Full wwPDB EM Validation Report ⓘ

Nov 8, 2022 – 05:32 AM JST

PDB ID	:	5Y0B
EMDB ID	:	EMD-6799
Title	:	PIG GASTRIC H+,K+ - ATPASE IN COMPLEX with BYK99
Authors	:	Abe, K.; Shimokawa, J.; Natio, M.; Munson, K.; Vagin, O.; Sachs, G.; Suzuki, H.; Tani, K.; Fujiyoshi, Y.
Deposited on	:	2017-07-16
Resolution	:	6.70 Å(reported)

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

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

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

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

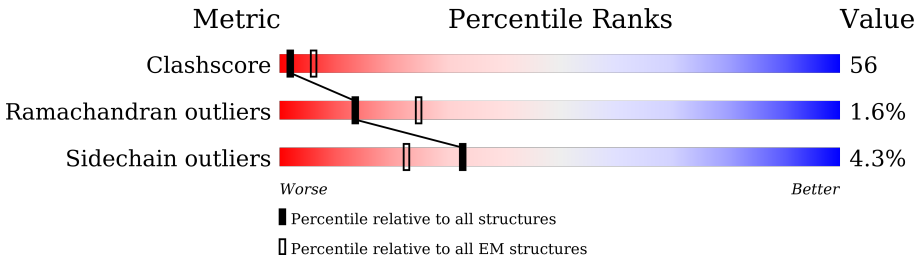
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 6.70 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	1034	28% 37% 55% · 5%
2	B	290	31% 19% 36% 5% 40%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9101 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 Potassium-transporting ATPase alpha chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	986	7658	4890	1294	1422	52	0	0

- Molecule 2 is a protein called Potassium-transporting ATPase subunit beta.

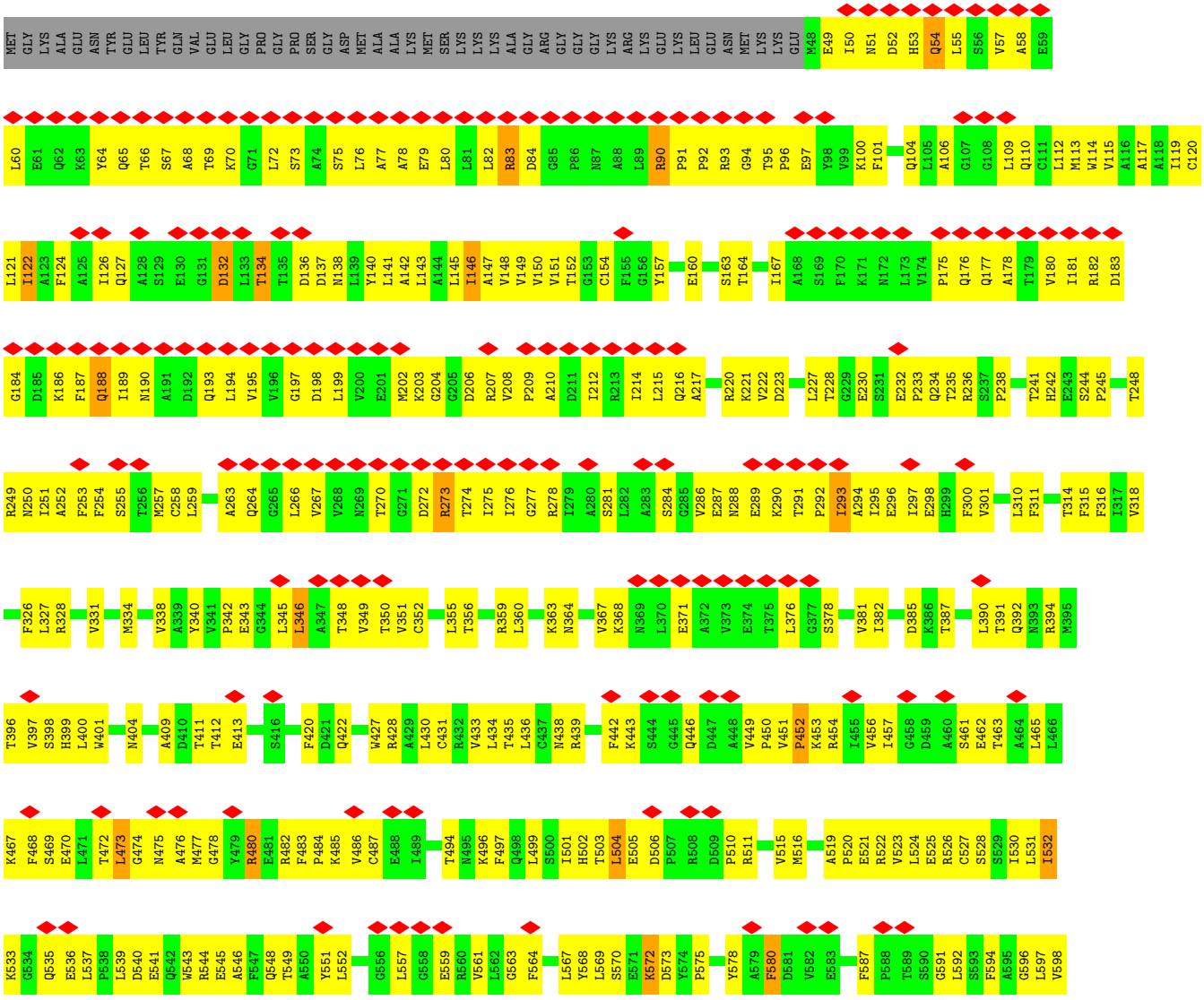
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	175	1443	949	237	249	8	0	0

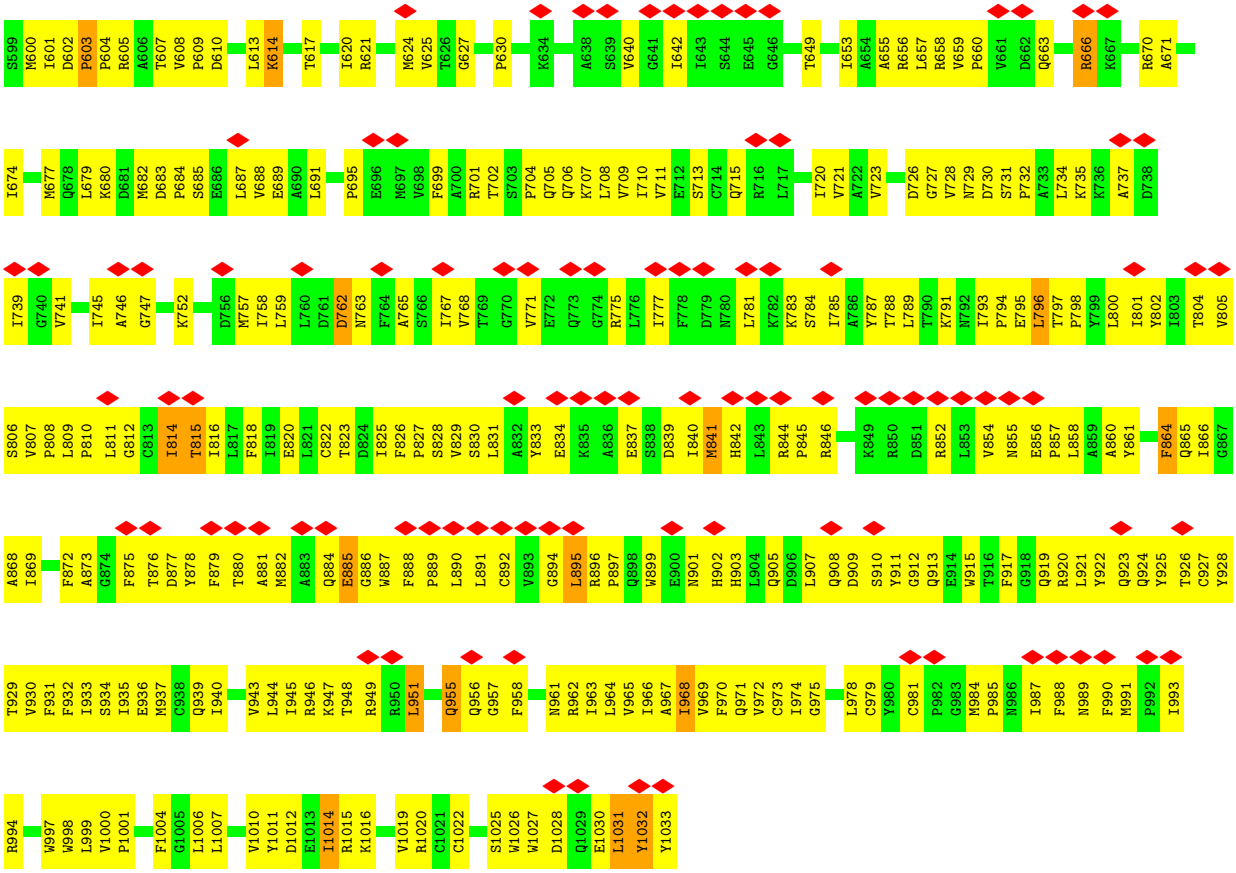
3 Residue-property plots (i)

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

- Molecule 1: Potassium-transporting ATPase alpha chain 1

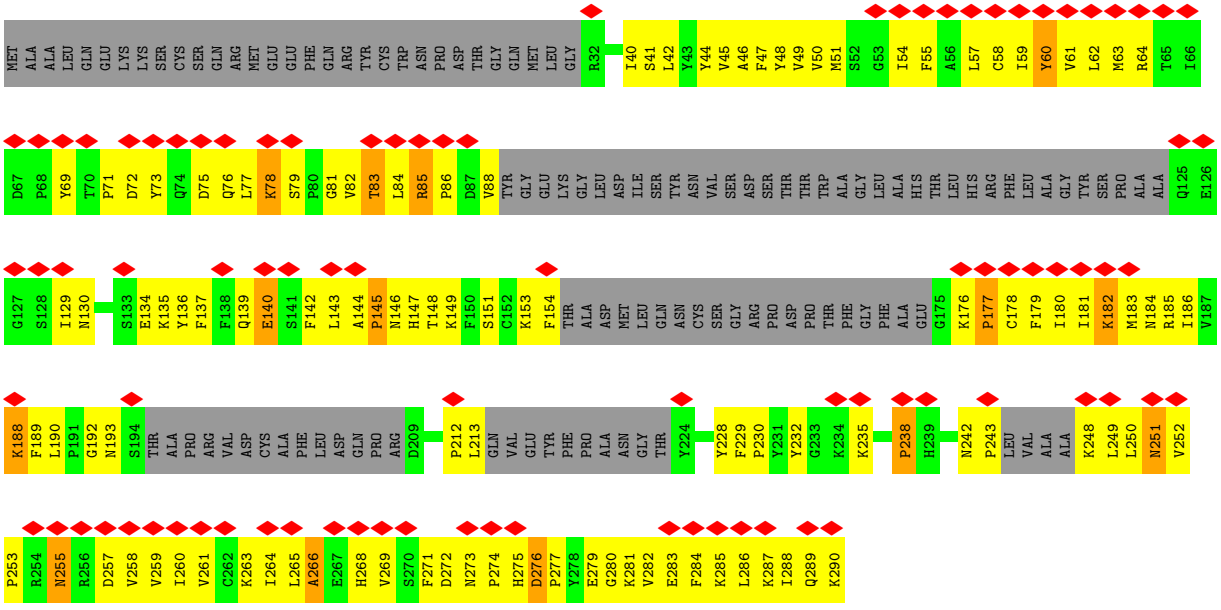
Chain A:





• Molecule 2: Potassium-transporting ATPase subunit beta

Chain B:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	CRYSTALLOGRAPHY	Depositor
Imposed symmetry	2D CRYSTAL, a=142.6 Å, b=112.0 Å, c=320 Å, γ=90°, space group=P 2 21 21	Depositor
Number of images used	Not provided	
Resolution determination method	DIFFRACTION PATTERN/LAYERLINES	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	JEOL KYOTO-3000SFF	Depositor
Voltage (kV)	300	Depositor
Electron dose (e^-/Å^2)	8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.023	Depositor
Minimum map value	-0.018	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	142.596, 111.997604, 319.9968	wwPDB
Map dimensions	289, 137, 105	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0485, 1.0769, 1.1111	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	0.26	0/7816	0.53	0/10616
2	B	0.29	0/1486	0.53	0/2008
All	All	0.27	0/9302	0.53	0/12624

There are no bond length outliers.

There are no bond angle outliers.

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	7658	0	7689	861	1
2	B	1443	0	1431	187	0
All	All	9101	0	9120	1018	1

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 56.

All (1018) 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:83:THR:HG23	2:B:182:LYS:HD3	1.28	1.10
1:A:837:GLU:HB3	1:A:951:LEU:HD21	1.32	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:951:LEU:HD23	1:A:951:LEU:H	1.15	1.08
1:A:1027:TRP:HB3	1:A:1031:LEU:CD1	1.84	1.06
1:A:431:CYS:HB3	1:A:473:LEU:HD13	1.32	1.04
1:A:220:ARG:HD3	1:A:236:ARG:HB2	1.39	1.04
1:A:469:SER:HA	1:A:473:LEU:HD21	1.34	1.03
1:A:1022:CYS:CB	1:A:1025:SER:HB3	1.90	1.01
1:A:53:HIS:HB3	1:A:251:ILE:HD11	1.41	1.00
1:A:951:LEU:HD12	1:A:956:GLN:HB2	1.44	1.00
1:A:784:SER:HA	1:A:946:ARG:HH21	1.27	1.00
1:A:1022:CYS:HB2	1:A:1025:SER:HB3	1.44	0.99
1:A:787:TYR:HB2	1:A:946:ARG:HD2	1.46	0.97
1:A:861:TYR:CE2	1:A:1031:LEU:HD23	2.00	0.97
1:A:907:LEU:HD22	1:A:920:ARG:HH11	1.31	0.96
2:B:134:GLU:HG2	2:B:135:LYS:H	1.31	0.95
1:A:80:LEU:HG	1:A:83:ARG:HH21	1.32	0.95
1:A:504:LEU:HG	1:A:510:PRO:HA	1.50	0.94
1:A:887:TRP:HH2	1:A:907:LEU:HG	1.31	0.94
1:A:473:LEU:HD23	1:A:473:LEU:H	1.34	0.93
1:A:220:ARG:HD2	1:A:263:ALA:HB2	1.49	0.93
1:A:273:ARG:HH11	1:A:273:ARG:HB3	1.34	0.93
1:A:113:MET:HE1	1:A:148:VAL:HB	1.48	0.92
1:A:392:GLN:NE2	1:A:603:PRO:HG2	1.83	0.92
1:A:1027:TRP:HB3	1:A:1031:LEU:HD11	1.50	0.92
1:A:273:ARG:HB3	1:A:273:ARG:NH1	1.85	0.91
1:A:828:SER:HA	1:A:946:ARG:HH22	1.35	0.90
2:B:143:LEU:HB3	2:B:145:PRO:HD2	1.52	0.90
2:B:85:ARG:HH21	2:B:86:PRO:HB3	1.37	0.89
1:A:1027:TRP:HB3	1:A:1031:LEU:HD12	1.52	0.89
1:A:907:LEU:HD22	1:A:920:ARG:NH1	1.87	0.88
1:A:784:SER:HA	1:A:946:ARG:NH2	1.89	0.88
1:A:570:SER:HB2	1:A:572:LYS:HD3	1.52	0.88
1:A:886:GLY:HA2	1:A:911:TYR:HE2	1.39	0.87
1:A:484:PRO:HD2	1:A:503:THR:HG22	1.54	0.87
2:B:88:VAL:HG21	2:B:284:PHE:CZ	2.10	0.86
1:A:391:THR:HA	1:A:604:PRO:HA	1.56	0.85
1:A:567:LEU:HD22	1:A:592:LEU:HD23	1.58	0.85
1:A:831:LEU:HG	1:A:946:ARG:NE	1.92	0.85
1:A:152:THR:HG23	1:A:350:THR:HG21	1.56	0.84
1:A:1015:ARG:HG2	1:A:1031:LEU:HD13	1.55	0.84
1:A:815:THR:CG2	1:A:932:PHE:HB2	2.08	0.84
1:A:113:MET:SD	1:A:346:LEU:HD22	2.18	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:81:GLY:HA2	2:B:280:GLY:H	1.43	0.83
1:A:422:GLN:HG3	1:A:427:TRP:HE1	1.40	0.83
1:A:925:TYR:HA	1:A:928:TYR:CD2	2.14	0.83
1:A:100:LYS:HE2	1:A:100:LYS:HA	1.59	0.83
1:A:431:CYS:SG	1:A:473:LEU:HD22	2.18	0.82
1:A:925:TYR:HA	1:A:928:TYR:HD2	1.43	0.82
1:A:220:ARG:HD2	1:A:263:ALA:CB	2.08	0.82
1:A:730:ASP:HB3	1:A:734:LEU:HD13	1.59	0.82
1:A:1000:VAL:HG13	1:A:1001:PRO:HD3	1.62	0.82
1:A:197:GLY:HA2	1:A:266:LEU:HD11	1.61	0.82
1:A:430:LEU:O	1:A:433:VAL:HG12	1.79	0.82
2:B:257:ASP:OD1	2:B:285:LYS:HB3	1.79	0.82
1:A:411:THR:O	1:A:603:PRO:HG3	1.80	0.81
1:A:422:GLN:HG3	1:A:427:TRP:NE1	1.94	0.81
1:A:787:TYR:HB2	1:A:946:ARG:CD	2.10	0.81
1:A:223:ASP:HB2	1:A:259:LEU:HD11	1.60	0.81
1:A:837:GLU:CB	1:A:951:LEU:HD21	2.09	0.81
1:A:666:ARG:H	1:A:666:ARG:HD3	1.46	0.81
1:A:601:ILE:HG12	1:A:602:ASP:H	1.45	0.81
2:B:186:ILE:HG23	2:B:189:PHE:HB3	1.63	0.81
1:A:442:PHE:CE2	1:A:470:GLU:HG3	2.17	0.80
2:B:176:LYS:H	2:B:288:ILE:HD13	1.45	0.80
1:A:948:THR:HG22	1:A:956:GLN:HE21	1.44	0.80
1:A:398:SER:H	1:A:600:MET:HA	1.45	0.80
1:A:997:TRP:O	1:A:1000:VAL:HG12	1.82	0.79
2:B:154:PHE:HD1	2:B:228:TYR:HH	1.28	0.79
1:A:815:THR:HA	1:A:990:PHE:HZ	1.47	0.79
1:A:981:CYS:HB3	1:A:984:MET:HG2	1.63	0.79
1:A:113:MET:HG3	1:A:346:LEU:HD13	1.65	0.79
1:A:486:VAL:HG11	1:A:580:PHE:HE1	1.47	0.78
1:A:1022:CYS:HB3	1:A:1025:SER:HB3	1.65	0.78
1:A:143:LEU:O	1:A:146:ILE:HG22	1.84	0.78
1:A:610:ASP:O	1:A:613:LEU:HG	1.83	0.78
1:A:887:TRP:CH2	1:A:907:LEU:HG	2.16	0.78
1:A:907:LEU:CD2	1:A:920:ARG:HH11	1.96	0.78
1:A:923:GLN:OE1	2:B:76:GLN:HG2	1.83	0.78
1:A:497:PHE:HB3	1:A:526:ARG:HH12	1.47	0.77
1:A:614:LYS:O	1:A:617:THR:HG22	1.84	0.77
1:A:294:ALA:O	1:A:297:ILE:HG22	1.83	0.77
1:A:706:GLN:O	1:A:709:VAL:HG22	1.85	0.77
1:A:923:GLN:NE2	2:B:76:GLN:HB3	1.99	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:937:MET:SD	1:A:1001:PRO:HG2	2.24	0.76
1:A:788:THR:O	1:A:791:LYS:HG2	1.84	0.76
1:A:607:THR:OG1	1:A:765:ALA:HB2	1.85	0.76
1:A:345:LEU:HA	1:A:348:THR:HG22	1.67	0.76
1:A:114:TRP:CZ3	1:A:146:ILE:HG12	2.20	0.76
1:A:837:GLU:HB3	1:A:951:LEU:CD2	2.15	0.75
1:A:298:GLU:O	1:A:301:VAL:HG22	1.87	0.75
1:A:947:LYS:HG2	1:A:958:PHE:CB	2.17	0.75
1:A:1027:TRP:HE3	1:A:1031:LEU:HD11	1.52	0.75
1:A:398:SER:N	1:A:600:MET:HA	2.01	0.74
1:A:823:THR:HB	1:A:971:GLN:HG3	1.68	0.74
1:A:866:ILE:HD12	1:A:866:ILE:H	1.52	0.74
1:A:220:ARG:CD	1:A:236:ARG:HB2	2.17	0.74
1:A:434:LEU:HD21	1:A:465:LEU:HB3	1.69	0.74
1:A:869:ILE:HD13	1:A:1007:LEU:HD12	1.70	0.74
1:A:199:LEU:HD11	1:A:264:GLN:HB2	1.67	0.73
1:A:818:PHE:O	1:A:822:CYS:HB3	1.88	0.73
1:A:965:VAL:HA	1:A:968:ILE:HD11	1.70	0.73
1:A:614:LYS:HG2	1:A:768:VAL:CG1	2.18	0.73
1:A:561:VAL:HG11	1:A:597:LEU:HD13	1.70	0.73
1:A:328:ARG:O	1:A:331:VAL:HG22	1.88	0.73
1:A:699:PHE:HB3	1:A:702:THR:HG21	1.71	0.72
1:A:947:LYS:HD3	1:A:964:LEU:HD12	1.70	0.72
1:A:96:PRO:HB3	1:A:100:LYS:HD2	1.70	0.72
1:A:53:HIS:CE1	1:A:54:GLN:HE22	2.08	0.72
1:A:114:TRP:HZ3	1:A:146:ILE:HG12	1.55	0.72
1:A:539:LEU:O	1:A:539:LEU:HD12	1.90	0.72
1:A:80:LEU:HG	1:A:83:ARG:NH2	2.05	0.72
1:A:895:LEU:HD11	1:A:907:LEU:HD21	1.70	0.72
2:B:45:VAL:O	2:B:49:VAL:HB	1.90	0.72
1:A:536:GLU:C	1:A:537:LEU:HD12	2.10	0.71
1:A:889:PRO:HG2	1:A:890:LEU:HD12	1.71	0.71
1:A:945:ILE:HB	1:A:1012:ASP:OD2	1.90	0.71
2:B:84:LEU:HG	2:B:181:ILE:HG12	1.72	0.71
1:A:948:THR:HG22	1:A:956:GLN:NE2	2.05	0.71
1:A:981:CYS:HB3	1:A:984:MET:CG	2.20	0.71
2:B:41:SER:O	2:B:45:VAL:HG23	1.90	0.71
1:A:815:THR:HG22	1:A:932:PHE:HB2	1.72	0.70
1:A:657:LEU:HD23	1:A:659:VAL:HG11	1.73	0.70
1:A:677:MET:O	1:A:680:LYS:HG2	1.90	0.70
2:B:189:PHE:HZ	2:B:268:HIS:HB3	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:801:ILE:HD12	1:A:875:PHE:CZ	2.26	0.70
1:A:73:SER:OG	1:A:76:LEU:HD13	1.91	0.70
1:A:886:GLY:HA2	1:A:911:TYR:CE2	2.24	0.70
1:A:115:VAL:O	1:A:119:ILE:HG13	1.91	0.70
2:B:85:ARG:NH2	2:B:86:PRO:HB3	2.07	0.70
2:B:261:VAL:HG22	2:B:283:GLU:OE1	1.92	0.70
1:A:655:ALA:O	1:A:658:ARG:HD2	1.91	0.70
1:A:1011:TYR:O	1:A:1014:ILE:HG22	1.91	0.69
1:A:572:LYS:H	1:A:572:LYS:HD2	1.56	0.69
2:B:178:CYS:HB2	2:B:248:LYS:HD2	1.72	0.69
2:B:213:LEU:HG	2:B:251:ASN:HB3	1.74	0.69
1:A:504:LEU:CG	1:A:510:PRO:HA	2.22	0.69
1:A:884:GLN:HG3	1:A:997:TRP:HH2	1.56	0.69
1:A:203:LYS:HG2	1:A:204:GLY:H	1.57	0.69
1:A:666:ARG:HD3	1:A:666:ARG:N	2.07	0.69
1:A:214:ILE:CD1	1:A:236:ARG:HB3	2.23	0.69
1:A:730:ASP:HB3	1:A:734:LEU:CD1	2.22	0.69
2:B:82:VAL:HG13	2:B:280:GLY:HA2	1.75	0.69
1:A:775:ARG:HD3	1:A:840:ILE:HG22	1.75	0.68
1:A:951:LEU:HD23	1:A:951:LEU:N	1.99	0.68
1:A:971:GLN:O	1:A:974:ILE:HG22	1.93	0.68
1:A:885:GLU:HB2	2:B:76:GLN:NE2	2.08	0.68
1:A:951:LEU:H	1:A:951:LEU:CD2	1.96	0.68
1:A:70:LYS:NZ	1:A:183:ASP:HA	2.09	0.68
2:B:83:THR:C	2:B:84:LEU:HD12	2.12	0.68
1:A:197:GLY:HA2	1:A:266:LEU:CD1	2.24	0.68
1:A:392:GLN:CD	1:A:603:PRO:HG2	2.14	0.68
1:A:450:PRO:HG3	1:A:453:LYS:HD2	1.74	0.68
1:A:745:ILE:HG13	1:A:746:ALA:N	2.09	0.68
1:A:828:SER:HA	1:A:946:ARG:NH2	2.08	0.68
1:A:852:ARG:HG3	1:A:852:ARG:HH11	1.58	0.68
1:A:939:GLN:O	1:A:943:VAL:HG23	1.94	0.68
1:A:917:PHE:O	1:A:921:LEU:HD23	1.94	0.68
2:B:142:PHE:HE2	2:B:232:TYR:HA	1.58	0.68
1:A:442:PHE:HE2	1:A:470:GLU:HG3	1.58	0.68
1:A:768:VAL:O	1:A:771:VAL:HG12	1.94	0.68
2:B:78:LYS:HG2	2:B:79:SER:N	2.08	0.68
1:A:293:ILE:HD13	1:A:293:ILE:O	1.93	0.68
1:A:397:VAL:HA	1:A:600:MET:HB3	1.75	0.68
1:A:451:VAL:HA	1:A:454:ARG:NE	2.08	0.68
1:A:486:VAL:HG11	1:A:580:PHE:CE1	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:570:SER:HB2	1:A:572:LYS:CD	2.24	0.68
1:A:94:GLY:C	1:A:96:PRO:HD3	2.14	0.67
1:A:181:ILE:HG12	1:A:186:LYS:HG2	1.74	0.67
1:A:146:ILE:HD13	1:A:146:ILE:O	1.95	0.67
1:A:1015:ARG:CG	1:A:1031:LEU:HD13	2.23	0.67
2:B:255:ASN:HD21	2:B:290:LYS:H	1.42	0.67
1:A:376:LEU:HB3	1:A:771:VAL:HA	1.75	0.67
1:A:791:LYS:O	1:A:795:GLU:HG3	1.94	0.67
1:A:666:ARG:H	1:A:666:ARG:CD	2.08	0.67
1:A:601:ILE:HG12	1:A:602:ASP:N	2.08	0.67
1:A:614:LYS:HG2	1:A:768:VAL:HG13	1.77	0.67
2:B:57:LEU:O	2:B:61:VAL:HG13	1.94	0.67
2:B:84:LEU:CG	2:B:181:ILE:HG12	2.23	0.67
1:A:908:GLN:HE21	1:A:912:GLY:HA2	1.59	0.67
1:A:911:TYR:CE2	2:B:71:PRO:HB3	2.29	0.67
1:A:420:PHE:CZ	1:A:472:THR:HG21	2.30	0.67
2:B:40:ILE:HG23	2:B:44:TYR:CE2	2.30	0.67
2:B:46:ALA:HA	2:B:49:VAL:CG1	2.24	0.67
2:B:130:ASN:OD1	2:B:153:LYS:HD2	1.94	0.67
1:A:110:GLN:H	1:A:110:GLN:NE2	1.92	0.66
1:A:524:LEU:HD11	1:A:544:ARG:HH21	1.59	0.66
1:A:212:ILE:HG13	1:A:252:ALA:HB3	1.77	0.66
1:A:884:GLN:HB3	2:B:73:TYR:CE2	2.31	0.66
1:A:834:GLU:OE2	1:A:947:LYS:HE3	1.96	0.66
1:A:908:GLN:HG3	1:A:912:GLY:HA2	1.78	0.66
1:A:826:PHE:O	1:A:829:VAL:HG12	1.96	0.66
1:A:97:GLU:O	1:A:100:LYS:HG2	1.96	0.66
1:A:923:GLN:HA	1:A:926:THR:HG22	1.78	0.66
2:B:134:GLU:HG2	2:B:135:LYS:N	2.08	0.66
1:A:223:ASP:HB2	1:A:259:LEU:CD1	2.26	0.66
1:A:949:ARG:HD2	1:A:1033:TYR:O	1.95	0.66
2:B:189:PHE:CZ	2:B:268:HIS:HB3	2.30	0.66
1:A:433:VAL:HG23	1:A:515:VAL:HB	1.78	0.65
1:A:476:ALA:O	1:A:480:ARG:HG2	1.96	0.65
1:A:902:HIS:HA	1:A:917:PHE:CD1	2.32	0.65
1:A:922:TYR:HA	1:A:991:MET:HE1	1.77	0.65
1:A:621:ARG:HD2	1:A:695:PRO:O	1.96	0.65
1:A:113:MET:HG3	1:A:346:LEU:CD1	2.26	0.65
1:A:294:ALA:HB2	1:A:371:GLU:OE1	1.97	0.65
1:A:1027:TRP:CE3	1:A:1031:LEU:HD11	2.31	0.65
2:B:273:ASN:HB3	2:B:274:PRO:HD3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:833:TYR:HB2	1:A:961:ASN:HD21	1.62	0.65
1:A:915:TRP:CH2	2:B:76:GLN:HB2	2.32	0.65
2:B:139:GLN:O	2:B:140:GLU:HB2	1.96	0.65
1:A:387:THR:HA	1:A:391:THR:OG1	1.97	0.65
1:A:1014:ILE:HD13	1:A:1014:ILE:O	1.96	0.65
1:A:884:GLN:HG3	1:A:997:TRP:CH2	2.32	0.64
1:A:504:LEU:O	1:A:504:LEU:HD22	1.98	0.64
1:A:784:SER:CA	1:A:946:ARG:HH21	2.04	0.64
2:B:134:GLU:CG	2:B:135:LYS:H	2.09	0.64
2:B:213:LEU:HA	2:B:251:ASN:CB	2.27	0.64
1:A:869:ILE:HG12	2:B:51:MET:CE	2.28	0.64
1:A:314:THR:O	1:A:318:VAL:HG23	1.97	0.64
1:A:497:PHE:HB3	1:A:526:ARG:NH1	2.11	0.64
1:A:605:ARG:HB2	1:A:608:VAL:HG23	1.79	0.64
2:B:275:HIS:CD2	2:B:276:ASP:H	2.15	0.64
1:A:987:ILE:HG13	1:A:988:PHE:N	2.13	0.64
1:A:944:LEU:HD22	1:A:958:PHE:CE1	2.33	0.64
2:B:85:ARG:HE	2:B:86:PRO:N	1.96	0.64
1:A:194:LEU:HD11	1:A:267:VAL:HG11	1.78	0.64
2:B:147:HIS:ND1	2:B:148:THR:HG22	2.12	0.64
1:A:890:LEU:HD12	1:A:890:LEU:H	1.61	0.64
2:B:78:LYS:HG2	2:B:79:SER:H	1.61	0.63
1:A:887:TRP:HH2	1:A:907:LEU:CG	2.09	0.63
1:A:978:LEU:HD12	1:A:984:MET:HE1	1.79	0.63
1:A:428:ARG:HB3	1:A:428:ARG:NH1	2.13	0.63
1:A:620:ILE:HD11	1:A:771:VAL:HG21	1.79	0.63
1:A:876:THR:O	1:A:880:THR:HG23	1.99	0.63
1:A:127:GLN:NE2	1:A:134:THR:HB	2.13	0.63
1:A:469:SER:HA	1:A:473:LEU:CD2	2.19	0.63
1:A:532:ILE:HD13	1:A:533:LYS:N	2.14	0.63
1:A:54:GLN:HG2	1:A:54:GLN:O	1.98	0.62
1:A:202:MET:HA	1:A:206:ASP:OD2	1.99	0.62
1:A:994:ARG:HD2	1:A:997:TRP:NE1	2.14	0.62
1:A:64:TYR:CD2	1:A:266:LEU:HD11	2.34	0.62
1:A:826:PHE:CE2	1:A:966:ILE:HG23	2.34	0.62
1:A:866:ILE:HD12	1:A:866:ILE:N	2.13	0.62
1:A:964:LEU:O	1:A:968:ILE:HD13	1.99	0.62
2:B:60:TYR:O	2:B:64:ARG:HG3	2.00	0.62
1:A:345:LEU:HD12	1:A:348:THR:CG2	2.28	0.62
1:A:79:GLU:O	1:A:83:ARG:HG3	2.00	0.62
1:A:828:SER:CA	1:A:946:ARG:HH22	2.11	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:176:LYS:HB3	2:B:249:LEU:O	2.00	0.62
1:A:53:HIS:HB2	1:A:250:ASN:HD21	1.64	0.62
1:A:310:LEU:O	1:A:314:THR:HG23	2.00	0.62
1:A:801:ILE:O	1:A:805:VAL:HG22	1.99	0.62
1:A:987:ILE:HG13	1:A:988:PHE:H	1.62	0.62
2:B:176:LYS:HB3	2:B:250:LEU:HA	1.81	0.62
1:A:685:SER:O	1:A:689:GLU:HG3	1.99	0.61
1:A:841:MET:HA	1:A:841:MET:HE3	1.82	0.61
2:B:259:VAL:HG12	2:B:285:LYS:HG2	1.81	0.61
2:B:213:LEU:HA	2:B:251:ASN:HB2	1.81	0.61
1:A:214:ILE:HD12	1:A:236:ARG:HB3	1.82	0.61
2:B:85:ARG:N	2:B:86:PRO:HD2	2.16	0.61
2:B:180:ILE:HD12	2:B:180:ILE:O	2.00	0.61
1:A:134:THR:HG1	1:A:138:ASN:HB2	1.65	0.61
1:A:504:LEU:HG	1:A:510:PRO:CA	2.29	0.61
1:A:563:GLY:HA2	1:A:597:LEU:HD23	1.82	0.61
1:A:964:LEU:O	1:A:967:ALA:HB3	2.01	0.61
2:B:229:PHE:HB3	2:B:230:PRO:HA	1.83	0.61
1:A:470:GLU:HA	1:A:474:GLY:O	2.00	0.61
2:B:85:ARG:CB	2:B:180:ILE:HG13	2.31	0.61
2:B:275:HIS:CG	2:B:276:ASP:H	2.19	0.61
1:A:442:PHE:CZ	1:A:470:GLU:HG3	2.36	0.61
2:B:84:LEU:HB3	2:B:86:PRO:HD2	1.83	0.61
1:A:486:VAL:CG1	1:A:501:ILE:HG23	2.30	0.60
1:A:1012:ASP:OD2	1:A:1016:LYS:HE3	2.00	0.60
1:A:679:LEU:HD12	1:A:702:THR:HG22	1.83	0.60
2:B:83:THR:HG22	2:B:184:ASN:OD1	2.00	0.60
1:A:434:LEU:CD2	1:A:465:LEU:HB3	2.30	0.60
1:A:436:LEU:HD23	1:A:480:ARG:HA	1.84	0.60
1:A:861:TYR:CE1	1:A:1031:LEU:HA	2.36	0.60
1:A:905:GLN:HB2	2:B:83:THR:HB	1.83	0.60
1:A:188:GLN:H	1:A:188:GLN:NE2	1.99	0.60
1:A:300:PHE:CD1	1:A:854:VAL:HG21	2.36	0.60
1:A:516:MET:CE	1:A:526:ARG:HD3	2.32	0.60
1:A:486:VAL:HG13	1:A:487:CYS:H	1.67	0.60
1:A:915:TRP:CZ3	2:B:76:GLN:HB2	2.37	0.60
1:A:80:LEU:HA	1:A:83:ARG:HE	1.66	0.60
1:A:861:TYR:CZ	1:A:1031:LEU:HD23	2.36	0.60
1:A:993:ILE:HG12	1:A:997:TRP:HB2	1.84	0.60
1:A:275:ILE:HG23	1:A:276:ILE:N	2.17	0.60
1:A:345:LEU:HD12	1:A:348:THR:HG21	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:ARG:HD3	1:A:505:GLU:OE1	2.01	0.60
1:A:516:MET:HE1	1:A:526:ARG:HD3	1.84	0.60
1:A:831:LEU:HG	1:A:946:ARG:CD	2.32	0.60
1:A:923:GLN:CD	2:B:76:GLN:HG2	2.22	0.60
2:B:136:TYR:CE2	2:B:190:LEU:HB3	2.36	0.59
2:B:255:ASN:ND2	2:B:290:LYS:H	2.00	0.59
1:A:966:ILE:HA	1:A:969:VAL:HG22	1.84	0.59
2:B:178:CYS:CB	2:B:248:LYS:HD2	2.33	0.59
1:A:106:ALA:O	1:A:110:GLN:HB2	2.03	0.59
1:A:203:LYS:NZ	1:A:203:LYS:HB3	2.17	0.59
1:A:450:PRO:HG2	1:A:453:LYS:HB2	1.84	0.59
1:A:504:LEU:HD13	1:A:504:LEU:H	1.66	0.59
2:B:249:LEU:HD12	2:B:286:LEU:HD12	1.84	0.59
1:A:504:LEU:H	1:A:504:LEU:CD1	2.14	0.59
1:A:614:LYS:HG2	1:A:768:VAL:HG11	1.84	0.59
1:A:411:THR:C	1:A:603:PRO:HG3	2.23	0.59
1:A:430:LEU:O	1:A:430:LEU:HD23	2.03	0.59
1:A:484:PRO:CD	1:A:503:THR:HG22	2.29	0.59
1:A:630:PRO:HD3	1:A:701:ARG:HG3	1.84	0.59
1:A:880:THR:HG22	2:B:62:LEU:HD22	1.85	0.59
1:A:885:GLU:OE1	1:A:923:GLN:HB3	2.02	0.59
2:B:188:LYS:HA	2:B:230:PRO:HB2	1.84	0.59
1:A:486:VAL:HG13	1:A:487:CYS:N	2.18	0.59
1:A:788:THR:HG23	1:A:791:LYS:HE3	1.84	0.59
1:A:1015:ARG:HG3	1:A:1031:LEU:HD22	1.85	0.59
1:A:1028:ASP:O	1:A:1032:TYR:HB3	2.03	0.59
2:B:75:ASP:O	2:B:78:LYS:HD2	2.03	0.59
1:A:806:SER:OG	1:A:896:ARG:HG2	2.02	0.58
2:B:183:MET:CE	2:B:264:ILE:HD13	2.33	0.58
1:A:964:LEU:O	1:A:964:LEU:HD23	2.02	0.58
2:B:252:VAL:HB	2:B:253:PRO:HD3	1.84	0.58
1:A:113:MET:CG	1:A:346:LEU:HD22	2.33	0.58
1:A:203:LYS:HG2	1:A:204:GLY:N	2.17	0.58
2:B:282:VAL:O	2:B:283:GLU:HG2	2.03	0.58
1:A:259:LEU:HD12	1:A:259:LEU:H	1.69	0.58
1:A:381:VAL:CG1	1:A:721:VAL:HG22	2.33	0.58
1:A:1026:TRP:CZ2	1:A:1030:GLU:HG3	2.37	0.58
1:A:120:CYS:HB2	1:A:142:ALA:HB2	1.86	0.58
1:A:351:VAL:O	1:A:355:LEU:HD23	2.04	0.58
2:B:282:VAL:HG12	2:B:283:GLU:N	2.18	0.58
1:A:807:VAL:HG23	1:A:892:CYS:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:885:GLU:HA	2:B:76:GLN:HE22	1.67	0.58
1:A:947:LYS:HG2	1:A:958:PHE:HB3	1.85	0.58
2:B:144:ALA:N	2:B:145:PRO:CD	2.66	0.58
1:A:190:ASN:HB3	1:A:193:GLN:HE21	1.67	0.58
1:A:434:LEU:C	1:A:434:LEU:HD23	2.24	0.58
1:A:520:PRO:HG2	1:A:551:TYR:CE1	2.39	0.58
1:A:220:ARG:HG3	1:A:220:ARG:O	2.03	0.58
1:A:483:PHE:HB3	1:A:502:HIS:HB3	1.86	0.58
1:A:292:PRO:O	1:A:295:ILE:HG12	2.04	0.58
2:B:46:ALA:HA	2:B:49:VAL:HG11	1.85	0.58
2:B:255:ASN:HD22	2:B:255:ASN:N	2.02	0.58
1:A:478:GLY:O	1:A:482:ARG:HG3	2.04	0.57
2:B:143:LEU:CB	2:B:145:PRO:HD2	2.31	0.57
1:A:212:ILE:C	1:A:212:ILE:HD12	2.24	0.57
1:A:266:LEU:HD13	1:A:267:VAL:N	2.18	0.57
1:A:624:MET:HB2	1:A:642:ILE:HD13	1.86	0.57
1:A:841:MET:HA	1:A:841:MET:CE	2.34	0.57
1:A:113:MET:CG	1:A:346:LEU:HD13	2.33	0.57
2:B:287:LYS:HE2	2:B:289:GLN:CG	2.34	0.57
1:A:70:LYS:CE	1:A:183:ASP:HA	2.35	0.57
1:A:163:SER:O	1:A:167:ILE:HG12	2.04	0.57
1:A:427:TRP:CZ2	1:A:431:CYS:SG	2.98	0.57
1:A:572:LYS:HD2	1:A:572:LYS:N	2.19	0.57
1:A:933:ILE:HD11	1:A:979:CYS:SG	2.45	0.57
1:A:951:LEU:CD1	1:A:956:GLN:HB2	2.26	0.57
2:B:177:PRO:HD3	2:B:288:ILE:HD11	1.86	0.57
1:A:865:GLN:OE1	1:A:1011:TYR:HE2	1.87	0.57
1:A:965:VAL:HA	1:A:968:ILE:CD1	2.33	0.57
2:B:154:PHE:HD1	2:B:228:TYR:OH	1.85	0.57
2:B:192:GLY:N	2:B:268:HIS:HD2	2.02	0.57
2:B:265:LEU:O	2:B:266:ALA:HB2	2.05	0.57
1:A:345:LEU:HA	1:A:348:THR:CG2	2.33	0.57
1:A:433:VAL:HG13	1:A:564:PHE:HD2	1.70	0.57
1:A:575:PRO:HG2	1:A:578:TYR:HB2	1.86	0.57
1:A:945:ILE:HA	1:A:1016:LYS:NZ	2.19	0.57
2:B:54:ILE:O	2:B:57:LEU:HB3	2.04	0.57
2:B:83:THR:O	2:B:182:LYS:HD2	2.04	0.57
1:A:557:LEU:HD23	1:A:559:GLU:CD	2.25	0.57
1:A:578:TYR:CE2	1:A:580:PHE:HB3	2.39	0.57
2:B:137:PHE:HD2	2:B:139:GLN:HE21	1.52	0.57
1:A:117:ALA:HA	1:A:145:LEU:HD12	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1012:ASP:O	1:A:1016:LYS:HG3	2.05	0.57
2:B:242:ASN:OD1	2:B:243:PRO:HD2	2.05	0.57
1:A:866:ILE:H	1:A:866:ILE:CD1	2.17	0.56
1:A:392:GLN:HE22	1:A:603:PRO:HG2	1.68	0.56
1:A:856:GLU:HB2	1:A:857:PRO:HD3	1.88	0.56
2:B:137:PHE:HD2	2:B:139:GLN:NE2	2.02	0.56
1:A:92:PRO:C	1:A:94:GLY:H	2.08	0.56
1:A:815:THR:CA	1:A:990:PHE:HZ	2.17	0.56
1:A:827:PRO:O	1:A:831:LEU:HD23	2.05	0.56
2:B:248:LYS:C	2:B:249:LEU:HD23	2.26	0.56
1:A:233:PRO:HB3	1:A:259:LEU:HD22	1.86	0.56
1:A:401:TRP:HB3	1:A:597:LEU:H	1.70	0.56
1:A:504:LEU:HD23	1:A:506:ASP:O	2.06	0.56
1:A:578:TYR:HE2	1:A:580:PHE:HB3	1.70	0.56
1:A:758:ILE:HD12	1:A:758:ILE:N	2.21	0.56
1:A:879:PHE:CD1	1:A:889:PRO:HB3	2.41	0.56
1:A:978:LEU:O	1:A:984:MET:HG3	2.06	0.56
2:B:85:ARG:HB3	2:B:180:ILE:HG13	1.86	0.56
1:A:806:SER:HA	1:A:896:ARG:HD3	1.88	0.56
1:A:1016:LYS:O	1:A:1020:ARG:HG3	2.05	0.56
2:B:88:VAL:HG21	2:B:284:PHE:CE1	2.39	0.56
2:B:186:ILE:HG23	2:B:189:PHE:CB	2.34	0.56
1:A:436:LEU:HB3	1:A:502:HIS:HE1	1.69	0.56
1:A:730:ASP:O	1:A:734:LEU:HD13	2.06	0.56
1:A:527:CYS:HG	1:A:594:PHE:HD2	1.54	0.56
1:A:801:ILE:HG22	1:A:805:VAL:HG22	1.87	0.56
2:B:82:VAL:HG22	2:B:281:LYS:N	2.20	0.56
2:B:88:VAL:HG11	2:B:284:PHE:CE1	2.41	0.56
2:B:139:GLN:O	2:B:140:GLU:CB	2.53	0.56
1:A:73:SER:HG	1:A:76:LEU:HD13	1.70	0.56
1:A:104:GLN:HG3	1:A:157:TYR:HB2	1.88	0.56
1:A:241:THR:HG21	1:A:249:ARG:HD2	1.88	0.56
1:A:532:ILE:HG22	1:A:537:LEU:CD1	2.36	0.56
1:A:825:ILE:HG23	1:A:826:PHE:N	2.21	0.56
2:B:85:ARG:HH21	2:B:86:PRO:CB	2.16	0.56
1:A:427:TRP:HH2	1:A:468:PHE:CE2	2.24	0.55
1:A:501:ILE:HD13	1:A:580:PHE:CZ	2.41	0.55
1:A:1030:GLU:CD	2:B:40:ILE:HD11	2.27	0.55
1:A:427:TRP:HH2	1:A:468:PHE:HE2	1.53	0.55
1:A:947:LYS:HG2	1:A:958:PHE:HB2	1.86	0.55
1:A:294:ALA:O	1:A:298:GLU:HG3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:ILE:CG1	1:A:252:ALA:HB3	2.36	0.55
1:A:523:VAL:HA	1:A:526:ARG:HD2	1.88	0.55
1:A:630:PRO:HD3	1:A:701:ARG:CG	2.36	0.55
1:A:752:LYS:HE3	1:A:758:ILE:HG21	1.87	0.55
1:A:831:LEU:HG	1:A:946:ARG:CZ	2.36	0.55
1:A:124:PHE:HA	1:A:127:GLN:HG2	1.89	0.55
1:A:826:PHE:HB3	1:A:827:PRO:HD3	1.88	0.55
1:A:49:GLU:OE2	1:A:278:ARG:HG3	2.07	0.55
1:A:90:ARG:H	1:A:90:ARG:HD3	1.71	0.55
1:A:704:PRO:HG3	1:A:729:ASN:HB2	1.88	0.55
1:A:711:VAL:O	1:A:715:GLN:HG3	2.06	0.55
1:A:75:SER:O	1:A:79:GLU:HG3	2.07	0.55
1:A:745:ILE:HG13	1:A:746:ALA:H	1.71	0.55
1:A:54:GLN:H	1:A:54:GLN:NE2	2.05	0.55
1:A:276:ILE:HG13	1:A:277:GLY:N	2.21	0.55
1:A:528:SER:OG	1:A:591:GLY:HA2	2.06	0.55
2:B:49:VAL:CG1	2:B:50:VAL:N	2.69	0.55
1:A:288:ASN:O	1:A:289:GLU:HB3	2.07	0.55
1:A:473:LEU:HD23	1:A:473:LEU:N	2.13	0.55
1:A:890:LEU:HD12	1:A:890:LEU:N	2.22	0.55
2:B:57:LEU:C	2:B:57:LEU:HD23	2.27	0.55
1:A:66:THR:OG1	1:A:72:LEU:HD21	2.07	0.54
1:A:134:THR:HA	1:A:137:ASP:HB2	1.88	0.54
1:A:212:ILE:CD1	1:A:214:ILE:HG13	2.37	0.54
1:A:931:PHE:O	1:A:935:ILE:HG13	2.06	0.54
2:B:277:PRO:O	2:B:281:LYS:HG3	2.08	0.54
1:A:72:LEU:HD12	1:A:198:ASP:HB3	1.89	0.54
1:A:233:PRO:HB3	1:A:259:LEU:CD2	2.38	0.54
1:A:653:ILE:O	1:A:656:ARG:HG2	2.07	0.54
1:A:869:ILE:HD13	1:A:1007:LEU:CD1	2.35	0.54
1:A:935:ILE:O	1:A:939:GLN:HG2	2.06	0.54
1:A:974:ILE:HG23	1:A:975:GLY:N	2.22	0.54
2:B:212:PRO:HB2	2:B:253:PRO:CG	2.38	0.54
1:A:443:LYS:HB2	1:A:446:GLN:OE1	2.08	0.54
2:B:142:PHE:CE2	2:B:232:TYR:HA	2.40	0.54
1:A:217:ALA:HB1	1:A:220:ARG:HG2	1.89	0.54
1:A:451:VAL:HG13	1:A:452:PRO:HD3	1.89	0.54
1:A:684:PRO:O	1:A:688:VAL:HG13	2.07	0.54
1:A:814:ILE:N	1:A:814:ILE:HD13	2.22	0.54
1:A:143:LEU:O	1:A:143:LEU:HD13	2.07	0.54
1:A:274:THR:O	1:A:278:ARG:HG2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:PHE:HE2	1:A:470:GLU:CG	2.20	0.54
1:A:613:LEU:HD12	1:A:614:LYS:N	2.22	0.54
1:A:921:LEU:HD13	1:A:924:GLN:NE2	2.22	0.54
2:B:146:ASN:HD21	2:B:149:LYS:HG2	1.71	0.54
2:B:265:LEU:N	2:B:265:LEU:HD12	2.22	0.54
1:A:124:PHE:HA	1:A:127:GLN:CG	2.38	0.54
1:A:270:THR:O	1:A:273:ARG:HG2	2.08	0.54
1:A:112:LEU:HD22	1:A:301:VAL:HG12	1.88	0.54
1:A:180:VAL:HG12	1:A:181:ILE:N	2.23	0.54
1:A:182:ARG:HH21	1:A:195:VAL:HG22	1.72	0.54
1:A:216:GLN:HA	1:A:238:PRO:HG3	1.88	0.54
1:A:469:SER:O	1:A:473:LEU:HG	2.07	0.54
1:A:523:VAL:HA	1:A:526:ARG:HG2	1.88	0.54
1:A:275:ILE:HG23	1:A:276:ILE:H	1.73	0.54
1:A:443:LYS:CE	1:A:457:ILE:HB	2.37	0.54
1:A:640:VAL:HG23	1:A:642:ILE:HG13	1.89	0.54
1:A:880:THR:HA	2:B:62:LEU:HD21	1.89	0.54
2:B:177:PRO:CD	2:B:288:ILE:HD11	2.38	0.54
1:A:53:HIS:HB2	1:A:250:ASN:ND2	2.22	0.54
1:A:124:PHE:HA	1:A:127:GLN:OE1	2.07	0.54
1:A:434:LEU:HD11	1:A:465:LEU:HD22	1.90	0.54
1:A:891:LEU:HD12	1:A:910:SER:HB3	1.89	0.54
1:A:929:THR:HG22	1:A:990:PHE:CD1	2.43	0.54
1:A:929:THR:HG21	1:A:991:MET:H	1.73	0.54
2:B:261:VAL:HG13	2:B:282:VAL:O	2.08	0.54
1:A:399:HIS:C	1:A:400:LEU:HD22	2.27	0.54
1:A:656:ARG:HG3	1:A:657:LEU:N	2.23	0.54
1:A:726:ASP:O	1:A:747:GLY:HA2	2.08	0.54
1:A:101:PHE:HE1	1:A:154:CYS:HA	1.73	0.53
1:A:340:TYR:O	1:A:342:PRO:HD3	2.08	0.53
1:A:613:LEU:HD12	1:A:613:LEU:C	2.28	0.53
1:A:151:VAL:HG13	1:A:152:THR:N	2.24	0.53
1:A:411:THR:HB	1:A:603:PRO:HB3	1.90	0.53
1:A:449:VAL:HG23	1:A:454:ARG:HB3	1.89	0.53
1:A:524:LEU:HD13	1:A:524:LEU:O	2.08	0.53
1:A:345:LEU:O	1:A:349:VAL:HG23	2.09	0.53
1:A:392:GLN:NE2	1:A:413:GLU:HG3	2.23	0.53
1:A:814:ILE:O	1:A:818:PHE:HD1	1.91	0.53
1:A:908:GLN:HA	1:A:913:GLN:O	2.09	0.53
1:A:909:ASP:OD2	1:A:911:TYR:HD2	1.92	0.53
1:A:113:MET:CE	1:A:148:VAL:HB	2.29	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:LYS:HD2	1:A:295:ILE:HG22	1.91	0.53
1:A:363:LYS:O	1:A:364:ASN:HB2	2.08	0.53
1:A:451:VAL:O	1:A:454:ARG:HG2	2.08	0.53
1:A:777:ILE:O	1:A:781:LEU:HG	2.08	0.53
1:A:974:ILE:O	1:A:978:LEU:HD23	2.07	0.53
2:B:282:VAL:HG13	2:B:284:PHE:CE2	2.43	0.53
1:A:401:TRP:HE3	1:A:596:GLY:HA2	1.74	0.53
1:A:877:ASP:CG	1:A:1000:VAL:HG13	2.29	0.53
2:B:177:PRO:HD3	2:B:288:ILE:CD1	2.39	0.53
1:A:122:ILE:O	1:A:126:ILE:HG12	2.08	0.53
1:A:940:ILE:O	1:A:944:LEU:HG	2.09	0.53
1:A:1022:CYS:HB2	1:A:1025:SER:CB	2.29	0.53
2:B:248:LYS:HB3	2:B:248:LYS:NZ	2.23	0.53
1:A:96:PRO:HB3	1:A:100:LYS:CD	2.39	0.53
1:A:625:VAL:HG12	1:A:707:LYS:HG2	1.91	0.53
1:A:993:ILE:CG1	1:A:997:TRP:HB2	2.38	0.53
1:A:434:LEU:CD1	1:A:465:LEU:HD22	2.38	0.53
1:A:930:VAL:HG22	1:A:993:ILE:CD1	2.38	0.53
1:A:245:PRO:O	1:A:248:THR:HG22	2.09	0.53
1:A:880:THR:O	1:A:884:GLN:HG2	2.09	0.53
1:A:78:ALA:O	1:A:82:LEU:HG	2.09	0.52
1:A:422:GLN:HG3	1:A:427:TRP:CD1	2.43	0.52
1:A:540:ASP:OD1	1:A:543:TRP:HB2	2.09	0.52
1:A:999:LEU:N	1:A:999:LEU:HD12	2.24	0.52
1:A:327:LEU:H	1:A:327:LEU:HD22	1.74	0.52
1:A:657:LEU:HD23	1:A:659:VAL:CG1	2.38	0.52
1:A:885:GLU:OE2	1:A:923:GLN:HG3	2.08	0.52
1:A:486:VAL:HG12	1:A:501:ILE:O	2.08	0.52
1:A:791:LYS:NZ	1:A:820:GLU:HA	2.24	0.52
1:A:828:SER:HA	1:A:946:ARG:HH12	1.74	0.52
1:A:856:GLU:CD	1:A:856:GLU:H	2.13	0.52
1:A:896:ARG:HA	1:A:899:TRP:HB3	1.90	0.52
2:B:178:CYS:HB2	2:B:248:LYS:CD	2.37	0.52
1:A:496:LYS:O	1:A:496:LYS:HG3	2.10	0.52
1:A:182:ARG:NH2	1:A:195:VAL:HG22	2.25	0.52
1:A:254:PHE:CD1	1:A:255:SER:N	2.78	0.52
1:A:428:ARG:HB3	1:A:428:ARG:CZ	2.40	0.52
2:B:179:PHE:HE2	2:B:249:LEU:HD11	1.74	0.52
2:B:248:LYS:HB3	2:B:248:LYS:HZ2	1.73	0.52
1:A:499:LEU:C	1:A:499:LEU:HD12	2.30	0.52
1:A:522:ARG:HG3	1:A:526:ARG:CZ	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:806:SER:HG	1:A:896:ARG:HG2	1.73	0.52
2:B:59:ILE:O	2:B:63:MET:HG2	2.10	0.52
1:A:390:LEU:O	1:A:608:VAL:HG21	2.10	0.52
1:A:625:VAL:CG1	1:A:707:LYS:HG2	2.39	0.52
1:A:76:LEU:O	1:A:80:LEU:HD13	2.09	0.52
1:A:295:ILE:HG13	1:A:296:GLU:N	2.24	0.52
1:A:420:PHE:HZ	1:A:472:THR:HG21	1.71	0.52
2:B:49:VAL:HG13	2:B:50:VAL:N	2.25	0.52
1:A:345:LEU:CA	1:A:348:THR:HG22	2.38	0.52
1:A:598:VAL:HG13	1:A:598:VAL:O	2.10	0.52
1:A:685:SER:O	1:A:688:VAL:HG22	2.10	0.52
1:A:929:THR:HG21	1:A:991:MET:N	2.24	0.52
1:A:1007:LEU:HD13	1:A:1007:LEU:C	2.30	0.52
1:A:427:TRP:CH2	1:A:468:PHE:HE2	2.27	0.52
2:B:275:HIS:CG	2:B:276:ASP:N	2.78	0.52
1:A:351:VAL:HG23	1:A:352:CYS:N	2.25	0.51
1:A:670:ARG:O	1:A:695:PRO:HD2	2.11	0.51
1:A:90:ARG:HD3	1:A:90:ARG:N	2.25	0.51
1:A:682:MET:HE3	1:A:687:LEU:HD22	1.92	0.51
1:A:827:PRO:HG3	1:A:967:ALA:HB1	1.92	0.51
2:B:190:LEU:N	2:B:190:LEU:HD12	2.26	0.51
1:A:95:THR:N	1:A:96:PRO:HD3	2.25	0.51
1:A:783:LYS:HD2	1:A:946:ARG:O	2.11	0.51
1:A:925:TYR:HB2	1:A:991:MET:HE1	1.93	0.51
2:B:213:LEU:HD11	2:B:249:LEU:HD13	1.93	0.51
1:A:356:THR:OG1	1:A:777:ILE:HD12	2.11	0.51
1:A:505:GLU:HG3	1:A:506:ASP:N	2.26	0.51
1:A:630:PRO:CD	1:A:701:ARG:HD2	2.40	0.51
1:A:660:PRO:HD2	1:A:663:GLN:NE2	2.25	0.51
2:B:72:ASP:OD2	2:B:73:TYR:CE1	2.63	0.51
1:A:486:VAL:CG1	1:A:580:PHE:HE1	2.19	0.51
1:A:483:PHE:HB3	1:A:502:HIS:CB	2.41	0.51
1:A:548:GLN:O	1:A:552:LEU:HD13	2.10	0.51
1:A:974:ILE:HG13	1:A:978:LEU:CD2	2.41	0.51
1:A:400:LEU:HD13	1:A:598:VAL:HG23	1.91	0.51
1:A:457:ILE:HG23	1:A:457:ILE:O	2.10	0.51
1:A:814:ILE:HG12	1:A:815:THR:N	2.26	0.51
1:A:827:PRO:HG2	1:A:971:GLN:OE1	2.11	0.51
1:A:880:THR:HA	2:B:62:LEU:CD2	2.41	0.51
1:A:461:SER:O	1:A:465:LEU:HG	2.11	0.51
1:A:787:TYR:CB	1:A:946:ARG:HD2	2.30	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:834:GLU:HG2	1:A:947:LYS:HD2	1.93	0.51
1:A:994:ARG:HD2	1:A:997:TRP:HE1	1.74	0.51
1:A:194:LEU:HD21	1:A:267:VAL:HG21	1.93	0.50
1:A:223:ASP:CB	1:A:259:LEU:HD11	2.35	0.50
1:A:400:LEU:CD1	1:A:598:VAL:HG23	2.41	0.50
1:A:868:ALA:O	1:A:872:PHE:HD1	1.93	0.50
1:A:723:VAL:HG23	1:A:737:ALA:HB2	1.93	0.50
1:A:852:ARG:HG3	1:A:852:ARG:NH1	2.26	0.50
1:A:436:LEU:HB3	1:A:502:HIS:CE1	2.45	0.50
2:B:75:ASP:O	2:B:78:LYS:HB3	2.11	0.50
1:A:392:GLN:CD	1:A:413:GLU:CG	2.80	0.50
1:A:924:GLN:O	1:A:927:CYS:HB3	2.11	0.50
1:A:120:CYS:SG	1:A:141:LEU:HD22	2.51	0.50
1:A:134:THR:OG1	1:A:138:ASN:HB2	2.10	0.50
1:A:533:LYS:O	1:A:533:LYS:HG2	2.11	0.50
1:A:691:LEU:HD11	1:A:713:SER:OG	2.12	0.50
1:A:112:LEU:O	1:A:115:VAL:HG12	2.10	0.50
1:A:291:THR:HG23	1:A:292:PRO:HD2	1.94	0.50
1:A:430:LEU:HD23	1:A:430:LEU:C	2.32	0.50
1:A:801:ILE:HG22	1:A:805:VAL:CG2	2.41	0.50
1:A:929:THR:O	1:A:932:PHE:HB3	2.12	0.50
1:A:291:THR:CG2	1:A:292:PRO:HD2	2.42	0.50
1:A:122:ILE:HG22	1:A:334:MET:HE2	1.94	0.50
1:A:993:ILE:HD11	1:A:997:TRP:CB	2.42	0.50
1:A:90:ARG:NH2	1:A:281:SER:HA	2.27	0.49
1:A:890:LEU:H	1:A:890:LEU:CD1	2.25	0.49
2:B:58:CYS:O	2:B:61:VAL:HG22	2.11	0.49
2:B:85:ARG:HB2	2:B:180:ILE:HD11	1.94	0.49
1:A:814:ILE:HD13	1:A:814:ILE:H	1.77	0.49
1:A:872:PHE:HD2	2:B:55:PHE:CG	2.30	0.49
1:A:327:LEU:O	1:A:331:VAL:HG13	2.13	0.49
1:A:68:ALA:HB1	1:A:215:LEU:CD2	2.43	0.49
1:A:100:LYS:HE2	1:A:100:LYS:CA	2.38	0.49
1:A:254:PHE:HD1	1:A:255:SER:N	2.10	0.49
1:A:878:TYR:CE1	1:A:882:MET:HG3	2.48	0.49
1:A:1027:TRP:CB	1:A:1031:LEU:HD12	2.33	0.49
2:B:261:VAL:HG22	2:B:283:GLU:CD	2.32	0.49
1:A:994:ARG:HB2	1:A:997:TRP:CD1	2.48	0.49
1:A:974:ILE:HG13	1:A:978:LEU:HD21	1.95	0.49
1:A:394:ARG:NH2	1:A:452:PRO:HB2	2.27	0.49
1:A:731:SER:OG	1:A:732:PRO:HD3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:264:ILE:C	2:B:265:LEU:HD12	2.33	0.49
1:A:175:PRO:O	1:A:176:GLN:HB2	2.13	0.49
1:A:378:SER:HB3	1:A:720:ILE:HD12	1.95	0.48
1:A:382:ILE:HG13	1:A:620:ILE:HG21	1.95	0.48
1:A:630:PRO:HD3	1:A:701:ARG:HD2	1.94	0.48
1:A:896:ARG:N	1:A:897:PRO:HD2	2.28	0.48
2:B:85:ARG:HB2	2:B:180:ILE:CG1	2.43	0.48
1:A:109:LEU:HD13	1:A:297:ILE:HD11	1.95	0.48
1:A:216:GLN:HB3	1:A:264:GLN:HG2	1.95	0.48
1:A:649:THR:HA	1:A:671:ALA:O	2.14	0.48
1:A:707:LYS:O	1:A:711:VAL:HG23	2.13	0.48
1:A:917:PHE:CE2	1:A:921:LEU:HG	2.47	0.48
1:A:933:ILE:HD13	1:A:936:GLU:OE1	2.13	0.48
2:B:212:PRO:HB2	2:B:253:PRO:HG2	1.95	0.48
1:A:739:ILE:HG23	1:A:739:ILE:O	2.14	0.48
1:A:837:GLU:CG	1:A:951:LEU:HD21	2.43	0.48
1:A:869:ILE:HG12	2:B:51:MET:HE1	1.96	0.48
2:B:85:ARG:HB2	2:B:180:ILE:HG13	1.96	0.48
1:A:66:THR:HG22	1:A:67:SER:N	2.28	0.48
1:A:145:LEU:HD21	1:A:343:GLU:CG	2.43	0.48
1:A:266:LEU:HD13	1:A:266:LEU:C	2.34	0.48
1:A:270:THR:HG23	1:A:273:ARG:HE	1.77	0.48
1:A:367:VAL:O	1:A:367:VAL:HG23	2.14	0.48
1:A:392:GLN:HB2	1:A:394:ARG:HG2	1.96	0.48
1:A:861:TYR:CD2	1:A:865:GLN:HG3	2.48	0.48
2:B:78:LYS:CG	2:B:79:SER:N	2.76	0.48
1:A:194:LEU:HD11	1:A:267:VAL:HG21	1.95	0.48
1:A:741:VAL:HG11	1:A:767:ILE:HD11	1.94	0.48
1:A:885:GLU:CG	1:A:887:TRP:HD1	2.26	0.48
1:A:963:ILE:HA	1:A:966:ILE:HG22	1.96	0.48
1:A:227:LEU:HD11	1:A:275:ILE:CG2	2.44	0.48
1:A:286:VAL:HB	1:A:735:LYS:HG2	1.95	0.48
1:A:443:LYS:HE3	1:A:457:ILE:HB	1.94	0.48
1:A:473:LEU:H	1:A:473:LEU:CD2	2.11	0.48
1:A:679:LEU:CD1	1:A:702:THR:HG22	2.43	0.48
1:A:801:ILE:HA	1:A:804:THR:OG1	2.13	0.48
1:A:396:THR:HG22	1:A:397:VAL:N	2.28	0.48
1:A:682:MET:HE3	1:A:687:LEU:HD13	1.95	0.48
1:A:805:VAL:O	1:A:806:SER:HB3	2.13	0.48
1:A:911:TYR:CG	2:B:71:PRO:HD3	2.48	0.48
1:A:925:TYR:CD1	1:A:989:ASN:HB3	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:ILE:HG12	1:A:51:ASN:N	2.29	0.48
1:A:222:VAL:HG23	1:A:236:ARG:HG3	1.96	0.48
1:A:401:TRP:CE3	1:A:596:GLY:HA2	2.48	0.48
1:A:796:LEU:CD1	1:A:800:LEU:HG	2.43	0.48
1:A:112:LEU:HD22	1:A:301:VAL:CG1	2.43	0.48
1:A:113:MET:CE	1:A:145:LEU:HA	2.44	0.48
1:A:504:LEU:HD22	1:A:504:LEU:C	2.34	0.48
1:A:532:ILE:HD13	1:A:532:ILE:C	2.34	0.48
1:A:532:ILE:HD13	1:A:533:LYS:HB2	1.95	0.48
1:A:947:LYS:HD3	1:A:964:LEU:CD1	2.41	0.48
1:A:96:PRO:HB3	1:A:100:LYS:CG	2.44	0.47
1:A:150:VAL:HG13	1:A:151:VAL:N	2.29	0.47
1:A:194:LEU:HD13	1:A:194:LEU:C	2.34	0.47
1:A:523:VAL:HA	1:A:526:ARG:CG	2.44	0.47
1:A:624:MET:HE2	1:A:642:ILE:HD12	1.96	0.47
1:A:255:SER:HB3	1:A:276:ILE:HD13	1.95	0.47
1:A:297:ILE:O	1:A:301:VAL:HG13	2.14	0.47
1:A:438:ASN:OD1	1:A:462:GLU:HG2	2.14	0.47
1:A:745:ILE:HG12	1:A:762:ASP:CG	2.35	0.47
1:A:993:ILE:HD11	1:A:997:TRP:HB3	1.95	0.47
1:A:1000:VAL:CG1	1:A:1001:PRO:HD3	2.37	0.47
2:B:180:ILE:HD12	2:B:180:ILE:C	2.34	0.47
1:A:439:ARG:HG2	1:A:462:GLU:CD	2.34	0.47
1:A:212:ILE:HD12	1:A:212:ILE:O	2.13	0.47
1:A:327:LEU:HD22	1:A:327:LEU:N	2.30	0.47
1:A:420:PHE:HE2	1:A:468:PHE:HZ	1.61	0.47
2:B:86:PRO:O	2:B:88:VAL:HG23	2.14	0.47
1:A:113:MET:HG3	1:A:346:LEU:HD22	1.96	0.47
1:A:797:THR:HB	1:A:798:PRO:HD3	1.96	0.47
1:A:901:ASN:O	1:A:920:ARG:NH2	2.48	0.47
2:B:46:ALA:HA	2:B:49:VAL:HG12	1.95	0.47
1:A:451:VAL:N	1:A:452:PRO:HD2	2.29	0.47
1:A:523:VAL:CG1	1:A:594:PHE:HE2	2.26	0.47
1:A:881:ALA:HA	1:A:997:TRP:CH2	2.49	0.47
1:A:978:LEU:HD12	1:A:984:MET:CE	2.45	0.47
2:B:213:LEU:HA	2:B:251:ASN:HB3	1.96	0.47
1:A:70:LYS:HE2	1:A:183:ASP:HA	1.97	0.47
1:A:121:LEU:HD23	1:A:121:LEU:O	2.15	0.47
1:A:434:LEU:O	1:A:438:ASN:ND2	2.48	0.47
1:A:974:ILE:CG2	1:A:975:GLY:N	2.78	0.47
2:B:44:TYR:HA	2:B:47:PHE:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:PRO:O	1:A:94:GLY:N	2.48	0.47
1:A:136:ASP:HA	1:A:140:TYR:CE1	2.50	0.47
1:A:286:VAL:HG12	1:A:287:GLU:N	2.30	0.47
1:A:409:ALA:HB1	1:A:468:PHE:HE1	1.80	0.47
1:A:869:ILE:HG23	2:B:51:MET:HE1	1.95	0.47
1:A:947:LYS:NZ	1:A:961:ASN:ND2	2.62	0.47
1:A:221:LYS:HA	1:A:235:THR:HA	1.97	0.47
1:A:524:LEU:HD13	1:A:524:LEU:C	2.35	0.47
1:A:149:VAL:HG23	1:A:150:VAL:N	2.30	0.47
1:A:917:PHE:CE1	1:A:921:LEU:HD21	2.50	0.47
1:A:919:GLN:HE22	2:B:78:LYS:NZ	2.12	0.47
1:A:90:ARG:HD2	1:A:272:ASP:OD2	2.15	0.46
1:A:143:LEU:HD13	1:A:143:LEU:C	2.36	0.46
1:A:706:GLN:O	1:A:710:ILE:HG13	2.14	0.46
1:A:858:LEU:C	1:A:858:LEU:HD23	2.35	0.46
1:A:896:ARG:HG3	1:A:897:PRO:N	2.30	0.46
1:A:947:LYS:HZ1	1:A:961:ASN:HD22	1.64	0.46
1:A:707:LYS:NZ	1:A:729:ASN:ND2	2.62	0.46
1:A:947:LYS:CD	1:A:964:LEU:HD12	2.41	0.46
2:B:249:LEU:C	2:B:251:ASN:H	2.18	0.46
1:A:316:PHE:HZ	1:A:326:PHE:CE1	2.32	0.46
1:A:356:THR:HG23	1:A:359:ARG:HH21	1.80	0.46
1:A:439:ARG:HG2	1:A:462:GLU:OE1	2.15	0.46
1:A:451:VAL:CG1	1:A:452:PRO:HD3	2.45	0.46
1:A:701:ARG:HB3	1:A:701:ARG:HH11	1.80	0.46
1:A:759:LEU:N	1:A:759:LEU:HD22	2.31	0.46
1:A:796:LEU:HD13	1:A:796:LEU:O	2.16	0.46
1:A:905:GLN:CB	2:B:83:THR:HB	2.44	0.46
1:A:923:GLN:O	1:A:926:THR:HG22	2.14	0.46
1:A:530:ILE:HD13	1:A:594:PHE:HB3	1.97	0.46
1:A:532:ILE:HG22	1:A:537:LEU:HD11	1.98	0.46
1:A:875:PHE:O	1:A:878:TYR:HB3	2.16	0.46
2:B:78:LYS:CG	2:B:79:SER:H	2.26	0.46
1:A:77:ALA:O	1:A:195:VAL:HG11	2.14	0.46
1:A:146:ILE:O	1:A:149:VAL:HG22	2.14	0.46
1:A:469:SER:OG	1:A:473:LEU:HD11	2.16	0.46
1:A:757:MET:C	1:A:758:ILE:HD12	2.36	0.46
1:A:811:LEU:HD13	1:A:931:PHE:CD1	2.51	0.46
2:B:83:THR:O	2:B:84:LEU:HD12	2.15	0.46
2:B:179:PHE:O	2:B:179:PHE:CD1	2.69	0.46
1:A:296:GLU:CD	1:A:846:ARG:HH12	2.18	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:531:LEU:HD12	1:A:535:GLN:O	2.16	0.46
1:A:873:ALA:HA	1:A:1004:PHE:CD2	2.51	0.46
1:A:1027:TRP:O	1:A:1031:LEU:N	2.47	0.46
2:B:85:ARG:HE	2:B:86:PRO:CA	2.29	0.46
1:A:127:GLN:HB2	1:A:132:ASP:OD2	2.16	0.46
1:A:212:ILE:HD11	1:A:252:ALA:CB	2.46	0.46
1:A:228:THR:CG2	1:A:230:GLU:HG3	2.46	0.46
1:A:345:LEU:O	1:A:348:THR:HG22	2.16	0.46
1:A:376:LEU:HD22	1:A:376:LEU:H	1.80	0.46
1:A:442:PHE:HE2	1:A:470:GLU:CD	2.20	0.46
1:A:494:THR:C	1:A:496:LYS:H	2.19	0.46
1:A:659:VAL:HG22	1:A:660:PRO:HD2	1.97	0.46
1:A:844:ARG:HB3	1:A:845:PRO:HD2	1.97	0.46
1:A:939:GLN:HA	1:A:939:GLN:OE1	2.16	0.46
2:B:259:VAL:HG23	2:B:259:VAL:O	2.16	0.46
1:A:522:ARG:HG3	1:A:526:ARG:NH2	2.31	0.46
1:A:607:THR:HG1	1:A:765:ALA:HB2	1.79	0.46
1:A:1000:VAL:HG13	1:A:1001:PRO:CD	2.41	0.46
2:B:148:THR:HG23	2:B:148:THR:O	2.16	0.46
1:A:160:GLU:O	1:A:164:THR:HG23	2.16	0.46
1:A:216:GLN:HA	1:A:238:PRO:CG	2.46	0.46
1:A:475:ASN:ND2	1:A:477:MET:HB2	2.31	0.46
1:A:815:THR:HA	1:A:990:PHE:CZ	2.38	0.46
1:A:860:ALA:O	1:A:864:PHE:HB3	2.16	0.46
1:A:923:GLN:CA	1:A:926:THR:HG22	2.44	0.46
1:A:930:VAL:HG22	1:A:993:ILE:HG13	1.97	0.46
1:A:141:LEU:HD23	1:A:145:LEU:HG	1.98	0.45
1:A:404:ASN:HD21	1:A:546:ALA:CB	2.28	0.45
1:A:674:ILE:HG23	1:A:674:ILE:O	2.16	0.45
1:A:833:TYR:CG	1:A:963:ILE:HD12	2.50	0.45
1:A:90:ARG:O	1:A:90:ARG:HG2	2.16	0.45
1:A:787:TYR:HB2	1:A:946:ARG:NE	2.30	0.45
1:A:924:GLN:HG2	1:A:928:TYR:CZ	2.52	0.45
1:A:392:GLN:CD	1:A:413:GLU:HG2	2.37	0.45
1:A:704:PRO:HG3	1:A:729:ASN:CB	2.46	0.45
1:A:855:ASN:CG	1:A:857:PRO:HD2	2.35	0.45
1:A:80:LEU:CG	1:A:83:ARG:HH21	2.15	0.45
1:A:148:VAL:HA	1:A:151:VAL:HG12	1.99	0.45
1:A:569:LEU:HD11	1:A:587:PHE:CD1	2.51	0.45
1:A:442:PHE:CD1	1:A:456:VAL:HG22	2.52	0.45
1:A:812:GLY:O	1:A:816:ILE:HG13	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:VAL:HB	1:A:253:PHE:O	2.17	0.45
1:A:945:ILE:HA	1:A:1016:LYS:HZ1	1.81	0.45
1:A:356:THR:O	1:A:360:LEU:HD13	2.16	0.45
1:A:806:SER:HA	1:A:896:ARG:CD	2.46	0.45
1:A:811:LEU:HA	1:A:928:TYR:HD1	1.82	0.45
1:A:969:VAL:HG23	1:A:970:PHE:N	2.31	0.45
1:A:401:TRP:CE2	1:A:404:ASN:HA	2.52	0.45
1:A:436:LEU:CD2	1:A:480:ARG:HA	2.45	0.45
1:A:449:VAL:CG2	1:A:454:ARG:HB3	2.46	0.45
1:A:807:VAL:HG22	1:A:808:PRO:HD2	1.98	0.45
1:A:872:PHE:CD2	2:B:55:PHE:HB2	2.52	0.45
1:A:925:TYR:HB2	1:A:991:MET:CE	2.47	0.45
2:B:249:LEU:CD1	2:B:260:ILE:HD13	2.47	0.45
2:B:282:VAL:CG1	2:B:283:GLU:N	2.80	0.45
1:A:726:ASP:CG	1:A:727:GLY:N	2.70	0.45
1:A:895:LEU:HD12	1:A:899:TRP:HB2	1.97	0.45
1:A:903:HIS:CD2	2:B:88:VAL:O	2.69	0.45
1:A:1030:GLU:OE1	2:B:40:ILE:HD11	2.17	0.45
1:A:207:ARG:HB3	1:A:257:MET:SD	2.57	0.45
1:A:443:LYS:HE2	1:A:457:ILE:HB	1.98	0.45
1:A:531:LEU:HD12	1:A:535:GLN:C	2.38	0.45
1:A:945:ILE:HG13	1:A:946:ARG:N	2.32	0.45
2:B:84:LEU:HD11	2:B:282:VAL:HG21	1.98	0.45
1:A:435:THR:HG23	1:A:476:ALA:HB1	1.97	0.44
1:A:541:GLU:O	1:A:545:GLU:HG3	2.17	0.44
1:A:674:ILE:HD11	1:A:682:MET:SD	2.57	0.44
1:A:831:LEU:HD13	1:A:947:LYS:HD2	1.99	0.44
1:A:815:THR:HG23	1:A:990:PHE:CZ	2.52	0.44
2:B:272:ASP:CG	2:B:275:HIS:HB3	2.37	0.44
1:A:96:PRO:HB3	1:A:100:LYS:HG3	2.00	0.44
1:A:288:ASN:O	1:A:289:GLU:CB	2.65	0.44
1:A:230:GLU:OE1	1:A:234:GLN:HG3	2.17	0.44
1:A:392:GLN:HG3	1:A:603:PRO:O	2.17	0.44
1:A:607:THR:HG21	1:A:763:ASN:OD1	2.17	0.44
1:A:839:ASP:HB3	1:A:842:HIS:HD2	1.82	0.44
1:A:997:TRP:CZ2	2:B:73:TYR:CE2	3.06	0.44
2:B:139:GLN:HG2	2:B:149:LYS:HB3	1.98	0.44
1:A:877:ASP:HA	1:A:1000:VAL:HG21	1.99	0.44
1:A:60:LEU:HD13	1:A:60:LEU:C	2.38	0.44
1:A:113:MET:HE1	1:A:148:VAL:CB	2.35	0.44
1:A:707:LYS:HZ1	1:A:729:ASN:ND2	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:77:LEU:O	2:B:77:LEU:HG	2.17	0.44
2:B:135:LYS:NZ	2:B:135:LYS:HB3	2.33	0.44
2:B:242:ASN:CG	2:B:243:PRO:HD2	2.38	0.44
1:A:222:VAL:HG12	1:A:223:ASP:N	2.31	0.44
1:A:398:SER:HB3	1:A:601:ILE:HG22	1.98	0.44
1:A:442:PHE:CE1	1:A:454:ARG:HD2	2.53	0.44
1:A:877:ASP:OD2	1:A:934:SER:HB2	2.18	0.44
1:A:888:PHE:HD2	1:A:910:SER:CB	2.30	0.44
2:B:140:GLU:OE1	2:B:140:GLU:HA	2.17	0.44
1:A:392:GLN:HE22	1:A:412:THR:HA	1.83	0.44
1:A:520:PRO:HA	1:A:523:VAL:HG12	2.00	0.44
1:A:567:LEU:HD22	1:A:592:LEU:CD2	2.39	0.44
1:A:947:LYS:HZ1	1:A:961:ASN:ND2	2.16	0.44
1:A:222:VAL:HA	1:A:258:CYS:HA	2.00	0.44
1:A:427:TRP:CE2	1:A:431:CYS:SG	3.11	0.44
1:A:781:LEU:O	1:A:785:ILE:HG13	2.18	0.44
1:A:92:PRO:C	1:A:94:GLY:N	2.71	0.43
1:A:327:LEU:H	1:A:327:LEU:CD2	2.30	0.43
1:A:815:THR:HG23	1:A:932:PHE:HB2	1.96	0.43
1:A:826:PHE:CD2	1:A:967:ALA:HA	2.52	0.43
1:A:895:LEU:C	1:A:897:PRO:HD2	2.37	0.43
1:A:911:TYR:CD1	2:B:71:PRO:HD3	2.53	0.43
2:B:40:ILE:HG23	2:B:44:TYR:HE2	1.82	0.43
2:B:266:ALA:O	2:B:269:VAL:HG22	2.18	0.43
1:A:178:ALA:HB2	1:A:209:PRO:HB3	2.01	0.43
1:A:334:MET:O	1:A:338:VAL:HG23	2.18	0.43
1:A:501:ILE:HG21	1:A:587:PHE:CZ	2.52	0.43
1:A:523:VAL:HA	1:A:526:ARG:CD	2.47	0.43
1:A:683:ASP:HB3	1:A:684:PRO:HD2	2.00	0.43
1:A:962:ARG:HH11	1:A:962:ARG:HG2	1.83	0.43
2:B:178:CYS:SG	2:B:248:LYS:HD2	2.57	0.43
1:A:68:ALA:HB1	1:A:215:LEU:HD21	2.00	0.43
1:A:69:THR:HG23	1:A:70:LYS:N	2.33	0.43
1:A:877:ASP:OD2	1:A:1001:PRO:HD3	2.19	0.43
1:A:988:PHE:O	1:A:989:ASN:HB2	2.18	0.43
2:B:147:HIS:CG	2:B:148:THR:H	2.36	0.43
1:A:227:LEU:HD11	1:A:275:ILE:HG21	2.00	0.43
1:A:630:PRO:HD3	1:A:701:ARG:CD	2.49	0.43
1:A:1019:VAL:HG13	1:A:1020:ARG:N	2.33	0.43
1:A:113:MET:HG3	1:A:346:LEU:CD2	2.49	0.43
1:A:857:PRO:O	1:A:861:TYR:HD1	2.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:919:GLN:O	1:A:922:TYR:HB3	2.19	0.43
1:A:932:PHE:HE2	1:A:975:GLY:HA2	1.84	0.43
1:A:134:THR:C	1:A:136:ASP:N	2.72	0.43
1:A:656:ARG:CG	1:A:657:LEU:N	2.82	0.43
1:A:66:THR:HG23	1:A:72:LEU:HD23	2.01	0.43
1:A:519:ALA:O	1:A:523:VAL:HG12	2.18	0.43
1:A:731:SER:N	1:A:732:PRO:HD2	2.33	0.43
2:B:77:LEU:HG	2:B:186:ILE:HD12	2.00	0.43
1:A:434:LEU:HD21	1:A:465:LEU:C	2.40	0.43
1:A:521:GLU:O	1:A:525:GLU:HG2	2.18	0.43
1:A:601:ILE:CG1	1:A:602:ASP:N	2.81	0.43
1:A:683:ASP:HB3	1:A:684:PRO:CD	2.48	0.43
1:A:858:LEU:HD23	1:A:858:LEU:O	2.18	0.43
1:A:889:PRO:HG2	1:A:890:LEU:CD1	2.46	0.43
2:B:263:LYS:HB2	2:B:271:PHE:HE2	1.84	0.43
1:A:147:ALA:O	1:A:151:VAL:HG12	2.19	0.43
1:A:434:LEU:CG	1:A:465:LEU:HB3	2.48	0.43
1:A:439:ARG:HB3	1:A:439:ARG:NH1	2.34	0.43
1:A:921:LEU:HD13	1:A:924:GLN:HE21	1.82	0.43
1:A:203:LYS:H	1:A:206:ASP:CG	2.22	0.42
1:A:293:ILE:HD13	1:A:293:ILE:C	2.39	0.42
1:A:839:ASP:CB	1:A:842:HIS:HD2	2.32	0.42
1:A:972:VAL:HG13	1:A:973:CYS:N	2.34	0.42
2:B:77:LEU:O	2:B:78:LYS:C	2.57	0.42
1:A:359:ARG:O	1:A:363:LYS:HD3	2.19	0.42
1:A:450:PRO:HB2	1:A:452:PRO:HD2	2.01	0.42
1:A:523:VAL:HG13	1:A:594:PHE:HE2	1.84	0.42
1:A:809:LEU:HA	1:A:810:PRO:HD3	1.88	0.42
1:A:1015:ARG:HE	1:A:1031:LEU:HB3	1.84	0.42
2:B:84:LEU:CD2	2:B:181:ILE:HG12	2.49	0.42
1:A:52:ASP:O	1:A:55:LEU:HG	2.19	0.42
1:A:109:LEU:HD13	1:A:297:ILE:CD1	2.50	0.42
1:A:127:GLN:HE22	1:A:134:THR:HB	1.84	0.42
1:A:141:LEU:HD23	1:A:141:LEU:O	2.19	0.42
1:A:381:VAL:HG11	1:A:721:VAL:HG22	1.99	0.42
1:A:811:LEU:HD13	1:A:931:PHE:HB3	2.00	0.42
1:A:994:ARG:HD2	1:A:997:TRP:CE2	2.53	0.42
2:B:82:VAL:HG23	2:B:82:VAL:O	2.18	0.42
1:A:101:PHE:HA	1:A:157:TYR:CD1	2.54	0.42
1:A:400:LEU:HD22	1:A:400:LEU:N	2.34	0.42
1:A:470:GLU:OE2	1:A:476:ALA:HB3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:50:VAL:O	2:B:54:ILE:HG13	2.19	0.42
1:A:420:PHE:HZ	1:A:427:TRP:CZ2	2.37	0.42
1:A:434:LEU:HA	1:A:564:PHE:HE2	1.83	0.42
1:A:551:TYR:HD2	1:A:552:LEU:HD12	1.83	0.42
1:A:640:VAL:CG2	1:A:642:ILE:HG13	2.49	0.42
1:A:947:LYS:CE	1:A:964:LEU:HD12	2.50	0.42
1:A:985:PRO:O	1:A:989:ASN:HA	2.19	0.42
1:A:65:GLN:O	1:A:65:GLN:HG2	2.19	0.42
1:A:203:LYS:HB3	1:A:203:LYS:HZ3	1.85	0.42
1:A:222:VAL:CG2	1:A:236:ARG:HG3	2.49	0.42
1:A:532:ILE:O	1:A:532:ILE:HG23	2.20	0.42
1:A:683:ASP:O	1:A:687:LEU:HD23	2.19	0.42
1:A:787:TYR:OH	1:A:939:GLN:HB3	2.20	0.42
1:A:878:TYR:CD2	1:A:927:CYS:SG	3.13	0.42
1:A:966:ILE:HA	1:A:969:VAL:CG2	2.49	0.42
2:B:77:LEU:HD21	2:B:186:ILE:HB	2.02	0.42
1:A:160:GLU:HG2	1:A:368:LYS:O	2.19	0.42
1:A:214:ILE:HD13	1:A:220:ARG:HD3	2.02	0.42
1:A:485:LYS:HA	1:A:502:HIS:CD2	2.55	0.42
1:A:802:TYR:CD1	1:A:807:VAL:O	2.73	0.42
1:A:814:ILE:H	1:A:814:ILE:CD1	2.32	0.42
1:A:141:LEU:HD23	1:A:141:LEU:C	2.40	0.42
1:A:496:LYS:HE3	1:A:496:LYS:HB2	1.83	0.42
1:A:784:SER:HA	1:A:946:ARG:CZ	2.47	0.42
1:A:997:TRP:CZ2	2:B:73:TYR:HE2	2.37	0.42
2:B:129:ILE:HG22	2:B:151:SER:O	2.19	0.42
1:A:57:VAL:HG13	1:A:58:ALA:N	2.35	0.42
1:A:212:ILE:CD1	1:A:252:ALA:HB3	2.50	0.42
1:A:385:ASP:O	1:A:390:LEU:HG	2.19	0.42
1:A:878:TYR:O	1:A:882:MET:HG2	2.20	0.42
1:A:520:PRO:HA	1:A:523:VAL:CG1	2.50	0.41
1:A:601:ILE:CG1	1:A:602:ASP:H	2.24	0.41
1:A:627:GLY:HA2	1:A:702:THR:H	1.83	0.41
1:A:830:SER:OG	1:A:963:ILE:HG22	2.20	0.41
1:A:869:ILE:HG12	2:B:51:MET:HE2	1.99	0.41
1:A:1006:LEU:O	1:A:1010:VAL:HG12	2.20	0.41
2:B:287:LYS:HE2	2:B:289:GLN:NE2	2.35	0.41
1:A:210:ALA:O	1:A:212:ILE:HG23	2.20	0.41
1:A:427:TRP:CZ2	1:A:472:THR:HG21	2.55	0.41
1:A:923:GLN:HA	1:A:926:THR:CG2	2.48	0.41
1:A:1007:LEU:HD13	1:A:1007:LEU:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:61:VAL:CG2	2:B:62:LEU:N	2.84	0.41
2:B:265:LEU:O	2:B:266:ALA:CB	2.68	0.41
1:A:793:ILE:HB	1:A:794:PRO:CD	2.50	0.41
2:B:69:TYR:HE1	2:B:235:LYS:NZ	2.18	0.41
1:A:463:THR:CG2	1:A:467:LYS:HE3	2.50	0.41
1:A:532:ILE:HG22	1:A:537:LEU:HD13	2.03	0.41
1:A:822:CYS:O	1:A:825:ILE:HG22	2.19	0.41
1:A:70:LYS:HZ3	1:A:183:ASP:HA	1.84	0.41
1:A:202:MET:HE1	1:A:212:ILE:HG21	2.03	0.41
1:A:485:LYS:HG3	1:A:502:HIS:CD2	2.56	0.41
1:A:504:LEU:HB3	1:A:511:ARG:O	2.20	0.41
1:A:608:VAL:N	1:A:609:PRO:HD2	2.34	0.41
1:A:857:PRO:HB3	1:A:1030:GLU:O	2.21	0.41
1:A:1026:TRP:CE2	1:A:1030:GLU:HG3	2.55	0.41
2:B:144:ALA:N	2:B:145:PRO:HD2	2.35	0.41
1:A:120:CYS:CB	1:A:142:ALA:HB2	2.50	0.41
1:A:345:LEU:C	1:A:348:THR:HG22	2.41	0.41
1:A:392:GLN:CD	1:A:413:GLU:HG3	2.40	0.41
1:A:439:ARG:HB3	1:A:439:ARG:CZ	2.50	0.41
1:A:545:GLU:O	1:A:549:THR:HG23	2.21	0.41
1:A:705:GLN:O	1:A:708:LEU:HB3	2.21	0.41
1:A:826:PHE:HD2	1:A:967:ALA:CB	2.33	0.41
1:A:242:HIS:CD2	1:A:244:SER:H	2.38	0.41
1:A:706:GLN:HA	1:A:709:VAL:HG22	2.03	0.41
1:A:968:ILE:HD13	1:A:968:ILE:H	1.86	0.41
2:B:185:ARG:HD3	2:B:242:ASN:HB2	2.01	0.41
1:A:220:ARG:NH1	1:A:263:ALA:HB3	2.35	0.41
1:A:404:ASN:HD21	1:A:546:ALA:HB1	1.86	0.41
1:A:516:MET:HE3	1:A:526:ARG:HD3	2.02	0.41
1:A:530:ILE:CD1	1:A:594:PHE:HB3	2.51	0.41
1:A:903:HIS:HB3	2:B:88:VAL:O	2.21	0.41
1:A:945:ILE:HA	1:A:1016:LYS:HZ2	1.85	0.41
2:B:85:ARG:HB2	2:B:180:ILE:CD1	2.51	0.41
1:A:50:ILE:O	1:A:51:ASN:ND2	2.54	0.41
1:A:189:ILE:HD12	1:A:193:GLN:HB2	2.02	0.41
1:A:214:ILE:CD1	1:A:236:ARG:CB	2.97	0.41
1:A:232:GLU:HB2	1:A:233:PRO:HD2	2.02	0.41
1:A:290:LYS:HE3	1:A:298:GLU:OE2	2.21	0.41
1:A:396:THR:O	1:A:600:MET:HB2	2.21	0.41
1:A:785:ILE:O	1:A:789:LEU:HG	2.20	0.41
1:A:812:GLY:N	1:A:928:TYR:CD1	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:833:TYR:CB	1:A:961:ASN:HD21	2.31	0.41
1:A:109:LEU:HG	1:A:346:LEU:CD2	2.51	0.41
1:A:563:GLY:HA2	1:A:597:LEU:CD2	2.50	0.41
1:A:944:LEU:HD22	1:A:958:PHE:CD1	2.55	0.41
1:A:993:ILE:HG23	1:A:998:TRP:NE1	2.35	0.41
1:A:997:TRP:HA	1:A:997:TRP:CE3	2.56	0.41
2:B:40:ILE:HG22	2:B:41:SER:N	2.34	0.41
1:A:775:ARG:HD2	1:A:841:MET:HE3	2.02	0.40
1:A:884:GLN:CB	2:B:73:TYR:CE2	3.02	0.40
1:A:966:ILE:CA	1:A:969:VAL:HG22	2.50	0.40
1:A:567:LEU:HG	1:A:568:TYR:O	2.21	0.40
1:A:806:SER:OG	1:A:894:GLY:HA2	2.20	0.40
1:A:1010:VAL:HG13	1:A:1011:TYR:N	2.37	0.40
2:B:148:THR:OG1	2:B:238:PRO:HD2	2.21	0.40
1:A:296:GLU:OE2	1:A:852:ARG:HA	2.22	0.40
1:A:376:LEU:HD22	1:A:376:LEU:N	2.36	0.40
1:A:572:LYS:HG2	1:A:573:ASP:N	2.36	0.40
1:A:726:ASP:CG	1:A:727:GLY:H	2.24	0.40
1:A:810:PRO:HG2	1:A:875:PHE:HE1	1.86	0.40
2:B:192:GLY:N	2:B:268:HIS:CD2	2.86	0.40
2:B:258:VAL:O	2:B:285:LYS:HA	2.22	0.40
1:A:70:LYS:HG3	1:A:184:GLY:N	2.36	0.40
1:A:145:LEU:HD21	1:A:343:GLU:HG3	2.03	0.40
1:A:311:PHE:O	1:A:315:PHE:HD1	2.04	0.40
1:A:745:ILE:CG1	1:A:746:ALA:N	2.83	0.40
1:A:826:PHE:HD2	1:A:967:ALA:HB2	1.86	0.40
1:A:920:ARG:HG3	1:A:921:LEU:HD22	2.03	0.40
1:A:1014:ILE:HD13	1:A:1014:ILE:C	2.42	0.40
1:A:194:LEU:HD13	1:A:195:VAL:O	2.22	0.40
1:A:275:ILE:CG2	1:A:276:ILE:N	2.84	0.40
1:A:427:TRP:CH2	1:A:431:CYS:SG	3.15	0.40
2:B:88:VAL:HG21	2:B:284:PHE:CE2	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:PHE:CZ	1:A:457:ILE:CD1[2_565]	1.04	1.16

5.3 Torsion angles

5.3.1 Protein backbone

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	984/1034 (95%)	913 (93%)	60 (6%)	11 (1%)	14 52
2	B	163/290 (56%)	135 (83%)	21 (13%)	7 (4%)	2 22
All	All	1147/1324 (87%)	1048 (91%)	81 (7%)	18 (2%)	13 44

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	140	GLU
2	B	251	ASN
1	A	93	ARG
1	A	134	THR
1	A	955	GLN
1	A	1031	LEU
2	B	266	ALA
2	B	279	GLU
1	A	84	ASP
2	B	193	ASN
1	A	83	ARG
1	A	284	SER
1	A	957	GLY
2	B	238	PRO
1	A	1032	TYR
2	B	177	PRO
1	A	91	PRO
1	A	452	PRO

5.3.2 Protein sidechains

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

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	833/869 (96%)	801 (96%)	32 (4%)	33	57
2	B	162/254 (64%)	151 (93%)	11 (7%)	16	41
All	All	995/1123 (89%)	952 (96%)	43 (4%)	33	54

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	90	ARG
1	A	122	ILE
1	A	132	ASP
1	A	146	ILE
1	A	177	GLN
1	A	188	GLN
1	A	273	ARG
1	A	293	ILE
1	A	346	LEU
1	A	473	LEU
1	A	480	ARG
1	A	504	LEU
1	A	532	ILE
1	A	572	LYS
1	A	580	PHE
1	A	603	PRO
1	A	614	LYS
1	A	666	ARG
1	A	728	VAL
1	A	762	ASP
1	A	796	LEU
1	A	814	ILE
1	A	815	THR
1	A	841	MET
1	A	864	PHE
1	A	885	GLU
1	A	895	LEU
1	A	951	LEU
1	A	955	GLN
1	A	968	ILE
1	A	1014	ILE
2	B	42	LEU

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Mol	Chain	Res	Type
2	B	48	TYR
2	B	60	TYR
2	B	78	LYS
2	B	83	THR
2	B	85	ARG
2	B	145	PRO
2	B	182	LYS
2	B	188	LYS
2	B	255	ASN
2	B	276	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	54	GLN
1	A	65	GLN
1	A	110	GLN
1	A	188	GLN
1	A	193	GLN
1	A	242	HIS
1	A	288	ASN
1	A	299	HIS
1	A	404	ASN
1	A	405	HIS
1	A	502	HIS
1	A	566	GLN
1	A	675	ASN
1	A	694	HIS
1	A	706	GLN
1	A	729	ASN
1	A	842	HIS
1	A	903	HIS
1	A	908	GLN
1	A	919	GLN
1	A	924	GLN
1	A	956	GLN
1	A	961	ASN
2	B	76	GLN
2	B	125	GLN
2	B	255	ASN
2	B	268	HIS

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Mol	Chain	Res	Type
2	B	275	HIS
2	B	289	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Map visualisation

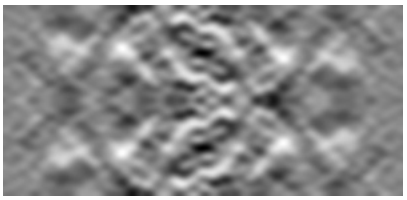
This section contains visualisations of the EMDB entry EMD-6799. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

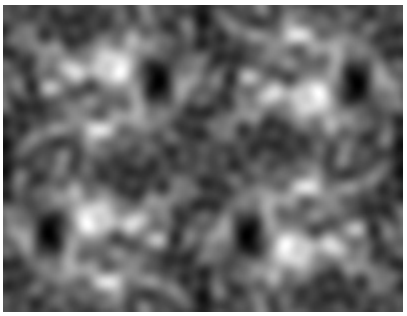
6.1 Orthogonal projections

6.1.1 Primary map

X



Y



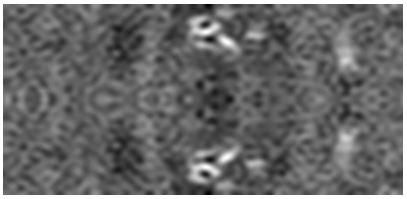
Z

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

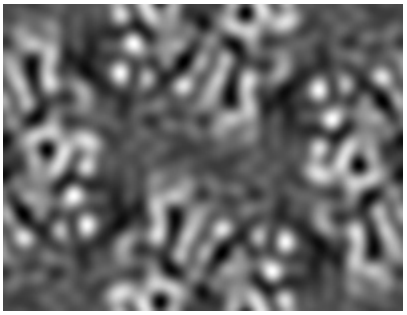
6.2 Central slices

6.2.1 Primary map

X Index: 68



Y Index: 52

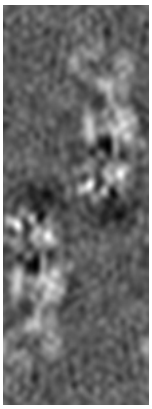


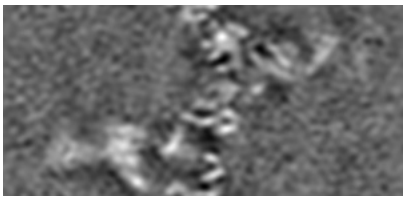
Z Index: 144

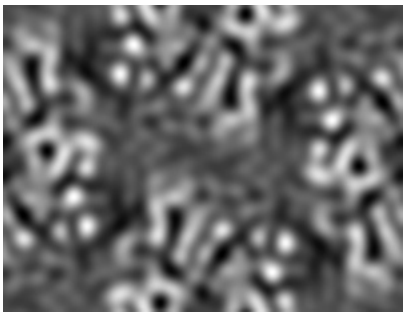
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map


X Index: 34


Y Index: 33


Z Index: 144

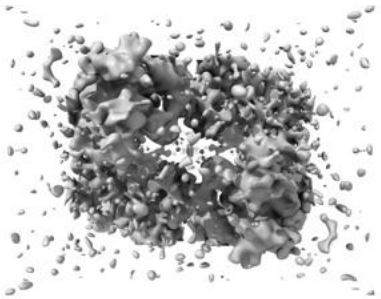
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map


X


Y


Z

The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

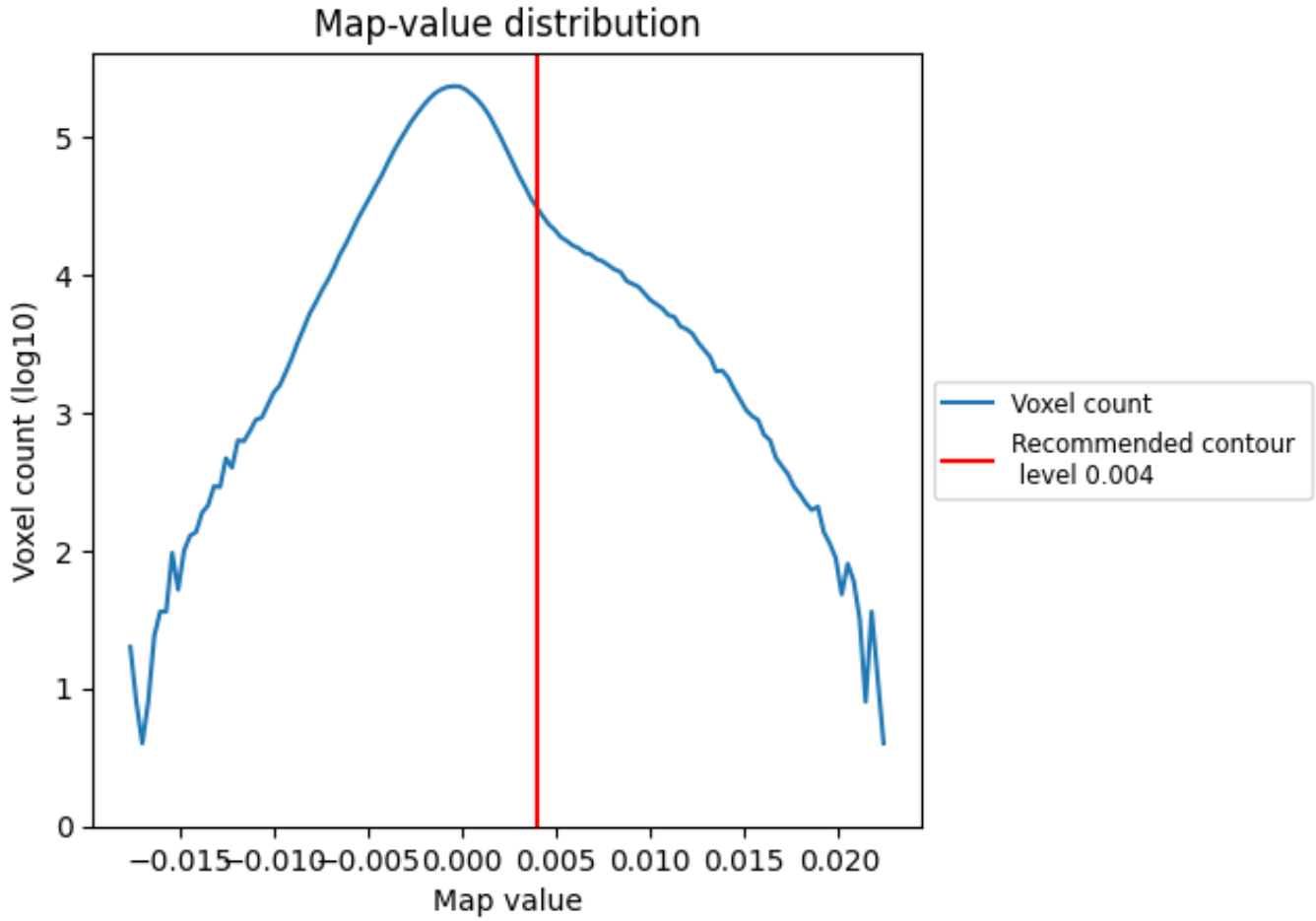
6.5 Mask visualisation (i)

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

7 Map analysis

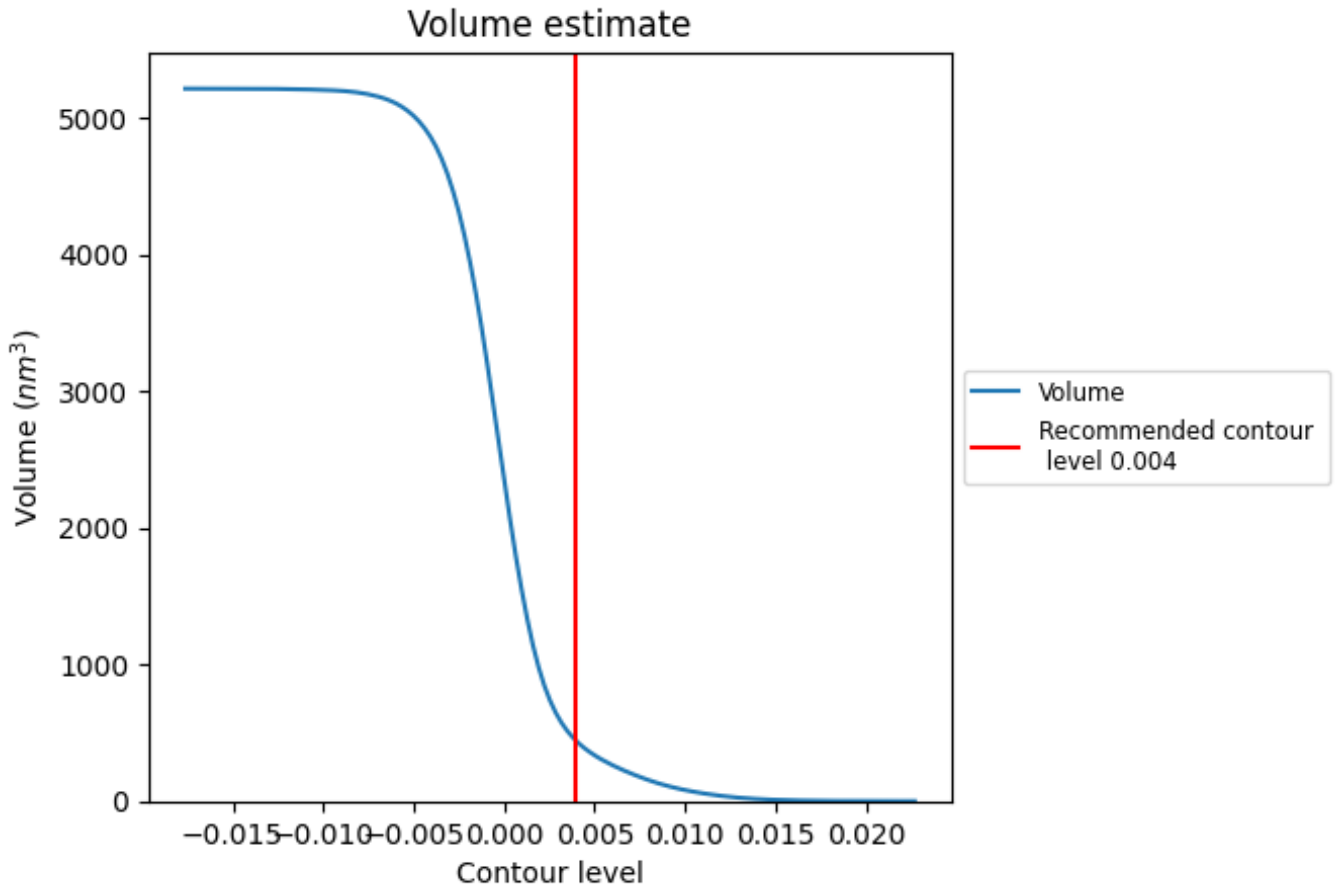
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

7.2 Volume estimate



The volume at the recommended contour level is 440 nm^3; this corresponds to an approximate mass of 398 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

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

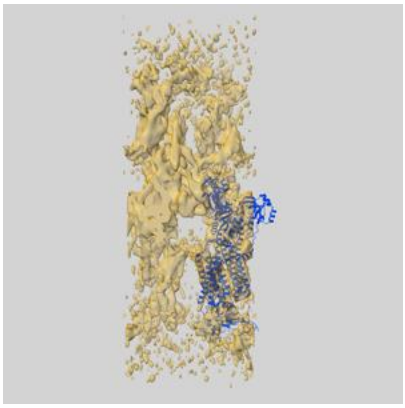
8 Fourier-Shell correlation (i)

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

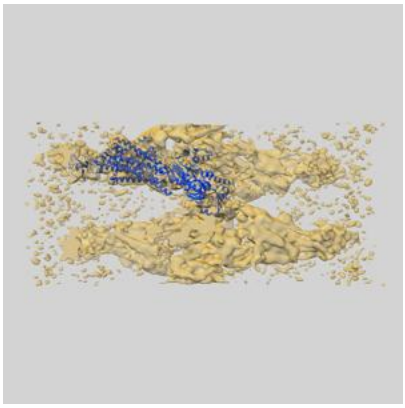
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-6799 and PDB model 5Y0B. Per-residue inclusion information can be found in section 3 on page 4.

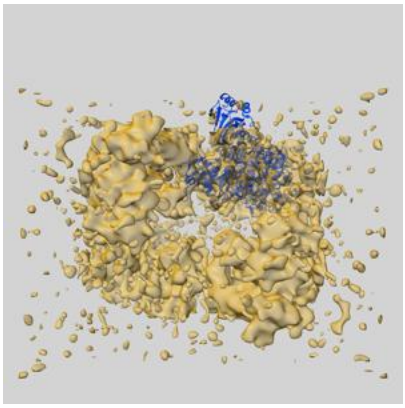
9.1 Map-model overlay



X



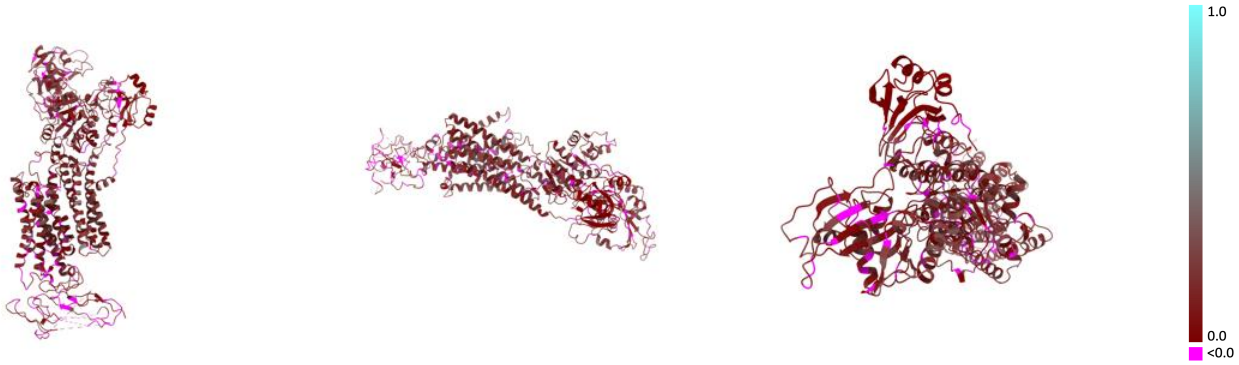
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.004 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.

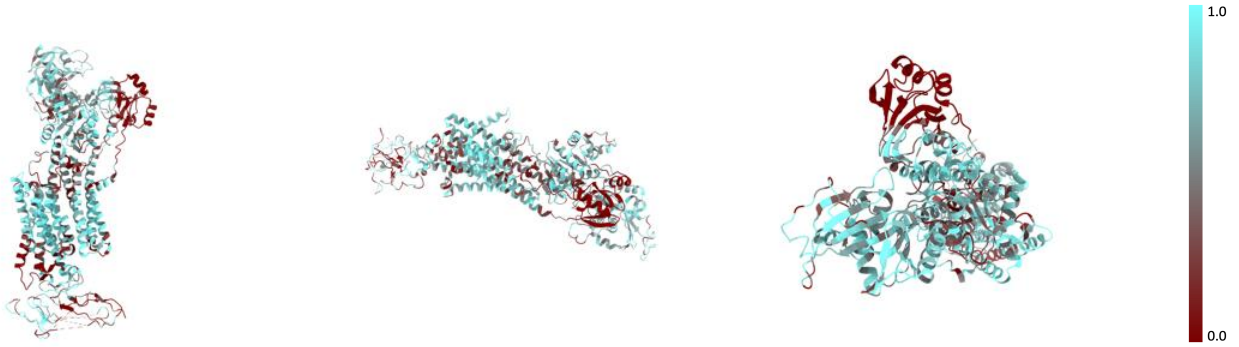
9.2 Q-score mapped to coordinate model



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.

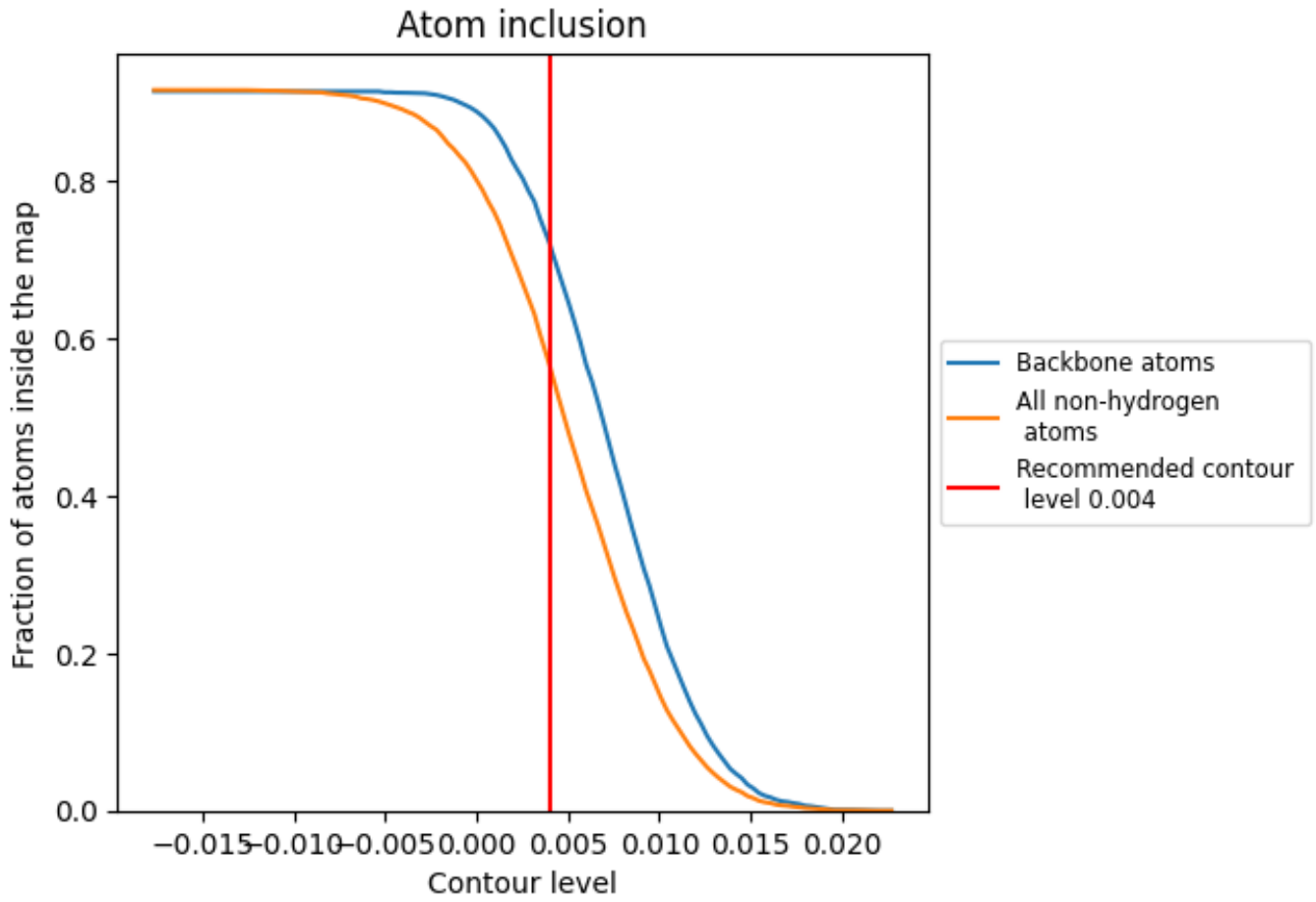
9.3 Atom inclusion mapped to coordinate model



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 (0.004).

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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5660	0.1150
A	0.5866	0.1240
B	0.4562	0.0670