



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 04:37 PM UTC

PDB ID : 7RYJ / pdb_00007ryj
EMDB ID : EMD-24741
Title : Cryo EM analysis reveals inherent flexibility of authentic murine papillomavirus capsids
Authors : Hartmann, S.R.; Hafenstein, S.
Deposited on : 2021-08-25
Resolution : 3.30 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:

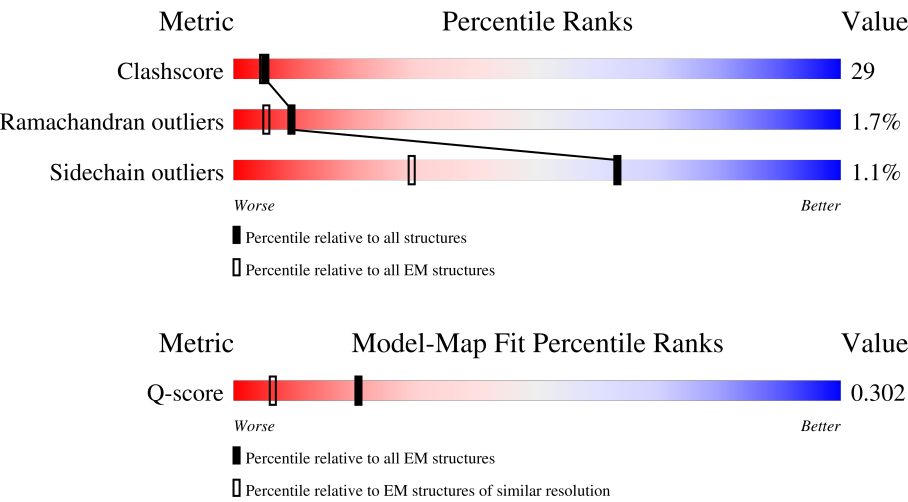
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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

Mol	Chain	Length	Quality of chain
1	A	509	
1	B	509	
1	C	509	
1	D	509	

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Mol	Chain	Length	Quality of chain
1	E	509	38% 75% 19% • 6%
1	F	509	39% 69% 23% • 5%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 22953 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.

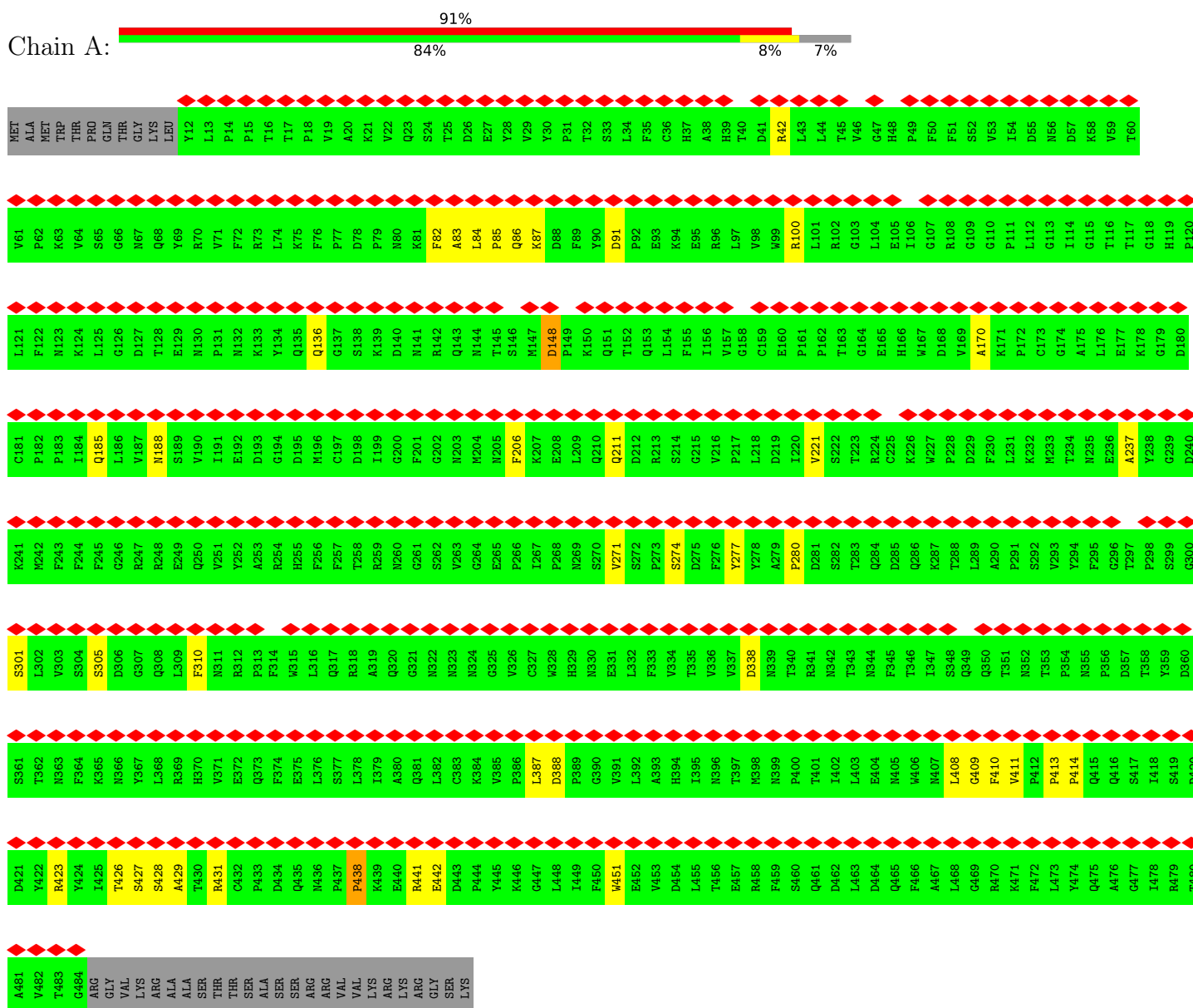
- Molecule 1 is a protein called Major capsid protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	473	Total	C	N	O	S	0	0
			3784	2399	651	719	15		
1	B	466	Total	C	N	O	S	0	0
			3732	2364	644	709	15		
1	C	482	Total	C	N	O	S	0	0
			3859	2449	663	730	17		
1	D	482	Total	C	N	O	S	0	0
			3859	2449	663	730	17		
1	E	481	Total	C	N	O	S	0	0
			3853	2445	662	730	16		
1	F	483	Total	C	N	O	S	0	0
			3866	2453	664	732	17		

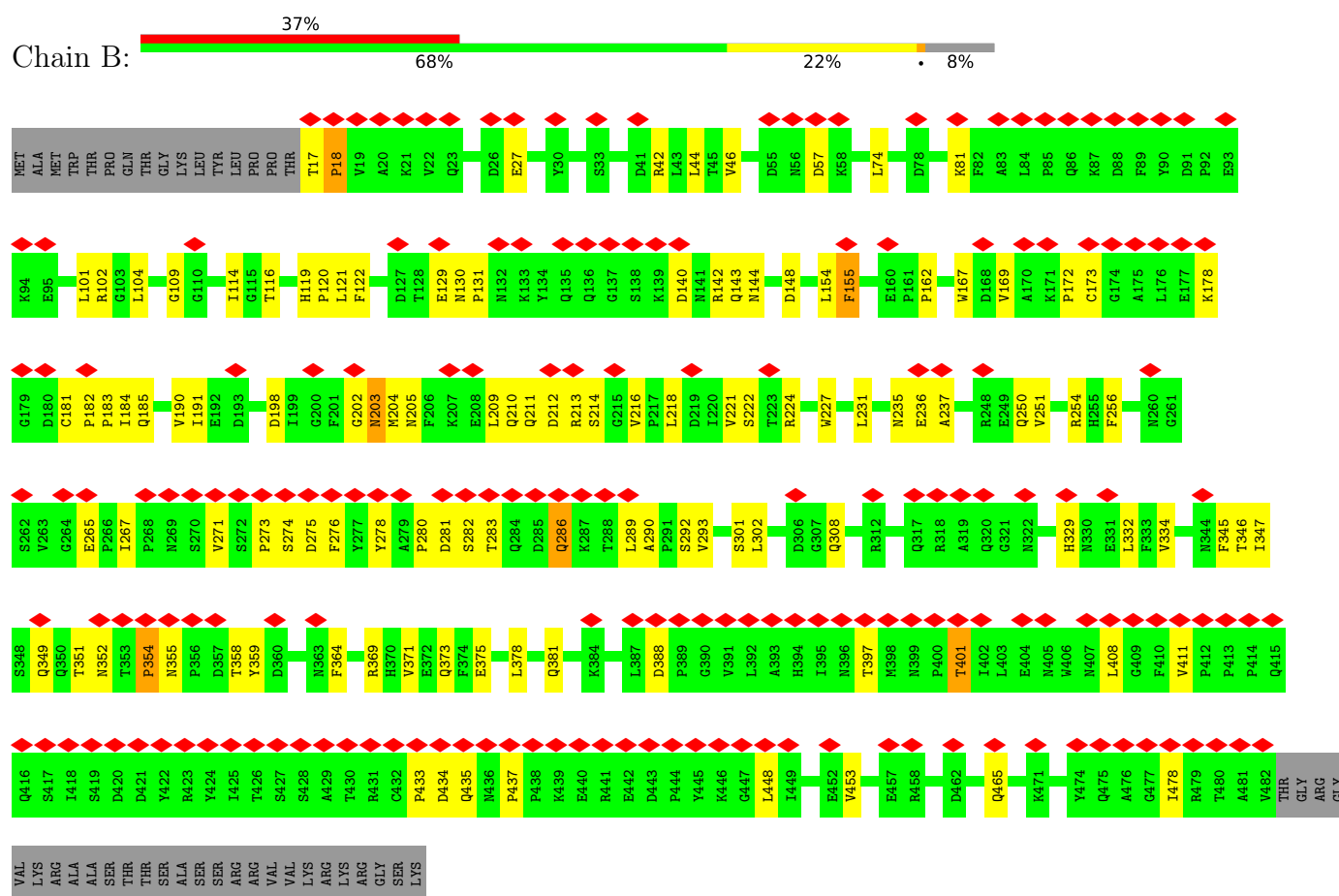
3 Residue-property plots

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

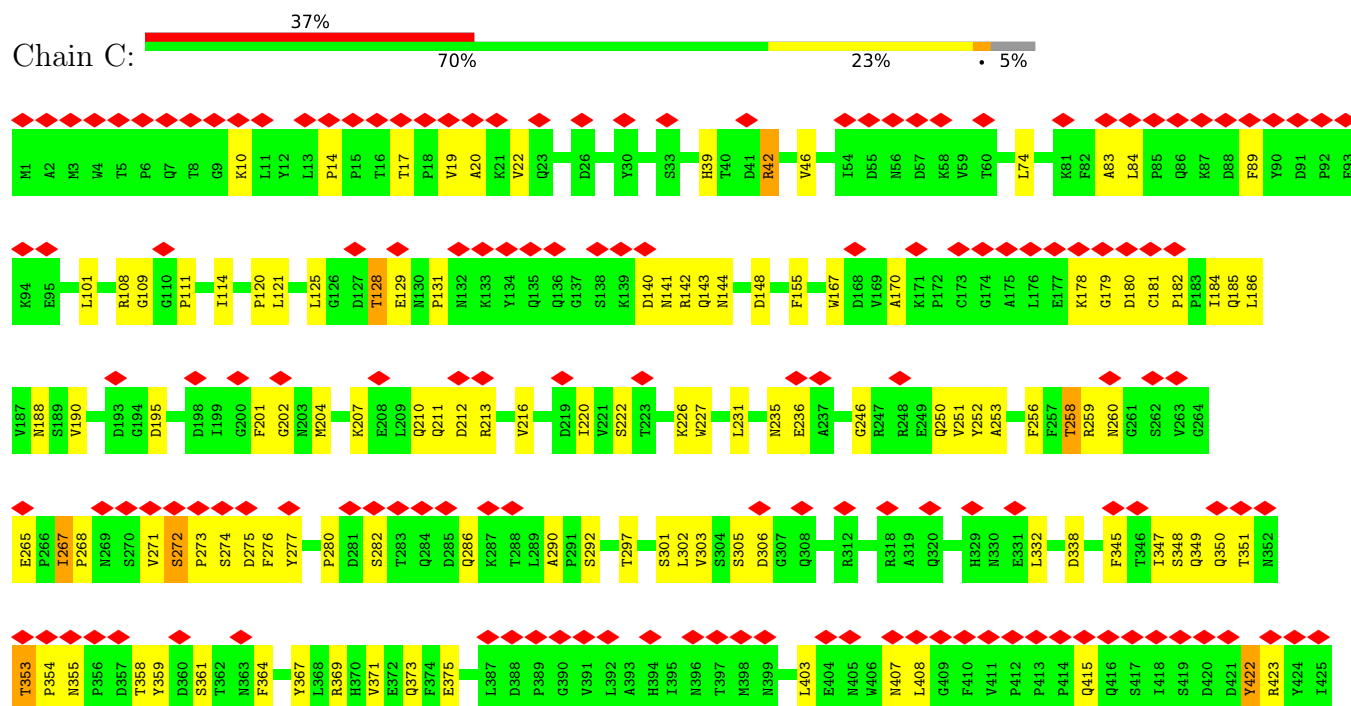
- Molecule 1: Major capsid protein L1

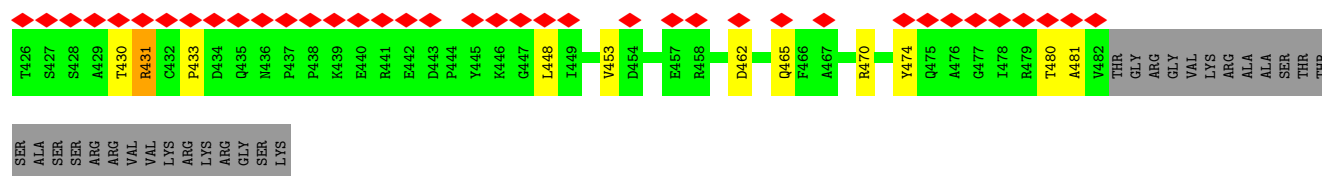


- Molecule 1: Major capsid protein L1

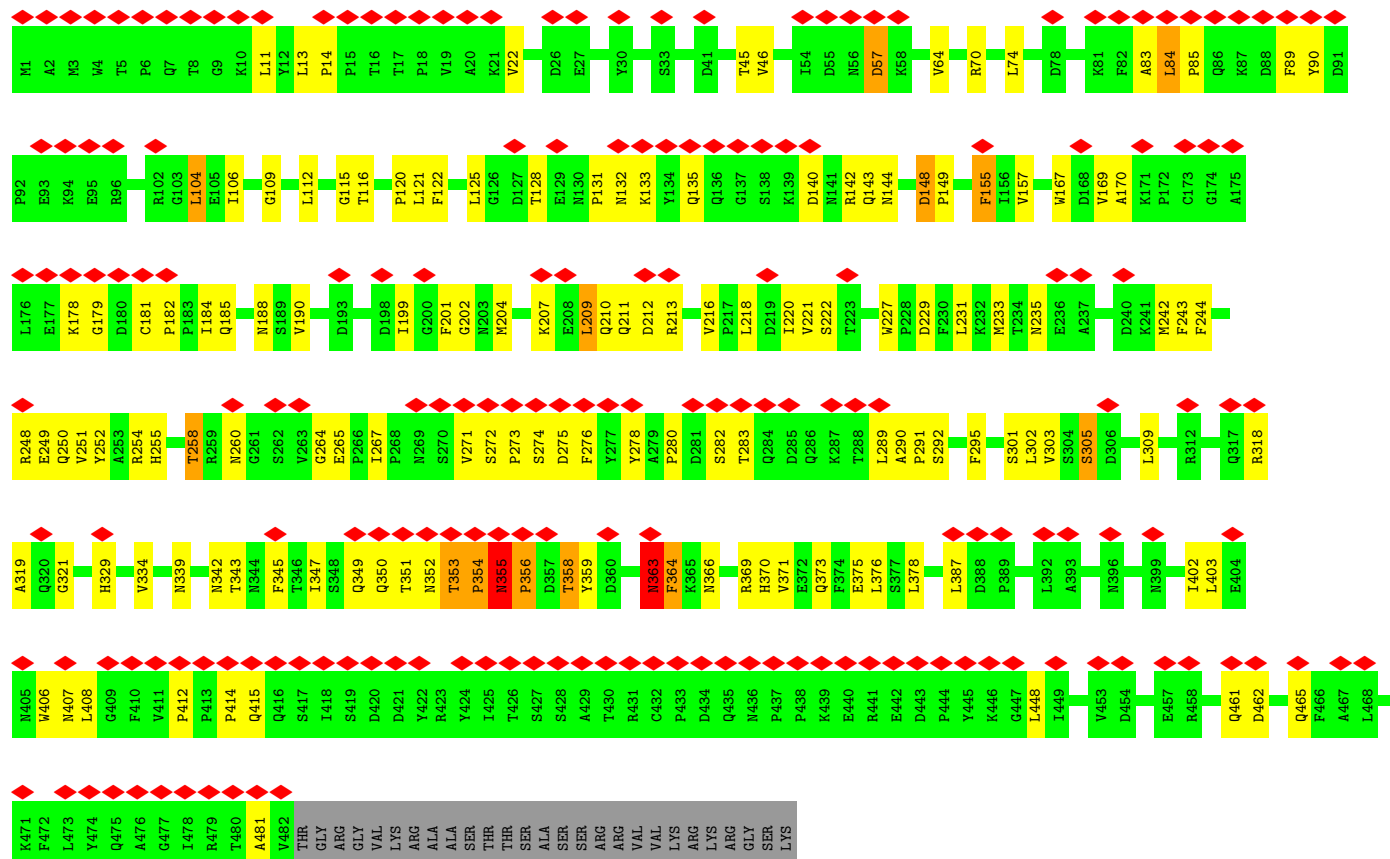


• Molecule 1: Major capsid protein L1

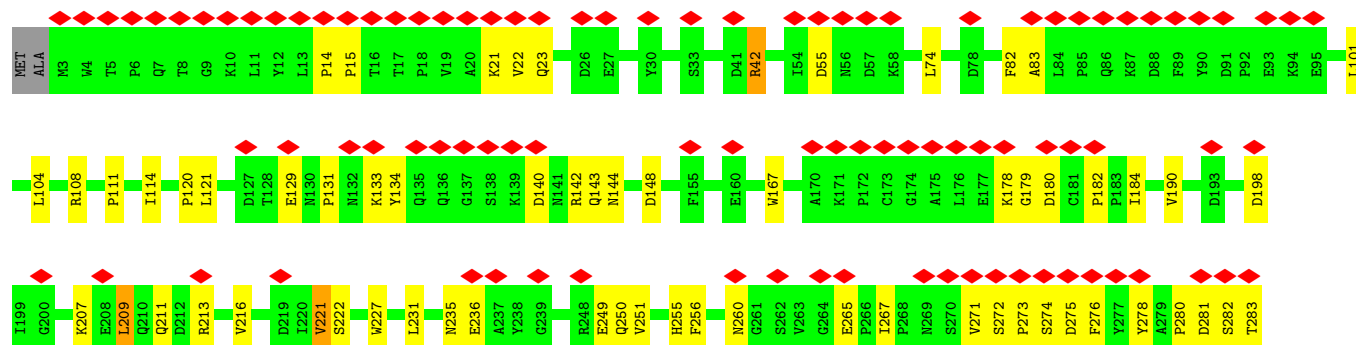
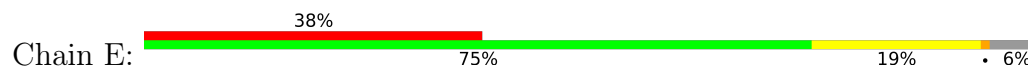


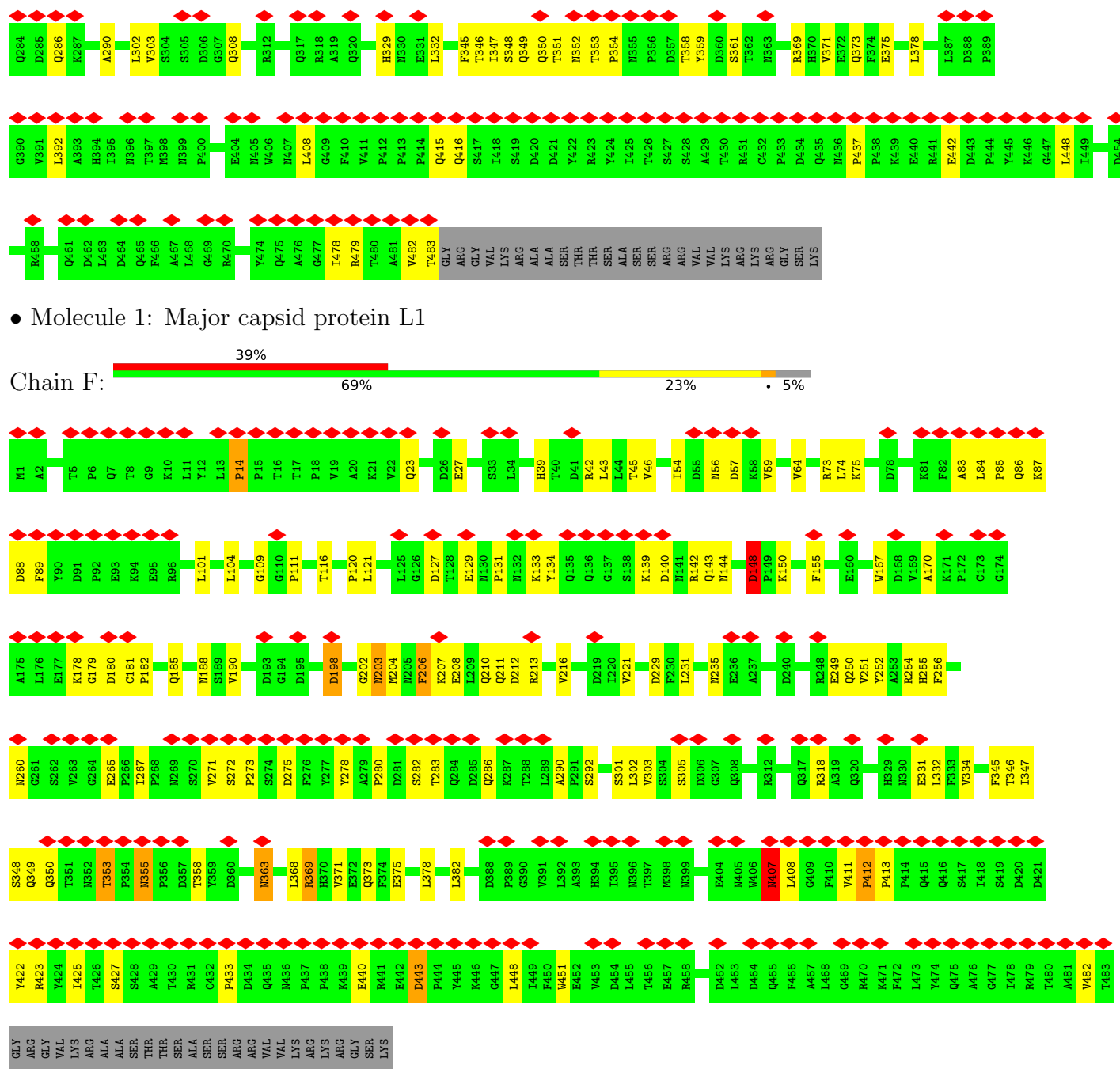


• Molecule 1: Major capsid protein L1



• Molecule 1: Major capsid protein L1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	10181	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	19.263	Depositor
Minimum map value	-12.272	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4	Depositor
Map size ($\text{\AA}$)	660.0, 660.0, 660.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	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	0.89	0/3893	1.40	20/5302 (0.4%)
1	B	0.83	0/3838	1.28	8/5224 (0.2%)
1	C	0.96	2/3971 (0.1%)	1.40	17/5408 (0.3%)
1	D	0.99	1/3971 (0.0%)	1.31	19/5408 (0.4%)
1	E	0.83	0/3965	1.26	5/5401 (0.1%)
1	F	0.88	1/3978 (0.0%)	1.39	12/5418 (0.2%)
All	All	0.90	4/23616 (0.0%)	1.34	81/32161 (0.3%)

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	3
1	B	1	3
1	C	0	2
1	D	1	3
1	E	1	1
1	F	1	2
All	All	4	14

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	353	THR	C-N	-10.43	1.21	1.33
1	C	267	ILE	CA-C	6.64	1.59	1.52
1	C	268	PRO	C-O	-5.39	1.17	1.23
1	F	363	ASN	N-CA	-5.16	1.39	1.46

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	353	THR	O-C-N	-11.07	111.31	121.05
1	D	363	ASN	N-CA-CB	-10.87	94.09	110.07
1	F	203	ASN	CA-CB-CG	-9.53	103.07	112.60
1	F	363	ASN	CA-CB-CG	9.44	122.04	112.60
1	D	363	ASN	OD1-CG-ND2	8.54	131.14	122.60
1	C	267	ILE	N-CA-CB	-8.42	99.42	111.21
1	D	57	ASP	CA-CB-CG	8.29	120.89	112.60
1	D	354	PRO	CA-C-O	-8.11	112.55	121.23
1	D	353	THR	CB-CA-C	-7.95	100.93	111.11
1	B	203	ASN	CA-CB-CG	-7.54	105.06	112.60
1	A	274	SER	CA-C-N	7.23	130.69	120.28
1	A	274	SER	C-N-CA	7.23	130.69	120.28
1	C	408	LEU	N-CA-C	7.20	118.77	111.07
1	A	338	ASP	CA-CB-CG	7.15	119.75	112.60
1	C	188	ASN	CA-CB-CG	-6.77	105.83	112.60
1	D	363	ASN	CB-CG-OD1	-6.43	107.94	120.80
1	A	413	PRO	CA-C-O	-6.32	116.35	120.90
1	A	280	PRO	CA-C-N	6.31	129.37	120.28
1	A	280	PRO	C-N-CA	6.31	129.37	120.28
1	D	353	THR	CA-CB-CG2	-6.28	99.82	110.50
1	C	236	GLU	CB-CG-CD	-6.24	102.00	112.60
1	F	148	ASP	CA-CB-CG	6.21	118.81	112.60
1	E	329	HIS	CA-CB-CG	6.19	119.99	113.80
1	C	481	ALA	CA-C-N	6.14	132.75	121.70
1	C	481	ALA	C-N-CA	6.14	132.75	121.70
1	B	286	GLN	CA-C-N	6.11	128.46	120.28
1	B	286	GLN	C-N-CA	6.11	128.46	120.28
1	D	353	THR	OG1-CB-CG2	6.11	121.52	109.30
1	C	354	PRO	CA-C-N	6.08	128.41	120.26
1	C	354	PRO	C-N-CA	6.08	128.41	120.26
1	C	272	SER	CA-C-N	6.04	127.15	120.45
1	C	272	SER	C-N-CA	6.04	127.15	120.45
1	F	305	SER	CA-C-N	6.00	128.32	120.28
1	F	305	SER	C-N-CA	6.00	128.32	120.28
1	E	308	GLN	N-CA-C	5.91	118.80	110.23
1	D	188	ASN	CA-CB-CG	-5.90	106.70	112.60
1	D	355	ASN	CA-CB-CG	5.87	118.47	112.60
1	E	437	PRO	CA-C-O	-5.85	112.08	120.56
1	C	148	ASP	CB-CA-C	5.84	117.54	108.61
1	A	388	ASP	CA-CB-CG	5.81	118.41	112.60
1	C	267	ILE	CA-CB-CG2	-5.79	100.65	110.50
1	D	258	THR	CB-CA-C	-5.72	98.97	110.30
1	F	407	ASN	CA-CB-CG	5.71	118.31	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148	ASP	CA-CB-CG	5.63	118.23	112.60
1	A	305	SER	CA-C-N	5.62	127.81	120.28
1	A	305	SER	C-N-CA	5.62	127.81	120.28
1	C	258	THR	CB-CA-C	-5.58	99.75	110.24
1	B	437	PRO	N-CA-C	5.54	117.46	110.70
1	D	364	PHE	N-CA-C	-5.53	100.22	109.24
1	F	148	ASP	CB-CA-C	5.53	116.66	108.87
1	A	310	PHE	CA-CB-CG	-5.44	108.36	113.80
1	A	91	ASP	CA-CB-CG	5.38	117.98	112.60
1	B	388	ASP	CA-C-N	5.37	124.82	119.24
1	B	388	ASP	C-N-CA	5.37	124.82	119.24
1	D	148	ASP	CA-CB-CG	5.36	117.96	112.60
1	A	206	PHE	CA-CB-CG	-5.35	108.45	113.80
1	B	237	ALA	N-CA-C	5.34	117.11	111.28
1	C	39	HIS	CB-CG-ND1	-5.34	114.69	122.70
1	D	329	HIS	ND1-CG-CD2	5.32	111.42	106.10
1	A	91	ASP	O-C-N	-5.31	116.93	121.23
1	A	237	ALA	N-CA-C	5.26	117.02	111.28
1	E	416	GLN	N-CA-C	5.24	117.02	108.63
1	C	128	THR	CA-CB-OG1	5.24	117.45	109.60
1	F	206	PHE	CA-CB-CG	-5.24	108.56	113.80
1	E	221	VAL	N-CA-C	5.21	115.93	110.62
1	F	353	THR	OG1-CB-CG2	-5.20	98.89	109.30
1	C	17	THR	O-C-N	-5.18	116.78	122.06
1	D	355	ASN	CA-C-N	5.16	126.30	119.84
1	D	355	ASN	C-N-CA	5.16	126.30	119.84
1	A	188	ASN	CA-CB-CG	-5.14	107.46	112.60
1	B	308	GLN	N-CA-C	5.12	117.12	109.59
1	F	355	ASN	CA-CB-CG	5.08	117.69	112.60
1	A	211	GLN	CA-C-N	5.06	127.31	120.38
1	A	211	GLN	C-N-CA	5.06	127.31	120.38
1	A	91	ASP	CB-CA-C	5.04	115.88	110.08
1	C	431	ARG	N-CA-C	5.04	121.53	110.80
1	F	39	HIS	CB-CG-ND1	-5.03	115.16	122.70
1	F	412	PRO	CB-CA-C	5.03	117.05	110.92
1	A	136	GLN	N-CA-C	5.01	114.91	108.34
1	D	84	LEU	CA-C-N	5.01	124.79	119.28
1	D	84	LEU	C-N-CA	5.01	124.79	119.28

All (4) chirality outliers are listed below:

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Mol	Chain	Res	Type	Atom
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Mol	Chain	Res	Type	Atom
1	B	57	ASP	CA
1	D	57	ASP	CA
1	E	56	ASN	CA
1	F	57	ASP	CA

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	100	ARG	Sidechain
1	A	277	TYR	Sidechain
1	A	441	ARG	Sidechain
1	B	155	PHE	Sidechain
1	B	411	VAL	Peptide
1	B	434	ASP	Peptide
1	C	422	TYR	Peptide
1	C	430	THR	Peptide
1	D	155	PHE	Sidechain
1	D	352	ASN	Peptide
1	D	363	ASN	Peptide
1	E	108	ARG	Sidechain
1	F	411	VAL	Peptide
1	F	412	PRO	Peptide

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	3784	0	3626	114	0
1	B	3732	0	3563	557	0
1	C	3859	0	3692	465	0
1	D	3859	0	3696	454	0
1	E	3853	0	3686	402	0
1	F	3866	0	3703	457	0
All	All	22953	0	21966	1283	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 29.

All (1283) 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:C:46:VAL:HG11	1:D:184:ILE:CD1	1.26	1.65
1:B:202:GLY:HA3	1:F:345:PHE:CE1	1.14	1.65
1:B:351:THR:CG2	1:C:179:GLY:HA3	1.19	1.63
1:B:121:LEU:HG	1:C:276:PHE:CD1	1.17	1.62
1:B:119:HIS:CE1	1:C:276:PHE:H	1.05	1.62
1:B:271:VAL:CG1	1:F:213:ARG:HB3	1.23	1.62
1:E:207:LYS:CG	1:F:273:PRO:HG3	1.18	1.62
1:E:207:LYS:HE3	1:F:273:PRO:CB	1.21	1.60
1:C:46:VAL:CG1	1:D:184:ILE:HD11	1.23	1.60
1:B:121:LEU:CG	1:C:276:PHE:HD1	1.11	1.60
1:B:345:PHE:CE1	1:C:202:GLY:HA3	1.10	1.58
1:B:271:VAL:HG11	1:F:213:ARG:CB	1.18	1.58
1:D:351:THR:CB	1:E:179:GLY:HA3	1.24	1.57
1:B:351:THR:HG22	1:C:179:GLY:CA	1.27	1.56
1:B:283:THR:CG2	1:F:140:ASP:HB3	1.27	1.56
1:B:46:VAL:CG1	1:C:184:ILE:HD11	1.29	1.55
1:B:281:ASP:CB	1:E:358:THR:CG2	1.80	1.55
1:D:213:ARG:CB	1:E:271:VAL:HG11	1.09	1.55
1:C:213:ARG:HB3	1:D:271:VAL:CG1	1.24	1.55
1:B:184:ILE:HD11	1:F:46:VAL:CG1	1.33	1.55
1:C:345:PHE:CE1	1:D:202:GLY:CA	1.83	1.55
1:A:411:VAL:HG13	1:B:18:PRO:CG	1.33	1.54
1:E:207:LYS:CG	1:F:273:PRO:CG	1.74	1.54
1:E:345:PHE:CE1	1:F:202:GLY:HA3	1.01	1.54
1:B:283:THR:CG2	1:F:140:ASP:CB	1.86	1.53
1:C:213:ARG:CG	1:D:274:SER:CB	1.83	1.53
1:E:345:PHE:CE1	1:F:202:GLY:CA	1.88	1.52
1:E:347:ILE:HD11	1:F:181:CYS:SG	1.48	1.52
1:D:46:VAL:CG1	1:E:184:ILE:HD11	1.06	1.51
1:B:283:THR:HG21	1:F:140:ASP:CB	1.37	1.50
1:D:46:VAL:HG11	1:E:184:ILE:CD1	1.41	1.50
1:B:218:LEU:CD2	1:C:273:PRO:HA	1.40	1.50
1:E:350:GLN:CD	1:F:211:GLN:HG3	1.30	1.50
1:A:411:VAL:CG1	1:B:18:PRO:HG2	1.37	1.49
1:B:46:VAL:HG11	1:C:184:ILE:CD1	1.44	1.48
1:B:218:LEU:CD2	1:C:273:PRO:C	1.87	1.48
1:C:350:GLN:NE2	1:D:211:GLN:HB3	1.28	1.47
1:C:213:ARG:CB	1:D:271:VAL:HG11	1.45	1.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:213:ARG:HB3	1:E:271:VAL:CG1	1.00	1.45
1:A:423:ARG:NH2	1:F:43:LEU:HB3	1.15	1.45
1:A:423:ARG:NH2	1:F:43:LEU:CB	1.78	1.44
1:E:207:LYS:CE	1:F:273:PRO:HB3	0.97	1.44
1:C:345:PHE:CE1	1:D:202:GLY:HA3	0.92	1.43
1:B:276:PHE:CE2	1:F:211:GLN:OE1	1.66	1.43
1:E:207:LYS:CD	1:F:273:PRO:HB3	1.49	1.43
1:E:350:GLN:OE1	1:F:211:GLN:CG	1.66	1.43
1:D:46:VAL:CG1	1:E:184:ILE:CD1	1.92	1.42
1:D:207:LYS:CG	1:E:275:ASP:OD2	1.66	1.41
1:A:411:VAL:CG1	1:B:18:PRO:CG	1.94	1.41
1:B:345:PHE:CE1	1:C:202:GLY:CA	2.02	1.41
1:B:345:PHE:CZ	1:C:202:GLY:HA3	1.51	1.41
1:B:203:ASN:ND2	1:F:111:PRO:HG3	1.32	1.40
1:B:109:GLY:O	1:C:227:TRP:CZ3	1.72	1.40
1:B:119:HIS:CD2	1:C:274:SER:CB	2.00	1.40
1:B:202:GLY:CA	1:F:345:PHE:CE1	2.02	1.39
1:B:119:HIS:CD2	1:C:274:SER:HB3	1.51	1.39
1:B:222:SER:CB	1:C:271:VAL:CG2	1.98	1.39
1:D:221:VAL:CG2	1:E:273:PRO:CG	2.01	1.38
1:B:184:ILE:CD1	1:F:46:VAL:CG1	1.99	1.38
1:D:351:THR:HG23	1:E:178:LYS:C	0.96	1.38
1:A:423:ARG:HH21	1:F:43:LEU:CD2	1.36	1.37
1:D:221:VAL:CG2	1:E:273:PRO:HG2	1.29	1.37
1:B:218:LEU:CD2	1:C:273:PRO:CA	2.00	1.37
1:B:281:ASP:HB2	1:E:358:THR:CG2	0.90	1.37
1:B:46:VAL:CG1	1:C:184:ILE:CD1	1.99	1.37
1:E:371:VAL:HG11	1:F:167:TRP:NE1	1.37	1.36
1:B:222:SER:HB3	1:C:271:VAL:CG2	1.53	1.36
1:E:207:LYS:HG3	1:F:273:PRO:CG	0.88	1.36
1:C:109:GLY:O	1:D:227:TRP:CZ3	1.79	1.35
1:C:213:ARG:HG3	1:D:274:SER:CB	1.48	1.35
1:C:46:VAL:CG1	1:D:184:ILE:CD1	1.87	1.34
1:C:213:ARG:CD	1:D:274:SER:OG	1.74	1.34
1:C:213:ARG:HG2	1:D:274:SER:CB	1.49	1.34
1:D:211:GLN:OE1	1:E:276:PHE:CE2	1.81	1.33
1:B:116:THR:HG21	1:C:256:PHE:CD1	1.63	1.33
1:B:142:ARG:NH2	1:C:280:PRO:HG3	1.43	1.33
1:D:109:GLY:O	1:E:227:TRP:CZ3	1.81	1.33
1:D:221:VAL:HG22	1:E:273:PRO:CG	1.57	1.33
1:D:351:THR:CB	1:E:179:GLY:CA	1.87	1.33

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:350:GLN:NE2	1:F:211:GLN:HG3	1.37	1.32
1:E:350:GLN:OE1	1:F:211:GLN:CB	1.75	1.32
1:B:358:THR:CG2	1:D:282:SER:HB3	1.57	1.32
1:B:184:ILE:CD1	1:F:46:VAL:HG11	1.55	1.31
1:E:479:ARG:NH2	1:F:318:ARG:HH22	1.29	1.31
1:E:111:PRO:HG3	1:F:203:ASN:OD1	1.24	1.31
1:B:211:GLN:HG3	1:F:350:GLN:CD	1.56	1.30
1:B:209:LEU:O	1:F:347:ILE:HG23	1.31	1.30
1:B:116:THR:HG21	1:C:256:PHE:CE1	1.64	1.29
1:B:281:ASP:CB	1:E:358:THR:HG22	1.50	1.29
1:D:140:ASP:HB3	1:E:283:THR:OG1	1.26	1.29
1:D:351:THR:OG1	1:E:179:GLY:N	1.59	1.29
1:E:371:VAL:HG11	1:F:167:TRP:CE2	1.33	1.28
1:E:347:ILE:CD1	1:F:181:CYS:SG	2.20	1.28
1:D:211:GLN:OE1	1:E:276:PHE:HE2	1.01	1.27
1:B:203:ASN:ND2	1:F:111:PRO:CG	1.96	1.27
1:B:358:THR:HG21	1:D:282:SER:CB	1.62	1.27
1:D:351:THR:O	1:E:178:LYS:HG2	1.30	1.27
1:B:218:LEU:HD23	1:C:273:PRO:C	1.46	1.27
1:D:213:ARG:CD	1:E:271:VAL:HB	1.63	1.27
1:E:350:GLN:HE22	1:F:211:GLN:CD	1.42	1.27
1:B:116:THR:CG2	1:C:256:PHE:CE1	2.18	1.26
1:C:345:PHE:HE1	1:D:202:GLY:CA	1.28	1.26
1:B:271:VAL:HB	1:F:213:ARG:CD	1.65	1.26
1:E:222:SER:HB2	1:F:273:PRO:CD	1.38	1.26
1:B:222:SER:CB	1:C:271:VAL:HG23	1.57	1.25
1:C:140:ASP:HB3	1:D:283:THR:CG2	1.66	1.25
1:B:271:VAL:CB	1:F:213:ARG:HD3	1.64	1.25
1:A:87:LYS:N	1:F:86:GLN:HG3	1.24	1.24
1:E:207:LYS:CB	1:F:273:PRO:HG3	1.65	1.24
1:E:222:SER:CB	1:F:273:PRO:CD	2.07	1.24
1:B:116:THR:CG2	1:C:256:PHE:HE1	1.49	1.24
1:C:282:SER:OG	1:F:358:THR:HG21	1.35	1.24
1:B:281:ASP:CB	1:E:358:THR:HG21	1.47	1.24
1:C:345:PHE:CZ	1:D:202:GLY:HA3	1.72	1.24
1:E:350:GLN:OE1	1:F:211:GLN:HG3	1.27	1.24
1:A:423:ARG:HH22	1:F:43:LEU:CB	1.43	1.23
1:E:345:PHE:CZ	1:F:202:GLY:HA3	1.72	1.23
1:B:273:PRO:O	1:F:206:PHE:O	1.53	1.23
1:C:350:GLN:CD	1:D:211:GLN:HB3	1.62	1.23
1:C:351:THR:HG23	1:D:178:LYS:O	1.37	1.23

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:345:PHE:CZ	1:F:202:GLY:CA	2.21	1.23
1:E:350:GLN:NE2	1:F:211:GLN:CG	2.02	1.22
1:E:371:VAL:CG1	1:F:167:TRP:CE2	2.22	1.22
1:B:140:ASP:OD2	1:C:280:PRO:HB3	1.33	1.22
1:B:283:THR:CB	1:F:140:ASP:HB3	1.70	1.22
1:C:282:SER:CB	1:F:358:THR:HG21	1.70	1.21
1:E:350:GLN:CD	1:F:211:GLN:CG	2.10	1.21
1:C:213:ARG:CB	1:D:274:SER:OG	1.88	1.21
1:C:46:VAL:CB	1:D:184:ILE:HD11	1.71	1.21
1:B:275:ASP:CG	1:F:207:LYS:CG	2.03	1.21
1:B:275:ASP:CG	1:F:207:LYS:HG2	1.61	1.21
1:E:207:LYS:CE	1:F:273:PRO:CB	1.91	1.21
1:B:202:GLY:HA3	1:F:345:PHE:CZ	1.75	1.20
1:B:276:PHE:CE1	1:E:354:PRO:HG3	1.76	1.20
1:D:221:VAL:HG22	1:E:273:PRO:CD	1.71	1.20
1:A:428:SER:HA	1:B:173:CYS:SG	1.81	1.20
1:D:207:LYS:CG	1:E:275:ASP:CG	2.05	1.20
1:B:119:HIS:HE1	1:C:276:PHE:N	1.13	1.20
1:A:411:VAL:HG21	1:B:397:THR:CG2	1.71	1.19
1:D:351:THR:OG1	1:E:179:GLY:C	1.83	1.19
1:C:350:GLN:HE21	1:D:211:GLN:CB	1.53	1.19
1:E:207:LYS:CD	1:F:273:PRO:CB	2.17	1.19
1:E:222:SER:CA	1:F:273:PRO:HD3	1.72	1.19
1:D:221:VAL:HG23	1:E:273:PRO:HG2	1.20	1.18
1:B:275:ASP:OD2	1:F:207:LYS:CG	1.90	1.18
1:B:283:THR:HG21	1:F:140:ASP:CA	1.74	1.17
1:B:211:GLN:HG3	1:F:350:GLN:OE1	1.02	1.17
1:C:350:GLN:HE21	1:D:211:GLN:CG	1.57	1.17
1:E:350:GLN:HE22	1:F:211:GLN:CG	1.55	1.17
1:B:211:GLN:CG	1:F:350:GLN:OE1	1.93	1.17
1:A:409:GLY:HA2	1:B:17:THR:N	1.57	1.17
1:B:221:VAL:HG11	1:C:274:SER:CA	1.74	1.16
1:D:213:ARG:HD3	1:E:271:VAL:CB	1.73	1.16
1:C:345:PHE:CZ	1:D:202:GLY:CA	2.29	1.16
1:B:275:ASP:OD2	1:F:207:LYS:HG2	1.00	1.16
1:B:358:THR:CG2	1:D:282:SER:CB	2.18	1.15
1:C:350:GLN:NE2	1:D:211:GLN:CB	2.06	1.15
1:E:222:SER:CB	1:F:273:PRO:HD3	1.71	1.15
1:B:203:ASN:HD21	1:F:111:PRO:CG	1.54	1.15
1:E:371:VAL:CG1	1:F:167:TRP:NE1	2.08	1.15
1:B:276:PHE:HE2	1:F:211:GLN:OE1	0.84	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:LEU:HD21	1:C:273:PRO:HA	1.22	1.14
1:B:222:SER:HB2	1:C:271:VAL:HG21	1.19	1.14
1:E:375:GLU:OE1	1:F:235:ASN:ND2	1.81	1.14
1:C:282:SER:OG	1:F:358:THR:CG2	1.96	1.14
1:A:423:ARG:HH21	1:F:43:LEU:CG	1.59	1.14
1:C:213:ARG:HD3	1:D:271:VAL:HB	1.21	1.14
1:A:411:VAL:HG21	1:B:397:THR:HG21	1.29	1.13
1:A:429:ALA:CA	1:B:172:PRO:HA	1.77	1.13
1:B:121:LEU:HD12	1:C:276:PHE:HA	1.20	1.13
1:B:122:PHE:HA	1:C:275:ASP:OD2	1.49	1.13
1:B:27:GLU:HG2	1:F:482:VAL:HG13	1.30	1.12
1:E:207:LYS:HG3	1:F:273:PRO:CB	1.77	1.12
1:E:350:GLN:OE1	1:F:211:GLN:HB2	1.48	1.12
1:A:411:VAL:HG13	1:B:18:PRO:CD	1.80	1.11
1:B:116:THR:HG22	1:C:256:PHE:HE1	1.11	1.11
1:D:375:GLU:OE1	1:E:235:ASN:ND2	1.83	1.11
1:B:214:SER:HA	1:C:275:ASP:CA	1.78	1.11
1:B:218:LEU:HD22	1:C:273:PRO:HA	1.15	1.10
1:B:202:GLY:CA	1:F:345:PHE:HE1	1.49	1.10
1:B:203:ASN:ND2	1:F:111:PRO:CD	2.15	1.10
1:B:184:ILE:HD11	1:F:46:VAL:CG2	1.82	1.10
1:C:144:ASN:HD22	1:D:290:ALA:HB3	1.10	1.09
1:A:423:ARG:HH21	1:F:43:LEU:HD22	1.08	1.09
1:B:184:ILE:HD11	1:F:46:VAL:CB	1.81	1.09
1:B:235:ASN:ND2	1:F:375:GLU:OE1	1.85	1.09
1:C:213:ARG:NH1	1:D:275:ASP:O	1.56	1.09
1:E:479:ARG:NH2	1:F:318:ARG:NH2	1.99	1.09
1:B:283:THR:HG23	1:F:140:ASP:CB	1.82	1.09
1:D:207:LYS:HG2	1:E:275:ASP:OD2	0.93	1.09
1:C:46:VAL:HG11	1:D:184:ILE:HD13	1.32	1.08
1:C:140:ASP:CB	1:D:283:THR:HG21	1.81	1.08
1:E:207:LYS:CG	1:F:273:PRO:CB	2.31	1.08
1:B:184:ILE:CD1	1:F:46:VAL:HG13	1.81	1.08
1:B:214:SER:HA	1:C:275:ASP:HA	1.35	1.08
1:A:83:ALA:CB	1:F:83:ALA:HA	1.83	1.08
1:A:83:ALA:HB2	1:F:83:ALA:HA	1.14	1.08
1:C:143:GLN:HE22	1:D:132:ASN:C	1.60	1.08
1:D:351:THR:CB	1:E:178:LYS:O	2.02	1.08
1:D:351:THR:O	1:E:178:LYS:CG	2.01	1.08
1:B:358:THR:HG21	1:D:282:SER:HB3	1.09	1.08
1:B:119:HIS:CE1	1:C:276:PHE:N	1.77	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:VAL:HG21	1:C:274:SER:HA	1.32	1.07
1:B:231:LEU:HD12	1:F:373:GLN:HE21	1.16	1.07
1:B:276:PHE:HE1	1:E:354:PRO:HG3	1.03	1.07
1:A:409:GLY:CA	1:B:17:THR:OG1	2.02	1.07
1:B:273:PRO:C	1:F:207:LYS:HA	1.80	1.06
1:C:213:ARG:HB3	1:D:271:VAL:CB	1.84	1.06
1:C:358:THR:HG21	1:E:282:SER:HB3	1.35	1.06
1:B:218:LEU:HA	1:C:274:SER:HB2	1.31	1.06
1:C:120:PRO:HG2	1:D:267:ILE:CD1	1.84	1.06
1:B:281:ASP:HB3	1:E:358:THR:HG21	1.36	1.06
1:B:345:PHE:CZ	1:C:202:GLY:CA	2.26	1.06
1:D:351:THR:HG22	1:E:178:LYS:O	1.48	1.06
1:A:411:VAL:CG1	1:B:18:PRO:CB	2.33	1.06
1:D:207:LYS:HG3	1:E:275:ASP:CG	1.77	1.05
1:B:218:LEU:HD21	1:C:273:PRO:C	1.64	1.05
1:D:46:VAL:HG11	1:E:184:ILE:CG1	1.85	1.05
1:B:222:SER:HB3	1:C:271:VAL:CB	1.87	1.05
1:B:283:THR:HG23	1:F:140:ASP:HB2	1.34	1.05
1:B:214:SER:OG	1:C:275:ASP:HA	1.55	1.05
1:B:227:TRP:CZ3	1:F:109:GLY:O	2.10	1.05
1:D:46:VAL:HG13	1:E:184:ILE:HD11	1.06	1.05
1:A:409:GLY:CA	1:B:17:THR:N	2.19	1.04
1:B:46:VAL:CB	1:C:184:ILE:HD11	1.86	1.04
1:B:256:PHE:HE2	1:F:254:ARG:CZ	1.69	1.04
1:D:221:VAL:HG13	1:E:273:PRO:HD3	1.32	1.04
1:D:351:THR:CG2	1:E:178:LYS:O	0.74	1.04
1:E:302:LEU:HD12	1:F:251:VAL:O	1.58	1.04
1:D:140:ASP:CB	1:E:283:THR:OG1	2.05	1.04
1:A:83:ALA:HB2	1:F:83:ALA:CA	1.86	1.03
1:A:423:ARG:NH2	1:F:43:LEU:CD2	2.21	1.03
1:B:375:GLU:OE1	1:C:235:ASN:ND2	1.90	1.03
1:B:121:LEU:CG	1:C:276:PHE:CD1	2.01	1.03
1:B:214:SER:CA	1:C:275:ASP:HA	1.86	1.03
1:A:87:LYS:N	1:F:86:GLN:CG	2.19	1.03
1:B:218:LEU:HD21	1:C:273:PRO:O	1.56	1.03
1:B:358:THR:HG21	1:D:282:SER:CA	1.89	1.03
1:D:221:VAL:HG22	1:E:273:PRO:HD2	1.39	1.03
1:A:429:ALA:HA	1:B:172:PRO:HA	1.03	1.03
1:B:218:LEU:HD21	1:C:273:PRO:CA	1.72	1.03
1:B:221:VAL:HG11	1:C:274:SER:HA	1.35	1.02
1:C:46:VAL:CG2	1:D:184:ILE:HD11	1.87	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:VAL:HG11	1:C:274:SER:N	1.74	1.02
1:D:221:VAL:HG22	1:E:273:PRO:HG2	1.12	1.02
1:C:350:GLN:CG	1:D:211:GLN:CB	2.37	1.02
1:B:221:VAL:HG13	1:C:271:VAL:O	1.59	1.01
1:A:423:ARG:NH2	1:F:43:LEU:HD22	1.73	1.01
1:B:119:HIS:HD2	1:C:274:SER:OG	1.40	1.01
1:E:142:ARG:NH2	1:F:280:PRO:HG3	1.76	1.01
1:D:351:THR:CB	1:E:178:LYS:C	2.33	1.01
1:E:111:PRO:CG	1:F:203:ASN:OD1	2.08	1.01
1:B:351:THR:CG2	1:C:179:GLY:CA	2.02	1.00
1:E:207:LYS:HE3	1:F:273:PRO:HB2	1.42	1.00
1:B:46:VAL:CG2	1:C:184:ILE:HD11	1.91	1.00
1:E:302:LEU:HD12	1:F:251:VAL:C	1.87	1.00
1:C:373:GLN:HE21	1:D:231:LEU:HD12	1.23	1.00
1:A:411:VAL:CG2	1:B:397:THR:HG21	1.91	1.00
1:C:375:GLU:OE1	1:D:235:ASN:ND2	1.94	1.00
1:E:483:THR:HB	1:F:23:GLN:HE22	1.26	0.99
1:B:119:HIS:CE1	1:C:273:PRO:O	2.15	0.99
1:B:222:SER:CB	1:C:271:VAL:HG21	1.79	0.99
1:B:46:VAL:HG13	1:C:184:ILE:CD1	1.92	0.99
1:D:351:THR:HG21	1:E:178:LYS:O	1.17	0.99
1:C:351:THR:HG23	1:D:178:LYS:C	1.85	0.99
1:D:349:GLN:CD	1:E:179:GLY:C	2.30	0.99
1:E:207:LYS:HG3	1:F:273:PRO:HG2	1.02	0.99
1:B:273:PRO:O	1:F:207:LYS:HA	1.63	0.98
1:B:256:PHE:CZ	1:F:254:ARG:NH1	2.31	0.98
1:A:411:VAL:HG11	1:B:18:PRO:HG2	1.45	0.98
1:D:302:LEU:HD12	1:E:251:VAL:O	1.63	0.98
1:B:222:SER:HB2	1:C:271:VAL:CG2	1.76	0.98
1:B:276:PHE:CD1	1:E:354:PRO:HB3	1.99	0.98
1:E:222:SER:N	1:F:272:SER:OG	1.93	0.98
1:E:345:PHE:HE1	1:F:202:GLY:C	1.70	0.98
1:B:273:PRO:HD3	1:F:221:VAL:HG13	1.45	0.98
1:D:351:THR:OG1	1:E:179:GLY:HA2	1.19	0.98
1:A:429:ALA:HA	1:B:172:PRO:CA	1.92	0.98
1:B:109:GLY:O	1:C:227:TRP:HZ3	1.41	0.98
1:B:221:VAL:CG2	1:C:274:SER:HA	1.93	0.97
1:C:345:PHE:HE1	1:D:202:GLY:C	1.70	0.97
1:E:345:PHE:HE1	1:F:202:GLY:CA	1.44	0.97
1:B:202:GLY:CA	1:F:345:PHE:CZ	2.40	0.97
1:B:283:THR:CG2	1:F:140:ASP:HB2	1.89	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:VAL:CG1	1:D:184:ILE:HD13	1.85	0.97
1:C:350:GLN:NE2	1:E:276:PHE:CE2	2.32	0.97
1:B:231:LEU:HD12	1:F:373:GLN:NE2	1.80	0.97
1:C:109:GLY:O	1:D:227:TRP:HZ3	1.40	0.97
1:C:46:VAL:HG13	1:D:184:ILE:CD1	1.90	0.97
1:B:345:PHE:HE1	1:C:202:GLY:CA	1.53	0.97
1:B:214:SER:OG	1:C:275:ASP:CA	2.13	0.96
1:E:373:GLN:HE21	1:F:231:LEU:HD12	1.26	0.96
1:A:411:VAL:CG1	1:B:18:PRO:HB2	1.95	0.96
1:B:27:GLU:HG2	1:F:482:VAL:CG1	1.95	0.96
1:C:143:GLN:NE2	1:D:132:ASN:C	2.23	0.96
1:D:46:VAL:HG13	1:E:184:ILE:CD1	1.74	0.96
1:B:121:LEU:CB	1:C:276:PHE:CD1	2.43	0.96
1:C:213:ARG:CB	1:D:271:VAL:CG1	2.16	0.96
1:B:121:LEU:CD1	1:C:276:PHE:HA	1.95	0.96
1:B:144:ASN:HD22	1:C:290:ALA:CB	1.77	0.96
1:B:202:GLY:C	1:F:345:PHE:HE1	1.73	0.96
1:C:213:ARG:NH1	1:D:276:PHE:CD1	2.15	0.96
1:E:345:PHE:CE1	1:F:202:GLY:C	2.43	0.96
1:C:213:ARG:CD	1:D:271:VAL:HB	1.96	0.96
1:B:276:PHE:CE1	1:E:354:PRO:CG	2.48	0.96
1:C:358:THR:CG2	1:E:282:SER:HB3	1.96	0.95
1:B:140:ASP:OD2	1:C:280:PRO:CB	2.13	0.95
1:B:256:PHE:CD1	1:F:116:THR:HG21	2.02	0.95
1:B:221:VAL:CG1	1:C:274:SER:HA	1.95	0.95
1:B:218:LEU:CD2	1:C:273:PRO:O	2.11	0.95
1:C:350:GLN:NE2	1:D:211:GLN:OE1	2.00	0.95
1:B:46:VAL:HG13	1:C:184:ILE:HD11	1.47	0.95
1:B:256:PHE:CZ	1:F:148:ASP:OD1	2.20	0.94
1:B:358:THR:CG2	1:D:282:SER:N	2.30	0.94
1:B:203:ASN:HD22	1:F:111:PRO:CD	1.76	0.94
1:B:281:ASP:HB2	1:E:358:THR:HG21	1.04	0.94
1:A:428:SER:HA	1:B:173:CYS:CB	1.96	0.94
1:B:203:ASN:ND2	1:F:111:PRO:HD3	1.81	0.94
1:A:429:ALA:HB1	1:B:183:PRO:CB	1.98	0.93
1:C:358:THR:HG21	1:E:282:SER:CB	1.97	0.93
1:D:481:ALA:HB1	1:E:23:GLN:OE1	1.67	0.93
1:D:221:VAL:HG13	1:E:273:PRO:CD	1.98	0.93
1:E:148:ASP:OD1	1:F:256:PHE:CZ	2.21	0.93
1:C:140:ASP:CB	1:D:283:THR:CG2	2.41	0.93
1:E:222:SER:HA	1:F:273:PRO:HD3	1.51	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:474:TYR:CE2	1:D:318:ARG:CZ	2.47	0.93
1:B:184:ILE:HD11	1:F:46:VAL:HG13	1.36	0.93
1:B:142:ARG:O	1:C:286:GLN:NE2	2.00	0.93
1:C:350:GLN:HE21	1:D:211:GLN:CD	1.77	0.93
1:A:409:GLY:HA2	1:B:17:THR:OG1	1.69	0.92
1:B:209:LEU:O	1:F:347:ILE:CG2	2.16	0.92
1:D:351:THR:CB	1:E:179:GLY:N	2.21	0.92
1:D:254:ARG:NH1	1:E:256:PHE:HE2	1.66	0.92
1:B:256:PHE:CE2	1:F:254:ARG:NH1	2.37	0.92
1:C:358:THR:CG2	1:E:282:SER:CB	2.48	0.92
1:C:350:GLN:CG	1:D:211:GLN:HB3	1.99	0.92
1:B:119:HIS:CD2	1:C:274:SER:OG	2.17	0.92
1:E:350:GLN:NE2	1:F:211:GLN:CD	2.25	0.92
1:E:361:SER:OG	1:F:260:ASN:ND2	2.02	0.92
1:A:409:GLY:HA3	1:B:17:THR:OG1	1.69	0.91
1:B:267:ILE:CD1	1:F:120:PRO:HG2	2.00	0.91
1:C:302:LEU:HD12	1:D:251:VAL:C	1.95	0.91
1:E:120:PRO:HG2	1:F:267:ILE:CD1	2.01	0.91
1:B:283:THR:OG1	1:F:140:ASP:HB3	1.70	0.91
1:B:358:THR:HG21	1:D:282:SER:N	1.84	0.91
1:C:361:SER:OG	1:D:260:ASN:OD1	1.88	0.91
1:C:140:ASP:HB3	1:D:283:THR:HG21	0.91	0.91
1:B:358:THR:HG22	1:D:282:SER:CB	1.99	0.91
1:D:221:VAL:CG2	1:E:273:PRO:CD	2.41	0.91
1:D:221:VAL:CG1	1:E:273:PRO:HD3	1.97	0.91
1:B:122:PHE:HA	1:C:275:ASP:CG	1.96	0.90
1:B:144:ASN:HD22	1:C:290:ALA:HB3	1.37	0.90
1:D:213:ARG:CB	1:E:271:VAL:CG1	1.93	0.90
1:D:213:ARG:NH1	1:E:276:PHE:CG	2.32	0.90
1:B:184:ILE:HD13	1:F:46:VAL:CG1	1.99	0.90
1:B:214:SER:CB	1:C:275:ASP:HA	2.00	0.90
1:A:86:GLN:C	1:F:86:GLN:HG3	1.97	0.90
1:B:182:PRO:HD3	1:F:349:GLN:CG	2.00	0.90
1:A:411:VAL:CG2	1:B:397:THR:CG2	2.50	0.90
1:C:143:GLN:NE2	1:D:132:ASN:O	2.05	0.90
1:B:256:PHE:CE2	1:F:254:ARG:CZ	2.54	0.90
1:B:211:GLN:CG	1:F:350:GLN:CD	2.42	0.90
1:C:46:VAL:HG11	1:D:184:ILE:CG1	2.02	0.89
1:C:474:TYR:HE2	1:D:318:ARG:CZ	1.79	0.89
1:D:120:PRO:HG2	1:E:267:ILE:CD1	2.00	0.89
1:D:349:GLN:CD	1:E:180:ASP:N	2.29	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:ARG:NH2	1:C:280:PRO:CG	2.35	0.89
1:B:27:GLU:CG	1:F:482:VAL:HG13	2.02	0.89
1:B:222:SER:HB3	1:C:271:VAL:HG23	1.26	0.89
1:B:273:PRO:O	1:F:207:LYS:CA	2.20	0.89
1:B:352:ASN:C	1:C:178:LYS:HD3	1.97	0.89
1:B:221:VAL:CG1	1:C:271:VAL:O	2.20	0.89
1:B:286:GLN:NE2	1:F:142:ARG:O	2.05	0.89
1:C:222:SER:N	1:D:272:SER:OG	1.98	0.89
1:D:109:GLY:O	1:E:227:TRP:HZ3	1.44	0.89
1:B:221:VAL:HG21	1:C:274:SER:CA	2.02	0.89
1:B:116:THR:HG22	1:C:256:PHE:CE1	1.98	0.89
1:E:345:PHE:CZ	1:F:202:GLY:HA2	2.06	0.88
1:B:116:THR:HG21	1:C:256:PHE:HD1	1.35	0.88
1:B:283:THR:HG22	1:F:139:LYS:O	1.73	0.88
1:C:358:THR:HG23	1:E:282:SER:H	1.36	0.88
1:D:351:THR:C	1:E:178:LYS:HG2	1.98	0.88
1:B:213:ARG:CB	1:C:277:TYR:HD2	1.85	0.88
1:E:479:ARG:HH21	1:F:318:ARG:NH2	1.65	0.88
1:B:273:PRO:O	1:F:206:PHE:C	2.17	0.88
1:B:273:PRO:CD	1:F:221:VAL:HG13	2.03	0.88
1:C:83:ALA:HB3	1:D:13:LEU:HD23	1.55	0.88
1:B:121:LEU:HD12	1:C:276:PHE:CA	2.02	0.88
1:E:351:THR:O	1:F:178:LYS:HE2	1.74	0.88
1:E:207:LYS:CD	1:F:273:PRO:HG3	2.03	0.88
1:C:213:ARG:CA	1:D:271:VAL:HG11	2.02	0.87
1:A:427:SER:O	1:B:173:CYS:SG	2.32	0.87
1:B:46:VAL:CG1	1:C:184:ILE:HD13	2.01	0.87
1:B:46:VAL:HG11	1:C:184:ILE:HD13	1.54	0.87
1:B:251:VAL:O	1:F:302:LEU:HD12	1.74	0.87
1:D:351:THR:CG2	1:E:178:LYS:C	1.78	0.87
1:D:302:LEU:HD12	1:E:251:VAL:C	1.98	0.87
1:A:411:VAL:HG12	1:B:18:PRO:HB2	1.56	0.87
1:B:251:VAL:C	1:F:302:LEU:HD12	1.99	0.87
1:C:375:GLU:OE2	1:D:231:LEU:HB3	1.74	0.86
1:B:121:LEU:CB	1:C:276:PHE:HD1	1.84	0.86
1:B:275:ASP:CG	1:F:207:LYS:HG3	1.98	0.86
1:C:347:ILE:HG21	1:D:182:PRO:HD2	1.58	0.86
1:A:409:GLY:HA2	1:B:17:THR:CA	2.05	0.86
1:B:142:ARG:HH21	1:C:280:PRO:HG3	1.07	0.86
1:D:213:ARG:HB3	1:E:271:VAL:CB	2.05	0.86
1:D:345:PHE:CE1	1:E:209:LEU:HD23	2.11	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:373:GLN:HE21	1:E:231:LEU:HD12	1.40	0.86
1:B:203:ASN:HD21	1:F:111:PRO:HG3	1.01	0.86
1:D:46:VAL:CB	1:E:184:ILE:HD11	2.05	0.86
1:B:184:ILE:CG1	1:F:46:VAL:HG11	2.04	0.86
1:B:358:THR:HG22	1:D:282:SER:HB3	1.54	0.86
1:C:222:SER:C	1:D:272:SER:HB2	1.71	0.86
1:B:144:ASN:ND2	1:C:290:ALA:HB3	1.91	0.85
1:C:213:ARG:HG2	1:D:274:SER:CA	2.05	0.85
1:B:359:TYR:HB2	1:D:278:TYR:CE2	2.11	0.85
1:D:46:VAL:HG11	1:E:184:ILE:HD11	0.91	0.85
1:A:87:LYS:H	1:F:86:GLN:HG3	1.38	0.85
1:B:46:VAL:HG11	1:C:184:ILE:HD11	1.02	0.85
1:A:423:ARG:NH2	1:F:43:LEU:CG	2.25	0.85
1:E:349:GLN:HG2	1:F:180:ASP:O	1.77	0.85
1:C:350:GLN:CG	1:D:211:GLN:HB2	2.05	0.85
1:C:359:TYR:CD1	1:E:278:TYR:HE2	1.95	0.85
1:C:144:ASN:HD22	1:D:290:ALA:CB	1.90	0.84
1:B:231:LEU:CD1	1:F:373:GLN:HE21	1.90	0.84
1:B:213:ARG:HB3	1:C:277:TYR:HD2	1.42	0.84
1:B:222:SER:HB3	1:C:271:VAL:HB	1.58	0.84
1:B:256:PHE:HD1	1:F:116:THR:HG21	1.39	0.84
1:B:375:GLU:OE2	1:C:231:LEU:HB3	1.77	0.84
1:E:207:LYS:CE	1:F:275:ASP:OD2	2.25	0.84
1:B:120:PRO:HG2	1:C:267:ILE:CD1	2.07	0.84
1:C:351:THR:CG2	1:D:178:LYS:O	2.24	0.84
1:D:465:GLN:HE22	1:E:22:VAL:H	1.23	0.84
1:B:218:LEU:HD23	1:C:274:SER:N	1.92	0.84
1:C:375:GLU:OE2	1:D:231:LEU:HD22	1.78	0.84
1:D:351:THR:HG23	1:E:178:LYS:CA	2.07	0.84
1:B:116:THR:CG2	1:C:256:PHE:CD1	2.53	0.83
1:C:345:PHE:CZ	1:D:202:GLY:HA2	2.12	0.83
1:E:347:ILE:HD11	1:F:181:CYS:HG	1.03	0.83
1:C:213:ARG:CD	1:D:274:SER:HG	1.74	0.83
1:B:283:THR:HG21	1:F:140:ASP:HB3	0.93	0.83
1:C:345:PHE:HD1	1:D:204:MET:SD	2.01	0.83
1:B:358:THR:HG23	1:D:282:SER:H	1.44	0.82
1:A:431:ARG:NH1	1:B:185:GLN:OE1	2.12	0.82
1:D:351:THR:O	1:E:178:LYS:CD	2.26	0.82
1:B:273:PRO:HD2	1:F:221:VAL:HG22	1.60	0.82
1:C:267:ILE:CG2	1:C:273:PRO:HB3	2.09	0.82
1:C:282:SER:HB3	1:F:358:THR:HG21	1.60	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:GLN:HE22	1:F:142:ARG:HB2	1.44	0.82
1:A:409:GLY:C	1:B:17:THR:N	2.37	0.82
1:E:345:PHE:HD1	1:F:204:MET:SD	2.03	0.81
1:D:349:GLN:NE2	1:E:180:ASP:N	2.28	0.81
1:E:351:THR:O	1:F:178:LYS:HG2	1.79	0.81
1:B:210:GLN:NE2	1:F:346:THR:O	2.13	0.81
1:D:347:ILE:HD12	1:E:182:PRO:HD2	1.60	0.81
1:B:278:TYR:CE2	1:E:359:TYR:HB2	2.16	0.81
1:D:213:ARG:CA	1:E:271:VAL:HG11	2.09	0.81
1:B:358:THR:CG2	1:D:282:SER:H	1.94	0.81
1:C:213:ARG:O	1:D:271:VAL:HG11	1.80	0.81
1:B:216:VAL:O	1:C:274:SER:OG	1.97	0.81
1:C:350:GLN:HG3	1:D:211:GLN:CB	2.08	0.81
1:B:184:ILE:CD1	1:F:46:VAL:CG2	2.59	0.80
1:C:350:GLN:NE2	1:D:211:GLN:CG	2.41	0.80
1:E:375:GLU:OE2	1:F:231:LEU:HB3	1.81	0.80
1:A:431:ARG:CZ	1:B:185:GLN:OE1	2.28	0.80
1:B:271:VAL:CG1	1:F:213:ARG:CB	2.09	0.80
1:D:349:GLN:NE2	1:E:179:GLY:H	1.79	0.80
1:D:351:THR:OG1	1:E:179:GLY:CA	0.50	0.80
1:A:411:VAL:HG21	1:B:397:THR:HG22	1.62	0.80
1:B:256:PHE:HZ	1:F:254:ARG:NH1	1.79	0.80
1:B:351:THR:HG23	1:C:179:GLY:CA	2.09	0.80
1:E:207:LYS:CG	1:F:273:PRO:HB3	2.05	0.80
1:B:286:GLN:HE22	1:F:142:ARG:CA	1.94	0.79
1:D:213:ARG:HB3	1:E:271:VAL:HG12	1.54	0.79
1:A:428:SER:HA	1:B:173:CYS:HB2	1.61	0.79
1:B:280:PRO:HG3	1:F:121:LEU:CD1	2.11	0.79
1:D:349:GLN:HG2	1:E:179:GLY:HA2	1.63	0.79
1:E:207:LYS:HE3	1:F:273:PRO:CA	2.13	0.79
1:C:345:PHE:CE1	1:D:202:GLY:C	2.51	0.79
1:E:347:ILE:HD12	1:F:182:PRO:HD2	1.62	0.79
1:B:345:PHE:HE1	1:C:202:GLY:C	1.91	0.79
1:B:221:VAL:CB	1:C:274:SER:HA	2.13	0.79
1:B:283:THR:OG1	1:F:140:ASP:CB	2.30	0.79
1:E:82:PHE:CD2	1:F:14:PRO:HG3	2.18	0.79
1:E:479:ARG:HH21	1:F:318:ARG:HH22	0.80	0.79
1:A:83:ALA:HB2	1:F:83:ALA:CB	2.12	0.78
1:A:87:LYS:HB3	1:F:85:PRO:C	2.06	0.78
1:B:119:HIS:CG	1:C:274:SER:HB3	2.18	0.78
1:B:119:HIS:CG	1:C:275:ASP:HB2	2.18	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:GLN:OE1	1:F:140:ASP:CG	2.26	0.78
1:B:271:VAL:CG1	1:F:213:ARG:CG	2.61	0.78
1:E:207:LYS:HE2	1:F:275:ASP:OD2	1.83	0.78
1:E:348:SER:OG	1:F:212:ASP:OD1	2.02	0.78
1:E:350:GLN:CD	1:F:211:GLN:CB	2.48	0.78
1:A:411:VAL:CG1	1:B:18:PRO:CD	2.50	0.78
1:D:143:GLN:OE1	1:E:134:TYR:N	2.16	0.78
1:B:148:ASP:OD1	1:C:256:PHE:CZ	2.37	0.78
1:D:199:ILE:HD11	1:D:220:ILE:HD13	1.65	0.78
1:A:428:SER:CA	1:B:173:CYS:SG	2.68	0.78
1:C:213:ARG:N	1:D:274:SER:HB3	1.99	0.78
1:B:286:GLN:HE22	1:F:142:ARG:CB	1.97	0.78
1:C:120:PRO:HG2	1:D:267:ILE:HD12	1.65	0.78
1:B:202:GLY:HA3	1:F:345:PHE:HE1	0.97	0.77
1:C:207:LYS:C	1:D:275:ASP:OD2	2.27	0.77
1:A:411:VAL:HG13	1:B:18:PRO:HG2	0.80	0.77
1:B:283:THR:CG2	1:F:139:LYS:O	2.32	0.77
1:A:408:LEU:O	1:B:17:THR:N	2.17	0.77
1:D:481:ALA:CB	1:E:23:GLN:OE1	2.32	0.77
1:B:218:LEU:HD22	1:C:273:PRO:CA	1.89	0.77
1:B:345:PHE:HD1	1:C:204:MET:SD	2.07	0.77
1:C:46:VAL:HG13	1:D:184:ILE:HD11	1.51	0.77
1:B:46:VAL:HG11	1:C:184:ILE:CG1	2.15	0.77
1:B:204:MET:SD	1:F:345:PHE:HD1	2.07	0.77
1:D:213:ARG:CG	1:E:271:VAL:CG1	2.63	0.76
1:D:254:ARG:NH1	1:E:256:PHE:CE2	2.53	0.76
1:B:280:PRO:HG3	1:F:121:LEU:HD13	1.68	0.76
1:C:121:LEU:HD13	1:D:280:PRO:HG3	1.65	0.76
1:D:140:ASP:HB3	1:E:283:THR:HG1	1.49	0.76
1:C:144:ASN:ND2	1:D:290:ALA:HB3	1.94	0.76
1:B:222:SER:OG	1:C:271:VAL:HG23	1.86	0.75
1:D:211:GLN:HA	1:E:274:SER:HB2	1.68	0.75
1:B:345:PHE:CD1	1:C:204:MET:SD	2.79	0.75
1:C:144:ASN:O	1:D:131:PRO:HG3	1.86	0.75
1:E:345:PHE:CD1	1:F:204:MET:SD	2.79	0.75
1:A:423:ARG:NH2	1:F:43:LEU:CA	2.48	0.75
1:B:221:VAL:CG1	1:C:274:SER:CA	2.57	0.75
1:B:271:VAL:HG11	1:F:213:ARG:CA	2.16	0.75
1:D:351:THR:CA	1:E:179:GLY:CA	2.65	0.74
1:A:411:VAL:HG12	1:B:18:PRO:CB	2.13	0.74
1:B:358:THR:HG22	1:D:282:SER:OG	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:PHE:N	1:B:17:THR:N	2.36	0.74
1:B:221:VAL:HG11	1:C:274:SER:H	1.46	0.74
1:C:213:ARG:C	1:D:271:VAL:HG11	2.12	0.74
1:D:207:LYS:HA	1:E:273:PRO:O	1.86	0.74
1:D:142:ARG:N	1:E:286:GLN:HE22	1.86	0.74
1:C:358:THR:OG1	1:E:281:ASP:HB2	1.88	0.74
1:A:411:VAL:HG11	1:B:18:PRO:CB	2.16	0.74
1:B:142:ARG:C	1:C:286:GLN:HE22	1.94	0.74
1:C:345:PHE:CD1	1:D:204:MET:SD	2.80	0.74
1:C:213:ARG:HD3	1:D:276:PHE:O	1.88	0.74
1:C:213:ARG:CG	1:D:274:SER:OG	0.44	0.74
1:C:213:ARG:O	1:D:271:VAL:CG1	2.36	0.74
1:C:46:VAL:CG2	1:D:184:ILE:CD1	2.63	0.74
1:B:214:SER:OG	1:C:275:ASP:O	2.06	0.73
1:E:148:ASP:OD1	1:F:256:PHE:HZ	1.69	0.73
1:E:373:GLN:NE2	1:F:231:LEU:HD12	2.04	0.73
1:A:429:ALA:HB1	1:B:183:PRO:CG	2.17	0.73
1:B:46:VAL:CG2	1:C:184:ILE:CD1	2.67	0.73
1:B:276:PHE:CD1	1:E:354:PRO:CB	2.71	0.73
1:D:350:GLN:OE1	1:E:211:GLN:HG3	1.87	0.73
1:B:256:PHE:CZ	1:F:148:ASP:CG	2.66	0.73
1:D:207:LYS:HA	1:E:273:PRO:C	2.14	0.73
1:E:371:VAL:CG1	1:F:167:TRP:HE1	2.01	0.73
1:C:213:ARG:HB3	1:D:271:VAL:HG11	0.75	0.73
1:B:213:ARG:CB	1:C:277:TYR:CD2	2.68	0.72
1:B:121:LEU:HB2	1:C:275:ASP:C	2.14	0.72
1:D:349:GLN:HE21	1:E:179:GLY:H	1.35	0.72
1:B:302:LEU:HD12	1:C:251:VAL:C	2.13	0.72
1:B:373:GLN:HE21	1:C:231:LEU:HD12	1.55	0.72
1:D:142:ARG:NH2	1:E:280:PRO:HG3	2.03	0.72
1:B:130:ASN:ND2	1:F:127:ASP:OD2	2.23	0.72
1:C:465:GLN:HE22	1:D:22:VAL:H	1.36	0.72
1:A:429:ALA:H	1:B:173:CYS:N	1.86	0.72
1:B:184:ILE:HD12	1:F:371:VAL:CG2	2.20	0.72
1:B:351:THR:CG2	1:C:179:GLY:HA2	2.14	0.72
1:B:271:VAL:CB	1:F:213:ARG:HB3	2.18	0.72
1:B:122:PHE:CA	1:C:275:ASP:OD2	2.35	0.72
1:C:373:GLN:NE2	1:D:231:LEU:HD12	2.03	0.72
1:B:119:HIS:HD2	1:C:274:SER:HG	1.36	0.72
1:B:286:GLN:NE2	1:F:142:ARG:C	2.48	0.72
1:D:104:LEU:HD12	1:D:155:PHE:CE2	2.24	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:144:ASN:O	1:F:131:PRO:HG3	1.89	0.71
1:E:222:SER:CB	1:F:273:PRO:HD2	2.16	0.71
1:A:411:VAL:CG1	1:B:18:PRO:HD2	2.20	0.71
1:B:218:LEU:HD22	1:C:272:SER:O	1.90	0.71
1:B:358:THR:HG23	1:D:282:SER:N	2.00	0.71
1:C:213:ARG:CD	1:D:276:PHE:O	2.38	0.71
1:C:348:SER:OG	1:D:210:GLN:HA	1.90	0.71
1:C:350:GLN:HG2	1:D:211:GLN:HB2	1.72	0.71
1:B:345:PHE:CE1	1:C:202:GLY:C	2.65	0.71
1:E:121:LEU:HD13	1:F:280:PRO:CG	2.20	0.71
1:E:142:ARG:HH21	1:F:280:PRO:HG3	1.51	0.71
1:E:369:ARG:NH2	1:F:265:GLU:OE2	2.24	0.71
1:B:271:VAL:HG11	1:F:213:ARG:CG	2.14	0.71
1:B:349:GLN:CG	1:C:182:PRO:HD3	2.21	0.71
1:C:282:SER:OG	1:F:358:THR:HG22	1.90	0.71
1:B:178:LYS:HE2	1:F:353:THR:N	2.06	0.71
1:B:184:ILE:HD11	1:F:46:VAL:HG11	1.24	0.71
1:D:371:VAL:HG21	1:E:167:TRP:CE2	2.26	0.71
1:D:462:ASP:OD2	1:E:21:LYS:NZ	2.21	0.70
1:E:207:LYS:HB2	1:F:273:PRO:HG3	1.66	0.70
1:E:351:THR:O	1:F:178:LYS:CE	2.39	0.70
1:B:144:ASN:ND2	1:C:290:ALA:CB	2.52	0.70
1:B:202:GLY:C	1:F:345:PHE:CE1	2.54	0.70
1:C:351:THR:O	1:D:178:LYS:HB3	1.91	0.70
1:B:184:ILE:HD13	1:F:46:VAL:HG11	1.63	0.70
1:D:213:ARG:HD3	1:E:271:VAL:HB	0.79	0.70
1:A:411:VAL:HG11	1:B:18:PRO:CG	2.05	0.70
1:B:184:ILE:CD1	1:F:371:VAL:HG22	2.21	0.70
1:C:358:THR:CG2	1:E:282:SER:H	2.03	0.70
1:E:207:LYS:CD	1:F:273:PRO:CG	2.48	0.70
1:A:429:ALA:H	1:B:173:CYS:H	1.37	0.70
1:A:429:ALA:CB	1:B:183:PRO:CB	2.70	0.70
1:B:286:GLN:NE2	1:F:142:ARG:HB2	2.06	0.70
1:C:350:GLN:NE2	1:E:276:PHE:HE2	1.84	0.70
1:B:101:LEU:HD22	1:B:332:LEU:HD21	1.73	0.70
1:B:144:ASN:HD22	1:C:290:ALA:HB1	1.55	0.69
1:B:184:ILE:HD13	1:F:46:VAL:HG13	1.65	0.69
1:B:351:THR:HG22	1:C:179:GLY:N	2.06	0.69
1:C:142:ARG:NH2	1:D:280:PRO:HG3	2.06	0.69
1:C:211:GLN:HA	1:D:274:SER:HB2	1.73	0.69
1:C:371:VAL:HG21	1:D:167:TRP:CE2	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:213:ARG:NE	1:F:271:VAL:HG21	2.06	0.69
1:A:409:GLY:HA2	1:B:17:THR:CB	2.22	0.69
1:A:411:VAL:HG13	1:B:18:PRO:HD2	1.69	0.69
1:B:364:PHE:CD1	1:C:212:ASP:OD1	2.45	0.69
1:E:345:PHE:CZ	1:F:203:ASN:N	2.60	0.69
1:A:429:ALA:HB1	1:B:183:PRO:HB2	1.72	0.69
1:A:423:ARG:CZ	1:F:43:LEU:HD22	2.23	0.69
1:B:214:SER:OG	1:C:275:ASP:C	2.36	0.69
1:D:369:ARG:NH2	1:E:265:GLU:OE2	2.25	0.69
1:B:281:ASP:CG	1:E:358:THR:HG22	2.18	0.69
1:D:46:VAL:HG11	1:E:184:ILE:HG12	1.75	0.69
1:C:302:LEU:HD12	1:D:251:VAL:O	1.92	0.69
1:C:351:THR:HA	1:D:179:GLY:N	2.06	0.69
1:A:423:ARG:NH1	1:F:451:TRP:HE1	1.91	0.68
1:D:213:ARG:HG2	1:E:274:SER:N	2.08	0.68
1:B:364:PHE:CG	1:C:212:ASP:OD1	2.46	0.68
1:D:199:ILE:CD1	1:D:220:ILE:HD13	2.23	0.68
1:E:120:PRO:HG2	1:F:267:ILE:HD13	1.74	0.68
1:B:276:PHE:CD2	1:F:211:GLN:OE1	2.43	0.68
1:C:46:VAL:HG21	1:D:184:ILE:CD1	2.24	0.68
1:C:358:THR:CG2	1:E:282:SER:N	2.57	0.68
1:D:349:GLN:NE2	1:E:179:GLY:N	2.41	0.68
1:E:213:ARG:CZ	1:F:271:VAL:HG22	2.23	0.68
1:E:302:LEU:CD1	1:F:251:VAL:C	2.66	0.68
1:D:358:THR:CG2	1:F:282:SER:OG	2.41	0.68
1:B:265:GLU:OE2	1:F:369:ARG:NH2	2.27	0.67
1:B:109:GLY:O	1:C:227:TRP:CE3	2.44	0.67
1:B:142:ARG:HH21	1:C:280:PRO:CG	1.95	0.67
1:B:46:VAL:HG21	1:C:184:ILE:HD11	1.74	0.67
1:B:184:ILE:HD12	1:F:371:VAL:HG22	1.77	0.67
1:E:207:LYS:HD2	1:F:273:PRO:CB	2.22	0.67
1:B:221:VAL:HB	1:C:274:SER:OG	1.95	0.67
1:B:155:PHE:CE1	1:B:334:VAL:HG13	2.30	0.67
1:B:211:GLN:HG3	1:F:350:GLN:NE2	2.09	0.67
1:D:144:ASN:HD22	1:E:290:ALA:HB3	1.59	0.67
1:D:221:VAL:CG1	1:E:273:PRO:CD	2.60	0.67
1:E:148:ASP:CG	1:F:256:PHE:HZ	2.02	0.67
1:B:281:ASP:HB2	1:E:358:THR:HG22	0.67	0.67
1:D:213:ARG:HE	1:E:274:SER:C	2.03	0.67
1:D:375:GLU:OE2	1:E:231:LEU:HB3	1.95	0.67
1:E:114:ILE:HD12	1:F:252:TYR:HA	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:143:GLN:OE1	1:E:133:LYS:C	2.37	0.66
1:D:351:THR:CA	1:E:179:GLY:N	2.58	0.66
1:E:345:PHE:HE1	1:F:202:GLY:HA3	0.93	0.66
1:B:276:PHE:CE1	1:E:354:PRO:HB3	2.29	0.66
1:C:120:PRO:CG	1:D:267:ILE:CD1	2.69	0.66
1:C:371:VAL:HG21	1:D:167:TRP:CD2	2.30	0.66
1:B:273:PRO:CD	1:F:221:VAL:CG1	2.70	0.66
1:B:214:SER:CB	1:C:275:ASP:CA	2.70	0.66
1:B:276:PHE:CE1	1:E:354:PRO:CB	2.79	0.66
1:D:148:ASP:OD1	1:E:256:PHE:CZ	2.48	0.66
1:D:199:ILE:HD11	1:D:220:ILE:CD1	2.26	0.66
1:E:207:LYS:CE	1:F:273:PRO:CA	2.72	0.66
1:B:256:PHE:HZ	1:F:148:ASP:CG	2.03	0.66
1:B:349:GLN:HG2	1:C:182:PRO:HD3	1.77	0.66
1:B:184:ILE:HD11	1:F:46:VAL:HG21	1.76	0.66
1:D:221:VAL:CG2	1:E:273:PRO:HD2	2.16	0.66
1:B:182:PRO:HD3	1:F:349:GLN:HG2	1.78	0.65
1:B:204:MET:SD	1:F:345:PHE:CD1	2.90	0.65
1:B:121:LEU:HB2	1:C:276:PHE:HA	1.79	0.65
1:C:42:ARG:NH2	1:D:229:ASP:OD1	2.29	0.65
1:C:46:VAL:HG21	1:D:184:ILE:HD11	1.73	0.65
1:C:213:ARG:HG3	1:D:274:SER:OG	0.83	0.65
1:B:302:LEU:HD12	1:C:251:VAL:O	1.96	0.65
1:C:120:PRO:HG2	1:D:267:ILE:HD11	1.72	0.65
1:D:213:ARG:CB	1:E:271:VAL:HG12	2.16	0.65
1:B:286:GLN:OE1	1:F:140:ASP:OD1	2.13	0.65
1:C:347:ILE:CG2	1:D:182:PRO:HD2	2.25	0.65
1:D:351:THR:CA	1:E:178:LYS:HG2	2.27	0.65
1:B:274:SER:HB2	1:F:211:GLN:HA	1.79	0.65
1:C:359:TYR:O	1:E:282:SER:OG	2.15	0.65
1:B:273:PRO:CD	1:F:221:VAL:HG22	1.99	0.65
1:C:358:THR:HG23	1:E:282:SER:N	2.09	0.65
1:E:213:ARG:CZ	1:F:271:VAL:CG2	2.74	0.65
1:B:273:PRO:HD3	1:F:221:VAL:CG1	2.18	0.65
1:D:120:PRO:HG2	1:E:267:ILE:HD12	1.79	0.65
1:A:423:ARG:CZ	1:F:451:TRP:HE1	2.09	0.64
1:C:101:LEU:HD22	1:C:332:LEU:HD21	1.78	0.64
1:D:359:TYR:CD1	1:F:278:TYR:HE2	2.14	0.64
1:B:129:GLU:HG2	1:F:255:HIS:CE1	2.33	0.64
1:B:345:PHE:HZ	1:C:202:GLY:CA	2.02	0.64
1:E:222:SER:HB3	1:F:273:PRO:CD	2.23	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:213:ARG:CD	1:E:271:VAL:CB	2.53	0.64
1:E:142:ARG:O	1:F:286:GLN:NE2	2.29	0.64
1:E:345:PHE:HZ	1:F:203:ASN:H	1.46	0.64
1:B:345:PHE:CE1	1:C:201:PHE:O	2.51	0.64
1:B:131:PRO:HG3	1:F:144:ASN:O	1.98	0.64
1:C:140:ASP:CB	1:D:283:THR:HG23	2.25	0.64
1:D:46:VAL:CG1	1:E:184:ILE:HD13	2.20	0.64
1:E:351:THR:O	1:F:178:LYS:CG	2.45	0.63
1:E:483:THR:CB	1:F:23:GLN:HE22	2.07	0.63
1:B:214:SER:HA	1:C:275:ASP:N	2.13	0.63
1:C:359:TYR:CD1	1:E:278:TYR:CE2	2.82	0.63
1:D:351:THR:O	1:E:178:LYS:HE2	1.99	0.63
1:D:351:THR:HB	1:E:179:GLY:HA3	1.64	0.63
1:A:411:VAL:HG11	1:B:18:PRO:HB2	1.75	0.63
1:B:359:TYR:CD1	1:D:278:TYR:HE2	2.17	0.63
1:B:121:LEU:CG	1:C:276:PHE:HA	2.28	0.63
1:B:256:PHE:CE1	1:F:116:THR:HG21	2.33	0.63
1:B:184:ILE:HG12	1:F:46:VAL:HG11	1.78	0.63
1:B:345:PHE:CZ	1:C:202:GLY:HA2	2.32	0.63
1:C:359:TYR:HD1	1:E:278:TYR:HE2	1.45	0.63
1:A:414:PRO:HG3	1:B:397:THR:O	1.98	0.63
1:D:120:PRO:CG	1:E:267:ILE:CD1	2.76	0.63
1:E:42:ARG:NH2	1:F:229:ASP:OD2	2.28	0.63
1:B:121:LEU:HG	1:C:276:PHE:CE1	2.14	0.63
1:D:45:THR:HG22	1:D:64:VAL:HG21	1.79	0.63
1:D:104:LEU:HD12	1:D:155:PHE:CZ	2.33	0.63
1:B:278:TYR:HE2	1:E:359:TYR:CD1	2.16	0.62
1:C:83:ALA:CB	1:D:13:LEU:HD23	2.27	0.62
1:C:210:GLN:O	1:D:274:SER:HB3	1.98	0.62
1:D:155:PHE:CE1	1:D:334:VAL:HG13	2.33	0.62
1:D:363:ASN:ND2	1:D:364:PHE:CE2	2.67	0.62
1:C:470:ARG:HH21	1:D:321:GLY:HA2	1.63	0.62
1:D:144:ASN:HD22	1:E:290:ALA:CB	2.11	0.62
1:B:283:THR:CG2	1:F:139:LYS:C	2.73	0.62
1:B:290:ALA:HB1	1:F:144:ASN:HD22	1.65	0.62
1:C:213:ARG:HG3	1:D:274:SER:HB2	1.68	0.62
1:D:350:GLN:CD	1:E:211:GLN:HG3	2.24	0.62
1:C:210:GLN:O	1:D:274:SER:HA	1.99	0.62
1:D:302:LEU:HD21	1:E:250:GLN:OE1	2.00	0.62
1:C:213:ARG:HB3	1:D:271:VAL:HB	1.80	0.62
1:B:351:THR:HG23	1:C:179:GLY:HA2	1.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:122:PHE:HA	1:C:275:ASP:CB	2.31	0.61
1:B:202:GLY:HA2	1:F:345:PHE:CZ	2.34	0.61
1:C:350:GLN:HG3	1:D:211:GLN:HG3	1.82	0.61
1:B:46:VAL:HG21	1:C:184:ILE:CD1	2.28	0.61
1:B:371:VAL:HG21	1:C:167:TRP:CE2	2.35	0.61
1:B:280:PRO:HG3	1:F:121:LEU:HD11	1.82	0.61
1:C:213:ARG:CD	1:D:276:PHE:C	2.73	0.61
1:A:429:ALA:N	1:B:172:PRO:HA	2.15	0.61
1:B:148:ASP:OD1	1:C:256:PHE:HZ	1.81	0.61
1:D:222:SER:HA	1:E:273:PRO:HA	1.82	0.61
1:B:221:VAL:HB	1:C:274:SER:CB	2.31	0.61
1:C:109:GLY:O	1:D:227:TRP:CE3	2.50	0.61
1:C:213:ARG:H	1:D:274:SER:HB3	1.65	0.61
1:C:302:LEU:HD11	1:D:251:VAL:N	2.16	0.61
1:D:142:ARG:HH21	1:E:280:PRO:HG3	1.65	0.61
1:C:213:ARG:CB	1:D:271:VAL:CB	2.70	0.61
1:E:213:ARG:NE	1:F:271:VAL:CG2	2.64	0.61
1:B:209:LEU:HD13	1:F:347:ILE:CD1	2.30	0.61
1:B:345:PHE:CD1	1:C:201:PHE:O	2.53	0.61
1:C:120:PRO:HG3	1:D:292:SER:HB2	1.81	0.61
1:B:27:GLU:HG2	1:F:482:VAL:HG22	1.83	0.61
1:C:120:PRO:CG	1:D:267:ILE:HD11	2.30	0.61
1:B:121:LEU:CG	1:C:276:PHE:CE1	2.79	0.60
1:E:345:PHE:HZ	1:F:202:GLY:CA	2.08	0.60
1:D:148:ASP:CG	1:E:256:PHE:HZ	2.09	0.60
1:D:143:GLN:HE22	1:E:134:TYR:H	1.49	0.60
1:D:351:THR:HA	1:E:178:LYS:HG2	1.83	0.60
1:B:184:ILE:CD1	1:F:46:VAL:HG21	2.27	0.60
1:E:121:LEU:HD13	1:F:280:PRO:HG3	1.82	0.60
1:C:213:ARG:CG	1:D:274:SER:HG	0.86	0.60
1:E:143:GLN:OE1	1:F:133:LYS:C	2.45	0.60
1:B:119:HIS:CG	1:C:275:ASP:CB	2.84	0.60
1:C:121:LEU:HD13	1:D:278:TYR:HE1	1.67	0.60
1:A:411:VAL:CB	1:B:397:THR:HG21	2.30	0.60
1:D:358:THR:HG21	1:F:282:SER:OG	2.02	0.60
1:D:143:GLN:NE2	1:E:133:LYS:HA	2.16	0.60
1:E:222:SER:HB2	1:F:273:PRO:HD3	1.36	0.60
1:D:349:GLN:OE1	1:E:179:GLY:C	2.44	0.59
1:D:351:THR:O	1:E:178:LYS:CE	2.51	0.59
1:B:203:ASN:HD21	1:F:111:PRO:CD	2.00	0.59
1:B:280:PRO:CG	1:F:121:LEU:HD11	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:350:GLN:HG3	1:D:211:GLN:CG	2.32	0.59
1:D:371:VAL:HG21	1:E:167:TRP:CD2	2.37	0.59
1:B:121:LEU:HB2	1:C:275:ASP:O	2.02	0.59
1:C:213:ARG:HB3	1:D:271:VAL:HG12	1.65	0.59
1:E:347:ILE:HD12	1:F:181:CYS:SG	2.36	0.59
1:E:371:VAL:HG11	1:F:167:TRP:CD1	2.31	0.59
1:E:375:GLU:OE2	1:F:231:LEU:HD22	2.01	0.59
1:D:371:VAL:HG22	1:E:184:ILE:HD12	1.84	0.59
1:B:204:MET:HE1	1:F:347:ILE:HG12	1.84	0.59
1:B:27:GLU:HG2	1:F:482:VAL:CG2	2.32	0.59
1:B:256:PHE:HZ	1:F:148:ASP:OD1	1.82	0.59
1:B:283:THR:OG1	1:F:140:ASP:CG	2.46	0.59
1:D:358:THR:HG21	1:F:282:SER:CB	2.32	0.59
1:A:423:ARG:NE	1:F:43:LEU:HD22	2.18	0.59
1:B:148:ASP:CG	1:C:256:PHE:HZ	2.11	0.59
1:C:125:LEU:HD13	1:C:260:ASN:HD22	1.68	0.59
1:C:350:GLN:NE2	1:D:211:GLN:CD	2.47	0.59
1:B:182:PRO:HD3	1:F:349:GLN:CD	2.28	0.59
1:B:209:LEU:C	1:F:347:ILE:HG23	2.23	0.58
1:C:369:ARG:NH1	1:D:181:CYS:SG	2.76	0.58
1:C:222:SER:O	1:D:272:SER:HB2	2.00	0.58
1:E:371:VAL:HG13	1:F:167:TRP:HE1	1.66	0.58
1:E:213:ARG:NH2	1:F:271:VAL:HG22	2.18	0.58
1:C:213:ARG:CB	1:D:274:SER:HG	1.93	0.58
1:D:207:LYS:CA	1:E:273:PRO:O	2.51	0.58
1:A:428:SER:CA	1:B:173:CYS:HB2	2.32	0.58
1:B:81:LYS:HD2	1:C:10:LYS:HE3	1.85	0.58
1:C:210:GLN:O	1:D:274:SER:CB	2.51	0.58
1:C:470:ARG:NH2	1:D:321:GLY:HA2	2.18	0.58
1:E:148:ASP:CG	1:F:256:PHE:CZ	2.81	0.58
1:C:358:THR:CG2	1:E:282:SER:OG	2.52	0.58
1:A:423:ARG:HE	1:F:43:LEU:HD22	1.69	0.57
1:D:190:VAL:HG11	1:D:448:LEU:HD13	1.86	0.57
1:F:73:ARG:HH22	1:F:443:ASP:CG	2.12	0.57
1:B:371:VAL:HG21	1:C:167:TRP:CD2	2.38	0.57
1:D:359:TYR:CG	1:F:278:TYR:OH	2.56	0.57
1:E:144:ASN:HD22	1:F:290:ALA:CB	2.16	0.57
1:E:349:GLN:CG	1:F:180:ASP:O	2.50	0.57
1:E:345:PHE:CZ	1:F:202:GLY:C	2.79	0.57
1:A:431:ARG:CZ	1:B:185:GLN:CD	2.78	0.57
1:E:483:THR:HB	1:F:23:GLN:NE2	2.08	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:210:GLN:O	1:D:274:SER:CA	2.53	0.57
1:E:350:GLN:NE2	1:F:211:GLN:OE1	2.38	0.57
1:E:482:VAL:HG12	1:F:27:GLU:CD	2.29	0.57
1:B:290:ALA:CB	1:F:144:ASN:HD22	2.17	0.57
1:C:302:LEU:CD1	1:D:251:VAL:C	2.74	0.57
1:D:211:GLN:HA	1:E:274:SER:CB	2.32	0.57
1:D:373:GLN:NE2	1:E:231:LEU:HD12	2.16	0.57
1:B:209:LEU:HD13	1:F:347:ILE:HD11	1.87	0.57
1:B:214:SER:CB	1:C:275:ASP:CB	2.82	0.57
1:B:346:THR:HG21	1:C:259:ARG:HE	1.70	0.57
1:B:221:VAL:HG21	1:C:274:SER:C	2.30	0.56
1:B:140:ASP:OD2	1:C:280:PRO:CG	2.53	0.56
1:E:349:GLN:HG3	1:F:179:GLY:HA2	1.85	0.56
1:A:87:LYS:HB3	1:F:85:PRO:O	2.04	0.56
1:A:431:ARG:CZ	1:B:185:GLN:HE22	2.18	0.56
1:D:358:THR:HG21	1:F:282:SER:HB3	1.87	0.56
1:E:371:VAL:HG13	1:F:167:TRP:NE1	2.11	0.56
1:C:353:THR:HG22	1:C:355:ASN:H	1.71	0.56
1:A:431:ARG:CZ	1:B:185:GLN:NE2	2.68	0.56
1:C:282:SER:H	1:F:358:THR:CG2	2.18	0.56
1:D:46:VAL:CG2	1:E:184:ILE:HD11	2.36	0.56
1:B:254:ARG:NH1	1:C:129:GLU:OE2	2.38	0.56
1:C:211:GLN:C	1:D:274:SER:HB2	2.31	0.56
1:D:351:THR:HA	1:E:179:GLY:N	2.20	0.56
1:B:129:GLU:HG2	1:F:255:HIS:HE1	1.69	0.56
1:B:218:LEU:CA	1:C:274:SER:HB2	2.21	0.56
1:E:222:SER:C	1:F:273:PRO:HD3	2.29	0.56
1:A:409:GLY:HA3	1:B:17:THR:HG1	1.70	0.56
1:C:114:ILE:HD12	1:D:252:TYR:HA	1.87	0.56
1:C:128:THR:CG2	1:C:258:THR:HG23	2.35	0.56
1:D:222:SER:N	1:E:272:SER:OG	2.35	0.56
1:A:83:ALA:CB	1:F:87:LYS:HD2	2.35	0.55
1:B:167:TRP:CD2	1:F:371:VAL:HG21	2.41	0.55
1:B:211:GLN:CD	1:F:350:GLN:NE2	2.64	0.55
1:C:211:GLN:CA	1:D:274:SER:HB2	2.36	0.55
1:C:358:THR:HG21	1:E:282:SER:CA	2.35	0.55
1:A:87:LYS:CE	1:F:89:PHE:HB3	2.36	0.55
1:D:116:THR:HG21	1:E:256:PHE:HD1	1.71	0.55
1:B:120:PRO:HG2	1:C:267:ILE:HD11	1.88	0.55
1:B:211:GLN:CD	1:F:350:GLN:HE22	2.15	0.55
1:B:214:SER:HG	1:C:275:ASP:C	2.13	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:TRP:CE2	1:F:371:VAL:HG21	2.41	0.55
1:B:369:ARG:NH2	1:C:265:GLU:OE2	2.40	0.55
1:C:42:ARG:HH22	1:D:229:ASP:CG	2.14	0.55
1:A:84:LEU:O	1:F:87:LYS:HB3	2.07	0.55
1:B:359:TYR:HB3	1:C:140:ASP:OD2	2.07	0.55
1:C:358:THR:HG22	1:E:282:SER:CB	2.36	0.55
1:D:302:LEU:HD11	1:E:251:VAL:N	2.21	0.55
1:E:348:SER:OG	1:F:212:ASP:CG	2.50	0.55
1:A:409:GLY:CA	1:B:17:THR:CB	2.84	0.54
1:D:371:VAL:CG2	1:E:184:ILE:HD12	2.36	0.54
1:B:184:ILE:CD1	1:F:371:VAL:CG2	2.83	0.54
1:B:358:THR:CG2	1:D:282:SER:OG	2.51	0.54
1:C:358:THR:HG22	1:E:282:SER:OG	2.08	0.54
1:D:349:GLN:CD	1:E:179:GLY:CA	2.79	0.54
1:B:214:SER:HG	1:C:275:ASP:CA	2.18	0.54
1:C:213:ARG:CA	1:D:274:SER:HB3	2.38	0.54
1:D:85:PRO:HD3	1:E:15:PRO:HD3	1.88	0.54
1:D:109:GLY:O	1:E:227:TRP:CE3	2.54	0.54
1:E:74:LEU:HD13	1:E:378:LEU:HD11	1.88	0.54
1:A:85:PRO:O	1:F:88:ASP:OD2	2.26	0.54
1:D:387:LEU:HD13	1:D:408:LEU:CD2	2.37	0.54
1:E:101:LEU:HD21	1:E:104:LEU:HD23	1.89	0.54
1:B:44:LEU:HD21	1:C:186:LEU:HD22	1.90	0.54
1:A:451:TRP:CD1	1:F:423:ARG:HH22	2.25	0.54
1:B:347:ILE:HG21	1:C:182:PRO:HD2	1.88	0.54
1:C:213:ARG:NE	1:D:274:SER:OG	2.36	0.54
1:D:116:THR:CG2	1:E:256:PHE:HD1	2.21	0.54
1:B:121:LEU:HB2	1:C:276:PHE:CA	2.38	0.54
1:B:27:GLU:CG	1:F:482:VAL:HG22	2.38	0.54
1:B:267:ILE:HD11	1:F:120:PRO:HG2	1.87	0.54
1:B:351:THR:HA	1:C:178:LYS:HG2	1.89	0.54
1:E:144:ASN:HD22	1:F:290:ALA:HB1	1.71	0.54
1:A:87:LYS:CB	1:F:85:PRO:C	2.74	0.54
1:B:251:VAL:C	1:F:302:LEU:CD1	2.77	0.54
1:D:121:LEU:HD13	1:E:280:PRO:HG3	1.89	0.54
1:B:358:THR:CG2	1:D:282:SER:CA	2.68	0.53
1:C:371:VAL:HG22	1:D:184:ILE:HD12	1.90	0.53
1:D:248:ARG:HG2	1:D:309:LEU:HD11	1.91	0.53
1:A:429:ALA:CB	1:B:183:PRO:HB3	2.39	0.53
1:C:359:TYR:HB2	1:E:278:TYR:CE2	2.43	0.53
1:C:350:GLN:HG3	1:D:211:GLN:HB2	1.76	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:303:VAL:HG22	1:E:251:VAL:HG13	1.89	0.53
1:A:423:ARG:NH2	1:F:43:LEU:HA	2.23	0.53
1:B:286:GLN:HE22	1:F:142:ARG:C	2.14	0.53
1:E:345:PHE:CE1	1:F:203:ASN:N	2.76	0.53
1:D:349:GLN:CG	1:E:179:GLY:HA2	2.35	0.53
1:C:375:GLU:OE2	1:D:231:LEU:CB	2.52	0.53
1:C:375:GLU:OE2	1:D:231:LEU:CD2	2.53	0.53
1:C:267:ILE:HG22	1:C:273:PRO:HB3	1.87	0.53
1:C:282:SER:H	1:F:358:THR:HG23	1.74	0.53
1:A:428:SER:CB	1:B:173:CYS:HB2	2.38	0.53
1:B:182:PRO:HD3	1:F:349:GLN:HG3	1.89	0.53
1:D:128:THR:HG23	1:D:258:THR:HG23	1.91	0.53
1:D:302:LEU:CD1	1:E:251:VAL:N	2.72	0.53
1:F:198:ASP:HB3	1:F:203:ASN:HD21	1.74	0.53
1:E:207:LYS:CB	1:F:273:PRO:CG	2.55	0.53
1:B:119:HIS:ND1	1:C:275:ASP:HB2	2.17	0.53
1:B:212:ASP:CG	1:F:348:SER:OG	2.52	0.53
1:C:83:ALA:HB2	1:D:11:LEU:CG	2.39	0.53
1:D:222:SER:HA	1:E:273:PRO:CA	2.20	0.53
1:D:349:GLN:NE2	1:E:179:GLY:C	2.65	0.53
1:D:351:THR:CA	1:E:178:LYS:C	2.81	0.53
1:B:251:VAL:N	1:F:302:LEU:HD11	2.24	0.52
1:E:207:LYS:HE3	1:F:275:ASP:OD2	2.07	0.52
1:C:140:ASP:HB2	1:D:283:THR:HG23	1.91	0.52
1:D:371:VAL:HG22	1:E:184:ILE:CD1	2.40	0.52
1:B:352:ASN:C	1:C:178:LYS:CD	2.61	0.52
1:B:465:GLN:HE22	1:C:22:VAL:HB	1.74	0.52
1:A:429:ALA:N	1:B:173:CYS:H	2.05	0.52
1:D:207:LYS:CD	1:E:275:ASP:OD2	2.38	0.52
1:A:86:GLN:C	1:F:86:GLN:CG	2.75	0.52
1:B:121:LEU:CB	1:C:276:PHE:HA	2.39	0.52
1:A:431:ARG:NE	1:B:185:GLN:OE1	2.43	0.52
1:F:101:LEU:HD21	1:F:104:LEU:HD23	1.92	0.52
1:B:256:PHE:CE1	1:F:116:THR:CG2	2.93	0.52
1:C:170:ALA:HB2	1:C:185:GLN:HB2	1.91	0.52
1:C:465:GLN:NE2	1:D:22:VAL:H	2.06	0.52
1:F:190:VAL:HG11	1:F:448:LEU:HD13	1.92	0.52
1:A:429:ALA:CB	1:B:183:PRO:HG3	2.40	0.52
1:D:213:ARG:HG2	1:E:274:SER:H	1.73	0.52
1:D:359:TYR:CD1	1:F:278:TYR:CE2	2.96	0.52
1:E:345:PHE:HZ	1:F:202:GLY:HA2	1.67	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:VAL:CB	1:C:274:SER:CB	2.88	0.51
1:A:423:ARG:NH1	1:F:451:TRP:NE1	2.56	0.51
1:B:184:ILE:HD12	1:F:371:VAL:HG21	1.93	0.51
1:B:203:ASN:N	1:F:345:PHE:CE1	2.77	0.51
1:B:267:ILE:HD12	1:F:120:PRO:HG2	1.89	0.51
1:C:345:PHE:CD1	1:D:201:PHE:O	2.63	0.51
1:D:112:LEU:HD22	1:E:249:GLU:HG3	1.91	0.51
1:D:305:SER:HB2	1:E:249:GLU:H	1.75	0.51
1:D:349:GLN:NE2	1:E:179:GLY:CA	2.73	0.51
1:B:211:GLN:CG	1:F:350:GLN:NE2	2.70	0.51
1:B:218:LEU:HA	1:C:274:SER:CB	2.22	0.51
1:C:271:VAL:C	1:C:273:PRO:HD2	2.35	0.51
1:C:358:THR:HG21	1:E:282:SER:N	2.24	0.51
1:B:231:LEU:HB3	1:F:375:GLU:OE2	2.10	0.51
1:E:120:PRO:HG3	1:F:292:SER:HB3	1.92	0.51
1:E:350:GLN:CB	1:E:353:THR:HB	2.40	0.51
1:B:273:PRO:O	1:F:207:LYS:N	2.43	0.51
1:D:148:ASP:OD1	1:E:256:PHE:HZ	1.89	0.51
1:D:255:HIS:CE1	1:E:129:GLU:HG2	2.45	0.51
1:B:155:PHE:HE1	1:B:334:VAL:HG13	1.76	0.51
1:B:271:VAL:CB	1:F:213:ARG:CD	2.51	0.51
1:D:351:THR:H	1:E:179:GLY:HA2	1.75	0.51
1:E:120:PRO:HG2	1:F:267:ILE:HD11	1.89	0.51
1:C:213:ARG:CB	1:D:271:VAL:HB	2.40	0.51
1:C:213:ARG:HG2	1:D:274:SER:N	2.25	0.51
1:C:345:PHE:HZ	1:D:202:GLY:HA2	1.71	0.51
1:F:353:THR:CG2	1:F:363:ASN:CG	2.84	0.51
1:B:369:ARG:NH1	1:C:181:CYS:SG	2.84	0.51
1:E:348:SER:HG	1:F:212:ASP:CG	2.16	0.51
1:A:429:ALA:HB1	1:B:183:PRO:HG3	1.90	0.50
1:B:184:ILE:HD11	1:F:46:VAL:HG22	1.85	0.50
1:C:371:VAL:CG2	1:D:167:TRP:CE2	2.89	0.50
1:D:349:GLN:NE2	1:E:180:ASP:H	2.09	0.50
1:E:207:LYS:HD2	1:F:273:PRO:CA	2.41	0.50
1:D:211:GLN:CA	1:E:274:SER:HB2	2.39	0.50
1:E:207:LYS:CD	1:F:273:PRO:CA	2.89	0.50
1:B:282:SER:O	1:F:139:LYS:HD3	2.11	0.50
1:E:352:ASN:HA	1:F:178:LYS:HE2	1.92	0.50
1:B:131:PRO:HG2	1:F:143:GLN:HB3	1.94	0.50
1:C:369:ARG:NH2	1:D:265:GLU:OE2	2.40	0.50
1:D:302:LEU:CD1	1:E:251:VAL:C	2.79	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:350:GLN:CD	1:F:211:GLN:HB3	2.36	0.50
1:F:74:LEU:HD13	1:F:378:LEU:HD11	1.93	0.50
1:C:302:LEU:CD1	1:D:251:VAL:N	2.74	0.50
1:D:216:VAL:HB	1:D:220:ILE:HD11	1.94	0.50
1:B:349:GLN:NE2	1:C:181:CYS:C	2.70	0.50
1:A:87:LYS:HB2	1:F:86:GLN:OE1	2.12	0.50
1:C:207:LYS:O	1:D:275:ASP:OD2	2.30	0.50
1:B:274:SER:HB3	1:F:210:GLN:O	2.11	0.49
1:B:256:PHE:CD1	1:F:116:THR:CG2	2.87	0.49
1:B:346:THR:O	1:C:210:GLN:NE2	2.45	0.49
1:C:74:LEU:HD12	1:C:332:LEU:HD23	1.93	0.49
1:B:273:PRO:HD2	1:F:221:VAL:HG13	1.93	0.49
1:B:347:ILE:CG2	1:C:182:PRO:HD2	2.42	0.49
1:B:371:VAL:HG22	1:C:184:ILE:HD12	1.95	0.49
1:C:207:LYS:HA	1:D:273:PRO:C	2.38	0.49
1:E:121:LEU:HD13	1:F:280:PRO:HG2	1.93	0.49
1:E:346:THR:O	1:F:210:GLN:NE2	2.46	0.49
1:B:190:VAL:HG11	1:B:448:LEU:HD13	1.95	0.49
1:B:209:LEU:HD22	1:F:347:ILE:HD13	1.93	0.49
1:C:474:TYR:CE2	1:D:318:ARG:CD	2.95	0.49
1:D:74:LEU:HD13	1:D:378:LEU:HD11	1.95	0.49
1:E:111:PRO:CD	1:F:203:ASN:OD1	2.60	0.49
1:B:251:VAL:N	1:F:302:LEU:CD1	2.76	0.49
1:C:121:LEU:HD13	1:D:280:PRO:CG	2.38	0.49
1:E:140:ASP:HB3	1:F:283:THR:OG1	2.12	0.49
1:A:411:VAL:CG2	1:B:397:THR:HG22	2.30	0.49
1:B:74:LEU:HD13	1:B:378:LEU:HD11	1.94	0.49
1:D:267:ILE:HD12	1:D:289:LEU:HD23	1.95	0.49
1:E:350:GLN:O	1:F:179:GLY:HA2	2.13	0.49
1:C:83:ALA:HB2	1:D:11:LEU:HG	1.93	0.48
1:C:474:TYR:HE2	1:D:318:ARG:NE	2.08	0.48
1:B:282:SER:H	1:E:358:THR:HB	1.77	0.48
1:D:359:TYR:HB2	1:F:278:TYR:CE2	2.47	0.48
1:F:155:PHE:CE1	1:F:334:VAL:HG13	2.48	0.48
1:B:144:ASN:O	1:C:131:PRO:HG3	2.12	0.48
1:B:227:TRP:CE3	1:F:109:GLY:O	2.64	0.48
1:B:329:HIS:CE1	1:B:401:THR:HG23	2.48	0.48
1:B:371:VAL:HG22	1:C:184:ILE:CD1	2.44	0.48
1:D:148:ASP:CG	1:E:256:PHE:CZ	2.91	0.48
1:E:213:ARG:HB3	1:F:271:VAL:HG12	1.36	0.48
1:C:121:LEU:CD1	1:D:278:TYR:HE1	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:474:TYR:CE2	1:D:318:ARG:HD2	2.48	0.48
1:D:120:PRO:CG	1:E:267:ILE:HD11	2.42	0.48
1:E:222:SER:HB3	1:F:273:PRO:HD2	1.88	0.48
1:A:410:PHE:H	1:B:17:THR:N	2.11	0.48
1:D:213:ARG:CA	1:E:271:VAL:CG1	2.82	0.48
1:E:213:ARG:CZ	1:F:271:VAL:HG21	2.42	0.48
1:E:352:ASN:HA	1:F:178:LYS:CE	2.44	0.48
1:B:221:VAL:HG11	1:C:274:SER:CB	2.42	0.48
1:B:354:PRO:CD	1:C:178:LYS:NZ	2.76	0.48
1:C:213:ARG:CG	1:D:271:VAL:HB	2.43	0.48
1:D:303:VAL:CG2	1:E:251:VAL:CG1	2.92	0.48
1:B:119:HIS:CD2	1:C:275:ASP:CB	2.93	0.48
1:B:121:LEU:HB2	1:C:276:PHE:N	2.29	0.48
1:B:119:HIS:CD2	1:C:274:SER:HG	2.20	0.47
1:B:267:ILE:HD11	1:F:120:PRO:CG	2.44	0.47
1:D:169:VAL:HG22	1:D:209:LEU:HD12	1.96	0.47
1:B:213:ARG:HB3	1:C:277:TYR:CD2	2.32	0.47
1:A:83:ALA:HB1	1:F:87:LYS:HD2	1.96	0.47
1:C:350:GLN:HG2	1:D:211:GLN:CB	2.30	0.47
1:D:402:ILE:HG23	1:D:406:TRP:CZ2	2.49	0.47
1:F:45:THR:HG22	1:F:64:VAL:HG21	1.96	0.47
1:E:302:LEU:HD11	1:F:251:VAL:N	2.28	0.47
1:B:184:ILE:CG1	1:F:46:VAL:HG21	2.45	0.47
1:C:121:LEU:CD1	1:D:280:PRO:CG	2.92	0.47
1:D:303:VAL:HG22	1:E:251:VAL:CG1	2.44	0.47
1:B:140:ASP:OD1	1:C:286:GLN:OE1	2.33	0.47
1:B:214:SER:CA	1:C:275:ASP:CA	2.54	0.47
1:B:221:VAL:CB	1:C:274:SER:CA	2.88	0.47
1:E:140:ASP:OD1	1:F:286:GLN:OE1	2.32	0.47
1:E:143:GLN:CD	1:F:133:LYS:HA	2.40	0.47
1:A:423:ARG:NH1	1:F:451:TRP:CZ2	2.83	0.47
1:B:251:VAL:HG12	1:F:303:VAL:CG2	2.44	0.47
1:B:280:PRO:HG2	1:B:286:GLN:O	2.15	0.47
1:B:302:LEU:HD11	1:C:250:GLN:HB2	1.96	0.47
1:D:106:ILE:HD12	1:D:376:LEU:HD22	1.96	0.47
1:D:157:VAL:HG12	1:D:244:PHE:HB3	1.96	0.47
1:D:221:VAL:HG13	1:E:273:PRO:HD2	1.91	0.47
1:D:128:THR:CG2	1:D:258:THR:HG23	2.45	0.47
1:D:204:MET:HE3	1:D:209:LEU:HD23	1.97	0.47
1:B:251:VAL:CG1	1:F:303:VAL:HG22	2.45	0.47
1:B:273:PRO:O	1:F:207:LYS:C	2.58	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:VAL:HG22	1:B:209:LEU:HD23	1.97	0.47
1:B:274:SER:C	1:F:213:ARG:HE	2.22	0.47
1:B:283:THR:HG21	1:F:140:ASP:C	2.36	0.47
1:C:195:ASP:CG	1:C:226:LYS:HE3	2.39	0.47
1:B:281:ASP:CG	1:E:358:THR:CG2	2.78	0.46
1:B:354:PRO:HD3	1:C:178:LYS:NZ	2.30	0.46
1:B:74:LEU:HD23	1:B:453:VAL:HB	1.98	0.46
1:B:267:ILE:CD1	1:F:120:PRO:CG	2.84	0.46
1:D:125:LEU:HB3	1:D:258:THR:OG1	2.16	0.46
1:D:351:THR:CG2	1:E:179:GLY:HA3	2.20	0.46
1:F:104:LEU:HD13	1:F:155:PHE:CE2	2.50	0.46
1:C:305:SER:HB2	1:D:249:GLU:H	1.81	0.46
1:C:474:TYR:CE2	1:D:318:ARG:NE	2.81	0.46
1:A:87:LYS:HE2	1:F:89:PHE:HD2	1.80	0.46
1:A:431:ARG:NH2	1:B:185:GLN:HE22	2.13	0.46
1:B:119:HIS:HD1	1:B:121:LEU:H	1.62	0.46
1:B:209:LEU:HD13	1:F:347:ILE:HD13	1.96	0.46
1:B:256:PHE:HE2	1:F:254:ARG:NH2	2.10	0.46
1:C:46:VAL:HG13	1:D:184:ILE:HD13	1.72	0.46
1:D:125:LEU:HD13	1:D:260:ASN:HD22	1.79	0.46
1:B:181:CYS:CA	1:F:349:GLN:CD	2.89	0.46
1:B:251:VAL:HG13	1:F:303:VAL:HG22	1.97	0.46
1:B:27:GLU:CB	1:F:482:VAL:HG13	2.46	0.46
1:B:184:ILE:HG13	1:F:46:VAL:HG21	1.96	0.46
1:E:221:VAL:CG1	1:F:272:SER:OG	2.64	0.46
1:A:451:TRP:NE1	1:F:423:ARG:HH22	2.11	0.46
1:D:83:ALA:O	1:E:14:PRO:C	2.58	0.46
1:D:125:LEU:CD2	1:D:291:PRO:HG2	2.46	0.46
1:B:274:SER:N	1:F:213:ARG:HG2	2.30	0.46
1:C:111:PRO:HB3	1:D:227:TRP:CD1	2.50	0.46
1:B:148:ASP:CG	1:C:256:PHE:CZ	2.92	0.45
1:B:227:TRP:HZ3	1:F:109:GLY:O	1.85	0.45
1:B:283:THR:CG2	1:F:140:ASP:CA	2.58	0.45
1:D:303:VAL:CG2	1:E:251:VAL:HG12	2.47	0.45
1:E:121:LEU:CD1	1:F:280:PRO:CG	2.91	0.45
1:B:104:LEU:C	1:B:104:LEU:HD12	2.41	0.45
1:C:83:ALA:HB2	1:D:11:LEU:HD11	1.98	0.45
1:C:361:SER:CB	1:D:260:ASN:OD1	2.63	0.45
1:C:371:VAL:HG22	1:D:184:ILE:CD1	2.45	0.45
1:D:213:ARG:CG	1:E:271:VAL:HG12	2.44	0.45
1:E:369:ARG:NH1	1:F:181:CYS:SG	2.90	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:ASN:N	1:F:345:PHE:CZ	2.84	0.45
1:B:211:GLN:CB	1:F:350:GLN:HB3	2.46	0.45
1:B:256:PHE:CE1	1:F:148:ASP:CG	2.94	0.45
1:C:349:GLN:HG2	1:D:179:GLY:HA2	1.37	0.45
1:A:427:SER:C	1:B:173:CYS:HG	2.17	0.45
1:C:213:ARG:CA	1:D:271:VAL:CG1	2.79	0.45
1:C:364:PHE:CG	1:D:212:ASP:OD1	2.70	0.45
1:B:211:GLN:OE1	1:F:350:GLN:NE2	2.50	0.45
1:D:342:ASN:HA	1:D:370:HIS:HE2	1.82	0.45
1:A:83:ALA:HB3	1:F:87:LYS:HD2	1.99	0.45
1:B:120:PRO:HG2	1:C:267:ILE:HD12	1.91	0.45
1:B:345:PHE:HZ	1:C:202:GLY:HA2	1.77	0.45
1:D:116:THR:CG2	1:E:256:PHE:CD1	2.99	0.45
1:A:170:ALA:HB2	1:A:185:GLN:HB2	1.98	0.45
1:B:283:THR:OG1	1:F:140:ASP:OD2	2.33	0.45
1:C:128:THR:HG21	1:C:258:THR:HG23	1.97	0.45
1:D:85:PRO:HD3	1:D:461:GLN:HE22	1.82	0.45
1:D:213:ARG:NH1	1:E:276:PHE:CD2	2.84	0.45
1:D:412:PRO:HG2	1:D:415:GLN:HG2	1.98	0.45
1:E:392:LEU:HD11	1:E:408:LEU:HD21	1.98	0.45
1:D:210:GLN:O	1:E:274:SER:HB3	2.17	0.45
1:E:121:LEU:CD1	1:F:280:PRO:HG2	2.47	0.45
1:B:283:THR:HG22	1:F:139:LYS:C	2.38	0.45
1:C:302:LEU:O	1:D:252:TYR:OH	2.20	0.45
1:B:283:THR:CG2	1:F:140:ASP:N	2.80	0.45
1:C:216:VAL:HB	1:C:220:ILE:HD11	1.99	0.45
1:D:213:ARG:NE	1:E:274:SER:C	2.74	0.45
1:C:19:VAL:HG23	1:C:20:ALA:H	1.82	0.44
1:D:387:LEU:HD13	1:D:408:LEU:HD22	1.98	0.44
1:E:190:VAL:HG11	1:E:448:LEU:HD13	1.98	0.44
1:C:143:GLN:HE22	1:D:132:ASN:CA	2.29	0.44
1:C:207:LYS:HA	1:D:273:PRO:O	2.16	0.44
1:B:254:ARG:NH2	1:C:253:ALA:O	2.50	0.44
1:D:144:ASN:O	1:E:131:PRO:HG3	2.16	0.44
1:A:438:PRO:HB2	1:A:442:GLU:HG3	2.00	0.44
1:D:143:GLN:CD	1:E:134:TYR:N	2.76	0.44
1:E:207:LYS:HD2	1:F:273:PRO:HA	2.00	0.44
1:B:271:VAL:CG1	1:F:213:ARG:CD	2.93	0.44
1:B:283:THR:HG21	1:F:140:ASP:N	2.28	0.44
1:D:351:THR:N	1:E:179:GLY:HA2	2.32	0.44
1:B:119:HIS:CD2	1:C:275:ASP:CG	2.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:VAL:CB	1:C:274:SER:OG	2.65	0.44
1:B:250:GLN:HB2	1:F:302:LEU:HD11	1.99	0.44
1:B:283:THR:HG21	1:F:139:LYS:O	2.17	0.44
1:D:115:GLY:H	1:D:342:ASN:ND2	2.16	0.44
1:F:84:LEU:HD21	1:F:382:LEU:HD22	1.98	0.44
1:F:353:THR:HG22	1:F:363:ASN:OD1	2.18	0.44
1:D:84:LEU:HD22	1:D:89:PHE:CE1	2.53	0.44
1:D:143:GLN:HE22	1:E:134:TYR:N	2.14	0.44
1:D:149:PRO:HG2	1:D:339:ASN:HD21	1.82	0.44
1:D:349:GLN:HE22	1:E:180:ASP:N	2.09	0.44
1:B:74:LEU:HD12	1:B:332:LEU:HD23	1.99	0.44
1:B:122:PHE:CG	1:C:275:ASP:OD2	2.71	0.44
1:E:82:PHE:CE2	1:F:14:PRO:HG3	2.52	0.44
1:C:371:VAL:CG2	1:D:184:ILE:HD12	2.49	0.43
1:D:345:PHE:HE1	1:E:209:LEU:HD23	1.74	0.43
1:D:354:PRO:O	1:D:355:ASN:CB	2.66	0.43
1:F:170:ALA:HB2	1:F:185:GLN:HB2	2.00	0.43
1:E:120:PRO:CG	1:F:267:ILE:HD11	2.48	0.43
1:B:286:GLN:OE1	1:F:140:ASP:O	2.36	0.43
1:E:303:VAL:O	1:F:250:GLN:HA	2.18	0.43
1:C:207:LYS:CA	1:D:273:PRO:O	2.66	0.43
1:D:349:GLN:HE22	1:E:180:ASP:H	1.67	0.43
1:A:429:ALA:CB	1:B:183:PRO:CG	2.91	0.43
1:B:359:TYR:O	1:D:282:SER:OG	2.33	0.43
1:D:218:LEU:HD11	1:E:267:ILE:CD1	2.49	0.43
1:B:286:GLN:HE22	1:F:142:ARG:N	2.17	0.43
1:B:351:THR:HG22	1:C:178:LYS:C	2.44	0.43
1:C:359:TYR:HB3	1:D:140:ASP:OD2	2.19	0.43
1:D:211:GLN:OE1	1:E:276:PHE:CD2	2.57	0.43
1:D:363:ASN:C	1:D:363:ASN:OD1	2.61	0.43
1:D:157:VAL:CG1	1:D:244:PHE:HB3	2.49	0.43
1:E:140:ASP:OD2	1:F:280:PRO:HB3	2.19	0.42
1:F:206:PHE:CE1	1:F:216:VAL:HG11	2.54	0.42
1:B:114:ILE:HD12	1:C:252:TYR:HA	2.01	0.42
1:B:273:PRO:HD2	1:F:221:VAL:CG2	2.35	0.42
1:D:351:THR:CA	1:E:179:GLY:HA2	2.43	0.42
1:C:303:VAL:O	1:D:250:GLN:HA	2.19	0.42
1:B:46:VAL:HG13	1:C:184:ILE:HD13	1.78	0.42
1:C:109:GLY:C	1:D:227:TRP:CZ3	2.80	0.42
1:D:170:ALA:HB2	1:D:185:GLN:HB2	2.01	0.42
1:E:143:GLN:OE1	1:F:134:TYR:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:353:THR:HG22	1:F:363:ASN:CG	2.45	0.42
1:B:282:SER:N	1:E:358:THR:HB	2.35	0.42
1:A:387:LEU:HD13	1:A:408:LEU:HD22	2.00	0.42
1:B:140:ASP:OD2	1:C:280:PRO:HG3	2.20	0.42
1:C:155:PHE:CZ	1:C:246:GLY:HA3	2.53	0.42
1:B:140:ASP:CG	1:C:286:GLN:OE1	2.63	0.42
1:C:273:PRO:HG2	1:C:277:TYR:HA	2.00	0.42
1:E:42:ARG:HH22	1:F:229:ASP:CG	2.24	0.42
1:B:120:PRO:CG	1:C:267:ILE:HD11	2.50	0.42
1:B:351:THR:HG22	1:C:178:LYS:O	2.20	0.42
1:C:74:LEU:HD23	1:C:453:VAL:HB	2.01	0.42
1:C:84:LEU:HD22	1:C:89:PHE:CE1	2.55	0.42
1:C:213:ARG:CA	1:D:274:SER:CB	2.96	0.42
1:D:122:PHE:HE1	1:D:295:PHE:CZ	2.37	0.42
1:D:243:PHE:HB2	1:D:319:ALA:HB1	2.02	0.42
1:B:143:GLN:HB3	1:C:131:PRO:HG2	2.01	0.42
1:B:289:LEU:HD22	1:F:120:PRO:HB2	2.02	0.42
1:B:293:VAL:HG13	1:F:368:LEU:HG	2.01	0.42
1:C:347:ILE:CG2	1:D:182:PRO:CD	2.96	0.42
1:D:128:THR:CG2	1:D:258:THR:CG2	2.98	0.42
1:D:143:GLN:OE1	1:E:134:TYR:CA	2.68	0.42
1:D:349:GLN:CG	1:E:179:GLY:CA	2.98	0.42
1:D:402:ILE:HG23	1:D:406:TRP:CH2	2.55	0.42
1:B:251:VAL:CG1	1:F:303:VAL:CG2	2.98	0.41
1:D:366:ASN:ND2	1:E:260:ASN:O	2.50	0.41
1:E:42:ARG:HH12	1:F:188:ASN:HD21	1.68	0.41
1:E:74:LEU:HD12	1:E:332:LEU:HD23	2.02	0.41
1:E:478:ILE:O	1:E:478:ILE:HG22	2.20	0.41
1:B:121:LEU:HD13	1:C:280:PRO:HD3	2.02	0.41
1:B:273:PRO:HB3	1:F:206:PHE:HB3	2.01	0.41
1:C:121:LEU:HD13	1:D:278:TYR:CE1	2.51	0.41
1:C:211:GLN:HA	1:D:274:SER:CB	2.48	0.41
1:D:213:ARG:CD	1:E:271:VAL:CG1	2.97	0.41
1:E:83:ALA:O	1:F:14:PRO:HD2	2.20	0.41
1:E:207:LYS:CG	1:F:273:PRO:HG2	1.93	0.41
1:B:347:ILE:HD13	1:C:204:MET:HE1	2.01	0.41
1:C:108:ARG:HH21	1:C:338:ASP:HB3	1.86	0.41
1:C:143:GLN:NE2	1:D:133:LYS:N	2.67	0.41
1:C:211:GLN:O	1:D:274:SER:HB2	2.21	0.41
1:E:104:LEU:C	1:E:104:LEU:HD12	2.45	0.41
1:E:255:HIS:HE1	1:F:129:GLU:HG2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:150:LYS:HE2	1:F:249:GLU:HB2	2.02	0.41
1:A:414:PRO:CG	1:B:397:THR:O	2.64	0.41
1:B:267:ILE:HD13	1:F:120:PRO:HG2	1.97	0.41
1:D:70:ARG:HA	1:D:70:ARG:HD3	1.90	0.41
1:E:350:GLN:HB2	1:E:353:THR:HB	2.02	0.41
1:B:212:ASP:CG	1:F:348:SER:HG	2.26	0.41
1:B:292:SER:HB2	1:F:120:PRO:HG3	2.03	0.41
1:C:272:SER:N	1:C:273:PRO:HD2	2.35	0.41
1:F:75:LYS:NZ	1:F:331:GLU:OE2	2.54	0.41
1:B:221:VAL:CG1	1:C:274:SER:CB	2.99	0.41
1:D:254:ARG:HH12	1:E:256:PHE:HE2	1.58	0.41
1:E:255:HIS:CE1	1:F:129:GLU:HG2	2.55	0.41
1:B:27:GLU:HG2	1:F:482:VAL:CB	2.50	0.41
1:B:102:ARG:HD3	1:B:381:GLN:HE21	1.86	0.41
1:B:359:TYR:CD1	1:D:278:TYR:CE2	3.02	0.41
1:B:371:VAL:CG2	1:C:184:ILE:HD12	2.50	0.41
1:C:364:PHE:HB3	1:D:212:ASP:OD1	2.20	0.41
1:D:169:VAL:CG2	1:D:209:LEU:HD12	2.50	0.41
1:E:302:LEU:CD1	1:F:251:VAL:N	2.84	0.41
1:C:213:ARG:O	1:D:271:VAL:HG13	2.16	0.41
1:D:302:LEU:HA	1:E:251:VAL:O	2.21	0.41
1:A:451:TRP:NE1	1:F:423:ARG:NH2	2.60	0.41
1:B:46:VAL:HG13	1:B:371:VAL:HG22	2.03	0.41
1:B:221:VAL:CG2	1:C:274:SER:OG	2.69	0.41
1:B:271:VAL:HB	1:F:213:ARG:HD3	0.70	0.41
1:B:465:GLN:HE22	1:C:22:VAL:N	2.19	0.41
1:C:358:THR:HG22	1:E:282:SER:HB3	1.90	0.41
1:D:155:PHE:CD1	1:D:155:PHE:C	2.96	0.41
1:B:352:ASN:CA	1:C:178:LYS:HD3	2.49	0.41
1:C:190:VAL:HG11	1:C:448:LEU:HD13	2.02	0.41
1:E:345:PHE:HZ	1:F:203:ASN:N	2.07	0.41
1:A:411:VAL:HB	1:B:397:THR:HG21	2.00	0.40
1:B:162:PRO:HG2	1:B:191:ILE:HB	2.02	0.40
1:C:83:ALA:HB2	1:D:11:LEU:CD1	2.51	0.40
1:F:104:LEU:HD13	1:F:155:PHE:CZ	2.56	0.40
1:B:205:ASN:ND2	1:B:224:ARG:HE	2.18	0.40
1:C:267:ILE:HD11	1:C:292:SER:HB2	2.03	0.40
1:D:233:MET:HB3	1:D:242:MET:HE2	2.02	0.40
1:D:353:THR:O	1:D:356:PRO:HD2	2.21	0.40
1:A:423:ARG:HH22	1:F:43:LEU:HB3	0.49	0.40
1:B:119:HIS:ND1	1:C:276:PHE:N	2.49	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:182:PRO:HD3	1:F:349:GLN:NE2	2.36	0.40
1:C:213:ARG:HG2	1:D:274:SER:H	1.87	0.40
1:C:367:TYR:CE2	1:D:264:GLY:HA3	2.57	0.40
1:D:104:LEU:HD12	1:D:155:PHE:HE2	1.84	0.40
1:D:349:GLN:HB3	1:E:179:GLY:O	2.21	0.40
1:D:403:LEU:CD2	1:D:408:LEU:HD23	2.52	0.40
1:F:54:ILE:HG22	1:F:59:VAL:HA	2.03	0.40
1:B:202:GLY:CA	1:F:345:PHE:HZ	2.24	0.40
1:B:275:ASP:OD2	1:F:208:GLU:OE2	2.38	0.40
1:C:277:TYR:CD1	1:C:277:TYR:C	3.00	0.40
1:D:213:ARG:HA	1:E:273:PRO:HB2	2.03	0.40
1:D:387:LEU:CD1	1:D:408:LEU:HD22	2.52	0.40
1:F:74:LEU:HD12	1:F:332:LEU:HD23	2.03	0.40
1:F:422:TYR:HB2	1:F:425:ILE:CG2	2.51	0.40
1:C:114:ILE:CD1	1:D:252:TYR:HA	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	471/509 (92%)	426 (90%)	40 (8%)	5 (1%)	11	39
1	B	464/509 (91%)	419 (90%)	35 (8%)	10 (2%)	5	26
1	C	480/509 (94%)	431 (90%)	38 (8%)	11 (2%)	5	25
1	D	480/509 (94%)	435 (91%)	37 (8%)	8 (2%)	7	30
1	E	479/509 (94%)	441 (92%)	34 (7%)	4 (1%)	16	45
1	F	481/509 (94%)	438 (91%)	32 (7%)	11 (2%)	5	25
All	All	2855/3054 (94%)	2590 (91%)	216 (8%)	49 (2%)	9	30

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	57	ASP
1	B	435	GLN
1	B	478	ILE
1	C	353	THR
1	C	433	PRO
1	D	57	ASP
1	D	355	ASN
1	F	42	ARG
1	F	57	ASP
1	F	355	ASN
1	F	407	ASN
1	A	42	ARG
1	A	271	VAL
1	B	42	ARG
1	B	301	SER
1	B	408	LEU
1	C	407	ASN
1	C	415	GLN
1	C	422	TYR
1	D	407	ASN
1	E	42	ARG
1	E	55	ASP
1	E	415	GLN
1	A	426	THR
1	C	431	ARG
1	C	480	THR
1	D	14	PRO
1	F	14	PRO
1	F	56	ASN
1	F	301	SER
1	F	413	PRO
1	F	433	PRO
1	C	42	ARG
1	C	301	SER
1	D	135	GLN
1	D	301	SER
1	E	442	GLU
1	A	301	SER
1	B	18	PRO
1	C	14	PRO
1	D	414	PRO
1	F	408	LEU
1	F	440	GLU

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Mol	Chain	Res	Type
1	B	354	PRO
1	B	433	PRO
1	C	423	ARG
1	B	355	ASN
1	D	356	PRO
1	A	438	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	423/452 (94%)	420 (99%)	3 (1%)	76	80
1	B	417/452 (92%)	413 (99%)	4 (1%)	68	76
1	C	431/452 (95%)	425 (99%)	6 (1%)	59	73
1	D	431/452 (95%)	425 (99%)	6 (1%)	59	73
1	E	431/452 (95%)	427 (99%)	4 (1%)	70	78
1	F	432/452 (96%)	426 (99%)	6 (1%)	59	73
All	All	2565/2712 (95%)	2536 (99%)	29 (1%)	63	76

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	PHE
1	A	148	ASP
1	A	221	VAL
1	B	154	LEU
1	B	198	ASP
1	B	236	GLU
1	B	401	THR
1	C	141	ASN
1	C	180	ASP
1	C	297	THR
1	C	306	ASP
1	C	403	LEU

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Mol	Chain	Res	Type
1	C	462	ASP
1	D	90	TYR
1	D	104	LEU
1	D	209	LEU
1	D	305	SER
1	D	343	THR
1	D	358	THR
1	E	198	ASP
1	E	209	LEU
1	E	216	VAL
1	E	236	GLU
1	F	148	ASP
1	F	198	ASP
1	F	369	ARG
1	F	407	ASN
1	F	427	SER
1	F	443	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	166	HIS
1	A	185	GLN
1	A	344	ASN
1	A	363	ASN
1	A	405	ASN
1	A	475	GLN
1	B	23	GLN
1	B	144	ASN
1	B	166	HIS
1	B	188	ASN
1	B	203	ASN
1	B	205	ASN
1	B	255	HIS
1	B	260	ASN
1	B	286	GLN
1	B	373	GLN
1	B	381	GLN
1	B	405	ASN
1	B	465	GLN
1	C	37	HIS

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Mol	Chain	Res	Type
1	C	39	HIS
1	C	67	ASN
1	C	143	GLN
1	C	144	ASN
1	C	166	HIS
1	C	185	GLN
1	C	211	GLN
1	C	255	HIS
1	C	286	GLN
1	C	308	GLN
1	C	339	ASN
1	C	344	ASN
1	C	350	GLN
1	C	352	ASN
1	C	373	GLN
1	C	465	GLN
1	D	166	HIS
1	D	211	GLN
1	D	255	HIS
1	D	284	GLN
1	D	308	GLN
1	D	320	GLN
1	D	373	GLN
1	D	461	GLN
1	D	465	GLN
1	E	67	ASN
1	E	144	ASN
1	E	166	HIS
1	E	210	GLN
1	E	255	HIS
1	E	308	GLN
1	E	330	ASN
1	E	339	ASN
1	E	373	GLN
1	E	461	GLN
1	E	465	GLN
1	F	23	GLN
1	F	37	HIS
1	F	144	ASN
1	F	188	ASN
1	F	210	GLN
1	F	255	HIS

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Mol	Chain	Res	Type
1	F	260	ASN
1	F	286	GLN
1	F	308	GLN
1	F	329	HIS
1	F	373	GLN
1	F	465	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

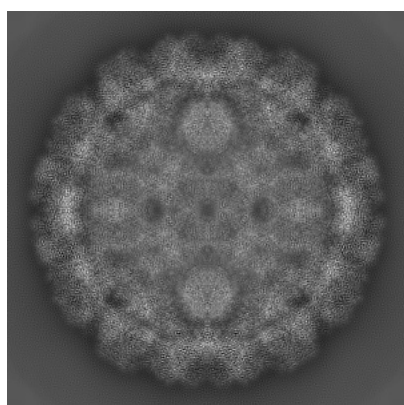
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24741. These allow visual inspection of the internal detail of the map and identification of artifacts.

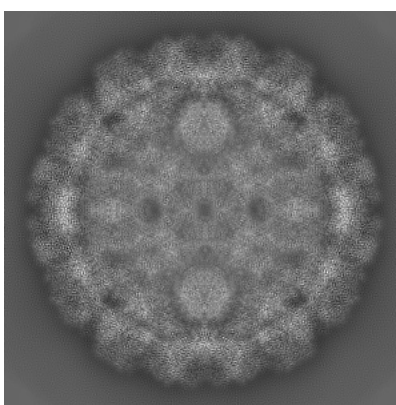
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

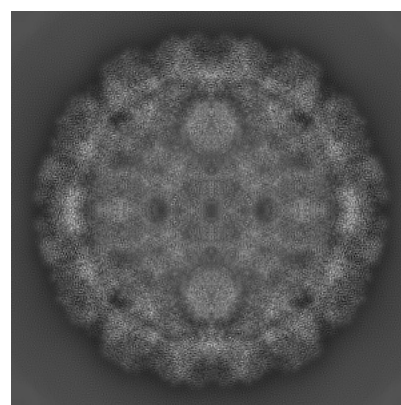
6.1.1 Primary map



X



Y

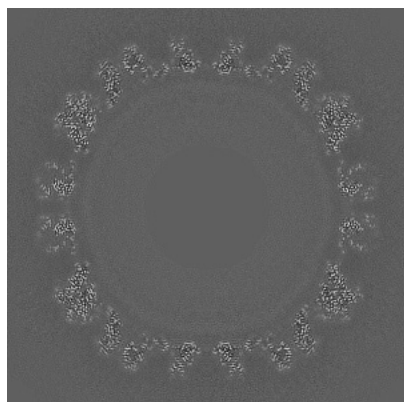


Z

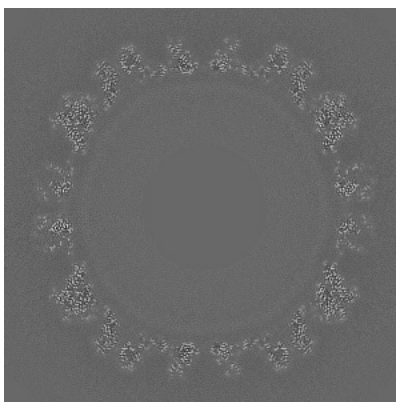
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

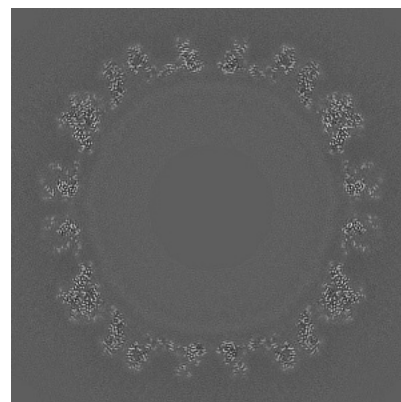
6.2.1 Primary map



X Index: 300



Y Index: 300

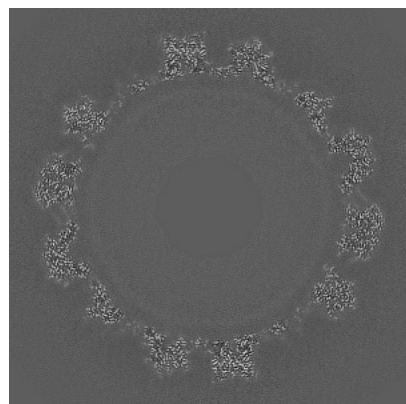


Z Index: 300

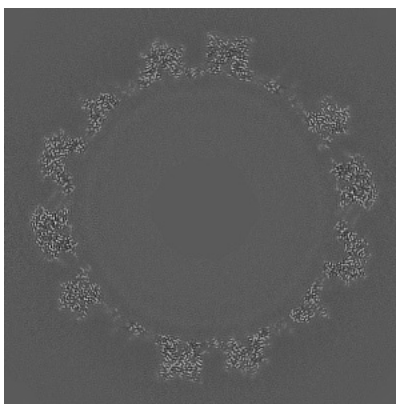
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

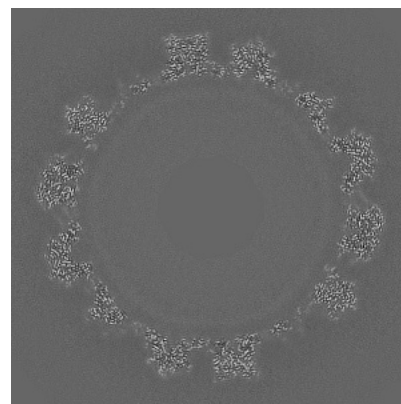
6.3.1 Primary map



X Index: 249



Y Index: 351

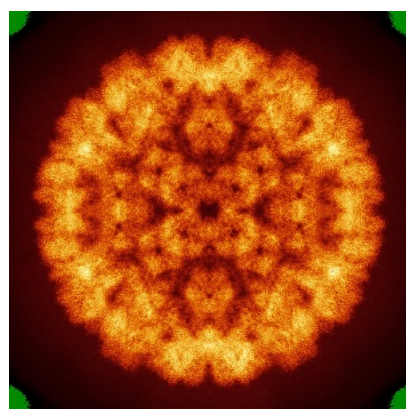


Z Index: 249

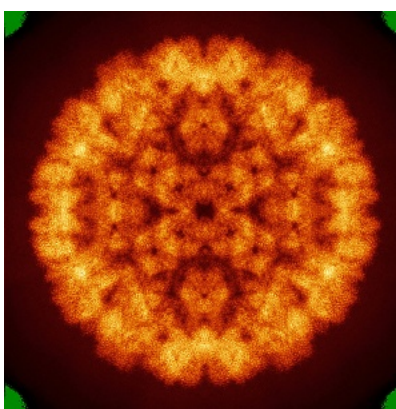
The images above show the largest variance slices of the map in three orthogonal directions.

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

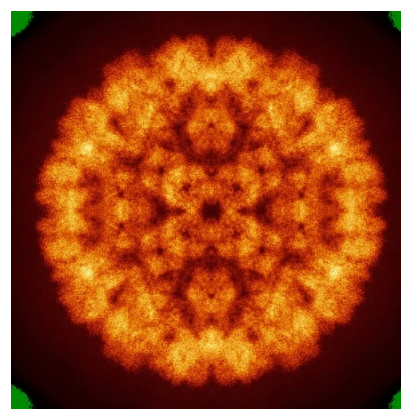
6.4.1 Primary map



X



Y

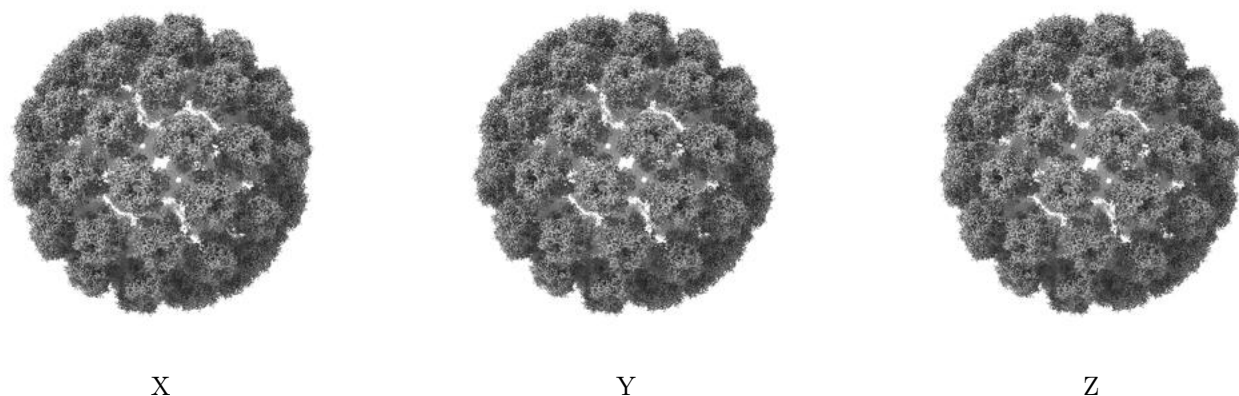


Z

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



The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

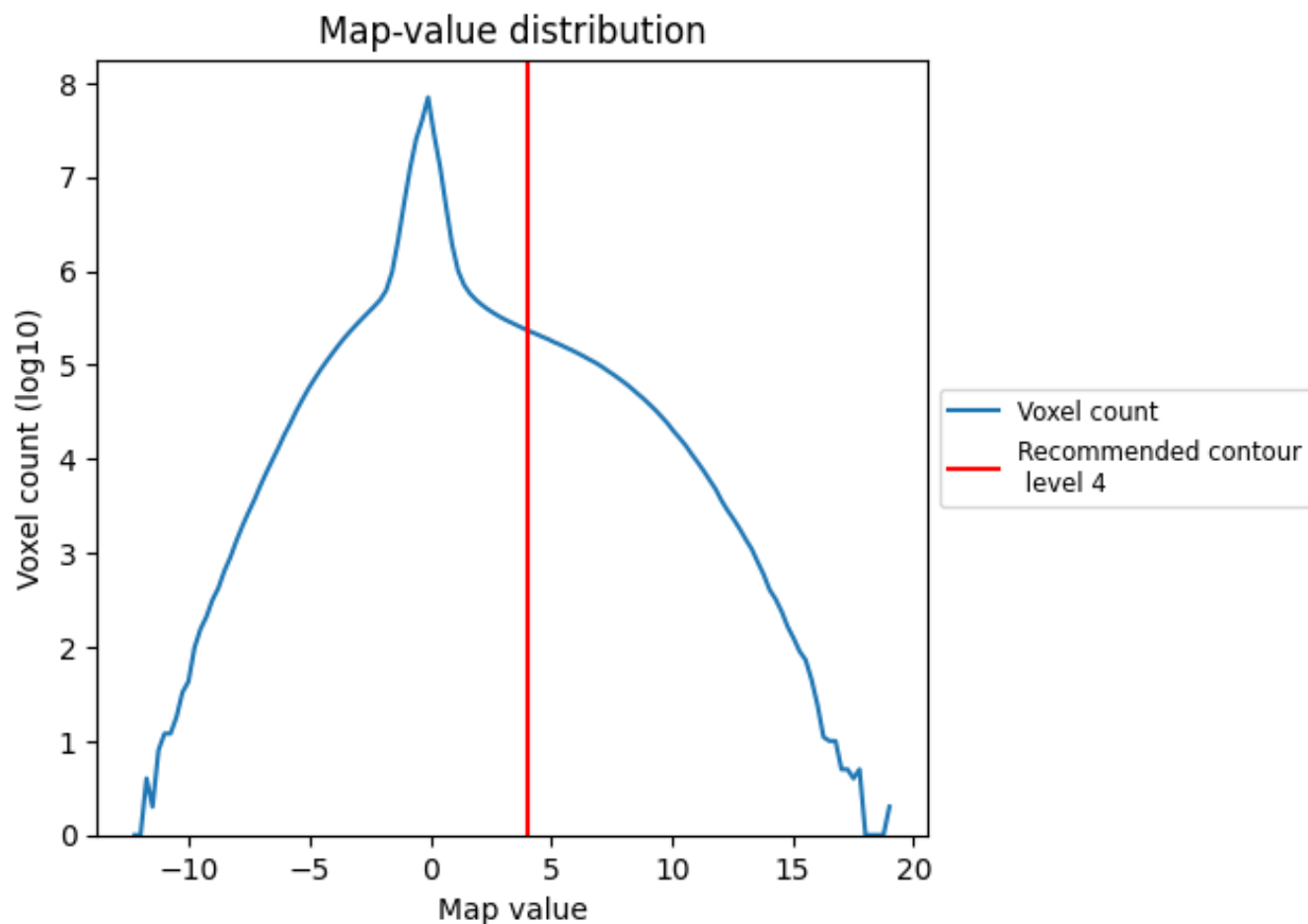
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

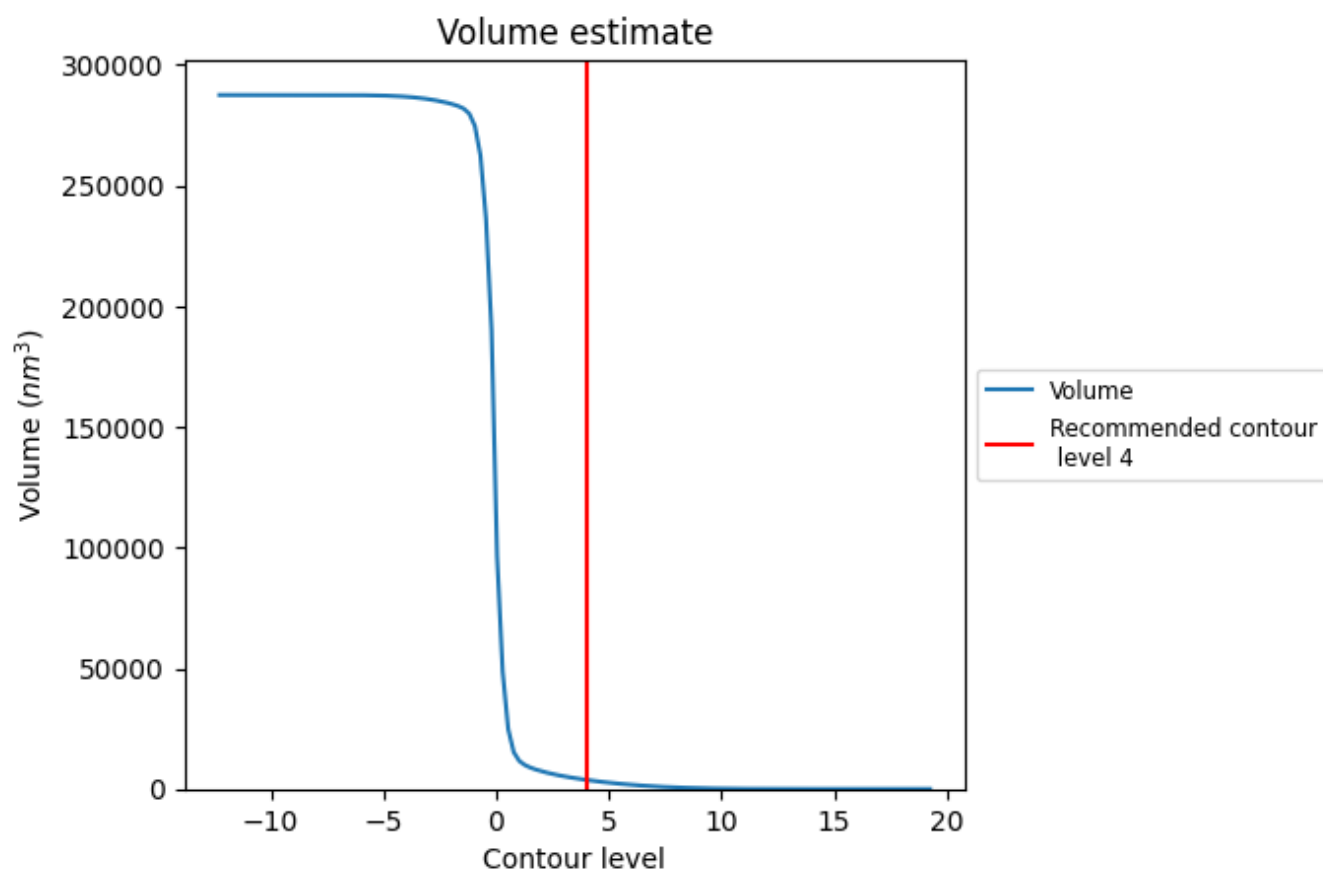
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

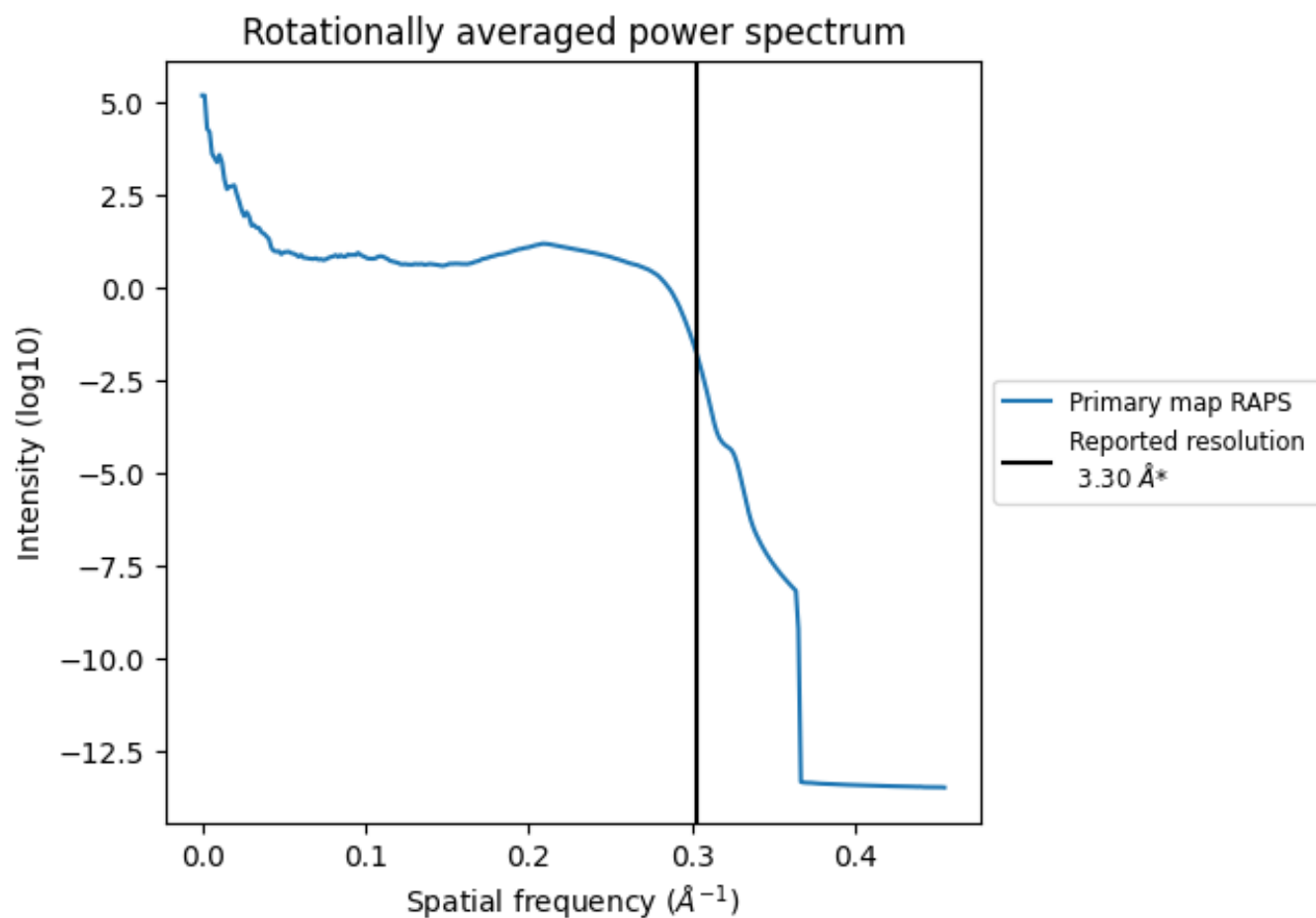
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3759 nm³; this corresponds to an approximate mass of 3396 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation ⓘ

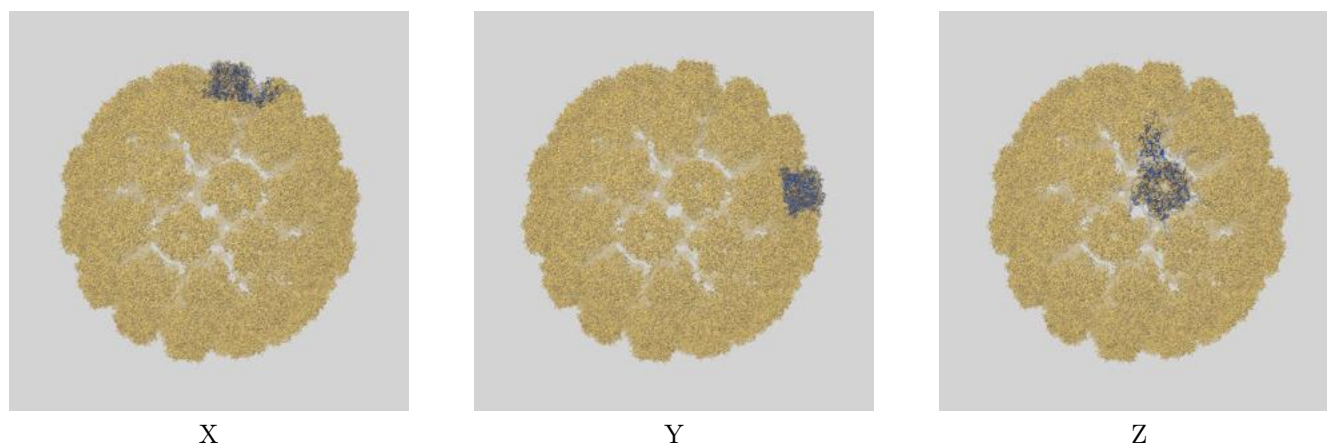
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

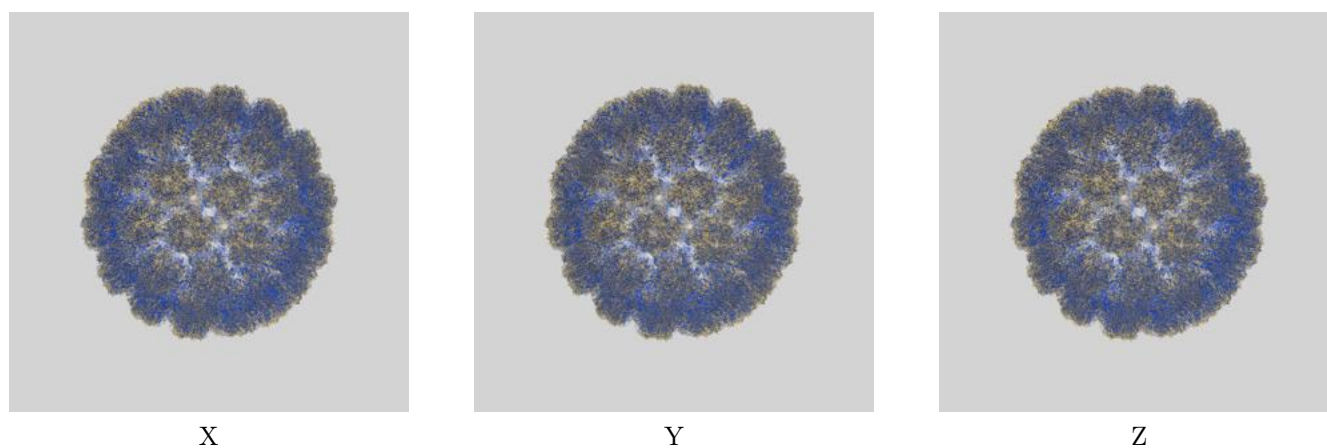
This section contains information regarding the fit between EMDB map EMD-24741 and PDB model 7RYJ. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

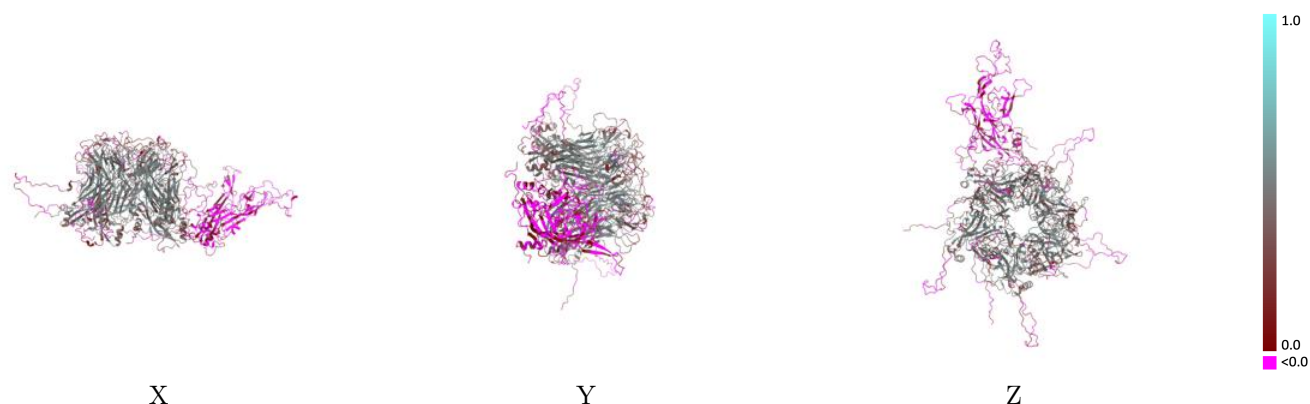


9.1.2 Map-model assembly overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



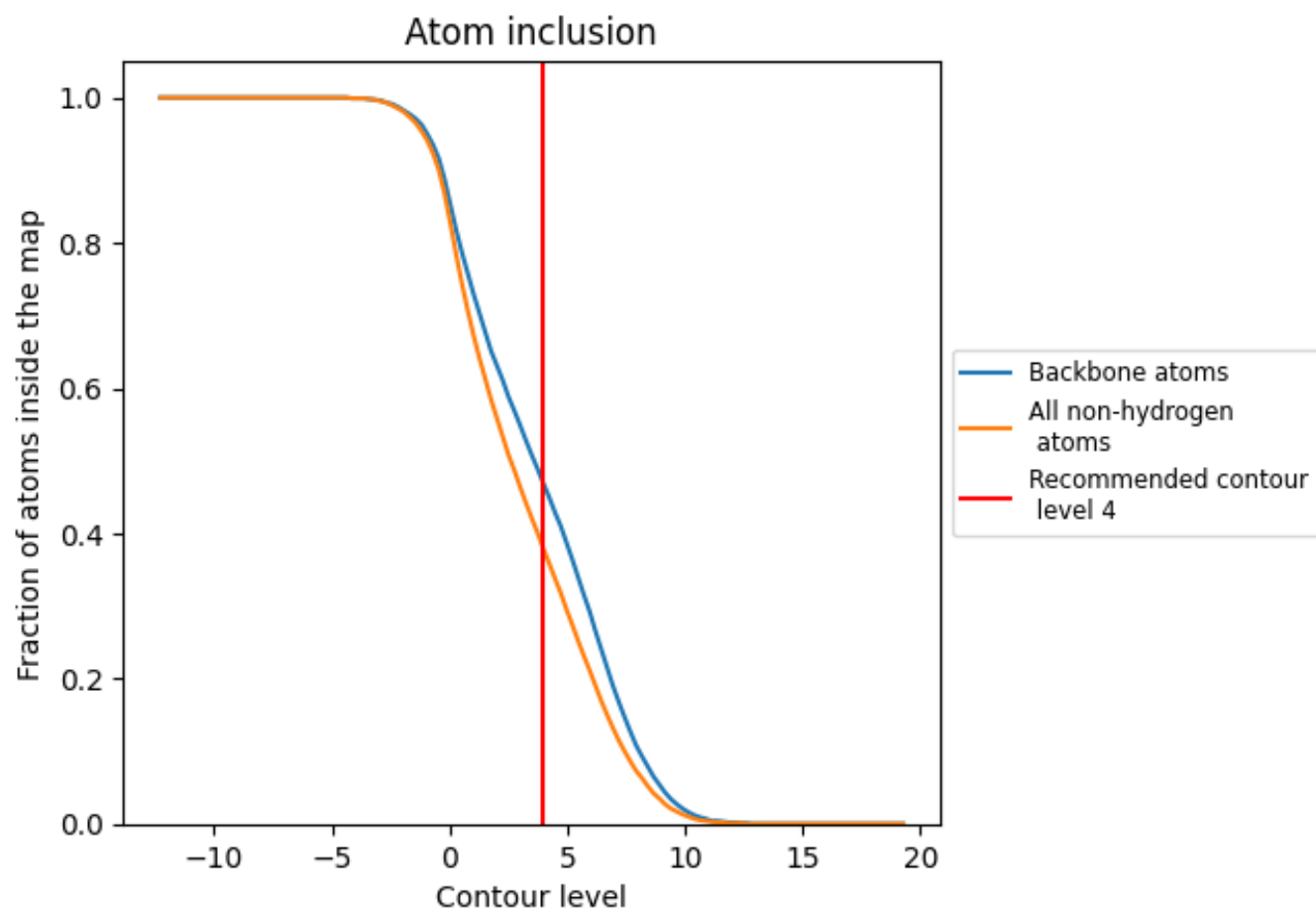
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 47% of all backbone atoms, 38% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3780	0.3020
A	0.0710	-0.0630
B	0.4370	0.3820
C	0.4580	0.3680
D	0.4490	0.3770
E	0.4250	0.3730
F	0.4230	0.3680

1.0
0.0
-0.0