



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 12:21 PM UTC

PDB ID : 3IZH / pdb_00003izh
EMDB ID : EMD-5244
Title : Mm-cpn D386A with ATP
Authors : Douglas, N.R.; Reissmann, S.; Zhang, J.; Chen, B.; Jakana, J.; Kumar, R.;
Chiu, W.; Frydman, J.
Deposited on : 2010-10-29
Resolution : 11.00 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:

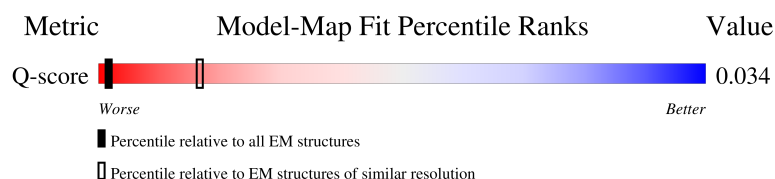
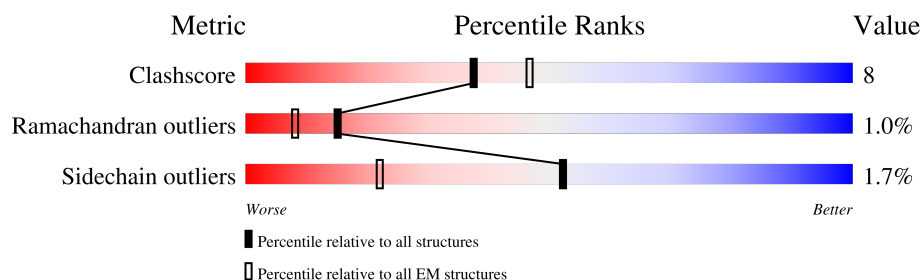
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 11.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	97 (10.50 - 11.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	513	29% 86% 13% .
1	B	513	28% 87% 12% .
1	C	513	29% 87% 12% .
1	D	513	28% 87% 12% .

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Mol	Chain	Length	Quality of chain
1	E	513	
1	F	513	
1	G	513	
1	H	513	
1	I	513	
1	J	513	
1	K	513	
1	L	513	
1	M	513	
1	N	513	
1	O	513	
1	P	513	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 61632 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 Chaperonin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	B	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	C	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	D	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	E	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	F	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	G	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	H	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	I	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	J	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	K	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	L	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	M	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	N	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	O	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		
1	P	513	Total	C	N	O	S	0	0
			3852	2391	664	772	25		

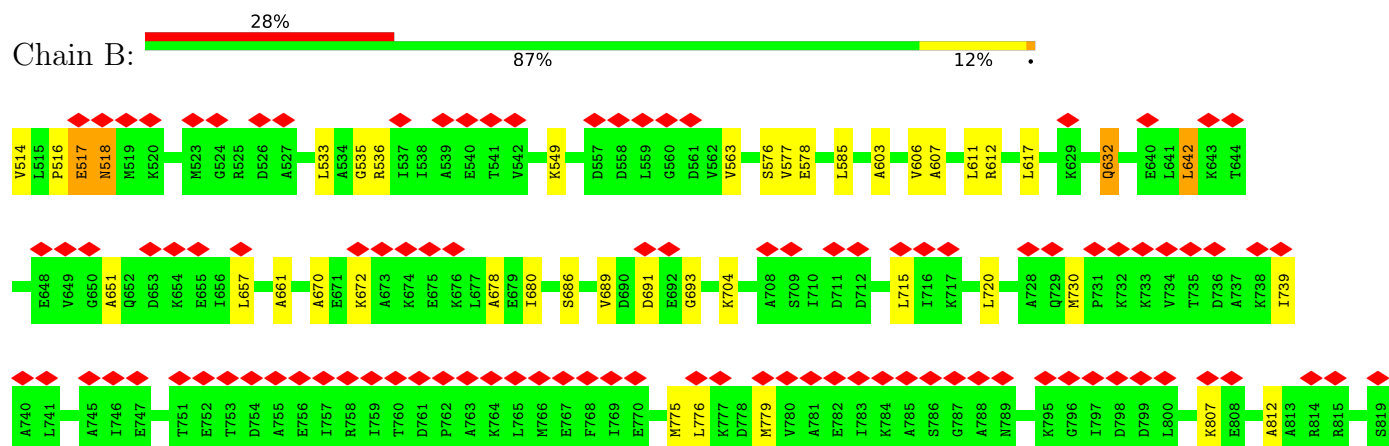
3 Residue-property plots

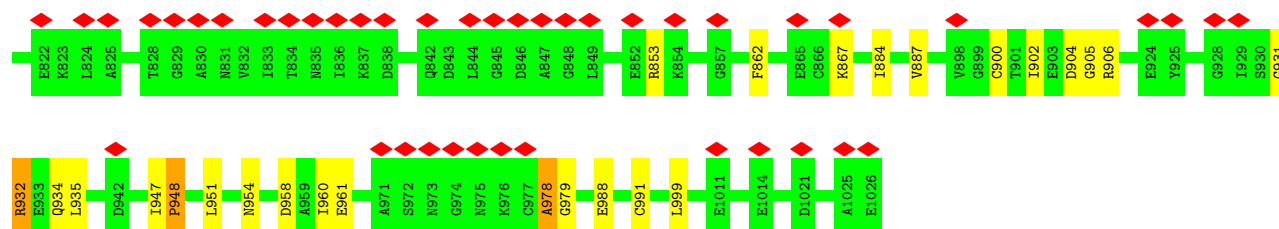
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Chaperonin

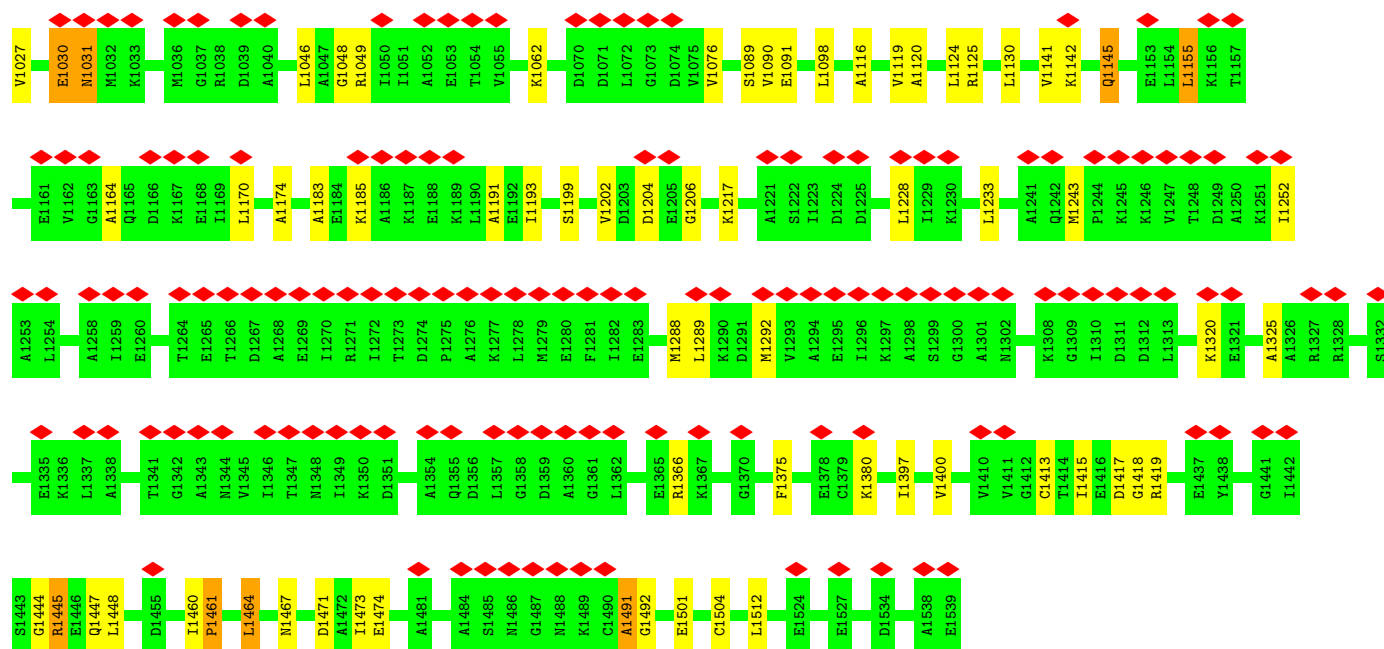
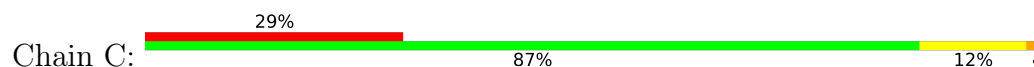


• Molecule 1: Chaperonin

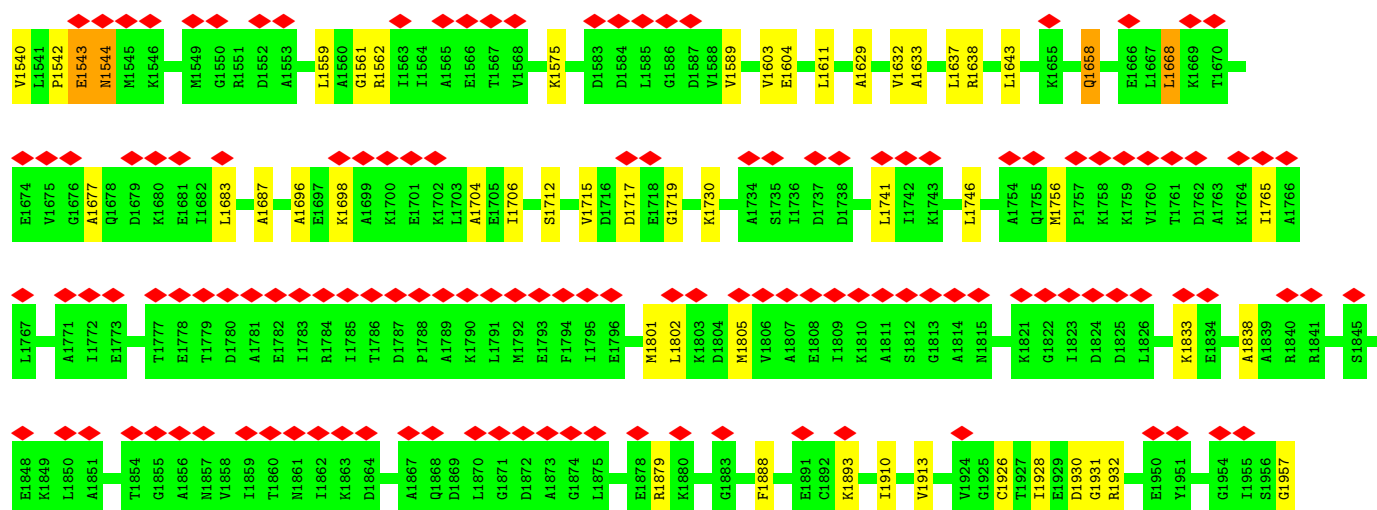
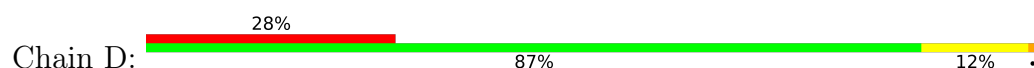


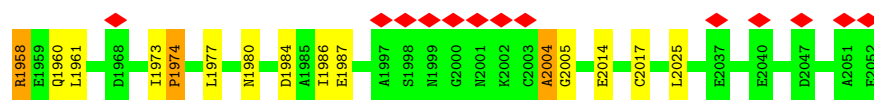


• Molecule 1: Chaperonin

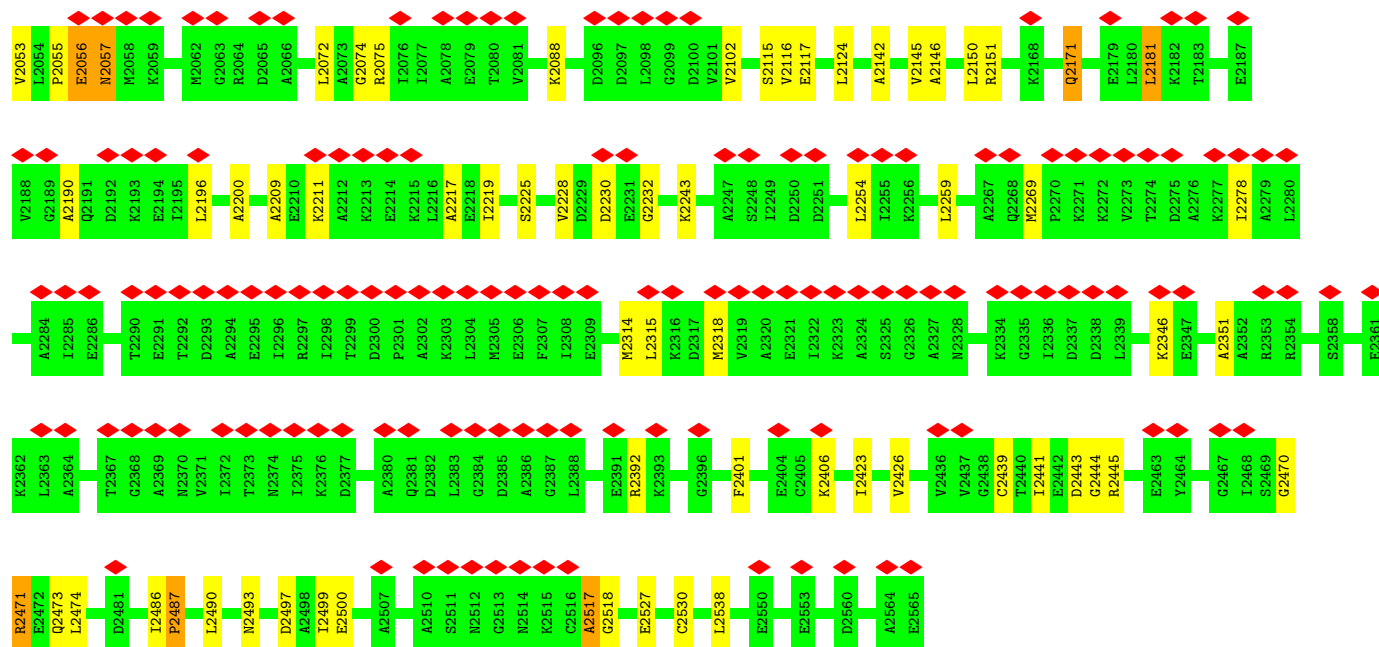
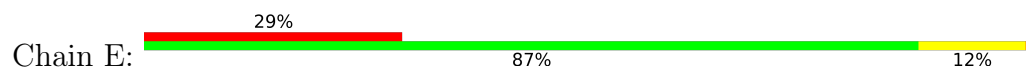


• Molecule 1: Chaperonin

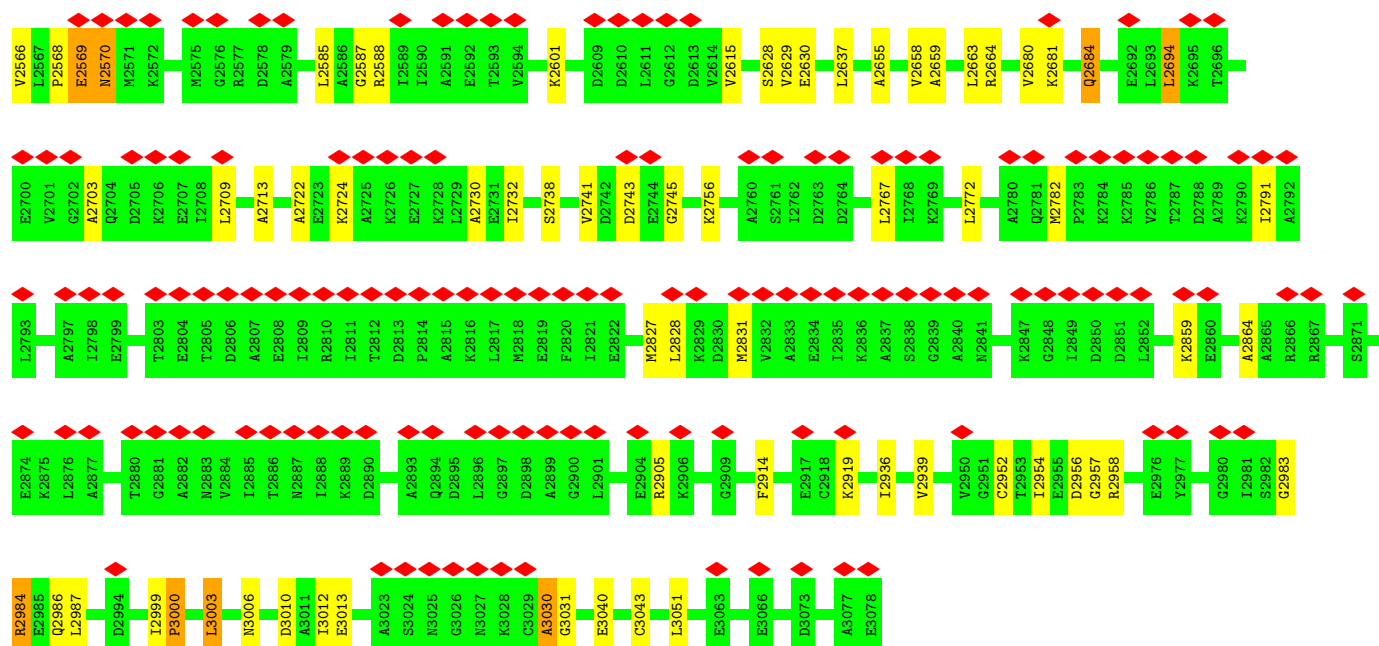
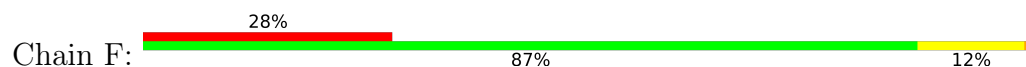




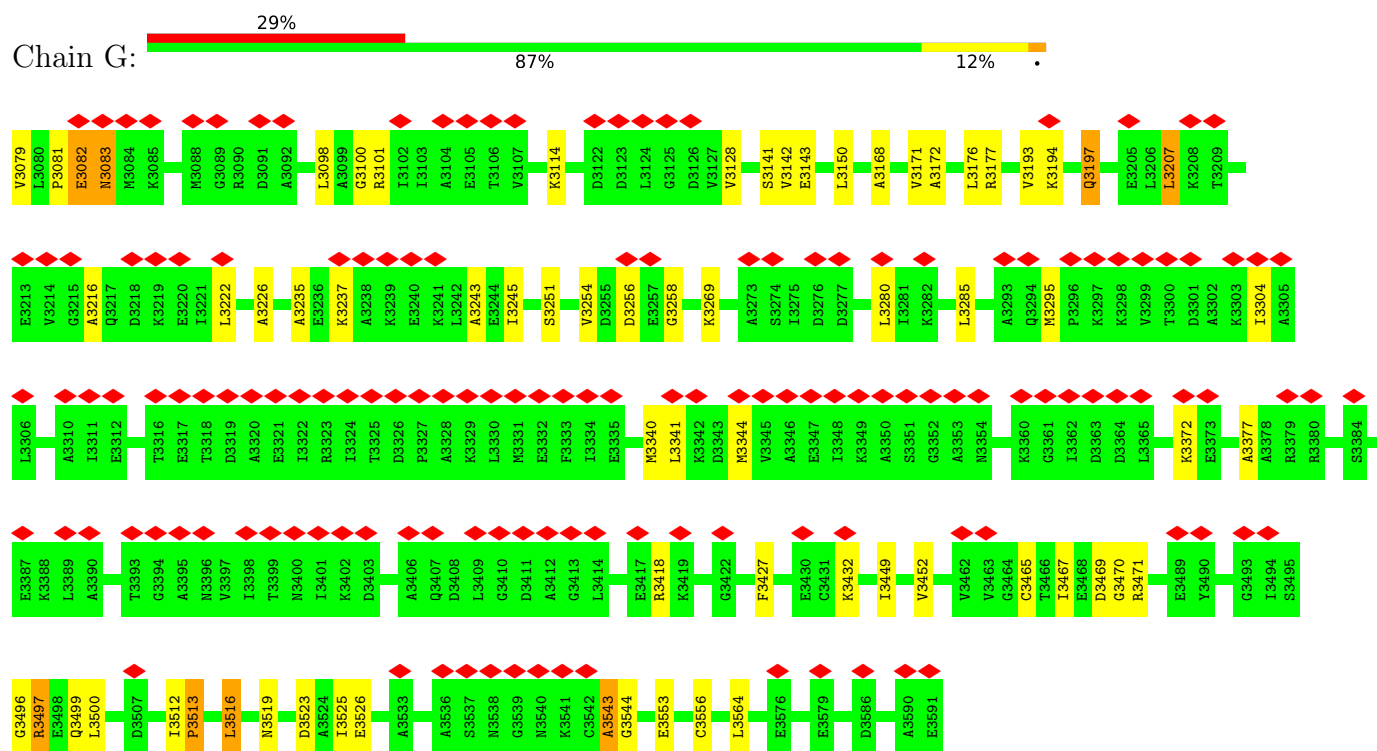
• Molecule 1: Chaperonin



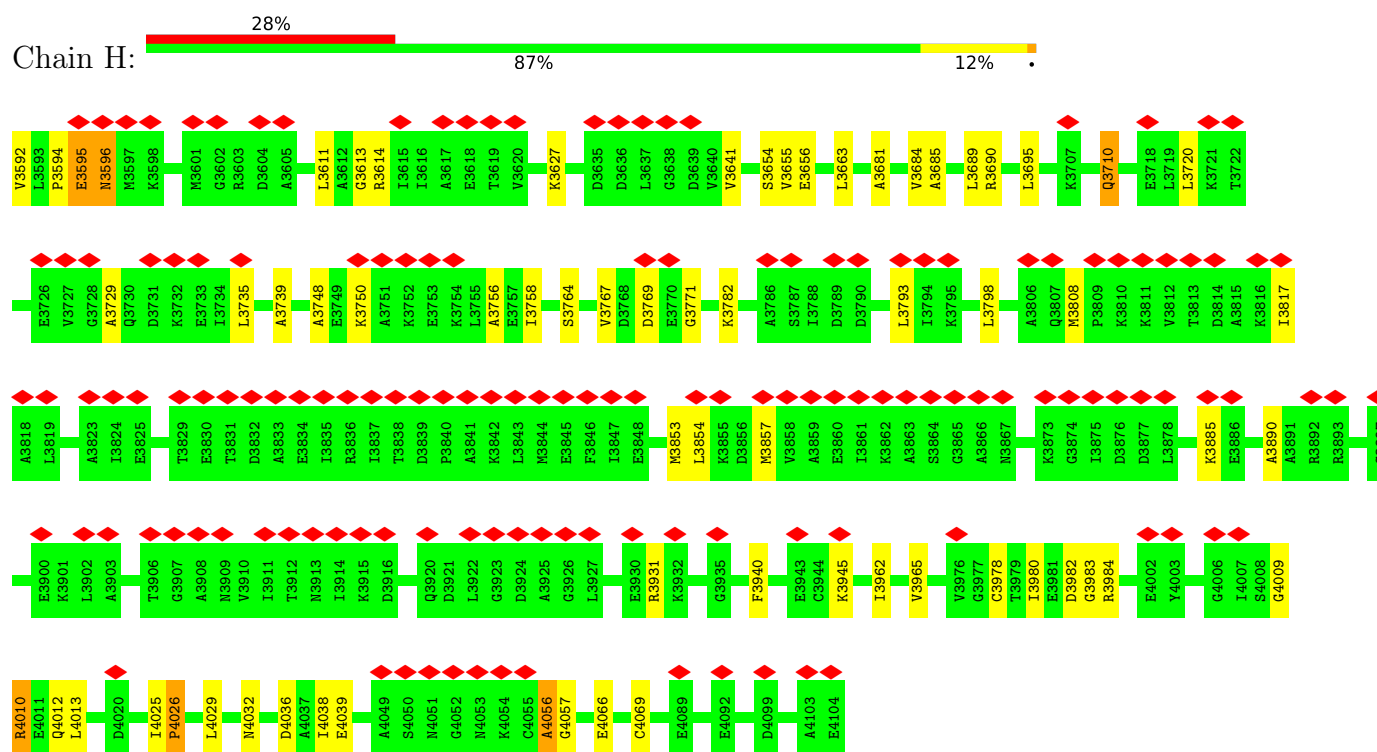
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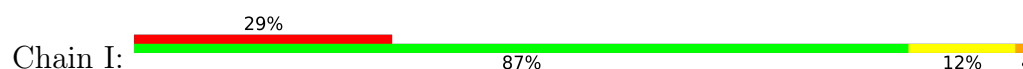
- Molecule 1: Chaperonin

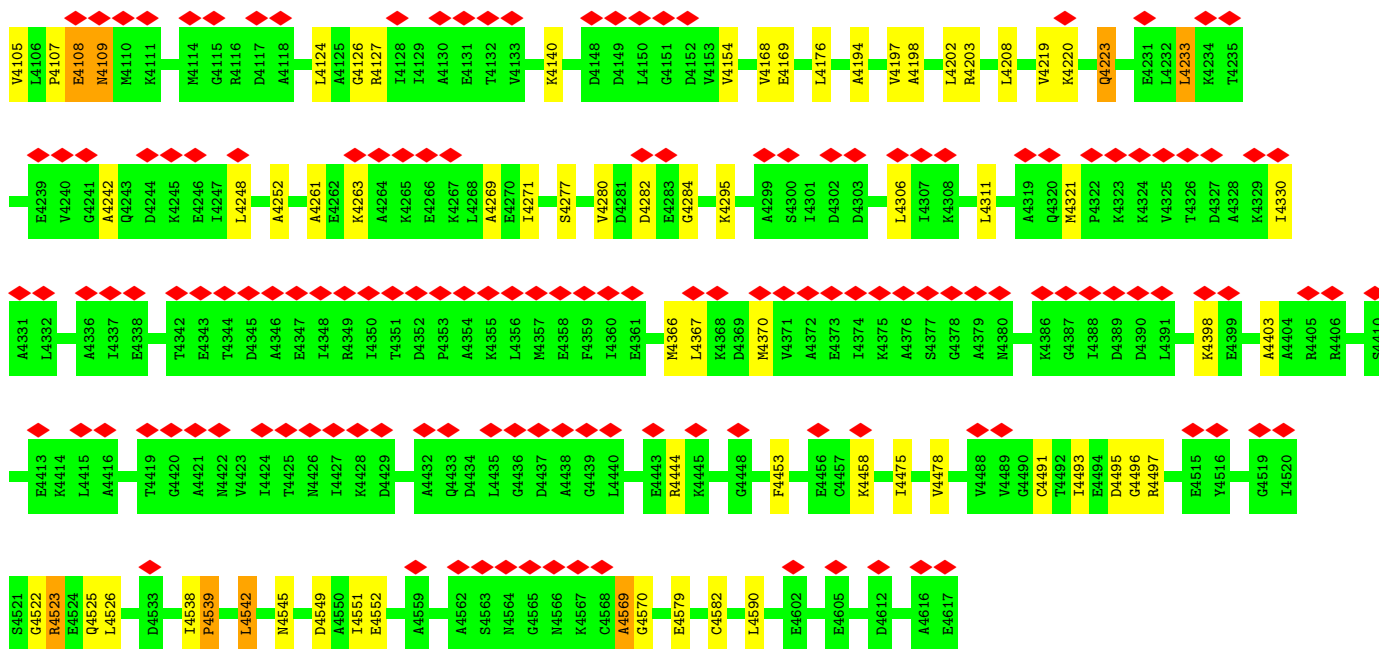


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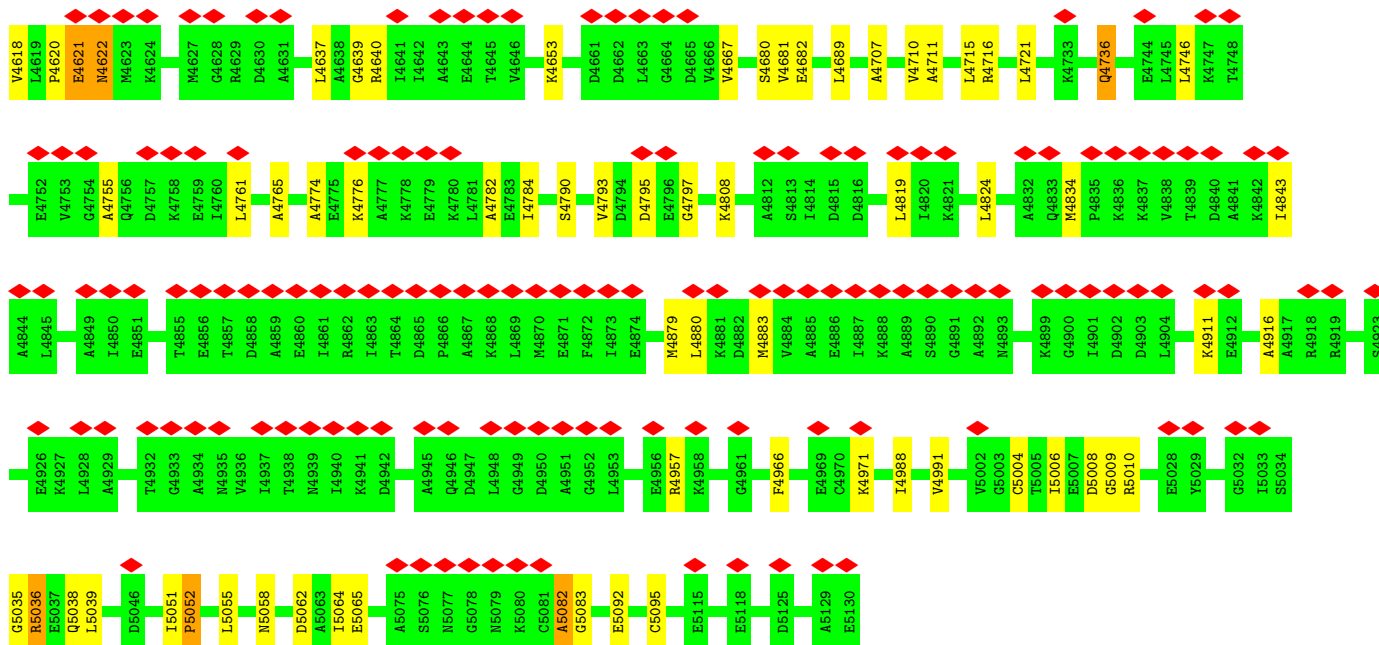
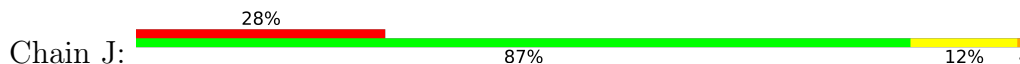


- Molecule 1: Chaperonin

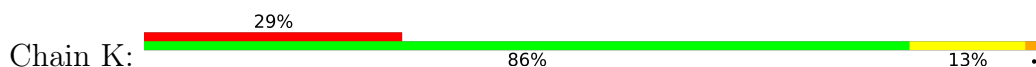


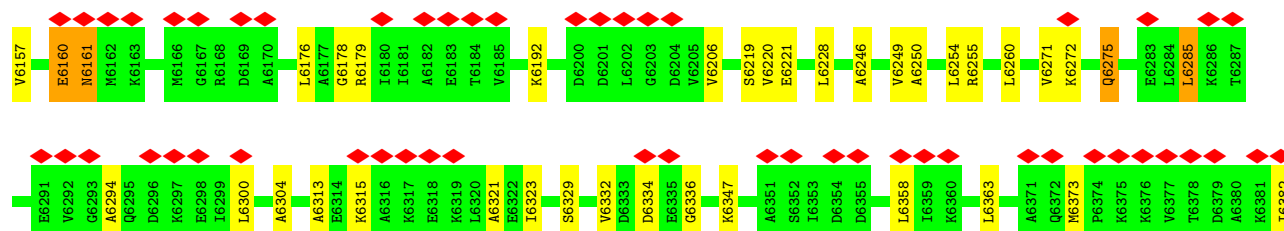


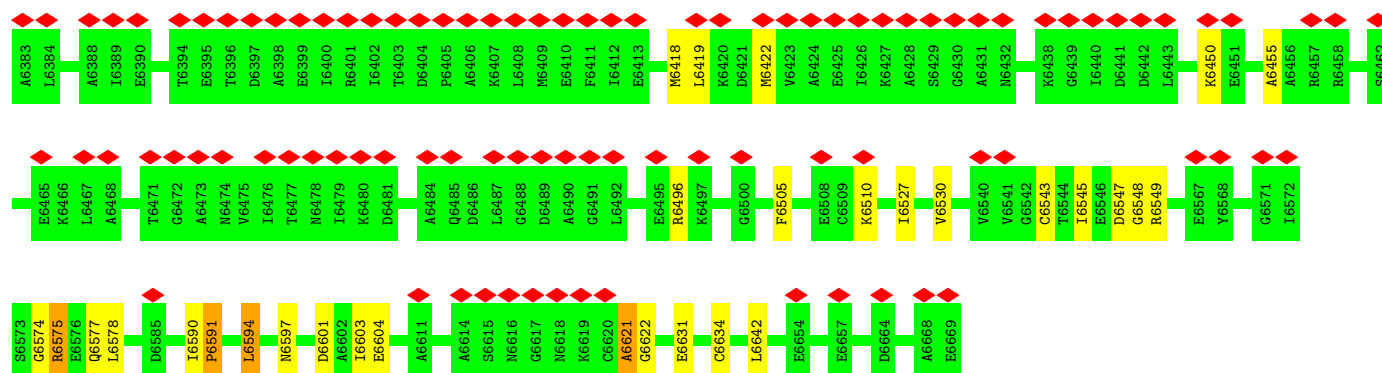
• Molecule 1: Chaperonin



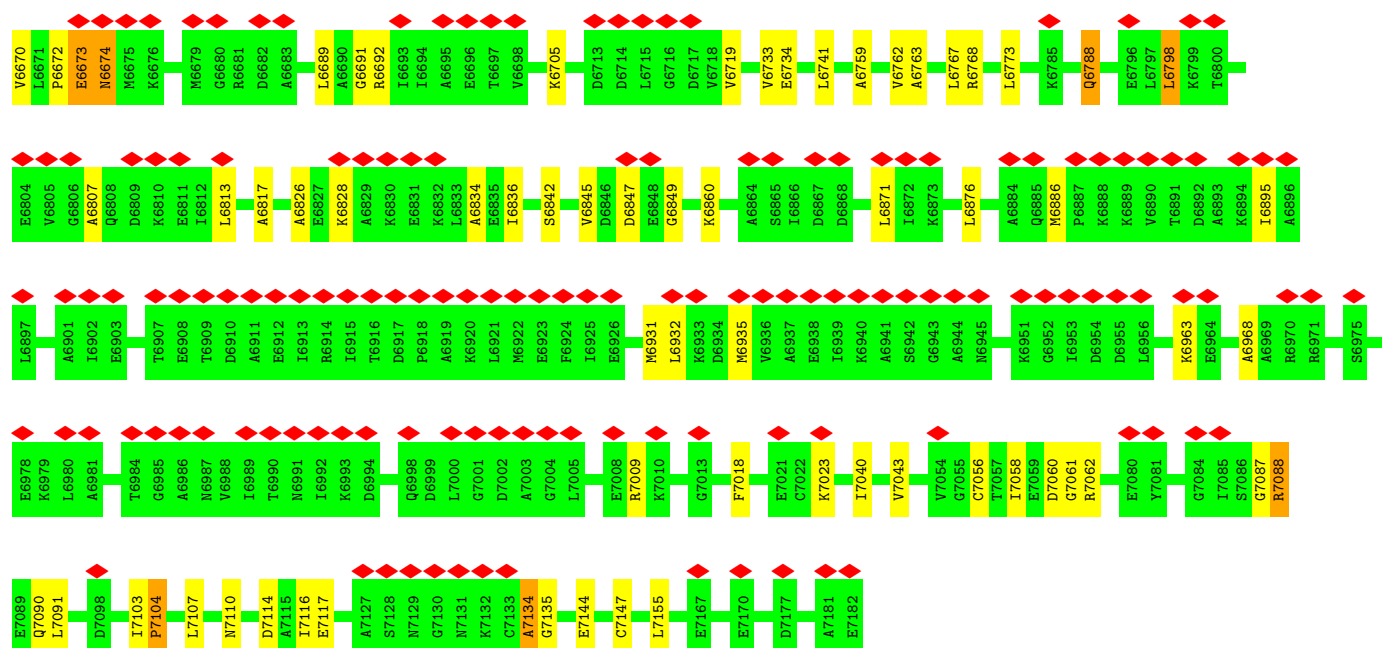
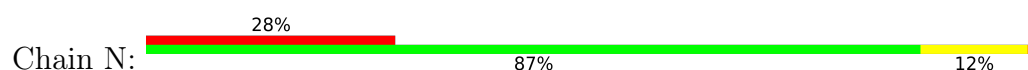
• Molecule 1: Chaperonin



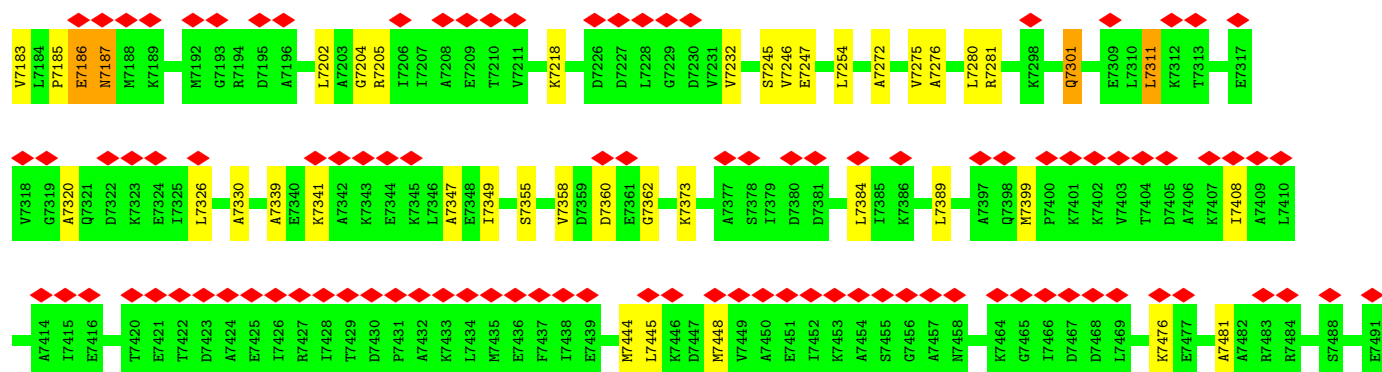
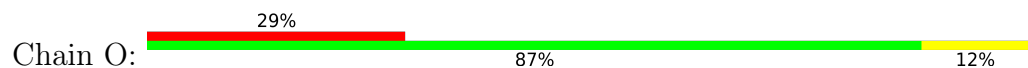


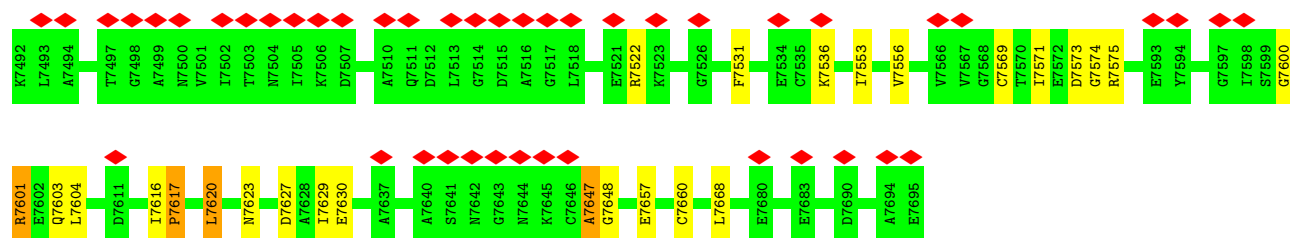


• Molecule 1: Chaperonin

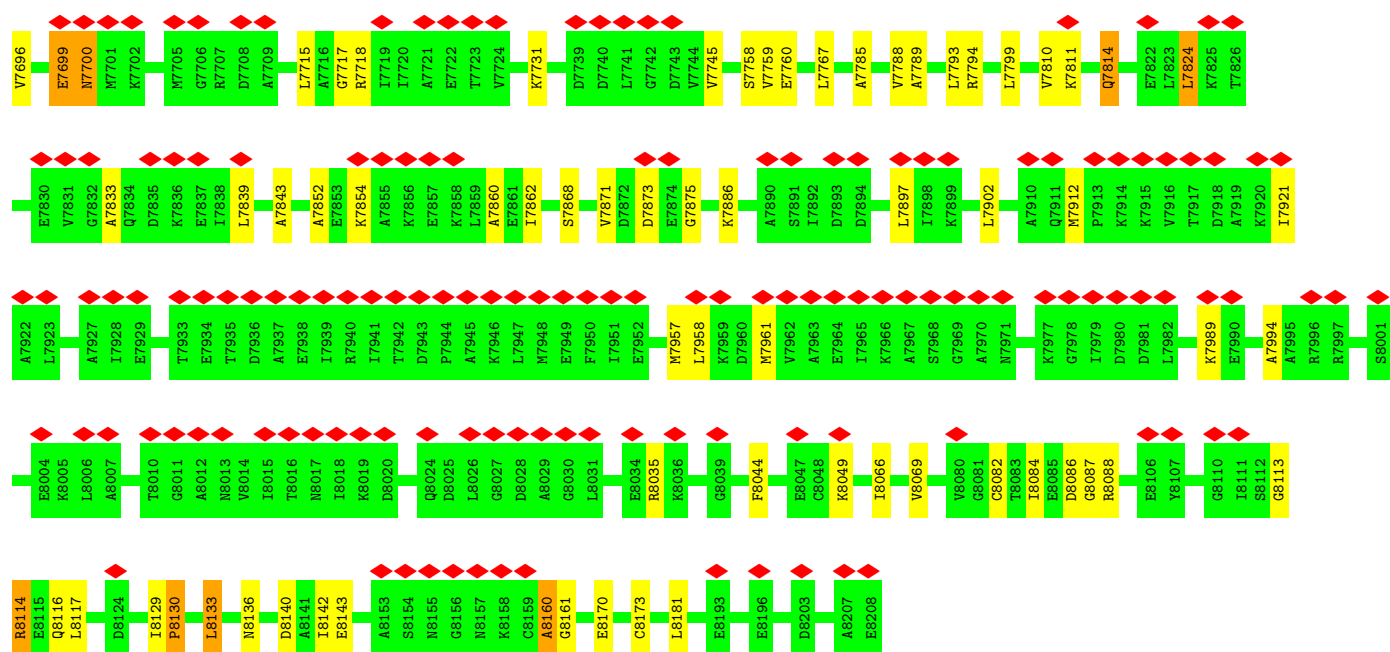
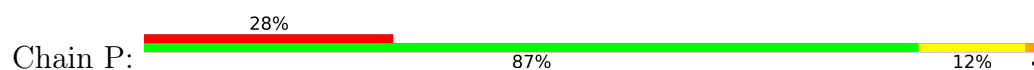


• Molecule 1: Chaperonin





• Molecule 1: Chaperonin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D8	Depositor
Number of particles used	Not provided	
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	JEOL 2010F	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	2.340	Depositor
Minimum map value	-0.420	Depositor
Average map value	0.071	Depositor
Map value standard deviation	0.257	Depositor
Recommended contour level	0.9	Depositor
Map size ($\text{\AA}$)	347.52, 347.52, 347.52	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.81, 1.81, 1.81	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	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	B	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	C	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	D	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	E	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	F	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	G	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	H	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	I	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	J	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	K	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	L	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	M	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	N	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	O	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
1	P	0.96	6/3875 (0.2%)	1.04	5/5214 (0.1%)
All	All	0.96	96/62000 (0.2%)	1.04	80/83424 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	3
1	C	0	3
1	D	0	3
1	E	0	3
1	F	0	3
1	G	0	3
1	H	0	3
1	I	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	J	0	3
1	K	0	3
1	L	0	3
1	M	0	3
1	N	0	3
1	O	0	3
1	P	0	3
All	All	0	48

All (96) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	4621	GLU	C-O	-9.56	1.12	1.23
1	L	5647	GLU	C-O	-9.56	1.12	1.23
1	N	6673	GLU	C-O	-9.56	1.12	1.23
1	P	7699	GLU	C-O	-9.56	1.12	1.23
1	K	5134	GLU	C-O	-9.54	1.12	1.23
1	M	6160	GLU	C-O	-9.54	1.12	1.23
1	I	4108	GLU	C-O	-9.52	1.12	1.23
1	O	7186	GLU	C-O	-9.52	1.12	1.23
1	A	4	GLU	C-O	-9.48	1.12	1.23
1	C	1030	GLU	C-O	-9.48	1.12	1.23
1	E	2056	GLU	C-O	-9.48	1.12	1.23
1	G	3082	GLU	C-O	-9.48	1.12	1.23
1	B	517	GLU	C-O	-9.48	1.12	1.23
1	D	1543	GLU	C-O	-9.48	1.12	1.23
1	F	2569	GLU	C-O	-9.48	1.12	1.23
1	H	3595	GLU	C-O	-9.48	1.12	1.23
1	M	6160	GLU	C-N	9.19	1.46	1.33
1	A	4	GLU	C-N	9.19	1.46	1.33
1	C	1030	GLU	C-N	9.19	1.46	1.33
1	E	2056	GLU	C-N	9.19	1.46	1.33
1	G	3082	GLU	C-N	9.19	1.46	1.33
1	K	5134	GLU	C-N	9.19	1.46	1.33
1	B	517	GLU	C-N	9.15	1.46	1.33
1	D	1543	GLU	C-N	9.15	1.46	1.33
1	F	2569	GLU	C-N	9.15	1.46	1.33
1	H	3595	GLU	C-N	9.15	1.46	1.33
1	J	4621	GLU	C-N	9.15	1.46	1.33
1	L	5647	GLU	C-N	9.15	1.46	1.33
1	I	4108	GLU	C-N	9.13	1.46	1.33
1	O	7186	GLU	C-N	9.13	1.46	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	6673	GLU	C-N	9.10	1.46	1.33
1	P	7699	GLU	C-N	9.10	1.46	1.33
1	B	978	ALA	C-O	-6.95	1.15	1.24
1	D	2004	ALA	C-O	-6.95	1.15	1.24
1	F	3030	ALA	C-O	-6.95	1.15	1.24
1	H	4056	ALA	C-O	-6.95	1.15	1.24
1	A	465	ALA	C-O	-6.90	1.15	1.24
1	C	1491	ALA	C-O	-6.90	1.15	1.24
1	E	2517	ALA	C-O	-6.90	1.15	1.24
1	G	3543	ALA	C-O	-6.90	1.15	1.24
1	I	4569	ALA	C-O	-6.90	1.15	1.24
1	K	5595	ALA	C-O	-6.90	1.15	1.24
1	J	5082	ALA	C-O	-6.86	1.15	1.24
1	L	6108	ALA	C-O	-6.86	1.15	1.24
1	N	7134	ALA	C-O	-6.86	1.15	1.24
1	P	8160	ALA	C-O	-6.86	1.15	1.24
1	M	6621	ALA	C-O	-6.84	1.15	1.24
1	O	7647	ALA	C-O	-6.84	1.15	1.24
1	J	4736	GLN	C-O	-6.65	1.16	1.24
1	P	7814	GLN	C-O	-6.65	1.16	1.24
1	L	5762	GLN	C-O	-6.58	1.16	1.24
1	N	6788	GLN	C-O	-6.58	1.16	1.24
1	A	119	GLN	C-O	-6.56	1.16	1.24
1	C	1145	GLN	C-O	-6.56	1.16	1.24
1	E	2171	GLN	C-O	-6.56	1.16	1.24
1	G	3197	GLN	C-O	-6.56	1.16	1.24
1	I	4223	GLN	C-O	-6.56	1.16	1.24
1	K	5249	GLN	C-O	-6.56	1.16	1.24
1	M	6275	GLN	C-O	-6.56	1.16	1.24
1	O	7301	GLN	C-O	-6.56	1.16	1.24
1	B	632	GLN	C-O	-6.55	1.16	1.24
1	D	1658	GLN	C-O	-6.55	1.16	1.24
1	F	2684	GLN	C-O	-6.55	1.16	1.24
1	H	3710	GLN	C-O	-6.55	1.16	1.24
1	A	119	GLN	C-N	5.41	1.40	1.33
1	C	1145	GLN	C-N	5.41	1.40	1.33
1	E	2171	GLN	C-N	5.41	1.40	1.33
1	G	3197	GLN	C-N	5.41	1.40	1.33
1	M	6275	GLN	C-N	5.41	1.40	1.33
1	O	7301	GLN	C-N	5.41	1.40	1.33
1	J	4736	GLN	C-N	5.36	1.40	1.33
1	P	7814	GLN	C-N	5.36	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	5249	GLN	C-N	5.35	1.40	1.33
1	B	948	PRO	N-CD	5.35	1.55	1.47
1	D	1974	PRO	N-CD	5.35	1.55	1.47
1	F	3000	PRO	N-CD	5.35	1.55	1.47
1	H	4026	PRO	N-CD	5.35	1.55	1.47
1	I	4223	GLN	C-N	5.35	1.40	1.33
1	J	5052	PRO	N-CD	5.35	1.55	1.47
1	L	6078	PRO	N-CD	5.35	1.55	1.47
1	M	6591	PRO	N-CD	5.35	1.55	1.47
1	O	7617	PRO	N-CD	5.35	1.55	1.47
1	B	632	GLN	C-N	5.32	1.40	1.33
1	D	1658	GLN	C-N	5.32	1.40	1.33
1	F	2684	GLN	C-N	5.32	1.40	1.33
1	H	3710	GLN	C-N	5.32	1.40	1.33
1	L	5762	GLN	C-N	5.32	1.40	1.33
1	N	6788	GLN	C-N	5.32	1.40	1.33
1	N	7104	PRO	N-CD	5.31	1.55	1.47
1	P	8130	PRO	N-CD	5.31	1.55	1.47
1	A	435	PRO	N-CD	5.28	1.55	1.47
1	C	1461	PRO	N-CD	5.28	1.55	1.47
1	E	2487	PRO	N-CD	5.28	1.55	1.47
1	G	3513	PRO	N-CD	5.28	1.55	1.47
1	I	4539	PRO	N-CD	5.28	1.55	1.47
1	K	5565	PRO	N-CD	5.28	1.55	1.47

All (80) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	4108	GLU	CA-C-O	-6.62	113.91	121.19
1	O	7186	GLU	CA-C-O	-6.62	113.91	121.19
1	N	6673	GLU	CA-C-O	-6.62	113.91	121.19
1	P	7699	GLU	CA-C-O	-6.62	113.91	121.19
1	J	4621	GLU	CA-C-O	-6.60	113.93	121.19
1	L	5647	GLU	CA-C-O	-6.60	113.93	121.19
1	A	4	GLU	CA-C-O	-6.58	113.96	121.19
1	C	1030	GLU	CA-C-O	-6.58	113.96	121.19
1	E	2056	GLU	CA-C-O	-6.58	113.96	121.19
1	G	3082	GLU	CA-C-O	-6.58	113.96	121.19
1	B	517	GLU	CA-C-O	-6.57	113.97	121.19
1	D	1543	GLU	CA-C-O	-6.57	113.97	121.19
1	F	2569	GLU	CA-C-O	-6.57	113.97	121.19
1	H	3595	GLU	CA-C-O	-6.57	113.97	121.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	5134	GLU	CA-C-O	-6.56	113.98	121.19
1	M	6160	GLU	CA-C-O	-6.56	113.98	121.19
1	K	5134	GLU	N-CA-C	-6.30	101.09	110.23
1	I	4108	GLU	N-CA-C	-6.29	101.11	110.23
1	M	6160	GLU	N-CA-C	-6.29	101.11	110.23
1	J	4621	GLU	N-CA-C	-6.28	101.12	110.23
1	L	5647	GLU	N-CA-C	-6.28	101.12	110.23
1	N	6673	GLU	N-CA-C	-6.28	101.12	110.23
1	P	7699	GLU	N-CA-C	-6.28	101.12	110.23
1	O	7186	GLU	N-CA-C	-6.28	101.12	110.23
1	B	517	GLU	N-CA-C	-6.27	101.14	110.23
1	D	1543	GLU	N-CA-C	-6.27	101.14	110.23
1	F	2569	GLU	N-CA-C	-6.27	101.14	110.23
1	H	3595	GLU	N-CA-C	-6.27	101.14	110.23
1	A	4	GLU	N-CA-C	-6.26	101.15	110.23
1	C	1030	GLU	N-CA-C	-6.26	101.15	110.23
1	E	2056	GLU	N-CA-C	-6.26	101.15	110.23
1	G	3082	GLU	N-CA-C	-6.26	101.15	110.23
1	J	5095	CYS	N-CA-CB	-5.33	102.34	110.07
1	L	6121	CYS	N-CA-CB	-5.33	102.34	110.07
1	N	7147	CYS	N-CA-CB	-5.33	102.34	110.07
1	P	8173	CYS	N-CA-CB	-5.33	102.34	110.07
1	I	4582	CYS	N-CA-CB	-5.33	102.34	110.07
1	K	5608	CYS	N-CA-CB	-5.33	102.34	110.07
1	M	6634	CYS	N-CA-CB	-5.33	102.34	110.07
1	O	7660	CYS	N-CA-CB	-5.33	102.34	110.07
1	B	991	CYS	N-CA-CB	-5.30	102.39	110.07
1	D	2017	CYS	N-CA-CB	-5.30	102.39	110.07
1	F	3043	CYS	N-CA-CB	-5.30	102.39	110.07
1	H	4069	CYS	N-CA-CB	-5.30	102.39	110.07
1	A	478	CYS	N-CA-CB	-5.29	102.39	110.07
1	C	1504	CYS	N-CA-CB	-5.29	102.39	110.07
1	E	2530	CYS	N-CA-CB	-5.29	102.39	110.07
1	G	3556	CYS	N-CA-CB	-5.29	102.39	110.07
1	L	5762	GLN	CA-C-O	-5.25	115.31	120.82
1	N	6788	GLN	CA-C-O	-5.25	115.31	120.82
1	B	632	GLN	CA-C-O	-5.21	115.35	120.82
1	D	1658	GLN	CA-C-O	-5.21	115.35	120.82
1	F	2684	GLN	CA-C-O	-5.21	115.35	120.82
1	H	3710	GLN	CA-C-O	-5.21	115.35	120.82
1	J	4736	GLN	CA-C-O	-5.20	115.36	120.82
1	P	7814	GLN	CA-C-O	-5.20	115.36	120.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	119	GLN	CA-C-O	-5.17	115.39	120.82
1	C	1145	GLN	CA-C-O	-5.17	115.39	120.82
1	E	2171	GLN	CA-C-O	-5.17	115.39	120.82
1	G	3197	GLN	CA-C-O	-5.17	115.39	120.82
1	I	4223	GLN	CA-C-O	-5.17	115.39	120.82
1	K	5249	GLN	CA-C-O	-5.17	115.39	120.82
1	M	6275	GLN	CA-C-O	-5.17	115.39	120.82
1	O	7301	GLN	CA-C-O	-5.17	115.39	120.82
1	K	5517	CYS	N-CA-CB	-5.10	102.62	110.12
1	M	6543	CYS	N-CA-CB	-5.10	102.62	110.12
1	B	900	CYS	N-CA-CB	-5.10	102.62	110.12
1	D	1926	CYS	N-CA-CB	-5.10	102.62	110.12
1	F	2952	CYS	N-CA-CB	-5.10	102.62	110.12
1	H	3978	CYS	N-CA-CB	-5.10	102.62	110.12
1	A	387	CYS	N-CA-CB	-5.09	102.63	110.12
1	C	1413	CYS	N-CA-CB	-5.09	102.63	110.12
1	E	2439	CYS	N-CA-CB	-5.09	102.63	110.12
1	G	3465	CYS	N-CA-CB	-5.09	102.63	110.12
1	I	4491	CYS	N-CA-CB	-5.09	102.64	110.12
1	O	7569	CYS	N-CA-CB	-5.09	102.64	110.12
1	J	5004	CYS	N-CA-CB	-5.09	102.64	110.12
1	L	6030	CYS	N-CA-CB	-5.09	102.64	110.12
1	N	7056	CYS	N-CA-CB	-5.09	102.64	110.12
1	P	8082	CYS	N-CA-CB	-5.09	102.64	110.12

There are no chirality outliers.

All (48) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	119	GLN	Mainchain
1	A	138	ALA	Mainchain
1	A	475	GLU	Mainchain
1	B	632	GLN	Mainchain
1	B	651	ALA	Mainchain
1	B	988	GLU	Mainchain
1	C	1145	GLN	Mainchain
1	C	1164	ALA	Mainchain
1	C	1501	GLU	Mainchain
1	D	1658	GLN	Mainchain
1	D	1677	ALA	Mainchain
1	D	2014	GLU	Mainchain
1	E	2171	GLN	Mainchain

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Mol	Chain	Res	Type	Group
1	E	2190	ALA	Mainchain
1	E	2527	GLU	Mainchain
1	F	2684	GLN	Mainchain
1	F	2703	ALA	Mainchain
1	F	3040	GLU	Mainchain
1	G	3197	GLN	Mainchain
1	G	3216	ALA	Mainchain
1	G	3553	GLU	Mainchain
1	H	3710	GLN	Mainchain
1	H	3729	ALA	Mainchain
1	H	4066	GLU	Mainchain
1	I	4223	GLN	Mainchain
1	I	4242	ALA	Mainchain
1	I	4579	GLU	Mainchain
1	J	4736	GLN	Mainchain
1	J	4755	ALA	Mainchain
1	J	5092	GLU	Mainchain
1	K	5249	GLN	Mainchain
1	K	5268	ALA	Mainchain
1	K	5605	GLU	Mainchain
1	L	5762	GLN	Mainchain
1	L	5781	ALA	Mainchain
1	L	6118	GLU	Mainchain
1	M	6275	GLN	Mainchain
1	M	6294	ALA	Mainchain
1	M	6631	GLU	Mainchain
1	N	6788	GLN	Mainchain
1	N	6807	ALA	Mainchain
1	N	7144	GLU	Mainchain
1	O	7301	GLN	Mainchain
1	O	7320	ALA	Mainchain
1	O	7657	GLU	Mainchain
1	P	7814	GLN	Mainchain
1	P	7833	ALA	Mainchain
1	P	8170	GLU	Mainchain

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	3852	0	3996	92	0
1	B	3852	0	3993	89	0
1	C	3852	0	3993	87	0
1	D	3852	0	3993	86	0
1	E	3852	0	3993	85	0
1	F	3852	0	3993	89	0
1	G	3852	0	3993	89	0
1	H	3852	0	3993	89	0
1	I	3852	0	3993	89	0
1	J	3852	0	3993	89	0
1	K	3852	0	3993	91	0
1	L	3852	0	3993	87	0
1	M	3852	0	3993	87	0
1	N	3852	0	3993	86	0
1	O	3852	0	3993	86	0
1	P	3852	0	3993	89	0
All	All	61632	0	63891	945	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 8.

All (945) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1984:ASP:OD1	1:N:7091:LEU:HD21	1.45	1.17
1:D:1961:LEU:HD21	1:N:7114:ASP:OD1	1.45	1.17
1:A:422:LEU:HD21	1:I:4549:ASP:OD1	1.44	1.16
1:G:3500:LEU:HD21	1:K:5575:ASP:OD1	1.44	1.16
1:A:445:ASP:OD1	1:I:4526:LEU:HD21	1.44	1.16
1:B:935:LEU:HD21	1:P:8140:ASP:OD1	1.45	1.16
1:G:3523:ASP:OD1	1:K:5552:LEU:HD21	1.44	1.16
1:H:4013:LEU:HD21	1:J:5062:ASP:OD1	1.45	1.16
1:F:3010:ASP:OD1	1:L:6065:LEU:HD21	1.45	1.16
1:H:4036:ASP:OD1	1:J:5039:LEU:HD21	1.45	1.16
1:F:2987:LEU:HD21	1:L:6088:ASP:OD1	1.45	1.15
1:B:958:ASP:OD1	1:P:8117:LEU:HD21	1.45	1.15
1:C:1448:LEU:HD21	1:O:7627:ASP:OD1	1.44	1.15
1:E:2497:ASP:OD1	1:M:6578:LEU:HD21	1.44	1.15
1:A:421:GLN:NE2	1:I:4552:GLU:OE2	1.81	1.14
1:G:3526:GLU:OE2	1:K:5551:GLN:NE2	1.81	1.14
1:E:2474:LEU:HD21	1:M:6601:ASP:OD1	1.44	1.13
1:C:1471:ASP:OD1	1:O:7604:LEU:HD21	1.44	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1447:GLN:NE2	1:O:7630:GLU:OE2	1.81	1.12
1:D:1987:GLU:OE2	1:N:7090:GLN:NE2	1.81	1.12
1:F:3013:GLU:OE2	1:L:6064:GLN:NE2	1.81	1.12
1:D:1960:GLN:NE2	1:N:7117:GLU:OE2	1.81	1.12
1:E:2500:GLU:OE2	1:M:6577:GLN:NE2	1.81	1.12
1:B:934:GLN:NE2	1:P:8143:GLU:OE2	1.81	1.12
1:A:448:GLU:OE2	1:I:4525:GLN:NE2	1.81	1.12
1:H:4012:GLN:NE2	1:J:5065:GLU:OE2	1.81	1.12
1:G:3499:GLN:NE2	1:K:5578:GLU:OE2	1.81	1.12
1:H:4039:GLU:OE2	1:J:5038:GLN:NE2	1.81	1.12
1:C:1474:GLU:OE2	1:O:7603:GLN:NE2	1.81	1.11
1:E:2473:GLN:NE2	1:M:6604:GLU:OE2	1.81	1.11
1:F:2986:GLN:NE2	1:L:6091:GLU:OE2	1.81	1.10
1:B:961:GLU:OE2	1:P:8116:GLN:NE2	1.81	1.10
1:F:2986:GLN:NE2	1:L:6091:GLU:CD	2.15	1.05
1:B:961:GLU:CD	1:P:8116:GLN:NE2	2.15	1.05
1:C:1447:GLN:NE2	1:O:7630:GLU:CD	2.15	1.05
1:D:1960:GLN:NE2	1:N:7117:GLU:CD	2.15	1.05
1:D:1987:GLU:CD	1:N:7090:GLN:NE2	2.15	1.05
1:E:2500:GLU:CD	1:M:6577:GLN:NE2	2.15	1.05
1:A:448:GLU:CD	1:I:4525:GLN:NE2	2.15	1.05
1:G:3499:GLN:NE2	1:K:5578:GLU:CD	2.15	1.04
1:E:2473:GLN:NE2	1:M:6604:GLU:CD	2.15	1.04
1:C:1474:GLU:CD	1:O:7603:GLN:NE2	2.15	1.04
1:H:4012:GLN:NE2	1:J:5065:GLU:CD	2.15	1.04
1:H:4039:GLU:CD	1:J:5038:GLN:NE2	2.15	1.04
1:F:3013:GLU:CD	1:L:6064:GLN:NE2	2.15	1.04
1:B:934:GLN:NE2	1:P:8143:GLU:CD	2.15	1.03
1:G:3526:GLU:CD	1:K:5551:GLN:NE2	2.15	1.03
1:A:421:GLN:NE2	1:I:4552:GLU:CD	2.15	1.02
1:D:1960:GLN:CD	1:N:7117:GLU:OE1	2.10	0.94
1:D:1987:GLU:OE1	1:N:7090:GLN:CD	2.10	0.94
1:A:421:GLN:CD	1:I:4552:GLU:OE1	2.10	0.94
1:G:3526:GLU:OE1	1:K:5551:GLN:CD	2.10	0.94
1:C:1447:GLN:CD	1:O:7630:GLU:OE1	2.10	0.94
1:E:2500:GLU:OE1	1:M:6577:GLN:CD	2.10	0.94
1:B:934:GLN:CD	1:P:8143:GLU:OE1	2.10	0.94
1:B:961:GLU:OE1	1:P:8116:GLN:CD	2.10	0.94
1:C:1474:GLU:OE1	1:O:7603:GLN:CD	2.10	0.94
1:E:2473:GLN:CD	1:M:6604:GLU:OE1	2.10	0.94
1:F:3013:GLU:OE1	1:L:6064:GLN:CD	2.10	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2986:GLN:CD	1:L:6091:GLU:OE1	2.10	0.94
1:A:448:GLU:OE1	1:I:4525:GLN:CD	2.10	0.93
1:H:4012:GLN:CD	1:J:5065:GLU:OE1	2.10	0.93
1:H:4039:GLU:OE1	1:J:5038:GLN:CD	2.10	0.93
1:G:3499:GLN:CD	1:K:5578:GLU:OE1	2.10	0.93
1:B:960:ILE:CB	1:P:8117:LEU:HG	2.05	0.87
1:C:1473:ILE:CB	1:O:7604:LEU:HG	2.05	0.87
1:A:422:LEU:HG	1:I:4551:ILE:CB	2.05	0.87
1:E:2474:LEU:HG	1:M:6603:ILE:CB	2.05	0.87
1:F:2987:LEU:HG	1:L:6090:ILE:CB	2.05	0.87
1:G:3525:ILE:CB	1:K:5552:LEU:HG	2.05	0.87
1:C:1473:ILE:HB	1:O:7604:LEU:HG	1.57	0.87
1:D:1961:LEU:HG	1:N:7116:ILE:CB	2.05	0.87
1:D:1986:ILE:CB	1:N:7091:LEU:HG	2.05	0.87
1:E:2474:LEU:HG	1:M:6603:ILE:HB	1.57	0.87
1:C:1448:LEU:HG	1:O:7629:ILE:CB	2.05	0.86
1:D:1961:LEU:HG	1:N:7116:ILE:HB	1.57	0.86
1:D:1986:ILE:HB	1:N:7091:LEU:HG	1.57	0.86
1:E:2499:ILE:CB	1:M:6578:LEU:HG	2.05	0.86
1:B:935:LEU:HG	1:P:8142:ILE:CB	2.05	0.86
1:G:3500:LEU:HG	1:K:5577:ILE:CB	2.05	0.86
1:F:2987:LEU:HG	1:L:6090:ILE:HB	1.57	0.86
1:A:447:ILE:CB	1:I:4526:LEU:HG	2.05	0.86
1:B:960:ILE:HB	1:P:8117:LEU:HG	1.57	0.86
1:F:3012:ILE:CB	1:L:6065:LEU:HG	2.05	0.86
1:H:4038:ILE:CB	1:J:5039:LEU:HG	2.05	0.86
1:H:4013:LEU:HG	1:J:5064:ILE:CB	2.05	0.86
1:C:1448:LEU:HG	1:O:7629:ILE:HB	1.57	0.86
1:E:2499:ILE:HB	1:M:6578:LEU:HG	1.57	0.85
1:A:422:LEU:CD2	1:I:4549:ASP:OD1	2.25	0.85
1:G:3523:ASP:OD1	1:K:5552:LEU:CD2	2.25	0.85
1:A:447:ILE:HB	1:I:4526:LEU:HG	1.57	0.85
1:G:3500:LEU:HG	1:K:5577:ILE:HB	1.57	0.85
1:B:935:LEU:HG	1:P:8142:ILE:HB	1.57	0.84
1:H:4013:LEU:CD2	1:J:5062:ASP:OD1	2.25	0.84
1:A:445:ASP:OD1	1:I:4526:LEU:CD2	2.25	0.84
1:F:3012:ILE:HB	1:L:6065:LEU:HG	1.57	0.84
1:H:4036:ASP:OD1	1:J:5039:LEU:CD2	2.25	0.84
1:G:3500:LEU:CD2	1:K:5575:ASP:OD1	2.25	0.84
1:H:4013:LEU:HG	1:J:5064:ILE:HB	1.57	0.84
1:H:4038:ILE:HB	1:J:5039:LEU:HG	1.57	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:LEU:HG	1:I:4551:ILE:HB	1.57	0.84
1:G:3525:ILE:HB	1:K:5552:LEU:HG	1.57	0.84
1:F:3010:ASP:OD1	1:L:6065:LEU:CD2	2.25	0.84
1:B:935:LEU:CD2	1:P:8140:ASP:OD1	2.25	0.84
1:C:1471:ASP:OD1	1:O:7604:LEU:CD2	2.25	0.83
1:E:2474:LEU:CD2	1:M:6601:ASP:OD1	2.25	0.83
1:C:1448:LEU:CG	1:O:7629:ILE:HB	2.09	0.83
1:C:1473:ILE:HB	1:O:7604:LEU:CG	2.09	0.83
1:E:2474:LEU:CG	1:M:6603:ILE:HB	2.09	0.83
1:E:2499:ILE:HB	1:M:6578:LEU:CG	2.09	0.83
1:B:960:ILE:HB	1:P:8117:LEU:CG	2.09	0.83
1:D:1961:LEU:CG	1:N:7116:ILE:HB	2.09	0.83
1:F:2987:LEU:CG	1:L:6090:ILE:HB	2.09	0.83
1:G:3500:LEU:CG	1:K:5577:ILE:HB	2.09	0.83
1:A:422:LEU:CG	1:I:4551:ILE:HB	2.09	0.83
1:A:447:ILE:HB	1:I:4526:LEU:CG	2.09	0.83
1:D:1986:ILE:HB	1:N:7091:LEU:CG	2.09	0.83
1:G:3525:ILE:HB	1:K:5552:LEU:CG	2.09	0.83
1:B:935:LEU:CG	1:P:8142:ILE:HB	2.09	0.82
1:D:1984:ASP:OD1	1:N:7091:LEU:CD2	2.25	0.82
1:D:1961:LEU:CD2	1:N:7114:ASP:OD1	2.25	0.82
1:F:3012:ILE:HB	1:L:6065:LEU:CG	2.09	0.82
1:H:4038:ILE:HB	1:J:5039:LEU:CG	2.09	0.82
1:H:4013:LEU:CG	1:J:5064:ILE:HB	2.09	0.82
1:B:958:ASP:OD1	1:P:8117:LEU:CD2	2.25	0.81
1:F:2987:LEU:CD2	1:L:6088:ASP:OD1	2.25	0.81
1:E:2497:ASP:OD1	1:M:6578:LEU:CD2	2.25	0.81
1:C:1448:LEU:CD2	1:O:7627:ASP:OD1	2.25	0.80
1:B:961:GLU:OE1	1:P:8116:GLN:NE2	2.17	0.77
1:F:2986:GLN:NE2	1:L:6091:GLU:OE1	2.17	0.77
1:C:1474:GLU:OE1	1:O:7603:GLN:NE2	2.17	0.77
1:E:2473:GLN:NE2	1:M:6604:GLU:OE1	2.17	0.77
1:D:1960:GLN:NE2	1:N:7117:GLU:OE1	2.17	0.77
1:E:2500:GLU:OE1	1:M:6577:GLN:NE2	2.17	0.77
1:D:1987:GLU:OE1	1:N:7090:GLN:NE2	2.17	0.76
1:C:1447:GLN:NE2	1:O:7630:GLU:OE1	2.17	0.76
1:G:3526:GLU:OE1	1:K:5551:GLN:NE2	2.17	0.76
1:A:421:GLN:NE2	1:I:4552:GLU:OE1	2.17	0.76
1:A:448:GLU:OE1	1:I:4525:GLN:NE2	2.17	0.76
1:G:3499:GLN:NE2	1:K:5578:GLU:OE1	2.17	0.76
1:H:4038:ILE:CG2	1:J:5039:LEU:HG	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:4013:LEU:HG	1:J:5064:ILE:CG2	2.19	0.73
1:B:960:ILE:CG2	1:P:8117:LEU:HG	2.19	0.73
1:F:2987:LEU:HG	1:L:6090:ILE:CG2	2.19	0.73
1:C:1473:ILE:CG2	1:O:7604:LEU:HG	2.19	0.73
1:E:2474:LEU:HG	1:M:6603:ILE:CG2	2.19	0.73
1:A:447:ILE:CG2	1:I:4526:LEU:HG	2.19	0.73
1:D:1961:LEU:HG	1:N:7116:ILE:CG2	2.19	0.73
1:D:1986:ILE:CG2	1:N:7091:LEU:HG	2.19	0.73
1:G:3500:LEU:HG	1:K:5577:ILE:CG2	2.19	0.73
1:M:6590:ILE:HB	1:M:6591:PRO:HD3	1.71	0.73
1:A:422:LEU:HG	1:I:4551:ILE:CG2	2.19	0.72
1:B:935:LEU:HG	1:P:8142:ILE:CG2	2.19	0.72
1:C:1460:ILE:HB	1:C:1461:PRO:HD3	1.71	0.72
1:F:3012:ILE:CG2	1:L:6065:LEU:HG	2.18	0.72
1:A:434:ILE:HB	1:A:435:PRO:HD3	1.71	0.72
1:K:5564:ILE:HB	1:K:5565:PRO:HD3	1.71	0.72
1:G:3525:ILE:CG2	1:K:5552:LEU:HG	2.19	0.72
1:C:1448:LEU:HG	1:O:7629:ILE:CG2	2.19	0.72
1:D:1973:ILE:HB	1:D:1974:PRO:HD3	1.71	0.72
1:N:7103:ILE:HB	1:N:7104:PRO:HD3	1.71	0.72
1:E:2499:ILE:CG2	1:M:6578:LEU:HG	2.19	0.72
1:F:2999:ILE:HB	1:F:3000:PRO:HD3	1.71	0.71
1:P:8129:ILE:HB	1:P:8130:PRO:HD3	1.71	0.71
1:B:947:ILE:HB	1:B:948:PRO:HD3	1.71	0.71
1:F:3013:GLU:OE1	1:L:6064:GLN:NE2	2.17	0.71
1:H:4039:GLU:OE1	1:J:5038:GLN:NE2	2.17	0.71
1:J:5051:ILE:HB	1:J:5052:PRO:HD3	1.71	0.71
1:I:4538:ILE:HB	1:I:4539:PRO:HD3	1.71	0.71
1:L:6077:ILE:HB	1:L:6078:PRO:HD3	1.71	0.71
1:G:3512:ILE:HB	1:G:3513:PRO:HD3	1.71	0.71
1:H:4025:ILE:HB	1:H:4026:PRO:HD3	1.71	0.71
1:B:934:GLN:NE2	1:P:8143:GLU:OE1	2.17	0.71
1:H:4012:GLN:NE2	1:J:5065:GLU:OE1	2.17	0.71
1:E:2486:ILE:HB	1:E:2487:PRO:HD3	1.71	0.70
1:O:7616:ILE:HB	1:O:7617:PRO:HD3	1.71	0.70
1:B:960:ILE:HB	1:P:8117:LEU:CD2	2.22	0.70
1:F:2987:LEU:CD2	1:L:6090:ILE:HB	2.22	0.70
1:H:4013:LEU:CD2	1:J:5064:ILE:HB	2.22	0.70
1:H:4038:ILE:HB	1:J:5039:LEU:CD2	2.22	0.69
1:A:447:ILE:HB	1:I:4526:LEU:CD2	2.22	0.69
1:G:3500:LEU:CD2	1:K:5577:ILE:HB	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1448:LEU:CD2	1:O:7629:ILE:HB	2.22	0.69
1:G:3525:ILE:HB	1:K:5552:LEU:CD2	2.22	0.69
1:A:422:LEU:CD2	1:I:4551:ILE:HB	2.22	0.69
1:D:1986:ILE:HB	1:N:7091:LEU:CD2	2.22	0.69
1:E:2474:LEU:CD2	1:M:6603:ILE:HB	2.22	0.69
1:E:2499:ILE:HB	1:M:6578:LEU:CD2	2.22	0.69
1:D:1961:LEU:CD2	1:N:7116:ILE:HB	2.22	0.69
1:F:3012:ILE:HB	1:L:6065:LEU:CD2	2.22	0.69
1:B:935:LEU:CD2	1:P:8142:ILE:HB	2.22	0.69
1:C:1473:ILE:HB	1:O:7604:LEU:CD2	2.22	0.69
1:B:960:ILE:HG21	1:P:8117:LEU:HG	1.77	0.66
1:F:2987:LEU:HG	1:L:6090:ILE:HG21	1.77	0.66
1:A:447:ILE:HG21	1:I:4526:LEU:HG	1.78	0.66
1:G:3500:LEU:HG	1:K:5577:ILE:HG21	1.78	0.66
1:H:4013:LEU:HG	1:J:5064:ILE:HG21	1.77	0.66
1:H:4038:ILE:HG21	1:J:5039:LEU:HG	1.77	0.66
1:A:422:LEU:HG	1:I:4551:ILE:HG21	1.77	0.66
1:L:5850:LEU:HD23	1:L:5850:LEU:C	2.21	0.66
1:G:3525:ILE:HG21	1:K:5552:LEU:HG	1.78	0.66
1:M:6363:LEU:C	1:M:6363:LEU:HD23	2.21	0.66
1:B:720:LEU:C	1:B:720:LEU:HD23	2.21	0.66
1:C:1233:LEU:C	1:C:1233:LEU:HD23	2.21	0.66
1:E:2259:LEU:HD23	1:E:2259:LEU:C	2.21	0.66
1:O:7389:LEU:C	1:O:7389:LEU:HD23	2.21	0.66
1:A:207:LEU:C	1:A:207:LEU:HD23	2.21	0.66
1:C:1473:ILE:HG21	1:O:7604:LEU:HG	1.78	0.66
1:E:2474:LEU:HG	1:M:6603:ILE:HG21	1.78	0.66
1:F:3012:ILE:HG21	1:L:6065:LEU:HG	1.77	0.65
1:K:5337:LEU:C	1:K:5337:LEU:HD23	2.21	0.65
1:N:6876:LEU:C	1:N:6876:LEU:HD23	2.21	0.65
1:B:935:LEU:HG	1:P:8142:ILE:HG21	1.77	0.65
1:P:7902:LEU:C	1:P:7902:LEU:HD23	2.21	0.65
1:D:1746:LEU:C	1:D:1746:LEU:HD23	2.21	0.65
1:F:2772:LEU:C	1:F:2772:LEU:HD23	2.21	0.65
1:I:4311:LEU:C	1:I:4311:LEU:HD23	2.21	0.65
1:D:1961:LEU:HG	1:N:7116:ILE:HG21	1.77	0.65
1:G:3285:LEU:HD23	1:G:3285:LEU:C	2.21	0.65
1:D:1986:ILE:HG21	1:N:7091:LEU:HG	1.77	0.65
1:H:3798:LEU:C	1:H:3798:LEU:HD23	2.21	0.65
1:J:4824:LEU:HD23	1:J:4824:LEU:C	2.21	0.65
1:C:1448:LEU:HG	1:O:7629:ILE:HG21	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2499:ILE:HG21	1:M:6578:LEU:HG	1.78	0.64
1:D:1698:LYS:HE2	1:D:1698:LYS:HA	1.81	0.63
1:N:6828:LYS:HE2	1:N:6828:LYS:HA	1.81	0.63
1:D:1961:LEU:HG	1:N:7116:ILE:CD1	2.29	0.63
1:D:1986:ILE:CD1	1:N:7091:LEU:HG	2.29	0.63
1:B:960:ILE:CD1	1:P:8117:LEU:HG	2.29	0.62
1:F:2724:LYS:HE2	1:F:2724:LYS:HA	1.81	0.62
1:F:2987:LEU:HG	1:L:6090:ILE:CD1	2.29	0.62
1:P:7854:LYS:HE2	1:P:7854:LYS:HA	1.81	0.62
1:A:447:ILE:CD1	1:I:4526:LEU:HG	2.30	0.62
1:G:3500:LEU:HG	1:K:5577:ILE:CD1	2.30	0.62
1:C:1185:LYS:HA	1:C:1185:LYS:HE2	1.81	0.62
1:C:1473:ILE:CD1	1:O:7604:LEU:HG	2.30	0.62
1:E:2474:LEU:HG	1:M:6603:ILE:CD1	2.30	0.62
1:G:3525:ILE:CD1	1:K:5552:LEU:HG	2.30	0.62
1:A:422:LEU:HG	1:I:4551:ILE:CD1	2.30	0.62
1:B:935:LEU:HD21	1:P:8142:ILE:HB	1.82	0.62
1:B:935:LEU:HG	1:P:8142:ILE:CD1	2.29	0.62
1:F:2987:LEU:HD21	1:L:6090:ILE:HB	1.82	0.62
1:F:3012:ILE:HB	1:L:6065:LEU:HD21	1.82	0.62
1:F:3012:ILE:CD1	1:L:6065:LEU:HG	2.29	0.62
1:B:960:ILE:HB	1:P:8117:LEU:HD21	1.82	0.62
1:M:6315:LYS:HE2	1:M:6315:LYS:HA	1.81	0.62
1:H:4013:LEU:HG	1:J:5064:ILE:CD1	2.29	0.62
1:D:1961:LEU:HD21	1:N:7116:ILE:HB	1.82	0.62
1:D:1986:ILE:HB	1:N:7091:LEU:HD21	1.82	0.62
1:G:3500:LEU:HD21	1:K:5577:ILE:HB	1.82	0.62
1:H:4038:ILE:CD1	1:J:5039:LEU:HG	2.29	0.62
1:I:4263:LYS:HE2	1:I:4263:LYS:HA	1.81	0.62
1:O:7341:LYS:HE2	1:O:7341:LYS:HA	1.81	0.62
1:A:447:ILE:HB	1:I:4526:LEU:HD21	1.82	0.61
1:C:1448:LEU:HD21	1:O:7629:ILE:HB	1.82	0.61
1:E:2499:ILE:HB	1:M:6578:LEU:HD21	1.82	0.61
1:G:3237:LYS:HE2	1:G:3237:LYS:HA	1.81	0.61
1:E:2211:LYS:HA	1:E:2211:LYS:HE2	1.81	0.61
1:L:5802:LYS:HA	1:L:5802:LYS:HE2	1.81	0.61
1:B:672:LYS:HE2	1:B:672:LYS:HA	1.81	0.61
1:E:2499:ILE:CD1	1:M:6578:LEU:HG	2.30	0.61
1:G:3525:ILE:HB	1:K:5552:LEU:HD21	1.82	0.61
1:A:422:LEU:HD21	1:I:4551:ILE:HB	1.82	0.61
1:C:1448:LEU:HG	1:O:7629:ILE:CD1	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1473:ILE:HB	1:O:7604:LEU:HD21	1.82	0.61
1:E:2474:LEU:HD21	1:M:6603:ILE:HB	1.82	0.61
1:H:3750:LYS:HE2	1:H:3750:LYS:HA	1.81	0.61
1:J:4776:LYS:HA	1:J:4776:LYS:HE2	1.81	0.61
1:A:159:LYS:HE2	1:A:159:LYS:HA	1.81	0.61
1:H:4013:LEU:HD21	1:J:5064:ILE:HB	1.82	0.60
1:K:5289:LYS:HE2	1:K:5289:LYS:HA	1.81	0.60
1:H:4038:ILE:HB	1:J:5039:LEU:HD21	1.82	0.60
1:E:2497:ASP:CG	1:M:6578:LEU:CD2	2.75	0.60
1:C:1448:LEU:CD2	1:O:7627:ASP:CG	2.75	0.60
1:B:958:ASP:CG	1:P:8117:LEU:CD2	2.75	0.60
1:F:2987:LEU:CD2	1:L:6088:ASP:CG	2.75	0.60
1:D:1961:LEU:CD2	1:N:7114:ASP:CG	2.75	0.60
1:D:1984:ASP:CG	1:N:7091:LEU:CD2	2.75	0.60
1:G:3523:ASP:CG	1:K:5552:LEU:CD2	2.75	0.59
1:A:422:LEU:CD2	1:I:4549:ASP:CG	2.75	0.59
1:A:445:ASP:CG	1:I:4526:LEU:HD21	2.25	0.59
1:G:3500:LEU:HD21	1:K:5575:ASP:CG	2.25	0.59
1:B:935:LEU:CD2	1:P:8140:ASP:CG	2.75	0.59
1:C:1471:ASP:CG	1:O:7604:LEU:CD2	2.75	0.59
1:F:3010:ASP:CG	1:L:6065:LEU:CD2	2.75	0.59
1:E:2474:LEU:CD2	1:M:6601:ASP:CG	2.75	0.59
1:A:422:LEU:HD21	1:I:4549:ASP:CG	2.25	0.59
1:H:4013:LEU:CD2	1:J:5062:ASP:CG	2.75	0.59
1:H:4036:ASP:CG	1:J:5039:LEU:CD2	2.75	0.59
1:G:3523:ASP:CG	1:K:5552:LEU:HD21	2.25	0.59
1:A:445:ASP:CG	1:I:4526:LEU:CD2	2.75	0.59
1:H:4036:ASP:CG	1:J:5039:LEU:HD21	2.26	0.58
1:G:3500:LEU:CD2	1:K:5575:ASP:CG	2.75	0.58
1:A:422:LEU:CD1	1:I:4551:ILE:CG2	2.82	0.58
1:A:447:ILE:CG2	1:I:4526:LEU:CD1	2.82	0.58
1:G:3500:LEU:CD1	1:K:5577:ILE:CG2	2.82	0.58
1:H:4013:LEU:HD21	1:J:5062:ASP:CG	2.26	0.58
1:B:935:LEU:CD1	1:P:8142:ILE:CG2	2.81	0.58
1:D:1961:LEU:CD1	1:N:7116:ILE:CG2	2.81	0.58
1:G:3525:ILE:CG2	1:K:5552:LEU:CD1	2.82	0.58
1:H:4013:LEU:CD1	1:J:5064:ILE:CG2	2.81	0.58
1:D:1986:ILE:CG2	1:N:7091:LEU:CD1	2.81	0.58
1:F:3012:ILE:CG2	1:L:6065:LEU:CD1	2.81	0.58
1:H:4038:ILE:CG2	1:J:5039:LEU:CD1	2.81	0.58
1:O:7445:LEU:HD23	1:O:7445:LEU:C	2.29	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1473:ILE:CG2	1:O:7604:LEU:CD1	2.82	0.58
1:E:2315:LEU:C	1:E:2315:LEU:HD23	2.29	0.58
1:E:2474:LEU:CD1	1:M:6603:ILE:CG2	2.82	0.58
1:N:6932:LEU:C	1:N:6932:LEU:HD23	2.29	0.57
1:C:1448:LEU:CD1	1:O:7629:ILE:CG2	2.82	0.57
1:F:2828:LEU:HD23	1:F:2828:LEU:C	2.29	0.57
1:P:7958:LEU:C	1:P:7958:LEU:HD23	2.29	0.57
1:E:2499:ILE:CG2	1:M:6578:LEU:CD1	2.82	0.57
1:B:960:ILE:CG2	1:P:8117:LEU:CD1	2.81	0.57
1:D:1802:LEU:C	1:D:1802:LEU:HD23	2.29	0.57
1:F:2987:LEU:CD1	1:L:6090:ILE:CG2	2.81	0.57
1:F:3010:ASP:CG	1:L:6065:LEU:HD21	2.26	0.57
1:A:445:ASP:OD2	1:I:4526:LEU:HD22	2.05	0.57
1:B:935:LEU:HD21	1:P:8140:ASP:CG	2.26	0.57
1:G:3500:LEU:HD22	1:K:5575:ASP:OD2	2.05	0.57
1:J:4880:LEU:HD23	1:J:4880:LEU:C	2.29	0.57
1:H:3854:LEU:HD23	1:H:3854:LEU:C	2.29	0.57
1:F:3010:ASP:OD2	1:L:6065:LEU:HD22	2.05	0.56
1:K:5393:LEU:C	1:K:5393:LEU:HD23	2.29	0.56
1:L:5906:LEU:C	1:L:5906:LEU:HD23	2.29	0.56
1:M:6419:LEU:HD23	1:M:6419:LEU:C	2.29	0.56
1:A:263:LEU:C	1:A:263:LEU:HD23	2.29	0.56
1:B:935:LEU:HD22	1:P:8140:ASP:OD2	2.05	0.56
1:B:958:ASP:CG	1:P:8117:LEU:HD21	2.26	0.56
1:F:2987:LEU:HD22	1:L:6088:ASP:OD2	2.05	0.56
1:A:422:LEU:HD22	1:I:4549:ASP:OD2	2.05	0.56
1:B:776:LEU:HD23	1:B:776:LEU:C	2.29	0.56
1:B:958:ASP:OD2	1:P:8117:LEU:HD22	2.05	0.56
1:C:1289:LEU:HD23	1:C:1289:LEU:C	2.29	0.56
1:G:3341:LEU:C	1:G:3341:LEU:HD23	2.29	0.56
1:I:4367:LEU:C	1:I:4367:LEU:HD23	2.29	0.56
1:F:2987:LEU:HD21	1:L:6088:ASP:CG	2.26	0.56
1:G:3523:ASP:OD2	1:K:5552:LEU:HD22	2.05	0.56
1:J:4639:GLY:HA2	1:J:4689:LEU:HD22	1.87	0.56
1:C:1448:LEU:HD22	1:O:7627:ASP:OD2	2.05	0.56
1:C:1471:ASP:OD2	1:O:7604:LEU:HD22	2.05	0.56
1:D:1961:LEU:HD22	1:N:7114:ASP:OD2	2.05	0.56
1:D:1984:ASP:OD2	1:N:7091:LEU:HD22	2.05	0.56
1:H:3613:GLY:HA2	1:H:3663:LEU:HD22	1.87	0.56
1:D:1561:GLY:HA2	1:D:1611:LEU:HD22	1.87	0.56
1:E:2474:LEU:HD22	1:M:6601:ASP:OD2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:2497:ASP:OD2	1:M:6578:LEU:HD22	2.05	0.56
1:I:4126:GLY:HA2	1:I:4176:LEU:HD22	1.87	0.56
1:N:6691:GLY:HA2	1:N:6741:LEU:HD22	1.87	0.56
1:G:3100:GLY:HA2	1:G:3150:LEU:HD22	1.87	0.56
1:H:4036:ASP:OD2	1:J:5039:LEU:HD22	2.05	0.56
1:L:5665:GLY:HA2	1:L:5715:LEU:HD22	1.87	0.55
1:A:22:GLY:HA2	1:A:72:LEU:HD22	1.87	0.55
1:B:535:GLY:HA2	1:B:585:LEU:HD22	1.87	0.55
1:H:4013:LEU:HD22	1:J:5062:ASP:OD2	2.05	0.55
1:K:5152:GLY:HA2	1:K:5202:LEU:HD22	1.87	0.55
1:D:1960:GLN:CD	1:N:7117:GLU:CD	2.68	0.55
1:D:1987:GLU:CD	1:N:7090:GLN:CD	2.68	0.55
1:O:7204:GLY:HA2	1:O:7254:LEU:HD22	1.87	0.55
1:C:1048:GLY:HA2	1:C:1098:LEU:HD22	1.87	0.55
1:E:2074:GLY:HA2	1:E:2124:LEU:HD22	1.87	0.55
1:B:934:GLN:CD	1:P:8143:GLU:CD	2.68	0.55
1:F:3013:GLU:CD	1:L:6064:GLN:CD	2.68	0.55
1:M:6178:GLY:HA2	1:M:6228:LEU:HD22	1.87	0.55
1:P:7717:GLY:HA2	1:P:7767:LEU:HD22	1.87	0.54
1:A:167:ILE:HB	1:A:202:LEU:HB2	1.89	0.54
1:B:680:ILE:HB	1:B:715:LEU:HB2	1.89	0.54
1:F:2587:GLY:HA2	1:F:2637:LEU:HD22	1.87	0.54
1:K:5297:ILE:HB	1:K:5332:LEU:HB2	1.89	0.54
1:L:5810:ILE:HB	1:L:5845:LEU:HB2	1.89	0.54
1:F:2732:ILE:HB	1:F:2767:LEU:HB2	1.89	0.54
1:P:7862:ILE:HB	1:P:7897:LEU:HB2	1.89	0.54
1:C:1193:ILE:HB	1:C:1228:LEU:HB2	1.89	0.54
1:O:7349:ILE:HB	1:O:7384:LEU:HB2	1.89	0.54
1:E:2219:ILE:HB	1:E:2254:LEU:HB2	1.89	0.54
1:H:3758:ILE:HB	1:H:3793:LEU:HB2	1.89	0.54
1:M:6323:ILE:HB	1:M:6358:LEU:HB2	1.89	0.54
1:J:4784:ILE:HB	1:J:4819:LEU:HB2	1.89	0.53
1:D:1706:ILE:HB	1:D:1741:LEU:HB2	1.89	0.53
1:N:6836:ILE:HB	1:N:6871:LEU:HB2	1.89	0.53
1:E:2497:ASP:CG	1:M:6578:LEU:HD21	2.25	0.53
1:I:4271:ILE:HB	1:I:4306:LEU:HB2	1.89	0.53
1:G:3245:ILE:HB	1:G:3280:LEU:HB2	1.89	0.53
1:C:1448:LEU:HD21	1:O:7627:ASP:CG	2.25	0.52
1:C:1474:GLU:CD	1:O:7603:GLN:CD	2.68	0.52
1:E:2473:GLN:CD	1:M:6604:GLU:CD	2.68	0.52
1:E:2230:ASP:O	1:E:2232:GLY:HA2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:7360:ASP:O	1:O:7362:GLY:HA2	2.10	0.52
1:F:2743:ASP:O	1:F:2745:GLY:HA2	2.10	0.52
1:D:1717:ASP:O	1:D:1719:GLY:HA2	2.10	0.52
1:D:1986:ILE:HG22	1:N:7091:LEU:CD1	2.39	0.52
1:N:6847:ASP:O	1:N:6849:GLY:HA2	2.10	0.52
1:P:7873:ASP:O	1:P:7875:GLY:HA2	2.10	0.52
1:D:1961:LEU:CD1	1:N:7116:ILE:HG22	2.40	0.52
1:C:1204:ASP:O	1:C:1206:GLY:HA2	2.09	0.52
1:M:6334:ASP:O	1:M:6336:GLY:HA2	2.10	0.52
1:B:935:LEU:CD1	1:P:8142:ILE:HG22	2.39	0.52
1:F:3012:ILE:HG22	1:L:6065:LEU:CD1	2.39	0.52
1:G:3256:ASP:O	1:G:3258:GLY:HA2	2.09	0.52
1:C:1448:LEU:CD1	1:O:7629:ILE:HG22	2.40	0.52
1:H:4013:LEU:CD1	1:J:5064:ILE:HG22	2.39	0.52
1:L:5821:ASP:O	1:L:5823:GLY:HA2	2.10	0.52
1:B:691:ASP:O	1:B:693:GLY:HA2	2.10	0.52
1:E:2499:ILE:HG22	1:M:6578:LEU:CD1	2.40	0.52
1:H:4038:ILE:HG22	1:J:5039:LEU:CD1	2.39	0.52
1:I:4282:ASP:O	1:I:4284:GLY:HA2	2.10	0.52
1:C:1471:ASP:CG	1:O:7604:LEU:HD21	2.25	0.52
1:C:1473:ILE:HG22	1:O:7604:LEU:CD1	2.40	0.51
1:F:2987:LEU:CG	1:L:6090:ILE:CG2	2.89	0.51
1:H:4038:ILE:CG2	1:J:5039:LEU:CG	2.89	0.51
1:A:422:LEU:CD1	1:I:4551:ILE:HG22	2.40	0.51
1:E:2474:LEU:HD21	1:M:6601:ASP:CG	2.25	0.51
1:E:2474:LEU:CD1	1:M:6603:ILE:HG22	2.40	0.51
1:H:4013:LEU:CG	1:J:5064:ILE:CG2	2.89	0.51
1:B:960:ILE:HG22	1:P:8117:LEU:CD1	2.39	0.51
1:H:3769:ASP:O	1:H:3771:GLY:HA2	2.10	0.51
1:G:3525:ILE:HG22	1:K:5552:LEU:CD1	2.40	0.51
1:H:4013:LEU:HD11	1:J:5064:ILE:HG22	1.93	0.51
1:K:5308:ASP:O	1:K:5310:GLY:HA2	2.10	0.51
1:A:447:ILE:HG22	1:I:4526:LEU:CD1	2.40	0.51
1:F:2987:LEU:CD1	1:L:6090:ILE:HG22	2.40	0.51
1:G:3500:LEU:CD1	1:K:5577:ILE:HG22	2.40	0.51
1:H:4038:ILE:HG22	1:J:5039:LEU:HD11	1.93	0.51
1:A:178:ASP:O	1:A:180:GLY:HA2	2.09	0.51
1:F:3012:ILE:CG2	1:L:6065:LEU:CG	2.89	0.51
1:J:4795:ASP:O	1:J:4797:GLY:HA2	2.10	0.51
1:A:445:ASP:OD2	1:I:4526:LEU:CD2	2.59	0.51
1:B:935:LEU:CG	1:P:8142:ILE:CG2	2.89	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3500:LEU:CD2	1:K:5575:ASP:OD2	2.59	0.51
1:K:5356:ILE:HD12	1:K:5356:ILE:N	2.26	0.51
1:A:422:LEU:CD2	1:I:4549:ASP:OD2	2.59	0.51
1:B:935:LEU:CD2	1:P:8140:ASP:OD2	2.59	0.51
1:C:1448:LEU:CD2	1:O:7627:ASP:OD2	2.59	0.51
1:G:3523:ASP:OD2	1:K:5552:LEU:CD2	2.59	0.51
1:L:5869:ILE:N	1:L:5869:ILE:HD12	2.26	0.51
1:M:6382:ILE:HD12	1:M:6382:ILE:N	2.26	0.51
1:N:6895:ILE:N	1:N:6895:ILE:HD12	2.26	0.51
1:A:226:ILE:HD12	1:A:226:ILE:N	2.27	0.50
1:B:739:ILE:N	1:B:739:ILE:HD12	2.27	0.50
1:C:1252:ILE:N	1:C:1252:ILE:HD12	2.27	0.50
1:D:1765:ILE:HD12	1:D:1765:ILE:N	2.27	0.50
1:D:1986:ILE:CG2	1:N:7091:LEU:CG	2.89	0.50
1:E:2497:ASP:OD2	1:M:6578:LEU:CD2	2.59	0.50
1:F:3010:ASP:OD2	1:L:6065:LEU:CD2	2.59	0.50
1:H:4036:ASP:OD2	1:J:5039:LEU:CD2	2.59	0.50
1:B:514:VAL:O	1:C:1090:VAL:HA	2.12	0.50
1:D:1540:VAL:O	1:E:2116:VAL:HA	2.12	0.50
1:D:1961:LEU:CG	1:N:7116:ILE:CG2	2.89	0.50
1:H:4013:LEU:CD2	1:J:5062:ASP:OD2	2.59	0.50
1:O:7408:ILE:N	1:O:7408:ILE:HD12	2.26	0.50
1:C:1471:ASP:OD2	1:O:7604:LEU:CD2	2.59	0.50
1:E:2278:ILE:N	1:E:2278:ILE:HD12	2.27	0.50
1:E:2474:LEU:CD2	1:M:6601:ASP:OD2	2.59	0.50
1:I:4105:VAL:O	1:J:4681:VAL:HA	2.12	0.50
1:L:5644:VAL:O	1:M:6220:VAL:HA	2.12	0.50
1:N:6670:VAL:O	1:O:7246:VAL:HA	2.12	0.50
1:A:64:VAL:HA	1:H:3592:VAL:O	2.12	0.50
1:D:1984:ASP:OD2	1:N:7091:LEU:CD2	2.59	0.50
1:D:1961:LEU:CD2	1:N:7114:ASP:OD2	2.59	0.50
1:G:3079:VAL:O	1:H:3655:VAL:HA	2.12	0.50
1:G:3114:LYS:HB2	1:G:3519:ASN:HB3	1.94	0.50
1:H:3817:ILE:N	1:H:3817:ILE:HD12	2.27	0.50
1:I:4140:LYS:HB2	1:I:4545:ASN:HB3	1.94	0.50
1:J:4843:ILE:N	1:J:4843:ILE:HD12	2.26	0.50
1:B:935:LEU:HD11	1:P:8142:ILE:HG22	1.93	0.50
1:D:1986:ILE:HG22	1:N:7091:LEU:HD11	1.93	0.50
1:F:2566:VAL:O	1:G:3142:VAL:HA	2.12	0.50
1:J:4618:VAL:O	1:K:5194:VAL:HA	2.12	0.50
1:D:1961:LEU:HD11	1:N:7116:ILE:HG22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2987:LEU:HD11	1:L:6090:ILE:HG22	1.93	0.50
1:F:3012:ILE:HG22	1:L:6065:LEU:HD11	1.93	0.50
1:L:6034:ASP:C	1:L:6036:ARG:H	2.20	0.50
1:A:447:ILE:CG2	1:I:4526:LEU:CG	2.89	0.50
1:B:958:ASP:OD2	1:P:8117:LEU:CD2	2.59	0.50
1:B:960:ILE:HG22	1:P:8117:LEU:HD11	1.93	0.50
1:F:2987:LEU:CD2	1:L:6088:ASP:OD2	2.59	0.50
1:I:4168:VAL:HA	1:P:7696:VAL:O	2.12	0.50
1:L:5647:GLU:O	1:L:5648:ASN:CB	2.60	0.50
1:B:517:GLU:O	1:B:518:ASN:CB	2.60	0.50
1:B:904:ASP:C	1:B:906:ARG:H	2.20	0.50
1:C:1473:ILE:CG2	1:O:7604:LEU:CG	2.89	0.49
1:E:2056:GLU:O	1:E:2057:ASN:CB	2.60	0.49
1:G:3304:ILE:N	1:G:3304:ILE:HD12	2.27	0.49
1:G:3500:LEU:CG	1:K:5577:ILE:CG2	2.89	0.49
1:I:4330:ILE:N	1:I:4330:ILE:HD12	2.26	0.49
1:K:5521:ASP:C	1:K:5523:ARG:H	2.20	0.49
1:M:6160:GLU:O	1:M:6161:ASN:CB	2.60	0.49
1:O:7183:VAL:O	1:P:7759:VAL:HA	2.12	0.49
1:P:7921:ILE:HD12	1:P:7921:ILE:N	2.26	0.49
1:A:391:ASP:C	1:A:393:ARG:H	2.20	0.49
1:C:1030:GLU:O	1:C:1031:ASN:CB	2.60	0.49
1:C:1448:LEU:HD11	1:O:7629:ILE:HG22	1.93	0.49
1:O:7186:GLU:O	1:O:7187:ASN:CB	2.60	0.49
1:E:2053:VAL:O	1:F:2629:VAL:HA	2.12	0.49
1:E:2499:ILE:HG22	1:M:6578:LEU:HD11	1.93	0.49
1:F:2791:ILE:HD12	1:F:2791:ILE:N	2.27	0.49
1:N:7060:ASP:C	1:N:7062:ARG:H	2.20	0.49
1:C:1027:VAL:O	1:D:1603:VAL:HA	2.12	0.49
1:D:1930:ASP:C	1:D:1932:ARG:H	2.20	0.49
1:E:2474:LEU:CG	1:M:6603:ILE:CG2	2.89	0.49
1:F:2601:LYS:HB2	1:F:3006:ASN:HB3	1.94	0.49
1:P:7731:LYS:HB2	1:P:8136:ASN:HB3	1.94	0.49
1:P:8086:ASP:C	1:P:8088:ARG:H	2.20	0.49
1:C:1473:ILE:HG22	1:O:7604:LEU:HD11	1.93	0.49
1:E:2474:LEU:HD11	1:M:6603:ILE:HG22	1.93	0.49
1:H:3627:LYS:HB2	1:H:4032:ASN:HB3	1.94	0.49
1:P:7699:GLU:O	1:P:7700:ASN:CB	2.60	0.49
1:A:447:ILE:HG22	1:I:4526:LEU:HD11	1.93	0.49
1:D:1575:LYS:HB2	1:D:1980:ASN:HB3	1.94	0.49
1:F:2569:GLU:O	1:F:2570:ASN:CB	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:5131:VAL:O	1:L:5707:VAL:HA	2.12	0.49
1:M:6547:ASP:C	1:M:6549:ARG:H	2.20	0.49
1:C:1417:ASP:C	1:C:1419:ARG:H	2.20	0.49
1:D:1543:GLU:O	1:D:1544:ASN:CB	2.60	0.49
1:E:2088:LYS:HB2	1:E:2493:ASN:HB3	1.94	0.49
1:F:2956:ASP:C	1:F:2958:ARG:H	2.20	0.49
1:J:5008:ASP:C	1:J:5010:ARG:H	2.20	0.49
1:M:6157:VAL:O	1:N:6733:VAL:HA	2.12	0.49
1:A:1:VAL:O	1:B:577:VAL:HA	2.12	0.49
1:A:4:GLU:O	1:A:5:ASN:CB	2.60	0.49
1:G:3500:LEU:HD11	1:K:5577:ILE:HG22	1.93	0.49
1:J:4653:LYS:HB2	1:J:5058:ASN:HB3	1.94	0.49
1:K:5166:LYS:HB2	1:K:5571:ASN:HB3	1.94	0.49
1:N:6673:GLU:O	1:N:6674:ASN:CB	2.60	0.49
1:N:6705:LYS:HB2	1:N:7110:ASN:HB3	1.94	0.49
1:O:7218:LYS:HB2	1:O:7623:ASN:HB3	1.94	0.49
1:H:3982:ASP:C	1:H:3984:ARG:H	2.20	0.49
1:K:5134:GLU:O	1:K:5135:ASN:CB	2.60	0.49
1:A:36:LYS:HB2	1:A:441:ASN:HB3	1.94	0.49
1:B:549:LYS:HB2	1:B:954:ASN:HB3	1.94	0.49
1:G:3469:ASP:C	1:G:3471:ARG:H	2.20	0.49
1:I:4108:GLU:O	1:I:4109:ASN:CB	2.60	0.49
1:I:4495:ASP:C	1:I:4497:ARG:H	2.20	0.49
1:L:5679:LYS:HB2	1:L:6084:ASN:HB3	1.94	0.49
1:A:422:LEU:HD11	1:I:4551:ILE:HG22	1.93	0.48
1:C:1062:LYS:HB2	1:C:1467:ASN:HB3	1.94	0.48
1:G:3082:GLU:O	1:G:3083:ASN:CB	2.60	0.48
1:G:3525:ILE:HG22	1:K:5552:LEU:HD11	1.93	0.48
1:M:6192:LYS:HB2	1:M:6597:ASN:HB3	1.94	0.48
1:G:3525:ILE:CG2	1:K:5552:LEU:CG	2.89	0.48
1:A:422:LEU:CG	1:I:4551:ILE:CG2	2.89	0.48
1:F:2986:GLN:CD	1:L:6091:GLU:CD	2.68	0.48
1:G:3499:GLN:CD	1:K:5578:GLU:CD	2.68	0.48
1:A:448:GLU:CD	1:I:4525:GLN:CD	2.68	0.48
1:B:961:GLU:CD	1:P:8116:GLN:CD	2.68	0.48
1:E:2499:ILE:CG2	1:M:6578:LEU:CG	2.89	0.48
1:D:1987:GLU:HG2	1:N:7088:ARG:NH2	2.29	0.48
1:H:3595:GLU:O	1:H:3596:ASN:CB	2.60	0.48
1:H:4039:GLU:HG2	1:J:5036:ARG:NH2	2.29	0.48
1:B:932:ARG:NH2	1:P:8143:GLU:HG2	2.29	0.48
1:C:1445:ARG:NH2	1:O:7630:GLU:HG2	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1448:LEU:CG	1:O:7629:ILE:CG2	2.89	0.48
1:E:2443:ASP:C	1:E:2445:ARG:H	2.20	0.48
1:E:2500:GLU:HG2	1:M:6575:ARG:NH2	2.29	0.48
1:F:2984:ARG:NH2	1:L:6091:GLU:HG2	2.29	0.48
1:H:4010:ARG:NH2	1:J:5065:GLU:HG2	2.29	0.48
1:J:4621:GLU:O	1:J:4622:ASN:CB	2.60	0.48
1:O:7573:ASP:C	1:O:7575:ARG:H	2.20	0.48
1:B:960:ILE:CG2	1:P:8117:LEU:CG	2.89	0.48
1:B:961:GLU:HG2	1:P:8114:ARG:NH2	2.29	0.48
1:D:1958:ARG:NH2	1:N:7117:GLU:HG2	2.29	0.48
1:F:3013:GLU:HG2	1:L:6062:ARG:NH2	2.29	0.48
1:G:3526:GLU:HG2	1:K:5549:ARG:NH2	2.29	0.47
1:A:419:ARG:NH2	1:I:4552:GLU:HG2	2.29	0.47
1:C:1474:GLU:HG2	1:O:7601:ARG:NH2	2.29	0.47
1:E:2471:ARG:NH2	1:M:6604:GLU:HG2	2.29	0.47
1:G:3497:ARG:NH2	1:K:5578:GLU:HG2	2.29	0.47
1:A:448:GLU:HG2	1:I:4523:ARG:NH2	2.29	0.47
1:A:421:GLN:CD	1:I:4552:GLU:CD	2.68	0.47
1:G:3526:GLU:CD	1:K:5551:GLN:CD	2.68	0.47
1:M:6373:MET:HE1	1:M:6455:ALA:HB3	1.97	0.47
1:O:7399:MET:HE1	1:O:7481:ALA:HB3	1.97	0.47
1:C:1243:MET:HE1	1:C:1325:ALA:HB3	1.97	0.47
1:E:2269:MET:HE1	1:E:2351:ALA:HB3	1.97	0.47
1:G:3295:MET:HE1	1:G:3377:ALA:HB3	1.97	0.46
1:I:4321:MET:HE1	1:I:4403:ALA:HB3	1.97	0.46
1:E:2243:LYS:HB2	1:E:2423:ILE:HD12	1.97	0.46
1:K:5347:MET:HE1	1:K:5429:ALA:HB3	1.97	0.46
1:O:7373:LYS:HB2	1:O:7553:ILE:HD12	1.97	0.46
1:A:217:MET:HE1	1:A:299:ALA:HB3	1.97	0.46
1:H:4012:GLN:CD	1:J:5065:GLU:CD	2.68	0.46
1:F:2756:LYS:HB2	1:F:2936:ILE:HD12	1.97	0.46
1:H:3782:LYS:HB2	1:H:3962:ILE:HD12	1.97	0.46
1:D:1730:LYS:HB2	1:D:1910:ILE:HD12	1.97	0.46
1:H:3854:LEU:HD23	1:H:3854:LEU:O	2.16	0.46
1:J:4808:LYS:HB2	1:J:4988:ILE:HD12	1.98	0.46
1:J:4880:LEU:HD23	1:J:4880:LEU:O	2.16	0.46
1:P:7886:LYS:HB2	1:P:8066:ILE:HD12	1.98	0.46
1:D:1801:MET:O	1:D:1805:MET:HG2	2.16	0.46
1:D:1984:ASP:CG	1:N:7091:LEU:HD21	2.26	0.46
1:K:5393:LEU:HD23	1:K:5393:LEU:O	2.16	0.46
1:M:6419:LEU:HD23	1:M:6419:LEU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:LEU:HD23	1:A:263:LEU:O	2.16	0.45
1:B:704:LYS:HB2	1:B:884:ILE:HD12	1.97	0.45
1:D:1802:LEU:HD23	1:D:1802:LEU:O	2.16	0.45
1:N:6860:LYS:HB2	1:N:7040:ILE:HD12	1.98	0.45
1:N:6931:MET:O	1:N:6935:MET:HG2	2.17	0.45
1:N:6932:LEU:HD23	1:N:6932:LEU:O	2.16	0.45
1:P:7852:ALA:HB2	1:P:8069:VAL:HG22	1.99	0.45
1:A:262:MET:O	1:A:266:MET:HG2	2.16	0.45
1:C:1289:LEU:HD23	1:C:1289:LEU:O	2.16	0.45
1:F:2722:ALA:HB2	1:F:2939:VAL:HG22	1.99	0.45
1:K:5392:MET:O	1:K:5396:MET:HG2	2.16	0.45
1:L:5834:LYS:HB2	1:L:6014:ILE:HD12	1.98	0.45
1:P:7912:MET:HE1	1:P:7994:ALA:HB3	1.97	0.45
1:B:730:MET:HE1	1:B:812:ALA:HB3	1.98	0.45
1:C:1288:MET:O	1:C:1292:MET:HG2	2.16	0.45
1:E:2209:ALA:HB2	1:E:2426:VAL:HG22	1.99	0.45
1:G:3341:LEU:HD23	1:G:3341:LEU:O	2.16	0.45
1:I:4367:LEU:HD23	1:I:4367:LEU:O	2.16	0.45
1:O:7339:ALA:HB2	1:O:7556:VAL:HG22	1.99	0.45
1:O:7444:MET:O	1:O:7448:MET:HG2	2.16	0.45
1:A:191:LYS:HB2	1:A:371:ILE:HD12	1.97	0.45
1:H:3748:ALA:HB2	1:H:3965:VAL:HG22	1.99	0.45
1:H:4039:GLU:CD	1:J:5038:GLN:CD	2.68	0.45
1:J:4774:ALA:HB2	1:J:4991:VAL:HG22	1.99	0.45
1:L:5860:MET:HE1	1:L:5942:ALA:HB3	1.97	0.45
1:M:6418:MET:O	1:M:6422:MET:HG2	2.16	0.45
1:D:1961:LEU:HD21	1:N:7114:ASP:CG	2.26	0.45
1:E:2314:MET:O	1:E:2318:MET:HG2	2.16	0.45
1:F:2782:MET:HE1	1:F:2864:ALA:HB3	1.98	0.45
1:J:4879:MET:O	1:J:4883:MET:HG2	2.16	0.45
1:K:5321:LYS:HB2	1:K:5501:ILE:HD12	1.97	0.45
1:L:5906:LEU:HD23	1:L:5906:LEU:O	2.16	0.45
1:M:6347:LYS:HB2	1:M:6527:ILE:HD12	1.97	0.45
1:C:1217:LYS:HB2	1:C:1397:ILE:HD12	1.97	0.45
1:D:1756:MET:HE1	1:D:1838:ALA:HB3	1.98	0.45
1:G:3235:ALA:HB2	1:G:3452:VAL:HG22	1.99	0.45
1:H:3853:MET:O	1:H:3857:MET:HG2	2.16	0.45
1:I:4261:ALA:HB2	1:I:4478:VAL:HG22	1.99	0.45
1:B:776:LEU:HD23	1:B:776:LEU:O	2.16	0.45
1:N:6886:MET:HE1	1:N:6968:ALA:HB3	1.97	0.45
1:E:2315:LEU:HD23	1:E:2315:LEU:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3269:LYS:HB2	1:G:3449:ILE:HD12	1.97	0.45
1:I:4295:LYS:HB2	1:I:4475:ILE:HD12	1.97	0.45
1:D:1696:ALA:HB2	1:D:1913:VAL:HG22	1.99	0.45
1:F:2828:LEU:HD23	1:F:2828:LEU:O	2.16	0.45
1:K:5287:ALA:HB2	1:K:5504:VAL:HG22	1.99	0.45
1:N:6826:ALA:HB2	1:N:7043:VAL:HG22	1.99	0.45
1:O:7445:LEU:HD23	1:O:7445:LEU:O	2.16	0.45
1:P:7958:LEU:HD23	1:P:7958:LEU:O	2.16	0.45
1:A:157:ALA:HB2	1:A:374:VAL:HG22	1.99	0.45
1:B:775:MET:O	1:B:779:MET:HG2	2.16	0.45
1:D:1629:ALA:O	1:D:1633:ALA:CB	2.66	0.45
1:N:6759:ALA:O	1:N:6763:ALA:CB	2.66	0.44
1:A:207:LEU:C	1:A:207:LEU:CD2	2.90	0.44
1:K:5337:LEU:C	1:K:5337:LEU:CD2	2.90	0.44
1:L:5905:MET:O	1:L:5909:MET:HG2	2.17	0.44
1:B:603:ALA:O	1:B:607:ALA:CB	2.66	0.44
1:H:3681:ALA:O	1:H:3685:ALA:CB	2.66	0.44
1:J:4834:MET:HE1	1:J:4916:ALA:HB3	1.97	0.44
1:L:5800:ALA:HB2	1:L:6017:VAL:HG22	1.99	0.44
1:M:6313:ALA:HB2	1:M:6530:VAL:HG22	1.99	0.44
1:P:7957:MET:O	1:P:7961:MET:HG2	2.16	0.44
1:B:670:ALA:HB2	1:B:887:VAL:HG22	1.99	0.44
1:H:3808:MET:HE1	1:H:3890:ALA:HB3	1.98	0.44
1:J:4707:ALA:O	1:J:4711:ALA:CB	2.66	0.44
1:L:5733:ALA:O	1:L:5737:ALA:CB	2.66	0.44
1:C:1183:ALA:HB2	1:C:1400:VAL:HG22	1.99	0.44
1:F:2827:MET:O	1:F:2831:MET:HG2	2.16	0.44
1:G:3340:MET:O	1:G:3344:MET:HG2	2.16	0.44
1:E:2142:ALA:O	1:E:2146:ALA:CB	2.65	0.44
1:F:2655:ALA:O	1:F:2659:ALA:CB	2.66	0.44
1:C:1116:ALA:O	1:C:1120:ALA:CB	2.65	0.44
1:I:4366:MET:O	1:I:4370:MET:HG2	2.16	0.44
1:O:7272:ALA:O	1:O:7276:ALA:CB	2.66	0.44
1:P:7785:ALA:O	1:P:7789:ALA:CB	2.66	0.44
1:K:5131:VAL:O	1:L:5708:GLU:N	2.51	0.44
1:M:6246:ALA:O	1:M:6250:ALA:CB	2.66	0.44
1:C:1447:GLN:CD	1:O:7630:GLU:CD	2.68	0.44
1:E:2500:GLU:CD	1:M:6577:GLN:CD	2.68	0.44
1:P:7902:LEU:C	1:P:7902:LEU:CD2	2.90	0.44
1:A:90:ALA:O	1:A:94:ALA:CB	2.65	0.43
1:B:514:VAL:O	1:C:1091:GLU:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2772:LEU:C	1:F:2772:LEU:CD2	2.90	0.43
1:K:5220:ALA:O	1:K:5224:ALA:CB	2.66	0.43
1:A:1:VAL:O	1:B:578:GLU:N	2.51	0.43
1:B:686:SER:O	1:B:689:VAL:HG12	2.19	0.43
1:C:1199:SER:O	1:C:1202:VAL:HG12	2.19	0.43
1:L:5816:SER:O	1:L:5819:VAL:HG12	2.19	0.43
1:E:2225:SER:O	1:E:2228:VAL:HG12	2.19	0.43
1:G:3168:ALA:O	1:G:3172:ALA:CB	2.65	0.43
1:G:3372:LYS:NZ	1:G:3372:LYS:HB3	2.34	0.43
1:I:4194:ALA:O	1:I:4198:ALA:CB	2.66	0.43
1:M:6157:VAL:O	1:N:6734:GLU:N	2.51	0.43
1:O:7355:SER:O	1:O:7358:VAL:HG12	2.18	0.43
1:A:173:SER:O	1:A:176:VAL:HG12	2.19	0.43
1:E:2346:LYS:NZ	1:E:2346:LYS:HB3	2.34	0.43
1:G:3285:LEU:C	1:G:3285:LEU:CD2	2.90	0.43
1:I:4311:LEU:C	1:I:4311:LEU:CD2	2.90	0.43
1:I:4398:LYS:NZ	1:I:4398:LYS:HB3	2.34	0.43
1:M:6329:SER:O	1:M:6332:VAL:HG12	2.19	0.43
1:O:7183:VAL:O	1:P:7760:GLU:N	2.51	0.43
1:A:294:LYS:HB3	1:A:294:LYS:NZ	2.34	0.43
1:C:1320:LYS:NZ	1:C:1320:LYS:HB3	2.34	0.43
1:K:5303:SER:O	1:K:5306:VAL:HG12	2.19	0.43
1:A:65:GLU:N	1:H:3592:VAL:O	2.51	0.43
1:C:1027:VAL:O	1:D:1604:GLU:N	2.51	0.43
1:D:1540:VAL:O	1:E:2117:GLU:N	2.51	0.43
1:K:5424:LYS:NZ	1:K:5424:LYS:HB3	2.34	0.43
1:L:5644:VAL:O	1:M:6221:GLU:N	2.52	0.43
1:O:7476:LYS:NZ	1:O:7476:LYS:HB3	2.34	0.43
1:C:1233:LEU:C	1:C:1233:LEU:CD2	2.90	0.43
1:K:5564:ILE:HB	1:K:5565:PRO:CD	2.46	0.43
1:M:6363:LEU:C	1:M:6363:LEU:CD2	2.90	0.43
1:M:6450:LYS:NZ	1:M:6450:LYS:HB3	2.34	0.43
1:D:1833:LYS:NZ	1:D:1833:LYS:HB3	2.34	0.43
1:E:2053:VAL:O	1:F:2630:GLU:N	2.51	0.43
1:N:6670:VAL:O	1:O:7247:GLU:N	2.52	0.43
1:N:6963:LYS:NZ	1:N:6963:LYS:HB3	2.34	0.43
1:A:434:ILE:HB	1:A:435:PRO:CD	2.46	0.43
1:F:2738:SER:O	1:F:2741:VAL:HG12	2.19	0.43
1:H:3764:SER:O	1:H:3767:VAL:HG12	2.19	0.43
1:I:4154:VAL:O	1:I:4154:VAL:HG13	2.19	0.43
1:J:4618:VAL:O	1:K:5195:GLU:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3251:SER:O	1:G:3254:VAL:HG12	2.19	0.43
1:H:4009:GLY:O	1:H:4012:GLN:HG2	2.19	0.43
1:I:4105:VAL:O	1:J:4682:GLU:N	2.51	0.43
1:I:4277:SER:O	1:I:4280:VAL:HG12	2.18	0.43
1:J:4790:SER:O	1:J:4793:VAL:HG12	2.19	0.43
1:M:6590:ILE:HB	1:M:6591:PRO:CD	2.46	0.43
1:P:7868:SER:O	1:P:7871:VAL:HG12	2.19	0.43
1:B:807:LYS:NZ	1:B:807:LYS:HB3	2.34	0.42
1:C:1460:ILE:HB	1:C:1461:PRO:CD	2.46	0.42
1:D:1632:VAL:CG1	1:D:1633:ALA:N	2.82	0.42
1:D:1957:GLY:O	1:D:1960:GLN:HG2	2.19	0.42
1:D:1986:ILE:HD12	1:N:7091:LEU:HG	2.01	0.42
1:F:2566:VAL:O	1:G:3143:GLU:N	2.51	0.42
1:F:2859:LYS:NZ	1:F:2859:LYS:HB3	2.34	0.42
1:G:3525:ILE:HD12	1:K:5552:LEU:HG	2.01	0.42
1:H:3684:VAL:CG1	1:H:3685:ALA:N	2.82	0.42
1:J:4710:VAL:CG1	1:J:4711:ALA:N	2.82	0.42
1:J:5035:GLY:O	1:J:5038:GLN:HG2	2.19	0.42
1:L:5937:LYS:NZ	1:L:5937:LYS:HB3	2.34	0.42
1:N:6762:VAL:CG1	1:N:6763:ALA:N	2.82	0.42
1:N:7087:GLY:O	1:N:7090:GLN:HG2	2.19	0.42
1:P:7745:VAL:HG13	1:P:7745:VAL:O	2.19	0.42
1:D:1961:LEU:HG	1:N:7116:ILE:HD12	2.01	0.42
1:E:2145:VAL:CG1	1:E:2146:ALA:N	2.82	0.42
1:F:2615:VAL:O	1:F:2615:VAL:HG13	2.19	0.42
1:F:2655:ALA:O	1:F:2659:ALA:HB2	2.20	0.42
1:G:3128:VAL:O	1:G:3128:VAL:HG13	2.19	0.42
1:N:6842:SER:O	1:N:6845:VAL:HG12	2.19	0.42
1:O:7275:VAL:CG1	1:O:7276:ALA:N	2.82	0.42
1:A:422:LEU:HG	1:I:4551:ILE:HD12	2.02	0.42
1:B:606:VAL:CG1	1:B:607:ALA:N	2.82	0.42
1:C:1444:GLY:O	1:C:1447:GLN:HG2	2.19	0.42
1:D:1629:ALA:O	1:D:1633:ALA:HB2	2.20	0.42
1:H:3641:VAL:O	1:H:3641:VAL:HG13	2.19	0.42
1:H:3885:LYS:NZ	1:H:3885:LYS:HB3	2.34	0.42
1:J:4667:VAL:O	1:J:4667:VAL:HG13	2.19	0.42
1:J:4911:LYS:HB3	1:J:4911:LYS:NZ	2.34	0.42
1:L:5736:VAL:CG1	1:L:5737:ALA:N	2.82	0.42
1:M:6574:GLY:O	1:M:6577:GLN:HG2	2.19	0.42
1:N:6876:LEU:C	1:N:6876:LEU:CD2	2.90	0.42
1:C:1366:ARG:HB2	1:C:1375:PHE:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1589:VAL:O	1:D:1589:VAL:HG13	2.19	0.42
1:D:1712:SER:O	1:D:1715:VAL:HG12	2.19	0.42
1:D:1746:LEU:C	1:D:1746:LEU:CD2	2.90	0.42
1:E:2392:ARG:HB2	1:E:2401:PHE:CE1	2.55	0.42
1:G:3079:VAL:O	1:H:3656:GLU:N	2.51	0.42
1:H:3931:ARG:HB2	1:H:3940:PHE:CE1	2.55	0.42
1:I:4169:GLU:N	1:P:7696:VAL:O	2.52	0.42
1:I:4194:ALA:O	1:I:4198:ALA:HB2	2.20	0.42
1:M:6496:ARG:HB2	1:M:6505:PHE:CE1	2.55	0.42
1:M:6594:LEU:HD12	1:M:6594:LEU:HA	1.86	0.42
1:N:6759:ALA:O	1:N:6763:ALA:HB2	2.20	0.42
1:O:7522:ARG:HB2	1:O:7531:PHE:CE1	2.55	0.42
1:P:7785:ALA:O	1:P:7789:ALA:HB2	2.20	0.42
1:B:603:ALA:O	1:B:607:ALA:HB2	2.20	0.42
1:B:853:ARG:HB2	1:B:862:PHE:CE1	2.55	0.42
1:D:1879:ARG:HB2	1:D:1888:PHE:CE1	2.55	0.42
1:E:2259:LEU:C	1:E:2259:LEU:CD2	2.90	0.42
1:F:2905:ARG:HB2	1:F:2914:PHE:CE1	2.55	0.42
1:G:3168:ALA:O	1:G:3172:ALA:HB2	2.20	0.42
1:J:4957:ARG:HB2	1:J:4966:PHE:CE1	2.55	0.42
1:K:5223:VAL:CG1	1:K:5224:ALA:N	2.82	0.42
1:L:5733:ALA:O	1:L:5737:ALA:HB2	2.20	0.42
1:N:6719:VAL:O	1:N:6719:VAL:HG13	2.19	0.42
1:N:7009:ARG:HB2	1:N:7018:PHE:CE1	2.55	0.42
1:P:7989:LYS:NZ	1:P:7989:LYS:HB3	2.34	0.42
1:G:3171:VAL:CG1	1:G:3172:ALA:N	2.82	0.42
1:L:5983:ARG:HB2	1:L:5992:PHE:CE1	2.55	0.42
1:P:8035:ARG:HB2	1:P:8044:PHE:CE1	2.55	0.42
1:P:8129:ILE:HB	1:P:8130:PRO:CD	2.46	0.42
1:A:93:VAL:CG1	1:A:94:ALA:N	2.82	0.42
1:C:1464:LEU:HD12	1:C:1464:LEU:HA	1.86	0.42
1:E:2102:VAL:O	1:E:2102:VAL:HG13	2.19	0.42
1:E:2142:ALA:O	1:E:2146:ALA:HB2	2.20	0.42
1:H:3681:ALA:O	1:H:3685:ALA:HB2	2.20	0.42
1:J:4707:ALA:O	1:J:4711:ALA:HB2	2.20	0.42
1:K:5220:ALA:O	1:K:5224:ALA:HB2	2.20	0.42
1:M:6249:VAL:CG1	1:M:6250:ALA:N	2.82	0.42
1:O:7232:VAL:HG13	1:O:7232:VAL:O	2.19	0.42
1:A:23:ARG:NH1	1:A:99:ARG:HD3	2.35	0.42
1:A:90:ALA:O	1:A:94:ALA:HB2	2.20	0.42
1:C:1119:VAL:CG1	1:C:1120:ALA:N	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2983:GLY:O	1:F:2986:GLN:HG2	2.19	0.42
1:H:4038:ILE:HG21	1:J:5039:LEU:CG	2.49	0.42
1:I:4197:VAL:CG1	1:I:4198:ALA:N	2.82	0.42
1:L:5850:LEU:C	1:L:5850:LEU:CD2	2.90	0.42
1:N:6817:ALA:HB1	1:N:6834:ALA:HA	2.02	0.42
1:O:7272:ALA:O	1:O:7276:ALA:HB2	2.20	0.42
1:O:7389:LEU:C	1:O:7389:LEU:CD2	2.90	0.42
1:B:720:LEU:C	1:B:720:LEU:CD2	2.90	0.42
1:B:960:ILE:HD12	1:P:8117:LEU:HG	2.01	0.42
1:D:1687:ALA:HB1	1:D:1704:ALA:HA	2.02	0.42
1:E:2474:LEU:CG	1:M:6603:ILE:CB	2.80	0.42
1:E:2499:ILE:HD12	1:M:6578:LEU:HG	2.01	0.42
1:H:4013:LEU:CG	1:J:5064:ILE:HG21	2.49	0.42
1:I:4522:GLY:O	1:I:4525:GLN:HG2	2.19	0.42
1:O:7600:GLY:O	1:O:7603:GLN:HG2	2.19	0.42
1:P:8113:GLY:O	1:P:8116:GLN:HG2	2.19	0.42
1:B:931:GLY:O	1:B:934:GLN:HG2	2.19	0.42
1:E:2470:GLY:O	1:E:2473:GLN:HG2	2.19	0.42
1:F:2999:ILE:HB	1:F:3000:PRO:CD	2.46	0.42
1:G:3496:GLY:O	1:G:3499:GLN:HG2	2.19	0.42
1:K:5153:ARG:NH1	1:K:5229:ARG:HD3	2.35	0.42
1:F:2987:LEU:HG	1:L:6090:ILE:HD12	2.01	0.41
1:G:3101:ARG:NH1	1:G:3177:ARG:HD3	2.35	0.41
1:K:5568:LEU:HD12	1:K:5568:LEU:HA	1.86	0.41
1:L:5693:VAL:O	1:L:5693:VAL:HG13	2.19	0.41
1:M:6246:ALA:O	1:M:6250:ALA:HB2	2.20	0.41
1:P:7718:ARG:NH1	1:P:7794:ARG:HD3	2.35	0.41
1:A:418:GLY:O	1:A:421:GLN:HG2	2.19	0.41
1:B:563:VAL:O	1:B:563:VAL:HG13	2.19	0.41
1:C:1116:ALA:O	1:C:1120:ALA:HB2	2.20	0.41
1:E:2200:ALA:HB1	1:E:2217:ALA:HA	2.02	0.41
1:F:2588:ARG:NH1	1:F:2664:ARG:HD3	2.35	0.41
1:I:4127:ARG:NH1	1:I:4203:ARG:HD3	2.35	0.41
1:L:6061:GLY:O	1:L:6064:GLN:HG2	2.19	0.41
1:O:7330:ALA:HB1	1:O:7347:ALA:HA	2.02	0.41
1:A:50:VAL:O	1:A:50:VAL:HG13	2.19	0.41
1:A:340:ARG:HB2	1:A:349:PHE:CE1	2.55	0.41
1:C:1448:LEU:HG	1:O:7629:ILE:HD12	2.02	0.41
1:G:3418:ARG:HB2	1:G:3427:PHE:CE1	2.55	0.41
1:I:4444:ARG:HB2	1:I:4453:PHE:CE1	2.55	0.41
1:K:5470:ARG:HB2	1:K:5479:PHE:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:5548:GLY:O	1:K:5551:GLN:HG2	2.19	0.41
1:M:6304:ALA:HB1	1:M:6321:ALA:HA	2.02	0.41
1:P:8133:LEU:HD12	1:P:8133:LEU:HA	1.86	0.41
1:A:438:LEU:HD12	1:A:438:LEU:HA	1.86	0.41
1:C:1049:ARG:NH1	1:C:1125:ARG:HD3	2.35	0.41
1:C:1076:VAL:O	1:C:1076:VAL:HG13	2.19	0.41
1:C:1174:ALA:HB1	1:C:1191:ALA:HA	2.02	0.41
1:C:1473:ILE:CB	1:O:7604:LEU:CG	2.80	0.41
1:K:5180:VAL:O	1:K:5180:VAL:HG13	2.19	0.41
1:M:6179:ARG:NH1	1:M:6255:ARG:HD3	2.35	0.41
1:P:7788:VAL:CG1	1:P:7789:ALA:N	2.82	0.41
1:B:960:ILE:HG21	1:P:8117:LEU:CG	2.49	0.41
1:E:2181:LEU:HB3	1:E:2538:LEU:HD11	2.03	0.41
1:F:3003:LEU:HD12	1:F:3003:LEU:HA	1.86	0.41
1:H:4038:ILE:HD12	1:J:5039:LEU:HG	2.01	0.41
1:M:6206:VAL:O	1:M:6206:VAL:HG13	2.19	0.41
1:A:63:SER:O	1:H:3594:PRO:HD3	2.21	0.41
1:B:536:ARG:NH1	1:B:612:ARG:HD3	2.35	0.41
1:B:661:ALA:HB1	1:B:678:ALA:HA	2.02	0.41
1:D:1542:PRO:HD3	1:E:2115:SER:O	2.21	0.41
1:D:1562:ARG:NH1	1:D:1638:ARG:HD3	2.35	0.41
1:F:2658:VAL:CG1	1:F:2659:ALA:N	2.82	0.41
1:F:2987:LEU:CG	1:L:6090:ILE:HG21	2.49	0.41
1:J:4640:ARG:NH1	1:J:4716:ARG:HD3	2.35	0.41
1:L:5791:ALA:HB1	1:L:5808:ALA:HA	2.02	0.41
1:O:7185:PRO:HD3	1:P:7758:SER:O	2.21	0.41
1:O:7311:LEU:HB3	1:O:7668:LEU:HD11	2.03	0.41
1:B:516:PRO:HD3	1:C:1089:SER:O	2.21	0.41
1:C:1155:LEU:HB3	1:C:1512:LEU:HD11	2.03	0.41
1:E:2055:PRO:HD3	1:F:2628:SER:O	2.21	0.41
1:H:3614:ARG:NH1	1:H:3690:ARG:HD3	2.35	0.41
1:H:4013:LEU:HG	1:J:5064:ILE:HD12	2.01	0.41
1:J:4824:LEU:C	1:J:4824:LEU:CD2	2.90	0.41
1:L:5666:ARG:NH1	1:L:5742:ARG:HD3	2.35	0.41
1:N:6692:ARG:NH1	1:N:6768:ARG:HD3	2.35	0.41
1:G:3081:PRO:HD3	1:H:3654:SER:O	2.21	0.41
1:H:3798:LEU:C	1:H:3798:LEU:CD2	2.90	0.41
1:I:4107:PRO:HD3	1:J:4680:SER:O	2.21	0.41
1:K:5132:LEU:HA	1:K:5133:PRO:HD3	1.95	0.41
1:L:5646:PRO:HD3	1:M:6219:SER:O	2.21	0.41
1:L:5772:LEU:HB3	1:L:6129:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:6285:LEU:HB3	1:M:6642:LEU:HD11	2.03	0.41
1:A:2:LEU:HA	1:A:3:PRO:HD3	1.95	0.41
1:A:422:LEU:CG	1:I:4551:ILE:CB	2.80	0.41
1:B:642:LEU:HB3	1:B:999:LEU:HD11	2.03	0.41
1:F:2680:VAL:HG13	1:F:2681:LYS:N	2.36	0.41
1:F:2713:ALA:HB1	1:F:2730:ALA:HA	2.02	0.41
1:J:4620:PRO:HD3	1:K:5193:SER:O	2.21	0.41
1:N:6672:PRO:HD3	1:O:7245:SER:O	2.21	0.41
1:N:6798:LEU:HB3	1:N:7155:LEU:HD11	2.03	0.41
1:A:3:PRO:HD3	1:B:576:SER:O	2.21	0.41
1:C:1141:VAL:HG13	1:C:1142:LYS:N	2.36	0.41
1:D:1668:LEU:HB3	1:D:2025:LEU:HD11	2.03	0.41
1:G:3207:LEU:HB3	1:G:3564:LEU:HD11	2.03	0.41
1:H:4013:LEU:CG	1:J:5064:ILE:CB	2.80	0.41
1:H:4038:ILE:HD11	1:J:4721:LEU:CD2	2.51	0.41
1:P:7810:VAL:HG13	1:P:7811:LYS:N	2.36	0.41
1:P:7843:ALA:HB1	1:P:7860:ALA:HA	2.02	0.41
1:A:129:LEU:HB3	1:A:486:LEU:HD11	2.03	0.40
1:F:3012:ILE:HD11	1:L:5747:LEU:CD2	2.51	0.40
1:H:3695:LEU:CD2	1:J:5064:ILE:HD11	2.52	0.40
1:I:4233:LEU:HB3	1:I:4590:LEU:HD11	2.03	0.40
1:I:4542:LEU:HD12	1:I:4542:LEU:HA	1.86	0.40
1:J:4765:ALA:HB1	1:J:4782:ALA:HA	2.02	0.40
1:K:5133:PRO:HD3	1:L:5706:SER:O	2.21	0.40
1:M:6271:VAL:HG13	1:M:6272:LYS:N	2.36	0.40
1:N:7103:ILE:HB	1:N:7104:PRO:CD	2.46	0.40
1:B:617:LEU:CD2	1:P:8142:ILE:HD11	2.52	0.40
1:G:3193:VAL:HG13	1:G:3194:LYS:N	2.36	0.40
1:H:3739:ALA:HB1	1:H:3756:ALA:HA	2.02	0.40
1:I:4219:VAL:HG13	1:I:4220:LYS:N	2.36	0.40
1:K:5259:LEU:HB3	1:K:5616:LEU:HD11	2.03	0.40
1:K:5278:ALA:HB1	1:K:5295:ALA:HA	2.02	0.40
1:A:148:ALA:HB1	1:A:165:ALA:HA	2.02	0.40
1:E:2075:ARG:NH1	1:E:2151:ARG:HD3	2.35	0.40
1:F:3012:ILE:HG21	1:L:6065:LEU:CG	2.49	0.40
1:L:5906:LEU:C	1:L:5906:LEU:CD2	2.95	0.40
1:P:7824:LEU:HB3	1:P:8181:LEU:HD11	2.03	0.40
1:A:32:THR:CG2	1:A:53:ASN:HB2	2.52	0.40
1:A:419:ARG:NE	1:I:4549:ASP:OD2	2.54	0.40
1:A:447:ILE:HD11	1:I:4208:LEU:CD2	2.52	0.40
1:B:606:VAL:HG13	1:B:607:ALA:N	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:776:LEU:C	1:B:776:LEU:CD2	2.95	0.40
1:B:935:LEU:CG	1:P:8142:ILE:HG21	2.49	0.40
1:C:1130:LEU:CD2	1:O:7629:ILE:HD11	2.52	0.40
1:D:1643:LEU:CD2	1:N:7116:ILE:HD11	2.52	0.40
1:D:1986:ILE:HD11	1:N:6773:LEU:CD2	2.51	0.40
1:E:2499:ILE:HD11	1:M:6260:LEU:CD2	2.52	0.40
1:F:2568:PRO:HD3	1:G:3141:SER:O	2.21	0.40
1:F:2694:LEU:HB3	1:F:3051:LEU:HD11	2.03	0.40
1:G:3516:LEU:HD12	1:G:3516:LEU:HA	1.86	0.40
1:I:4367:LEU:C	1:I:4367:LEU:CD2	2.95	0.40
1:K:5162:THR:CG2	1:K:5183:ASN:HB2	2.52	0.40
1:O:7205:ARG:NH1	1:O:7281:ARG:HD3	2.35	0.40
1:O:7620:LEU:HD12	1:O:7620:LEU:HA	1.86	0.40
1:A:104:LEU:CD2	1:I:4551:ILE:HD11	2.52	0.40
1:A:115:VAL:HG13	1:A:116:LYS:N	2.36	0.40
1:B:960:ILE:HD11	1:P:7799:LEU:CD2	2.51	0.40
1:D:1973:ILE:HB	1:D:1974:PRO:CD	2.46	0.40
1:G:3226:ALA:HB1	1:G:3243:ALA:HA	2.02	0.40
1:G:3341:LEU:C	1:G:3341:LEU:CD2	2.95	0.40
1:G:3523:ASP:OD2	1:K:5549:ARG:NE	2.54	0.40
1:G:3525:ILE:CB	1:K:5552:LEU:CG	2.80	0.40
1:G:3525:ILE:HD11	1:K:5234:LEU:CD2	2.52	0.40
1:H:4038:ILE:CB	1:J:5039:LEU:CG	2.80	0.40
1:I:4252:ALA:HB1	1:I:4269:ALA:HA	2.02	0.40
1:K:5245:VAL:HG13	1:K:5246:LYS:N	2.36	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	A	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12 49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	C	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	D	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	E	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	F	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	G	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	H	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	I	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	J	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	K	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	L	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	M	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	N	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	O	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
1	P	511/513 (100%)	486 (95%)	20 (4%)	5 (1%)	12	49
All	All	8176/8208 (100%)	7776 (95%)	320 (4%)	80 (1%)	15	49

All (80) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	B	518	ASN
1	C	1031	ASN
1	D	1544	ASN
1	E	2057	ASN
1	F	2570	ASN
1	G	3083	ASN
1	H	3596	ASN
1	I	4109	ASN
1	J	4622	ASN
1	K	5135	ASN
1	L	5648	ASN
1	M	6161	ASN
1	N	6674	ASN
1	O	7187	ASN
1	P	7700	ASN
1	A	354	LYS

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Mol	Chain	Res	Type
1	A	465	ALA
1	A	466	GLY
1	B	867	LYS
1	B	978	ALA
1	B	979	GLY
1	C	1380	LYS
1	C	1491	ALA
1	C	1492	GLY
1	D	1893	LYS
1	D	2004	ALA
1	D	2005	GLY
1	E	2406	LYS
1	E	2517	ALA
1	E	2518	GLY
1	F	2919	LYS
1	F	3030	ALA
1	F	3031	GLY
1	G	3432	LYS
1	G	3543	ALA
1	G	3544	GLY
1	H	3945	LYS
1	H	4056	ALA
1	H	4057	GLY
1	I	4458	LYS
1	I	4569	ALA
1	I	4570	GLY
1	J	4971	LYS
1	J	5082	ALA
1	J	5083	GLY
1	K	5484	LYS
1	K	5595	ALA
1	K	5596	GLY
1	L	5997	LYS
1	L	6108	ALA
1	L	6109	GLY
1	M	6510	LYS
1	M	6621	ALA
1	M	6622	GLY
1	N	7023	LYS
1	N	7134	ALA
1	N	7135	GLY
1	O	7536	LYS

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Mol	Chain	Res	Type
1	O	7647	ALA
1	O	7648	GLY
1	P	8049	LYS
1	P	8160	ALA
1	P	8161	GLY
1	A	392	GLY
1	B	905	GLY
1	C	1418	GLY
1	D	1931	GLY
1	E	2444	GLY
1	F	2957	GLY
1	G	3470	GLY
1	H	3983	GLY
1	I	4496	GLY
1	J	5009	GLY
1	K	5522	GLY
1	L	6035	GLY
1	M	6548	GLY
1	N	7061	GLY
1	O	7574	GLY
1	P	8087	GLY

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	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	B	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	C	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	D	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	E	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	F	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	G	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	H	414/414 (100%)	407 (98%)	7 (2%)	53	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	J	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	K	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	L	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	M	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	N	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	O	414/414 (100%)	407 (98%)	7 (2%)	53	69
1	P	414/414 (100%)	407 (98%)	7 (2%)	53	69
All	All	6624/6624 (100%)	6512 (98%)	112 (2%)	52	69

All (112) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LEU
1	A	98	LEU
1	A	129	LEU
1	A	144	LEU
1	A	389	ILE
1	A	419	ARG
1	A	438	LEU
1	B	533	LEU
1	B	611	LEU
1	B	642	LEU
1	B	657	LEU
1	B	902	ILE
1	B	932	ARG
1	B	951	LEU
1	C	1046	LEU
1	C	1124	LEU
1	C	1155	LEU
1	C	1170	LEU
1	C	1415	ILE
1	C	1445	ARG
1	C	1464	LEU
1	D	1559	LEU
1	D	1637	LEU
1	D	1668	LEU
1	D	1683	LEU
1	D	1928	ILE

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Mol	Chain	Res	Type
1	D	1958	ARG
1	D	1977	LEU
1	E	2072	LEU
1	E	2150	LEU
1	E	2181	LEU
1	E	2196	LEU
1	E	2441	ILE
1	E	2471	ARG
1	E	2490	LEU
1	F	2585	LEU
1	F	2663	LEU
1	F	2694	LEU
1	F	2709	LEU
1	F	2954	ILE
1	F	2984	ARG
1	F	3003	LEU
1	G	3098	LEU
1	G	3176	LEU
1	G	3207	LEU
1	G	3222	LEU
1	G	3467	ILE
1	G	3497	ARG
1	G	3516	LEU
1	H	3611	LEU
1	H	3689	LEU
1	H	3720	LEU
1	H	3735	LEU
1	H	3980	ILE
1	H	4010	ARG
1	H	4029	LEU
1	I	4124	LEU
1	I	4202	LEU
1	I	4233	LEU
1	I	4248	LEU
1	I	4493	ILE
1	I	4523	ARG
1	I	4542	LEU
1	J	4637	LEU
1	J	4715	LEU
1	J	4746	LEU
1	J	4761	LEU
1	J	5006	ILE

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Mol	Chain	Res	Type
1	J	5036	ARG
1	J	5055	LEU
1	K	5150	LEU
1	K	5228	LEU
1	K	5259	LEU
1	K	5274	LEU
1	K	5519	ILE
1	K	5549	ARG
1	K	5568	LEU
1	L	5663	LEU
1	L	5741	LEU
1	L	5772	LEU
1	L	5787	LEU
1	L	6032	ILE
1	L	6062	ARG
1	L	6081	LEU
1	M	6176	LEU
1	M	6254	LEU
1	M	6285	LEU
1	M	6300	LEU
1	M	6545	ILE
1	M	6575	ARG
1	M	6594	LEU
1	N	6689	LEU
1	N	6767	LEU
1	N	6798	LEU
1	N	6813	LEU
1	N	7058	ILE
1	N	7088	ARG
1	N	7107	LEU
1	O	7202	LEU
1	O	7280	LEU
1	O	7311	LEU
1	O	7326	LEU
1	O	7571	ILE
1	O	7601	ARG
1	O	7620	LEU
1	P	7715	LEU
1	P	7793	LEU
1	P	7824	LEU
1	P	7839	LEU
1	P	8084	ILE

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Mol	Chain	Res	Type
1	P	8114	ARG
1	P	8133	LEU

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

Mol	Chain	Res	Type
1	A	139	GLN
1	A	462	ASN
1	B	652	GLN
1	B	975	ASN
1	C	1165	GLN
1	D	1678	GLN
1	D	1908	HIS
1	D	2001	ASN
1	E	2191	GLN
1	E	2421	HIS
1	E	2514	ASN
1	F	2704	GLN
1	F	3027	ASN
1	G	3540	ASN
1	H	3730	GLN
1	H	4053	ASN
1	I	4566	ASN
1	J	4756	GLN
1	J	5079	ASN
1	K	5269	GLN
1	K	5592	ASN
1	L	5782	GLN
1	L	6105	ASN
1	M	6295	GLN
1	N	6808	GLN
1	N	7038	HIS
1	N	7131	ASN
1	O	7321	GLN
1	O	7551	HIS
1	O	7644	ASN
1	P	7834	GLN
1	P	8064	HIS
1	P	8157	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

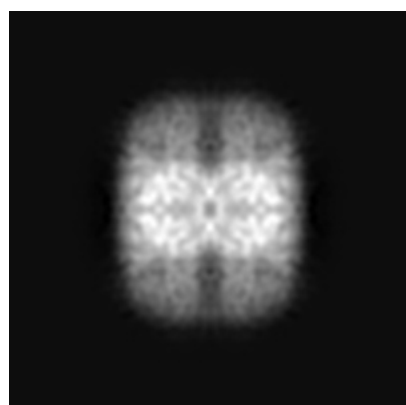
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5244. These allow visual inspection of the internal detail of the map and identification of artifacts.

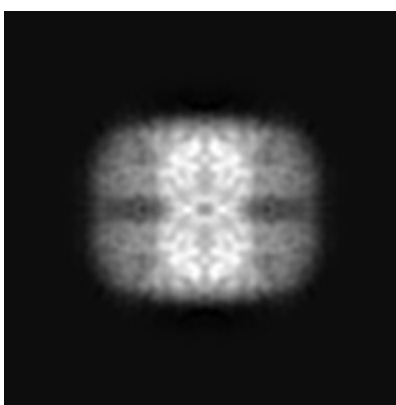
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

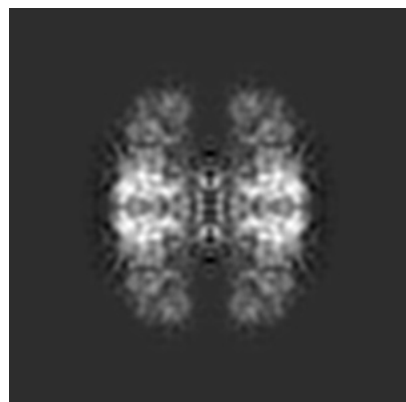


Z

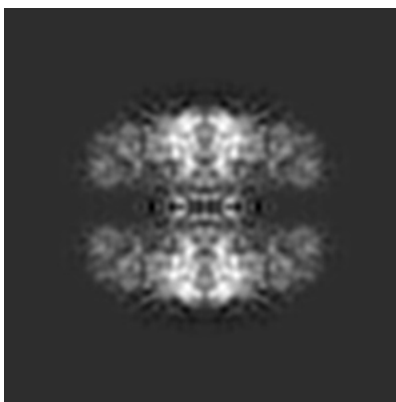
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 96



Y Index: 96

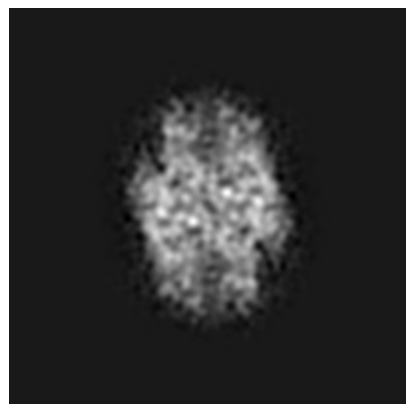


Z Index: 96

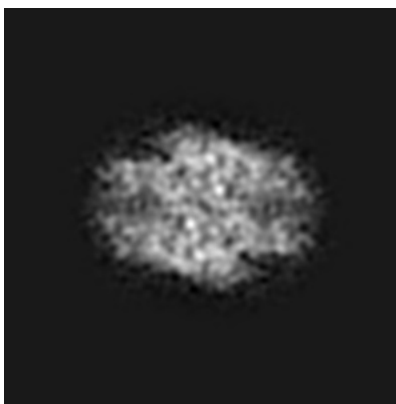
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

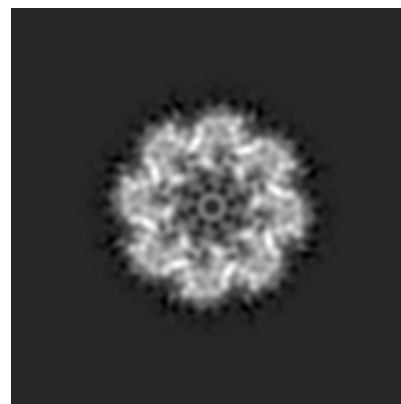
6.3.1 Primary map



X Index: 66



Y Index: 126

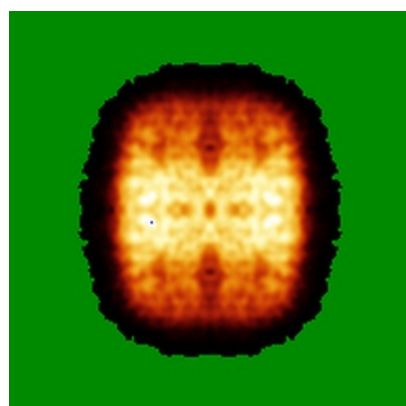


Z Index: 90

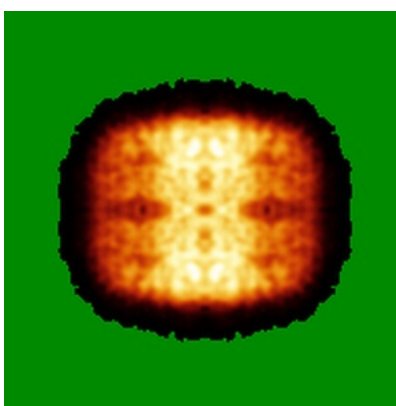
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

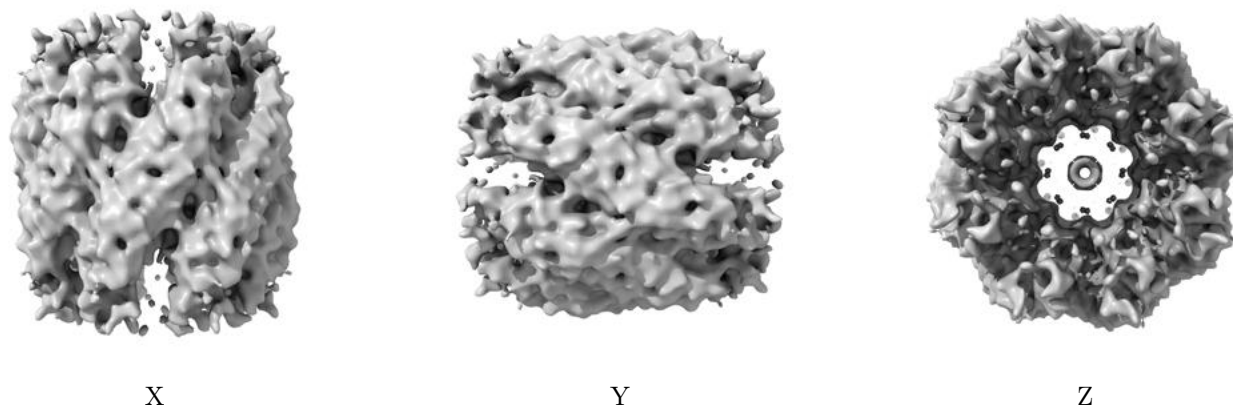


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

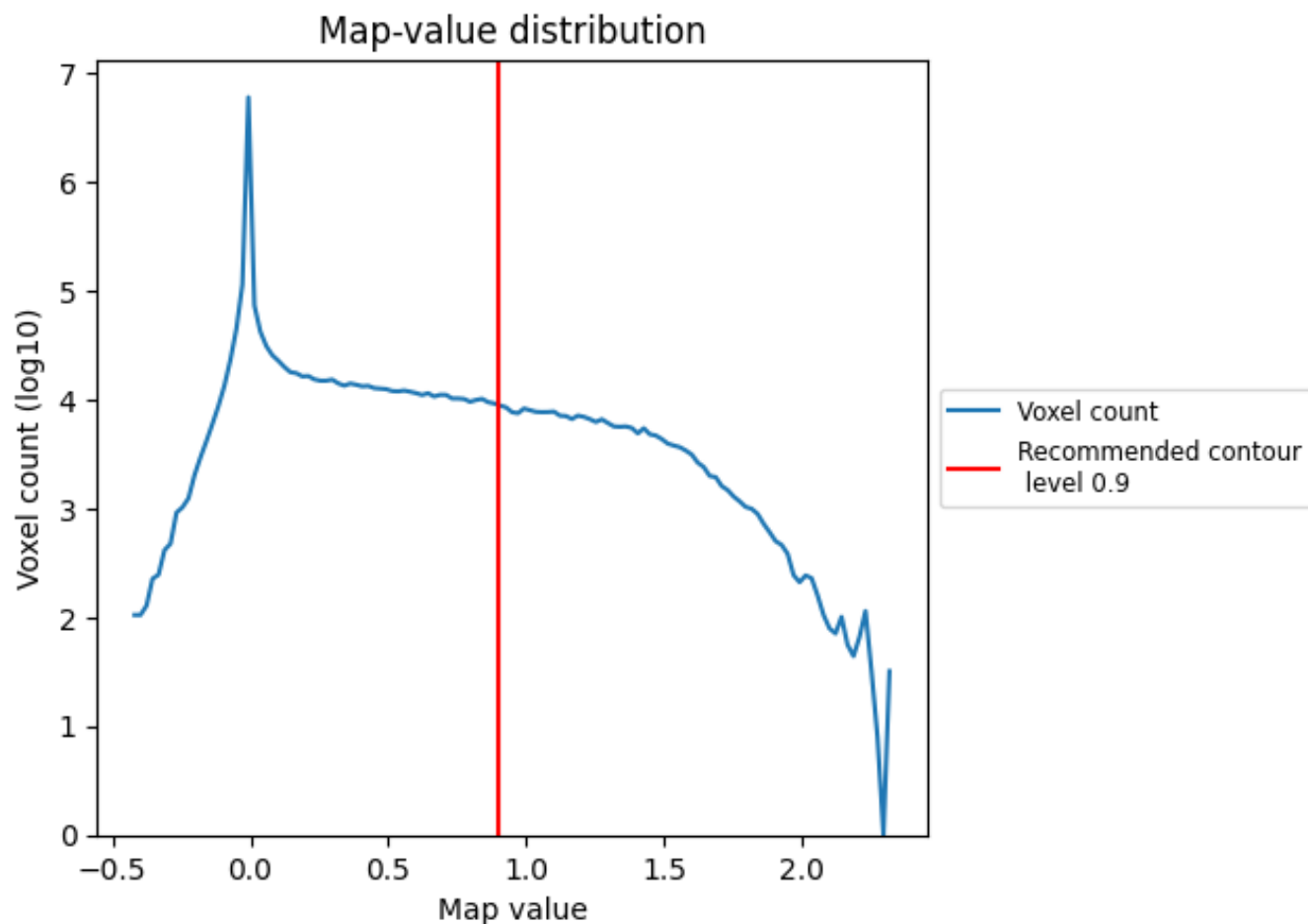
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

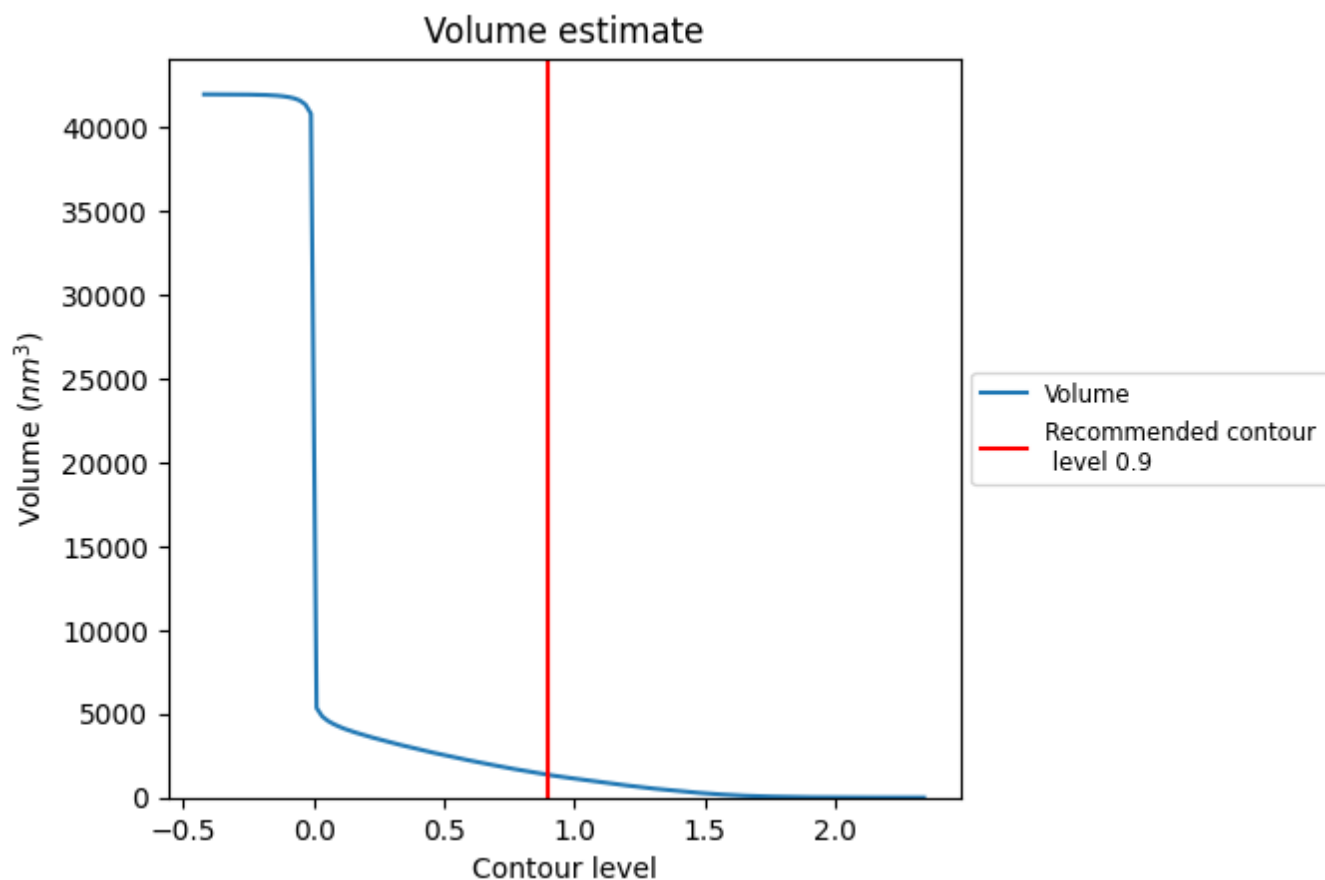
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

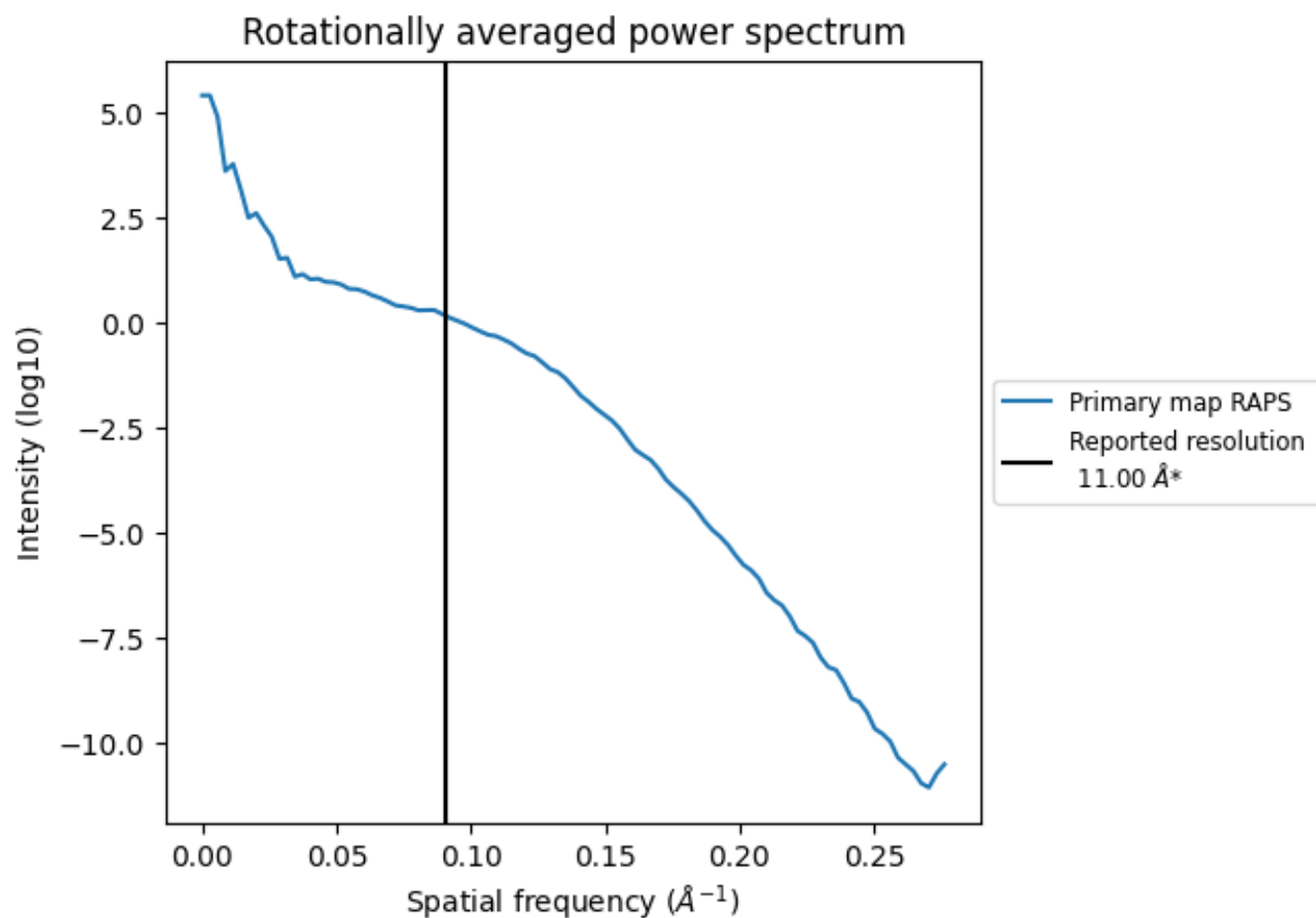
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1356 nm³; this corresponds to an approximate mass of 1225 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.091 Å⁻¹

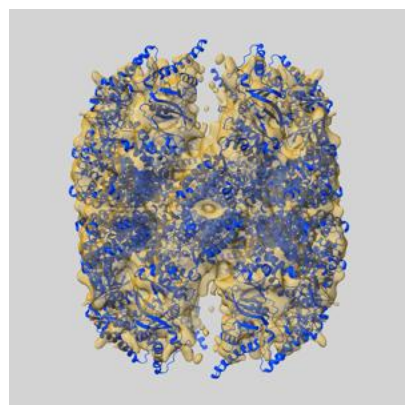
8 Fourier-Shell correlation ⓘ

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

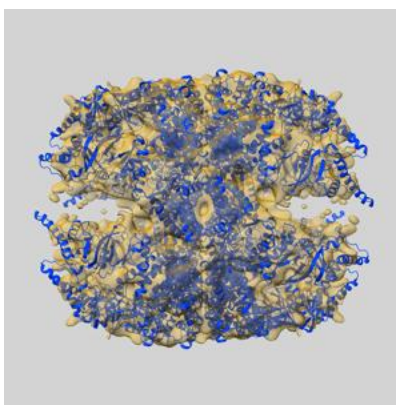
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5244 and PDB model 3IZH. Per-residue inclusion information can be found in section [3](#) on page [5](#).

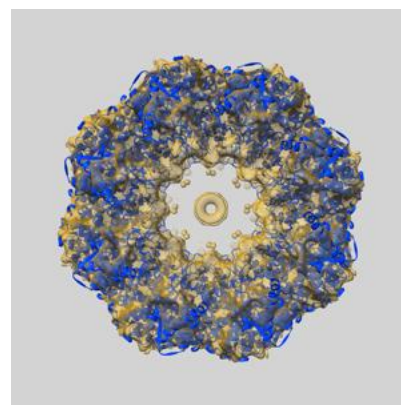
9.1 Map-model overlay [i](#)



X



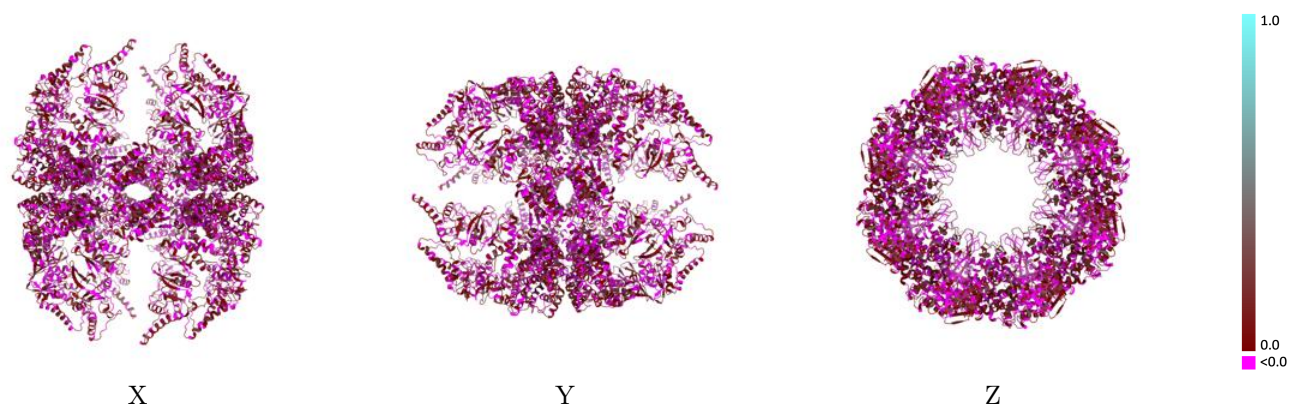
Y



Z

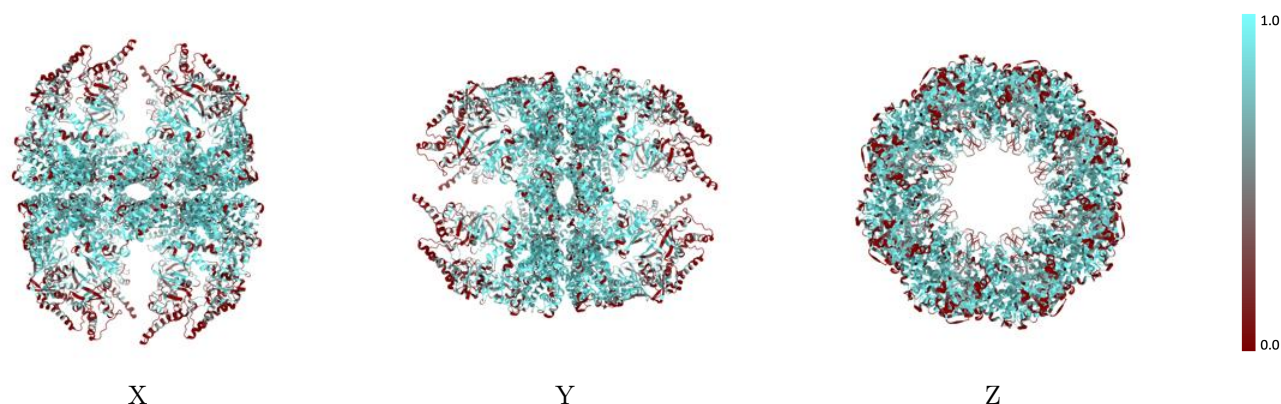
The images above show the 3D surface view of the map at the recommended contour level 0.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



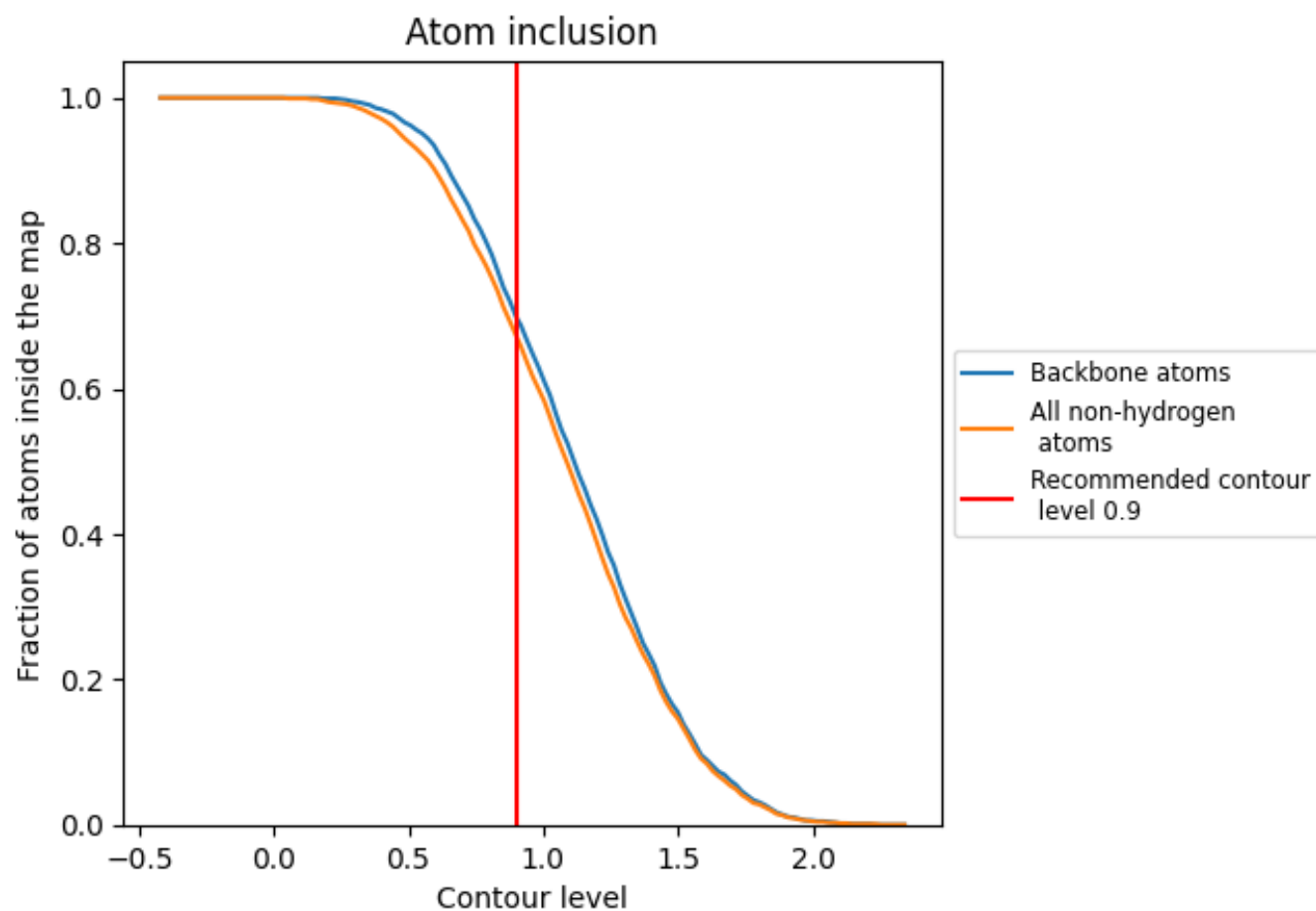
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 67% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6720	0.0340
A	0.6720	0.0350
B	0.6720	0.0340
C	0.6720	0.0350
D	0.6710	0.0350
E	0.6720	0.0340
F	0.6710	0.0330
G	0.6720	0.0330
H	0.6720	0.0330
I	0.6720	0.0330
J	0.6710	0.0330
K	0.6720	0.0330
L	0.6720	0.0320
M	0.6720	0.0340
N	0.6720	0.0340
O	0.6720	0.0340
P	0.6720	0.0350

1.0

0.0

<0.0