Full wwPDB EM Validation Report

Mar 20, 2024 – 01:51 PM JST

PDB ID	:	7D3K
EMDB ID	:	EMD-30558
Title	:	FOOT AND MOUTH DISEASE VIRUS O/TIBET/99-BOUND THE SINGLE CHAIN FRAGMEN ANTIBODY B77
Authors	:	He, Y.; Lou, Z.
Deposited on	:	2020-09-19
Resolution	:	3.90 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:

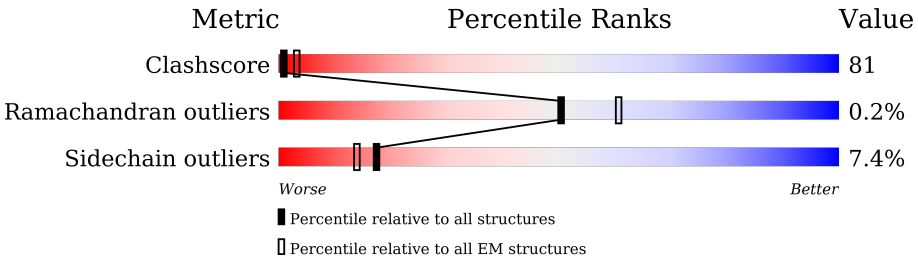
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.90 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	1	213	32% 47% 6% 14%
2	2	218	32% 51% 10% 6%
3	3	220	50% 45%
4	4	85	31% 19% 48%
5	H	124	8% 33% 42% 11% 12%
6	L	123	5% 20% 31% 18% 31%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6515 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 O/TIBET/99 VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	183	Total	C	N	O	S	0	0
			1432	907	256	266	3		

- Molecule 2 is a protein called O/TIBET/99 VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	206	Total	C	N	O	S	0	0
			1617	1031	276	303	7		

- Molecule 3 is a protein called O/TIBET/99 VP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	219	Total	C	N	O	S	0	0
			1673	1073	272	319	9		

- Molecule 4 is a protein called O/TIBET/99 VP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	44	Total	C	N	O	S	0	0
			337	214	54	67	2		

- Molecule 5 is a protein called B77 VH.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	109	Total	C	N	O	S	0	0
			819	516	138	161	4		

- Molecule 6 is a protein called B77 VL.

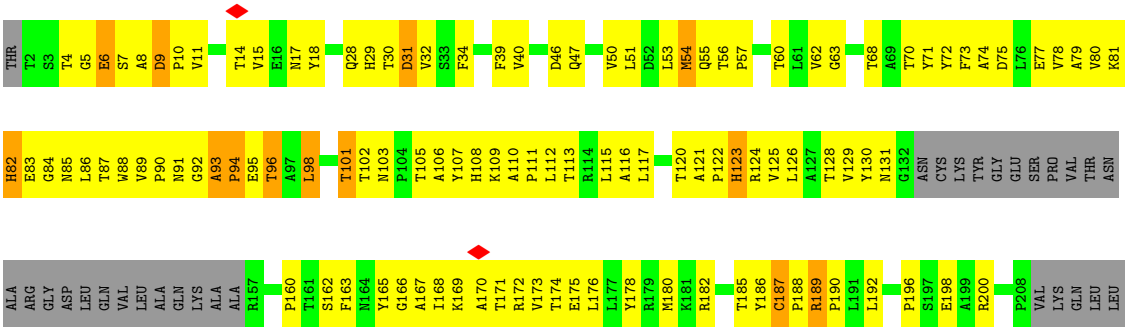
Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	85	Total	C	N	O	S	0	0
			637	395	109	131	2		

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.

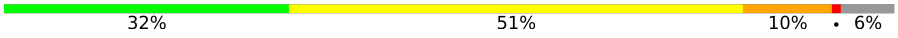
• Molecule 1: O/TIBET/99 VP1

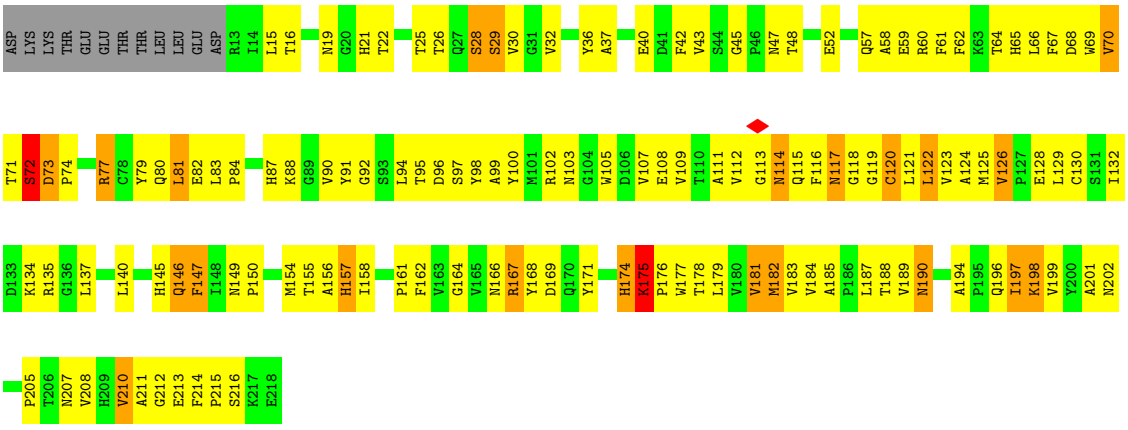
Chain 1:



• Molecule 2: O/TIBET/99 VP2

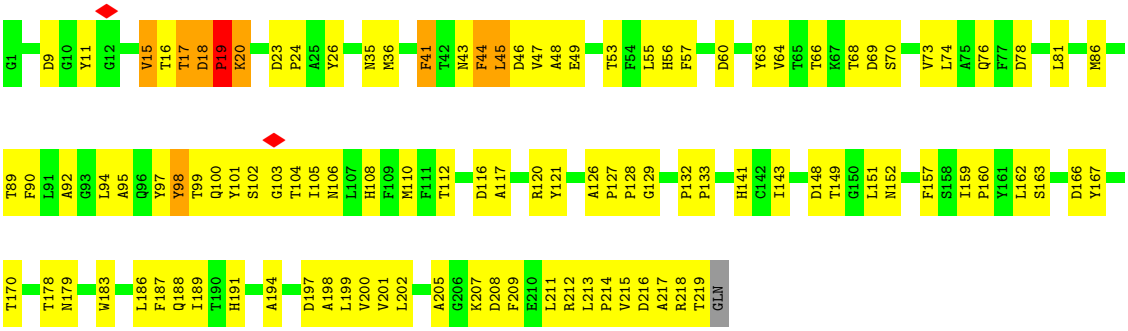
Chain 2:



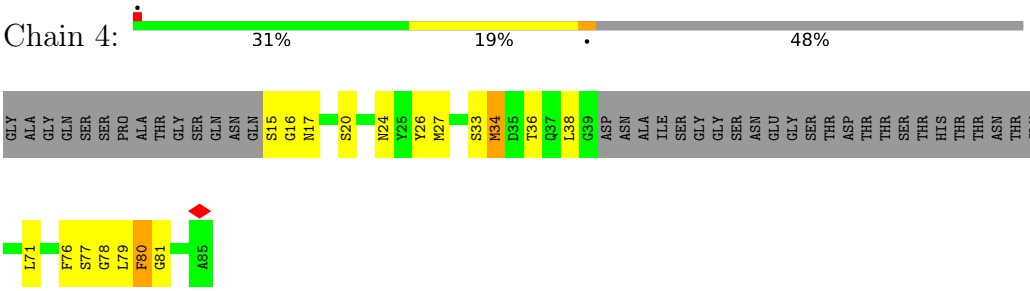


• Molecule 3: O/TIBET/99 VP3

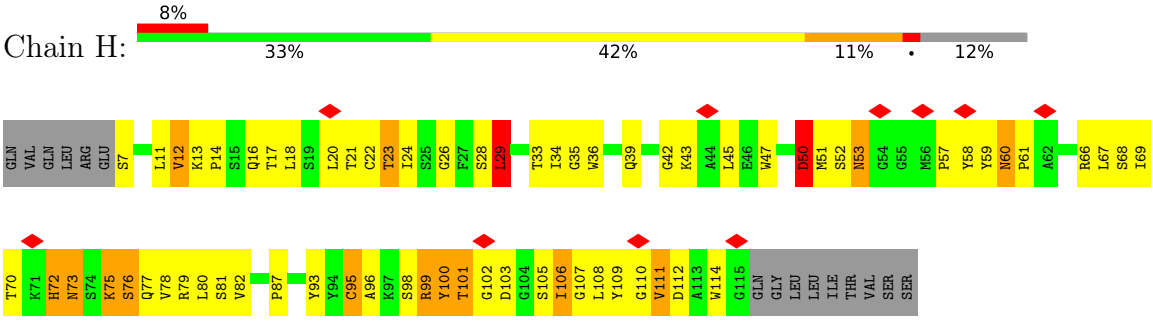
Chain 3:



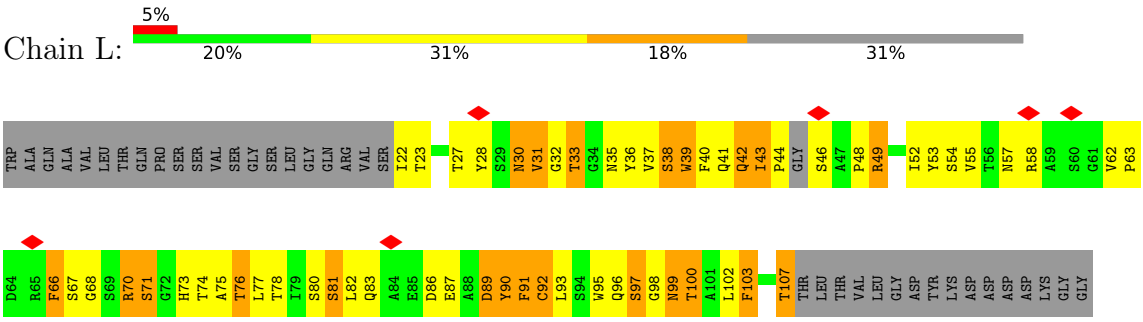
• Molecule 4: O/TIBET/99 VP4



• Molecule 5: B77 VH



• Molecule 6: B77 VL



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, POINT	Depositor
Number of particles used	15460, 15460	Depositor
Resolution determination method	FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	1.63	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.086	Depositor
Minimum map value	-0.054	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.009	Depositor
Map size (Å)	372.0, 372.0, 372.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	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	1	0.50	0/1466	1.03	16/2005 (0.8%)
2	2	0.48	0/1661	0.98	22/2269 (1.0%)
3	3	0.50	1/1723 (0.1%)	0.95	19/2355 (0.8%)
4	4	0.40	0/343	0.69	1/459 (0.2%)
5	H	0.49	0/839	1.06	12/1140 (1.1%)
6	L	0.59	0/651	1.69	22/886 (2.5%)
All	All	0.50	1/6683 (0.0%)	1.07	92/9114 (1.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	3	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	3	127	PRO	N-CD	5.33	1.55	1.47

All (92) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	L	39	TRP	N-CA-CB	15.54	138.57	110.60
6	L	75	ALA	CB-CA-C	14.07	131.20	110.10
2	2	211	ALA	N-CA-C	13.70	148.00	111.00
1	1	93	ALA	C-N-CD	-11.23	95.90	120.60
6	L	107	THR	N-CA-CB	10.77	130.76	110.30
6	L	76	THR	N-CA-CB	10.46	130.17	110.30
1	1	82	HIS	CB-CA-C	-9.83	90.75	110.40
1	1	31	ASP	N-CA-C	-9.82	84.48	111.00
6	L	80	SER	CB-CA-C	-9.79	91.49	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	2	211	ALA	CB-CA-C	-9.78	95.43	110.10
3	3	45	LEU	CB-CA-C	-9.64	91.89	110.20
6	L	39	TRP	N-CA-C	-9.58	85.13	111.00
5	H	23	THR	N-CA-CB	9.39	128.15	110.30
6	L	75	ALA	N-CA-C	-9.35	85.74	111.00
1	1	103	ASN	N-CA-C	-9.28	85.94	111.00
5	H	99	ARG	N-CA-C	-9.16	86.27	111.00
3	3	19	PRO	CB-CA-C	-9.15	89.12	112.00
1	1	30	THR	N-CA-C	-9.13	86.36	111.00
5	H	100	TYR	N-CA-CB	-9.06	94.29	110.60
6	L	81	SER	N-CA-CB	-8.92	97.12	110.50
6	L	33	THR	CB-CA-C	-8.71	88.08	111.60
2	2	212	GLY	N-CA-C	-8.67	91.43	113.10
6	L	70	ARG	CB-CA-C	-8.61	93.19	110.40
3	3	148	ASP	CB-CA-C	-8.38	93.64	110.40
3	3	16	THR	CB-CA-C	8.15	133.62	111.60
6	L	89	ASP	CB-CA-C	-8.09	94.21	110.40
5	H	22	CYS	N-CA-C	-8.03	89.31	111.00
1	1	83	GLU	N-CA-C	8.01	132.63	111.00
1	1	188	PRO	N-CA-C	7.72	132.18	112.10
1	1	188	PRO	CB-CA-C	-7.71	92.73	112.00
1	1	83	GLU	CB-CA-C	-7.61	95.18	110.40
3	3	99	THR	N-CA-C	7.52	131.31	111.00
3	3	20	LYS	N-CA-C	-7.41	90.98	111.00
1	1	31	ASP	N-CA-CB	7.23	123.61	110.60
2	2	147	PHE	N-CA-CB	7.21	123.57	110.60
2	2	156	ALA	CB-CA-C	-7.14	99.39	110.10
1	1	39	PHE	CB-CA-C	-6.90	96.59	110.40
3	3	149	THR	N-CA-CB	-6.87	97.24	110.30
1	1	189	ARG	N-CA-CB	-6.83	98.31	110.60
3	3	15	VAL	CB-CA-C	-6.81	98.46	111.40
3	3	17	THR	N-CA-C	6.76	129.24	111.00
2	2	29	SER	N-CA-CB	6.71	120.56	110.50
3	3	98	TYR	CB-CA-C	-6.57	97.25	110.40
1	1	123	HIS	N-CA-CB	-6.57	98.77	110.60
2	2	181	VAL	N-CA-C	-6.56	93.29	111.00
2	2	21	HIS	CB-CA-C	-6.54	97.31	110.40
2	2	182	MET	N-CA-C	-6.52	93.39	111.00
2	2	72	SER	CB-CA-C	6.52	122.48	110.10
5	H	50	ASP	CB-CA-C	-6.46	97.48	110.40
6	L	71	SER	N-CA-CB	-6.46	100.82	110.50
6	L	97	SER	CB-CA-C	6.32	122.11	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	2	28	SER	CB-CA-C	6.27	122.02	110.10
2	2	73	ASP	N-CA-C	6.26	127.91	111.00
3	3	151	LEU	CB-CA-C	-6.20	98.42	110.20
5	H	28	SER	N-CA-CB	-6.20	101.20	110.50
6	L	38	SER	N-CA-C	-6.20	94.27	111.00
5	H	96	ALA	N-CA-CB	6.19	118.77	110.10
5	H	100	TYR	N-CA-C	6.19	127.71	111.00
2	2	146	GLN	N-CA-C	-6.18	94.31	111.00
2	2	210	VAL	CB-CA-C	-6.03	99.95	111.40
2	2	70	VAL	CB-CA-C	-6.00	100.01	111.40
4	4	34	MET	CB-CA-C	-5.98	98.44	110.40
3	3	18	ASP	CB-CA-C	-5.92	98.56	110.40
6	L	90	TYR	N-CA-CB	-5.84	100.09	110.60
5	H	29	LEU	N-CA-C	-5.75	95.48	111.00
2	2	164	GLY	N-CA-C	-5.62	99.04	113.10
5	H	95	CYS	N-CA-C	-5.62	95.84	111.00
6	L	98	GLY	C-N-CA	5.60	135.69	121.70
1	1	75	ASP	N-CA-C	-5.59	95.90	111.00
1	1	187	CYS	N-CA-C	5.56	126.00	111.00
3	3	99	THR	N-CA-CB	-5.52	99.81	110.30
3	3	46	ASP	N-CA-C	-5.51	96.13	111.00
6	L	42	GLN	N-CA-C	-5.47	96.23	111.00
6	L	43	ILE	C-N-CD	5.46	139.88	128.40
5	H	23	THR	N-CA-C	-5.42	96.38	111.00
6	L	98	GLY	N-CA-C	5.41	126.62	113.10
6	L	49	ARG	N-CA-CB	-5.40	100.88	110.60
6	L	81	SER	N-CA-C	5.38	125.52	111.00
3	3	20	LYS	N-CA-CB	5.34	120.20	110.60
5	H	99	ARG	CB-CA-C	-5.31	99.79	110.40
2	2	126	VAL	C-N-CD	5.28	139.48	128.40
2	2	157	HIS	N-CA-CB	-5.24	101.17	110.60
2	2	22	THR	N-CA-CB	5.22	120.22	110.30
2	2	146	GLN	CB-CA-C	5.21	120.83	110.40
3	3	16	THR	N-CA-C	-5.20	96.97	111.00
3	3	126	ALA	CB-CA-C	5.15	117.82	110.10
2	2	175	LYS	C-N-CD	5.15	139.21	128.40
2	2	59	GLU	N-CA-CB	-5.12	101.39	110.60
3	3	17	THR	CB-CA-C	-5.12	97.78	111.60
6	L	76	THR	N-CA-C	-5.03	97.43	111.00
1	1	175	GLU	CB-CA-C	5.01	120.42	110.40
3	3	152	ASN	N-CA-CB	5.00	119.61	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3	19	PRO	Mainchain

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	1	1432	0	1436	211	0
2	2	1617	0	1572	314	0
3	3	1673	0	1600	168	0
4	4	337	0	314	23	0
5	H	819	0	805	214	0
6	L	637	0	590	216	0
All	All	6515	0	6317	1036	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 81.

All (1036) 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)
5:H:20:LEU:HD12	5:H:36:TRP:CH2	1.20	1.66
6:L:40:PHE:CB	6:L:52:ILE:HG23	1.21	1.66
2:2:69:TRP:CZ3	2:2:121:LEU:HD22	1.28	1.63
6:L:39:TRP:CB	6:L:93:LEU:HD23	1.19	1.62
1:1:86:LEU:CA	1:1:170:ALA:HB2	1.22	1.61
3:3:45:LEU:HD21	3:3:211:LEU:CD1	1.25	1.60
6:L:66:PHE:HZ	6:L:90:TYR:CE2	1.17	1.59
3:3:45:LEU:HD11	3:3:209:PHE:CE2	1.30	1.59
6:L:66:PHE:CZ	6:L:90:TYR:CZ	1.90	1.58
3:3:110:MET:CE	3:3:200:VAL:HG11	1.33	1.58
5:H:17:THR:CG2	5:H:82:VAL:H	1.11	1.57
3:3:117:ALA:CB	3:3:194:ALA:HB2	1.16	1.56
3:3:45:LEU:CD2	3:3:211:LEU:HD13	1.33	1.55
6:L:66:PHE:CZ	6:L:90:TYR:CE2	1.94	1.54
1:1:86:LEU:HA	1:1:170:ALA:CB	1.11	1.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:59:TYR:CD2	5:H:67:LEU:CD2	1.95	1.50
2:2:69:TRP:CZ3	2:2:121:LEU:CD2	1.93	1.48
1:1:88:TRP:HE1	1:1:117:LEU:CD1	1.25	1.47
2:2:69:TRP:CZ3	2:2:121:LEU:HB2	1.50	1.46
6:L:40:PHE:HB3	6:L:52:ILE:CG2	1.00	1.46
5:H:72:HIS:CE1	5:H:77:GLN:HB2	1.48	1.45
6:L:52:ILE:HD11	6:L:62:VAL:CG1	1.48	1.43
1:1:84:GLY:HA3	1:1:171:THR:CG2	1.47	1.43
3:3:110:MET:CE	3:3:200:VAL:CG1	1.97	1.43
1:1:91:ASN:HD22	1:1:121:ALA:CA	1.30	1.43
5:H:72:HIS:CE1	5:H:77:GLN:CB	2.02	1.42
6:L:28:TYR:HA	6:L:73:HIS:CE1	1.55	1.40
6:L:76:THR:HG21	6:L:92:CYS:SG	1.62	1.38
6:L:96:GLN:NE2	6:L:103:PHE:HB3	1.38	1.37
3:3:45:LEU:CD1	3:3:209:PHE:HE2	1.34	1.37
6:L:40:PHE:CE1	6:L:42:GLN:NE2	1.93	1.36
5:H:17:THR:HG23	5:H:82:VAL:N	1.37	1.36
1:1:84:GLY:CA	1:1:171:THR:HG21	1.57	1.35
2:2:79:TYR:CE1	6:L:33:THR:HG23	1.61	1.34
6:L:28:TYR:CA	6:L:73:HIS:HE1	1.40	1.34
5:H:20:LEU:CD1	5:H:36:TRP:HH2	1.40	1.34
6:L:40:PHE:HE1	6:L:42:GLN:NE2	1.23	1.33
2:2:83:LEU:HD11	2:2:105:TRP:CZ3	1.64	1.33
5:H:110:GLY:O	6:L:36:TYR:CB	1.77	1.33
1:1:130:TYR:OH	2:2:174:HIS:CD2	1.82	1.32
3:3:117:ALA:CB	3:3:194:ALA:CB	2.06	1.32
5:H:17:THR:CG2	5:H:82:VAL:N	1.83	1.32
1:1:86:LEU:CA	1:1:170:ALA:CB	1.86	1.31
3:3:110:MET:HE2	3:3:200:VAL:CG1	1.53	1.31
1:1:51:LEU:HD22	1:1:178:TYR:CE1	1.64	1.31
2:2:69:TRP:HZ3	2:2:121:LEU:CG	1.43	1.31
1:1:88:TRP:NE1	1:1:117:LEU:CD1	1.91	1.31
5:H:20:LEU:CD1	5:H:36:TRP:CH2	2.13	1.30
2:2:118:GLY:H	2:2:189:VAL:CG2	1.44	1.30
5:H:72:HIS:HE1	5:H:77:GLN:CB	1.42	1.30
5:H:72:HIS:HE1	5:H:77:GLN:CA	1.44	1.29
1:1:91:ASN:ND2	1:1:121:ALA:HA	0.98	1.29
2:2:120:CYS:H	2:2:185:ALA:CB	1.43	1.29
6:L:28:TYR:CA	6:L:73:HIS:CE1	2.13	1.29
2:2:69:TRP:CE3	2:2:121:LEU:HD22	1.67	1.28
2:2:69:TRP:CZ3	2:2:121:LEU:CB	2.17	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:53:LEU:HD12	1:1:72:TYR:CE2	1.67	1.27
2:2:69:TRP:HZ3	2:2:121:LEU:CD2	1.33	1.27
6:L:66:PHE:CE2	6:L:90:TYR:OH	1.71	1.26
1:1:51:LEU:HD23	1:1:178:TYR:OH	1.33	1.26
3:3:117:ALA:HB1	3:3:194:ALA:CB	1.65	1.26
2:2:69:TRP:CH2	2:2:121:LEU:HB2	1.71	1.25
6:L:39:TRP:CB	6:L:93:LEU:CD2	2.15	1.24
2:2:98:TYR:CD2	2:2:210:VAL:HB	1.70	1.23
1:1:51:LEU:CD2	1:1:178:TYR:CE1	2.21	1.22
1:1:88:TRP:NE1	1:1:117:LEU:HD13	1.45	1.21
2:2:47:ASN:ND2	2:2:167:ARG:HG3	1.53	1.21
6:L:39:TRP:HB3	6:L:93:LEU:CD2	1.68	1.21
2:2:125:MET:CE	2:2:179:LEU:HD23	1.71	1.20
1:1:91:ASN:ND2	1:1:122:PRO:CD	2.05	1.19
6:L:43:ILE:O	6:L:46:SER:HA	1.41	1.19
6:L:96:GLN:NE2	6:L:103:PHE:CB	2.03	1.19
6:L:53:TYR:CE2	6:L:55:VAL:CG2	2.26	1.19
1:1:91:ASN:ND2	1:1:122:PRO:HD3	1.57	1.18
5:H:23:THR:HG21	5:H:77:GLN:HA	1.26	1.18
1:1:130:TYR:CZ	2:2:174:HIS:CD2	2.31	1.17
1:1:88:TRP:CE2	1:1:117:LEU:HD22	1.80	1.16
2:2:129:LEU:CD2	2:2:178:THR:HG21	1.76	1.16
5:H:110:GLY:O	6:L:36:TYR:HB3	1.46	1.16
1:1:91:ASN:ND2	1:1:121:ALA:CA	1.91	1.15
2:2:71:THR:HA	2:2:188:THR:HG22	1.27	1.14
3:3:103:GLY:HA3	3:3:208:ASP:O	1.45	1.14
5:H:59:TYR:CD2	5:H:67:LEU:HD23	1.66	1.14
2:2:118:GLY:H	2:2:189:VAL:HG21	1.11	1.14
2:2:68:ASP:CB	2:2:198:LYS:HA	1.78	1.13
5:H:106:ILE:HG21	6:L:100:THR:OG1	1.49	1.13
5:H:18:LEU:HG	5:H:82:VAL:CG1	1.79	1.13
3:3:74:LEU:HB2	3:3:186:LEU:O	1.50	1.12
3:3:20:LYS:NZ	4:4:26:TYR:OH	1.82	1.12
2:2:118:GLY:N	2:2:189:VAL:CG2	2.11	1.12
6:L:52:ILE:HD11	6:L:62:VAL:HG11	1.21	1.12
2:2:125:MET:HE2	2:2:125:MET:HA	1.32	1.12
5:H:107:GLY:O	6:L:102:LEU:HD11	1.48	1.11
6:L:53:TYR:CE2	6:L:55:VAL:HG23	1.84	1.11
2:2:47:ASN:CG	2:2:167:ARG:HG3	1.69	1.11
2:2:118:GLY:N	2:2:189:VAL:HG21	1.65	1.10
1:1:82:HIS:O	1:1:82:HIS:CD2	2.04	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:19:PRO:O	3:3:19:PRO:HG2	1.40	1.10
5:H:110:GLY:O	6:L:36:TYR:HB2	1.45	1.10
6:L:66:PHE:CZ	6:L:90:TYR:OH	1.86	1.10
6:L:52:ILE:HD11	6:L:62:VAL:HG12	1.33	1.09
2:2:98:TYR:HD2	2:2:210:VAL:CB	1.65	1.09
5:H:12:VAL:HG23	5:H:87:PRO:HA	1.30	1.09
5:H:72:HIS:CE1	5:H:77:GLN:C	2.26	1.09
2:2:100:TYR:O	2:2:168:TYR:CD1	2.04	1.09
1:1:53:LEU:CD1	1:1:72:TYR:HE2	1.65	1.09
2:2:129:LEU:HD21	2:2:178:THR:HG21	1.12	1.08
3:3:45:LEU:HB2	3:3:94:LEU:HD23	1.11	1.08
1:1:6:GLU:CD	2:2:149:ASN:OD1	1.91	1.08
3:3:103:GLY:CA	3:3:208:ASP:O	2.02	1.08
3:3:110:MET:HE3	3:3:200:VAL:CG1	1.70	1.08
1:1:91:ASN:HD21	1:1:122:PRO:CD	1.63	1.07
2:2:68:ASP:HB3	2:2:198:LYS:HA	1.12	1.07
3:3:45:LEU:HD21	3:3:211:LEU:HD11	1.30	1.07
6:L:39:TRP:HB2	6:L:93:LEU:HD23	1.23	1.07
1:1:6:GLU:OE2	2:2:149:ASN:OD1	1.72	1.07
6:L:66:PHE:HZ	6:L:90:TYR:CZ	1.43	1.06
2:2:125:MET:HE3	2:2:179:LEU:HD23	1.36	1.06
2:2:120:CYS:N	2:2:185:ALA:HB2	1.67	1.06
5:H:72:HIS:CE1	5:H:77:GLN:CA	2.36	1.06
6:L:40:PHE:CB	6:L:52:ILE:CG2	1.94	1.05
1:1:51:LEU:CD2	1:1:178:TYR:CZ	2.39	1.05
2:2:97:SER:O	2:2:98:TYR:CD1	2.08	1.05
2:2:71:THR:HA	2:2:188:THR:CG2	1.86	1.05
2:2:137:LEU:HD23	2:2:182:MET:HE3	1.36	1.05
5:H:59:TYR:HD2	5:H:67:LEU:HD21	0.96	1.05
6:L:39:TRP:CG	6:L:93:LEU:HD23	1.91	1.04
2:2:134:LYS:HA	2:2:137:LEU:HD13	1.36	1.04
2:2:79:TYR:CZ	6:L:33:THR:HG23	1.91	1.04
1:1:88:TRP:CD1	1:1:117:LEU:HD11	1.92	1.04
3:3:110:MET:HE2	3:3:200:VAL:HG13	1.34	1.03
3:3:117:ALA:HB1	3:3:194:ALA:HB2	1.06	1.03
5:H:18:LEU:HG	5:H:82:VAL:HG12	1.39	1.03
1:1:88:TRP:NE1	1:1:117:LEU:CD2	2.21	1.03
5:H:72:HIS:HE1	5:H:77:GLN:C	1.61	1.03
2:2:73:ASP:OD2	2:2:183:VAL:HG11	1.58	1.03
3:3:110:MET:HE3	3:3:200:VAL:HG11	1.10	1.02
2:2:118:GLY:CA	2:2:189:VAL:HG21	1.89	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:51:LEU:CD2	1:1:178:TYR:OH	2.08	1.01
5:H:17:THR:HG23	5:H:82:VAL:H	0.85	1.01
2:2:120:CYS:SG	2:2:149:ASN:ND2	2.31	1.01
6:L:40:PHE:HB3	6:L:52:ILE:HG21	1.37	1.01
3:3:17:THR:HG22	3:3:17:THR:O	1.58	1.01
5:H:17:THR:HG23	5:H:82:VAL:CA	1.89	1.01
6:L:52:ILE:CD1	6:L:62:VAL:CG1	2.39	1.01
6:L:53:TYR:CZ	6:L:55:VAL:CG2	2.43	1.01
1:1:84:GLY:CA	1:1:171:THR:CG2	2.25	1.00
5:H:17:THR:HG21	5:H:82:VAL:N	1.69	1.00
5:H:106:ILE:HD13	5:H:106:ILE:H	1.24	1.00
3:3:19:PRO:O	3:3:19:PRO:CG	2.02	1.00
3:3:104:THR:HG23	3:3:160:PRO:HA	1.40	1.00
6:L:28:TYR:N	6:L:73:HIS:HE1	1.59	1.00
6:L:40:PHE:HE1	6:L:42:GLN:CD	1.64	1.00
3:3:74:LEU:HD13	3:3:186:LEU:HD23	1.44	1.00
5:H:17:THR:HA	5:H:82:VAL:O	1.62	1.00
2:2:129:LEU:HD22	2:2:178:THR:OG1	1.61	1.00
3:3:45:LEU:HD23	3:3:211:LEU:HD13	1.41	1.00
6:L:41:GLN:OE1	6:L:43:ILE:HB	1.61	1.00
1:1:112:LEU:HD21	3:3:9:ASP:HB2	1.44	0.99
2:2:79:TYR:CE1	6:L:33:THR:CG2	2.45	0.99
1:1:87:THR:HA	1:1:105:THR:HG22	1.43	0.99
5:H:59:TYR:HD2	5:H:67:LEU:CD2	1.51	0.99
6:L:96:GLN:CD	6:L:103:PHE:HB3	1.81	0.99
1:1:6:GLU:OE1	2:2:149:ASN:OD1	1.81	0.99
3:3:74:LEU:HB3	3:3:186:LEU:HB3	1.42	0.99
6:L:96:GLN:HE22	6:L:103:PHE:CB	1.67	0.99
6:L:28:TYR:N	6:L:73:HIS:CE1	2.31	0.98
1:1:130:TYR:OH	2:2:174:HIS:NE2	1.78	0.98
5:H:107:GLY:O	6:L:102:LEU:CD1	2.10	0.98
1:1:51:LEU:HD22	1:1:178:TYR:CZ	1.97	0.98
2:2:97:SER:C	2:2:98:TYR:HD1	1.66	0.98
3:3:74:LEU:HB2	3:3:186:LEU:C	1.83	0.98
2:2:69:TRP:HZ3	2:2:121:LEU:CB	1.62	0.98
3:3:45:LEU:HG	3:3:45:LEU:O	1.61	0.98
2:2:69:TRP:CH2	2:2:121:LEU:CB	2.42	0.98
2:2:120:CYS:H	2:2:185:ALA:HB2	0.86	0.97
1:1:85:ASN:OD1	1:1:107:TYR:CE1	2.17	0.97
1:1:34:PHE:CZ	4:4:17:ASN:ND2	2.32	0.97
2:2:125:MET:HE1	2:2:179:LEU:HD23	1.43	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:33:THR:HG22	5:H:52:SER:HA	1.47	0.97
2:2:113:GLY:CA	2:2:150:PRO:HB3	1.94	0.96
2:2:120:CYS:N	2:2:185:ALA:CB	2.26	0.96
2:2:98:TYR:CD2	2:2:210:VAL:CB	2.43	0.96
6:L:39:TRP:HB3	6:L:93:LEU:HD23	0.97	0.96
5:H:59:TYR:CG	5:H:67:LEU:CD2	2.49	0.96
1:1:51:LEU:CD2	1:1:178:TYR:HE1	1.72	0.96
6:L:53:TYR:HE2	6:L:55:VAL:HG23	1.23	0.95
2:2:68:ASP:HB3	2:2:198:LYS:CA	1.97	0.95
2:2:120:CYS:HB2	2:2:149:ASN:ND2	1.82	0.95
2:2:100:TYR:OH	3:3:128:PRO:CD	2.13	0.95
2:2:216:SER:OG	3:3:141:HIS:CD2	2.18	0.95
2:2:98:TYR:HD2	2:2:210:VAL:HB	0.81	0.95
5:H:59:TYR:CB	5:H:67:LEU:HD22	1.96	0.95
6:L:66:PHE:CE1	6:L:90:TYR:CE2	2.55	0.95
1:1:91:ASN:HD21	1:1:122:PRO:HD2	1.27	0.94
1:1:34:PHE:CE2	4:4:17:ASN:ND2	2.35	0.94
2:2:47:ASN:ND2	2:2:167:ARG:CG	2.31	0.94
1:1:85:ASN:OD1	1:1:107:TYR:CD1	2.20	0.94
2:2:125:MET:CE	2:2:125:MET:HA	1.97	0.94
5:H:95:CYS:O	6:L:49:ARG:HD2	1.68	0.94
2:2:45:GLY:HA3	2:2:167:ARG:HD2	1.50	0.94
1:1:85:ASN:C	1:1:170:ALA:HB1	1.88	0.93
5:H:59:TYR:HB3	5:H:67:LEU:HD22	1.50	0.93
5:H:95:CYS:O	6:L:49:ARG:CD	2.17	0.93
3:3:45:LEU:O	3:3:45:LEU:CG	2.17	0.93
2:2:26:THR:HG22	2:2:28:SER:O	1.67	0.93
6:L:53:TYR:CE2	6:L:55:VAL:HG22	2.02	0.93
6:L:89:ASP:CB	6:L:107:THR:HG21	1.99	0.93
1:1:53:LEU:HD22	1:1:180:MET:SD	2.08	0.92
3:3:117:ALA:HB3	3:3:194:ALA:CB	1.81	0.92
1:1:84:GLY:HA3	1:1:171:THR:HG21	0.93	0.92
5:H:23:THR:HB	5:H:76:SER:O	1.70	0.92
5:H:102:GLY:HA3	5:H:114:TRP:HE1	1.35	0.92
3:3:117:ALA:HB3	3:3:194:ALA:HB2	0.93	0.92
1:1:110:ALA:HB1	3:3:9:ASP:HB3	1.51	0.92
6:L:52:ILE:CD1	6:L:62:VAL:HG11	1.99	0.92
1:1:88:TRP:NE1	1:1:117:LEU:HD22	1.83	0.92
6:L:53:TYR:CZ	6:L:55:VAL:HG22	2.05	0.92
1:1:112:LEU:CD2	3:3:9:ASP:HB2	2.00	0.91
2:2:120:CYS:CB	2:2:149:ASN:ND2	2.33	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:88:TRP:CD1	1:1:117:LEU:HD21	2.04	0.91
3:3:45:LEU:HB2	3:3:94:LEU:CD2	2.01	0.91
5:H:23:THR:CG2	5:H:77:GLN:HA	2.00	0.91
5:H:107:GLY:C	6:L:102:LEU:HD21	1.90	0.90
6:L:66:PHE:HZ	6:L:90:TYR:HE2	1.04	0.90
5:H:58:TYR:HB2	5:H:105:SER:O	1.71	0.90
2:2:118:GLY:HA3	2:2:189:VAL:HG21	1.51	0.90
5:H:45:LEU:HD11	6:L:91:PHE:CD2	2.06	0.90
3:3:45:LEU:CB	3:3:94:LEU:HD23	2.02	0.90
6:L:31:VAL:O	6:L:35:ASN:HB2	1.72	0.90
6:L:66:PHE:HE2	6:L:90:TYR:HH	0.97	0.90
3:3:45:LEU:CD2	3:3:211:LEU:CD1	2.13	0.90
6:L:40:PHE:CD1	6:L:52:ILE:HG21	2.06	0.90
1:1:88:TRP:CD1	1:1:117:LEU:CD1	2.51	0.89
1:1:53:LEU:HD12	1:1:72:TYR:HE2	0.74	0.89
1:1:98:LEU:HD12	1:1:98:LEU:H	1.37	0.89
1:1:86:LEU:N	1:1:170:ALA:CB	2.34	0.89
5:H:107:GLY:O	6:L:102:LEU:CG	2.20	0.89
5:H:75:LYS:CE	5:H:75:LYS:HA	2.02	0.89
2:2:129:LEU:HD21	2:2:178:THR:CG2	2.02	0.88
2:2:100:TYR:OH	3:3:128:PRO:HD2	1.74	0.88
5:H:12:VAL:CG2	5:H:87:PRO:HA	2.03	0.88
2:2:98:TYR:CE2	2:2:210:VAL:HG21	2.07	0.88
5:H:59:TYR:CD2	5:H:67:LEU:HD21	1.78	0.88
2:2:97:SER:C	2:2:98:TYR:CD1	2.45	0.88
6:L:40:PHE:CD1	6:L:52:ILE:HD13	2.08	0.88
1:1:86:LEU:CA	1:1:170:ALA:HB3	2.04	0.88
2:2:129:LEU:CD2	2:2:178:THR:CG2	2.51	0.88
3:3:74:LEU:CB	3:3:186:LEU:HB3	2.03	0.88
5:H:51:MET:SD	5:H:57:PRO:HB3	2.13	0.88
2:2:26:THR:CG2	2:2:28:SER:O	2.22	0.88
2:2:100:TYR:O	2:2:168:TYR:HD1	1.52	0.87
2:2:47:ASN:HD21	2:2:167:ARG:CB	1.87	0.87
5:H:59:TYR:CG	5:H:67:LEU:HD22	2.10	0.87
5:H:75:LYS:HA	5:H:75:LYS:HE2	1.55	0.87
5:H:24:ILE:HD12	5:H:26:GLY:H	1.39	0.87
1:1:91:ASN:HB2	1:1:120:THR:HG23	1.57	0.87
2:2:118:GLY:H	2:2:189:VAL:HG23	1.37	0.87
2:2:45:GLY:HA3	2:2:167:ARG:CD	2.05	0.86
5:H:17:THR:HG21	5:H:81:SER:HA	1.57	0.86
5:H:23:THR:HG21	5:H:77:GLN:CA	2.04	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:53:TYR:OH	6:L:55:VAL:HG21	1.76	0.86
2:2:48:THR:HG21	2:2:168:TYR:CE2	2.09	0.86
4:4:20:SER:OG	4:4:24:ASN:OD1	1.94	0.86
6:L:76:THR:CG2	6:L:92:CYS:SG	2.58	0.85
1:1:51:LEU:HD21	1:1:178:TYR:HE1	1.39	0.85
6:L:52:ILE:CD1	6:L:62:VAL:HG12	2.03	0.85
5:H:23:THR:OG1	5:H:77:GLN:HG2	1.77	0.85
6:L:39:TRP:CG	6:L:93:LEU:CD2	2.56	0.85
6:L:28:TYR:HA	6:L:73:HIS:HE1	0.93	0.84
1:1:86:LEU:CB	1:1:170:ALA:HB3	2.07	0.84
1:1:88:TRP:CD1	1:1:117:LEU:CD2	2.61	0.84
1:1:84:GLY:N	1:1:171:THR:HG21	1.92	0.84
5:H:17:THR:HG23	5:H:82:VAL:C	1.97	0.84
2:2:113:GLY:HA2	2:2:150:PRO:HB3	1.60	0.84
5:H:68:SER:O	5:H:81:SER:N	2.08	0.84
2:2:47:ASN:HD21	2:2:167:ARG:CG	1.90	0.84
1:1:86:LEU:CB	1:1:170:ALA:CB	2.55	0.84
5:H:45:LEU:HD11	6:L:91:PHE:CE2	2.13	0.84
5:H:69:ILE:HG12	5:H:80:LEU:HD13	1.60	0.83
1:1:81:LYS:O	1:1:174:THR:OG1	1.96	0.83
1:1:7:SER:HB3	1:1:9:ASP:OD1	1.77	0.83
5:H:18:LEU:CD2	5:H:82:VAL:HG11	2.09	0.82
1:1:91:ASN:HB3	1:1:120:THR:O	1.79	0.82
2:2:83:LEU:CD1	2:2:105:TRP:CZ3	2.58	0.82
2:2:47:ASN:HD21	2:2:167:ARG:HG3	1.45	0.81
3:3:45:LEU:CD1	3:3:209:PHE:CE2	2.24	0.81
6:L:71:SER:OG	6:L:73:HIS:O	1.98	0.81
6:L:99:ASN:ND2	6:L:99:ASN:O	2.14	0.81
6:L:40:PHE:CG	6:L:52:ILE:HG21	2.16	0.80
5:H:72:HIS:NE2	5:H:77:GLN:HB2	1.95	0.80
6:L:31:VAL:HA	6:L:35:ASN:CB	2.11	0.80
3:3:101:TYR:HD2	3:3:170:THR:HG22	1.47	0.80
5:H:18:LEU:O	5:H:18:LEU:HD12	1.82	0.80
3:3:110:MET:O	3:3:199:LEU:HD12	1.81	0.80
2:2:48:THR:HG23	3:3:163:SER:H	1.47	0.79
2:2:166:ASN:HB3	2:2:167:ARG:HH12	1.47	0.79
6:L:40:PHE:CG	6:L:52:ILE:CG2	2.64	0.79
3:3:95:ALA:O	3:3:98:TYR:O	2.01	0.79
2:2:113:GLY:HA3	2:2:150:PRO:HB3	1.61	0.79
2:2:60:ARG:HD3	2:2:90:VAL:CG1	2.13	0.78
2:2:98:TYR:HE2	2:2:210:VAL:HG21	1.47	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:111:VAL:HA	6:L:36:TYR:HD1	1.49	0.78
1:1:88:TRP:NE1	1:1:117:LEU:CG	2.45	0.78
6:L:37:VAL:CG1	6:L:70:ARG:HG3	2.14	0.78
2:2:134:LYS:HA	2:2:137:LEU:CD1	2.12	0.78
6:L:62:VAL:HG22	6:L:66:PHE:HB2	1.65	0.78
3:3:76:GLN:NE2	3:3:132:PRO:HB2	1.97	0.78
5:H:72:HIS:CE1	5:H:77:GLN:HB3	2.16	0.78
2:2:81:LEU:O	2:2:81:LEU:HD23	1.84	0.77
2:2:83:LEU:HD12	2:2:84:PRO:HA	1.66	0.77
5:H:17:THR:HG21	5:H:81:SER:CA	2.13	0.77
5:H:72:HIS:CE1	5:H:77:GLN:O	2.37	0.77
6:L:81:SER:O	6:L:82:LEU:HG	1.84	0.77
6:L:96:GLN:CD	6:L:99:ASN:HD21	1.87	0.77
2:2:115:GLN:OE1	2:2:115:GLN:N	2.17	0.77
3:3:104:THR:CG2	3:3:159:ILE:O	2.33	0.77
6:L:31:VAL:HA	6:L:35:ASN:HB2	1.66	0.77
6:L:43:ILE:O	6:L:46:SER:CA	2.28	0.77
5:H:107:GLY:CA	6:L:102:LEU:HD11	2.15	0.76
5:H:47:TRP:CE2	5:H:109:TYR:CE2	2.72	0.76
5:H:33:THR:HA	5:H:51:MET:O	1.85	0.76
6:L:40:PHE:HB2	6:L:52:ILE:HG23	1.59	0.76
6:L:62:VAL:HG22	6:L:66:PHE:CB	2.16	0.76
2:2:167:ARG:HH11	2:2:167:ARG:HA	1.51	0.76
3:3:186:LEU:O	3:3:187:PHE:CD1	2.39	0.76
2:2:125:MET:CE	2:2:179:LEU:CD2	2.58	0.76
1:1:70:THR:HG22	1:1:189:ARG:HE	1.50	0.76
6:L:96:GLN:CD	6:L:103:PHE:CB	2.49	0.76
1:1:98:LEU:HD12	1:1:98:LEU:N	2.01	0.76
2:2:79:TYR:CZ	6:L:33:THR:CG2	2.66	0.76
1:1:84:GLY:HA3	1:1:171:THR:HG23	1.60	0.76
1:1:7:SER:HA	2:2:146:GLN:HE22	1.51	0.75
1:1:88:TRP:HE1	1:1:117:LEU:HD13	0.59	0.75
2:2:45:GLY:HA3	2:2:167:ARG:NE	2.01	0.75
3:3:103:GLY:HA3	3:3:209:PHE:HA	1.67	0.75
1:1:53:LEU:CD1	1:1:72:TYR:CE2	2.53	0.75
1:1:85:ASN:O	1:1:170:ALA:HB1	1.86	0.75
4:4:78:GLY:C	4:4:79:LEU:HD12	2.05	0.75
2:2:37:ALA:HB3	2:2:161:PRO:HG2	1.67	0.75
6:L:76:THR:HG21	6:L:92:CYS:HG	1.52	0.75
2:2:69:TRP:CZ3	2:2:121:LEU:CG	2.35	0.75
5:H:107:GLY:C	6:L:102:LEU:HD11	2.07	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:28:TYR:CB	6:L:73:HIS:CE1	2.69	0.75
1:1:86:LEU:N	1:1:170:ALA:HB1	1.97	0.75
1:1:106:ALA:HB2	3:3:15:VAL:HG12	1.69	0.75
2:2:84:PRO:HB3	2:2:105:TRP:HH2	1.51	0.74
5:H:109:TYR:CE2	6:L:102:LEU:HD23	2.22	0.74
6:L:95:TRP:HZ3	6:L:97:SER:CA	2.00	0.74
5:H:18:LEU:CG	5:H:82:VAL:CG1	2.63	0.74
6:L:22:ILE:N	6:L:22:ILE:HD12	2.02	0.74
2:2:120:CYS:CB	2:2:149:ASN:HD22	1.98	0.74
3:3:117:ALA:CB	3:3:194:ALA:CA	2.66	0.74
3:3:103:GLY:HA2	3:3:208:ASP:O	1.87	0.74
6:L:89:ASP:HB2	6:L:107:THR:CG2	2.18	0.74
2:2:100:TYR:HB3	2:2:168:TYR:CB	2.18	0.73
5:H:18:LEU:CD1	5:H:80:LEU:CB	2.66	0.73
5:H:95:CYS:O	6:L:49:ARG:HD3	1.88	0.73
2:2:83:LEU:HD11	2:2:105:TRP:CE3	2.21	0.73
3:3:106:ASN:OD1	3:3:157:PHE:O	2.05	0.73
5:H:72:HIS:O	5:H:72:HIS:ND1	2.19	0.73
5:H:57:PRO:HA	5:H:103:ASP:OD2	1.89	0.73
2:2:125:MET:HE1	2:2:179:LEU:CD2	2.16	0.73
6:L:31:VAL:CA	6:L:35:ASN:HB2	2.19	0.73
1:1:130:TYR:CZ	2:2:174:HIS:NE2	2.49	0.73
5:H:18:LEU:HD12	5:H:80:LEU:CB	2.19	0.73
6:L:89:ASP:HB3	6:L:107:THR:HG21	1.70	0.73
5:H:47:TRP:CD2	5:H:109:TYR:HE2	2.07	0.73
5:H:72:HIS:NE2	5:H:77:GLN:CB	2.50	0.73
2:2:198:LYS:NZ	2:2:198:LYS:HB3	2.04	0.72
6:L:66:PHE:HE2	6:L:90:TYR:OH	1.39	0.72
1:1:17:ASN:OD1	1:1:18:TYR:N	2.22	0.72
1:1:82:HIS:O	1:1:82:HIS:HD2	1.70	0.72
5:H:106:ILE:HG21	6:L:100:THR:HG1	1.52	0.72
5:H:18:LEU:HG	5:H:82:VAL:HG11	1.72	0.72
5:H:12:VAL:HG23	5:H:87:PRO:CA	2.15	0.72
6:L:40:PHE:CB	6:L:52:ILE:HG21	1.99	0.72
2:2:72:SER:HB2	5:H:111:VAL:HG21	1.71	0.72
6:L:31:VAL:HA	6:L:35:ASN:ND2	2.04	0.72
6:L:92:CYS:C	6:L:93:LEU:HD22	2.09	0.72
1:1:6:GLU:O	2:2:146:GLN:NE2	2.22	0.72
2:2:83:LEU:HD11	2:2:105:TRP:CH2	2.25	0.72
5:H:17:THR:HG21	5:H:81:SER:C	2.09	0.72
5:H:17:THR:CA	5:H:82:VAL:O	2.38	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:101:THR:HG23	1:1:105:THR:HG21	1.71	0.72
3:3:74:LEU:HD13	3:3:186:LEU:CD2	2.19	0.72
5:H:59:TYR:HB3	5:H:67:LEU:CD2	2.19	0.72
1:1:89:VAL:HG23	1:1:167:ALA:N	2.05	0.71
2:2:100:TYR:O	2:2:168:TYR:HB3	1.90	0.71
2:2:216:SER:OG	3:3:141:HIS:CG	2.43	0.71
2:2:107:VAL:HG21	2:2:179:LEU:HD21	1.70	0.71
2:2:111:ALA:HB1	2:2:197:ILE:HD11	1.72	0.71
6:L:31:VAL:HA	6:L:35:ASN:HD22	1.55	0.71
4:4:79:LEU:HD12	4:4:79:LEU:N	2.06	0.71
1:1:6:GLU:OE2	2:2:149:ASN:CG	2.29	0.71
5:H:17:THR:HG23	5:H:82:VAL:O	1.90	0.71
6:L:30:ASN:C	6:L:30:ASN:HD22	1.92	0.71
3:3:89:THR:HG23	3:3:92:ALA:H	1.53	0.71
6:L:76:THR:HG22	6:L:77:LEU:H	1.55	0.71
1:1:87:THR:HG22	1:1:105:THR:HG21	1.71	0.71
2:2:174:HIS:O	2:2:174:HIS:ND1	2.23	0.71
6:L:57:ASN:HD21	6:L:67:SER:HB2	1.56	0.71
2:2:52:GLU:HB3	2:2:168:TYR:OH	1.91	0.71
2:2:100:TYR:HB3	2:2:168:TYR:HB3	1.72	0.71
3:3:45:LEU:H	3:3:48:ALA:HB3	1.56	0.71
5:H:18:LEU:CD1	5:H:80:LEU:HB3	2.20	0.71
2:2:118:GLY:CA	2:2:189:VAL:CG2	2.62	0.70
5:H:47:TRP:O	5:H:60:ASN:OD1	2.08	0.70
6:L:41:GLN:O	6:L:90:TYR:CE1	2.44	0.70
1:1:88:TRP:CE2	1:1:117:LEU:CD2	2.62	0.70
5:H:59:TYR:CE2	5:H:67:LEU:HD23	2.26	0.70
6:L:40:PHE:CE1	6:L:90:TYR:CE1	2.79	0.70
6:L:53:TYR:OH	6:L:55:VAL:CG2	2.36	0.70
5:H:106:ILE:HD13	5:H:106:ILE:N	2.01	0.70
2:2:47:ASN:OD1	2:2:167:ARG:HG3	1.90	0.70
5:H:111:VAL:HA	6:L:36:TYR:CD1	2.26	0.70
2:2:57:GLN:OE1	2:2:90:VAL:HG23	1.92	0.70
5:H:47:TRP:CD2	5:H:109:TYR:CE2	2.79	0.70
2:2:116:PHE:C	2:2:117:ASN:HD22	1.95	0.70
5:H:102:GLY:HA3	5:H:114:TRP:NE1	2.04	0.70
6:L:62:VAL:HG21	6:L:66:PHE:CD2	2.27	0.69
1:1:85:ASN:ND2	1:1:107:TYR:HE1	1.89	0.69
3:3:17:THR:O	3:3:17:THR:CG2	2.32	0.69
5:H:102:GLY:CA	5:H:114:TRP:HE1	2.05	0.69
2:2:114:ASN:HD22	2:2:194:ALA:H	1.39	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:84:PRO:HB3	2:2:105:TRP:CH2	2.27	0.69
2:2:71:THR:CA	2:2:188:THR:CG2	2.69	0.69
3:3:81:LEU:HD21	3:3:105:ILE:HD11	1.74	0.69
1:1:84:GLY:CA	1:1:171:THR:HG23	2.19	0.68
1:1:85:ASN:HD21	1:1:107:TYR:HE1	1.41	0.68
2:2:16:THR:HA	2:2:25:THR:HG22	1.73	0.68
2:2:122:LEU:HD23	2:2:122:LEU:C	2.14	0.68
5:H:51:MET:SD	5:H:57:PRO:CB	2.82	0.68
2:2:121:LEU:CD1	2:2:183:VAL:HA	2.23	0.68
1:1:82:HIS:O	1:1:82:HIS:CG	2.44	0.68
1:1:85:ASN:ND2	1:1:107:TYR:CE1	2.62	0.68
2:2:100:TYR:O	2:2:168:TYR:CG	2.47	0.68
5:H:29:LEU:O	5:H:29:LEU:HD23	1.94	0.68
6:L:89:ASP:HB2	6:L:107:THR:HG21	1.76	0.68
3:3:49:GLU:HB3	3:3:205:ALA:HB3	1.75	0.68
3:3:117:ALA:HB1	3:3:194:ALA:CA	2.24	0.68
4:4:80:PHE:CD1	4:4:81:GLY:N	2.62	0.67
5:H:61:PRO:HG3	6:L:100:THR:HG23	1.76	0.67
3:3:104:THR:HG22	3:3:159:ILE:O	1.94	0.67
3:3:186:LEU:O	3:3:187:PHE:HD1	1.77	0.67
6:L:96:GLN:NE2	6:L:103:PHE:HB2	2.09	0.67
3:3:18:ASP:OD1	3:3:18:ASP:C	2.32	0.67
6:L:40:PHE:CE1	6:L:90:TYR:HE1	2.11	0.67
2:2:137:LEU:HB3	2:2:182:MET:HE1	1.75	0.67
5:H:24:ILE:HD12	5:H:24:ILE:O	1.95	0.67
6:L:96:GLN:HE22	6:L:103:PHE:HB2	1.56	0.67
2:2:94:LEU:C	2:2:94:LEU:HD23	2.15	0.67
5:H:18:LEU:CG	5:H:82:VAL:HG11	2.25	0.67
3:3:45:LEU:CD1	3:3:45:LEU:O	2.42	0.67
6:L:83:GLN:HA	6:L:83:GLN:OE1	1.92	0.67
1:1:8:ALA:HB1	2:2:145:HIS:NE2	2.10	0.67
3:3:55:LEU:HD13	3:3:201:VAL:HG23	1.77	0.66
1:1:169:LYS:HG2	1:1:169:LYS:O	1.96	0.66
1:1:95:GLU:OE1	1:1:95:GLU:HA	1.95	0.66
6:L:28:TYR:HB2	6:L:73:HIS:CE1	2.30	0.66
3:3:108:HIS:HB2	3:3:202:LEU:HB2	1.78	0.66
5:H:50:ASP:N	5:H:50:ASP:OD1	2.28	0.66
2:2:98:TYR:CE2	2:2:210:VAL:CG2	2.78	0.66
2:2:82:GLU:OE2	2:2:82:GLU:HA	1.95	0.66
6:L:96:GLN:CG	6:L:99:ASN:HD21	2.09	0.66
1:1:85:ASN:CG	1:1:107:TYR:CE1	2.69	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:110:GLY:C	6:L:36:TYR:HB2	2.15	0.66
6:L:89:ASP:CB	6:L:107:THR:CG2	2.71	0.66
2:2:66:LEU:HD11	2:2:201:ALA:HB3	1.76	0.66
3:3:74:LEU:HD11	3:3:188:GLN:NE2	2.10	0.66
3:3:104:THR:HG23	3:3:159:ILE:O	1.96	0.66
6:L:95:TRP:HZ3	6:L:97:SER:HA	1.61	0.66
3:3:73:VAL:HG23	3:3:187:PHE:HE1	1.60	0.65
5:H:23:THR:CB	5:H:76:SER:O	2.43	0.65
5:H:107:GLY:O	6:L:102:LEU:HD21	1.96	0.65
1:1:85:ASN:O	1:1:170:ALA:CB	2.44	0.65
2:2:125:MET:HE1	2:2:179:LEU:HA	1.78	0.65
5:H:24:ILE:HD12	5:H:24:ILE:C	2.15	0.65
1:1:86:LEU:HB3	1:1:170:ALA:HB3	1.78	0.65
3:3:23:ASP:N	3:3:24:PRO:HD3	2.12	0.65
2:2:117:ASN:HD22	2:2:117:ASN:N	1.94	0.65
6:L:93:LEU:HD22	6:L:93:LEU:N	2.11	0.65
3:3:45:LEU:HD21	3:3:211:LEU:HD13	0.80	0.65
3:3:110:MET:CE	3:3:200:VAL:HG13	1.98	0.65
6:L:102:LEU:CD1	6:L:102:LEU:H	2.10	0.65
5:H:29:LEU:HD23	5:H:29:LEU:C	2.17	0.65
5:H:33:THR:HG22	5:H:52:SER:CA	2.25	0.65
1:1:91:ASN:HD21	1:1:121:ALA:HA	1.43	0.65
3:3:73:VAL:HG23	3:3:187:PHE:CE1	2.32	0.65
6:L:40:PHE:CZ	6:L:90:TYR:CE1	2.85	0.65
5:H:45:LEU:HD11	6:L:91:PHE:HD2	1.58	0.65
6:L:95:TRP:CZ3	6:L:97:SER:HA	2.32	0.65
2:2:47:ASN:HD21	2:2:167:ARG:HB2	1.63	0.64
1:1:85:ASN:C	1:1:170:ALA:CB	2.60	0.64
1:1:91:ASN:HD22	1:1:121:ALA:C	2.00	0.64
1:1:10:PRO:HG3	4:4:71:LEU:HG	1.79	0.64
2:2:58:ALA:O	2:2:91:TYR:HB2	1.97	0.64
2:2:69:TRP:CZ3	2:2:121:LEU:HD23	2.23	0.64
2:2:176:PRO:HG2	2:2:177:TRP:HD1	1.63	0.64
6:L:31:VAL:C	6:L:35:ASN:HB2	2.17	0.64
2:2:80:GLN:OE1	2:2:129:LEU:HD11	1.97	0.64
2:2:125:MET:HE3	2:2:179:LEU:CD2	2.22	0.64
5:H:107:GLY:O	6:L:102:LEU:HG	1.97	0.64
1:1:55:GLN:O	1:1:55:GLN:HG2	1.98	0.63
6:L:87:GLU:N	6:L:87:GLU:OE1	2.31	0.63
1:1:7:SER:CB	1:1:9:ASP:OD1	2.45	0.63
1:1:9:ASP:OD1	1:1:9:ASP:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:56:THR:OG1	1:1:63:GLY:CA	2.47	0.63
1:1:89:VAL:CG2	1:1:167:ALA:N	2.61	0.63
1:1:112:LEU:CD2	3:3:9:ASP:CB	2.75	0.63
1:1:130:TYR:OH	2:2:174:HIS:HD2	1.71	0.63
2:2:68:ASP:HB2	2:2:198:LYS:HA	1.76	0.63
6:L:95:TRP:HZ3	6:L:97:SER:HB2	1.63	0.63
6:L:73:HIS:O	6:L:74:THR:C	2.37	0.63
1:1:88:TRP:HD1	1:1:117:LEU:HD11	1.62	0.63
5:H:45:LEU:HD12	6:L:93:LEU:HD11	1.80	0.63
2:2:166:ASN:C	2:2:167:ARG:NH1	2.52	0.62
1:1:160:PRO:HD2	1:1:163:PHE:HE2	1.64	0.62
1:1:187:CYS:SG	1:1:187:CYS:O	2.57	0.62
6:L:102:LEU:N	6:L:102:LEU:HD12	2.13	0.62
1:1:78:VAL:HG13	1:1:115:LEU:HB2	1.80	0.62
1:1:98:LEU:H	1:1:98:LEU:CD1	2.11	0.62
2:2:98:TYR:CD2	2:2:210:VAL:CG2	2.82	0.62
5:H:107:GLY:O	6:L:102:LEU:CD2	2.47	0.62
6:L:30:ASN:O	6:L:35:ASN:ND2	2.32	0.62
2:2:114:ASN:HD21	2:2:194:ALA:HB3	1.64	0.62
5:H:24:ILE:HD12	5:H:26:GLY:N	2.11	0.62
1:1:53:LEU:CD2	1:1:180:MET:SD	2.85	0.62
2:2:64:THR:O	2:2:66:LEU:HD12	2.00	0.62
2:2:122:LEU:HD23	2:2:122:LEU:O	1.99	0.62
5:H:36:TRP:HD1	5:H:69:ILE:HD13	1.65	0.62
6:L:96:GLN:NE2	6:L:103:PHE:CG	2.66	0.62
2:2:197:ILE:HG12	2:2:197:ILE:O	1.99	0.62
5:H:23:THR:CG2	5:H:78:VAL:HG22	2.30	0.62
3:3:45:LEU:O	3:3:45:LEU:HD12	2.00	0.62
6:L:96:GLN:HG3	6:L:99:ASN:HD21	1.64	0.61
6:L:102:LEU:H	6:L:102:LEU:HD12	1.65	0.61
1:1:47:GLN:O	1:1:169:LYS:HG3	2.00	0.61
1:1:51:LEU:HD21	1:1:176:LEU:HD21	1.82	0.61
1:1:88:TRP:CH2	1:1:90:PRO:HA	2.34	0.61
5:H:59:TYR:CZ	5:H:68:SER:HA	2.34	0.61
3:3:81:LEU:HD23	3:3:101:TYR:CD2	2.34	0.61
2:2:69:TRP:HH2	2:2:121:LEU:CB	2.12	0.61
2:2:95:THR:O	2:2:98:TYR:O	2.18	0.61
3:3:74:LEU:HD11	3:3:188:GLN:HE21	1.64	0.61
1:1:92:GLY:O	1:1:94:PRO:HD3	2.01	0.61
2:2:99:ALA:HB2	2:2:214:PHE:HE1	1.63	0.61
2:2:176:PRO:HG2	2:2:177:TRP:CD1	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:35:GLY:HA2	5:H:50:ASP:HA	1.81	0.61
6:L:41:GLN:O	6:L:90:TYR:CD1	2.54	0.61
1:1:112:LEU:HD23	1:1:112:LEU:O	2.00	0.61
6:L:95:TRP:HZ3	6:L:97:SER:CB	2.14	0.61
5:H:18:LEU:HD12	5:H:80:LEU:HB2	1.82	0.61
6:L:31:VAL:CA	6:L:35:ASN:HD22	2.13	0.61
6:L:96:GLN:HG3	6:L:99:ASN:ND2	2.15	0.60
1:1:87:THR:HG22	1:1:105:THR:CG2	2.31	0.60
1:1:131:ASN:O	2:2:174:HIS:HB2	2.01	0.60
5:H:75:LYS:HB3	5:H:77:GLN:HG3	1.83	0.60
2:2:213:GLU:OE1	2:2:213:GLU:N	2.34	0.60
5:H:18:LEU:HD11	5:H:80:LEU:HB3	1.82	0.60
6:L:62:VAL:O	6:L:62:VAL:HG13	2.01	0.60
1:1:102:THR:HG22	1:1:102:THR:O	2.01	0.60
2:2:122:LEU:HA	2:2:147:PHE:HB2	1.83	0.60
5:H:20:LEU:O	5:H:36:TRP:CZ2	2.54	0.60
5:H:58:TYR:CB	5:H:105:SER:O	2.46	0.60
2:2:122:LEU:HB2	2:2:147:PHE:HB2	1.82	0.60
5:H:20:LEU:CD1	5:H:36:TRP:CZ3	2.83	0.60
5:H:24:ILE:CD1	5:H:26:GLY:H	2.14	0.60
2:2:48:THR:HG21	2:2:168:TYR:HE2	1.65	0.60
3:3:110:MET:HE2	3:3:200:VAL:HG11	1.18	0.60
6:L:40:PHE:CE1	6:L:52:ILE:HD13	2.37	0.60
2:2:73:ASP:O	2:2:187:LEU:HA	2.01	0.60
1:1:15:VAL:HG12	1:1:15:VAL:O	2.02	0.60
1:1:96:THR:HG23	1:1:96:THR:O	2.02	0.60
5:H:23:THR:CB	5:H:77:GLN:HA	2.32	0.60
5:H:101:THR:HG23	5:H:101:THR:O	2.02	0.60
6:L:46:SER:O	6:L:48:PRO:HD3	2.00	0.60
2:2:216:SER:HG	3:3:141:HIS:CD2	2.20	0.59
1:1:124:ARG:NH2	4:4:36:THR:OG1	2.35	0.59
2:2:57:GLN:OE1	2:2:90:VAL:CG2	2.50	0.59
3:3:44:PHE:O	3:3:45:LEU:HB3	2.02	0.59
1:1:6:GLU:OE2	2:2:149:ASN:HB2	2.02	0.59
2:2:125:MET:CE	2:2:179:LEU:HA	2.32	0.59
5:H:47:TRP:O	5:H:60:ASN:ND2	2.36	0.59
1:1:128:THR:HG23	1:1:129:VAL:HG23	1.85	0.59
2:2:69:TRP:CH2	2:2:121:LEU:HB3	2.36	0.59
2:2:100:TYR:O	2:2:168:TYR:CB	2.50	0.59
1:1:84:GLY:N	1:1:171:THR:CG2	2.59	0.59
1:1:106:ALA:CB	3:3:15:VAL:HG12	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:7:SER:CA	2:2:146:GLN:HE22	2.15	0.58
1:1:101:THR:CG2	1:1:105:THR:HG21	2.33	0.58
2:2:26:THR:HG21	2:2:28:SER:O	2.02	0.58
2:2:137:LEU:HB3	2:2:182:MET:CE	2.32	0.58
3:3:104:THR:CG2	3:3:160:PRO:HA	2.23	0.58
6:L:66:PHE:CZ	6:L:90:TYR:HE2	1.84	0.58
2:2:42:PHE:HD2	4:4:38:LEU:HB2	1.67	0.58
3:3:47:VAL:HG12	3:3:47:VAL:O	2.03	0.58
3:3:117:ALA:HB1	3:3:194:ALA:N	2.17	0.58
2:2:103:ASN:HB3	2:2:208:VAL:HG12	1.85	0.58
3:3:207:LYS:HG3	3:3:208:ASP:N	2.19	0.58
5:H:18:LEU:HD12	5:H:80:LEU:HB3	1.83	0.58
5:H:59:TYR:CE2	5:H:68:SER:HA	2.39	0.58
1:1:79:ALA:HA	1:1:113:THR:O	2.04	0.58
2:2:112:VAL:O	2:2:197:ILE:HD12	2.04	0.58
5:H:108:LEU:HA	6:L:95:TRP:HD1	1.69	0.58
1:1:91:ASN:CG	1:1:122:PRO:HD3	2.21	0.57
2:2:129:LEU:HD22	2:2:178:THR:CB	2.33	0.57
5:H:106:ILE:H	5:H:106:ILE:CD1	2.06	0.57
6:L:40:PHE:CG	6:L:52:ILE:HD13	2.40	0.57
1:1:110:ALA:CB	3:3:9:ASP:HB3	2.28	0.57
2:2:71:THR:HA	2:2:188:THR:HG21	1.85	0.57
2:2:100:TYR:CB	2:2:168:TYR:HB3	2.35	0.57
1:1:73:PHE:HE2	1:1:182:ARG:HH12	1.52	0.57
1:1:89:VAL:O	1:1:166:GLY:HA3	2.05	0.57
1:1:6:GLU:OE2	2:2:149:ASN:CB	2.52	0.57
2:2:111:ALA:O	2:2:154:MET:HB2	2.05	0.57
3:3:18:ASP:OD1	3:3:18:ASP:O	2.23	0.57
1:1:8:ALA:HB1	2:2:145:HIS:CE1	2.40	0.56
5:H:17:THR:CB	5:H:82:VAL:O	2.53	0.56
2:2:119:GLY:H	2:2:189:VAL:HG22	1.70	0.56
2:2:119:GLY:HA2	2:2:185:ALA:HB1	1.86	0.56
4:4:15:SER:OG	4:4:16:GLY:N	2.37	0.56
2:2:121:LEU:HD13	2:2:183:VAL:HA	1.87	0.56
5:H:18:LEU:HD21	5:H:82:VAL:HG11	1.84	0.56
1:1:87:THR:OG1	1:1:98:LEU:HB3	2.04	0.56
1:1:124:ARG:HG3	1:1:125:VAL:HG23	1.88	0.56
2:2:26:THR:HG22	2:2:28:SER:H	1.69	0.56
1:1:7:SER:HB3	1:1:9:ASP:CG	2.25	0.56
2:2:99:ALA:HB2	2:2:214:PHE:CE1	2.40	0.56
2:2:129:LEU:HD22	2:2:178:THR:HG1	1.66	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:167:ARG:HH11	2:2:167:ARG:CA	2.16	0.56
2:2:130:CYS:O	2:2:132:ILE:HD13	2.05	0.56
3:3:74:LEU:HD12	3:3:186:LEU:HG	1.87	0.56
5:H:23:THR:HG21	5:H:77:GLN:C	2.26	0.55
5:H:68:SER:O	5:H:81:SER:HB3	2.06	0.55
3:3:74:LEU:CD1	3:3:186:LEU:HB3	2.37	0.55
6:L:62:VAL:CG2	6:L:66:PHE:CD2	2.89	0.55
5:H:16:GLN:HA	5:H:16:GLN:OE1	2.05	0.55
5:H:18:LEU:CD1	5:H:80:LEU:HG	2.37	0.55
5:H:61:PRO:HD3	5:H:106:ILE:HG22	1.87	0.55
2:2:60:ARG:HD3	2:2:90:VAL:HG12	1.89	0.55
6:L:95:TRP:CZ3	6:L:97:SER:HB2	2.41	0.55
6:L:68:GLY:HA3	6:L:77:LEU:HB2	1.89	0.55
2:2:121:LEU:HD12	2:2:183:VAL:HA	1.89	0.55
6:L:67:SER:O	6:L:78:THR:O	2.25	0.55
2:2:65:HIS:NE2	6:L:97:SER:OG	2.35	0.55
1:1:40:VAL:HG23	1:1:60:THR:HG21	1.89	0.55
2:2:100:TYR:OH	3:3:128:PRO:HD3	2.03	0.55
5:H:11:LEU:HB3	5:H:14:PRO:CG	2.37	0.55
5:H:20:LEU:CG	5:H:36:TRP:CH2	2.89	0.55
5:H:36:TRP:CD1	5:H:69:ILE:HD13	2.42	0.55
3:3:18:ASP:HB2	3:3:19:PRO:HD2	1.88	0.54
3:3:76:GLN:NE2	3:3:132:PRO:CB	2.70	0.54
1:1:200:ARG:O	1:1:200:ARG:HG2	2.08	0.54
5:H:110:GLY:HA2	6:L:53:TYR:HE1	1.70	0.54
6:L:39:TRP:HB2	6:L:93:LEU:CD2	2.10	0.54
6:L:89:ASP:HB2	6:L:107:THR:HG22	1.89	0.54
2:2:79:TYR:HE1	6:L:33:THR:HG23	1.55	0.54
3:3:76:GLN:O	3:3:76:GLN:HG2	2.06	0.54
5:H:18:LEU:HD11	5:H:80:LEU:CB	2.36	0.54
5:H:45:LEU:HD21	6:L:91:PHE:HE2	1.72	0.54
5:H:47:TRP:HB2	6:L:102:LEU:HD22	1.89	0.54
1:1:109:LYS:O	1:1:109:LYS:HG2	2.08	0.54
2:2:134:LYS:HD2	2:2:134:LYS:O	2.08	0.54
5:H:17:THR:CG2	5:H:82:VAL:O	2.56	0.54
2:2:80:GLN:HA	2:2:179:LEU:O	2.07	0.54
5:H:42:GLY:O	5:H:43:LYS:HG3	2.07	0.54
6:L:40:PHE:CE1	6:L:42:GLN:CD	2.57	0.54
6:L:66:PHE:CZ	6:L:90:TYR:HH	1.60	0.54
1:1:88:TRP:CZ2	1:1:117:LEU:HD22	2.40	0.54
1:1:91:ASN:ND2	1:1:121:ALA:C	2.61	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:216:ASP:OD1	3:3:217:ALA:N	2.40	0.54
2:2:198:LYS:HB3	2:2:198:LYS:HZ1	1.73	0.53
6:L:39:TRP:CD1	6:L:93:LEU:HD21	2.43	0.53
6:L:41:GLN:CD	6:L:43:ILE:HB	2.28	0.53
6:L:43:ILE:CG2	6:L:44:PRO:HD3	2.38	0.53
1:1:46:ASP:HA	1:1:173:VAL:HG22	1.89	0.53
2:2:214:PHE:CZ	3:3:129:GLY:HA3	2.43	0.53
5:H:34:ILE:O	5:H:51:MET:N	2.38	0.53
6:L:38:SER:HB3	6:L:53:TYR:CE1	2.44	0.53
2:2:154:MET:HG3	2:2:155:THR:HG23	1.91	0.53
6:L:30:ASN:C	6:L:30:ASN:ND2	2.58	0.53
2:2:120:CYS:SG	2:2:184:VAL:CG1	2.96	0.53
2:2:98:TYR:CD2	2:2:210:VAL:CG1	2.92	0.53
2:2:162:PHE:CE1	2:2:169:ASP:OD2	2.62	0.53
5:H:68:SER:HB3	5:H:81:SER:HB3	1.90	0.53
6:L:95:TRP:CZ3	6:L:97:SER:CA	2.86	0.53
3:3:108:HIS:N	3:3:202:LEU:O	2.41	0.53
4:4:80:PHE:HD1	4:4:81:GLY:N	2.07	0.52
5:H:61:PRO:HD3	5:H:106:ILE:CG2	2.39	0.52
5:H:12:VAL:CG2	5:H:87:PRO:CA	2.80	0.52
6:L:27:THR:C	6:L:73:HIS:HE1	2.11	0.52
2:2:69:TRP:HH2	2:2:121:LEU:HB3	1.74	0.52
2:2:87:HIS:HB3	2:2:92:GLY:HA2	1.92	0.52
5:H:68:SER:O	5:H:81:SER:CA	2.57	0.52
3:3:212:ARG:HG3	3:3:213:LEU:H	1.75	0.52
2:2:81:LEU:HD23	2:2:81:LEU:C	2.30	0.52
3:3:43:ASN:OD1	3:3:47:VAL:HB	2.08	0.52
1:1:130:TYR:CE2	2:2:174:HIS:CD2	2.94	0.52
2:2:32:VAL:HG12	2:2:157:HIS:CG	2.45	0.52
3:3:74:LEU:CD1	3:3:186:LEU:CG	2.88	0.52
5:H:18:LEU:HD11	5:H:80:LEU:CG	2.40	0.52
5:H:11:LEU:HD13	5:H:14:PRO:HG3	1.91	0.52
6:L:96:GLN:OE1	6:L:99:ASN:ND2	2.43	0.52
1:1:196:PRO:HB2	1:1:198:GLU:O	2.10	0.52
4:4:79:LEU:N	4:4:79:LEU:CD1	2.73	0.52
6:L:42:GLN:OE1	6:L:90:TYR:HE1	1.93	0.52
2:2:122:LEU:HB2	2:2:147:PHE:CB	2.40	0.51
1:1:172:ARG:HH11	1:1:172:ARG:HB2	1.75	0.51
3:3:104:THR:HG23	3:3:160:PRO:CA	2.28	0.51
1:1:7:SER:O	2:2:146:GLN:OE1	2.28	0.51
1:1:34:PHE:CD2	4:4:17:ASN:HB2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:91:ASN:HB2	1:1:120:THR:CG2	2.37	0.51
2:2:43:VAL:HG13	2:2:102:ARG:NH2	2.25	0.51
5:H:18:LEU:HD11	5:H:80:LEU:HG	1.92	0.51
5:H:45:LEU:HD11	6:L:91:PHE:HE2	1.73	0.51
2:2:112:VAL:HG12	2:2:114:ASN:OD1	2.10	0.51
5:H:70:THR:HB	5:H:79:ARG:H	1.76	0.51
1:1:172:ARG:NH1	1:1:172:ARG:CB	2.73	0.51
1:1:70:THR:HG22	1:1:189:ARG:NE	2.20	0.51
2:2:129:LEU:CD2	2:2:178:THR:CB	2.88	0.51
6:L:28:TYR:HA	6:L:73:HIS:ND1	2.13	0.51
6:L:37:VAL:O	6:L:37:VAL:HG13	2.11	0.51
3:3:121:TYR:CE2	3:3:199:LEU:HD22	2.46	0.50
1:1:130:TYR:HA	2:2:128:GLU:OE1	2.10	0.50
3:3:66:THR:HG23	3:3:188:GLN:OE1	2.11	0.50
2:2:64:THR:O	2:2:66:LEU:CD1	2.60	0.50
5:H:59:TYR:CB	5:H:67:LEU:CD2	2.72	0.50
2:2:68:ASP:CB	2:2:198:LYS:CA	2.67	0.50
2:2:122:LEU:CB	2:2:147:PHE:HB2	2.41	0.50
5:H:23:THR:CG2	5:H:76:SER:O	2.59	0.50
5:H:59:TYR:HE2	5:H:69:ILE:N	2.09	0.50
6:L:42:GLN:OE1	6:L:90:TYR:CE1	2.65	0.50
2:2:99:ALA:C	2:2:100:TYR:CD2	2.85	0.50
2:2:129:LEU:HD22	2:2:178:THR:CG2	2.41	0.50
6:L:27:THR:C	6:L:73:HIS:CE1	2.85	0.50
1:1:123:HIS:HE1	1:1:162:SER:HB2	1.77	0.50
1:1:88:TRP:CZ3	1:1:89:VAL:C	2.85	0.50
1:1:112:LEU:HD23	1:1:112:LEU:H	1.76	0.50
2:2:166:ASN:HB3	2:2:167:ARG:NH1	2.21	0.50
3:3:36:MET:O	3:3:36:MET:HG2	2.12	0.50
5:H:47:TRP:CG	5:H:109:TYR:HE2	2.29	0.50
5:H:98:SER:C	5:H:99:ARG:O	2.42	0.50
1:1:192:LEU:HD11	2:2:135:ARG:HG3	1.94	0.49
5:H:18:LEU:HD22	5:H:93:TYR:CE2	2.47	0.49
6:L:82:LEU:HD12	6:L:83:GLN:HB2	1.94	0.49
2:2:102:ARG:HD2	2:2:162:PHE:HD2	1.77	0.49
4:4:80:PHE:CD1	4:4:80:PHE:C	2.86	0.49
5:H:47:TRP:CZ2	5:H:109:TYR:CD2	3.00	0.49
5:H:59:TYR:CE2	5:H:69:ILE:N	2.80	0.49
2:2:15:LEU:HD21	2:2:157:HIS:HD2	1.77	0.49
2:2:100:TYR:CA	2:2:168:TYR:HB3	2.42	0.49
3:3:101:TYR:CD2	3:3:170:THR:HG22	2.36	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:76:PHE:CD1	4:4:77:SER:N	2.80	0.49
5:H:47:TRP:O	5:H:60:ASN:CG	2.51	0.49
1:1:5:GLY:O	1:1:6:GLU:HB2	2.13	0.49
1:1:5:GLY:O	1:1:6:GLU:CB	2.58	0.49
1:1:51:LEU:CD2	1:1:176:LEU:HD21	2.42	0.49
2:2:122:LEU:CA	2:2:147:PHE:HB2	2.42	0.49
3:3:81:LEU:HD23	3:3:101:TYR:CE2	2.47	0.49
1:1:77:GLU:OE1	1:1:116:ALA:HA	2.12	0.49
3:3:98:TYR:HD2	3:3:211:LEU:HD22	1.77	0.49
2:2:108:GLU:O	2:2:202:ASN:N	2.44	0.49
2:2:123:VAL:HG23	2:2:181:VAL:HG22	1.95	0.49
2:2:137:LEU:CD2	2:2:182:MET:HE3	2.25	0.49
6:L:40:PHE:CA	6:L:52:ILE:CG2	2.85	0.49
3:3:73:VAL:HA	3:3:187:PHE:CE1	2.48	0.49
1:1:91:ASN:ND2	1:1:122:PRO:N	2.59	0.49
2:2:68:ASP:HB3	2:2:198:LYS:CB	2.41	0.49
3:3:74:LEU:HD13	3:3:186:LEU:CG	2.41	0.49
3:3:102:SER:HB2	3:3:167:TYR:CD1	2.48	0.49
1:1:78:VAL:CG1	1:1:115:LEU:HB2	2.42	0.48
2:2:94:LEU:HD23	2:2:94:LEU:O	2.12	0.48
5:H:17:THR:HG22	5:H:82:VAL:H	1.47	0.48
5:H:68:SER:N	5:H:81:SER:O	2.46	0.48
2:2:45:GLY:HA3	2:2:167:ARG:HE	1.74	0.48
2:2:67:PHE:HD2	2:2:79:TYR:CD2	2.31	0.48
6:L:62:VAL:CG2	6:L:66:PHE:HD2	2.26	0.48
1:1:56:THR:OG1	1:1:63:GLY:HA2	2.13	0.48
1:1:160:PRO:HD2	1:1:163:PHE:CE2	2.48	0.48
2:2:67:PHE:O	2:2:199:VAL:HG12	2.12	0.48
2:2:120:CYS:SG	2:2:184:VAL:HG13	2.53	0.48
1:1:7:SER:HA	2:2:146:GLN:NE2	2.24	0.48
2:2:120:CYS:CA	2:2:185:ALA:HB2	2.41	0.48
5:H:109:TYR:CE2	6:L:102:LEU:CD2	2.93	0.48
1:1:71:TYR:HB2	1:1:186:TYR:HB2	1.95	0.48
6:L:39:TRP:CG	6:L:93:LEU:HD21	2.45	0.48
2:2:47:ASN:ND2	3:3:166:ASP:OD1	2.47	0.48
5:H:75:LYS:HZ3	5:H:75:LYS:CA	2.27	0.48
6:L:22:ILE:HG22	6:L:23:THR:N	2.29	0.48
1:1:82:HIS:CD2	1:1:82:HIS:C	2.76	0.48
1:1:172:ARG:CZ	1:1:172:ARG:HB3	2.43	0.48
2:2:100:TYR:OH	3:3:128:PRO:CG	2.61	0.48
3:3:117:ALA:CB	3:3:194:ALA:N	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:87:THR:CA	1:1:105:THR:HG22	2.31	0.48
2:2:120:CYS:SG	2:2:147:PHE:HD2	2.37	0.48
2:2:196:GLN:HE22	5:H:106:ILE:HD12	1.78	0.48
2:2:215:PRO:HG2	3:3:133:PRO:HD3	1.95	0.48
3:3:35:ASN:O	3:3:36:MET:HB3	2.14	0.48
3:3:178:THR:HG1	3:3:183:TRP:HH2	1.62	0.48
2:2:29:SER:OG	2:2:30:VAL:N	2.47	0.47
6:L:28:TYR:O	6:L:32:GLY:CA	2.61	0.47
2:2:190:ASN:C	2:2:190:ASN:HD22	2.16	0.47
5:H:75:LYS:HA	5:H:75:LYS:NZ	2.29	0.47
6:L:38:SER:HB3	6:L:53:TYR:CD1	2.48	0.47
6:L:93:LEU:CD2	6:L:93:LEU:N	2.77	0.47
3:3:120:ARG:HG2	3:3:189:ILE:HD11	1.95	0.47
6:L:96:GLN:OE1	6:L:103:PHE:CB	2.62	0.47
2:2:47:ASN:OD1	2:2:167:ARG:CG	2.60	0.47
2:2:47:ASN:OD1	2:2:48:THR:N	2.47	0.47
3:3:74:LEU:CD1	3:3:186:LEU:HG	2.43	0.47
3:3:215:VAL:HG22	3:3:216:ASP:H	1.79	0.47
6:L:37:VAL:HG12	6:L:70:ARG:HG3	1.93	0.47
6:L:96:GLN:OE1	6:L:103:PHE:HB2	2.14	0.47
1:1:29:HIS:CG	1:1:29:HIS:O	2.68	0.47
2:2:66:LEU:HD12	2:2:66:LEU:N	2.29	0.47
2:2:114:ASN:ND2	2:2:194:ALA:H	2.10	0.47
2:2:167:ARG:HH11	2:2:167:ARG:N	2.12	0.47
5:H:72:HIS:NE2	5:H:77:GLN:HB3	2.24	0.47
6:L:31:VAL:HA	6:L:35:ASN:CG	2.33	0.47
6:L:38:SER:HA	6:L:54:SER:OG	2.15	0.47
1:1:14:THR:HG22	1:1:14:THR:O	2.14	0.47
1:1:34:PHE:CE2	4:4:17:ASN:CG	2.88	0.47
1:1:111:PRO:HD2	3:3:9:ASP:OD2	2.15	0.47
3:3:100:GLN:HA	3:3:170:THR:HG23	1.97	0.47
5:H:33:THR:HG22	5:H:52:SER:CB	2.45	0.47
5:H:114:TRP:CE3	5:H:114:TRP:C	2.88	0.47
6:L:57:ASN:HD21	6:L:67:SER:CB	2.26	0.47
6:L:62:VAL:N	6:L:63:PRO:HD3	2.29	0.47
6:L:95:TRP:CZ3	6:L:96:GLN:C	2.88	0.47
1:1:7:SER:O	1:1:8:ALA:HB3	2.14	0.47
5:H:75:LYS:HZ3	5:H:75:LYS:C	2.18	0.47
1:1:126:LEU:HD12	1:1:163:PHE:HB3	1.96	0.47
3:3:55:LEU:HB2	3:3:201:VAL:HG23	1.97	0.47
5:H:18:LEU:CD1	5:H:80:LEU:CG	2.93	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:81:LEU:CD2	3:3:105:ILE:HD11	2.43	0.46
2:2:196:GLN:OE1	5:H:106:ILE:CD1	2.63	0.46
3:3:53:THR:HG1	3:3:89:THR:HG1	1.56	0.46
3:3:112:THR:O	3:3:112:THR:HG22	2.15	0.46
2:2:117:ASN:N	2:2:117:ASN:ND2	2.60	0.46
2:2:167:ARG:O	2:2:168:TYR:CG	2.68	0.46
5:H:7:SER:HA	5:H:93:TYR:O	2.15	0.46
6:L:68:GLY:HA2	6:L:78:THR:O	2.16	0.46
6:L:102:LEU:CD1	6:L:102:LEU:N	2.73	0.46
6:L:103:PHE:CD1	6:L:103:PHE:C	2.89	0.46
1:1:172:ARG:HB2	1:1:172:ARG:NH1	2.30	0.46
2:2:58:ALA:O	2:2:91:TYR:CB	2.64	0.46
5:H:24:ILE:CD1	5:H:26:GLY:N	2.76	0.46
5:H:107:GLY:CA	6:L:102:LEU:HD21	2.45	0.46
1:1:40:VAL:HB	1:1:62:VAL:HG12	1.98	0.46
1:1:187:CYS:HG	2:2:36:TYR:HH	1.64	0.46
3:3:86:MET:O	3:3:89:THR:HG22	2.16	0.46
5:H:110:GLY:O	6:L:36:TYR:CG	2.62	0.46
2:2:60:ARG:HD3	2:2:90:VAL:HG13	1.96	0.46
3:3:41:PHE:N	3:3:41:PHE:CD1	2.82	0.46
3:3:56:HIS:CE1	3:3:60:ASP:HA	2.51	0.46
5:H:72:HIS:HD1	5:H:72:HIS:C	2.13	0.46
2:2:96:ASP:O	2:2:214:PHE:CD2	2.69	0.46
2:2:123:VAL:O	2:2:123:VAL:HG13	2.16	0.46
3:3:73:VAL:CG2	3:3:187:PHE:HE1	2.28	0.46
5:H:106:ILE:CG2	6:L:100:THR:OG1	2.41	0.46
5:H:112:ASP:C	5:H:114:TRP:H	2.18	0.46
6:L:66:PHE:CE1	6:L:90:TYR:CZ	2.84	0.46
1:1:89:VAL:CG2	1:1:167:ALA:H	2.27	0.45
3:3:110:MET:HE3	3:3:200:VAL:HG12	1.81	0.45
5:H:111:VAL:HG22	5:H:114:TRP:HB3	1.98	0.45
1:1:89:VAL:HG22	1:1:167:ALA:O	2.16	0.45
2:2:120:CYS:O	2:2:184:VAL:HG13	2.17	0.45
1:1:51:LEU:HD21	1:1:178:TYR:CE1	2.19	0.45
1:1:89:VAL:HG23	1:1:167:ALA:H	1.77	0.45
5:H:13:LYS:N	5:H:14:PRO:HD2	2.31	0.45
5:H:102:GLY:CA	5:H:114:TRP:NE1	2.74	0.45
6:L:40:PHE:CZ	6:L:42:GLN:NE2	2.55	0.45
2:2:107:VAL:HG12	2:2:158:ILE:HB	1.99	0.45
2:2:120:CYS:HB2	2:2:149:ASN:HD22	1.58	0.45
2:2:166:ASN:C	2:2:167:ARG:HH11	2.18	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:74:LEU:CD1	3:3:188:GLN:HE21	2.29	0.45
3:3:186:LEU:HD12	3:3:186:LEU:HA	1.80	0.45
5:H:23:THR:HG23	5:H:78:VAL:HG22	1.99	0.45
6:L:42:GLN:OE1	6:L:42:GLN:HA	2.16	0.45
1:1:87:THR:HG22	1:1:101:THR:HG23	1.98	0.45
5:H:53:ASN:HB3	5:H:100:TYR:OH	2.17	0.45
6:L:28:TYR:O	6:L:32:GLY:N	2.50	0.45
6:L:41:GLN:O	6:L:90:TYR:HE1	1.99	0.45
2:2:66:LEU:CD1	2:2:201:ALA:HB3	2.45	0.45
2:2:167:ARG:HH21	4:4:38:LEU:HD11	1.82	0.45
3:3:101:TYR:O	3:3:101:TYR:CD1	2.70	0.45
1:1:17:ASN:OD1	1:1:18:TYR:CD2	2.70	0.45
1:1:50:VAL:O	1:1:50:VAL:HG23	2.17	0.45
1:1:82:HIS:CE1	1:1:86:LEU:HD22	2.52	0.45
2:2:69:TRP:CD1	2:2:69:TRP:O	2.70	0.45
5:H:39:GLN:HG2	5:H:45:LEU:HD22	2.00	0.44
2:2:58:ALA:HB1	2:2:91:TYR:HB2	1.99	0.44
3:3:63:TYR:HB2	3:3:198:ALA:HB1	1.99	0.44
3:3:108:HIS:HB2	3:3:202:LEU:CB	2.45	0.44
5:H:114:TRP:CE3	5:H:114:TRP:O	2.70	0.44
2:2:70:VAL:HG21	5:H:108:LEU:CD2	2.47	0.44
2:2:91:TYR:O	2:2:91:TYR:CD2	2.70	0.44
2:2:99:ALA:O	2:2:100:TYR:CD2	2.70	0.44
2:2:102:ARG:HD2	2:2:162:PHE:CD2	2.52	0.44
2:2:114:ASN:OD1	2:2:114:ASN:N	2.51	0.44
2:2:126:VAL:HG13	2:2:178:THR:OG1	2.17	0.44
4:4:33:SER:OG	4:4:34:MET:N	2.50	0.44
6:L:95:TRP:CZ3	6:L:96:GLN:O	2.70	0.44
1:1:28:GLN:O	1:1:29:HIS:HB3	2.17	0.44
1:1:129:VAL:O	2:2:128:GLU:OE1	2.35	0.44
1:1:93:ALA:HA	1:1:94:PRO:HD2	1.49	0.44
2:2:91:TYR:O	2:2:91:TYR:CG	2.70	0.44
5:H:17:THR:CG2	5:H:82:VAL:C	2.79	0.44
5:H:75:LYS:CE	5:H:75:LYS:CA	2.85	0.44
2:2:48:THR:HG21	2:2:168:TYR:CD2	2.52	0.44
1:1:68:THR:O	1:1:189:ARG:N	2.40	0.44
1:1:168:ILE:O	1:1:168:ILE:HG13	2.18	0.44
2:2:114:ASN:C	2:2:116:PHE:H	2.21	0.44
1:1:130:TYR:CE1	2:2:174:HIS:NE2	2.85	0.44
2:2:120:CYS:SG	2:2:147:PHE:CD2	3.11	0.44
2:2:174:HIS:O	2:2:174:HIS:CG	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:23:THR:HG21	5:H:78:VAL:N	2.33	0.44
2:2:118:GLY:HA3	2:2:189:VAL:CG2	2.33	0.44
1:1:74:ALA:HB3	1:1:165:TYR:OH	2.18	0.43
2:2:120:CYS:N	2:2:185:ALA:HB3	2.24	0.43
2:2:126:VAL:CG1	2:2:178:THR:OG1	2.66	0.43
3:3:64:VAL:HG21	3:3:74:LEU:HD22	1.99	0.43
6:L:103:PHE:CD1	6:L:103:PHE:O	2.70	0.43
2:2:71:THR:CA	2:2:188:THR:HG21	2.47	0.43
5:H:109:TYR:HB3	5:H:114:TRP:CH2	2.53	0.43
6:L:43:ILE:HG23	6:L:44:PRO:HD3	1.99	0.43
2:2:77:ARG:HH21	2:2:77:ARG:HB2	1.83	0.43
2:2:100:TYR:HB3	2:2:168:TYR:HB2	1.99	0.43
1:1:57:PRO:HG2	1:1:60:THR:OG1	2.18	0.43
1:1:91:ASN:HB3	1:1:120:THR:OG1	2.19	0.43
2:2:124:ALA:HB3	2:2:140:LEU:HD21	2.00	0.43
2:2:166:ASN:CB	2:2:167:ARG:HH12	2.24	0.43
3:3:74:LEU:CD1	3:3:186:LEU:CB	2.96	0.43
3:3:166:ASP:O	3:3:167:TYR:HD1	2.00	0.43
3:3:132:PRO:HG3	3:3:183:TRP:CE2	2.53	0.43
5:H:68:SER:O	5:H:81:SER:CB	2.67	0.43
6:L:43:ILE:HG22	6:L:44:PRO:HD3	2.01	0.43
1:1:54:MET:SD	1:1:54:MET:C	2.97	0.43
1:1:112:LEU:CD2	1:1:112:LEU:H	2.31	0.43
2:2:167:ARG:NH1	2:2:167:ARG:N	2.67	0.43
1:1:80:VAL:O	1:1:113:THR:HG22	2.19	0.43
1:1:189:ARG:HG3	1:1:190:PRO:HD2	2.00	0.43
3:3:110:MET:O	3:3:199:LEU:CD1	2.62	0.43
3:3:218:ARG:HD2	3:3:218:ARG:HA	1.74	0.43
5:H:20:LEU:HG	5:H:36:TRP:CZ3	2.54	0.43
6:L:33:THR:O	6:L:33:THR:HG22	2.19	0.43
6:L:43:ILE:HG23	6:L:44:PRO:CD	2.48	0.43
2:2:74:PRO:HG3	5:H:112:ASP:OD2	2.18	0.43
2:2:122:LEU:HA	2:2:147:PHE:CB	2.49	0.42
2:2:45:GLY:CA	2:2:167:ARG:HD2	2.35	0.42
5:H:72:HIS:ND1	5:H:77:GLN:O	2.52	0.42
3:3:68:THR:HG22	3:3:191:HIS:NE2	2.33	0.42
2:2:67:PHE:O	2:2:67:PHE:CG	2.71	0.42
2:2:84:PRO:HG3	2:2:171:TYR:CD2	2.54	0.42
3:3:18:ASP:OD1	3:3:20:LYS:N	2.52	0.42
3:3:20:LYS:CE	4:4:26:TYR:OH	2.65	0.42
5:H:47:TRP:CE2	5:H:109:TYR:CD2	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:H:68:SER:CB	5:H:81:SER:HB3	2.49	0.42
5:H:73:ASN:C	5:H:73:ASN:ND2	2.73	0.42
2:2:42:PHE:CD2	4:4:38:LEU:HB2	2.51	0.42
2:2:125:MET:HE2	2:2:178:THR:O	2.20	0.42
3:3:74:LEU:HD12	3:3:186:LEU:CG	2.50	0.42
1:1:82:HIS:NE2	1:1:108:HIS:HB2	2.35	0.42
2:2:98:TYR:CD1	2:2:98:TYR:N	2.85	0.42
2:2:190:ASN:C	2:2:190:ASN:ND2	2.73	0.42
1:1:46:ASP:OD1	1:1:46:ASP:N	2.48	0.42
1:1:91:ASN:CB	1:1:120:THR:O	2.60	0.42
1:1:56:THR:OG1	1:1:63:GLY:HA3	2.20	0.42
2:2:57:GLN:CD	2:2:90:VAL:HG21	2.39	0.42
2:2:103:ASN:N	2:2:103:ASN:OD1	2.52	0.42
2:2:119:GLY:HA2	2:2:185:ALA:CB	2.49	0.42
2:2:126:VAL:HG11	2:2:129:LEU:HD13	2.02	0.42
2:2:174:HIS:ND1	2:2:174:HIS:C	2.73	0.42
1:1:32:VAL:HG21	1:1:185:THR:HG23	2.00	0.42
1:1:112:LEU:HD21	3:3:9:ASP:CB	2.32	0.42
2:2:120:CYS:SG	2:2:184:VAL:HG11	2.60	0.42
3:3:110:MET:CG	3:3:200:VAL:HG13	2.50	0.41
5:H:21:THR:O	5:H:21:THR:HG22	2.20	0.41
2:2:19:ASN:ND2	2:2:61:PHE:HE1	2.18	0.41
2:2:65:HIS:HE1	2:2:198:LYS:HE3	1.85	0.41
3:3:74:LEU:HD13	3:3:186:LEU:HB3	2.00	0.41
4:4:27:MET:SD	4:4:27:MET:N	2.92	0.41
5:H:18:LEU:HD12	5:H:18:LEU:C	2.38	0.41
6:L:95:TRP:CE3	6:L:96:GLN:C	2.94	0.41
1:1:123:HIS:CE1	1:1:162:SER:HB2	2.55	0.41
3:3:57:PHE:CD2	3:3:64:VAL:HB	2.55	0.41
1:1:54:MET:SD	1:1:54:MET:O	2.78	0.41
1:1:192:LEU:HA	1:1:192:LEU:HD12	1.82	0.41
2:2:74:PRO:HG3	5:H:112:ASP:CG	2.41	0.41
3:3:44:PHE:HA	3:3:48:ALA:HB2	2.01	0.41
3:3:69:ASP:OD1	3:3:70:SER:N	2.53	0.41
3:3:76:GLN:HE21	3:3:132:PRO:CB	2.32	0.41
3:3:98:TYR:HD1	3:3:214:PRO:HA	1.85	0.41
2:2:72:SER:CB	5:H:111:VAL:HG21	2.45	0.41
2:2:198:LYS:NZ	2:2:198:LYS:CB	2.73	0.41
3:3:49:GLU:CB	3:3:205:ALA:HB3	2.47	0.41
3:3:53:THR:HG21	3:3:90:PHE:CB	2.51	0.41
2:2:98:TYR:HE2	2:2:210:VAL:CG2	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:114:ASN:C	2:2:116:PHE:N	2.73	0.41
3:3:78:ASP:OD2	3:3:179:ASN:ND2	2.54	0.41
6:L:62:VAL:CG2	6:L:66:PHE:HB2	2.45	0.41
3:3:74:LEU:CB	3:3:186:LEU:O	2.42	0.41
3:3:97:TYR:CE1	3:3:219:THR:HG21	2.55	0.41
2:2:80:GLN:OE1	2:2:129:LEU:CD1	2.68	0.41
3:3:53:THR:HG21	3:3:90:PHE:HB2	2.03	0.41
5:H:66:ARG:O	5:H:82:VAL:HA	2.21	0.41
5:H:112:ASP:C	5:H:114:TRP:N	2.75	0.41
5:H:114:TRP:O	5:H:114:TRP:CD2	2.74	0.41
6:L:28:TYR:O	6:L:32:GLY:HA3	2.20	0.41
1:1:11:VAL:HG23	4:4:76:PHE:HB3	2.02	0.41
1:1:94:PRO:HG3	3:3:215:VAL:HG11	2.02	0.41
2:2:57:GLN:O	2:2:90:VAL:HG21	2.21	0.41
2:2:82:GLU:HB3	2:2:175:LYS:HD3	2.02	0.41
2:2:109:VAL:HG21	2:2:123:VAL:HG11	2.02	0.41
6:L:62:VAL:HG22	6:L:66:PHE:HB3	1.98	0.41
6:L:73:HIS:CG	6:L:74:THR:H	2.38	0.41
2:2:40:GLU:OE2	2:2:207:ASN:HB3	2.19	0.40
2:2:100:TYR:C	2:2:168:TYR:HB3	2.40	0.40
2:2:122:LEU:CB	2:2:147:PHE:CB	2.99	0.40
3:3:18:ASP:O	3:3:18:ASP:CG	2.55	0.40
5:H:33:THR:CA	5:H:51:MET:O	2.61	0.40
2:2:19:ASN:HD22	2:2:61:PHE:HE1	1.69	0.40
2:2:47:ASN:ND2	3:3:163:SER:OG	2.54	0.40
2:2:134:LYS:O	2:2:134:LYS:CG	2.70	0.40
5:H:60:ASN:OD1	5:H:60:ASN:N	2.55	0.40
2:2:62:PHE:HE1	2:2:205:PRO:HD3	1.86	0.40
2:2:118:GLY:N	2:2:189:VAL:HG22	2.25	0.40
3:3:97:TYR:CZ	3:3:219:THR:HG21	2.56	0.40
1:1:88:TRP:CE3	1:1:89:VAL:N	2.90	0.40
1:1:110:ALA:HB1	3:3:9:ASP:CB	2.37	0.40
2:2:65:HIS:CE1	2:2:198:LYS:HE3	2.56	0.40
2:2:196:GLN:OE1	5:H:106:ILE:HD11	2.22	0.40
3:3:162:LEU:H	3:3:162:LEU:HD23	1.86	0.40
5:H:106:ILE:CG2	6:L:100:THR:HG1	2.28	0.40
3:3:44:PHE:CD1	3:3:44:PHE:N	2.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	1	179/213 (84%)	160 (89%)	18 (10%)	1 (1%)	25 63
2	2	204/218 (94%)	188 (92%)	16 (8%)	0	100 100
3	3	217/220 (99%)	201 (93%)	15 (7%)	1 (0%)	29 67
4	4	40/85 (47%)	37 (92%)	3 (8%)	0	100 100
5	H	107/124 (86%)	98 (92%)	9 (8%)	0	100 100
6	L	81/123 (66%)	64 (79%)	17 (21%)	0	100 100
All	All	828/983 (84%)	748 (90%)	78 (9%)	2 (0%)	50 79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	94	PRO
3	3	19	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	1	154/178 (86%)	146 (95%)	8 (5%)	23 53
2	2	178/190 (94%)	164 (92%)	14 (8%)	12 41
3	3	174/175 (99%)	167 (96%)	7 (4%)	31 58
4	4	35/67 (52%)	34 (97%)	1 (3%)	42 65
5	H	91/105 (87%)	79 (87%)	12 (13%)	4 22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
6	L	70/100 (70%)	60 (86%)	10 (14%)	3 20
All	All	702/815 (86%)	650 (93%)	52 (7%)	17 43

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	4	THR
1	1	6	GLU
1	1	9	ASP
1	1	31	ASP
1	1	54	MET
1	1	96	THR
1	1	98	LEU
1	1	101	THR
2	2	72	SER
2	2	77	ARG
2	2	81	LEU
2	2	88	LYS
2	2	114	ASN
2	2	117	ASN
2	2	120	CYS
2	2	122	LEU
2	2	167	ARG
2	2	174	HIS
2	2	175	LYS
2	2	190	ASN
2	2	197	ILE
2	2	198	LYS
3	3	11	TYR
3	3	26	TYR
3	3	41	PHE
3	3	44	PHE
3	3	116	ASP
3	3	143	ILE
3	3	197	ASP
4	4	80	PHE
5	H	12	VAL
5	H	29	LEU
5	H	50	ASP
5	H	53	ASN
5	H	60	ASN
5	H	72	HIS

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Mol	Chain	Res	Type
5	H	73	ASN
5	H	75	LYS
5	H	76	SER
5	H	101	THR
5	H	106	ILE
5	H	111	VAL
6	L	30	ASN
6	L	31	VAL
6	L	58	ARG
6	L	66	PHE
6	L	86	ASP
6	L	91	PHE
6	L	92	CYS
6	L	99	ASN
6	L	100	THR
6	L	103	PHE

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

Mol	Chain	Res	Type
1	1	82	HIS
1	1	85	ASN
1	1	91	ASN
1	1	123	HIS
2	2	19	ASN
2	2	117	ASN
2	2	146	GLN
2	2	149	ASN
2	2	157	HIS
2	2	190	ASN
3	3	56	HIS
3	3	76	GLN
3	3	141	HIS
3	3	144	HIS
3	3	179	ASN
3	3	188	GLN
5	H	53	ASN
5	H	72	HIS
5	H	73	ASN
6	L	30	ASN
6	L	35	ASN
6	L	57	ASN

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Mol	Chain	Res	Type
6	L	73	HIS
6	L	96	GLN
6	L	99	ASN

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-30558. 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

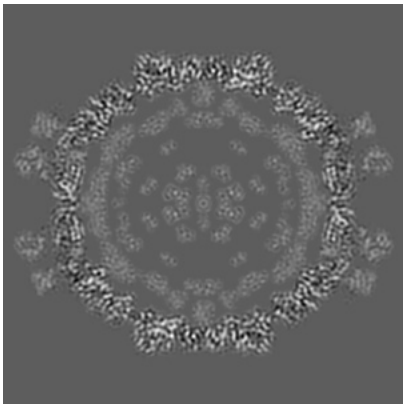
Y

Z

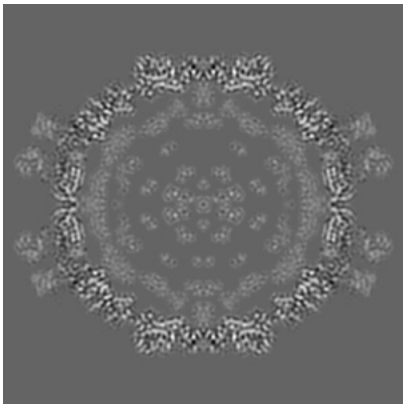
The images above show the map projected in three orthogonal directions.

6.2 Central slices

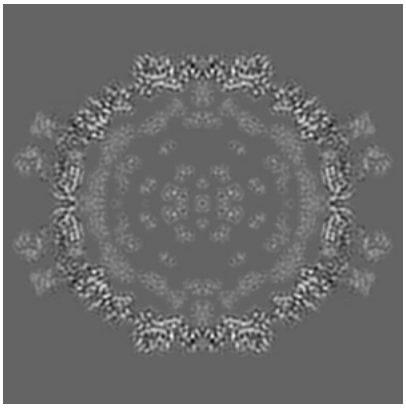
6.2.1 Primary map



X Index: 200



Y Index: 200

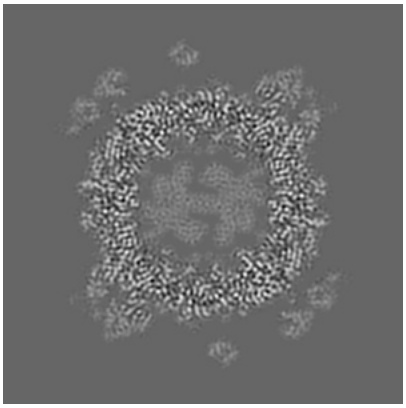


Z Index: 200

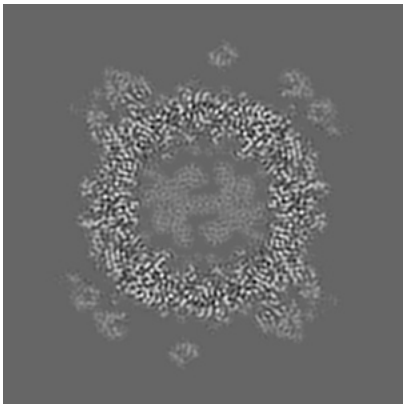
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

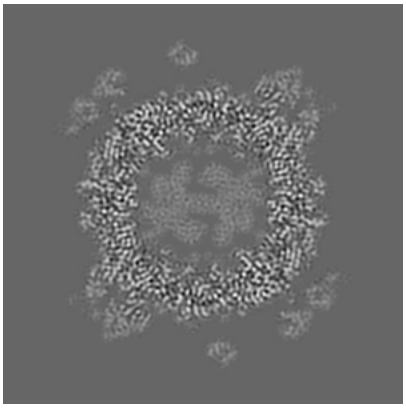
6.3.1 Primary map



X Index: 300



Y Index: 99

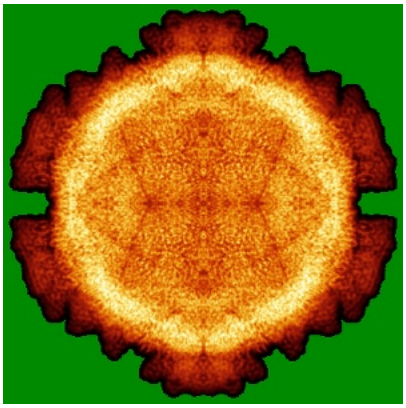


Z Index: 301

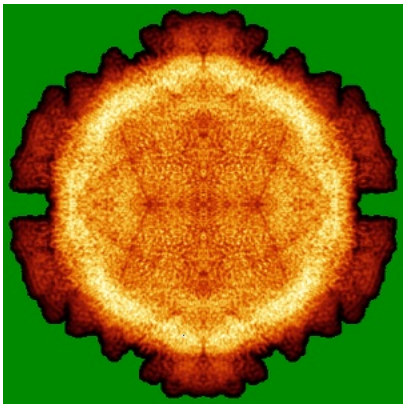
The images above show the largest variance slices of the map in three orthogonal directions.

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

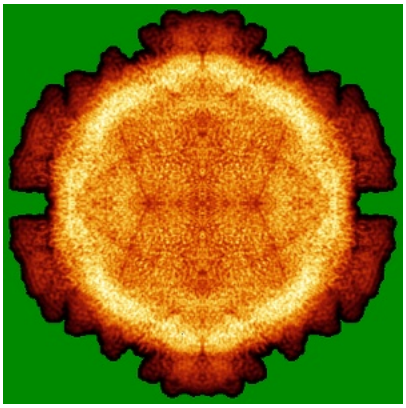
6.4.1 Primary map



X



Y

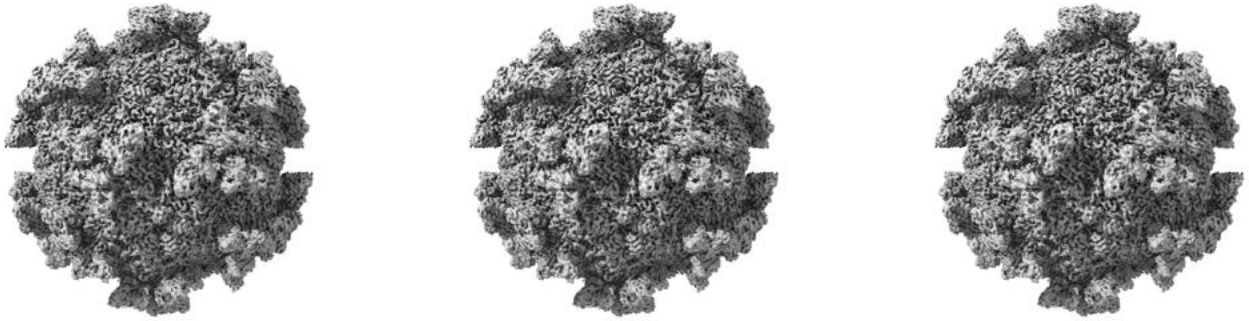


Z

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

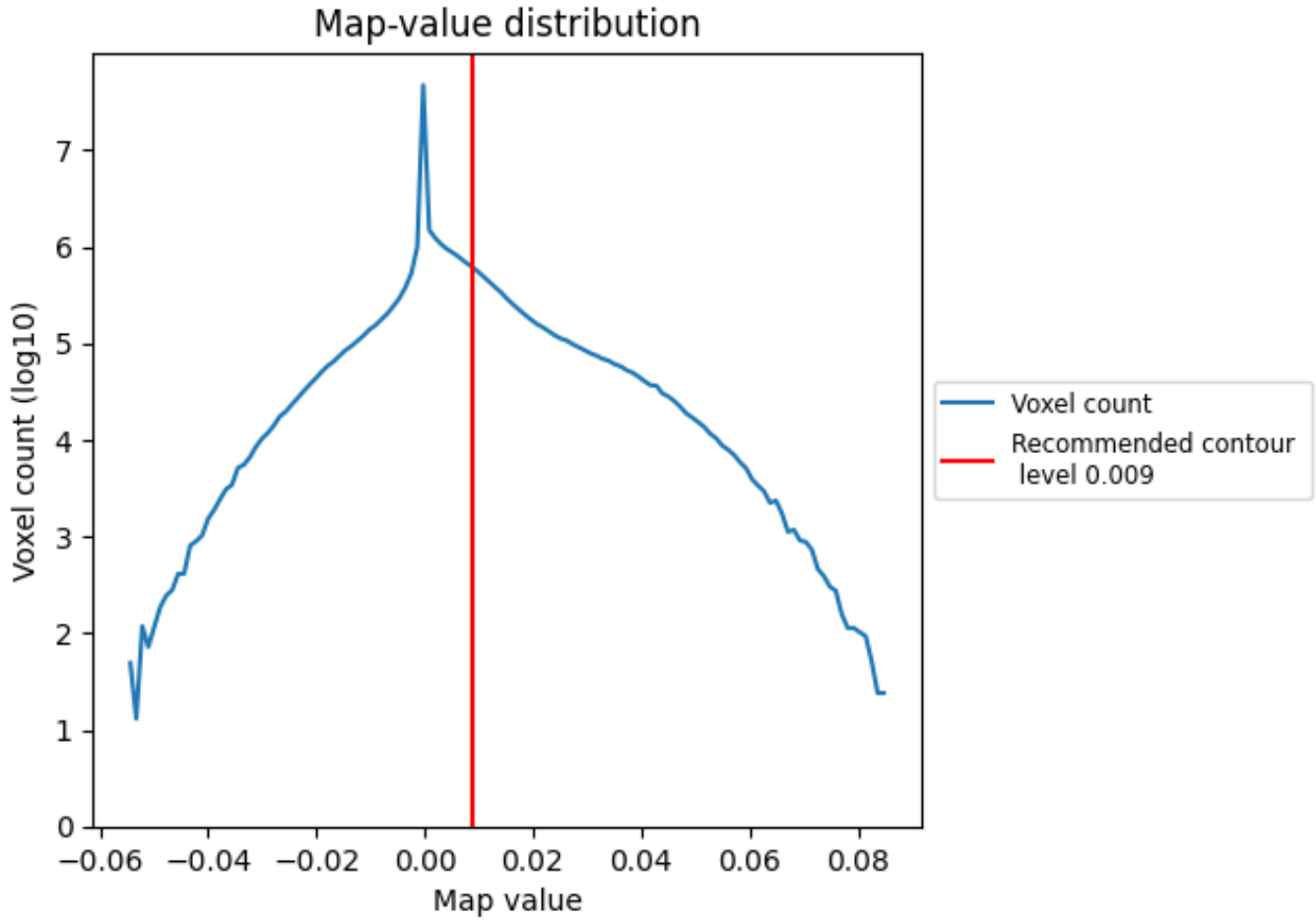
6.6 Mask visualisation (i)

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

7 Map analysis

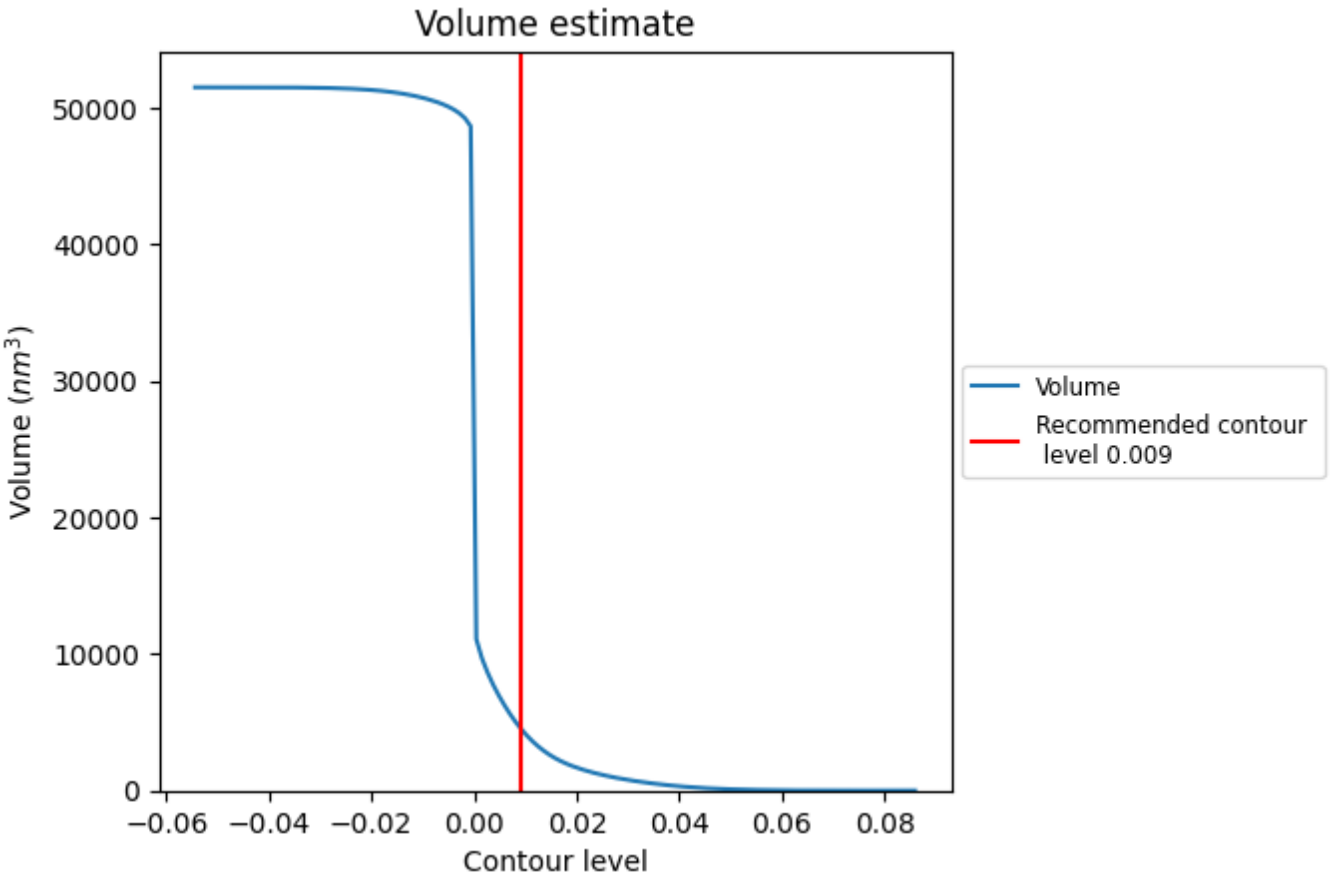
This section contains the results of statistical analysis of the map.

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.

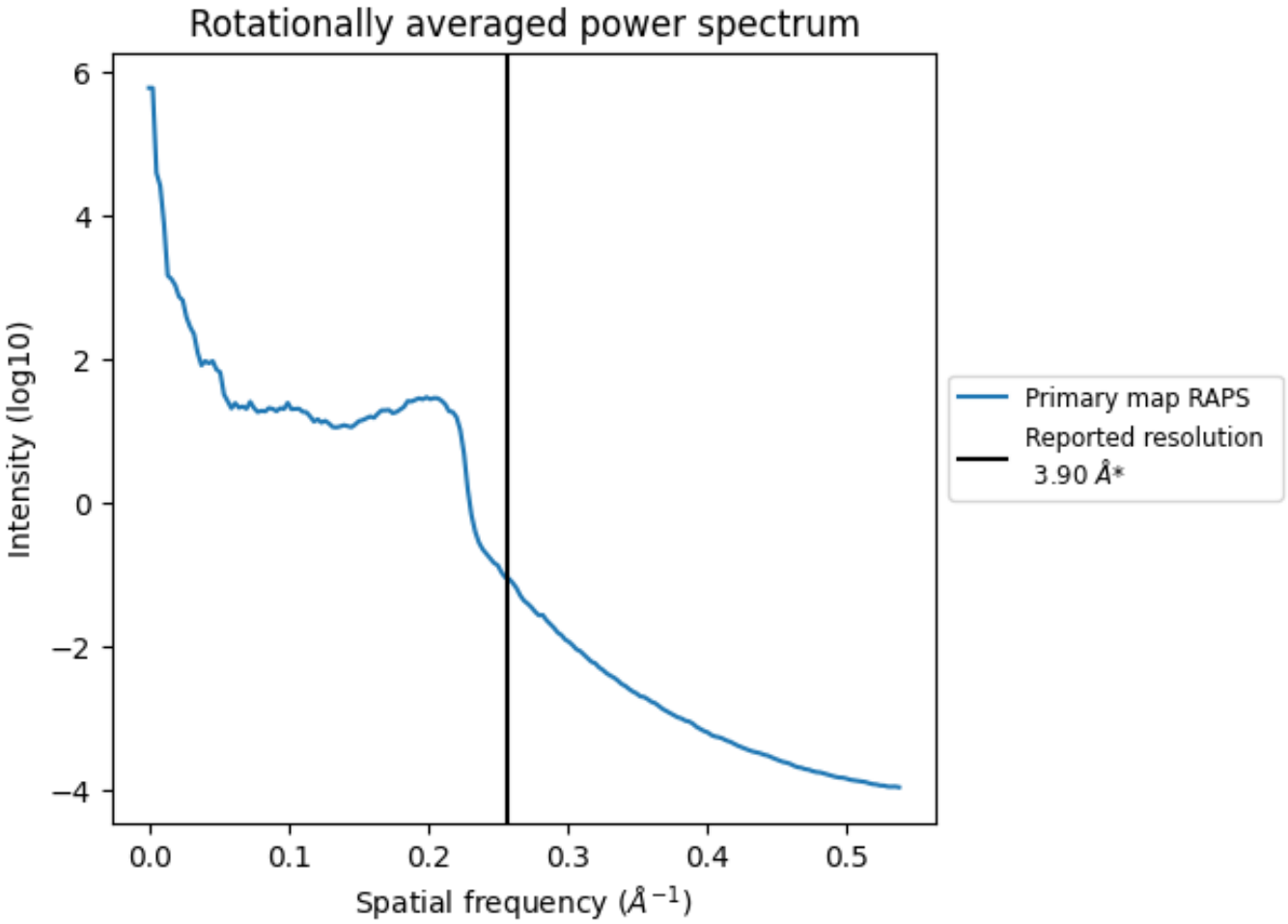
7.2 Volume estimate



The volume at the recommended contour level is 4593 nm^3; this corresponds to an approximate mass of 4149 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 0.256 Å^{-1}

8 Fourier-Shell correlation (i)

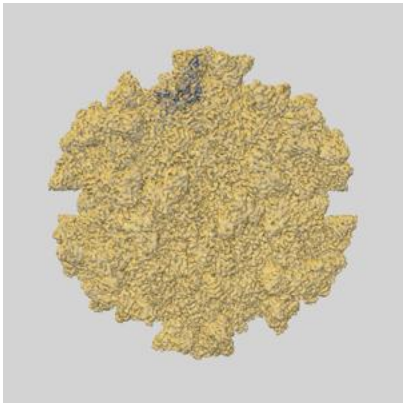
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

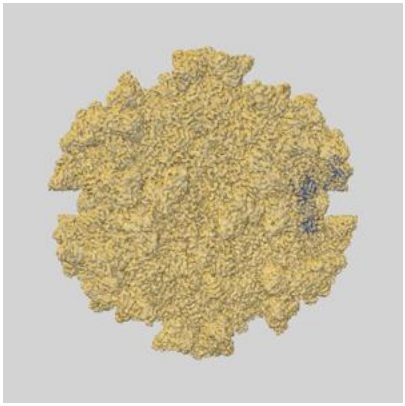
This section contains information regarding the fit between EMDB map EMD-30558 and PDB model 7D3K. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlays

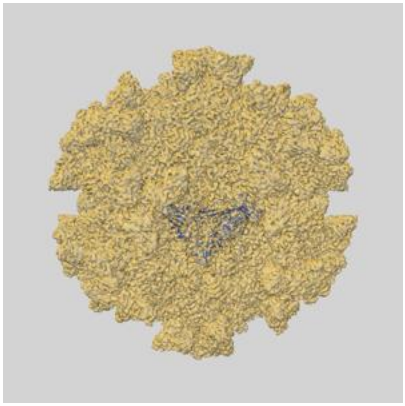
9.1.1 Map-model overlay



X

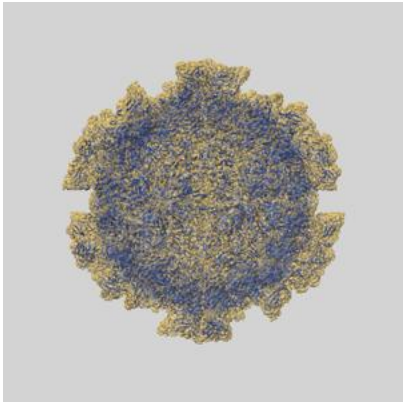


Y

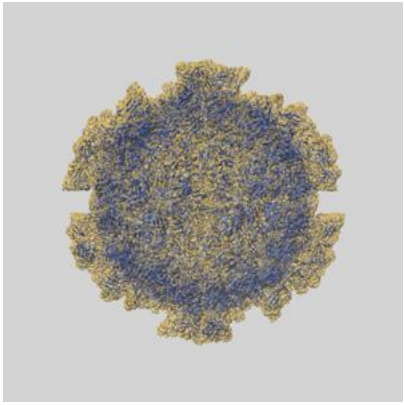


Z

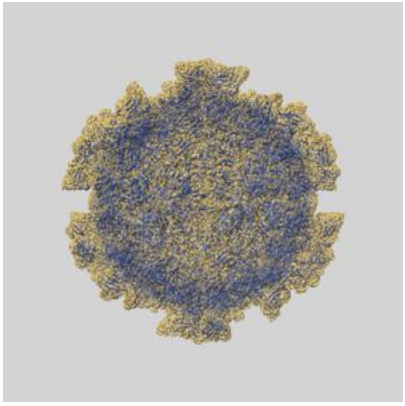
9.1.2 Map-model assembly overlay



X



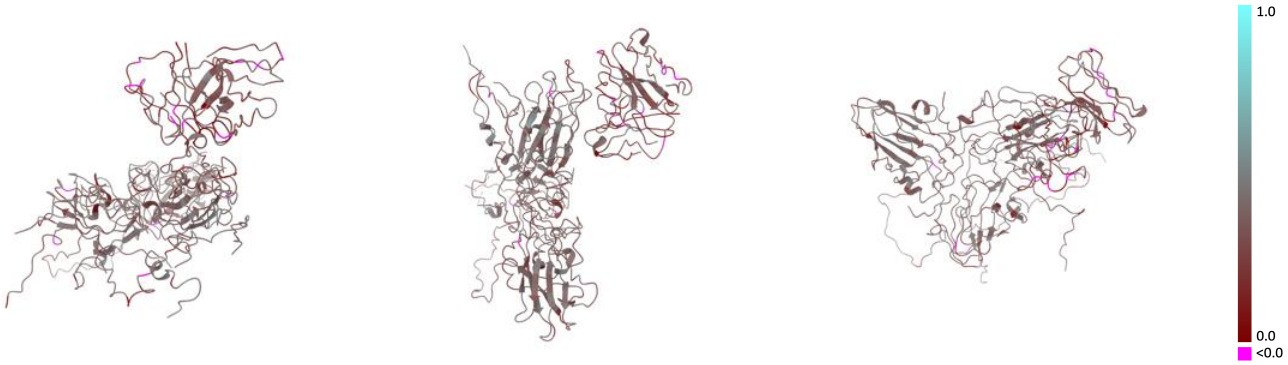
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.009 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.

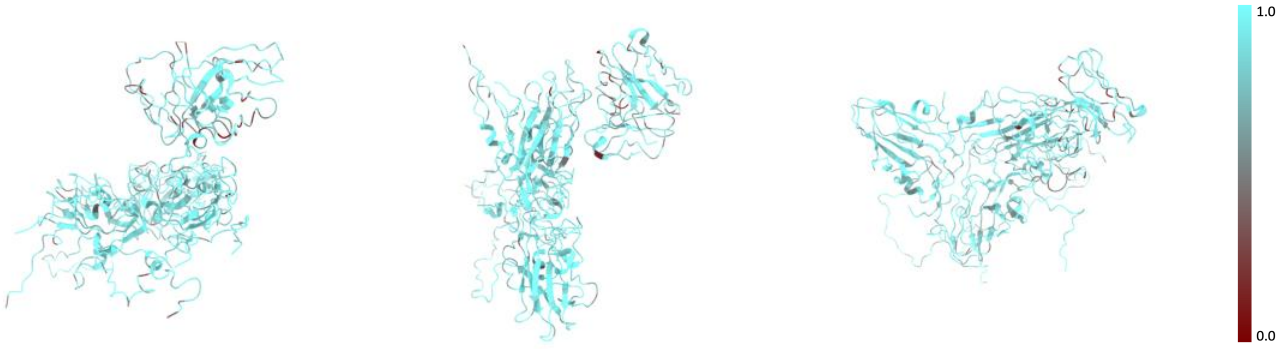
9.2 Q-score mapped to coordinate model (i)



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.

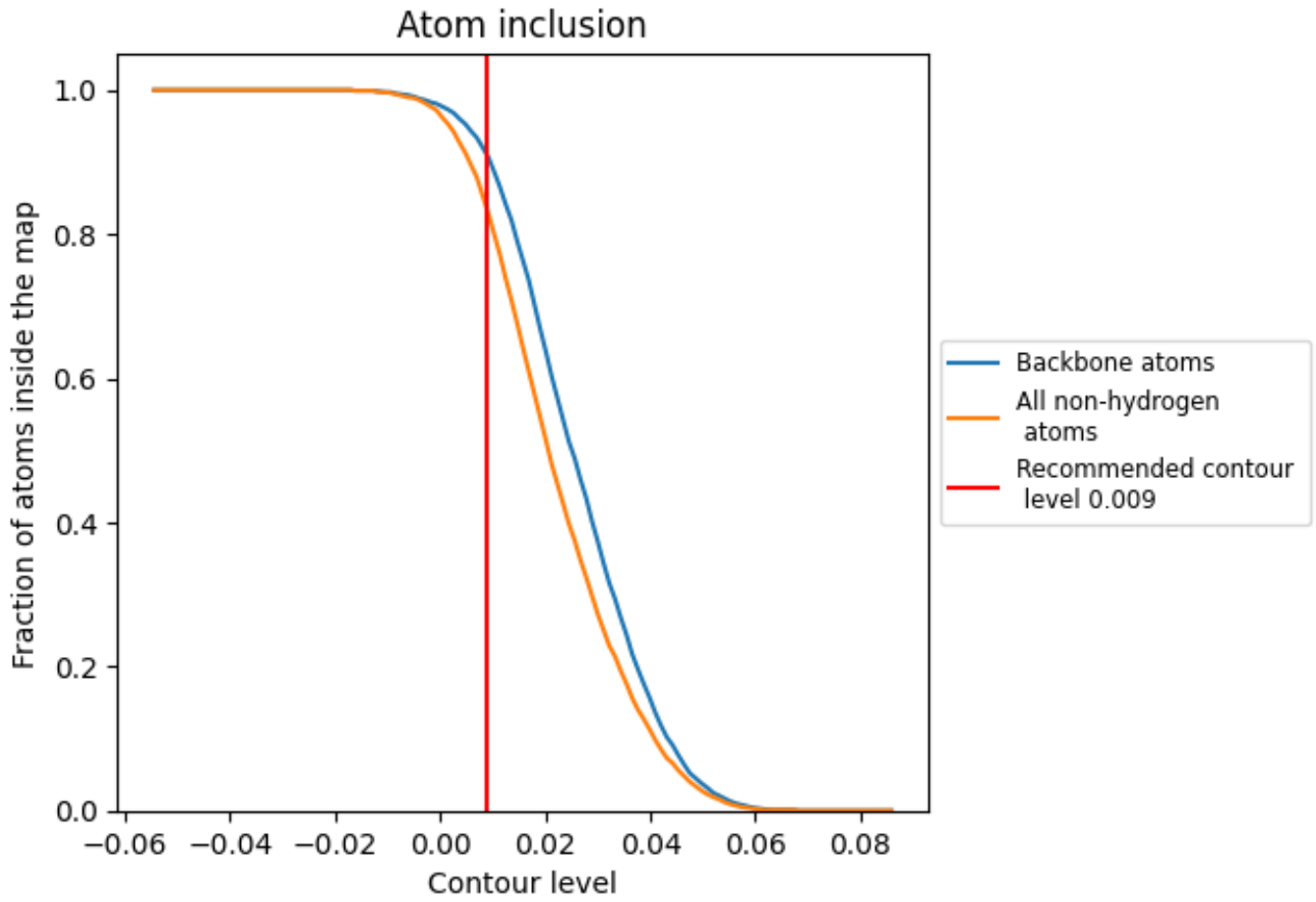
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.009).

9.4 Atom inclusion (i)



At the recommended contour level, 91% of all backbone atoms, 83% 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 (0.009) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8330	0.3520
1	0.8560	0.3680
2	0.8430	0.3790
3	0.8650	0.3700
4	0.8230	0.4010
H	0.7730	0.2920
L	0.7610	0.2510