Full wwPDB EM Validation Report ⓘ

Dec 11, 2022 – 09:36 pm GMT

PDB ID	:	6TA5
EMDB ID	:	EMD-10372
Title	:	OprM-MexA complex from the MexAB-OprM Pseudomonas aeruginosa whole assembly reconstituted in nanodiscs
Authors	:	Glavier, M.; Schoehn, G.; Taveau, J.C.; Phan, G.; Daury, L.; Lambert, O.; Broutin, I.
Deposited on	:	2019-10-29
Resolution	:	3.20 Å(reported)
Based on initial models	:	3D5K, 6TA6

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

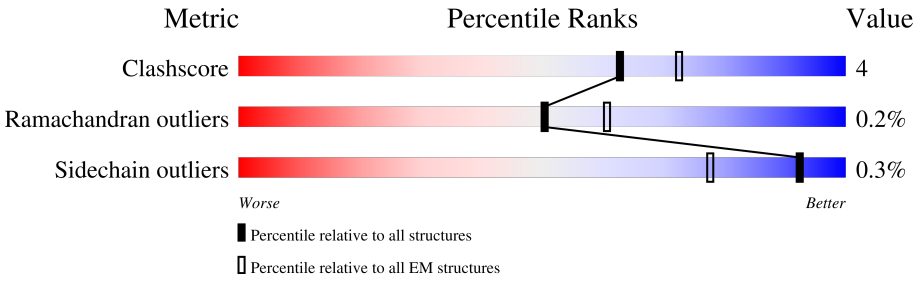
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

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 3.20 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	474	89% 7% ·
1	B	474	87% 9% ·
1	C	474	90% 6% ·
2	D	366	5% 84% 10% 6%
2	E	366	12% 83% 11% 6%
2	F	366	5% 85% 9% 6%
2	G	366	13% 83% 11% 6%
2	H	366	84% 9% · 6%

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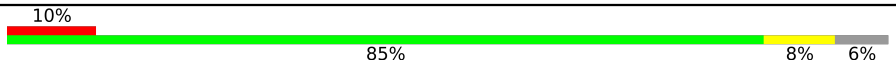
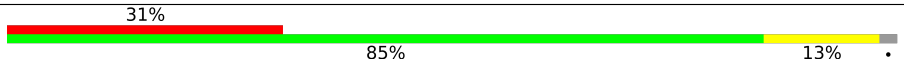
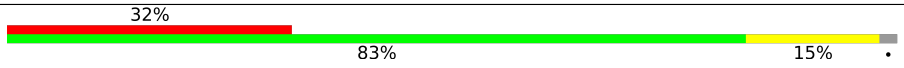
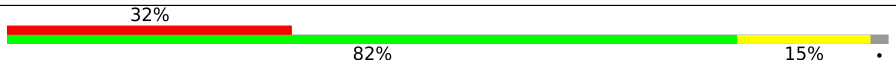
Mol	Chain	Length	Quality of chain
2	I	366	
3	J	1052	
3	K	1052	
3	L	1052	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 49554 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 Outer membrane protein OprM.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	455	Total	C	N	O	S	0	0
			3487	2182	621	681	3		
1	B	455	Total	C	N	O	S	0	0
			3487	2182	621	681	3		
1	C	455	Total	C	N	O	S	0	0
			3487	2182	621	681	3		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	469	HIS	-	expression tag	UNP Q51487
A	470	HIS	-	expression tag	UNP Q51487
A	471	HIS	-	expression tag	UNP Q51487
A	472	HIS	-	expression tag	UNP Q51487
A	473	HIS	-	expression tag	UNP Q51487
A	474	HIS	-	expression tag	UNP Q51487
B	469	HIS	-	expression tag	UNP Q51487
B	470	HIS	-	expression tag	UNP Q51487
B	471	HIS	-	expression tag	UNP Q51487
B	472	HIS	-	expression tag	UNP Q51487
B	473	HIS	-	expression tag	UNP Q51487
B	474	HIS	-	expression tag	UNP Q51487
C	469	HIS	-	expression tag	UNP Q51487
C	470	HIS	-	expression tag	UNP Q51487
C	471	HIS	-	expression tag	UNP Q51487
C	472	HIS	-	expression tag	UNP Q51487
C	473	HIS	-	expression tag	UNP Q51487
C	474	HIS	-	expression tag	UNP Q51487

- Molecule 2 is a protein called MexA family multidrug efflux RND transporter periplasmic adaptor subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	345	Total	C	N	O	S	0	0
			2615	1631	468	513	3		
2	E	343	Total	C	N	O	S	0	0
			2604	1625	466	510	3		
2	F	345	Total	C	N	O	S	0	0
			2615	1631	468	513	3		
2	G	343	Total	C	N	O	S	0	0
			2604	1625	466	510	3		
2	H	345	Total	C	N	O	S	0	0
			2615	1631	468	513	3		
2	I	343	Total	C	N	O	S	0	0
			2604	1625	466	510	3		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	361	HIS	-	expression tag	UNP A0A2V3GTR8
D	362	HIS	-	expression tag	UNP A0A2V3GTR8
D	363	HIS	-	expression tag	UNP A0A2V3GTR8
D	364	HIS	-	expression tag	UNP A0A2V3GTR8
D	365	HIS	-	expression tag	UNP A0A2V3GTR8
D	366	HIS	-	expression tag	UNP A0A2V3GTR8
E	361	HIS	-	expression tag	UNP A0A2V3GTR8
E	362	HIS	-	expression tag	UNP A0A2V3GTR8
E	363	HIS	-	expression tag	UNP A0A2V3GTR8
E	364	HIS	-	expression tag	UNP A0A2V3GTR8
E	365	HIS	-	expression tag	UNP A0A2V3GTR8
E	366	HIS	-	expression tag	UNP A0A2V3GTR8
F	361	HIS	-	expression tag	UNP A0A2V3GTR8
F	362	HIS	-	expression tag	UNP A0A2V3GTR8
F	363	HIS	-	expression tag	UNP A0A2V3GTR8
F	364	HIS	-	expression tag	UNP A0A2V3GTR8
F	365	HIS	-	expression tag	UNP A0A2V3GTR8
F	366	HIS	-	expression tag	UNP A0A2V3GTR8
G	361	HIS	-	expression tag	UNP A0A2V3GTR8
G	362	HIS	-	expression tag	UNP A0A2V3GTR8
G	363	HIS	-	expression tag	UNP A0A2V3GTR8
G	364	HIS	-	expression tag	UNP A0A2V3GTR8
G	365	HIS	-	expression tag	UNP A0A2V3GTR8
G	366	HIS	-	expression tag	UNP A0A2V3GTR8
H	361	HIS	-	expression tag	UNP A0A2V3GTR8
H	362	HIS	-	expression tag	UNP A0A2V3GTR8
H	363	HIS	-	expression tag	UNP A0A2V3GTR8
H	364	HIS	-	expression tag	UNP A0A2V3GTR8

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Chain	Residue	Modelled	Actual	Comment	Reference
H	365	HIS	-	expression tag	UNP A0A2V3GTR8
H	366	HIS	-	expression tag	UNP A0A2V3GTR8
I	361	HIS	-	expression tag	UNP A0A2V3GTR8
I	362	HIS	-	expression tag	UNP A0A2V3GTR8
I	363	HIS	-	expression tag	UNP A0A2V3GTR8
I	364	HIS	-	expression tag	UNP A0A2V3GTR8
I	365	HIS	-	expression tag	UNP A0A2V3GTR8
I	366	HIS	-	expression tag	UNP A0A2V3GTR8

- Molecule 3 is a protein called Efflux pump membrane transporter.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	1030	Total	C	N	O	S	0	0
			7812	5027	1298	1447	40		
3	K	1030	Total	C	N	O	S	0	0
			7812	5027	1298	1447	40		
3	L	1030	Total	C	N	O	S	0	0
			7812	5027	1298	1447	40		

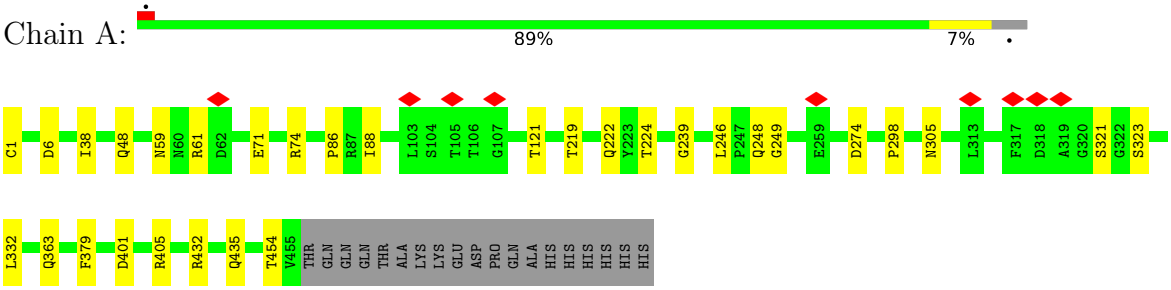
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1047	HIS	-	expression tag	UNP A0A069Q9M6
J	1048	HIS	-	expression tag	UNP A0A069Q9M6
J	1049	HIS	-	expression tag	UNP A0A069Q9M6
J	1050	HIS	-	expression tag	UNP A0A069Q9M6
J	1051	HIS	-	expression tag	UNP A0A069Q9M6
J	1052	HIS	-	expression tag	UNP A0A069Q9M6
K	1047	HIS	-	expression tag	UNP A0A069Q9M6
K	1048	HIS	-	expression tag	UNP A0A069Q9M6
K	1049	HIS	-	expression tag	UNP A0A069Q9M6
K	1050	HIS	-	expression tag	UNP A0A069Q9M6
K	1051	HIS	-	expression tag	UNP A0A069Q9M6
K	1052	HIS	-	expression tag	UNP A0A069Q9M6
L	1047	HIS	-	expression tag	UNP A0A069Q9M6
L	1048	HIS	-	expression tag	UNP A0A069Q9M6
L	1049	HIS	-	expression tag	UNP A0A069Q9M6
L	1050	HIS	-	expression tag	UNP A0A069Q9M6
L	1051	HIS	-	expression tag	UNP A0A069Q9M6
L	1052	HIS	-	expression tag	UNP A0A069Q9M6

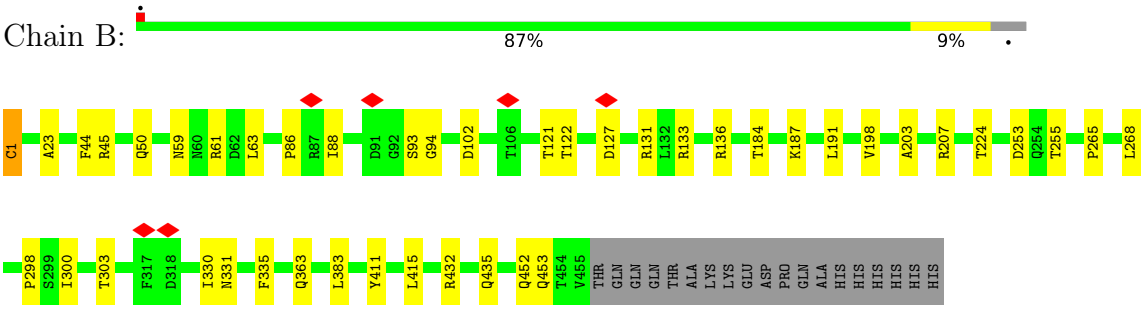
3 Residue-property plots (i)

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.

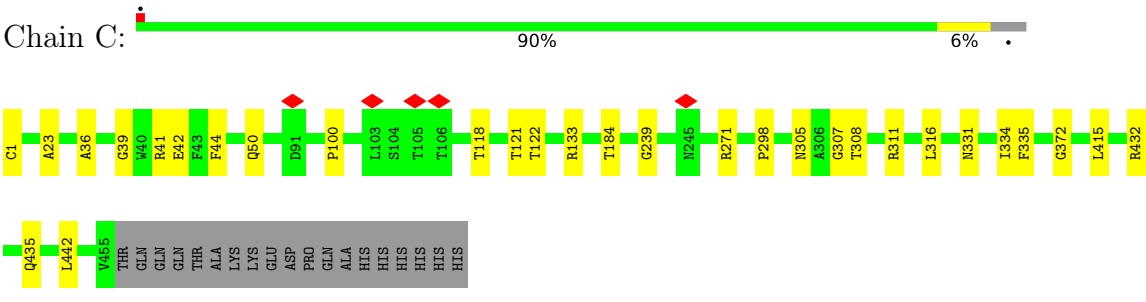
• Molecule 1: Outer membrane protein OprM



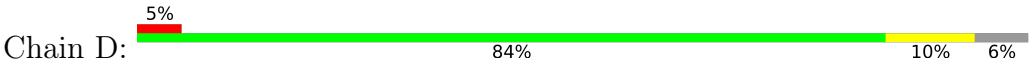
• Molecule 1: Outer membrane protein OprM

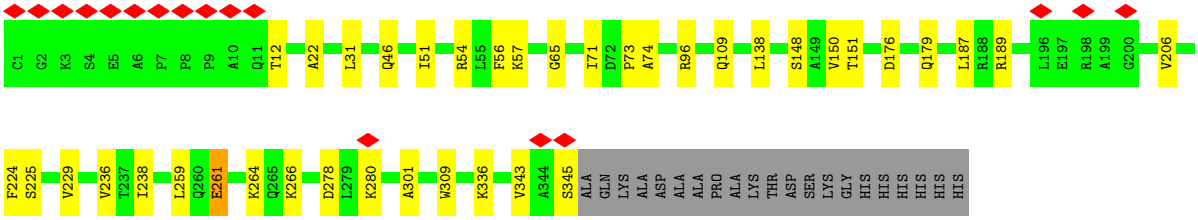


• Molecule 1: Outer membrane protein OprM



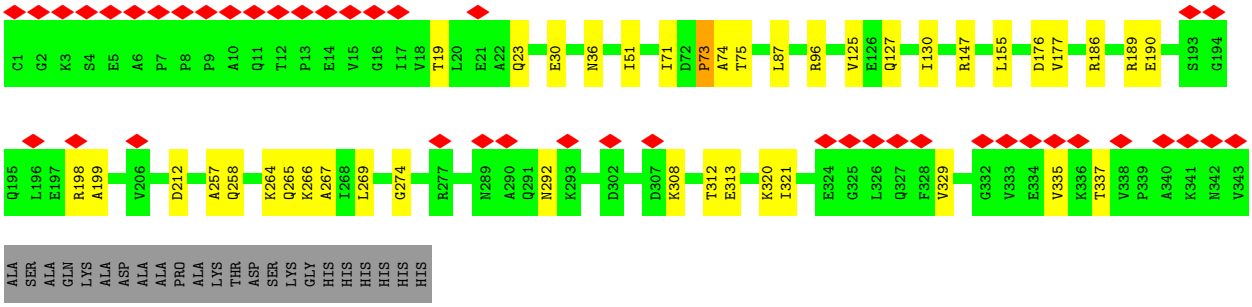
• Molecule 2: MexA family multidrug efflux RND transporter periplasmic adaptor subunit





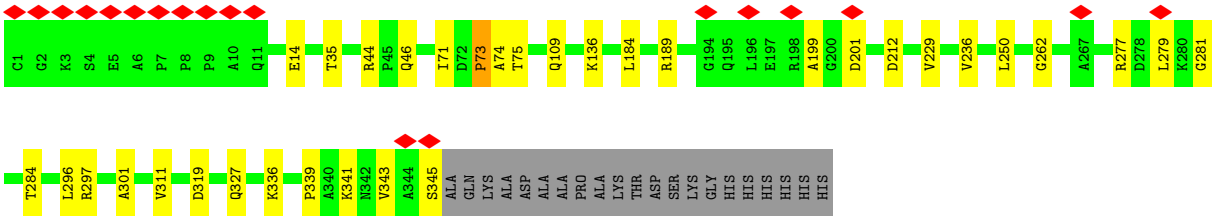
• Molecule 2: MexA family multidrug efflux RND transporter periplasmic adaptor subunit

Chain E:



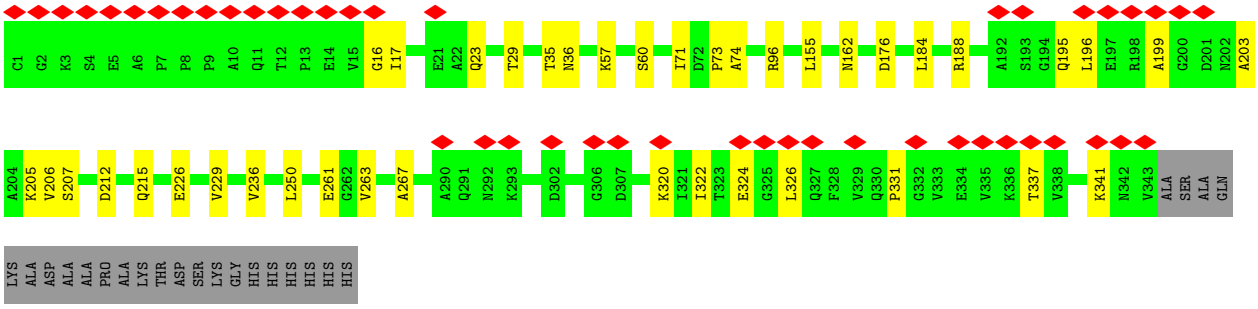
• Molecule 2: MexA family multidrug efflux RND transporter periplasmic adaptor subunit

Chain F:



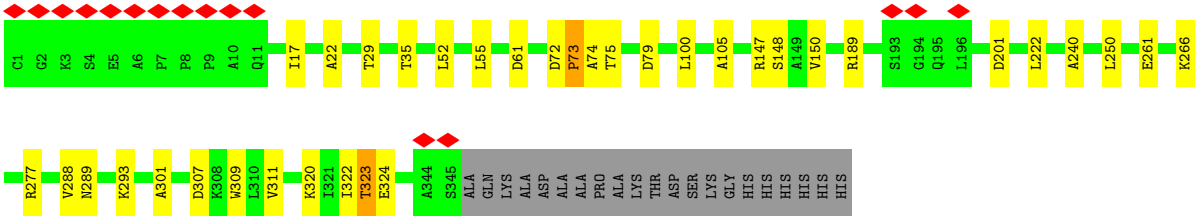
• Molecule 2: MexA family multidrug efflux RND transporter periplasmic adaptor subunit

Chain G:

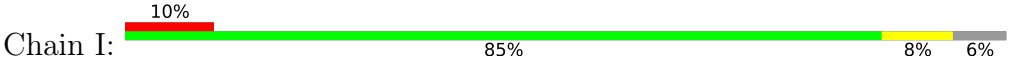


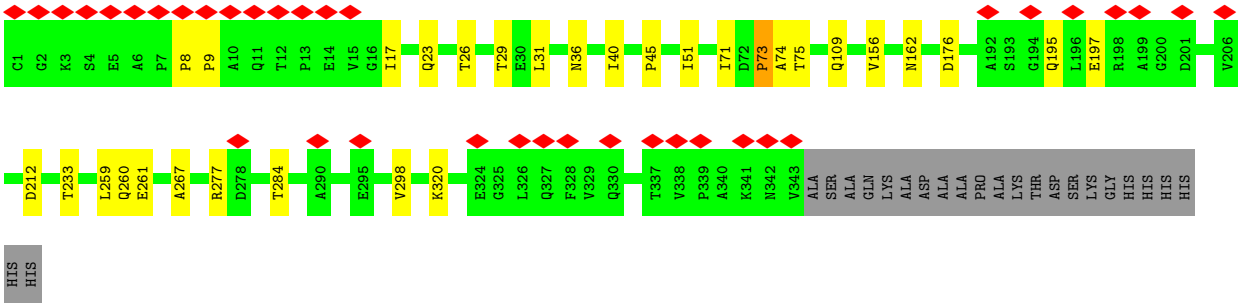
• Molecule 2: MexA family multidrug efflux RND transporter periplasmic adaptor subunit

Chain H:

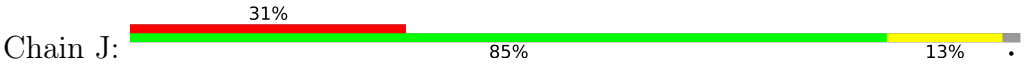


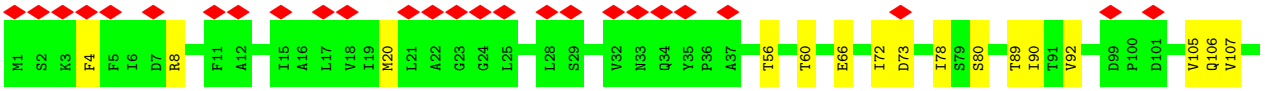
• Molecule 2: MexA family multidrug efflux RND transporter periplasmic adaptor subunit

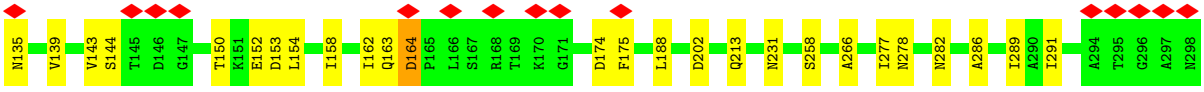


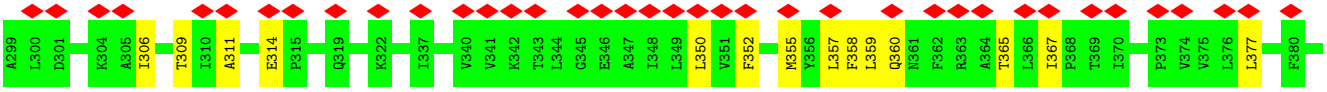


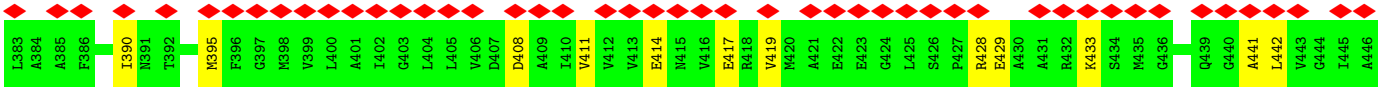
• Molecule 3: Efflux pump membrane transporter

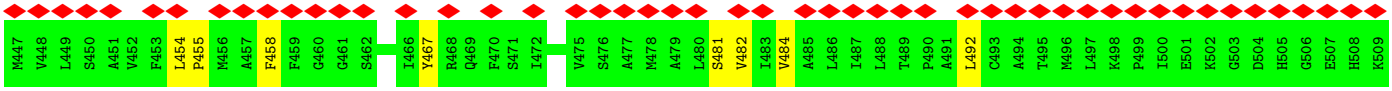


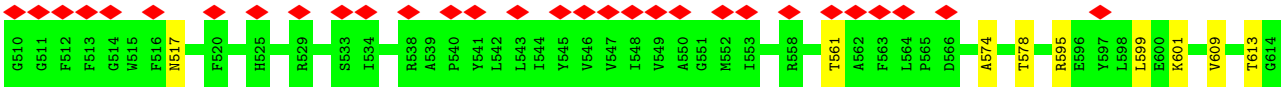


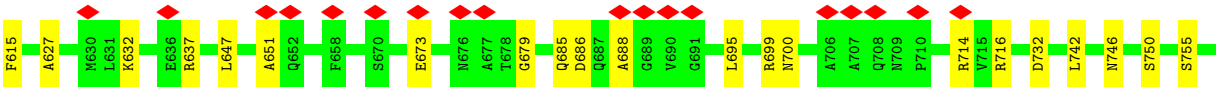


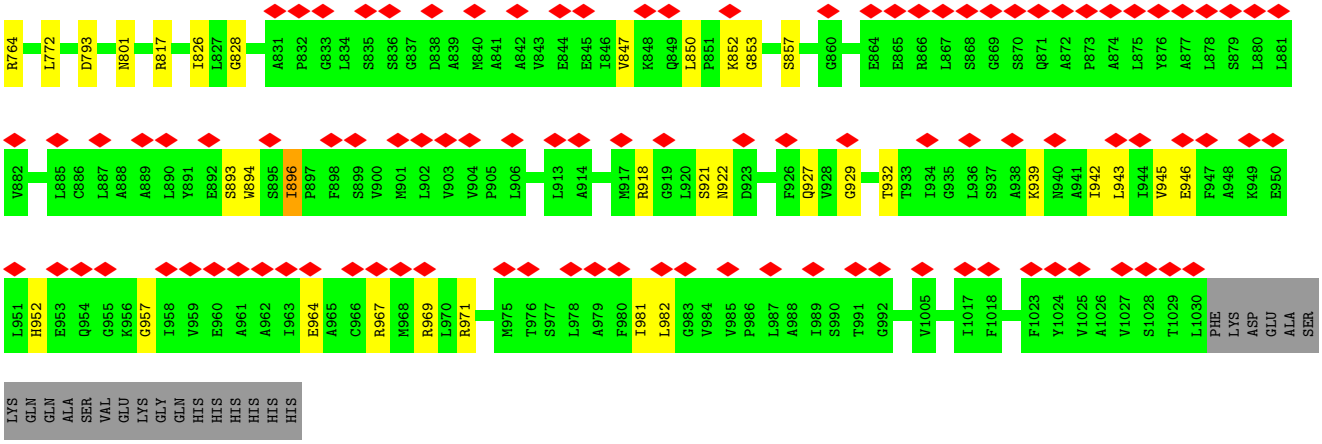






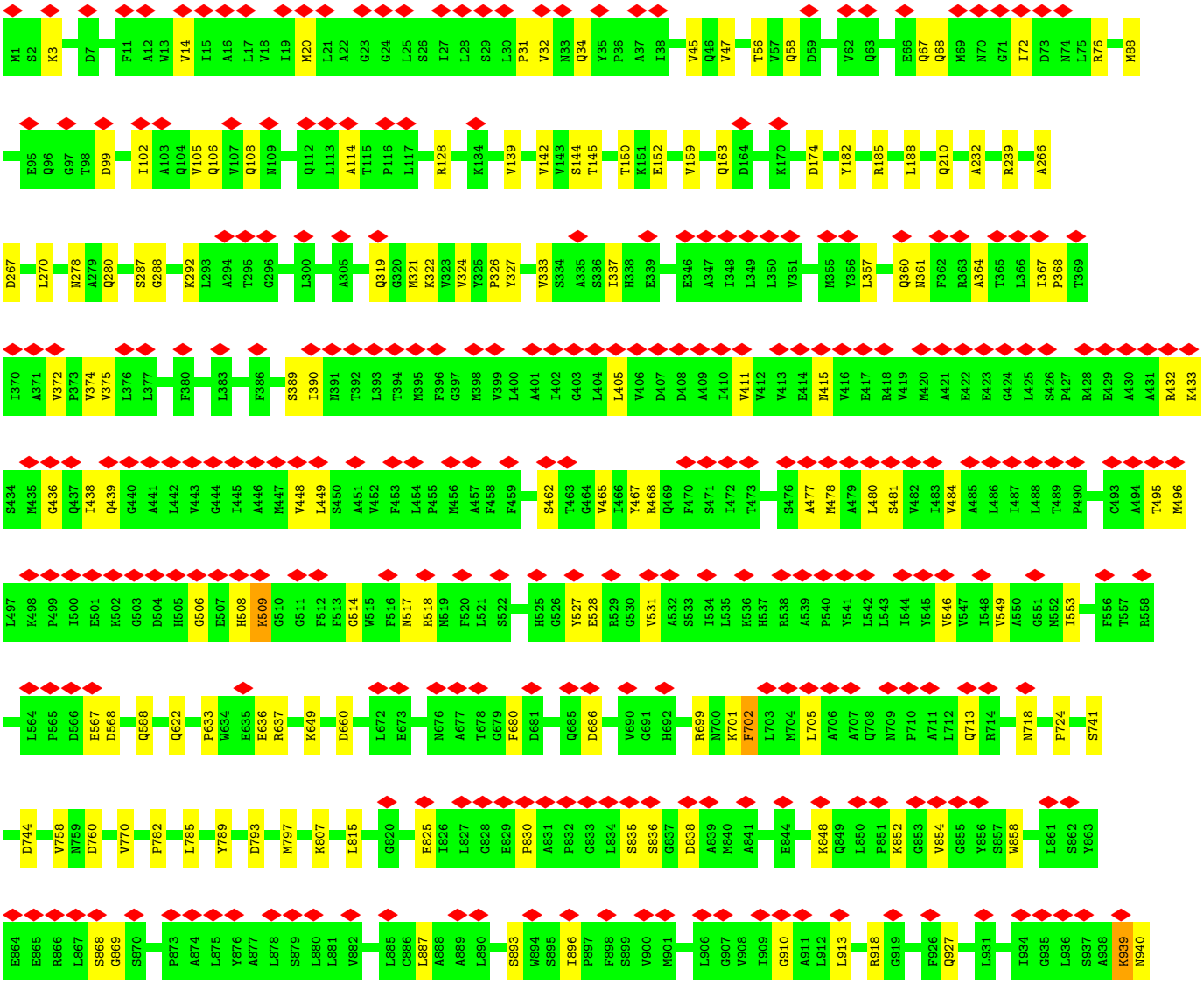


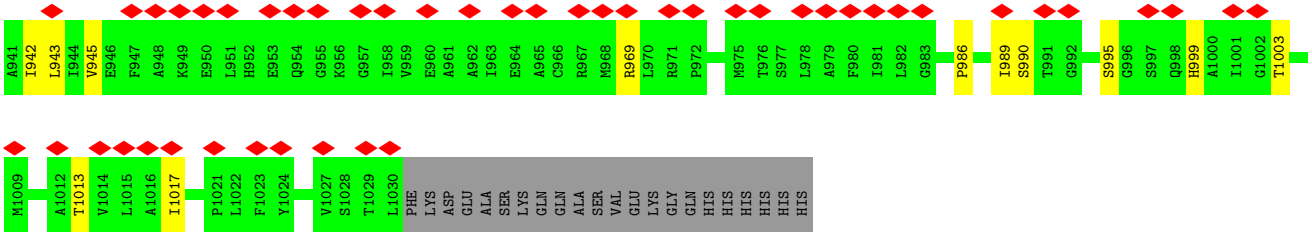




• Molecule 3: Efflux pump membrane transporter

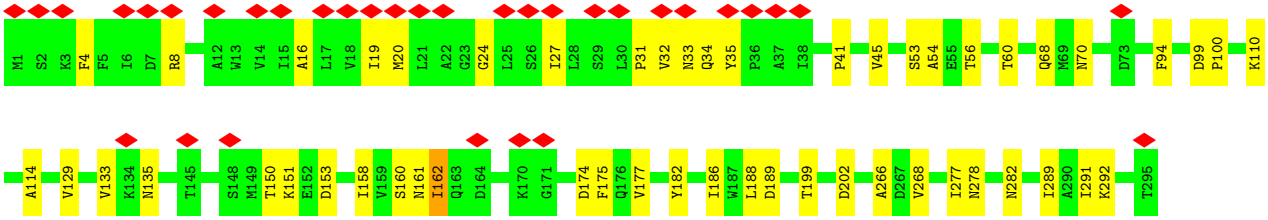
Chain K:

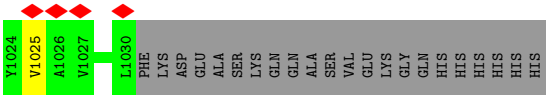




• Molecule 3: Efflux pump membrane transporter

Chain L:




V1024
V1025
A1026
V1027
L1030
PHE
LYS
ASP
GLU
ALA
SER
LYS
GLN
GLN
ALA
SER
VAL
GLU
LYS
GLY
GLN
HIS
HIS
HIS
HIS
HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	35819	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 ($e^-/Å^2$)	42	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.175	Depositor
Minimum map value	-0.098	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.028	Depositor
Map size (Å)	696.32, 696.32, 696.32	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.30	0/3543	0.44	0/4819
1	B	0.30	0/3543	0.46	0/4819
1	C	0.30	0/3543	0.45	0/4819
2	D	0.32	0/2649	0.55	0/3597
2	E	0.32	0/2638	0.54	0/3582
2	F	0.32	0/2649	0.58	3/3597 (0.1%)
2	G	0.31	0/2638	0.56	2/3582 (0.1%)
2	H	0.32	0/2649	0.54	1/3597 (0.0%)
2	I	0.32	0/2638	0.54	0/3582
3	J	0.30	0/7971	0.60	1/10833 (0.0%)
3	K	0.31	0/7971	0.59	0/10833
3	L	0.30	0/7971	0.59	5/10833 (0.0%)
All	All	0.31	0/50403	0.55	12/68493 (0.0%)

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
3	L	0	1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	201	ASP	CB-CG-OD1	7.00	124.60	118.30
2	F	279	LEU	CA-CB-CG	6.73	130.79	115.30
3	J	454	LEU	CA-CB-CG	6.73	130.78	115.30
2	G	196	LEU	CA-CB-CG	6.68	130.66	115.30
3	L	978	LEU	CA-CB-CG	5.79	128.61	115.30
3	L	357	LEU	CA-CB-CG	5.76	128.54	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	71	ILE	CG1-CB-CG2	-5.27	99.81	111.40
2	F	71	ILE	CG1-CB-CG2	-5.20	99.97	111.40
3	L	162	ILE	CG1-CB-CG2	-5.17	100.03	111.40
3	L	902	LEU	CA-CB-CG	5.17	127.18	115.30
2	H	55	LEU	CA-CB-CG	5.14	127.11	115.30
3	L	931	LEU	CA-CB-CG	5.12	127.08	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	L	348	ILE	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	3487	0	3466	20	0
1	B	3487	0	3466	28	0
1	C	3487	0	3466	20	0
2	D	2615	0	2666	26	0
2	E	2604	0	2656	25	0
2	F	2615	0	2666	20	0
2	G	2604	0	2656	25	0
2	H	2615	0	2666	27	0
2	I	2604	0	2656	19	0
3	J	7812	0	7944	83	0
3	K	7812	0	7944	94	0
3	L	7812	0	7944	91	0
All	All	49554	0	50196	438	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 4.

All (438) 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)
3:J:679:GLY:HA3	3:J:828:GLY:O	1.80	0.82
2:H:29:THR:CG2	2:H:261:GLU:CD	2.57	0.73
3:J:163:GLN:HG2	3:K:67:GLN:HE22	1.54	0.72
2:H:29:THR:HG23	2:H:261:GLU:CD	2.14	0.67
2:F:46:GLN:HE21	2:G:155:LEU:HD13	1.62	0.64
3:L:32:VAL:HG12	3:L:390:ILE:HD11	1.79	0.63
3:K:150:THR:HG23	3:K:152:GLU:H	1.63	0.63
3:J:213:GLN:HE21	3:K:56:THR:HG22	1.65	0.62
1:A:86:PRO:HB2	1:A:121:THR:HG21	1.81	0.61
2:G:229:VAL:HG12	2:G:236:VAL:HG22	1.83	0.61
2:E:23:GLN:O	2:E:267:ALA:N	2.26	0.61
3:L:931:LEU:HA	3:L:934:ILE:HG12	1.83	0.60
2:H:324:GLU:HG2	3:K:660:ASP:HB3	1.82	0.60
3:K:68:GLN:HE22	3:K:114:ALA:HB2	1.66	0.60
3:J:143:VAL:HG23	3:J:286:ALA:HB2	1.84	0.60
2:D:225:SER:HB3	2:E:147:ARG:HB3	1.84	0.59
2:D:229:VAL:HG12	2:D:236:VAL:HG22	1.85	0.58
2:E:36:ASN:ND2	2:E:176:ASP:OD2	2.37	0.58
3:L:158:ILE:HD13	3:L:162:ILE:HD13	1.85	0.58
3:L:679:GLY:HA3	3:L:828:GLY:O	2.04	0.57
2:G:322:ILE:HB	2:G:326:LEU:HD21	1.87	0.57
3:K:782:PRO:O	3:K:785:LEU:HB2	2.05	0.57
3:K:102:ILE:HA	3:K:105:VAL:HG22	1.87	0.57
3:K:367:ILE:HG23	3:K:368:PRO:HD3	1.86	0.57
3:J:441:ALA:HB2	3:J:946:GLU:HG3	1.87	0.57
2:F:229:VAL:HG12	2:F:236:VAL:HG22	1.87	0.57
3:L:509:LYS:HE3	3:L:514:GLY:HA2	1.86	0.56
3:K:942:ILE:HA	3:K:945:VAL:HG12	1.87	0.56
3:L:405:LEU:HD11	3:L:477:ALA:HB1	1.88	0.56
3:K:99:ASP:HB3	3:K:102:ILE:HG12	1.87	0.56
1:A:239:GLY:O	1:B:363:GLN:NE2	2.38	0.56
2:G:23:GLN:O	2:G:267:ALA:HB3	2.05	0.56
1:A:363:GLN:NE2	1:C:239:GLY:O	2.39	0.56
2:D:343:VAL:HG13	2:D:345:SER:H	1.71	0.55
2:H:29:THR:CG2	2:H:261:GLU:OE1	2.54	0.55
3:J:352:PHE:HA	3:J:355:MET:HG2	1.87	0.55
3:K:411:VAL:O	3:K:415:ASN:ND2	2.39	0.55
3:J:350:LEU:HD22	3:J:982:LEU:HG	1.89	0.55
3:K:509:LYS:HG2	3:K:517:ASN:HD21	1.71	0.55
1:A:379:PHE:HB3	1:A:435:GLN:HG3	1.88	0.55
1:A:432:ARG:NH1	1:A:435:GLN:OE1	2.40	0.55
1:B:432:ARG:NH1	1:B:435:GLN:OE1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:22:ALA:HB1	2:H:266:LYS:HB3	1.87	0.55
1:B:133:ARG:HG2	1:B:136:ARG:HH21	1.71	0.55
2:E:87:LEU:HD22	2:E:125:VAL:HG11	1.88	0.55
3:K:182:TYR:HB3	3:K:270:LEU:HD22	1.89	0.55
3:K:509:LYS:HE3	3:K:514:GLY:HA2	1.87	0.55
2:G:199:ALA:HB3	2:G:203:ALA:HB2	1.89	0.55
2:I:36:ASN:ND2	2:I:176:ASP:OD2	2.40	0.55
3:J:714:ARG:O	3:J:716:ARG:NH1	2.38	0.55
3:K:943:LEU:O	3:K:969:ARG:NH1	2.40	0.55
3:L:844:GLU:O	3:L:848:LYS:NZ	2.39	0.55
3:J:144:SER:HB3	3:J:154:LEU:HD11	1.87	0.55
3:J:358:PHE:O	3:J:971:ARG:NH2	2.39	0.55
3:J:150:THR:HG23	3:J:152:GLU:H	1.72	0.54
3:K:76:ARG:HH22	3:K:462:SER:HB2	1.72	0.54
2:G:207:SER:OG	2:G:215:GLN:NE2	2.40	0.54
3:J:20:MET:HA	3:J:377:LEU:HD11	1.89	0.54
3:J:442:LEU:HG	3:J:482:VAL:HG23	1.88	0.54
2:G:331:PRO:O	3:K:319:GLN:NE2	2.34	0.54
2:H:288:VAL:HG13	2:H:322:ILE:HD11	1.89	0.54
3:J:408:ASP:HA	3:J:411:VAL:HG22	1.88	0.54
3:L:817:ARG:NH2	3:L:820:GLY:O	2.39	0.54
3:L:277:ILE:HD12	3:L:615:PHE:HB2	1.89	0.54
2:D:22:ALA:HB1	2:D:266:LYS:HB2	1.89	0.54
3:K:986:PRO:HA	3:K:989:ILE:HG12	1.90	0.54
3:L:367:ILE:HG13	3:L:368:PRO:HD3	1.90	0.54
2:E:189:ARG:NH1	2:F:212:ASP:OD2	2.41	0.54
3:K:14:VAL:HG23	3:L:885:LEU:HB2	1.90	0.54
1:B:102:ASP:O	1:C:311:ARG:NH2	2.42	0.53
3:J:517:ASN:OD1	3:J:517:ASN:N	2.41	0.53
3:K:686:ASP:HA	3:K:854:VAL:HA	1.90	0.53
3:L:457:ALA:O	3:L:468:ARG:NH1	2.41	0.53
3:K:528:GLU:HA	3:K:531:VAL:HG12	1.89	0.53
1:A:71:GLU:HG2	1:A:74:ARG:HH21	1.74	0.53
2:E:127:GLN:HA	2:E:130:ILE:HD12	1.89	0.53
3:K:280:GLN:OE1	3:K:588:GLN:NE2	2.41	0.53
2:D:31:LEU:HD13	2:D:179:GLN:HB2	1.89	0.53
2:G:195:GLN:NE2	2:G:263:VAL:O	2.38	0.53
3:L:33:ASN:ND2	3:L:35:TYR:O	2.40	0.53
1:C:36:ALA:HB3	1:C:271:ARG:HD3	1.89	0.53
2:G:205:LYS:NZ	2:G:206:VAL:O	2.33	0.53
2:I:277:ARG:O	3:J:764:ARG:NH2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:164:ASP:OD1	3:J:164:ASP:N	2.35	0.53
3:J:647:LEU:HD12	3:J:651:ALA:HB3	1.91	0.53
3:L:943:LEU:HG	3:L:944:ILE:HG23	1.89	0.53
3:J:357:LEU:O	3:J:360:GLN:NE2	2.42	0.53
3:J:202:ASP:OD1	3:J:202:ASP:N	2.36	0.52
3:J:896:ILE:HD11	3:J:945:VAL:HB	1.91	0.52
1:B:86:PRO:HB2	1:B:121:THR:HG21	1.92	0.52
1:B:452:GLN:HG2	1:B:453:GLN:HE21	1.74	0.52
1:C:118:THR:HA	1:C:307:GLY:HA3	1.91	0.52
3:K:34:GLN:HB3	3:K:333:VAL:HG13	1.91	0.52
3:L:20:MET:HB3	3:L:374:VAL:HG23	1.91	0.52
2:G:17:ILE:HG23	2:G:320:LYS:HB3	1.91	0.52
3:J:73:ASP:OD1	3:J:106:GLN:NE2	2.42	0.52
2:F:109:GLN:OE1	2:G:96:ARG:NH1	2.42	0.52
3:J:282:ASN:HD21	3:J:609:VAL:H	1.57	0.52
3:K:835:SER:OG	3:K:836:SER:N	2.42	0.52
2:D:151:THR:HG21	2:I:40:ILE:H	1.75	0.52
2:D:176:ASP:OD2	2:E:147:ARG:NH1	2.42	0.52
3:K:372:VAL:HG23	3:K:405:LEU:HD11	1.92	0.52
3:J:428:ARG:NH1	3:J:429:GLU:OE2	2.42	0.52
3:L:472:ILE:HA	3:L:475:VAL:HG22	1.91	0.52
3:L:538:ARG:HG2	3:L:1022:LEU:HD11	1.91	0.52
2:D:187:LEU:HD13	2:D:261:GLU:OE1	2.10	0.52
2:E:186:ARG:NH1	2:E:190:GLU:OE2	2.42	0.52
2:H:79:ASP:OD1	2:H:79:ASP:N	2.43	0.51
3:L:45:VAL:HG22	3:L:129:VAL:HG22	1.92	0.51
3:K:139:VAL:HG23	3:K:326:PRO:HD2	1.92	0.51
3:L:177:VAL:HA	3:L:289:ILE:HA	1.92	0.51
3:J:390:ILE:HD11	3:J:395:MET:HB3	1.91	0.51
3:L:715:VAL:HG12	3:L:828:GLY:HA3	1.91	0.51
1:B:93:SER:OG	1:B:94:GLY:N	2.44	0.51
3:K:893:SER:HB3	3:K:896:ILE:HG12	1.92	0.51
1:C:432:ARG:NH1	1:C:435:GLN:OE1	2.43	0.51
3:K:32:VAL:HA	3:K:390:ILE:HG23	1.91	0.51
3:K:72:ILE:HD12	3:K:106:GLN:HG2	1.92	0.51
3:L:186:ILE:HG12	3:L:268:VAL:HG13	1.93	0.51
1:B:253:ASP:OD1	1:B:253:ASP:N	2.44	0.51
2:F:189:ARG:NH1	2:G:212:ASP:OD2	2.44	0.51
3:L:300:LEU:HD21	3:L:333:VAL:HG11	1.92	0.50
2:E:274:GLY:HA3	2:E:321:ILE:HD12	1.92	0.50
3:K:633:PRO:HG2	3:K:636:GLU:HG3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:741:SER:OG	3:K:744:ASP:OD2	2.29	0.50
1:B:1:CYS:O	1:B:133:ARG:NH2	2.45	0.50
3:L:577:GLN:O	3:L:661:ALA:HA	2.11	0.50
1:A:248:GLN:NE2	1:A:249:GLY:O	2.44	0.50
3:J:105:VAL:HG11	3:K:105:VAL:HB	1.93	0.50
3:L:400:LEU:HD11	3:L:1005:VAL:HG11	1.94	0.50
2:I:284:THR:HG22	2:I:298:VAL:HG12	1.92	0.50
3:K:20:MET:HB2	3:K:374:VAL:HG23	1.93	0.50
3:K:232:ALA:HB1	3:L:725:GLN:HA	1.94	0.50
1:B:45:ARG:NH2	1:B:255:THR:OG1	2.44	0.50
3:K:918:ARG:HD2	3:K:1003:THR:HG21	1.93	0.50
2:H:277:ARG:HB2	3:K:724:PRO:HB3	1.94	0.50
3:J:80:SER:HA	3:J:89:THR:O	2.11	0.50
3:J:417:GLU:OE2	3:J:971:ARG:NH1	2.44	0.50
3:J:943:LEU:HD13	3:J:969:ARG:HE	1.76	0.50
3:K:105:VAL:HA	3:K:108:GLN:HB2	1.93	0.50
1:A:59:ASN:O	1:A:61:ARG:NH1	2.45	0.49
1:B:298:PRO:HA	1:B:331:ASN:O	2.12	0.49
2:F:297:ARG:NH1	2:F:319:ASP:OD2	2.45	0.49
3:K:465:VAL:HA	3:K:468:ARG:HD2	1.93	0.49
3:K:239:ARG:NH1	3:K:760:ASP:O	2.45	0.49
3:K:449:LEU:HB3	3:K:478:MET:HE3	1.93	0.49
3:J:561:THR:HA	3:J:922:ASN:HB3	1.94	0.49
3:J:278:ASN:HB3	3:J:613:THR:HG23	1.94	0.49
3:L:344:LEU:HD13	3:L:399:VAL:HG12	1.94	0.49
1:B:59:ASN:O	1:B:61:ARG:NH1	2.45	0.49
3:L:521:LEU:O	3:L:525:HIS:ND1	2.44	0.49
3:L:291:ILE:HD13	3:L:306:ILE:HD12	1.94	0.49
3:L:416:VAL:HA	3:L:419:VAL:HG22	1.94	0.49
1:A:6:ASP:OD1	1:A:6:ASP:N	2.44	0.49
2:G:36:ASN:ND2	2:G:176:ASP:OD2	2.44	0.49
2:H:73:PRO:O	2:H:75:THR:N	2.43	0.49
3:J:574:ALA:HB3	3:J:627:ALA:HB3	1.94	0.49
3:K:436:GLY:HA2	3:K:439:GLN:HB2	1.95	0.49
3:L:410:ILE:HA	3:L:413:VAL:HG12	1.94	0.49
1:B:191:LEU:HD11	1:B:411:TYR:HD2	1.77	0.48
3:K:713:GLN:NE2	3:K:830:PRO:O	2.44	0.48
3:L:278:ASN:OD1	3:L:278:ASN:N	2.46	0.48
2:H:61:ASP:OD1	2:H:61:ASP:N	2.41	0.48
2:H:100:LEU:HB3	2:H:105:ALA:HB3	1.94	0.48
2:I:17:ILE:HG23	2:I:320:LYS:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:699:ARG:HG3	3:J:826:ILE:HD11	1.94	0.48
3:K:701:LYS:HA	3:K:705:LEU:HB2	1.94	0.48
2:G:184:LEU:HD21	2:G:236:VAL:HG21	1.96	0.48
1:B:187:LYS:HB3	1:B:415:LEU:HD21	1.96	0.48
2:D:189:ARG:NH1	2:E:212:ASP:OD2	2.41	0.48
3:K:357:LEU:O	3:K:360:GLN:NE2	2.46	0.48
1:A:323:SER:HB2	1:C:100:PRO:HD3	1.95	0.48
3:L:41:PRO:HG2	3:L:94:PHE:HB2	1.94	0.48
2:I:29:THR:CG2	2:I:261:GLU:OE2	2.61	0.48
3:J:231:ASN:OD1	3:K:622:GLN:NE2	2.47	0.48
2:F:281:GLY:H	3:L:810:TYR:HE1	1.62	0.48
3:J:80:SER:HB3	3:J:90:ILE:HG23	1.96	0.48
3:K:159:VAL:HA	3:K:163:GLN:HB2	1.96	0.48
3:K:477:ALA:O	3:K:481:SER:OG	2.32	0.48
3:K:568:ASP:OD1	3:K:637:ARG:NH2	2.47	0.48
3:K:718:ASN:HB3	3:K:825:GLU:HB2	1.95	0.48
2:I:29:THR:HG21	2:I:261:GLU:OE2	2.13	0.47
3:L:31:PRO:O	3:L:389:SER:OG	2.32	0.47
3:J:685:GLN:NE2	3:J:857:SER:OG	2.46	0.47
3:J:4:PHE:HB2	3:J:8:ARG:HD2	1.96	0.47
3:K:278:ASN:N	3:K:278:ASN:OD1	2.47	0.47
3:L:448:VAL:HA	3:L:886:CYS:HB3	1.96	0.47
2:H:301:ALA:HB2	2:H:311:VAL:HG22	1.95	0.47
2:I:51:ILE:HD13	2:I:71:ILE:HG23	1.96	0.47
3:L:425:LEU:HD13	3:L:429:GLU:HB3	1.95	0.47
2:D:148:SER:OG	2:D:150:VAL:O	2.32	0.47
3:L:403:GLY:HA3	3:L:980:PHE:HB2	1.97	0.47
3:L:871:GLN:HB3	3:L:874:ALA:HB3	1.95	0.47
2:F:35:THR:OG1	2:F:250:LEU:O	2.32	0.47
2:H:52:LEU:HG	2:H:72:ASP:HB2	1.97	0.47
3:J:188:LEU:HD23	3:J:266:ALA:HB2	1.97	0.47
3:K:142:VAL:HB	3:K:324:VAL:HG22	1.96	0.47
3:K:990:SER:O	3:K:999:HIS:NE2	2.47	0.47
1:C:121:THR:OG1	1:C:122:THR:N	2.48	0.47
3:L:342:LYS:HD2	3:L:342:LYS:HA	1.71	0.47
3:L:719:GLY:HA2	3:L:814:LYS:HD3	1.95	0.47
2:D:46:GLN:HE21	2:E:155:LEU:HD13	1.80	0.47
3:K:567:GLU:OE2	3:K:995:SER:N	2.48	0.47
3:K:838:ASP:OD1	3:K:838:ASP:N	2.45	0.47
3:L:413:VAL:HA	3:L:416:VAL:HG22	1.97	0.47
1:B:198:VAL:HG12	2:E:96:ARG:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:17:ILE:HG13	2:G:337:THR:HG23	1.97	0.46
3:L:357:LEU:HD12	3:L:513:PHE:HE1	1.81	0.46
1:C:184:THR:HG23	1:C:415:LEU:HD22	1.96	0.46
2:D:12:THR:O	2:D:336:LYS:NZ	2.48	0.46
2:H:288:VAL:HG23	2:H:320:LYS:HE2	1.96	0.46
1:B:127:ASP:OD1	1:B:131:ARG:N	2.48	0.46
3:L:150:THR:OG1	3:L:151:LYS:N	2.48	0.46
3:L:366:LEU:HA	3:L:369:THR:HB	1.97	0.46
2:H:29:THR:HG21	2:H:261:GLU:OE1	2.16	0.46
3:L:784:ASP:O	3:L:787:LYS:HB2	2.15	0.46
3:L:981:ILE:HA	3:L:984:VAL:HG22	1.97	0.46
2:D:109:GLN:OE1	2:E:96:ARG:NH1	2.44	0.46
3:J:732:ASP:HB3	3:J:742:LEU:HD21	1.98	0.46
3:J:801:ASN:OD1	3:J:801:ASN:N	2.49	0.46
2:G:16:GLY:HA3	2:G:324:GLU:HG2	1.97	0.46
3:J:355:MET:O	3:J:359:LEU:HB2	2.15	0.46
3:J:964:GLU:OE2	3:J:967:ARG:NH2	2.41	0.46
3:J:72:ILE:HD13	3:J:107:VAL:HG12	1.97	0.46
3:J:929:GLY:O	3:J:932:THR:OG1	2.34	0.46
3:J:952:HIS:ND1	3:J:957:GLY:O	2.49	0.46
3:K:287:SER:OG	3:K:288:GLY:N	2.48	0.46
3:L:562:ALA:HB3	3:L:923:ASP:HB3	1.97	0.46
3:L:606:VAL:HA	3:L:631:LEU:HA	1.98	0.46
1:B:300:ILE:HG12	1:B:330:ILE:HG22	1.96	0.46
3:J:66:GLU:OE1	3:J:817:ARG:NE	2.45	0.46
3:J:153:ASP:N	3:J:153:ASP:OD1	2.44	0.46
1:A:305:ASN:OD1	1:A:305:ASN:N	2.50	0.45
2:E:312:THR:OG1	2:E:313:GLU:OE1	2.32	0.45
3:J:174:ASP:N	3:J:174:ASP:OD1	2.48	0.45
3:L:153:ASP:OD1	3:L:182:TYR:OH	2.29	0.45
3:L:160:SER:OG	3:L:161:ASN:OD1	2.34	0.45
3:K:45:VAL:HA	3:K:128:ARG:O	2.16	0.45
3:L:174:ASP:HB3	3:L:292:LYS:HB2	1.98	0.45
3:L:763:ASP:HB3	3:L:768:LYS:HD2	1.99	0.45
3:J:367:ILE:HG13	3:J:492:LEU:HD22	1.99	0.45
3:J:699:ARG:HH21	3:J:700:ASN:HD21	1.64	0.45
3:L:70:ASN:O	3:L:110:LYS:NZ	2.44	0.45
1:A:219:THR:HA	1:A:222:GLN:HG2	1.98	0.45
3:K:210:GLN:HG2	3:L:742:LEU:HD22	1.99	0.45
3:L:68:GLN:HG3	3:L:114:ALA:HB2	1.98	0.45
3:J:755:SER:HA	3:J:772:LEU:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K:940:ASN:HD21	3:K:1013:THR:HG22	1.82	0.45
3:K:3:LYS:NZ	3:K:432:ARG:O	2.45	0.45
2:I:233:THR:HG21	3:J:258:SER:HB2	1.98	0.45
3:J:139:VAL:HA	3:J:289:ILE:O	2.17	0.45
3:K:47:VAL:HG12	3:K:88:MET:HG2	1.99	0.45
3:K:939:LYS:HA	3:K:942:ILE:HG12	1.99	0.45
3:J:306:ILE:HA	3:J:309:THR:HG22	1.97	0.45
1:B:184:THR:HG23	1:B:415:LEU:HG	1.98	0.45
2:F:44:ARG:NH2	2:G:155:LEU:O	2.45	0.45
2:F:343:VAL:HG12	2:F:345:SER:H	1.82	0.45
2:H:148:SER:OG	2:H:150:VAL:O	2.30	0.45
2:H:189:ARG:NH1	2:I:212:ASP:OD2	2.50	0.45
3:K:185:ARG:HD2	3:K:185:ARG:HA	1.82	0.45
2:F:277:ARG:HB2	3:L:724:PRO:HB3	1.99	0.44
3:J:78:ILE:HG23	3:J:92:VAL:HG12	1.99	0.44
3:J:595:ARG:O	3:J:599:LEU:HB2	2.17	0.44
3:K:758:VAL:HG23	3:K:770:VAL:HG13	1.98	0.44
1:C:298:PRO:HA	1:C:331:ASN:O	2.18	0.44
1:C:308:THR:OG1	1:C:316:LEU:O	2.28	0.44
3:J:467:TYR:OH	3:J:927:GLN:NE2	2.38	0.44
3:J:793:ASP:OD1	3:J:793:ASP:N	2.49	0.44
3:K:142:VAL:HG11	3:K:324:VAL:HG13	2.00	0.44
3:L:685:GLN:HA	3:L:823:ALA:HA	2.00	0.44
2:D:54:ARG:NH1	2:D:56:PHE:O	2.51	0.44
2:E:51:ILE:HD13	2:E:71:ILE:HG23	2.00	0.44
2:H:17:ILE:HD12	2:H:320:LYS:HB3	1.99	0.44
3:J:893:SER:OG	3:J:894:TRP:N	2.50	0.44
3:L:189:ASP:OD2	3:L:775:ARG:NH1	2.51	0.44
2:G:29:THR:HG23	2:G:261:GLU:HG3	2.00	0.44
2:G:162:ASN:N	2:G:162:ASN:OD1	2.49	0.44
2:I:23:GLN:O	2:I:267:ALA:N	2.50	0.44
3:L:409:ALA:HA	3:L:412:VAL:HG22	1.99	0.44
1:A:224:THR:HG22	1:B:23:ALA:HB2	2.00	0.44
2:E:30:GLU:HG2	2:E:258:GLN:HB3	1.98	0.44
2:E:177:VAL:HG11	2:E:257:ALA:HB3	2.00	0.44
2:E:329:VAL:HA	2:E:335:VAL:HG11	1.99	0.44
2:H:222:LEU:HA	2:H:240:ALA:HA	1.99	0.44
3:J:135:ASN:HB3	3:J:673:GLU:HG3	2.00	0.44
3:J:175:PHE:HB3	3:J:291:ILE:HG22	2.00	0.44
3:L:350:LEU:HD21	3:L:983:GLY:HA2	1.99	0.44
3:L:423:GLU:HB2	3:L:425:LEU:HD23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:96:ARG:NH1	2:I:109:GLN:OE1	2.51	0.44
2:F:339:PRO:O	2:F:341:LYS:NZ	2.50	0.44
2:F:184:LEU:HD21	2:F:236:VAL:HG21	1.99	0.43
3:J:355:MET:HG3	3:J:365:THR:HG22	2.00	0.43
1:C:372:GLY:HA3	1:C:442:LEU:HD13	1.99	0.43
2:E:19:THR:HA	2:E:320:LYS:HA	2.00	0.43
2:F:327:GLN:HG3	3:L:579:PRO:HG3	1.99	0.43
3:J:56:THR:O	3:J:60:THR:OG1	2.29	0.43
3:L:368:PRO:HB3	3:L:409:ALA:HB3	1.99	0.43
1:A:88:ILE:HB	1:B:335:PHE:HB3	2.00	0.43
3:K:144:SER:HA	3:K:321:MET:HA	2.00	0.43
3:K:793:ASP:N	3:K:793:ASP:OD1	2.50	0.43
1:B:122:THR:HA	1:B:303:THR:HG23	2.00	0.43
3:L:595:ARG:NH2	3:L:596:GLU:OE2	2.45	0.43
2:G:57:LYS:O	2:G:60:SER:OG	2.33	0.43
3:J:352:PHE:HB2	3:J:365:THR:HB	2.01	0.43
3:L:572:LEU:HB3	3:L:629:ILE:HB	2.00	0.43
3:L:872:ALA:HA	3:L:875:LEU:HG	2.01	0.43
2:E:198:ARG:HH11	2:E:199:ALA:H	1.67	0.43
2:F:301:ALA:HB2	2:F:311:VAL:HG12	2.01	0.43
2:I:73:PRO:O	2:I:75:THR:N	2.46	0.43
3:J:632:LYS:O	3:J:637:ARG:NE	2.38	0.43
3:J:969:ARG:HD2	3:J:969:ARG:HA	1.79	0.43
3:L:34:GLN:O	3:L:392:THR:OG1	2.34	0.43
1:A:298:PRO:HG3	1:A:332:LEU:HD13	2.01	0.43
1:C:39:GLY:N	1:C:42:GLU:OE2	2.51	0.43
2:G:17:ILE:HD13	2:G:17:ILE:HA	1.91	0.43
3:J:601:LYS:HD3	3:J:601:LYS:HA	1.90	0.43
2:D:206:VAL:HG12	2:D:259:LEU:HB3	2.01	0.43
2:G:35:THR:OG1	2:G:250:LEU:O	2.25	0.43
2:I:31:LEU:HD12	2:I:259:LEU:HD13	2.00	0.43
3:L:759:ASN:OD1	3:L:759:ASN:N	2.51	0.43
2:F:14:GLU:HB3	2:F:336:LYS:HB3	2.01	0.43
3:K:188:LEU:HD23	3:K:266:ALA:HB2	2.00	0.43
3:L:546:VAL:HA	3:L:549:VAL:HG12	2.01	0.43
3:L:952:HIS:HA	3:L:956:LYS:HB2	2.00	0.43
1:A:38:ILE:HA	1:A:454:THR:HG23	2.00	0.42
1:A:321:SER:HA	1:C:100:PRO:HB3	2.01	0.42
2:I:26:THR:OG1	2:I:260:GLN:OE1	2.37	0.42
3:J:419:VAL:HG21	3:J:433:LYS:HG2	2.00	0.42
1:B:224:THR:HG22	1:C:23:ALA:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:158:ILE:HA	3:J:162:ILE:HB	2.01	0.42
3:K:139:VAL:HG22	3:K:327:TYR:HB3	2.01	0.42
3:K:910:GLY:HA2	3:K:913:LEU:HB2	2.01	0.42
2:I:162:ASN:OD1	2:I:162:ASN:N	2.52	0.42
3:K:495:THR:OG1	3:K:496:MET:N	2.52	0.42
3:L:392:THR:HA	3:L:395:MET:HG2	2.02	0.42
3:L:660:ASP:OD1	3:L:660:ASP:N	2.45	0.42
2:H:289:ASN:HD21	2:H:293:LYS:HB2	1.84	0.42
3:J:981:ILE:HD13	3:J:981:ILE:HA	1.91	0.42
3:K:789:TYR:HB3	3:K:797:MET:HB3	2.01	0.42
3:L:535:LEU:HD11	3:L:1025:VAL:HG21	2.02	0.42
1:A:48:GLN:HE21	1:A:246:LEU:HD13	1.83	0.42
3:L:282:ASN:HD21	3:L:609:VAL:H	1.67	0.42
1:A:274:ASP:OD1	1:A:274:ASP:N	2.52	0.42
1:B:265:PRO:O	1:B:268:LEU:HB2	2.19	0.42
1:C:44:PHE:O	1:C:50:GLN:NE2	2.49	0.42
2:D:278:ASP:N	2:D:278:ASP:OD1	2.53	0.42
3:J:455:PRO:O	3:J:458:PHE:HB2	2.20	0.42
3:K:361:ASN:HB3	3:K:364:ALA:HB3	2.01	0.42
3:K:481:SER:HA	3:K:484:VAL:HG22	2.01	0.42
2:H:301:ALA:HB1	2:H:309:TRP:HB3	2.02	0.42
3:K:58:GLN:HG2	3:K:815:LEU:HD22	2.01	0.42
3:K:145:THR:HG22	3:K:322:LYS:HD3	2.01	0.42
3:K:553:ILE:HD13	3:K:553:ILE:HA	1.94	0.42
3:L:99:ASP:HA	3:L:100:PRO:HD3	1.85	0.42
3:L:509:LYS:HD3	3:L:517:ASN:HD22	1.85	0.42
2:E:73:PRO:O	2:E:75:THR:N	2.45	0.42
2:G:226:GLU:HG2	2:H:147:ARG:HD3	2.02	0.42
3:J:686:ASP:HB2	3:J:695:LEU:HD22	2.02	0.42
3:K:267:ASP:OD1	3:K:267:ASP:N	2.50	0.42
1:C:305:ASN:OD1	1:C:305:ASN:N	2.53	0.41
2:D:65:GLY:HA2	2:D:138:LEU:HB3	2.02	0.41
2:H:307:ASP:OD1	2:H:307:ASP:N	2.46	0.41
2:I:8:PRO:HA	2:I:9:PRO:HD3	1.87	0.41
2:I:195:GLN:NE2	2:I:197:GLU:OE2	2.40	0.41
3:J:311:ALA:HA	3:J:314:GLU:HB2	2.02	0.41
1:A:401:ASP:OD1	1:A:405:ARG:NH1	2.53	0.41
1:B:383:LEU:HD23	1:B:383:LEU:HA	1.87	0.41
3:J:481:SER:HA	3:J:484:VAL:HG22	2.02	0.41
3:K:546:VAL:HA	3:K:549:VAL:HG22	2.01	0.41
1:C:41:ARG:O	1:C:50:GLN:NE2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:269:LEU:HB3	2:E:308:LYS:HD3	2.01	0.41
2:G:23:GLN:N	2:G:267:ALA:O	2.51	0.41
2:H:261:GLU:O	2:H:261:GLU:HG3	2.20	0.41
3:K:174:ASP:HB3	3:K:292:LYS:HD2	2.02	0.41
3:K:527:TYR:OH	3:K:1017:ILE:O	2.32	0.41
3:L:641:GLU:OE2	3:L:642:ASN:ND2	2.53	0.41
1:B:203:ALA:HB1	1:B:207:ARG:HH11	1.85	0.41
3:J:414:GLU:OE2	3:J:969:ARG:NH1	2.53	0.41
3:K:438:ILE:HD12	3:K:438:ILE:HG23	1.91	0.41
3:K:467:TYR:OH	3:K:927:GLN:OE1	2.37	0.41
3:L:188:LEU:HD23	3:L:266:ALA:HB2	2.02	0.41
1:C:334:ILE:HD13	1:C:334:ILE:HA	1.95	0.41
3:K:699:ARG:HA	3:K:702:PHE:HB3	2.02	0.41
2:D:51:ILE:HD13	2:D:71:ILE:HG23	2.03	0.41
2:H:201:ASP:OD1	2:H:201:ASP:N	2.49	0.41
2:I:45:PRO:HG3	2:I:156:VAL:HB	2.02	0.41
3:J:163:GLN:O	3:K:67:GLN:NE2	2.54	0.41
3:K:848:LYS:HA	3:K:848:LYS:HD2	1.81	0.41
2:E:264:LYS:NZ	2:E:265:GLN:O	2.46	0.41
2:G:341:LYS:HD3	2:G:341:LYS:HA	1.88	0.41
2:H:323:THR:HB	2:H:324:GLU:H	1.71	0.41
3:J:688:ALA:HB2	3:J:853:GLY:HA3	2.03	0.41
3:J:847:VAL:HA	3:J:850:LEU:HD13	2.02	0.41
3:K:31:PRO:O	3:K:389:SER:OG	2.31	0.41
3:K:508:HIS:HA	3:K:518:ARG:HH21	1.86	0.41
3:L:755:SER:HA	3:L:772:LEU:O	2.20	0.41
2:D:264:LYS:HA	2:D:264:LYS:HD2	1.83	0.41
3:J:746:ASN:O	3:J:750:SER:OG	2.30	0.41
3:K:337:ILE:HD13	3:K:337:ILE:HA	1.93	0.41
3:K:807:LYS:HB3	3:K:807:LYS:HE2	1.88	0.41
3:L:24:GLY:HA2	3:L:27:ILE:HG12	2.03	0.41
3:L:53:SER:OG	3:L:54:ALA:N	2.54	0.41
1:B:88:ILE:HB	1:C:335:PHE:HB3	2.03	0.41
2:D:57:LYS:HB2	2:D:57:LYS:HE2	1.89	0.41
2:D:224:PHE:HE1	2:D:238:ILE:HG12	1.86	0.41
2:E:266:LYS:HB3	2:E:266:LYS:HE3	1.81	0.41
2:H:35:THR:OG1	2:H:250:LEU:O	2.31	0.41
3:J:918:ARG:HD2	3:J:918:ARG:HA	1.91	0.41
3:K:680:PHE:HB2	3:K:858:TRP:HZ3	1.85	0.41
3:L:4:PHE:HD2	3:L:8:ARG:HD2	1.86	0.41
3:L:16:ALA:HA	3:L:19:ILE:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:693:GLU:OE1	3:L:697:GLN:NE2	2.48	0.41
3:K:375:VAL:HG23	3:K:480:LEU:HG	2.03	0.41
3:L:135:ASN:HD21	3:L:672:LEU:HB3	1.86	0.41
3:L:199:THR:OG1	3:L:202:ASP:OD1	2.36	0.41
1:B:63:LEU:HD12	1:B:63:LEU:HA	1.94	0.40
1:C:1:CYS:O	1:C:133:ARG:NH2	2.47	0.40
2:D:12:THR:O	2:D:12:THR:OG1	2.38	0.40
2:F:199:ALA:HA	2:F:262:GLY:HA2	2.02	0.40
3:K:506:GLY:HA2	3:K:509:LYS:HB3	2.02	0.40
3:L:32:VAL:HG23	3:L:300:LEU:HG	2.02	0.40
2:F:73:PRO:O	2:F:75:THR:N	2.47	0.40
3:L:175:PHE:HB2	3:L:289:ILE:HD11	2.03	0.40
1:B:44:PHE:O	1:B:50:GLN:NE2	2.55	0.40
2:D:261:GLU:HG3	2:D:261:GLU:O	2.22	0.40
2:D:301:ALA:HB1	2:D:309:TRP:HB3	2.03	0.40
2:E:292:ASN:ND2	2:E:337:THR:OG1	2.55	0.40
2:F:136:LYS:HB2	2:F:136:LYS:HE2	1.94	0.40
2:F:284:THR:HB	2:F:296:LEU:HD11	2.02	0.40
3:J:939:LYS:HA	3:J:942:ILE:HG22	2.03	0.40
3:L:568:ASP:OD2	3:L:637:ARG:NH2	2.46	0.40
2:D:261:GLU:O	2:D:261:GLU:CG	2.69	0.40
3:J:277:ILE:HD12	3:J:615:PHE:HB2	2.03	0.40
3:J:921:SER:OG	3:J:922:ASN:N	2.53	0.40
3:K:448:VAL:HB	3:K:887:LEU:HD11	2.03	0.40
3:K:868:SER:OG	3:K:869:GLY:N	2.54	0.40
3:L:56:THR:O	3:L:60:THR:OG1	2.26	0.40
3:L:843:VAL:O	3:L:847:VAL:HG23	2.21	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	453/474 (96%)	449 (99%)	4 (1%)	0	100	100
1	B	453/474 (96%)	450 (99%)	3 (1%)	0	100	100
1	C	453/474 (96%)	448 (99%)	5 (1%)	0	100	100
2	D	343/366 (94%)	312 (91%)	29 (8%)	2 (1%)	25	64
2	E	341/366 (93%)	309 (91%)	30 (9%)	2 (1%)	25	64
2	F	343/366 (94%)	311 (91%)	30 (9%)	2 (1%)	25	64
2	G	341/366 (93%)	308 (90%)	31 (9%)	2 (1%)	25	64
2	H	343/366 (94%)	313 (91%)	27 (8%)	3 (1%)	17	56
2	I	341/366 (93%)	315 (92%)	24 (7%)	2 (1%)	25	64
3	J	1028/1052 (98%)	972 (95%)	56 (5%)	0	100	100
3	K	1028/1052 (98%)	964 (94%)	64 (6%)	0	100	100
3	L	1028/1052 (98%)	966 (94%)	61 (6%)	1 (0%)	51	83
All	All	6495/6774 (96%)	6117 (94%)	364 (6%)	14 (0%)	50	79

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	74	ALA
2	E	74	ALA
2	F	74	ALA
2	H	74	ALA
2	F	73	PRO
2	G	74	ALA
2	I	74	ALA
2	D	73	PRO
2	G	73	PRO
2	H	73	PRO
2	H	323	THR
2	E	73	PRO
2	I	73	PRO
3	L	133	VAL

5.3.2 Protein sidechains (i)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	358/375 (96%)	357 (100%)	1 (0%)	92 96
1	B	358/375 (96%)	357 (100%)	1 (0%)	92 96
1	C	358/375 (96%)	358 (100%)	0	100 100
2	D	278/293 (95%)	276 (99%)	2 (1%)	84 94
2	E	277/293 (94%)	277 (100%)	0	100 100
2	F	278/293 (95%)	278 (100%)	0	100 100
2	G	277/293 (94%)	276 (100%)	1 (0%)	91 95
2	H	278/293 (95%)	278 (100%)	0	100 100
2	I	277/293 (94%)	277 (100%)	0	100 100
3	J	841/860 (98%)	837 (100%)	4 (0%)	88 95
3	K	841/860 (98%)	835 (99%)	6 (1%)	84 94
3	L	841/860 (98%)	839 (100%)	2 (0%)	93 98
All	All	5262/5463 (96%)	5245 (100%)	17 (0%)	92 96

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	CYS
1	B	1	CYS
2	D	261	GLU
2	D	280	LYS
2	G	188	ARG
3	J	164	ASP
3	J	578	THR
3	J	852	LYS
3	J	896	ILE
3	K	433	LYS
3	K	509	LYS
3	K	649	LYS
3	K	702	PHE
3	K	852	LYS
3	K	939	LYS
3	L	716	ARG
3	L	931	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (74) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	GLN
1	A	248	GLN
1	A	350	GLN
1	A	427	GLN
1	A	441	ASN
1	B	20	GLN
1	B	26	GLN
1	B	80	GLN
1	B	453	GLN
1	C	26	GLN
1	C	60	ASN
1	C	80	GLN
1	C	386	GLN
2	D	11	GLN
2	D	36	ASN
2	D	46	GLN
2	D	91	GLN
2	D	95	GLN
2	D	316	ASN
2	E	70	GLN
2	E	91	GLN
2	E	169	GLN
2	E	292	ASN
2	F	36	ASN
2	F	46	GLN
2	G	215	GLN
2	G	247	ASN
2	G	330	GLN
2	H	70	GLN
2	H	95	GLN
2	H	179	GLN
2	H	256	HIS
2	I	23	GLN
2	I	28	ASN
2	I	104	GLN
2	I	260	GLN
3	J	46	GLN
3	J	67	GLN
3	J	74	ASN
3	J	229	GLN
3	J	282	ASN
3	J	577	GLN
3	J	685	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	J	700	ASN
3	J	725	GLN
3	J	819	ASN
3	J	871	GLN
3	K	46	GLN
3	K	67	GLN
3	K	68	GLN
3	K	70	ASN
3	K	208	GLN
3	K	218	GLN
3	K	229	GLN
3	K	248	ASN
3	K	254	ASN
3	K	280	GLN
3	K	588	GLN
3	K	622	GLN
3	K	692	HIS
3	K	725	GLN
3	L	125	GLN
3	L	208	GLN
3	L	248	ASN
3	L	282	ASN
3	L	298	ASN
3	L	415	ASN
3	L	437	GLN
3	L	517	ASN
3	L	622	GLN
3	L	642	ASN
3	L	652	GLN
3	L	819	ASN
3	L	940	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 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.

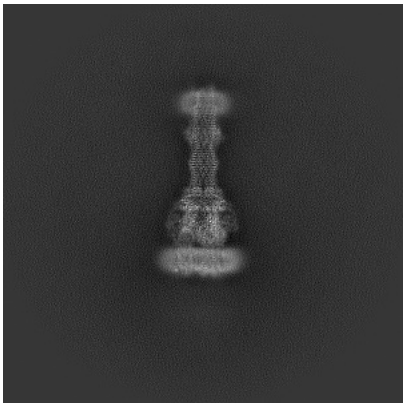
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10372. These allow visual inspection of the internal detail of the map and identification of artifacts.

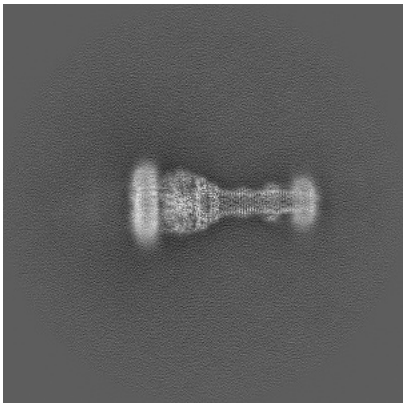
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

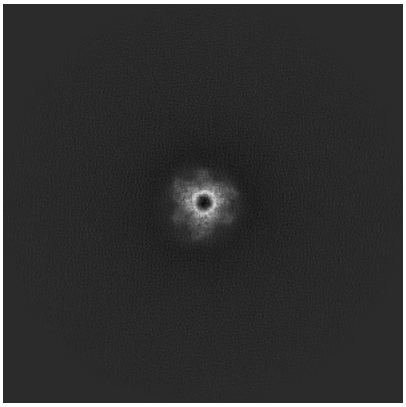
6.1.1 Primary map



X



Y

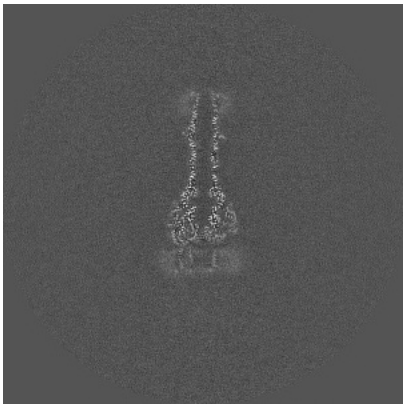


Z

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

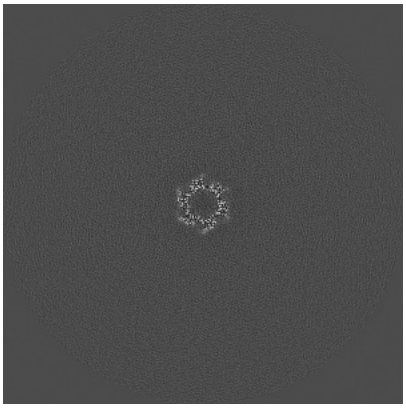
6.2 Central slices

6.2.1 Primary map



X Index: 256

Y Index: 256

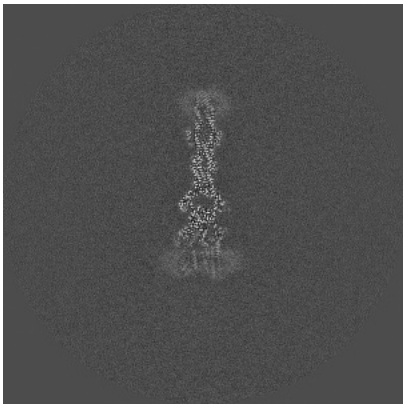


Z Index: 256

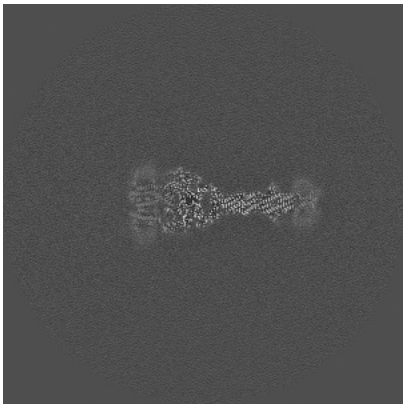
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

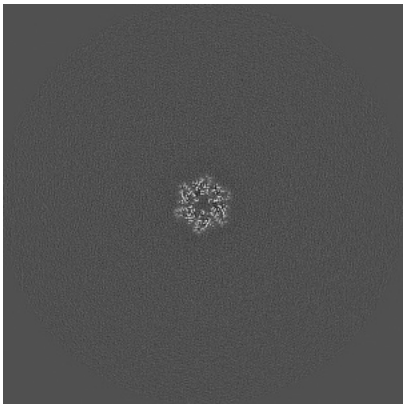
6.3.1 Primary map



X Index: 268



Y Index: 269

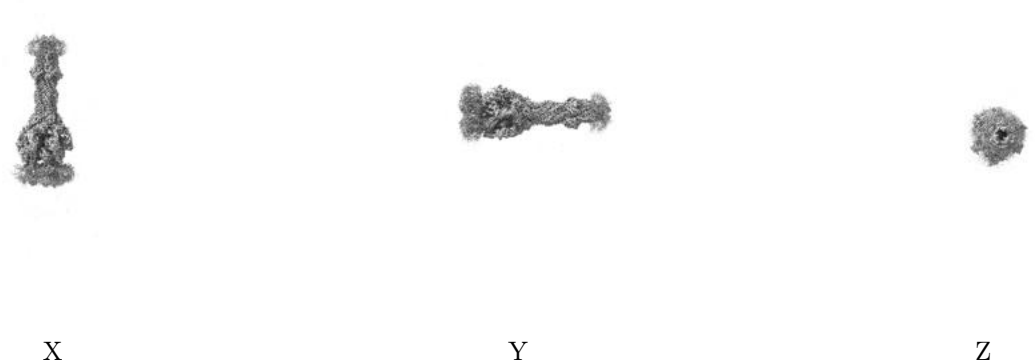


Z Index: 251

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 0.028. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

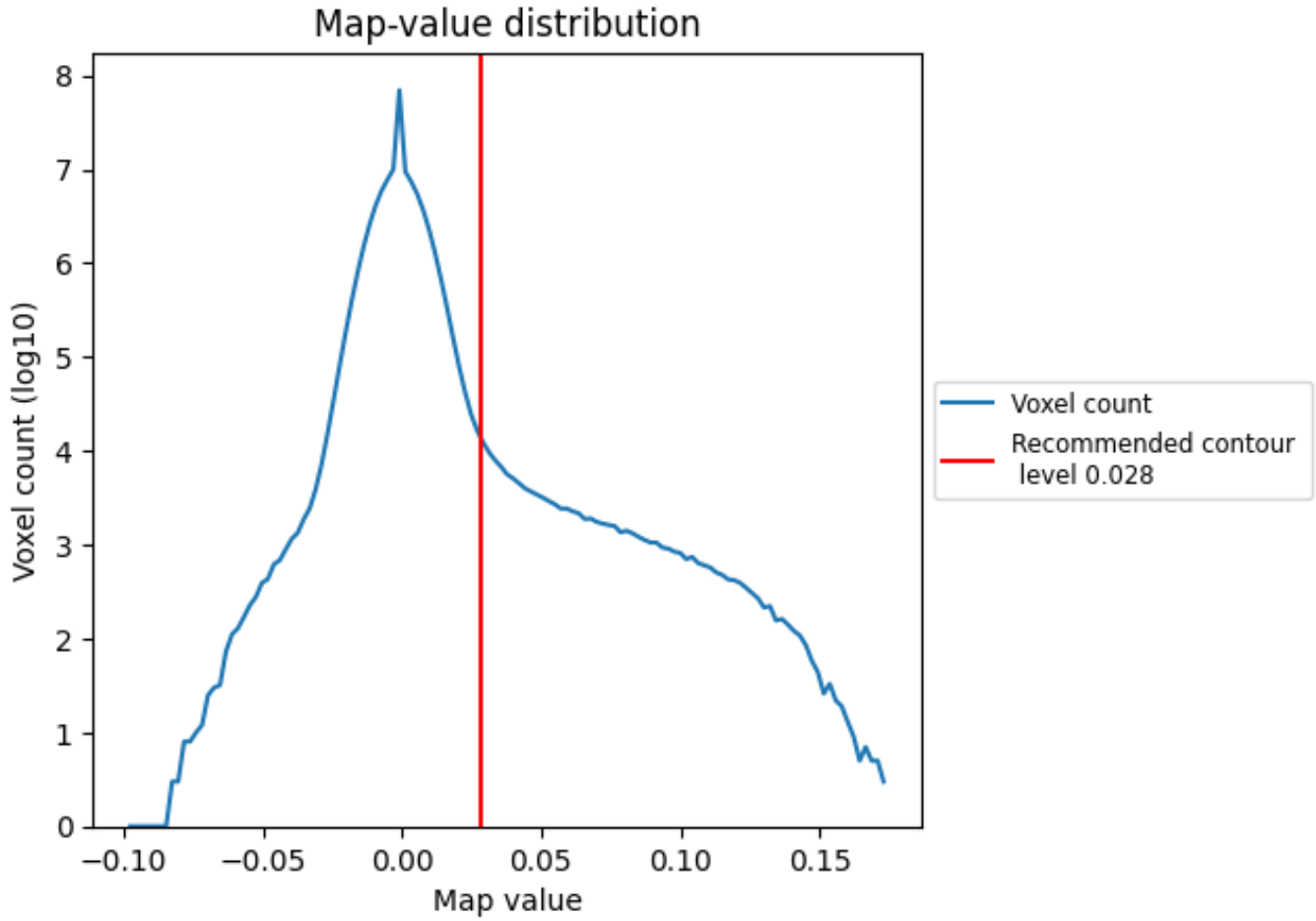
6.5 Mask visualisation (i)

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

7 Map analysis

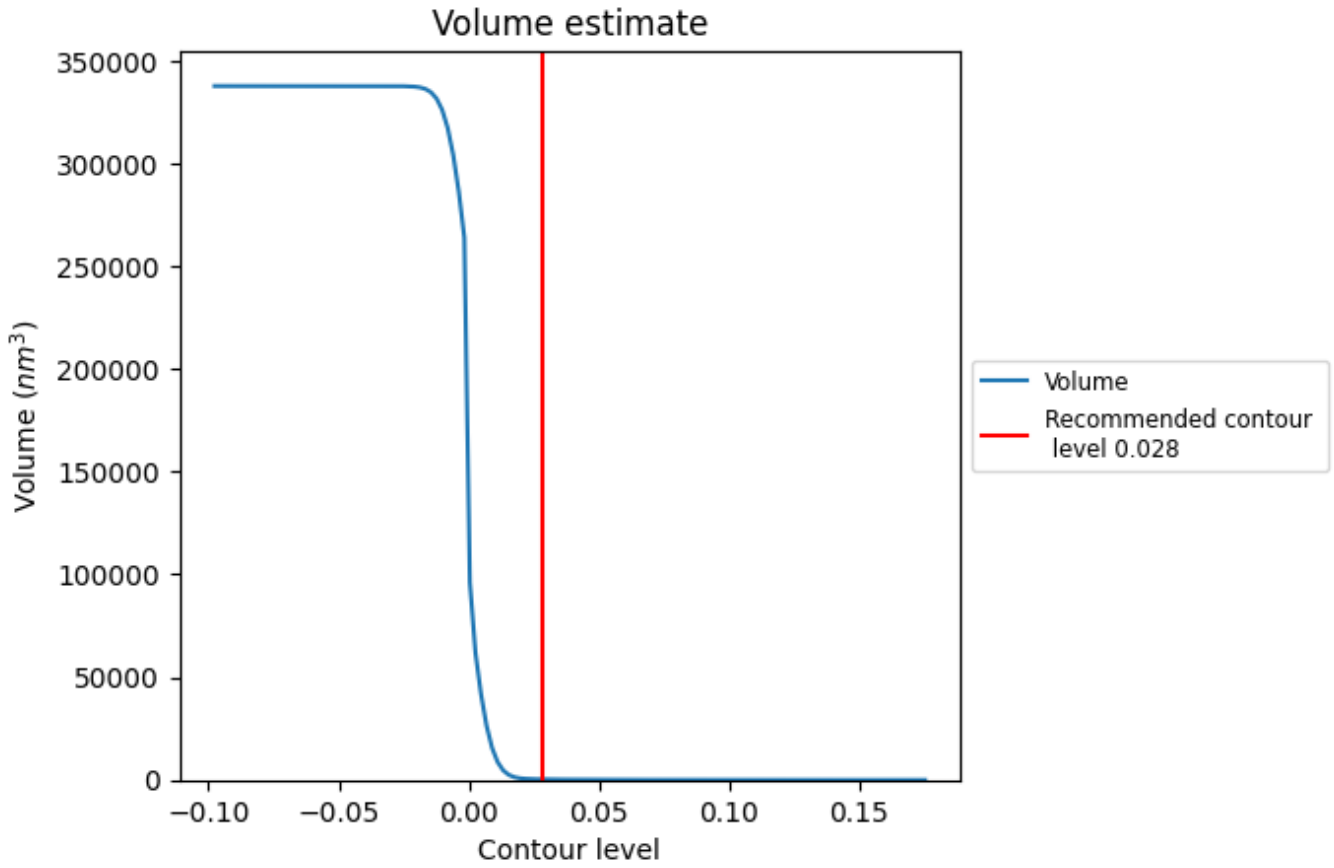
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

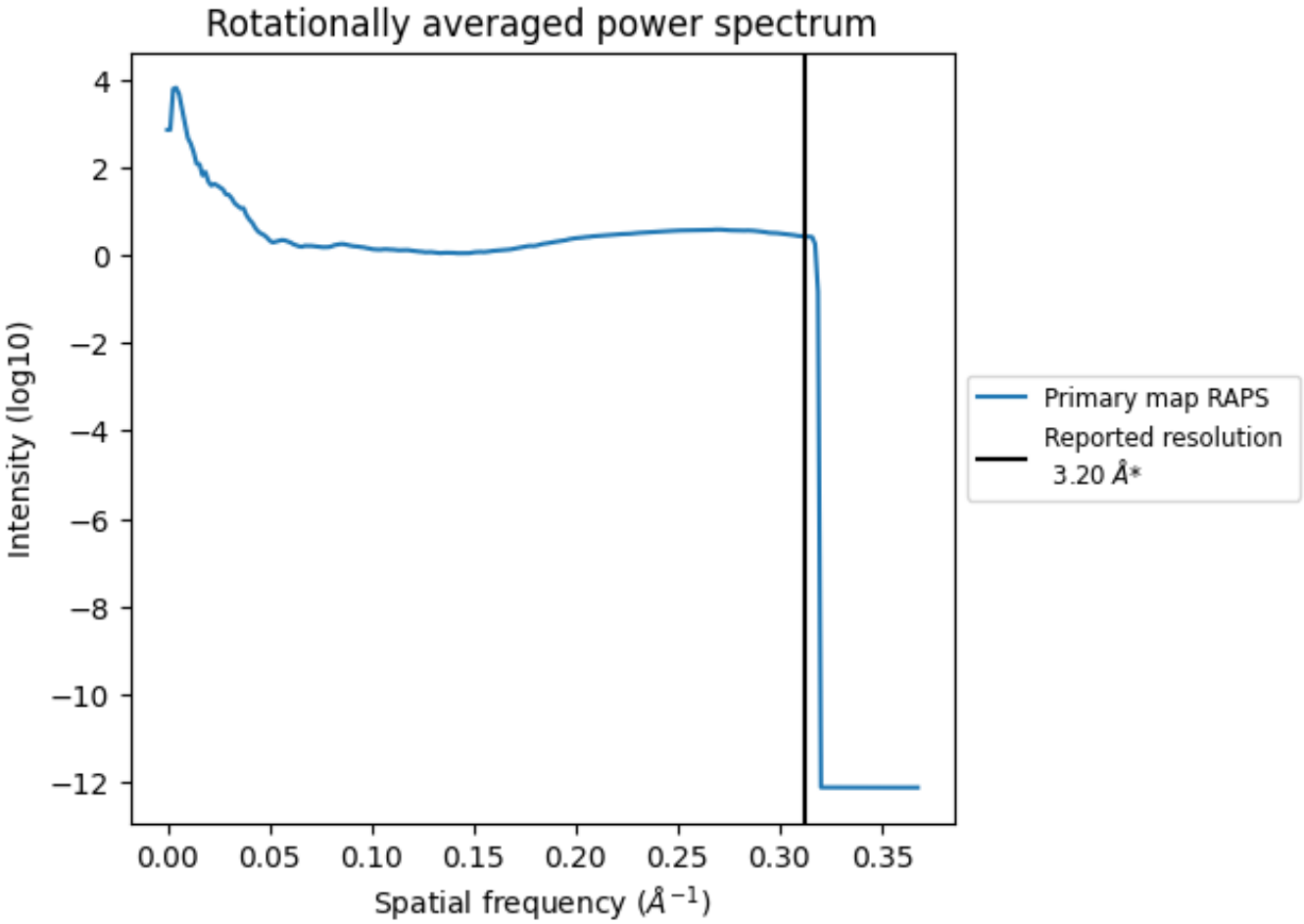
7.2 Volume estimate



The volume at the recommended contour level is 302 nm^3; this corresponds to an approximate mass of 273 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)

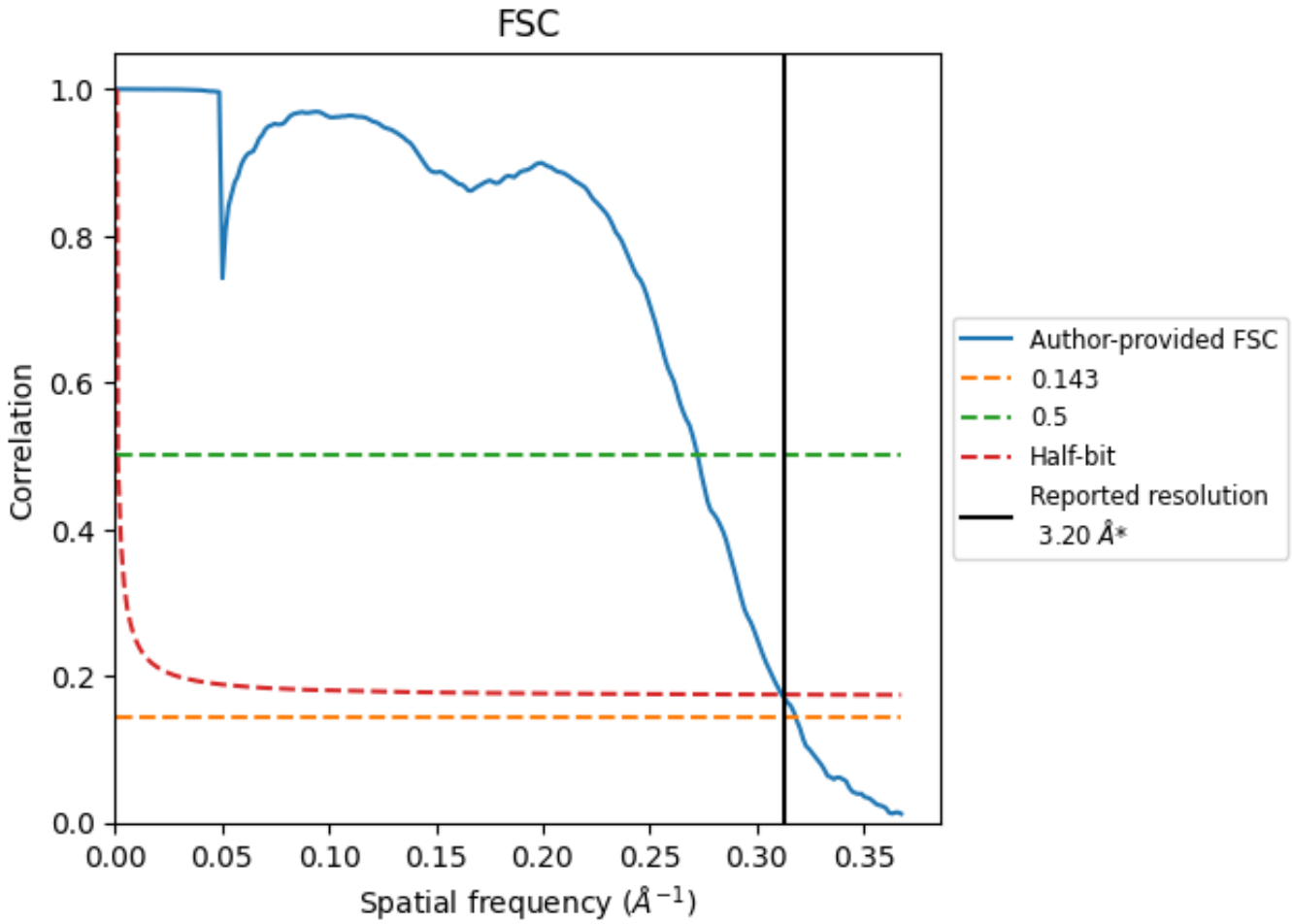


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.14	3.67	3.21
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

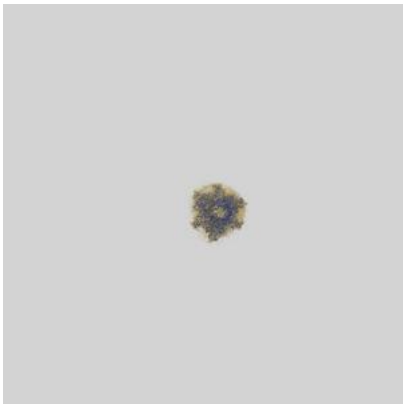
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-10372 and PDB model 6TA5. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay

X

Y



Z

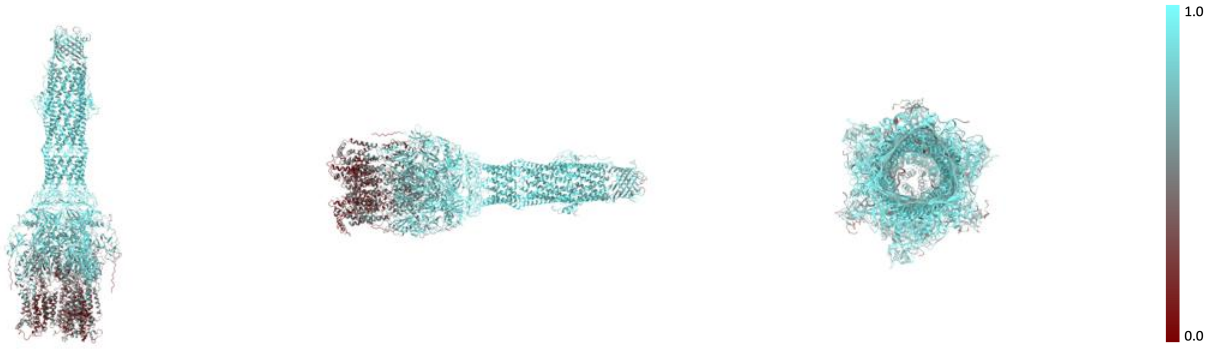
The images above show the 3D surface view of the map at the recommended contour level 0.028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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.

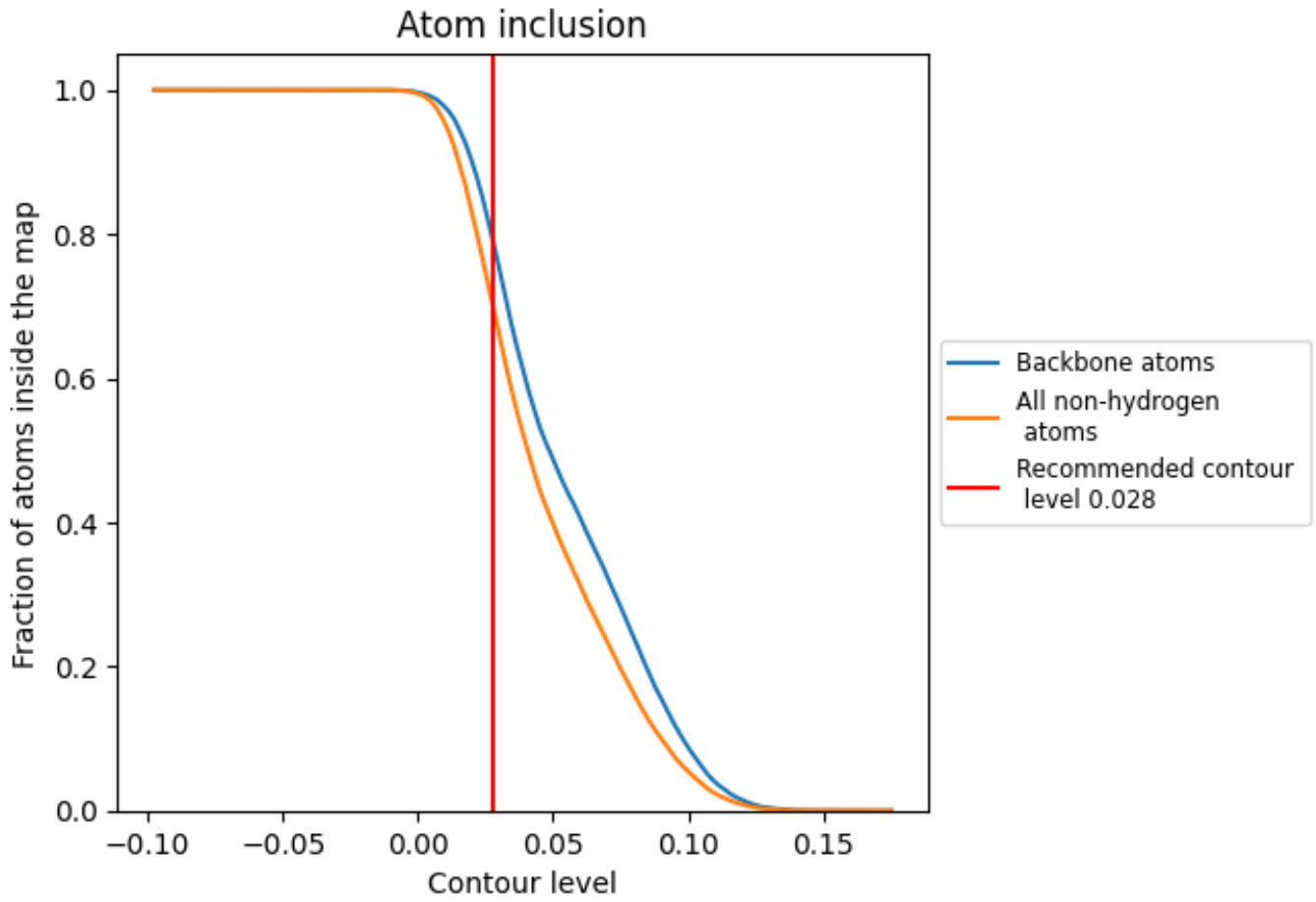
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.028).

9.4 Atom inclusion (i)



At the recommended contour level, 79% of all backbone atoms, 69% 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 (0.028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6947	0.4810
A	0.8227	0.5350
B	0.8244	0.5390
C	0.8368	0.5410
D	0.8237	0.5340
E	0.7478	0.5110
F	0.8174	0.5290
G	0.7525	0.4990
H	0.8330	0.5350
I	0.7635	0.5160
J	0.5828	0.4390
K	0.5640	0.4230
L	0.5705	0.4240