:TYR:CE1	2.31	0.65
1:K:290:SER:CB	1:L:344:VAL:HG11	2.26	0.65
1:J:367:GLU:HG2	1:K:376:TYR:CE1	2.29	0.65
1:H:367:GLU:HG2	1:I:376:TYR:CE1	2.31	0.65
1:E:439:LEU:HB2	1:F:473:ALA:HB2	1.78	0.65
1:G:112:MET:HE2	1:H:97:LEU:HD22	1.78	0.65
1:E:150:PRO:HG2	1:E:411:THR:HG21	1.79	0.65
1:A:301:ASN:HD21	1:L:323:ARG:HG3	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:150:PRO:HG2	1:C:411:THR:HG21	1.79	0.64
1:D:150:PRO:HG2	1:D:411:THR:HG21	1.79	0.64
1:F:150:PRO:HG2	1:F:411:THR:HG21	1.79	0.64
1:A:112:MET:HE2	1:B:97:LEU:HD22	1.78	0.64
1:A:329:PHE:CE2	1:B:332:LEU:CD2	2.80	0.64
1:C:327:ILE:HD12	1:D:330:LEU:HD12	1.80	0.64
1:I:291:MET:CG	1:J:282:LEU:HD11	2.25	0.64
1:A:6:THR:O	1:A:6:THR:OG1	2.09	0.64
1:C:327:ILE:HD12	1:D:330:LEU:CD1	2.26	0.64
1:H:291:MET:CG	1:I:282:LEU:HD11	2.27	0.64
1:B:150:PRO:HG2	1:B:411:THR:HG21	1.79	0.64
1:H:190:LEU:HB3	1:H:195:ARG:HG3	1.79	0.64
1:I:190:LEU:HB3	1:I:195:ARG:HG3	1.79	0.64
1:J:323:ARG:HG3	1:K:301:ASN:HD21	1.59	0.64
1:F:291:MET:CG	1:G:282:LEU:HD11	2.26	0.64
1:J:290:SER:CB	1:K:344:VAL:HG11	2.28	0.64
1:J:293:SER:OG	1:K:337:ASP:CB	2.45	0.64
1:G:190:LEU:HB3	1:G:195:ARG:HG3	1.79	0.64
1:D:190:LEU:HB3	1:D:195:ARG:HG3	1.79	0.64
1:F:413:GLN:CB	1:G:93:ALA:CB	2.74	0.64
1:G:150:PRO:HG2	1:G:411:THR:HG21	1.79	0.64
1:H:291:MET:HG2	1:I:282:LEU:HD13	1.77	0.64
1:B:291:MET:HG2	1:C:282:LEU:HD13	1.77	0.64
1:J:369:VAL:HB	1:K:375:ARG:HG2	1.80	0.64
1:A:439:LEU:HB2	1:B:473:ALA:HB2	1.78	0.64
1:C:190:LEU:HB3	1:C:195:ARG:HG3	1.79	0.64
1:F:293:SER:OG	1:G:337:ASP:CB	2.45	0.64
1:H:293:SER:OG	1:I:337:ASP:CB	2.46	0.64
1:I:327:ILE:HD12	1:J:330:LEU:CD1	2.27	0.64
1:J:190:LEU:HB3	1:J:195:ARG:HG3	1.79	0.64
1:B:190:LEU:HB3	1:B:195:ARG:HG3	1.79	0.64
1:I:168:VAL:HG22	1:I:179:MET:HB3	1.81	0.64
1:J:115:ARG:NH2	1:K:476:ILE:N	2.46	0.64
1:E:190:LEU:HB3	1:E:195:ARG:HG3	1.79	0.63
1:F:291:MET:HG2	1:G:282:LEU:HD13	1.76	0.63
1:A:150:PRO:HG2	1:A:411:THR:HG21	1.79	0.63
1:D:367:GLU:HG2	1:E:376:TYR:CE1	2.30	0.63
1:L:168:VAL:HG22	1:L:179:MET:HB3	1.81	0.63
1:A:291:MET:CG	1:B:282:LEU:HD11	2.24	0.63
1:B:293:SER:OG	1:C:337:ASP:CB	2.47	0.63
1:D:369:VAL:HB	1:E:375:ARG:HG2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:327:ILE:HD12	1:H:330:LEU:HD12	1.80	0.63
1:H:413:GLN:HB2	1:I:93:ALA:HB1	1.80	0.63
1:H:150:PRO:HG2	1:H:411:THR:HG21	1.79	0.63
1:I:112:MET:HG2	1:J:97:LEU:HD21	1.80	0.63
1:B:413:GLN:HB2	1:C:93:ALA:HB1	1.79	0.63
1:D:290:SER:CB	1:E:344:VAL:HG11	2.28	0.63
1:D:367:GLU:HB3	1:E:376:TYR:CE1	2.33	0.63
1:J:291:MET:CG	1:K:282:LEU:HD11	2.25	0.63
1:B:367:GLU:HB3	1:C:376:TYR:CE1	2.34	0.63
1:F:190:LEU:HB3	1:F:195:ARG:HG3	1.79	0.63
1:K:168:VAL:HG22	1:K:179:MET:HB3	1.81	0.63
1:B:367:GLU:HG2	1:C:376:TYR:CE1	2.30	0.63
1:C:329:PHE:CE2	1:D:332:LEU:CD2	2.81	0.63
1:F:168:VAL:HG22	1:F:179:MET:HB3	1.80	0.63
1:G:294:SER:HB2	1:H:285:ALA:CB	2.29	0.63
1:K:190:LEU:HB3	1:K:195:ARG:HG3	1.79	0.63
1:F:323:ARG:HG3	1:G:301:ASN:HD21	1.61	0.63
1:A:190:LEU:HB3	1:A:195:ARG:HG3	1.79	0.62
1:A:327:ILE:HD12	1:B:330:LEU:HD12	1.81	0.62
1:A:376:TYR:CE1	1:L:367:GLU:HB3	2.34	0.62
1:G:291:MET:CG	1:H:282:LEU:HD11	2.25	0.62
1:H:168:VAL:HG22	1:H:179:MET:HB3	1.81	0.62
1:I:150:PRO:HG2	1:I:411:THR:HG21	1.79	0.62
1:J:168:VAL:HG22	1:J:179:MET:HB3	1.80	0.62
1:K:150:PRO:HG2	1:K:411:THR:HG21	1.79	0.62
1:L:150:PRO:HG2	1:L:411:THR:HG21	1.79	0.62
1:A:282:LEU:HD11	1:L:291:MET:CG	2.28	0.62
1:D:293:SER:OG	1:E:337:ASP:CB	2.47	0.62
1:H:323:ARG:HG3	1:I:301:ASN:HD21	1.62	0.62
1:I:327:ILE:HD12	1:J:330:LEU:HD12	1.81	0.62
1:L:190:LEU:HB3	1:L:195:ARG:HG3	1.79	0.62
1:B:64:ARG:HE	1:B:358:LEU:HD21	1.64	0.62
1:C:6:THR:O	1:C:6:THR:OG1	2.09	0.62
1:G:168:VAL:HG22	1:G:179:MET:HB3	1.81	0.62
1:K:311:LEU:HD11	1:L:299:LEU:HD21	1.81	0.62
1:C:168:VAL:HG22	1:C:179:MET:HB3	1.81	0.62
1:D:323:ARG:HG3	1:E:301:ASN:HD21	1.60	0.62
1:E:367:GLU:HG2	1:F:376:TYR:HE1	1.64	0.62
1:F:115:ARG:NH2	1:G:476:ILE:N	2.47	0.62
1:H:64:ARG:HE	1:H:358:LEU:HD21	1.64	0.62
1:K:439:LEU:HB2	1:L:473:ALA:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:VAL:HG22	1:B:179:MET:HB3	1.81	0.62
1:G:64:ARG:HE	1:G:358:LEU:HD21	1.64	0.62
1:J:150:PRO:HG2	1:J:411:THR:HG21	1.79	0.62
1:A:344:VAL:HG11	1:L:290:SER:CB	2.29	0.62
1:A:376:TYR:CE1	1:L:367:GLU:HG2	2.31	0.62
1:F:413:GLN:HB2	1:G:93:ALA:HB1	1.78	0.62
1:I:329:PHE:CE2	1:J:332:LEU:CD2	2.82	0.62
1:E:168:VAL:HG22	1:E:179:MET:HB3	1.80	0.62
1:I:64:ARG:HE	1:I:358:LEU:HD21	1.64	0.62
1:I:439:LEU:CD1	1:J:473:ALA:CB	2.78	0.62
1:J:413:GLN:HB2	1:K:93:ALA:HB1	1.79	0.62
1:J:413:GLN:CB	1:K:93:ALA:CB	2.76	0.62
1:D:291:MET:CG	1:E:282:LEU:HD11	2.27	0.62
1:F:64:ARG:HE	1:F:358:LEU:HD21	1.64	0.62
1:K:64:ARG:HE	1:K:358:LEU:HD21	1.64	0.62
1:C:293:SER:OG	1:D:337:ASP:CB	2.48	0.61
1:E:327:ILE:HD12	1:F:330:LEU:CD1	2.30	0.61
1:J:367:GLU:HB3	1:K:376:TYR:CE1	2.35	0.61
1:A:168:VAL:HG22	1:A:179:MET:HB3	1.81	0.61
1:F:131:PHE:HE2	1:G:387:GLY:CA	2.02	0.61
1:H:323:ARG:HG3	1:I:301:ASN:HD22	1.65	0.61
1:I:367:GLU:HG2	1:J:376:TYR:HE1	1.64	0.61
1:C:311:LEU:HD11	1:D:299:LEU:HD21	1.80	0.61
1:E:64:ARG:HE	1:E:358:LEU:HD21	1.64	0.61
1:H:115:ARG:NH2	1:I:476:ILE:N	2.49	0.61
1:K:367:GLU:HG2	1:L:376:TYR:HE1	1.64	0.61
1:L:64:ARG:HE	1:L:358:LEU:HD21	1.64	0.61
1:A:64:ARG:HE	1:A:358:LEU:HD21	1.64	0.61
1:E:311:LEU:HD11	1:F:299:LEU:HD21	1.82	0.61
1:I:311:LEU:HD11	1:J:299:LEU:HD21	1.82	0.61
1:J:64:ARG:HE	1:J:358:LEU:HD21	1.64	0.61
1:D:168:VAL:HG22	1:D:179:MET:HB3	1.80	0.61
1:D:442:LEU:HB3	1:E:470:ILE:CD1	2.29	0.61
1:H:367:GLU:HB3	1:I:376:TYR:CE1	2.35	0.61
1:A:476:ILE:N	1:L:115:ARG:NH2	2.49	0.61
1:A:367:GLU:HG2	1:B:376:TYR:HE1	1.66	0.61
1:K:327:ILE:HD12	1:L:330:LEU:CD1	2.30	0.61
1:A:294:SER:HB2	1:B:285:ALA:CB	2.30	0.61
1:A:375:ARG:HG2	1:L:369:VAL:HB	1.82	0.61
1:B:413:GLN:CB	1:C:93:ALA:CB	2.75	0.61
1:G:367:GLU:HG2	1:H:376:TYR:HE1	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:369:VAL:HB	1:C:375:ARG:HG2	1.83	0.61
1:J:186:ALA:HB2	1:K:171:ASP:CB	2.31	0.61
1:B:323:ARG:HG3	1:C:301:ASN:HD21	1.63	0.60
1:E:327:ILE:HD12	1:F:330:LEU:HD12	1.83	0.60
1:C:294:SER:HB2	1:D:285:ALA:CB	2.31	0.60
1:I:294:SER:HB2	1:J:285:ALA:CB	2.31	0.60
1:B:115:ARG:NH2	1:C:476:ILE:N	2.48	0.60
1:D:64:ARG:HE	1:D:358:LEU:HD21	1.64	0.60
1:A:293:SER:OG	1:B:337:ASP:CB	2.49	0.60
1:C:112:MET:HG2	1:D:97:LEU:HD21	1.83	0.60
1:G:449:TRP:CH2	1:H:461:ILE:HG12	2.36	0.60
1:C:64:ARG:HE	1:C:358:LEU:HD21	1.64	0.60
1:D:115:ARG:NH2	1:E:476:ILE:N	2.48	0.60
1:G:293:SER:OG	1:H:337:ASP:CB	2.50	0.60
1:K:327:ILE:HD12	1:L:330:LEU:HD12	1.83	0.60
1:B:131:PHE:HE2	1:C:387:GLY:CA	2.02	0.60
1:B:323:ARG:HG3	1:C:301:ASN:HD22	1.64	0.60
1:C:367:GLU:HG2	1:D:376:TYR:HE1	1.65	0.60
1:F:367:GLU:HB3	1:G:376:TYR:CE1	2.35	0.60
1:F:369:VAL:HB	1:G:375:ARG:HG2	1.82	0.60
1:G:21:LYS:HG3	1:G:24:ARG:HH12	1.67	0.60
1:I:449:TRP:CH2	1:J:461:ILE:HG12	2.36	0.60
1:J:21:LYS:HG3	1:J:24:ARG:HH12	1.67	0.60
1:L:442:LEU:O	1:L:446:VAL:HG12	2.02	0.60
1:A:21:LYS:HG3	1:A:24:ARG:HH12	1.67	0.60
1:C:439:LEU:CD1	1:D:473:ALA:CB	2.80	0.60
1:G:256:MET:HA	1:G:256:MET:HE2	1.84	0.60
1:H:256:MET:HE2	1:H:256:MET:HA	1.84	0.60
1:K:329:PHE:CE2	1:L:332:LEU:CD2	2.85	0.60
1:K:442:LEU:O	1:K:446:VAL:HG12	2.02	0.60
1:K:115:ARG:NH2	1:L:476:ILE:N	2.50	0.60
1:A:470:ILE:CD1	1:L:442:LEU:HB3	2.30	0.60
1:A:337:ASP:CB	1:L:293:SER:OG	2.48	0.59
1:E:112:MET:HG2	1:F:97:LEU:HD21	1.83	0.59
1:F:186:ALA:HB2	1:G:171:ASP:CB	2.30	0.59
1:F:323:ARG:HG3	1:G:301:ASN:HD22	1.64	0.59
1:H:290:SER:CB	1:I:344:VAL:HG11	2.32	0.59
1:F:442:LEU:O	1:F:446:VAL:HG12	2.02	0.59
1:H:369:VAL:HB	1:I:375:ARG:HG2	1.83	0.59
1:J:131:PHE:HE2	1:K:387:GLY:CA	2.04	0.59
1:A:442:LEU:O	1:A:446:VAL:HG12	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:442:LEU:O	1:C:446:VAL:HG12	2.02	0.59
1:D:256:MET:HE2	1:D:256:MET:HA	1.85	0.59
1:E:21:LYS:HG3	1:E:24:ARG:HH12	1.67	0.59
1:E:256:MET:HE2	1:E:256:MET:HA	1.85	0.59
1:E:329:PHE:CE2	1:F:332:LEU:CD2	2.84	0.59
1:E:442:LEU:O	1:E:446:VAL:HG12	2.02	0.59
1:G:442:LEU:O	1:G:446:VAL:HG12	2.02	0.59
1:I:256:MET:HE2	1:I:256:MET:HA	1.84	0.59
1:I:293:SER:OG	1:J:337:ASP:CB	2.50	0.59
1:A:20:LEU:CB	1:A:167:VAL:HG21	2.33	0.59
1:A:115:ARG:NH2	1:B:476:ILE:N	2.50	0.59
1:B:442:LEU:O	1:B:446:VAL:HG12	2.02	0.59
1:C:21:LYS:HG3	1:C:24:ARG:HH12	1.67	0.59
1:D:442:LEU:O	1:D:446:VAL:HG12	2.02	0.59
1:F:256:MET:HE2	1:F:256:MET:HA	1.84	0.59
1:G:112:MET:HG2	1:H:97:LEU:HD21	1.83	0.59
1:J:294:SER:HB2	1:K:285:ALA:CB	2.33	0.59
1:L:21:LYS:HG3	1:L:24:ARG:HH12	1.67	0.59
1:B:20:LEU:CB	1:B:167:VAL:HG21	2.33	0.59
1:C:256:MET:HE2	1:C:256:MET:HA	1.84	0.59
1:C:449:TRP:CH2	1:D:461:ILE:HG12	2.37	0.59
1:E:291:MET:CG	1:F:282:LEU:HD11	2.26	0.59
1:F:413:GLN:CB	1:G:93:ALA:HB3	2.27	0.59
1:G:329:PHE:CE2	1:H:332:LEU:HD22	2.38	0.59
1:K:21:LYS:HG3	1:K:24:ARG:HH12	1.67	0.59
1:K:293:SER:OG	1:L:337:ASP:CB	2.48	0.59
1:C:20:LEU:CB	1:C:167:VAL:HG21	2.33	0.59
1:H:442:LEU:O	1:H:446:VAL:HG12	2.02	0.59
1:I:21:LYS:HG3	1:I:24:ARG:HH12	1.67	0.59
1:K:20:LEU:CB	1:K:167:VAL:HG21	2.33	0.59
1:L:20:LEU:CB	1:L:167:VAL:HG21	2.33	0.59
1:D:439:LEU:HB2	1:E:473:ALA:HB2	1.85	0.59
1:E:115:ARG:NH2	1:F:476:ILE:N	2.50	0.59
1:E:294:SER:HB2	1:F:285:ALA:CB	2.33	0.59
1:F:122:GLU:HG2	1:G:427:SER:HB3	1.84	0.59
1:H:21:LYS:HG3	1:H:24:ARG:HH12	1.67	0.59
1:H:186:ALA:HB2	1:I:171:ASP:CB	2.32	0.59
1:A:449:TRP:CH2	1:B:461:ILE:HG12	2.37	0.59
1:B:122:GLU:HG2	1:C:427:SER:HB3	1.84	0.59
1:B:186:ALA:HB2	1:C:171:ASP:CB	2.32	0.59
1:J:142:ASN:HB2	1:J:163:LEU:HD13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:256:MET:HA	1:J:256:MET:HE2	1.84	0.59
1:J:323:ARG:HG3	1:K:301:ASN:HD22	1.65	0.59
1:J:442:LEU:O	1:J:446:VAL:HG12	2.02	0.59
1:A:427:SER:HB3	1:L:122:GLU:HG2	1.85	0.59
1:C:142:ASN:HB2	1:C:163:LEU:HD13	1.84	0.59
1:D:21:LYS:HG3	1:D:24:ARG:HH12	1.67	0.59
1:D:142:ASN:HB2	1:D:163:LEU:HD13	1.84	0.59
1:D:294:SER:HB2	1:E:285:ALA:CB	2.33	0.59
1:F:290:SER:CB	1:G:344:VAL:HG11	2.32	0.59
1:J:20:LEU:CB	1:J:167:VAL:HG21	2.33	0.59
1:K:294:SER:HB2	1:L:285:ALA:CB	2.32	0.59
1:B:142:ASN:HB2	1:B:163:LEU:HD13	1.84	0.59
1:D:20:LEU:CB	1:D:167:VAL:HG21	2.33	0.59
1:F:21:LYS:HG3	1:F:24:ARG:HH12	1.67	0.59
1:I:442:LEU:O	1:I:446:VAL:HG12	2.02	0.59
1:B:256:MET:HA	1:B:256:MET:HE2	1.84	0.58
1:D:439:LEU:HD12	1:E:473:ALA:HB3	1.85	0.58
1:G:115:ARG:NH2	1:H:476:ILE:N	2.50	0.58
1:J:144:LEU:HD11	1:J:251:TYR:HB3	1.85	0.58
1:K:144:LEU:HD11	1:K:251:TYR:HB3	1.85	0.58
1:E:20:LEU:CB	1:E:167:VAL:HG21	2.33	0.58
1:K:256:MET:HE2	1:K:256:MET:HA	1.84	0.58
1:L:144:LEU:HD11	1:L:251:TYR:HB3	1.85	0.58
1:A:171:ASP:CB	1:L:186:ALA:HB2	2.33	0.58
1:A:256:MET:HE2	1:A:256:MET:HA	1.84	0.58
1:E:142:ASN:HB2	1:E:163:LEU:HD13	1.84	0.58
1:H:122:GLU:HG2	1:I:427:SER:HB3	1.85	0.58
1:I:20:LEU:CB	1:I:167:VAL:HG21	2.33	0.58
1:I:144:LEU:HD11	1:I:251:TYR:HB3	1.85	0.58
1:K:142:ASN:HB2	1:K:163:LEU:HD13	1.85	0.58
1:A:144:LEU:HD11	1:A:251:TYR:HB3	1.85	0.58
1:B:80:MET:HE3	1:C:430:LEU:HD23	1.84	0.58
1:L:256:MET:HE2	1:L:256:MET:HA	1.84	0.58
1:G:142:ASN:HB2	1:G:163:LEU:HD13	1.85	0.58
1:H:131:PHE:HE2	1:I:387:GLY:CA	2.03	0.58
1:I:142:ASN:HB2	1:I:163:LEU:HD13	1.84	0.58
1:A:93:ALA:CB	1:L:413:GLN:CB	2.79	0.58
1:A:112:MET:HG2	1:B:97:LEU:HD21	1.84	0.58
1:A:142:ASN:HB2	1:A:163:LEU:HD13	1.84	0.58
1:A:372:GLU:C	1:A:374:ILE:N	2.60	0.58
1:H:144:LEU:HD11	1:H:251:TYR:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:LEU:HD11	1:B:251:TYR:HB3	1.85	0.58
1:D:413:GLN:HB2	1:E:93:ALA:HB1	1.83	0.58
1:E:449:TRP:CH2	1:F:461:ILE:HG12	2.38	0.58
1:F:20:LEU:CB	1:F:167:VAL:HG21	2.33	0.58
1:H:80:MET:HE3	1:I:430:LEU:HD23	1.85	0.58
1:J:122:GLU:HG2	1:K:427:SER:HB3	1.84	0.58
1:A:311:LEU:HD11	1:B:299:LEU:HD21	1.84	0.58
1:A:439:LEU:CD1	1:B:473:ALA:CB	2.82	0.58
1:F:80:MET:HE3	1:G:430:LEU:HD23	1.84	0.58
1:G:439:LEU:CD1	1:H:473:ALA:CB	2.81	0.58
1:J:442:LEU:HB3	1:K:470:ILE:CD1	2.31	0.58
1:B:290:SER:CB	1:C:344:VAL:HG11	2.33	0.58
1:G:20:LEU:CB	1:G:167:VAL:HG21	2.33	0.58
1:B:21:LYS:HG3	1:B:24:ARG:HH12	1.67	0.58
1:D:122:GLU:HG2	1:E:427:SER:HB3	1.85	0.58
1:F:142:ASN:HB2	1:F:163:LEU:HD13	1.85	0.58
1:G:144:LEU:HD11	1:G:251:TYR:HB3	1.85	0.58
1:H:413:GLN:CB	1:I:93:ALA:CB	2.76	0.58
1:B:228:ARG:HD2	1:B:244:TYR:HE2	1.69	0.57
1:C:228:ARG:HD2	1:C:244:TYR:HE2	1.69	0.57
1:G:372:GLU:C	1:G:374:ILE:N	2.60	0.57
1:H:20:LEU:CB	1:H:167:VAL:HG21	2.33	0.57
1:H:142:ASN:HB2	1:H:163:LEU:HD13	1.84	0.57
1:A:473:ALA:HB3	1:L:439:LEU:HD12	1.84	0.57
1:B:291:MET:CG	1:C:282:LEU:HD11	2.28	0.57
1:C:144:LEU:HD11	1:C:251:TYR:HB3	1.86	0.57
1:D:228:ARG:HD2	1:D:244:TYR:HE2	1.69	0.57
1:A:228:ARG:HD2	1:A:244:TYR:HE2	1.69	0.57
1:B:442:LEU:HB3	1:C:470:ILE:CD1	2.34	0.57
1:D:122:GLU:HG2	1:E:427:SER:CB	2.35	0.57
1:D:144:LEU:HD11	1:D:251:TYR:HB3	1.85	0.57
1:E:293:SER:OG	1:F:337:ASP:CB	2.51	0.57
1:F:144:LEU:HD11	1:F:251:TYR:HB3	1.85	0.57
1:G:311:LEU:HD11	1:H:299:LEU:HD21	1.86	0.57
1:K:186:ALA:HB2	1:L:171:ASP:CB	2.35	0.57
1:D:131:PHE:HE2	1:E:387:GLY:CA	2.05	0.57
1:K:41:SER:HB3	1:L:271:GLU:OE1	2.04	0.57
1:L:142:ASN:HB2	1:L:163:LEU:HD13	1.84	0.57
1:A:301:ASN:HD22	1:L:323:ARG:HG3	1.68	0.57
1:D:186:ALA:HB2	1:E:171:ASP:CB	2.33	0.57
1:E:144:LEU:HD11	1:E:251:TYR:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:228:ARG:HD2	1:E:244:TYR:HE2	1.69	0.57
1:I:442:LEU:HB3	1:J:470:ILE:HD11	1.87	0.57
1:F:41:SER:HB3	1:G:271:GLU:OE1	2.05	0.57
1:I:228:ARG:HD2	1:I:244:TYR:HE2	1.69	0.57
1:J:41:SER:HB3	1:K:271:GLU:OE1	2.05	0.57
1:K:449:TRP:CH2	1:L:461:ILE:HG12	2.40	0.57
1:E:442:LEU:HB3	1:F:470:ILE:HD11	1.87	0.57
1:H:228:ARG:HD2	1:H:244:TYR:HE2	1.69	0.57
1:J:122:GLU:HG2	1:K:427:SER:CB	2.35	0.57
1:F:294:SER:HB2	1:G:285:ALA:CB	2.35	0.57
1:I:467:LYS:HD3	1:J:460:ASP:HB3	1.87	0.57
1:L:228:ARG:HD2	1:L:244:TYR:HE2	1.70	0.57
1:A:41:SER:HB3	1:B:271:GLU:OE1	2.05	0.56
1:A:427:SER:CB	1:L:122:GLU:HG2	2.35	0.56
1:A:387:GLY:CA	1:L:131:PHE:HE2	2.05	0.56
1:C:372:GLU:C	1:C:374:ILE:N	2.60	0.56
1:F:228:ARG:HD2	1:F:244:TYR:HE2	1.69	0.56
1:H:413:GLN:CB	1:I:93:ALA:HB3	2.28	0.56
1:A:329:PHE:CE2	1:B:332:LEU:HD22	2.40	0.56
1:B:294:SER:HB2	1:C:285:ALA:CB	2.36	0.56
1:G:41:SER:HB3	1:H:271:GLU:OE1	2.05	0.56
1:G:228:ARG:HD2	1:G:244:TYR:HE2	1.69	0.56
1:H:126:TYR:HE1	1:H:158:MET:H	1.53	0.56
1:J:228:ARG:HD2	1:J:244:TYR:HE2	1.69	0.56
1:A:285:ALA:CB	1:L:294:SER:HB2	2.35	0.56
1:B:8:LEU:HD21	1:B:219:LEU:O	2.06	0.56
1:C:41:SER:HB3	1:D:271:GLU:OE1	2.05	0.56
1:C:329:PHE:CE2	1:D:332:LEU:HD22	2.41	0.56
1:J:126:TYR:HE1	1:J:158:MET:H	1.53	0.56
1:K:112:MET:HG2	1:L:97:LEU:HD21	1.87	0.56
1:B:413:GLN:CB	1:C:93:ALA:HB3	2.27	0.56
1:J:329:PHE:CE2	1:K:332:LEU:CD2	2.88	0.56
1:L:372:GLU:C	1:L:374:ILE:N	2.60	0.56
1:D:323:ARG:HG3	1:E:301:ASN:HD22	1.66	0.56
1:E:41:SER:HB3	1:F:271:GLU:OE1	2.04	0.56
1:I:41:SER:HB3	1:J:271:GLU:OE1	2.05	0.56
1:J:80:MET:HE3	1:K:430:LEU:HD23	1.88	0.56
1:K:126:TYR:HE1	1:K:158:MET:H	1.53	0.56
1:B:439:LEU:HD12	1:C:473:ALA:HB3	1.87	0.56
1:D:8:LEU:HD21	1:D:219:LEU:O	2.06	0.56
1:F:8:LEU:HD21	1:F:219:LEU:O	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:372:GLU:C	1:F:374:ILE:N	2.60	0.56
1:H:8:LEU:HD21	1:H:219:LEU:O	2.06	0.56
1:I:329:PHE:CE2	1:J:332:LEU:HD22	2.41	0.56
1:K:8:LEU:HD21	1:K:219:LEU:O	2.06	0.56
1:H:439:LEU:HD12	1:I:473:ALA:HB3	1.86	0.56
1:J:372:GLU:C	1:J:374:ILE:N	2.60	0.56
1:J:413:GLN:H	1:K:93:ALA:HB3	1.70	0.56
1:K:372:GLU:C	1:K:374:ILE:N	2.60	0.56
1:C:8:LEU:HD21	1:C:219:LEU:O	2.06	0.56
1:C:115:ARG:NH2	1:D:476:ILE:N	2.53	0.56
1:C:467:LYS:HD3	1:D:460:ASP:HB3	1.88	0.56
1:D:329:PHE:CE2	1:E:332:LEU:CD2	2.88	0.56
1:E:30:ARG:HH12	1:E:266:ARG:NH2	2.04	0.56
1:H:294:SER:HB2	1:I:285:ALA:CB	2.36	0.56
1:L:8:LEU:HD21	1:L:219:LEU:O	2.06	0.56
1:L:30:ARG:HH12	1:L:266:ARG:NH2	2.04	0.56
1:G:17:TYR:HB2	1:G:180:VAL:HG11	1.88	0.56
1:I:8:LEU:HD21	1:I:219:LEU:O	2.06	0.56
1:I:17:TYR:HB2	1:I:180:VAL:HG11	1.88	0.56
1:I:30:ARG:HH12	1:I:266:ARG:NH2	2.04	0.56
1:B:122:GLU:HG2	1:C:427:SER:CB	2.36	0.55
1:D:112:MET:HG2	1:E:97:LEU:HD21	1.88	0.55
1:D:126:TYR:HE1	1:D:158:MET:H	1.53	0.55
1:E:8:LEU:HD21	1:E:219:LEU:O	2.06	0.55
1:H:30:ARG:HH12	1:H:266:ARG:NH2	2.04	0.55
1:A:30:ARG:HH12	1:A:266:ARG:NH2	2.04	0.55
1:F:30:ARG:HH12	1:F:266:ARG:NH2	2.04	0.55
1:F:442:LEU:HB3	1:G:470:ILE:CD1	2.35	0.55
1:G:30:ARG:HH12	1:G:266:ARG:NH2	2.04	0.55
1:A:186:ALA:HB2	1:B:171:ASP:CB	2.37	0.55
1:C:126:TYR:HE1	1:C:158:MET:H	1.53	0.55
1:D:30:ARG:HH12	1:D:266:ARG:NH2	2.04	0.55
1:F:122:GLU:HG2	1:G:427:SER:CB	2.36	0.55
1:F:126:TYR:HE1	1:F:158:MET:H	1.53	0.55
1:K:228:ARG:HD2	1:K:244:TYR:HE2	1.69	0.55
1:A:8:LEU:HD21	1:A:219:LEU:O	2.06	0.55
1:A:473:ALA:HB2	1:L:439:LEU:HB2	1.85	0.55
1:D:80:MET:SD	1:E:431:GLU:HA	2.47	0.55
1:G:126:TYR:HE1	1:G:158:MET:H	1.53	0.55
1:I:126:TYR:HE1	1:I:158:MET:H	1.53	0.55
1:I:367:GLU:HB3	1:J:376:TYR:CE1	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:372:GLU:C	1:I:374:ILE:N	2.60	0.55
1:J:17:TYR:HB2	1:J:180:VAL:HG11	1.88	0.55
1:A:126:TYR:HE1	1:A:158:MET:H	1.53	0.55
1:B:17:TYR:HB2	1:B:180:VAL:HG11	1.88	0.55
1:D:413:GLN:H	1:E:93:ALA:HB3	1.72	0.55
1:F:17:TYR:HB2	1:F:180:VAL:HG11	1.88	0.55
1:K:30:ARG:HH12	1:K:266:ARG:NH2	2.04	0.55
1:A:430:LEU:HD23	1:L:80:MET:HE3	1.89	0.55
1:B:126:TYR:HE1	1:B:158:MET:H	1.53	0.55
1:L:126:TYR:HE1	1:L:158:MET:H	1.53	0.55
1:J:30:ARG:HH12	1:J:266:ARG:NH2	2.04	0.55
1:A:17:TYR:HB2	1:A:180:VAL:HG11	1.88	0.55
1:A:133:ALA:HB1	1:A:143:VAL:HG11	1.89	0.55
1:C:17:TYR:HB2	1:C:180:VAL:HG11	1.88	0.55
1:G:8:LEU:HD21	1:G:219:LEU:O	2.06	0.55
1:L:133:ALA:HB1	1:L:143:VAL:HG11	1.89	0.55
1:A:93:ALA:HB1	1:L:413:GLN:HB2	1.83	0.55
1:B:372:GLU:C	1:B:374:ILE:N	2.60	0.55
1:F:115:ARG:NH2	1:G:475:GLY:C	2.65	0.55
1:G:442:LEU:HB3	1:H:470:ILE:HD11	1.89	0.55
1:H:122:GLU:HG2	1:I:427:SER:CB	2.36	0.55
1:A:93:ALA:HB3	1:L:413:GLN:H	1.72	0.55
1:A:271:GLU:OE1	1:L:41:SER:HB3	2.07	0.55
1:A:431:GLU:HA	1:L:80:MET:SD	2.47	0.55
1:B:41:SER:HB3	1:C:271:GLU:OE1	2.06	0.55
1:B:133:ALA:HB1	1:B:143:VAL:HG11	1.89	0.55
1:E:17:TYR:HB2	1:E:180:VAL:HG11	1.88	0.55
1:E:439:LEU:CD1	1:F:473:ALA:CB	2.84	0.55
1:K:17:TYR:HB2	1:K:180:VAL:HG11	1.88	0.55
1:K:133:ALA:HB1	1:K:143:VAL:HG11	1.89	0.55
1:E:126:TYR:HE1	1:E:158:MET:H	1.53	0.54
1:F:413:GLN:H	1:G:93:ALA:HB3	1.72	0.54
1:F:439:LEU:HD12	1:G:473:ALA:HB3	1.89	0.54
1:H:442:LEU:HB3	1:I:470:ILE:CD1	2.34	0.54
1:J:133:ALA:HB1	1:J:143:VAL:HG11	1.89	0.54
1:K:129:THR:HG21	1:K:158:MET:O	2.07	0.54
1:K:439:LEU:CD1	1:L:473:ALA:CB	2.85	0.54
1:B:30:ARG:HH12	1:B:266:ARG:NH2	2.04	0.54
1:C:30:ARG:HH12	1:C:266:ARG:NH2	2.04	0.54
1:D:17:TYR:HB2	1:D:180:VAL:HG11	1.88	0.54
1:F:108:GLU:HB3	1:F:112:MET:HE3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:108:GLU:HB3	1:G:112:MET:HE3	1.90	0.54
1:H:17:TYR:HB2	1:H:180:VAL:HG11	1.88	0.54
1:J:8:LEU:HD21	1:J:219:LEU:O	2.06	0.54
1:L:17:TYR:HB2	1:L:180:VAL:HG11	1.88	0.54
1:A:129:THR:HG21	1:A:158:MET:O	2.07	0.54
1:H:41:SER:HB3	1:I:271:GLU:OE1	2.06	0.54
1:H:108:GLU:HB3	1:H:112:MET:HE3	1.90	0.54
1:I:115:ARG:NH2	1:J:476:ILE:N	2.56	0.54
1:I:108:GLU:HB3	1:I:112:MET:HE3	1.90	0.54
1:J:129:THR:HG21	1:J:158:MET:O	2.07	0.54
1:L:108:GLU:HB3	1:L:112:MET:HE3	1.90	0.54
1:B:108:GLU:HB3	1:B:112:MET:HE3	1.90	0.54
1:E:108:GLU:HB3	1:E:112:MET:HE3	1.90	0.54
1:E:186:ALA:HB2	1:F:171:ASP:CB	2.36	0.54
1:I:129:THR:HG21	1:I:158:MET:O	2.07	0.54
1:J:108:GLU:HB3	1:J:112:MET:HE3	1.90	0.54
1:K:108:GLU:HB3	1:K:112:MET:HE3	1.90	0.54
1:L:17:TYR:CZ	1:L:182:ARG:HG3	2.43	0.54
1:A:332:LEU:CD2	1:L:329:PHE:CE2	2.91	0.54
1:C:133:ALA:HB1	1:C:143:VAL:HG11	1.89	0.54
1:C:186:ALA:HB2	1:D:171:ASP:CB	2.37	0.54
1:D:41:SER:HB3	1:E:271:GLU:OE1	2.06	0.54
1:F:413:GLN:CB	1:G:93:ALA:HB1	2.37	0.54
1:K:17:TYR:CZ	1:K:182:ARG:HG3	2.43	0.54
1:A:17:TYR:CZ	1:A:182:ARG:HG3	2.43	0.54
1:A:108:GLU:HB3	1:A:112:MET:HE3	1.90	0.54
1:C:108:GLU:HB3	1:C:112:MET:HE3	1.90	0.54
1:H:372:GLU:C	1:H:374:ILE:N	2.60	0.54
1:I:133:ALA:HB1	1:I:143:VAL:HG11	1.89	0.54
1:A:97:LEU:HD21	1:L:112:MET:HG2	1.89	0.54
1:E:372:GLU:C	1:E:374:ILE:N	2.60	0.54
1:J:17:TYR:CZ	1:J:182:ARG:HG3	2.43	0.54
1:J:115:ARG:NH2	1:K:475:GLY:C	2.66	0.54
1:B:17:TYR:CZ	1:B:182:ARG:HG3	2.43	0.54
1:C:17:TYR:CZ	1:C:182:ARG:HG3	2.43	0.54
1:E:329:PHE:CE2	1:F:332:LEU:HD22	2.43	0.54
1:F:129:THR:HG21	1:F:158:MET:O	2.07	0.54
1:I:122:GLU:HG2	1:J:427:SER:CB	2.38	0.54
1:D:108:GLU:HB3	1:D:112:MET:HE3	1.90	0.54
1:G:467:LYS:HD3	1:H:460:ASP:HB3	1.90	0.54
1:H:133:ALA:HB1	1:H:143:VAL:HG11	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:439:LEU:HD12	1:K:473:ALA:HB3	1.89	0.54
1:D:17:TYR:CZ	1:D:182:ARG:HG3	2.43	0.53
1:D:413:GLN:CB	1:E:93:ALA:HB3	2.31	0.53
1:I:17:TYR:CZ	1:I:182:ARG:HG3	2.43	0.53
1:B:129:THR:HG21	1:B:158:MET:O	2.07	0.53
1:E:17:TYR:CZ	1:E:182:ARG:HG3	2.43	0.53
1:F:133:ALA:HB1	1:F:143:VAL:HG11	1.89	0.53
1:H:129:THR:HG21	1:H:158:MET:O	2.07	0.53
1:I:122:GLU:HG2	1:J:427:SER:OG	2.08	0.53
1:A:467:LYS:HD3	1:B:460:ASP:HB3	1.91	0.53
1:C:439:LEU:CD1	1:D:473:ALA:HB3	2.38	0.53
1:D:129:THR:HG21	1:D:158:MET:O	2.07	0.53
1:B:80:MET:SD	1:C:431:GLU:HA	2.48	0.53
1:B:413:GLN:H	1:C:93:ALA:HB3	1.73	0.53
1:C:367:GLU:HB3	1:D:376:TYR:CE1	2.43	0.53
1:C:442:LEU:HB3	1:D:470:ILE:HD11	1.89	0.53
1:E:129:THR:HG21	1:E:158:MET:O	2.07	0.53
1:G:133:ALA:HB1	1:G:143:VAL:HG11	1.89	0.53
1:H:413:GLN:H	1:I:93:ALA:HB3	1.74	0.53
1:K:413:GLN:HB2	1:L:93:ALA:HB1	1.89	0.53
1:D:133:ALA:HB1	1:D:143:VAL:HG11	1.89	0.53
1:D:413:GLN:CB	1:E:93:ALA:CB	2.79	0.53
1:E:133:ALA:HB1	1:E:143:VAL:HG11	1.89	0.53
1:H:17:TYR:CZ	1:H:182:ARG:HG3	2.43	0.53
1:L:129:THR:HG21	1:L:158:MET:O	2.07	0.53
1:C:108:GLU:O	1:C:112:MET:HG3	2.09	0.53
1:C:129:THR:HG21	1:C:158:MET:O	2.07	0.53
1:F:17:TYR:CZ	1:F:182:ARG:HG3	2.43	0.53
1:G:17:TYR:CZ	1:G:182:ARG:HG3	2.43	0.53
1:B:413:GLN:CB	1:C:93:ALA:HB1	2.39	0.53
1:D:108:GLU:O	1:D:112:MET:HG3	2.09	0.53
1:A:442:LEU:HB3	1:B:470:ILE:HD11	1.90	0.53
1:D:80:MET:HE3	1:E:430:LEU:HD23	1.90	0.53
1:A:108:GLU:O	1:A:112:MET:HG3	2.09	0.53
1:H:311:LEU:HD11	1:I:299:LEU:HD21	1.91	0.53
1:F:112:MET:SD	1:F:415:PRO:HB3	2.49	0.53
1:K:367:GLU:HB3	1:L:376:TYR:CE1	2.44	0.53
1:D:112:MET:SD	1:D:415:PRO:HB3	2.49	0.52
1:E:108:GLU:O	1:E:112:MET:HG3	2.09	0.52
1:E:122:GLU:HG2	1:F:427:SER:CB	2.39	0.52
1:H:80:MET:SD	1:I:431:GLU:HA	2.49	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:413:GLN:CB	1:I:93:ALA:HB1	2.39	0.52
1:I:112:MET:HG2	1:J:97:LEU:CD2	2.39	0.52
1:J:439:LEU:HB2	1:K:473:ALA:HB2	1.87	0.52
1:L:108:GLU:O	1:L:112:MET:HG3	2.09	0.52
1:A:367:GLU:HB3	1:B:376:TYR:CE1	2.45	0.52
1:K:108:GLU:O	1:K:112:MET:HG3	2.09	0.52
1:B:108:GLU:O	1:B:112:MET:HG3	2.09	0.52
1:C:112:MET:SD	1:C:415:PRO:HB3	2.49	0.52
1:E:367:GLU:HB3	1:F:376:TYR:CE1	2.44	0.52
1:G:129:THR:HG21	1:G:158:MET:O	2.07	0.52
1:G:367:GLU:HB3	1:H:376:TYR:CE1	2.44	0.52
1:H:115:ARG:NH2	1:I:475:GLY:C	2.68	0.52
1:K:112:MET:SD	1:K:415:PRO:HB3	2.49	0.52
1:K:323:ARG:HG3	1:L:301:ASN:HD22	1.73	0.52
1:B:115:ARG:NH2	1:C:475:GLY:C	2.67	0.52
1:J:80:MET:SD	1:K:431:GLU:HA	2.49	0.52
1:D:363:GLN:HB3	1:D:376:TYR:HE2	1.75	0.52
1:G:186:ALA:HB2	1:H:171:ASP:CB	2.38	0.52
1:H:329:PHE:CE2	1:I:332:LEU:CD2	2.93	0.52
1:J:108:GLU:O	1:J:112:MET:HG3	2.09	0.52
1:J:112:MET:SD	1:J:415:PRO:HB3	2.49	0.52
1:K:442:LEU:HB3	1:L:470:ILE:HD11	1.90	0.52
1:D:44:PRO:HB3	1:D:54:TYR:OH	2.10	0.52
1:E:112:MET:SD	1:E:415:PRO:HB3	2.49	0.52
1:F:80:MET:SD	1:G:431:GLU:HA	2.50	0.52
1:F:142:ASN:HD21	1:F:255:ARG:HG2	1.75	0.52
1:F:329:PHE:CE2	1:G:332:LEU:CD2	2.92	0.52
1:G:44:PRO:HB3	1:G:54:TYR:OH	2.10	0.52
1:H:44:PRO:HB3	1:H:54:TYR:OH	2.10	0.52
1:H:363:GLN:HB3	1:H:376:TYR:HE2	1.75	0.52
1:I:44:PRO:HB3	1:I:54:TYR:OH	2.10	0.52
1:L:363:GLN:HB3	1:L:376:TYR:HE2	1.75	0.52
1:E:142:ASN:HD21	1:E:255:ARG:HG2	1.75	0.52
1:F:44:PRO:HB3	1:F:54:TYR:OH	2.10	0.52
1:K:122:GLU:HG2	1:L:427:SER:HB3	1.92	0.52
1:K:363:GLN:HB3	1:K:376:TYR:HE2	1.75	0.52
1:E:122:GLU:HG2	1:F:427:SER:HB3	1.90	0.52
1:E:363:GLN:HB3	1:E:376:TYR:HE2	1.75	0.52
1:H:142:ASN:HD21	1:H:255:ARG:HG2	1.75	0.52
1:A:363:GLN:HB3	1:A:376:TYR:HE2	1.75	0.52
1:G:112:MET:SD	1:G:415:PRO:HB3	2.49	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:142:ASN:HD21	1:G:255:ARG:HG2	1.75	0.52
1:G:329:PHE:CE2	1:H:332:LEU:HD23	2.44	0.52
1:F:108:GLU:O	1:F:112:MET:HG3	2.09	0.52
1:F:115:ARG:HH22	1:G:475:GLY:C	2.18	0.52
1:F:311:LEU:HD11	1:G:299:LEU:HD21	1.91	0.52
1:F:363:GLN:HB3	1:F:376:TYR:HE2	1.75	0.52
1:G:363:GLN:HB3	1:G:376:TYR:HE2	1.75	0.52
1:H:112:MET:SD	1:H:415:PRO:HB3	2.49	0.52
1:I:112:MET:SD	1:I:415:PRO:HB3	2.49	0.52
1:A:369:VAL:HG12	1:A:370:THR:H	1.76	0.51
1:D:142:ASN:HD21	1:D:255:ARG:HG2	1.75	0.51
1:G:112:MET:HG2	1:H:97:LEU:CD2	2.40	0.51
1:H:108:GLU:O	1:H:112:MET:HG3	2.09	0.51
1:I:122:GLU:HG2	1:J:427:SER:HB3	1.91	0.51
1:K:44:PRO:HB3	1:K:54:TYR:OH	2.10	0.51
1:L:112:MET:SD	1:L:415:PRO:HB3	2.49	0.51
1:A:112:MET:SD	1:A:415:PRO:HB3	2.49	0.51
1:C:363:GLN:HB3	1:C:376:TYR:HE2	1.75	0.51
1:G:323:ARG:HG3	1:H:301:ASN:HD22	1.74	0.51
1:C:369:VAL:HG12	1:C:370:THR:H	1.76	0.51
1:D:372:GLU:C	1:D:374:ILE:N	2.60	0.51
1:I:363:GLN:HB3	1:I:376:TYR:HE2	1.75	0.51
1:C:44:PRO:HB3	1:C:54:TYR:OH	2.10	0.51
1:F:115:ARG:HH21	1:G:476:ILE:N	2.09	0.51
1:G:108:GLU:O	1:G:112:MET:HG3	2.09	0.51
1:J:115:ARG:HH21	1:K:476:ILE:N	2.07	0.51
1:J:413:GLN:CB	1:K:93:ALA:HB1	2.39	0.51
1:K:329:PHE:CE2	1:L:332:LEU:HD22	2.44	0.51
1:K:369:VAL:HG12	1:K:370:THR:H	1.76	0.51
1:A:142:ASN:HD21	1:A:255:ARG:HG2	1.75	0.51
1:B:112:MET:SD	1:B:415:PRO:HB3	2.49	0.51
1:B:311:LEU:HD11	1:C:299:LEU:HD21	1.93	0.51
1:B:329:PHE:CE2	1:C:332:LEU:CD2	2.93	0.51
1:F:369:VAL:HG12	1:F:370:THR:H	1.75	0.51
1:G:439:LEU:CD1	1:H:473:ALA:HB3	2.40	0.51
1:I:108:GLU:O	1:I:112:MET:HG3	2.09	0.51
1:I:369:VAL:HG12	1:I:370:THR:H	1.75	0.51
1:A:329:PHE:CE2	1:B:332:LEU:HD23	2.45	0.51
1:B:44:PRO:HB3	1:B:54:TYR:OH	2.10	0.51
1:C:142:ASN:HD21	1:C:255:ARG:HG2	1.75	0.51
1:D:112:MET:HG2	1:E:97:LEU:CD2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:369:VAL:HG12	1:E:370:THR:H	1.76	0.51
1:J:369:VAL:HG12	1:J:370:THR:H	1.76	0.51
1:D:122:GLU:HG2	1:E:427:SER:OG	2.10	0.51
1:D:369:VAL:HG12	1:D:370:THR:H	1.76	0.51
1:E:112:MET:HG2	1:F:97:LEU:CD2	2.39	0.51
1:G:122:GLU:HG2	1:H:427:SER:CB	2.41	0.51
1:I:142:ASN:HD21	1:I:255:ARG:HG2	1.75	0.51
1:J:363:GLN:HB3	1:J:376:TYR:HE2	1.75	0.51
1:A:44:PRO:HB3	1:A:54:TYR:OH	2.10	0.51
1:E:122:GLU:HG2	1:F:427:SER:OG	2.11	0.51
1:J:112:MET:HG2	1:K:97:LEU:HD21	1.91	0.51
1:A:427:SER:OG	1:L:122:GLU:HG2	2.10	0.51
1:B:142:ASN:HD21	1:B:255:ARG:HG2	1.75	0.51
1:B:369:VAL:HG12	1:B:370:THR:H	1.76	0.51
1:C:122:GLU:HG2	1:D:427:SER:HB3	1.93	0.51
1:H:369:VAL:HG12	1:H:370:THR:H	1.76	0.51
1:K:80:MET:HE3	1:L:430:LEU:HD23	1.92	0.51
1:B:363:GLN:HB3	1:B:376:TYR:HE2	1.75	0.51
1:C:122:GLU:HG2	1:D:427:SER:OG	2.11	0.51
1:E:44:PRO:HB3	1:E:54:TYR:OH	2.10	0.51
1:J:142:ASN:HD21	1:J:255:ARG:HG2	1.75	0.51
1:I:67:ASN:ND2	1:J:386:GLY:HA2	2.26	0.50
1:J:413:GLN:CB	1:K:93:ALA:HB3	2.30	0.50
1:K:122:GLU:HG2	1:L:427:SER:CB	2.41	0.50
1:K:165:SER:O	1:K:165:SER:OG	2.30	0.50
1:A:357:MET:HB2	1:A:385:LEU:HD21	1.94	0.50
1:B:340:VAL:O	1:B:344:VAL:HG12	2.12	0.50
1:B:357:MET:HB2	1:B:385:LEU:HD21	1.94	0.50
1:H:357:MET:HB2	1:H:385:LEU:HD21	1.94	0.50
1:I:357:MET:HB2	1:I:385:LEU:HD21	1.94	0.50
1:J:44:PRO:HB3	1:J:54:TYR:OH	2.10	0.50
1:L:44:PRO:HB3	1:L:54:TYR:OH	2.10	0.50
1:E:340:VAL:O	1:E:344:VAL:HG12	2.12	0.50
1:I:340:VAL:O	1:I:344:VAL:HG12	2.12	0.50
1:I:439:LEU:CD1	1:J:473:ALA:HB3	2.36	0.50
1:J:115:ARG:HH22	1:K:475:GLY:C	2.19	0.50
1:L:357:MET:HB2	1:L:385:LEU:HD21	1.94	0.50
1:A:122:GLU:HG2	1:B:427:SER:HB3	1.94	0.50
1:G:369:VAL:HG12	1:G:370:THR:H	1.76	0.50
1:H:340:VAL:O	1:H:344:VAL:HG12	2.12	0.50
1:J:357:MET:HB2	1:J:385:LEU:HD21	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:340:VAL:O	1:L:344:VAL:HG12	2.12	0.50
1:C:357:MET:HB2	1:C:385:LEU:HD21	1.94	0.50
1:G:122:GLU:HG2	1:H:427:SER:OG	2.11	0.50
1:K:340:VAL:O	1:K:344:VAL:HG12	2.12	0.50
1:A:340:VAL:O	1:A:344:VAL:HG12	2.12	0.50
1:C:122:GLU:HG2	1:D:427:SER:CB	2.41	0.50
1:C:329:PHE:CE2	1:D:332:LEU:HD23	2.46	0.50
1:D:115:ARG:NH2	1:E:475:GLY:C	2.70	0.50
1:F:340:VAL:O	1:F:344:VAL:HG12	2.12	0.50
1:G:357:MET:HB2	1:G:385:LEU:HD21	1.94	0.50
1:K:142:ASN:HD21	1:K:255:ARG:HG2	1.75	0.50
1:L:142:ASN:HD21	1:L:255:ARG:HG2	1.75	0.50
1:A:323:ARG:HG3	1:B:301:ASN:HD22	1.74	0.50
1:D:126:TYR:HE1	1:D:158:MET:N	2.10	0.50
1:K:357:MET:HB2	1:K:385:LEU:HD21	1.94	0.50
1:L:126:TYR:HE1	1:L:158:MET:N	2.10	0.50
1:L:369:VAL:HG12	1:L:370:THR:H	1.76	0.50
1:A:126:TYR:HE1	1:A:158:MET:N	2.10	0.50
1:A:299:LEU:HD21	1:L:311:LEU:HD11	1.93	0.50
1:B:126:TYR:HE1	1:B:158:MET:N	2.10	0.50
1:B:439:LEU:HB2	1:C:473:ALA:HB2	1.90	0.50
1:C:126:TYR:HE1	1:C:158:MET:N	2.10	0.50
1:C:340:VAL:O	1:C:344:VAL:HG12	2.12	0.50
1:D:165:SER:O	1:D:165:SER:OG	2.30	0.50
1:F:126:TYR:HE1	1:F:158:MET:N	2.10	0.50
1:H:439:LEU:HB2	1:I:473:ALA:HB2	1.89	0.50
1:I:186:ALA:HB2	1:J:171:ASP:CB	2.39	0.50
1:K:126:TYR:HE1	1:K:158:MET:N	2.10	0.50
1:A:93:ALA:HB3	1:L:413:GLN:CB	2.30	0.50
1:D:340:VAL:O	1:D:344:VAL:HG12	2.12	0.50
1:E:126:TYR:HE1	1:E:158:MET:N	2.10	0.50
1:E:413:GLN:HB2	1:F:93:ALA:HB1	1.92	0.50
1:F:357:MET:HB2	1:F:385:LEU:HD21	1.94	0.50
1:H:126:TYR:HE1	1:H:158:MET:N	2.10	0.50
1:J:126:TYR:HE1	1:J:158:MET:N	2.10	0.50
1:A:97:LEU:CD2	1:L:112:MET:HG2	2.41	0.49
1:A:475:GLY:C	1:L:115:ARG:NH2	2.70	0.49
1:C:112:MET:HG2	1:D:97:LEU:CD2	2.41	0.49
1:D:357:MET:HB2	1:D:385:LEU:HD21	1.94	0.49
1:G:126:TYR:HE1	1:G:158:MET:N	2.10	0.49
1:H:115:ARG:HH22	1:I:475:GLY:C	2.20	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:80:MET:SD	1:J:431:GLU:HA	2.52	0.49
1:I:126:TYR:HE1	1:I:158:MET:N	2.10	0.49
1:A:122:GLU:HG2	1:B:427:SER:CB	2.42	0.49
1:G:67:ASN:ND2	1:H:386:GLY:HA2	2.27	0.49
1:A:439:LEU:CD1	1:B:473:ALA:HB3	2.41	0.49
1:D:327:ILE:HD12	1:E:330:LEU:CD1	2.42	0.49
1:J:172:ALA:HA	1:J:261:GLY:HA2	1.95	0.49
1:I:172:ALA:HA	1:I:261:GLY:HA2	1.95	0.49
1:I:329:PHE:CE2	1:J:332:LEU:HD23	2.47	0.49
1:J:112:MET:HG2	1:K:97:LEU:CD2	2.42	0.49
1:J:340:VAL:O	1:J:344:VAL:HG12	2.12	0.49
1:K:172:ALA:HA	1:K:261:GLY:HA2	1.95	0.49
1:A:93:ALA:HB1	1:L:413:GLN:CB	2.42	0.49
1:B:61:VAL:HG22	1:B:64:ARG:HH22	1.78	0.49
1:B:112:MET:HG2	1:C:97:LEU:HD21	1.94	0.49
1:E:357:MET:HB2	1:E:385:LEU:HD21	1.94	0.49
1:E:467:LYS:HD3	1:F:460:ASP:HB3	1.93	0.49
1:J:311:LEU:HD11	1:K:299:LEU:HD21	1.94	0.49
1:K:467:LYS:HD3	1:L:460:ASP:HB3	1.94	0.49
1:B:115:ARG:HH22	1:C:475:GLY:C	2.20	0.49
1:B:115:ARG:HH21	1:C:476:ILE:N	2.10	0.49
1:I:61:VAL:HG22	1:I:64:ARG:HH22	1.78	0.49
1:J:327:ILE:HD12	1:K:330:LEU:CD1	2.42	0.49
1:A:97:LEU:HD21	1:L:112:MET:SD	2.53	0.49
1:A:122:GLU:HG2	1:B:427:SER:OG	2.12	0.49
1:D:311:LEU:HD11	1:E:299:LEU:HD21	1.95	0.49
1:G:340:VAL:O	1:G:344:VAL:HG12	2.12	0.49
1:D:112:MET:SD	1:E:97:LEU:HD21	2.53	0.49
1:H:112:MET:HG2	1:I:97:LEU:HD21	1.93	0.49
1:J:203:GLY:O	1:J:205:LYS:HG2	2.13	0.49
1:K:61:VAL:HG22	1:K:64:ARG:HH22	1.78	0.49
1:L:172:ALA:HA	1:L:261:GLY:HA2	1.95	0.49
1:G:165:SER:O	1:G:165:SER:OG	2.30	0.49
1:H:172:ALA:HA	1:H:261:GLY:HA2	1.95	0.49
1:J:122:GLU:HG2	1:K:427:SER:OG	2.12	0.49
1:L:61:VAL:HG22	1:L:64:ARG:HH22	1.78	0.49
1:A:112:MET:HG2	1:B:97:LEU:CD2	2.41	0.49
1:E:67:ASN:ND2	1:F:386:GLY:HA2	2.28	0.49
1:G:122:GLU:HG2	1:H:427:SER:HB3	1.94	0.49
1:D:392:LEU:HD12	1:D:392:LEU:HA	1.61	0.48
1:E:413:GLN:H	1:F:93:ALA:HB3	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:112:MET:HG2	1:G:97:LEU:HD21	1.95	0.48
1:G:61:VAL:HG22	1:G:64:ARG:HH22	1.78	0.48
1:D:172:ALA:HA	1:D:261:GLY:HA2	1.95	0.48
1:E:61:VAL:HG22	1:E:64:ARG:HH22	1.78	0.48
1:E:80:MET:HE3	1:F:430:LEU:HD23	1.95	0.48
1:F:439:LEU:HB2	1:G:473:ALA:HB2	1.91	0.48
1:G:158:MET:HE3	1:G:158:MET:HB3	1.60	0.48
1:A:67:ASN:ND2	1:B:386:GLY:HA2	2.28	0.48
1:A:172:ALA:HA	1:A:261:GLY:HA2	1.95	0.48
1:A:203:GLY:O	1:A:205:LYS:HG2	2.13	0.48
1:A:351:ARG:O	1:A:352:LEU:C	2.56	0.48
1:B:351:ARG:O	1:B:352:LEU:C	2.56	0.48
1:D:61:VAL:HG22	1:D:64:ARG:HH22	1.78	0.48
1:F:203:GLY:O	1:F:205:LYS:HG2	2.13	0.48
1:H:115:ARG:HH21	1:I:476:ILE:N	2.11	0.48
1:J:329:PHE:CE2	1:K:332:LEU:HD22	2.49	0.48
1:A:461:ILE:HG12	1:L:449:TRP:CH2	2.48	0.48
1:C:61:VAL:HG22	1:C:64:ARG:HH22	1.78	0.48
1:C:67:ASN:ND2	1:D:386:GLY:HA2	2.28	0.48
1:C:172:ALA:HA	1:C:261:GLY:HA2	1.95	0.48
1:C:351:ARG:O	1:C:352:LEU:C	2.56	0.48
1:D:449:TRP:CH2	1:E:461:ILE:HG12	2.48	0.48
1:F:61:VAL:HG22	1:F:64:ARG:HH22	1.78	0.48
1:K:115:ARG:HH22	1:L:475:GLY:C	2.20	0.48
1:L:203:GLY:O	1:L:205:LYS:HG2	2.13	0.48
1:E:172:ALA:HA	1:E:261:GLY:HA2	1.95	0.48
1:E:203:GLY:O	1:E:205:LYS:HG2	2.13	0.48
1:B:122:GLU:HG2	1:C:427:SER:OG	2.13	0.48
1:C:203:GLY:O	1:C:205:LYS:HG2	2.13	0.48
1:E:323:ARG:HG3	1:F:301:ASN:HD22	1.76	0.48
1:G:319:PHE:CD2	1:H:298:GLY:HA3	2.48	0.48
1:H:61:VAL:HG22	1:H:64:ARG:HH22	1.78	0.48
1:J:76:ALA:HA	1:J:374:ILE:HD11	1.96	0.48
1:K:76:ALA:HA	1:K:374:ILE:HD11	1.96	0.48
1:A:115:ARG:HH22	1:B:475:GLY:C	2.22	0.48
1:A:413:GLN:HB2	1:B:93:ALA:HB1	1.91	0.48
1:E:319:PHE:CD2	1:F:298:GLY:HA3	2.49	0.48
1:H:203:GLY:O	1:H:205:LYS:HG2	2.13	0.48
1:J:351:ARG:O	1:J:352:LEU:C	2.56	0.48
1:K:203:GLY:O	1:K:205:LYS:HG2	2.13	0.48
1:L:76:ALA:HA	1:L:374:ILE:HD11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:GLY:HA3	1:L:319:PHE:CD2	2.49	0.48
1:D:413:GLN:CB	1:E:93:ALA:HB1	2.42	0.48
1:H:122:GLU:HG2	1:I:427:SER:OG	2.13	0.48
1:I:76:ALA:HA	1:I:374:ILE:HD11	1.96	0.48
1:K:112:MET:HG2	1:L:97:LEU:CD2	2.43	0.48
1:K:122:GLU:HG2	1:L:427:SER:OG	2.13	0.48
1:A:76:ALA:HA	1:A:374:ILE:HD11	1.96	0.48
1:B:172:ALA:HA	1:B:261:GLY:HA2	1.95	0.48
1:D:329:PHE:CE2	1:E:332:LEU:HD22	2.48	0.48
1:D:351:ARG:O	1:D:352:LEU:C	2.56	0.48
1:E:80:MET:SD	1:F:431:GLU:HA	2.54	0.48
1:I:203:GLY:O	1:I:205:LYS:HG2	2.13	0.48
1:B:203:GLY:O	1:B:205:LYS:HG2	2.13	0.48
1:C:80:MET:HE3	1:D:430:LEU:HD23	1.95	0.48
1:E:115:ARG:HH22	1:F:475:GLY:C	2.22	0.47
1:H:76:ALA:HA	1:H:374:ILE:HD11	1.96	0.47
1:H:165:SER:O	1:H:165:SER:OG	2.29	0.47
1:A:61:VAL:HG22	1:A:64:ARG:HH22	1.78	0.47
1:A:469:ARG:HA	1:A:469:ARG:HD2	1.67	0.47
1:B:76:ALA:HA	1:B:374:ILE:HD11	1.96	0.47
1:F:172:ALA:HA	1:F:261:GLY:HA2	1.94	0.47
1:G:203:GLY:O	1:G:205:LYS:HG2	2.13	0.47
1:J:61:VAL:HG22	1:J:64:ARG:HH22	1.78	0.47
1:K:351:ARG:O	1:K:352:LEU:C	2.56	0.47
1:D:203:GLY:O	1:D:205:LYS:HG2	2.13	0.47
1:F:122:GLU:HG2	1:G:427:SER:OG	2.14	0.47
1:A:476:ILE:N	1:L:115:ARG:HH21	2.11	0.47
1:C:323:ARG:HG3	1:D:301:ASN:HD22	1.74	0.47
1:D:115:ARG:HH21	1:E:476:ILE:N	2.11	0.47
1:E:351:ARG:O	1:E:352:LEU:C	2.56	0.47
1:G:172:ALA:HA	1:G:261:GLY:HA2	1.95	0.47
1:A:330:LEU:CD1	1:L:327:ILE:HD12	2.44	0.47
1:C:76:ALA:HA	1:C:374:ILE:HD11	1.96	0.47
1:E:108:GLU:C	1:E:112:MET:HE3	2.40	0.47
1:F:108:GLU:C	1:F:112:MET:HE3	2.40	0.47
1:J:112:MET:SD	1:K:97:LEU:HD21	2.55	0.47
1:A:319:PHE:CD2	1:B:298:GLY:HA3	2.49	0.47
1:D:319:PHE:CD2	1:E:298:GLY:HA3	2.49	0.47
1:G:76:ALA:HA	1:G:374:ILE:HD11	1.96	0.47
1:J:258:ARG:HE	1:J:258:ARG:HB2	1.45	0.47
1:K:108:GLU:C	1:K:112:MET:HE3	2.40	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:GLU:C	1:B:112:MET:HE3	2.40	0.47
1:D:76:ALA:HA	1:D:374:ILE:HD11	1.96	0.47
1:D:464:ALA:O	1:E:460:ASP:OD2	2.33	0.47
1:E:329:PHE:CE2	1:F:332:LEU:HD23	2.50	0.47
1:F:76:ALA:HA	1:F:374:ILE:HD11	1.96	0.47
1:H:80:MET:HE2	1:H:80:MET:HB2	1.49	0.47
1:H:108:GLU:C	1:H:112:MET:HE3	2.40	0.47
1:I:108:GLU:C	1:I:112:MET:HE3	2.40	0.47
1:J:319:PHE:CD2	1:K:298:GLY:HA3	2.50	0.47
1:A:80:MET:HE3	1:B:430:LEU:HD23	1.96	0.47
1:D:115:ARG:HH22	1:E:475:GLY:C	2.23	0.47
1:E:76:ALA:HA	1:E:374:ILE:HD11	1.96	0.47
1:E:170:ARG:H	1:E:263:SER:HB3	1.80	0.47
1:I:170:ARG:H	1:I:263:SER:HB3	1.80	0.47
1:K:392:LEU:HD12	1:K:392:LEU:HA	1.61	0.47
1:B:418:PRO:HB2	1:B:420:GLU:OE1	2.15	0.47
1:C:108:GLU:C	1:C:112:MET:HE3	2.40	0.47
1:D:170:ARG:H	1:D:263:SER:HB3	1.80	0.47
1:E:439:LEU:CD1	1:F:473:ALA:HB3	2.42	0.47
1:H:112:MET:HG2	1:I:97:LEU:CD2	2.45	0.47
1:I:158:MET:HB3	1:I:158:MET:HE3	1.59	0.47
1:J:108:GLU:C	1:J:112:MET:HE3	2.40	0.47
1:J:413:GLN:H	1:K:93:ALA:CB	2.28	0.47
1:K:80:MET:HE2	1:K:80:MET:HB2	1.49	0.47
1:K:418:PRO:HB2	1:K:420:GLU:OE1	2.15	0.47
1:L:108:GLU:C	1:L:112:MET:HE3	2.40	0.47
1:B:433:ILE:HD12	1:B:433:ILE:HA	1.83	0.47
1:C:80:MET:SD	1:D:431:GLU:HA	2.54	0.47
1:C:158:MET:HE3	1:C:158:MET:HB3	1.59	0.47
1:G:108:GLU:C	1:G:112:MET:HE3	2.40	0.47
1:G:115:ARG:HH22	1:H:475:GLY:C	2.23	0.47
1:J:449:TRP:CH2	1:K:461:ILE:HG12	2.49	0.47
1:K:329:PHE:CE2	1:L:332:LEU:HD23	2.49	0.47
1:A:413:GLN:H	1:B:93:ALA:HB3	1.80	0.46
1:C:180:VAL:HA	1:C:215:THR:O	2.15	0.46
1:E:180:VAL:HA	1:E:215:THR:O	2.15	0.46
1:F:59:GLN:CA	1:G:351:ARG:HH22	2.25	0.46
1:G:413:GLN:HB2	1:H:93:ALA:HB1	1.92	0.46
1:G:413:GLN:H	1:H:93:ALA:HB3	1.80	0.46
1:J:170:ARG:H	1:J:263:SER:HB3	1.80	0.46
1:K:413:GLN:H	1:L:93:ALA:HB3	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:LEU:HD22	1:L:329:PHE:CE2	2.50	0.46
1:A:418:PRO:HB2	1:A:420:GLU:OE1	2.16	0.46
1:E:165:SER:O	1:E:165:SER:OG	2.29	0.46
1:F:469:ARG:HA	1:F:469:ARG:HD2	1.67	0.46
1:G:180:VAL:HA	1:G:215:THR:O	2.15	0.46
1:H:170:ARG:H	1:H:263:SER:HB3	1.80	0.46
1:J:469:ARG:HD2	1:J:469:ARG:HA	1.67	0.46
1:L:418:PRO:HB2	1:L:420:GLU:OE1	2.15	0.46
1:A:170:ARG:H	1:A:263:SER:HB3	1.80	0.46
1:B:112:MET:SD	1:C:97:LEU:HD21	2.56	0.46
1:D:67:ASN:ND2	1:E:386:GLY:HA2	2.31	0.46
1:D:108:GLU:C	1:D:112:MET:HE3	2.40	0.46
1:D:180:VAL:HA	1:D:215:THR:O	2.15	0.46
1:E:418:PRO:HB2	1:E:420:GLU:OE1	2.15	0.46
1:F:430:LEU:O	1:F:433:ILE:HG22	2.16	0.46
1:I:319:PHE:CD2	1:J:298:GLY:HA3	2.49	0.46
1:J:381:LEU:HD23	1:J:381:LEU:HA	1.71	0.46
1:K:170:ARG:H	1:K:263:SER:HB3	1.80	0.46
1:L:180:VAL:HA	1:L:215:THR:O	2.15	0.46
1:A:180:VAL:HA	1:A:215:THR:O	2.15	0.46
1:A:460:ASP:OD2	1:L:464:ALA:O	2.34	0.46
1:A:473:ALA:CB	1:L:439:LEU:HD12	2.45	0.46
1:B:25:ALA:O	1:B:29:THR:HG23	2.16	0.46
1:B:170:ARG:H	1:B:263:SER:HB3	1.80	0.46
1:C:413:GLN:HB2	1:D:93:ALA:HB1	1.94	0.46
1:C:418:PRO:HB2	1:C:420:GLU:OE1	2.15	0.46
1:G:430:LEU:O	1:G:433:ILE:HG22	2.16	0.46
1:I:80:MET:CE	1:J:431:GLU:OE1	2.58	0.46
1:J:322:GLY:O	1:K:300:VAL:O	2.33	0.46
1:K:67:ASN:ND2	1:L:386:GLY:HA2	2.31	0.46
1:K:180:VAL:HA	1:K:215:THR:O	2.15	0.46
1:L:351:ARG:O	1:L:352:LEU:C	2.56	0.46
1:A:108:GLU:C	1:A:112:MET:HE3	2.40	0.46
1:D:430:LEU:O	1:D:433:ILE:HG22	2.16	0.46
1:D:433:ILE:HD12	1:D:433:ILE:HA	1.83	0.46
1:G:25:ALA:O	1:G:29:THR:HG23	2.16	0.46
1:H:327:ILE:HD12	1:I:330:LEU:CD1	2.46	0.46
1:H:418:PRO:HB2	1:H:420:GLU:OE1	2.15	0.46
1:I:25:ALA:O	1:I:29:THR:HG23	2.16	0.46
1:I:431:GLU:H	1:I:431:GLU:HG2	1.22	0.46
1:K:413:GLN:CB	1:L:93:ALA:CB	2.88	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:GLY:C	1:L:115:ARG:HH22	2.22	0.46
1:D:25:ALA:O	1:D:29:THR:HG23	2.16	0.46
1:D:418:PRO:HB2	1:D:420:GLU:OE1	2.15	0.46
1:F:112:MET:HG2	1:G:97:LEU:CD2	2.46	0.46
1:F:351:ARG:O	1:F:352:LEU:C	2.56	0.46
1:F:392:LEU:HD12	1:F:392:LEU:HA	1.61	0.46
1:H:258:ARG:HE	1:H:258:ARG:HB2	1.45	0.46
1:I:180:VAL:HA	1:I:215:THR:O	2.15	0.46
1:K:110:LEU:O	1:K:114:GLU:N	2.46	0.46
1:K:146:TYR:O	1:K:148:PRO:HD3	2.16	0.46
1:L:146:TYR:O	1:L:148:PRO:HD3	2.16	0.46
1:A:146:TYR:O	1:A:148:PRO:HD3	2.16	0.46
1:B:165:SER:O	1:B:165:SER:OG	2.29	0.46
1:D:431:GLU:H	1:D:431:GLU:HG2	1.22	0.46
1:E:367:GLU:HG2	1:F:376:TYR:CE1	2.49	0.46
1:F:322:GLY:O	1:G:300:VAL:O	2.33	0.46
1:I:430:LEU:O	1:I:433:ILE:HG22	2.16	0.46
1:J:418:PRO:HB2	1:J:420:GLU:OE1	2.16	0.46
1:J:426:ILE:H	1:J:426:ILE:HG13	1.59	0.46
1:A:80:MET:SD	1:B:431:GLU:HA	2.56	0.46
1:B:322:GLY:O	1:C:300:VAL:O	2.34	0.46
1:E:369:VAL:HB	1:F:375:ARG:HG2	1.98	0.46
1:E:381:LEU:HD23	1:E:381:LEU:HA	1.71	0.46
1:F:327:ILE:HD12	1:G:330:LEU:CD1	2.46	0.46
1:G:170:ARG:H	1:G:263:SER:HB3	1.80	0.46
1:H:227:LEU:HD23	1:H:227:LEU:HA	1.83	0.46
1:H:322:GLY:O	1:I:300:VAL:O	2.34	0.46
1:J:180:VAL:HA	1:J:215:THR:O	2.15	0.46
1:J:413:GLN:O	1:K:93:ALA:HB1	2.16	0.46
1:K:115:ARG:NH2	1:L:475:GLY:C	2.74	0.46
1:L:25:ALA:O	1:L:29:THR:HG23	2.16	0.46
1:A:386:GLY:HA2	1:L:67:ASN:ND2	2.31	0.46
1:D:442:LEU:CB	1:E:470:ILE:HD11	2.41	0.46
1:F:146:TYR:O	1:F:148:PRO:HD3	2.16	0.46
1:F:180:VAL:HA	1:F:215:THR:O	2.15	0.46
1:G:146:TYR:O	1:G:148:PRO:HD3	2.16	0.46
1:H:146:TYR:O	1:H:148:PRO:HD3	2.16	0.46
1:H:430:LEU:O	1:H:433:ILE:HG22	2.16	0.46
1:J:146:TYR:O	1:J:148:PRO:HD3	2.16	0.46
1:B:146:TYR:O	1:B:148:PRO:HD3	2.16	0.46
1:E:25:ALA:O	1:E:29:THR:HG23	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:80:MET:HE2	1:E:80:MET:HB2	1.49	0.46
1:E:430:LEU:O	1:E:433:ILE:HG22	2.16	0.46
1:F:158:MET:HB3	1:F:158:MET:HE3	1.60	0.46
1:F:418:PRO:HB2	1:F:420:GLU:OE1	2.16	0.46
1:H:112:MET:SD	1:I:97:LEU:HD21	2.56	0.46
1:I:146:TYR:O	1:I:148:PRO:HD3	2.16	0.46
1:I:351:ARG:O	1:I:352:LEU:C	2.56	0.46
1:I:469:ARG:HD2	1:I:469:ARG:HA	1.67	0.46
1:K:25:ALA:O	1:K:29:THR:HG23	2.16	0.46
1:K:80:MET:SD	1:L:431:GLU:HA	2.56	0.46
1:B:112:MET:HG2	1:C:97:LEU:CD2	2.45	0.45
1:B:180:VAL:HA	1:B:215:THR:O	2.15	0.45
1:D:146:TYR:O	1:D:148:PRO:HD3	2.16	0.45
1:D:413:GLN:O	1:E:93:ALA:HB1	2.15	0.45
1:E:392:LEU:HD12	1:E:392:LEU:HA	1.61	0.45
1:F:170:ARG:H	1:F:263:SER:HB3	1.80	0.45
1:G:80:MET:HE1	1:H:431:GLU:OE2	2.16	0.45
1:H:319:PHE:CD2	1:I:298:GLY:HA3	2.51	0.45
1:I:165:SER:O	1:I:165:SER:OG	2.30	0.45
1:J:25:ALA:O	1:J:29:THR:HG23	2.16	0.45
1:K:386:GLY:C	1:K:388:VAL:H	2.24	0.45
1:L:431:GLU:H	1:L:431:GLU:HG2	1.22	0.45
1:C:430:LEU:O	1:C:433:ILE:HG22	2.16	0.45
1:D:322:GLY:O	1:E:300:VAL:O	2.34	0.45
1:D:442:LEU:CB	1:E:470:ILE:CD1	2.93	0.45
1:F:25:ALA:O	1:F:29:THR:HG23	2.16	0.45
1:F:381:LEU:HD23	1:F:381:LEU:HA	1.71	0.45
1:G:418:PRO:HB2	1:G:420:GLU:OE1	2.15	0.45
1:H:25:ALA:O	1:H:29:THR:HG23	2.16	0.45
1:H:351:ARG:O	1:H:352:LEU:C	2.56	0.45
1:H:386:GLY:C	1:H:388:VAL:H	2.25	0.45
1:I:418:PRO:HB2	1:I:420:GLU:OE1	2.15	0.45
1:K:430:LEU:O	1:K:433:ILE:HG22	2.16	0.45
1:L:170:ARG:H	1:L:263:SER:HB3	1.80	0.45
1:A:93:ALA:HB1	1:L:413:GLN:O	2.15	0.45
1:A:431:GLU:H	1:A:431:GLU:HG2	1.22	0.45
1:C:319:PHE:CD2	1:D:298:GLY:HA3	2.51	0.45
1:C:392:LEU:HD12	1:C:392:LEU:HA	1.61	0.45
1:D:413:GLN:O	1:E:93:ALA:CB	2.64	0.45
1:D:439:LEU:HD12	1:E:473:ALA:CB	2.46	0.45
1:E:146:TYR:O	1:E:148:PRO:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:413:GLN:H	1:G:93:ALA:CB	2.29	0.45
1:G:392:LEU:HA	1:G:392:LEU:HD12	1.61	0.45
1:G:469:ARG:HA	1:G:469:ARG:HD2	1.67	0.45
1:I:80:MET:CE	1:J:431:GLU:CD	2.75	0.45
1:A:80:MET:HE2	1:A:80:MET:HB2	1.49	0.45
1:A:93:ALA:CB	1:L:413:GLN:O	2.64	0.45
1:A:386:GLY:C	1:A:388:VAL:H	2.24	0.45
1:B:439:LEU:HD12	1:C:473:ALA:CB	2.46	0.45
1:C:146:TYR:O	1:C:148:PRO:HD3	2.16	0.45
1:E:227:LEU:HD23	1:E:227:LEU:HA	1.83	0.45
1:F:112:MET:SD	1:G:97:LEU:HD21	2.56	0.45
1:F:412:GLN:HB3	1:F:413:GLN:H	1.57	0.45
1:G:80:MET:SD	1:H:431:GLU:HA	2.55	0.45
1:I:381:LEU:HD23	1:I:381:LEU:HA	1.71	0.45
1:K:372:GLU:C	1:K:374:ILE:H	2.25	0.45
1:C:170:ARG:H	1:C:263:SER:HB3	1.80	0.45
1:C:412:GLN:HB3	1:C:413:GLN:H	1.57	0.45
1:G:80:MET:HE3	1:H:430:LEU:HD23	1.97	0.45
1:I:367:GLU:HG2	1:J:376:TYR:CE1	2.49	0.45
1:J:413:GLN:O	1:K:93:ALA:CB	2.65	0.45
1:K:319:PHE:CD2	1:L:298:GLY:HA3	2.51	0.45
1:A:430:LEU:O	1:A:433:ILE:HG22	2.16	0.45
1:B:374:ILE:HD12	1:B:374:ILE:HA	1.82	0.45
1:B:386:GLY:C	1:B:388:VAL:H	2.24	0.45
1:B:430:LEU:O	1:B:433:ILE:HG22	2.16	0.45
1:D:327:ILE:HD12	1:E:330:LEU:HD12	1.99	0.45
1:D:374:ILE:HD12	1:D:374:ILE:HA	1.82	0.45
1:F:227:LEU:HD23	1:F:227:LEU:HA	1.83	0.45
1:I:80:MET:HE3	1:J:430:LEU:HD23	1.96	0.45
1:K:158:MET:HB3	1:K:158:MET:HE3	1.59	0.45
1:L:372:GLU:C	1:L:374:ILE:H	2.25	0.45
1:B:413:GLN:O	1:C:93:ALA:CB	2.65	0.45
1:D:227:LEU:HD23	1:D:227:LEU:HA	1.83	0.45
1:F:431:GLU:H	1:F:431:GLU:HG2	1.22	0.45
1:A:158:MET:HE3	1:A:158:MET:HB3	1.60	0.45
1:G:367:GLU:HG2	1:H:376:TYR:CE1	2.51	0.45
1:G:369:VAL:HB	1:H:375:ARG:HG2	1.99	0.45
1:G:386:GLY:C	1:G:388:VAL:H	2.25	0.45
1:H:180:VAL:HA	1:H:215:THR:O	2.15	0.45
1:J:110:LEU:O	1:J:114:GLU:N	2.46	0.45
1:J:386:GLY:C	1:J:388:VAL:H	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:442:LEU:CB	1:K:470:ILE:CD1	2.95	0.45
1:L:430:LEU:O	1:L:433:ILE:HG22	2.16	0.45
1:A:396:LEU:HD23	1:A:396:LEU:HA	1.82	0.45
1:B:431:GLU:H	1:B:431:GLU:HG2	1.22	0.45
1:C:25:ALA:O	1:C:29:THR:HG23	2.16	0.45
1:C:115:ARG:HH22	1:D:475:GLY:C	2.25	0.45
1:G:351:ARG:O	1:G:352:LEU:C	2.56	0.45
1:H:158:MET:HE3	1:H:158:MET:HB3	1.60	0.45
1:H:311:LEU:HD13	1:H:311:LEU:HA	1.84	0.45
1:H:439:LEU:HD12	1:I:473:ALA:CB	2.45	0.45
1:A:25:ALA:O	1:A:29:THR:HG23	2.16	0.45
1:A:311:LEU:HA	1:A:311:LEU:HD13	1.84	0.45
1:C:80:MET:HE1	1:D:431:GLU:OE2	2.16	0.45
1:C:433:ILE:HD12	1:C:433:ILE:HA	1.83	0.45
1:A:392:LEU:HD12	1:A:392:LEU:HA	1.61	0.44
1:F:413:GLN:O	1:G:93:ALA:HB1	2.17	0.44
1:I:369:VAL:HB	1:J:375:ARG:HG2	1.99	0.44
1:A:206:LYS:H	1:A:206:LYS:HG2	1.52	0.44
1:A:322:GLY:O	1:B:300:VAL:O	2.35	0.44
1:B:128:VAL:O	1:B:132:GLU:HG2	2.18	0.44
1:C:416:GLU:H	1:C:416:GLU:HG2	1.65	0.44
1:E:386:GLY:C	1:E:388:VAL:H	2.25	0.44
1:J:372:GLU:C	1:J:374:ILE:H	2.25	0.44
1:A:372:GLU:C	1:A:374:ILE:H	2.25	0.44
1:B:206:LYS:H	1:B:206:LYS:HG2	1.52	0.44
1:D:413:GLN:H	1:E:93:ALA:CB	2.31	0.44
1:D:474:ILE:H	1:D:474:ILE:HG12	1.67	0.44
1:E:115:ARG:NH2	1:F:475:GLY:C	2.76	0.44
1:J:430:LEU:O	1:J:433:ILE:HG22	2.16	0.44
1:A:467:LYS:CB	1:B:460:ASP:OD2	2.64	0.44
1:F:165:SER:O	1:F:165:SER:OG	2.30	0.44
1:B:327:ILE:HD12	1:C:330:LEU:CD1	2.47	0.44
1:D:128:VAL:O	1:D:132:GLU:HG2	2.18	0.44
1:F:319:PHE:CD2	1:G:298:GLY:HA3	2.52	0.44
1:F:413:GLN:O	1:G:93:ALA:CB	2.65	0.44
1:F:439:LEU:HD12	1:G:473:ALA:CB	2.47	0.44
1:G:416:GLU:H	1:G:416:GLU:HG2	1.65	0.44
1:H:388:VAL:O	1:H:389:TYR:C	2.59	0.44
1:I:372:GLU:C	1:I:374:ILE:H	2.25	0.44
1:I:467:LYS:CB	1:J:460:ASP:OD2	2.60	0.44
1:L:128:VAL:O	1:L:132:GLU:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:GLU:OE1	1:L:80:MET:CE	2.60	0.44
1:B:319:PHE:CD2	1:C:298:GLY:HA3	2.52	0.44
1:D:381:LEU:HD23	1:D:381:LEU:HA	1.72	0.44
1:H:413:GLN:O	1:I:93:ALA:CB	2.66	0.44
1:I:227:LEU:HD23	1:I:227:LEU:HA	1.83	0.44
1:J:67:ASN:ND2	1:K:386:GLY:HA2	2.33	0.44
1:J:327:ILE:HD12	1:K:330:LEU:HD12	1.99	0.44
1:B:449:TRP:CH2	1:C:461:ILE:HG12	2.53	0.44
1:C:227:LEU:HD23	1:C:227:LEU:HA	1.83	0.44
1:D:369:VAL:HB	1:E:375:ARG:CG	2.48	0.44
1:E:388:VAL:O	1:E:389:TYR:C	2.59	0.44
1:F:388:VAL:O	1:F:389:TYR:C	2.59	0.44
1:G:372:GLU:C	1:G:374:ILE:H	2.25	0.44
1:K:396:LEU:HD23	1:K:396:LEU:HA	1.82	0.44
1:A:93:ALA:CB	1:L:413:GLN:H	2.31	0.44
1:A:227:LEU:HD23	1:A:227:LEU:HA	1.83	0.44
1:C:80:MET:HE2	1:C:80:MET:HB2	1.49	0.44
1:C:258:ARG:HE	1:C:258:ARG:HB2	1.45	0.44
1:D:258:ARG:HE	1:D:258:ARG:HB2	1.45	0.44
1:G:322:GLY:O	1:H:300:VAL:O	2.35	0.44
1:H:372:GLU:C	1:H:374:ILE:H	2.25	0.44
1:J:186:ALA:CB	1:K:171:ASP:HB3	2.47	0.44
1:K:369:VAL:HB	1:L:375:ARG:HG2	1.99	0.44
1:B:426:ILE:H	1:B:426:ILE:HG13	1.59	0.44
1:C:322:GLY:O	1:D:300:VAL:O	2.35	0.44
1:D:388:VAL:O	1:D:389:TYR:C	2.59	0.44
1:E:469:ARG:HD2	1:E:469:ARG:HA	1.67	0.44
1:H:59:GLN:CA	1:I:351:ARG:HH22	2.27	0.44
1:H:449:TRP:CH2	1:I:461:ILE:HG12	2.52	0.44
1:J:329:PHE:CE2	1:K:332:LEU:HD23	2.53	0.44
1:K:128:VAL:O	1:K:132:GLU:HG2	2.18	0.44
1:A:470:ILE:CD1	1:L:442:LEU:CB	2.95	0.43
1:D:329:PHE:CE2	1:E:332:LEU:HD23	2.53	0.43
1:D:386:GLY:C	1:D:388:VAL:H	2.25	0.43
1:F:314:ALA:HB1	1:F:318:ASP:HB3	2.00	0.43
1:G:227:LEU:HD23	1:G:227:LEU:HA	1.83	0.43
1:I:80:MET:HE2	1:I:80:MET:HB2	1.49	0.43
1:I:413:GLN:H	1:J:93:ALA:HB3	1.83	0.43
1:J:464:ALA:O	1:K:460:ASP:OD2	2.36	0.43
1:L:206:LYS:H	1:L:206:LYS:HG2	1.52	0.43
1:F:372:GLU:C	1:F:374:ILE:H	2.25	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:329:PHE:CE2	1:I:332:LEU:HD22	2.53	0.43
1:J:128:VAL:O	1:J:132:GLU:HG2	2.18	0.43
1:K:322:GLY:O	1:L:300:VAL:O	2.36	0.43
1:A:115:ARG:NH2	1:B:475:GLY:C	2.76	0.43
1:A:128:VAL:O	1:A:132:GLU:HG2	2.18	0.43
1:B:258:ARG:HE	1:B:258:ARG:HB2	1.45	0.43
1:B:413:GLN:O	1:C:93:ALA:HB1	2.18	0.43
1:B:464:ALA:O	1:C:460:ASP:OD2	2.36	0.43
1:D:167:VAL:HG23	1:D:264:TYR:OH	2.19	0.43
1:D:335:GLN:HE22	1:E:336:ALA:HB1	1.83	0.43
1:D:416:GLU:H	1:D:416:GLU:HG2	1.65	0.43
1:F:128:VAL:O	1:F:132:GLU:HG2	2.18	0.43
1:F:416:GLU:H	1:F:416:GLU:HG2	1.65	0.43
1:G:433:ILE:HD12	1:G:433:ILE:HA	1.83	0.43
1:J:335:GLN:HE22	1:K:336:ALA:HB1	1.82	0.43
1:K:372:GLU:O	1:K:373:GLU:C	2.61	0.43
1:B:80:MET:CE	1:C:431:GLU:OE1	2.59	0.43
1:B:413:GLN:H	1:C:93:ALA:CB	2.31	0.43
1:E:314:ALA:HB1	1:E:318:ASP:HB3	2.00	0.43
1:E:372:GLU:O	1:E:373:GLU:C	2.61	0.43
1:G:314:ALA:HB1	1:G:318:ASP:HB3	2.00	0.43
1:H:186:ALA:CB	1:I:171:ASP:HB3	2.46	0.43
1:L:372:GLU:O	1:L:373:GLU:C	2.61	0.43
1:A:330:LEU:HD12	1:L:327:ILE:HD12	2.00	0.43
1:A:372:GLU:O	1:A:373:GLU:C	2.61	0.43
1:G:24:ARG:O	1:G:25:ALA:C	2.62	0.43
1:G:128:VAL:O	1:G:132:GLU:HG2	2.18	0.43
1:G:374:ILE:HD12	1:G:374:ILE:HA	1.82	0.43
1:H:8:LEU:HD23	1:H:8:LEU:H	1.83	0.43
1:H:128:VAL:O	1:H:132:GLU:HG2	2.18	0.43
1:H:417:LEU:HA	1:H:418:PRO:HD3	1.90	0.43
1:J:59:GLN:CA	1:K:351:ARG:HH22	2.25	0.43
1:K:80:MET:CE	1:L:431:GLU:OE1	2.61	0.43
1:K:408:LEU:HD23	1:K:408:LEU:HA	1.86	0.43
1:L:314:ALA:HB1	1:L:318:ASP:HB3	2.00	0.43
1:L:386:GLY:C	1:L:388:VAL:H	2.24	0.43
1:L:461:ILE:HD12	1:L:461:ILE:HA	1.95	0.43
1:B:372:GLU:C	1:B:374:ILE:H	2.25	0.43
1:C:388:VAL:O	1:C:389:TYR:C	2.59	0.43
1:D:314:ALA:HB1	1:D:318:ASP:HB3	2.00	0.43
1:H:413:GLN:H	1:I:93:ALA:CB	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:8:LEU:H	1:J:8:LEU:HD23	1.83	0.43
1:K:8:LEU:HD23	1:K:8:LEU:H	1.83	0.43
1:K:381:LEU:HD23	1:K:381:LEU:HA	1.72	0.43
1:K:426:ILE:H	1:K:426:ILE:HG13	1.59	0.43
1:K:474:ILE:H	1:K:474:ILE:HG12	1.66	0.43
1:L:412:GLN:HB3	1:L:413:GLN:H	1.57	0.43
1:A:314:ALA:HB1	1:A:318:ASP:HB3	2.00	0.43
1:A:461:ILE:HD12	1:A:461:ILE:HA	1.95	0.43
1:B:167:VAL:HG23	1:B:264:TYR:OH	2.19	0.43
1:B:440:ASP:O	1:B:443:GLU:HG3	2.19	0.43
1:B:461:ILE:HD12	1:B:461:ILE:HA	1.95	0.43
1:C:413:GLN:H	1:D:93:ALA:HB3	1.83	0.43
1:D:434:GLY:O	1:D:435:ARG:HD2	2.19	0.43
1:E:412:GLN:HB3	1:E:413:GLN:H	1.57	0.43
1:F:24:ARG:O	1:F:25:ALA:C	2.62	0.43
1:F:27:TYR:CZ	1:F:264:TYR:HB2	2.54	0.43
1:F:329:PHE:CE2	1:G:332:LEU:HD22	2.53	0.43
1:F:449:TRP:CH2	1:G:461:ILE:HG12	2.53	0.43
1:G:27:TYR:CZ	1:G:264:TYR:HB2	2.54	0.43
1:G:396:LEU:HD23	1:G:396:LEU:HA	1.82	0.43
1:H:71:SER:OG	1:I:383:ASP:OD1	2.29	0.43
1:K:367:GLU:HG2	1:L:376:TYR:CE1	2.50	0.43
1:L:440:ASP:O	1:L:443:GLU:HG3	2.19	0.43
1:A:220:ASP:HB3	1:A:223:SER:O	2.19	0.43
1:B:434:GLY:O	1:B:435:ARG:HD2	2.19	0.43
1:C:128:VAL:O	1:C:132:GLU:HG2	2.18	0.43
1:C:220:ASP:HB3	1:C:223:SER:O	2.19	0.43
1:D:158:MET:HE3	1:D:158:MET:HB3	1.59	0.43
1:D:372:GLU:O	1:D:373:GLU:C	2.61	0.43
1:E:8:LEU:HD23	1:E:8:LEU:H	1.83	0.43
1:F:80:MET:CE	1:G:431:GLU:OE1	2.60	0.43
1:F:440:ASP:O	1:F:443:GLU:HG3	2.19	0.43
1:G:115:ARG:NH2	1:H:475:GLY:C	2.77	0.43
1:G:167:VAL:HG23	1:G:264:TYR:OH	2.19	0.43
1:H:24:ARG:O	1:H:25:ALA:C	2.62	0.43
1:H:67:ASN:ND2	1:I:386:GLY:HA2	2.34	0.43
1:H:220:ASP:HB3	1:H:223:SER:O	2.19	0.43
1:I:110:LEU:O	1:I:114:GLU:N	2.46	0.43
1:J:372:GLU:O	1:J:373:GLU:C	2.61	0.43
1:K:314:ALA:HB1	1:K:318:ASP:HB3	2.00	0.43
1:L:8:LEU:HD23	1:L:8:LEU:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:SER:O	1:A:165:SER:OG	2.30	0.43
1:A:369:VAL:HB	1:B:375:ARG:HG2	2.00	0.43
1:B:372:GLU:O	1:B:373:GLU:C	2.61	0.43
1:C:206:LYS:H	1:C:206:LYS:HG2	1.52	0.43
1:E:416:GLU:H	1:E:416:GLU:HG2	1.65	0.43
1:F:167:VAL:HG23	1:F:264:TYR:OH	2.19	0.43
1:F:335:GLN:HE22	1:G:336:ALA:HB1	1.84	0.43
1:H:27:TYR:CZ	1:H:264:TYR:HB2	2.54	0.43
1:H:413:GLN:O	1:I:93:ALA:HB1	2.18	0.43
1:I:128:VAL:O	1:I:132:GLU:HG2	2.18	0.43
1:J:412:GLN:HB3	1:J:413:GLN:H	1.57	0.43
1:A:8:LEU:HD23	1:A:8:LEU:H	1.83	0.43
1:A:412:GLN:HB3	1:A:413:GLN:H	1.57	0.43
1:B:24:ARG:O	1:B:25:ALA:C	2.62	0.43
1:B:27:TYR:CZ	1:B:264:TYR:HB2	2.54	0.43
1:B:227:LEU:HD23	1:B:227:LEU:HA	1.83	0.43
1:C:27:TYR:CZ	1:C:264:TYR:HB2	2.54	0.43
1:C:367:GLU:HG2	1:D:376:TYR:CE1	2.51	0.43
1:C:369:VAL:HB	1:D:375:ARG:HG2	2.00	0.43
1:C:372:GLU:O	1:C:373:GLU:C	2.62	0.43
1:C:413:GLN:CB	1:D:93:ALA:CB	2.92	0.43
1:D:220:ASP:HB3	1:D:223:SER:O	2.19	0.43
1:E:27:TYR:CZ	1:E:264:TYR:HB2	2.54	0.43
1:E:128:VAL:O	1:E:132:GLU:HG2	2.18	0.43
1:F:434:GLY:O	1:F:435:ARG:HD2	2.19	0.43
1:H:314:ALA:HB1	1:H:318:ASP:HB3	2.00	0.43
1:I:8:LEU:HD23	1:I:8:LEU:H	1.83	0.43
1:I:386:GLY:C	1:I:388:VAL:H	2.25	0.43
1:J:311:LEU:HD13	1:J:311:LEU:HA	1.84	0.43
1:B:329:PHE:CE2	1:C:332:LEU:HD22	2.54	0.42
1:B:396:LEU:HD23	1:B:396:LEU:HA	1.82	0.42
1:C:167:VAL:HG23	1:C:264:TYR:OH	2.19	0.42
1:C:467:LYS:CB	1:D:460:ASP:OD2	2.61	0.42
1:C:474:ILE:H	1:C:474:ILE:HG12	1.66	0.42
1:D:8:LEU:HD23	1:D:8:LEU:H	1.83	0.42
1:D:27:TYR:CZ	1:D:264:TYR:HB2	2.54	0.42
1:E:372:GLU:C	1:E:374:ILE:H	2.25	0.42
1:G:381:LEU:HD23	1:G:381:LEU:HA	1.71	0.42
1:I:220:ASP:HB3	1:I:223:SER:O	2.19	0.42
1:J:314:ALA:HB1	1:J:318:ASP:HB3	2.00	0.42
1:J:374:ILE:HD12	1:J:374:ILE:HA	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:388:VAL:O	1:J:389:TYR:C	2.59	0.42
1:K:440:ASP:O	1:K:443:GLU:HG3	2.19	0.42
1:A:375:ARG:CG	1:L:369:VAL:HB	2.49	0.42
1:E:167:VAL:HG23	1:E:264:TYR:OH	2.19	0.42
1:E:440:ASP:O	1:E:443:GLU:HG3	2.19	0.42
1:F:8:LEU:HD23	1:F:8:LEU:H	1.83	0.42
1:G:388:VAL:O	1:G:389:TYR:C	2.59	0.42
1:A:27:TYR:CZ	1:A:264:TYR:HB2	2.54	0.42
1:B:67:ASN:ND2	1:C:386:GLY:HA2	2.33	0.42
1:C:186:ALA:CB	1:D:171:ASP:HB3	2.47	0.42
1:C:314:ALA:HB1	1:C:318:ASP:HB3	2.00	0.42
1:E:112:MET:CG	1:F:97:LEU:HD21	2.50	0.42
1:F:80:MET:HB2	1:F:80:MET:HE2	1.49	0.42
1:I:24:ARG:O	1:I:25:ALA:C	2.62	0.42
1:I:27:TYR:CZ	1:I:264:TYR:HB2	2.54	0.42
1:L:24:ARG:O	1:L:25:ALA:C	2.62	0.42
1:B:314:ALA:HB1	1:B:318:ASP:HB3	2.00	0.42
1:B:335:GLN:HE22	1:C:336:ALA:HB1	1.85	0.42
1:C:8:LEU:HD23	1:C:8:LEU:H	1.83	0.42
1:E:434:GLY:O	1:E:435:ARG:HD2	2.19	0.42
1:F:327:ILE:HD12	1:G:330:LEU:HD12	2.02	0.42
1:G:220:ASP:HB3	1:G:223:SER:O	2.19	0.42
1:G:440:ASP:O	1:G:443:GLU:HG3	2.19	0.42
1:H:434:GLY:O	1:H:435:ARG:HD2	2.19	0.42
1:I:434:GLY:O	1:I:435:ARG:HD2	2.19	0.42
1:K:220:ASP:HB3	1:K:223:SER:O	2.19	0.42
1:K:240:SER:O	1:K:241:ASP:C	2.63	0.42
1:L:392:LEU:HD12	1:L:392:LEU:HA	1.61	0.42
1:A:167:VAL:HG23	1:A:264:TYR:OH	2.19	0.42
1:A:434:GLY:O	1:A:435:ARG:HD2	2.19	0.42
1:C:440:ASP:O	1:C:443:GLU:HG3	2.19	0.42
1:E:80:MET:HE1	1:F:431:GLU:OE2	2.19	0.42
1:F:220:ASP:HB3	1:F:223:SER:O	2.19	0.42
1:I:80:MET:HE1	1:J:431:GLU:OE2	2.15	0.42
1:I:112:MET:CG	1:J:97:LEU:HD21	2.48	0.42
1:J:167:VAL:HG23	1:J:264:TYR:OH	2.19	0.42
1:J:227:LEU:HD23	1:J:227:LEU:HA	1.83	0.42
1:A:80:MET:HE1	1:B:431:GLU:OE2	2.17	0.42
1:B:8:LEU:HD23	1:B:8:LEU:H	1.83	0.42
1:B:186:ALA:CB	1:C:171:ASP:HB3	2.47	0.42
1:B:220:ASP:HB3	1:B:223:SER:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:434:GLY:O	1:C:435:ARG:HD2	2.19	0.42
1:D:80:MET:HE2	1:D:80:MET:HB2	1.49	0.42
1:E:110:LEU:O	1:E:114:GLU:N	2.46	0.42
1:E:220:ASP:HB3	1:E:223:SER:O	2.19	0.42
1:E:467:LYS:CB	1:F:460:ASP:OD2	2.65	0.42
1:F:381:LEU:HD22	1:F:385:LEU:HG	2.02	0.42
1:G:8:LEU:H	1:G:8:LEU:HD23	1.83	0.42
1:G:381:LEU:HD22	1:G:385:LEU:HG	2.02	0.42
1:G:467:LYS:CB	1:H:460:ASP:OD2	2.63	0.42
1:H:80:MET:CE	1:I:431:GLU:OE1	2.59	0.42
1:I:167:VAL:HG23	1:I:264:TYR:OH	2.19	0.42
1:I:314:ALA:HB1	1:I:318:ASP:HB3	2.00	0.42
1:I:322:GLY:O	1:J:300:VAL:O	2.37	0.42
1:I:381:LEU:HD22	1:I:385:LEU:HG	2.02	0.42
1:J:165:SER:O	1:J:165:SER:OG	2.29	0.42
1:J:452:LEU:O	1:J:456:ARG:NH1	2.53	0.42
1:L:27:TYR:CZ	1:L:264:TYR:HB2	2.54	0.42
1:L:434:GLY:O	1:L:435:ARG:HD2	2.19	0.42
1:B:388:VAL:O	1:B:389:TYR:C	2.59	0.42
1:B:392:LEU:HA	1:B:392:LEU:HD12	1.61	0.42
1:C:386:GLY:C	1:C:388:VAL:H	2.25	0.42
1:D:469:ARG:HA	1:D:469:ARG:HD2	1.67	0.42
1:E:381:LEU:HD22	1:E:385:LEU:HG	2.02	0.42
1:G:434:GLY:O	1:G:435:ARG:HD2	2.19	0.42
1:H:256:MET:HB3	1:H:266:ARG:O	2.20	0.42
1:H:327:ILE:HD12	1:I:330:LEU:HD12	2.02	0.42
1:H:381:LEU:HD22	1:H:385:LEU:HG	2.02	0.42
1:H:440:ASP:O	1:H:443:GLU:HG3	2.19	0.42
1:I:440:ASP:O	1:I:443:GLU:HG3	2.19	0.42
1:J:440:ASP:O	1:J:443:GLU:HG3	2.19	0.42
1:K:388:VAL:O	1:K:389:TYR:C	2.59	0.42
1:K:452:LEU:O	1:K:456:ARG:NH1	2.53	0.42
1:L:388:VAL:O	1:L:389:TYR:C	2.59	0.42
1:A:440:ASP:O	1:A:443:GLU:HG3	2.19	0.42
1:B:474:ILE:H	1:B:474:ILE:HG12	1.67	0.42
1:C:372:GLU:C	1:C:374:ILE:H	2.25	0.42
1:C:381:LEU:HD23	1:C:381:LEU:HA	1.71	0.42
1:D:372:GLU:C	1:D:374:ILE:H	2.25	0.42
1:E:126:TYR:CE1	1:E:158:MET:N	2.88	0.42
1:E:258:ARG:HE	1:E:258:ARG:HB2	1.45	0.42
1:E:413:GLN:CB	1:F:93:ALA:CB	2.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:186:ALA:CB	1:G:171:ASP:HB3	2.45	0.42
1:F:464:ALA:O	1:G:460:ASP:OD2	2.37	0.42
1:I:372:GLU:O	1:I:373:GLU:C	2.61	0.42
1:I:392:LEU:HD12	1:I:392:LEU:HA	1.61	0.42
1:J:24:ARG:O	1:J:25:ALA:C	2.62	0.42
1:J:240:SER:O	1:J:241:ASP:C	2.63	0.42
1:J:256:MET:HB3	1:J:266:ARG:O	2.20	0.42
1:J:396:LEU:HD23	1:J:396:LEU:HA	1.82	0.42
1:J:434:GLY:O	1:J:435:ARG:HD2	2.19	0.42
1:K:167:VAL:HG23	1:K:264:TYR:OH	2.19	0.42
1:L:256:MET:HB3	1:L:266:ARG:O	2.20	0.42
1:A:300:VAL:O	1:L:322:GLY:O	2.36	0.42
1:A:474:ILE:H	1:A:474:ILE:HG12	1.67	0.42
1:D:367:GLU:CG	1:E:376:TYR:CE1	3.01	0.42
1:D:440:ASP:O	1:D:443:GLU:HG3	2.19	0.42
1:G:352:LEU:HD13	1:G:352:LEU:HA	1.90	0.42
1:I:452:LEU:O	1:I:456:ARG:NH1	2.53	0.42
1:J:27:TYR:CZ	1:J:264:TYR:HB2	2.54	0.42
1:J:381:LEU:HD22	1:J:385:LEU:HG	2.02	0.42
1:K:206:LYS:H	1:K:206:LYS:HG2	1.52	0.42
1:L:94:LYS:HE3	1:L:94:LYS:HB3	1.93	0.42
1:L:220:ASP:HB3	1:L:223:SER:O	2.19	0.42
1:L:452:LEU:O	1:L:456:ARG:NH1	2.53	0.42
1:B:95:GLN:HE21	1:B:95:GLN:HB2	1.73	0.42
1:D:24:ARG:O	1:D:25:ALA:C	2.62	0.42
1:E:186:ALA:CB	1:F:171:ASP:HB3	2.47	0.42
1:E:256:MET:HB3	1:E:266:ARG:O	2.20	0.42
1:F:367:GLU:CG	1:G:376:TYR:CE1	3.02	0.42
1:F:386:GLY:C	1:F:388:VAL:H	2.25	0.42
1:H:167:VAL:HG23	1:H:264:TYR:OH	2.19	0.42
1:H:452:LEU:O	1:H:456:ARG:NH1	2.53	0.42
1:L:167:VAL:HG23	1:L:264:TYR:OH	2.19	0.42
1:A:431:GLU:CD	1:L:80:MET:CE	2.81	0.41
1:B:59:GLN:CA	1:C:351:ARG:HH22	2.27	0.41
1:B:256:MET:HB3	1:B:266:ARG:O	2.20	0.41
1:D:112:MET:CG	1:E:97:LEU:HD21	2.50	0.41
1:E:443:GLU:OE2	1:E:444:ARG:HG3	2.20	0.41
1:F:126:TYR:CE1	1:F:158:MET:N	2.88	0.41
1:F:256:MET:HB3	1:F:266:ARG:O	2.20	0.41
1:F:413:GLN:N	1:G:93:ALA:HB3	2.35	0.41
1:H:110:LEU:O	1:H:114:GLU:N	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:367:GLU:CG	1:I:376:TYR:CE1	3.02	0.41
1:H:392:LEU:HD12	1:H:392:LEU:HA	1.61	0.41
1:I:442:LEU:HB3	1:J:470:ILE:CD1	2.49	0.41
1:I:474:ILE:H	1:I:474:ILE:HG12	1.67	0.41
1:J:94:LYS:HE3	1:J:94:LYS:HB3	1.93	0.41
1:J:220:ASP:HB3	1:J:223:SER:O	2.19	0.41
1:L:158:MET:HB3	1:L:158:MET:HE3	1.59	0.41
1:A:244:TYR:HA	1:A:245:PRO:HD3	1.95	0.41
1:A:452:LEU:O	1:A:456:ARG:NH1	2.53	0.41
1:C:256:MET:HB3	1:C:266:ARG:O	2.20	0.41
1:D:381:LEU:HD22	1:D:385:LEU:HG	2.02	0.41
1:H:464:ALA:O	1:I:460:ASP:OD2	2.36	0.41
1:I:311:LEU:HA	1:I:311:LEU:HD13	1.84	0.41
1:I:412:GLN:HB3	1:I:413:GLN:H	1.57	0.41
1:I:443:GLU:OE2	1:I:444:ARG:HG3	2.21	0.41
1:J:376:TYR:C	1:J:378:ALA:N	2.78	0.41
1:K:24:ARG:O	1:K:25:ALA:C	2.62	0.41
1:K:27:TYR:CZ	1:K:264:TYR:HB2	2.54	0.41
1:A:94:LYS:HE3	1:A:94:LYS:HB3	1.93	0.41
1:A:381:LEU:HD23	1:A:381:LEU:HA	1.71	0.41
1:B:56:THR:HG21	1:C:274:GLY:H	1.85	0.41
1:B:469:ARG:HD2	1:B:469:ARG:HA	1.67	0.41
1:D:256:MET:HB3	1:D:266:ARG:O	2.20	0.41
1:E:95:GLN:HE21	1:E:95:GLN:HB2	1.72	0.41
1:E:413:GLN:O	1:F:93:ALA:HB1	2.20	0.41
1:F:443:GLU:OE2	1:F:444:ARG:HG3	2.20	0.41
1:I:396:LEU:HD23	1:I:396:LEU:HA	1.82	0.41
1:K:381:LEU:HD22	1:K:385:LEU:HG	2.02	0.41
1:K:434:GLY:O	1:K:435:ARG:HD2	2.19	0.41
1:L:227:LEU:HD23	1:L:227:LEU:HA	1.83	0.41
1:L:376:TYR:C	1:L:378:ALA:N	2.78	0.41
1:A:258:ARG:HE	1:A:258:ARG:HB2	1.45	0.41
1:G:121:ILE:HD12	1:G:121:ILE:HA	1.87	0.41
1:G:443:GLU:OE2	1:G:444:ARG:HG3	2.20	0.41
1:H:381:LEU:HA	1:H:381:LEU:HD23	1.72	0.41
1:J:392:LEU:HA	1:J:392:LEU:HD12	1.61	0.41
1:J:443:GLU:OE2	1:J:444:ARG:HG3	2.20	0.41
1:K:227:LEU:HD23	1:K:227:LEU:HA	1.83	0.41
1:K:443:GLU:OE2	1:K:444:ARG:HG3	2.20	0.41
1:L:469:ARG:HA	1:L:469:ARG:HD2	1.67	0.41
1:C:426:ILE:H	1:C:426:ILE:HG13	1.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:452:LEU:O	1:C:456:ARG:NH1	2.53	0.41
1:D:240:SER:O	1:D:241:ASP:C	2.63	0.41
1:D:311:LEU:HA	1:D:311:LEU:HD13	1.84	0.41
1:D:443:GLU:OE2	1:D:444:ARG:HG3	2.20	0.41
1:F:67:ASN:ND2	1:G:386:GLY:HA2	2.35	0.41
1:F:396:LEU:HA	1:F:396:LEU:HD23	1.82	0.41
1:G:452:LEU:O	1:G:456:ARG:NH1	2.53	0.41
1:I:413:GLN:HB2	1:J:93:ALA:HB1	1.97	0.41
1:L:381:LEU:HD23	1:L:381:LEU:HA	1.71	0.41
1:A:24:ARG:O	1:A:25:ALA:C	2.62	0.41
1:A:367:GLU:HG2	1:B:376:TYR:CE1	2.51	0.41
1:A:381:LEU:HD22	1:A:385:LEU:HG	2.02	0.41
1:A:388:VAL:O	1:A:389:TYR:C	2.59	0.41
1:B:408:LEU:HA	1:B:408:LEU:HD23	1.87	0.41
1:B:452:LEU:O	1:B:456:ARG:NH1	2.53	0.41
1:E:452:LEU:O	1:E:456:ARG:NH1	2.53	0.41
1:L:474:ILE:H	1:L:474:ILE:HG12	1.67	0.41
1:B:367:GLU:CG	1:C:376:TYR:CE1	3.01	0.41
1:C:240:SER:O	1:C:241:ASP:C	2.63	0.41
1:D:59:GLN:CA	1:E:351:ARG:HH22	2.27	0.41
1:E:112:MET:SD	1:F:97:LEU:HD21	2.61	0.41
1:F:452:LEU:O	1:F:456:ARG:NH1	2.53	0.41
1:G:256:MET:HB3	1:G:266:ARG:O	2.20	0.41
1:H:95:GLN:HE21	1:H:95:GLN:HB2	1.72	0.41
1:H:442:LEU:CB	1:I:470:ILE:CD1	2.99	0.41
1:I:240:SER:O	1:I:241:ASP:C	2.63	0.41
1:J:439:LEU:HD12	1:K:473:ALA:CB	2.49	0.41
1:K:430:LEU:O	1:K:431:GLU:C	2.63	0.41
1:L:381:LEU:HD22	1:L:385:LEU:HG	2.02	0.41
1:A:171:ASP:HB3	1:L:186:ALA:CB	2.49	0.41
1:B:240:SER:O	1:B:241:ASP:C	2.63	0.41
1:B:352:LEU:HD13	1:B:352:LEU:HA	1.89	0.41
1:B:381:LEU:HD22	1:B:385:LEU:HG	2.02	0.41
1:D:206:LYS:H	1:D:206:LYS:HG2	1.52	0.41
1:D:352:LEU:HD13	1:D:352:LEU:HA	1.90	0.41
1:D:413:GLN:N	1:E:93:ALA:HB3	2.36	0.41
1:E:240:SER:O	1:E:241:ASP:C	2.63	0.41
1:G:290:SER:HB3	1:H:344:VAL:HG11	2.02	0.41
1:H:372:GLU:O	1:H:373:GLU:C	2.61	0.41
1:H:408:LEU:HD23	1:H:408:LEU:HA	1.86	0.41
1:I:256:MET:HB3	1:I:266:ARG:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:95:GLN:HE21	1:L:95:GLN:HB2	1.73	0.41
1:B:130:LEU:HD12	1:B:130:LEU:HA	1.96	0.41
1:B:412:GLN:HB3	1:B:413:GLN:H	1.57	0.41
1:C:24:ARG:O	1:C:25:ALA:C	2.62	0.41
1:C:115:ARG:NH2	1:D:475:GLY:C	2.79	0.41
1:C:381:LEU:HD22	1:C:385:LEU:HG	2.02	0.41
1:D:452:LEU:O	1:D:456:ARG:NH1	2.53	0.41
1:E:322:GLY:O	1:F:300:VAL:O	2.39	0.41
1:E:413:GLN:O	1:F:93:ALA:CB	2.69	0.41
1:H:335:GLN:HE22	1:I:336:ALA:HB1	1.85	0.41
1:H:443:GLU:OE2	1:H:444:ARG:HG3	2.20	0.41
1:I:56:THR:HG21	1:J:274:GLY:H	1.86	0.41
1:J:431:GLU:H	1:J:431:GLU:HG2	1.22	0.41
1:K:256:MET:HB3	1:K:266:ARG:O	2.20	0.41
1:K:413:GLN:CB	1:L:93:ALA:HB1	2.51	0.41
1:L:443:GLU:OE2	1:L:444:ARG:HG3	2.20	0.41
1:A:97:LEU:HD21	1:L:112:MET:CG	2.51	0.41
1:A:256:MET:HB3	1:A:266:ARG:O	2.20	0.41
1:B:327:ILE:HD12	1:C:330:LEU:HD12	2.03	0.41
1:C:311:LEU:HD13	1:C:311:LEU:HA	1.84	0.41
1:C:461:ILE:HD12	1:C:461:ILE:HA	1.95	0.41
1:E:474:ILE:H	1:E:474:ILE:HG12	1.67	0.41
1:F:56:THR:HG21	1:G:274:GLY:H	1.86	0.41
1:H:196:LYS:HE3	1:H:196:LYS:HB3	1.91	0.41
1:H:396:LEU:HD23	1:H:396:LEU:HA	1.82	0.41
1:I:453:ALA:N	1:I:454:PRO:HD2	2.36	0.41
1:K:386:GLY:C	1:K:388:VAL:N	2.78	0.41
1:B:386:GLY:C	1:B:388:VAL:N	2.78	0.40
1:C:396:LEU:HD23	1:C:396:LEU:HA	1.82	0.40
1:E:196:LYS:HE3	1:E:196:LYS:HB3	1.91	0.40
1:F:240:SER:O	1:F:241:ASP:C	2.63	0.40
1:G:80:MET:CE	1:H:431:GLU:OE1	2.62	0.40
1:G:112:MET:CG	1:H:97:LEU:HD21	2.51	0.40
1:H:453:ALA:N	1:H:454:PRO:HD2	2.36	0.40
1:I:388:VAL:O	1:I:389:TYR:C	2.59	0.40
1:I:467:LYS:CD	1:J:460:ASP:HB3	2.49	0.40
1:J:453:ALA:N	1:J:454:PRO:HD2	2.36	0.40
1:K:94:LYS:HE3	1:K:94:LYS:HB3	1.93	0.40
1:L:80:MET:HE2	1:L:80:MET:HB2	1.49	0.40
1:L:386:GLY:C	1:L:388:VAL:N	2.78	0.40
1:A:470:ILE:HD11	1:L:442:LEU:CB	2.44	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:430:LEU:O	1:B:431:GLU:C	2.63	0.40
1:B:442:LEU:CB	1:C:470:ILE:CD1	2.98	0.40
1:B:443:GLU:OE2	1:B:444:ARG:HG3	2.20	0.40
1:F:112:MET:SD	1:F:415:PRO:CB	3.10	0.40
1:I:115:ARG:HH22	1:J:475:GLY:C	2.28	0.40
1:J:408:LEU:HD23	1:J:408:LEU:HA	1.86	0.40
1:L:426:ILE:H	1:L:426:ILE:HG13	1.59	0.40
1:C:442:LEU:HB3	1:D:470:ILE:CD1	2.51	0.40
1:D:95:GLN:HE21	1:D:95:GLN:HB2	1.73	0.40
1:D:112:MET:SD	1:D:415:PRO:CB	3.10	0.40
1:G:240:SER:O	1:G:241:ASP:C	2.63	0.40
1:G:453:ALA:N	1:G:454:PRO:HD2	2.36	0.40
1:H:56:THR:HG21	1:I:274:GLY:H	1.87	0.40
1:I:293:SER:HG	1:J:337:ASP:HB3	1.84	0.40
1:I:323:ARG:HG3	1:J:301:ASN:HD22	1.75	0.40
1:J:73:LEU:HG	1:J:134:LEU:HD11	2.03	0.40
1:K:73:LEU:HG	1:K:134:LEU:HD11	2.03	0.40
1:L:417:LEU:HA	1:L:418:PRO:HD3	1.90	0.40
1:A:186:ALA:CB	1:B:171:ASP:HB3	2.47	0.40
1:F:442:LEU:CB	1:G:470:ILE:CD1	2.99	0.40
1:G:110:LEU:O	1:G:114:GLU:N	2.46	0.40
1:G:112:MET:SD	1:G:415:PRO:CB	3.10	0.40
1:G:376:TYR:C	1:G:378:ALA:N	2.78	0.40
1:H:433:ILE:HD12	1:H:433:ILE:HA	1.83	0.40
1:I:112:MET:SD	1:I:415:PRO:CB	3.10	0.40
1:I:186:ALA:O	1:I:187:PHE:C	2.65	0.40
1:I:430:LEU:O	1:I:431:GLU:C	2.63	0.40
1:L:112:MET:SD	1:L:415:PRO:CB	3.10	0.40
1:A:59:GLN:OE1	1:A:61:VAL:N	2.55	0.40
1:A:386:GLY:C	1:A:388:VAL:N	2.78	0.40
1:A:417:LEU:HA	1:A:418:PRO:HD3	1.90	0.40
1:A:443:GLU:OE2	1:A:444:ARG:HG3	2.21	0.40
1:B:158:MET:HB3	1:B:158:MET:HE3	1.59	0.40
1:C:112:MET:SD	1:C:415:PRO:CB	3.10	0.40
1:D:453:ALA:N	1:D:454:PRO:HD2	2.36	0.40
1:E:442:LEU:HB3	1:F:470:ILE:CD1	2.50	0.40
1:F:59:GLN:OE1	1:F:61:VAL:N	2.55	0.40
1:F:329:PHE:CE2	1:G:332:LEU:HD23	2.56	0.40
1:G:282:LEU:HD12	1:G:282:LEU:HA	1.95	0.40
1:H:376:TYR:C	1:H:378:ALA:N	2.78	0.40
1:I:112:MET:SD	1:J:97:LEU:HD21	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:386:GLY:C	1:J:388:VAL:N	2.79	0.40
1:K:412:GLN:HB3	1:K:413:GLN:H	1.57	0.40
1:K:469:ARG:HD2	1:K:469:ARG:HA	1.67	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	B	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	C	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	D	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	E	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	F	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	G	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	H	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	I	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	J	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	K	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
1	L	465/536 (87%)	436 (94%)	28 (6%)	1 (0%)	44	78
All	All	5580/6432 (87%)	5232 (94%)	336 (6%)	12 (0%)	45	78

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	388	VAL

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Mol	Chain	Res	Type
1	B	388	VAL
1	C	388	VAL
1	D	388	VAL
1	H	388	VAL
1	E	388	VAL
1	F	388	VAL
1	G	388	VAL
1	I	388	VAL
1	J	388	VAL
1	K	388	VAL
1	L	388	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	B	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	C	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	D	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	E	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	F	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	G	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	H	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	I	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	J	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	K	396/442 (90%)	330 (83%)	66 (17%)	2	11
1	L	396/442 (90%)	330 (83%)	66 (17%)	2	11
All	All	4752/5304 (90%)	3960 (83%)	792 (17%)	4	11

All (792) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	THR
1	A	15	SER
1	A	34	CYS
1	A	38	THR
1	A	52	THR
1	A	56	THR
1	A	75	LEU
1	A	86	LEU
1	A	88	ILE
1	A	95	GLN
1	A	96	LEU
1	A	106	VAL
1	A	108	GLU
1	A	116	ILE
1	A	121	ILE
1	A	124	ASN
1	A	129	THR
1	A	130	LEU
1	A	138	VAL
1	A	139	VAL
1	A	147	LEU
1	A	158	MET
1	A	160	LEU
1	A	164	SER
1	A	165	SER
1	A	179	MET
1	A	193	ASP
1	A	206	LYS
1	A	210	THR
1	A	217	ILE
1	A	221	GLU
1	A	223	SER
1	A	227	LEU
1	A	237	VAL
1	A	238	GLN
1	A	243	THR
1	A	256	MET
1	A	259	LEU
1	A	263	SER
1	A	275	ASP
1	A	282	LEU
1	A	286	ILE
1	A	297	ILE

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Mol	Chain	Res	Type
1	A	307	GLN
1	A	311	LEU
1	A	313	LYS
1	A	321	THR
1	A	326	ASP
1	A	351	ARG
1	A	352	LEU
1	A	353	SER
1	A	357	MET
1	A	368	ARG
1	A	369	VAL
1	A	389	TYR
1	A	397	GLN
1	A	399	PRO
1	A	403	VAL
1	A	412	GLN
1	A	416	GLU
1	A	417	LEU
1	A	422	VAL
1	A	431	GLU
1	A	446	VAL
1	A	452	LEU
1	A	474	ILE
1	B	6	THR
1	B	15	SER
1	B	34	CYS
1	B	38	THR
1	B	52	THR
1	B	56	THR
1	B	75	LEU
1	B	86	LEU
1	B	88	ILE
1	B	95	GLN
1	B	96	LEU
1	B	106	VAL
1	B	108	GLU
1	B	116	ILE
1	B	121	ILE
1	B	124	ASN
1	B	129	THR
1	B	130	LEU
1	B	138	VAL

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Mol	Chain	Res	Type
1	B	139	VAL
1	B	147	LEU
1	B	158	MET
1	B	160	LEU
1	B	164	SER
1	B	165	SER
1	B	179	MET
1	B	193	ASP
1	B	206	LYS
1	B	210	THR
1	B	217	ILE
1	B	221	GLU
1	B	223	SER
1	B	227	LEU
1	B	237	VAL
1	B	238	GLN
1	B	243	THR
1	B	256	MET
1	B	259	LEU
1	B	263	SER
1	B	275	ASP
1	B	282	LEU
1	B	286	ILE
1	B	297	ILE
1	B	307	GLN
1	B	311	LEU
1	B	313	LYS
1	B	321	THR
1	B	326	ASP
1	B	351	ARG
1	B	352	LEU
1	B	353	SER
1	B	357	MET
1	B	368	ARG
1	B	369	VAL
1	B	389	TYR
1	B	397	GLN
1	B	399	PRO
1	B	403	VAL
1	B	412	GLN
1	B	416	GLU
1	B	417	LEU

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Mol	Chain	Res	Type
1	B	422	VAL
1	B	431	GLU
1	B	446	VAL
1	B	452	LEU
1	B	474	ILE
1	C	6	THR
1	C	15	SER
1	C	34	CYS
1	C	38	THR
1	C	52	THR
1	C	56	THR
1	C	75	LEU
1	C	86	LEU
1	C	88	ILE
1	C	95	GLN
1	C	96	LEU
1	C	106	VAL
1	C	108	GLU
1	C	116	ILE
1	C	121	ILE
1	C	124	ASN
1	C	129	THR
1	C	130	LEU
1	C	138	VAL
1	C	139	VAL
1	C	147	LEU
1	C	158	MET
1	C	160	LEU
1	C	164	SER
1	C	165	SER
1	C	179	MET
1	C	193	ASP
1	C	206	LYS
1	C	210	THR
1	C	217	ILE
1	C	221	GLU
1	C	223	SER
1	C	227	LEU
1	C	237	VAL
1	C	238	GLN
1	C	243	THR
1	C	256	MET

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Mol	Chain	Res	Type
1	C	259	LEU
1	C	263	SER
1	C	275	ASP
1	C	282	LEU
1	C	286	ILE
1	C	297	ILE
1	C	307	GLN
1	C	311	LEU
1	C	313	LYS
1	C	321	THR
1	C	326	ASP
1	C	351	ARG
1	C	352	LEU
1	C	353	SER
1	C	357	MET
1	C	368	ARG
1	C	369	VAL
1	C	389	TYR
1	C	397	GLN
1	C	399	PRO
1	C	403	VAL
1	C	412	GLN
1	C	416	GLU
1	C	417	LEU
1	C	422	VAL
1	C	431	GLU
1	C	446	VAL
1	C	452	LEU
1	C	474	ILE
1	D	6	THR
1	D	15	SER
1	D	34	CYS
1	D	38	THR
1	D	52	THR
1	D	56	THR
1	D	75	LEU
1	D	86	LEU
1	D	88	ILE
1	D	95	GLN
1	D	96	LEU
1	D	106	VAL
1	D	108	GLU

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Mol	Chain	Res	Type
1	D	116	ILE
1	D	121	ILE
1	D	124	ASN
1	D	129	THR
1	D	130	LEU
1	D	138	VAL
1	D	139	VAL
1	D	147	LEU
1	D	158	MET
1	D	160	LEU
1	D	164	SER
1	D	165	SER
1	D	179	MET
1	D	193	ASP
1	D	206	LYS
1	D	210	THR
1	D	217	ILE
1	D	221	GLU
1	D	223	SER
1	D	227	LEU
1	D	237	VAL
1	D	238	GLN
1	D	243	THR
1	D	256	MET
1	D	259	LEU
1	D	263	SER
1	D	275	ASP
1	D	282	LEU
1	D	286	ILE
1	D	297	ILE
1	D	307	GLN
1	D	311	LEU
1	D	313	LYS
1	D	321	THR
1	D	326	ASP
1	D	351	ARG
1	D	352	LEU
1	D	353	SER
1	D	357	MET
1	D	368	ARG
1	D	369	VAL
1	D	389	TYR

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Mol	Chain	Res	Type
1	D	397	GLN
1	D	399	PRO
1	D	403	VAL
1	D	412	GLN
1	D	416	GLU
1	D	417	LEU
1	D	422	VAL
1	D	431	GLU
1	D	446	VAL
1	D	452	LEU
1	D	474	ILE
1	E	6	THR
1	E	15	SER
1	E	34	CYS
1	E	38	THR
1	E	52	THR
1	E	56	THR
1	E	75	LEU
1	E	86	LEU
1	E	88	ILE
1	E	95	GLN
1	E	96	LEU
1	E	106	VAL
1	E	108	GLU
1	E	116	ILE
1	E	121	ILE
1	E	124	ASN
1	E	129	THR
1	E	130	LEU
1	E	138	VAL
1	E	139	VAL
1	E	147	LEU
1	E	158	MET
1	E	160	LEU
1	E	164	SER
1	E	165	SER
1	E	179	MET
1	E	193	ASP
1	E	206	LYS
1	E	210	THR
1	E	217	ILE
1	E	221	GLU

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Mol	Chain	Res	Type
1	E	223	SER
1	E	227	LEU
1	E	237	VAL
1	E	238	GLN
1	E	243	THR
1	E	256	MET
1	E	259	LEU
1	E	263	SER
1	E	275	ASP
1	E	282	LEU
1	E	286	ILE
1	E	297	ILE
1	E	307	GLN
1	E	311	LEU
1	E	313	LYS
1	E	321	THR
1	E	326	ASP
1	E	351	ARG
1	E	352	LEU
1	E	353	SER
1	E	357	MET
1	E	368	ARG
1	E	369	VAL
1	E	389	TYR
1	E	397	GLN
1	E	399	PRO
1	E	403	VAL
1	E	412	GLN
1	E	416	GLU
1	E	417	LEU
1	E	422	VAL
1	E	431	GLU
1	E	446	VAL
1	E	452	LEU
1	E	474	ILE
1	F	6	THR
1	F	15	SER
1	F	34	CYS
1	F	38	THR
1	F	52	THR
1	F	56	THR
1	F	75	LEU

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Mol	Chain	Res	Type
1	F	86	LEU
1	F	88	ILE
1	F	95	GLN
1	F	96	LEU
1	F	106	VAL
1	F	108	GLU
1	F	116	ILE
1	F	121	ILE
1	F	124	ASN
1	F	129	THR
1	F	130	LEU
1	F	138	VAL
1	F	139	VAL
1	F	147	LEU
1	F	158	MET
1	F	160	LEU
1	F	164	SER
1	F	165	SER
1	F	179	MET
1	F	193	ASP
1	F	206	LYS
1	F	210	THR
1	F	217	ILE
1	F	221	GLU
1	F	223	SER
1	F	227	LEU
1	F	237	VAL
1	F	238	GLN
1	F	243	THR
1	F	256	MET
1	F	259	LEU
1	F	263	SER
1	F	275	ASP
1	F	282	LEU
1	F	286	ILE
1	F	297	ILE
1	F	307	GLN
1	F	311	LEU
1	F	313	LYS
1	F	321	THR
1	F	326	ASP
1	F	351	ARG

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Mol	Chain	Res	Type
1	F	352	LEU
1	F	353	SER
1	F	357	MET
1	F	368	ARG
1	F	369	VAL
1	F	389	TYR
1	F	397	GLN
1	F	399	PRO
1	F	403	VAL
1	F	412	GLN
1	F	416	GLU
1	F	417	LEU
1	F	422	VAL
1	F	431	GLU
1	F	446	VAL
1	F	452	LEU
1	F	474	ILE
1	G	6	THR
1	G	15	SER
1	G	34	CYS
1	G	38	THR
1	G	52	THR
1	G	56	THR
1	G	75	LEU
1	G	86	LEU
1	G	88	ILE
1	G	95	GLN
1	G	96	LEU
1	G	106	VAL
1	G	108	GLU
1	G	116	ILE
1	G	121	ILE
1	G	124	ASN
1	G	129	THR
1	G	130	LEU
1	G	138	VAL
1	G	139	VAL
1	G	147	LEU
1	G	158	MET
1	G	160	LEU
1	G	164	SER
1	G	165	SER

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Mol	Chain	Res	Type
1	G	179	MET
1	G	193	ASP
1	G	206	LYS
1	G	210	THR
1	G	217	ILE
1	G	221	GLU
1	G	223	SER
1	G	227	LEU
1	G	237	VAL
1	G	238	GLN
1	G	243	THR
1	G	256	MET
1	G	259	LEU
1	G	263	SER
1	G	275	ASP
1	G	282	LEU
1	G	286	ILE
1	G	297	ILE
1	G	307	GLN
1	G	311	LEU
1	G	313	LYS
1	G	321	THR
1	G	326	ASP
1	G	351	ARG
1	G	352	LEU
1	G	353	SER
1	G	357	MET
1	G	368	ARG
1	G	369	VAL
1	G	389	TYR
1	G	397	GLN
1	G	399	PRO
1	G	403	VAL
1	G	412	GLN
1	G	416	GLU
1	G	417	LEU
1	G	422	VAL
1	G	431	GLU
1	G	446	VAL
1	G	452	LEU
1	G	474	ILE
1	H	6	THR

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Mol	Chain	Res	Type
1	H	15	SER
1	H	34	CYS
1	H	38	THR
1	H	52	THR
1	H	56	THR
1	H	75	LEU
1	H	86	LEU
1	H	88	ILE
1	H	95	GLN
1	H	96	LEU
1	H	106	VAL
1	H	108	GLU
1	H	116	ILE
1	H	121	ILE
1	H	124	ASN
1	H	129	THR
1	H	130	LEU
1	H	138	VAL
1	H	139	VAL
1	H	147	LEU
1	H	158	MET
1	H	160	LEU
1	H	164	SER
1	H	165	SER
1	H	179	MET
1	H	193	ASP
1	H	206	LYS
1	H	210	THR
1	H	217	ILE
1	H	221	GLU
1	H	223	SER
1	H	227	LEU
1	H	237	VAL
1	H	238	GLN
1	H	243	THR
1	H	256	MET
1	H	259	LEU
1	H	263	SER
1	H	275	ASP
1	H	282	LEU
1	H	286	ILE
1	H	297	ILE

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Mol	Chain	Res	Type
1	H	307	GLN
1	H	311	LEU
1	H	313	LYS
1	H	321	THR
1	H	326	ASP
1	H	351	ARG
1	H	352	LEU
1	H	353	SER
1	H	357	MET
1	H	368	ARG
1	H	369	VAL
1	H	389	TYR
1	H	397	GLN
1	H	399	PRO
1	H	403	VAL
1	H	412	GLN
1	H	416	GLU
1	H	417	LEU
1	H	422	VAL
1	H	431	GLU
1	H	446	VAL
1	H	452	LEU
1	H	474	ILE
1	I	6	THR
1	I	15	SER
1	I	34	CYS
1	I	38	THR
1	I	52	THR
1	I	56	THR
1	I	75	LEU
1	I	86	LEU
1	I	88	ILE
1	I	95	GLN
1	I	96	LEU
1	I	106	VAL
1	I	108	GLU
1	I	116	ILE
1	I	121	ILE
1	I	124	ASN
1	I	129	THR
1	I	130	LEU
1	I	138	VAL

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Mol	Chain	Res	Type
1	I	139	VAL
1	I	147	LEU
1	I	158	MET
1	I	160	LEU
1	I	164	SER
1	I	165	SER
1	I	179	MET
1	I	193	ASP
1	I	206	LYS
1	I	210	THR
1	I	217	ILE
1	I	221	GLU
1	I	223	SER
1	I	227	LEU
1	I	237	VAL
1	I	238	GLN
1	I	243	THR
1	I	256	MET
1	I	259	LEU
1	I	263	SER
1	I	275	ASP
1	I	282	LEU
1	I	286	ILE
1	I	297	ILE
1	I	307	GLN
1	I	311	LEU
1	I	313	LYS
1	I	321	THR
1	I	326	ASP
1	I	351	ARG
1	I	352	LEU
1	I	353	SER
1	I	357	MET
1	I	368	ARG
1	I	369	VAL
1	I	389	TYR
1	I	397	GLN
1	I	399	PRO
1	I	403	VAL
1	I	412	GLN
1	I	416	GLU
1	I	417	LEU

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Mol	Chain	Res	Type
1	I	422	VAL
1	I	431	GLU
1	I	446	VAL
1	I	452	LEU
1	I	474	ILE
1	J	6	THR
1	J	15	SER
1	J	34	CYS
1	J	38	THR
1	J	52	THR
1	J	56	THR
1	J	75	LEU
1	J	86	LEU
1	J	88	ILE
1	J	95	GLN
1	J	96	LEU
1	J	106	VAL
1	J	108	GLU
1	J	116	ILE
1	J	121	ILE
1	J	124	ASN
1	J	129	THR
1	J	130	LEU
1	J	138	VAL
1	J	139	VAL
1	J	147	LEU
1	J	158	MET
1	J	160	LEU
1	J	164	SER
1	J	165	SER
1	J	179	MET
1	J	193	ASP
1	J	206	LYS
1	J	210	THR
1	J	217	ILE
1	J	221	GLU
1	J	223	SER
1	J	227	LEU
1	J	237	VAL
1	J	238	GLN
1	J	243	THR
1	J	256	MET

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Mol	Chain	Res	Type
1	J	259	LEU
1	J	263	SER
1	J	275	ASP
1	J	282	LEU
1	J	286	ILE
1	J	297	ILE
1	J	307	GLN
1	J	311	LEU
1	J	313	LYS
1	J	321	THR
1	J	326	ASP
1	J	351	ARG
1	J	352	LEU
1	J	353	SER
1	J	357	MET
1	J	368	ARG
1	J	369	VAL
1	J	389	TYR
1	J	397	GLN
1	J	399	PRO
1	J	403	VAL
1	J	412	GLN
1	J	416	GLU
1	J	417	LEU
1	J	422	VAL
1	J	431	GLU
1	J	446	VAL
1	J	452	LEU
1	J	474	ILE
1	K	6	THR
1	K	15	SER
1	K	34	CYS
1	K	38	THR
1	K	52	THR
1	K	56	THR
1	K	75	LEU
1	K	86	LEU
1	K	88	ILE
1	K	95	GLN
1	K	96	LEU
1	K	106	VAL
1	K	108	GLU

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Mol	Chain	Res	Type
1	K	116	ILE
1	K	121	ILE
1	K	124	ASN
1	K	129	THR
1	K	130	LEU
1	K	138	VAL
1	K	139	VAL
1	K	147	LEU
1	K	158	MET
1	K	160	LEU
1	K	164	SER
1	K	165	SER
1	K	179	MET
1	K	193	ASP
1	K	206	LYS
1	K	210	THR
1	K	217	ILE
1	K	221	GLU
1	K	223	SER
1	K	227	LEU
1	K	237	VAL
1	K	238	GLN
1	K	243	THR
1	K	256	MET
1	K	259	LEU
1	K	263	SER
1	K	275	ASP
1	K	282	LEU
1	K	286	ILE
1	K	297	ILE
1	K	307	GLN
1	K	311	LEU
1	K	313	LYS
1	K	321	THR
1	K	326	ASP
1	K	351	ARG
1	K	352	LEU
1	K	353	SER
1	K	357	MET
1	K	368	ARG
1	K	369	VAL
1	K	389	TYR

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Mol	Chain	Res	Type
1	K	397	GLN
1	K	399	PRO
1	K	403	VAL
1	K	412	GLN
1	K	416	GLU
1	K	417	LEU
1	K	422	VAL
1	K	431	GLU
1	K	446	VAL
1	K	452	LEU
1	K	474	ILE
1	L	6	THR
1	L	15	SER
1	L	34	CYS
1	L	38	THR
1	L	52	THR
1	L	56	THR
1	L	75	LEU
1	L	86	LEU
1	L	88	ILE
1	L	95	GLN
1	L	96	LEU
1	L	106	VAL
1	L	108	GLU
1	L	116	ILE
1	L	121	ILE
1	L	124	ASN
1	L	129	THR
1	L	130	LEU
1	L	138	VAL
1	L	139	VAL
1	L	147	LEU
1	L	158	MET
1	L	160	LEU
1	L	164	SER
1	L	165	SER
1	L	179	MET
1	L	193	ASP
1	L	206	LYS
1	L	210	THR
1	L	217	ILE
1	L	221	GLU

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Mol	Chain	Res	Type
1	L	223	SER
1	L	227	LEU
1	L	237	VAL
1	L	238	GLN
1	L	243	THR
1	L	256	MET
1	L	259	LEU
1	L	263	SER
1	L	275	ASP
1	L	282	LEU
1	L	286	ILE
1	L	297	ILE
1	L	307	GLN
1	L	311	LEU
1	L	313	LYS
1	L	321	THR
1	L	326	ASP
1	L	351	ARG
1	L	352	LEU
1	L	353	SER
1	L	357	MET
1	L	368	ARG
1	L	369	VAL
1	L	389	TYR
1	L	397	GLN
1	L	399	PRO
1	L	403	VAL
1	L	412	GLN
1	L	416	GLU
1	L	417	LEU
1	L	422	VAL
1	L	431	GLU
1	L	446	VAL
1	L	452	LEU
1	L	474	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	95	GLN
1	A	156	ASN

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Mol	Chain	Res	Type
1	A	397	GLN
1	B	55	GLN
1	B	95	GLN
1	B	156	ASN
1	B	335	GLN
1	B	397	GLN
1	C	55	GLN
1	C	95	GLN
1	C	156	ASN
1	C	397	GLN
1	D	55	GLN
1	D	95	GLN
1	D	156	ASN
1	D	335	GLN
1	D	397	GLN
1	E	55	GLN
1	E	95	GLN
1	E	156	ASN
1	E	397	GLN
1	F	55	GLN
1	F	95	GLN
1	F	156	ASN
1	F	335	GLN
1	F	397	GLN
1	G	55	GLN
1	G	95	GLN
1	G	156	ASN
1	G	397	GLN
1	H	55	GLN
1	H	95	GLN
1	H	156	ASN
1	H	335	GLN
1	H	397	GLN
1	I	55	GLN
1	I	95	GLN
1	I	156	ASN
1	I	397	GLN
1	J	55	GLN
1	J	95	GLN
1	J	156	ASN
1	J	397	GLN
1	K	55	GLN

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Mol	Chain	Res	Type
1	K	95	GLN
1	K	156	ASN
1	K	397	GLN
1	L	55	GLN
1	L	95	GLN
1	L	156	ASN
1	L	397	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

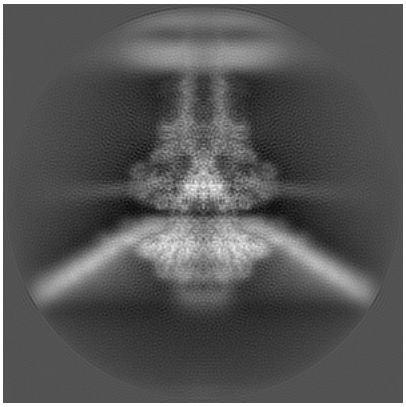
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-31321. These allow visual inspection of the internal detail of the map and identification of artifacts.

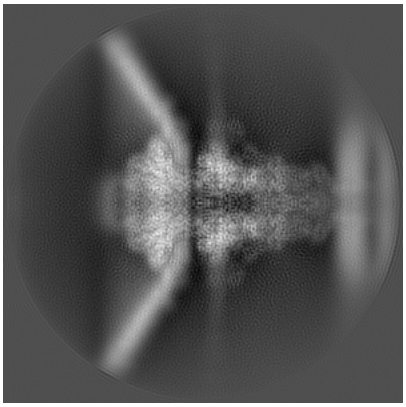
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

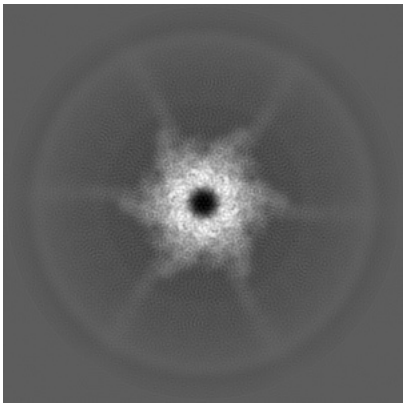
6.1.1 Primary map



X



Y

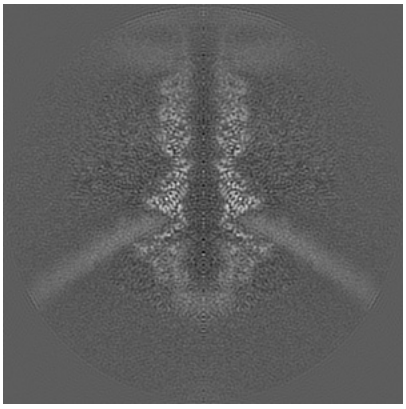


Z

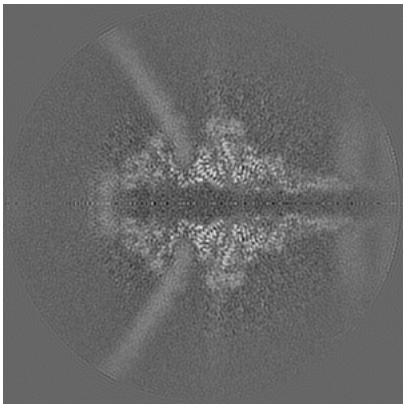
The images above show the map projected in three orthogonal directions.

6.2 Central slices

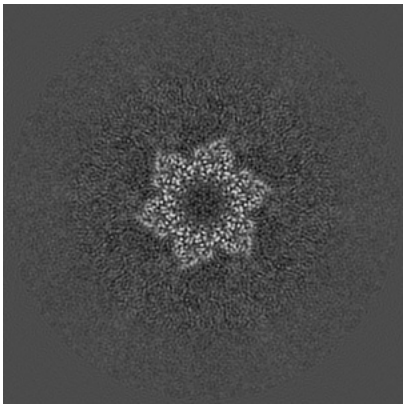
6.2.1 Primary map



X Index: 200



Y Index: 200

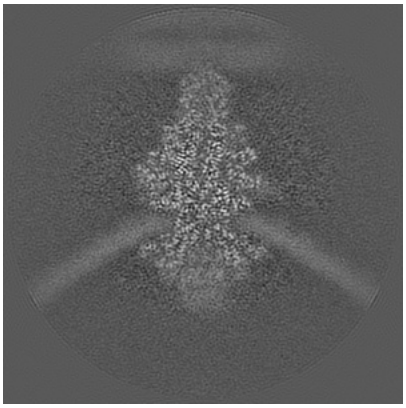


Z Index: 200

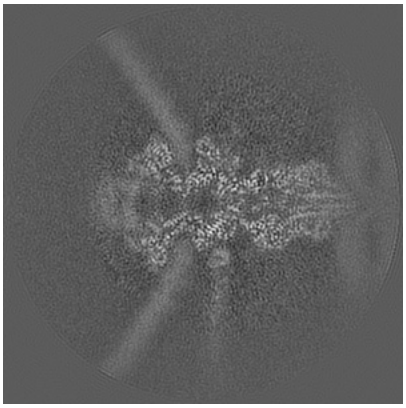
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

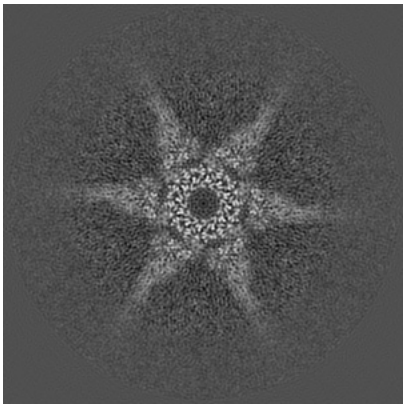
6.3.1 Primary map



X Index: 177



Y Index: 216

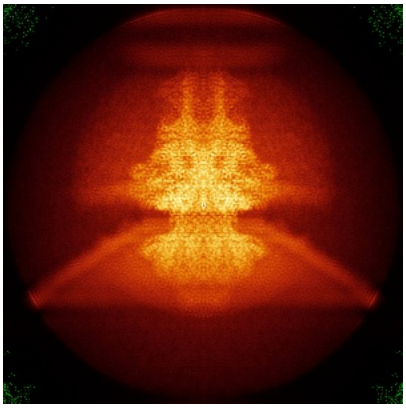


Z Index: 217

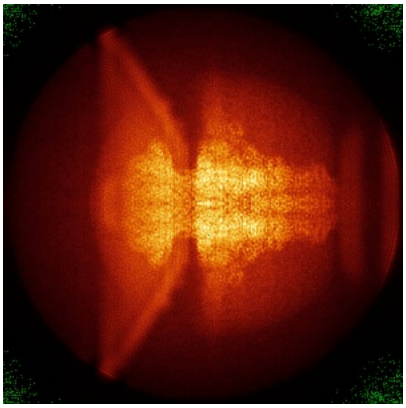
The images above show the largest variance slices of the map in three orthogonal directions.

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

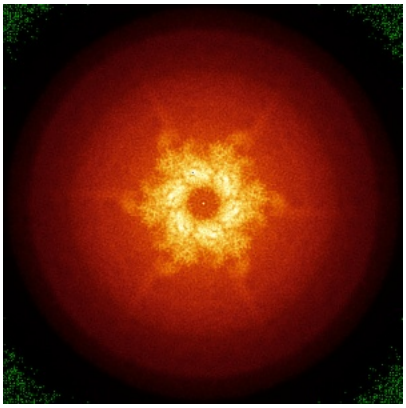
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 8.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

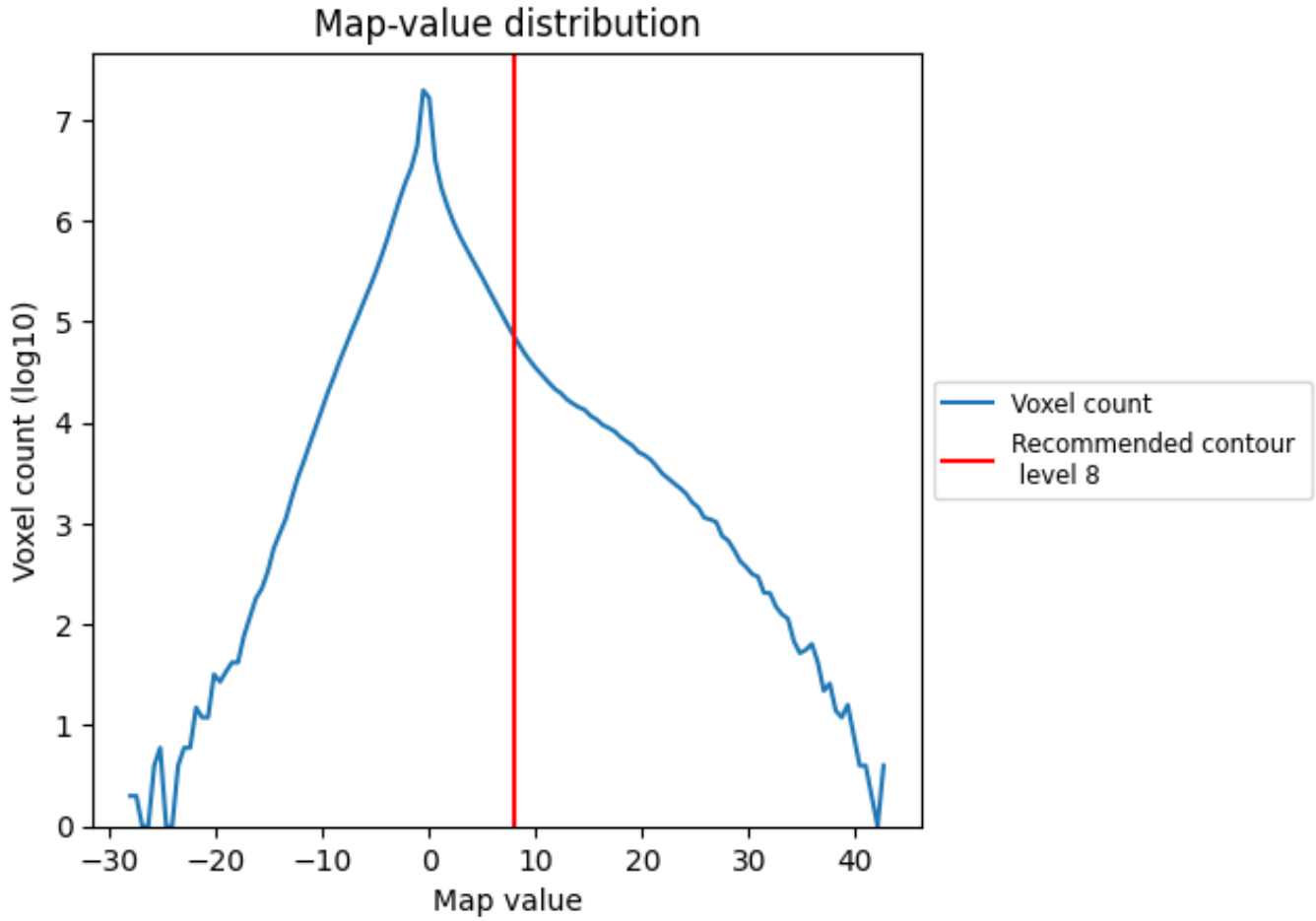
6.6 Mask visualisation (i)

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

7 Map analysis

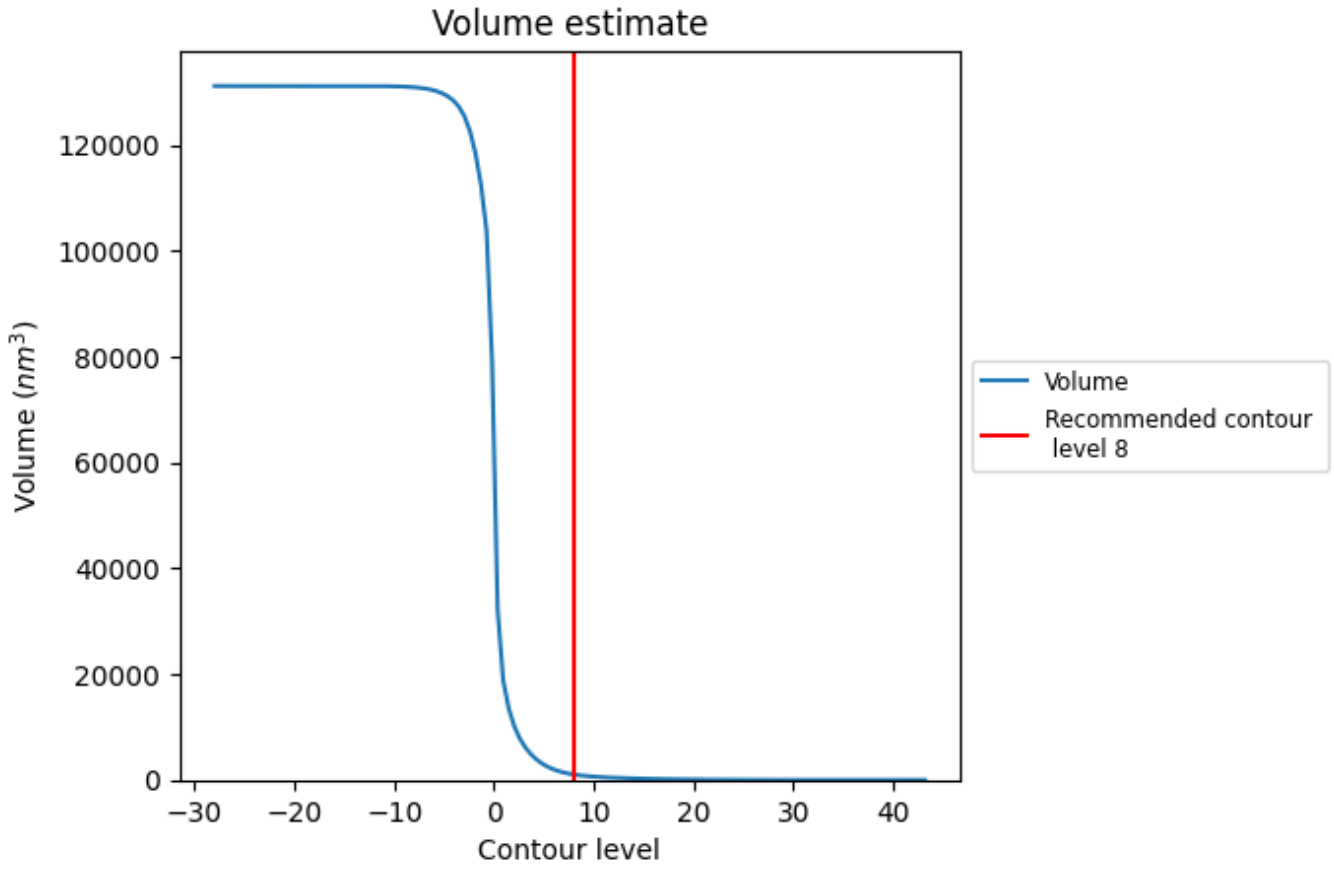
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

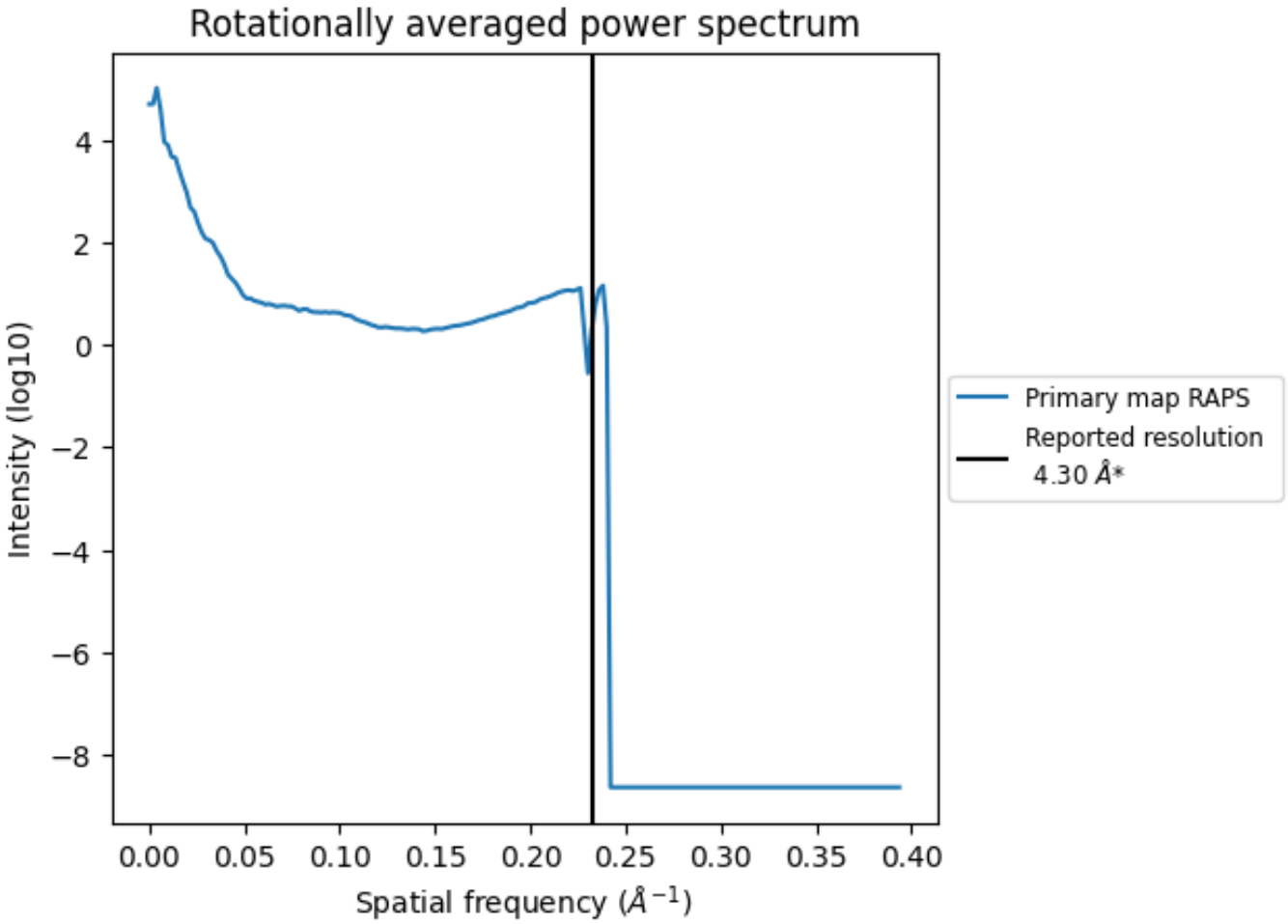
7.2 Volume estimate



The volume at the recommended contour level is 1038 nm^3; this corresponds to an approximate mass of 938 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

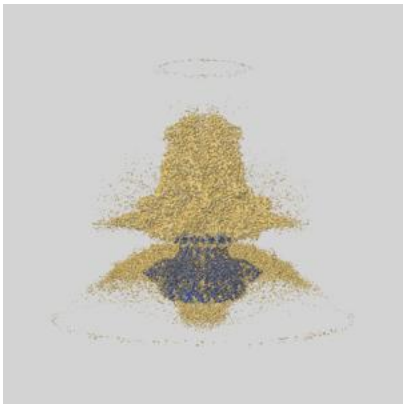
8 Fourier-Shell correlation

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

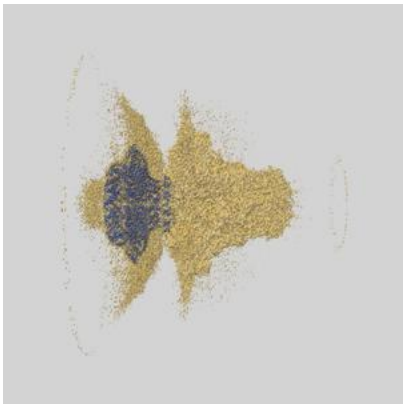
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-31321 and PDB model 7EY6. Per-residue inclusion information can be found in section 3 on page 5.

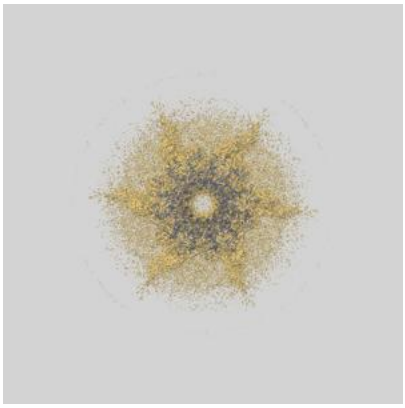
9.1 Map-model overlay



X



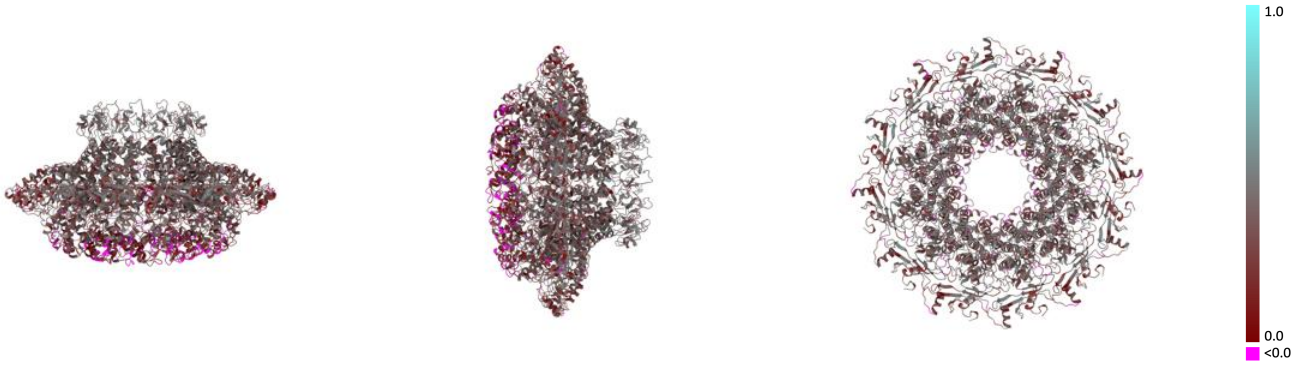
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 8.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

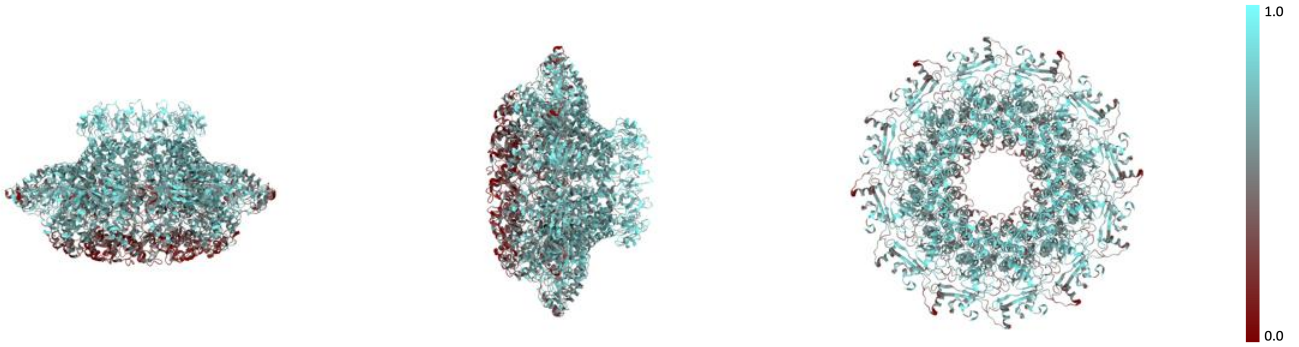
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

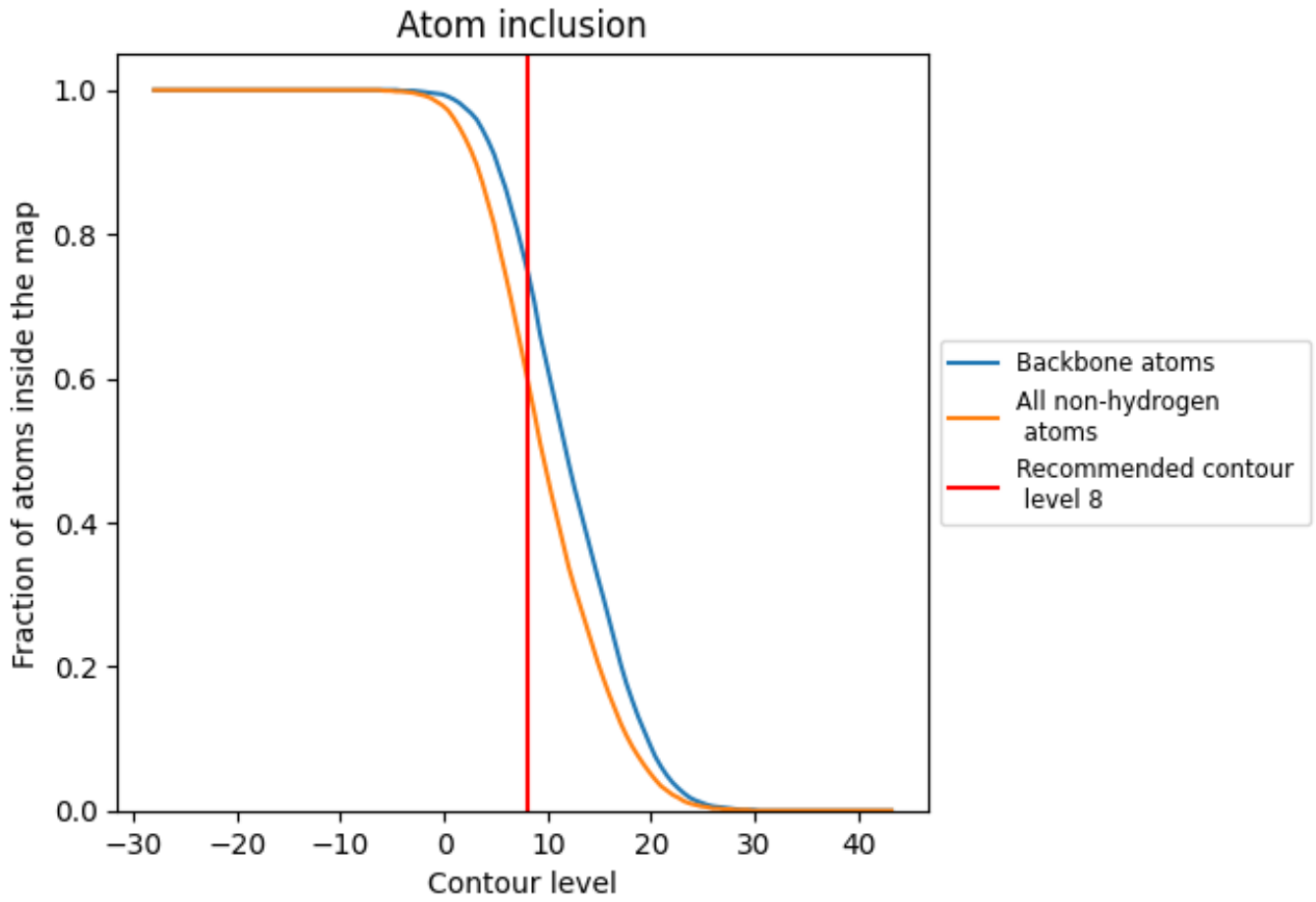
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (8).

9.4 Atom inclusion (i)



At the recommended contour level, 75% of all backbone atoms, 60% 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 (8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6020	0.3220
A	0.5880	0.3050
B	0.6180	0.3400
C	0.5860	0.3040
D	0.6170	0.3380
E	0.5880	0.3060
F	0.6180	0.3390
G	0.5870	0.3050
H	0.6190	0.3390
I	0.5860	0.3050
J	0.6180	0.3390
K	0.5870	0.3050
L	0.6170	0.3380