



Full wwPDB EM Validation Report ⓘ

Mar 30, 2026 – 03:05 PM UTC

PDB ID : 6ZG5 / pdb_00006zg5
EMDB ID : EMD-11193
Title : COPII on membranes, outer coat right-handed rod, class1
Authors : Zanetti, G.; Hutchings, J.
Deposited on : 2020-06-18
Resolution : 40.00 Å(reported)
Based on initial model : 2PM6

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:

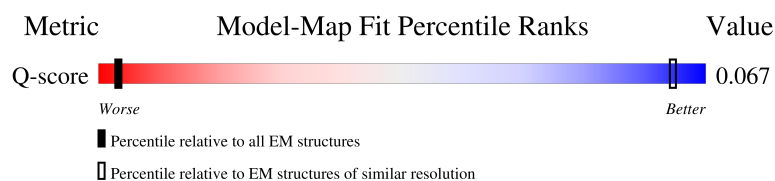
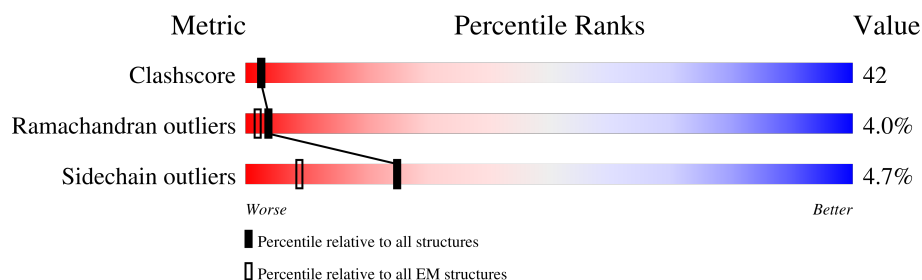
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 40.00 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	18 (40.00 - 40.00)

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	1273	 13% 12% • 73%
1	C	1273	 5% 14% 11% • 73%
2	B	297	 7% 42% 49% • 6%
3	F	297	 14% 23% 56% 15% 6%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9971 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 Protein transport protein SEC31.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	340	Total	C	N	O	S	0	0
			2684	1696	443	540	5		
1	C	342	Total	C	N	O	S	0	0
			2701	1707	446	543	5		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	367	SER	THR	conflict	UNP P38968
C	367	SER	THR	conflict	UNP P38968

- Molecule 2 is a protein called Protein transport protein SEC13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	279	Total	C	N	O	S	0	0
			2196	1403	375	415	3		

- Molecule 3 is a protein called Protein transport protein SEC13.

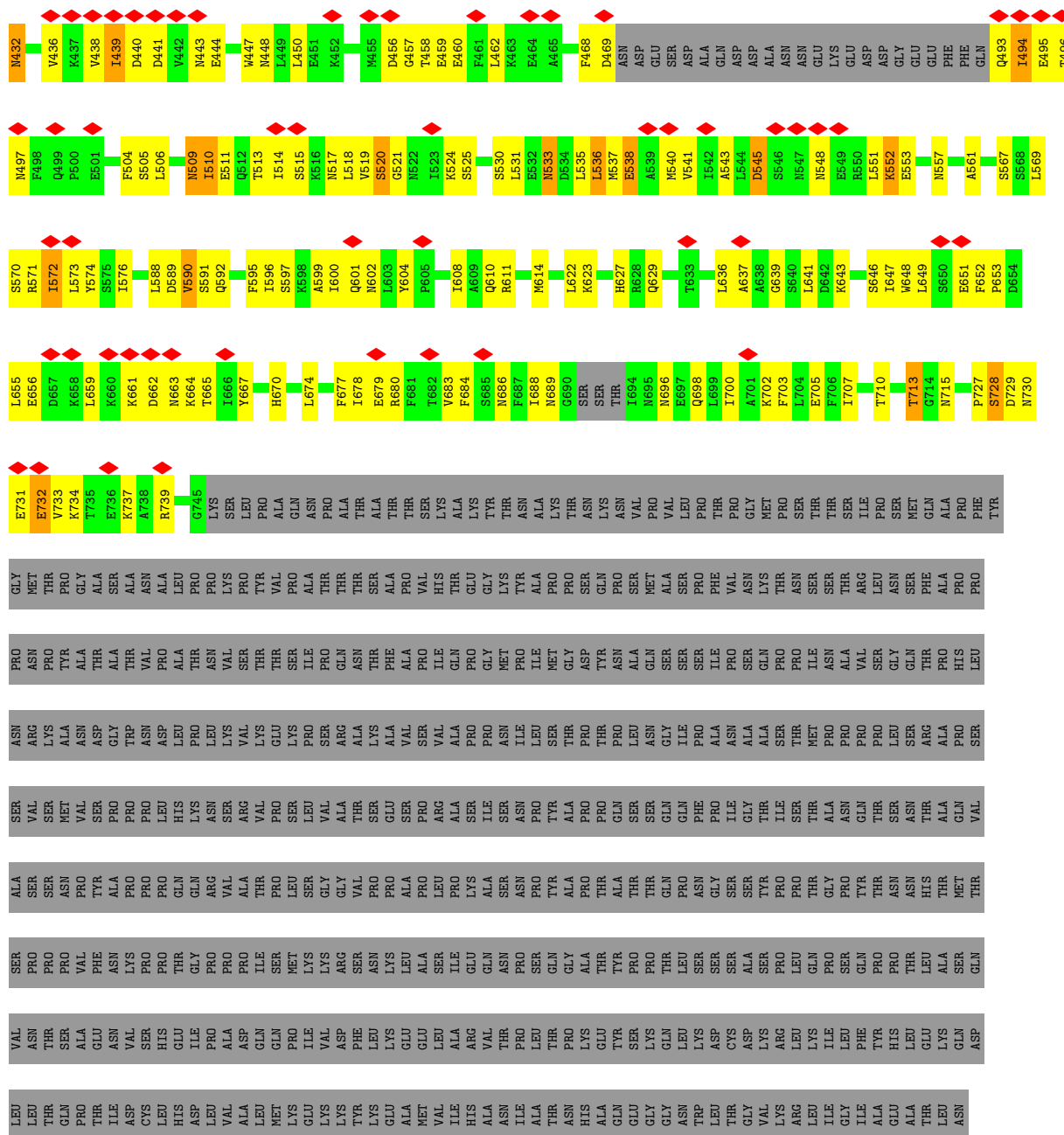
Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	280	Total	C	N	O	S	0	0
			2205	1402	376	418	9		

There are 6 discrepancies between the modelled and reference sequences:

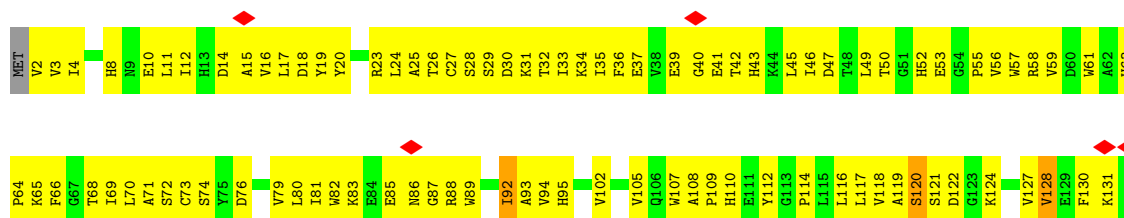
Chain	Residue	Modelled	Actual	Comment	Reference
F	11	MET	LEU	conflict	UNP Q04491
F	17	MET	LEU	conflict	UNP Q04491
F	24	MET	LEU	conflict	UNP Q04491
F	80	MET	LEU	conflict	UNP Q04491
F	115	MET	LEU	conflict	UNP Q04491
F	222	MET	LEU	conflict	UNP Q04491

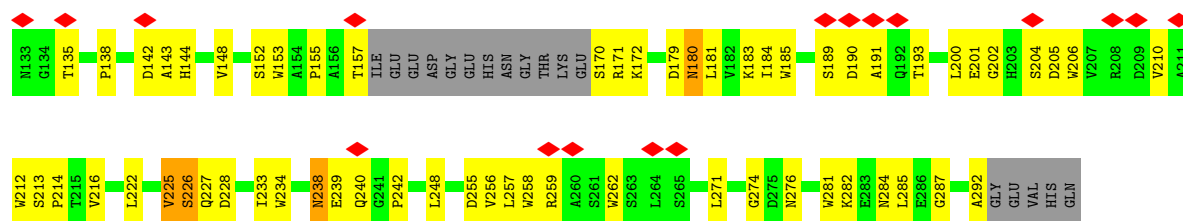
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		AltConf
4	A	27	Total 27	O 27	0
4	B	79	Total 79	O 79	0
4	C	47	Total 47	O 47	0
4	F	32	Total 32	O 32	0

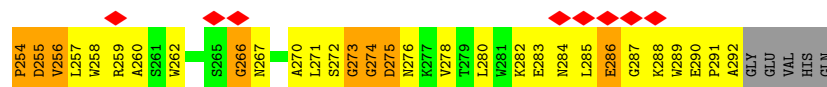
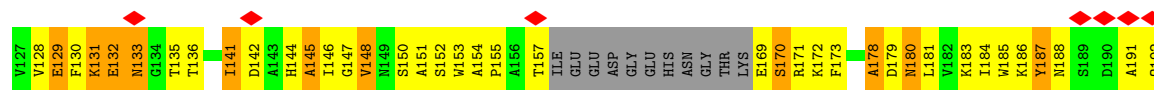
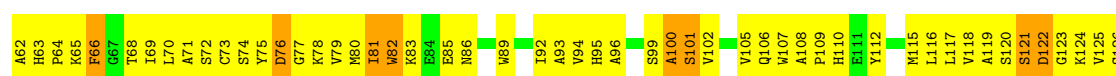


● Molecule 2: Protein transport protein SEC13





• Molecule 3: Protein transport protein SEC13



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, Not provided	
Number of subtomograms used	192	Depositor
Resolution determination method	Not provided	
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; 3d ctf correction	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.634	Depositor
Minimum map value	-5.132	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.225	Depositor
Recommended contour level	3.5	Depositor
Map size ($\text{\AA}$)	340.48, 340.48, 340.48	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.66, 2.66, 2.66	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	0.39	0/2724	0.90	10/3674 (0.3%)
1	C	0.46	1/2741 (0.0%)	0.92	9/3697 (0.2%)
2	B	0.47	0/2256	0.99	6/3079 (0.2%)
3	F	0.48	0/2265	1.01	9/3085 (0.3%)
All	All	0.45	1/9986 (0.0%)	0.95	34/13535 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	384	ALA	CA-CB	-5.12	1.45	1.53

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	178	ALA	N-CA-C	-9.64	101.52	113.28
3	F	275	ASP	N-CA-C	-8.34	103.22	113.15
2	B	226	SER	N-CA-C	7.96	121.26	109.24
1	C	713	THR	N-CA-C	-7.17	104.53	113.20
2	B	128	VAL	N-CA-C	7.05	118.27	108.12
1	C	533	ASN	N-CA-C	-6.76	99.21	109.95
3	F	122	ASP	N-CA-C	-6.59	105.55	112.93
2	B	120	SER	N-CA-C	6.56	119.86	109.50
3	F	121	SER	N-CA-C	-6.55	105.36	113.15
1	A	608	ILE	N-CA-C	6.43	117.18	110.62
1	C	386	TRP	N-CA-C	-6.42	101.27	110.59
2	B	143	ALA	N-CA-C	6.13	121.69	113.72
1	C	406	ASN	CA-C-N	6.11	127.47	119.84
1	C	406	ASN	C-N-CA	6.11	127.47	119.84
3	F	266	GLY	N-CA-C	-6.09	107.29	115.21
2	B	179	ASP	N-CA-C	-5.86	105.72	112.92
3	F	226	SER	N-CA-C	5.79	117.05	108.60
3	F	3	VAL	N-CA-C	5.77	117.93	109.63
1	C	441	ASP	N-CA-C	5.67	117.47	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	536	LEU	N-CA-C	5.57	117.05	110.97
1	C	732	GLU	N-CA-C	-5.55	104.05	112.04
3	F	181	LEU	N-CA-C	5.50	117.92	109.07
1	A	600	ILE	N-CA-C	-5.45	107.12	111.81
1	A	533	ASN	N-CA-C	-5.43	100.67	108.60
3	F	36	PHE	N-CA-C	5.40	117.19	109.14
2	B	287	GLY	N-CA-C	-5.32	107.68	115.72
1	A	384	ALA	N-CA-C	5.32	117.15	110.24
1	A	547	ASN	N-CA-C	-5.31	107.35	113.88
1	A	453	LEU	N-CA-C	-5.04	105.91	111.71
1	A	406	ASN	CA-C-N	5.02	125.01	119.89
1	A	406	ASN	C-N-CA	5.02	125.01	119.89
1	A	396	THR	CA-C-N	5.02	124.80	119.28
1	A	396	THR	C-N-CA	5.02	124.80	119.28
1	C	648	TRP	N-CA-C	5.02	116.83	111.36

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	2684	0	2668	219	0
1	C	2701	0	2685	229	0
2	B	2196	0	2138	176	0
3	F	2205	0	2131	298	0
4	A	27	0	0	15	0
4	B	79	0	0	25	0
4	C	47	0	0	5	0
4	F	32	0	0	5	0
All	All	9971	0	9622	823	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 42.

All (823) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:739:ARG:HA	3:F:20:TYR:CE1	1.28	1.65
1:C:664:LYS:C	3:F:285:LEU:HD21	1.30	1.56
1:C:739:ARG:CA	3:F:20:TYR:HE1	1.28	1.46
1:C:665:THR:N	3:F:285:LEU:HD21	1.38	1.34
1:C:665:THR:HA	3:F:285:LEU:CD2	1.58	1.33
1:C:663:ASN:C	3:F:285:LEU:HD11	1.53	1.29
1:C:663:ASN:C	3:F:285:LEU:CD1	2.13	1.21
1:C:665:THR:CA	3:F:285:LEU:CD2	2.19	1.19
1:C:664:LYS:N	3:F:285:LEU:HD11	1.65	1.12
1:C:664:LYS:C	3:F:285:LEU:CD2	2.24	1.11
1:C:665:THR:N	3:F:285:LEU:CD2	2.14	1.09
1:C:665:THR:CA	3:F:285:LEU:HD23	1.81	1.06
3:F:256:VAL:HG12	3:F:257:LEU:H	1.11	1.06
1:C:665:THR:HA	3:F:285:LEU:HD23	1.09	1.06
1:C:739:ARG:CA	3:F:20:TYR:CE1	2.15	1.06
3:F:184:ILE:HD11	3:F:222:MET:HE1	1.34	1.06
1:C:665:THR:CA	3:F:285:LEU:HD21	1.83	1.05
3:F:46:ILE:HG22	3:F:47:ASP:H	1.20	1.04
3:F:24:MET:HG2	3:F:25:ALA:H	1.18	1.03
1:C:664:LYS:O	3:F:285:LEU:HD21	1.58	1.02
1:C:688:ILE:HG13	1:C:689:ASN:H	1.21	1.01
1:C:425:LYS:HE2	1:C:686:ASN:HD21	1.21	1.01
1:C:663:ASN:O	3:F:285:LEU:CD1	2.08	1.01
2:B:11:LEU:O	2:B:28:SER:HB2	1.61	1.00
1:C:408:LYS:HD3	1:C:408:LYS:H	1.22	1.00
3:F:69:ILE:HD11	3:F:83:LYS:HE2	1.43	1.00
1:C:623:LYS:HE3	1:C:647:ILE:HD12	1.44	0.99
1:A:431:ILE:HD11	1:A:683:VAL:HG11	1.42	0.99
3:F:80:MET:HG2	3:F:94:VAL:HG23	1.43	0.99
3:F:69:ILE:HG12	3:F:83:LYS:HG2	1.45	0.98
1:A:438:VAL:HG23	1:A:443:ASN:HD22	1.28	0.97
2:B:128:VAL:HG22	2:B:138:PRO:HB3	1.43	0.97
1:C:535:LEU:HB3	1:C:538:GLU:HG3	1.49	0.95
1:A:720:THR:HA	1:A:723:LEU:HD12	1.46	0.95
1:C:407:PRO:HD2	4:C:1302:HOH:O	1.67	0.94
3:F:233:ILE:H	3:F:233:ILE:HD12	1.33	0.93
1:A:639:GLY:HA2	1:A:688:ILE:HD11	1.51	0.92
1:C:664:LYS:CA	3:F:285:LEU:HD11	2.00	0.91
1:C:739:ARG:CB	3:F:20:TYR:HE1	1.83	0.90
1:A:428:LYS:HB2	1:A:429:PRO:HD3	1.54	0.89
1:C:420:GLU:O	1:C:423:LYS:HG2	1.70	0.89
1:C:649:LEU:HD22	1:C:698:GLN:HG2	1.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:180:ASN:HD22	3:F:180:ASN:N	1.72	0.88
2:B:81:ILE:HB	4:B:303:HOH:O	1.73	0.88
1:A:536:LEU:HD23	1:C:537:MET:HE1	1.55	0.87
1:C:739:ARG:HA	3:F:20:TYR:CD1	2.08	0.87
1:A:496:THR:HG23	1:C:557:ASN:HB3	1.54	0.87
3:F:249:LYS:HE3	3:F:251:GLU:HB2	1.54	0.87
2:B:81:ILE:HD13	2:B:93:ALA:HB3	1.54	0.87
4:A:1317:HOH:O	1:C:602:ASN:HB3	1.75	0.86
1:A:412:LEU:HD21	1:A:713:THR:HG22	1.57	0.86
1:C:663:ASN:O	3:F:285:LEU:HD11	1.69	0.86
1:A:592:GLN:HE21	1:C:506:LEU:HD12	1.40	0.86
1:C:425:LYS:O	1:C:425:LYS:HD3	1.75	0.86
2:B:83:LYS:O	2:B:89:TRP:HA	1.76	0.85
1:C:663:ASN:O	3:F:285:LEU:HD12	1.74	0.85
3:F:73:CYS:HB3	3:F:79:VAL:HG12	1.59	0.85
1:C:494:ILE:HG13	1:C:495:GLU:H	1.42	0.84
1:C:703:PHE:O	1:C:707:ILE:HG12	1.78	0.84
2:B:257:LEU:HD13	2:B:271:LEU:HD21	1.59	0.84
2:B:12:ILE:HA	2:B:28:SER:HB3	1.59	0.84
3:F:24:MET:CG	3:F:25:ALA:H	1.90	0.84
3:F:69:ILE:CD1	3:F:83:LYS:HE2	2.07	0.83
1:C:665:THR:HG22	3:F:285:LEU:HA	1.61	0.83
1:C:524:LYS:HG3	1:C:525:SER:H	1.43	0.82
1:C:383:ALA:HB1	4:F:302:HOH:O	1.80	0.82
3:F:83:LYS:HG3	3:F:92:ILE:HD13	1.62	0.82
3:F:150:SER:OG	3:F:209:ASP:HA	1.80	0.82
3:F:79:VAL:HG23	3:F:95:HIS:HB3	1.60	0.81
3:F:46:ILE:HG22	3:F:47:ASP:N	1.95	0.81
1:C:427:PHE:O	1:C:431:ILE:HG12	1.81	0.81
1:C:380:PRO:HG3	3:F:11:MET:CE	2.09	0.81
3:F:24:MET:HG2	3:F:25:ALA:N	1.96	0.80
1:C:439:ILE:HG21	1:C:659:LEU:HD21	1.63	0.80
1:C:652:PHE:HB3	1:C:653:PRO:HD3	1.64	0.80
1:A:518:LEU:HB3	1:C:576:ILE:HD13	1.63	0.79
1:A:420:GLU:HA	1:A:423:LYS:HE2	1.63	0.79
1:A:505:SER:HB3	1:C:589:ASP:HB2	1.63	0.78
1:C:688:ILE:HG13	1:C:689:ASN:N	1.98	0.78
3:F:37:GLU:HG2	3:F:46:ILE:HD11	1.65	0.78
1:A:590:VAL:HG13	1:A:622:LEU:HD23	1.65	0.78
1:C:380:PRO:HG3	3:F:11:MET:HE1	1.67	0.76
3:F:33:ILE:HB	3:F:49:LEU:HD12	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:513:THR:HB	4:C:1304:HOH:O	1.84	0.76
1:C:739:ARG:HG3	3:F:20:TYR:CE1	2.20	0.76
3:F:256:VAL:CG1	3:F:257:LEU:H	1.94	0.76
3:F:154:ALA:HB2	3:F:212:TRP:CZ3	2.21	0.75
1:A:393:VAL:HG22	1:A:404:ILE:HG13	1.67	0.75
2:B:10:GLU:HB2	4:B:311:HOH:O	1.86	0.75
1:A:719:ALA:O	1:A:723:LEU:HG	1.87	0.75
1:C:592:GLN:HG3	1:C:595:PHE:HB3	1.69	0.75
1:C:524:LYS:HG3	1:C:525:SER:N	2.01	0.75
1:A:589:ASP:HB2	1:C:505:SER:HB3	1.67	0.75
3:F:65:LYS:HD3	3:F:110:HIS:HB2	1.68	0.75
3:F:71:ALA:HB2	3:F:81:ILE:HG22	1.67	0.75
2:B:117:LEU:HA	4:B:306:HOH:O	1.86	0.74
1:A:652:PHE:HB3	1:A:653:PRO:HD3	1.69	0.74
3:F:52:HIS:CE1	3:F:80:MET:HE3	2.22	0.74
1:A:723:LEU:HD11	1:A:740:VAL:HG21	1.69	0.74
1:C:428:LYS:HB2	1:C:429:PRO:HD3	1.69	0.74
3:F:83:LYS:HG3	3:F:92:ILE:HG21	1.69	0.74
3:F:282:LYS:HA	4:F:305:HOH:O	1.87	0.74
1:C:425:LYS:HE2	1:C:686:ASN:ND2	2.02	0.73
3:F:117:LEU:HD23	3:F:151:ALA:O	1.86	0.73
3:F:29:SER:C	3:F:31:LYS:H	1.95	0.73
3:F:224:SER:HB2	3:F:234:TRP:HE1	1.53	0.73
3:F:225:VAL:HG22	3:F:257:LEU:HB3	1.70	0.73
2:B:255:ASP:OD2	2:B:274:GLY:HA3	1.89	0.72
3:F:16:VAL:HG12	3:F:61:TRP:HD1	1.54	0.72
3:F:225:VAL:HG22	3:F:257:LEU:HD13	1.72	0.72
1:C:739:ARG:CB	3:F:20:TYR:CE1	2.64	0.72
1:A:393:VAL:HG21	2:B:17:LEU:HG	1.69	0.72
1:A:578:LYS:O	1:A:580:GLU:HG3	1.88	0.72
3:F:256:VAL:HG12	3:F:257:LEU:N	1.92	0.72
1:C:664:LYS:O	3:F:285:LEU:CD2	2.31	0.72
3:F:46:ILE:HD12	3:F:46:ILE:N	2.04	0.71
1:C:548:ASN:O	1:C:552:LYS:HB2	1.89	0.71
1:C:510:ILE:HD12	1:C:510:ILE:H	1.55	0.71
3:F:196:LEU:HD11	3:F:198:SER:O	1.90	0.71
1:A:420:GLU:HG3	1:A:423:LYS:HE2	1.72	0.71
1:A:431:ILE:HD13	1:A:447:TRP:HZ3	1.55	0.71
1:A:496:THR:O	1:A:497:ASN:HB2	1.89	0.71
1:A:388:PHE:HB2	1:A:739:ARG:HH21	1.56	0.71
3:F:82:TRP:O	3:F:89:TRP:HZ3	1.74	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:428:LYS:NZ	1:A:455:MET:HG2	2.06	0.70
1:C:408:LYS:HD3	1:C:408:LYS:N	1.97	0.70
2:B:74:SER:HB3	2:B:76:ASP:OD1	1.91	0.70
3:F:73:CYS:CB	3:F:79:VAL:HG12	2.20	0.70
1:A:518:LEU:HD13	1:C:576:ILE:HD12	1.73	0.70
1:C:567:SER:HB3	1:C:570:SER:HB2	1.73	0.70
3:F:154:ALA:HB2	3:F:212:TRP:CE3	2.26	0.70
1:A:665:THR:OG1	1:A:668:GLU:HG3	1.91	0.70
1:A:595:PHE:CZ	1:C:515:SER:HB2	2.28	0.69
1:A:727:PRO:C	1:A:729:ASP:H	2.01	0.69
2:B:144:HIS:CE1	2:B:183:LYS:HD2	2.28	0.69
2:B:53:GLU:HG3	4:B:328:HOH:O	1.93	0.69
1:C:444:GLU:HG2	1:C:448:ASN:ND2	2.08	0.69
2:B:274:GLY:C	2:B:276:ASN:H	2.00	0.68
3:F:233:ILE:HD12	3:F:233:ILE:N	2.05	0.68
1:A:736:GLU:O	1:A:740:VAL:HG23	1.93	0.68
3:F:227:GLN:HA	3:F:256:VAL:HG13	1.75	0.68
3:F:16:VAL:HG12	3:F:61:TRP:CD1	2.29	0.68
2:B:105:VAL:HG23	2:B:118:VAL:HG22	1.73	0.68
1:A:590:VAL:HG13	1:A:622:LEU:CD2	2.23	0.68
1:C:509:ASN:N	1:C:509:ASN:HD22	1.92	0.68
1:A:402:VAL:HG11	2:B:24:LEU:HD21	1.76	0.68
1:A:427:PHE:O	1:A:431:ILE:HG12	1.94	0.68
3:F:105:VAL:HG22	3:F:116:LEU:HD11	1.75	0.67
1:A:528:LYS:HG3	1:C:493:GLN:HE22	1.58	0.67
1:C:439:ILE:HG13	1:C:440:ASP:H	1.60	0.67
3:F:153:TRP:O	3:F:212:TRP:HB3	1.95	0.67
3:F:274:GLY:C	3:F:276:ASN:H	2.03	0.67
2:B:24:LEU:HB3	2:B:36:PHE:HB2	1.75	0.67
3:F:200:LEU:HB3	3:F:234:TRP:CZ3	2.30	0.67
1:C:590:VAL:HG13	1:C:622:LEU:CD2	2.25	0.66
2:B:157:THR:OG1	2:B:170:SER:HB2	1.95	0.66
3:F:75:TYR:CD1	3:F:101:SER:HB2	2.31	0.66
2:B:3:VAL:C	2:B:4:ILE:HD12	2.21	0.66
1:A:639:GLY:CA	1:A:688:ILE:HD11	2.26	0.66
2:B:233:ILE:HD11	2:B:248:LEU:HD13	1.76	0.66
1:C:519:VAL:C	1:C:521:GLY:H	2.02	0.66
1:C:535:LEU:HB3	1:C:538:GLU:CG	2.23	0.66
3:F:144:HIS:HB2	3:F:147:GLY:O	1.95	0.66
1:A:414:SER:OG	1:A:715:ASN:HB2	1.96	0.66
1:A:557:ASN:HB3	1:C:496:THR:HG23	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:498:PHE:HB2	1:C:561:ALA:HA	1.77	0.65
1:A:427:PHE:CD2	1:A:683:VAL:HG22	2.31	0.65
2:B:238:ASN:HD22	2:B:240:GLN:H	1.45	0.65
3:F:233:ILE:H	3:F:233:ILE:CD1	2.09	0.65
3:F:2:VAL:HG13	3:F:41:GLU:HA	1.79	0.65
1:C:416:THR:HG22	1:C:420:GLU:OE2	1.96	0.65
1:A:536:LEU:O	1:A:540:MET:HG3	1.96	0.65
1:A:557:ASN:HB3	1:C:496:THR:CG2	2.27	0.65
3:F:225:VAL:CG2	3:F:257:LEU:HB3	2.26	0.65
1:C:647:ILE:O	1:C:651:GLU:HG3	1.96	0.64
1:C:400:LYS:O	3:F:7:ALA:N	2.29	0.64
1:A:438:VAL:HG23	1:A:443:ASN:ND2	2.07	0.64
1:A:608:ILE:HB	1:A:611:ARG:HH12	1.62	0.64
2:B:102:VAL:CG2	4:B:304:HOH:O	2.45	0.64
1:A:519:VAL:C	1:A:521:GLY:H	2.05	0.64
1:A:608:ILE:HD13	1:A:611:ARG:HH11	1.62	0.64
3:F:49:LEU:HD22	3:F:82:TRP:CD2	2.33	0.64
1:A:592:GLN:HG3	1:A:595:PHE:HB3	1.80	0.64
3:F:184:ILE:CD1	3:F:222:MET:HE1	2.21	0.64
1:A:519:VAL:HG13	1:C:599:ALA:HA	1.79	0.64
2:B:40:GLY:N	4:B:305:HOH:O	2.30	0.64
1:A:537:MET:HE1	1:C:536:LEU:HD23	1.78	0.63
1:C:727:PRO:C	1:C:729:ASP:H	2.06	0.63
3:F:224:SER:CB	3:F:234:TRP:HE1	2.11	0.63
1:C:739:ARG:CG	3:F:20:TYR:CE1	2.82	0.63
2:B:18:ASP:HB2	4:B:337:HOH:O	1.98	0.63
2:B:23:ARG:NH1	2:B:68:THR:HG21	2.14	0.63
1:C:395:ILE:HD13	3:F:12:ILE:O	1.98	0.63
1:A:458:THR:HG23	1:A:459:GLU:N	2.14	0.62
3:F:207:VAL:HA	3:F:226:SER:HB2	1.78	0.62
1:C:639:GLY:HA2	1:C:688:ILE:HD11	1.81	0.62
1:C:661:LYS:C	1:C:663:ASN:H	2.06	0.62
3:F:105:VAL:CG2	3:F:116:LEU:HD11	2.28	0.62
3:F:225:VAL:CG2	3:F:257:LEU:HD13	2.28	0.62
1:A:592:GLN:HG3	1:A:592:GLN:O	1.99	0.62
1:A:596:ILE:O	1:A:600:ILE:HG12	2.00	0.62
2:B:68:THR:C	2:B:69:ILE:HD12	2.23	0.62
3:F:69:ILE:HD11	3:F:83:LYS:CE	2.25	0.62
1:A:703:PHE:HA	4:A:1303:HOH:O	2.00	0.62
1:C:408:LYS:H	1:C:408:LYS:CD	2.05	0.62
3:F:115:MET:HG2	3:F:129:GLU:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:233:ILE:HD11	3:F:248:LEU:HD13	1.81	0.62
2:B:257:LEU:CD1	2:B:271:LEU:HD21	2.30	0.61
3:F:27:CYS:HB2	3:F:56:VAL:HG11	1.82	0.61
2:B:33:ILE:HD11	2:B:56:VAL:HG11	1.80	0.61
2:B:66:PHE:HE1	2:B:114:PRO:HD3	1.65	0.61
1:C:510:ILE:HA	4:C:1304:HOH:O	1.99	0.61
2:B:157:THR:HG22	2:B:157:THR:O	2.00	0.61
3:F:118:VAL:O	3:F:125:VAL:HG13	2.00	0.61
3:F:147:GLY:N	3:F:178:ALA:HB3	2.15	0.61
1:A:559:TYR:CD2	1:C:541:VAL:HG21	2.36	0.61
1:C:458:THR:HG23	1:C:459:GLU:H	1.65	0.61
3:F:249:LYS:CE	3:F:251:GLU:HB2	2.28	0.61
2:B:155:PRO:HG3	2:B:214:PRO:HA	1.83	0.61
1:A:608:ILE:CD1	1:A:611:ARG:HH11	2.14	0.61
3:F:23:ARG:HA	3:F:36:PHE:O	2.01	0.61
3:F:81:ILE:HD13	3:F:81:ILE:H	1.66	0.61
1:A:392:LEU:HD13	4:A:1301:HOH:O	2.00	0.61
1:A:675:THR:O	1:A:679:GLU:HG3	2.01	0.61
1:C:641:LEU:HD13	1:C:688:ILE:HG21	1.82	0.61
1:A:514:ILE:HA	1:A:517:ASN:HD22	1.65	0.60
2:B:4:ILE:HG13	2:B:43:HIS:ND1	2.16	0.60
2:B:30:ASP:OD1	2:B:32:THR:N	2.34	0.60
2:B:128:VAL:CG2	2:B:138:PRO:HB3	2.27	0.60
2:B:200:LEU:HB3	2:B:234:TRP:CZ3	2.36	0.60
3:F:106:GLN:O	3:F:116:LEU:HD12	2.01	0.60
1:A:742:ILE:HB	2:B:20:TYR:CD2	2.36	0.60
3:F:196:LEU:HD12	3:F:197:GLU:H	1.66	0.60
1:A:517:ASN:ND2	1:A:529:ASN:HD22	1.98	0.60
1:A:709:LEU:O	1:A:713:THR:HG23	2.02	0.60
1:A:386:TRP:HA	4:A:1301:HOH:O	2.01	0.60
1:C:665:THR:HG22	3:F:285:LEU:CA	2.30	0.60
1:C:553:GLU:HG2	1:C:557:ASN:HD21	1.67	0.60
2:B:52:HIS:HA	4:B:328:HOH:O	2.01	0.60
1:C:739:ARG:HG3	3:F:20:TYR:CD1	2.36	0.60
3:F:28:SER:OG	3:F:29:SER:N	2.35	0.60
3:F:14:ASP:OD2	3:F:59:VAL:HG22	2.01	0.60
3:F:172:LYS:HA	3:F:185:TRP:O	2.01	0.60
2:B:12:ILE:HA	2:B:28:SER:CB	2.30	0.60
3:F:219:ARG:HG3	3:F:221:TYR:CE1	2.37	0.60
3:F:247:LEU:HD13	3:F:249:LYS:O	2.02	0.60
1:C:604:TYR:CE1	1:C:610:GLN:HG2	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:189:SER:C	2:B:191:ALA:H	2.09	0.59
1:A:396:THR:HG23	4:A:1312:HOH:O	2.02	0.59
2:B:37:GLU:HG2	2:B:46:ILE:HG13	1.82	0.59
3:F:225:VAL:HG22	3:F:257:LEU:CD1	2.32	0.59
1:C:667:TYR:CE2	3:F:266:GLY:HA2	2.37	0.59
3:F:169:GLU:HG2	3:F:187:TYR:HD2	1.67	0.59
1:A:388:PHE:CD1	1:A:739:ARG:CZ	2.86	0.59
1:A:537:MET:O	1:A:541:VAL:HG23	2.02	0.59
3:F:4:ILE:N	3:F:4:ILE:HD12	2.18	0.59
3:F:249:LYS:HG2	3:F:251:GLU:OE1	2.03	0.59
2:B:102:VAL:HG23	4:B:304:HOH:O	2.00	0.59
2:B:216:VAL:HG12	2:B:216:VAL:O	2.03	0.59
1:C:399:GLY:O	3:F:12:ILE:HG13	2.01	0.59
1:A:458:THR:HG23	1:A:459:GLU:H	1.66	0.59
1:C:438:VAL:HG23	1:C:443:ASN:HD22	1.68	0.59
3:F:29:SER:C	3:F:31:LYS:N	2.59	0.59
2:B:180:ASN:N	2:B:180:ASN:HD22	2.00	0.59
1:C:670:HIS:HE1	1:C:705:GLU:OE1	1.86	0.59
2:B:19:TYR:CD2	2:B:64:PRO:HG2	2.38	0.58
1:C:665:THR:CG2	3:F:285:LEU:HD23	2.33	0.58
3:F:17:MET:C	3:F:61:TRP:CD1	2.81	0.58
2:B:29:SER:HA	2:B:55:PRO:HB3	1.84	0.58
1:C:386:TRP:CZ2	3:F:280:LEU:HD22	2.37	0.58
1:A:511:GLU:HG3	4:A:1314:HOH:O	2.03	0.58
1:A:674:LEU:O	1:A:678:ILE:HG12	2.03	0.58
3:F:52:HIS:N	4:F:301:HOH:O	2.29	0.58
3:F:147:GLY:H	3:F:178:ALA:HB3	1.66	0.58
1:C:592:GLN:HG3	1:C:595:PHE:CB	2.33	0.58
3:F:81:ILE:HD13	3:F:81:ILE:N	2.18	0.58
1:A:496:THR:O	1:A:497:ASN:CB	2.51	0.58
1:A:584:LEU:HD12	1:A:584:LEU:N	2.18	0.58
1:C:386:TRP:HZ2	3:F:280:LEU:HD22	1.68	0.58
2:B:83:LYS:HB2	2:B:92:ILE:HD13	1.85	0.58
2:B:225:VAL:HG13	2:B:257:LEU:HB2	1.84	0.58
1:A:518:LEU:HB3	1:C:576:ILE:CD1	2.31	0.58
1:A:612:ASN:O	1:A:616:ILE:HG12	2.03	0.58
2:B:120:SER:HB3	2:B:122:ASP:OD1	2.03	0.58
3:F:187:TYR:CG	3:F:188:ASN:N	2.71	0.58
2:B:108:ALA:HB1	2:B:109:PRO:CD	2.34	0.58
3:F:130:PHE:HA	3:F:136:THR:HG22	1.86	0.58
3:F:37:GLU:HB2	3:F:44:LYS:HB3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:LYS:HG3	1:A:424:THR:HG23	1.86	0.57
1:A:551:LEU:C	1:A:553:GLU:H	2.11	0.57
1:A:509:ASN:N	1:A:509:ASN:HD22	2.01	0.57
2:B:4:ILE:HG13	2:B:43:HIS:CG	2.40	0.57
3:F:29:SER:O	3:F:31:LYS:N	2.37	0.57
1:A:730:ASN:O	1:A:733:VAL:HB	2.03	0.57
1:C:656:GLU:OE2	1:C:670:HIS:HA	2.04	0.57
3:F:25:ALA:HB1	3:F:70:LEU:HD21	1.86	0.57
2:B:222:LEU:HB2	2:B:234:TRP:HB2	1.85	0.57
1:A:731:GLU:O	1:A:734:LYS:HB3	2.04	0.57
1:A:593:TRP:C	1:A:595:PHE:H	2.12	0.57
1:A:468:PHE:CE1	1:A:598:LYS:HE3	2.40	0.57
1:A:496:THR:HG23	1:C:557:ASN:CB	2.32	0.57
3:F:10:GLU:HG3	3:F:30:ASP:HB3	1.87	0.56
3:F:196:LEU:HG	3:F:197:GLU:N	2.20	0.56
2:B:255:ASP:CG	2:B:256:VAL:H	2.14	0.56
1:C:380:PRO:HG3	3:F:11:MET:SD	2.43	0.56
1:C:430:LEU:HD11	1:C:679:GLU:HG2	1.86	0.56
3:F:180:ASN:CG	3:F:205:ASP:O	2.49	0.56
1:A:647:ILE:O	1:A:651:GLU:HG3	2.04	0.56
2:B:24:LEU:HG	2:B:25:ALA:N	2.20	0.56
2:B:56:VAL:HA	2:B:74:SER:HB2	1.87	0.56
1:C:519:VAL:C	1:C:521:GLY:N	2.62	0.56
3:F:282:LYS:NZ	4:F:303:HOH:O	2.38	0.56
1:A:418:LEU:HG	1:A:718:LEU:HD11	1.87	0.56
3:F:4:ILE:HG22	3:F:4:ILE:O	2.04	0.56
1:A:509:ASN:N	1:A:509:ASN:ND2	2.54	0.56
3:F:239:GLU:N	4:F:304:HOH:O	2.38	0.56
1:A:531:LEU:C	1:A:533:ASN:H	2.13	0.56
1:C:462:LEU:HD22	1:C:637:ALA:HB2	1.87	0.56
3:F:81:ILE:HG12	3:F:92:ILE:HG13	1.88	0.56
2:B:8:HIS:ND1	2:B:30:ASP:OD2	2.39	0.56
2:B:66:PHE:CE1	2:B:114:PRO:HD3	2.41	0.56
3:F:150:SER:HB2	3:F:210:VAL:HG22	1.88	0.56
3:F:155:PRO:HG2	3:F:214:PRO:HA	1.88	0.56
3:F:257:LEU:HD23	3:F:273:GLY:HA2	1.86	0.56
1:A:434:ARG:HG3	1:A:447:TRP:CZ2	2.41	0.55
1:A:438:VAL:HG22	1:A:439:ILE:N	2.20	0.55
1:C:535:LEU:HD22	1:C:538:GLU:HG3	1.88	0.55
1:A:616:ILE:HD11	1:A:640:SER:HB2	1.88	0.55
2:B:69:ILE:HD12	2:B:69:ILE:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:519:VAL:HG23	1:C:520:SER:N	2.21	0.55
3:F:80:MET:CG	3:F:94:VAL:HG23	2.27	0.55
2:B:180:ASN:N	2:B:180:ASN:ND2	2.53	0.55
1:C:431:ILE:HD11	1:C:683:VAL:HG11	1.88	0.55
1:C:667:TYR:CD2	3:F:266:GLY:HA2	2.41	0.55
1:A:418:LEU:HD23	1:A:718:LEU:HD21	1.89	0.55
1:A:730:ASN:HB3	1:A:733:VAL:CG2	2.36	0.55
1:A:431:ILE:HD13	1:A:447:TRP:CZ3	2.40	0.55
2:B:4:ILE:HD12	2:B:4:ILE:N	2.20	0.55
1:C:494:ILE:HG13	1:C:495:GLU:N	2.18	0.55
1:A:537:MET:HE1	1:C:536:LEU:CD2	2.36	0.55
1:C:509:ASN:N	1:C:509:ASN:ND2	2.51	0.55
3:F:39:GLU:O	3:F:41:GLU:N	2.33	0.55
2:B:73:CYS:HB2	2:B:102:VAL:CG1	2.37	0.55
3:F:145:ALA:HB3	3:F:179:ASP:HB3	1.89	0.55
1:A:517:ASN:HD21	1:A:529:ASN:ND2	2.04	0.55
1:A:584:LEU:HD12	1:A:584:LEU:H	1.71	0.55
3:F:74:SER:HB3	3:F:76:ASP:OD1	2.06	0.55
3:F:183:LYS:HB2	3:F:185:TRP:HE1	1.72	0.55
1:A:510:ILE:HB	4:A:1314:HOH:O	2.06	0.54
3:F:79:VAL:CG2	3:F:95:HIS:HB3	2.35	0.54
1:C:551:LEU:HD23	1:C:551:LEU:C	2.33	0.54
3:F:92:ILE:HG13	3:F:93:ALA:H	1.72	0.54
3:F:184:ILE:HG12	3:F:198:SER:HB2	1.88	0.54
1:C:733:VAL:O	1:C:737:LYS:HG3	2.07	0.54
1:C:402:VAL:HG11	3:F:24:MET:SD	2.47	0.54
3:F:283:GLU:HA	3:F:288:LYS:O	2.07	0.54
1:A:420:GLU:HG3	1:A:423:LYS:CE	2.37	0.54
2:B:45:LEU:O	2:B:46:ILE:HD13	2.08	0.54
1:C:444:GLU:HG2	1:C:448:ASN:HD21	1.71	0.54
3:F:25:ALA:HA	3:F:34:LYS:O	2.08	0.54
3:F:208:ARG:H	3:F:226:SER:HA	1.72	0.54
2:B:80:LEU:HD23	2:B:94:VAL:HG23	1.90	0.54
3:F:2:VAL:HG12	3:F:2:VAL:O	2.07	0.54
3:F:225:VAL:HG22	3:F:257:LEU:CB	2.37	0.54
2:B:80:LEU:CD2	2:B:94:VAL:HG23	2.38	0.54
1:C:696:ASN:O	1:C:700:ILE:HG13	2.08	0.54
1:A:593:TRP:C	1:A:595:PHE:N	2.66	0.54
3:F:46:ILE:N	3:F:46:ILE:CD1	2.71	0.54
1:A:528:LYS:HG3	1:C:493:GLN:NE2	2.21	0.54
1:C:604:TYR:CZ	1:C:610:GLN:HG2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:590:VAL:HG13	1:C:622:LEU:HD23	1.90	0.53
3:F:215:THR:HG23	3:F:215:THR:O	2.08	0.53
1:A:623:LYS:HE3	1:A:647:ILE:HD12	1.89	0.53
3:F:59:VAL:HG12	3:F:72:SER:HA	1.89	0.53
1:C:614:MET:HA	1:C:614:MET:HE2	1.90	0.53
3:F:75:TYR:C	3:F:77:GLY:H	2.17	0.53
3:F:155:PRO:CG	3:F:214:PRO:HA	2.37	0.53
3:F:229:ARG:HG2	3:F:256:VAL:HA	1.90	0.53
2:B:29:SER:C	2:B:31:LYS:H	2.16	0.53
1:C:386:TRP:NE1	3:F:270:ALA:HB2	2.24	0.53
1:C:707:ILE:O	1:C:710:THR:HB	2.09	0.53
3:F:260:ALA:HA	3:F:271:LEU:HD12	1.89	0.53
1:C:510:ILE:HG21	1:C:533:ASN:ND2	2.23	0.53
1:A:723:LEU:HA	4:A:1319:HOH:O	2.08	0.53
2:B:25:ALA:HB2	2:B:61:TRP:CZ2	2.44	0.53
2:B:39:GLU:HB2	4:B:305:HOH:O	2.08	0.53
1:A:439:ILE:HG21	1:A:659:LEU:HD21	1.90	0.53
2:B:49:LEU:HB3	2:B:82:TRP:CZ3	2.44	0.53
1:C:665:THR:HG22	3:F:285:LEU:HD23	1.91	0.53
3:F:236:GLN:HG2	3:F:237:ASP:N	2.22	0.53
3:F:78:LYS:HG2	3:F:96:ALA:CB	2.39	0.53
3:F:184:ILE:CG1	3:F:198:SER:HB2	2.38	0.53
3:F:71:ALA:CB	3:F:81:ILE:HG22	2.37	0.52
2:B:117:LEU:HD12	4:B:306:HOH:O	2.08	0.52
3:F:188:ASN:HB3	3:F:191:ALA:HB3	1.92	0.52
1:A:451:GLU:O	1:A:454:SER:HB3	2.09	0.52
3:F:108:ALA:HB2	3:F:153:TRP:CZ2	2.44	0.52
1:A:688:ILE:HD13	1:A:689:ASN:N	2.25	0.52
1:A:540:MET:HE1	1:C:541:VAL:HG23	1.91	0.52
1:C:423:LYS:CG	1:C:424:THR:N	2.71	0.52
3:F:119:ALA:HB2	3:F:151:ALA:HB2	1.91	0.52
3:F:206:TRP:N	3:F:206:TRP:CD1	2.78	0.52
1:A:519:VAL:CG1	1:C:599:ALA:HA	2.40	0.52
2:B:33:ILE:CD1	2:B:56:VAL:HG11	2.39	0.52
1:A:742:ILE:H	1:A:742:ILE:HD12	1.73	0.52
1:C:727:PRO:C	1:C:729:ASP:N	2.67	0.52
3:F:231:CYS:HB3	3:F:248:LEU:HD22	1.92	0.52
1:A:388:PHE:CD1	1:A:739:ARG:NH2	2.77	0.52
1:A:584:LEU:H	1:A:584:LEU:CD1	2.22	0.52
3:F:99:SER:O	3:F:100:ALA:CB	2.58	0.52
1:A:412:LEU:C	1:A:412:LEU:HD23	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:649:LEU:HB3	1:A:698:GLN:OE1	2.09	0.51
3:F:274:GLY:C	3:F:276:ASN:N	2.66	0.51
2:B:238:ASN:HD22	2:B:240:GLN:N	2.08	0.51
1:C:408:LYS:HE2	3:F:292:ALA:O	2.10	0.51
1:C:674:LEU:HD21	1:C:705:GLU:HB3	1.91	0.51
3:F:27:CYS:HB2	3:F:56:VAL:CG1	2.41	0.51
3:F:23:ARG:NH1	3:F:68:THR:CG2	2.74	0.51
3:F:71:ALA:HB2	3:F:81:ILE:CG2	2.40	0.51
1:A:608:ILE:HD13	1:A:611:ARG:NH1	2.24	0.51
3:F:123:GLY:HA2	3:F:147:GLY:HA2	1.92	0.51
3:F:180:ASN:N	3:F:180:ASN:ND2	2.46	0.51
2:B:33:ILE:HB	2:B:49:LEU:HB2	1.92	0.51
2:B:105:VAL:CG2	2:B:116:LEU:HD21	2.41	0.51
3:F:29:SER:HA	3:F:55:PRO:HB3	1.93	0.51
1:A:505:SER:CB	1:C:589:ASP:HB2	2.37	0.51
3:F:259:ARG:HG3	3:F:259:ARG:HH11	1.76	0.51
3:F:233:ILE:HG21	3:F:289:TRP:CZ2	2.46	0.51
1:A:432:ASN:O	1:A:436:VAL:HG23	2.11	0.50
1:C:636:LEU:HD12	1:C:688:ILE:HD12	1.93	0.50
3:F:92:ILE:HG13	3:F:93:ALA:N	2.27	0.50
1:A:537:MET:HE2	1:C:540:MET:SD	2.51	0.50
2:B:30:ASP:OD1	2:B:30:ASP:C	2.55	0.50
1:C:430:LEU:HD23	1:C:430:LEU:O	2.11	0.50
1:C:677:PHE:CD2	1:C:678:ILE:HD12	2.46	0.50
3:F:63:HIS:ND1	3:F:64:PRO:HD2	2.26	0.50
3:F:78:LYS:HG2	3:F:96:ALA:HB1	1.94	0.50
3:F:286:GLU:HG3	3:F:288:LYS:HD2	1.94	0.50
1:A:664:LYS:HA	1:A:668:GLU:OE1	2.11	0.50
1:A:524:LYS:HG3	1:A:525:SER:N	2.26	0.50
2:B:95:HIS:CE1	2:B:128:VAL:HG21	2.46	0.50
2:B:200:LEU:HD13	2:B:234:TRP:CE3	2.47	0.50
1:C:400:LYS:O	3:F:6:ASN:HA	2.11	0.50
3:F:85:GLU:O	3:F:86:ASN:HB2	2.11	0.50
1:A:543:ALA:C	1:A:545:ASP:H	2.19	0.50
1:C:601:GLN:HE22	1:C:611:ARG:HD3	1.77	0.50
3:F:171:ARG:O	3:F:186:LYS:HA	2.11	0.50
2:B:69:ILE:HG22	2:B:70:LEU:N	2.25	0.50
2:B:274:GLY:C	2:B:276:ASN:N	2.69	0.50
1:C:494:ILE:HG23	1:C:495:GLU:N	2.26	0.50
3:F:94:VAL:O	3:F:94:VAL:HG13	2.11	0.50
1:A:496:THR:HG22	1:A:497:ASN:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:663:ASN:HA	2:B:285:LEU:HD11	1.94	0.50
3:F:121:SER:C	3:F:123:GLY:H	2.20	0.50
3:F:131:LYS:HB3	3:F:132:GLU:OE2	2.12	0.50
2:B:259:ARG:HG3	2:B:259:ARG:HH11	1.77	0.50
3:F:65:LYS:CD	3:F:110:HIS:HB2	2.40	0.50
3:F:284:ASN:HB3	3:F:290:GLU:CD	2.36	0.50
1:A:608:ILE:HB	1:A:611:ARG:NH1	2.27	0.49
1:A:540:MET:HE1	1:C:541:VAL:CG2	2.42	0.49
2:B:148:VAL:O	4:B:301:HOH:O	2.20	0.49
2:B:95:HIS:HE1	2:B:138:PRO:HG3	1.77	0.49
1:A:731:GLU:HA	1:A:734:LYS:HB3	1.93	0.49
2:B:112:TYR:CZ	2:B:171:ARG:HG2	2.46	0.49
1:A:567:SER:HB3	1:A:570:SER:HB2	1.93	0.49
2:B:4:ILE:O	2:B:4:ILE:HG22	2.11	0.49
1:C:530:SER:O	1:C:533:ASN:O	2.31	0.49
3:F:69:ILE:CG1	3:F:83:LYS:HG2	2.32	0.49
2:B:184:ILE:N	2:B:184:ILE:HD12	2.28	0.49
1:C:439:ILE:HG13	1:C:440:ASP:N	2.27	0.49
3:F:240:GLN:O	3:F:241:GLY:C	2.55	0.49
1:A:568:SER:HB2	1:C:511:GLU:OE1	2.13	0.49
2:B:8:HIS:CE1	2:B:34:LYS:HE2	2.48	0.49
2:B:74:SER:C	2:B:76:ASP:N	2.71	0.49
1:C:439:ILE:CG2	1:C:659:LEU:HD21	2.39	0.49
1:C:733:VAL:HG12	1:C:737:LYS:HE3	1.95	0.49
3:F:10:GLU:CG	3:F:30:ASP:HB3	2.43	0.49
1:A:466:LEU:O	1:A:598:LYS:HE2	2.13	0.49
2:B:233:ILE:CD1	2:B:248:LEU:HD13	2.43	0.49
3:F:59:VAL:HA	3:F:71:ALA:O	2.12	0.49
1:A:514:ILE:HA	1:A:517:ASN:ND2	2.28	0.48
1:A:555:VAL:O	1:A:558:ALA:HB3	2.12	0.48
1:A:585:VAL:HA	1:A:596:ILE:HG21	1.95	0.48
2:B:26:THR:O	2:B:33:ILE:HG23	2.12	0.48
2:B:63:HIS:CD2	4:B:312:HOH:O	2.65	0.48
3:F:179:ASP:C	3:F:180:ASN:HD22	2.20	0.48
1:A:519:VAL:C	1:A:521:GLY:N	2.71	0.48
2:B:57:TRP:O	2:B:58:ARG:HG2	2.14	0.48
2:B:172:LYS:HA	2:B:185:TRP:O	2.14	0.48
1:C:665:THR:HG22	3:F:285:LEU:N	2.27	0.48
3:F:52:HIS:ND1	3:F:74:SER:HB2	2.28	0.48
3:F:108:ALA:HB3	3:F:115:MET:HB2	1.96	0.48
3:F:24:MET:HB3	3:F:36:PHE:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:551:LEU:C	1:A:553:GLU:N	2.71	0.48
1:C:664:LYS:C	3:F:285:LEU:HD11	2.38	0.48
3:F:102:VAL:HA	3:F:120:SER:HA	1.95	0.48
1:A:426:ASP:OD1	1:A:429:PRO:HD3	2.14	0.48
2:B:29:SER:C	2:B:31:LYS:N	2.70	0.48
2:B:59:VAL:HA	2:B:71:ALA:O	2.14	0.48
2:B:72:SER:O	2:B:79:VAL:HG13	2.14	0.48
2:B:108:ALA:HA	2:B:153:TRP:CD1	2.49	0.48
1:C:424:THR:O	1:C:425:LYS:CB	2.62	0.48
3:F:47:ASP:OD2	3:F:89:TRP:HB2	2.12	0.48
3:F:95:HIS:CE1	3:F:128:VAL:HG21	2.48	0.48
1:A:430:LEU:O	1:A:430:LEU:HD23	2.13	0.48
3:F:196:LEU:CG	3:F:197:GLU:N	2.77	0.48
2:B:18:ASP:OD2	2:B:23:ARG:HB3	2.14	0.48
1:C:553:GLU:HG2	1:C:557:ASN:ND2	2.28	0.48
1:C:661:LYS:C	1:C:663:ASN:N	2.72	0.48
3:F:259:ARG:HB2	3:F:272:SER:HB2	1.95	0.48
1:A:517:ASN:HD21	1:A:529:ASN:HD22	1.61	0.48
2:B:34:LYS:HB3	2:B:36:PHE:HE1	1.79	0.48
1:C:388:PHE:CE1	1:C:739:ARG:HD3	2.49	0.48
3:F:82:TRP:N	3:F:82:TRP:CD1	2.82	0.48
3:F:157:THR:HB	3:F:170:SER:OG	2.14	0.48
1:A:412:LEU:CD2	1:A:713:THR:HG22	2.38	0.47
1:A:639:GLY:HA2	1:A:688:ILE:CD1	2.35	0.47
1:A:644:VAL:HG11	1:A:684:PHE:CE2	2.48	0.47
2:B:37:GLU:HG2	2:B:46:ILE:CG1	2.44	0.47
2:B:225:VAL:HG13	2:B:257:LEU:CB	2.44	0.47
1:C:456:ASP:O	1:C:460:GLU:HB2	2.14	0.47
3:F:141:ILE:HD13	3:F:141:ILE:O	2.14	0.47
1:A:420:GLU:CA	1:A:423:LYS:HE2	2.38	0.47
1:A:542:ILE:HD11	1:C:573:LEU:CD2	2.44	0.47
2:B:69:ILE:CG2	2:B:70:LEU:N	2.77	0.47
1:C:536:LEU:O	1:C:537:MET:C	2.57	0.47
3:F:109:PRO:HD2	3:F:112:TYR:CD2	2.49	0.47
3:F:131:LYS:HD2	3:F:135:THR:O	2.14	0.47
2:B:119:ALA:HB1	2:B:148:VAL:HG12	1.96	0.47
2:B:212:TRP:CD2	2:B:222:LEU:HD21	2.49	0.47
1:C:535:LEU:CB	1:C:538:GLU:HG3	2.31	0.47
3:F:24:MET:O	3:F:61:TRP:HZ2	1.96	0.47
1:A:402:VAL:HG11	2:B:24:LEU:CD2	2.42	0.47
2:B:87:GLY:C	2:B:88:ARG:HG3	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:514:ILE:HA	1:C:517:ASN:HD22	1.79	0.47
1:A:593:TRP:O	1:A:595:PHE:N	2.48	0.47
1:A:739:ARG:HD2	2:B:19:TYR:CZ	2.50	0.47
2:B:15:ALA:HA	2:B:25:ALA:O	2.14	0.47
2:B:119:ALA:HB1	2:B:148:VAL:CG1	2.45	0.47
2:B:124:LYS:HE2	2:B:142:ASP:OD1	2.15	0.47
2:B:255:ASP:CG	2:B:256:VAL:N	2.72	0.47
2:B:259:ARG:HG3	2:B:259:ARG:NH1	2.30	0.47
1:C:728:SER:HB3	1:C:737:LYS:NZ	2.29	0.47
3:F:205:ASP:H	3:F:228:ASP:HB3	1.78	0.47
3:F:250:GLU:C	3:F:251:GLU:OE1	2.58	0.47
1:A:517:ASN:ND2	1:A:529:ASN:ND2	2.63	0.47
1:A:536:LEU:CD2	1:C:537:MET:HE1	2.38	0.47
1:A:664:LYS:HB3	1:A:668:GLU:HB2	1.96	0.47
3:F:23:ARG:NH1	3:F:68:THR:HG21	2.29	0.47
3:F:146:ILE:HB	3:F:178:ALA:HB3	1.96	0.47
2:B:29:SER:O	2:B:31:LYS:HG3	2.14	0.47
1:C:688:ILE:CG1	1:C:689:ASN:H	2.09	0.47
1:A:727:PRO:C	1:A:729:ASP:N	2.69	0.47
1:C:674:LEU:O	1:C:678:ILE:HD13	2.15	0.47
1:A:608:ILE:CD1	1:A:611:ARG:NH1	2.78	0.46
1:C:382:PRO:CB	3:F:278:VAL:HG23	2.46	0.46
1:C:412:LEU:CD2	1:C:713:THR:HG22	2.45	0.46
1:C:731:GLU:HA	1:C:734:LYS:HB3	1.97	0.46
3:F:40:GLY:O	3:F:41:GLU:CG	2.62	0.46
3:F:216:VAL:HG12	3:F:216:VAL:O	2.15	0.46
1:A:392:LEU:CD1	4:A:1301:HOH:O	2.61	0.46
1:C:386:TRP:HZ3	4:C:1302:HOH:O	1.98	0.46
1:C:438:VAL:HG21	1:C:444:GLU:HA	1.96	0.46
1:C:641:LEU:HD12	1:C:684:PHE:HE2	1.80	0.46
3:F:46:ILE:CG2	3:F:47:ASP:N	2.66	0.46
2:B:18:ASP:CG	2:B:23:ARG:HB3	2.39	0.46
2:B:109:PRO:HD2	2:B:112:TYR:CD2	2.50	0.46
1:C:589:ASP:C	1:C:591:SER:H	2.23	0.46
3:F:31:LYS:HB3	3:F:52:HIS:O	2.15	0.46
3:F:118:VAL:HB	3:F:126:SER:OG	2.15	0.46
3:F:152:SER:CB	3:F:211:ALA:HA	2.45	0.46
1:A:542:ILE:HD11	1:C:573:LEU:HD21	1.96	0.46
1:A:563:TYR:C	1:A:565:SER:H	2.24	0.46
2:B:27:CYS:HB2	2:B:56:VAL:CG1	2.44	0.46
3:F:129:GLU:HG2	3:F:130:PHE:N	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:200:LEU:HD13	3:F:234:TRP:CE3	2.51	0.46
3:F:209:ASP:HB2	3:F:258:TRP:O	2.15	0.46
3:F:99:SER:O	3:F:100:ALA:HB2	2.15	0.46
3:F:224:SER:HB2	3:F:234:TRP:NE1	2.28	0.46
1:A:572:ILE:CD1	1:C:504:PHE:HE2	2.28	0.46
2:B:74:SER:CB	2:B:76:ASP:OD1	2.61	0.46
3:F:52:HIS:NE2	3:F:80:MET:HE3	2.30	0.46
1:A:462:LEU:HD13	1:A:637:ALA:HB2	1.97	0.46
2:B:200:LEU:HB3	2:B:234:TRP:CH2	2.50	0.46
1:A:564:GLY:HA2	1:A:570:SER:OG	2.16	0.46
2:B:93:ALA:HB1	4:B:336:HOH:O	2.14	0.46
1:C:438:VAL:HG23	1:C:443:ASN:ND2	2.30	0.46
1:A:392:LEU:HA	4:A:1301:HOH:O	2.16	0.46
1:A:663:ASN:CA	2:B:285:LEU:HD11	2.46	0.46
3:F:14:ASP:HB3	3:F:27:CYS:SG	2.55	0.46
3:F:75:TYR:O	3:F:77:GLY:N	2.49	0.46
3:F:210:VAL:HG23	3:F:210:VAL:O	2.14	0.46
3:F:37:GLU:O	3:F:43:HIS:HA	2.15	0.46
3:F:124:LYS:HG2	3:F:142:ASP:OD1	2.15	0.46
1:A:441:ASP:HA	4:A:1305:HOH:O	2.15	0.45
2:B:284:ASN:HB2	4:B:347:HOH:O	2.16	0.45
3:F:85:GLU:HG2	3:F:86:ASN:ND2	2.31	0.45
3:F:194:TYR:HD1	3:F:194:TYR:H	1.63	0.45
3:F:247:LEU:C	3:F:249:LYS:N	2.74	0.45
2:B:66:PHE:CD1	2:B:114:PRO:HB3	2.51	0.45
2:B:117:LEU:HB2	2:B:153:TRP:NE1	2.31	0.45
1:C:641:LEU:HD12	1:C:684:PHE:CE2	2.51	0.45
1:C:431:ILE:HD13	1:C:447:TRP:HZ3	1.82	0.45
1:C:432:ASN:O	1:C:436:VAL:HG23	2.16	0.45
1:A:551:LEU:C	1:A:551:LEU:HD23	2.41	0.45
2:B:121:SER:HA	4:B:301:HOH:O	2.15	0.45
3:F:255:ASP:HB2	3:F:275:ASP:HB3	1.98	0.45
1:A:559:TYR:CE2	1:C:541:VAL:HG21	2.52	0.45
1:C:596:ILE:O	1:C:600:ILE:HG13	2.16	0.45
1:A:504:PHE:CZ	1:C:588:LEU:HD13	2.52	0.45
2:B:31:LYS:O	4:B:302:HOH:O	2.20	0.45
2:B:35:ILE:HG13	2:B:89:TRP:CE2	2.52	0.45
1:C:622:LEU:O	1:C:627:HIS:HB2	2.16	0.45
3:F:196:LEU:CD1	3:F:197:GLU:H	2.30	0.45
3:F:59:VAL:HG12	3:F:72:SER:CB	2.46	0.45
3:F:191:ALA:C	3:F:192:GLN:HG2	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:226:SER:OG	3:F:227:GLN:N	2.49	0.45
1:A:428:LYS:HB2	1:A:429:PRO:CD	2.38	0.45
1:A:449:LEU:O	1:A:453:LEU:HB2	2.17	0.45
1:A:581:VAL:HG11	1:A:600:ILE:HD13	1.98	0.45
1:A:601:GLN:HE22	1:A:611:ARG:HD3	1.82	0.45
1:C:590:VAL:O	1:C:590:VAL:CG1	2.64	0.45
3:F:120:SER:O	3:F:148:VAL:HG23	2.16	0.45
1:A:688:ILE:HG12	1:A:689:ASN:H	1.82	0.45
1:A:718:LEU:O	1:A:722:PHE:HD1	1.98	0.45
2:B:127:VAL:HA	4:B:306:HOH:O	2.15	0.45
2:B:239:GLU:HG3	4:B:346:HOH:O	2.16	0.45
1:C:412:LEU:C	1:C:412:LEU:HD23	2.41	0.45
1:C:727:PRO:O	1:C:729:ASP:N	2.50	0.44
2:B:4:ILE:HG21	2:B:36:PHE:CE2	2.52	0.44
1:C:497:ASN:CG	1:C:497:ASN:O	2.59	0.44
3:F:257:LEU:HD23	3:F:257:LEU:HA	1.80	0.44
1:A:538:GLU:O	1:A:539:ALA:C	2.60	0.44
1:A:573:LEU:HD23	1:C:518:LEU:CD1	2.47	0.44
1:A:584:LEU:N	1:A:584:LEU:CD1	2.81	0.44
1:A:595:PHE:C	1:A:597:SER:N	2.72	0.44
2:B:105:VAL:HG22	2:B:116:LEU:HD11	1.99	0.44
1:C:665:THR:CG2	3:F:285:LEU:N	2.80	0.44
3:F:3:VAL:C	3:F:4:ILE:HD12	2.42	0.44
1:A:511:GLU:HG2	1:C:569:LEU:HB2	2.00	0.44
1:A:399:GLY:O	2:B:11:LEU:HD12	2.17	0.44
1:A:436:VAL:HG12	1:A:436:VAL:O	2.16	0.44
1:A:496:THR:CG2	1:A:497:ASN:N	2.81	0.44
3:F:38:VAL:HA	3:F:42:THR:O	2.18	0.44
2:B:181:LEU:CD2	2:B:201:GLU:HG2	2.47	0.44
2:B:189:SER:C	2:B:191:ALA:N	2.76	0.44
2:B:191:ALA:HB1	2:B:193:THR:HG22	1.99	0.44
2:B:213:SER:HB2	2:B:262:TRP:CE2	2.53	0.44
1:C:457:GLY:O	1:C:458:THR:C	2.59	0.44
1:C:652:PHE:HB3	1:C:653:PRO:CD	2.42	0.44
1:A:504:PHE:CE2	1:C:588:LEU:HD13	2.53	0.44
3:F:52:HIS:ND1	3:F:74:SER:CB	2.81	0.44
2:B:14:ASP:HB3	2:B:27:CYS:SG	2.58	0.44
2:B:74:SER:C	2:B:76:ASP:H	2.26	0.44
1:C:551:LEU:C	1:C:553:GLU:N	2.76	0.44
3:F:72:SER:O	3:F:79:VAL:HA	2.17	0.44
3:F:271:LEU:HD12	3:F:271:LEU:HA	1.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:GLU:HG2	2:B:258:TRP:CZ2	2.53	0.43
2:B:63:HIS:CE1	2:B:65:LYS:HB3	2.53	0.43
1:A:423:LYS:HG3	1:A:424:THR:N	2.32	0.43
2:B:85:GLU:O	2:B:86:ASN:HB2	2.18	0.43
2:B:281:TRP:CD1	2:B:281:TRP:N	2.87	0.43
1:C:543:ALA:C	1:C:545:ASP:H	2.26	0.43
1:C:571:ARG:O	1:C:574:TYR:HB3	2.18	0.43
3:F:213:SER:OG	3:F:214:PRO:HD2	2.18	0.43
1:A:438:VAL:CG2	1:A:439:ILE:N	2.81	0.43
2:B:30:ASP:OD1	2:B:32:THR:HG23	2.17	0.43
1:A:604:TYR:N	1:A:605:PRO:CD	2.81	0.43
1:C:458:THR:HG23	1:C:459:GLU:N	2.30	0.43
1:C:519:VAL:O	1:C:521:GLY:N	2.51	0.43
3:F:63:HIS:HB3	3:F:66:PHE:CE1	2.53	0.43
1:A:537:MET:HE1	1:C:536:LEU:CG	2.48	0.43
1:A:688:ILE:CG1	1:A:689:ASN:H	2.31	0.43
2:B:112:TYR:N	2:B:112:TYR:CD1	2.86	0.43
2:B:248:LEU:HD12	2:B:248:LEU:HA	1.86	0.43
1:C:608:ILE:HD13	1:C:611:ARG:NH1	2.33	0.43
1:C:677:PHE:HD2	1:C:678:ILE:HD12	1.83	0.43
3:F:259:ARG:HG3	3:F:259:ARG:NH1	2.33	0.43
2:B:64:PRO:HD2	4:B:312:HOH:O	2.18	0.43
1:A:429:PRO:HD2	4:A:1313:HOH:O	2.19	0.43
1:A:549:GLU:HA	1:A:552:LYS:HB3	2.01	0.43
1:A:639:GLY:C	1:A:688:ILE:HD11	2.44	0.43
2:B:46:ILE:O	2:B:46:ILE:HG22	2.19	0.43
2:B:102:VAL:HG22	4:B:304:HOH:O	2.14	0.43
2:B:226:SER:HB3	2:B:228:ASP:OD1	2.19	0.43
3:F:184:ILE:O	3:F:196:LEU:HD12	2.18	0.43
3:F:233:ILE:HD11	3:F:248:LEU:CD1	2.47	0.43
1:A:706:PHE:CB	4:A:1303:HOH:O	2.66	0.43
2:B:238:ASN:HD22	2:B:238:ASN:C	2.26	0.43
1:C:590:VAL:HG13	1:C:622:LEU:HD22	1.99	0.43
1:C:636:LEU:HD12	1:C:688:ILE:CD1	2.48	0.43
3:F:26:THR:O	3:F:33:ILE:HA	2.18	0.43
3:F:109:PRO:O	3:F:110:HIS:C	2.61	0.43
3:F:219:ARG:CG	3:F:221:TYR:CE1	3.02	0.43
2:B:25:ALA:HB2	2:B:61:TRP:HZ2	1.81	0.43
1:C:551:LEU:C	1:C:553:GLU:H	2.27	0.43
3:F:201:GLU:O	3:F:234:TRP:HH2	2.02	0.43
2:B:107:TRP:CH2	2:B:130:PHE:HE2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:227:GLN:HA	2:B:256:VAL:HG13	2.01	0.43
1:C:424:THR:O	1:C:425:LYS:HB3	2.18	0.43
1:C:531:LEU:C	1:C:533:ASN:N	2.77	0.43
3:F:233:ILE:HG21	3:F:289:TRP:HZ2	1.82	0.43
2:B:63:HIS:CD2	2:B:110:HIS:HB3	2.54	0.42
1:C:379:GLU:HB3	3:F:258:TRP:CZ2	2.54	0.42
1:C:412:LEU:HD21	1:C:713:THR:HG22	2.01	0.42
1:C:420:GLU:HA	1:C:423:LYS:HD3	2.01	0.42
1:C:639:GLY:HA2	1:C:688:ILE:CD1	2.47	0.42
3:F:206:TRP:O	3:F:226:SER:OG	2.23	0.42
1:A:422:LEU:CD2	1:A:721:GLU:HG2	2.49	0.42
1:A:500:PRO:O	1:A:501:GLU:HG2	2.20	0.42
2:B:49:LEU:HA	4:B:334:HOH:O	2.20	0.42
1:A:399:GLY:HA3	2:B:11:LEU:CD1	2.49	0.42
2:B:4:ILE:N	2:B:4:ILE:CD1	2.83	0.42
2:B:16:VAL:HG12	2:B:61:TRP:HD1	1.84	0.42
3:F:23:ARG:HD3	3:F:61:TRP:CH2	2.54	0.42
1:A:497:ASN:OD1	1:A:498:PHE:N	2.53	0.42
1:C:468:PHE:O	1:C:469:ASP:C	2.62	0.42
1:C:739:ARG:CD	3:F:19:TYR:CE2	2.71	0.42
3:F:68:THR:HG22	3:F:89:TRP:CH2	2.54	0.42
1:C:493:GLN:HG3	1:C:494:ILE:N	2.35	0.42
3:F:39:GLU:HB2	3:F:42:THR:OG1	2.19	0.42
3:F:62:ALA:HB2	3:F:107:TRP:CE2	2.55	0.42
1:A:388:PHE:CE2	1:A:716:PHE:HE2	2.37	0.42
1:A:694:ILE:HG23	1:A:699:LEU:HD23	2.02	0.42
2:B:238:ASN:ND2	2:B:240:GLN:H	2.14	0.42
3:F:58:ARG:HE	3:F:58:ARG:HB2	1.60	0.42
1:A:404:ILE:N	1:A:404:ILE:HD12	2.34	0.42
1:A:439:ILE:HG13	1:A:440:ASP:H	1.85	0.42
1:A:733:VAL:HG13	4:A:1319:HOH:O	2.19	0.42
2:B:52:HIS:CD2	2:B:56:VAL:HG22	2.55	0.42
1:C:420:GLU:HA	1:C:423:LYS:CD	2.50	0.42
3:F:231:CYS:HB2	3:F:271:LEU:HD21	2.00	0.42
1:A:431:ILE:HG21	1:A:451:GLU:HA	2.02	0.42
1:A:519:VAL:O	1:A:521:GLY:N	2.52	0.42
1:A:610:GLN:HA	1:A:610:GLN:OE1	2.20	0.42
3:F:194:TYR:CD1	3:F:194:TYR:N	2.88	0.42
3:F:232:ILE:HG21	3:F:234:TRP:CZ2	2.55	0.42
3:F:262:TRP:CE3	3:F:262:TRP:HA	2.55	0.42
1:A:420:GLU:O	1:A:423:LYS:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:TRP:O	1:A:451:GLU:N	2.53	0.41
1:A:497:ASN:O	1:A:498:PHE:HB3	2.20	0.41
1:A:556:LYS:C	1:A:558:ALA:N	2.78	0.41
2:B:233:ILE:HD12	2:B:233:ILE:N	2.35	0.41
3:F:35:ILE:HG13	3:F:89:TRP:NE1	2.35	0.41
3:F:105:VAL:HG21	3:F:116:LEU:HD21	2.02	0.41
3:F:247:LEU:C	3:F:249:LYS:H	2.27	0.41
2:B:30:ASP:OD1	2:B:32:THR:OG1	2.36	0.41
2:B:152:SER:OG	2:B:210:VAL:O	2.33	0.41
2:B:282:LYS:HB3	2:B:292:ALA:HB2	2.02	0.41
1:C:438:VAL:HG21	1:C:444:GLU:CA	2.50	0.41
1:C:447:TRP:CE3	1:C:450:LEU:HD12	2.55	0.41
3:F:33:ILE:HD13	3:F:72:SER:HB3	2.02	0.41
1:A:608:ILE:HA	1:A:611:ARG:NH1	2.34	0.41
3:F:24:MET:CG	3:F:25:ALA:N	2.60	0.41
3:F:60:ASP:O	3:F:107:TRP:NE1	2.52	0.41
3:F:102:VAL:HG22	3:F:120:SER:HB2	2.02	0.41
3:F:253:PHE:HA	3:F:254:PRO:HD2	1.87	0.41
1:A:430:LEU:C	1:A:430:LEU:CD2	2.94	0.41
1:A:444:GLU:HG2	1:A:448:ASN:ND2	2.36	0.41
1:A:644:VAL:HG21	1:A:684:PHE:CZ	2.55	0.41
1:C:510:ILE:O	1:C:511:GLU:C	2.63	0.41
3:F:3:VAL:HG12	3:F:5:ALA:N	2.35	0.41
3:F:112:TYR:HA	3:F:171:ARG:NH2	2.36	0.41
1:A:434:ARG:HG3	1:A:447:TRP:CH2	2.55	0.41
1:A:458:THR:CG2	1:A:459:GLU:N	2.81	0.41
1:A:653:PRO:O	1:A:656:GLU:N	2.54	0.41
2:B:225:VAL:CG1	2:B:257:LEU:O	2.69	0.41
1:A:412:LEU:HD23	1:A:413:GLU:N	2.35	0.41
1:A:537:MET:CE	1:C:536:LEU:HD23	2.48	0.41
1:A:563:TYR:C	1:A:565:SER:N	2.77	0.41
3:F:10:GLU:HG3	3:F:30:ASP:CA	2.51	0.41
3:F:23:ARG:NH1	3:F:68:THR:OG1	2.51	0.41
3:F:49:LEU:HD22	3:F:82:TRP:CG	2.55	0.41
3:F:213:SER:OG	3:F:215:THR:HG22	2.20	0.41
2:B:213:SER:HB2	2:B:262:TRP:CD2	2.55	0.41
1:C:400:LYS:C	3:F:12:ILE:HD11	2.45	0.41
1:A:706:PHE:HB2	4:A:1303:HOH:O	2.19	0.41
2:B:46:ILE:O	2:B:47:ASP:HB2	2.21	0.41
2:B:121:SER:CA	4:B:301:HOH:O	2.68	0.41
2:B:205:ASP:O	2:B:206:TRP:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:679:GLU:O	1:C:680:ARG:C	2.62	0.41
3:F:152:SER:O	3:F:173:PHE:HB2	2.21	0.41
1:A:388:PHE:HB2	1:A:739:ARG:NH2	2.30	0.41
1:A:598:LYS:O	1:A:602:ASN:HB2	2.20	0.41
2:B:120:SER:C	2:B:122:ASP:H	2.29	0.41
1:C:646:SER:O	1:C:647:ILE:C	2.62	0.41
3:F:30:ASP:O	3:F:31:LYS:HB2	2.21	0.41
3:F:59:VAL:HG12	3:F:72:SER:CA	2.50	0.41
3:F:247:LEU:HD23	3:F:247:LEU:HA	1.79	0.41
1:A:541:VAL:HG23	1:C:540:MET:HE1	2.03	0.41
1:A:592:GLN:O	1:A:595:PHE:HB3	2.21	0.41
1:A:614:MET:HA	1:A:614:MET:HE2	2.03	0.41
2:B:155:PRO:CG	2:B:214:PRO:HA	2.49	0.41
1:C:596:ILE:O	1:C:597:SER:C	2.63	0.41
1:C:702:LYS:HA	1:C:705:GLU:HB2	2.03	0.41
3:F:4:ILE:HG13	3:F:43:HIS:HB3	2.03	0.41
2:B:17:LEU:HD23	2:B:24:LEU:HA	2.03	0.40
2:B:42:THR:N	4:B:305:HOH:O	2.41	0.40
2:B:238:ASN:HB2	4:B:346:HOH:O	2.20	0.40
1:C:592:GLN:NE2	4:C:1309:HOH:O	2.53	0.40
3:F:105:VAL:HG13	3:F:105:VAL:O	2.21	0.40
3:F:120:SER:OG	3:F:121:SER:N	2.53	0.40
3:F:224:SER:O	3:F:231:CYS:HA	2.21	0.40
1:A:727:PRO:O	1:A:729:ASP:N	2.54	0.40
1:C:551:LEU:O	1:C:553:GLU:N	2.54	0.40
1:C:572:ILE:HG22	1:C:573:LEU:N	2.35	0.40
1:C:589:ASP:C	1:C:591:SER:N	2.80	0.40
1:C:730:ASN:C	1:C:732:GLU:H	2.29	0.40
1:C:730:ASN:C	1:C:732:GLU:N	2.79	0.40
3:F:83:LYS:CG	3:F:92:ILE:HG21	2.45	0.40
2:B:225:VAL:CG2	2:B:271:LEU:HD11	2.50	0.40
1:C:423:LYS:HG2	1:C:424:THR:H	1.86	0.40
1:C:643:LYS:O	1:C:647:ILE:HG12	2.21	0.40
1:A:387:ALA:O	1:A:388:PHE:C	2.65	0.40
1:A:581:VAL:O	1:A:582:ASP:C	2.63	0.40
1:A:704:LEU:O	1:A:707:ILE:HB	2.21	0.40
2:B:2:VAL:HG13	2:B:41:GLU:HA	2.03	0.40
1:A:421:ALA:O	1:A:425:LYS:HA	2.21	0.40
1:A:578:LYS:HD3	1:A:580:GLU:OE2	2.21	0.40
2:B:23:ARG:NH1	2:B:68:THR:CG2	2.83	0.40
2:B:212:TRP:HA	2:B:222:LEU:HD23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:422:LEU:HD12	1:C:422:LEU:HA	1.87	0.40
3:F:227:GLN:C	3:F:229:ARG:H	2.27	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	334/1273 (26%)	280 (84%)	43 (13%)	11 (3%)	3	21
1	C	336/1273 (26%)	293 (87%)	34 (10%)	9 (3%)	4	25
2	B	275/297 (93%)	241 (88%)	30 (11%)	4 (2%)	8	40
3	F	276/297 (93%)	214 (78%)	37 (13%)	25 (9%)	0	8
All	All	1221/3140 (39%)	1028 (84%)	144 (12%)	49 (4%)	4	18

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	497	ASN
2	B	131	LYS
1	C	715	ASN
3	F	76	ASP
3	F	100	ALA
3	F	131	LYS
1	A	388	PHE
1	A	425	LYS
1	A	518	LEU
2	B	135	THR
1	C	425	LYS
3	F	30	ASP
3	F	41	GLU

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Mol	Chain	Res	Type
3	F	133	ASN
3	F	241	GLY
3	F	254	PRO
3	F	256	VAL
3	F	273	GLY
1	A	520	SER
1	A	728	SER
2	B	190	ASP
1	C	439	ILE
1	C	552	LYS
1	C	728	SER
3	F	40	GLY
3	F	47	ASP
3	F	101	SER
3	F	145	ALA
3	F	240	GLN
3	F	291	PRO
1	A	439	ILE
1	A	498	PHE
1	A	561	ALA
2	B	202	GLY
1	C	407	PRO
3	F	46	ILE
3	F	218	LEU
3	F	267	ASN
3	F	274	GLY
1	A	548	ASN
1	A	653	PRO
1	C	520	SER
1	C	662	ASP
3	F	51	GLY
3	F	170	SER
3	F	187	TYR
3	F	21	GLY
3	F	287	GLY
1	C	494	ILE

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	302/1113 (27%)	294 (97%)	8 (3%)	40	62
1	C	304/1113 (27%)	291 (96%)	13 (4%)	26	47
2	B	237/252 (94%)	230 (97%)	7 (3%)	36	57
3	F	238/252 (94%)	215 (90%)	23 (10%)	8	24
All	All	1081/2730 (40%)	1030 (95%)	51 (5%)	25	45

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

Mol	Chain	Res	Type
1	A	430	LEU
1	A	509	ASN
1	A	537	MET
1	A	545	ASP
1	A	572	ILE
1	A	688	ILE
1	A	703	PHE
1	A	720	THR
2	B	50	THR
2	B	92	ILE
2	B	180	ASN
2	B	204	SER
2	B	225	VAL
2	B	238	ASN
2	B	242	PRO
1	C	381	SER
1	C	407	PRO
1	C	408	LYS
1	C	413	GLU
1	C	432	ASN
1	C	509	ASN
1	C	510	ILE
1	C	538	GLU
1	C	545	ASP
1	C	572	ILE
1	C	590	VAL
1	C	629	GLN
1	C	655	LEU
3	F	33	ILE
3	F	38	VAL

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Mol	Chain	Res	Type
3	F	43	HIS
3	F	46	ILE
3	F	66	PHE
3	F	81	ILE
3	F	82	TRP
3	F	122	ASP
3	F	129	GLU
3	F	132	GLU
3	F	133	ASN
3	F	141	ILE
3	F	148	VAL
3	F	180	ASN
3	F	199	THR
3	F	200	LEU
3	F	206	TRP
3	F	225	VAL
3	F	233	ILE
3	F	237	ASP
3	F	247	LEU
3	F	255	ASP
3	F	286	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	433	GLN
1	A	443	ASN
1	A	448	ASN
1	A	509	ASN
1	A	512	GLN
1	A	517	ASN
1	A	529	ASN
1	A	592	GLN
1	A	601	GLN
1	A	612	ASN
2	B	91	GLN
2	B	95	HIS
2	B	149	ASN
2	B	180	ASN
2	B	238	ASN
2	B	240	GLN
1	C	443	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	448	ASN
1	C	493	GLN
1	C	509	ASN
1	C	512	GLN
1	C	517	ASN
1	C	522	ASN
1	C	557	ASN
1	C	601	GLN
1	C	602	ASN
1	C	606	ASN
1	C	612	ASN
1	C	670	HIS
1	C	686	ASN
3	F	86	ASN
3	F	149	ASN
3	F	180	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 ⓘ

There are no chain breaks in this entry.

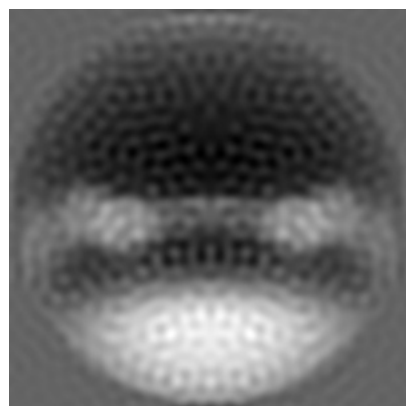
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11193. These allow visual inspection of the internal detail of the map and identification of artifacts.

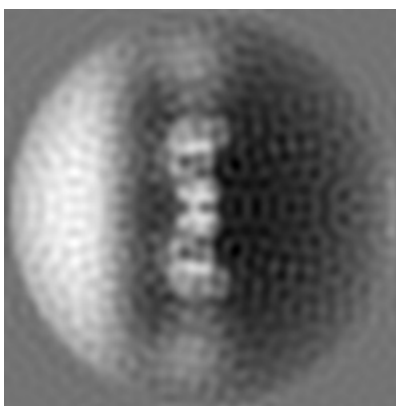
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

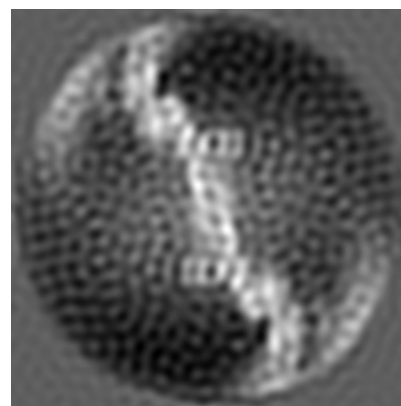
6.1.1 Primary map



X



Y

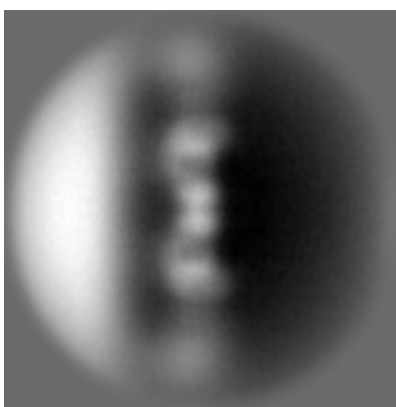


Z

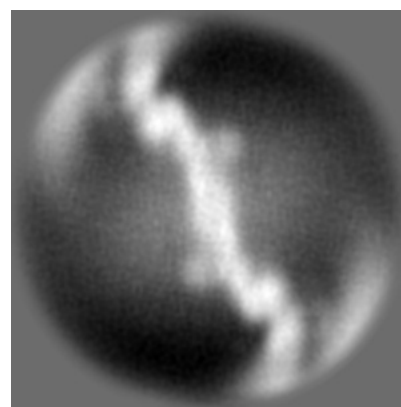
6.1.2 Raw map



X



Y

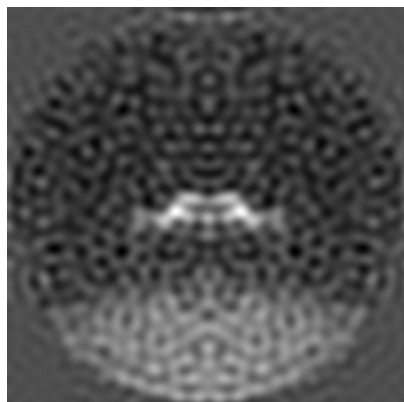


Z

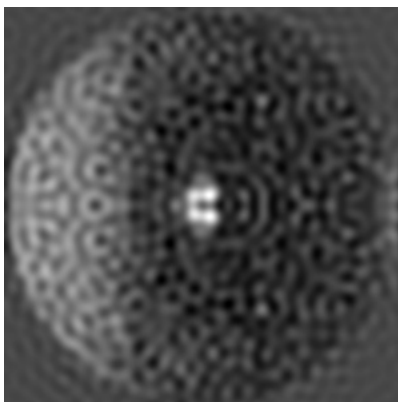
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

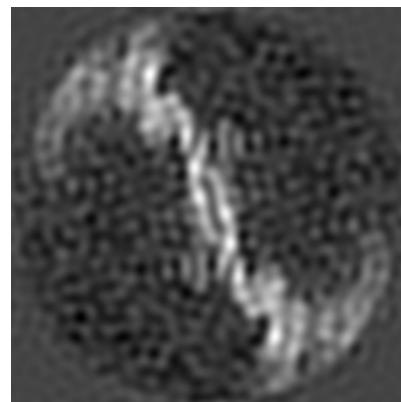
6.2.1 Primary map



X Index: 64

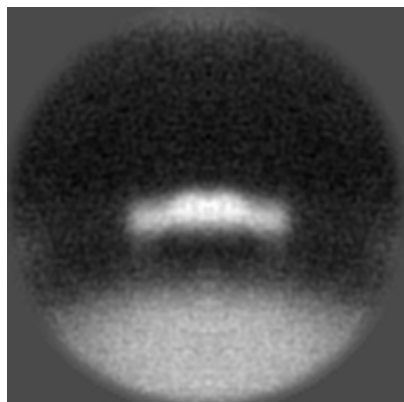


Y Index: 64

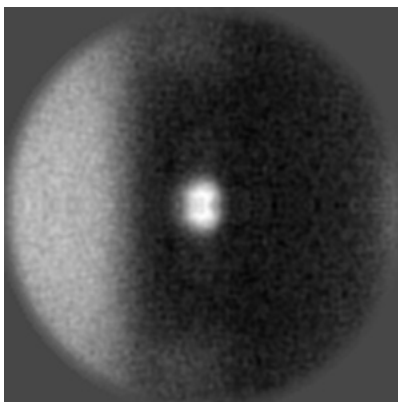


Z Index: 64

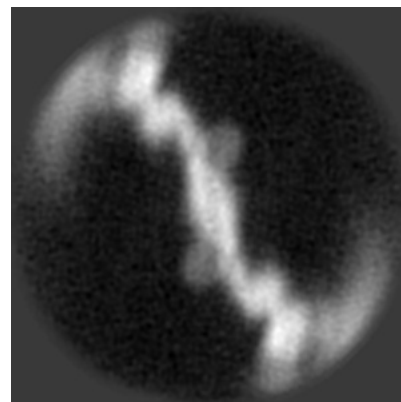
6.2.2 Raw map



X Index: 64



Y Index: 64

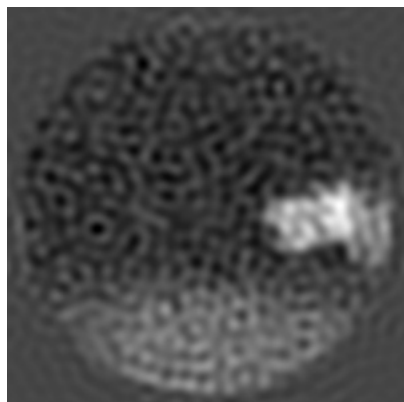


Z Index: 64

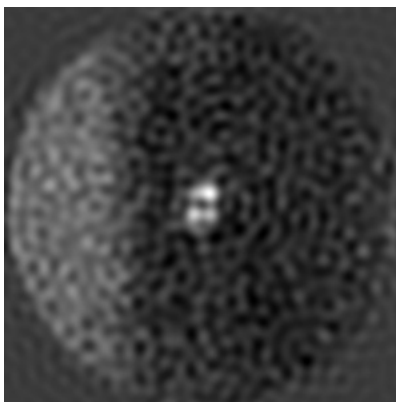
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

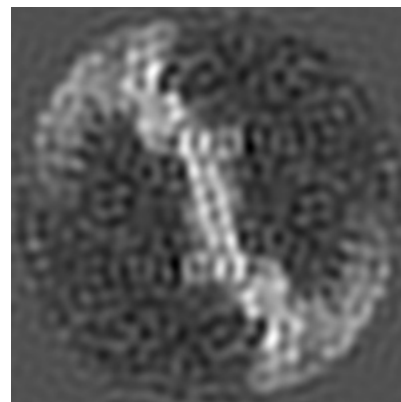
6.3.1 Primary map



X Index: 44

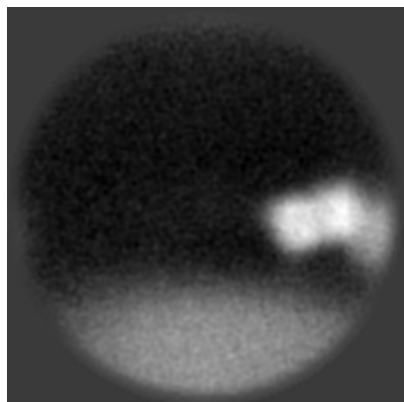


Y Index: 62

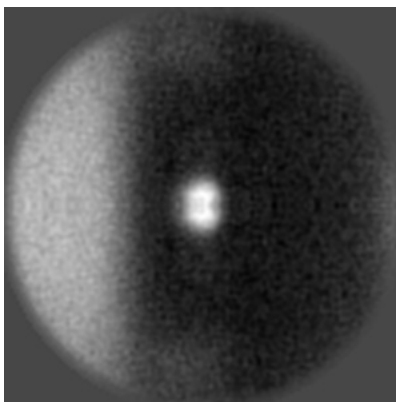


Z Index: 61

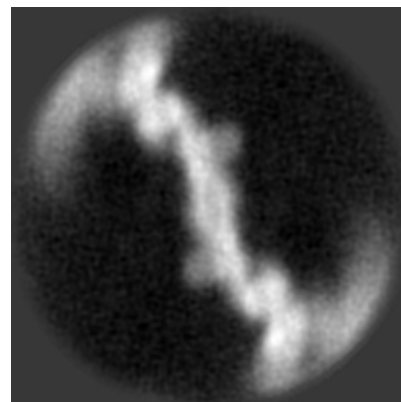
6.3.2 Raw map



X Index: 44



Y Index: 64

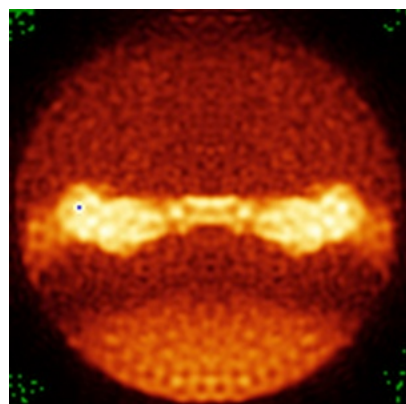


Z Index: 61

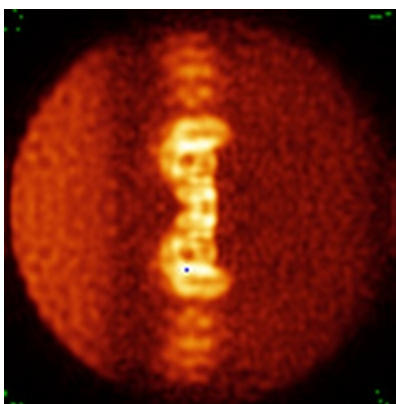
The images above show the largest variance slices of the map in three orthogonal directions.

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

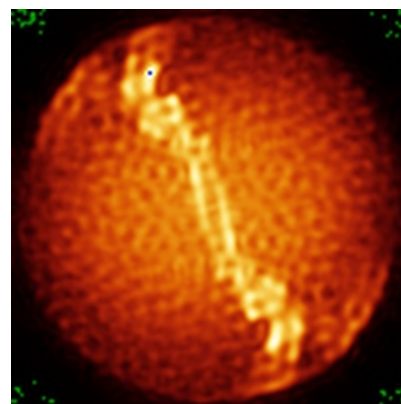
6.4.1 Primary map



X

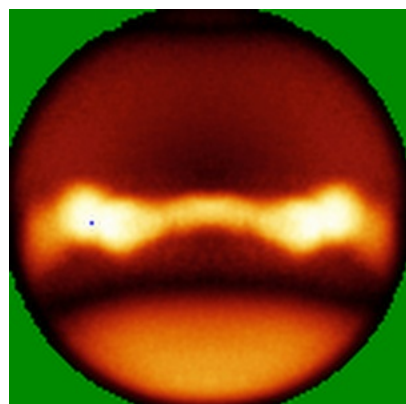


Y

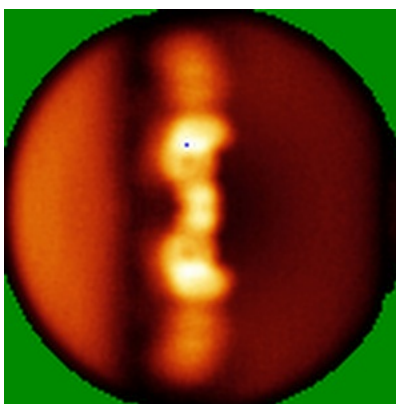


Z

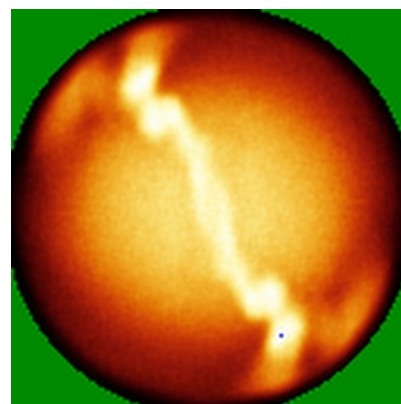
6.4.2 Raw map



X



Y

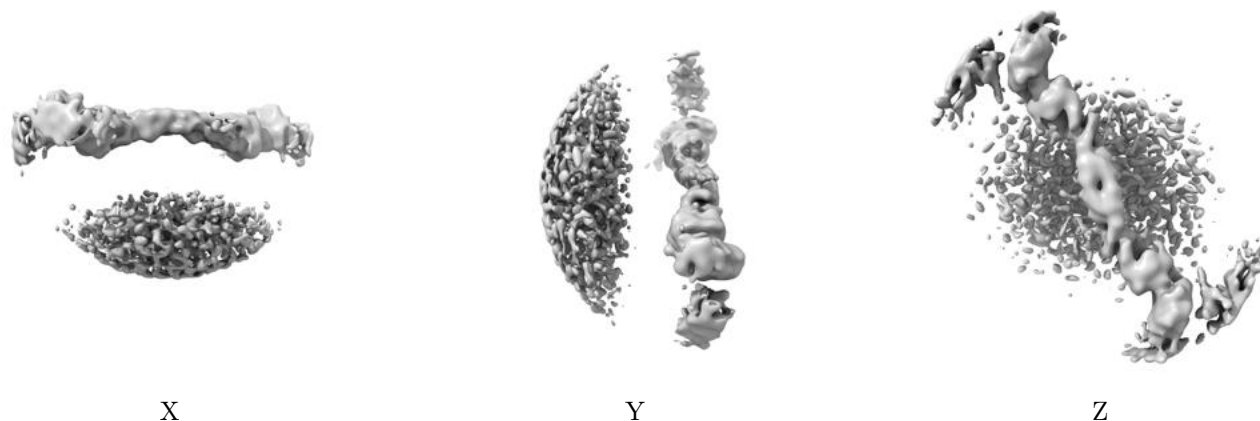


Z

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

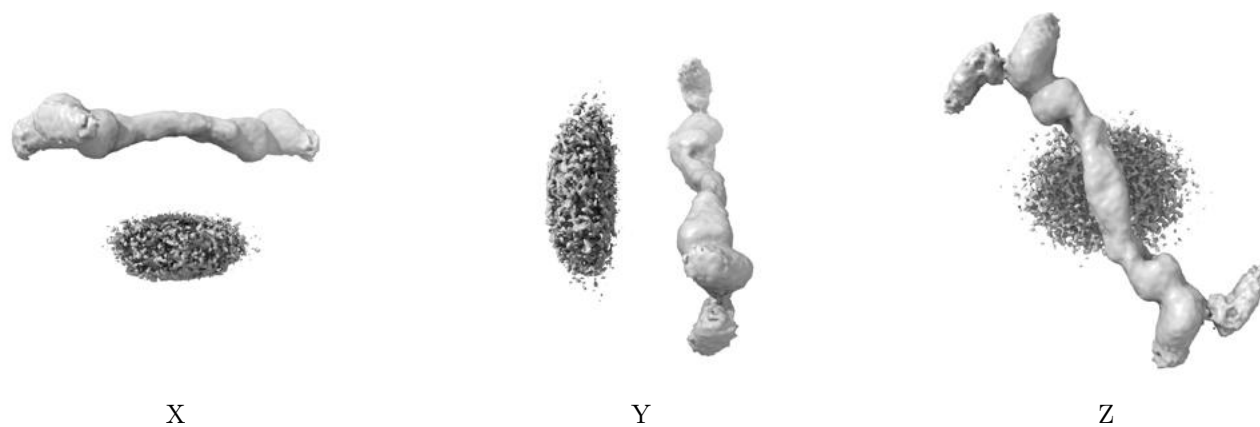
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

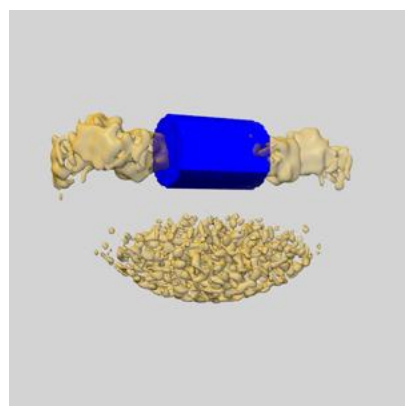
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

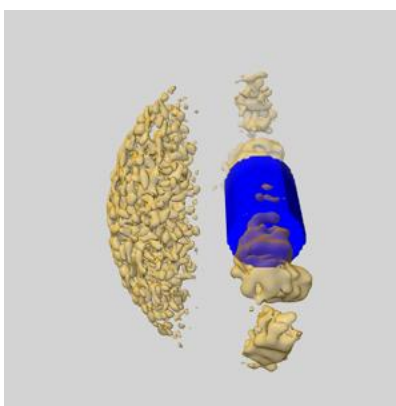
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

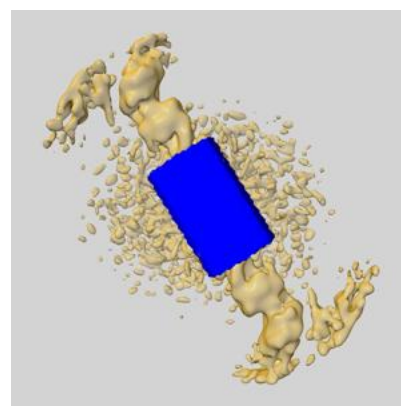
6.6.1 emd_11193_msk_1.map [i](#)



X



Y

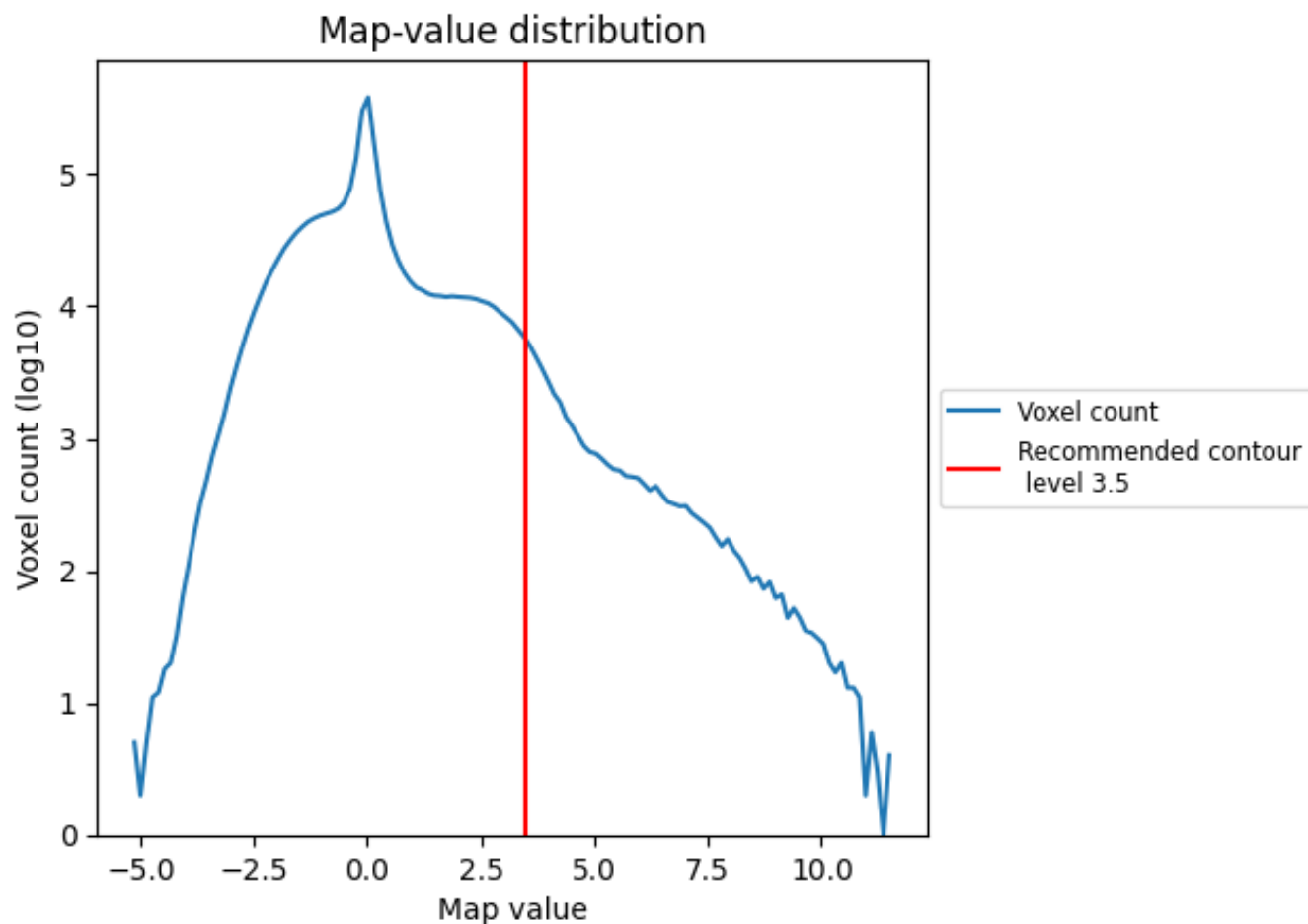


Z

7 Map analysis [i](#)

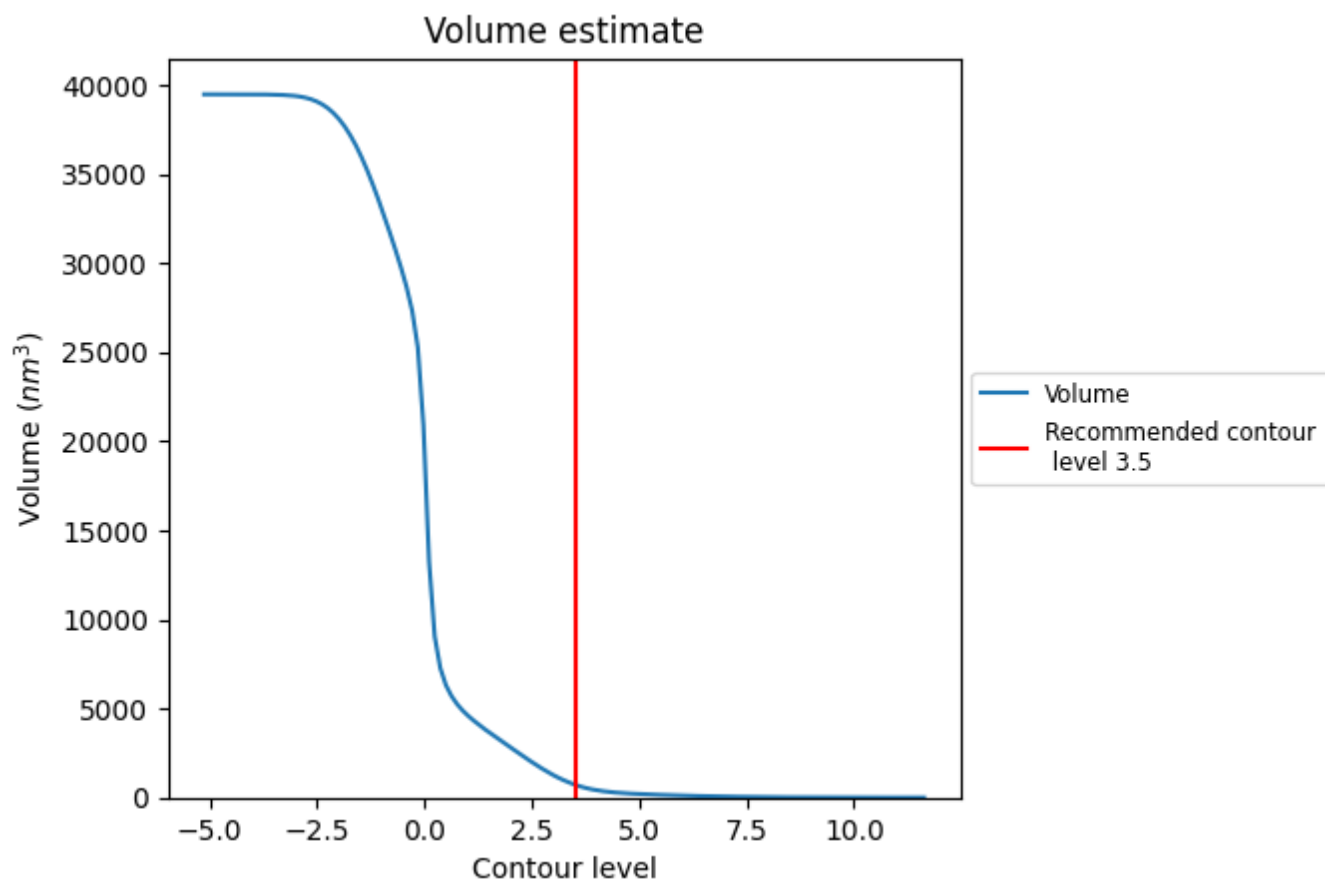
This section contains the results of statistical analysis of the map.

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.

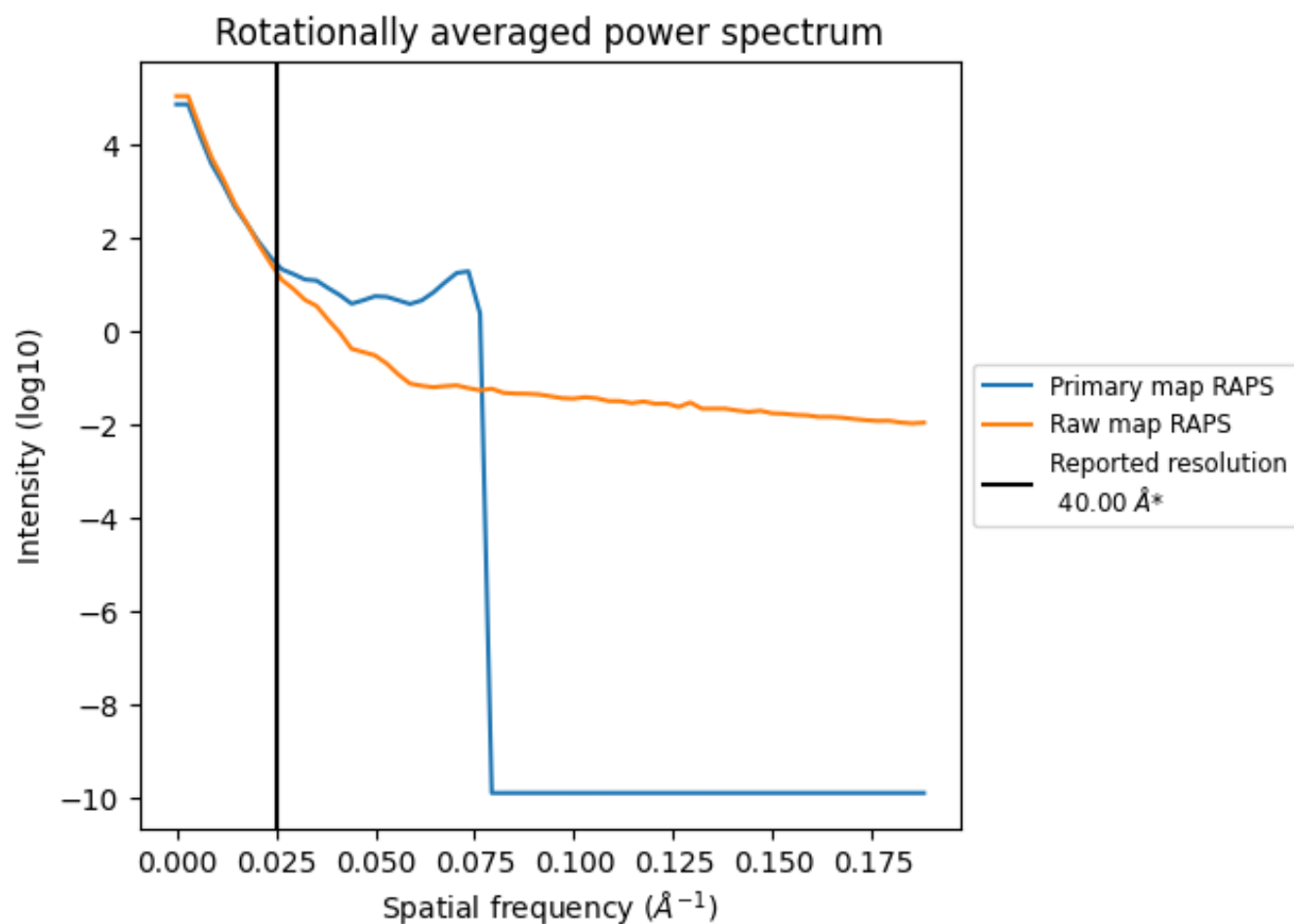
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 728 nm³; this corresponds to an approximate mass of 657 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

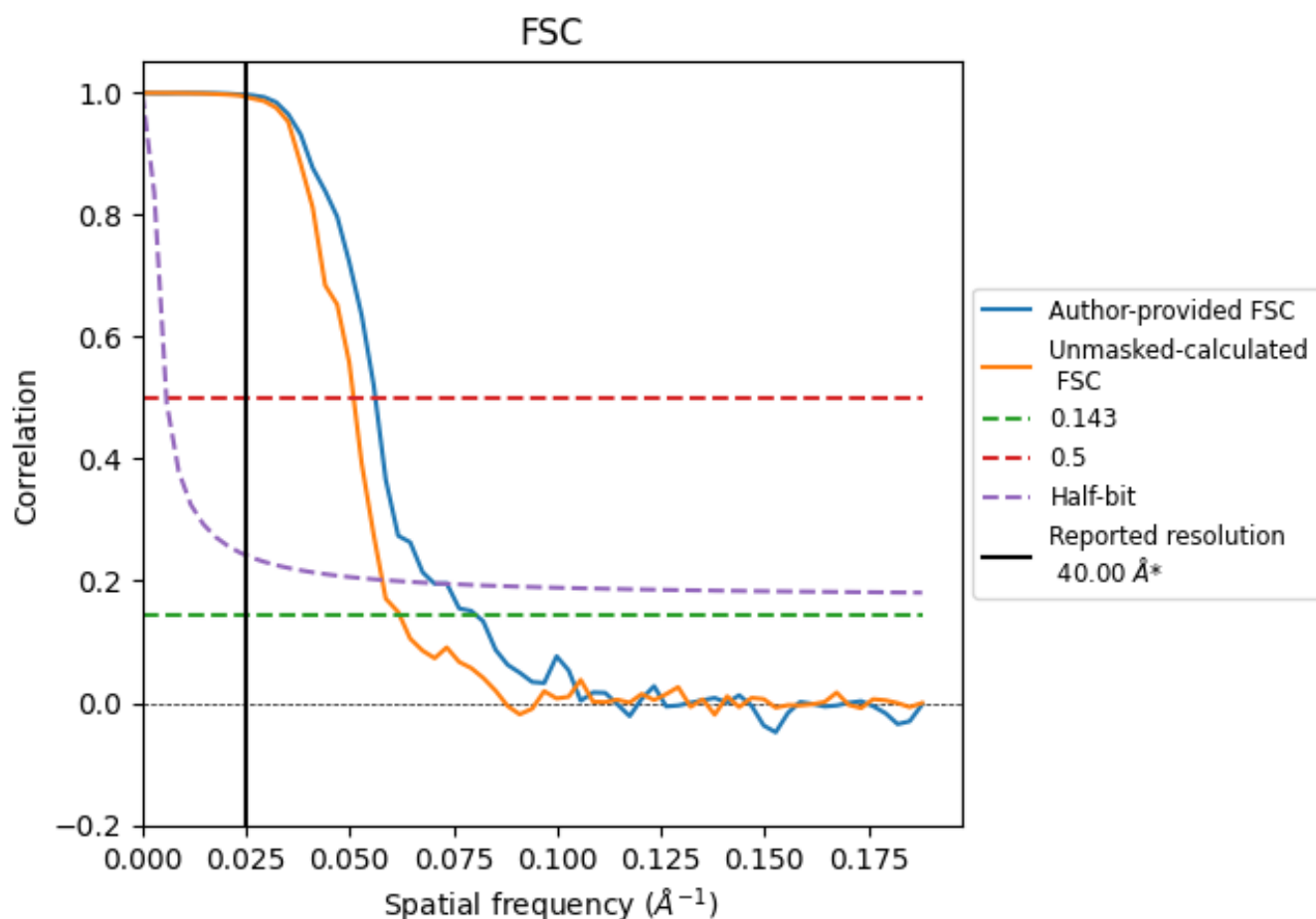


*Reported resolution corresponds to spatial frequency of 0.025 Å⁻¹

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.025 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

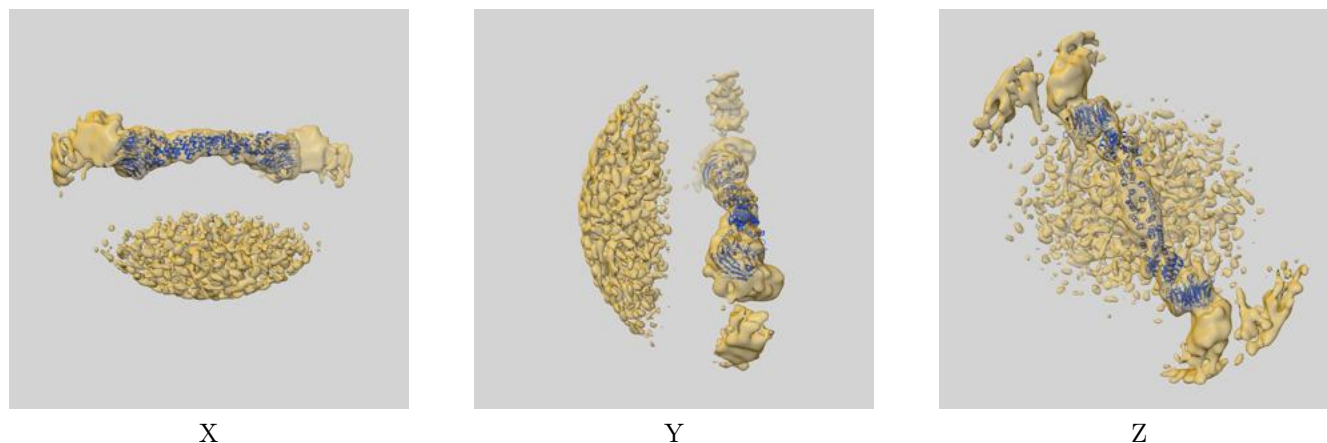
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	-	-	-
Author-provided FSC curve	12.41	17.79	13.61
Unmasked-calculated*	16.10	19.61	17.27

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

9 Map-model fit [i](#)

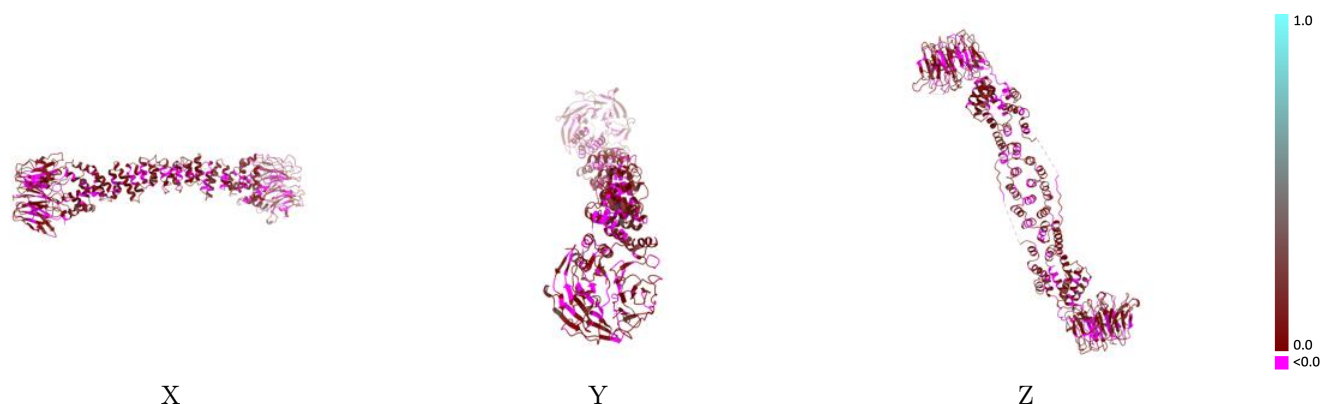
This section contains information regarding the fit between EMDB map EMD-11193 and PDB model 6ZG5. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



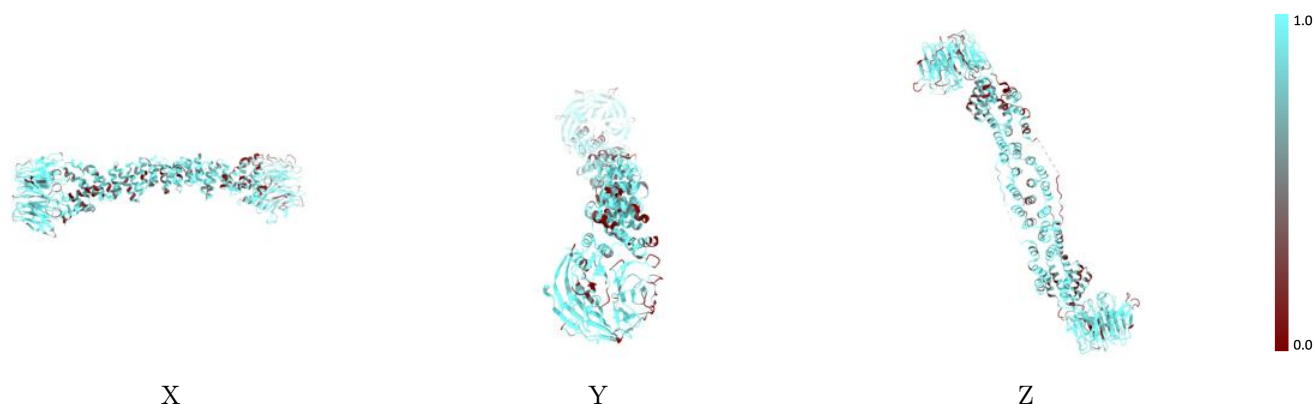
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



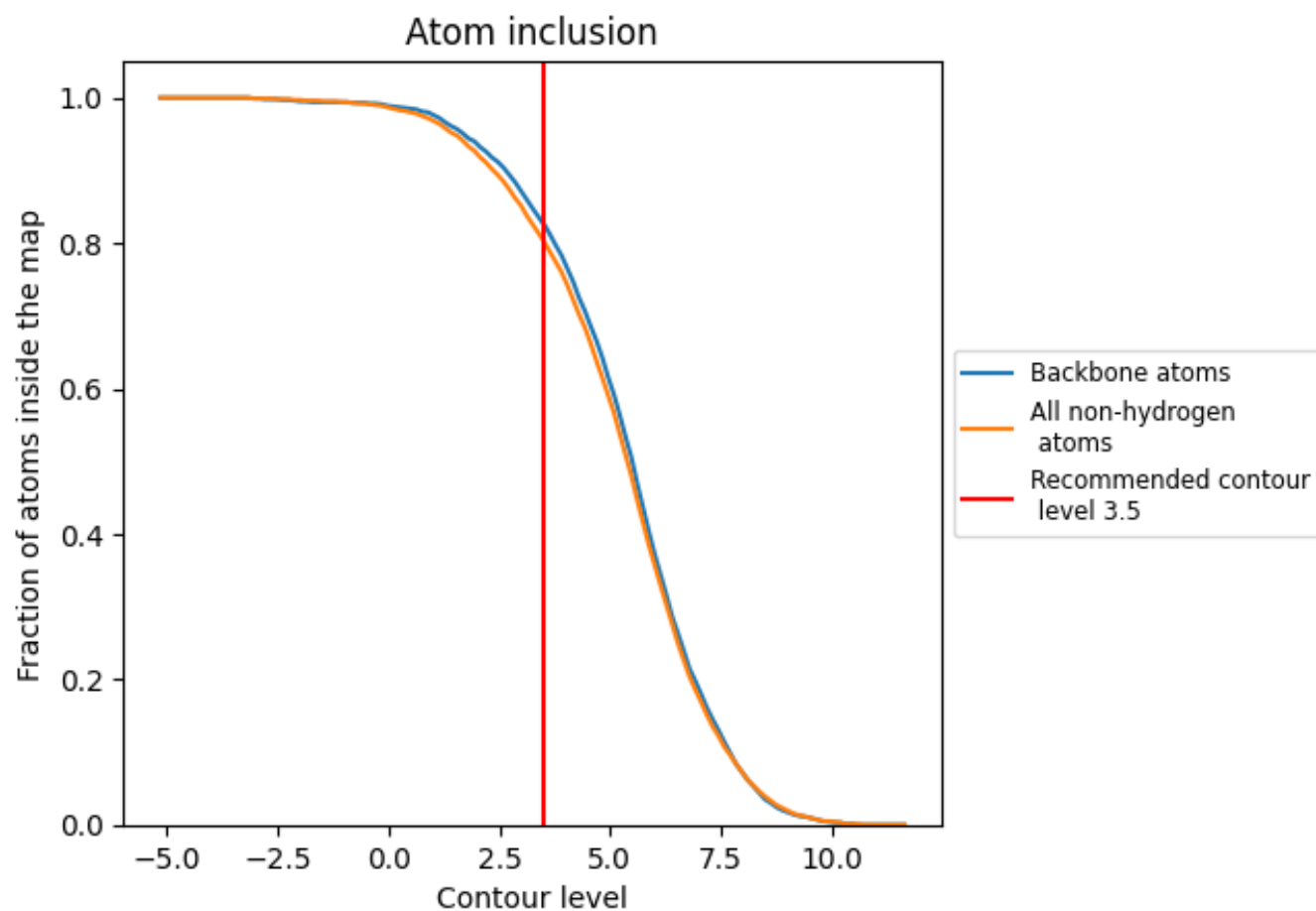
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 80% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8030	0.0670
A	0.8030	0.0800
B	0.8830	0.0700
C	0.7370	0.0600
F	0.8060	0.0590

