Full wwPDB EM Validation Report (i)

Nov 15, 2022 – 12:06 PM JST

PDB ID	:	6L31
EMDB ID	:	EMD-0816
Title	:	L1 protein of human papillomavirus 6
Authors	:	Li, S.W.; Liu, X.L.; Gu, Y.
Deposited on	:	2019-10-07
Resolution	:	4.18 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 (i) 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 (i)) were used in the production of this report:

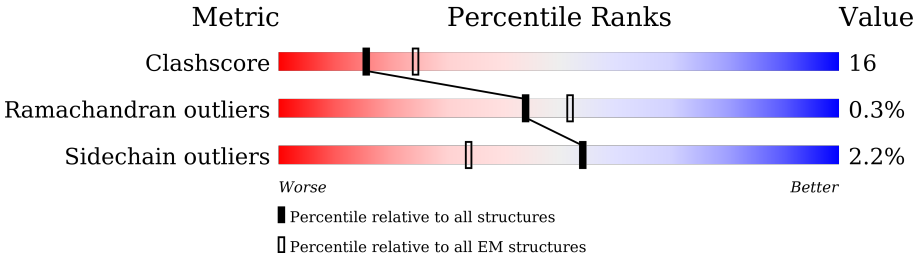
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 4.18 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	447	35% 66% 32% ••
1	B	447	36% 65% 32% •
1	C	447	31% 68% 30% •
1	D	447	41% 68% 30% •
1	E	447	38% 66% 32% ••
1	F	447	31% 69% 30% ••

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 20905 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.

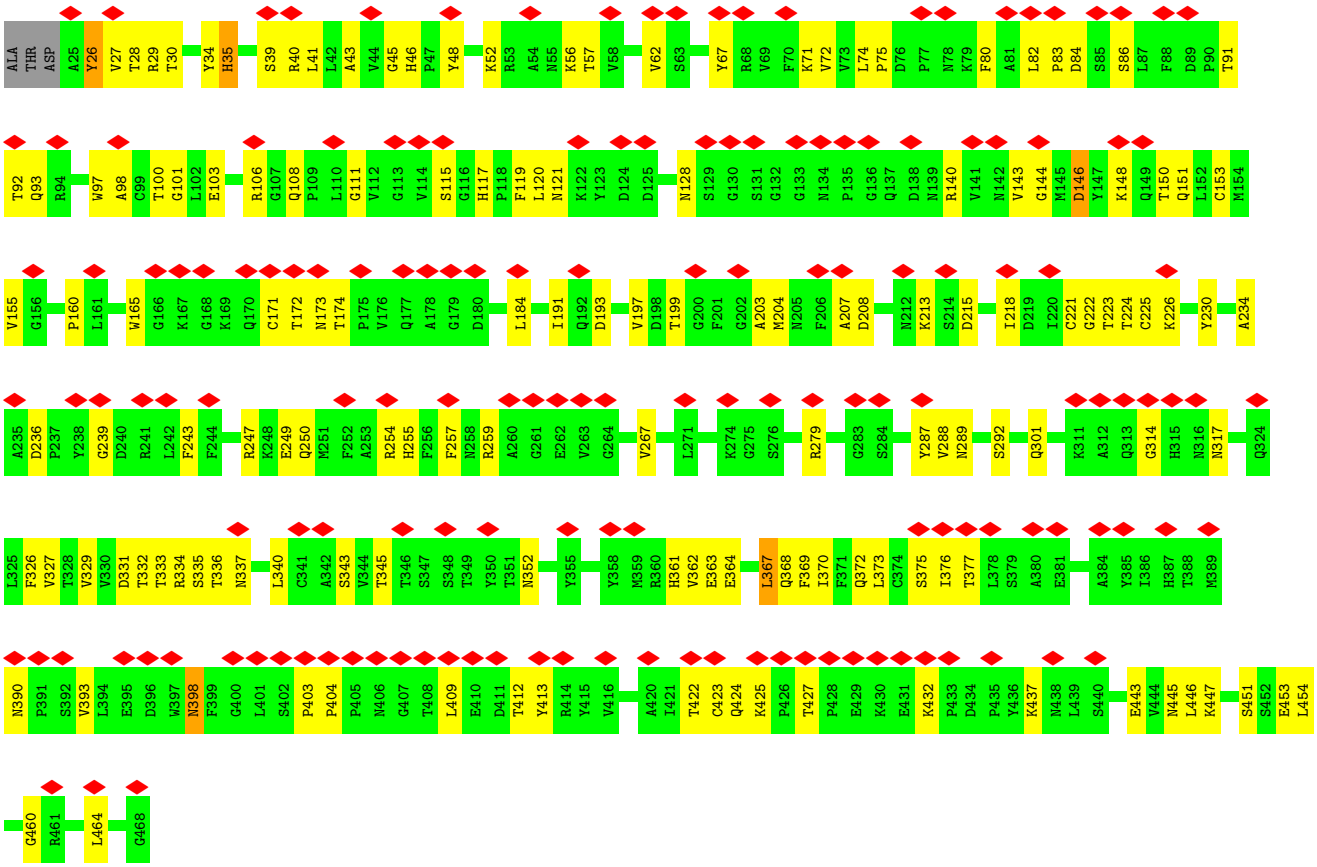
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	444	3477	2204	585	667	21	0	0
1	B	447	3497	2215	588	673	21	0	0
1	C	447	3497	2215	588	673	21	0	0
1	D	445	3485	2208	586	670	21	0	0
1	E	443	3472	2201	584	666	21	0	0
1	F	444	3477	2204	585	667	21	0	0

3 Residue-property plots (i)

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

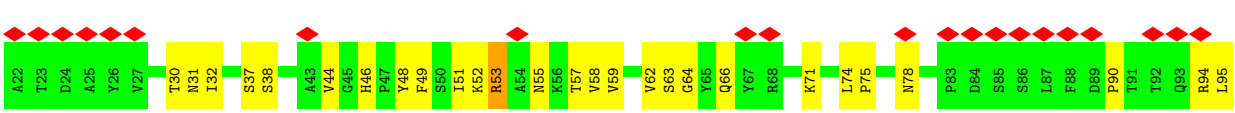
• Molecule 1: Major capsid protein L1

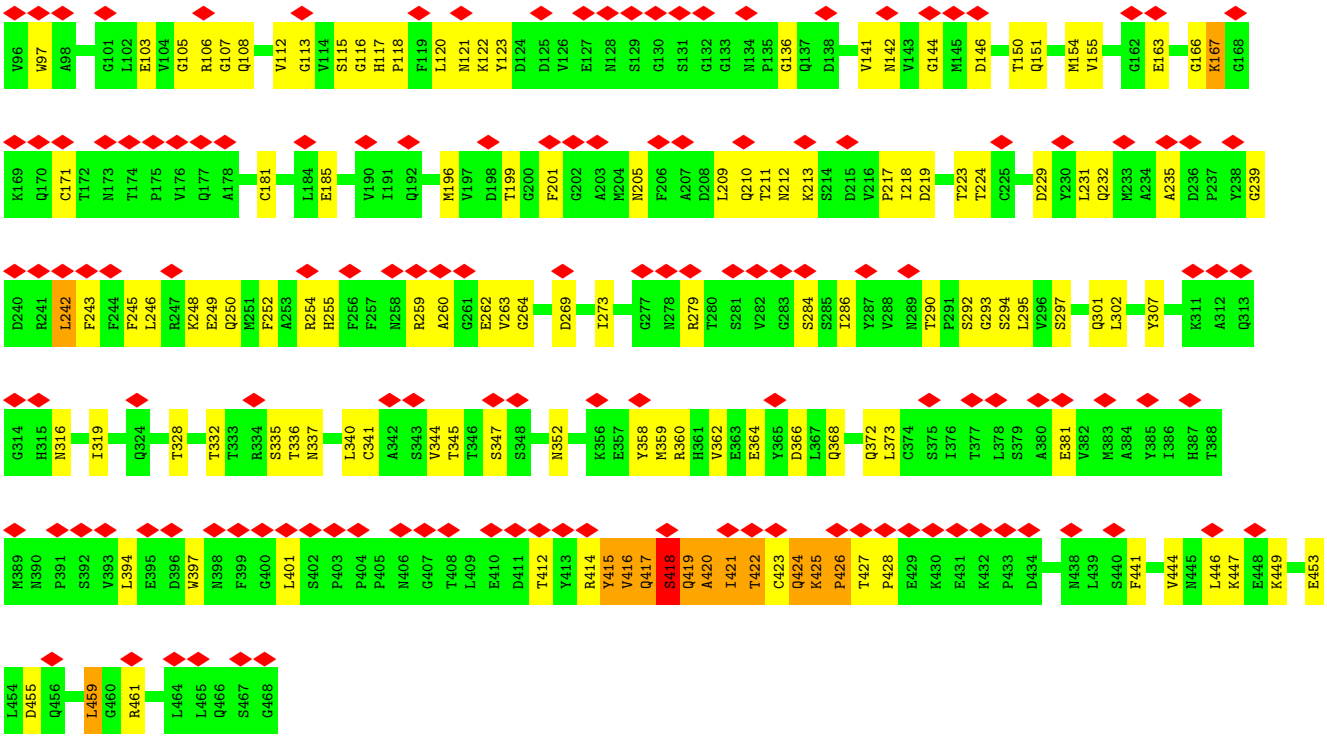
Chain A: 35% 66% 32%



• Molecule 1: Major capsid protein L1

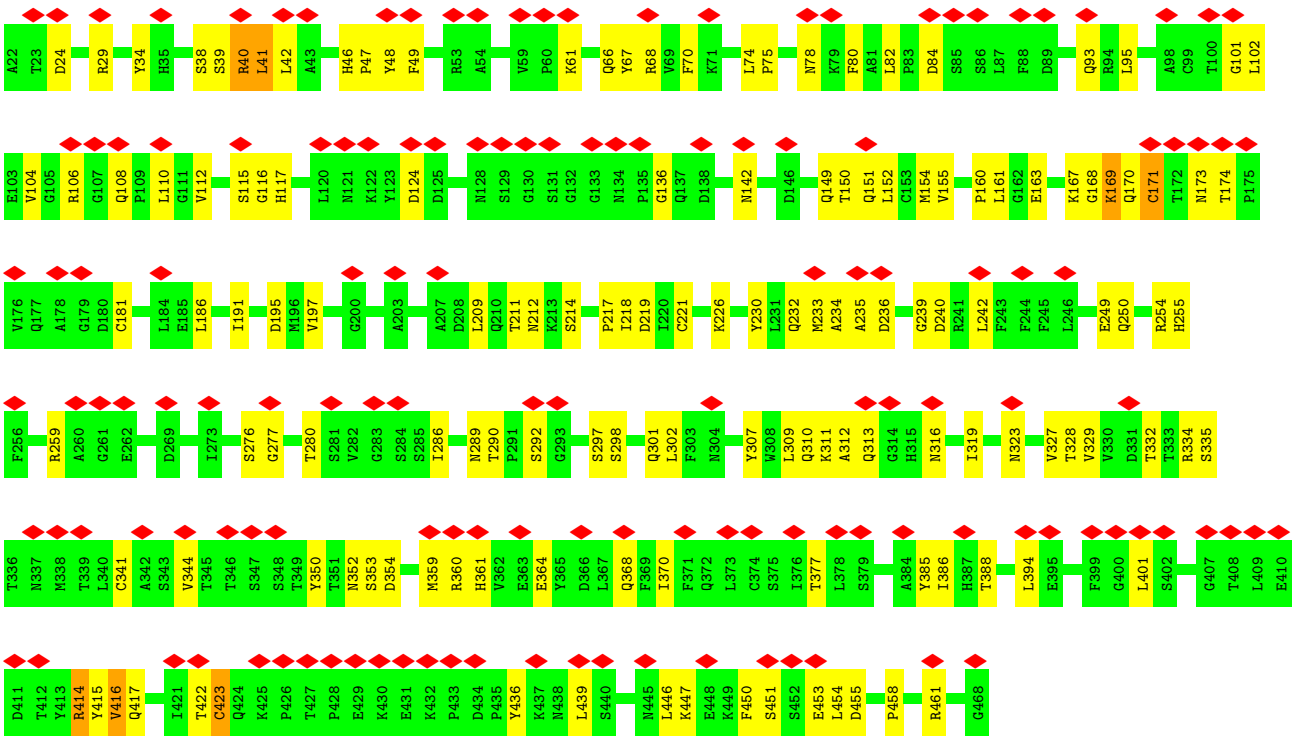
Chain B: 36% 65% 32%





- Molecule 1: Major capsid protein L1

Chain C: 31% 68% 30%

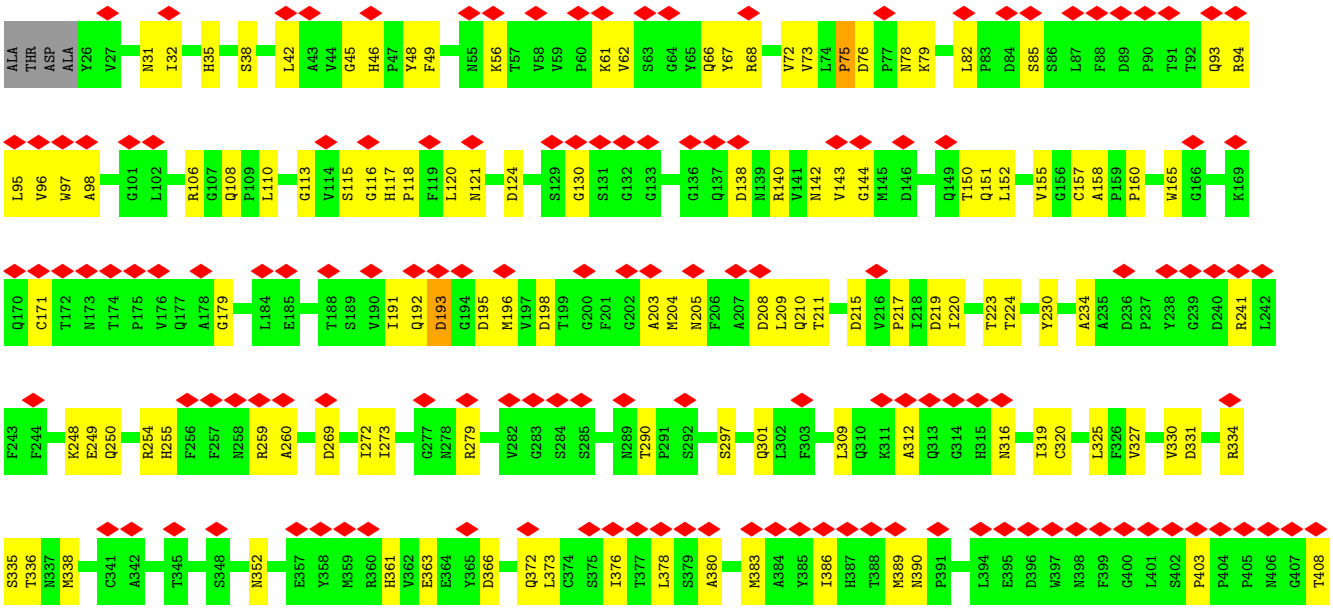


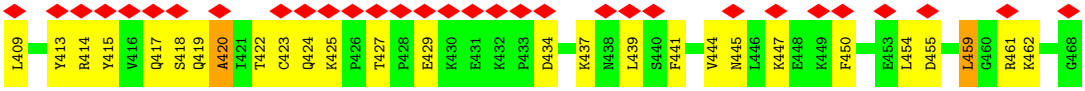
- Molecule 1: Major capsid protein L1

Chain D:

- Molecule 1: Major capsid protein L1

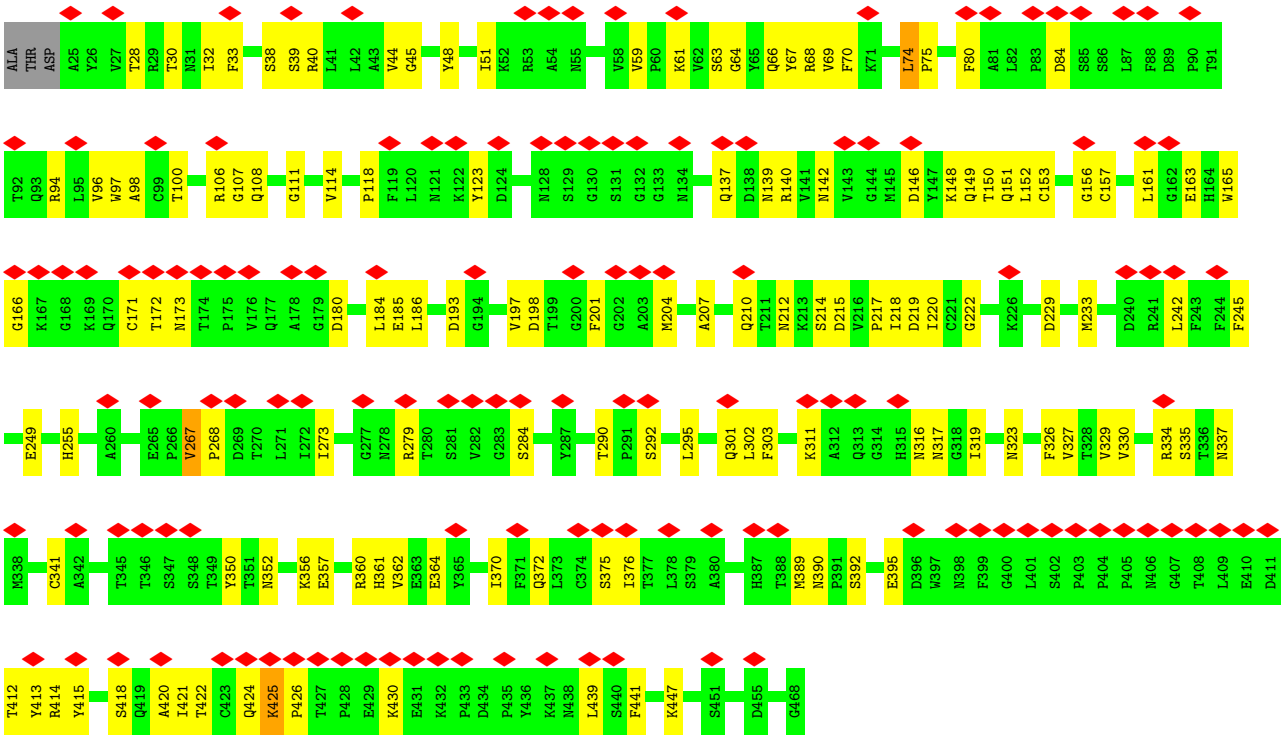
Chain E:





• Molecule 1: Major capsid protein L1

Chain F:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	173490	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	30	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	12.593	Depositor
Minimum map value	-8.978	Depositor
Average map value	0.005	Depositor
Map value standard deviation	1.105	Depositor
Recommended contour level	3.0	Depositor
Map size (Å)	470.4, 470.4, 470.4	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.12, 1.12, 1.12	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.44	0/3569	0.72	1/4855 (0.0%)
1	B	0.39	0/3589	0.71	8/4883 (0.2%)
1	C	0.39	0/3589	0.66	3/4883 (0.1%)
1	D	0.38	0/3577	0.64	1/4866 (0.0%)
1	E	0.39	0/3564	0.65	1/4848 (0.0%)
1	F	0.39	0/3569	0.61	1/4855 (0.0%)
All	All	0.40	0/21457	0.66	15/29190 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	8
1	C	0	2
1	E	0	3
1	F	0	1
All	All	0	14

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	418	SER	N-CA-CB	15.05	133.07	110.50
1	D	409	LEU	CA-CB-CG	8.45	134.73	115.30
1	C	169	LYS	N-CA-C	7.59	131.50	111.00
1	B	415	TYR	N-CA-CB	7.50	124.09	110.60
1	C	401	LEU	CA-CB-CG	7.26	131.99	115.30
1	B	417	GLN	CA-C-N	-6.83	102.17	117.20
1	B	446	LEU	CA-CB-CG	6.16	129.47	115.30
1	B	417	GLN	CB-CA-C	5.76	121.93	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	242	LEU	CA-CB-CG	5.42	127.76	115.30
1	B	401	LEU	C-N-CA	5.38	135.15	121.70
1	B	417	GLN	C-N-CA	5.27	134.87	121.70
1	F	74	LEU	CA-CB-CG	5.23	127.33	115.30
1	C	171	CYS	N-CA-CB	5.16	119.89	110.60
1	E	75	PRO	C-N-CA	5.09	134.43	121.70
1	A	409	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	128	ASN	Peptide
1	A	146	ASP	Peptide
1	A	267	VAL	Peptide
1	A	340	LEU	Peptide
1	A	35	HIS	Peptide
1	A	398	ASN	Peptide
1	A	403	PRO	Peptide
1	A	404	PRO	Peptide
1	C	422	THR	Peptide
1	C	423	CYS	Peptide
1	E	403	PRO	Peptide
1	E	418	SER	Peptide
1	E	427	THR	Peptide
1	F	413	TYR	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	3477	0	3358	95	0
1	B	3497	0	3374	170	0
1	C	3497	0	3375	118	0
1	D	3485	0	3363	124	0
1	E	3472	0	3353	106	0
1	F	3477	0	3359	100	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	20905	0	20182	669	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 16.

All (669) 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:B:419:GLN:NE2	1:B:421:ILE:H	1.10	1.41
1:B:414:ARG:HB2	1:B:424:GLN:NE2	1.39	1.38
1:B:419:GLN:HE22	1:B:421:ILE:N	1.23	1.37
1:C:41:LEU:O	1:C:42:LEU:HD12	1.24	1.31
1:A:26:TYR:O	1:A:376:ILE:HD13	1.10	1.27
1:B:414:ARG:CB	1:B:424:GLN:NE2	2.00	1.25
1:B:422:THR:O	1:B:423:CYS:SG	1.99	1.21
1:A:26:TYR:O	1:A:376:ILE:CD1	1.94	1.16
1:D:425:LYS:HG3	1:D:426:PRO:HD3	1.26	1.14
1:B:419:GLN:CD	1:B:421:ILE:HG12	1.69	1.12
1:D:418:SER:OG	1:D:421:ILE:CG2	2.03	1.07
1:A:27:VAL:O	1:A:375:SER:O	1.74	1.04
1:C:41:LEU:C	1:C:42:LEU:HD12	1.77	1.03
1:D:418:SER:HA	1:D:421:ILE:HG21	1.37	1.03
1:D:418:SER:CA	1:D:421:ILE:CG2	2.40	0.99
1:B:414:ARG:HB3	1:B:424:GLN:CD	1.83	0.98
1:D:418:SER:OG	1:D:421:ILE:HG23	1.63	0.98
1:D:418:SER:HA	1:D:421:ILE:CG2	1.92	0.98
1:D:418:SER:CA	1:D:421:ILE:HG21	1.94	0.98
1:C:416:VAL:HG13	1:C:417:GLN:H	1.34	0.92
1:C:416:VAL:HG13	1:C:417:GLN:N	1.83	0.91
1:B:419:GLN:CD	1:B:421:ILE:H	1.71	0.91
1:B:425:LYS:NZ	1:B:428:PRO:HD3	1.86	0.91
1:B:414:ARG:CB	1:B:424:GLN:HE22	1.84	0.90
1:D:425:LYS:HG3	1:D:426:PRO:CD	2.02	0.89
1:B:425:LYS:HZ1	1:B:428:PRO:HD3	1.36	0.89
1:B:419:GLN:CD	1:B:420:ALA:N	2.28	0.87
1:B:419:GLN:OE1	1:B:421:ILE:HG12	1.74	0.87
1:D:418:SER:CB	1:D:421:ILE:CG2	2.53	0.86
1:B:416:VAL:O	1:B:417:GLN:CD	2.14	0.85
1:B:414:ARG:HB3	1:B:424:GLN:NE2	1.88	0.85
1:B:424:GLN:C	1:B:426:PRO:HD3	1.97	0.85
1:B:414:ARG:CB	1:B:424:GLN:CD	2.43	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:418:SER:CB	1:D:421:ILE:HG21	2.07	0.84
1:C:40:ARG:HB3	1:C:40:ARG:CZ	2.08	0.83
1:D:418:SER:CA	1:D:421:ILE:HG22	2.08	0.83
1:D:425:LYS:HD2	1:D:426:PRO:N	1.94	0.83
1:B:425:LYS:N	1:B:426:PRO:HD3	1.95	0.82
1:C:416:VAL:CG1	1:C:417:GLN:N	2.42	0.81
1:B:419:GLN:NE2	1:B:421:ILE:N	1.94	0.80
1:B:419:GLN:NE2	1:B:421:ILE:HG12	1.95	0.80
1:B:419:GLN:HE22	1:B:421:ILE:CA	1.94	0.80
1:B:414:ARG:HB3	1:B:424:GLN:OE1	1.81	0.79
1:A:28:THR:O	1:A:29:ARG:HD3	1.82	0.79
1:C:170:GLN:HG3	1:C:173:ASN:HB2	1.62	0.79
1:B:414:ARG:HB2	1:B:424:GLN:HE22	1.44	0.79
1:B:419:GLN:O	1:B:420:ALA:CB	2.32	0.78
1:D:418:SER:C	1:D:421:ILE:HG22	2.04	0.78
1:B:416:VAL:C	1:B:417:GLN:OE1	2.22	0.77
1:B:424:GLN:NE2	1:B:424:GLN:H	1.82	0.77
1:B:63:SER:H	1:B:66:GLN:HE22	1.34	0.76
1:B:419:GLN:O	1:B:420:ALA:HB2	1.86	0.75
1:B:419:GLN:OE1	1:B:421:ILE:CD1	2.35	0.75
1:B:425:LYS:CE	1:B:428:PRO:HD3	2.19	0.73
1:D:425:LYS:CG	1:D:426:PRO:HD3	2.14	0.72
1:E:255:HIS:H	1:E:290:THR:HB	1.55	0.71
1:B:419:GLN:OE1	1:B:421:ILE:CG1	2.39	0.71
1:A:82:LEU:HG	1:A:84:ASP:H	1.54	0.71
1:C:41:LEU:O	1:C:42:LEU:CD1	2.20	0.71
1:D:151:GLN:HE22	1:D:302:LEU:H	1.39	0.70
1:B:419:GLN:OE1	1:B:420:ALA:N	2.24	0.70
1:F:420:ALA:C	1:F:421:ILE:HD13	2.11	0.70
1:D:139:ASN:HD22	1:E:279:ARG:HH21	1.37	0.70
1:F:165:TRP:HB2	1:F:204:MET:HG3	1.73	0.69
1:B:414:ARG:CD	1:B:424:GLN:HE22	2.04	0.69
1:C:169:LYS:HE2	1:C:170:GLN:NE2	2.08	0.69
1:C:416:VAL:O	1:C:417:GLN:NE2	2.26	0.68
1:C:167:LYS:NZ	1:C:168:GLY:O	2.26	0.68
1:C:169:LYS:NZ	1:C:170:GLN:O	2.16	0.68
1:B:425:LYS:HZ1	1:B:427:THR:N	1.91	0.68
1:B:255:HIS:H	1:B:290:THR:HB	1.60	0.67
1:B:416:VAL:O	1:B:417:GLN:OE1	2.13	0.66
1:B:419:GLN:CD	1:B:420:ALA:H	1.99	0.66
1:E:155:VAL:HG12	1:E:327:VAL:HG12	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:LYS:HG2	1:A:57:THR:HB	1.77	0.66
1:A:35:HIS:HB2	1:A:370:ILE:HA	1.79	0.65
1:D:119:PHE:HB3	1:D:140:ARG:HD2	1.78	0.65
1:D:425:LYS:CD	1:D:426:PRO:HG3	2.27	0.65
1:B:425:LYS:NZ	1:B:427:THR:N	2.45	0.65
1:B:205:ASN:HB2	1:B:209:LEU:HD23	1.78	0.65
1:F:74:LEU:HD12	1:F:75:PRO:HD2	1.79	0.64
1:F:418:SER:OG	1:F:421:ILE:HB	1.97	0.64
1:F:421:ILE:HD13	1:F:421:ILE:N	2.11	0.64
1:C:167:LYS:NZ	1:C:168:GLY:C	2.50	0.64
1:D:63:SER:O	1:D:68:ARG:NH2	2.31	0.64
1:B:103:GLU:HB3	1:B:368:GLN:HB2	1.79	0.64
1:B:425:LYS:HE2	1:B:428:PRO:HG3	1.78	0.64
1:D:425:LYS:HE2	1:D:426:PRO:HG3	1.80	0.64
1:B:53:ARG:HG2	1:B:55:ASN:H	1.62	0.64
1:D:164:HIS:HB3	1:D:226:LYS:HG2	1.78	0.64
1:C:39:SER:C	1:C:40:ARG:HG2	2.19	0.63
1:D:55:ASN:HB2	1:D:56:LYS:HE3	1.79	0.63
1:E:151:GLN:HE22	1:E:301:GLN:HA	1.63	0.63
1:B:252:PHE:HB3	1:F:295:LEU:HA	1.81	0.63
1:D:340:LEU:HD22	1:E:209:LEU:HD12	1.80	0.63
1:D:425:LYS:CE	1:D:426:PRO:HG3	2.28	0.63
1:F:30:THR:HG22	1:F:32:ILE:H	1.63	0.63
1:A:43:ALA:HB3	1:A:363:GLU:HB2	1.81	0.62
1:C:40:ARG:HG2	1:C:40:ARG:HH11	1.64	0.62
1:D:141:VAL:HG13	1:E:130:GLY:HA2	1.81	0.62
1:B:394:LEU:HA	1:B:397:TRP:HB2	1.81	0.62
1:F:421:ILE:HG22	1:F:421:ILE:O	2.00	0.62
1:D:106:ARG:NH1	1:D:364:GLU:O	2.32	0.62
1:A:257:PHE:HB3	1:A:288:VAL:HG23	1.82	0.62
1:C:39:SER:O	1:C:40:ARG:HG2	1.99	0.62
1:B:419:GLN:OE1	1:B:421:ILE:N	2.33	0.61
1:A:93:GLN:NE2	1:A:377:THR:OG1	2.32	0.61
1:C:170:GLN:CG	1:C:173:ASN:HB2	2.30	0.61
1:C:255:HIS:H	1:C:290:THR:HB	1.65	0.61
1:C:40:ARG:HB3	1:C:40:ARG:NH1	2.14	0.61
1:B:352:ASN:ND2	1:C:136:GLY:O	2.32	0.61
1:C:40:ARG:HH11	1:C:40:ARG:CG	2.13	0.61
1:C:219:ASP:OD1	1:C:219:ASP:N	2.34	0.61
1:B:118:PRO:HD3	1:B:218:ILE:HD11	1.82	0.61
1:C:41:LEU:C	1:C:42:LEU:CD1	2.62	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:TRP:HB3	1:A:184:LEU:HD11	1.81	0.60
1:C:455:ASP:O	1:C:461:ARG:NH2	2.34	0.60
1:C:151:GLN:HE22	1:C:301:GLN:HA	1.66	0.60
1:A:150:THR:HG23	1:A:249:GLU:HG3	1.83	0.60
1:F:212:ASN:ND2	1:F:215:ASP:OD1	2.35	0.60
1:B:46:HIS:HD2	1:B:359:MET:HB2	1.67	0.60
1:B:78:ASN:ND2	1:B:95:LEU:O	2.35	0.60
1:E:67:TYR:HD1	1:E:330:VAL:HG21	1.66	0.60
1:A:121:ASN:OD1	1:A:259:ARG:NH1	2.34	0.60
1:D:120:LEU:HD12	1:D:143:VAL:HB	1.84	0.59
1:A:45:GLY:HA3	1:A:62:VAL:H	1.67	0.59
1:A:80:PHE:HA	1:F:80:PHE:HA	1.85	0.59
1:B:146:ASP:OD1	1:B:293:GLY:N	2.34	0.59
1:B:414:ARG:HD2	1:B:424:GLN:HE22	1.66	0.59
1:C:67:TYR:O	1:C:68:ARG:NH1	2.36	0.59
1:C:297:SER:O	1:C:301:GLN:NE2	2.36	0.59
1:E:248:LYS:O	1:E:250:GLN:NE2	2.36	0.59
1:F:118:PRO:HD3	1:F:218:ILE:HD11	1.84	0.59
1:D:148:LYS:NZ	1:D:149:GLN:O	2.36	0.59
1:B:425:LYS:HE2	1:B:428:PRO:CG	2.33	0.58
1:B:425:LYS:HE3	1:B:425:LYS:O	2.03	0.58
1:A:331:ASP:OD2	1:A:334:ARG:NH1	2.34	0.58
1:B:419:GLN:CD	1:B:421:ILE:N	2.44	0.58
1:C:436:TYR:HA	1:C:439:LEU:HD13	1.85	0.58
1:F:153:CYS:HA	1:F:329:VAL:HG22	1.85	0.58
1:C:169:LYS:HD2	1:C:170:GLN:OE1	2.03	0.58
1:E:93:GLN:O	1:E:94:ARG:NH1	2.36	0.58
1:B:211:THR:O	1:B:213:LYS:NZ	2.35	0.58
1:A:39:SER:HB3	1:F:414:ARG:HH11	1.67	0.58
1:D:294:SER:OG	1:D:295:LEU:N	2.35	0.58
1:B:167:LYS:HB3	1:B:209:LEU:HD11	1.85	0.58
1:C:46:HIS:ND1	1:C:49:PHE:O	2.31	0.58
1:E:110:LEU:HD13	1:E:334:ARG:HG2	1.85	0.58
1:F:255:HIS:H	1:F:290:THR:HB	1.68	0.58
1:A:106:ARG:NH1	1:A:364:GLU:O	2.37	0.58
1:A:26:TYR:HD1	1:A:27:VAL:HG13	1.69	0.58
1:E:35:HIS:HB3	1:E:454:LEU:HD11	1.86	0.58
1:C:352:ASN:HB3	1:D:136:GLY:HA3	1.86	0.57
1:A:115:SER:OG	1:A:146:ASP:OD1	2.21	0.57
1:C:218:ILE:HD12	1:C:221:CYS:HB3	1.86	0.57
1:B:425:LYS:N	1:B:426:PRO:CD	2.66	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:51:ILE:HB	1:F:59:VAL:HB	1.87	0.57
1:C:38:SER:HB2	1:C:446:LEU:HD21	1.86	0.57
1:D:425:LYS:CG	1:D:426:PRO:CD	2.76	0.57
1:A:218:ILE:O	1:A:222:GLY:N	2.37	0.57
1:E:117:HIS:HB3	1:E:120:LEU:HG	1.85	0.57
1:E:75:PRO:O	1:E:97:TRP:NE1	2.38	0.57
1:F:152:LEU:HD21	1:F:330:VAL:H	1.70	0.57
1:B:107:GLY:N	1:B:364:GLU:OE2	2.37	0.57
1:B:150:THR:HA	1:B:249:GLU:HG3	1.87	0.57
1:E:297:SER:O	1:E:301:GLN:NE2	2.37	0.57
1:A:333:THR:OG1	1:A:334:ARG:NH1	2.37	0.56
1:A:225:CYS:SG	1:A:226:LYS:N	2.78	0.56
1:B:90:PRO:O	1:B:94:ARG:NH1	2.39	0.56
1:B:294:SER:OG	1:B:295:LEU:N	2.38	0.56
1:F:106:ARG:NH1	1:F:364:GLU:O	2.38	0.56
1:B:52:LYS:NZ	1:B:57:THR:OG1	2.36	0.56
1:C:169:LYS:HD2	1:C:170:GLN:N	2.21	0.56
1:C:212:ASN:ND2	1:C:214:SER:OG	2.38	0.56
1:E:61:LYS:NZ	1:E:219:ASP:O	2.39	0.56
1:E:108:GLN:O	1:E:334:ARG:NH1	2.34	0.56
1:E:223:THR:OG1	1:E:224:THR:N	2.38	0.56
1:F:172:THR:O	1:F:172:THR:OG1	2.20	0.56
1:C:112:VAL:O	1:D:289:ASN:ND2	2.38	0.56
1:D:149:GLN:NE2	1:D:332:THR:OG1	2.38	0.56
1:D:425:LYS:HD2	1:D:426:PRO:CG	2.35	0.56
1:F:70:PHE:HB2	1:F:327:VAL:HG23	1.87	0.56
1:B:112:VAL:N	1:B:336:THR:OG1	2.39	0.56
1:B:259:ARG:HH11	1:B:286:ILE:HD11	1.69	0.56
1:B:419:GLN:NE2	1:B:420:ALA:H	2.03	0.56
1:F:412:THR:HA	1:F:414:ARG:HH21	1.71	0.56
1:C:230:TYR:O	1:C:234:ALA:N	2.39	0.56
1:D:424:GLN:OE1	1:D:424:GLN:N	2.37	0.56
1:E:98:ALA:O	1:E:372:GLN:N	2.38	0.56
1:C:332:THR:HG22	1:C:335:SER:HB3	1.86	0.56
1:B:418:SER:CB	1:B:422:THR:HB	2.36	0.56
1:C:106:ARG:NH1	1:C:364:GLU:OE2	2.39	0.56
1:A:460:GLY:O	1:A:464:LEU:N	2.39	0.55
1:F:75:PRO:HD3	1:F:447:LYS:HA	1.88	0.55
1:A:34:TYR:HA	1:A:454:LEU:HD21	1.88	0.55
1:C:78:ASN:HD21	1:C:95:LEU:H	1.53	0.55
1:E:117:HIS:HB2	1:E:217:PRO:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:67:TYR:O	1:E:68:ARG:NH1	2.39	0.55
1:F:67:TYR:O	1:F:68:ARG:NH1	2.40	0.55
1:C:67:TYR:HE1	1:C:197:VAL:HG23	1.72	0.55
1:F:98:ALA:N	1:F:372:GLN:O	2.40	0.55
1:C:24:ASP:OD1	1:C:29:ARG:NH2	2.40	0.55
1:E:230:TYR:O	1:E:234:ALA:N	2.39	0.55
1:B:273:ILE:HG22	1:F:140:ARG:HH22	1.72	0.55
1:E:423:CYS:O	1:E:425:LYS:NZ	2.36	0.55
1:B:297:SER:O	1:B:301:GLN:NE2	2.34	0.55
1:B:340:LEU:HD11	1:B:358:TYR:HB2	1.89	0.55
1:B:414:ARG:HB2	1:B:424:GLN:HE21	1.58	0.55
1:B:461:ARG:NH2	1:C:313:GLN:O	2.39	0.55
1:D:425:LYS:N	1:D:426:PRO:CD	2.70	0.55
1:F:316:ASN:ND2	1:F:319:ILE:O	2.40	0.55
1:E:66:GLN:OE1	1:E:68:ARG:NH2	2.40	0.55
1:F:148:LYS:NZ	1:F:150:THR:OG1	2.40	0.55
1:B:302:LEU:O	1:B:307:TYR:OH	2.24	0.54
1:E:455:ASP:O	1:E:461:ARG:NH1	2.38	0.54
1:B:181:CYS:HB2	1:F:360:ARG:HH21	1.73	0.54
1:D:425:LYS:HD2	1:D:426:PRO:HG3	1.88	0.54
1:B:116:GLY:HA3	1:B:144:GLY:HA2	1.87	0.54
1:B:106:ARG:HH12	1:B:108:GLN:HE22	1.56	0.54
1:C:154:MET:HB2	1:C:328:THR:HB	1.90	0.54
1:D:116:GLY:HA3	1:D:144:GLY:HA2	1.90	0.54
1:F:38:SER:OG	1:F:39:SER:N	2.41	0.54
1:B:239:GLY:HA2	1:B:242:LEU:HG	1.90	0.54
1:D:150:THR:HA	1:D:249:GLU:HG3	1.89	0.54
1:E:417:GLN:NE2	1:E:419:GLN:OE1	2.41	0.54
1:F:61:LYS:O	1:F:66:GLN:NE2	2.36	0.54
1:D:425:LYS:HD2	1:D:426:PRO:CA	2.38	0.54
1:E:192:GLN:HG2	1:E:439:LEU:HD12	1.89	0.54
1:F:75:PRO:O	1:F:97:TRP:NE1	2.38	0.54
1:A:119:PHE:HB3	1:A:140:ARG:HD2	1.89	0.53
1:C:386:ILE:HG13	1:C:394:LEU:HD11	1.90	0.53
1:E:76:ASP:OD2	1:E:79:LYS:N	2.41	0.53
1:A:29:ARG:NH2	1:A:317:ASN:OD1	2.42	0.53
1:B:196:MET:HG3	1:B:223:THR:HG21	1.89	0.53
1:C:117:HIS:HB2	1:C:217:PRO:HA	1.89	0.53
1:D:75:PRO:HD3	1:D:447:LYS:HA	1.89	0.53
1:E:113:GLY:N	1:E:335:SER:OG	2.41	0.53
1:E:116:GLY:HA3	1:E:144:GLY:HA2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:361:HIS:NE2	1:E:363:GLU:OE2	2.37	0.53
1:B:264:GLY:HA2	1:F:356:LYS:HE3	1.89	0.53
1:D:409:LEU:HG	1:D:412:THR:HA	1.90	0.53
1:B:425:LYS:HZ1	1:B:426:PRO:C	2.11	0.53
1:C:160:PRO:HB2	1:C:191:ILE:HD12	1.91	0.53
1:D:425:LYS:O	1:D:428:PRO:HD2	2.09	0.53
1:F:207:ALA:HB2	1:F:222:GLY:HA2	1.91	0.53
1:B:37:SER:O	1:B:449:LYS:NZ	2.37	0.53
1:D:463:PHE:O	1:D:466:GLN:NE2	2.41	0.53
1:F:161:LEU:H	1:F:233:MET:HE1	1.74	0.53
1:F:166:GLY:N	1:F:185:GLU:O	2.42	0.53
1:A:413:TYR:O	1:F:40:ARG:NH2	2.40	0.53
1:F:165:TRP:HA	1:F:186:LEU:HA	1.91	0.53
1:A:218:ILE:HA	1:A:221:CYS:HB3	1.90	0.53
1:D:117:HIS:HB2	1:D:217:PRO:HA	1.90	0.53
1:B:166:GLY:O	1:B:185:GLU:N	2.42	0.53
1:C:47:PRO:HG3	1:C:361:HIS:HB2	1.91	0.52
1:D:424:GLN:O	1:D:427:THR:HG23	2.09	0.52
1:A:111:GLY:H	1:A:334:ARG:HA	1.72	0.52
1:B:113:GLY:N	1:B:335:SER:O	2.43	0.52
1:B:422:THR:C	1:B:423:CYS:SG	2.84	0.52
1:C:254:ARG:HB2	1:C:292:SER:HB3	1.91	0.52
1:B:425:LYS:HZ2	1:B:426:PRO:N	2.07	0.52
1:C:316:ASN:OD1	1:C:319:ILE:N	2.35	0.52
1:D:72:VAL:HB	1:D:325:LEU:HB2	1.91	0.52
1:A:103:GLU:HB3	1:A:368:GLN:HE21	1.74	0.52
1:B:344:VAL:HG13	1:B:345:THR:HG22	1.90	0.52
1:C:40:ARG:NH1	1:C:40:ARG:CB	2.73	0.52
1:F:108:GLN:H	1:F:334:ARG:HE	1.57	0.52
1:F:114:VAL:O	1:F:337:ASN:ND2	2.41	0.52
1:B:46:HIS:O	1:B:62:VAL:N	2.43	0.52
1:A:111:GLY:O	1:A:335:SER:N	2.40	0.52
1:B:51:ILE:HB	1:B:59:VAL:HB	1.91	0.52
1:B:30:THR:OG1	1:B:372:GLN:NE2	2.43	0.52
1:B:71:LYS:HD3	1:B:441:PHE:HE1	1.74	0.52
1:E:386:ILE:HA	1:E:389:MET:HG2	1.92	0.52
1:A:148:LYS:HE3	1:A:199:THR:HA	1.91	0.52
1:F:150:THR:HA	1:F:249:GLU:HG3	1.92	0.52
1:B:48:TYR:HH	1:B:115:SER:HG	1.58	0.51
1:D:297:SER:O	1:D:301:GLN:NE2	2.43	0.51
1:C:74:LEU:H	1:C:323:ASN:HB3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:74:LEU:HB3	1:F:323:ASN:HB3	1.93	0.51
1:F:389:MET:SD	1:F:390:ASN:N	2.83	0.51
1:B:262:GLU:HB3	1:F:356:LYS:HZ2	1.76	0.51
1:D:238:TYR:HA	1:D:315:HIS:HB2	1.92	0.51
1:D:258:ASN:ND2	1:D:286:ILE:O	2.44	0.51
1:D:298:SER:OG	1:E:248:LYS:O	2.24	0.51
1:B:229:ASP:HB3	1:B:232:GLN:HE21	1.75	0.51
1:B:425:LYS:NZ	1:B:428:PRO:CD	2.66	0.51
1:E:73:VAL:HG23	1:E:447:LYS:HG3	1.93	0.51
1:E:115:SER:OG	1:E:116:GLY:N	2.44	0.51
1:A:208:ASP:OD1	1:A:208:ASP:N	2.40	0.51
1:D:155:VAL:HG12	1:D:327:VAL:HG22	1.93	0.51
1:E:215:ASP:O	1:E:259:ARG:NH1	2.43	0.51
1:B:424:GLN:CD	1:B:424:GLN:H	2.12	0.51
1:C:34:TYR:HB3	1:C:450:PHE:HB3	1.92	0.51
1:E:98:ALA:HB3	1:E:372:GLN:HB3	1.92	0.51
1:E:422:THR:HG22	1:E:425:LYS:HZ1	1.76	0.51
1:A:390:ASN:HB3	1:A:393:VAL:HG23	1.92	0.51
1:D:76:ASP:HB3	1:D:79:LYS:HD3	1.93	0.51
1:D:343:SER:OG	1:D:345:THR:OG1	2.29	0.51
1:E:151:GLN:NE2	1:E:301:GLN:OE1	2.43	0.51
1:F:66:GLN:OE1	1:F:68:ARG:NH2	2.36	0.51
1:A:30:THR:HG21	1:A:373:LEU:HG	1.91	0.51
1:A:451:SER:OG	1:A:453:GLU:O	2.28	0.51
1:E:408:THR:OG1	1:E:409:LEU:N	2.43	0.51
1:C:75:PRO:HD3	1:C:447:LYS:HA	1.92	0.50
1:F:217:PRO:HD2	1:F:220:ILE:HD11	1.93	0.50
1:B:166:GLY:N	1:B:185:GLU:O	2.44	0.50
1:D:205:ASN:HA	1:D:224:THR:HG22	1.93	0.50
1:A:230:TYR:O	1:A:234:ALA:N	2.45	0.50
1:A:239:GLY:HA3	1:A:314:GLY:HA3	1.93	0.50
1:A:432:LYS:HD2	1:A:437:LYS:HD2	1.93	0.50
1:D:358:TYR:OH	1:E:179:GLY:O	2.27	0.50
1:D:421:ILE:HD11	1:D:425:LYS:HA	1.93	0.50
1:E:219:ASP:OD1	1:E:219:ASP:N	2.45	0.50
1:F:214:SER:O	1:F:214:SER:OG	2.28	0.50
1:A:425:LYS:HG3	1:A:427:THR:HG22	1.92	0.50
1:C:236:ASP:OD1	1:C:239:GLY:N	2.44	0.50
1:F:96:VAL:HG12	1:F:376:ILE:HD11	1.93	0.50
1:B:44:VAL:HG22	1:B:362:VAL:HG23	1.93	0.50
1:C:169:LYS:HG3	1:C:170:GLN:O	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:453:GLU:OE2	1:C:454:LEU:N	2.43	0.50
1:D:425:LYS:CD	1:D:426:PRO:N	2.71	0.50
1:E:46:HIS:ND1	1:E:49:PHE:O	2.43	0.50
1:B:113:GLY:HA2	1:C:289:ASN:HD21	1.76	0.50
1:B:219:ASP:N	1:B:219:ASP:OD1	2.45	0.50
1:B:223:THR:OG1	1:B:224:THR:N	2.44	0.50
1:D:99:CYS:HA	1:D:371:PHE:HD1	1.77	0.50
1:F:30:THR:O	1:F:372:GLN:NE2	2.45	0.50
1:E:75:PRO:HD3	1:E:447:LYS:HA	1.93	0.50
1:F:48:TYR:HB3	1:F:218:ILE:HG21	1.93	0.50
1:A:215:ASP:HB3	1:A:259:ARG:HH22	1.77	0.50
1:C:142:ASN:ND2	1:D:284:SER:O	2.45	0.50
1:D:333:THR:OG1	1:D:334:ARG:NH1	2.45	0.50
1:B:154:MET:N	1:B:328:THR:O	2.36	0.50
1:B:155:VAL:HG23	1:B:243:PHE:HB2	1.94	0.50
1:D:127:GLU:HB2	1:D:256:PHE:HD2	1.77	0.50
1:C:70:PHE:N	1:C:327:VAL:O	2.42	0.49
1:E:120:LEU:HD12	1:E:143:VAL:HB	1.93	0.49
1:C:232:GLN:HA	1:C:235:ALA:HB3	1.94	0.49
1:D:108:GLN:HB2	1:D:334:ARG:HD3	1.94	0.49
1:B:118:PRO:HA	1:B:142:ASN:HD22	1.77	0.49
1:E:46:HIS:O	1:E:62:VAL:N	2.43	0.49
1:B:418:SER:OG	1:B:422:THR:HB	2.12	0.49
1:E:82:LEU:O	1:E:85:SER:OG	2.30	0.49
1:F:63:SER:OG	1:F:64:GLY:N	2.45	0.49
1:D:166:GLY:N	1:D:185:GLU:O	2.42	0.49
1:D:206:PHE:HE2	1:D:225:CYS:H	1.61	0.49
1:F:69:VAL:N	1:F:193:ASP:OD2	2.41	0.49
1:F:303:PHE:HE1	1:F:329:VAL:HG11	1.77	0.49
1:B:163:GLU:OE1	1:B:229:ASP:N	2.39	0.49
1:B:163:GLU:OE2	1:B:232:GLN:NE2	2.45	0.49
1:E:316:ASN:ND2	1:E:319:ILE:O	2.45	0.49
1:F:165:TRP:HB3	1:F:184:LEU:HD11	1.93	0.49
1:C:163:GLU:HB2	1:C:186:LEU:HD11	1.94	0.49
1:D:29:ARG:NH1	1:D:372:GLN:OE1	2.44	0.49
1:D:146:ASP:OD2	1:D:293:GLY:N	2.45	0.49
1:D:417:GLN:HG3	1:D:419:GLN:OE1	2.13	0.49
1:E:140:ARG:NH2	1:F:273:ILE:O	2.46	0.49
1:E:198:ASP:OD1	1:E:198:ASP:N	2.45	0.49
1:E:417:GLN:HE21	1:E:419:GLN:HB3	1.77	0.49
1:A:422:THR:HG22	1:A:424:GLN:HG2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:284:SER:O	1:F:142:ASN:ND2	2.38	0.49
1:C:298:SER:OG	1:D:249:GLU:N	2.43	0.49
1:E:434:ASP:HB3	1:E:437:LYS:HD3	1.95	0.49
1:D:126:VAL:O	1:D:129:SER:OG	2.30	0.49
1:D:394:LEU:HD12	1:D:397:TRP:HB2	1.95	0.49
1:A:39:SER:OG	1:A:40:ARG:N	2.45	0.48
1:B:286:ILE:HD12	1:F:357:GLU:HG3	1.95	0.48
1:C:302:LEU:O	1:C:307:TYR:OH	2.29	0.48
1:C:385:TYR:O	1:C:388:THR:OG1	2.26	0.48
1:A:151:GLN:NE2	1:A:332:THR:OG1	2.33	0.48
1:B:199:THR:HG23	1:B:201:PHE:HD2	1.78	0.48
1:B:360:ARG:HH22	1:C:181:CYS:HB2	1.78	0.48
1:D:452:SER:OG	1:D:453:GLU:N	2.46	0.48
1:F:418:SER:OG	1:F:421:ILE:CB	2.62	0.48
1:A:28:THR:O	1:A:29:ARG:CD	2.60	0.48
1:C:46:HIS:CE1	1:C:49:PHE:H	2.31	0.48
1:C:240:ASP:OD1	1:C:316:ASN:ND2	2.45	0.48
1:F:148:LYS:NZ	1:F:149:GLN:O	2.40	0.48
1:B:46:HIS:CD2	1:B:359:MET:HB2	2.48	0.48
1:F:439:LEU:HD13	1:F:441:PHE:HE1	1.79	0.48
1:A:223:THR:OG1	1:A:224:THR:N	2.46	0.48
1:B:31:ASN:H	1:B:32:ILE:HD12	1.78	0.48
1:B:250:GLN:HE21	1:F:295:LEU:HB2	1.79	0.48
1:E:160:PRO:HG2	1:E:191:ILE:HD12	1.94	0.48
1:F:242:LEU:HA	1:F:245:PHE:HE2	1.78	0.48
1:A:445:ASN:HD21	1:A:447:LYS:HE2	1.79	0.48
1:D:46:HIS:CE1	1:D:49:PHE:H	2.32	0.48
1:A:67:TYR:CZ	1:A:197:VAL:HG22	2.49	0.48
1:B:263:VAL:O	1:F:356:LYS:NZ	2.46	0.48
1:C:115:SER:OG	1:C:116:GLY:N	2.47	0.48
1:A:35:HIS:CD2	1:A:369:PHE:H	2.32	0.47
1:B:151:GLN:HE22	1:B:301:GLN:HA	1.79	0.47
1:B:341:CYS:SG	1:C:211:THR:N	2.86	0.47
1:B:425:LYS:HZ2	1:B:425:LYS:C	2.17	0.47
1:E:193:ASP:HB2	1:E:441:PHE:HA	1.96	0.47
1:B:419:GLN:HE22	1:B:422:THR:N	2.13	0.47
1:B:419:GLN:OE1	1:B:420:ALA:CA	2.62	0.47
1:F:267:VAL:HG22	1:F:268:PRO:HD2	1.97	0.47
1:A:86:SER:OG	1:F:84:ASP:OD1	2.31	0.47
1:B:78:ASN:HD21	1:B:95:LEU:H	1.63	0.47
1:B:427:THR:O	1:B:427:THR:OG1	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:390:ASN:OD1	1:D:392:SER:OG	2.30	0.47
1:B:229:ASP:O	1:B:232:GLN:NE2	2.47	0.47
1:D:425:LYS:HD2	1:D:426:PRO:CD	2.45	0.47
1:B:284:SER:OG	1:B:286:ILE:O	2.33	0.47
1:E:309:LEU:HD21	1:E:312:ALA:HB2	1.97	0.47
1:F:198:ASP:OD1	1:F:201:PHE:N	2.47	0.47
1:B:51:ILE:HG22	1:B:58:VAL:HB	1.97	0.47
1:C:40:ARG:NH1	1:C:40:ARG:CG	2.73	0.47
1:C:49:PHE:HA	1:C:61:LYS:HE2	1.96	0.47
1:C:169:LYS:CE	1:C:170:GLN:NE2	2.75	0.47
1:D:240:ASP:N	1:D:240:ASP:OD1	2.47	0.47
1:D:339:THR:HG21	1:E:259:ARG:HH21	1.79	0.47
1:E:38:SER:OG	1:E:366:ASP:OD1	2.27	0.47
1:E:152:LEU:HD21	1:E:330:VAL:HB	1.96	0.47
1:C:353:SER:O	1:C:353:SER:OG	2.30	0.47
1:D:444:VAL:HG13	1:D:446:LEU:HD11	1.97	0.47
1:F:156:GLY:O	1:F:326:PHE:N	2.46	0.47
1:A:86:SER:OG	1:A:86:SER:O	2.32	0.47
1:B:212:ASN:ND2	1:F:350:TYR:OH	2.47	0.47
1:D:420:ALA:O	1:D:423:CYS:SG	2.73	0.47
1:C:93:GLN:HE21	1:C:377:THR:HA	1.80	0.47
1:D:425:LYS:N	1:D:426:PRO:HD3	2.29	0.47
1:B:38:SER:OG	1:B:366:ASP:OD1	2.29	0.46
1:D:418:SER:OG	1:D:421:ILE:HG22	2.08	0.46
1:E:97:TRP:HA	1:E:373:LEU:HD13	1.98	0.46
1:A:120:LEU:HD13	1:A:143:VAL:HG23	1.97	0.46
1:D:149:GLN:NE2	1:D:150:THR:O	2.48	0.46
1:E:56:LYS:HA	1:E:56:LYS:HD3	1.77	0.46
1:E:72:VAL:HG12	1:E:325:LEU:HB2	1.97	0.46
1:E:338:MET:HE2	1:E:361:HIS:HA	1.97	0.46
1:F:197:VAL:HG21	1:F:330:VAL:HG11	1.96	0.46
1:D:158:ALA:HB3	1:D:241:ARG:HD3	1.97	0.46
1:E:269:ASP:HA	1:E:272:ILE:HG12	1.97	0.46
1:C:101:GLY:HA3	1:C:370:ILE:HB	1.97	0.46
1:C:359:MET:O	1:C:360:ARG:NH1	2.44	0.46
1:E:78:ASN:HD21	1:E:95:LEU:H	1.63	0.46
1:B:418:SER:HB3	1:B:422:THR:HB	1.97	0.46
1:D:93:GLN:HB2	1:D:376:ILE:HG13	1.97	0.46
1:D:305:LYS:HD3	1:D:307:TYR:HE1	1.81	0.46
1:D:448:GLU:HG2	1:D:449:LYS:HG2	1.98	0.46
1:D:421:ILE:O	1:D:421:ILE:HD12	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:75:PRO:HG2	1:E:450:PHE:HE2	1.80	0.46
1:E:151:GLN:HG2	1:E:248:LYS:HB2	1.97	0.46
1:E:124:ASP:N	1:E:124:ASP:OD1	2.49	0.46
1:A:257:PHE:H	1:A:287:TYR:HE1	1.63	0.46
1:B:210:GLN:OE1	1:B:210:GLN:N	2.49	0.46
1:D:140:ARG:HH12	1:E:273:ILE:HB	1.81	0.46
1:E:94:ARG:HG2	1:E:378:LEU:HD11	1.98	0.46
1:E:210:GLN:NE2	1:E:215:ASP:OD2	2.43	0.46
1:E:217:PRO:HD2	1:E:220:ILE:HD11	1.98	0.46
1:C:108:GLN:HB2	1:C:334:ARG:HG2	1.97	0.46
1:B:44:VAL:HG13	1:B:362:VAL:HB	1.97	0.45
1:C:451:SER:OG	1:C:453:GLU:O	2.34	0.45
1:D:198:ASP:OD1	1:D:201:PHE:N	2.40	0.45
1:E:380:ALA:HA	1:E:383:MET:HB2	1.98	0.45
1:B:121:ASN:HB3	1:B:260:ALA:H	1.81	0.45
1:B:151:GLN:HB2	1:B:248:LYS:HB2	1.97	0.45
1:C:149:GLN:OE1	1:C:250:GLN:NE2	2.50	0.45
1:B:424:GLN:H	1:B:424:GLN:HE21	1.61	0.45
1:C:167:LYS:HZ2	1:C:168:GLY:C	2.18	0.45
1:A:333:THR:HG1	1:A:334:ARG:NH1	2.14	0.45
1:B:332:THR:O	1:B:335:SER:OG	2.28	0.45
1:F:33:PHE:HB3	1:F:372:GLN:HG3	1.99	0.45
1:A:39:SER:H	1:F:415:TYR:HD2	1.63	0.45
1:A:160:PRO:HG2	1:A:191:ILE:HB	1.99	0.45
1:C:254:ARG:HG2	1:C:255:HIS:CD2	2.52	0.45
1:A:72:VAL:HG23	1:A:446:LEU:HD23	1.99	0.45
1:B:453:GLU:OE2	1:B:455:ASP:N	2.49	0.45
1:E:31:ASN:HB3	1:E:32:ILE:HD12	1.99	0.45
1:E:150:THR:HA	1:E:249:GLU:HA	1.99	0.45
1:E:419:GLN:HG2	1:E:420:ALA:H	1.79	0.45
1:F:210:GLN:NE2	1:F:215:ASP:OD2	2.40	0.45
1:A:74:LEU:HD21	1:A:97:TRP:HD1	1.81	0.45
1:A:155:VAL:HA	1:A:327:VAL:HG12	1.99	0.45
1:B:231:LEU:O	1:B:235:ALA:N	2.50	0.45
1:D:425:LYS:CD	1:D:425:LYS:C	2.85	0.45
1:E:121:ASN:HB3	1:E:260:ALA:H	1.81	0.45
1:E:352:ASN:HB3	1:F:137:GLN:HA	1.99	0.45
1:A:91:THR:HG23	1:A:92:THR:HG22	1.99	0.45
1:A:117:HIS:H	1:A:144:GLY:HA3	1.80	0.45
1:B:316:ASN:OD1	1:B:319:ILE:N	2.50	0.45
1:D:95:LEU:HB3	1:D:375:SER:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:150:THR:OG1	1:D:151:GLN:N	2.49	0.45
1:D:454:LEU:HA	1:D:457:TYR:HD2	1.81	0.45
1:E:49:PHE:HA	1:E:61:LYS:HD2	1.99	0.45
1:E:195:ASP:N	1:E:195:ASP:OD1	2.48	0.45
1:A:249:GLU:O	1:A:250:GLN:NE2	2.50	0.45
1:B:425:LYS:CE	1:B:425:LYS:C	2.86	0.45
1:E:45:GLY:O	1:E:361:HIS:N	2.49	0.45
1:F:108:GLN:N	1:F:364:GLU:OE2	2.49	0.45
1:A:225:CYS:O	1:A:226:LYS:NZ	2.41	0.44
1:C:150:THR:HA	1:C:249:GLU:HG3	1.99	0.44
1:D:66:GLN:O	1:D:68:ARG:NE	2.48	0.44
1:D:73:VAL:HG23	1:D:446:LEU:H	1.82	0.44
1:D:320:CYS:HB2	1:D:324:GLN:H	1.82	0.44
1:D:198:ASP:OD1	1:D:200:GLY:N	2.50	0.44
1:A:41:LEU:HD11	1:A:367:LEU:HD11	1.98	0.44
1:D:219:ASP:N	1:D:219:ASP:OD1	2.39	0.44
1:E:248:LYS:HA	1:E:248:LYS:HD3	1.82	0.44
1:A:56:LYS:HD2	1:A:56:LYS:HA	1.79	0.44
1:B:211:THR:N	1:F:341:CYS:SG	2.91	0.44
1:E:46:HIS:CE1	1:E:48:TYR:HB2	2.52	0.44
1:E:68:ARG:HA	1:E:68:ARG:HD3	1.82	0.44
1:E:150:THR:HG23	1:E:249:GLU:HG3	2.00	0.44
1:C:104:VAL:HG21	1:C:329:VAL:HG21	1.99	0.44
1:C:259:ARG:HB3	1:C:286:ILE:HG21	2.00	0.44
1:D:425:LYS:HD2	1:D:425:LYS:C	2.36	0.44
1:F:163:GLU:OE2	1:F:229:ASP:N	2.51	0.44
1:F:219:ASP:OD1	1:F:219:ASP:N	2.51	0.44
1:A:74:LEU:HD12	1:A:75:PRO:HD2	1.98	0.44
1:C:102:LEU:HD23	1:C:155:VAL:HG11	1.99	0.44
1:C:170:GLN:O	1:C:170:GLN:HG2	2.17	0.44
1:F:45:GLY:O	1:F:361:HIS:N	2.51	0.44
1:F:94:ARG:HB3	1:F:376:ILE:HB	2.00	0.44
1:A:98:ALA:HB3	1:A:372:GLN:HB3	2.00	0.44
1:A:343:SER:OG	1:A:345:THR:O	2.35	0.44
1:B:122:LYS:HA	1:B:122:LYS:HD3	1.81	0.44
1:B:279:ARG:HH21	1:F:139:ASN:HD22	1.66	0.44
1:B:368:GLN:HB3	1:B:459:LEU:HD22	1.99	0.44
1:D:120:LEU:N	1:D:141:VAL:O	2.48	0.44
1:F:28:THR:OG1	1:F:375:SER:OG	2.31	0.44
1:F:430:LYS:HA	1:F:430:LYS:HD2	1.76	0.44
1:C:169:LYS:HE2	1:C:170:GLN:HE22	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:350:TYR:HE2	1:D:138:ASP:HA	1.83	0.43
1:E:158:ALA:HB3	1:E:241:ARG:HA	2.00	0.43
1:A:100:THR:OG1	1:A:101:GLY:N	2.51	0.43
1:C:82:LEU:HD23	1:C:84:ASP:H	1.83	0.43
1:C:310:GLN:HE22	1:C:311:LYS:HE3	1.82	0.43
1:D:162:GLY:N	1:D:189:SER:O	2.50	0.43
1:D:341:CYS:HG	1:E:211:THR:H	1.65	0.43
1:C:161:LEU:HG	1:C:233:MET:HE3	2.00	0.43
1:D:343:SER:HA	1:D:355:TYR:HA	2.01	0.43
1:E:68:ARG:H	1:E:330:VAL:HG22	1.83	0.43
1:A:71:LYS:HB2	1:A:443:GLU:HA	2.01	0.43
1:A:155:VAL:HG13	1:A:243:PHE:HB2	2.00	0.43
1:C:61:LYS:HG3	1:C:66:GLN:NE2	2.32	0.43
1:B:74:LEU:O	1:B:447:LYS:NZ	2.51	0.43
1:C:108:GLN:H	1:C:334:ARG:NH1	2.15	0.43
1:A:86:SER:HA	1:F:84:ASP:HA	2.01	0.43
1:B:424:GLN:NE2	1:B:424:GLN:N	2.60	0.43
1:C:39:SER:C	1:C:40:ARG:CG	2.84	0.43
1:B:46:HIS:CE1	1:B:49:PHE:H	2.37	0.43
1:B:105:GLY:N	1:B:366:ASP:O	2.48	0.43
1:B:242:LEU:HA	1:B:245:PHE:HZ	1.83	0.43
1:F:32:ILE:HD13	1:F:32:ILE:HA	1.88	0.43
1:B:154:MET:HB2	1:B:328:THR:HB	2.01	0.43
1:C:209:LEU:HD23	1:C:209:LEU:HA	1.87	0.43
1:D:369:PHE:HB3	1:D:371:PHE:CE2	2.53	0.43
1:E:66:GLN:HA	1:E:196:MET:HA	2.00	0.43
1:F:123:TYR:HE2	1:F:284:SER:H	1.67	0.43
1:B:381:GLU:H	1:B:381:GLU:HG3	1.67	0.43
1:D:104:VAL:HB	1:D:303:PHE:HD1	1.84	0.43
1:E:165:TRP:N	1:E:203:ALA:O	2.52	0.43
1:A:412:THR:O	1:A:412:THR:OG1	2.37	0.42
1:A:447:LYS:HB2	1:A:447:LYS:HE3	1.85	0.42
1:D:120:LEU:HD23	1:D:120:LEU:HA	1.84	0.42
1:F:111:GLY:O	1:F:335:SER:N	2.49	0.42
1:A:148:LYS:HD3	1:A:150:THR:HB	2.01	0.42
1:C:414:ARG:HE	1:C:414:ARG:HB3	1.55	0.42
1:E:78:ASN:ND2	1:E:95:LEU:O	2.51	0.42
1:E:254:ARG:HG2	1:E:255:HIS:CD2	2.54	0.42
1:A:236:ASP:N	1:A:236:ASP:OD1	2.51	0.42
1:B:75:PRO:HD3	1:B:447:LYS:HA	2.02	0.42
1:B:246:LEU:HD12	1:B:302:LEU:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:94:ARG:CZ	1:D:399:PHE:HB2	2.49	0.42
1:D:424:GLN:N	1:D:424:GLN:CD	2.72	0.42
1:A:71:LYS:HB3	1:A:326:PHE:HD1	1.85	0.42
1:A:193:ASP:N	1:A:193:ASP:OD1	2.52	0.42
1:B:425:LYS:NZ	1:B:425:LYS:C	2.73	0.42
1:C:67:TYR:N	1:C:195:ASP:O	2.52	0.42
1:E:205:ASN:HB3	1:E:208:ASP:H	1.84	0.42
1:F:44:VAL:HG22	1:F:362:VAL:HG23	2.02	0.42
1:F:204:MET:HB2	1:F:204:MET:HE2	1.83	0.42
1:F:392:SER:OG	1:F:395:GLU:OE2	2.32	0.42
1:C:169:LYS:HD2	1:C:170:GLN:H	1.84	0.42
1:C:276:SER:OG	1:C:277:GLY:N	2.52	0.42
1:C:309:LEU:HD21	1:C:312:ALA:HB2	2.01	0.42
1:E:118:PRO:HA	1:E:142:ASN:HA	2.01	0.42
1:A:82:LEU:HD12	1:A:83:PRO:HD2	2.02	0.42
1:A:148:LYS:HG2	1:A:199:THR:HG23	2.02	0.42
1:A:352:ASN:OD1	1:A:352:ASN:N	2.46	0.42
1:B:46:HIS:CE1	1:B:48:TYR:H	2.37	0.42
1:F:107:GLY:H	1:F:364:GLU:CD	2.22	0.42
1:F:311:LYS:HE3	1:F:317:ASN:HD21	1.84	0.42
1:B:63:SER:OG	1:B:64:GLY:N	2.52	0.42
1:E:459:LEU:H	1:E:459:LEU:HD23	1.85	0.42
1:A:153:CYS:HA	1:A:329:VAL:HG22	2.02	0.42
1:B:103:GLU:HB3	1:B:368:GLN:HE21	1.85	0.42
1:B:337:ASN:HD21	1:B:359:MET:HB3	1.84	0.42
1:C:46:HIS:HA	1:C:47:PRO:HD3	1.81	0.42
1:E:106:ARG:NH2	1:E:331:ASP:OD2	2.49	0.42
1:B:136:GLY:O	1:F:352:ASN:ND2	2.46	0.42
1:C:110:LEU:HD13	1:C:334:ARG:HG3	2.02	0.42
1:C:302:LEU:HD13	1:C:302:LEU:HA	1.95	0.42
1:D:213:LYS:HB3	1:E:273:ILE:HD11	2.01	0.42
1:E:72:VAL:HG23	1:E:444:VAL:HG12	2.02	0.42
1:F:301:GLN:HE21	1:F:303:PHE:HB2	1.83	0.42
1:C:276:SER:HA	1:C:280:THR:HB	2.02	0.41
1:C:341:CYS:SG	1:D:212:ASN:N	2.92	0.41
1:A:207:ALA:HB1	1:A:213:LYS:HG3	2.01	0.41
1:B:425:LYS:CE	1:B:428:PRO:CD	2.95	0.41
1:E:138:ASP:O	1:F:279:ARG:NE	2.53	0.41
1:E:165:TRP:HB2	1:E:204:MET:HG3	2.01	0.41
1:F:151:GLN:NE2	1:F:302:LEU:H	2.18	0.41
1:B:58:VAL:HG12	1:B:59:VAL:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:344:VAL:HB	1:C:354:ASP:HA	2.03	0.41
1:D:153:CYS:HA	1:D:329:VAL:HG22	2.02	0.41
1:F:311:LYS:HA	1:F:311:LYS:HD3	1.87	0.41
1:A:254:ARG:HG2	1:A:292:SER:HB3	2.01	0.41
1:A:423:CYS:HB3	1:B:171:CYS:HB3	1.78	0.41
1:D:197:VAL:HG21	1:D:330:VAL:HG11	2.03	0.41
1:D:373:LEU:HD12	1:D:373:LEU:HA	1.88	0.41
1:F:418:SER:OG	1:F:421:ILE:HG12	2.20	0.41
1:A:165:TRP:HD1	1:A:203:ALA:H	1.67	0.41
1:C:242:LEU:HD23	1:C:242:LEU:HA	1.85	0.41
1:C:414:ARG:C	1:C:414:ARG:NE	2.73	0.41
1:E:73:VAL:HG22	1:E:445:ASN:HA	2.01	0.41
1:A:336:THR:OG1	1:A:337:ASN:N	2.53	0.41
1:B:254:ARG:HB2	1:B:292:SER:HB3	2.01	0.41
1:B:341:CYS:SG	1:C:212:ASN:N	2.86	0.41
1:F:100:THR:OG1	1:F:370:ILE:O	2.32	0.41
1:D:151:GLN:HE22	1:D:302:LEU:N	2.12	0.41
1:D:383:MET:HA	1:D:386:ILE:HG22	2.03	0.41
1:D:394:LEU:HA	1:D:397:TRP:HE3	1.86	0.41
1:E:336:THR:O	1:E:361:HIS:ND1	2.54	0.41
1:E:459:LEU:HA	1:E:462:LYS:HD3	2.03	0.41
1:B:97:TRP:HA	1:B:373:LEU:HD13	2.02	0.41
1:B:421:ILE:O	1:B:422:THR:C	2.59	0.41
1:D:94:ARG:HH12	1:D:378:LEU:HD22	1.85	0.41
1:D:425:LYS:CD	1:D:426:PRO:CG	2.95	0.41
1:A:279:ARG:HA	1:A:279:ARG:HD2	1.95	0.41
1:C:93:GLN:HG3	1:C:377:THR:HA	2.02	0.41
1:C:352:ASN:OD1	1:C:352:ASN:N	2.53	0.41
1:D:36:ALA:HB2	1:D:450:PHE:HE1	1.86	0.41
1:D:145:MET:N	1:D:145:MET:SD	2.93	0.41
1:D:218:ILE:H	1:D:218:ILE:HG12	1.68	0.41
1:D:339:THR:OG1	1:D:357:GLU:OE2	2.30	0.41
1:E:96:VAL:HB	1:E:376:ILE:HD11	2.02	0.41
1:E:372:GLN:HG2	1:E:373:LEU:H	1.86	0.41
1:B:117:HIS:HB2	1:B:217:PRO:HA	2.02	0.41
1:B:120:LEU:N	1:B:141:VAL:O	2.42	0.41
1:C:195:ASP:OD2	1:C:226:LYS:NZ	2.38	0.41
1:B:316:ASN:ND2	1:B:319:ILE:O	2.37	0.40
1:C:152:LEU:HD13	1:C:154:MET:HG2	2.02	0.40
1:F:74:LEU:HD23	1:F:323:ASN:HA	2.03	0.40
1:A:46:HIS:CE1	1:A:48:TYR:HB2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:CYS:SG	1:A:171:CYS:O	2.79	0.40
1:A:301:GLN:H	1:A:301:GLN:HG3	1.71	0.40
1:B:71:LYS:O	1:B:444:VAL:N	2.53	0.40
1:B:123:TYR:CD2	1:B:284:SER:HB2	2.56	0.40
1:C:368:GLN:HE22	1:C:458:PRO:HG2	1.86	0.40
1:E:157:CYS:HB3	1:E:320:CYS:SG	2.61	0.40
1:B:345:THR:HG1	1:B:347:SER:HG	1.68	0.40
1:B:419:GLN:NE2	1:B:422:THR:N	2.69	0.40
1:C:360:ARG:HA	1:C:360:ARG:HD3	1.86	0.40
1:D:238:TYR:O	1:D:315:HIS:N	2.54	0.40
1:E:386:ILE:O	1:E:390:ASN:N	2.40	0.40
1:B:425:LYS:HE2	1:B:428:PRO:CD	2.52	0.40
1:C:48:TYR:HE1	1:C:115:SER:HA	1.86	0.40
1:E:414:ARG:NH1	1:E:429:GLU:OE1	2.55	0.40
1:F:273:ILE:HD13	1:F:273:ILE:HA	1.95	0.40
1:A:108:GLN:HB3	1:A:334:ARG:HD3	2.04	0.40
1:A:254:ARG:NH1	1:A:255:HIS:HB2	2.36	0.40
1:A:337:ASN:ND2	1:A:361:HIS:HD2	2.18	0.40
1:C:124:ASP:N	1:C:124:ASP:OD1	2.53	0.40
1:F:146:ASP:HB3	1:F:292:SER:HA	2.03	0.40
1:F:157:CYS:SG	1:F:316:ASN:ND2	2.95	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	442/447 (99%)	384 (87%)	57 (13%)	1 (0%)	47 80
1	B	445/447 (100%)	399 (90%)	42 (9%)	4 (1%)	17 55
1	C	445/447 (100%)	389 (87%)	55 (12%)	1 (0%)	47 80
1	D	443/447 (99%)	386 (87%)	57 (13%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	441/447 (99%)	388 (88%)	52 (12%)	1 (0%)	47	80
1	F	442/447 (99%)	393 (89%)	47 (11%)	2 (0%)	29	68
All	All	2658/2682 (99%)	2339 (88%)	310 (12%)	9 (0%)	44	75

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	420	ALA
1	A	289	ASN
1	F	426	PRO
1	B	418	SER
1	B	422	THR
1	B	426	PRO
1	C	416	VAL
1	E	420	ALA
1	F	425	LYS

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	388/390 (100%)	379 (98%)	9 (2%)	50	69
1	B	390/390 (100%)	379 (97%)	11 (3%)	43	65
1	C	390/390 (100%)	382 (98%)	8 (2%)	53	71
1	D	389/390 (100%)	380 (98%)	9 (2%)	50	69
1	E	388/390 (100%)	381 (98%)	7 (2%)	59	76
1	F	388/390 (100%)	381 (98%)	7 (2%)	59	76
All	All	2333/2340 (100%)	2282 (98%)	51 (2%)	54	70

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	TYR

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Mol	Chain	Res	Type
1	A	172	THR
1	A	173	ASN
1	A	174	THR
1	A	204	MET
1	A	247	ARG
1	A	362	VAL
1	A	367	LEU
1	A	398	ASN
1	B	53	ARG
1	B	167	LYS
1	B	269	ASP
1	B	412	THR
1	B	415	TYR
1	B	416	VAL
1	B	419	GLN
1	B	421	ILE
1	B	424	GLN
1	B	425	LYS
1	B	459	LEU
1	C	40	ARG
1	C	41	LEU
1	C	80	PHE
1	C	171	CYS
1	C	174	THR
1	C	414	ARG
1	C	415	TYR
1	C	423	CYS
1	D	165	TRP
1	D	241	ARG
1	D	243	PHE
1	D	412	THR
1	D	421	ILE
1	D	422	THR
1	D	423	CYS
1	D	425	LYS
1	D	454	LEU
1	E	42	LEU
1	E	171	CYS
1	E	193	ASP
1	E	413	TYR
1	E	415	TYR
1	E	424	GLN

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Mol	Chain	Res	Type
1	E	459	LEU
1	F	171	CYS
1	F	173	ASN
1	F	180	ASP
1	F	267	VAL
1	F	422	THR
1	F	424	GLN
1	F	425	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	93	GLN
1	A	250	GLN
1	A	258	ASN
1	A	289	ASN
1	A	337	ASN
1	A	361	HIS
1	A	372	GLN
1	B	55	ASN
1	B	142	ASN
1	B	149	GLN
1	B	212	ASN
1	B	232	GLN
1	B	372	GLN
1	B	424	GLN
1	C	78	ASN
1	C	139	ASN
1	C	173	ASN
1	C	210	GLN
1	C	212	ASN
1	C	417	GLN
1	C	419	GLN
1	D	139	ASN
1	D	149	GLN
1	D	258	ASN
1	E	139	ASN
1	E	212	ASN
1	E	289	ASN
1	E	315	HIS
1	E	337	ASN
1	E	372	GLN

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Mol	Chain	Res	Type
1	E	417	GLN
1	F	31	ASN
1	F	139	ASN
1	F	301	GLN
1	F	316	ASN
1	F	317	ASN
1	F	424	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 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)

There are no chain breaks in this entry.

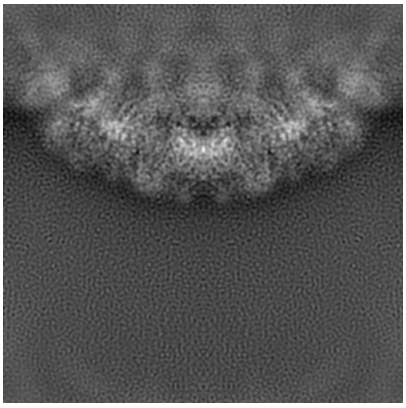
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-0816. These allow visual inspection of the internal detail of the map and identification of artifacts.

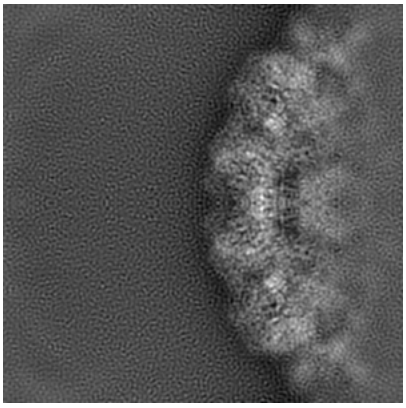
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

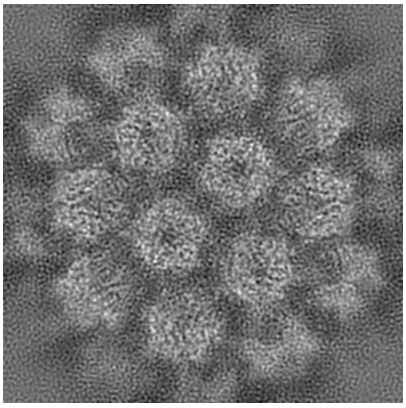
6.1.1 Primary map



X



Y

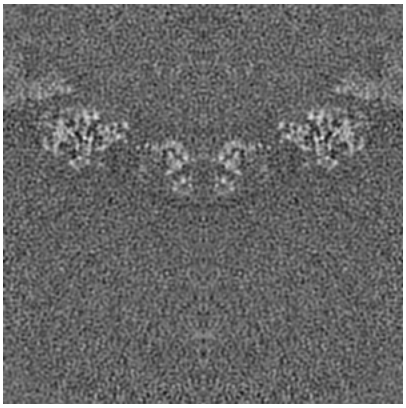


Z

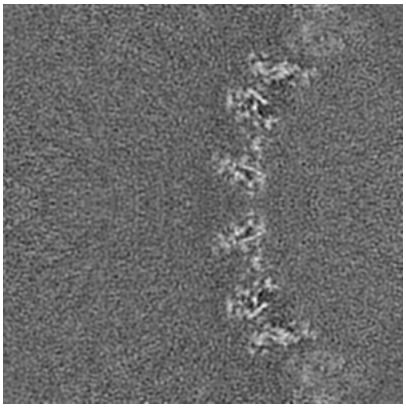
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

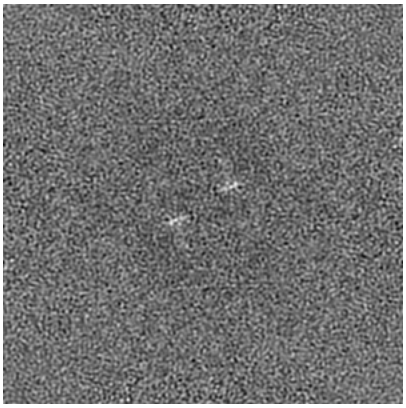
6.2.1 Primary map



X Index: 210



Y Index: 210

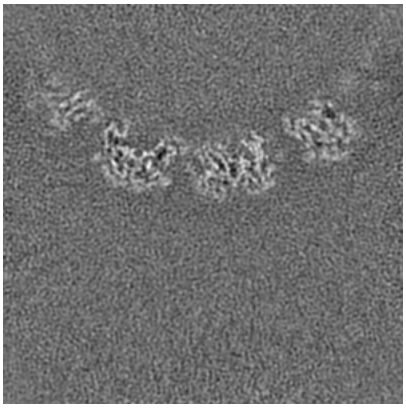


Z Index: 210

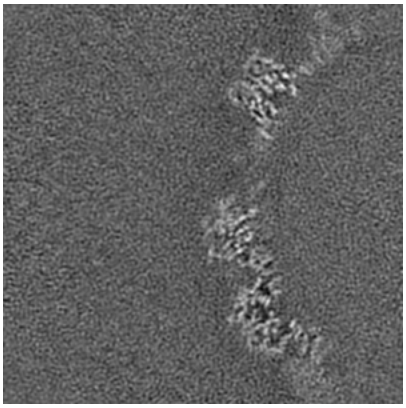
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

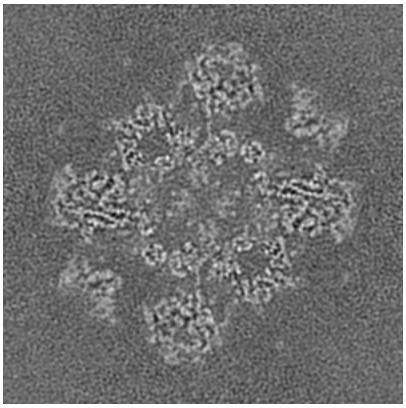
6.3.1 Primary map



X Index: 259



Y Index: 196

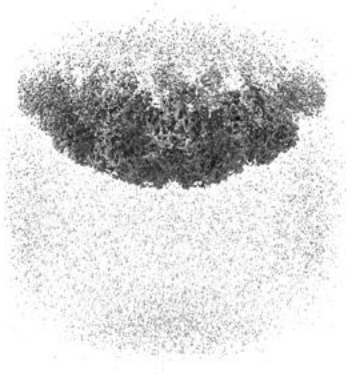


Z Index: 272

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

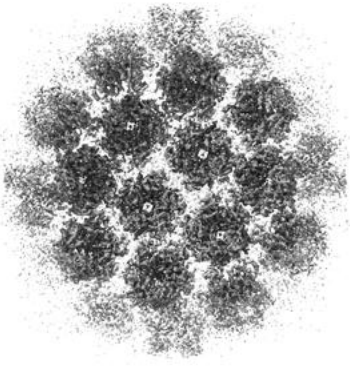
6.4 Orthogonal surface views (i)

6.4.1 Primary map



X

Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

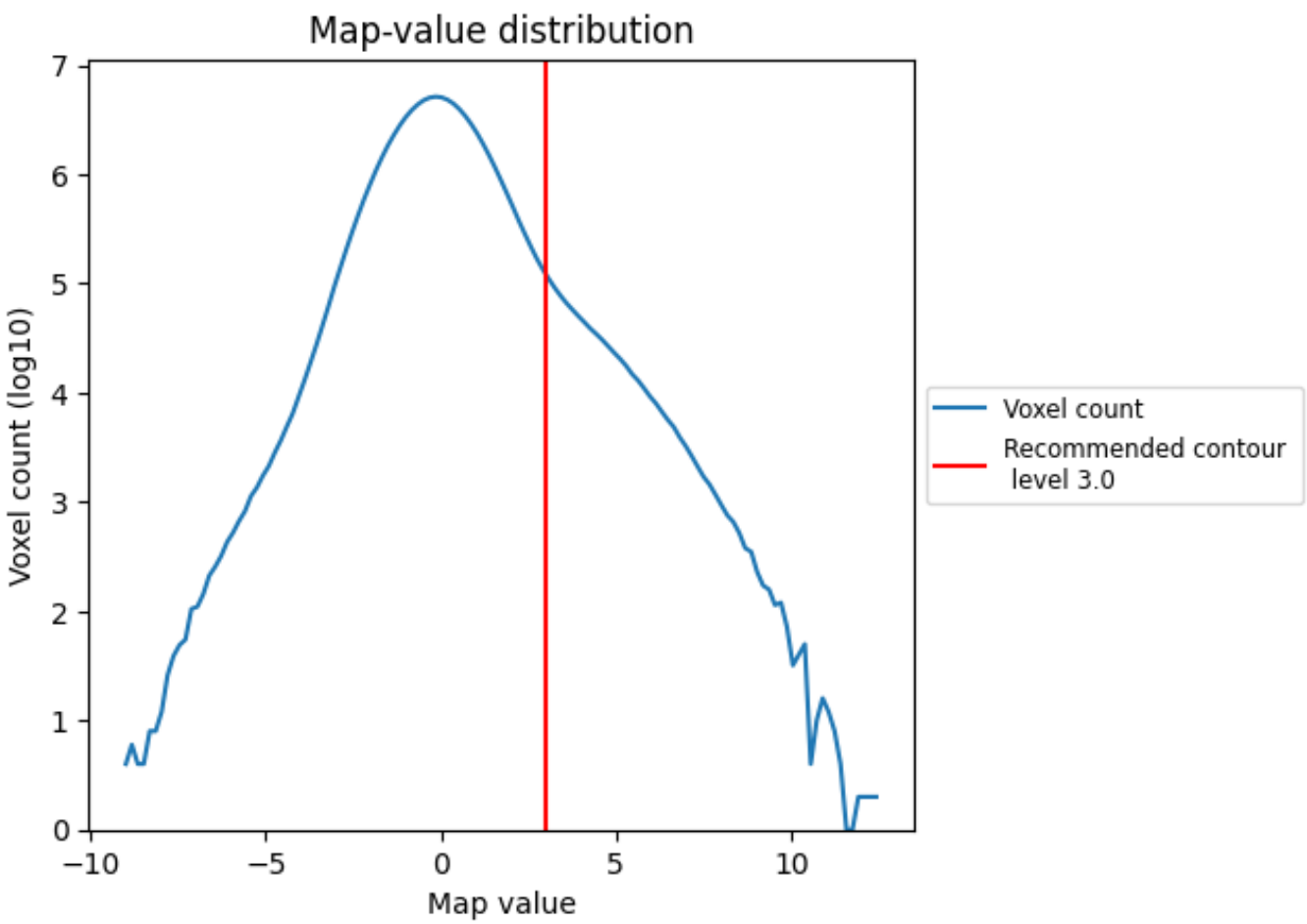
6.5 Mask visualisation (i)

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

7 Map analysis (i)

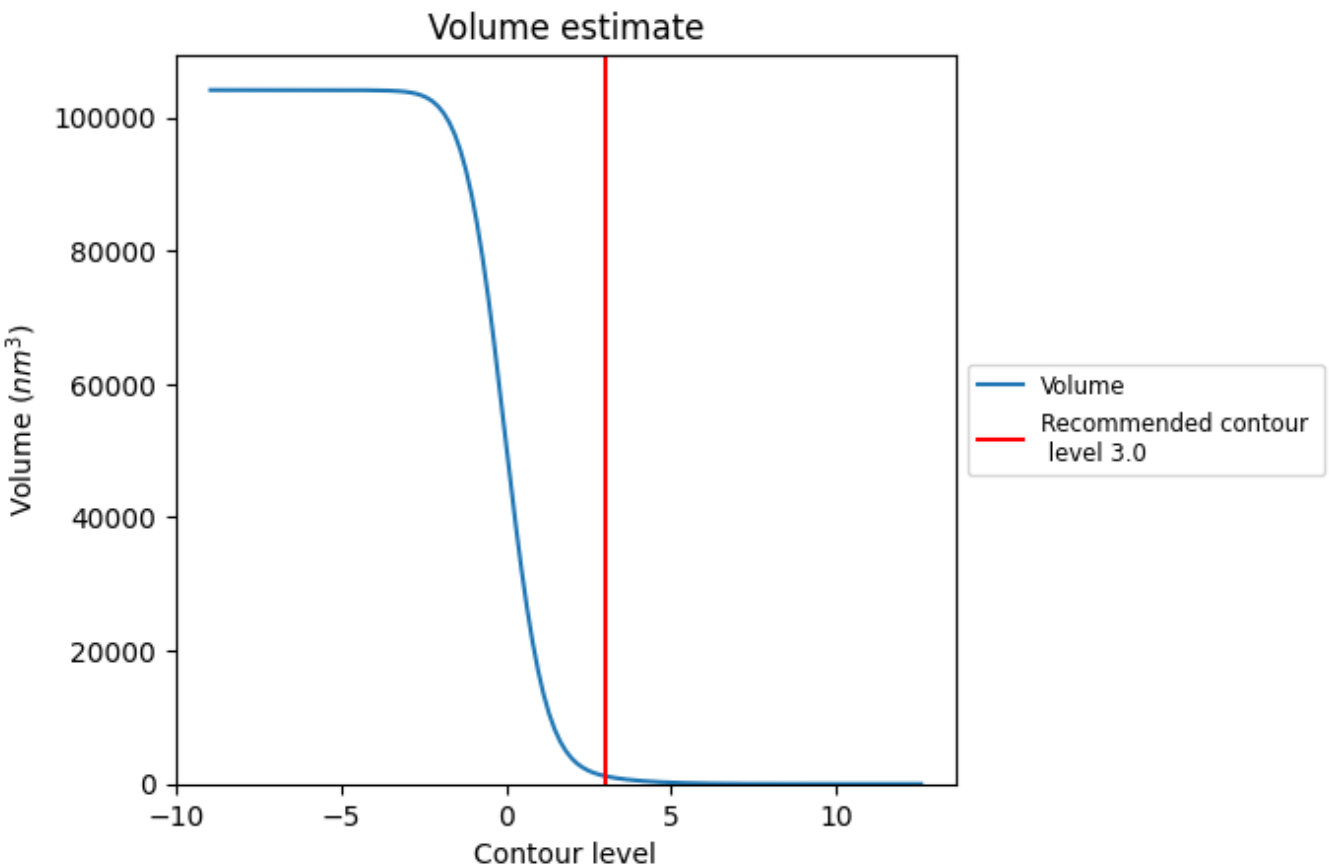
This section contains the results of statistical analysis of the map.

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.

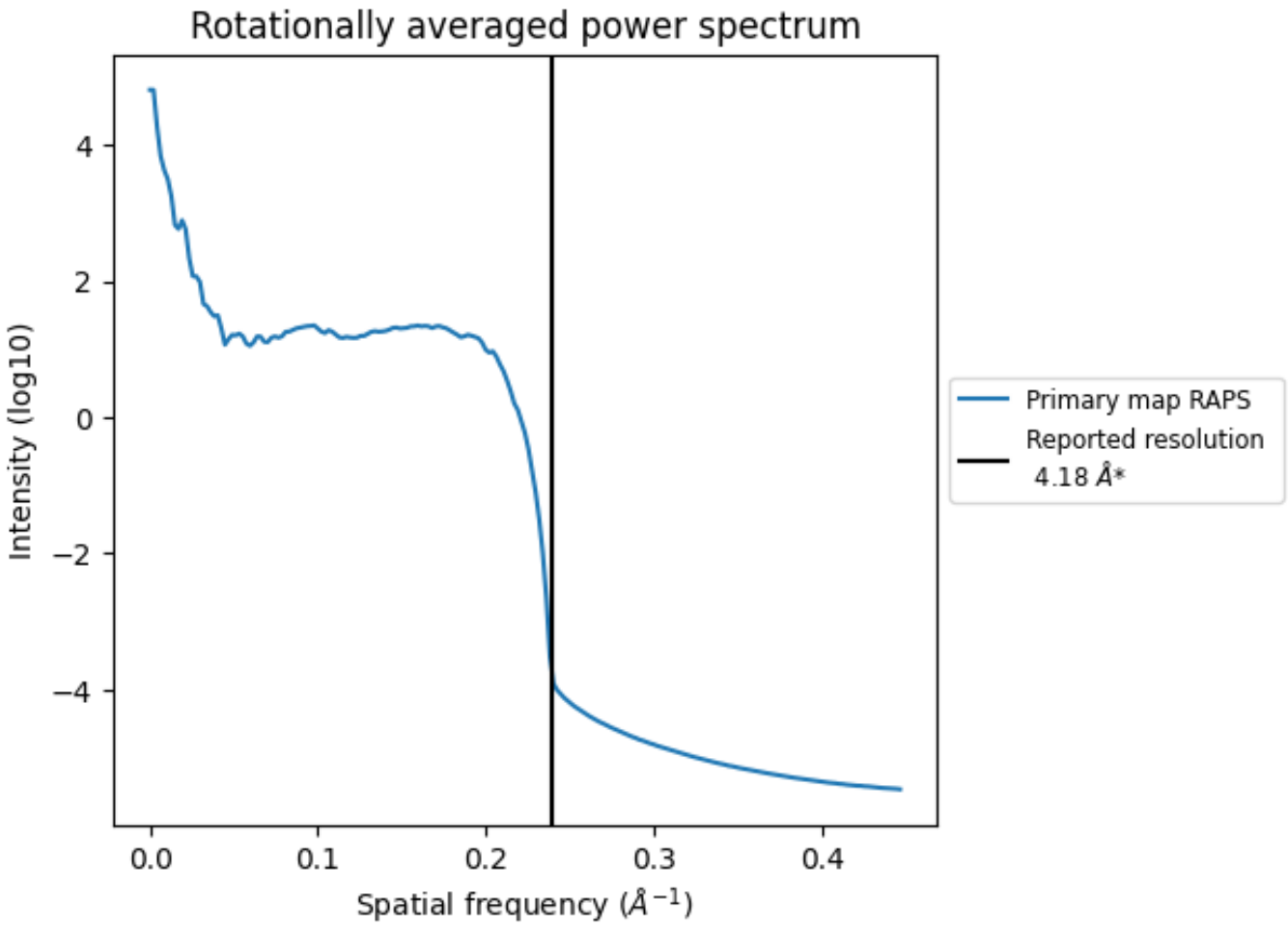
7.2 Volume estimate (i)



The volume at the recommended contour level is 1186 nm^3; this corresponds to an approximate mass of 1072 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.239 Å^{-1}

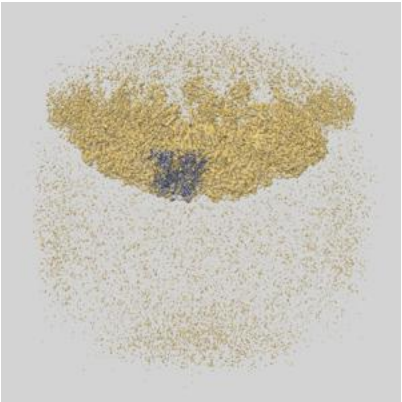
8 Fourier-Shell correlation (i)

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

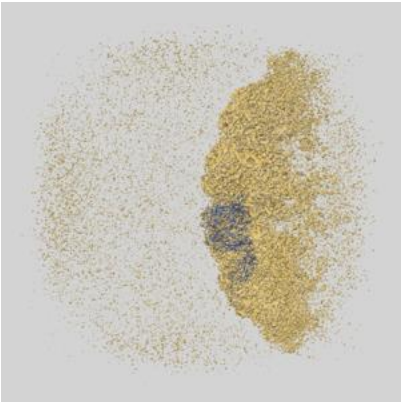
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-0816 and PDB model 6L31. Per-residue inclusion information can be found in section 3 on page 4.

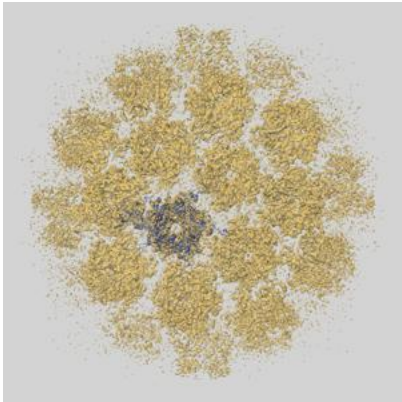
9.1 Map-model overlay (i)



X



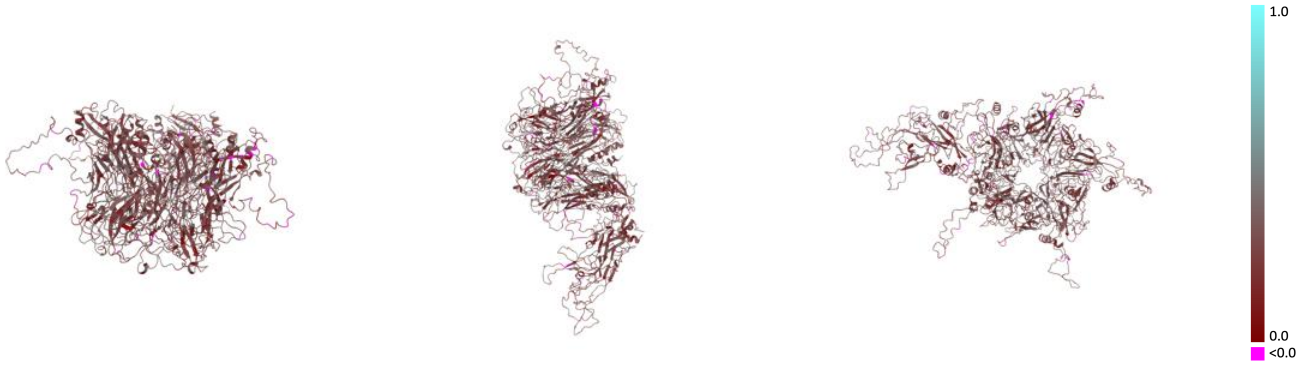
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

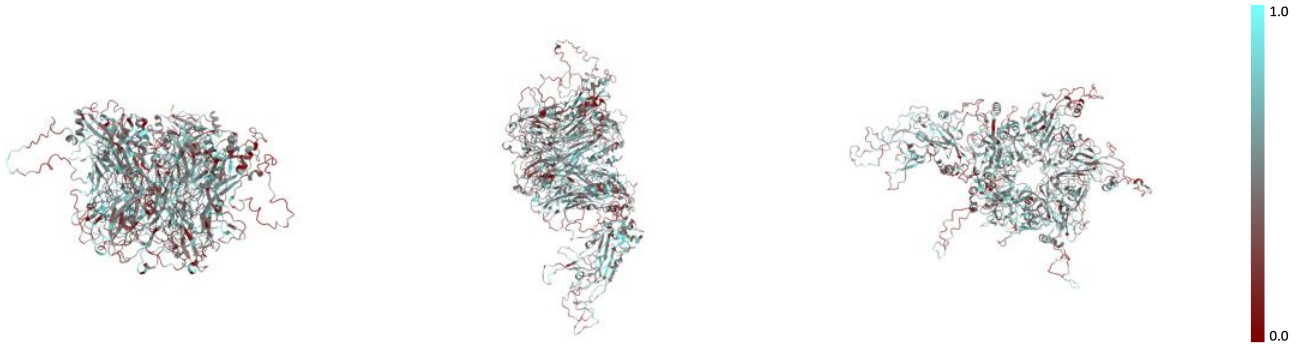
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

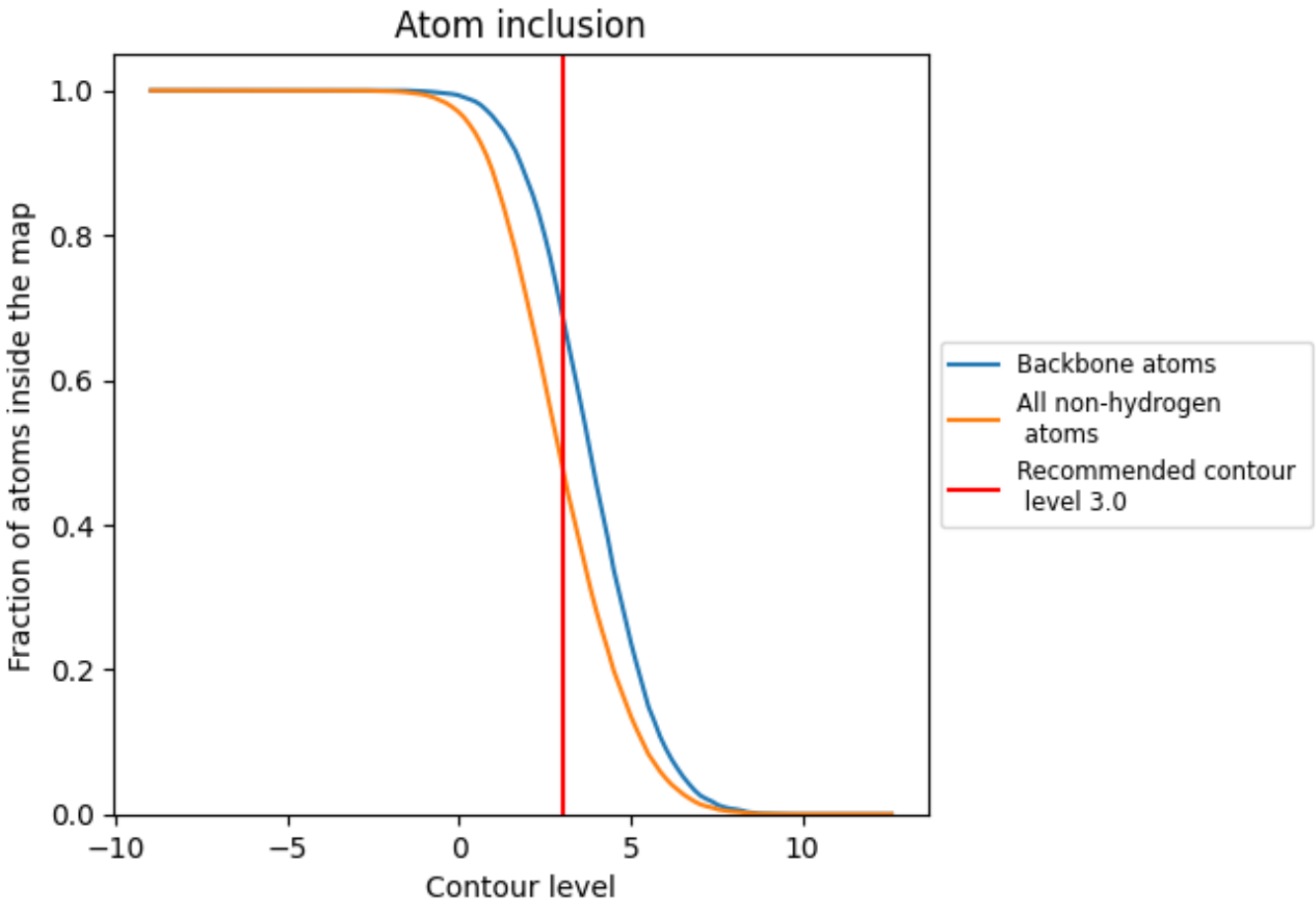
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.0).

9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 48% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4808	0.2880
A	0.4892	0.2740
B	0.4872	0.2920
C	0.5076	0.3060
D	0.4460	0.2870
E	0.4568	0.2800
F	0.4980	0.2910