



Full wwPDB EM Validation Report ⓘ

Nov 27, 2022 – 01:04 AM EST

PDB ID : 5KEQ
EMDB ID : EMD-6619
Title : High resolution cryo-EM maps of Human papillomavirus 16 reveal L2 location and heparin-induced conformational changes
Authors : Guan, J.; Bywaters, S.M.; Brendle, S.A.; Ashley, R.E.; Makhov, A.M.; Conway, J.F.; Christensen, N.D.; Hafenstein, S.
Deposited on : 2016-06-10
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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

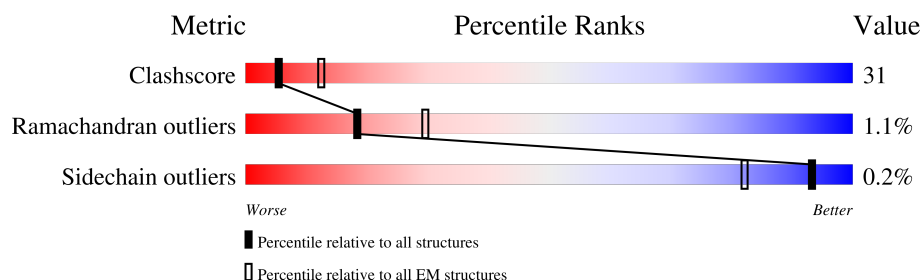
1 Overall quality at a glance i

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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	483	44% 53% ...
1	B	483	51% 42% . .
1	C	483	47% 48% . .
1	D	483	51% 44% . .
1	E	483	53% 45% .
1	F	483	53% 42% ...

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 22267 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.

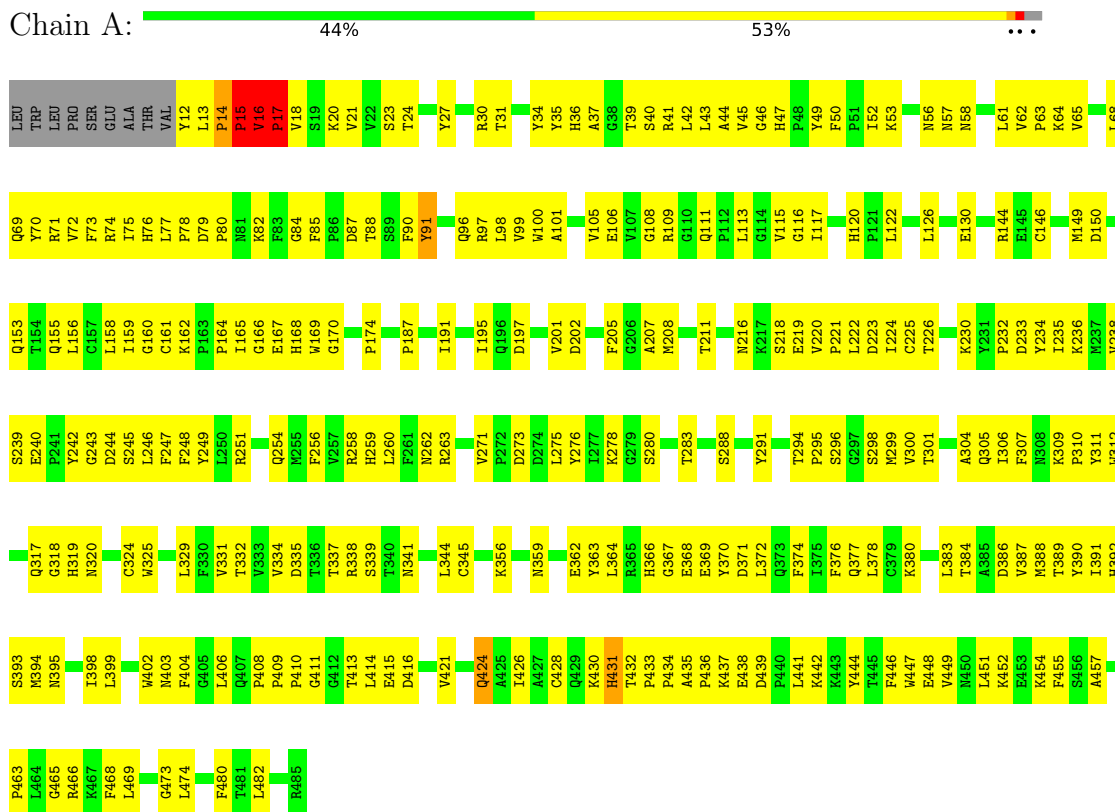
- Molecule 1 is a protein called Major capsid protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	474	Total	C	N	O	S	0	0
			3725	2380	627	697	21		
1	B	463	Total	C	N	O	S	0	0
			3638	2321	612	684	21		
1	C	472	Total	C	N	O	S	0	0
			3705	2368	621	695	21		
1	D	471	Total	C	N	O	S	0	0
			3700	2365	620	694	21		
1	E	482	Total	C	N	O	S	0	0
			3785	2422	633	709	21		
1	F	473	Total	C	N	O	S	0	0
			3714	2373	622	698	21		

3 Residue-property plots

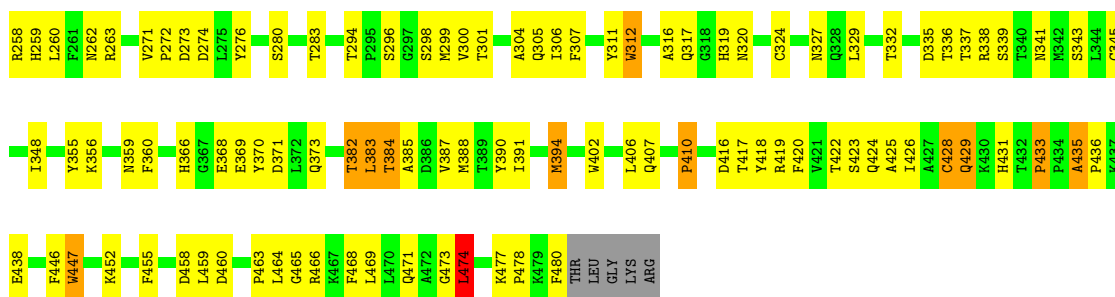
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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: Major capsid protein L1



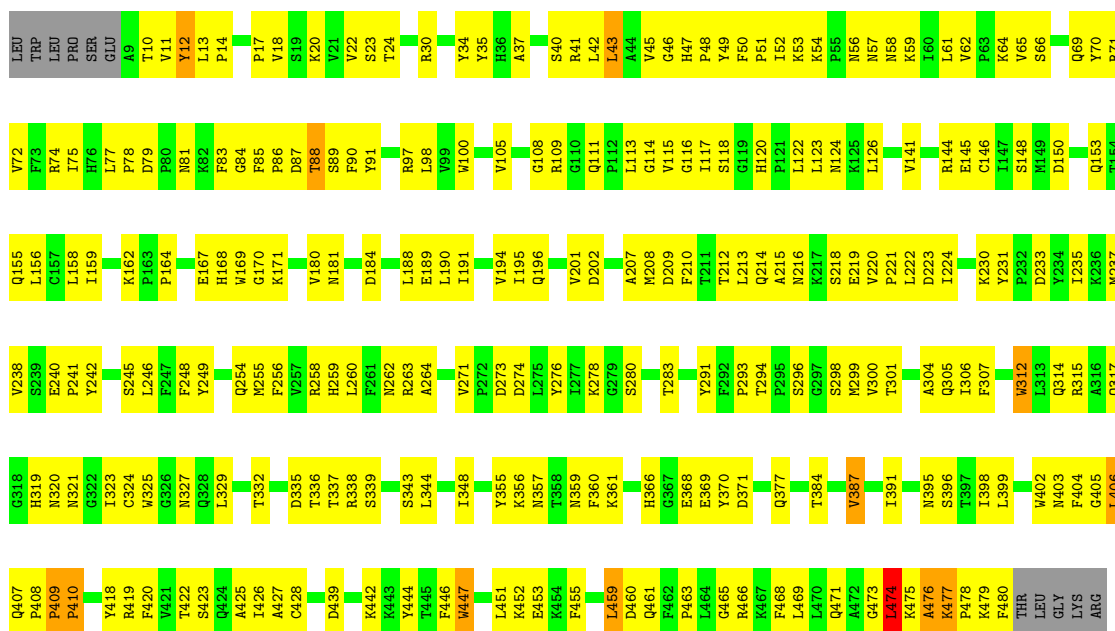
• Molecule 1: Major capsid protein L1





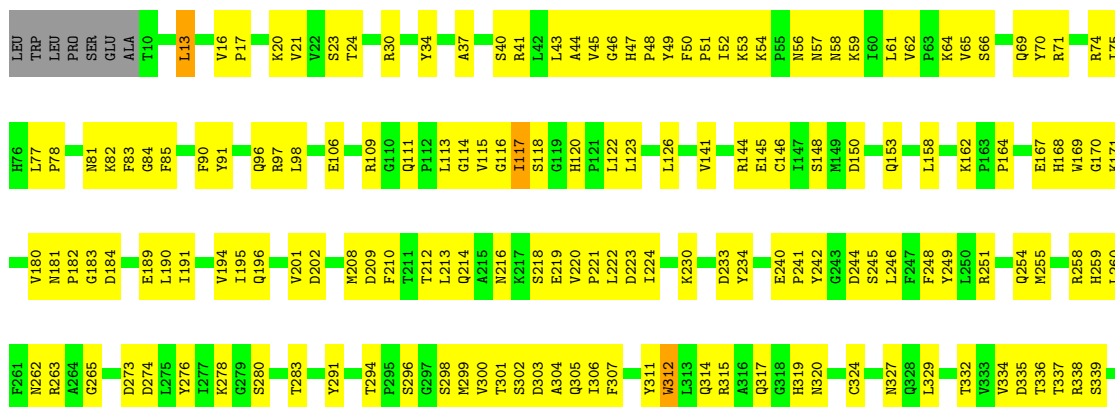
• Molecule 1: Major capsid protein L1

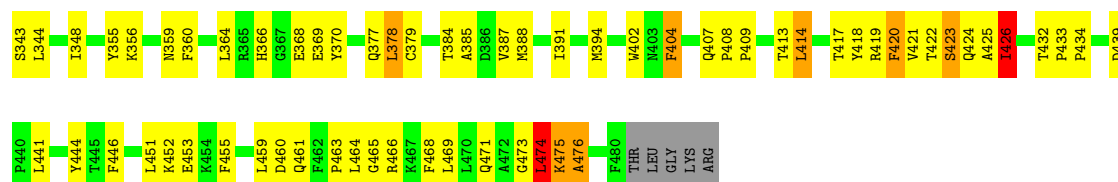
Chain C: 47% 48%



• Molecule 1: Major capsid protein L1

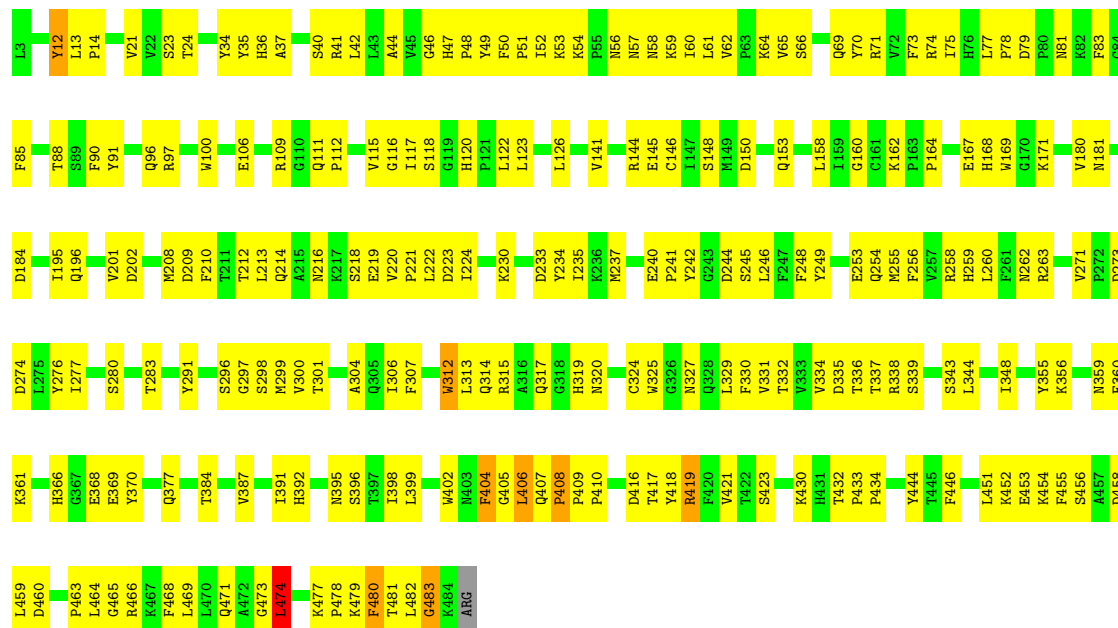
Chain D: 51% 44%





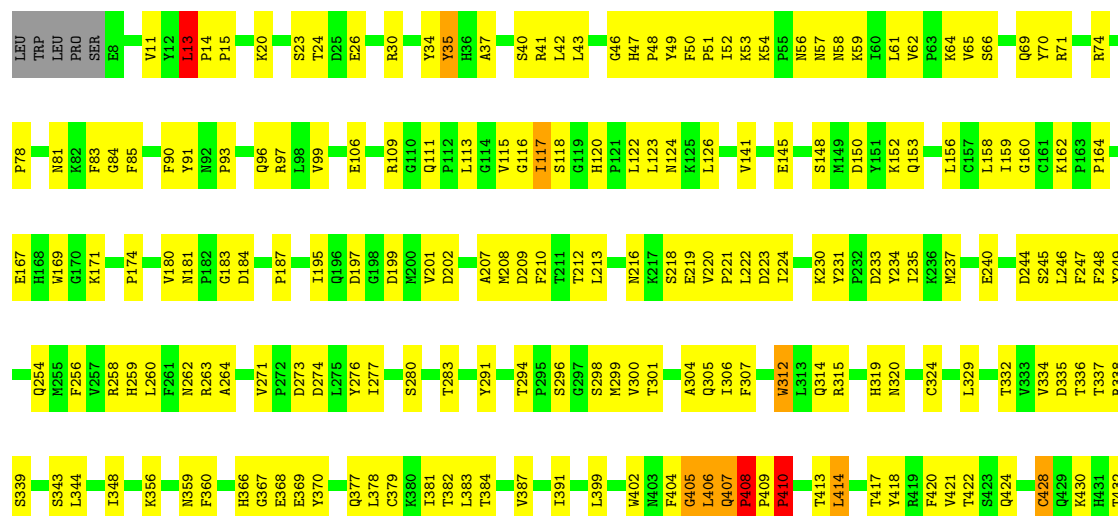
• Molecule 1: Major capsid protein L1

Chain E: 53% 45%



• Molecule 1: Major capsid protein L1

Chain F: 53% 42%



D439	P440	F446	W447	K452	F455	D458	L459	D460	Q461	F462	P463	L464	G465	R466	K467	F468	L469	L470	Q471	A472	G473	L474	P478	K479	F480	THR	LEU	GLY	LYS	ARG
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	51422	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	7	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.50	0/3827	0.68	8/5209 (0.2%)
1	B	0.57	2/3736 (0.1%)	0.67	6/5083 (0.1%)
1	C	0.64	4/3807 (0.1%)	0.74	7/5185 (0.1%)
1	D	0.60	3/3802 (0.1%)	0.78	11/5178 (0.2%)
1	E	0.60	4/3890 (0.1%)	0.67	6/5299 (0.1%)
1	F	0.69	8/3816 (0.2%)	0.78	16/5197 (0.3%)
All	All	0.60	21/22878 (0.1%)	0.72	54/31151 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
1	B	0	7
1	C	0	4
1	D	0	3
1	E	0	5
1	F	0	6
All	All	0	31

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	408	PRO	N-CA	15.98	1.74	1.47
1	F	409	PRO	N-CA	11.28	1.66	1.47
1	F	409	PRO	C-N	10.84	1.54	1.34
1	C	409	PRO	C-N	-8.11	1.18	1.34
1	E	404	PHE	CB-CG	-7.85	1.38	1.51
1	E	404	PHE	CD2-CE2	-7.02	1.25	1.39
1	F	428	CYS	CB-SG	-6.91	1.70	1.82
1	F	35	TYR	CD1-CE1	-6.43	1.29	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	420	PHE	CE1-CZ	-6.28	1.25	1.37
1	F	312	TRP	CB-CG	-6.13	1.39	1.50
1	C	428	CYS	CB-SG	-5.96	1.72	1.81
1	D	16	VAL	C-N	-5.86	1.23	1.34
1	C	312	TRP	CB-CG	-5.78	1.39	1.50
1	B	447	TRP	CB-CG	-5.47	1.40	1.50
1	B	312	TRP	CB-CG	-5.43	1.40	1.50
1	E	404	PHE	CD1-CE1	-5.37	1.28	1.39
1	F	35	TYR	CB-CG	-5.31	1.43	1.51
1	F	35	TYR	CD2-CE2	-5.15	1.31	1.39
1	E	312	TRP	CB-CG	-5.11	1.41	1.50
1	C	447	TRP	CB-CG	-5.07	1.41	1.50
1	D	312	TRP	CB-CG	-5.01	1.41	1.50

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	426	ILE	CG1-CB-CG2	-16.52	75.05	111.40
1	F	13	LEU	CB-CG-CD1	-12.63	89.52	111.00
1	D	426	ILE	CB-CG1-CD1	-12.57	78.71	113.90
1	D	378	LEU	CB-CG-CD2	-9.98	94.03	111.00
1	D	474	LEU	CA-C-O	8.64	138.24	120.10
1	C	474	LEU	CA-C-O	8.53	138.01	120.10
1	F	407	GLN	N-CA-C	8.51	133.99	111.00
1	E	474	LEU	CA-C-O	8.49	137.93	120.10
1	F	474	LEU	CA-C-O	8.46	137.86	120.10
1	B	474	LEU	CA-C-O	8.42	137.78	120.10
1	A	16	VAL	CA-CB-CG1	8.25	123.27	110.90
1	D	414	LEU	CB-CG-CD2	-8.01	97.38	111.00
1	F	406	LEU	CA-CB-CG	7.92	133.52	115.30
1	F	405	GLY	N-CA-C	7.61	132.12	113.10
1	D	13	LEU	CA-CB-CG	-7.58	97.87	115.30
1	E	474	LEU	CA-C-N	-7.53	100.64	117.20
1	C	459	LEU	CA-CB-CG	-7.50	98.05	115.30
1	C	474	LEU	CA-C-N	-7.49	100.73	117.20
1	B	474	LEU	CA-C-N	-7.44	100.84	117.20
1	F	474	LEU	CA-C-N	-7.42	100.87	117.20
1	D	474	LEU	CA-C-N	-7.42	100.88	117.20
1	A	16	VAL	CB-CA-C	-7.29	97.55	111.40
1	F	406	LEU	C-N-CA	7.25	139.83	121.70
1	F	410	PRO	CA-N-CD	-7.06	101.62	111.50
1	A	15	PRO	C-N-CA	6.85	138.81	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	414	LEU	CA-CB-CG	-6.66	99.97	115.30
1	A	17	PRO	N-CA-CB	-6.47	95.48	102.60
1	D	474	LEU	O-C-N	-6.47	112.35	122.70
1	A	13	LEU	C-N-CD	-6.39	106.53	120.60
1	F	13	LEU	CB-CG-CD2	-6.38	100.16	111.00
1	C	43	LEU	CA-CB-CG	6.37	129.94	115.30
1	F	408	PRO	O-C-N	-6.33	109.07	121.10
1	F	474	LEU	O-C-N	-6.28	112.65	122.70
1	C	474	LEU	O-C-N	-6.28	112.66	122.70
1	F	407	GLN	C-N-CD	-6.24	106.87	120.60
1	E	474	LEU	O-C-N	-6.24	112.72	122.70
1	B	474	LEU	O-C-N	-6.21	112.76	122.70
1	C	410	PRO	CA-N-CD	-6.11	102.95	111.50
1	B	312	TRP	CA-CB-CG	-5.92	102.44	113.70
1	D	426	ILE	CB-CA-C	-5.85	99.90	111.60
1	A	16	VAL	CA-CB-CG2	5.75	119.53	110.90
1	E	12	TYR	C-N-CA	5.60	135.71	121.70
1	C	188	LEU	CA-CB-CG	5.53	128.02	115.30
1	F	409	PRO	C-N-CD	5.50	139.95	128.40
1	F	409	PRO	N-CA-C	5.49	126.38	112.10
1	F	407	GLN	N-CA-CB	-5.40	100.88	110.60
1	A	17	PRO	N-CA-C	5.35	126.00	112.10
1	B	410	PRO	C-N-CA	5.32	133.48	122.30
1	A	14	PRO	N-CA-C	5.25	125.75	112.10
1	D	378	LEU	CA-CB-CG	-5.21	103.32	115.30
1	E	483	GLY	N-CA-C	-5.11	100.32	113.10
1	D	426	ILE	CA-CB-CG1	5.10	120.70	111.00
1	B	459	LEU	CA-CB-CG	-5.02	103.75	115.30
1	E	406	LEU	CB-CG-CD2	-5.00	102.50	111.00

There are no chirality outliers.

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	PRO	Peptide
1	A	415	GLU	Peptide
1	A	424	GLN	Peptide
1	A	430	LYS	Peptide
1	A	431	HIS	Peptide
1	A	91	TYR	Peptide
1	B	423	SER	Peptide
1	B	425	ALA	Peptide

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Mol	Chain	Res	Type	Group
1	B	428	CYS	Peptide
1	B	429	GLN	Peptide
1	B	433	PRO	Peptide
1	B	435	ALA	Peptide
1	B	474	LEU	Mainchain
1	C	12	TYR	Peptide
1	C	14	PRO	Peptide
1	C	406	LEU	Peptide
1	C	474	LEU	Mainchain
1	D	404	PHE	Peptide
1	D	423	SER	Peptide
1	D	474	LEU	Mainchain
1	E	408	PRO	Peptide
1	E	418	TYR	Peptide
1	E	419	ARG	Peptide
1	E	474	LEU	Mainchain
1	E	480	PHE	Peptide
1	F	405	GLY	Peptide
1	F	406	LEU	Peptide,Mainchain
1	F	408	PRO	Peptide
1	F	413	THR	Peptide
1	F	474	LEU	Mainchain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3725	0	3648	256	0
1	B	3638	0	3551	233	0
1	C	3705	0	3622	278	0
1	D	3700	0	3617	250	0
1	E	3785	0	3706	236	0
1	F	3714	0	3628	227	0
All	All	22267	0	21772	1373	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 31.

All (1373) 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:D:469:LEU:HA	1:D:474:LEU:CD2	1.44	1.48
1:D:469:LEU:CA	1:D:474:LEU:HD21	1.48	1.41
1:F:408:PRO:N	1:F:408:PRO:CA	1.74	1.31
1:E:455:PHE:HB2	1:F:13:LEU:HD11	1.15	1.10
1:C:475:LYS:O	1:C:477:LYS:N	1.89	1.03
1:D:97:ARG:HH22	1:D:404:PHE:HB2	1.27	0.99
1:A:16:VAL:HB	1:A:17:PRO:CD	1.90	0.98
1:D:312:TRP:HH2	1:D:468:PHE:HD1	1.13	0.96
1:C:170:GLY:O	1:C:189:GLU:N	2.00	0.94
1:E:312:TRP:HH2	1:E:471:GLN:HB3	1.32	0.94
1:B:44:ALA:HB3	1:B:368:GLU:HB2	1.46	0.93
1:B:219:GLU:OE1	1:B:263:ARG:NH1	2.02	0.92
1:F:81:ASN:HD21	1:F:97:ARG:HB3	1.36	0.91
1:B:81:ASN:HD21	1:B:98:LEU:H	1.16	0.91
1:C:399:LEU:HB3	1:C:404:PHE:CE1	2.06	0.91
1:C:312:TRP:HH2	1:C:468:PHE:HD1	1.12	0.91
1:F:312:TRP:HH2	1:F:468:PHE:HD1	1.14	0.90
1:E:37:ALA:HB2	1:E:455:PHE:HA	1.54	0.90
1:E:312:TRP:CH2	1:E:471:GLN:HB3	2.05	0.90
1:F:109:ARG:NH1	1:F:369:GLU:O	2.05	0.90
1:B:419:ARG:O	1:B:422:THR:OG1	1.90	0.90
1:C:219:GLU:OE1	1:C:263:ARG:NH1	2.05	0.90
1:B:406:LEU:HA	1:B:407:GLN:HB2	1.53	0.89
1:B:383:LEU:O	1:B:387:VAL:HB	1.72	0.88
1:C:312:TRP:CH2	1:C:468:PHE:HD1	1.90	0.88
1:D:74:ARG:HB2	1:D:446:PHE:HE1	1.39	0.88
1:E:417:THR:HB	1:E:419:ARG:HE	1.39	0.88
1:F:219:GLU:OE1	1:F:263:ARG:NH1	2.07	0.87
1:B:109:ARG:NH1	1:B:369:GLU:O	2.07	0.87
1:D:219:GLU:OE1	1:D:263:ARG:NH1	2.07	0.87
1:D:312:TRP:CH2	1:D:468:PHE:HD1	1.93	0.87
1:E:83:PHE:HA	1:F:11:VAL:HG21	1.57	0.86
1:A:111:GLN:HB2	1:A:338:ARG:HD3	1.56	0.86
1:E:219:GLU:OE1	1:E:263:ARG:NH1	2.08	0.86
1:F:74:ARG:HB2	1:F:446:PHE:HE1	1.40	0.86
1:F:93:PRO:O	1:F:97:ARG:NH1	2.09	0.86
1:A:15:PRO:HG3	1:A:389:THR:HB	1.58	0.86
1:F:312:TRP:HH2	1:F:468:PHE:CD1	1.95	0.85
1:B:111:GLN:HB2	1:B:338:ARG:HD3	1.58	0.85
1:F:312:TRP:CH2	1:F:468:PHE:HD1	1.94	0.84
1:A:439:ASP:HB3	1:A:442:LYS:HB2	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:ARG:HB2	1:B:446:PHE:HE1	1.41	0.84
1:E:406:LEU:HB3	1:E:407:GLN:HG3	1.59	0.84
1:E:109:ARG:NH1	1:E:369:GLU:O	2.11	0.83
1:D:312:TRP:HH2	1:D:468:PHE:CD1	1.98	0.82
1:B:263:ARG:NH2	1:F:343:SER:OG	2.11	0.82
1:C:74:ARG:HB2	1:C:446:PHE:HE1	1.44	0.82
1:F:74:ARG:NH1	1:F:439:ASP:OD2	2.12	0.81
1:A:80:PRO:HB2	1:A:98:LEU:HB2	1.61	0.81
1:A:240:GLU:OE1	1:A:245:SER:N	2.12	0.81
1:A:411:GLY:O	1:B:19:SER:OG	1.98	0.81
1:D:421:VAL:HG12	1:D:422:THR:H	1.45	0.81
1:C:111:GLN:HB2	1:C:338:ARG:HD3	1.61	0.81
1:A:259:HIS:H	1:A:294:THR:HB	1.45	0.81
1:C:43:LEU:HA	1:C:368:GLU:O	1.80	0.81
1:B:258:ARG:NH2	1:B:296:SER:OG	2.14	0.81
1:A:85:PHE:HD2	1:A:88:THR:HG22	1.46	0.80
1:E:37:ALA:HB2	1:E:455:PHE:HD1	1.46	0.80
1:E:74:ARG:HB2	1:E:446:PHE:HE1	1.45	0.80
1:E:399:LEU:HB3	1:E:404:PHE:CE2	2.16	0.79
1:E:474:LEU:HD12	1:E:474:LEU:O	1.81	0.79
1:C:312:TRP:HH2	1:C:468:PHE:CD1	1.98	0.79
1:A:101:ALA:HB3	1:A:377:GLN:HB3	1.63	0.79
1:D:258:ARG:NH2	1:D:296:SER:OG	2.16	0.79
1:A:37:ALA:HB1	1:A:454:LYS:HB2	1.65	0.79
1:E:47:HIS:HE1	1:E:49:TYR:HB2	1.48	0.79
1:A:63:PRO:HG3	1:F:424:GLN:OE1	1.83	0.78
1:C:109:ARG:NH1	1:C:369:GLU:O	2.16	0.78
1:A:39:THR:HG23	1:A:451:LEU:HD21	1.66	0.78
1:D:473:GLY:O	1:D:474:LEU:HG	1.82	0.78
1:E:158:LEU:HB2	1:E:332:THR:HB	1.65	0.78
1:A:428:CYS:HB3	1:A:432:THR:HG23	1.66	0.78
1:C:53:LYS:HA	1:C:61:LEU:H	1.48	0.78
1:C:406:LEU:HB3	1:C:407:GLN:HG3	1.64	0.78
1:A:16:VAL:HB	1:A:17:PRO:HD2	1.64	0.78
1:A:16:VAL:HG23	1:A:18:VAL:H	1.48	0.78
1:A:399:LEU:HA	1:A:404:PHE:CE2	2.20	0.77
1:B:83:PHE:HE1	1:C:13:LEU:HD22	1.48	0.77
1:F:47:HIS:HE1	1:F:49:TYR:HB2	1.47	0.77
1:B:158:LEU:HB2	1:B:332:THR:HB	1.66	0.77
1:C:403:ASN:C	1:C:405:GLY:HA2	2.04	0.77
1:E:51:PRO:HD3	1:E:64:LYS:HD2	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:476:ALA:O	1:C:477:LYS:HG2	1.85	0.77
1:C:11:VAL:HG13	1:C:13:LEU:HD11	1.63	0.77
1:D:158:LEU:HB2	1:D:332:THR:HB	1.67	0.77
1:F:35:TYR:HE2	1:F:85:PHE:HE1	1.30	0.77
1:F:116:GLY:N	1:F:339:SER:OG	2.15	0.77
1:F:51:PRO:HD3	1:F:64:LYS:HD2	1.65	0.76
1:E:473:GLY:O	1:E:474:LEU:HG	1.85	0.76
1:C:81:ASN:HD21	1:C:98:LEU:H	1.30	0.76
1:E:258:ARG:NH2	1:E:296:SER:OG	2.18	0.76
1:A:85:PHE:CD2	1:A:88:THR:HG22	2.20	0.76
1:D:460:ASP:OD1	1:E:319:HIS:NE2	2.16	0.76
1:C:126:LEU:HB3	1:C:262:ASN:HB2	1.66	0.76
1:A:159:ILE:HG12	1:A:331:VAL:HG22	1.68	0.76
1:D:126:LEU:HB3	1:D:262:ASN:HB2	1.68	0.76
1:F:420:PHE:HB3	1:F:430:LYS:HE2	1.68	0.76
1:F:164:PRO:HB2	1:F:195:ILE:HD12	1.68	0.75
1:B:44:ALA:CB	1:B:368:GLU:HB2	2.15	0.75
1:D:111:GLN:HB2	1:D:338:ARG:HD3	1.66	0.75
1:E:120:HIS:HB2	1:E:221:PRO:HA	1.69	0.75
1:A:164:PRO:HB2	1:A:195:ILE:HD12	1.67	0.75
1:C:406:LEU:HB3	1:C:407:GLN:CG	2.17	0.75
1:F:478:PRO:HG2	1:F:480:PHE:HE2	1.51	0.75
1:F:126:LEU:HB3	1:F:262:ASN:HB2	1.69	0.74
1:C:158:LEU:HB2	1:C:332:THR:HB	1.70	0.74
1:A:64:LYS:O	1:A:69:GLN:NE2	2.21	0.74
1:A:390:TYR:O	1:A:394:MET:N	2.20	0.74
1:C:169:TRP:HB2	1:C:208:MET:HB3	1.69	0.74
1:B:120:HIS:HB2	1:B:221:PRO:HA	1.70	0.74
1:C:47:HIS:HE1	1:C:49:TYR:HB2	1.53	0.74
1:D:312:TRP:NE1	1:D:471:GLN:OE1	2.21	0.74
1:A:111:GLN:NE2	1:A:369:GLU:OE1	2.21	0.74
1:E:169:TRP:HB2	1:E:208:MET:HB3	1.69	0.74
1:C:476:ALA:O	1:C:477:LYS:CB	2.36	0.73
1:E:52:ILE:HB	1:E:62:VAL:HB	1.68	0.73
1:B:85:PHE:H	1:B:88:THR:HG22	1.54	0.73
1:B:463:PRO:HA	1:B:466:ARG:HH12	1.52	0.73
1:E:126:LEU:HB3	1:E:262:ASN:HB2	1.71	0.73
1:E:396:SER:O	1:E:399:LEU:HB2	1.89	0.73
1:D:463:PRO:HA	1:D:466:ARG:HH12	1.54	0.73
1:D:465:GLY:O	1:D:468:PHE:N	2.21	0.73
1:E:53:LYS:HA	1:E:61:LEU:H	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:312:TRP:CH2	1:C:468:PHE:CD1	2.76	0.73
1:D:109:ARG:NH1	1:D:369:GLU:O	2.22	0.73
1:A:164:PRO:HG2	1:A:195:ILE:HB	1.71	0.72
1:B:42:LEU:O	1:B:370:TYR:N	2.18	0.72
1:C:150:ASP:OD1	1:C:296:SER:HA	1.89	0.72
1:E:162:LYS:HB2	1:E:245:SER:HA	1.72	0.72
1:B:74:ARG:HB2	1:B:446:PHE:CE1	2.24	0.72
1:D:96:GLN:O	1:D:97:ARG:NH1	2.23	0.72
1:C:52:ILE:HB	1:C:62:VAL:HB	1.71	0.72
1:B:22:VAL:HG11	1:F:480:PHE:CD2	2.25	0.72
1:B:44:ALA:HB3	1:B:368:GLU:CB	2.20	0.72
1:C:465:GLY:O	1:C:468:PHE:N	2.23	0.72
1:B:42:LEU:HB2	1:B:370:TYR:HB2	1.71	0.72
1:C:109:ARG:HG3	1:C:307:PHE:HD2	1.55	0.72
1:C:258:ARG:NH2	1:C:296:SER:OG	2.23	0.71
1:B:164:PRO:HB2	1:B:195:ILE:HD12	1.72	0.71
1:C:54:LYS:HB3	1:C:57:ASN:HB3	1.71	0.71
1:E:421:VAL:HB	1:E:430:LYS:HZ1	1.56	0.71
1:F:258:ARG:NH2	1:F:296:SER:OG	2.22	0.71
1:A:24:THR:OG1	1:A:319:HIS:O	2.04	0.71
1:B:57:ASN:OD1	1:B:58:ASN:N	2.22	0.71
1:B:126:LEU:HB3	1:B:262:ASN:HB2	1.70	0.71
1:D:169:TRP:HB2	1:D:208:MET:HB3	1.72	0.71
1:C:169:TRP:HA	1:C:189:GLU:O	1.90	0.71
1:E:57:ASN:OD1	1:E:58:ASN:N	2.24	0.71
1:B:312:TRP:CE2	1:B:471:GLN:NE2	2.57	0.71
1:F:428:CYS:HB3	1:F:432:THR:HG21	1.72	0.71
1:B:51:PRO:HD3	1:B:64:LYS:HD2	1.72	0.71
1:F:35:TYR:CE2	1:F:85:PHE:HE1	2.08	0.71
1:D:240:GLU:OE1	1:D:245:SER:N	2.22	0.71
1:D:425:ALA:O	1:D:426:ILE:HB	1.91	0.71
1:C:476:ALA:O	1:C:477:LYS:CG	2.38	0.70
1:F:57:ASN:OD1	1:F:58:ASN:N	2.23	0.70
1:B:116:GLY:N	1:B:339:SER:OG	2.19	0.70
1:F:463:PRO:HA	1:F:466:ARG:HH12	1.54	0.70
1:C:407:GLN:HB2	1:C:410:PRO:CD	2.21	0.70
1:E:463:PRO:HA	1:E:466:ARG:HH12	1.55	0.70
1:B:53:LYS:HA	1:B:61:LEU:H	1.56	0.69
1:C:116:GLY:N	1:C:339:SER:OG	2.18	0.69
1:A:406:LEU:HD22	1:A:409:PRO:HA	1.74	0.69
1:D:57:ASN:OD1	1:D:58:ASN:N	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:116:GLY:N	1:E:339:SER:OG	2.18	0.69
1:F:158:LEU:HB2	1:F:332:THR:HB	1.73	0.69
1:A:69:GLN:OE1	1:A:71:ARG:NH2	2.25	0.69
1:A:101:ALA:N	1:A:377:GLN:O	2.22	0.69
1:B:259:HIS:H	1:B:294:THR:HB	1.56	0.69
1:C:406:LEU:HB3	1:C:407:GLN:CD	2.12	0.69
1:D:475:LYS:O	1:D:476:ALA:HB3	1.92	0.69
1:B:312:TRP:CH2	1:B:468:PHE:HD1	2.10	0.69
1:C:162:LYS:HB2	1:C:245:SER:HA	1.75	0.69
1:F:41:ARG:HH21	1:F:369:GLU:HG3	1.56	0.69
1:F:312:TRP:CH2	1:F:468:PHE:CD1	2.76	0.69
1:F:384:THR:H	1:F:387:VAL:HB	1.58	0.69
1:D:144:ARG:HH12	1:E:277:ILE:HB	1.57	0.69
1:F:54:LYS:HB3	1:F:57:ASN:HB3	1.75	0.69
1:C:164:PRO:HB2	1:C:195:ILE:HD12	1.74	0.69
1:E:71:ARG:HG3	1:E:370:TYR:OH	1.93	0.69
1:A:16:VAL:HG23	1:A:18:VAL:N	2.08	0.68
1:F:71:ARG:HG3	1:F:370:TYR:OH	1.93	0.68
1:F:81:ASN:ND2	1:F:97:ARG:HB3	2.08	0.68
1:A:162:LYS:HB2	1:A:245:SER:HA	1.75	0.68
1:D:52:ILE:HB	1:D:62:VAL:HB	1.75	0.68
1:B:465:GLY:O	1:B:468:PHE:N	2.26	0.68
1:B:324:CYS:SG	1:B:329:LEU:HD12	2.33	0.68
1:D:51:PRO:HD3	1:D:64:LYS:HD2	1.74	0.68
1:B:82:LYS:HB3	1:C:12:TYR:CE1	2.29	0.68
1:C:301:THR:HG23	1:C:304:ALA:H	1.59	0.68
1:E:74:ARG:HB2	1:E:446:PHE:CE1	2.29	0.68
1:B:463:PRO:HA	1:B:466:ARG:NH1	2.09	0.68
1:E:46:GLY:HA3	1:E:65:VAL:HB	1.76	0.68
1:F:463:PRO:HA	1:F:466:ARG:NH1	2.09	0.68
1:B:47:HIS:HE1	1:B:49:TYR:HB2	1.58	0.68
1:F:312:TRP:NE1	1:F:471:GLN:OE1	2.27	0.68
1:C:57:ASN:OD1	1:C:58:ASN:N	2.27	0.67
1:D:150:ASP:OD1	1:D:296:SER:HA	1.93	0.67
1:E:455:PHE:CB	1:F:13:LEU:HD11	2.08	0.67
1:A:258:ARG:NH2	1:A:296:SER:OG	2.26	0.67
1:B:54:LYS:HB3	1:B:57:ASN:HB3	1.75	0.67
1:B:428:CYS:C	1:B:429:GLN:HG3	2.14	0.67
1:F:169:TRP:HB2	1:F:208:MET:HB3	1.75	0.67
1:A:437:LYS:HG2	1:A:438:GLU:H	1.59	0.67
1:E:111:GLN:HB2	1:E:338:ARG:HD3	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:465:GLY:O	1:E:468:PHE:N	2.27	0.67
1:F:11:VAL:HG12	1:F:13:LEU:H	1.60	0.67
1:F:47:HIS:CE1	1:F:49:TYR:HB2	2.30	0.67
1:F:111:GLN:HB2	1:F:338:ARG:HD3	1.77	0.67
1:F:117:ILE:HG12	1:F:118:SER:H	1.59	0.67
1:E:164:PRO:HB2	1:E:195:ILE:HD12	1.76	0.67
1:C:65:VAL:HG13	1:C:71:ARG:HH22	1.60	0.67
1:E:47:HIS:CE1	1:E:49:TYR:HB2	2.30	0.67
1:E:463:PRO:HA	1:E:466:ARG:NH1	2.10	0.67
1:F:74:ARG:HB2	1:F:446:PHE:CE1	2.27	0.67
1:A:258:ARG:HG2	1:A:259:HIS:ND1	2.10	0.67
1:B:42:LEU:HD22	1:B:447:TRP:HZ2	1.60	0.67
1:C:18:VAL:HG12	1:C:20:LYS:H	1.60	0.67
1:E:109:ARG:NH2	1:E:338:ARG:HD2	2.10	0.67
1:A:73:PHE:HB2	1:A:331:VAL:HB	1.77	0.66
1:A:463:PRO:HA	1:A:466:ARG:NH1	2.10	0.66
1:C:407:GLN:CG	1:C:410:PRO:HG3	2.26	0.66
1:D:74:ARG:HB2	1:D:446:PHE:CE1	2.25	0.66
1:E:97:ARG:HG3	1:E:402:TRP:CE3	2.30	0.66
1:A:399:LEU:HA	1:A:404:PHE:HE2	1.58	0.66
1:A:406:LEU:HB2	1:A:408:PRO:O	1.96	0.66
1:D:164:PRO:HB2	1:D:195:ILE:HD12	1.77	0.66
1:A:169:TRP:HB2	1:A:208:MET:HB3	1.77	0.66
1:C:65:VAL:HA	1:C:69:GLN:OE1	1.95	0.66
1:D:57:ASN:OD1	1:D:59:LYS:N	2.28	0.66
1:C:120:HIS:HB2	1:C:221:PRO:HA	1.78	0.66
1:D:54:LYS:HB3	1:D:57:ASN:HB3	1.77	0.66
1:F:150:ASP:OD1	1:F:296:SER:HA	1.96	0.66
1:F:162:LYS:HB2	1:F:245:SER:HA	1.78	0.66
1:A:56:ASN:OD1	1:A:57:ASN:N	2.28	0.66
1:B:150:ASP:OD1	1:B:296:SER:HA	1.95	0.66
1:C:463:PRO:HA	1:C:466:ARG:NH1	2.11	0.66
1:E:150:ASP:OD1	1:E:296:SER:HA	1.95	0.66
1:B:46:GLY:HA3	1:B:65:VAL:HB	1.77	0.66
1:D:171:LYS:HB2	1:D:213:LEU:HD11	1.77	0.66
1:C:312:TRP:NE1	1:C:471:GLN:OE1	2.29	0.66
1:C:404:PHE:HB2	1:C:406:LEU:N	2.10	0.66
1:E:70:TYR:OH	1:E:230:LYS:O	2.13	0.65
1:F:41:ARG:NH2	1:F:369:GLU:HG3	2.11	0.65
1:A:57:ASN:OD1	1:A:58:ASN:N	2.26	0.65
1:D:418:TYR:HB3	1:D:419:ARG:HB3	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:312:TRP:CZ3	1:B:468:PHE:HD1	2.14	0.65
1:A:52:ILE:N	1:A:62:VAL:O	2.23	0.65
1:B:162:LYS:HB2	1:B:245:SER:HA	1.78	0.65
1:C:124:ASN:HA	1:C:144:ARG:HG2	1.79	0.65
1:A:108:GLY:HA3	1:A:371:ASP:HB3	1.77	0.65
1:B:109:ARG:HG3	1:B:307:PHE:HD2	1.62	0.65
1:C:475:LYS:C	1:C:477:LYS:H	1.96	0.65
1:F:24:THR:HG21	1:F:320:ASN:HA	1.79	0.65
1:A:130:GLU:HB2	1:A:260:LEU:HB2	1.79	0.65
1:A:404:PHE:HB2	1:A:406:LEU:O	1.97	0.65
1:F:421:VAL:O	1:F:422:THR:HG23	1.97	0.64
1:F:465:GLY:O	1:F:468:PHE:N	2.29	0.64
1:E:77:LEU:HD22	1:E:455:PHE:CZ	2.31	0.64
1:C:77:LEU:HD22	1:C:455:PHE:HZ	1.60	0.64
1:F:70:TYR:OH	1:F:230:LYS:O	2.16	0.64
1:F:301:THR:HG23	1:F:304:ALA:H	1.63	0.64
1:A:52:ILE:HB	1:A:62:VAL:HB	1.79	0.64
1:C:108:GLY:HA3	1:C:371:ASP:HB3	1.79	0.64
1:D:475:LYS:CG	1:D:476:ALA:H	2.09	0.64
1:A:276:TYR:OH	1:A:278:LYS:NZ	2.31	0.64
1:A:408:PRO:HG2	1:A:410:PRO:HG2	1.79	0.64
1:D:475:LYS:HG2	1:D:476:ALA:H	1.63	0.64
1:E:36:HIS:O	1:E:456:SER:N	2.31	0.64
1:C:473:GLY:C	1:C:474:LEU:HG	2.17	0.64
1:C:455:PHE:HB2	1:D:13:LEU:HD11	1.79	0.63
1:F:37:ALA:HB2	1:F:455:PHE:HA	1.80	0.63
1:D:97:ARG:NH2	1:D:404:PHE:HB2	2.06	0.63
1:D:312:TRP:CH2	1:D:468:PHE:CD1	2.78	0.63
1:B:301:THR:HG23	1:B:304:ALA:H	1.63	0.63
1:F:53:LYS:HA	1:F:61:LEU:H	1.63	0.63
1:C:407:GLN:HB2	1:C:410:PRO:HD2	1.78	0.63
1:D:324:CYS:SG	1:D:329:LEU:HD12	2.38	0.63
1:A:387:VAL:O	1:A:390:TYR:N	2.30	0.63
1:F:120:HIS:HB2	1:F:221:PRO:HA	1.81	0.63
1:C:56:ASN:OD1	1:C:57:ASN:N	2.32	0.63
1:D:162:LYS:HB2	1:D:245:SER:HA	1.78	0.63
1:E:408:PRO:HG2	1:E:409:PRO:CD	2.29	0.63
1:E:421:VAL:O	1:E:430:LYS:NZ	2.30	0.63
1:C:51:PRO:HD3	1:C:64:LYS:HD2	1.79	0.63
1:D:463:PRO:HA	1:D:466:ARG:NH1	2.12	0.63
1:A:126:LEU:HB3	1:A:262:ASN:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:74:ARG:HB2	1:C:446:PHE:CE1	2.29	0.63
1:C:87:ASP:O	1:C:89:SER:N	2.32	0.63
1:F:387:VAL:O	1:F:391:ILE:HD12	1.99	0.63
1:B:23:SER:HA	1:B:319:HIS:HB3	1.81	0.63
1:C:387:VAL:O	1:C:391:ILE:HD12	1.99	0.63
1:C:476:ALA:O	1:C:477:LYS:HB2	1.98	0.63
1:E:399:LEU:HB3	1:E:404:PHE:HE2	1.61	0.63
1:F:111:GLN:N	1:F:369:GLU:OE1	2.31	0.63
1:B:37:ALA:HB2	1:B:455:PHE:HA	1.81	0.62
1:B:43:LEU:HD23	1:B:44:ALA:N	2.14	0.62
1:C:324:CYS:SG	1:C:329:LEU:HD12	2.39	0.62
1:E:301:THR:HG23	1:E:304:ALA:H	1.64	0.62
1:C:474:LEU:HD22	1:C:479:LYS:O	1.99	0.62
1:D:469:LEU:O	1:D:473:GLY:N	2.32	0.62
1:B:120:HIS:CD2	1:B:222:LEU:HD12	2.34	0.62
1:C:71:ARG:HG3	1:C:370:TYR:OH	1.99	0.62
1:C:85:PHE:H	1:C:88:THR:CG2	2.12	0.62
1:D:120:HIS:HB2	1:D:221:PRO:HA	1.81	0.62
1:F:234:TYR:HA	1:F:237:MET:HE3	1.79	0.62
1:A:53:LYS:HA	1:A:61:LEU:H	1.64	0.62
1:D:77:LEU:HD22	1:D:455:PHE:CZ	2.35	0.62
1:E:77:LEU:HD22	1:E:455:PHE:HZ	1.65	0.62
1:B:81:ASN:ND2	1:B:98:LEU:H	1.92	0.62
1:B:169:TRP:HB2	1:B:208:MET:HB3	1.81	0.62
1:D:223:ASP:OD1	1:D:224:ILE:N	2.32	0.62
1:E:56:ASN:OD1	1:E:57:ASN:N	2.33	0.62
1:B:117:ILE:HD11	1:C:260:LEU:HG	1.82	0.62
1:C:37:ALA:HB2	1:C:455:PHE:HA	1.82	0.62
1:C:77:LEU:HD22	1:C:455:PHE:CZ	2.35	0.62
1:A:75:ILE:HG21	1:A:451:LEU:HD12	1.80	0.62
1:A:160:GLY:HA3	1:A:246:LEU:HA	1.81	0.62
1:A:221:PRO:HD2	1:A:224:ILE:HD11	1.81	0.62
1:A:469:LEU:O	1:A:473:GLY:N	2.32	0.62
1:C:407:GLN:CB	1:C:410:PRO:HG3	2.30	0.61
1:F:254:GLN:NE2	1:F:298:SER:HB3	2.15	0.61
1:B:458:ASP:OD2	1:C:20:LYS:HE2	1.99	0.61
1:C:46:GLY:HA3	1:C:65:VAL:HB	1.82	0.61
1:F:324:CYS:SG	1:F:329:LEU:HD12	2.40	0.61
1:C:240:GLU:OE1	1:C:245:SER:N	2.31	0.61
1:C:406:LEU:CB	1:C:407:GLN:HG3	2.31	0.61
1:E:335:ASP:OD1	1:E:336:THR:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:HIS:HB2	1:A:221:PRO:HA	1.82	0.61
1:B:387:VAL:O	1:B:391:ILE:HD12	2.01	0.61
1:A:242:TYR:CZ	1:A:394:MET:HG3	2.34	0.61
1:B:43:LEU:HD21	1:C:169:TRP:HH2	1.65	0.61
1:B:223:ASP:OD1	1:B:224:ILE:N	2.33	0.61
1:D:258:ARG:HG2	1:D:259:HIS:ND1	2.14	0.61
1:A:47:HIS:HE1	1:A:49:TYR:HB2	1.64	0.61
1:A:166:GLY:HA2	1:A:232:PRO:HA	1.83	0.61
1:C:210:PHE:HE2	1:C:224:ILE:HD12	1.64	0.61
1:D:109:ARG:NH2	1:D:338:ARG:HD2	2.16	0.61
1:E:223:ASP:OD1	1:E:224:ILE:N	2.34	0.61
1:A:126:LEU:HD22	1:A:288:SER:HB3	1.82	0.61
1:B:20:LYS:HB2	1:F:461:GLN:CD	2.21	0.61
1:E:324:CYS:SG	1:E:329:LEU:HD12	2.40	0.61
1:F:35:TYR:HH	1:F:85:PHE:HD1	1.48	0.61
1:A:301:THR:HG23	1:A:304:ALA:H	1.66	0.61
1:D:56:ASN:OD1	1:D:57:ASN:N	2.34	0.61
1:D:71:ARG:HG3	1:D:370:TYR:OH	2.00	0.61
1:B:335:ASP:OD1	1:B:336:THR:N	2.34	0.60
1:C:407:GLN:HB2	1:C:410:PRO:CG	2.30	0.60
1:E:83:PHE:CD1	1:F:11:VAL:HG11	2.35	0.60
1:A:122:LEU:HD22	1:A:144:ARG:HB2	1.82	0.60
1:A:130:GLU:HA	1:A:260:LEU:HD22	1.82	0.60
1:C:408:PRO:HG2	1:C:409:PRO:HD3	1.82	0.60
1:D:37:ALA:HB2	1:D:455:PHE:HA	1.81	0.60
1:A:37:ALA:HB2	1:A:455:PHE:HD1	1.66	0.60
1:B:474:LEU:HD12	1:B:474:LEU:O	2.01	0.60
1:D:301:THR:HG23	1:D:304:ALA:H	1.66	0.60
1:A:310:PRO:HB2	1:A:312:TRP:CZ2	2.36	0.60
1:B:240:GLU:OE1	1:B:245:SER:N	2.34	0.60
1:C:81:ASN:ND2	1:C:98:LEU:H	1.99	0.60
1:C:366:HIS:CE1	1:C:368:GLU:OE2	2.55	0.60
1:E:144:ARG:HH12	1:F:277:ILE:HB	1.66	0.60
1:F:223:ASP:OD1	1:F:224:ILE:N	2.34	0.60
1:E:54:LYS:HB3	1:E:57:ASN:HB3	1.84	0.60
1:B:43:LEU:HG	1:B:368:GLU:O	2.02	0.60
1:B:71:ARG:HG3	1:B:370:TYR:OH	2.01	0.60
1:C:399:LEU:HB3	1:C:404:PHE:HE1	1.59	0.60
1:D:83:PHE:CE2	1:D:85:PHE:HD1	2.20	0.60
1:E:23:SER:HA	1:E:319:HIS:HB3	1.84	0.60
1:C:356:LYS:HA	1:D:141:VAL:HG13	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:418:TYR:HB3	1:C:420:PHE:CE2	2.37	0.60
1:D:421:VAL:HG12	1:D:422:THR:N	2.16	0.60
1:F:23:SER:HA	1:F:319:HIS:HB3	1.84	0.60
1:D:65:VAL:HG13	1:D:71:ARG:HH22	1.67	0.59
1:D:241:PRO:HG2	1:D:242:TYR:CD2	2.37	0.59
1:B:167:GLU:CD	1:B:233:ASP:HB2	2.22	0.59
1:C:109:ARG:NH2	1:C:338:ARG:HD2	2.18	0.59
1:C:171:LYS:HB2	1:C:213:LEU:HD11	1.84	0.59
1:C:223:ASP:OD1	1:C:224:ILE:N	2.36	0.59
1:D:335:ASP:OD1	1:D:336:THR:N	2.34	0.59
1:C:238:VAL:HG13	1:C:317:GLN:HG3	1.85	0.59
1:D:210:PHE:HE2	1:D:224:ILE:HD12	1.67	0.59
1:D:53:LYS:HA	1:D:61:LEU:H	1.66	0.59
1:D:109:ARG:HG3	1:D:307:PHE:HD2	1.67	0.59
1:A:15:PRO:HD3	1:A:386:ASP:O	2.02	0.59
1:A:280:SER:N	1:A:283:THR:OG1	2.27	0.59
1:B:52:ILE:HB	1:B:62:VAL:HB	1.83	0.59
1:A:120:HIS:ND1	1:A:122:LEU:O	2.35	0.59
1:A:413:THR:HG22	1:B:18:VAL:HA	1.83	0.59
1:C:155:GLN:NE2	1:C:306:ILE:HG12	2.18	0.59
1:B:56:ASN:OD1	1:B:57:ASN:N	2.35	0.59
1:E:85:PHE:H	1:E:88:THR:HG22	1.68	0.59
1:A:40:SER:OG	1:A:41:ARG:HG2	2.03	0.58
1:C:37:ALA:HB2	1:C:455:PHE:HD1	1.67	0.58
1:D:97:ARG:HG3	1:D:402:TRP:CE3	2.37	0.58
1:E:109:ARG:HG3	1:E:307:PHE:HD2	1.67	0.58
1:C:117:ILE:HD11	1:D:260:LEU:HG	1.84	0.58
1:D:423:SER:OG	1:D:424:GLN:N	2.36	0.58
1:E:258:ARG:HG2	1:E:259:HIS:ND1	2.18	0.58
1:F:120:HIS:CD2	1:F:222:LEU:HD12	2.38	0.58
1:A:408:PRO:HD2	1:A:411:GLY:HA2	1.84	0.58
1:B:109:ARG:NH2	1:B:338:ARG:HD2	2.18	0.58
1:C:254:GLN:NE2	1:C:298:SER:HB3	2.19	0.58
1:E:109:ARG:HG3	1:E:307:PHE:CD2	2.37	0.58
1:E:234:TYR:HA	1:E:237:MET:HE3	1.84	0.58
1:F:78:PRO:HD3	1:F:452:LYS:HG2	1.84	0.58
1:F:83:PHE:CG	1:F:84:GLY:N	2.71	0.58
1:A:73:PHE:N	1:A:331:VAL:O	2.35	0.58
1:B:153:GLN:NE2	1:B:300:VAL:HG12	2.18	0.58
1:B:210:PHE:HE2	1:B:224:ILE:HD12	1.67	0.58
1:D:170:GLY:O	1:D:189:GLU:N	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:469:LEU:HD22	1:A:474:LEU:HD21	1.86	0.58
1:D:65:VAL:HA	1:D:69:GLN:OE1	2.03	0.58
1:D:81:ASN:HD21	1:D:97:ARG:HB3	1.69	0.58
1:D:120:HIS:CD2	1:D:222:LEU:HD12	2.38	0.58
1:E:96:GLN:O	1:E:97:ARG:NH1	2.35	0.58
1:F:474:LEU:O	1:F:474:LEU:HD12	2.02	0.58
1:D:65:VAL:HG13	1:D:71:ARG:NH2	2.18	0.58
1:D:70:TYR:OH	1:D:230:LYS:O	2.21	0.58
1:A:174:PRO:HD3	1:A:187:PRO:HG3	1.84	0.58
1:B:469:LEU:O	1:B:473:GLY:N	2.36	0.58
1:C:47:HIS:CE1	1:C:49:TYR:HB2	2.38	0.58
1:C:85:PHE:HB3	1:C:86:PRO:HD2	1.86	0.58
1:C:463:PRO:HA	1:C:466:ARG:HH12	1.67	0.58
1:D:77:LEU:HD22	1:D:455:PHE:HZ	1.68	0.58
1:E:387:VAL:O	1:E:391:ILE:HD12	2.04	0.58
1:B:24:THR:HG21	1:B:320:ASN:HA	1.85	0.58
1:F:35:TYR:HE2	1:F:85:PHE:CE1	2.18	0.58
1:F:244:ASP:OD1	1:F:320:ASN:ND2	2.30	0.58
1:F:469:LEU:O	1:F:473:GLY:N	2.37	0.58
1:C:120:HIS:ND1	1:C:122:LEU:O	2.37	0.57
1:F:48:PRO:HA	1:F:66:SER:HB2	1.85	0.57
1:C:65:VAL:HG13	1:C:71:ARG:NH2	2.18	0.57
1:D:47:HIS:CD2	1:D:364:LEU:HB2	2.39	0.57
1:D:387:VAL:O	1:D:391:ILE:HD12	2.04	0.57
1:E:24:THR:HG21	1:E:320:ASN:HA	1.85	0.57
1:F:259:HIS:H	1:F:294:THR:HB	1.69	0.57
1:C:153:GLN:NE2	1:C:300:VAL:HG12	2.19	0.57
1:C:419:ARG:C	1:C:420:PHE:CD1	2.78	0.57
1:E:35:TYR:HD2	1:E:100:TRP:HH2	1.52	0.57
1:E:65:VAL:HG13	1:E:71:ARG:HH22	1.70	0.57
1:E:83:PHE:HD2	1:E:85:PHE:CE1	2.22	0.57
1:E:402:TRP:HE3	1:E:404:PHE:HE1	1.52	0.57
1:E:421:VAL:HG12	1:E:423:SER:H	1.69	0.57
1:C:120:HIS:CD2	1:C:222:LEU:HD12	2.39	0.57
1:A:234:TYR:O	1:A:238:VAL:N	2.28	0.57
1:A:15:PRO:CG	1:A:389:THR:HB	2.33	0.57
1:B:366:HIS:CE1	1:B:368:GLU:OE2	2.59	0.56
1:D:97:ARG:HH22	1:D:404:PHE:CB	2.11	0.56
1:D:475:LYS:O	1:D:476:ALA:CB	2.50	0.56
1:E:384:THR:H	1:E:387:VAL:HB	1.69	0.56
1:F:167:GLU:CD	1:F:233:ASP:HB2	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:43:LEU:HD21	1:C:169:TRP:CH2	2.39	0.56
1:C:109:ARG:HG3	1:C:307:PHE:CD2	2.38	0.56
1:A:30:ARG:HD2	1:A:377:GLN:NE2	2.20	0.56
1:A:88:THR:HB	1:A:91:TYR:CE1	2.40	0.56
1:A:356:LYS:HB2	1:A:359:ASN:HB2	1.86	0.56
1:B:181:ASN:N	1:B:184:ASP:OD2	2.35	0.56
1:B:273:ASP:HA	1:B:276:TYR:CE2	2.40	0.56
1:D:83:PHE:HE2	1:D:85:PHE:HD1	1.53	0.56
1:D:421:VAL:CG1	1:D:422:THR:H	2.18	0.56
1:E:35:TYR:HD2	1:E:100:TRP:CH2	2.24	0.56
1:F:407:GLN:HB3	1:F:408:PRO:HD3	1.87	0.56
1:A:47:HIS:CE1	1:A:49:TYR:HB2	2.40	0.56
1:A:344:LEU:O	1:A:363:TYR:N	2.38	0.56
1:B:77:LEU:HD22	1:B:455:PHE:CZ	2.41	0.56
1:B:234:TYR:HA	1:B:237:MET:HE3	1.88	0.56
1:E:83:PHE:HD2	1:E:85:PHE:HE1	1.52	0.56
1:F:65:VAL:HG13	1:F:71:ARG:NH2	2.20	0.56
1:A:74:ARG:HD3	1:A:448:GLU:OE2	2.04	0.56
1:A:153:GLN:HE22	1:A:300:VAL:HA	1.71	0.56
1:A:153:GLN:OE1	1:A:254:GLN:NE2	2.38	0.56
1:E:65:VAL:HG13	1:E:71:ARG:NH2	2.20	0.56
1:E:455:PHE:O	1:F:13:LEU:HD21	2.06	0.56
1:B:48:PRO:HA	1:B:66:SER:HB2	1.87	0.56
1:C:43:LEU:HD12	1:C:368:GLU:C	2.26	0.56
1:A:47:HIS:CD2	1:A:364:LEU:HB2	2.41	0.56
1:A:243:GLY:HA3	1:A:318:GLY:HA3	1.87	0.56
1:A:388:MET:HA	1:A:391:ILE:HD13	1.88	0.56
1:E:120:HIS:CD2	1:E:222:LEU:HD12	2.41	0.56
1:F:46:GLY:HA3	1:F:65:VAL:HB	1.88	0.56
1:F:56:ASN:OD1	1:F:57:ASN:N	2.39	0.56
1:A:45:VAL:HA	1:A:366:HIS:O	2.06	0.56
1:B:416:ASP:HB3	1:B:418:TYR:CE2	2.41	0.56
1:F:417:THR:HG1	1:F:418:TYR:HD2	1.54	0.56
1:A:24:THR:HA	1:A:27:TYR:CE2	2.41	0.55
1:A:317:GLN:OE1	1:A:317:GLN:N	2.30	0.55
1:A:366:HIS:ND1	1:A:367:GLY:O	2.39	0.55
1:B:47:HIS:CE1	1:B:49:TYR:HB2	2.41	0.55
1:B:91:TYR:CZ	1:B:98:LEU:HD11	2.40	0.55
1:B:148:SER:OG	1:C:260:LEU:HD23	2.07	0.55
1:B:260:LEU:HD23	1:F:148:SER:OG	2.07	0.55
1:B:356:LYS:HA	1:C:141:VAL:HG13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43:LEU:HD12	1:C:368:GLU:O	2.06	0.55
1:C:407:GLN:HB2	1:C:410:PRO:HG3	1.89	0.55
1:E:81:ASN:HD21	1:E:97:ARG:HB3	1.71	0.55
1:B:109:ARG:HG3	1:B:307:PHE:CD2	2.40	0.55
1:A:34:TYR:CE1	1:A:377:GLN:HG3	2.42	0.55
1:A:335:ASP:OD1	1:A:337:THR:N	2.35	0.55
1:A:384:THR:OG1	1:A:386:ASP:HB2	2.06	0.55
1:B:70:TYR:OH	1:B:230:LYS:O	2.24	0.55
1:B:77:LEU:HD22	1:B:455:PHE:HZ	1.71	0.55
1:E:273:ASP:HA	1:E:276:TYR:CE2	2.42	0.55
1:C:461:GLN:HE22	1:D:21:VAL:HG23	1.71	0.55
1:D:153:GLN:NE2	1:D:300:VAL:HG12	2.21	0.55
1:A:390:TYR:HA	1:A:393:SER:HB2	1.89	0.55
1:D:83:PHE:CG	1:D:84:GLY:N	2.75	0.55
1:E:153:GLN:NE2	1:E:300:VAL:HG12	2.22	0.55
1:B:42:LEU:HD13	1:B:447:TRP:HE1	1.70	0.55
1:C:384:THR:H	1:C:387:VAL:HB	1.71	0.55
1:C:469:LEU:HD21	1:C:477:LYS:HE3	1.88	0.55
1:B:144:ARG:NH1	1:B:218:SER:OG	2.40	0.55
1:E:466:ARG:HH21	1:F:319:HIS:CE1	2.24	0.55
1:A:301:THR:HG23	1:A:304:ALA:N	2.22	0.55
1:C:23:SER:HA	1:C:319:HIS:HB3	1.89	0.55
1:A:96:GLN:HA	1:A:383:LEU:HG	1.89	0.54
1:C:280:SER:O	1:C:283:THR:OG1	2.20	0.54
1:D:116:GLY:N	1:D:339:SER:OG	2.22	0.54
1:D:120:HIS:ND1	1:D:122:LEU:O	2.40	0.54
1:D:148:SER:OG	1:E:260:LEU:HD23	2.07	0.54
1:E:83:PHE:CD2	1:E:85:PHE:HE1	2.25	0.54
1:A:106:GLU:OE1	1:A:310:PRO:HA	2.07	0.54
1:C:258:ARG:HG2	1:C:259:HIS:ND1	2.23	0.54
1:C:335:ASP:OD1	1:C:336:THR:N	2.39	0.54
1:C:120:HIS:CE1	1:C:122:LEU:H	2.26	0.54
1:E:148:SER:OG	1:F:260:LEU:HD23	2.07	0.54
1:E:273:ASP:OD1	1:E:274:ASP:N	2.40	0.54
1:B:96:GLN:HG2	1:B:382:THR:HA	1.88	0.54
1:E:171:LYS:HB2	1:E:213:LEU:HD11	1.88	0.54
1:F:13:LEU:HB2	1:F:14:PRO:HD3	1.90	0.54
1:C:460:ASP:O	1:C:466:ARG:NH2	2.40	0.54
1:D:181:ASN:N	1:D:184:ASP:OD2	2.35	0.54
1:F:335:ASP:OD1	1:F:336:THR:N	2.40	0.54
1:A:24:THR:HG21	1:A:320:ASN:HA	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:HIS:CG	1:A:37:ALA:N	2.76	0.54
1:A:165:ILE:HG21	1:A:236:LYS:NZ	2.22	0.54
1:A:168:HIS:HB3	1:A:230:LYS:HG2	1.90	0.54
1:A:421:VAL:HA	1:A:424:GLN:NE2	2.23	0.54
1:B:466:ARG:HH21	1:C:319:HIS:CE1	2.26	0.54
1:A:52:ILE:O	1:A:62:VAL:N	2.30	0.54
1:B:65:VAL:HG13	1:B:71:ARG:HH22	1.73	0.54
1:D:216:ASN:ND2	1:D:219:GLU:OE2	2.40	0.54
1:E:65:VAL:HA	1:E:69:GLN:OE1	2.08	0.54
1:E:83:PHE:HA	1:F:11:VAL:CG2	2.36	0.54
1:F:78:PRO:HD2	1:F:455:PHE:CZ	2.43	0.54
1:A:306:ILE:HG22	1:A:311:TYR:OH	2.07	0.54
1:A:325:TRP:HB3	1:A:398:ILE:HD11	1.90	0.54
1:A:432:THR:N	1:A:433:PRO:HD2	2.21	0.54
1:C:273:ASP:OD1	1:C:274:ASP:N	2.41	0.54
1:D:57:ASN:CG	1:D:59:LYS:H	2.10	0.54
1:D:83:PHE:CE2	1:D:85:PHE:CD1	2.96	0.54
1:E:83:PHE:CE1	1:F:13:LEU:HD12	2.43	0.54
1:F:408:PRO:O	1:F:410:PRO:HD3	2.08	0.54
1:C:52:ILE:O	1:C:61:LEU:N	2.41	0.54
1:D:97:ARG:HG3	1:D:402:TRP:CZ3	2.43	0.54
1:F:153:GLN:NE2	1:F:300:VAL:HG12	2.22	0.54
1:A:431:HIS:HB3	1:A:433:PRO:O	2.08	0.53
1:F:220:VAL:HB	1:F:224:ILE:HD11	1.90	0.53
1:B:35:TYR:HD2	1:B:100:TRP:CH2	2.26	0.53
1:B:258:ARG:HG2	1:B:259:HIS:ND1	2.22	0.53
1:E:52:ILE:O	1:E:61:LEU:N	2.41	0.53
1:F:210:PHE:HE2	1:F:224:ILE:HD12	1.73	0.53
1:F:258:ARG:HG2	1:F:259:HIS:ND1	2.23	0.53
1:A:99:VAL:HG12	1:A:100:TRP:O	2.08	0.53
1:A:219:GLU:OE1	1:A:263:ARG:NH1	2.41	0.53
1:C:54:LYS:HD2	1:C:57:ASN:HB2	1.90	0.53
1:A:202:ASP:OD1	1:A:202:ASP:N	2.41	0.53
1:B:120:HIS:ND1	1:B:122:LEU:O	2.40	0.53
1:D:23:SER:HA	1:D:319:HIS:HB3	1.90	0.53
1:D:115:VAL:HG12	1:D:116:GLY:O	2.09	0.53
1:F:366:HIS:CE1	1:F:368:GLU:OE2	2.61	0.53
1:A:35:TYR:CE2	1:A:457:ALA:HA	2.44	0.53
1:A:71:ARG:HG3	1:A:370:TYR:OH	2.08	0.53
1:E:120:HIS:ND1	1:E:122:LEU:O	2.42	0.53
1:B:247:PHE:HB2	1:B:316:ALA:HB1	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:PRO:HG2	1:C:18:VAL:HG23	1.89	0.53
1:C:408:PRO:C	1:C:410:PRO:HD2	2.28	0.53
1:B:83:PHE:CE1	1:C:13:LEU:HD22	2.38	0.53
1:B:171:LYS:HB2	1:B:213:LEU:HD11	1.90	0.53
1:B:220:VAL:HB	1:B:224:ILE:HD11	1.90	0.53
1:C:220:VAL:HB	1:C:224:ILE:HD11	1.91	0.53
1:E:109:ARG:HH21	1:E:338:ARG:HD2	1.72	0.53
1:E:432:THR:C	1:E:434:PRO:HD2	2.29	0.53
1:F:117:ILE:CG1	1:F:118:SER:H	2.22	0.53
1:A:109:ARG:HB3	1:A:338:ARG:CZ	2.39	0.53
1:D:85:PHE:CE2	1:D:378:LEU:HD21	2.44	0.53
1:E:83:PHE:HE1	1:F:13:LEU:HD12	1.74	0.53
1:F:335:ASP:OD2	1:F:337:THR:OG1	2.23	0.53
1:D:419:ARG:HG3	1:D:420:PHE:N	2.24	0.53
1:F:78:PRO:HD3	1:F:452:LYS:HA	1.91	0.53
1:F:478:PRO:HG2	1:F:480:PHE:CE2	2.37	0.53
1:A:271:VAL:HG13	1:A:275:LEU:HD12	1.89	0.52
1:B:71:ARG:HA	1:B:197:ASP:OD1	2.10	0.52
1:B:72:VAL:O	1:B:447:TRP:HB3	2.09	0.52
1:C:395:ASN:HB3	1:C:398:ILE:HD12	1.91	0.52
1:D:37:ALA:HB2	1:D:455:PHE:HD1	1.74	0.52
1:D:220:VAL:HB	1:D:224:ILE:HD11	1.90	0.52
1:D:273:ASP:HA	1:D:276:TYR:CE2	2.43	0.52
1:E:432:THR:OG1	1:E:433:PRO:HD3	2.09	0.52
1:F:120:HIS:ND1	1:F:122:LEU:O	2.42	0.52
1:A:50:PHE:HE1	1:A:52:ILE:HD11	1.73	0.52
1:D:90:PHE:CE1	1:D:91:TYR:HD2	2.27	0.52
1:E:52:ILE:HG22	1:E:61:LEU:HB3	1.90	0.52
1:F:348:ILE:HG22	1:F:359:ASN:O	2.09	0.52
1:A:248:PHE:CG	1:A:249:TYR:N	2.76	0.52
1:D:273:ASP:OD1	1:D:274:ASP:N	2.41	0.52
1:E:355:TYR:HE1	1:E:360:PHE:CE2	2.27	0.52
1:C:45:VAL:HG12	1:C:46:GLY:N	2.25	0.52
1:C:83:PHE:CE2	1:C:85:PHE:CD1	2.98	0.52
1:E:396:SER:HA	1:E:399:LEU:HD12	1.91	0.52
1:A:116:GLY:N	1:A:339:SER:OG	2.34	0.52
1:A:392:HIS:HB2	1:A:399:LEU:HD21	1.90	0.52
1:B:280:SER:O	1:B:283:THR:OG1	2.21	0.52
1:E:325:TRP:CE3	1:E:398:ILE:HG21	2.45	0.52
1:F:70:TYR:HE1	1:F:201:VAL:HG22	1.74	0.52
1:C:109:ARG:HH21	1:C:338:ARG:HD2	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:148:SER:OG	1:D:260:LEU:HD23	2.09	0.52
1:C:404:PHE:N	1:C:405:GLY:HA2	2.24	0.52
1:D:83:PHE:CD2	1:D:85:PHE:CD1	2.97	0.52
1:D:466:ARG:HH21	1:E:319:HIS:CE1	2.28	0.52
1:E:460:ASP:OD1	1:F:319:HIS:NE2	2.30	0.52
1:A:155:GLN:HE22	1:A:305:GLN:HA	1.74	0.52
1:B:83:PHE:HD2	1:B:85:PHE:HE1	1.56	0.52
1:C:24:THR:HG21	1:C:320:ASN:HA	1.92	0.52
1:A:72:VAL:HB	1:A:446:PHE:HB2	1.92	0.52
1:C:396:SER:O	1:C:399:LEU:HB2	2.10	0.52
1:D:366:HIS:CE1	1:D:368:GLU:OE2	2.63	0.52
1:F:273:ASP:OD1	1:F:274:ASP:N	2.43	0.52
1:F:312:TRP:CE2	1:F:471:GLN:OE1	2.63	0.52
1:F:422:THR:O	1:F:430:LYS:NZ	2.41	0.52
1:A:85:PHE:HB2	1:A:88:THR:CG2	2.40	0.52
1:A:109:ARG:HD2	1:A:369:GLU:O	2.10	0.52
1:A:160:GLY:HA2	1:A:247:PHE:CE2	2.45	0.52
1:A:404:PHE:O	1:A:406:LEU:HG	2.09	0.52
1:B:42:LEU:HD22	1:B:447:TRP:CZ2	2.43	0.52
1:E:48:PRO:HA	1:E:66:SER:HB2	1.90	0.52
1:F:117:ILE:HG12	1:F:118:SER:N	2.24	0.52
1:B:78:PRO:HD3	1:B:452:LYS:HA	1.92	0.52
1:F:210:PHE:CE2	1:F:220:VAL:HG11	2.45	0.52
1:A:324:CYS:SG	1:A:329:LEU:HD12	2.50	0.51
1:B:209:ASP:OD2	1:B:212:THR:HG23	2.11	0.51
1:D:344:LEU:HB2	1:E:213:LEU:O	2.10	0.51
1:D:432:THR:HA	1:D:434:PRO:HD2	1.92	0.51
1:E:40:SER:OG	1:E:41:ARG:N	2.43	0.51
1:E:117:ILE:HD11	1:F:260:LEU:HG	1.92	0.51
1:A:235:ILE:O	1:A:239:SER:N	2.41	0.51
1:B:273:ASP:OD1	1:B:274:ASP:N	2.43	0.51
1:A:74:ARG:O	1:A:75:ILE:HD13	2.11	0.51
1:B:73:PHE:HZ	1:B:370:TYR:CD2	2.29	0.51
1:D:30:ARG:HD3	1:D:379:CYS:SG	2.50	0.51
1:D:356:LYS:HA	1:E:141:VAL:HG13	1.92	0.51
1:F:65:VAL:HG13	1:F:71:ARG:HH22	1.74	0.51
1:A:31:THR:OG1	1:A:378:LEU:HB3	2.11	0.51
1:B:355:TYR:HE1	1:B:360:PHE:CE2	2.28	0.51
1:C:83:PHE:HE2	1:C:85:PHE:CD1	2.28	0.51
1:D:47:HIS:CG	1:D:48:PRO:HD2	2.45	0.51
1:E:395:ASN:HB3	1:E:398:ILE:HD12	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ASP:HA	1:A:276:TYR:CE1	2.46	0.51
1:D:34:TYR:HE1	1:D:377:GLN:HG3	1.75	0.51
1:E:167:GLU:CD	1:E:233:ASP:HB2	2.31	0.51
1:E:78:PRO:HD3	1:E:452:LYS:HA	1.92	0.51
1:E:344:LEU:HD22	1:F:213:LEU:HD23	1.91	0.51
1:D:240:GLU:HG3	1:D:241:PRO:HD2	1.92	0.51
1:D:425:ALA:O	1:D:426:ILE:CB	2.57	0.51
1:E:280:SER:O	1:E:283:THR:OG1	2.21	0.51
1:A:18:VAL:HG11	1:A:20:LYS:HG3	1.93	0.51
1:A:23:SER:HA	1:A:319:HIS:CD2	2.45	0.51
1:A:76:HIS:O	1:A:77:LEU:HD23	2.11	0.51
1:A:97:ARG:HH21	1:A:404:PHE:N	2.08	0.51
1:D:109:ARG:HG3	1:D:307:PHE:CD2	2.45	0.51
1:F:171:LYS:HB2	1:F:213:LEU:HD11	1.93	0.51
1:F:233:ASP:N	1:F:237:MET:HE2	2.26	0.51
1:A:113:LEU:HD21	1:A:305:GLN:CD	2.31	0.51
1:C:466:ARG:O	1:C:469:LEU:HB2	2.11	0.51
1:E:356:LYS:HA	1:F:141:VAL:HG13	1.92	0.51
1:F:52:ILE:HB	1:F:62:VAL:HB	1.92	0.51
1:B:478:PRO:HG2	1:B:480:PHE:CE2	2.45	0.51
1:A:34:TYR:HE1	1:A:377:GLN:HG3	1.75	0.50
1:A:153:GLN:NE2	1:A:300:VAL:HA	2.25	0.50
1:A:403:ASN:CG	1:B:18:VAL:HG21	2.32	0.50
1:D:30:ARG:HB3	1:D:377:GLN:NE2	2.26	0.50
1:E:150:ASP:CG	1:E:297:GLY:H	2.15	0.50
1:F:109:ARG:NH2	1:F:338:ARG:HD2	2.26	0.50
1:F:109:ARG:HH21	1:F:338:ARG:HD2	1.76	0.50
1:D:242:TYR:CZ	1:D:394:MET:HG3	2.46	0.50
1:D:298:SER:OG	1:D:299:MET:N	2.45	0.50
1:E:455:PHE:HB2	1:F:13:LEU:CD1	2.10	0.50
1:F:153:GLN:CD	1:F:300:VAL:HG12	2.32	0.50
1:D:413:THR:O	1:D:414:LEU:HB2	2.11	0.50
1:F:65:VAL:HA	1:F:69:GLN:OE1	2.12	0.50
1:F:420:PHE:HB3	1:F:430:LYS:CE	2.39	0.50
1:D:280:SER:O	1:D:283:THR:OG1	2.21	0.50
1:B:417:THR:HG21	1:B:426:ILE:HG21	1.94	0.50
1:D:97:ARG:HE	1:D:402:TRP:HB3	1.77	0.50
1:A:155:GLN:OE1	1:A:306:ILE:N	2.38	0.50
1:A:372:LEU:HD22	1:A:374:PHE:CZ	2.47	0.50
1:B:108:GLY:HA3	1:B:371:ASP:HB3	1.94	0.50
1:C:466:ARG:HH21	1:D:319:HIS:CE1	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:77:LEU:O	1:D:327:ASN:HB3	2.11	0.50
1:B:335:ASP:OD1	1:B:337:THR:HG23	2.12	0.50
1:C:115:VAL:HG12	1:C:116:GLY:O	2.11	0.50
1:E:83:PHE:CD2	1:E:85:PHE:CE1	3.00	0.50
1:A:156:LEU:HG	1:A:334:VAL:HB	1.93	0.50
1:C:189:GLU:HG2	1:C:190:LEU:N	2.26	0.50
1:C:460:ASP:OD1	1:D:319:HIS:NE2	2.26	0.50
1:E:44:ALA:HB3	1:E:368:GLU:HB2	1.93	0.50
1:F:70:TYR:HD2	1:F:199:ASP:HB2	1.77	0.50
1:A:158:LEU:HD22	1:A:246:LEU:HD22	1.94	0.50
1:B:153:GLN:CD	1:B:300:VAL:HG12	2.32	0.50
1:B:168:HIS:HB3	1:B:230:LYS:HG2	1.94	0.50
1:E:41:ARG:HH21	1:E:369:GLU:HG3	1.77	0.50
1:E:407:GLN:O	1:E:410:PRO:HD3	2.11	0.49
1:A:61:LEU:HG	1:A:62:VAL:HG23	1.94	0.49
1:D:44:ALA:HB3	1:D:368:GLU:HB2	1.94	0.49
1:E:421:VAL:HB	1:E:430:LYS:NZ	2.27	0.49
1:F:43:LEU:HD12	1:F:368:GLU:O	2.12	0.49
1:F:113:LEU:HD21	1:F:305:GLN:NE2	2.26	0.49
1:F:421:VAL:N	1:F:430:LYS:HE3	2.27	0.49
1:A:44:ALA:H	1:A:368:GLU:HB2	1.76	0.49
1:A:71:ARG:HA	1:A:197:ASP:OD1	2.12	0.49
1:A:437:LYS:O	1:A:438:GLU:HG3	2.13	0.49
1:B:113:LEU:HD21	1:B:305:GLN:NE2	2.27	0.49
1:C:167:GLU:CD	1:C:233:ASP:HB2	2.33	0.49
1:A:235:ILE:O	1:A:239:SER:OG	2.28	0.49
1:C:70:TYR:HE1	1:C:201:VAL:HG22	1.77	0.49
1:E:37:ALA:HB2	1:E:455:PHE:CD1	2.37	0.49
1:F:181:ASN:N	1:F:184:ASP:OD2	2.38	0.49
1:B:65:VAL:HG13	1:B:71:ARG:NH2	2.28	0.49
1:B:78:PRO:HD2	1:B:455:PHE:CZ	2.48	0.49
1:B:83:PHE:HD2	1:B:85:PHE:CE1	2.30	0.49
1:D:52:ILE:O	1:D:61:LEU:N	2.44	0.49
1:D:70:TYR:CD1	1:D:334:VAL:HG21	2.48	0.49
1:D:47:HIS:HE1	1:D:49:TYR:HB2	1.77	0.49
1:D:109:ARG:HH21	1:D:338:ARG:HD2	1.78	0.49
1:D:335:ASP:OD1	1:D:337:THR:HG23	2.13	0.49
1:B:233:ASP:N	1:B:237:MET:HE2	2.28	0.49
1:C:153:GLN:CD	1:C:300:VAL:HG12	2.33	0.49
1:C:164:PRO:HG2	1:C:195:ILE:HB	1.95	0.49
1:C:399:LEU:C	1:C:404:PHE:HE1	2.16	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:ALA:HB1	1:A:230:LYS:HA	1.94	0.49
1:A:435:ALA:HB1	1:A:436:PRO:HD2	1.94	0.49
1:B:317:GLN:OE1	1:B:317:GLN:N	2.41	0.49
1:F:51:PRO:HB3	1:F:64:LYS:HB2	1.95	0.49
1:F:109:ARG:HG3	1:F:307:PHE:HD2	1.78	0.49
1:A:43:LEU:HA	1:A:368:GLU:O	2.13	0.49
1:A:85:PHE:HB2	1:A:88:THR:HG22	1.95	0.49
1:B:43:LEU:HA	1:B:368:GLU:O	2.13	0.49
1:B:65:VAL:HA	1:B:69:GLN:OE1	2.13	0.49
1:B:360:PHE:CE2	1:C:216:ASN:HA	2.48	0.49
1:C:259:HIS:H	1:C:294:THR:HB	1.78	0.49
1:C:439:ASP:HB3	1:C:442:LYS:HB2	1.94	0.49
1:C:466:ARG:NH2	1:D:319:HIS:CE1	2.81	0.49
1:E:109:ARG:NH1	1:E:370:TYR:CE1	2.81	0.49
1:E:181:ASN:N	1:E:184:ASP:OD2	2.42	0.49
1:E:402:TRP:CE3	1:E:404:PHE:HE1	2.30	0.49
1:D:419:ARG:HG3	1:D:420:PHE:H	1.78	0.48
1:E:408:PRO:HG2	1:E:409:PRO:HD3	1.94	0.48
1:F:382:THR:O	1:F:387:VAL:HG11	2.13	0.48
1:A:79:ASP:OD2	1:A:82:LYS:HG2	2.12	0.48
1:A:307:PHE:N	1:A:307:PHE:CD1	2.79	0.48
1:B:115:VAL:HG12	1:B:116:GLY:O	2.13	0.48
1:C:50:PHE:HA	1:C:64:LYS:HD2	1.94	0.48
1:D:385:ALA:HA	1:D:388:MET:HB2	1.95	0.48
1:E:41:ARG:NH2	1:E:369:GLU:OE2	2.47	0.48
1:E:416:ASP:O	1:E:417:THR:OG1	2.30	0.48
1:B:422:THR:O	1:B:424:GLN:N	2.45	0.48
1:E:70:TYR:HE1	1:E:201:VAL:HG22	1.78	0.48
1:E:210:PHE:HE2	1:E:224:ILE:HD12	1.79	0.48
1:F:42:LEU:HD13	1:F:447:TRP:HE1	1.78	0.48
1:A:403:ASN:OD1	1:B:18:VAL:HG21	2.13	0.48
1:B:146:CYS:HG	1:C:291:TYR:HH	1.59	0.48
1:B:348:ILE:HG22	1:B:359:ASN:O	2.13	0.48
1:B:391:ILE:O	1:B:394:MET:N	2.46	0.48
1:D:120:HIS:CE1	1:D:122:LEU:H	2.31	0.48
1:D:245:SER:OG	1:D:246:LEU:N	2.46	0.48
1:E:50:PHE:CE2	1:F:271:VAL:HG22	2.48	0.48
1:E:458:ASP:OD2	1:F:20:LYS:HE2	2.14	0.48
1:A:431:HIS:HA	1:A:433:PRO:HD2	1.96	0.48
1:B:82:LYS:HB3	1:C:12:TYR:HE1	1.78	0.48
1:D:258:ARG:HG2	1:D:259:HIS:CE1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:276:TYR:HE1	1:D:278:LYS:HD2	1.78	0.48
1:E:280:SER:N	1:E:283:THR:OG1	2.34	0.48
1:E:451:LEU:O	1:E:453:GLU:N	2.47	0.48
1:A:389:THR:O	1:A:392:HIS:HB3	2.13	0.48
1:B:210:PHE:CE2	1:B:220:VAL:HG11	2.48	0.48
1:E:233:ASP:N	1:E:237:MET:HE2	2.28	0.48
1:E:482:LEU:HD13	1:F:26:GLU:OE1	2.13	0.48
1:A:44:ALA:N	1:A:368:GLU:HB2	2.29	0.48
1:B:37:ALA:HB2	1:B:455:PHE:HD1	1.78	0.48
1:B:319:HIS:CE1	1:F:466:ARG:HH21	2.30	0.48
1:C:97:ARG:HG3	1:C:402:TRP:CE3	2.48	0.48
1:A:244:ASP:OD1	1:A:320:ASN:HB2	2.13	0.48
1:B:478:PRO:HG2	1:B:480:PHE:HE2	1.78	0.48
1:C:196:GLN:HE21	1:C:444:TYR:HD1	1.61	0.48
1:C:466:ARG:HA	1:C:469:LEU:HD12	1.96	0.48
1:D:109:ARG:NH1	1:D:370:TYR:CE1	2.81	0.48
1:E:408:PRO:C	1:E:410:PRO:CD	2.82	0.48
1:F:13:LEU:HB2	1:F:14:PRO:CD	2.43	0.48
1:F:335:ASP:OD1	1:F:337:THR:HG23	2.13	0.48
1:A:236:LYS:O	1:A:239:SER:HB2	2.13	0.48
1:B:355:TYR:CG	1:C:144:ARG:NH2	2.82	0.48
1:C:83:PHE:HE2	1:C:85:PHE:CG	2.32	0.48
1:D:24:THR:HG21	1:D:320:ASN:HA	1.96	0.48
1:D:30:ARG:HD2	1:D:377:GLN:NE2	2.29	0.48
1:E:402:TRP:HB2	1:E:404:PHE:CE1	2.49	0.48
1:E:407:GLN:C	1:E:410:PRO:HD3	2.34	0.48
1:A:211:THR:OG1	1:A:226:THR:O	2.27	0.48
1:B:109:ARG:HH21	1:B:338:ARG:HD2	1.76	0.48
1:B:436:PRO:O	1:B:438:GLU:HG3	2.13	0.48
1:C:335:ASP:OD1	1:C:337:THR:HG23	2.13	0.48
1:D:259:HIS:H	1:D:294:THR:HB	1.79	0.48
1:E:109:ARG:HB3	1:E:338:ARG:CZ	2.43	0.48
1:A:68:LEU:O	1:A:201:VAL:HG23	2.14	0.47
1:A:111:GLN:O	1:A:338:ARG:NE	2.46	0.47
1:B:216:ASN:C	1:B:218:SER:H	2.17	0.47
1:C:78:PRO:HD3	1:C:452:LYS:HA	1.96	0.47
1:E:399:LEU:HA	1:E:404:PHE:HZ	1.78	0.47
1:A:325:TRP:CE3	1:A:398:ILE:HD13	2.49	0.47
1:B:35:TYR:HD2	1:B:100:TRP:HH2	1.61	0.47
1:B:167:GLU:OE2	1:B:233:ASP:HB2	2.14	0.47
1:C:74:ARG:O	1:C:75:ILE:HD13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:77:LEU:O	1:C:327:ASN:HB3	2.13	0.47
1:C:109:ARG:NH1	1:C:370:TYR:CE1	2.82	0.47
1:D:97:ARG:NH2	1:D:404:PHE:HD2	2.13	0.47
1:E:70:TYR:CD1	1:E:334:VAL:HG21	2.49	0.47
1:F:14:PRO:HA	1:F:15:PRO:HA	1.44	0.47
1:F:85:PHE:CZ	1:F:378:LEU:HD22	2.50	0.47
1:A:16:VAL:HG12	1:A:17:PRO:HD2	1.96	0.47
1:C:43:LEU:HD12	1:C:368:GLU:H	1.79	0.47
1:C:47:HIS:CE1	1:C:49:TYR:H	2.32	0.47
1:C:113:LEU:HD21	1:C:305:GLN:NE2	2.28	0.47
1:C:475:LYS:C	1:C:477:LYS:N	2.56	0.47
1:D:48:PRO:HA	1:D:66:SER:HB2	1.95	0.47
1:D:78:PRO:HD3	1:D:452:LYS:HA	1.95	0.47
1:D:83:PHE:CD2	1:D:84:GLY:N	2.82	0.47
1:D:240:GLU:CG	1:D:241:PRO:HD2	2.44	0.47
1:E:469:LEU:O	1:E:473:GLY:N	2.47	0.47
1:E:168:HIS:HB3	1:E:230:LYS:HG2	1.95	0.47
1:F:99:VAL:N	1:F:379:CYS:O	2.30	0.47
1:A:399:LEU:HA	1:A:404:PHE:CZ	2.50	0.47
1:C:35:TYR:HD2	1:C:100:TRP:CH2	2.33	0.47
1:C:216:ASN:C	1:C:218:SER:H	2.18	0.47
1:D:254:GLN:NE2	1:D:298:SER:HB3	2.30	0.47
1:E:482:LEU:HD12	1:E:483:GLY:H	1.79	0.47
1:F:57:ASN:CG	1:F:59:LYS:H	2.17	0.47
1:A:108:GLY:CA	1:A:371:ASP:HB3	2.43	0.47
1:A:325:TRP:HE3	1:A:398:ILE:HD13	1.80	0.47
1:B:406:LEU:HA	1:B:407:GLN:CB	2.35	0.47
1:D:306:ILE:O	1:D:311:TYR:OH	2.23	0.47
1:E:399:LEU:C	1:E:404:PHE:CE2	2.88	0.47
1:A:40:SER:OG	1:A:41:ARG:N	2.47	0.47
1:A:70:TYR:CZ	1:A:201:VAL:HG22	2.49	0.47
1:B:70:TYR:HE1	1:B:201:VAL:HG22	1.80	0.47
1:B:418:TYR:HB3	1:B:419:ARG:HG2	1.97	0.47
1:C:90:PHE:CE1	1:C:91:TYR:HD2	2.32	0.47
1:C:123:LEU:H	1:C:145:GLU:H	1.62	0.47
1:C:194:VAL:O	1:C:230:LYS:NZ	2.48	0.47
1:C:476:ALA:C	1:C:477:LYS:HG2	2.35	0.47
1:D:74:ARG:O	1:D:75:ILE:HD13	2.15	0.47
1:D:82:LYS:O	1:E:12:TYR:CD2	2.68	0.47
1:D:153:GLN:CD	1:D:300:VAL:HG12	2.35	0.47
1:D:168:HIS:CE1	1:D:191:ILE:HB	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:196:GLN:HE21	1:D:444:TYR:HD1	1.61	0.47
1:D:276:TYR:CE1	1:D:278:LYS:HD2	2.49	0.47
1:F:90:PHE:CE1	1:F:91:TYR:HD2	2.31	0.47
1:A:115:VAL:HG12	1:A:116:GLY:O	2.15	0.47
1:A:447:TRP:HE1	1:A:449:VAL:HG23	1.78	0.47
1:B:216:ASN:ND2	1:B:219:GLU:OE2	2.43	0.47
1:C:105:VAL:HG21	1:C:159:ILE:HD13	1.96	0.47
1:D:118:SER:O	1:D:148:SER:HB2	2.15	0.47
1:D:466:ARG:NH1	1:E:317:GLN:O	2.48	0.47
1:F:42:LEU:HD22	1:F:447:TRP:HZ2	1.78	0.47
1:F:109:ARG:HG3	1:F:307:PHE:CD2	2.50	0.47
1:F:428:CYS:CB	1:F:432:THR:HG21	2.42	0.47
1:C:168:HIS:HB3	1:C:230:LYS:HG2	1.96	0.47
1:C:245:SER:OG	1:C:246:LEU:N	2.48	0.47
1:C:344:LEU:HB2	1:D:213:LEU:O	2.14	0.47
1:E:348:ILE:HG22	1:E:359:ASN:O	2.14	0.47
1:B:141:VAL:HG13	1:F:356:LYS:HA	1.96	0.47
1:C:403:ASN:O	1:C:405:GLY:HA2	2.14	0.47
1:D:40:SER:OG	1:D:41:ARG:N	2.47	0.47
1:E:146:CYS:SG	1:F:291:TYR:OH	2.69	0.47
1:E:432:THR:O	1:E:434:PRO:HD2	2.15	0.47
1:F:57:ASN:OD1	1:F:59:LYS:N	2.44	0.47
1:A:245:SER:OG	1:A:246:LEU:N	2.45	0.46
1:A:414:LEU:N	1:A:416:ASP:OD1	2.46	0.46
1:B:21:VAL:HG13	1:B:390:TYR:OH	2.15	0.46
1:B:79:ASP:HA	1:B:327:ASN:OD1	2.15	0.46
1:B:420:PHE:CE1	1:B:429:GLN:NE2	2.71	0.46
1:C:35:TYR:HD2	1:C:100:TRP:HH2	1.63	0.46
1:E:220:VAL:HB	1:E:224:ILE:HD11	1.95	0.46
1:A:84:GLY:HA2	1:F:84:GLY:HA2	1.97	0.46
1:A:109:ARG:HB3	1:A:338:ARG:NH1	2.31	0.46
1:A:117:ILE:HG13	1:A:149:MET:O	2.15	0.46
1:B:312:TRP:CZ3	1:B:468:PHE:CD1	3.01	0.46
1:C:42:LEU:HD13	1:C:447:TRP:CZ2	2.50	0.46
1:D:109:ARG:HB3	1:D:338:ARG:CZ	2.45	0.46
1:D:348:ILE:HG22	1:D:359:ASN:O	2.15	0.46
1:E:70:TYR:CE1	1:E:201:VAL:HG22	2.51	0.46
1:A:413:THR:HA	1:B:18:VAL:N	2.30	0.46
1:B:433:PRO:O	1:B:435:ALA:N	2.49	0.46
1:C:406:LEU:HA	1:C:407:GLN:HA	1.44	0.46
1:C:451:LEU:O	1:C:453:GLU:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:302:SER:OG	1:E:253:GLU:N	2.45	0.46
1:D:343:SER:OG	1:E:263:ARG:NH2	2.43	0.46
1:F:216:ASN:C	1:F:218:SER:H	2.19	0.46
1:F:402:TRP:C	1:F:404:PHE:H	2.17	0.46
1:C:123:LEU:N	1:C:145:GLU:O	2.49	0.46
1:D:50:PHE:CE2	1:E:271:VAL:HG22	2.50	0.46
1:D:216:ASN:C	1:D:218:SER:H	2.17	0.46
1:D:461:GLN:HE22	1:E:21:VAL:H	1.62	0.46
1:A:43:LEU:HG	1:A:44:ALA:N	2.31	0.46
1:A:372:LEU:HD22	1:A:374:PHE:HZ	1.80	0.46
1:A:392:HIS:ND1	1:A:399:LEU:HD11	2.31	0.46
1:B:466:ARG:NH2	1:C:319:HIS:CE1	2.84	0.46
1:C:233:ASP:N	1:C:237:MET:HE2	2.30	0.46
1:C:357:ASN:HB3	1:D:265:GLY:HA2	1.97	0.46
1:D:34:TYR:CE1	1:D:377:GLN:HG3	2.51	0.46
1:D:70:TYR:HD1	1:D:334:VAL:HG21	1.79	0.46
1:E:34:TYR:HE1	1:E:377:GLN:HG3	1.80	0.46
1:E:258:ARG:HG2	1:E:259:HIS:CE1	2.50	0.46
1:F:120:HIS:CE1	1:F:122:LEU:H	2.33	0.46
1:A:258:ARG:HB2	1:A:296:SER:HB2	1.98	0.46
1:B:298:SER:OG	1:B:299:MET:N	2.48	0.46
1:D:70:TYR:HE1	1:D:201:VAL:HG22	1.79	0.46
1:E:73:PHE:HZ	1:E:370:TYR:CD2	2.33	0.46
1:E:298:SER:OG	1:E:299:MET:N	2.47	0.46
1:E:480:PHE:O	1:E:481:THR:HG23	2.16	0.46
1:F:216:ASN:ND2	1:F:219:GLU:OE2	2.42	0.46
1:A:77:LEU:HD22	1:A:455:PHE:CZ	2.51	0.46
1:B:246:LEU:HD12	1:B:317:GLN:NE2	2.31	0.46
1:C:41:ARG:HH21	1:C:369:GLU:HG3	1.79	0.46
1:D:78:PRO:HD2	1:D:455:PHE:CZ	2.51	0.46
1:D:123:LEU:N	1:D:145:GLU:O	2.48	0.46
1:D:248:PHE:CG	1:D:249:TYR:N	2.83	0.46
1:E:97:ARG:HG3	1:E:402:TRP:CZ3	2.51	0.46
1:E:335:ASP:OD1	1:E:337:THR:HG23	2.15	0.46
1:F:109:ARG:NH1	1:F:370:TYR:CE1	2.84	0.46
1:F:164:PRO:HG2	1:F:195:ILE:HB	1.97	0.46
1:A:413:THR:HG22	1:B:18:VAL:CA	2.45	0.46
1:A:465:GLY:O	1:A:468:PHE:HB3	2.16	0.46
1:B:385:ALA:HA	1:B:388:MET:CE	2.46	0.46
1:C:146:CYS:SG	1:D:291:TYR:OH	2.71	0.46
1:C:181:ASN:N	1:C:184:ASP:OD2	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:392:HIS:HA	1:E:399:LEU:HD11	1.97	0.46
1:F:258:ARG:HG2	1:F:259:HIS:CE1	2.51	0.46
1:B:383:LEU:HD21	1:B:388:MET:SD	2.55	0.46
1:C:120:HIS:HD2	1:C:222:LEU:HD12	1.81	0.46
1:C:209:ASP:OD2	1:C:212:THR:HG23	2.16	0.46
1:C:459:LEU:HD23	1:C:459:LEU:HA	1.50	0.46
1:D:414:LEU:HD23	1:D:414:LEU:HA	1.57	0.46
1:D:451:LEU:O	1:D:453:GLU:N	2.49	0.46
1:E:112:PRO:HB3	1:F:231:TYR:CD1	2.51	0.46
1:F:298:SER:OG	1:F:299:MET:N	2.48	0.46
1:D:50:PHE:HA	1:D:64:LYS:HD2	1.98	0.46
1:F:248:PHE:CG	1:F:249:TYR:N	2.84	0.46
1:B:256:PHE:HB3	1:F:299:MET:HA	1.98	0.45
1:B:416:ASP:O	1:B:418:TYR:N	2.49	0.45
1:F:13:LEU:CB	1:F:14:PRO:HD3	2.47	0.45
1:A:105:VAL:HG13	1:A:374:PHE:CE1	2.52	0.45
1:A:150:ASP:OD1	1:A:296:SER:HA	2.17	0.45
1:A:240:GLU:OE1	1:A:244:ASP:N	2.49	0.45
1:B:345:CYS:SG	1:C:215:ALA:N	2.90	0.45
1:B:418:TYR:HA	1:B:419:ARG:HA	1.73	0.45
1:C:79:ASP:HA	1:C:327:ASN:OD1	2.16	0.45
1:F:115:VAL:HG12	1:F:116:GLY:O	2.16	0.45
1:F:414:LEU:HD23	1:F:414:LEU:HA	1.65	0.45
1:A:298:SER:OG	1:A:299:MET:N	2.49	0.45
1:B:45:VAL:HA	1:B:366:HIS:O	2.16	0.45
1:C:72:VAL:O	1:C:447:TRP:HB3	2.17	0.45
1:C:111:GLN:N	1:C:369:GLU:OE1	2.49	0.45
1:C:219:GLU:OE1	1:C:263:ARG:CZ	2.65	0.45
1:C:256:PHE:HE2	1:C:298:SER:HB2	1.80	0.45
1:C:406:LEU:HD22	1:C:407:GLN:HG3	1.97	0.45
1:D:246:LEU:HD12	1:D:246:LEU:O	2.16	0.45
1:E:210:PHE:CE2	1:E:220:VAL:HG11	2.51	0.45
1:A:480:PHE:O	1:A:482:LEU:HG	2.16	0.45
1:D:180:VAL:HG13	1:D:184:ASP:HB2	1.98	0.45
1:B:18:VAL:C	1:B:20:LYS:N	2.70	0.45
1:C:34:TYR:CE2	1:C:468:PHE:HZ	2.35	0.45
1:C:52:ILE:HG22	1:C:61:LEU:HB3	1.97	0.45
1:C:85:PHE:HD2	1:C:88:THR:HG22	1.81	0.45
1:D:13:LEU:HA	1:D:13:LEU:HD23	1.60	0.45
1:D:123:LEU:H	1:D:145:GLU:H	1.65	0.45
1:E:313:LEU:HA	1:E:313:LEU:HD23	1.72	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:473:GLY:C	1:E:474:LEU:HG	2.35	0.45
1:A:37:ALA:HB2	1:A:455:PHE:CD1	2.47	0.45
1:A:88:THR:HA	1:A:90:PHE:CE2	2.51	0.45
1:D:113:LEU:HD21	1:D:305:GLN:NE2	2.32	0.45
1:D:114:GLY:HA2	1:E:255:MET:CE	2.47	0.45
1:D:299:MET:HA	1:E:256:PHE:HB3	1.98	0.45
1:D:469:LEU:HB3	1:D:474:LEU:CG	2.46	0.45
1:D:469:LEU:HB3	1:D:474:LEU:HG	1.98	0.45
1:F:314:GLN:HG3	1:F:315:ARG:N	2.32	0.45
1:A:259:HIS:N	1:A:294:THR:HB	2.22	0.45
1:B:43:LEU:HD23	1:B:44:ALA:H	1.81	0.45
1:B:50:PHE:CE2	1:C:271:VAL:HG22	2.51	0.45
1:D:210:PHE:CE2	1:D:220:VAL:HG11	2.51	0.45
1:D:469:LEU:CB	1:D:474:LEU:CG	2.92	0.45
1:E:180:VAL:HG13	1:E:184:ASP:HB2	1.98	0.45
1:F:96:GLN:HG2	1:F:382:THR:HA	1.99	0.45
1:F:439:ASP:OD1	1:F:440:PRO:HD2	2.17	0.45
1:A:97:ARG:HG3	1:A:98:LEU:H	1.82	0.45
1:A:197:ASP:HB3	1:A:446:PHE:HA	1.98	0.45
1:B:244:ASP:OD1	1:B:320:ASN:ND2	2.39	0.45
1:B:271:VAL:HG22	1:F:50:PHE:CE2	2.52	0.45
1:C:423:SER:C	1:C:425:ALA:H	2.20	0.45
1:D:43:LEU:HD12	1:D:368:GLU:O	2.17	0.45
1:E:83:PHE:CE1	1:F:11:VAL:HG11	2.52	0.45
1:E:153:GLN:CD	1:E:300:VAL:HG12	2.37	0.45
1:E:246:LEU:HD12	1:E:317:GLN:NE2	2.32	0.45
1:C:20:LYS:O	1:C:22:VAL:HG13	2.17	0.45
1:C:298:SER:OG	1:C:299:MET:N	2.50	0.45
1:E:240:GLU:OE1	1:E:245:SER:N	2.47	0.45
1:F:96:GLN:HG2	1:F:381:ILE:O	2.17	0.45
1:C:11:VAL:CG1	1:C:13:LEU:HD11	2.39	0.45
1:C:48:PRO:HA	1:C:66:SER:HB2	1.99	0.45
1:C:248:PHE:CG	1:C:249:TYR:N	2.85	0.45
1:D:47:HIS:CE1	1:D:49:TYR:HB2	2.52	0.45
1:D:97:ARG:CZ	1:D:404:PHE:HD2	2.30	0.45
1:D:167:GLU:CD	1:D:233:ASP:HB2	2.38	0.45
1:D:201:VAL:HG12	1:D:202:ASP:O	2.16	0.45
1:D:391:ILE:O	1:D:394:MET:N	2.49	0.45
1:E:158:LEU:O	1:E:331:VAL:HA	2.17	0.45
1:E:343:SER:OG	1:F:263:ARG:NH2	2.49	0.45
1:A:106:GLU:OE2	1:A:309:LYS:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:109:ARG:NH1	1:B:370:TYR:CE1	2.85	0.44
1:B:417:THR:OG1	1:B:420:PHE:CZ	2.71	0.44
1:C:53:LYS:HA	1:C:61:LEU:N	2.26	0.44
1:D:34:TYR:HE1	1:D:377:GLN:CG	2.30	0.44
1:E:241:PRO:HG2	1:E:242:TYR:CD2	2.52	0.44
1:A:87:ASP:O	1:A:90:PHE:HE2	1.99	0.44
1:B:162:LYS:HG2	1:B:244:ASP:HB3	1.98	0.44
1:B:385:ALA:HA	1:B:388:MET:HE3	1.99	0.44
1:D:280:SER:N	1:D:283:THR:OG1	2.35	0.44
1:E:408:PRO:CA	1:E:410:PRO:HD3	2.47	0.44
1:E:459:LEU:HD23	1:E:459:LEU:HA	1.81	0.44
1:F:314:GLN:HG3	1:F:315:ARG:H	1.82	0.44
1:F:459:LEU:HD23	1:F:459:LEU:HA	1.76	0.44
1:A:72:VAL:HA	1:A:332:THR:OG1	2.17	0.44
1:D:146:CYS:HG	1:E:291:TYR:HH	1.64	0.44
1:D:417:THR:O	1:D:418:TYR:CG	2.71	0.44
1:E:85:PHE:HB2	1:E:88:THR:HG22	1.98	0.44
1:E:248:PHE:CG	1:E:249:TYR:N	2.85	0.44
1:E:482:LEU:HG	1:E:483:GLY:N	2.33	0.44
1:F:162:LYS:HG2	1:F:244:ASP:HB3	2.00	0.44
1:A:75:ILE:HG22	1:A:76:HIS:N	2.33	0.44
1:B:109:ARG:HD2	1:B:369:GLU:O	2.17	0.44
1:B:384:THR:O	1:B:388:MET:HG3	2.16	0.44
1:C:384:THR:OG1	1:C:387:VAL:HG23	2.17	0.44
1:F:152:LYS:HD3	1:F:202:ASP:OD1	2.17	0.44
1:F:240:GLU:OE1	1:F:245:SER:N	2.47	0.44
1:A:18:VAL:CG1	1:A:20:LYS:HG3	2.48	0.44
1:A:155:GLN:OE1	1:A:306:ILE:HG12	2.17	0.44
1:B:54:LYS:HD2	1:B:57:ASN:HB2	1.98	0.44
1:B:90:PHE:CE1	1:B:91:TYR:HD2	2.35	0.44
1:C:111:GLN:HG2	1:C:369:GLU:HB3	1.98	0.44
1:C:210:PHE:CE2	1:C:220:VAL:HG11	2.52	0.44
1:C:256:PHE:CE2	1:C:298:SER:HB2	2.53	0.44
1:D:246:LEU:HD12	1:D:317:GLN:NE2	2.32	0.44
1:D:312:TRP:CE2	1:D:471:GLN:OE1	2.70	0.44
1:A:388:MET:O	1:A:391:ILE:HB	2.18	0.44
1:A:447:TRP:NE1	1:A:449:VAL:HG23	2.32	0.44
1:B:120:HIS:CE1	1:B:122:LEU:H	2.34	0.44
1:B:306:ILE:O	1:B:311:TYR:OH	2.34	0.44
1:C:114:GLY:HA2	1:D:255:MET:CE	2.48	0.44
1:E:37:ALA:CB	1:E:455:PHE:HD1	2.22	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:24:THR:CG2	1:F:320:ASN:HA	2.47	0.44
1:A:78:PRO:HD3	1:A:452:LYS:HG2	2.00	0.44
1:A:174:PRO:CD	1:A:187:PRO:HG3	2.48	0.44
1:C:314:GLN:HG3	1:C:315:ARG:N	2.32	0.44
1:D:209:ASP:OD2	1:D:212:THR:HG23	2.18	0.44
1:E:35:TYR:CD2	1:E:100:TRP:HH2	2.35	0.44
1:F:160:GLY:HA2	1:F:247:PHE:CE2	2.52	0.44
1:F:167:GLU:OE2	1:F:233:ASP:HB2	2.17	0.44
1:F:402:TRP:C	1:F:404:PHE:N	2.70	0.44
1:B:170:GLY:O	1:B:189:GLU:N	2.51	0.44
1:C:41:ARG:NH2	1:C:369:GLU:OE2	2.51	0.44
1:D:244:ASP:OD1	1:D:320:ASN:HB2	2.18	0.44
1:E:79:ASP:HA	1:E:327:ASN:OD1	2.17	0.44
1:E:97:ARG:HH21	1:E:404:PHE:H	1.66	0.44
1:F:40:SER:OG	1:F:41:ARG:N	2.50	0.44
1:F:280:SER:O	1:F:283:THR:OG1	2.21	0.44
1:A:23:SER:HA	1:A:319:HIS:HD2	1.83	0.44
1:C:168:HIS:CE1	1:C:191:ILE:HB	2.53	0.44
1:D:426:ILE:HD13	1:D:426:ILE:HG21	1.27	0.44
1:D:439:ASP:OD1	1:D:441:LEU:N	2.48	0.44
1:E:74:ARG:O	1:E:75:ILE:HD13	2.18	0.44
1:F:70:TYR:CE1	1:F:201:VAL:HG22	2.52	0.44
1:B:77:LEU:O	1:B:327:ASN:HB3	2.18	0.43
1:B:159:ILE:HG22	1:B:247:PHE:CZ	2.53	0.43
1:B:312:TRP:CD2	1:B:471:GLN:NE2	2.83	0.43
1:C:473:GLY:C	1:C:474:LEU:CG	2.86	0.43
1:D:34:TYR:CE2	1:D:468:PHE:HZ	2.36	0.43
1:D:210:PHE:O	1:D:214:GLN:N	2.41	0.43
1:D:240:GLU:OE2	1:D:244:ASP:HB2	2.17	0.43
1:D:384:THR:O	1:D:388:MET:HG3	2.17	0.43
1:F:35:TYR:CE2	1:F:85:PHE:CE1	2.97	0.43
1:A:45:VAL:HG12	1:A:46:GLY:N	2.33	0.43
1:A:52:ILE:HG22	1:A:61:LEU:HB3	1.99	0.43
1:A:240:GLU:HG2	1:A:242:TYR:H	1.83	0.43
1:A:280:SER:H	1:A:283:THR:HG1	1.61	0.43
1:B:64:LYS:O	1:B:69:GLN:NE2	2.32	0.43
1:B:114:GLY:HA2	1:C:255:MET:CE	2.49	0.43
1:D:314:GLN:HG3	1:D:315:ARG:N	2.33	0.43
1:F:34:TYR:O	1:F:35:TYR:CD1	2.72	0.43
1:F:37:ALA:HB2	1:F:455:PHE:HD1	1.83	0.43
1:F:306:ILE:HG22	1:F:306:ILE:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:ARG:HH21	1:A:296:SER:HG	1.63	0.43
1:B:416:ASP:HB3	1:B:418:TYR:CZ	2.53	0.43
1:B:431:HIS:O	1:B:433:PRO:HD2	2.17	0.43
1:C:11:VAL:O	1:C:12:TYR:CD1	2.72	0.43
1:D:47:HIS:CE1	1:D:49:TYR:H	2.35	0.43
1:D:109:ARG:CZ	1:D:338:ARG:HD2	2.48	0.43
1:A:71:ARG:O	1:A:332:THR:HG23	2.17	0.43
1:D:355:TYR:HE1	1:D:360:PHE:CE2	2.37	0.43
1:E:115:VAL:HG12	1:E:116:GLY:O	2.19	0.43
1:E:306:ILE:O	1:E:306:ILE:HG22	2.18	0.43
1:A:262:ASN:ND2	1:A:291:TYR:HA	2.34	0.43
1:C:201:VAL:HG12	1:C:202:ASP:O	2.18	0.43
1:C:246:LEU:O	1:C:246:LEU:HD12	2.18	0.43
1:E:201:VAL:HG12	1:E:202:ASP:O	2.18	0.43
1:E:216:ASN:C	1:E:218:SER:H	2.21	0.43
1:F:30:ARG:HB3	1:F:377:GLN:NE2	2.33	0.43
1:A:99:VAL:HG22	1:A:402:TRP:HZ2	1.84	0.43
1:A:374:PHE:HB3	1:A:376:PHE:CE2	2.54	0.43
1:B:246:LEU:O	1:B:317:GLN:NE2	2.52	0.43
1:C:348:ILE:HG13	1:D:182:PRO:HB2	2.01	0.43
1:E:246:LEU:HD12	1:E:246:LEU:O	2.19	0.43
1:F:169:TRP:O	1:F:208:MET:HA	2.19	0.43
1:F:366:HIS:CE1	1:F:367:GLY:O	2.72	0.43
1:C:240:GLU:HG3	1:C:241:PRO:HD2	2.01	0.43
1:D:167:GLU:OE2	1:D:233:ASP:HB2	2.18	0.43
1:E:109:ARG:CZ	1:E:338:ARG:HD2	2.49	0.43
1:F:273:ASP:HA	1:F:276:TYR:CE2	2.53	0.43
1:B:81:ASN:HD21	1:B:98:LEU:N	1.99	0.43
1:C:426:ILE:HG22	1:C:427:ALA:N	2.34	0.43
1:D:70:TYR:CE1	1:D:201:VAL:HG22	2.54	0.43
1:D:408:PRO:N	1:D:409:PRO:CD	2.82	0.43
1:F:207:ALA:HB1	1:F:230:LYS:HA	2.01	0.43
1:A:74:ARG:HE	1:A:76:HIS:CE1	2.37	0.43
1:A:223:ASP:OD1	1:A:223:ASP:N	2.52	0.43
1:B:20:LYS:NZ	1:F:458:ASP:HB2	2.34	0.43
1:B:213:LEU:HD23	1:F:344:LEU:HD22	2.01	0.43
1:B:366:HIS:HE1	1:B:368:GLU:OE2	2.00	0.43
1:C:195:ILE:HA	1:C:230:LYS:NZ	2.34	0.43
1:C:210:PHE:HB3	1:C:214:GLN:OE1	2.19	0.43
1:D:194:VAL:O	1:D:230:LYS:NZ	2.52	0.43
1:D:475:LYS:CG	1:D:476:ALA:N	2.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:314:GLN:HG3	1:E:315:ARG:N	2.34	0.43
1:F:83:PHE:CD2	1:F:84:GLY:N	2.87	0.43
1:A:256:PHE:HE1	1:A:298:SER:HA	1.83	0.43
1:B:341:ASN:OD1	1:B:366:HIS:HD2	2.02	0.43
1:B:417:THR:HB	1:B:426:ILE:HG12	1.99	0.43
1:C:70:TYR:OH	1:C:230:LYS:O	2.35	0.43
1:C:109:ARG:HD2	1:C:369:GLU:O	2.18	0.43
1:C:120:HIS:ND1	1:C:122:LEU:N	2.62	0.43
1:E:210:PHE:O	1:E:214:GLN:N	2.43	0.43
1:E:301:THR:CG2	1:E:304:ALA:H	2.29	0.43
1:E:417:THR:HB	1:E:419:ARG:NE	2.19	0.43
1:A:109:ARG:NH2	1:A:338:ARG:HD2	2.33	0.42
1:B:156:LEU:HD12	1:B:156:LEU:C	2.39	0.42
1:C:42:LEU:HD13	1:C:447:TRP:HZ2	1.84	0.42
1:C:83:PHE:CG	1:C:84:GLY:N	2.87	0.42
1:C:325:TRP:CE3	1:C:398:ILE:HG21	2.54	0.42
1:A:335:ASP:OD1	1:A:337:THR:OG1	2.29	0.42
1:C:207:ALA:HB1	1:C:230:LYS:HA	2.01	0.42
1:C:258:ARG:HG2	1:C:259:HIS:CE1	2.53	0.42
1:C:280:SER:N	1:C:283:THR:OG1	2.33	0.42
1:E:50:PHE:HE2	1:F:271:VAL:HG22	1.83	0.42
1:A:170:GLY:HA3	1:A:191:ILE:HD12	2.00	0.42
1:A:216:ASN:C	1:A:218:SER:H	2.22	0.42
1:A:220:VAL:HG23	1:A:225:CYS:HA	2.00	0.42
1:A:391:ILE:O	1:A:395:ASN:N	2.49	0.42
1:B:85:PHE:H	1:B:88:THR:CG2	2.28	0.42
1:C:477:LYS:HB2	1:C:478:PRO:HD3	2.00	0.42
1:E:85:PHE:H	1:E:88:THR:CG2	2.30	0.42
1:F:34:TYR:HE1	1:F:377:GLN:HG3	1.85	0.42
1:B:207:ALA:HB1	1:B:230:LYS:HA	2.02	0.42
1:C:344:LEU:HD22	1:D:213:LEU:HD23	2.00	0.42
1:C:407:GLN:HG2	1:C:410:PRO:HG3	2.00	0.42
1:E:57:ASN:CG	1:E:59:LYS:H	2.21	0.42
1:E:90:PHE:CE1	1:E:91:TYR:HD2	2.38	0.42
1:E:118:SER:O	1:E:148:SER:HB2	2.19	0.42
1:F:109:ARG:HD2	1:F:369:GLU:O	2.20	0.42
1:A:80:PRO:HB2	1:A:98:LEU:CB	2.41	0.42
1:C:57:ASN:OD1	1:C:59:LYS:N	2.46	0.42
1:C:57:ASN:CG	1:C:59:LYS:H	2.23	0.42
1:D:83:PHE:HE2	1:D:85:PHE:HA	1.84	0.42
1:E:384:THR:O	1:E:387:VAL:HB	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:51:PRO:CB	1:F:64:LYS:HB2	2.48	0.42
1:A:70:TYR:CE2	1:A:201:VAL:HA	2.54	0.42
1:A:120:HIS:CD2	1:A:222:LEU:HD12	2.55	0.42
1:A:169:TRP:N	1:A:207:ALA:O	2.30	0.42
1:B:70:TYR:HD2	1:B:199:ASP:HB2	1.84	0.42
1:C:34:TYR:HE1	1:C:377:GLN:HG3	1.85	0.42
1:C:71:ARG:HG3	1:C:370:TYR:CZ	2.55	0.42
1:C:273:ASP:HA	1:C:276:TYR:CE2	2.54	0.42
1:C:343:SER:OG	1:D:263:ARG:NH2	2.48	0.42
1:D:301:THR:CG2	1:D:304:ALA:H	2.31	0.42
1:F:209:ASP:OD2	1:F:212:THR:HG23	2.20	0.42
1:A:15:PRO:HB3	1:A:390:TYR:HB2	2.01	0.42
1:C:312:TRP:CD1	1:C:471:GLN:OE1	2.73	0.42
1:E:162:LYS:N	1:E:244:ASP:O	2.51	0.42
1:E:451:LEU:O	1:E:454:LYS:N	2.41	0.42
1:C:40:SER:OG	1:C:41:ARG:N	2.53	0.42
1:C:312:TRP:CE2	1:C:471:GLN:OE1	2.72	0.42
1:C:355:TYR:HE1	1:C:360:PHE:CE2	2.38	0.42
1:D:117:ILE:HD12	1:D:150:ASP:HB3	2.01	0.42
1:D:469:LEU:CA	1:D:474:LEU:CD2	2.38	0.42
1:E:209:ASP:OD2	1:E:212:THR:HG23	2.19	0.42
1:E:360:PHE:CE2	1:F:216:ASN:HA	2.54	0.42
1:B:114:GLY:HA2	1:C:255:MET:HE2	2.01	0.42
1:B:168:HIS:CE1	1:B:191:ILE:HB	2.55	0.42
1:B:272:PRO:HD3	1:F:50:PHE:CE1	2.55	0.42
1:B:343:SER:OG	1:C:263:ARG:NH2	2.50	0.42
1:C:170:GLY:N	1:C:189:GLU:O	2.53	0.42
1:D:306:ILE:O	1:D:306:ILE:HG22	2.19	0.42
1:F:124:ASN:ND2	1:F:264:ALA:H	2.17	0.42
1:F:159:ILE:HG22	1:F:247:PHE:CZ	2.55	0.42
1:A:42:LEU:O	1:A:369:GLU:HA	2.19	0.42
1:A:120:HIS:O	1:A:146:CYS:HA	2.19	0.42
1:B:271:VAL:HG22	1:F:50:PHE:HE2	1.84	0.42
1:C:321:ASN:O	1:C:323:ILE:HG12	2.20	0.42
1:E:196:GLN:HE21	1:E:444:TYR:HD1	1.67	0.42
1:A:17:PRO:O	1:A:18:VAL:O	2.38	0.41
1:A:234:TYR:OH	1:A:251:ARG:HD3	2.20	0.41
1:B:78:PRO:HD3	1:B:452:LYS:HG2	2.02	0.41
1:C:241:PRO:HG2	1:C:242:TYR:CD2	2.54	0.41
1:D:234:TYR:CE2	1:D:251:ARG:HD3	2.55	0.41
1:A:428:CYS:HB3	1:A:432:THR:CG2	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:SER:O	1:B:26:GLU:HG2	2.20	0.41
1:C:118:SER:O	1:C:148:SER:HB2	2.20	0.41
1:C:465:GLY:O	1:C:468:PHE:HB3	2.20	0.41
1:E:219:GLU:OE1	1:E:263:ARG:CZ	2.66	0.41
1:E:466:ARG:NH2	1:F:319:HIS:CE1	2.88	0.41
1:F:180:VAL:HG13	1:F:184:ASP:HB2	2.01	0.41
1:A:371:ASP:O	1:A:372:LEU:HD23	2.21	0.41
1:B:216:ASN:HA	1:F:360:PHE:CE2	2.55	0.41
1:C:10:THR:OG1	1:C:11:VAL:N	2.53	0.41
1:C:156:LEU:C	1:C:156:LEU:HD12	2.41	0.41
1:C:422:THR:HA	1:C:426:ILE:HD12	2.02	0.41
1:E:123:LEU:H	1:E:145:GLU:H	1.68	0.41
1:E:478:PRO:HG2	1:E:480:PHE:HD2	1.85	0.41
1:F:70:TYR:HD1	1:F:334:VAL:HG21	1.85	0.41
1:F:106:GLU:HB2	1:F:464:LEU:HD11	2.03	0.41
1:A:35:TYR:HE2	1:A:457:ALA:HA	1.85	0.41
1:A:46:GLY:HA3	1:A:65:VAL:HB	2.03	0.41
1:B:42:LEU:HD23	1:B:42:LEU:HA	1.88	0.41
1:C:43:LEU:HD22	1:D:190:LEU:HD22	2.03	0.41
1:C:83:PHE:HE1	1:D:13:LEU:CB	2.33	0.41
1:C:167:GLU:OE2	1:C:233:ASP:HB2	2.20	0.41
1:D:106:GLU:HB2	1:D:464:LEU:HD11	2.02	0.41
1:D:117:ILE:HG13	1:D:150:ASP:HA	2.02	0.41
1:D:314:GLN:NE2	1:D:315:ARG:NH1	2.68	0.41
1:E:74:ARG:CB	1:E:446:PHE:HE1	2.24	0.41
1:E:314:GLN:HG3	1:E:315:ARG:H	1.85	0.41
1:E:344:LEU:HB2	1:F:213:LEU:O	2.21	0.41
1:E:477:LYS:O	1:E:479:LYS:N	2.48	0.41
1:F:117:ILE:CG1	1:F:118:SER:N	2.83	0.41
1:A:246:LEU:O	1:A:317:GLN:NE2	2.53	0.41
1:A:345:CYS:HB3	1:A:362:GLU:CD	2.41	0.41
1:A:408:PRO:O	1:A:411:GLY:N	2.54	0.41
1:B:280:SER:N	1:B:283:THR:OG1	2.38	0.41
1:D:469:LEU:HA	1:D:474:LEU:CG	2.34	0.41
1:E:13:LEU:HB3	1:E:14:PRO:HD2	2.03	0.41
1:E:54:LYS:HD2	1:E:57:ASN:HB2	2.01	0.41
1:F:13:LEU:HA	1:F:13:LEU:HD23	1.86	0.41
1:B:52:ILE:O	1:B:61:LEU:N	2.54	0.41
1:B:97:ARG:HE	1:B:402:TRP:HB3	1.85	0.41
1:E:71:ARG:HG3	1:E:370:TYR:CZ	2.54	0.41
1:A:97:ARG:HG3	1:A:98:LEU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:ARG:HG2	1:A:402:TRP:CD2	2.56	0.41
1:B:480:PHE:CE2	1:C:22:VAL:HG11	2.56	0.41
1:C:74:ARG:CB	1:C:446:PHE:HE1	2.24	0.41
1:C:348:ILE:HG22	1:C:359:ASN:O	2.21	0.41
1:D:259:HIS:C	1:D:260:LEU:HD12	2.41	0.41
1:D:312:TRP:CD1	1:D:471:GLN:OE1	2.74	0.41
1:E:405:GLY:O	1:E:408:PRO:HD2	2.21	0.41
1:F:383:LEU:HD23	1:F:387:VAL:HG11	2.02	0.41
1:A:404:PHE:C	1:A:406:LEU:N	2.74	0.41
1:A:433:PRO:HB2	1:A:434:PRO:HD2	2.02	0.41
1:B:73:PHE:CD1	1:B:447:TRP:HD1	2.39	0.41
1:B:164:PRO:HG2	1:B:195:ILE:HB	2.01	0.41
1:B:235:ILE:O	1:B:239:SER:N	2.52	0.41
1:B:247:PHE:HB2	1:B:316:ALA:CB	2.51	0.41
1:C:30:ARG:HB3	1:C:377:GLN:OE1	2.21	0.41
1:C:169:TRP:O	1:C:208:MET:HA	2.20	0.41
1:C:407:GLN:CB	1:C:410:PRO:CD	2.95	0.41
1:D:57:ASN:ND2	1:D:59:LYS:HB3	2.35	0.41
1:E:42:LEU:HD23	1:E:42:LEU:HA	1.89	0.41
1:E:254:GLN:NE2	1:E:298:SER:HB3	2.35	0.41
1:E:366:HIS:NE2	1:E:368:GLU:OE2	2.53	0.41
1:E:404:PHE:HB2	1:E:406:LEU:HD12	2.03	0.41
1:A:153:GLN:NE2	1:A:300:VAL:HG12	2.35	0.41
1:A:205:PHE:CE1	1:A:295:PRO:HG3	2.56	0.41
1:A:262:ASN:HD22	1:A:291:TYR:HA	1.85	0.41
1:B:109:ARG:HB3	1:B:338:ARG:CZ	2.51	0.41
1:B:111:GLN:HG2	1:B:369:GLU:HB3	2.02	0.41
1:B:112:PRO:HB3	1:C:231:TYR:CD1	2.56	0.41
1:B:112:PRO:HB2	1:C:202:ASP:OD2	2.20	0.41
1:B:117:ILE:HG21	1:C:293:PRO:HD3	2.03	0.41
1:B:406:LEU:HA	1:B:406:LEU:HD23	1.87	0.41
1:C:276:TYR:HE1	1:C:278:LYS:HD2	1.85	0.41
1:C:406:LEU:CD2	1:C:407:GLN:HG3	2.51	0.41
1:C:406:LEU:HD13	1:C:407:GLN:NE2	2.36	0.41
1:D:71:ARG:HG3	1:D:370:TYR:CZ	2.56	0.41
1:D:240:GLU:HG2	1:D:242:TYR:H	1.86	0.41
1:D:408:PRO:N	1:D:409:PRO:HD2	2.36	0.41
1:F:118:SER:O	1:F:148:SER:HB2	2.21	0.41
1:F:399:LEU:HA	1:F:399:LEU:HD23	1.87	0.41
1:A:98:LEU:HD23	1:A:380:LYS:HA	2.03	0.41
1:B:70:TYR:CE1	1:B:201:VAL:HG22	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:201:VAL:HG12	1:B:202:ASP:O	2.21	0.41
1:B:306:ILE:HD12	1:B:306:ILE:HG23	1.92	0.41
1:C:124:ASN:ND2	1:C:264:ALA:H	2.19	0.41
1:D:116:GLY:O	1:D:117:ILE:HB	2.20	0.41
1:D:301:THR:HG23	1:D:303:ASP:N	2.36	0.41
1:E:60:ILE:O	1:E:60:ILE:HG13	2.21	0.41
1:F:123:LEU:H	1:F:145:GLU:H	1.69	0.41
1:F:156:LEU:C	1:F:156:LEU:HD12	2.41	0.41
1:A:41:ARG:HA	1:A:370:TYR:O	2.21	0.40
1:A:167:GLU:CD	1:A:233:ASP:HB2	2.41	0.40
1:B:74:ARG:O	1:B:75:ILE:HD13	2.20	0.40
1:B:418:TYR:HB3	1:B:419:ARG:CG	2.51	0.40
1:D:34:TYR:CE2	1:D:468:PHE:CZ	3.09	0.40
1:F:158:LEU:HD22	1:F:246:LEU:HD22	2.02	0.40
1:F:256:PHE:HE2	1:F:298:SER:HB2	1.86	0.40
1:A:12:TYR:O	1:A:386:ASP:HA	2.21	0.40
1:A:469:LEU:HD22	1:A:474:LEU:CD2	2.50	0.40
1:D:91:TYR:CE2	1:D:98:LEU:HD11	2.55	0.40
1:D:258:ARG:HE	1:D:296:SER:HB2	1.87	0.40
1:D:459:LEU:HD23	1:D:459:LEU:HA	1.77	0.40
1:E:123:LEU:N	1:E:145:GLU:O	2.54	0.40
1:F:71:ARG:HA	1:F:197:ASP:OD1	2.21	0.40
1:F:246:LEU:HD12	1:F:246:LEU:O	2.21	0.40
1:F:259:HIS:C	1:F:260:LEU:HD12	2.42	0.40
1:A:161:CYS:SG	1:A:244:ASP:HB3	2.61	0.40
1:B:312:TRP:CH2	1:B:468:PHE:CD1	3.00	0.40
1:C:180:VAL:HG13	1:C:184:ASP:HB2	2.04	0.40
1:C:361:LYS:HD2	1:D:183:GLY:O	2.21	0.40
1:C:474:LEU:CD2	1:C:480:PHE:O	2.69	0.40
1:D:120:HIS:ND1	1:D:122:LEU:N	2.64	0.40
1:E:57:ASN:OD1	1:E:59:LYS:N	2.49	0.40
1:E:160:GLY:O	1:E:330:PHE:HB2	2.22	0.40
1:A:384:THR:O	1:A:388:MET:N	2.40	0.40
1:A:388:MET:HA	1:A:391:ILE:CD1	2.50	0.40
1:A:441:LEU:O	1:A:444:TYR:N	2.54	0.40
1:B:71:ARG:HG3	1:B:370:TYR:CZ	2.57	0.40
1:B:258:ARG:HG2	1:B:259:HIS:CE1	2.57	0.40
1:B:460:ASP:CG	1:B:477:LYS:HE2	2.42	0.40
1:C:144:ARG:NH1	1:C:216:ASN:OD1	2.55	0.40
1:C:171:LYS:HB2	1:C:213:LEU:CD1	2.51	0.40
1:D:45:VAL:HA	1:D:366:HIS:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:46:GLY:CA	1:D:65:VAL:HB	2.51	0.40
1:D:194:VAL:HG21	1:D:444:TYR:CE2	2.56	0.40
1:D:210:PHE:CE2	1:D:224:ILE:HD12	2.53	0.40
1:D:407:GLN:HA	1:D:408:PRO:HD2	1.99	0.40
1:E:51:PRO:HB3	1:E:64:LYS:HB2	2.04	0.40
1:E:106:GLU:HB2	1:E:464:LEU:HD11	2.04	0.40
1:E:259:HIS:C	1:E:260:LEU:HD12	2.42	0.40
1:E:355:TYR:CE1	1:F:216:ASN:OD1	2.74	0.40
1:E:361:LYS:HD2	1:F:183:GLY:O	2.22	0.40
1:F:13:LEU:CB	1:F:14:PRO:CD	2.99	0.40
1:A:341:ASN:OD1	1:A:366:HIS:HB2	2.21	0.40
1:A:345:CYS:HB3	1:A:362:GLU:OE2	2.22	0.40
1:B:312:TRP:HH2	1:B:468:PHE:HD1	1.65	0.40
1:B:373:GLN:OE1	1:B:464:LEU:HB2	2.22	0.40
1:C:259:HIS:C	1:C:260:LEU:HD12	2.40	0.40
1:D:47:HIS:HE1	1:D:49:TYR:CD2	2.40	0.40
1:D:54:LYS:HD2	1:D:57:ASN:HB2	2.04	0.40
1:D:246:LEU:O	1:D:317:GLN:NE2	2.55	0.40
1:E:169:TRP:O	1:E:208:MET:HA	2.21	0.40
1:F:174:PRO:HA	1:F:187:PRO:HG3	2.04	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	472/483 (98%)	434 (92%)	33 (7%)	5 (1%)	14	52
1	B	461/483 (95%)	428 (93%)	26 (6%)	7 (2%)	10	46
1	C	470/483 (97%)	428 (91%)	37 (8%)	5 (1%)	14	52
1	D	469/483 (97%)	426 (91%)	36 (8%)	7 (2%)	10	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	480/483 (99%)	439 (92%)	39 (8%)	2 (0%)	34	72
1	F	471/483 (98%)	438 (93%)	29 (6%)	4 (1%)	19	60
All	All	2823/2898 (97%)	2593 (92%)	200 (7%)	30 (1%)	18	52

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	384	THR
1	C	476	ALA
1	C	477	LYS
1	D	474	LEU
1	E	474	LEU
1	A	15	PRO
1	C	88	THR
1	F	117	ILE
1	B	21	VAL
1	D	426	ILE
1	D	476	ALA
1	F	410	PRO
1	B	383	LEU
1	A	17	PRO
1	B	382	THR
1	B	394	MET
1	D	17	PRO
1	D	20	LYS
1	A	21	VAL
1	D	433	PRO
1	B	235	ILE
1	E	235	ILE
1	F	235	ILE
1	B	410	PRO
1	C	235	ILE
1	F	13	LEU
1	A	426	ILE
1	C	387	VAL
1	D	117	ILE
1	A	14	PRO

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	412/420 (98%)	411 (100%)	1 (0%)	93	96
1	B	402/420 (96%)	401 (100%)	1 (0%)	93	96
1	C	410/420 (98%)	409 (100%)	1 (0%)	93	96
1	D	410/420 (98%)	408 (100%)	2 (0%)	88	93
1	E	419/420 (100%)	419 (100%)	0	100	100
1	F	411/420 (98%)	410 (100%)	1 (0%)	93	96
All	All	2464/2520 (98%)	2458 (100%)	6 (0%)	93	96

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	VAL
1	B	474	LEU
1	C	474	LEU
1	D	474	LEU
1	D	475	LYS
1	F	474	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	319	HIS
1	B	366	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	409:PRO	C	410:PRO	N	1.18

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6619. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal surface views

This section was not generated.

6.5 Mask visualisation

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 ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.