Full wwPDB EM Validation Report

Apr 23, 2024 – 08:37 am BST

PDB ID	:	7BLP
EMDB ID	:	EMD-12223
Title	:	Vps35/Vps29 arch of fungal membrane-assembled retromer:Grd19 complex
Authors	:	Leneva, N.; Kovtun, O.; Morado, D.R.; Briggs, J.A.G.; Owen, D.J.
Deposited on	:	2021-01-18
Resolution	:	9.50 Å(reported)

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

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

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

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

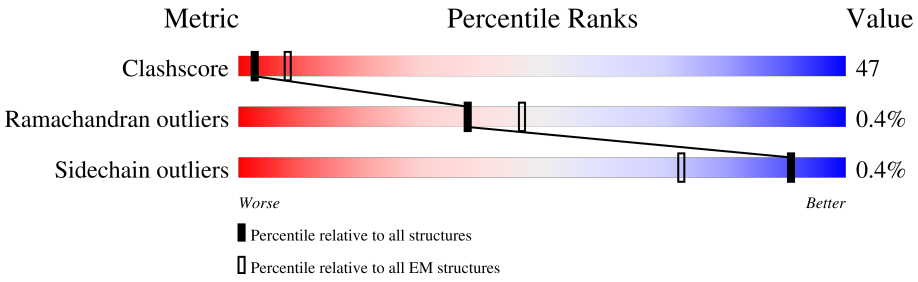
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 9.50 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	869	26% 29% 56% · 14%
1	C	869	27% 30% 54% · 14%
2	B	202	39% 30% 62% 7%
2	D	202	34% 23% 68% · 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14950 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 Vacuolar protein sorting-associated protein 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	748	Total	C	N	O	S	0	0
			6011	3804	1050	1126	31		
1	C	748	Total	C	N	O	S	0	0
			6011	3804	1050	1126	31		

- Molecule 2 is a protein called Vacuolar protein sorting-associated protein 29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	187	Total	C	N	O	S	0	0
			1464	946	238	271	9		
2	D	187	Total	C	N	O	S	0	0
			1464	946	238	271	9		

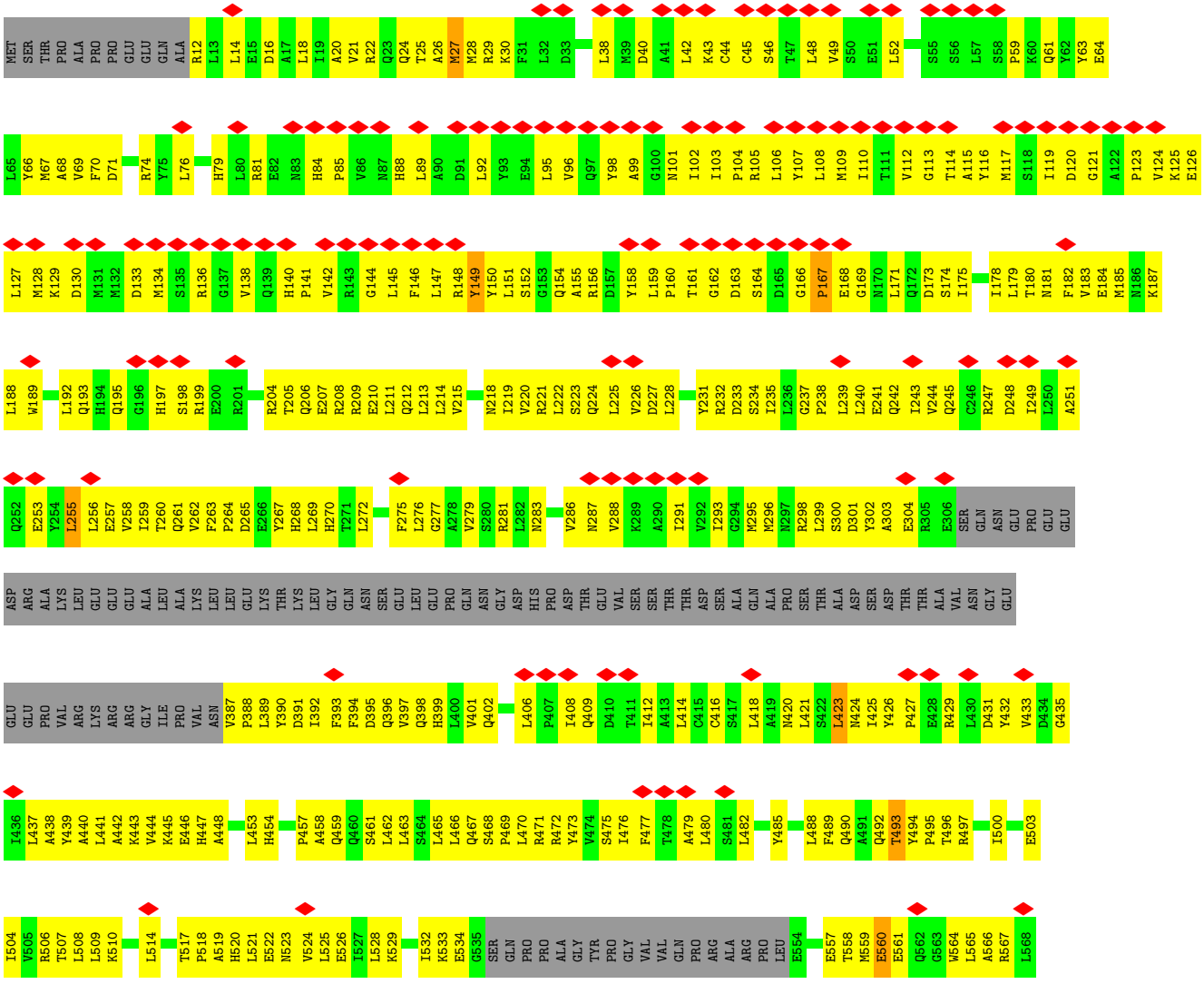
There are 2 discrepancies between the modelled and reference sequences:

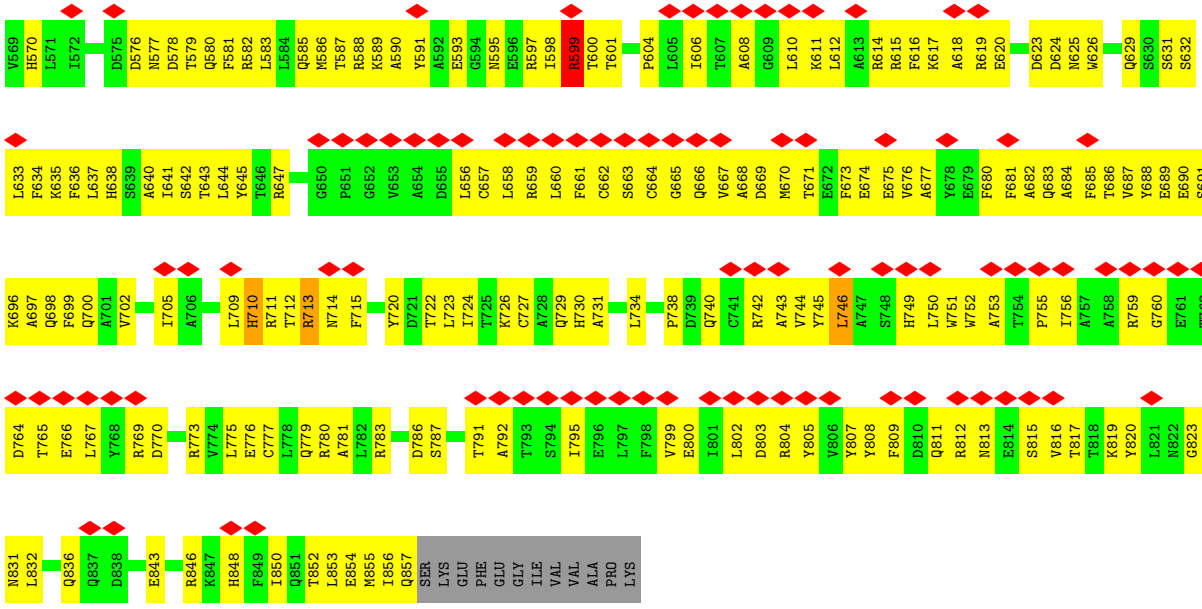
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	SER	-	expression tag	UNP G0RZB5
D	0	SER	-	expression tag	UNP G0RZB5

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.

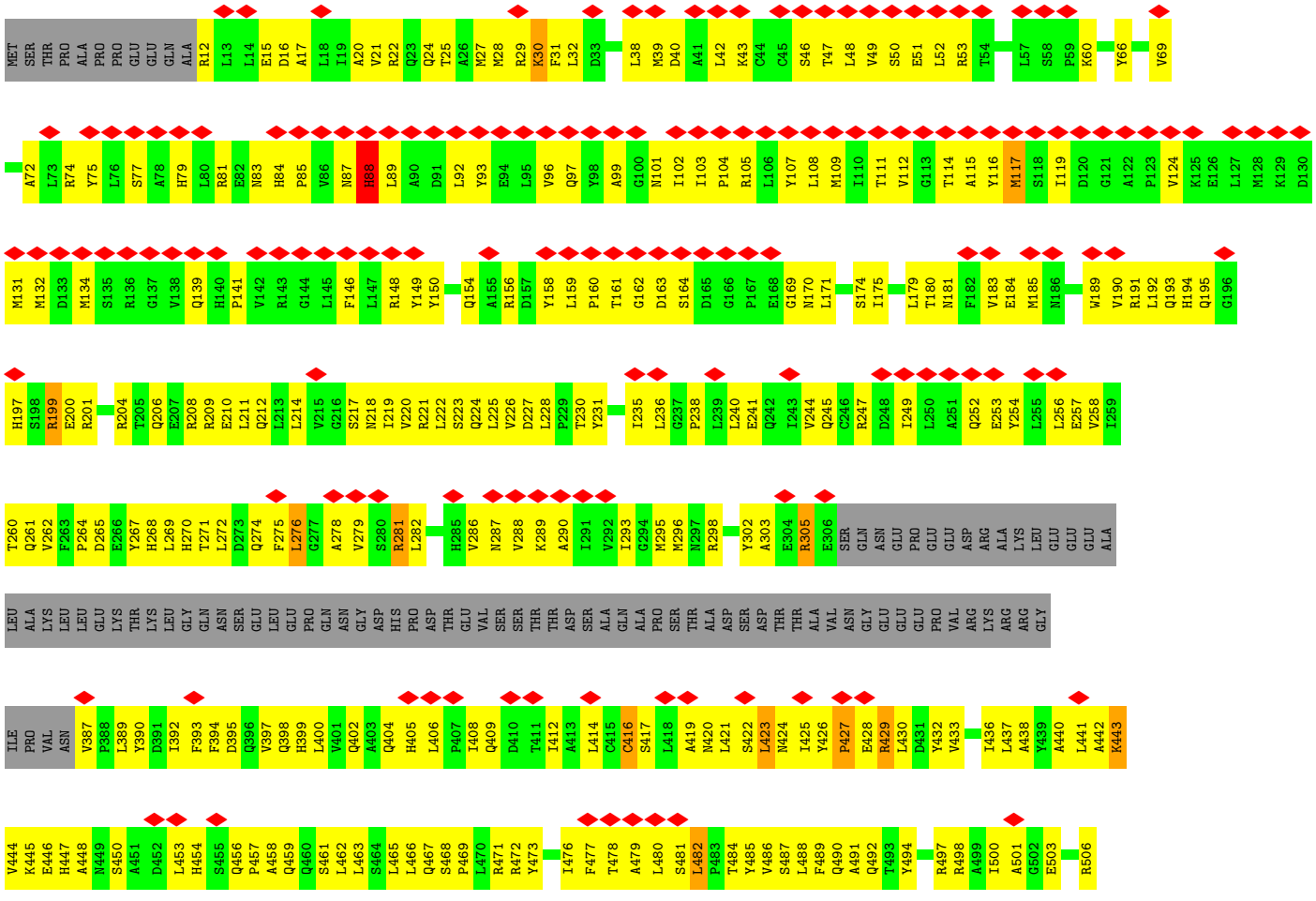
- Molecule 1: Vacuolar protein sorting-associated protein 35

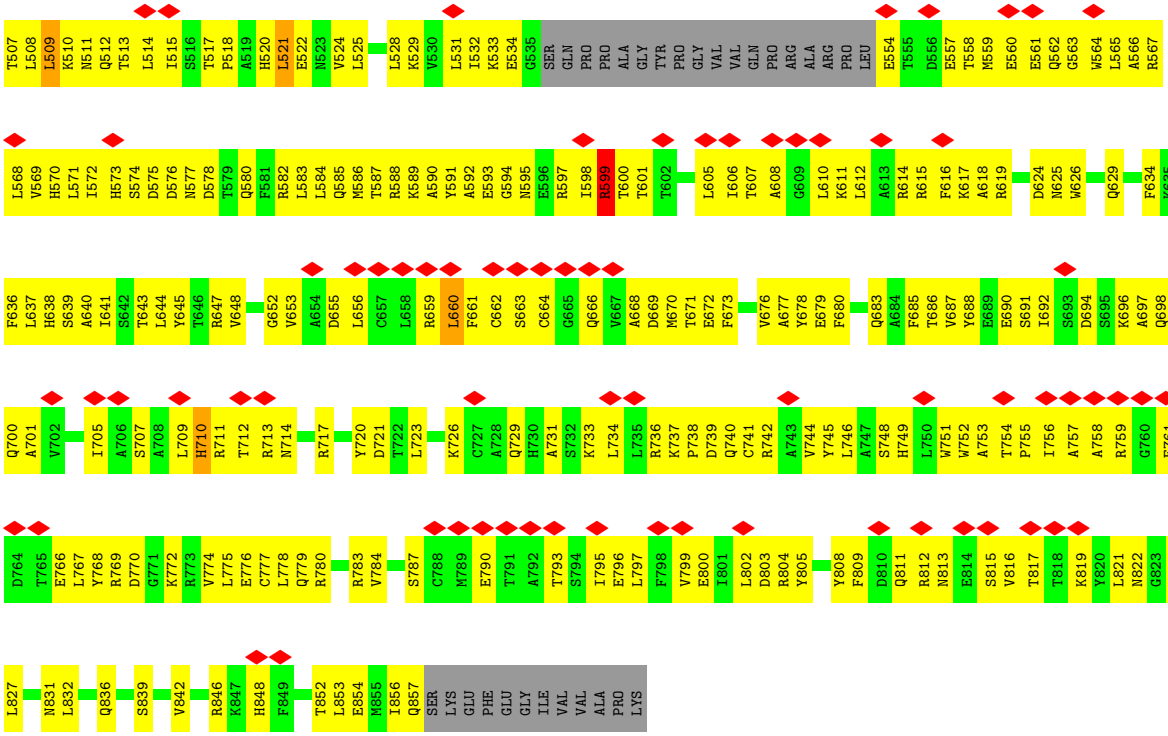




• Molecule 1: Vacuolar protein sorting-associated protein 35

Chain C:



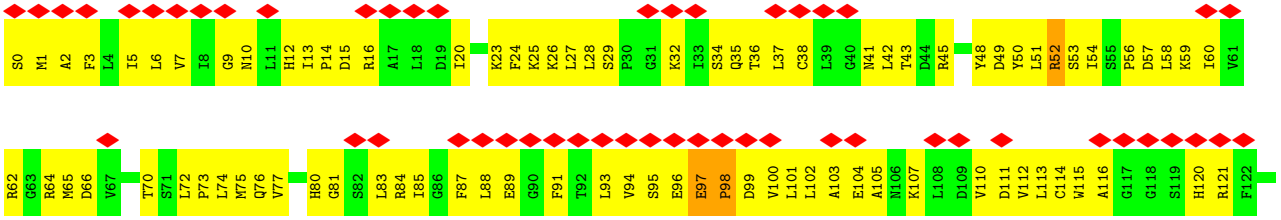


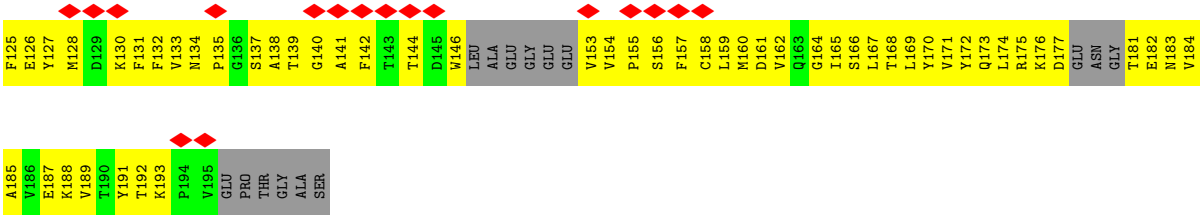
• Molecule 2: Vacuolar protein sorting-associated protein 29

Chain B:

• Molecule 2: Vacuolar protein sorting-associated protein 29

Chain D:




F125 E126 Y127 M128 D129 K130 F131 F132 V133 N134 P135 G136 S137 A138 T139 G140 A141 F142 T143 T144 D145 W146 LEU ALA GLU GLY GLU GLU V153 V154 P155 S156 F157 C158 L159 M160 D161 V162 Q163 G164 I165 S166 L167 T168 L169 Y170 V171 Y172 Q173 L174 R175 K176 D177 GLU ASN GLY T181 E182 N183 V184
A185 V186 E187 K188 V189 T190 Y191 T192 K193 P194 V195 GLU PRO THR GLY ALA SER

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	46633	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 ($e^-/Å^2$)	3	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	0.114	Depositor
Minimum map value	-0.097	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.024	Depositor
Map size (Å)	286.832, 286.832, 286.832	wwPDB
Map dimensions	104, 104, 104	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.758, 2.758, 2.758	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	0.42	1/6125 (0.0%)	0.75	9/8302 (0.1%)
1	C	0.42	1/6125 (0.0%)	0.77	10/8302 (0.1%)
2	B	0.33	0/1494	0.62	0/2027
2	D	0.37	0/1494	0.67	0/2027
All	All	0.41	2/15238 (0.0%)	0.74	19/20658 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	C	0	5
2	B	0	1
2	D	0	1
All	All	0	11

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	416	CYS	CB-SG	-5.90	1.72	1.81
1	A	149	TYR	CD2-CE2	-5.09	1.31	1.39

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	599	ARG	CD-NE-CZ	13.70	142.78	123.60
1	C	599	ARG	CD-NE-CZ	12.93	141.71	123.60
1	A	423	LEU	CA-CB-CG	-8.74	95.20	115.30
1	C	599	ARG	NE-CZ-NH1	-8.43	116.08	120.30
1	A	746	LEU	CB-CG-CD2	-7.90	97.57	111.00
1	A	27	MET	CA-CB-CG	7.40	125.89	113.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	599	ARG	NE-CZ-NH1	-7.30	116.65	120.30
1	C	423	LEU	CA-CB-CG	-7.05	99.09	115.30
1	C	276	LEU	CA-CB-CG	-6.07	101.34	115.30
1	A	149	TYR	CB-CG-CD2	-6.01	117.39	121.00
1	A	255	LEU	CA-CB-CG	-5.59	102.44	115.30
1	C	482	LEU	CA-CB-CG	5.57	128.12	115.30
1	A	167	PRO	CA-N-CD	-5.56	103.71	111.50
1	C	660	LEU	CB-CG-CD2	-5.36	101.89	111.00
1	C	660	LEU	CB-CG-CD1	5.32	120.05	111.00
1	A	658	LEU	CA-CB-CG	5.20	127.25	115.30
1	C	521	LEU	CA-CB-CG	-5.08	103.61	115.30
1	C	509	LEU	CA-CB-CG	5.04	126.88	115.30
1	C	117	MET	CB-CG-SD	5.02	127.45	112.40

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	493	THR	Peptide
1	A	560	GLU	Peptide
1	A	599	ARG	Sidechain
1	A	88	HIS	Peptide
2	B	1	MET	Peptide
1	C	305	ARG	Peptide
1	C	427	PRO	Peptide
1	C	429	ARG	Peptide
1	C	599	ARG	Sidechain
1	C	88	HIS	Peptide
2	D	96	GLU	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	6011	0	5999	571	0
1	C	6011	0	5999	568	0
2	B	1464	0	1484	125	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1464	0	1484	145	0
All	All	14950	0	14966	1393	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 47.

All (1393) 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)
2:B:1:MET:HG3	2:B:162:VAL:H	1.22	1.02
1:A:463:LEU:HD13	1:A:500:ILE:HG12	1.42	0.97
1:C:749:HIS:HB3	1:C:755:PRO:HD3	1.47	0.95
1:C:737:LYS:NZ	1:C:787:SER:OG	1.99	0.94
1:A:261:GLN:HG3	1:A:298:ARG:HH21	1.33	0.92
1:C:221:ARG:HD2	1:C:224:GLN:HE21	1.35	0.91
1:C:753:ALA:HA	1:C:767:LEU:HB2	1.52	0.90
1:C:161:THR:H	1:C:164:SER:HB3	1.36	0.89
1:C:585:GLN:OE1	1:C:589:LYS:NZ	2.05	0.89
1:C:648:VAL:HA	1:C:653:VAL:HG11	1.53	0.89
1:C:688:TYR:HA	1:C:692:ILE:HD13	1.54	0.89
1:A:606:ILE:HG21	1:A:660:LEU:HD22	1.55	0.88
1:A:566:ALA:HB2	2:B:18:LEU:HG	1.55	0.88
1:C:737:LYS:HE2	1:C:784:VAL:HG13	1.53	0.88
1:C:156:ARG:HH22	1:C:220:VAL:HG23	1.36	0.87
1:C:89:LEU:HD23	1:C:92:LEU:HD13	1.55	0.87
1:A:566:ALA:O	1:A:570:HIS:ND1	2.06	0.87
1:C:742:ARG:HA	1:C:745:TYR:CE1	2.09	0.87
1:A:473:TYR:HE2	1:A:479:ALA:HB2	1.37	0.87
1:C:423:LEU:HB3	1:C:472:ARG:HG2	1.56	0.86
1:C:517:THR:OG1	1:C:520:HIS:ND1	2.09	0.85
1:C:508:LEU:O	1:C:567:ARG:NH1	2.08	0.85
1:A:24:GLN:HA	1:A:27:MET:SD	2.17	0.84
1:A:18:LEU:HD22	1:A:22:ARG:HH22	1.43	0.84
1:A:742:ARG:HA	1:A:745:TYR:CE1	2.12	0.84
1:A:753:ALA:HA	1:A:767:LEU:HB3	1.59	0.84
1:C:99:ALA:O	1:C:105:ARG:NH2	2.11	0.84
1:C:506:ARG:HD2	1:C:557:GLU:HG2	1.60	0.84
1:A:490:GLN:O	1:A:497:ARG:NH1	2.11	0.84
1:A:494:TYR:HB2	1:A:497:ARG:HH21	1.42	0.83
1:A:682:ALA:HA	1:A:685:PHE:CD2	2.14	0.82
2:D:26:LYS:O	2:D:32:LYS:NZ	2.12	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:498:ARG:NH2	1:C:531:LEU:O	2.12	0.82
1:A:228:LEU:HD13	1:A:267:TYR:HA	1.60	0.82
1:C:74:ARG:NH1	1:C:154:GLN:OE1	2.12	0.82
2:D:36:THR:HG21	2:D:51:LEU:HD11	1.62	0.82
2:B:20:ILE:O	2:B:25:LYS:NZ	2.12	0.82
1:A:522:GLU:OE2	1:A:523:ASN:ND2	2.13	0.82
1:A:666:GLN:OE1	1:A:711:ARG:NH1	2.13	0.82
1:A:427:PRO:HG3	1:A:472:ARG:HE	1.43	0.81
1:A:724:ILE:HD12	1:A:750:LEU:HB3	1.63	0.81
1:A:398:GLN:O	1:A:402:GLN:NE2	2.14	0.81
1:C:399:HIS:O	1:C:402:GLN:NE2	2.14	0.80
1:C:588:ARG:HE	1:C:640:ALA:HB2	1.46	0.80
1:A:532:ILE:HB	1:A:593:GLU:HG3	1.63	0.80
1:C:395:ASP:O	1:C:399:HIS:ND1	2.11	0.80
1:A:683:GLN:O	1:A:686:THR:OG1	1.99	0.80
1:A:805:TYR:HD1	1:A:816:VAL:HG13	1.47	0.80
1:C:238:PRO:O	1:C:241:GLU:HG2	1.81	0.80
1:C:509:LEU:HA	1:C:567:ARG:NH1	1.96	0.80
1:A:662:CYS:SG	1:A:711:ARG:NE	2.55	0.79
1:A:585:GLN:HG3	1:A:589:LYS:HZ3	1.47	0.79
1:A:161:THR:HG23	1:A:163:ASP:H	1.48	0.79
2:B:36:THR:HG21	2:B:51:LEU:HD11	1.65	0.79
2:D:7:VAL:HB	2:D:158:CYS:HB2	1.64	0.79
1:A:751:TRP:HB3	1:A:770:ASP:HB2	1.65	0.79
1:C:607:THR:HA	1:C:610:LEU:HG	1.65	0.79
1:A:641:ILE:O	1:A:644:LEU:HG	1.83	0.78
1:A:779:GLN:OE1	1:A:805:TYR:OH	2.01	0.78
1:C:577:ASN:HB3	1:C:615:ARG:HG3	1.65	0.78
1:C:302:TYR:HA	1:C:305:ARG:HH22	1.47	0.78
2:D:57:ASP:OD1	2:D:59:LYS:NZ	2.16	0.78
2:B:169:LEU:N	2:B:189:VAL:O	2.15	0.78
1:C:400:LEU:O	1:C:404:GLN:N	2.17	0.78
1:A:105:ARG:HG2	1:A:109:MET:HE1	1.64	0.77
1:A:760:GLY:H	1:A:763:GLU:HB2	1.47	0.77
1:C:193:GLN:O	1:C:201:ARG:NH2	2.11	0.77
1:C:598:ILE:HD11	1:C:647:ARG:HD2	1.67	0.77
1:A:506:ARG:HH12	1:A:560:GLU:HA	1.49	0.77
1:A:803:ASP:OD2	1:A:848:HIS:NE2	2.18	0.77
2:D:165:ILE:HB	2:D:193:LYS:HB3	1.66	0.77
1:C:423:LEU:HA	1:C:427:PRO:HG3	1.67	0.77
1:A:727:CYS:HA	1:A:730:HIS:NE2	2.00	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:HIS:O	1:A:204:ARG:NH1	2.16	0.77
1:A:780:ARG:HB2	1:A:783:ARG:HH11	1.50	0.77
1:C:720:TYR:OH	1:C:757:ALA:O	2.03	0.77
2:B:63:GLY:HA2	2:B:89:GLU:HG3	1.66	0.76
1:C:734:LEU:HD21	1:C:740:GLN:HA	1.66	0.76
2:D:23:LYS:HA	2:D:26:LYS:HZ2	1.50	0.76
2:D:5:ILE:HB	2:D:160:MET:HB2	1.66	0.76
2:D:10:ASN:O	2:D:139:THR:OG1	2.03	0.76
1:A:509:LEU:O	1:A:567:ARG:NH1	2.18	0.76
1:A:561:GLU:HB3	1:A:565:LEU:HD23	1.68	0.75
2:D:102:LEU:HD13	2:D:128:MET:HG3	1.68	0.75
1:C:40:ASP:HA	1:C:43:LYS:HE2	1.69	0.75
1:C:421:LEU:O	1:C:425:ILE:HG12	1.87	0.75
1:C:529:LYS:HD3	1:C:532:ILE:HD11	1.69	0.75
1:C:617:LYS:NZ	1:C:670:MET:O	2.19	0.75
1:C:758:ALA:O	1:C:768:TYR:N	2.20	0.75
1:C:258:VAL:HA	1:C:261:GLN:HE21	1.49	0.75
1:A:467:GLN:NE2	1:A:503:GLU:OE2	2.20	0.75
2:B:3:PHE:HE1	2:B:35:GLN:HB2	1.52	0.74
1:A:303:ALA:HB2	1:A:421:LEU:HD12	1.69	0.74
1:A:753:ALA:HB2	1:A:769:ARG:HG3	1.69	0.74
1:C:729:GLN:HE22	1:C:733:LYS:HD3	1.52	0.74
2:D:10:ASN:HD21	2:D:120:HIS:CD2	2.06	0.74
1:C:558:THR:HB	1:C:563:GLY:H	1.50	0.74
2:D:23:LYS:HA	2:D:26:LYS:NZ	2.02	0.74
1:C:52:LEU:HD11	1:C:69:VAL:HG21	1.69	0.73
1:C:228:LEU:HD13	1:C:267:TYR:HA	1.70	0.73
1:A:489:PHE:HA	1:A:492:GLN:HG2	1.71	0.73
1:A:727:CYS:HA	1:A:730:HIS:CD2	2.24	0.73
1:C:53:ARG:HH22	1:C:103:ILE:H	1.34	0.73
1:C:595:ASN:HA	1:C:647:ARG:HD3	1.70	0.73
1:C:197:HIS:O	1:C:204:ARG:NH2	2.21	0.73
1:C:302:TYR:HA	1:C:305:ARG:NH2	2.03	0.73
1:C:711:ARG:NH2	2:D:144:THR:OG1	2.22	0.73
1:A:182:PHE:HD1	1:A:185:MET:HE3	1.53	0.73
1:A:599:ARG:HG2	1:A:600:THR:HG23	1.70	0.73
1:A:800:GLU:O	1:A:804:ARG:NH1	2.21	0.72
2:B:52:ARG:NH2	2:B:55:SER:O	2.22	0.72
1:C:592:ALA:N	1:C:593:GLU:OE2	2.23	0.72
1:A:473:TYR:CE2	1:A:479:ALA:HB2	2.23	0.72
1:A:480:LEU:HD21	1:A:520:HIS:HA	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:854:GLU:O	1:C:857:GLN:NE2	2.22	0.72
1:C:171:LEU:HD22	1:C:226:VAL:HG12	1.70	0.72
1:C:160:PRO:HB2	1:C:169:GLY:HA3	1.71	0.72
2:D:0:SER:N	2:D:161:ASP:OD2	2.23	0.72
1:C:139:GLN:OE1	1:C:191:ARG:NH1	2.23	0.71
1:C:736:ARG:O	1:C:740:GLN:N	2.23	0.71
1:A:303:ALA:HB1	1:A:424:ASN:HB2	1.71	0.71
2:D:97:GLU:HB2	2:D:98:PRO:HD3	1.71	0.71
1:C:634:PHE:HA	1:C:637:LEU:HG	1.70	0.71
1:C:532:ILE:O	1:C:597:ARG:NH2	2.22	0.71
1:C:751:TRP:HB3	1:C:770:ASP:HB2	1.71	0.71
1:A:74:ARG:NH1	1:A:154:GLN:OE1	2.23	0.71
1:A:426:TYR:HB3	1:A:429:ARG:HB2	1.73	0.71
1:C:402:GLN:O	1:C:405:HIS:NE2	2.23	0.71
1:C:561:GLU:O	1:C:565:LEU:N	2.20	0.70
1:C:717:ARG:HD3	1:C:761:GLU:H	1.55	0.70
1:A:770:ASP:OD2	1:A:773:ARG:NH2	2.23	0.70
1:C:575:ASP:O	1:C:580:GLN:NE2	2.23	0.70
1:C:578:ASP:OD2	1:C:582:ARG:NH2	2.21	0.70
2:D:62:ARG:NE	2:D:72:LEU:O	2.17	0.70
2:D:35:GLN:NE2	2:D:57:ASP:OD2	2.23	0.70
2:B:98:PRO:HB3	2:B:127:TYR:HE2	1.55	0.70
1:A:40:ASP:HA	1:A:43:LYS:HG2	1.74	0.70
2:D:88:LEU:O	2:D:115:TRP:HA	1.91	0.70
1:A:560:GLU:HG3	1:A:564:TRP:CE2	2.26	0.70
1:C:652:GLY:HA2	1:C:655:ASP:HB2	1.72	0.70
2:B:8:ILE:HD12	2:B:11:LEU:HD21	1.72	0.70
2:B:161:ASP:N	2:B:168:THR:O	2.23	0.70
1:A:667:VAL:HA	1:A:670:MET:HG3	1.74	0.69
1:C:195:GLN:O	1:C:204:ARG:HD3	1.91	0.69
1:C:32:LEU:HD22	1:C:79:HIS:CG	2.28	0.69
1:A:525:LEU:HD23	1:A:528:LEU:HD12	1.74	0.69
1:C:573:HIS:CE1	1:C:611:LYS:HE3	2.27	0.69
1:C:561:GLU:HB3	1:C:564:TRP:HB3	1.74	0.69
1:A:424:ASN:OD1	1:A:471:ARG:NH2	2.15	0.69
1:A:585:GLN:HG3	1:A:589:LYS:NZ	2.08	0.69
1:C:244:VAL:HG12	1:C:281:ARG:HE	1.57	0.69
1:A:517:THR:O	1:A:521:LEU:N	2.20	0.69
1:A:559:MET:HB3	1:A:560:GLU:HB3	1.75	0.68
1:A:641:ILE:HG22	1:A:645:TYR:CE2	2.28	0.68
1:C:467:GLN:NE2	1:C:503:GLU:OE2	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:631:SER:HA	1:A:673:PHE:CE2	2.27	0.68
2:D:49:ASP:O	2:D:52:ARG:HD3	1.92	0.68
1:A:152:SER:HA	1:A:156:ARG:HB2	1.74	0.68
2:D:169:LEU:N	2:D:189:VAL:O	2.22	0.68
1:C:25:THR:HA	1:C:28:MET:HG2	1.75	0.68
1:C:754:THR:HA	1:C:767:LEU:HD13	1.75	0.68
1:A:713:ARG:HB2	1:A:760:GLY:HA2	1.76	0.68
1:C:489:PHE:HE2	1:C:501:ALA:HB2	1.58	0.68
1:C:436:ILE:O	1:C:441:LEU:N	2.27	0.67
1:C:492:GLN:HB2	1:C:497:ARG:HG3	1.75	0.67
2:D:173:GLN:OE1	2:D:175:ARG:NH2	2.22	0.67
2:B:112:VAL:HG21	2:B:167:LEU:HD13	1.76	0.67
1:C:490:GLN:N	1:C:490:GLN:OE1	2.25	0.67
1:A:615:ARG:HG3	1:A:619:ARG:HH22	1.59	0.67
1:A:777:CYS:SG	1:A:780:ARG:NH2	2.68	0.67
1:C:236:LEU:HG	1:C:240:LEU:HG	1.76	0.67
1:A:46:SER:HA	1:A:104:PRO:HB3	1.76	0.67
2:B:129:ASP:HB3	2:B:194:PRO:HG3	1.77	0.67
1:C:717:ARG:NH2	1:C:762:THR:OG1	2.27	0.67
1:A:720:TYR:HA	1:A:723:LEU:HD12	1.77	0.67
1:C:723:LEU:HA	1:C:726:LYS:HG2	1.77	0.67
1:A:52:LEU:HD11	1:A:69:VAL:HG21	1.77	0.66
1:A:387:VAL:O	1:A:389:LEU:N	2.28	0.66
1:C:652:GLY:O	1:C:656:LEU:N	2.22	0.66
2:B:10:ASN:HB2	2:B:137:SER:HA	1.77	0.66
1:C:796:GLU:HG3	1:C:800:GLU:OE1	1.95	0.66
1:C:513:THR:H	1:C:567:ARG:NH2	1.93	0.66
1:A:561:GLU:HA	1:A:564:TRP:HB3	1.77	0.66
1:C:162:GLY:H	1:C:171:LEU:HD23	1.60	0.66
1:A:454:HIS:NE2	1:A:493:THR:OG1	2.28	0.66
1:C:387:VAL:O	1:C:389:LEU:N	2.29	0.66
1:C:507:THR:O	1:C:511:ASN:ND2	2.29	0.66
1:A:390:TYR:O	1:A:394:PHE:CB	2.44	0.66
1:C:805:TYR:HB3	1:C:821:LEU:HD11	1.78	0.66
1:A:506:ARG:NH1	1:A:559:MET:HG3	2.10	0.66
1:A:272:LEU:HA	1:A:275:PHE:HD1	1.59	0.65
2:D:175:ARG:N	2:D:183:ASN:O	2.27	0.65
1:A:642:SER:HA	1:A:645:TYR:HD2	1.59	0.65
2:B:19:ASP:OD1	2:B:20:ILE:N	2.29	0.65
1:C:49:VAL:HG13	1:C:52:LEU:HD12	1.79	0.65
1:A:509:LEU:HB3	1:A:567:ARG:CZ	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:578:ASP:OD2	1:A:582:ARG:NH2	2.30	0.65
1:C:156:ARG:NH2	1:C:220:VAL:HG23	2.10	0.65
1:C:408:ILE:HD13	1:C:450:SER:HA	1.79	0.65
1:A:780:ARG:HB2	1:A:783:ARG:NH1	2.10	0.65
1:C:289:LYS:HE2	1:C:406:LEU:HD13	1.77	0.65
1:C:389:LEU:HD22	1:C:393:PHE:CE2	2.32	0.65
1:C:746:LEU:HA	1:C:749:HIS:HD2	1.61	0.65
1:A:149:TYR:CE1	1:A:214:LEU:HA	2.32	0.65
1:A:702:VAL:HA	1:A:705:ILE:HD12	1.79	0.65
1:C:822:ASN:O	1:C:825:ILE:HG12	1.97	0.65
2:D:29:SER:HG	2:D:32:LYS:NZ	1.95	0.65
2:D:75:MET:HG2	2:D:87:PHE:H	1.62	0.65
1:A:116:TYR:HA	1:A:119:ILE:HG22	1.77	0.64
1:A:441:LEU:HG	1:A:488:LEU:HD13	1.79	0.64
1:A:699:PHE:HE1	1:A:734:LEU:HD13	1.62	0.64
1:C:22:ARG:HH11	1:C:25:THR:HG21	1.62	0.64
1:C:269:LEU:HA	1:C:272:LEU:HG	1.78	0.64
1:A:745:TYR:HE2	2:B:94:VAL:HG11	1.61	0.64
1:A:125:LYS:HB2	1:A:168:GLU:HB3	1.80	0.64
1:A:243:ILE:HG21	1:A:256:LEU:HD21	1.80	0.64
1:A:249:ILE:HG12	1:A:287:ASN:H	1.63	0.64
1:A:752:TRP:CG	1:A:753:ALA:N	2.66	0.64
2:B:77:VAL:HA	2:B:86:GLY:HA2	1.79	0.64
1:C:256:LEU:HD11	1:C:275:PHE:HE1	1.62	0.64
1:C:445:LYS:HG3	1:C:491:ALA:HB1	1.79	0.64
1:A:577:ASN:HD21	1:A:619:ARG:NH1	1.96	0.64
1:C:12:ARG:HA	1:C:15:GLU:OE2	1.97	0.64
1:C:49:VAL:HB	1:C:104:PRO:HG3	1.79	0.64
1:C:582:ARG:O	1:C:585:GLN:NE2	2.29	0.64
1:A:222:LEU:HA	1:A:225:LEU:HD12	1.80	0.64
2:B:29:SER:OG	2:B:32:LYS:NZ	2.25	0.63
2:B:88:LEU:HD11	2:B:93:LEU:HB2	1.79	0.63
1:C:488:LEU:O	1:C:492:GLN:NE2	2.31	0.63
1:A:99:ALA:O	1:A:105:ARG:NH2	2.30	0.63
1:C:12:ARG:NH1	1:C:16:ASP:OD1	2.31	0.63
1:C:423:LEU:HD22	1:C:472:ARG:HB3	1.79	0.63
1:C:228:LEU:CD1	1:C:267:TYR:HA	2.27	0.63
1:A:746:LEU:HA	1:A:749:HIS:HD2	1.64	0.63
1:C:427:PRO:HB2	1:C:428:GLU:HG3	1.80	0.63
2:D:50:TYR:CE2	2:D:54:ILE:HD11	2.34	0.63
2:D:101:LEU:HD13	2:D:125:PHE:HZ	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:529:LYS:HB3	1:A:533:LYS:NZ	2.14	0.63
1:C:240:LEU:HD11	1:C:274:GLN:HB3	1.81	0.63
1:C:272:LEU:HD13	1:C:389:LEU:HD21	1.81	0.63
1:C:588:ARG:HA	1:C:591:TYR:HD2	1.63	0.63
1:C:610:LEU:HD13	1:C:614:ARG:HH22	1.63	0.63
1:A:588:ARG:HH21	1:A:640:ALA:HA	1.64	0.63
2:B:42:LEU:HD22	2:B:48:TYR:HD1	1.63	0.63
1:C:252:GLN:NE2	1:C:281:ARG:HH12	1.96	0.63
1:C:276:LEU:HD21	1:C:393:PHE:CE1	2.34	0.63
1:C:422:SER:O	1:C:426:TYR:N	2.28	0.63
1:C:425:ILE:HG22	1:C:426:TYR:HD2	1.63	0.62
1:C:813:ASN:ND2	1:C:816:VAL:HG23	2.14	0.62
1:A:669:ASP:HB2	1:A:714:ASN:HD22	1.64	0.62
2:B:16:ARG:HD2	2:B:120:HIS:HE1	1.65	0.62
2:B:64:ARG:HG3	2:B:65:MET:SD	2.39	0.62
1:C:426:TYR:CD1	1:C:432:TYR:HD2	2.18	0.62
1:C:453:LEU:HD22	1:C:458:ALA:HB3	1.81	0.62
2:D:84:ARG:HH11	2:D:110:VAL:HG12	1.64	0.62
1:A:149:TYR:OH	1:A:213:LEU:HG	1.99	0.62
1:C:261:GLN:NE2	1:C:262:VAL:HG23	2.13	0.62
1:C:692:ILE:HG22	1:C:698:GLN:HG2	1.81	0.62
1:C:748:SER:HG	1:C:777:CYS:HG	1.42	0.62
2:D:29:SER:OG	2:D:32:LYS:NZ	2.31	0.62
1:A:665:GLY:O	1:A:714:ASN:ND2	2.32	0.62
2:B:28:LEU:HD22	2:B:33:ILE:HD11	1.81	0.62
1:C:440:ALA:HA	1:C:443:LYS:HE3	1.79	0.62
1:A:175:ILE:HD11	1:A:226:VAL:HG21	1.82	0.62
1:C:141:PRO:HG2	1:C:195:GLN:HB3	1.81	0.62
1:A:577:ASN:HD21	1:A:619:ARG:HH12	1.48	0.62
1:A:471:ARG:HD2	1:A:472:ARG:N	2.14	0.62
1:A:614:ARG:HG2	1:A:670:MET:HE3	1.80	0.62
1:A:726:LYS:O	1:A:729:GLN:HG3	2.00	0.62
2:B:34:SER:HA	2:B:56:PRO:HD2	1.81	0.62
1:A:24:GLN:HB2	1:A:48:LEU:HD12	1.81	0.62
1:A:427:PRO:HG3	1:A:472:ARG:NE	2.14	0.62
1:C:752:TRP:CG	1:C:753:ALA:N	2.68	0.62
1:C:582:ARG:HA	1:C:585:GLN:HG3	1.82	0.62
1:C:468:SER:HA	1:C:471:ARG:HG2	1.81	0.61
2:D:20:ILE:HG12	2:D:25:LYS:NZ	2.15	0.61
1:C:240:LEU:HD22	1:C:278:ALA:HB2	1.80	0.61
1:A:182:PHE:HA	1:A:185:MET:HG2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:477:PHE:HA	1:C:480:LEU:HD12	1.82	0.61
1:A:253:GLU:HA	1:A:291:ILE:HD13	1.82	0.61
1:A:601:THR:O	1:A:604:PRO:HG2	2.00	0.61
1:A:792:ALA:HA	1:A:836:GLN:HE21	1.63	0.61
1:C:492:GLN:HB2	1:C:497:ARG:CG	2.31	0.61
2:D:5:ILE:N	2:D:160:MET:O	2.30	0.61
1:A:852:THR:HA	1:A:855:MET:HG2	1.83	0.61
2:B:52:ARG:HH12	2:B:58:LEU:H	1.48	0.61
1:C:809:PHE:O	1:C:812:ARG:NH1	2.34	0.61
2:D:62:ARG:HB3	2:D:74:LEU:HD23	1.83	0.61
2:D:120:HIS:HB3	2:D:137:SER:HB2	1.82	0.61
1:A:623:ASP:OD1	1:A:624:ASP:N	2.34	0.61
2:B:22:PRO:HA	2:B:25:LYS:HG2	1.82	0.61
2:B:30:PRO:HG3	2:B:54:ILE:HA	1.81	0.61
1:C:245:GLN:HA	1:C:247:ARG:NH1	2.16	0.61
1:A:220:VAL:O	1:A:224:GLN:NE2	2.34	0.61
1:C:577:ASN:HB3	1:C:615:ARG:CG	2.31	0.61
1:A:390:TYR:O	1:A:394:PHE:HB2	2.01	0.60
1:A:145:LEU:HB3	1:A:214:LEU:HD23	1.83	0.60
1:A:746:LEU:HD21	2:B:94:VAL:CG1	2.31	0.60
1:A:494:TYR:HA	1:A:497:ARG:HE	1.66	0.60
2:B:26:LYS:O	2:B:32:LYS:NZ	2.31	0.60
1:A:409:GLN:HG2	1:A:457:PRO:HG2	1.83	0.60
1:A:593:GLU:HB2	1:A:597:ARG:HD2	1.83	0.60
2:B:42:LEU:HD22	2:B:48:TYR:CD1	2.36	0.60
2:D:41:ASN:N	2:D:66:ASP:OD2	2.34	0.60
1:C:484:THR:O	1:C:487:SER:OG	2.12	0.60
1:C:564:TRP:CE3	1:C:567:ARG:HD3	2.36	0.60
1:A:395:ASP:OD1	1:A:396:GLN:N	2.35	0.60
2:B:120:HIS:ND1	2:B:142:PHE:O	2.34	0.60
1:C:389:LEU:HD22	1:C:393:PHE:HE2	1.67	0.60
1:C:454:HIS:HA	1:C:459:GLN:HG3	1.82	0.60
1:C:742:ARG:HA	1:C:745:TYR:CD1	2.35	0.60
1:C:853:LEU:HA	1:C:856:ILE:HG12	1.84	0.60
2:B:13:ILE:HG23	2:B:18:LEU:HD13	1.84	0.60
1:A:223:SER:HB3	1:A:262:VAL:HG12	1.84	0.60
1:A:529:LYS:HB3	1:A:533:LYS:HZ2	1.66	0.60
1:A:560:GLU:HG3	1:A:564:TRP:CD2	2.36	0.60
1:A:595:ASN:OD1	1:A:647:ARG:NE	2.35	0.60
1:C:637:LEU:HD13	1:C:664:CYS:SG	2.42	0.60
1:C:729:GLN:NE2	1:C:733:LYS:HD3	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:595:ASN:HA	1:A:647:ARG:HE	1.66	0.60
1:A:687:VAL:HA	1:A:690:GLU:OE1	2.02	0.60
1:A:776:GLU:OE1	1:A:780:ARG:NH1	2.20	0.60
2:B:112:VAL:HG22	2:B:131:PHE:HB3	1.83	0.60
2:D:111:ASP:O	2:D:131:PHE:N	2.34	0.59
2:B:86:GLY:HA3	2:B:110:VAL:HG11	1.83	0.59
1:C:723:LEU:HA	1:C:726:LYS:HE3	1.83	0.59
1:A:260:THR:HG21	1:A:298:ARG:HD3	1.83	0.59
1:A:699:PHE:CE1	1:A:734:LEU:HD13	2.37	0.59
1:C:81:ARG:HG2	1:C:115:ALA:HA	1.84	0.59
1:C:737:LYS:HE2	1:C:784:VAL:CG1	2.28	0.59
1:A:21:VAL:O	1:A:25:THR:HG23	2.02	0.59
1:C:21:VAL:O	1:C:25:THR:HG23	2.02	0.59
1:A:171:LEU:HD13	1:A:226:VAL:HG12	1.85	0.59
1:A:437:LEU:HD11	1:A:485:TYR:HA	1.85	0.59
1:A:670:MET:SD	1:A:671:THR:HG23	2.43	0.59
1:C:494:TYR:HA	1:C:497:ARG:HE	1.68	0.59
1:C:634:PHE:HA	1:C:637:LEU:CG	2.32	0.59
1:A:525:LEU:HB3	1:A:529:LYS:NZ	2.17	0.59
1:A:598:ILE:HA	1:A:601:THR:OG1	2.02	0.59
1:C:28:MET:O	1:C:32:LEU:HG	2.02	0.59
1:C:286:VAL:O	1:C:288:VAL:N	2.33	0.59
1:C:554:GLU:O	1:C:554:GLU:HG2	2.02	0.59
1:A:416:CYS:SG	1:A:461:SER:HB3	2.42	0.59
1:A:753:ALA:HB1	1:A:767:LEU:HD13	1.84	0.59
2:B:5:ILE:HA	2:B:35:GLN:O	2.03	0.59
1:C:192:LEU:HD11	1:C:211:LEU:HD12	1.83	0.59
1:C:303:ALA:HB3	1:C:424:ASN:HB3	1.83	0.59
1:C:564:TRP:O	1:C:568:LEU:HG	2.03	0.59
1:A:99:ALA:O	1:A:105:ARG:HD3	2.02	0.59
1:A:709:LEU:HD12	1:A:712:THR:HB	1.84	0.59
1:C:32:LEU:HD22	1:C:79:HIS:CD2	2.38	0.59
1:C:102:ILE:HG22	1:C:105:ARG:NH1	2.18	0.59
1:C:114:THR:OG1	1:C:154:GLN:HB3	2.02	0.59
1:A:468:SER:HA	1:A:471:ARG:HG3	1.85	0.59
1:C:420:ASN:OD1	1:C:471:ARG:NH1	2.31	0.59
1:A:12:ARG:NH1	1:A:16:ASP:OD1	2.36	0.59
2:B:126:GLU:HG2	2:B:131:PHE:HD1	1.68	0.59
2:D:113:LEU:N	2:D:131:PHE:O	2.32	0.58
1:A:525:LEU:O	1:A:529:LYS:HD2	2.03	0.58
2:B:78:VAL:N	2:B:85:ILE:O	2.28	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:221:ARG:HD2	1:C:224:GLN:NE2	2.14	0.58
1:C:221:ARG:NH1	1:C:224:GLN:HG3	2.18	0.58
1:C:533:LYS:HA	1:C:534:GLU:C	2.21	0.58
1:C:171:LEU:HD13	1:C:230:THR:HG21	1.85	0.58
1:A:506:ARG:HB3	1:A:510:LYS:HZ3	1.67	0.58
1:A:529:LYS:HA	1:A:532:ILE:HG12	1.83	0.58
1:A:265:ASP:HA	1:A:268:HIS:CD2	2.39	0.58
1:A:770:ASP:CG	1:A:773:ARG:HH21	2.06	0.58
2:B:24:PHE:HE1	2:B:184:VAL:HG13	1.68	0.58
2:B:161:ASP:O	2:B:168:THR:N	2.25	0.58
1:C:734:LEU:HD11	1:C:739:ASP:O	2.04	0.58
1:C:803:ASP:OD2	1:C:848:HIS:NE2	2.37	0.58
1:A:586:MET:HA	1:A:589:LYS:HE2	1.85	0.58
1:C:390:TYR:HD1	1:C:425:ILE:HG21	1.69	0.58
1:A:221:ARG:NH1	1:A:224:GLN:OE1	2.37	0.58
2:B:103:ALA:O	2:B:107:LYS:HD3	2.03	0.58
1:C:39:MET:SD	1:C:39:MET:N	2.76	0.58
1:C:394:PHE:HE1	1:C:440:ALA:HB2	1.68	0.58
1:C:438:ALA:O	1:C:442:ALA:HB3	2.04	0.58
1:C:741:CYS:SG	1:C:797:LEU:HD21	2.42	0.58
1:A:786:ASP:OD1	1:A:787:SER:N	2.37	0.58
2:B:9:GLY:HA2	2:B:39:LEU:HB2	1.85	0.58
2:D:171:VAL:CG1	2:D:187:GLU:HB3	2.34	0.58
2:D:12:HIS:O	2:D:16:ARG:N	2.26	0.58
2:D:62:ARG:HH21	2:D:73:PRO:HA	1.69	0.58
1:A:63:TYR:CD1	1:A:146:PHE:HZ	2.22	0.58
1:A:205:THR:O	1:A:209:ARG:HG3	2.03	0.58
1:A:283:ASN:HB2	1:A:286:VAL:HG22	1.86	0.58
1:A:468:SER:HA	1:A:471:ARG:HE	1.68	0.58
1:A:435:GLY:O	1:A:439:TYR:HB2	2.03	0.57
1:A:695:SER:HA	1:A:698:GLN:CD	2.24	0.57
1:A:795:ILE:HD11	1:A:831:ASN:HB3	1.84	0.57
1:C:161:THR:HG23	1:C:163:ASP:H	1.68	0.57
2:D:12:HIS:HA	2:D:15:ASP:HB3	1.85	0.57
1:C:117:MET:HG3	1:C:124:VAL:HG22	1.86	0.57
1:C:228:LEU:HD11	1:C:270:HIS:HB3	1.85	0.57
1:C:437:LEU:HA	1:C:441:LEU:HD12	1.85	0.57
1:C:625:ASN:O	1:C:629:GLN:N	2.26	0.57
1:A:625:ASN:O	1:A:629:GLN:N	2.30	0.57
1:C:102:ILE:HG22	1:C:105:ARG:HH12	1.68	0.57
2:D:115:TRP:CH2	2:D:132:PHE:HB3	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:722:THR:HG22	1:A:726:LYS:NZ	2.19	0.57
1:A:817:THR:H	1:A:820:TYR:HD2	1.53	0.57
2:B:1:MET:HE3	2:B:4:LEU:HA	1.86	0.57
1:C:161:THR:HG23	1:C:163:ASP:N	2.20	0.57
1:C:197:HIS:CG	1:C:199:ARG:HH11	2.22	0.57
2:B:131:PHE:HB2	2:B:191:TYR:CD1	2.40	0.57
1:C:79:HIS:CD2	1:C:83:ASN:HD21	2.23	0.57
1:C:599:ARG:HG3	1:C:600:THR:HG23	1.87	0.57
1:A:96:VAL:HG11	1:A:112:VAL:HG21	1.85	0.57
1:A:853:LEU:HA	1:A:856:ILE:HG12	1.87	0.57
1:C:486:VAL:O	1:C:489:PHE:N	2.28	0.57
1:C:598:ILE:HA	1:C:601:THR:OG1	2.05	0.57
2:D:9:GLY:H	2:D:138:ALA:HB3	1.68	0.57
1:A:293:ILE:HA	1:A:414:LEU:HD21	1.87	0.57
1:A:519:ALA:O	1:A:522:GLU:HG3	2.03	0.57
2:B:28:LEU:HD21	2:B:157:PHE:CE1	2.39	0.57
1:C:477:PHE:HZ	1:C:513:THR:HA	1.69	0.57
1:C:780:ARG:O	1:C:783:ARG:HG2	2.05	0.57
1:A:68:ALA:HA	1:A:71:ASP:OD2	2.05	0.57
1:C:752:TRP:CE2	1:C:808:TYR:HD1	2.23	0.57
1:A:193:GLN:OE1	1:A:208:ARG:NH1	2.32	0.56
1:A:219:ILE:HG23	1:A:263:PHE:CE2	2.40	0.56
1:A:14:LEU:HD22	1:A:61:GLN:HA	1.86	0.56
1:A:493:THR:HG23	1:A:496:THR:OG1	2.05	0.56
1:A:775:LEU:HD22	1:A:815:SER:HB2	1.86	0.56
1:A:807:TYR:HB2	2:B:99:ASP:OD2	2.04	0.56
1:C:231:TYR:HA	1:C:235:ILE:HD12	1.87	0.56
1:C:710:HIS:O	1:C:756:ILE:HB	2.05	0.56
1:A:463:LEU:O	1:A:467:GLN:HG2	2.06	0.56
1:C:25:THR:HB	1:C:29:ARG:HH22	1.69	0.56
1:C:27:MET:HA	1:C:30:LYS:HG3	1.85	0.56
1:C:257:GLU:O	1:C:261:GLN:HG3	2.06	0.56
2:D:169:LEU:HB3	2:D:189:VAL:HB	1.88	0.56
2:D:20:ILE:HD12	2:D:24:PHE:HB3	1.88	0.56
2:D:49:ASP:HA	2:D:52:ARG:CD	2.36	0.56
2:D:81:GLY:HA3	2:D:164:GLY:HA2	1.87	0.56
1:A:64:GLU:HA	1:A:67:MET:HG2	1.87	0.56
1:A:577:ASN:ND2	1:A:619:ARG:HH12	2.03	0.56
2:B:169:LEU:HB3	2:B:189:VAL:HB	1.87	0.56
2:B:7:VAL:HB	2:B:158:CYS:HB2	1.87	0.56
1:C:507:THR:HA	1:C:510:LYS:HE2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:GLN:HB3	1:A:402:GLN:HE22	1.71	0.56
1:A:564:TRP:HD1	1:A:565:LEU:HD22	1.70	0.56
1:A:657:CYS:HB3	1:A:661:PHE:CE1	2.40	0.56
1:C:21:VAL:HG22	1:C:48:LEU:HG	1.88	0.56
1:C:506:ARG:HE	1:C:509:LEU:HD12	1.71	0.56
1:C:515:ILE:HD12	1:C:574:SER:HB3	1.88	0.56
1:A:184:GLU:HA	1:A:187:LYS:HG2	1.87	0.55
1:C:564:TRP:O	1:C:567:ARG:HG2	2.05	0.55
1:A:49:VAL:HB	1:A:104:PRO:HG3	1.89	0.55
1:A:242:GLN:HA	1:A:245:GLN:HE21	1.70	0.55
1:A:490:GLN:NE2	1:A:526:GLU:OE2	2.39	0.55
2:B:75:MET:HG3	2:B:88:LEU:HB3	1.88	0.55
1:C:281:ARG:NH2	1:C:282:LEU:HD23	2.21	0.55
1:C:509:LEU:HA	1:C:567:ARG:HH12	1.69	0.55
1:A:125:LYS:CB	1:A:168:GLU:HB3	2.37	0.55
2:D:42:LEU:HD22	2:D:45:ARG:HH21	1.71	0.55
1:A:149:TYR:OH	1:A:214:LEU:HA	2.05	0.55
1:A:467:GLN:HA	1:A:470:LEU:HD12	1.87	0.55
1:A:686:THR:HA	1:A:689:GLU:OE1	2.07	0.55
1:A:819:LYS:H	1:A:819:LYS:HD3	1.72	0.55
2:B:5:ILE:HB	2:B:160:MET:SD	2.46	0.55
1:C:566:ALA:O	1:C:570:HIS:ND1	2.39	0.55
1:A:477:PHE:CE2	1:A:514:LEU:HB2	2.41	0.55
1:A:657:CYS:HB3	1:A:661:PHE:CZ	2.40	0.55
2:B:46:ALA:O	2:B:49:ASP:OD1	2.23	0.55
1:C:513:THR:H	1:C:567:ARG:HH22	1.55	0.55
1:A:89:LEU:HD23	1:A:92:LEU:HD22	1.87	0.55
1:A:742:ARG:HA	1:A:745:TYR:CD1	2.42	0.55
1:A:823:GLY:O	1:A:826:GLU:HG3	2.07	0.55
1:C:25:THR:HB	1:C:29:ARG:NH2	2.22	0.55
1:C:217:SER:HA	1:C:220:VAL:HG22	1.89	0.55
1:C:489:PHE:O	1:C:497:ARG:HD3	2.05	0.55
1:C:46:SER:HA	1:C:104:PRO:HB3	1.89	0.55
1:C:500:ILE:HA	1:C:503:GLU:HG3	1.89	0.55
1:C:518:PRO:O	1:C:522:GLU:OE1	2.25	0.55
1:A:128:MET:SD	1:A:160:PRO:HD3	2.46	0.55
1:A:695:SER:HA	1:A:698:GLN:NE2	2.21	0.55
1:C:736:ARG:O	1:C:740:GLN:HG2	2.07	0.55
1:C:557:GLU:HB3	1:C:559:MET:HG3	1.89	0.55
2:D:10:ASN:HD21	2:D:120:HIS:CG	2.25	0.55
2:B:11:LEU:O	2:B:139:THR:OG1	2.16	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:423:LEU:CD1	1:C:468:SER:HB3	2.36	0.55
1:C:423:LEU:CB	1:C:472:ARG:HG2	2.34	0.55
1:C:529:LYS:NZ	1:C:590:ALA:O	2.30	0.55
1:C:640:ALA:O	1:C:643:THR:HB	2.07	0.55
1:C:805:TYR:O	1:C:816:VAL:HG11	2.07	0.55
2:B:137:SER:OG	2:B:141:ALA:N	2.35	0.54
1:C:42:LEU:HD22	1:C:108:LEU:HD22	1.90	0.54
1:A:577:ASN:HB2	1:A:612:LEU:HD13	1.88	0.54
1:A:777:CYS:O	1:A:780:ARG:HG2	2.07	0.54
1:C:441:LEU:HD13	1:C:488:LEU:HD21	1.88	0.54
1:C:752:TRP:HD1	1:C:754:THR:HG22	1.72	0.54
2:D:173:GLN:O	2:D:185:ALA:N	2.23	0.54
1:A:123:PRO:HB3	1:A:126:GLU:OE2	2.07	0.54
1:A:401:VAL:HG13	1:A:406:LEU:HD12	1.89	0.54
1:A:656:LEU:HD12	1:A:657:CYS:N	2.22	0.54
1:A:713:ARG:NH2	1:A:714:ASN:HB3	2.22	0.54
2:B:83:LEU:HD12	2:B:162:VAL:HG13	1.87	0.54
2:B:168:THR:HG21	2:B:188:LYS:HE2	1.88	0.54
1:C:269:LEU:HD23	1:C:272:LEU:HD11	1.88	0.54
1:A:164:SER:OG	1:A:169:GLY:O	2.19	0.54
1:A:303:ALA:O	1:A:424:ASN:HB3	2.06	0.54
2:B:74:LEU:HB3	2:B:92:THR:HG21	1.89	0.54
1:C:417:SER:HA	1:C:420:ASN:HD22	1.71	0.54
1:C:500:ILE:O	1:C:503:GLU:HG3	2.08	0.54
2:D:115:TRP:O	2:D:135:PRO:HD2	2.06	0.54
1:A:228:LEU:HD11	1:A:270:HIS:HB3	1.89	0.54
2:B:171:VAL:CG1	2:B:187:GLU:HB3	2.37	0.54
2:D:140:GLY:HA2	2:D:153:VAL:HB	1.89	0.54
1:A:26:ALA:HB1	1:A:30:LYS:HZ1	1.72	0.54
1:A:454:HIS:HD2	1:A:496:THR:HG23	1.72	0.54
1:C:53:ARG:HH12	1:C:103:ILE:CG1	2.20	0.54
1:C:148:ARG:NH1	1:C:184:GLU:HB2	2.22	0.54
1:C:394:PHE:O	1:C:398:GLN:NE2	2.41	0.54
1:C:427:PRO:O	1:C:433:VAL:HG22	2.08	0.54
1:C:752:TRP:CZ2	1:C:811:GLN:HB2	2.42	0.54
1:A:149:TYR:CZ	1:A:214:LEU:HA	2.42	0.54
1:A:241:GLU:O	1:A:245:GLN:HG3	2.07	0.54
1:C:477:PHE:CD1	1:C:514:LEU:HD22	2.43	0.54
1:A:408:ILE:HD13	1:A:448:ALA:HA	1.90	0.54
1:A:585:GLN:NE2	1:A:636:PHE:HD2	2.05	0.54
1:A:269:LEU:HA	1:A:272:LEU:HG	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:60:LYS:HZ1	1:C:209:ARG:HH12	1.55	0.54
1:C:607:THR:HA	1:C:610:LEU:CG	2.37	0.54
2:D:3:PHE:HA	2:D:34:SER:HB2	1.90	0.54
2:D:131:PHE:HB2	2:D:191:TYR:CZ	2.43	0.54
1:A:710:HIS:O	1:A:756:ILE:HB	2.07	0.54
1:C:231:TYR:CD2	1:C:267:TYR:HB3	2.43	0.54
1:C:822:ASN:O	1:C:826:GLU:OE1	2.26	0.54
1:A:192:LEU:O	1:A:204:ARG:HD2	2.07	0.53
1:A:219:ILE:HG21	1:A:258:VAL:HG12	1.90	0.53
1:A:390:TYR:HB2	1:A:426:TYR:HE2	1.73	0.53
1:A:668:ALA:HB1	1:A:674:GLU:HA	1.90	0.53
2:B:156:SER:HB3	2:B:173:GLN:HG2	1.90	0.53
1:C:104:PRO:O	1:C:108:LEU:HG	2.08	0.53
1:C:179:LEU:O	1:C:183:VAL:HG13	2.06	0.53
1:C:737:LYS:CE	1:C:784:VAL:HG13	2.32	0.53
1:C:751:TRP:HZ3	1:C:777:CYS:HB2	1.73	0.53
2:D:167:LEU:N	2:D:191:TYR:O	2.25	0.53
2:D:24:PHE:HE1	2:D:184:VAL:HG13	1.74	0.53
2:D:89:GLU:HA	2:D:116:ALA:H	1.73	0.53
1:C:102:ILE:HG13	1:C:103:ILE:N	2.23	0.53
1:C:685:PHE:CE2	1:C:726:LYS:HD2	2.44	0.53
1:C:775:LEU:HD22	1:C:815:SER:HB2	1.91	0.53
1:A:198:SER:HA	1:A:204:ARG:HH22	1.74	0.53
1:A:577:ASN:O	1:A:580:GLN:HB2	2.08	0.53
1:C:181:ASN:ND2	1:C:218:ASN:OD1	2.39	0.53
1:C:275:PHE:O	1:C:279:VAL:HG23	2.09	0.53
1:C:752:TRP:CH2	1:C:813:ASN:HB2	2.43	0.53
2:D:97:GLU:CB	2:D:98:PRO:HD3	2.37	0.53
1:A:155:ALA:HA	1:A:158:TYR:HD2	1.74	0.53
1:A:802:LEU:HD22	1:A:852:THR:HG21	1.89	0.53
2:D:154:VAL:HG13	2:D:174:LEU:O	2.08	0.53
1:C:275:PHE:HZ	1:C:295:MET:HG2	1.73	0.53
1:C:423:LEU:HB3	1:C:472:ARG:CG	2.33	0.53
2:D:1:MET:H	2:D:161:ASP:CG	2.11	0.53
1:A:59:PRO:HG3	1:A:207:GLU:OE2	2.09	0.53
1:A:211:LEU:O	1:A:214:LEU:HB2	2.09	0.53
1:A:791:THR:HG22	1:A:836:GLN:HG2	1.90	0.53
1:C:223:SER:HB3	1:C:262:VAL:HG12	1.90	0.53
1:C:430:LEU:HD11	1:C:482:LEU:HD23	1.91	0.53
1:A:233:ASP:OD1	1:A:234:SER:N	2.42	0.53
1:A:261:GLN:NE2	1:A:298:ARG:HE	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:303:ALA:CB	1:C:424:ASN:HB3	2.39	0.53
1:A:577:ASN:HB2	1:A:612:LEU:CD1	2.39	0.53
1:C:116:TYR:HA	1:C:119:ILE:HG22	1.91	0.53
1:A:189:TRP:NE1	1:A:251:ALA:HB2	2.25	0.52
1:C:161:THR:HA	1:C:170:ASN:C	2.30	0.52
1:C:416:CYS:O	1:C:420:ASN:ND2	2.41	0.52
1:C:477:PHE:CZ	1:C:513:THR:HA	2.44	0.52
1:C:678:TYR:CE1	1:C:723:LEU:HG	2.44	0.52
1:A:800:GLU:O	1:A:804:ARG:HG2	2.09	0.52
2:B:12:HIS:O	2:B:15:ASP:N	2.42	0.52
1:C:93:TYR:HE2	1:C:134:MET:HE1	1.75	0.52
1:A:288:VAL:HA	1:A:291:ILE:HG22	1.92	0.52
1:A:390:TYR:O	1:A:394:PHE:HB3	2.08	0.52
1:C:190:VAL:HG12	1:C:194:HIS:HE1	1.75	0.52
1:C:468:SER:HA	1:C:471:ARG:NE	2.24	0.52
1:C:774:VAL:O	1:C:778:LEU:HG	2.08	0.52
2:D:52:ARG:NH1	2:D:53:SER:HB3	2.24	0.52
2:D:62:ARG:HB2	2:D:72:LEU:O	2.09	0.52
2:D:171:VAL:HG13	2:D:187:GLU:HB3	1.91	0.52
1:A:608:ALA:O	1:A:611:LYS:HG2	2.09	0.52
1:A:666:GLN:HG3	1:A:713:ARG:NH1	2.24	0.52
1:A:738:PRO:O	1:A:742:ARG:HG3	2.09	0.52
1:C:595:ASN:CA	1:C:647:ARG:HD3	2.38	0.52
1:C:832:LEU:HD12	1:C:836:GLN:OE1	2.10	0.52
1:A:25:THR:HA	1:A:28:MET:HE3	1.90	0.52
1:A:208:ARG:HH22	1:A:248:ASP:CG	2.13	0.52
1:A:623:ASP:OD1	1:A:625:ASN:N	2.42	0.52
1:A:641:ILE:HD13	1:A:661:PHE:HE2	1.73	0.52
1:A:696:LYS:HA	1:A:699:PHE:HD2	1.74	0.52
1:A:809:PHE:O	1:A:812:ARG:NH1	2.42	0.52
2:B:16:ARG:HD2	2:B:120:HIS:CE1	2.44	0.52
2:B:158:CYS:HB3	2:B:169:LEU:HD11	1.91	0.52
1:C:560:GLU:OE2	1:C:597:ARG:NH1	2.42	0.52
1:C:713:ARG:NH2	1:C:714:ASN:HB3	2.24	0.52
1:A:110:ILE:HG21	1:A:151:LEU:HA	1.92	0.52
1:A:480:LEU:O	1:A:480:LEU:HD23	2.10	0.52
1:C:587:THR:O	1:C:591:TYR:CD2	2.63	0.52
2:B:52:ARG:NH1	2:B:58:LEU:H	2.07	0.52
1:C:564:TRP:HA	1:C:567:ARG:HG2	1.92	0.52
1:A:429:ARG:NH2	1:A:431:ASP:OD2	2.42	0.52
1:A:656:LEU:HA	1:A:659:ARG:NH1	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:21:VAL:HG13	1:C:48:LEU:HD11	1.92	0.52
2:D:34:SER:HA	2:D:56:PRO:HD2	1.90	0.52
2:D:105:ALA:HB1	2:D:130:LYS:CD	2.39	0.52
1:A:408:ILE:O	1:A:412:ILE:HG12	2.10	0.52
1:A:494:TYR:HA	1:A:497:ARG:HB2	1.92	0.52
1:A:744:VAL:HG12	1:A:781:ALA:HB2	1.92	0.52
1:A:795:ILE:O	1:A:799:VAL:HG23	2.10	0.52
1:C:506:ARG:O	1:C:510:LYS:HD3	2.10	0.52
1:C:804:ARG:HE	1:C:804:ARG:HA	1.75	0.52
1:A:21:VAL:HG13	1:A:48:LEU:HD11	1.92	0.52
1:A:257:GLU:O	1:A:261:GLN:OE1	2.28	0.52
1:A:587:THR:HB	1:A:591:TYR:CZ	2.44	0.52
1:C:92:LEU:O	1:C:96:VAL:HG22	2.10	0.52
1:C:409:GLN:HG3	1:C:457:PRO:HG2	1.91	0.52
1:C:494:TYR:HB2	1:C:497:ARG:HH21	1.74	0.52
1:C:790:GLU:OE1	1:C:793:THR:N	2.43	0.52
1:C:804:ARG:HA	1:C:804:ARG:NE	2.25	0.52
1:A:473:TYR:CD2	1:A:476:ILE:HA	2.45	0.51
1:A:713:ARG:HB2	1:A:760:GLY:CA	2.40	0.51
2:B:155:PRO:HD2	2:B:174:LEU:O	2.10	0.51
1:C:161:THR:HB	1:C:174:SER:OG	2.11	0.51
1:A:221:ARG:HA	1:A:224:GLN:OE1	2.10	0.51
1:A:389:LEU:HD22	1:A:393:PHE:CE2	2.45	0.51
1:C:399:HIS:HA	1:C:402:GLN:HG3	1.92	0.51
2:D:77:VAL:HG13	2:D:85:ILE:H	1.75	0.51
1:A:114:THR:OG1	1:A:154:GLN:HB3	2.09	0.51
1:C:731:ALA:O	1:C:734:LEU:HD22	2.10	0.51
1:A:221:ARG:HH12	1:A:224:GLN:HB2	1.76	0.51
1:A:619:ARG:O	1:A:623:ASP:N	2.42	0.51
1:A:697:ALA:HA	1:A:700:GLN:NE2	2.26	0.51
2:B:10:ASN:ND2	2:B:120:HIS:HA	2.24	0.51
1:C:96:VAL:HG23	1:C:109:MET:CE	2.40	0.51
1:C:425:ILE:HG22	1:C:426:TYR:CD2	2.44	0.51
1:A:70:PHE:HE1	1:A:150:TYR:HA	1.76	0.51
1:A:125:LYS:NZ	1:A:173:ASP:OD2	2.44	0.51
1:A:632:SER:HA	1:A:635:LYS:HG2	1.92	0.51
2:B:63:GLY:H	2:B:66:ASP:HB2	1.75	0.51
2:D:5:ILE:O	2:D:160:MET:N	2.39	0.51
2:D:12:HIS:CA	2:D:15:ASP:HB3	2.40	0.51
2:D:126:GLU:HG2	2:D:131:PHE:HD1	1.76	0.51
1:A:579:THR:OG1	1:A:582:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:755:PRO:O	1:C:767:LEU:HD22	2.10	0.51
1:A:120:ASP:HB3	1:A:123:PRO:HD2	1.93	0.51
1:A:424:ASN:HA	1:A:472:ARG:NE	2.26	0.51
1:C:599:ARG:HG3	1:C:600:THR:N	2.25	0.51
1:A:105:ARG:HG2	1:A:109:MET:CE	2.38	0.51
1:A:117:MET:SD	1:A:128:MET:HE2	2.51	0.51
1:A:136:ARG:NH1	1:A:184:GLU:HG2	2.26	0.51
1:A:304:GLU:HG2	1:A:424:ASN:ND2	2.26	0.51
1:A:506:ARG:HH12	1:A:560:GLU:CA	2.21	0.51
1:A:598:ILE:HD11	1:A:647:ARG:HD3	1.92	0.51
1:A:804:ARG:HG2	1:A:804:ARG:HH11	1.76	0.51
1:C:66:TYR:HA	1:C:69:VAL:HG22	1.93	0.51
1:C:797:LEU:HA	1:C:800:GLU:OE2	2.11	0.51
1:A:272:LEU:HB3	1:A:393:PHE:HZ	1.76	0.51
1:A:656:LEU:HA	1:A:659:ARG:HH11	1.75	0.51
1:A:688:TYR:CE2	1:A:730:HIS:HB2	2.46	0.51
1:C:389:LEU:O	1:C:393:PHE:HB2	2.11	0.51
1:C:520:HIS:O	1:C:524:VAL:HG23	2.10	0.51
1:C:561:GLU:HB3	1:C:564:TRP:CD1	2.46	0.51
1:C:813:ASN:HB3	1:C:816:VAL:HB	1.93	0.51
1:A:644:LEU:HD11	1:A:657:CYS:SG	2.50	0.51
1:C:31:PHE:CE2	1:C:40:ASP:HB3	2.46	0.51
1:C:432:TYR:O	1:C:436:ILE:HG12	2.10	0.51
1:C:443:LYS:HA	1:C:446:GLU:HG2	1.92	0.51
1:C:598:ILE:HD12	1:C:644:LEU:HD23	1.93	0.51
2:D:51:LEU:HG	2:D:58:LEU:HD13	1.93	0.51
1:A:18:LEU:O	1:A:22:ARG:HD3	2.11	0.50
2:B:101:LEU:O	2:B:104:GLU:HG3	2.11	0.50
1:C:96:VAL:HG23	1:C:109:MET:HE1	1.93	0.50
1:C:669:ASP:O	1:C:713:ARG:NH1	2.44	0.50
1:C:678:TYR:HE1	1:C:723:LEU:HG	1.75	0.50
2:D:83:LEU:HG	2:D:164:GLY:O	2.12	0.50
1:A:634:PHE:HE1	1:A:664:CYS:HB3	1.77	0.50
1:A:687:VAL:O	1:A:691:SER:OG	2.12	0.50
1:A:808:TYR:HB2	1:A:816:VAL:HG21	1.93	0.50
1:C:29:ARG:HA	1:C:32:LEU:HD12	1.94	0.50
1:C:99:ALA:O	1:C:105:ARG:HD3	2.10	0.50
1:C:737:LYS:NZ	1:C:787:SER:O	2.45	0.50
1:A:454:HIS:HE2	1:A:495:PRO:HD2	1.76	0.50
1:A:466:LEU:O	1:A:469:PRO:HD2	2.11	0.50
2:B:8:ILE:O	2:B:39:LEU:HD13	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:127:TYR:HB3	2:B:132:PHE:HE2	1.76	0.50
1:A:189:TRP:CH2	1:A:208:ARG:O	2.65	0.50
1:A:272:LEU:HA	1:A:275:PHE:CD1	2.45	0.50
1:A:412:ILE:HG21	1:A:462:LEU:HG	1.93	0.50
1:A:685:PHE:HZ	1:A:723:LEU:HD22	1.77	0.50
1:A:763:GLU:HB3	1:A:766:GLU:O	2.12	0.50
2:B:3:PHE:CE1	2:B:35:GLN:HB2	2.41	0.50
2:B:114:CYS:HA	2:B:133:VAL:O	2.11	0.50
1:C:219:ILE:HG21	1:C:258:VAL:HG12	1.94	0.50
1:C:512:GLN:HA	1:C:567:ARG:HH22	1.75	0.50
1:C:672:GLU:HA	1:C:714:ASN:ND2	2.26	0.50
1:A:113:GLY:O	1:A:117:MET:HG2	2.12	0.50
1:A:682:ALA:HA	1:A:685:PHE:CE2	2.47	0.50
1:C:437:LEU:HA	1:C:441:LEU:HB2	1.93	0.50
1:C:717:ARG:O	1:C:721:ASP:HB2	2.11	0.50
2:D:166:SER:HA	2:D:192:THR:HA	1.92	0.50
1:A:264:PRO:HG2	1:A:267:TYR:CG	2.47	0.50
1:A:409:GLN:HA	1:A:458:ALA:HB2	1.93	0.50
2:B:16:ARG:HB2	2:B:141:ALA:HB1	1.93	0.50
1:C:185:MET:CE	1:C:218:ASN:HD21	2.24	0.50
1:C:509:LEU:HA	1:C:567:ARG:HH11	1.72	0.50
2:D:6:LEU:HB3	2:D:36:THR:HG23	1.93	0.50
2:D:105:ALA:HB1	2:D:130:LYS:HD2	1.93	0.50
1:A:272:LEU:HB3	1:A:393:PHE:CZ	2.47	0.50
1:A:420:ASN:OD1	1:A:471:ARG:NH1	2.45	0.50
1:A:490:GLN:N	1:A:490:GLN:OE1	2.40	0.50
1:A:587:THR:HB	1:A:591:TYR:OH	2.12	0.50
1:A:638:HIS:ND1	1:A:680:PHE:HE1	2.10	0.50
1:C:189:TRP:NE1	1:C:208:ARG:O	2.32	0.50
1:C:416:CYS:SG	1:C:461:SER:HB3	2.52	0.50
1:C:437:LEU:HD21	1:C:484:THR:HB	1.93	0.50
1:C:525:LEU:HD22	1:C:590:ALA:CB	2.41	0.50
1:C:805:TYR:CD1	1:C:816:VAL:HG22	2.46	0.50
2:D:88:LEU:HG	2:D:89:GLU:H	1.76	0.50
2:D:97:GLU:HB2	2:D:98:PRO:CD	2.42	0.50
1:A:152:SER:HB3	1:A:156:ARG:NH2	2.26	0.50
1:C:734:LEU:HG	1:C:740:GLN:OE1	2.11	0.50
1:A:26:ALA:HB1	1:A:30:LYS:NZ	2.27	0.49
1:C:249:ILE:O	1:C:253:GLU:OE1	2.30	0.49
1:C:669:ASP:OD2	1:C:713:ARG:NE	2.45	0.49
1:C:752:TRP:HZ2	1:C:811:GLN:HB2	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:LEU:HB3	1:A:281:ARG:HH12	1.77	0.49
1:A:443:LYS:HD3	1:A:443:LYS:N	2.27	0.49
1:A:453:LEU:O	1:A:493:THR:HG21	2.11	0.49
1:A:557:GLU:HB2	1:A:559:MET:CE	2.42	0.49
1:C:161:THR:OG1	1:C:171:LEU:HA	2.11	0.49
1:C:276:LEU:HD21	1:C:393:PHE:CZ	2.47	0.49
1:C:577:ASN:OD1	1:C:619:ARG:NH2	2.44	0.49
1:C:748:SER:OG	1:C:777:CYS:SG	2.60	0.49
1:C:775:LEU:O	1:C:779:GLN:HG2	2.11	0.49
1:A:421:LEU:O	1:A:425:ILE:HG12	2.12	0.49
1:A:453:LEU:O	1:A:453:LEU:HD12	2.11	0.49
1:A:493:THR:O	1:A:496:THR:OG1	2.24	0.49
1:C:228:LEU:HD13	1:C:267:TYR:CD1	2.47	0.49
1:C:281:ARG:HH21	1:C:282:LEU:HA	1.77	0.49
1:C:591:TYR:CZ	1:C:605:LEU:HD11	2.47	0.49
2:D:13:ILE:O	2:D:43:THR:N	2.44	0.49
2:B:12:HIS:HB3	2:B:16:ARG:H	1.76	0.49
1:A:482:LEU:HB2	1:A:485:TYR:HB2	1.93	0.49
1:C:473:TYR:HB3	1:C:476:ILE:HA	1.95	0.49
1:C:528:LEU:HD23	1:C:531:LEU:HD12	1.94	0.49
1:C:529:LYS:HA	1:C:532:ILE:HG12	1.93	0.49
1:C:637:LEU:HD12	1:C:638:HIS:N	2.27	0.49
1:C:795:ILE:O	1:C:799:VAL:HG23	2.13	0.49
1:A:26:ALA:O	1:A:30:LYS:HE2	2.11	0.49
1:A:114:THR:HB	1:A:154:GLN:HE21	1.77	0.49
1:A:232:ARG:NH1	1:A:270:HIS:O	2.38	0.49
1:A:269:LEU:HD23	1:A:272:LEU:HD11	1.93	0.49
1:A:802:LEU:HD22	1:A:852:THR:CG2	2.43	0.49
1:C:567:ARG:O	1:C:570:HIS:HB2	2.12	0.49
1:A:724:ILE:HG23	1:A:750:LEU:HD13	1.93	0.49
1:C:281:ARG:NH2	1:C:282:LEU:HA	2.28	0.49
1:C:445:LYS:NZ	1:C:462:LEU:HD21	2.28	0.49
1:A:106:LEU:HD22	1:A:134:MET:HE1	1.94	0.49
1:A:117:MET:SD	1:A:124:VAL:HA	2.51	0.49
1:A:237:GLY:O	1:A:241:GLU:OE1	2.30	0.49
1:A:389:LEU:O	1:A:393:PHE:HB2	2.12	0.49
1:A:802:LEU:HD11	1:A:825:ILE:HG22	1.95	0.49
2:D:103:ALA:O	2:D:107:LYS:HG3	2.13	0.49
1:A:395:ASP:O	1:A:399:HIS:ND1	2.45	0.49
1:A:581:PHE:HB2	1:A:612:LEU:HD21	1.95	0.49
2:D:89:GLU:OE1	2:D:89:GLU:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:LEU:HD22	1:A:22:ARG:NH2	2.21	0.49
1:A:140:HIS:CE1	1:A:142:VAL:HB	2.47	0.49
1:A:525:LEU:HB3	1:A:529:LYS:HZ2	1.78	0.49
2:B:24:PHE:CG	2:B:157:PHE:HE2	2.31	0.49
1:C:258:VAL:HA	1:C:261:GLN:NE2	2.25	0.49
1:A:84:HIS:HB2	1:A:85:PRO:HD3	1.94	0.48
1:A:390:TYR:HB2	1:A:426:TYR:CE2	2.47	0.48
1:C:200:GLU:HB2	1:C:204:ARG:NH2	2.27	0.48
1:C:244:VAL:HG12	1:C:281:ARG:NE	2.27	0.48
1:C:416:CYS:SG	1:C:461:SER:O	2.70	0.48
2:D:20:ILE:HG12	2:D:25:LYS:HZ3	1.76	0.48
2:D:80:HIS:HB2	2:D:162:VAL:HG12	1.95	0.48
1:A:195:GLN:O	1:A:204:ARG:HD3	2.13	0.48
1:C:584:LEU:HD12	1:C:612:LEU:HD22	1.95	0.48
1:C:624:ASP:HA	1:C:626:TRP:HD1	1.78	0.48
2:D:10:ASN:HB3	2:D:141:ALA:CB	2.43	0.48
2:D:115:TRP:CZ3	2:D:132:PHE:HB3	2.48	0.48
1:C:659:ARG:NH1	2:D:64:ARG:NH1	2.60	0.48
2:D:127:TYR:HB3	2:D:132:PHE:CE2	2.48	0.48
1:A:238:PRO:HA	1:A:241:GLU:CD	2.34	0.48
1:A:389:LEU:HD22	1:A:393:PHE:HE2	1.77	0.48
1:A:521:LEU:CD1	1:A:583:LEU:HD13	2.44	0.48
1:C:583:LEU:O	1:C:587:THR:HG23	2.13	0.48
2:D:28:LEU:HD21	2:D:157:PHE:CE1	2.48	0.48
2:D:137:SER:HB3	2:D:153:VAL:HG21	1.96	0.48
1:A:130:ASP:O	1:A:134:MET:HG3	2.12	0.48
1:A:394:PHE:HZ	1:A:439:TYR:HB2	1.78	0.48
1:C:221:ARG:O	1:C:225:LEU:HG	2.14	0.48
1:C:839:SER:O	1:C:842:VAL:N	2.46	0.48
2:D:83:LEU:HG	2:D:165:ILE:HA	1.95	0.48
2:D:93:LEU:HD21	2:D:104:GLU:HG3	1.96	0.48
2:B:169:LEU:O	2:B:189:VAL:N	2.36	0.48
1:C:617:LYS:HD2	1:C:671:THR:HA	1.96	0.48
1:A:440:ALA:O	1:A:444:VAL:HG23	2.13	0.48
1:A:759:ARG:HA	1:A:765:THR:HA	1.94	0.48
1:C:87:ASN:O	1:C:88:HIS:HB2	2.14	0.48
1:C:408:ILE:O	1:C:412:ILE:HG12	2.14	0.48
1:C:696:LYS:O	1:C:700:GLN:OE1	2.31	0.48
2:B:45:ARG:HD2	2:B:48:TYR:HD2	1.79	0.48
2:B:89:GLU:HB2	2:B:91:PHE:HD1	1.79	0.48
1:C:532:ILE:HB	1:C:597:ARG:NH1	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:585:GLN:HA	1:C:636:PHE:HE2	1.79	0.48
1:A:744:VAL:HG11	1:A:780:ARG:HG3	1.96	0.48
1:C:84:HIS:HB2	1:C:85:PRO:HD3	1.96	0.48
1:C:265:ASP:OD1	1:C:268:HIS:HD2	1.97	0.48
1:C:503:GLU:O	1:C:507:THR:HG23	2.14	0.48
1:C:752:TRP:HA	1:C:752:TRP:CE3	2.49	0.48
1:A:133:ASP:O	1:A:136:ARG:HB2	2.13	0.48
1:A:206:GLN:O	1:A:210:GLU:HG3	2.13	0.48
1:A:412:ILE:HG13	1:A:458:ALA:HB1	1.95	0.48
1:A:631:SER:HA	1:A:673:PHE:CZ	2.49	0.48
1:C:66:TYR:HE1	1:C:107:TYR:HH	1.58	0.48
1:C:245:GLN:HA	1:C:247:ARG:HH11	1.78	0.48
1:A:503:GLU:O	1:A:507:THR:HG23	2.13	0.47
1:A:685:PHE:O	1:A:689:GLU:OE1	2.32	0.47
1:C:444:VAL:O	1:C:448:ALA:N	2.46	0.47
1:C:586:MET:HA	1:C:589:LYS:NZ	2.29	0.47
1:C:683:GLN:O	1:C:687:VAL:HG23	2.14	0.47
1:A:388:PRO:HB2	1:A:391:ASP:HB2	1.96	0.47
1:A:433:VAL:HG12	1:A:482:LEU:HD11	1.96	0.47
1:A:517:THR:O	1:A:520:HIS:N	2.47	0.47
2:B:165:ILE:HG12	2:B:193:LYS:HB3	1.96	0.47
1:C:192:LEU:O	1:C:204:ARG:HD2	2.13	0.47
1:C:206:GLN:HA	1:C:209:ARG:HG3	1.96	0.47
1:C:426:TYR:CG	1:C:432:TYR:HD2	2.31	0.47
1:C:509:LEU:CD2	1:C:564:TRP:HE3	2.27	0.47
2:D:88:LEU:N	2:D:114:CYS:O	2.40	0.47
1:A:178:ILE:HG21	1:A:222:LEU:HG	1.94	0.47
1:A:409:GLN:HG3	1:A:458:ALA:HB2	1.95	0.47
1:A:459:GLN:HG3	1:A:496:THR:HG21	1.97	0.47
2:B:102:LEU:HB2	2:B:128:MET:HE3	1.95	0.47
1:C:60:LYS:HZ1	1:C:209:ARG:NH1	2.11	0.47
1:C:612:LEU:HG	1:C:616:PHE:CE2	2.49	0.47
1:A:232:ARG:HD2	1:A:270:HIS:CD2	2.49	0.47
1:A:521:LEU:HA	1:A:524:VAL:HG22	1.96	0.47
1:A:777:CYS:HA	1:A:780:ARG:CZ	2.44	0.47
2:B:171:VAL:HG13	2:B:187:GLU:HB3	1.97	0.47
1:C:697:ALA:HA	1:C:700:GLN:OE1	2.14	0.47
2:D:27:LEU:HD13	2:D:172:TYR:CD2	2.50	0.47
2:D:158:CYS:HB3	2:D:169:LEU:HD11	1.97	0.47
1:A:576:ASP:OD1	1:A:579:THR:HB	2.14	0.47
1:C:38:LEU:HD13	1:C:79:HIS:CD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:269:LEU:HA	1:C:272:LEU:CG	2.44	0.47
1:C:305:ARG:CZ	1:C:305:ARG:HB3	2.44	0.47
2:D:10:ASN:OD1	2:D:137:SER:HA	2.14	0.47
1:A:42:LEU:HD23	1:A:76:LEU:HD21	1.96	0.47
1:A:89:LEU:HD23	1:A:92:LEU:HD13	1.96	0.47
1:A:102:ILE:O	1:A:106:LEU:HG	2.15	0.47
1:A:180:THR:O	1:A:183:VAL:HG22	2.15	0.47
2:B:45:ARG:HA	2:B:48:TYR:CD2	2.49	0.47
2:D:176:LYS:HG2	2:D:182:GLU:OE2	2.14	0.47
1:A:454:HIS:NE2	1:A:495:PRO:HD2	2.28	0.47
1:A:454:HIS:CD2	1:A:496:THR:HG23	2.49	0.47
1:A:576:ASP:O	1:A:580:GLN:HG3	2.15	0.47
1:A:685:PHE:O	1:A:688:TYR:HB3	2.14	0.47
1:A:832:LEU:HD12	1:A:836:GLN:OE1	2.14	0.47
2:B:51:LEU:HD23	2:B:60:ILE:HD11	1.96	0.47
2:B:52:ARG:HH22	2:B:57:ASP:N	2.13	0.47
1:C:97:GLN:HG2	1:C:109:MET:SD	2.55	0.47
1:C:149:TYR:HB2	1:C:214:LEU:HG	1.96	0.47
1:C:228:LEU:HD11	1:C:270:HIS:CB	2.44	0.47
1:C:478:THR:O	1:C:481:SER:OG	2.23	0.47
1:C:733:LYS:HG2	1:C:733:LYS:O	2.15	0.47
1:C:767:LEU:O	1:C:768:TYR:C	2.53	0.47
2:D:23:LYS:HZ2	2:D:27:LEU:HD11	1.78	0.47
1:A:161:THR:OG1	1:A:162:GLY:N	2.47	0.47
1:A:299:LEU:O	1:A:302:TYR:HB3	2.15	0.47
1:A:409:GLN:HG3	1:A:458:ALA:H	1.80	0.47
1:A:429:ARG:HD3	1:A:432:TYR:CD2	2.50	0.47
1:A:760:GLY:O	1:A:764:ASP:N	2.47	0.47
1:A:783:ARG:O	1:A:786:ASP:OD1	2.33	0.47
1:C:47:THR:O	1:C:50:SER:HB2	2.15	0.47
1:C:161:THR:HB	1:C:174:SER:CB	2.45	0.47
1:C:560:GLU:HG2	1:C:561:GLU:OE2	2.15	0.47
1:C:710:HIS:CD2	1:C:755:PRO:HG2	2.50	0.47
2:D:120:HIS:CB	2:D:137:SER:HB2	2.45	0.47
2:B:62:ARG:HD2	2:B:72:LEU:HB2	1.97	0.47
2:B:163:GLN:NE2	2:B:168:THR:OG1	2.40	0.47
2:D:160:MET:HA	2:D:168:THR:O	2.15	0.47
1:A:265:ASP:OD1	1:A:268:HIS:HD2	1.98	0.47
1:A:477:PHE:HE2	1:A:514:LEU:HB2	1.79	0.47
2:B:6:LEU:HD13	2:B:28:LEU:HD22	1.96	0.47
1:C:576:ASP:O	1:C:580:GLN:HG3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:767:LEU:O	1:C:769:ARG:N	2.47	0.47
1:A:509:LEU:HB3	1:A:567:ARG:NH1	2.30	0.46
1:A:509:LEU:HD11	1:A:564:TRP:CE3	2.50	0.46
1:A:663:SER:HA	1:A:711:ARG:HH22	1.79	0.46
2:B:1:MET:HE1	2:B:5:ILE:H	1.79	0.46
2:B:58:LEU:HD21	2:B:60:ILE:HD11	1.97	0.46
2:B:127:TYR:HB3	2:B:132:PHE:CE2	2.51	0.46
1:A:81:ARG:O	1:A:85:PRO:HG2	2.15	0.46
1:A:189:TRP:CH2	1:A:212:GLN:HA	2.50	0.46
1:A:557:GLU:C	1:A:559:MET:H	2.18	0.46
1:A:802:LEU:HD11	1:A:825:ILE:CG2	2.45	0.46
2:B:1:MET:HG3	2:B:162:VAL:N	2.07	0.46
1:C:222:LEU:O	1:C:225:LEU:HB2	2.16	0.46
1:C:445:LYS:HZ3	1:C:462:LEU:HD11	1.81	0.46
1:C:610:LEU:HD12	1:C:611:LYS:N	2.29	0.46
2:D:87:PHE:HB2	2:D:114:CYS:HB2	1.96	0.46
1:A:244:VAL:HG21	1:A:281:ARG:NH2	2.31	0.46
1:A:696:LYS:O	1:A:700:GLN:OE1	2.33	0.46
1:C:53:ARG:HH21	1:C:101:ASN:HB3	1.80	0.46
1:C:105:ARG:O	1:C:109:MET:HG2	2.16	0.46
1:C:217:SER:O	1:C:220:VAL:HG22	2.16	0.46
1:C:533:LYS:NZ	1:C:593:GLU:HA	2.30	0.46
1:C:562:GLN:N	1:C:562:GLN:OE1	2.48	0.46
1:C:751:TRP:O	1:C:768:TYR:HB2	2.14	0.46
1:C:800:GLU:HG3	1:C:848:HIS:HE1	1.80	0.46
2:D:112:VAL:HA	2:D:131:PHE:HB3	1.97	0.46
1:A:675:GLU:OE2	1:A:676:VAL:HG13	2.15	0.46
1:A:780:ARG:CB	1:A:783:ARG:HH11	2.26	0.46
2:B:115:TRP:CZ2	2:B:134:ASN:HB2	2.50	0.46
1:C:261:GLN:CD	1:C:262:VAL:HG23	2.35	0.46
1:C:453:LEU:O	1:C:453:LEU:HD12	2.16	0.46
2:D:58:LEU:HG	2:D:60:ILE:HD11	1.97	0.46
2:D:113:LEU:O	2:D:133:VAL:N	2.42	0.46
1:A:21:VAL:HG22	1:A:48:LEU:HG	1.96	0.46
1:A:408:ILE:HA	1:A:447:HIS:HE1	1.78	0.46
1:C:659:ARG:HH22	2:D:64:ARG:HD3	1.80	0.46
2:D:138:ALA:HA	2:D:156:SER:OG	2.16	0.46
2:B:41:ASN:OD1	2:B:65:MET:HB2	2.16	0.46
2:B:156:SER:CB	2:B:173:GLN:HG2	2.45	0.46
1:C:244:VAL:HA	1:C:281:ARG:HH11	1.81	0.46
1:C:607:THR:O	1:C:610:LEU:HG	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:PHE:O	1:A:398:GLN:OE1	2.33	0.46
1:A:656:LEU:O	1:A:660:LEU:HG	2.16	0.46
1:C:752:TRP:C	1:C:754:THR:H	2.18	0.46
1:A:121:GLY:O	1:A:124:VAL:HG23	2.15	0.46
1:A:633:LEU:O	1:A:637:LEU:HG	2.16	0.46
1:A:715:PHE:CD1	1:A:723:LEU:HD11	2.50	0.46
2:B:174:LEU:HD12	2:B:183:ASN:C	2.36	0.46
1:C:253:GLU:HG2	1:C:254:TYR:N	2.31	0.46
2:D:75:MET:SD	2:D:76:GLN:N	2.89	0.46
1:A:25:THR:HB	1:A:29:ARG:NH2	2.31	0.46
1:A:103:ILE:O	1:A:107:TYR:HD2	1.99	0.46
1:A:475:SER:OG	1:A:477:PHE:HB2	2.16	0.46
2:B:42:LEU:HD23	2:B:47:THR:HG22	1.98	0.46
2:B:42:LEU:N	2:B:43:THR:HA	2.31	0.46
1:C:79:HIS:CD2	1:C:83:ASN:ND2	2.84	0.46
1:C:200:GLU:HB2	1:C:204:ARG:HH22	1.80	0.46
1:C:626:TRP:HZ3	1:C:671:THR:HB	1.81	0.46
1:A:25:THR:HA	1:A:28:MET:CE	2.46	0.46
1:A:466:LEU:HD22	1:A:489:PHE:CZ	2.51	0.46
1:A:506:ARG:O	1:A:510:LYS:HD3	2.16	0.46
1:C:659:ARG:NH2	2:D:65:MET:HG2	2.31	0.46
1:C:672:GLU:OE1	1:C:714:ASN:ND2	2.36	0.46
1:C:780:ARG:HA	1:C:783:ARG:HG2	1.97	0.46
1:A:42:LEU:HD22	1:A:108:LEU:HD22	1.98	0.45
1:A:141:PRO:HA	1:A:188:LEU:HD22	1.97	0.45
1:A:480:LEU:HG	1:A:523:ASN:CB	2.46	0.45
1:A:494:TYR:OH	1:A:534:GLU:OE1	2.32	0.45
1:A:620:GLU:HA	1:A:626:TRP:CD1	2.51	0.45
1:A:695:SER:HA	1:A:698:GLN:OE1	2.17	0.45
1:C:101:ASN:HB3	1:C:104:PRO:HD2	1.99	0.45
1:C:512:GLN:HA	1:C:567:ARG:NH2	2.31	0.45
1:C:591:TYR:HA	1:C:593:GLU:HG2	1.98	0.45
1:C:194:HIS:HA	1:C:201:ARG:NH2	2.31	0.45
1:C:529:LYS:HZ3	1:C:590:ALA:HB1	1.80	0.45
1:C:694:ASP:O	1:C:698:GLN:HG3	2.15	0.45
1:C:734:LEU:HD11	1:C:739:ASP:C	2.37	0.45
1:C:839:SER:H	1:C:842:VAL:HB	1.82	0.45
1:A:238:PRO:HA	1:A:241:GLU:OE2	2.16	0.45
1:A:583:LEU:O	1:A:586:MET:HG3	2.17	0.45
2:B:115:TRP:O	2:B:134:ASN:HA	2.16	0.45
2:B:121:ARG:NH2	2:B:153:VAL:HG13	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:607:THR:CA	1:C:610:LEU:HG	2.42	0.45
1:C:763:GLU:CD	1:C:768:TYR:HA	2.37	0.45
1:C:93:TYR:CE1	1:C:131:MET:HE2	2.52	0.45
1:C:161:THR:HB	1:C:174:SER:HB2	1.99	0.45
1:C:440:ALA:O	1:C:444:VAL:HG23	2.16	0.45
1:C:645:TYR:O	1:C:648:VAL:HG13	2.16	0.45
1:C:755:PRO:HG3	2:D:94:VAL:O	2.16	0.45
1:A:583:LEU:HA	1:A:586:MET:HG3	1.99	0.45
2:B:8:ILE:HG22	2:B:157:PHE:HB2	1.98	0.45
1:C:111:THR:OG1	1:C:150:TYR:OH	2.17	0.45
1:C:206:GLN:O	1:C:210:GLU:HG3	2.16	0.45
1:C:209:ARG:O	1:C:212:GLN:HG2	2.17	0.45
1:C:289:LYS:CE	1:C:406:LEU:HD13	2.45	0.45
1:C:506:ARG:HH21	1:C:557:GLU:HG2	1.82	0.45
1:C:634:PHE:HA	1:C:637:LEU:CD2	2.46	0.45
2:D:35:GLN:HA	2:D:57:ASP:O	2.16	0.45
1:A:161:THR:OG1	1:A:171:LEU:HD23	2.17	0.45
1:A:221:ARG:NH1	1:A:224:GLN:HB2	2.31	0.45
1:C:24:GLN:HB2	1:C:48:LEU:HB2	1.99	0.45
1:C:260:THR:HG21	1:C:298:ARG:HD3	1.98	0.45
1:C:529:LYS:HD3	1:C:529:LYS:HA	1.82	0.45
2:D:16:ARG:NH1	2:D:142:PHE:O	2.48	0.45
1:A:193:GLN:O	1:A:204:ARG:NE	2.50	0.45
1:A:259:ILE:HG23	1:A:263:PHE:CD2	2.51	0.45
1:A:480:LEU:HD22	1:A:520:HIS:CD2	2.52	0.45
1:A:529:LYS:HE3	1:A:590:ALA:HB1	1.99	0.45
1:A:647:ARG:HD2	1:A:647:ARG:N	2.32	0.45
1:A:803:ASP:HB3	1:A:804:ARG:NH2	2.31	0.45
1:A:807:TYR:O	1:A:811:GLN:HG2	2.17	0.45
1:A:808:TYR:HB3	1:A:813:ASN:HB3	1.97	0.45
1:C:221:ARG:HH11	1:C:224:GLN:HG3	1.81	0.45
1:C:463:LEU:O	1:C:467:GLN:HG2	2.16	0.45
1:C:638:HIS:ND1	1:C:680:PHE:CZ	2.83	0.45
1:C:659:ARG:HH22	2:D:65:MET:HG2	1.82	0.45
1:C:758:ALA:HB3	1:C:767:LEU:HB3	1.99	0.45
1:A:14:LEU:HB2	1:A:61:GLN:HB3	1.98	0.45
1:A:106:LEU:CD2	1:A:134:MET:HE1	2.47	0.45
1:A:220:VAL:HG12	1:A:224:GLN:HE22	1.81	0.45
1:A:245:GLN:O	1:A:247:ARG:HG2	2.16	0.45
1:A:390:TYR:OH	1:A:432:TYR:O	2.21	0.45
1:A:641:ILE:HG23	1:A:644:LEU:HD21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:723:LEU:HA	1:A:726:LYS:HE2	1.97	0.45
1:A:808:TYR:HB3	1:A:813:ASN:CB	2.46	0.45
2:D:10:ASN:HB3	2:D:141:ALA:HB3	1.99	0.45
2:D:126:GLU:HG2	2:D:131:PHE:CD1	2.52	0.45
1:A:300:SER:HB3	1:A:420:ASN:HD22	1.82	0.45
1:A:468:SER:HA	1:A:471:ARG:NE	2.32	0.45
1:C:423:LEU:HA	1:C:423:LEU:HD23	1.75	0.45
1:C:445:LYS:HZ3	1:C:462:LEU:HD21	1.81	0.45
1:A:92:LEU:HA	1:A:95:LEU:HB2	1.98	0.45
1:A:110:ILE:HG22	1:A:154:GLN:HG3	1.99	0.45
1:A:138:VAL:HG11	1:A:144:GLY:CA	2.46	0.45
1:A:533:LYS:HB3	1:A:534:GLU:HA	1.98	0.45
1:A:661:PHE:CD1	1:A:684:ALA:HB2	2.52	0.45
2:B:165:ILE:CG1	2:B:193:LYS:HB3	2.46	0.45
1:C:72:ALA:HA	1:C:75:TYR:HD2	1.81	0.45
1:A:24:GLN:CB	1:A:48:LEU:HB2	2.47	0.44
1:A:96:VAL:HG11	1:A:112:VAL:CG2	2.47	0.44
1:A:745:TYR:CE2	2:B:94:VAL:HG11	2.48	0.44
1:C:221:ARG:HA	1:C:224:GLN:HG2	1.99	0.44
1:C:709:LEU:O	1:C:712:THR:N	2.42	0.44
1:C:709:LEU:C	1:C:711:ARG:H	2.19	0.44
2:D:5:ILE:HG23	2:D:37:LEU:HG	1.99	0.44
1:A:152:SER:HB3	1:A:156:ARG:NE	2.32	0.44
1:A:235:ILE:O	1:A:239:LEU:HG	2.17	0.44
1:A:277:GLY:O	1:A:281:ARG:HG3	2.17	0.44
1:A:303:ALA:HA	1:A:425:ILE:HD11	2.00	0.44
2:B:42:LEU:HB3	2:B:47:THR:HB	2.00	0.44
1:C:406:LEU:HD12	1:C:414:LEU:HD11	1.99	0.44
1:C:780:ARG:O	1:C:784:VAL:HG23	2.17	0.44
1:A:159:LEU:HB3	1:A:174:SER:OG	2.18	0.44
1:C:736:ARG:C	1:C:740:GLN:HG2	2.38	0.44
1:C:799:VAL:HG12	1:C:848:HIS:CE1	2.52	0.44
1:A:264:PRO:HG2	1:A:267:TYR:CD2	2.53	0.44
1:A:442:ALA:O	1:A:446:GLU:OE1	2.36	0.44
2:B:96:GLU:HA	2:B:101:LEU:HD21	2.00	0.44
2:B:173:GLN:OE1	2:B:175:ARG:NH2	2.47	0.44
1:C:463:LEU:HD13	1:C:500:ILE:HG12	1.99	0.44
1:C:466:LEU:O	1:C:469:PRO:HD2	2.17	0.44
2:D:115:TRP:CE2	2:D:134:ASN:HB2	2.53	0.44
1:A:152:SER:HB3	1:A:156:ARG:HH21	1.81	0.44
1:A:182:PHE:HE2	1:A:242:GLN:CB	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:VAL:HG12	1:A:255:LEU:HD21	1.99	0.44
1:A:500:ILE:HA	1:A:503:GLU:HG3	2.00	0.44
1:A:610:LEU:O	1:A:614:ARG:HG3	2.17	0.44
1:A:800:GLU:HG2	1:A:848:HIS:HE1	1.81	0.44
2:B:161:ASP:HB3	2:B:168:THR:HB	1.99	0.44
1:C:272:LEU:HD13	1:C:389:LEU:HD11	1.99	0.44
1:C:662:CYS:O	1:C:666:GLN:OE1	2.34	0.44
1:C:802:LEU:HD12	1:C:824:LEU:HB3	1.99	0.44
2:D:12:HIS:HB3	2:D:16:ARG:N	2.32	0.44
2:B:173:GLN:O	2:B:185:ALA:N	2.37	0.44
1:C:244:VAL:HA	1:C:281:ARG:HE	1.83	0.44
1:C:437:LEU:O	1:C:442:ALA:N	2.41	0.44
1:C:739:ASP:OD1	1:C:742:ARG:NH1	2.51	0.44
1:A:283:ASN:HB2	1:A:286:VAL:HG13	1.99	0.44
1:A:438:ALA:O	1:A:443:LYS:NZ	2.35	0.44
1:A:468:SER:HA	1:A:471:ARG:CG	2.46	0.44
1:A:612:LEU:HG	1:A:616:PHE:CE2	2.53	0.44
1:A:683:GLN:O	1:A:687:VAL:HG23	2.18	0.44
1:A:709:LEU:HD21	1:A:724:ILE:HD13	1.98	0.44
2:B:13:ILE:O	2:B:43:THR:HG23	2.18	0.44
2:B:16:ARG:NH1	2:B:142:PHE:O	2.38	0.44
1:C:24:GLN:CB	1:C:48:LEU:HB2	2.48	0.44
1:C:265:ASP:HA	1:C:268:HIS:CD2	2.53	0.44
1:C:749:HIS:NE2	2:D:94:VAL:HG11	2.33	0.44
2:D:62:ARG:NH2	2:D:73:PRO:HA	2.32	0.44
1:A:126:GLU:OE2	1:A:127:LEU:HG	2.18	0.44
1:A:843:GLU:OE2	1:A:846:ARG:NH2	2.51	0.44
1:A:149:TYR:OH	1:A:214:LEU:HD12	2.18	0.43
1:A:232:ARG:HD2	1:A:270:HIS:HD2	1.83	0.43
1:A:751:TRP:HZ3	1:A:777:CYS:HB2	1.82	0.43
2:B:117:GLY:O	2:B:120:HIS:HD2	2.00	0.43
1:C:222:LEU:HA	1:C:225:LEU:HD12	2.00	0.43
1:C:257:GLU:OE2	1:C:258:VAL:HG23	2.18	0.43
1:C:276:LEU:HD13	1:C:392:ILE:CG2	2.48	0.43
1:C:532:ILE:HG13	1:C:533:LYS:HG3	1.99	0.43
1:C:679:GLU:HG3	1:C:680:PHE:N	2.33	0.43
1:A:231:TYR:HA	1:A:235:ILE:HD12	1.99	0.43
1:A:392:ILE:O	1:A:395:ASP:OD1	2.36	0.43
1:A:494:TYR:O	1:A:497:ARG:HB2	2.18	0.43
1:A:850:ILE:O	1:A:854:GLU:HG3	2.17	0.43
1:C:103:ILE:O	1:C:107:TYR:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:471:ARG:HG3	1:C:472:ARG:N	2.33	0.43
1:C:663:SER:HA	1:C:666:GLN:OE1	2.19	0.43
1:C:709:LEU:C	1:C:711:ARG:N	2.71	0.43
2:D:38:CYS:HB3	2:D:51:LEU:HD21	2.00	0.43
1:A:304:GLU:CD	1:A:420:ASN:HD21	2.21	0.43
1:A:412:ILE:HG21	1:A:458:ALA:O	2.18	0.43
1:A:500:ILE:O	1:A:503:GLU:HG3	2.19	0.43
2:B:172:TYR:CD2	2:B:186:VAL:HG22	2.53	0.43
1:C:276:LEU:HA	1:C:276:LEU:HD23	1.76	0.43
1:C:279:VAL:O	1:C:400:LEU:HD21	2.18	0.43
1:C:763:GLU:O	1:C:766:GLU:HB3	2.18	0.43
2:D:174:LEU:HD12	2:D:183:ASN:C	2.37	0.43
1:A:66:TYR:CD1	1:A:146:PHE:HB3	2.54	0.43
1:A:746:LEU:HD21	2:B:94:VAL:HG12	1.99	0.43
2:B:13:ILE:HG12	2:B:18:LEU:HA	1.99	0.43
1:C:20:ALA:O	1:C:24:GLN:HG2	2.18	0.43
1:C:185:MET:HE3	1:C:218:ASN:HD21	1.82	0.43
1:C:506:ARG:HD2	1:C:557:GLU:CG	2.37	0.43
1:C:606:ILE:HG13	1:C:660:LEU:CD2	2.48	0.43
1:C:759:ARG:HG3	1:C:767:LEU:HD23	2.00	0.43
1:A:66:TYR:HA	1:A:69:VAL:HG22	2.00	0.43
1:A:585:GLN:C	1:A:589:LYS:HZ3	2.21	0.43
1:C:201:ARG:NH2	1:C:204:ARG:NE	2.66	0.43
1:C:296:MET:SD	1:C:421:LEU:HB2	2.59	0.43
1:C:393:PHE:O	1:C:397:VAL:HG23	2.18	0.43
1:C:561:GLU:CB	1:C:564:TRP:HB3	2.45	0.43
1:C:617:LYS:HD2	1:C:671:THR:HG22	2.00	0.43
1:C:617:LYS:C	1:C:619:ARG:H	2.22	0.43
2:D:7:VAL:HG21	2:D:160:MET:CE	2.49	0.43
1:A:85:PRO:HA	1:A:119:ILE:HD13	1.99	0.43
1:A:140:HIS:HE1	1:A:142:VAL:HB	1.82	0.43
1:A:185:MET:SD	1:A:218:ASN:ND2	2.92	0.43
1:A:276:LEU:HD21	1:A:393:PHE:CD1	2.53	0.43
1:A:688:TYR:CZ	1:A:730:HIS:HB2	2.54	0.43
1:C:171:LEU:CD2	1:C:226:VAL:HG12	2.45	0.43
2:D:77:VAL:HG21	2:D:84:ARG:CZ	2.48	0.43
1:A:211:LEU:HB3	1:A:214:LEU:HD22	1.99	0.43
1:A:470:LEU:CD1	1:A:504:ILE:HG12	2.49	0.43
1:A:723:LEU:HA	1:A:726:LYS:NZ	2.34	0.43
1:C:453:LEU:HB2	1:C:456:GLN:HB2	2.01	0.43
1:C:690:GLU:OE1	1:C:691:SER:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:6:LEU:HD12	2:D:158:CYS:O	2.18	0.43
1:A:27:MET:HG2	1:A:44:CYS:SG	2.59	0.43
1:A:48:LEU:HD21	1:A:69:VAL:HG12	2.01	0.43
1:A:95:LEU:HD23	1:A:98:TYR:CE2	2.53	0.43
1:C:296:MET:HE3	1:C:417:SER:HB2	2.00	0.43
1:C:587:THR:O	1:C:590:ALA:N	2.52	0.43
1:C:676:VAL:O	1:C:680:PHE:CD1	2.72	0.43
1:C:822:ASN:HA	1:C:825:ILE:HG12	2.00	0.43
1:A:20:ALA:O	1:A:24:GLN:HG2	2.18	0.43
1:A:222:LEU:O	1:A:225:LEU:HB2	2.18	0.43
2:B:75:MET:SD	2:B:92:THR:OG1	2.55	0.43
1:C:588:ARG:HH21	1:C:640:ALA:N	2.17	0.43
1:C:634:PHE:CA	1:C:637:LEU:HG	2.44	0.43
1:C:641:ILE:HG12	1:C:660:LEU:HD23	2.00	0.43
1:C:656:LEU:O	1:C:660:LEU:HD13	2.19	0.43
1:C:713:ARG:HD2	1:C:714:ASN:HB3	2.00	0.43
2:D:5:ILE:O	2:D:159:LEU:HA	2.19	0.43
1:A:24:GLN:O	1:A:28:MET:HG3	2.19	0.43
1:A:470:LEU:HD23	1:A:476:ILE:HG23	2.00	0.43
1:A:749:HIS:O	1:A:755:PRO:HD3	2.17	0.43
1:A:804:ARG:O	1:A:807:TYR:HB3	2.18	0.43
1:C:96:VAL:HG11	1:C:112:VAL:HG21	1.99	0.43
1:C:249:ILE:HD13	1:C:287:ASN:HB2	2.01	0.43
1:C:506:ARG:HE	1:C:509:LEU:CD1	2.29	0.43
2:D:23:LYS:HD2	2:D:184:VAL:HG21	2.00	0.43
2:D:42:LEU:CD2	2:D:48:TYR:HB2	2.49	0.43
2:D:177:ASP:OD1	2:D:181:THR:N	2.52	0.43
1:A:81:ARG:HG2	1:A:115:ALA:HA	2.01	0.42
1:A:265:ASP:HA	1:A:268:HIS:HB2	2.01	0.42
1:A:518:PRO:HA	1:A:521:LEU:HB2	2.00	0.42
1:A:557:GLU:O	1:A:558:THR:OG1	2.31	0.42
2:B:12:HIS:HE1	2:B:64:ARG:NH2	2.17	0.42
1:C:477:PHE:HE1	1:C:513:THR:OG1	2.02	0.42
1:C:713:ARG:HD2	1:C:714:ASN:N	2.34	0.42
1:A:129:LYS:HA	1:A:129:LYS:HD2	1.90	0.42
1:A:160:PRO:O	1:A:174:SER:OG	2.35	0.42
1:A:291:ILE:O	1:A:295:MET:HG2	2.19	0.42
1:C:161:THR:HA	1:C:170:ASN:O	2.18	0.42
1:C:521:LEU:O	1:C:525:LEU:HG	2.18	0.42
2:D:5:ILE:HA	2:D:35:GLN:O	2.19	0.42
1:A:14:LEU:O	1:A:18:LEU:HG	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:LEU:HD21	1:A:270:HIS:CG	2.54	0.42
1:A:470:LEU:HD11	1:A:504:ILE:HG12	2.01	0.42
1:A:503:GLU:OE2	1:A:504:ILE:HG13	2.19	0.42
1:A:588:ARG:NH2	1:A:643:THR:OG1	2.52	0.42
1:A:669:ASP:CB	1:A:713:ARG:HH22	2.32	0.42
1:A:852:THR:O	1:A:855:MET:HG2	2.19	0.42
1:C:97:GLN:O	1:C:105:ARG:HD2	2.19	0.42
1:C:180:THR:HA	1:C:183:VAL:HG22	2.00	0.42
1:C:249:ILE:HG12	1:C:286:VAL:HG13	2.00	0.42
1:C:419:ALA:O	1:C:423:LEU:HG	2.19	0.42
1:A:25:THR:HB	1:A:29:ARG:HH22	1.85	0.42
1:A:152:SER:CA	1:A:156:ARG:HB2	2.46	0.42
1:A:160:PRO:HB2	1:A:169:GLY:HA2	2.01	0.42
1:A:520:HIS:O	1:A:524:VAL:HG22	2.19	0.42
1:C:48:LEU:HD21	1:C:69:VAL:HA	2.01	0.42
1:C:482:LEU:HD22	1:C:484:THR:OG1	2.19	0.42
1:A:412:ILE:HD12	1:A:462:LEU:HD21	2.01	0.42
1:A:720:TYR:O	1:A:724:ILE:HG12	2.20	0.42
2:B:176:LYS:HA	2:B:181:THR:O	2.19	0.42
1:C:132:MET:HE3	1:C:184:GLU:OE2	2.19	0.42
1:C:149:TYR:CD1	1:C:214:LEU:HG	2.54	0.42
1:C:567:ARG:O	1:C:571:LEU:HG	2.19	0.42
1:A:420:ASN:HA	1:A:471:ARG:NH1	2.34	0.42
1:A:443:LYS:HD3	1:A:443:LYS:H	1.83	0.42
1:A:480:LEU:CD2	1:A:520:HIS:HA	2.43	0.42
2:B:0:SER:N	2:B:163:GLN:HA	2.34	0.42
2:B:101:LEU:HA	2:B:104:GLU:HG3	2.02	0.42
1:C:709:LEU:HA	1:C:712:THR:OG1	2.20	0.42
1:A:179:LEU:O	1:A:183:VAL:HG13	2.18	0.42
1:A:437:LEU:CD1	1:A:488:LEU:HD12	2.50	0.42
2:B:90:GLY:HA2	2:B:93:LEU:HB3	2.02	0.42
1:C:81:ARG:O	1:C:85:PRO:HG2	2.19	0.42
1:C:290:ALA:HA	1:C:293:ILE:HG12	2.01	0.42
1:C:409:GLN:HG3	1:C:457:PRO:HB2	2.01	0.42
1:C:744:VAL:O	1:C:777:CYS:SG	2.78	0.42
2:D:0:SER:C	2:D:2:ALA:H	2.23	0.42
2:D:93:LEU:HD22	2:D:100:VAL:CG1	2.49	0.42
1:A:64:GLU:O	1:A:67:MET:HG2	2.19	0.42
1:A:161:THR:HB	1:A:174:SER:OG	2.19	0.42
1:A:238:PRO:HA	1:A:241:GLU:OE1	2.20	0.42
1:A:197:HIS:ND1	1:A:199:ARG:HG2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:LEU:HD22	1:A:396:GLN:OE1	2.20	0.42
1:A:476:ILE:HG21	1:A:508:LEU:HD21	2.02	0.42
1:A:634:PHE:HB2	1:A:673:PHE:HE2	1.84	0.42
1:A:677:ALA:O	1:A:681:PHE:HD2	2.03	0.42
1:C:159:LEU:HB3	1:C:174:SER:OG	2.20	0.42
1:A:149:TYR:HE1	1:A:214:LEU:HA	1.82	0.42
1:A:183:VAL:C	1:A:187:LYS:HZ2	2.23	0.42
1:A:393:PHE:O	1:A:397:VAL:HG23	2.20	0.42
1:A:629:GLN:O	1:A:633:LEU:HD13	2.20	0.42
1:C:222:LEU:HD21	1:C:235:ILE:HG12	2.02	0.42
1:C:446:GLU:HG3	1:C:447:HIS:N	2.35	0.42
1:C:479:ALA:O	1:C:485:TYR:HB2	2.20	0.42
1:A:148:ARG:NH1	1:A:181:ASN:OD1	2.52	0.41
1:A:175:ILE:HD11	1:A:226:VAL:CG2	2.49	0.41
1:A:301:ASP:C	1:A:303:ALA:H	2.23	0.41
1:A:395:ASP:HA	1:A:398:GLN:OE1	2.20	0.41
1:A:433:VAL:CG1	1:A:482:LEU:HD11	2.50	0.41
2:B:137:SER:OG	2:B:140:GLY:N	2.53	0.41
1:C:25:THR:HG22	1:C:72:ALA:HB2	2.02	0.41
1:C:236:LEU:CD2	1:C:271:THR:HB	2.50	0.41
1:A:110:ILE:HD12	1:A:147:LEU:HD11	2.02	0.41
1:A:145:LEU:HB3	1:A:214:LEU:CD2	2.49	0.41
1:A:227:ASP:HA	1:A:267:TYR:OH	2.20	0.41
1:A:269:LEU:HD21	1:A:302:TYR:OH	2.19	0.41
1:A:423:LEU:HD23	1:A:423:LEU:HA	1.59	0.41
1:A:597:ARG:O	1:A:601:THR:HG23	2.20	0.41
1:A:616:PHE:HD1	1:A:619:ARG:HH11	1.68	0.41
1:A:682:ALA:HA	1:A:685:PHE:HD2	1.73	0.41
2:B:62:ARG:CD	2:B:72:LEU:HB2	2.50	0.41
1:C:804:ARG:O	1:C:808:TYR:CD2	2.73	0.41
1:C:808:TYR:O	1:C:813:ASN:N	2.39	0.41
2:D:41:ASN:OD1	2:D:65:MET:N	2.53	0.41
2:D:88:LEU:HG	2:D:89:GLU:N	2.35	0.41
1:A:454:HIS:CD2	1:A:493:THR:HG1	2.36	0.41
2:B:10:ASN:CG	2:B:116:ALA:HB1	2.40	0.41
1:C:53:ARG:HH22	1:C:103:ILE:N	2.10	0.41
1:C:201:ARG:NH2	1:C:204:ARG:HE	2.18	0.41
1:C:275:PHE:CZ	1:C:295:MET:HG2	2.54	0.41
1:C:437:LEU:O	1:C:441:LEU:HB2	2.20	0.41
1:C:661:PHE:HD1	1:C:680:PHE:CD2	2.38	0.41
1:A:96:VAL:CG1	1:A:112:VAL:HG21	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:445:LYS:HE2	1:A:445:LYS:HA	2.02	0.41
1:C:463:LEU:CD1	1:C:500:ILE:HG12	2.50	0.41
1:C:473:TYR:CB	1:C:476:ILE:HG12	2.50	0.41
1:C:683:GLN:O	1:C:686:THR:HB	2.20	0.41
1:C:802:LEU:HD22	1:C:852:THR:CG2	2.50	0.41
2:D:13:ILE:HA	2:D:14:PRO:HA	1.77	0.41
2:D:89:GLU:OE2	2:D:91:PHE:HE2	2.03	0.41
2:D:121:ARG:HH12	2:D:146:TRP:C	2.23	0.41
1:A:101:ASN:HB3	1:A:104:PRO:HD2	2.02	0.41
1:A:299:LEU:HA	1:A:302:TYR:HB3	2.03	0.41
1:A:615:ARG:O	1:A:619:ARG:NH2	2.53	0.41
1:A:620:GLU:HA	1:A:626:TRP:NE1	2.34	0.41
1:A:752:TRP:HE1	1:A:811:GLN:HG3	1.84	0.41
1:C:264:PRO:HG2	1:C:267:TYR:CG	2.54	0.41
1:C:668:ALA:O	1:C:673:PHE:N	2.53	0.41
1:C:672:GLU:OE2	1:C:713:ARG:NH1	2.43	0.41
1:C:707:SER:O	1:C:710:HIS:HB2	2.20	0.41
1:A:81:ARG:HD3	1:A:114:THR:HG22	2.03	0.41
1:A:259:ILE:HG23	1:A:263:PHE:HD2	1.86	0.41
1:A:260:THR:HG22	1:A:298:ARG:NH1	2.35	0.41
1:A:740:GLN:O	1:A:744:VAL:HG23	2.21	0.41
1:A:752:TRP:HE1	1:A:811:GLN:CB	2.33	0.41
2:B:4:LEU:HD12	2:B:32:LYS:O	2.21	0.41
1:C:400:LEU:HA	1:C:400:LEU:HD23	1.83	0.41
1:C:426:TYR:CD1	1:C:429:ARG:HG2	2.55	0.41
1:C:559:MET:HA	1:C:560:GLU:HA	1.36	0.41
1:A:52:LEU:HD21	1:A:66:TYR:HA	2.03	0.41
1:A:166:GLY:N	1:A:167:PRO:HD3	2.35	0.41
1:C:465:LEU:O	1:C:468:SER:HB2	2.21	0.41
2:D:168:THR:HG21	2:D:188:LYS:NZ	2.36	0.41
1:A:260:THR:HG22	1:A:298:ARG:CZ	2.51	0.41
1:A:559:MET:HA	1:A:560:GLU:HA	1.66	0.41
1:A:641:ILE:HG22	1:A:645:TYR:HE2	1.80	0.41
1:A:668:ALA:HB3	1:A:677:ALA:HB2	2.02	0.41
1:C:117:MET:HB3	1:C:158:TYR:CD1	2.55	0.41
1:C:594:GLY:O	1:C:598:ILE:HG12	2.21	0.41
1:C:616:PHE:CD1	1:C:629:GLN:HB3	2.55	0.41
1:C:668:ALA:HB3	1:C:677:ALA:HB2	2.02	0.41
1:C:737:LYS:HB3	1:C:738:PRO:HD3	2.03	0.41
1:C:749:HIS:ND1	1:C:754:THR:HG23	2.36	0.41
1:C:754:THR:OG1	2:D:95:SER:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:795:ILE:CD1	1:C:831:ASN:HB3	2.51	0.41
1:C:846:ARG:CZ	1:C:846:ARG:HB2	2.51	0.41
2:D:77:VAL:HG22	2:D:85:ILE:O	2.20	0.41
1:A:389:LEU:HD23	1:A:389:LEU:HA	1.72	0.41
1:A:416:CYS:SG	1:A:465:LEU:HB2	2.61	0.41
1:A:466:LEU:HD13	1:A:489:PHE:CE2	2.56	0.41
1:A:560:GLU:HB2	1:A:564:TRP:CE3	2.56	0.41
1:A:566:ALA:C	1:A:570:HIS:HD1	2.11	0.41
1:A:685:PHE:HZ	1:A:723:LEU:CD2	2.34	0.41
1:A:696:LYS:HA	1:A:699:PHE:CD2	2.54	0.41
1:C:25:THR:HA	1:C:28:MET:CG	2.49	0.41
1:C:175:ILE:HD11	1:C:226:VAL:HG21	2.03	0.41
1:C:225:LEU:HB3	1:C:226:VAL:H	1.74	0.41
1:C:482:LEU:HB2	1:C:485:TYR:HB2	2.03	0.41
1:C:518:PRO:HA	1:C:583:LEU:HD21	2.02	0.41
1:C:569:VAL:HG13	1:C:608:ALA:HB2	2.03	0.41
1:C:593:GLU:O	1:C:597:ARG:HD2	2.20	0.41
1:C:610:LEU:HD13	1:C:614:ARG:NH2	2.33	0.41
1:C:701:ALA:O	1:C:705:ILE:HG13	2.21	0.41
1:C:827:LEU:O	1:C:831:ASN:ND2	2.54	0.41
2:D:83:LEU:HD21	2:D:193:LYS:HB2	2.01	0.41
2:D:98:PRO:HD2	2:D:99:ASP:H	1.85	0.41
2:D:161:ASP:HB3	2:D:168:THR:HB	2.03	0.41
1:A:45:CYS:O	1:A:49:VAL:HG23	2.21	0.41
1:A:243:ILE:HD13	1:A:256:LEU:CD2	2.51	0.41
1:A:302:TYR:O	1:A:302:TYR:CD2	2.73	0.41
2:B:64:ARG:HB3	2:B:91:PHE:HB3	2.02	0.41
2:B:111:ASP:HB3	2:B:191:TYR:OH	2.21	0.41
1:C:132:MET:HE1	1:C:181:ASN:N	2.36	0.41
1:C:436:ILE:O	1:C:440:ALA:HB3	2.21	0.41
1:C:473:TYR:HB3	1:C:476:ILE:HG12	2.02	0.41
1:C:772:LYS:HD3	1:C:815:SER:HB3	2.03	0.41
1:C:805:TYR:HD1	1:C:816:VAL:HG13	1.86	0.41
2:D:156:SER:HA	2:D:172:TYR:O	2.21	0.41
1:A:99:ALA:HB3	1:A:105:ARG:HB2	2.04	0.40
1:A:166:GLY:N	1:A:167:PRO:CD	2.84	0.40
1:A:583:LEU:O	1:A:587:THR:HG23	2.20	0.40
1:A:746:LEU:HD11	2:B:94:VAL:HG13	2.03	0.40
1:C:17:ALA:O	1:C:21:VAL:HG23	2.22	0.40
1:C:66:TYR:CG	1:C:146:PHE:CD1	3.09	0.40
1:C:509:LEU:HD23	1:C:567:ARG:HH11	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:515:ILE:CD1	1:C:574:SER:HB3	2.51	0.40
1:C:705:ILE:O	1:C:709:LEU:HD23	2.20	0.40
1:C:751:TRP:HA	1:C:768:TYR:HD2	1.86	0.40
2:D:114:CYS:HA	2:D:133:VAL:O	2.21	0.40
2:D:155:PRO:HG2	2:D:174:LEU:HD23	2.02	0.40
2:D:159:LEU:HB2	2:D:170:TYR:HB2	2.02	0.40
1:A:38:LEU:HD13	1:A:79:HIS:CD2	2.56	0.40
1:A:275:PHE:O	1:A:279:VAL:HG23	2.20	0.40
1:A:855:MET:O	1:A:857:GLN:NE2	2.30	0.40
2:B:52:ARG:HH22	2:B:58:LEU:N	2.19	0.40
1:C:77:SER:HA	1:C:111:THR:HG23	2.03	0.40
1:C:161:THR:O	1:C:164:SER:HB3	2.21	0.40
1:C:227:ASP:O	1:C:231:TYR:N	2.45	0.40
1:C:583:LEU:HA	1:C:586:MET:HG3	2.03	0.40
1:C:625:ASN:O	1:C:629:GLN:HG3	2.22	0.40
1:A:215:VAL:CG1	1:A:255:LEU:HD21	2.51	0.40
1:A:286:VAL:O	1:A:288:VAL:N	2.52	0.40
1:C:27:MET:HA	1:C:30:LYS:CG	2.50	0.40
1:C:268:HIS:HA	1:C:271:THR:OG1	2.21	0.40
1:C:521:LEU:HD23	1:C:521:LEU:HA	1.75	0.40
1:C:679:GLU:HG3	1:C:680:PHE:H	1.86	0.40
1:C:710:HIS:HA	1:C:757:ALA:H	1.86	0.40
1:C:817:THR:OG1	1:C:819:LYS:HG2	2.21	0.40
2:D:52:ARG:HH11	2:D:53:SER:HB3	1.87	0.40
1:A:189:TRP:CD1	1:A:251:ALA:HB2	2.56	0.40
1:A:296:MET:HE2	1:A:418:LEU:HA	2.03	0.40
1:A:507:THR:HA	1:A:510:LYS:HE2	2.04	0.40
1:A:617:LYS:C	1:A:619:ARG:H	2.25	0.40
1:A:644:LEU:HD12	1:A:645:TYR:N	2.36	0.40
1:A:720:TYR:O	1:A:723:LEU:HB2	2.22	0.40
1:A:731:ALA:HB1	1:A:743:ALA:HB1	2.03	0.40
1:A:777:CYS:HA	1:A:780:ARG:HG2	2.02	0.40
2:B:25:LYS:HE3	2:B:25:LYS:HB3	1.76	0.40
1:C:156:ARG:NH1	1:C:221:ARG:HB2	2.36	0.40
1:C:569:VAL:HA	1:C:572:ILE:HD12	2.02	0.40
1:C:588:ARG:HH21	1:C:639:SER:C	2.24	0.40
1:C:607:THR:CG2	2:D:142:PHE:HZ	2.34	0.40
1:C:668:ALA:CB	1:C:677:ALA:HB2	2.51	0.40
1:C:723:LEU:CA	1:C:726:LYS:HG2	2.49	0.40
1:C:759:ARG:HG3	1:C:767:LEU:CD2	2.50	0.40
1:C:772:LYS:O	1:C:776:GLU:HG3	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:62:ARG:HD3	2:D:70:THR:HA	2.04	0.40
1:A:710:HIS:HA	1:A:755:PRO:CG	2.52	0.40
1:A:722:THR:HG22	1:A:726:LYS:HZ3	1.85	0.40
1:C:17:ALA:HB1	1:C:51:GLU:HB3	2.04	0.40
1:C:436:ILE:O	1:C:441:LEU:HG	2.20	0.40
1:C:669:ASP:HA	1:C:714:ASN:ND2	2.37	0.40
2:D:37:LEU:CD2	2:D:59:LYS:HB2	2.52	0.40
2:D:101:LEU:HD23	2:D:101:LEU:HA	1.94	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	742/869 (85%)	700 (94%)	40 (5%)	2 (0%)	41 77
1	C	742/869 (85%)	700 (94%)	39 (5%)	3 (0%)	34 72
2	B	181/202 (90%)	177 (98%)	4 (2%)	0	100 100
2	D	181/202 (90%)	170 (94%)	9 (5%)	2 (1%)	14 52
All	All	1846/2142 (86%)	1747 (95%)	92 (5%)	7 (0%)	38 72

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	98	PRO
1	C	88	HIS
1	C	710	HIS
1	A	710	HIS
1	C	618	ALA
1	A	618	ALA
2	D	97	GLU

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	660/762 (87%)	658 (100%)	2 (0%)	92 95
1	C	660/762 (87%)	656 (99%)	4 (1%)	86 92
2	B	165/175 (94%)	165 (100%)	0	100 100
2	D	165/175 (94%)	164 (99%)	1 (1%)	86 92
All	All	1650/1874 (88%)	1643 (100%)	7 (0%)	91 94

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	599	ARG
1	A	713	ARG
1	C	30	LYS
1	C	199	ARG
1	C	281	ARG
1	C	443	LYS
2	D	52	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	ASN
1	A	242	GLN
1	A	245	GLN
1	A	270	HIS
1	A	402	GLN
1	A	447	HIS
1	A	467	GLN
1	A	577	ASN
1	A	749	HIS
2	B	10	ASN
2	B	120	HIS
1	C	79	HIS

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Mol	Chain	Res	Type
1	C	83	ASN
1	C	181	ASN
1	C	218	ASN
1	C	224	GLN
1	C	252	GLN
1	C	261	GLN
1	C	398	GLN
1	C	573	HIS
1	C	580	GLN
1	C	649	ASN
1	C	710	HIS
1	C	857	GLN
2	D	120	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation

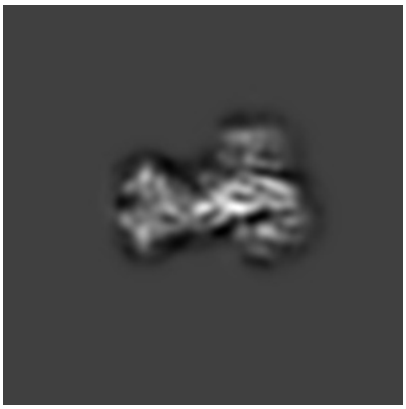
This section contains visualisations of the EMDB entry EMD-12223. These allow visual inspection of the internal detail of the map and identification of artifacts.

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.

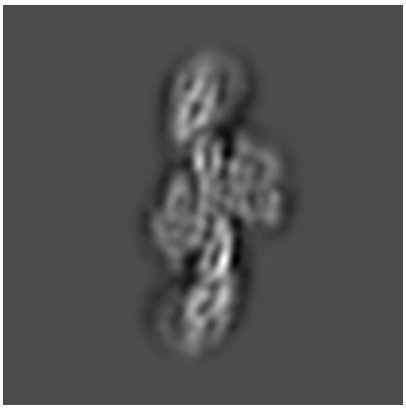
6.1 Orthogonal projections

6.1.1 Primary map

X

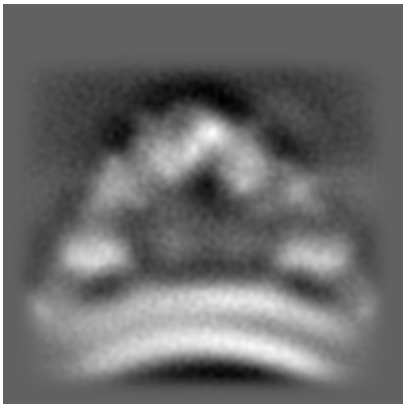


Y

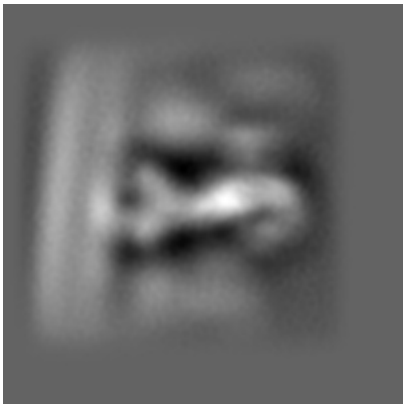


Z

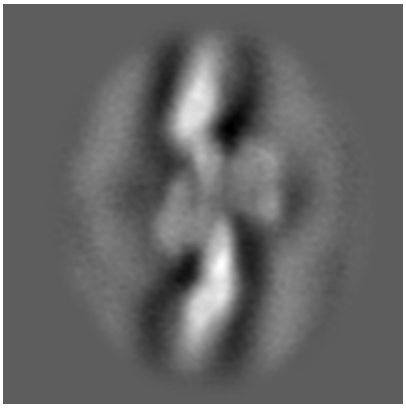
6.1.2 Raw map



X



Y

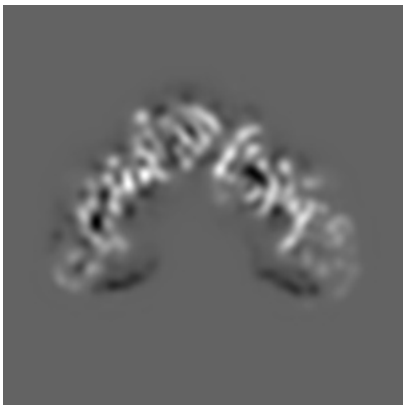


Z

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

6.2 Central slices (i)

6.2.1 Primary map

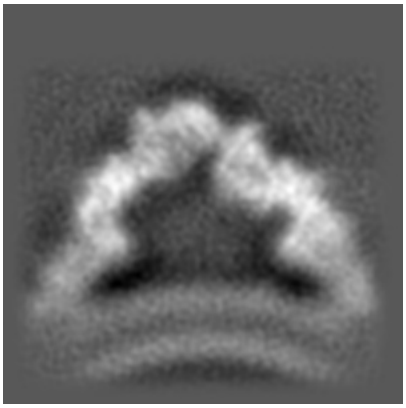


X Index: 52

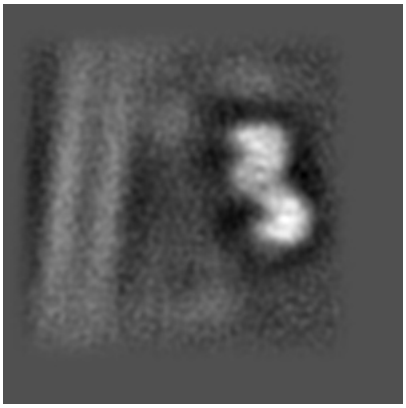
Y Index: 52

Z Index: 52

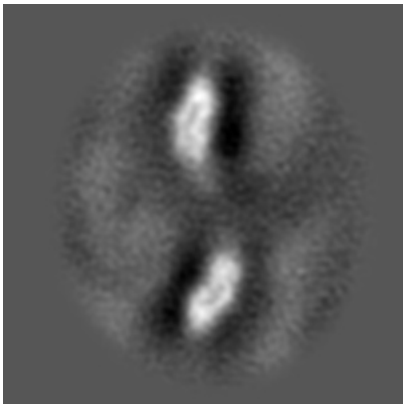
6.2.2 Raw map



X Index: 52



Y Index: 52

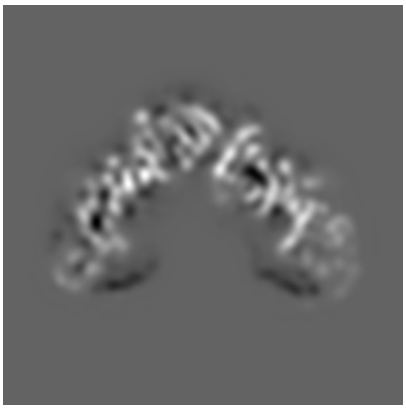


Z Index: 52

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

6.3 Largest variance slices (i)

6.3.1 Primary map

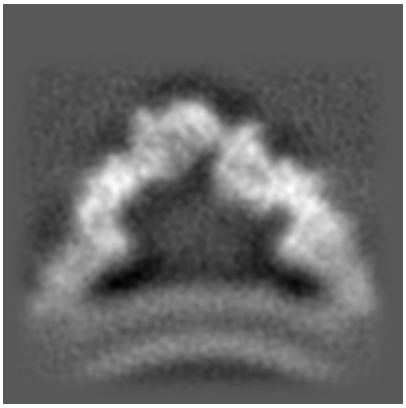


X Index: 52

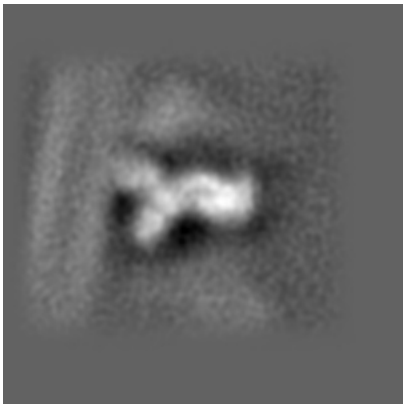
Y Index: 36

Z Index: 62

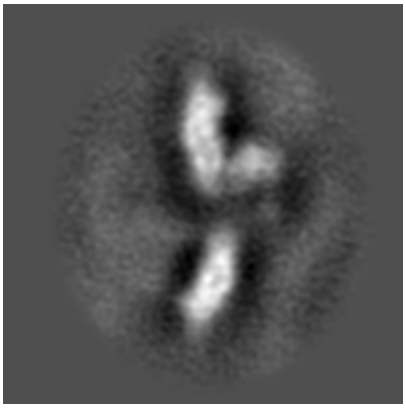
6.3.2 Raw map



X Index: 52



Y Index: 28

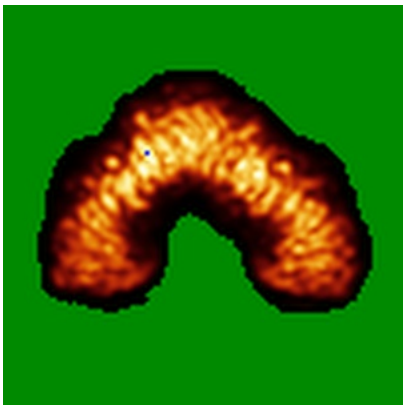


Z Index: 57

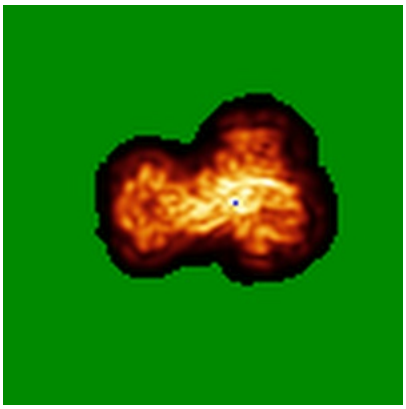
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

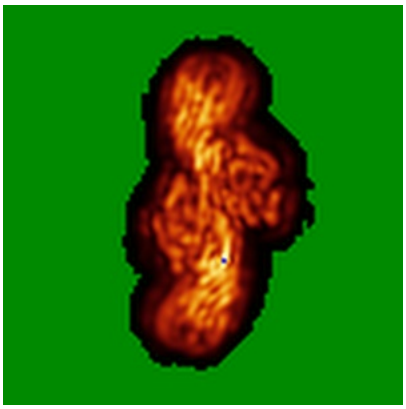
6.4.1 Primary map



X

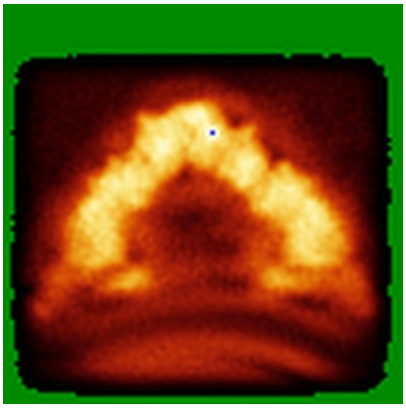


Y

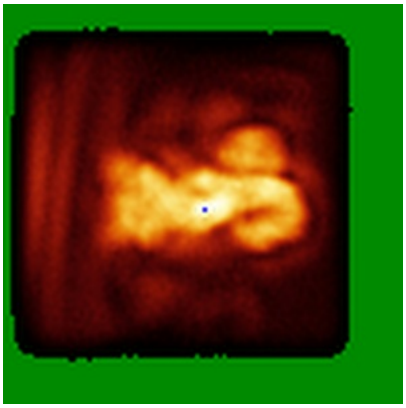


Z

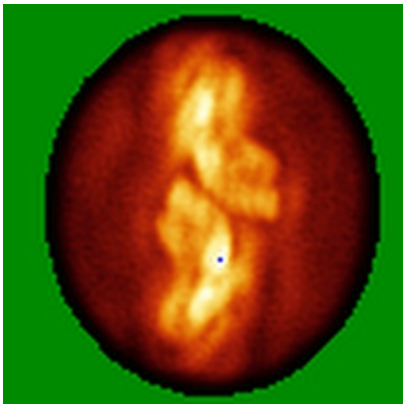
6.4.2 Raw map



X



Y

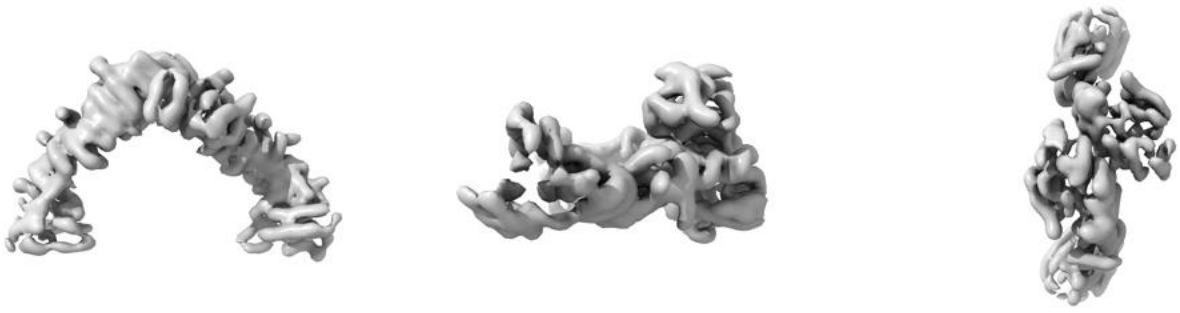


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.024. 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

X Y Z

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.

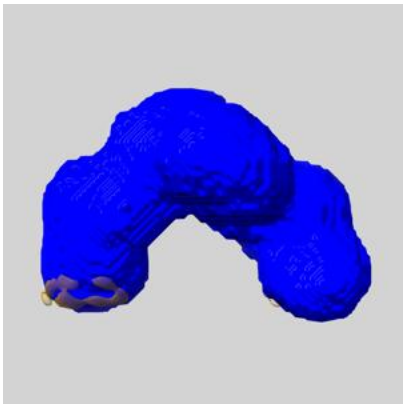
6.6 Mask visualisation

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

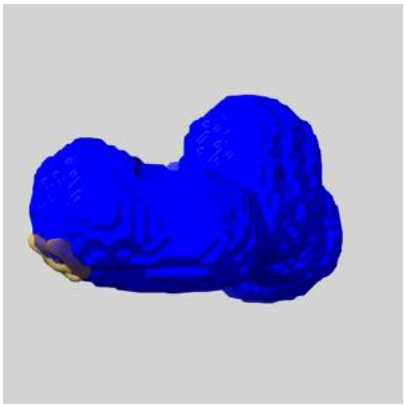
A mask typically either:

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

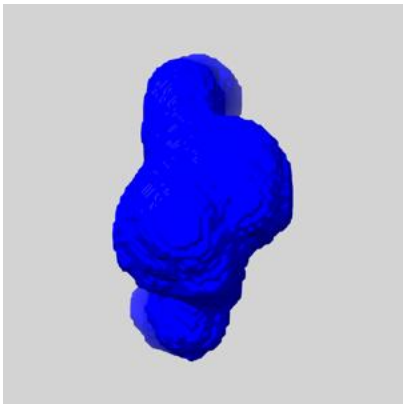
6.6.1 emd_12223_msk_1.map



X



Y

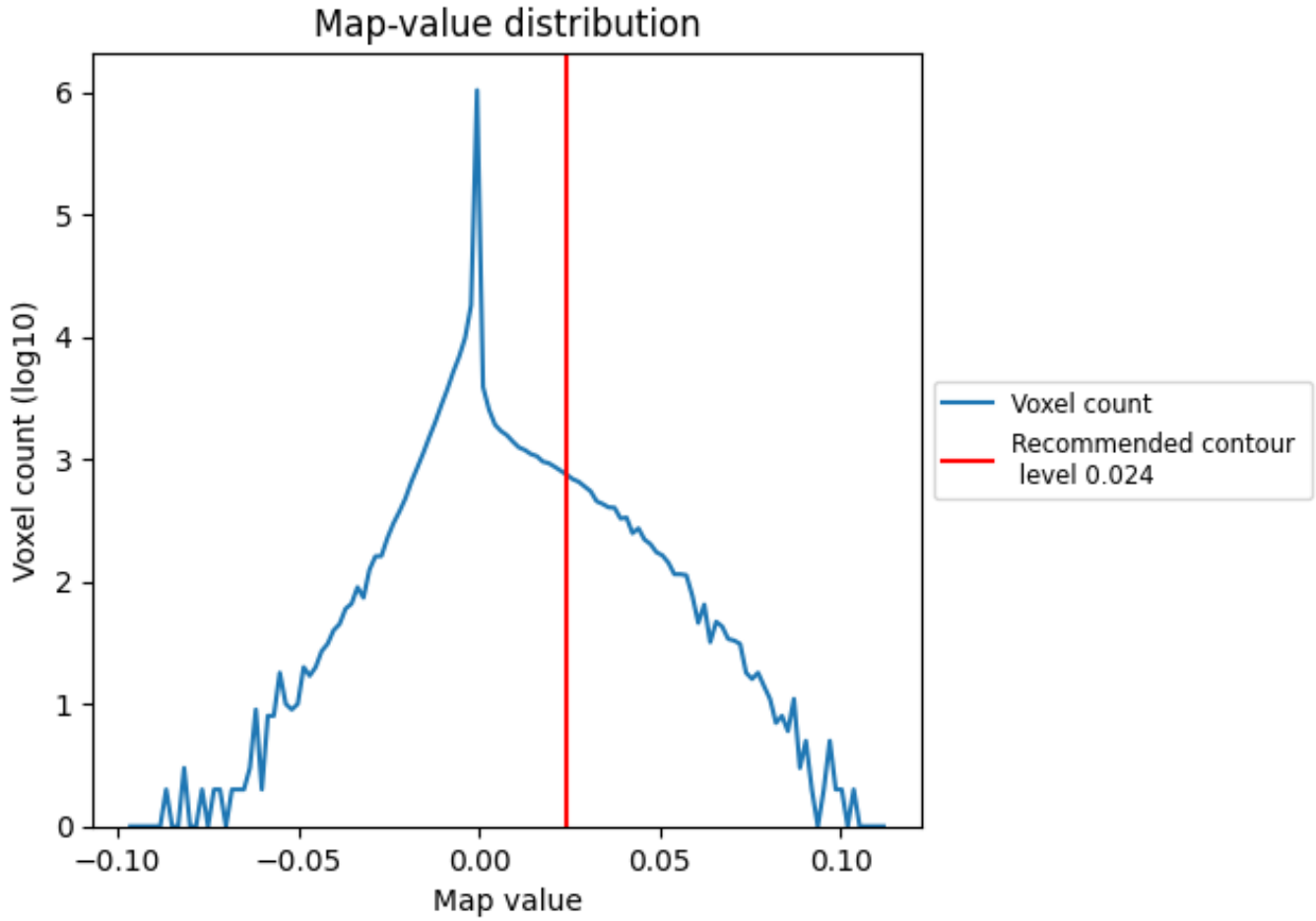


Z

7 Map analysis

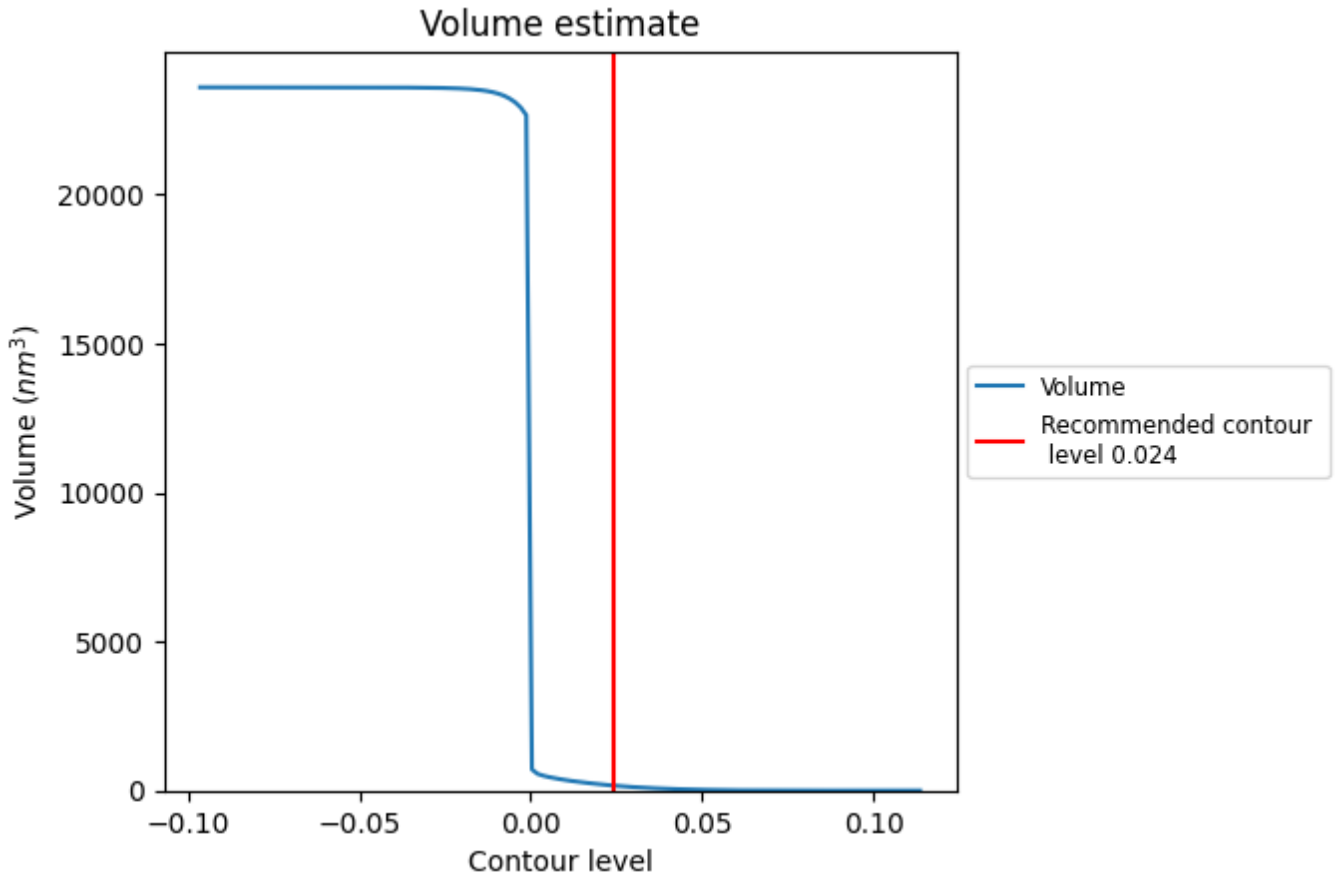
This section contains the results of statistical analysis of the map.

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.

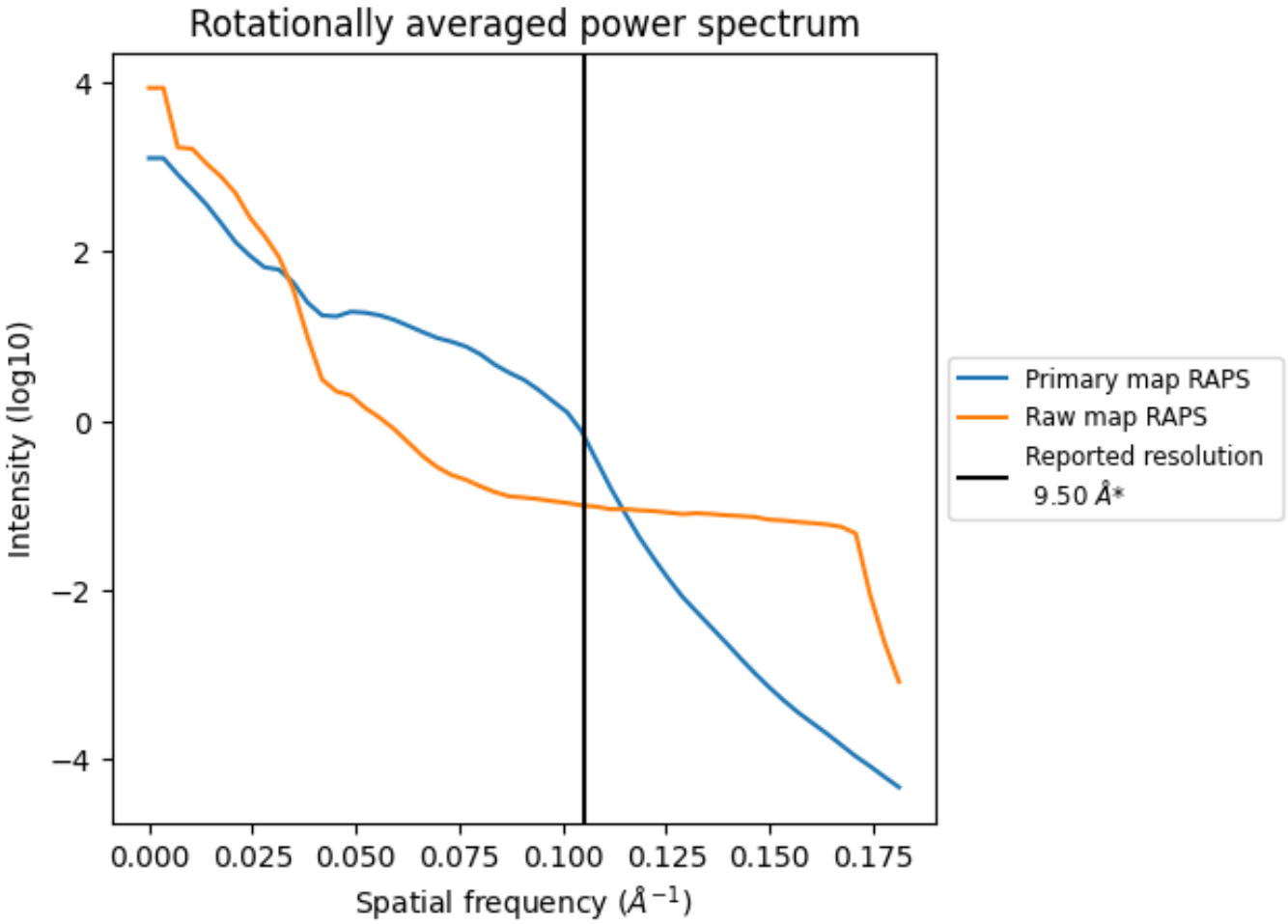
7.2 Volume estimate



The volume at the recommended contour level is 168 nm^3; this corresponds to an approximate mass of 152 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)

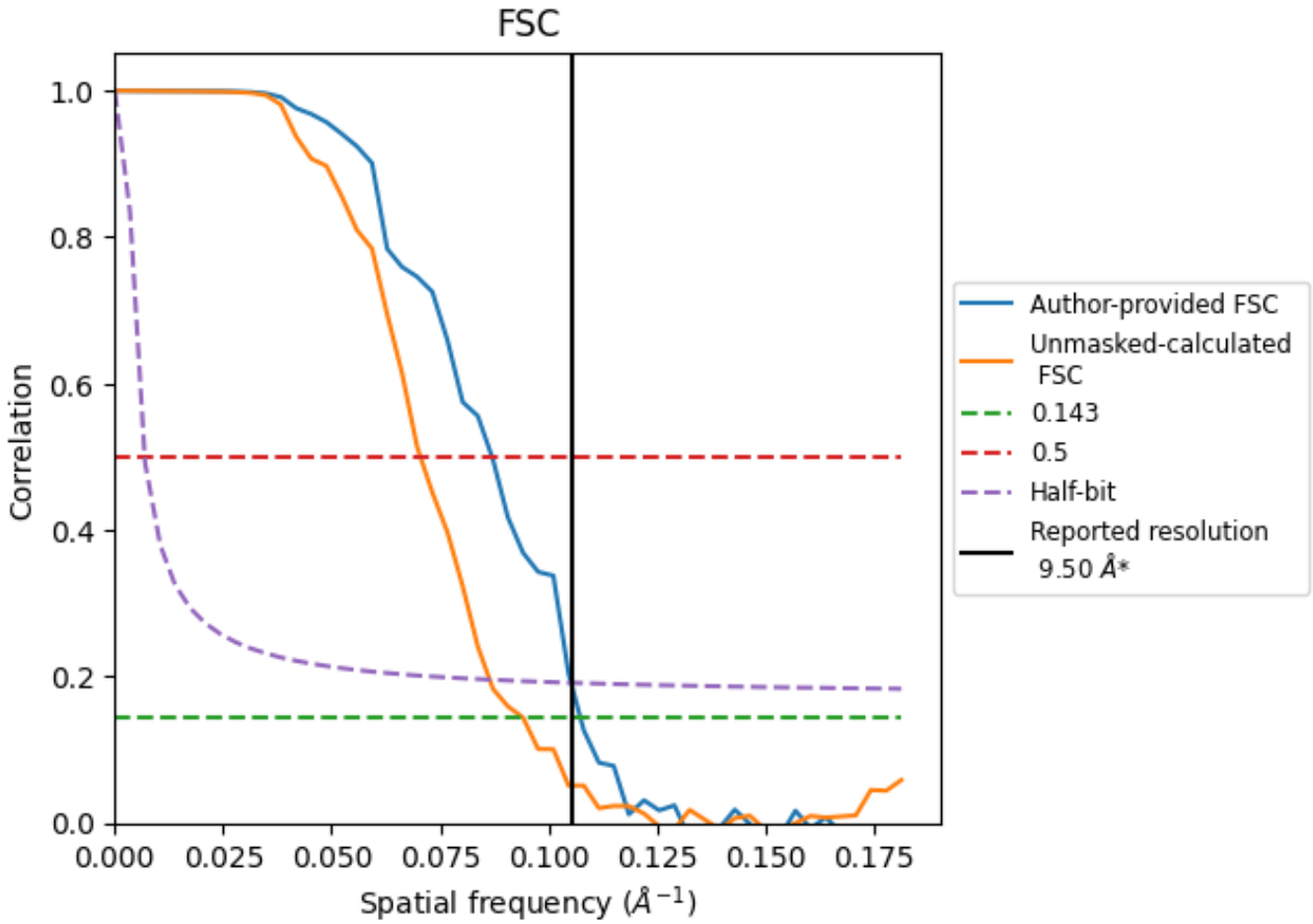


*Reported resolution corresponds to spatial frequency of 0.105 Å^{-1}

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 0.105 Å^{-1}

8.2 Resolution estimates (i)

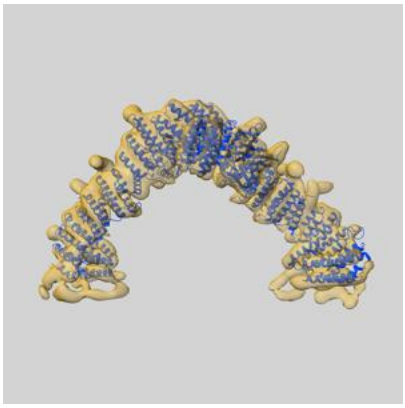
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.50	-	-
Author-provided FSC curve	9.32	11.51	9.51
Unmasked-calculated*	10.62	14.18	11.57

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 10.62 differs from the reported value 9.5 by more than 10 %

9 Map-model fit

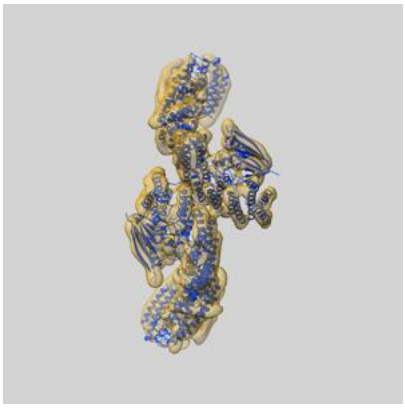
This section contains information regarding the fit between EMDB map EMD-12223 and PDB model 7BLP. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay



X

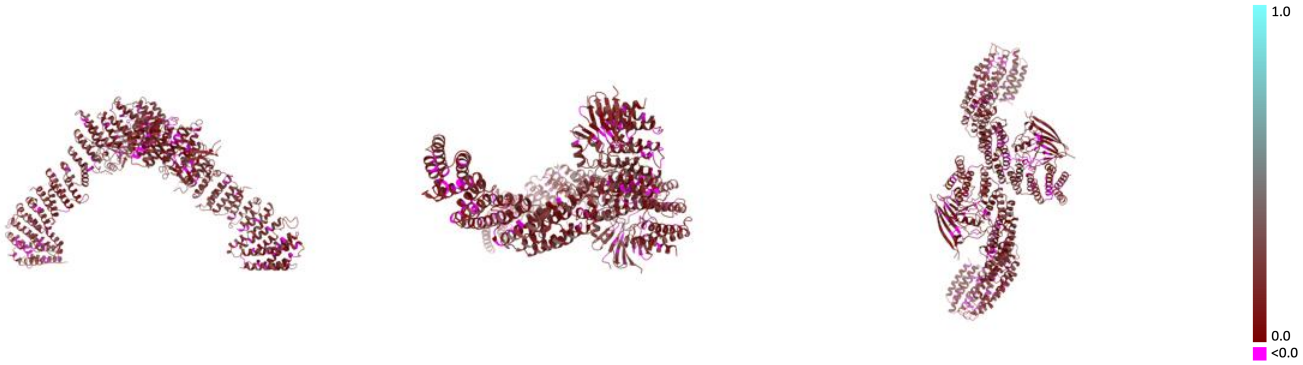
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.024 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.

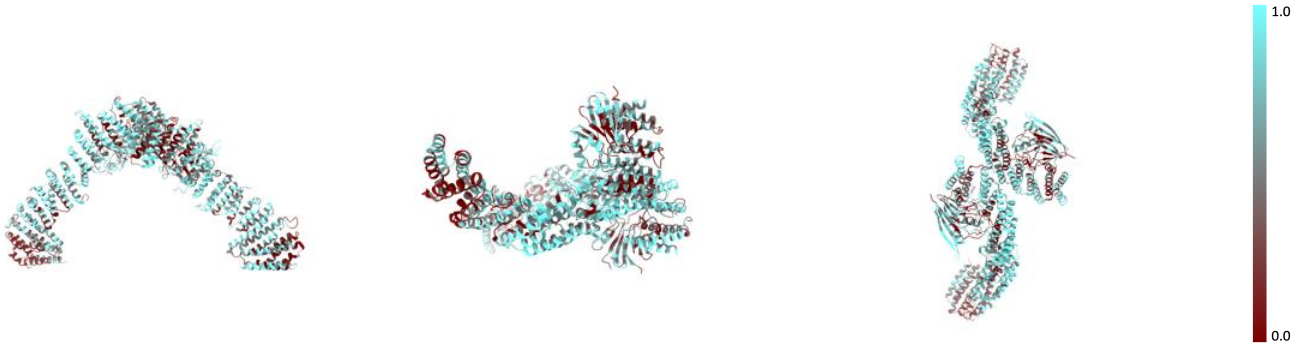
9.2 Q-score mapped to coordinate model (i)



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.

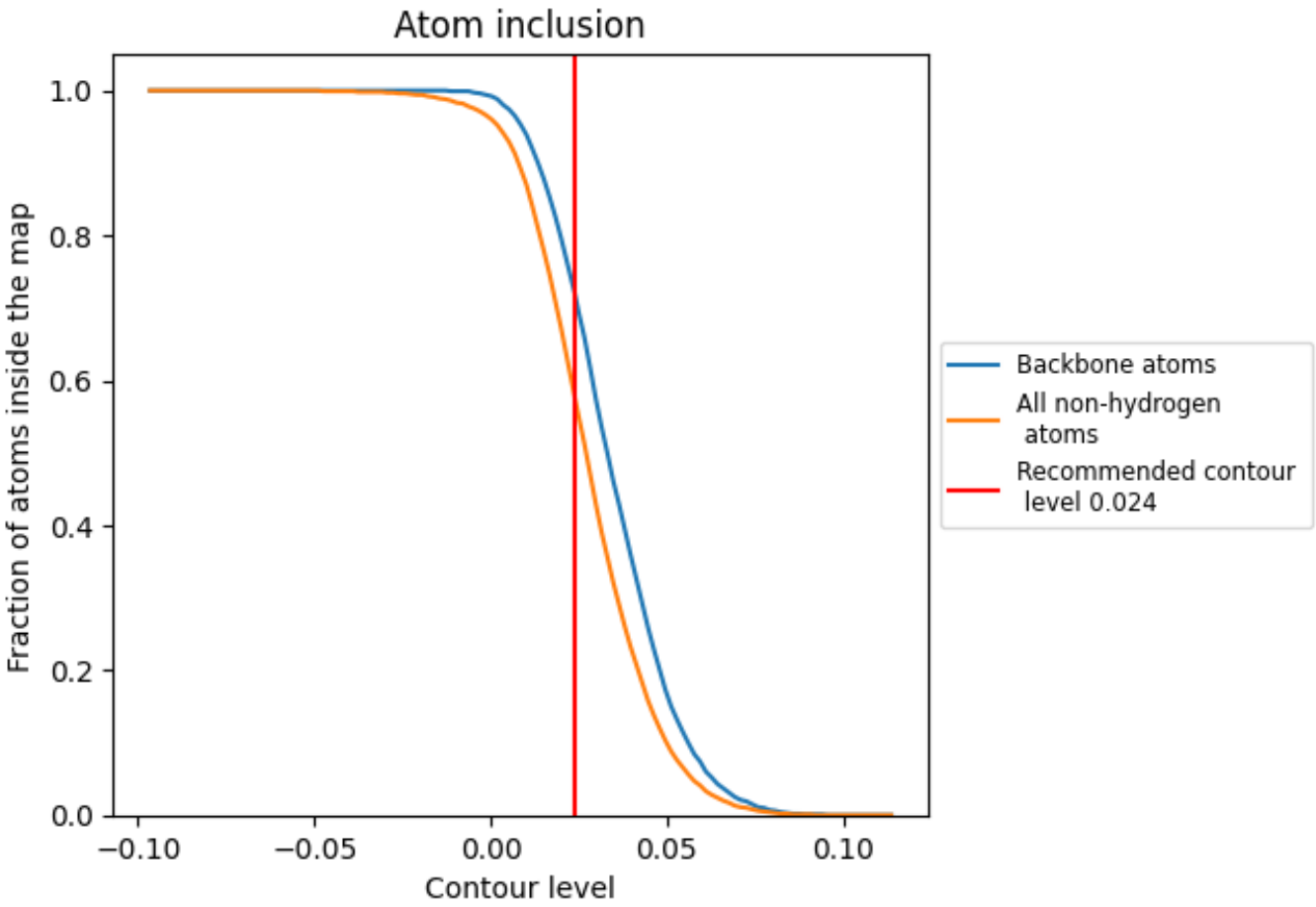
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.024).

9.4 Atom inclusion (i)



At the recommended contour level, 72% of all backbone atoms, 57% 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 (0.024) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5740	0.1420
A	0.5880	0.1470
B	0.4750	0.1260
C	0.5910	0.1440
D	0.5460	0.1270