



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 05:40 AM UTC

PDB ID : 7JZH / pdb_00007jzh
EMDB ID : EMD-22531
Title : The Cryo-EM structure of the Glutamate decarboxylase from Escherichia coli
Authors : Su, C.-C.
Deposited on : 2020-09-02
Resolution : 3.59 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

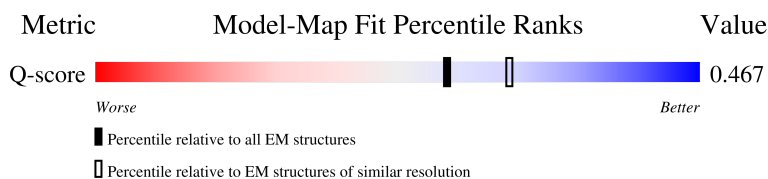
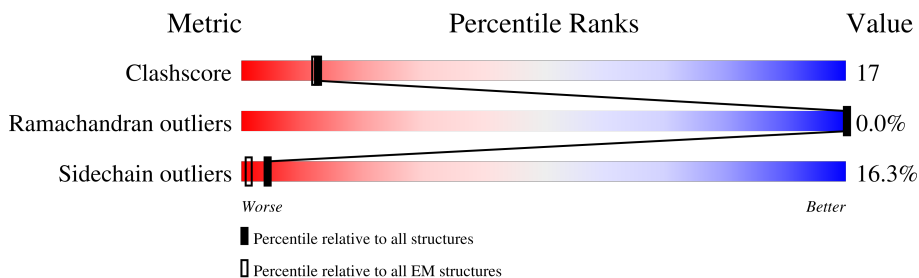
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.59 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	12565 (3.09 - 4.09)

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	466	20% 55% 31% 6% 8%
1	B	466	20% 56% 29% 6% 8%
1	C	466	20% 54% 32% 5% 8%
1	D	466	20% 54% 33% 5% 8%

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Mol	Chain	Length	Quality of chain
1	E	466	19% 56% 31% 5% 8%
1	F	466	19% 55% 31% 6% 8%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 20328 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.

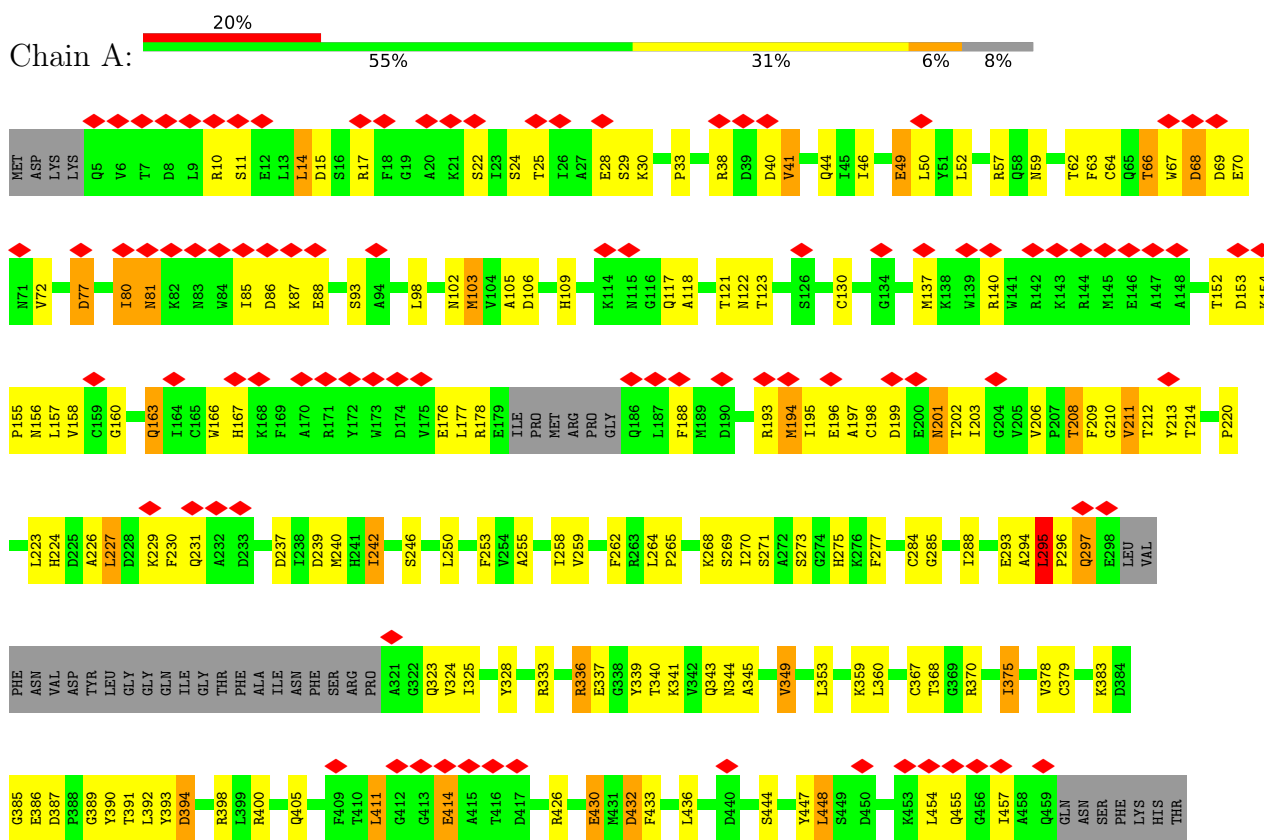
- Molecule 1 is a protein called Glutamate decarboxylase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	427	Total	C	N	O	S	0	0
			3388	2158	576	631	23		
1	B	427	Total	C	N	O	S	0	0
			3388	2158	576	631	23		
1	C	427	Total	C	N	O	S	0	0
			3388	2158	576	631	23		
1	D	427	Total	C	N	O	S	0	0
			3388	2158	576	631	23		
1	E	427	Total	C	N	O	S	0	0
			3388	2158	576	631	23		
1	F	427	Total	C	N	O	S	0	0
			3388	2158	576	631	23		

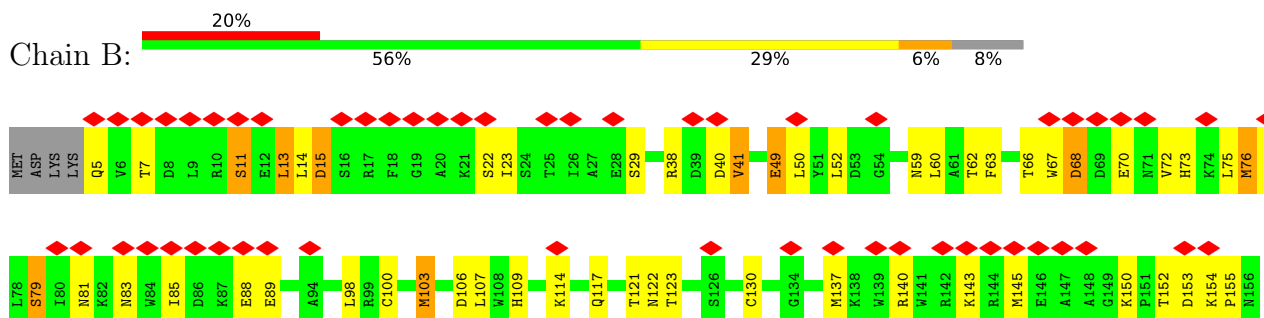
3 Residue-property plots

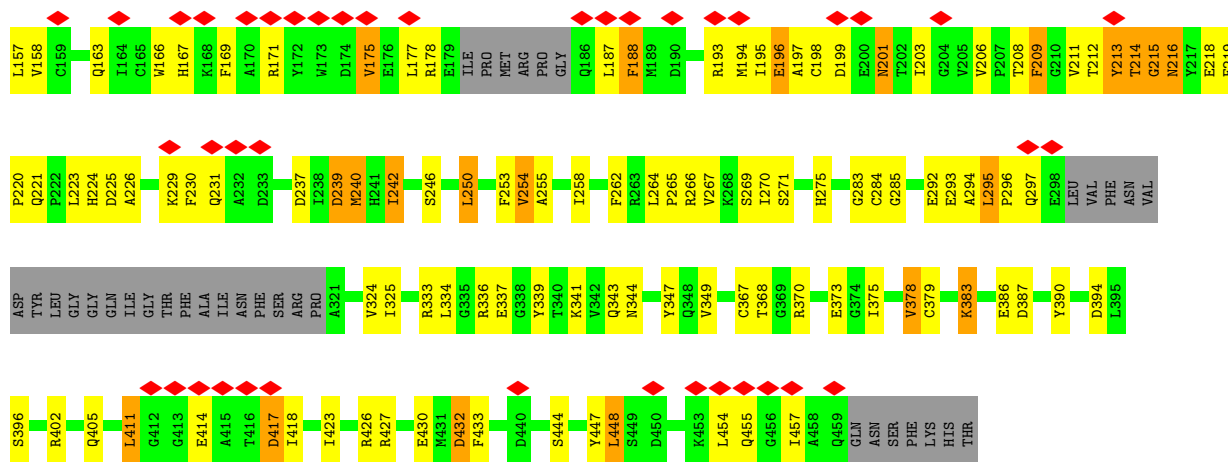
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Glutamate decarboxylase

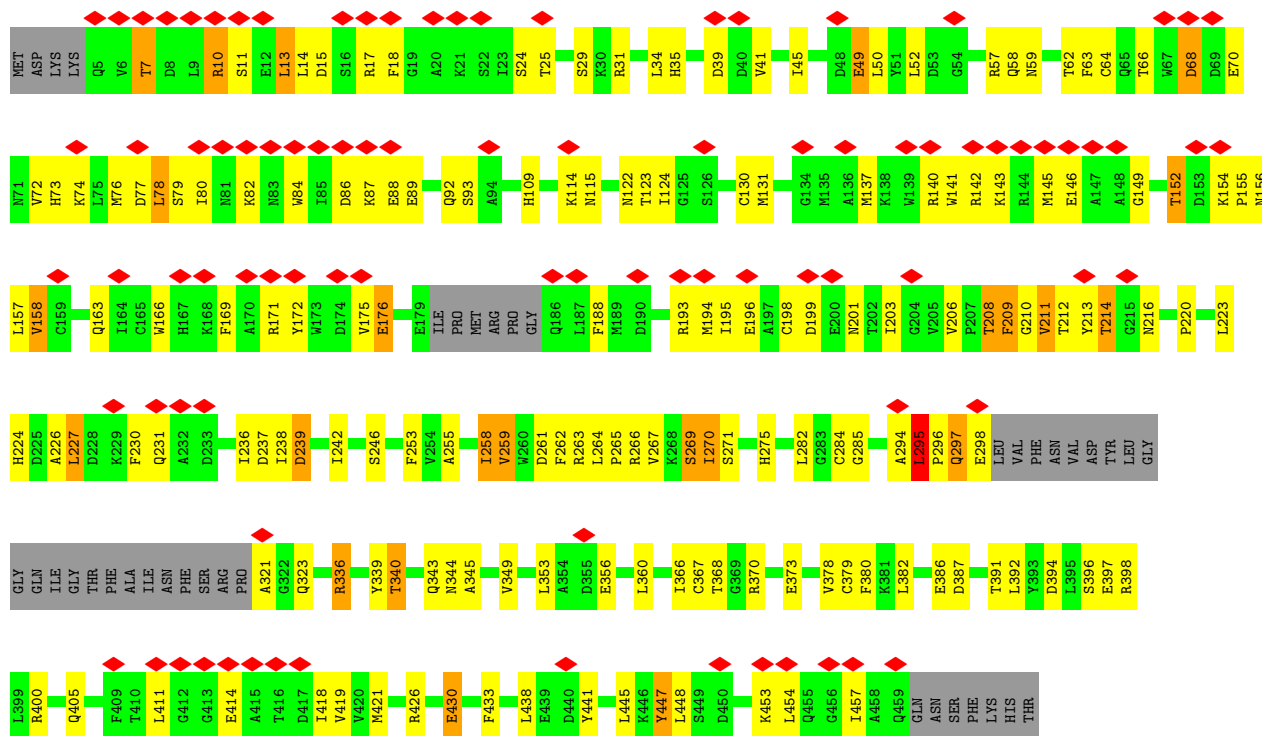


• Molecule 1: Glutamate decarboxylase

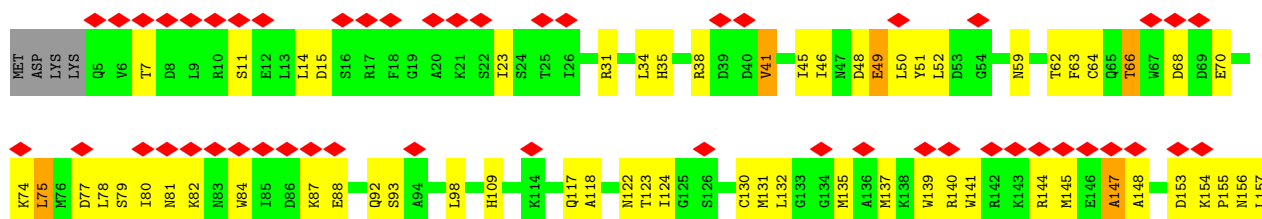


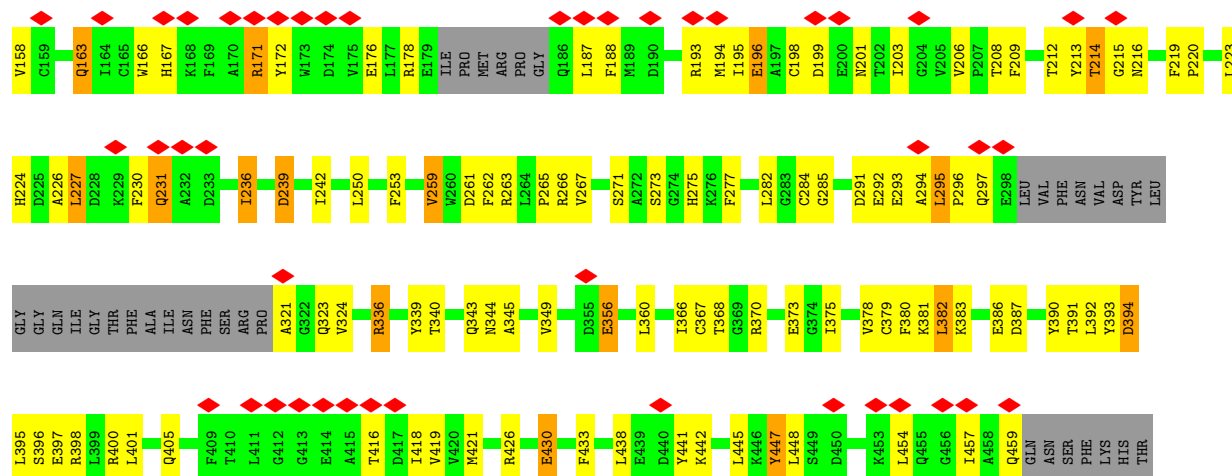


• Molecule 1: Glutamate decarboxylase

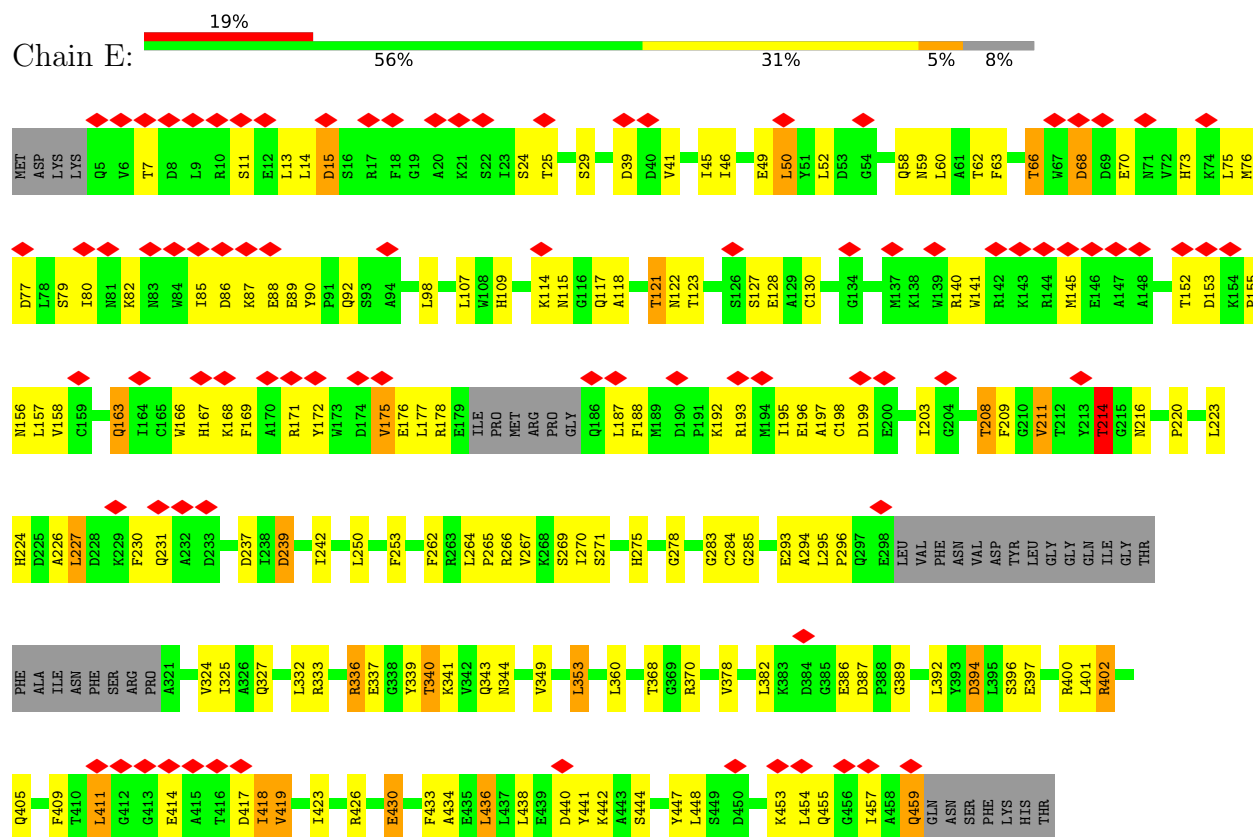


• Molecule 1: Glutamate decarboxylase

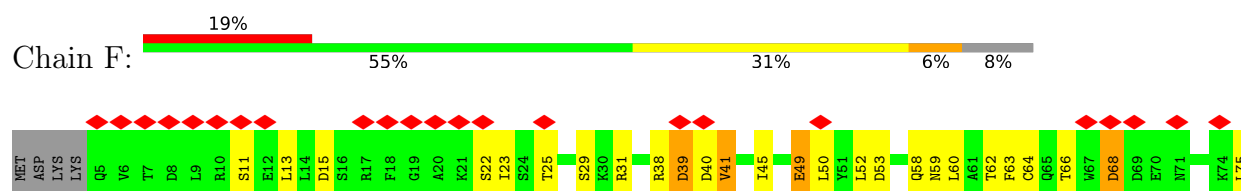


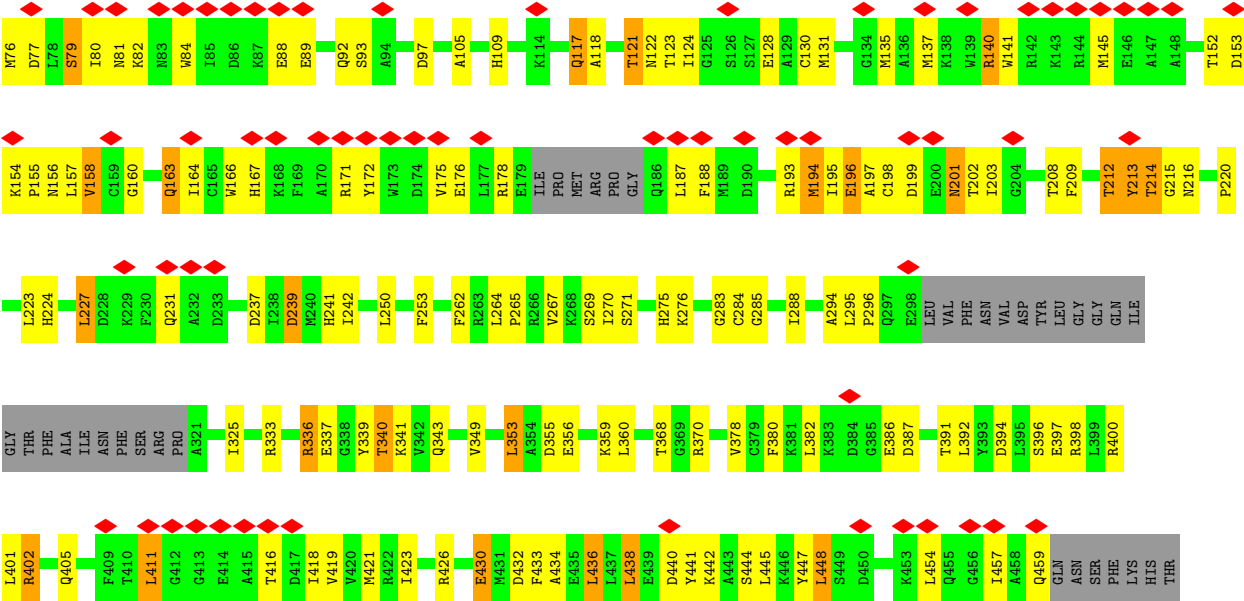


• Molecule 1: Glutamate decarboxylase



• Molecule 1: Glutamate decarboxylase





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32005	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.103	Depositor
Minimum map value	-1.476	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.166	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	150.12001, 150.12001, 93.96001	wwPDB
Map dimensions	139, 139, 87	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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	0.30	0/3471	0.58	2/4703 (0.0%)
1	B	0.30	0/3471	0.61	5/4703 (0.1%)
1	C	0.31	0/3471	0.60	5/4703 (0.1%)
1	D	0.31	0/3471	0.62	4/4703 (0.1%)
1	E	0.29	0/3471	0.56	1/4703 (0.0%)
1	F	0.30	0/3471	0.59	4/4703 (0.1%)
All	All	0.30	0/20826	0.59	21/28218 (0.1%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	259	VAL	N-CA-C	8.61	121.17	107.73
1	C	259	VAL	N-CA-C	8.04	118.27	106.85
1	F	215	GLY	N-CA-C	7.95	122.95	112.77
1	A	295	LEU	CA-C-N	7.88	127.77	120.21
1	A	295	LEU	C-N-CA	7.88	127.77	120.21
1	B	215	GLY	N-CA-C	7.83	122.79	112.77
1	C	295	LEU	CA-C-N	7.80	127.70	120.21
1	C	295	LEU	C-N-CA	7.80	127.70	120.21
1	B	88	GLU	N-CA-C	7.72	119.70	111.28
1	D	213	TYR	N-CA-C	7.56	119.60	111.36
1	B	295	LEU	CA-C-N	7.34	127.79	120.52
1	B	295	LEU	C-N-CA	7.34	127.79	120.52
1	E	214	THR	N-CA-C	-7.21	99.15	109.96
1	F	212	THR	N-CA-C	6.52	118.05	111.07
1	C	213	TYR	N-CA-C	6.51	118.46	111.36
1	C	149	GLY	N-CA-C	6.15	123.80	115.32
1	B	213	TYR	N-CA-C	5.96	119.02	111.69
1	D	212	THR	N-CA-C	5.83	117.31	111.07
1	D	147	ALA	N-CA-C	-5.56	105.31	111.71
1	F	213	TYR	N-CA-C	5.18	118.06	111.69
1	F	276	LYS	N-CA-C	5.12	116.67	111.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3388	0	3287	120	0
1	B	3388	0	3287	121	0
1	C	3388	0	3287	131	0
1	D	3388	0	3287	121	0
1	E	3388	0	3287	111	0
1	F	3388	0	3287	104	0
All	All	20328	0	19722	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 17.

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:295:LEU:HD12	1:B:296:PRO:CD	1.63	1.28
1:B:295:LEU:CD1	1:B:296:PRO:HD2	1.63	1.28
1:C:208:THR:HB	1:C:211:VAL:HG21	1.34	1.05
1:C:208:THR:HB	1:C:211:VAL:CG2	1.92	1.00
1:B:143:LYS:CE	1:B:297:GLN:HE22	1.80	0.94
1:D:261:ASP:OD1	1:D:263:ARG:HG3	1.70	0.91
1:A:212:THR:HG23	1:A:213:TYR:HD1	1.37	0.88
1:C:261:ASP:OD1	1:C:263:ARG:HG3	1.73	0.87
1:C:208:THR:CB	1:C:211:VAL:HG21	2.05	0.87
1:B:89:GLU:OE1	1:B:89:GLU:N	2.10	0.85
1:C:208:THR:CB	1:C:211:VAL:CG2	2.54	0.84
1:B:143:LYS:HE3	1:B:297:GLN:HE22	1.41	0.84
1:C:195:ILE:HA	1:C:198:CYS:HB3	1.62	0.82
1:F:195:ILE:HA	1:F:198:CYS:HB3	1.60	0.82
1:C:360:LEU:HD13	1:C:445:LEU:HD11	1.58	0.82
1:F:193:ARG:HA	1:F:196:GLU:HB2	1.62	0.81
1:D:137:MET:SD	1:D:140:ARG:NH2	2.54	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:297:GLN:HE21	1:C:297:GLN:HA	1.47	0.80
1:D:360:LEU:HD21	1:D:442:LYS:HE2	1.63	0.80
1:C:295:LEU:HD12	1:C:295:LEU:O	1.82	0.79
1:A:17:ARG:HD3	1:A:44:GLN:HG3	1.64	0.79
1:E:86:ASP:OD1	1:E:87:LYS:N	2.16	0.79
1:D:295:LEU:HD12	1:D:295:LEU:O	1.82	0.79
1:E:195:ILE:HA	1:E:198:CYS:HB3	1.63	0.79
1:A:295:LEU:HD12	1:A:295:LEU:O	1.83	0.78
1:B:143:LYS:CE	1:B:297:GLN:NE2	2.46	0.78
1:D:398:ARG:HG3	1:D:448:LEU:HD21	1.66	0.77
1:A:86:ASP:OD1	1:A:87:LYS:N	2.18	0.77
1:D:195:ILE:HA	1:D:198:CYS:HB3	1.64	0.77
1:D:398:ARG:HD2	1:D:448:LEU:HD21	1.66	0.77
1:C:398:ARG:CD	1:C:448:LEU:HD21	2.15	0.77
1:C:143:LYS:HD2	1:C:143:LYS:C	2.11	0.76
1:B:193:ARG:HA	1:B:196:GLU:HB2	1.68	0.76
1:D:193:ARG:HA	1:D:196:GLU:HB2	1.67	0.76
1:D:398:ARG:CD	1:D:448:LEU:HD21	2.15	0.75
1:C:130:CYS:HB3	1:C:166:TRP:NE1	2.01	0.75
1:D:140:ARG:HD3	1:D:294:ALA:O	1.87	0.75
1:E:163:GLN:O	1:E:167:HIS:ND1	2.20	0.75
1:D:297:GLN:NE2	1:D:297:GLN:HA	2.02	0.74
1:B:195:ILE:HA	1:B:198:CYS:HB3	1.69	0.74
1:D:130:CYS:HB3	1:D:166:TRP:NE1	2.04	0.73
1:C:208:THR:OG1	1:C:211:VAL:HG23	1.89	0.73
1:E:360:LEU:HD21	1:E:442:LYS:HE2	1.71	0.73
1:B:297:GLN:OE1	1:B:297:GLN:N	2.18	0.72
1:B:212:THR:HG23	1:B:213:TYR:N	2.04	0.72
1:E:75:LEU:HD11	1:E:325:ILE:HG12	1.69	0.72
1:A:163:GLN:O	1:A:167:HIS:ND1	2.23	0.71
1:E:193:ARG:HA	1:E:196:GLU:HB2	1.71	0.71
1:A:102:ASN:OD1	1:A:117:GLN:NE2	2.24	0.71
1:B:140:ARG:NH2	1:B:293:GLU:O	2.23	0.71
1:D:297:GLN:HA	1:D:297:GLN:HE21	1.56	0.71
1:C:143:LYS:HD2	1:C:143:LYS:O	1.90	0.71
1:D:360:LEU:HD13	1:D:445:LEU:HD11	1.71	0.71
1:B:59:ASN:O	1:B:426:ARG:NH2	2.24	0.71
1:F:59:ASN:O	1:F:426:ARG:NH2	2.24	0.71
1:A:391:THR:HG22	1:A:393:TYR:H	1.55	0.70
1:C:59:ASN:O	1:C:426:ARG:NH2	2.24	0.70
1:C:398:ARG:HH22	1:C:447:TYR:HD1	1.39	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:THR:HG22	1:A:392:LEU:N	2.07	0.70
1:D:59:ASN:O	1:D:426:ARG:NH2	2.24	0.70
1:E:122:ASN:OD1	1:E:123:THR:N	2.25	0.70
1:A:253:PHE:HB3	1:A:340:THR:HG22	1.74	0.69
1:C:398:ARG:HD2	1:C:448:LEU:HD21	1.73	0.69
1:C:398:ARG:NH2	1:C:447:TYR:CD1	2.60	0.69
1:D:398:ARG:CG	1:D:448:LEU:HD21	2.23	0.68
1:E:59:ASN:O	1:E:426:ARG:NH2	2.26	0.68
1:D:139:TRP:CZ3	1:D:297:GLN:HB2	2.29	0.68
1:A:122:ASN:OD1	1:A:123:THR:N	2.27	0.68
1:B:77:ASP:OD2	1:C:73:HIS:NE2	2.27	0.68
1:B:140:ARG:NE	1:B:294:ALA:O	2.28	0.67
1:D:398:ARG:HD2	1:D:448:LEU:CD2	2.24	0.67
1:F:360:LEU:HD21	1:F:442:LYS:HE2	1.76	0.67
1:C:297:GLN:HE21	1:C:297:GLN:CA	2.07	0.67
1:F:212:THR:HG23	1:F:213:TYR:N	2.09	0.67
1:B:122:ASN:HD22	1:B:324:VAL:HG13	1.60	0.67
1:C:59:ASN:HA	1:C:405:GLN:HB2	1.77	0.66
1:C:193:ARG:HA	1:C:196:GLU:HB2	1.78	0.66
1:A:212:THR:HG23	1:A:213:TYR:N	2.11	0.66
1:F:59:ASN:HA	1:F:405:GLN:HB2	1.78	0.66
1:B:75:LEU:HD11	1:B:325:ILE:HG12	1.78	0.66
1:B:83:ASN:HB3	1:B:85:ILE:HG22	1.78	0.66
1:C:208:THR:OG1	1:C:211:VAL:CG2	2.44	0.66
1:D:398:ARG:NH2	1:D:447:TYR:CD1	2.64	0.66
1:E:353:LEU:HD21	1:E:434:ALA:HB1	1.78	0.66
1:D:139:TRP:HZ3	1:D:297:GLN:HB2	1.60	0.65
1:E:59:ASN:HA	1:E:405:GLN:HB2	1.77	0.65
1:E:178:ARG:HD3	1:E:197:ALA:HB1	1.79	0.65
1:A:178:ARG:HD3	1:A:197:ALA:HB1	1.78	0.65
1:D:59:ASN:HA	1:D:405:GLN:HB2	1.77	0.65
1:B:122:ASN:OD1	1:B:123:THR:N	2.30	0.64
1:C:298:GLU:HA	1:C:298:GLU:OE1	1.97	0.64
1:D:145:MET:O	1:D:148:ALA:HB3	1.95	0.64
1:A:154:LYS:O	1:A:201:ASN:ND2	2.30	0.64
1:D:122:ASN:OD1	1:D:123:THR:N	2.29	0.64
1:A:195:ILE:O	1:A:199:ASP:N	2.29	0.64
1:A:155:PRO:HB2	1:A:203:ILE:HD11	1.80	0.64
1:B:38:ARG:HG2	1:E:14:LEU:HD22	1.78	0.64
1:C:78:LEU:O	1:C:82:LYS:NZ	2.30	0.64
1:E:46:ILE:HG21	1:F:75:LEU:HD21	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:ILE:HA	1:A:198:CYS:HB3	1.77	0.64
1:C:398:ARG:NH2	1:C:447:TYR:HD1	1.94	0.64
1:F:353:LEU:HD21	1:F:434:ALA:HB1	1.78	0.64
1:B:284:CYS:SG	1:B:285:GLY:N	2.71	0.63
1:A:59:ASN:HA	1:A:405:GLN:HB2	1.81	0.63
1:B:143:LYS:NZ	1:B:297:GLN:HE22	1.97	0.63
1:E:117:GLN:OE1	1:E:118:ALA:N	2.31	0.63
1:B:67:TRP:O	1:B:427:ARG:NH2	2.31	0.63
1:D:78:LEU:O	1:D:82:LYS:NZ	2.25	0.63
1:B:337:GLU:OE1	1:C:35:HIS:ND1	2.29	0.62
1:A:430:GLU:HB3	1:B:23:ILE:HD11	1.81	0.62
1:F:154:LYS:O	1:F:201:ASN:ND2	2.32	0.62
1:C:195:ILE:HD12	1:C:230:PHE:HD2	1.65	0.62
1:C:360:LEU:HD13	1:C:445:LEU:CD1	2.30	0.62
1:B:38:ARG:NH2	1:B:40:ASP:OD2	2.33	0.62
1:F:295:LEU:HD12	1:F:296:PRO:HD2	1.82	0.62
1:C:284:CYS:SG	1:C:285:GLY:N	2.72	0.62
1:B:212:THR:CG2	1:B:213:TYR:N	2.63	0.61
1:D:209:PHE:HE1	1:D:220:PRO:HD3	1.65	0.61
1:D:259:VAL:HG23	1:D:259:VAL:O	1.99	0.61
1:F:117:GLN:OE1	1:F:118:ALA:N	2.33	0.61
1:A:59:ASN:O	1:A:426:ARG:NH2	2.33	0.61
1:F:40:ASP:OD1	1:F:41:VAL:N	2.33	0.61
1:C:259:VAL:HG23	1:C:259:VAL:O	2.00	0.61
1:B:154:LYS:O	1:B:201:ASN:ND2	2.33	0.61
1:E:208:THR:OG1	1:E:211:VAL:HG22	2.00	0.61
1:B:212:THR:HG23	1:B:213:TYR:HD1	1.66	0.61
1:B:339:TYR:O	1:B:343:GLN:HG2	2.01	0.61
1:E:411:LEU:HD21	1:E:418:ILE:HG13	1.82	0.61
1:C:122:ASN:OD1	1:C:123:THR:N	2.33	0.61
1:F:284:CYS:SG	1:F:285:GLY:N	2.73	0.60
1:A:336:ARG:O	1:A:340:THR:HG23	2.01	0.60
1:F:122:ASN:OD1	1:F:123:THR:N	2.34	0.60
1:D:284:CYS:SG	1:D:285:GLY:N	2.74	0.60
1:E:62:THR:HG22	1:E:426:ARG:HH21	1.67	0.60
1:A:325:ILE:HD12	1:D:50:LEU:HD21	1.84	0.60
1:B:297:GLN:H	1:B:297:GLN:CD	2.08	0.60
1:F:62:THR:HG22	1:F:426:ARG:HH21	1.67	0.60
1:F:214:THR:HG22	1:F:214:THR:O	2.02	0.60
1:E:284:CYS:SG	1:E:285:GLY:N	2.75	0.60
1:B:178:ARG:HD3	1:B:197:ALA:HB1	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:339:TYR:O	1:C:343:GLN:HG2	2.01	0.60
1:C:295:LEU:HD12	1:C:295:LEU:C	2.27	0.59
1:D:158:VAL:HG11	1:D:198:CYS:HB2	1.83	0.59
1:D:295:LEU:HD12	1:D:295:LEU:C	2.27	0.59
1:A:284:CYS:SG	1:A:285:GLY:N	2.75	0.59
1:C:68:ASP:OD1	1:C:68:ASP:N	2.34	0.59
1:A:122:ASN:HD22	1:A:324:VAL:HG13	1.67	0.59
1:D:171:ARG:HG3	1:D:172:TYR:CD1	2.38	0.59
1:B:214:THR:O	1:B:214:THR:HG22	2.03	0.59
1:C:209:PHE:HE1	1:C:220:PRO:HD3	1.68	0.59
1:E:209:PHE:HE1	1:E:220:PRO:HD3	1.66	0.59
1:E:195:ILE:HD12	1:E:230:PHE:HD2	1.68	0.59
1:A:295:LEU:HD12	1:A:295:LEU:C	2.28	0.59
1:B:224:HIS:CE1	1:B:265:PRO:HD2	2.38	0.58
1:F:209:PHE:HE1	1:F:220:PRO:HD3	1.67	0.58
1:A:193:ARG:HA	1:A:196:GLU:HB3	1.86	0.58
1:A:208:THR:OG1	1:A:211:VAL:HG22	2.03	0.58
1:C:214:THR:HG22	1:C:214:THR:O	2.02	0.58
1:A:224:HIS:CE1	1:A:265:PRO:HD2	2.38	0.58
1:D:339:TYR:O	1:D:343:GLN:HG2	2.04	0.58
1:F:171:ARG:HG3	1:F:172:TYR:CE1	2.38	0.58
1:F:178:ARG:HD3	1:F:197:ALA:HB1	1.86	0.58
1:B:414:GLU:H	1:B:414:GLU:CD	2.12	0.58
1:D:400:ARG:NH2	1:D:405:GLN:OE1	2.37	0.58
1:D:214:THR:HG22	1:D:214:THR:O	2.02	0.58
1:B:195:ILE:O	1:B:199:ASP:N	2.37	0.57
1:E:295:LEU:HD12	1:E:296:PRO:HD2	1.86	0.57
1:B:143:LYS:NZ	1:B:297:GLN:NE2	2.52	0.57
1:C:114:LYS:H	1:C:114:LYS:HZ3	1.53	0.57
1:D:398:ARG:NH2	1:D:447:TYR:HD1	2.01	0.57
1:A:17:ARG:HB2	1:A:17:ARG:NH1	2.19	0.57
1:A:339:TYR:O	1:A:343:GLN:HG2	2.04	0.57
1:B:70:GLU:OE1	1:B:70:GLU:N	2.28	0.57
1:C:13:LEU:HD11	1:F:13:LEU:HD23	1.87	0.57
1:F:253:PHE:CE2	1:F:339:TYR:HD2	2.22	0.57
1:A:40:ASP:OD1	1:A:41:VAL:N	2.38	0.57
1:A:106:ASP:OD2	1:D:31:ARG:HG2	2.03	0.57
1:A:140:ARG:NH1	1:A:293:GLU:O	2.37	0.57
1:D:291:ASP:OD1	1:D:293:GLU:HB3	2.04	0.57
1:D:418:ILE:HD12	1:D:418:ILE:O	2.05	0.57
1:F:88:GLU:CD	1:F:88:GLU:H	2.13	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:109:HIS:O	1:F:262:PHE:HB2	2.05	0.57
1:D:223:LEU:O	1:D:227:LEU:HD12	2.03	0.57
1:A:212:THR:HG23	1:A:213:TYR:CD1	2.30	0.57
1:B:430:GLU:CD	1:B:430:GLU:H	2.13	0.57
1:C:224:HIS:CE1	1:C:265:PRO:HD2	2.40	0.57
1:B:106:ASP:OD2	1:C:31:ARG:HG2	2.04	0.57
1:B:432:ASP:OD1	1:B:432:ASP:N	2.34	0.57
1:B:155:PRO:HB2	1:B:203:ILE:HD11	1.87	0.56
1:C:140:ARG:HD3	1:C:294:ALA:O	2.05	0.56
1:E:253:PHE:HE2	1:E:339:TYR:HD2	1.53	0.56
1:E:223:LEU:O	1:E:227:LEU:HD12	2.05	0.56
1:F:339:TYR:O	1:F:343:GLN:HG2	2.06	0.56
1:C:210:GLY:O	1:C:246:SER:OG	2.24	0.56
1:C:77:ASP:HA	1:C:80:ILE:HG23	1.88	0.56
1:A:454:LEU:HB3	1:A:457:ILE:HD11	1.88	0.56
1:B:122:ASN:ND2	1:B:324:VAL:HG13	2.20	0.56
1:C:391:THR:OG1	1:C:394:ASP:OD2	2.23	0.56
1:E:454:LEU:HB3	1:E:457:ILE:HD11	1.88	0.56
1:A:444:SER:O	1:A:448:LEU:HG	2.06	0.56
1:B:40:ASP:OD1	1:B:41:VAL:N	2.38	0.56
1:E:60:LEU:HD23	1:E:423:ILE:HG23	1.87	0.56
1:C:10:ARG:HH12	1:C:14:LEU:HD22	1.72	0.55
1:F:153:ASP:C	1:F:155:PRO:HD3	2.31	0.55
1:B:444:SER:O	1:B:448:LEU:HG	2.06	0.55
1:E:109:HIS:O	1:E:262:PHE:HB2	2.05	0.55
1:D:224:HIS:CE1	1:D:265:PRO:HD2	2.42	0.55
1:A:137:MET:HE1	1:A:239:ASP:HB2	1.87	0.55
1:A:210:GLY:O	1:A:246:SER:OG	2.22	0.55
1:C:400:ARG:NH2	1:C:405:GLN:OE1	2.39	0.55
1:E:253:PHE:CE2	1:E:339:TYR:HD2	2.25	0.55
1:B:143:LYS:HE3	1:B:297:GLN:NE2	2.17	0.55
1:E:122:ASN:HD22	1:E:324:VAL:HG13	1.71	0.55
1:E:224:HIS:CE1	1:E:265:PRO:HD2	2.41	0.54
1:F:224:HIS:CE1	1:F:265:PRO:HD2	2.42	0.54
1:B:98:LEU:HB3	1:B:117:GLN:NE2	2.22	0.54
1:E:400:ARG:NH2	1:E:405:GLN:OE1	2.40	0.54
1:E:414:GLU:H	1:E:414:GLU:CD	2.15	0.54
1:F:123:THR:HB	1:F:128:GLU:OE1	2.06	0.54
1:F:400:ARG:NH2	1:F:405:GLN:OE1	2.41	0.54
1:B:333:ARG:O	1:B:333:ARG:NH1	2.39	0.54
1:F:68:ASP:OD1	1:F:68:ASP:N	2.39	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:ARG:NH2	1:A:405:GLN:OE1	2.40	0.54
1:F:223:LEU:O	1:F:227:LEU:HD12	2.07	0.54
1:D:131:MET:HE2	1:D:135:MET:HE1	1.90	0.54
1:A:109:HIS:O	1:A:262:PHE:HB2	2.07	0.54
1:A:391:THR:CG2	1:A:392:LEU:N	2.71	0.54
1:F:155:PRO:HB2	1:F:203:ILE:HD11	1.90	0.54
1:C:418:ILE:O	1:C:418:ILE:HD12	2.08	0.53
1:D:132:LEU:HA	1:D:135:MET:HE2	1.88	0.53
1:D:163:GLN:O	1:D:167:HIS:ND1	2.42	0.53
1:A:253:PHE:CE2	1:A:339:TYR:HD2	2.26	0.53
1:A:209:PHE:HE1	1:A:220:PRO:HD3	1.73	0.53
1:D:391:THR:HB	1:D:394:ASP:OD1	2.08	0.53
1:E:208:THR:OG1	1:E:211:VAL:CG2	2.55	0.53
1:A:70:GLU:OE2	1:A:70:GLU:N	2.35	0.53
1:E:226:ALA:HB1	1:E:230:PHE:CE2	2.44	0.53
1:B:109:HIS:O	1:B:262:PHE:HB2	2.09	0.53
1:E:339:TYR:O	1:E:343:GLN:HG2	2.08	0.53
1:E:73:HIS:NE2	1:F:77:ASP:OD2	2.41	0.53
1:A:17:ARG:HB2	1:A:17:ARG:HH11	1.74	0.53
1:F:253:PHE:HE2	1:F:339:TYR:HD2	1.55	0.53
1:F:382:LEU:HG	1:F:392:LEU:HD11	1.91	0.53
1:C:41:VAL:O	1:C:45:ILE:HG23	2.08	0.53
1:E:275:HIS:HB3	1:E:283:GLY:HA2	1.91	0.53
1:F:397:GLU:HA	1:F:400:ARG:HB3	1.90	0.53
1:A:223:LEU:O	1:A:227:LEU:HD12	2.09	0.53
1:A:250:LEU:HD21	1:A:277:PHE:CD2	2.44	0.53
1:B:14:LEU:HD22	1:D:38:ARG:HG3	1.91	0.52
1:C:155:PRO:HB2	1:C:203:ILE:HD11	1.92	0.52
1:C:356:GLU:HB3	1:C:438:LEU:HD11	1.91	0.52
1:F:212:THR:CG2	1:F:213:TYR:N	2.72	0.52
1:E:76:MET:HE1	1:F:76:MET:SD	2.50	0.52
1:A:195:ILE:HD12	1:A:230:PHE:HD2	1.73	0.52
1:B:137:MET:HE1	1:B:239:ASP:HB2	1.91	0.52
1:B:221:GLN:NE2	1:B:225:ASP:OD1	2.42	0.52
1:E:121:THR:OG1	1:E:122:ASN:O	2.27	0.52
1:E:155:PRO:HB2	1:E:203:ILE:HD11	1.90	0.52
1:F:41:VAL:O	1:F:45:ILE:HG23	2.09	0.52
1:E:70:GLU:OE2	1:E:70:GLU:N	2.40	0.52
1:B:68:ASP:N	1:B:68:ASP:OD1	2.43	0.52
1:D:391:THR:HG22	1:D:393:TYR:H	1.75	0.52
1:E:140:ARG:NH1	1:E:293:GLU:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:CYS:HG	1:C:275:HIS:CD2	2.28	0.52
1:C:454:LEU:HB3	1:C:457:ILE:HD11	1.92	0.52
1:E:122:ASN:HD22	1:E:324:VAL:CG1	2.23	0.52
1:F:444:SER:O	1:F:448:LEU:HG	2.10	0.52
1:B:216:ASN:OD1	1:B:216:ASN:N	2.39	0.52
1:A:337:GLU:OE1	1:D:35:HIS:ND1	2.42	0.52
1:D:454:LEU:HB3	1:D:457:ILE:HD11	1.91	0.52
1:E:168:LYS:HA	1:E:168:LYS:HE3	1.90	0.52
1:C:145:MET:CA	1:C:145:MET:HE2	2.40	0.51
1:D:41:VAL:O	1:D:45:ILE:HG23	2.10	0.51
1:E:153:ASP:C	1:E:155:PRO:HD3	2.36	0.51
1:F:391:THR:OG1	1:F:394:ASP:OD1	2.22	0.51
1:A:153:ASP:C	1:A:155:PRO:HD3	2.35	0.51
1:A:226:ALA:HB1	1:A:230:PHE:HE2	1.75	0.51
1:C:79:SER:O	1:C:79:SER:OG	2.24	0.51
1:D:23:ILE:HD11	1:F:430:GLU:HB3	1.92	0.51
1:E:41:VAL:O	1:E:45:ILE:HG23	2.10	0.51
1:C:414:GLU:H	1:C:414:GLU:CD	2.19	0.51
1:C:430:GLU:OE1	1:C:430:GLU:N	2.38	0.51
1:D:209:PHE:CE1	1:D:220:PRO:HD3	2.46	0.51
1:D:253:PHE:HE2	1:D:339:TYR:HD2	1.59	0.51
1:F:60:LEU:HD23	1:F:423:ILE:HG23	1.93	0.51
1:D:430:GLU:OE1	1:D:430:GLU:N	2.41	0.51
1:E:333:ARG:HG3	1:F:39:ASP:HB3	1.92	0.51
1:A:333:ARG:O	1:A:333:ARG:NH1	2.42	0.51
1:B:253:PHE:CE2	1:B:339:TYR:HD2	2.29	0.51
1:B:325:ILE:HD11	1:C:50:LEU:HD11	1.93	0.51
1:C:223:LEU:O	1:C:227:LEU:HD12	2.11	0.51
1:E:336:ARG:O	1:E:340:THR:OG1	2.29	0.51
1:A:122:ASN:ND2	1:A:324:VAL:HG13	2.25	0.51
1:B:79:SER:O	1:B:79:SER:OG	2.29	0.51
1:B:122:ASN:HD22	1:B:324:VAL:CG1	2.24	0.51
1:B:158:VAL:HA	1:B:178:ARG:O	2.11	0.51
1:B:254:VAL:HG11	1:B:343:GLN:HB2	1.93	0.51
1:C:109:HIS:O	1:C:262:PHE:HB2	2.11	0.51
1:B:73:HIS:NE2	1:C:77:ASP:OD2	2.44	0.50
1:E:92:GLN:OE1	1:F:49:GLU:HB3	2.10	0.50
1:F:411:LEU:HD21	1:F:418:ILE:HG13	1.92	0.50
1:A:226:ALA:HB1	1:A:230:PHE:CE2	2.46	0.50
1:F:171:ARG:HG3	1:F:172:TYR:CD1	2.47	0.50
1:D:139:TRP:HZ3	1:D:297:GLN:CB	2.24	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:250:LEU:HD11	1:D:277:PHE:CG	2.47	0.50
1:A:130:CYS:HB3	1:A:166:TRP:NE1	2.27	0.50
1:A:212:THR:CG2	1:A:213:TYR:N	2.74	0.50
1:F:121:THR:OG1	1:F:122:ASN:O	2.29	0.50
1:F:336:ARG:O	1:F:340:THR:OG1	2.30	0.50
1:B:253:PHE:HE2	1:B:339:TYR:HD2	1.60	0.50
1:D:46:ILE:O	1:D:50:LEU:HD12	2.12	0.50
1:A:253:PHE:HE2	1:A:339:TYR:HD2	1.60	0.50
1:B:153:ASP:C	1:B:155:PRO:HD3	2.37	0.50
1:C:15:ASP:OD2	1:E:341:LYS:NZ	2.43	0.50
1:D:158:VAL:HG12	1:D:178:ARG:O	2.11	0.50
1:E:50:LEU:HD21	1:F:325:ILE:HD13	1.93	0.50
1:F:79:SER:O	1:F:79:SER:OG	2.30	0.50
1:B:169:PHE:CE1	1:B:175:VAL:HG21	2.47	0.49
1:F:194:MET:HE1	1:F:223:LEU:HB2	1.94	0.49
1:A:88:GLU:CD	1:A:88:GLU:H	2.20	0.49
1:A:391:THR:HG22	1:A:392:LEU:H	1.77	0.49
1:E:79:SER:HA	1:E:82:LYS:NZ	2.28	0.49
1:A:295:LEU:C	1:A:295:LEU:CD1	2.86	0.49
1:C:209:PHE:CE1	1:C:220:PRO:HD3	2.48	0.49
1:D:155:PRO:HB2	1:D:203:ILE:HD11	1.95	0.49
1:D:397:GLU:HA	1:D:400:ARG:HB3	1.94	0.49
1:C:86:ASP:OD1	1:C:87:LYS:N	2.45	0.49
1:E:430:GLU:H	1:E:430:GLU:CD	2.19	0.49
1:E:444:SER:O	1:E:448:LEU:HG	2.13	0.49
1:A:122:ASN:HD22	1:A:324:VAL:CG1	2.26	0.49
1:B:215:GLY:O	1:B:375:ILE:HG12	2.12	0.49
1:B:231:GLN:HG2	1:B:237:ASP:OD1	2.12	0.49
1:E:49:GLU:HB3	1:F:92:GLN:OE1	2.12	0.49
1:F:137:MET:HE1	1:F:241:HIS:HB2	1.95	0.49
1:A:10:ARG:HH11	1:A:14:LEU:HD11	1.78	0.48
1:C:253:PHE:CE2	1:C:339:TYR:HD2	2.31	0.48
1:E:123:THR:HB	1:E:128:GLU:OE1	2.12	0.48
1:C:255:ALA:O	1:C:258:ILE:CG2	2.61	0.48
1:E:231:GLN:HG2	1:E:237:ASP:CG	2.38	0.48
1:A:81:ASN:ND2	1:D:66:THR:O	2.46	0.48
1:C:158:VAL:HG11	1:C:198:CYS:HB2	1.95	0.48
1:B:209:PHE:HE1	1:B:220:PRO:HD3	1.77	0.48
1:D:141:TRP:HD1	1:D:145:MET:HE3	1.79	0.48
1:D:291:ASP:O	1:D:292:GLU:C	2.56	0.48
1:D:430:GLU:HB3	1:F:23:ILE:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:295:LEU:C	1:D:295:LEU:CD1	2.86	0.48
1:B:100:CYS:HA	1:B:103:MET:HG3	1.95	0.48
1:C:239:ASP:N	1:C:239:ASP:OD1	2.43	0.48
1:D:79:SER:HA	1:D:82:LYS:NZ	2.28	0.48
1:A:430:GLU:H	1:A:430:GLU:CD	2.19	0.48
1:D:109:HIS:O	1:D:262:PHE:HB2	2.14	0.48
1:A:258:ILE:HD12	1:A:259:VAL:H	1.79	0.48
1:C:52:LEU:HA	1:E:58:GLN:HE22	1.78	0.48
1:C:226:ALA:HB1	1:C:230:PHE:CE2	2.49	0.48
1:D:226:ALA:HB1	1:D:230:PHE:HE2	1.79	0.48
1:A:198:CYS:HG	1:A:202:THR:HG1	1.62	0.47
1:B:367:CYS:SG	1:B:379:CYS:HB2	2.54	0.47
1:C:146:GLU:OE1	1:C:146:GLU:HA	2.14	0.47
1:D:367:CYS:SG	1:D:379:CYS:HB2	2.55	0.47
1:F:203:ILE:HD12	1:F:203:ILE:H	1.79	0.47
1:C:295:LEU:C	1:C:295:LEU:CD1	2.86	0.47
1:E:158:VAL:HG11	1:E:198:CYS:HB2	1.96	0.47
1:F:402:ARG:HG2	1:F:440:ASP:OD2	2.13	0.47
1:A:67:TRP:CZ2	1:A:69:ASP:HA	2.49	0.47
1:A:432:ASP:OD1	1:A:432:ASP:N	2.40	0.47
1:D:360:LEU:HD13	1:D:445:LEU:CD1	2.43	0.47
1:A:414:GLU:CD	1:A:414:GLU:H	2.23	0.47
1:B:411:LEU:H	1:B:411:LEU:HG	1.40	0.47
1:C:171:ARG:HG3	1:C:172:TYR:CE1	2.48	0.47
1:C:171:ARG:HG3	1:C:172:TYR:CD1	2.49	0.47
1:C:297:GLN:CA	1:C:297:GLN:NE2	2.73	0.47
1:D:253:PHE:CE2	1:D:339:TYR:HD2	2.33	0.47
1:C:336:ARG:O	1:C:340:THR:OG1	2.32	0.47
1:C:345:ALA:O	1:C:349:VAL:HG23	2.14	0.47
1:D:297:GLN:NE2	1:D:297:GLN:CA	2.73	0.47
1:E:66:THR:O	1:F:81:ASN:ND2	2.48	0.47
1:B:130:CYS:HB3	1:B:166:TRP:NE1	2.29	0.47
1:C:367:CYS:SG	1:C:379:CYS:HB2	2.54	0.47
1:D:77:ASP:O	1:D:80:ILE:HG13	2.15	0.47
1:D:144:ARG:O	1:D:147:ALA:HB3	2.14	0.47
1:A:208:THR:OG1	1:A:211:VAL:CG2	2.62	0.47
1:B:231:GLN:HG2	1:B:237:ASP:CG	2.40	0.47
1:B:325:ILE:HD12	1:C:50:LEU:HD21	1.96	0.47
1:D:345:ALA:O	1:D:349:VAL:HG23	2.14	0.47
1:E:401:LEU:HB2	1:E:402:ARG:HH12	1.79	0.47
1:A:167:HIS:NE2	1:A:177:LEU:HD11	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:LEU:H	1:A:411:LEU:HG	1.38	0.47
1:F:275:HIS:HB3	1:F:283:GLY:HA2	1.96	0.47
1:F:178:ARG:HH11	1:F:178:ARG:HG3	1.80	0.47
1:A:68:ASP:OD1	1:A:68:ASP:N	2.49	0.46
1:E:167:HIS:CD2	1:E:177:LEU:HD11	2.49	0.46
1:C:269:SER:O	1:C:270:ILE:HG13	2.15	0.46
1:C:398:ARG:HD2	1:C:448:LEU:CD2	2.42	0.46
1:E:397:GLU:HA	1:E:400:ARG:HB3	1.95	0.46
1:A:77:ASP:O	1:A:80:ILE:HG13	2.16	0.46
1:E:360:LEU:HD23	1:E:360:LEU:HA	1.70	0.46
1:F:80:ILE:HG23	1:F:81:ASN:OD1	2.14	0.46
1:F:140:ARG:NE	1:F:294:ALA:O	2.46	0.46
1:B:171:ARG:HG2	1:B:171:ARG:HH11	1.80	0.46
1:C:7:THR:O	1:C:10:ARG:HG3	2.16	0.46
1:D:216:ASN:HB2	1:D:373:GLU:OE2	2.14	0.46
1:F:131:MET:HG2	1:F:135:MET:HE2	1.98	0.46
1:C:392:LEU:HB3	1:C:421:MET:HE2	1.97	0.46
1:D:292:GLU:OE2	1:D:292:GLU:N	2.41	0.46
1:E:203:ILE:HD12	1:E:203:ILE:H	1.79	0.46
1:A:66:THR:O	1:D:81:ASN:ND2	2.48	0.46
1:A:156:ASN:HA	1:A:176:GLU:O	2.16	0.46
1:A:240:MET:HE3	1:A:240:MET:HB3	1.85	0.46
1:E:171:ARG:HG3	1:E:172:TYR:CD1	2.50	0.46
1:A:49:GLU:HB3	1:D:92:GLN:OE1	2.15	0.46
1:A:390:TYR:CG	1:A:448:LEU:HD13	2.51	0.46
1:D:11:SER:O	1:D:15:ASP:HB2	2.15	0.46
1:F:231:GLN:HG2	1:F:237:ASP:CG	2.41	0.46
1:B:89:GLU:HA	1:C:405:GLN:HE22	1.80	0.46
1:B:417:ASP:C	1:B:418:ILE:HD13	2.41	0.46
1:C:13:LEU:HD22	1:C:14:LEU:HD12	1.98	0.46
1:E:79:SER:O	1:E:79:SER:OG	2.32	0.46
1:D:52:LEU:O	1:D:52:LEU:HD13	2.16	0.45
1:D:64:CYS:HG	1:D:275:HIS:CD2	2.31	0.45
1:A:295:LEU:HB2	1:A:296:PRO:HD2	1.97	0.45
1:B:224:HIS:CD2	1:B:264:LEU:HB3	2.51	0.45
1:B:264:LEU:HB2	1:B:267:VAL:HG23	1.97	0.45
1:D:70:GLU:O	1:D:74:LYS:HG2	2.16	0.45
1:A:140:ARG:NH1	1:A:294:ALA:O	2.43	0.45
1:B:167:HIS:CE1	1:B:177:LEU:HD21	2.52	0.45
1:C:140:ARG:HG3	1:C:140:ARG:HH11	1.81	0.45
1:D:139:TRP:HZ3	1:D:297:GLN:CG	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:398:ARG:HH11	1:D:401:LEU:CD1	2.30	0.45
1:F:79:SER:HA	1:F:82:LYS:HZ1	1.81	0.45
1:F:360:LEU:HD23	1:F:360:LEU:HA	1.65	0.45
1:A:28:GLU:HG2	1:A:33:PRO:HG3	1.99	0.45
1:B:333:ARG:HG3	1:C:39:ASP:HB3	1.99	0.45
1:C:171:ARG:HH11	1:C:172:TYR:HE1	1.64	0.45
1:D:137:MET:SD	1:D:140:ARG:NH1	2.90	0.45
1:F:158:VAL:HG11	1:F:198:CYS:HB2	1.99	0.45
1:D:226:ALA:HB1	1:D:230:PHE:CE2	2.52	0.45
1:F:164:ILE:HA	1:F:167:HIS:HB2	1.99	0.45
1:A:367:CYS:SG	1:A:379:CYS:HB2	2.57	0.45
1:D:117:GLN:HG3	1:D:118:ALA:N	2.32	0.45
1:E:11:SER:O	1:E:15:ASP:HB2	2.17	0.45
1:B:333:ARG:HD3	1:B:334:LEU:HG	1.99	0.45
1:C:195:ILE:O	1:C:199:ASP:N	2.50	0.45
1:E:98:LEU:HB3	1:E:117:GLN:NE2	2.31	0.45
1:C:360:LEU:HD23	1:C:360:LEU:HA	1.68	0.45
1:D:356:GLU:HB3	1:D:438:LEU:HD11	1.99	0.45
1:E:75:LEU:HD11	1:E:325:ILE:CG1	2.44	0.45
1:E:171:ARG:HG3	1:E:172:TYR:CE1	2.51	0.45
1:F:269:SER:O	1:F:270:ILE:HG13	2.17	0.45
1:F:356:GLU:HA	1:F:359:LYS:HG2	1.99	0.45
1:D:360:LEU:HA	1:D:360:LEU:HD23	1.71	0.45
1:A:38:ARG:NH1	1:A:40:ASP:OD2	2.51	0.44
1:B:275:HIS:HB3	1:B:283:GLY:HA2	1.99	0.44
1:C:295:LEU:HB2	1:C:296:PRO:HD2	1.99	0.44
1:E:140:ARG:HD2	1:E:294:ALA:O	2.18	0.44
1:F:198:CYS:SG	1:F:202:THR:HG21	2.57	0.44
1:C:216:ASN:HB2	1:C:373:GLU:OE1	2.17	0.44
1:D:156:ASN:HA	1:D:176:GLU:O	2.18	0.44
1:D:390:TYR:CD2	1:D:390:TYR:O	2.70	0.44
1:A:337:GLU:O	1:A:341:LYS:HG3	2.16	0.44
1:B:203:ILE:H	1:B:203:ILE:HD12	1.83	0.44
1:C:70:GLU:OE1	1:C:70:GLU:N	2.29	0.44
1:D:137:MET:SD	1:D:140:ARG:CZ	3.05	0.44
1:D:381:LYS:HG3	1:D:382:LEU:O	2.17	0.44
1:F:64:CYS:HG	1:F:275:HIS:CD2	2.33	0.44
1:D:98:LEU:O	1:D:117:GLN:NE2	2.49	0.44
1:D:195:ILE:HD12	1:D:230:PHE:HD2	1.82	0.44
1:F:457:ILE:HD12	1:F:457:ILE:H	1.83	0.44
1:A:137:MET:HB3	1:A:137:MET:HE3	1.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:GLU:O	1:C:74:LYS:HG3	2.18	0.44
1:C:397:GLU:HA	1:C:400:ARG:HB3	1.99	0.44
1:E:39:ASP:HB3	1:F:333:ARG:HG3	2.00	0.44
1:E:239:ASP:N	1:E:239:ASP:OD1	2.49	0.44
1:A:323:GLN:H	1:A:323:GLN:HG2	1.61	0.44
1:B:62:THR:HG22	1:B:426:ARG:HH21	1.83	0.44
1:C:86:ASP:CG	1:C:87:LYS:H	2.26	0.44
1:C:114:LYS:HE2	1:C:114:LYS:HB2	1.86	0.44
1:F:454:LEU:HB3	1:F:457:ILE:HD11	1.99	0.44
1:B:13:LEU:HD23	1:E:13:LEU:HD21	2.00	0.44
1:D:231:GLN:HG2	1:D:266:ARG:NH1	2.33	0.44
1:B:98:LEU:HB3	1:B:117:GLN:HE22	1.82	0.44
1:F:84:TRP:NE1	1:F:97:ASP:OD2	2.51	0.44
1:F:253:PHE:HB3	1:F:340:THR:HG23	1.98	0.44
1:C:11:SER:O	1:C:15:ASP:HB2	2.18	0.43
1:C:398:ARG:CD	1:C:448:LEU:CD2	2.91	0.43
1:E:269:SER:O	1:E:270:ILE:HG13	2.18	0.43
1:B:59:ASN:HA	1:B:405:GLN:HB2	2.00	0.43
1:C:62:THR:HG22	1:C:426:ARG:HH21	1.83	0.43
1:D:416:THR:O	1:D:416:THR:HG22	2.18	0.43
1:A:11:SER:O	1:A:15:ASP:HB2	2.17	0.43
1:A:224:HIS:CD2	1:A:264:LEU:HB3	2.53	0.43
1:B:337:GLU:O	1:B:341:LYS:HG3	2.18	0.43
1:D:239:ASP:OD1	1:D:239:ASP:N	2.48	0.43
1:E:89:GLU:HG2	1:E:90:TYR:CD2	2.54	0.43
1:E:107:LEU:HD21	1:E:253:PHE:CZ	2.54	0.43
1:E:167:HIS:NE2	1:E:177:LEU:HD11	2.32	0.43
1:B:114:LYS:H	1:B:114:LYS:NZ	2.17	0.43
1:C:226:ALA:HB1	1:C:230:PHE:HE2	1.84	0.43
1:C:143:LYS:C	1:C:143:LYS:CD	2.85	0.43
1:D:140:ARG:HG3	1:D:140:ARG:HH11	1.82	0.43
1:E:436:LEU:HD13	1:E:436:LEU:HA	1.90	0.43
1:A:46:ILE:HG21	1:D:75:LEU:HD21	2.01	0.43
1:B:11:SER:O	1:B:15:ASP:HB2	2.18	0.43
1:C:224:HIS:CE1	1:C:266:ARG:HG3	2.54	0.43
1:C:253:PHE:HE2	1:C:339:TYR:HD2	1.66	0.43
1:D:62:THR:HG22	1:D:426:ARG:HH21	1.83	0.43
1:A:436:LEU:HD23	1:B:52:LEU:HG	2.00	0.43
1:B:246:SER:O	1:B:250:LEU:HD12	2.19	0.43
1:B:390:TYR:CG	1:B:448:LEU:HD13	2.53	0.43
1:C:193:ARG:HA	1:C:196:GLU:CB	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:253:PHE:HB3	1:E:340:THR:HG23	2.01	0.43
1:F:231:GLN:HG2	1:F:237:ASP:OD1	2.19	0.43
1:A:360:LEU:HD23	1:A:360:LEU:HA	1.74	0.43
1:C:156:ASN:HA	1:C:176:GLU:O	2.18	0.43
1:D:391:THR:HG22	1:D:392:LEU:N	2.34	0.43
1:E:169:PHE:CE1	1:E:175:VAL:HG21	2.54	0.43
1:F:224:HIS:CD2	1:F:264:LEU:HB3	2.54	0.43
1:F:401:LEU:HB2	1:F:402:ARG:HH12	1.84	0.43
1:F:416:THR:O	1:F:416:THR:HG22	2.18	0.43
1:F:432:ASP:OD1	1:F:432:ASP:N	2.46	0.43
1:A:117:GLN:HE21	1:A:118:ALA:N	2.17	0.43
1:C:57:ARG:HD2	1:C:57:ARG:HA	1.85	0.43
1:C:224:HIS:CD2	1:C:264:LEU:HB3	2.53	0.43
1:C:231:GLN:HG2	1:C:237:ASP:OD1	2.18	0.43
1:E:122:ASN:ND2	1:E:324:VAL:HG13	2.33	0.43
1:A:255:ALA:O	1:A:258:ILE:HG22	2.17	0.43
1:A:268:LYS:HA	1:A:268:LYS:HD3	1.81	0.43
1:A:391:THR:CG2	1:A:392:LEU:H	2.31	0.43
1:B:137:MET:HB3	1:B:137:MET:HE3	1.64	0.43
1:C:76:MET:O	1:C:80:ILE:HG23	2.18	0.43
1:C:142:ARG:NH1	1:C:152:THR:HG21	2.34	0.43
1:C:380:PHE:CZ	1:C:421:MET:HE3	2.54	0.43
1:D:215:GLY:O	1:D:375:ILE:HG12	2.19	0.43
1:A:10:ARG:NH1	1:A:14:LEU:HD11	2.34	0.42
1:B:254:VAL:HG21	1:B:347:TYR:CE2	2.53	0.42
1:E:156:ASN:HA	1:E:176:GLU:O	2.19	0.42
1:A:223:LEU:O	1:A:226:ALA:HB3	2.19	0.42
1:B:171:ARG:HG2	1:B:171:ARG:NH1	2.33	0.42
1:F:158:VAL:HA	1:F:178:ARG:O	2.19	0.42
1:A:105:ALA:HB2	1:A:288:ILE:HD12	2.02	0.42
1:B:49:GLU:HB3	1:C:92:GLN:OE1	2.19	0.42
1:B:223:LEU:O	1:B:226:ALA:HB3	2.19	0.42
1:E:130:CYS:HB3	1:E:166:TRP:NE1	2.34	0.42
1:E:224:HIS:CD2	1:E:264:LEU:HB3	2.54	0.42
1:F:11:SER:O	1:F:15:ASP:HB2	2.18	0.42
1:B:150:LYS:HA	1:B:150:LYS:HD3	1.88	0.42
1:C:194:MET:HB2	1:C:194:MET:HE2	1.81	0.42
1:E:68:ASP:OD1	1:E:68:ASP:N	2.52	0.42
1:E:253:PHE:CE2	1:E:339:TYR:CD2	3.07	0.42
1:E:389:GLY:O	1:E:455:GLN:HG3	2.20	0.42
1:E:411:LEU:H	1:E:411:LEU:HG	1.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:PHE:HA	1:B:220:PRO:HD3	1.92	0.42
1:D:48:ASP:O	1:D:51:TYR:HB2	2.19	0.42
1:D:398:ARG:CD	1:D:448:LEU:CD2	2.89	0.42
1:B:52:LEU:HD13	1:B:52:LEU:O	2.19	0.42
1:B:216:ASN:HB2	1:B:373:GLU:OE2	2.20	0.42
1:F:438:LEU:HD23	1:F:438:LEU:HA	1.88	0.42
1:A:375:ILE:H	1:A:375:ILE:HG12	1.58	0.42
1:B:81:ASN:OD1	1:B:81:ASN:N	2.53	0.42
1:B:226:ALA:O	1:B:230:PHE:CD2	2.73	0.42
1:C:49:GLU:H	1:C:49:GLU:HG2	1.56	0.42
1:C:137:MET:HE2	1:C:137:MET:HB2	1.92	0.42
1:D:87:LYS:HG3	1:D:88:GLU:H	1.82	0.42
1:E:187:LEU:HD12	1:E:187:LEU:H	1.85	0.42
1:E:214:THR:O	1:E:214:THR:HG22	2.20	0.42
1:A:62:THR:HG22	1:A:426:ARG:HH21	1.85	0.42
1:A:353:LEU:HD23	1:A:353:LEU:HA	1.89	0.42
1:B:292:GLU:H	1:B:292:GLU:CD	2.23	0.42
1:B:383:LYS:HE3	1:B:383:LYS:HB3	1.97	0.42
1:D:366:ILE:HG13	1:D:367:CYS:N	2.35	0.42
1:E:195:ILE:HD12	1:E:230:PHE:CD2	2.52	0.42
1:E:332:LEU:HD13	1:F:45:ILE:HD11	2.02	0.42
1:B:375:ILE:HG12	1:B:375:ILE:H	1.67	0.42
1:C:58:GLN:HE22	1:E:52:LEU:HA	1.84	0.42
1:C:145:MET:HE2	1:C:145:MET:N	2.35	0.42
1:D:79:SER:HA	1:D:82:LYS:HZ3	1.84	0.42
1:D:380:PHE:CZ	1:D:421:MET:HE3	2.55	0.42
1:E:337:GLU:O	1:E:340:THR:OG1	2.31	0.42
1:F:50:LEU:HA	1:F:53:ASP:HB2	2.01	0.42
1:C:353:LEU:HD23	1:C:353:LEU:HA	1.84	0.42
1:E:394:ASP:HB2	1:E:457:ILE:HD12	2.02	0.42
1:E:409:PHE:O	1:E:419:VAL:HG23	2.20	0.42
1:F:124:ILE:HD12	1:F:124:ILE:H	1.84	0.42
1:F:380:PHE:CZ	1:F:421:MET:HE3	2.55	0.42
1:A:297:GLN:OE1	1:A:297:GLN:N	2.53	0.41
1:E:52:LEU:HD13	1:E:52:LEU:O	2.20	0.41
1:F:156:ASN:HA	1:F:176:GLU:O	2.19	0.41
1:A:390:TYR:HB2	1:A:394:ASP:OD2	2.20	0.41
1:B:255:ALA:HB1	1:B:258:ILE:HD11	2.00	0.41
1:C:366:ILE:HG13	1:C:367:CYS:N	2.35	0.41
1:D:250:LEU:HD22	1:D:375:ILE:HG22	2.03	0.41
1:E:278:GLY:O	1:E:327:GLN:NE2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:160:GLY:HA2	1:F:163:GLN:OE1	2.20	0.41
1:F:212:THR:HG23	1:F:213:TYR:HD1	1.85	0.41
1:A:201:ASN:O	1:A:202:THR:OG1	2.38	0.41
1:B:122:ASN:OD1	1:B:122:ASN:C	2.63	0.41
1:C:84:TRP:N	1:C:321:ALA:HB2	2.35	0.41
1:C:142:ARG:HH11	1:C:152:THR:HG21	1.84	0.41
1:E:13:LEU:HG	1:E:14:LEU:HD23	2.02	0.41
1:E:87:LYS:HE2	1:E:88:GLU:HG2	2.01	0.41
1:B:76:MET:HE2	1:B:76:MET:HB2	1.74	0.41
1:B:242:ILE:HB	1:B:270:ILE:HD13	2.03	0.41
1:C:453:LYS:HZ2	1:C:453:LYS:HG2	1.71	0.41
1:D:79:SER:O	1:D:79:SER:OG	2.30	0.41
1:A:160:GLY:O	1:A:167:HIS:HE1	2.04	0.41
1:A:231:GLN:HG2	1:A:237:ASP:OD1	2.19	0.41
1:B:224:HIS:CE1	1:B:266:ARG:HG3	2.56	0.41
1:E:459:GLN:H	1:E:459:GLN:HG3	1.67	0.41
1:F:84:TRP:O	1:F:84:TRP:CG	2.73	0.41
1:F:130:CYS:HB3	1:F:166:TRP:NE1	2.36	0.41
1:A:122:ASN:OD1	1:A:122:ASN:C	2.63	0.41
1:C:52:LEU:HA	1:E:58:GLN:NE2	2.34	0.41
1:D:49:GLU:H	1:D:49:GLU:HG2	1.55	0.41
1:D:253:PHE:CE2	1:D:339:TYR:CD2	3.09	0.41
1:B:114:LYS:H	1:B:114:LYS:HZ3	1.69	0.41
1:B:240:MET:HE3	1:B:240:MET:HB3	1.70	0.41
1:C:89:GLU:OE2	1:C:89:GLU:N	2.42	0.41
1:C:398:ARG:CG	1:C:448:LEU:HD21	2.51	0.41
1:D:52:LEU:HA	1:F:58:GLN:HE22	1.86	0.41
1:E:114:LYS:H	1:E:114:LYS:NZ	2.19	0.41
1:F:145:MET:HE2	1:F:145:MET:HB2	1.91	0.41
1:A:194:MET:HE1	1:A:223:LEU:HB2	2.02	0.41
1:A:389:GLY:O	1:A:455:GLN:NE2	2.53	0.41
1:B:107:LEU:HD21	1:B:253:PHE:CZ	2.56	0.41
1:B:188:PHE:HB3	1:B:218:GLU:HG3	2.03	0.41
1:D:84:TRP:N	1:D:321:ALA:HB2	2.36	0.41
1:E:76:MET:O	1:E:80:ILE:HG23	2.20	0.41
1:E:145:MET:HE2	1:E:145:MET:HB2	1.89	0.41
1:A:158:VAL:HG11	1:A:198:CYS:HB2	2.03	0.41
1:A:253:PHE:CE2	1:A:339:TYR:CD2	3.08	0.41
1:B:13:LEU:HD22	1:B:13:LEU:HA	1.84	0.41
1:B:229:LYS:HB3	1:B:229:LYS:HE2	1.79	0.41
1:D:336:ARG:O	1:D:340:THR:OG1	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:171:ARG:C	1:F:172:TYR:HD1	2.29	0.41
1:F:239:ASP:OD1	1:F:239:ASP:N	2.53	0.41
1:A:103:MET:HE2	1:A:328:TYR:CE1	2.56	0.41
1:A:203:ILE:H	1:A:203:ILE:HD12	1.86	0.41
1:A:297:GLN:N	1:A:297:GLN:CD	2.79	0.41
1:D:219:PHE:HA	1:D:220:PRO:HD3	1.89	0.41
1:E:402:ARG:HG2	1:E:440:ASP:OD2	2.20	0.41
1:F:337:GLU:O	1:F:341:LYS:HG3	2.22	0.41
1:F:411:LEU:H	1:F:411:LEU:HG	1.39	0.41
1:F:436:LEU:HD13	1:F:436:LEU:HA	1.89	0.41
1:A:57:ARG:HA	1:A:57:ARG:HD2	1.86	0.40
1:A:98:LEU:HB3	1:A:117:GLN:OE1	2.20	0.40
1:B:145:MET:HE2	1:B:145:MET:HB2	1.85	0.40
1:C:169:PHE:CE1	1:C:175:VAL:HG21	2.56	0.40
1:D:153:ASP:C	1:D:155:PRO:HD3	2.47	0.40
1:D:236:ILE:H	1:D:236:ILE:HG12	1.62	0.40
1:C:17:ARG:HG3	1:C:18:PHE:CD2	2.56	0.40
1:F:156:ASN:OD1	1:F:156:ASN:N	2.53	0.40
1:A:345:ALA:O	1:A:349:VAL:HG12	2.21	0.40
1:A:383:LYS:HG3	1:A:385:GLY:H	1.86	0.40
1:C:140:ARG:HG3	1:C:140:ARG:NH1	2.36	0.40
1:C:198:CYS:O	1:C:198:CYS:SG	2.79	0.40
1:C:282:LEU:HD22	1:C:323:GLN:N	2.37	0.40
1:B:60:LEU:HD23	1:B:423:ILE:HG23	2.03	0.40
1:B:378:VAL:HG13	1:B:423:ILE:HB	2.02	0.40
1:B:454:LEU:HB3	1:B:457:ILE:HD11	2.02	0.40
1:E:224:HIS:NE2	1:E:266:ARG:HG3	2.36	0.40
1:F:178:ARG:HG3	1:F:178:ARG:NH1	2.37	0.40
1:A:64:CYS:HG	1:A:275:HIS:CD2	2.36	0.40
1:A:242:ILE:HB	1:A:270:ILE:HD13	2.02	0.40
1:D:122:ASN:HD22	1:D:324:VAL:CG1	2.34	0.40
1:D:282:LEU:HD22	1:D:323:GLN:N	2.36	0.40
1:E:158:VAL:HA	1:E:178:ARG:O	2.22	0.40
1:E:262:PHE:HA	1:E:267:VAL:HG13	2.03	0.40
1:E:382:LEU:HG	1:E:392:LEU:CD1	2.51	0.40
1:F:89:GLU:OE2	1:F:89:GLU:N	2.54	0.40
1:F:105:ALA:HB2	1:F:288:ILE:HD12	2.04	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	421/466 (90%)	385 (91%)	36 (9%)	0	100	100
1	B	421/466 (90%)	380 (90%)	41 (10%)	0	100	100
1	C	421/466 (90%)	384 (91%)	37 (9%)	0	100	100
1	D	421/466 (90%)	386 (92%)	34 (8%)	1 (0%)	43	72
1	E	421/466 (90%)	386 (92%)	35 (8%)	0	100	100
1	F	421/466 (90%)	385 (91%)	36 (9%)	0	100	100
All	All	2526/2796 (90%)	2306 (91%)	219 (9%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	296	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	355/390 (91%)	297 (84%)	58 (16%)	2	15
1	B	355/390 (91%)	296 (83%)	59 (17%)	2	14
1	C	355/390 (91%)	294 (83%)	61 (17%)	2	12
1	D	355/390 (91%)	303 (85%)	52 (15%)	3	18
1	E	355/390 (91%)	299 (84%)	56 (16%)	2	15
1	F	355/390 (91%)	293 (82%)	62 (18%)	2	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2130/2340 (91%)	1782 (84%)	348 (16%)	4 15

All (348) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LEU
1	A	22	SER
1	A	24	SER
1	A	25	THR
1	A	29	SER
1	A	30	LYS
1	A	41	VAL
1	A	49	GLU
1	A	50	LEU
1	A	52	LEU
1	A	63	PHE
1	A	66	THR
1	A	68	ASP
1	A	72	VAL
1	A	77	ASP
1	A	80	ILE
1	A	81	ASN
1	A	85	ILE
1	A	93	SER
1	A	103	MET
1	A	121	THR
1	A	152	THR
1	A	157	LEU
1	A	163	GLN
1	A	188	PHE
1	A	194	MET
1	A	201	ASN
1	A	206	VAL
1	A	208	THR
1	A	211	VAL
1	A	214	THR
1	A	227	LEU
1	A	229	LYS
1	A	242	ILE
1	A	269	SER
1	A	271	SER
1	A	273	SER

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Mol	Chain	Res	Type
1	A	295	LEU
1	A	297	GLN
1	A	336	ARG
1	A	344	ASN
1	A	349	VAL
1	A	359	LYS
1	A	368	THR
1	A	370	ARG
1	A	375	ILE
1	A	378	VAL
1	A	386	GLU
1	A	387	ASP
1	A	394	ASP
1	A	398	ARG
1	A	411	LEU
1	A	414	GLU
1	A	430	GLU
1	A	432	ASP
1	A	433	PHE
1	A	447	TYR
1	A	448	LEU
1	B	5	GLN
1	B	7	THR
1	B	11	SER
1	B	13	LEU
1	B	15	ASP
1	B	22	SER
1	B	29	SER
1	B	41	VAL
1	B	49	GLU
1	B	50	LEU
1	B	63	PHE
1	B	66	THR
1	B	68	ASP
1	B	72	VAL
1	B	76	MET
1	B	79	SER
1	B	103	MET
1	B	121	THR
1	B	152	THR
1	B	157	LEU
1	B	163	GLN

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Mol	Chain	Res	Type
1	B	175	VAL
1	B	187	LEU
1	B	188	PHE
1	B	194	MET
1	B	196	GLU
1	B	201	ASN
1	B	206	VAL
1	B	208	THR
1	B	209	PHE
1	B	211	VAL
1	B	214	THR
1	B	216	ASN
1	B	239	ASP
1	B	240	MET
1	B	242	ILE
1	B	250	LEU
1	B	254	VAL
1	B	269	SER
1	B	271	SER
1	B	336	ARG
1	B	344	ASN
1	B	349	VAL
1	B	368	THR
1	B	370	ARG
1	B	378	VAL
1	B	383	LYS
1	B	386	GLU
1	B	387	ASP
1	B	394	ASP
1	B	396	SER
1	B	402	ARG
1	B	411	LEU
1	B	417	ASP
1	B	432	ASP
1	B	433	PHE
1	B	447	TYR
1	B	448	LEU
1	B	455	GLN
1	C	7	THR
1	C	10	ARG
1	C	13	LEU
1	C	24	SER

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Mol	Chain	Res	Type
1	C	25	THR
1	C	29	SER
1	C	34	LEU
1	C	49	GLU
1	C	63	PHE
1	C	66	THR
1	C	68	ASP
1	C	72	VAL
1	C	78	LEU
1	C	88	GLU
1	C	93	SER
1	C	115	ASN
1	C	124	ILE
1	C	131	MET
1	C	141	TRP
1	C	152	THR
1	C	154	LYS
1	C	157	LEU
1	C	158	VAL
1	C	163	GLN
1	C	176	GLU
1	C	188	PHE
1	C	201	ASN
1	C	206	VAL
1	C	208	THR
1	C	209	PHE
1	C	211	VAL
1	C	212	THR
1	C	214	THR
1	C	227	LEU
1	C	236	ILE
1	C	238	ILE
1	C	239	ASP
1	C	242	ILE
1	C	258	ILE
1	C	267	VAL
1	C	269	SER
1	C	270	ILE
1	C	271	SER
1	C	295	LEU
1	C	297	GLN
1	C	336	ARG

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Mol	Chain	Res	Type
1	C	340	THR
1	C	344	ASN
1	C	368	THR
1	C	370	ARG
1	C	378	VAL
1	C	382	LEU
1	C	386	GLU
1	C	387	ASP
1	C	396	SER
1	C	411	LEU
1	C	419	VAL
1	C	430	GLU
1	C	433	PHE
1	C	441	TYR
1	C	447	TYR
1	D	7	THR
1	D	14	LEU
1	D	34	LEU
1	D	41	VAL
1	D	49	GLU
1	D	63	PHE
1	D	66	THR
1	D	68	ASP
1	D	75	LEU
1	D	93	SER
1	D	124	ILE
1	D	154	LYS
1	D	157	LEU
1	D	163	GLN
1	D	171	ARG
1	D	187	LEU
1	D	188	PHE
1	D	194	MET
1	D	196	GLU
1	D	199	ASP
1	D	201	ASN
1	D	206	VAL
1	D	208	THR
1	D	214	THR
1	D	227	LEU
1	D	231	GLN
1	D	236	ILE

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Mol	Chain	Res	Type
1	D	239	ASP
1	D	242	ILE
1	D	267	VAL
1	D	271	SER
1	D	273	SER
1	D	295	LEU
1	D	336	ARG
1	D	344	ASN
1	D	356	GLU
1	D	368	THR
1	D	370	ARG
1	D	378	VAL
1	D	382	LEU
1	D	383	LYS
1	D	386	GLU
1	D	387	ASP
1	D	394	ASP
1	D	395	LEU
1	D	396	SER
1	D	419	VAL
1	D	430	GLU
1	D	433	PHE
1	D	441	TYR
1	D	447	TYR
1	D	459	GLN
1	E	7	THR
1	E	15	ASP
1	E	24	SER
1	E	25	THR
1	E	29	SER
1	E	50	LEU
1	E	63	PHE
1	E	66	THR
1	E	68	ASP
1	E	77	ASP
1	E	85	ILE
1	E	115	ASN
1	E	121	THR
1	E	127	SER
1	E	141	TRP
1	E	152	THR
1	E	157	LEU

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Mol	Chain	Res	Type
1	E	163	GLN
1	E	175	VAL
1	E	188	PHE
1	E	192	LYS
1	E	199	ASP
1	E	208	THR
1	E	211	VAL
1	E	214	THR
1	E	216	ASN
1	E	227	LEU
1	E	239	ASP
1	E	242	ILE
1	E	250	LEU
1	E	271	SER
1	E	336	ARG
1	E	340	THR
1	E	344	ASN
1	E	349	VAL
1	E	353	LEU
1	E	368	THR
1	E	370	ARG
1	E	378	VAL
1	E	386	GLU
1	E	387	ASP
1	E	394	ASP
1	E	396	SER
1	E	402	ARG
1	E	411	LEU
1	E	417	ASP
1	E	418	ILE
1	E	419	VAL
1	E	430	GLU
1	E	433	PHE
1	E	436	LEU
1	E	438	LEU
1	E	441	TYR
1	E	447	TYR
1	E	453	LYS
1	E	459	GLN
1	F	22	SER
1	F	25	THR
1	F	29	SER

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Mol	Chain	Res	Type
1	F	31	ARG
1	F	38	ARG
1	F	39	ASP
1	F	41	VAL
1	F	49	GLU
1	F	52	LEU
1	F	63	PHE
1	F	66	THR
1	F	68	ASP
1	F	79	SER
1	F	93	SER
1	F	117	GLN
1	F	121	THR
1	F	140	ARG
1	F	141	TRP
1	F	152	THR
1	F	157	LEU
1	F	158	VAL
1	F	163	GLN
1	F	175	VAL
1	F	187	LEU
1	F	188	PHE
1	F	194	MET
1	F	196	GLU
1	F	199	ASP
1	F	201	ASN
1	F	208	THR
1	F	214	THR
1	F	216	ASN
1	F	227	LEU
1	F	239	ASP
1	F	242	ILE
1	F	250	LEU
1	F	267	VAL
1	F	271	SER
1	F	336	ARG
1	F	340	THR
1	F	349	VAL
1	F	353	LEU
1	F	355	ASP
1	F	368	THR
1	F	370	ARG

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Mol	Chain	Res	Type
1	F	378	VAL
1	F	386	GLU
1	F	387	ASP
1	F	396	SER
1	F	398	ARG
1	F	402	ARG
1	F	411	LEU
1	F	419	VAL
1	F	430	GLU
1	F	433	PHE
1	F	436	LEU
1	F	438	LEU
1	F	441	TYR
1	F	445	LEU
1	F	447	TYR
1	F	448	LEU
1	F	459	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	GLN
1	A	231	GLN
1	A	455	GLN
1	B	59	ASN
1	B	65	GLN
1	B	297	GLN
1	B	344	ASN
1	C	59	ASN
1	C	109	HIS
1	C	297	GLN
1	D	59	ASN
1	D	115	ASN
1	D	297	GLN
1	E	59	ASN
1	E	344	ASN
1	F	59	ASN
1	F	201	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

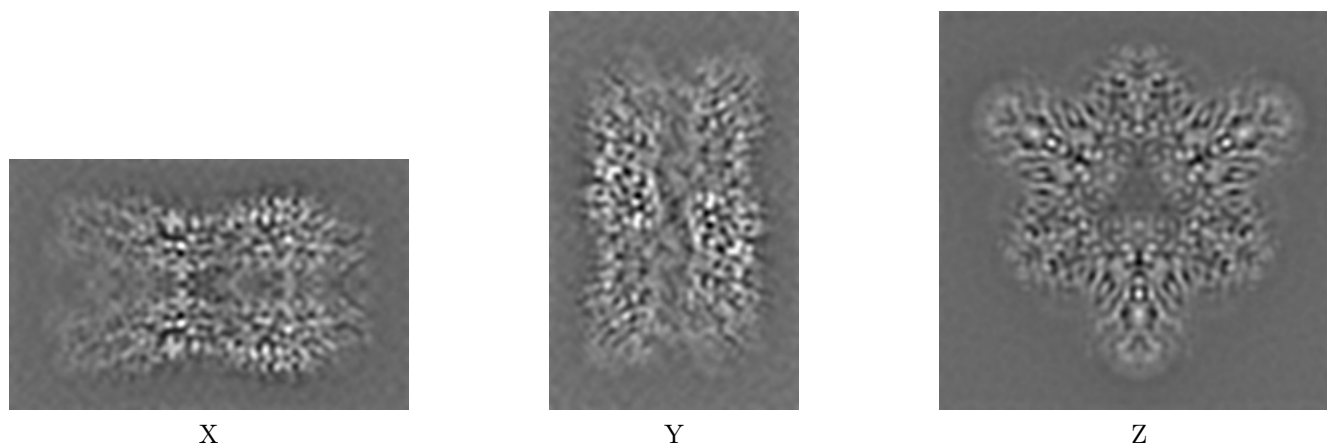
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22531. 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](#)

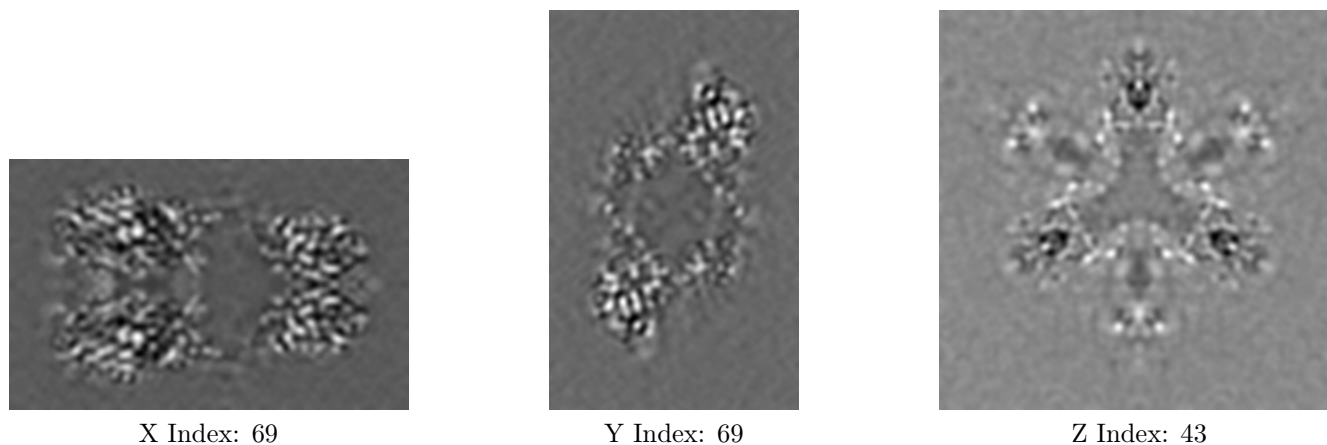
6.1.1 Primary map



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

6.2 Central slices [i](#)

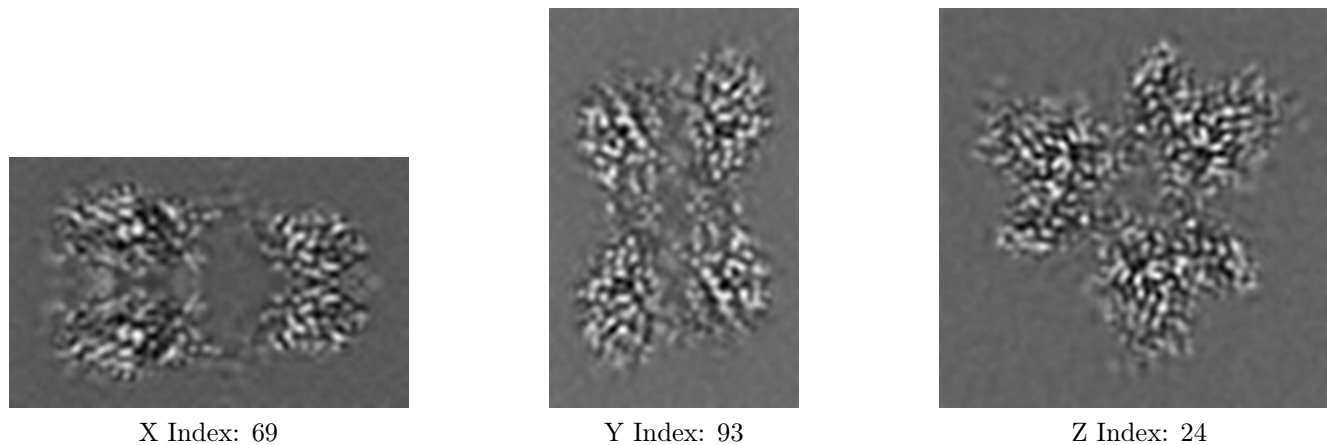
6.2.1 Primary map



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

6.3 Largest variance slices [i](#)

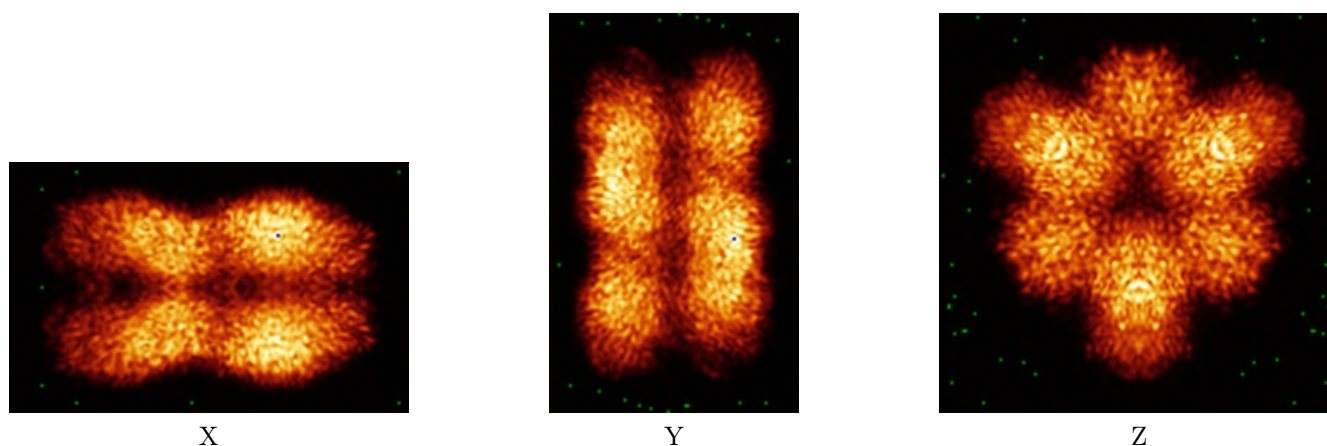
6.3.1 Primary map



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

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

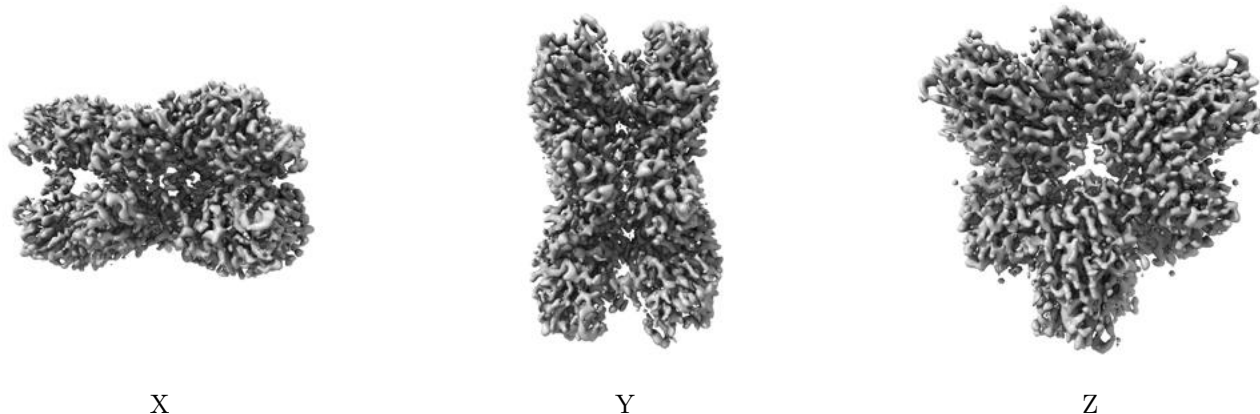
6.4.1 Primary map



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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

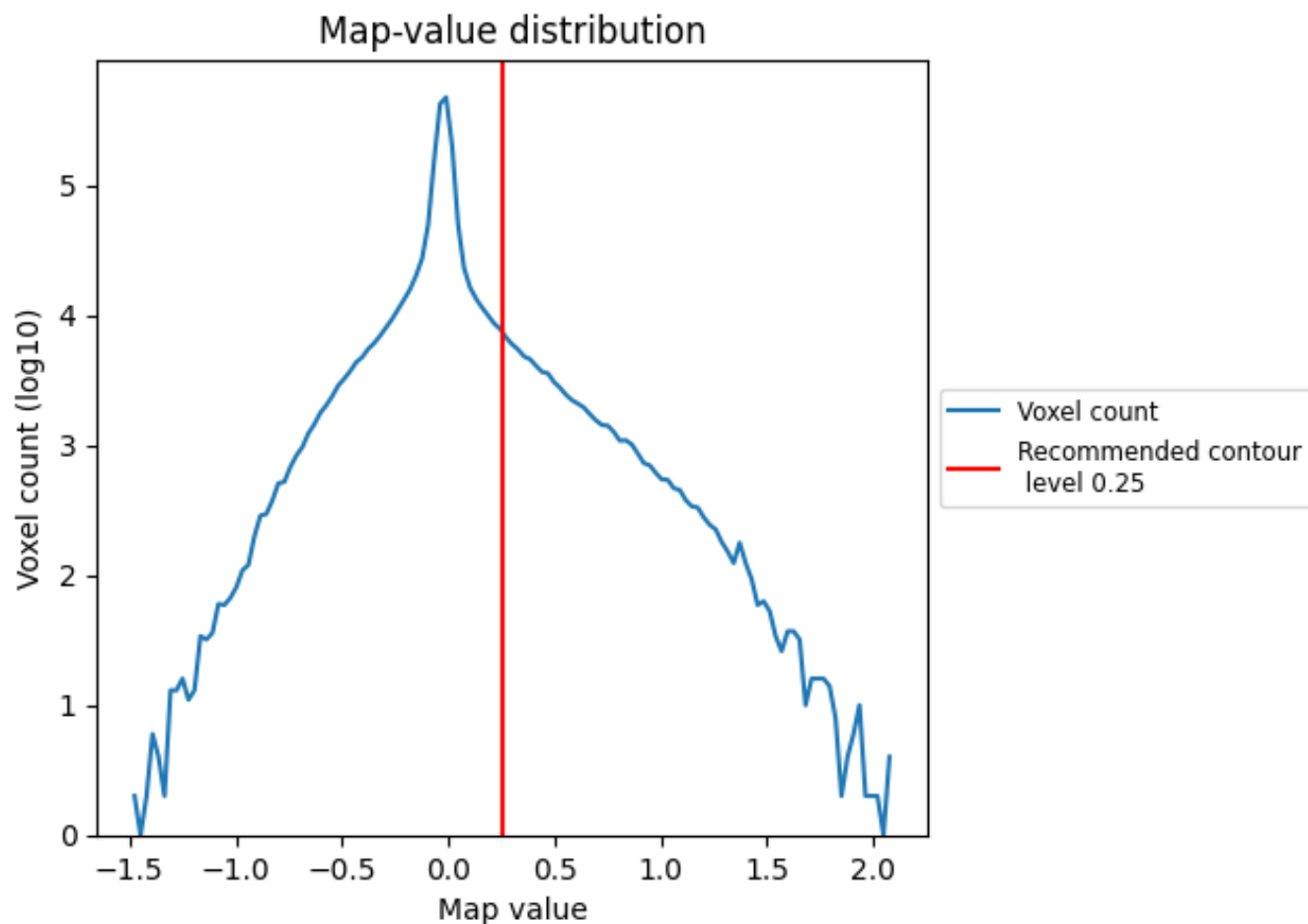
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

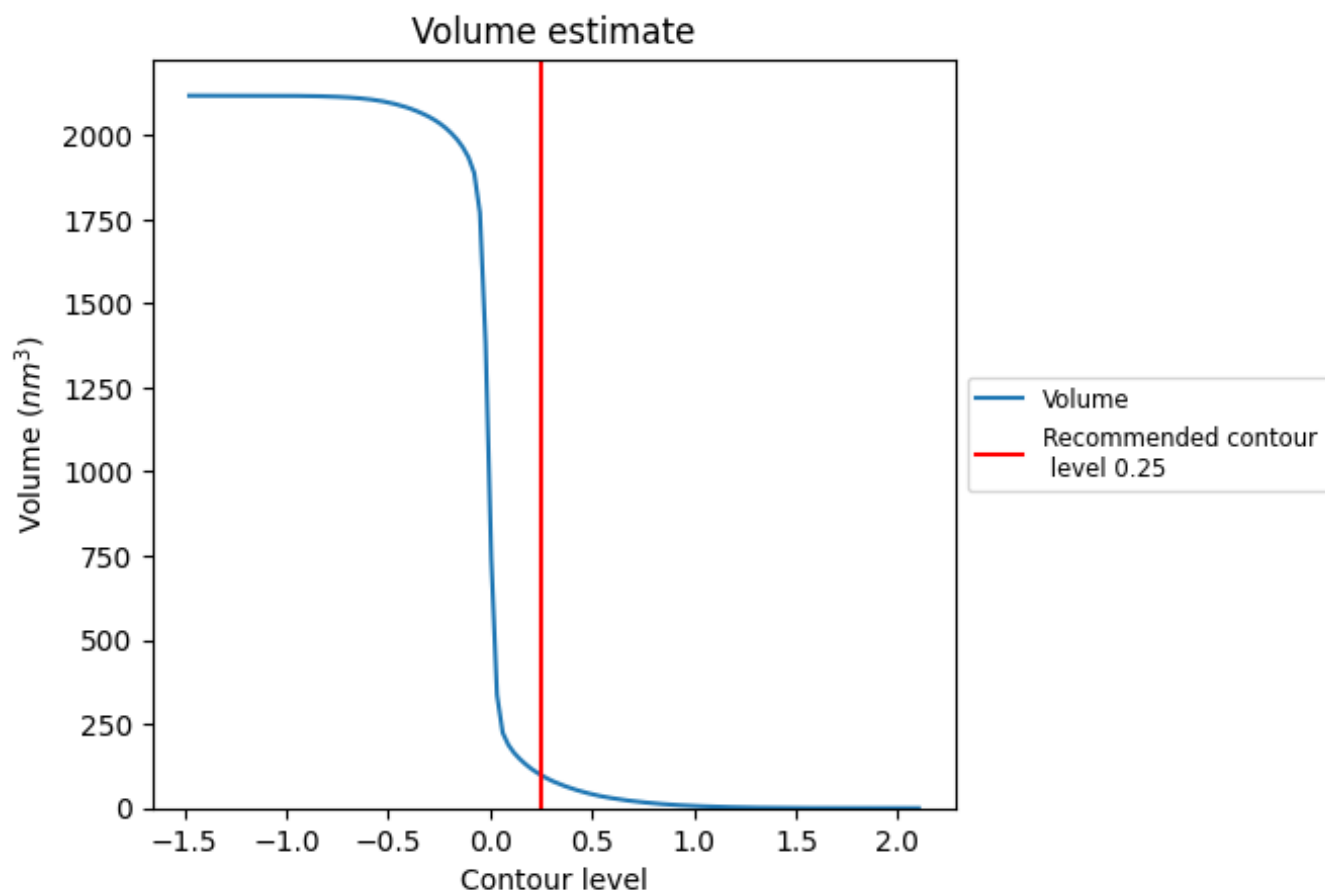
This section contains the results of statistical analysis of the map.

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 98 nm³; this corresponds to an approximate mass of 89 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

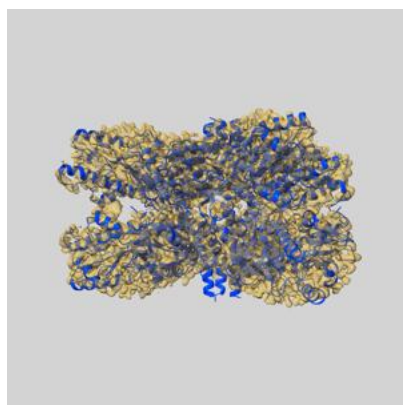
8 Fourier-Shell correlation

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

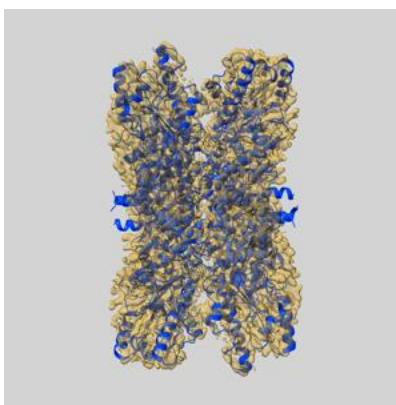
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22531 and PDB model 7JZH. Per-residue inclusion information can be found in section [3](#) on page [5](#).

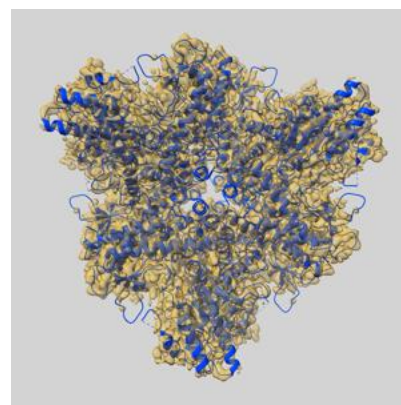
9.1 Map-model overlay [i](#)



X



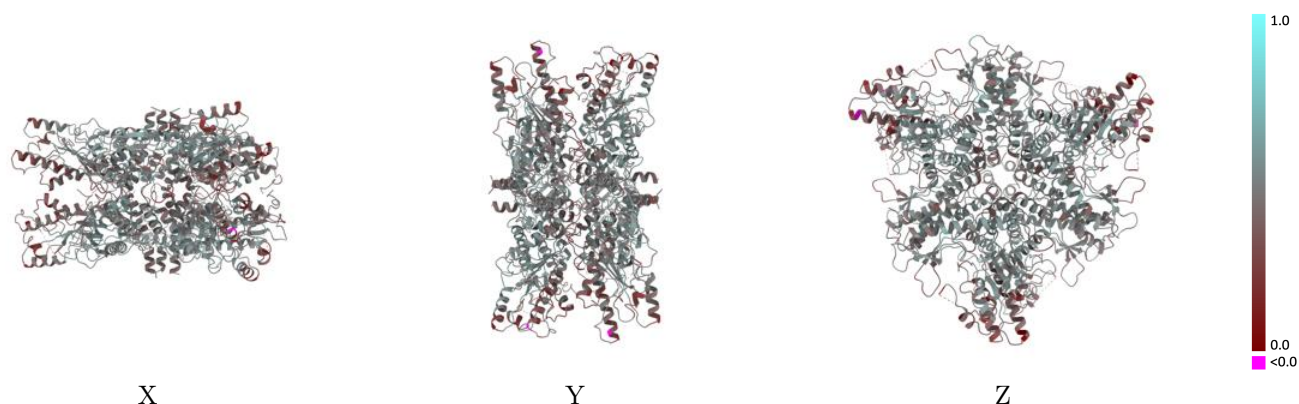
Y



Z

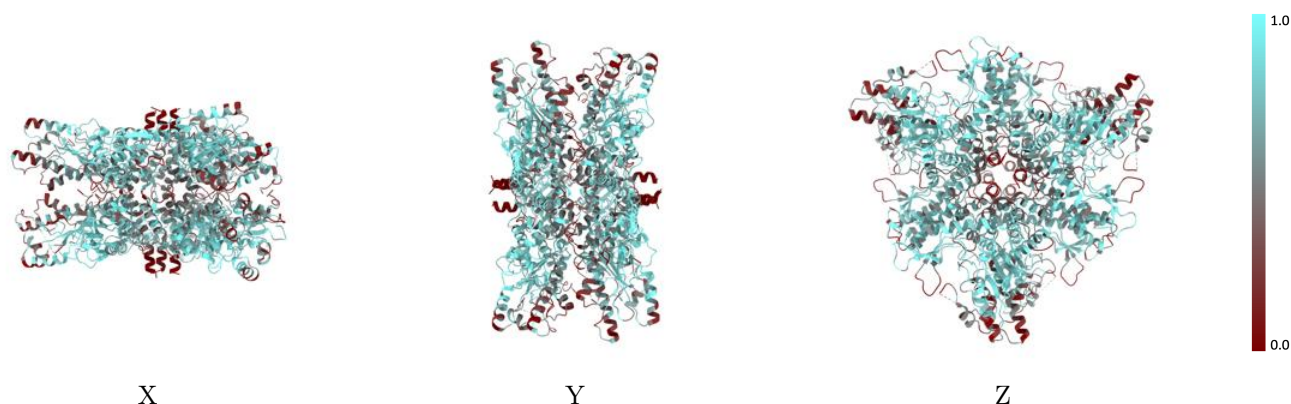
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



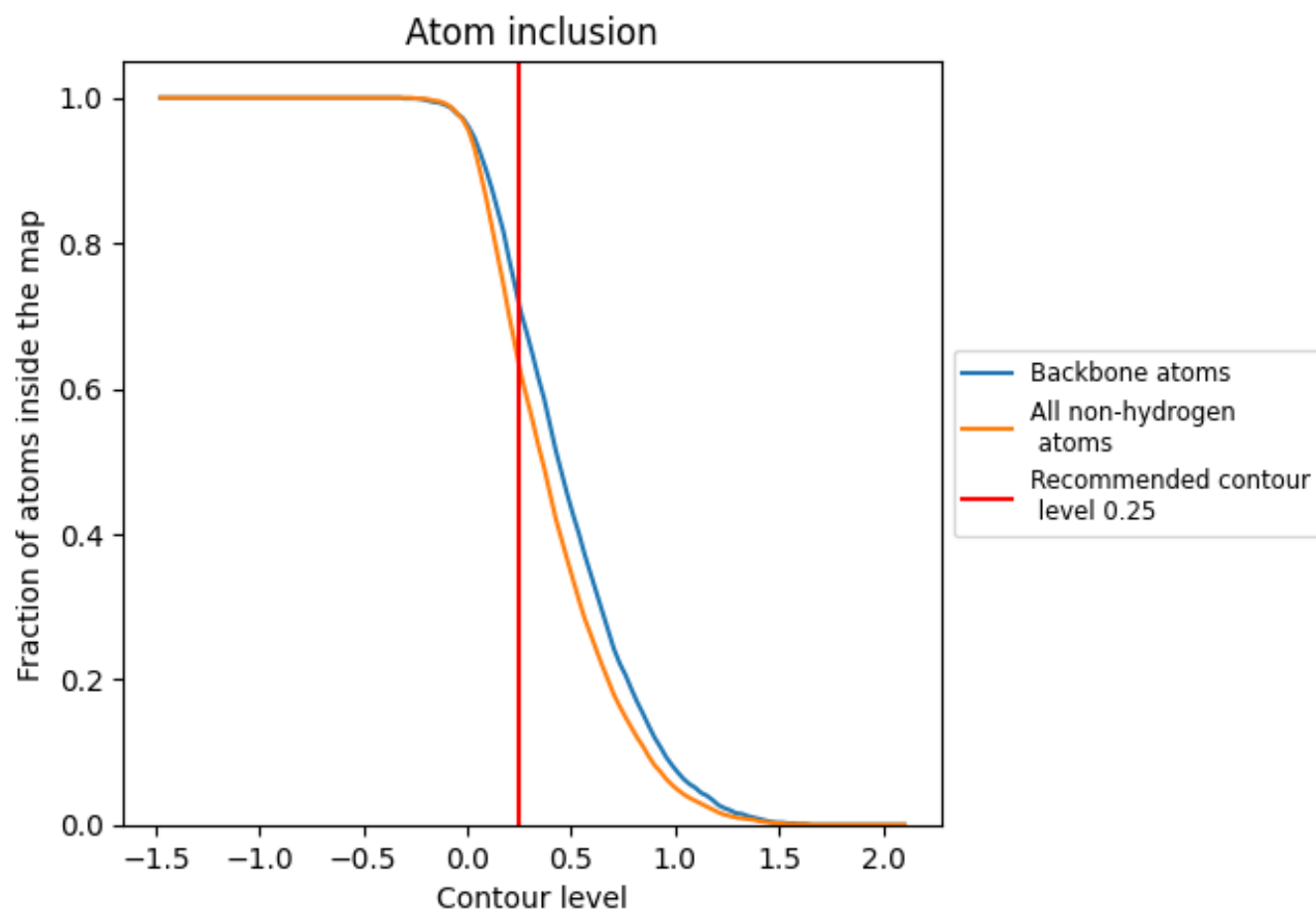
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 63% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6300	0.4670
A	0.6310	0.4660
B	0.6320	0.4660
C	0.6290	0.4670
D	0.6280	0.4680
E	0.6300	0.4660
F	0.6320	0.4680

1.0

0.0

<0.0