Full wwPDB EM Validation Report (i)

Mar 8, 2026 – 03:53 AM UTC

PDB ID	:	5W0S / pdb_00005w0s
EMDB ID	:	EMD-8750
Title	:	GroEL using cryoEM
Authors	:	Roh, S.H.; Chiu, W.
Deposited on	:	2017-05-31
Resolution	:	3.50 Å(reported)

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

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

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

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

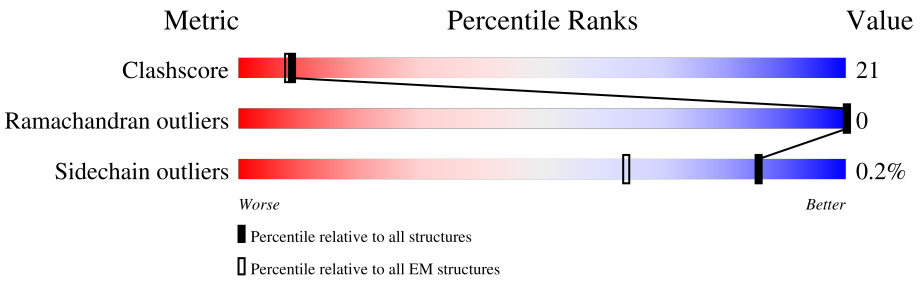
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh &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

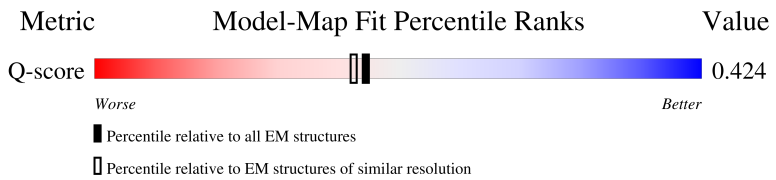
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.50 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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-A	524	15% 81% 19%
1	1-B	524	15% 81% 19%
1	1-C	524	16% 80% 20%
1	1-D	524	15% 80% 20%

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Mol	Chain	Length	Quality of chain
1	1-E	524	16% 80% 20%
1	1-F	524	16% 81% 19%
1	1-G	524	16% 80% 20%
1	1-H	524	16% 80% 20%
1	1-I	524	15% 81% 19%
1	1-J	524	15% 81% 19%
1	1-K	524	16% 80% 20%
1	1-L	524	15% 80% 20%
1	1-M	524	15% 80% 20%
1	1-N	524	15% 80% 20%
1	2-A	524	50% 50%
1	2-B	524	100%
1	2-C	524	100%
1	2-D	524	100%
1	2-E	524	100%
1	2-F	524	100%
1	2-G	524	100%
1	2-H	524	100%
1	2-I	524	100%
1	2-J	524	100%
1	2-K	524	100%
1	2-L	524	100%
1	2-M	524	100%
1	2-N	524	100%
1	3-A	524	56% 44%

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Mol	Chain	Length	Quality of chain
1	3-B	524	100%
1	3-C	524	100%
1	3-D	524	100%
1	3-E	524	100%
1	3-F	524	100%
1	3-G	524	100%
1	3-H	524	100%
1	3-I	524	100%
1	3-J	524	100%
1	3-K	524	100%
1	3-L	524	100%
1	3-M	524	100%
1	3-N	524	100%
1	4-A	524	61% 39%
1	4-B	524	100%
1	4-C	524	100%
1	4-D	524	100%
1	4-E	524	100%
1	4-F	524	100%
1	4-G	524	100%
1	4-H	524	100%
1	4-I	524	100%
1	4-J	524	100%
1	4-K	524	100%
1	4-L	524	100%

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Mol	Chain	Length	Quality of chain
1	4-M	524	100%
1	4-N	524	100%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 65574 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 60 kDa chaperonin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	1-A	524	3851	2395	662	774	20	0	0
1	2-A	524	3851	2395	662	774	20	0	0
1	3-A	524	3851	2395	662	774	20	0	0
1	4-A	524	3851	2395	662	774	20	0	0
1	1-B	524	3851	2395	662	774	20	0	0
1	1-C	524	3851	2395	662	774	20	0	0
1	1-D	524	3851	2395	662	774	20	0	0
1	1-E	524	3851	2395	662	774	20	0	0
1	1-F	524	3851	2395	662	774	20	0	0
1	1-G	524	3851	2395	662	774	20	0	0
1	1-H	524	3851	2395	662	774	20	0	0
1	1-I	524	3851	2395	662	774	20	0	0
1	1-J	524	3851	2395	662	774	20	0	0
1	1-K	524	3851	2395	662	774	20	0	0
1	1-L	524	3851	2395	662	774	20	0	0
1	1-M	524	3851	2395	662	774	20	0	0
1	1-N	524	3851	2395	662	774	20	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	GLY	ARG	conflict	UNP Q6Q099
B	13	GLY	ARG	conflict	UNP Q6Q099
C	13	GLY	ARG	conflict	UNP Q6Q099
D	13	GLY	ARG	conflict	UNP Q6Q099
E	13	GLY	ARG	conflict	UNP Q6Q099
F	13	GLY	ARG	conflict	UNP Q6Q099
G	13	GLY	ARG	conflict	UNP Q6Q099
H	13	GLY	ARG	conflict	UNP Q6Q099
I	13	GLY	ARG	conflict	UNP Q6Q099
J	13	GLY	ARG	conflict	UNP Q6Q099
K	13	GLY	ARG	conflict	UNP Q6Q099
L	13	GLY	ARG	conflict	UNP Q6Q099
M	13	GLY	ARG	conflict	UNP Q6Q099
N	13	GLY	ARG	conflict	UNP Q6Q099

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		AltConf
			Total	O	
2	1-A	19	19	19	0
			Total	O	
2	1-B	12	12	12	0
			Total	O	
2	1-C	14	14	14	0
			Total	O	
2	1-D	14	14	14	0
			Total	O	
2	1-E	10	10	10	0
			Total	O	
2	1-F	6	6	6	0
			Total	O	
2	1-G	13	13	13	0
			Total	O	
2	1-H	1	1	1	0
			Total	O	
2	1-I	3	3	3	0
			Total	O	
2	1-J	5	5	5	0
			Total	O	
2	1-K	1	1	1	0
			Total	O	
2	1-L	2	2	2	0

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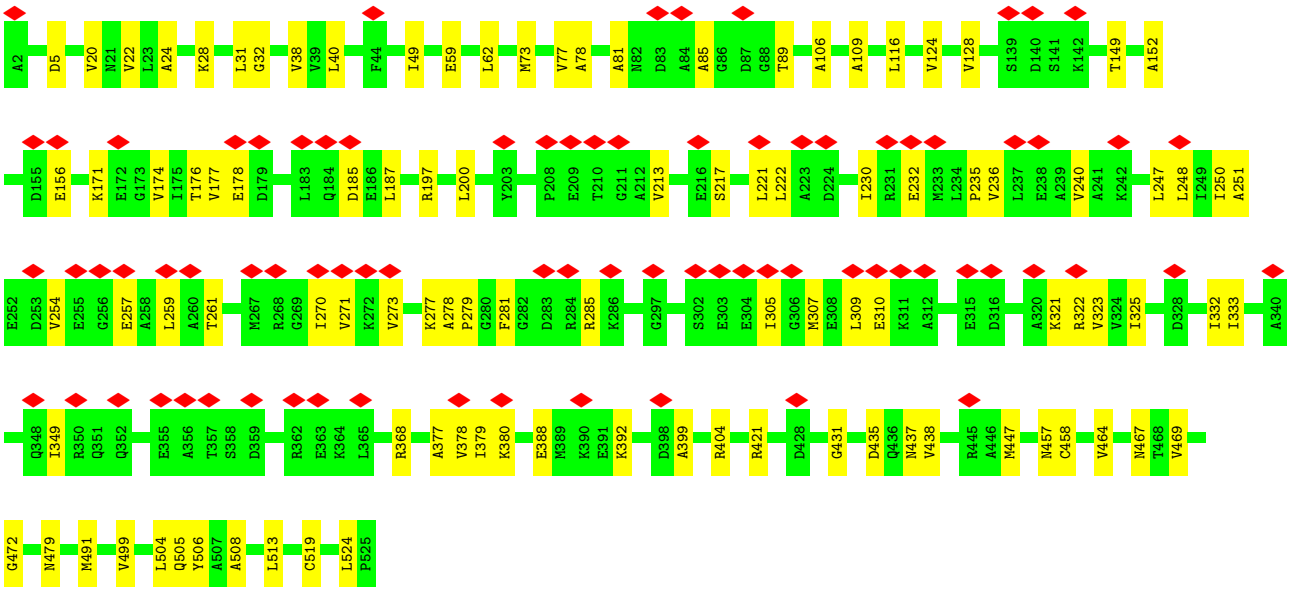
Mol	Chain	Residues	Atoms		AltConf
			Total	O	
2	1-M	5	5	5	0
			Total	O	
2	1-N	2	2	2	0

3 Residue-property plots (i)

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

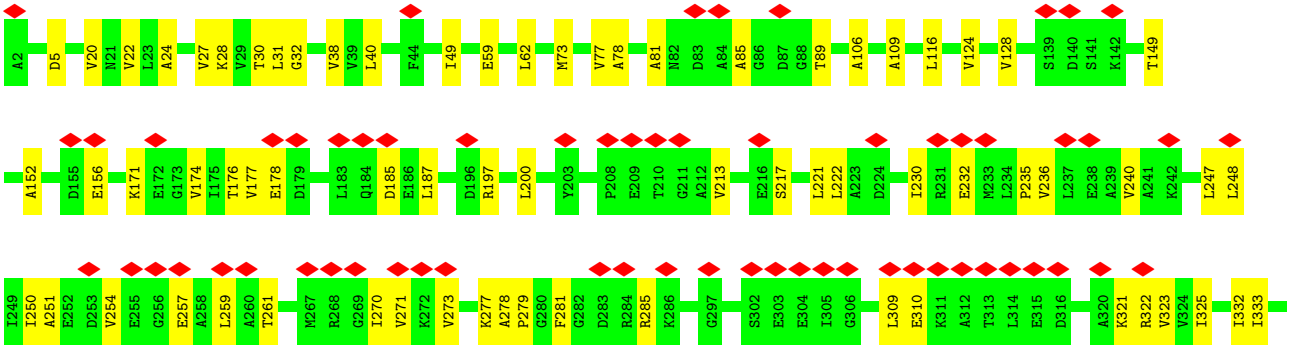
- Molecule 1: 60 kDa chaperonin

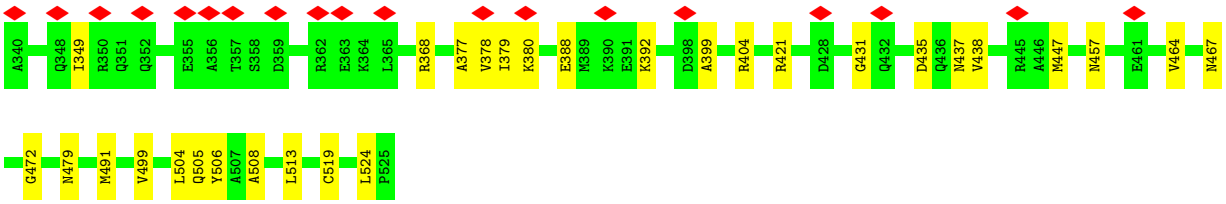
Chain 1-A:



- Molecule 1: 60 kDa chaperonin

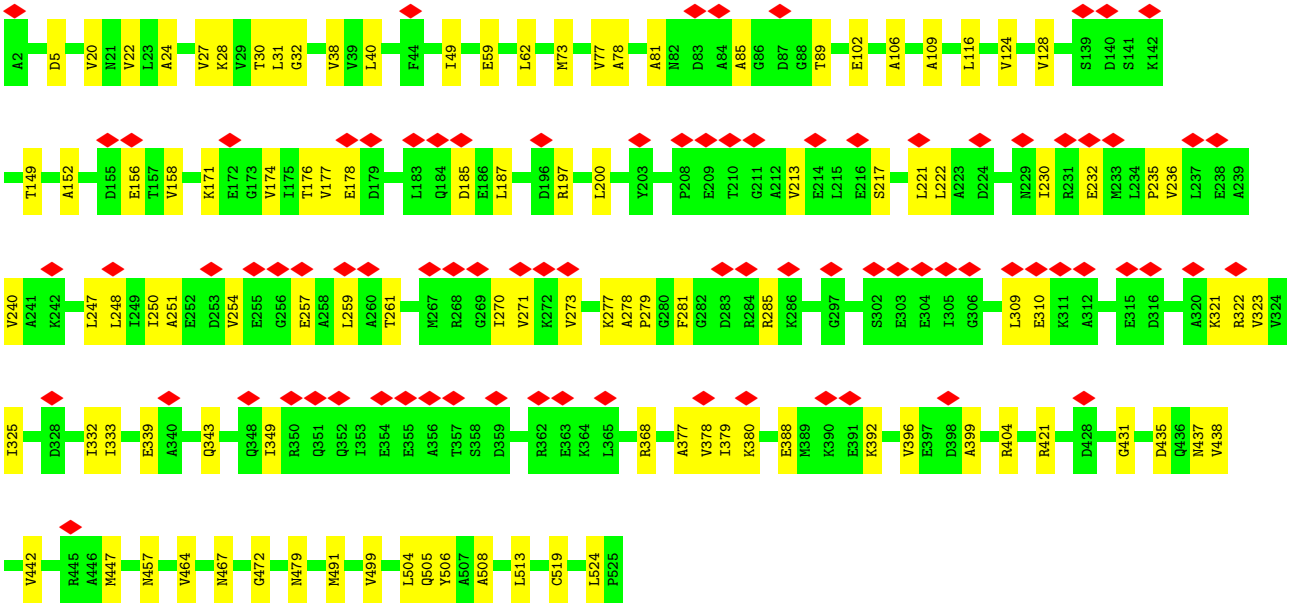
Chain 1-B:





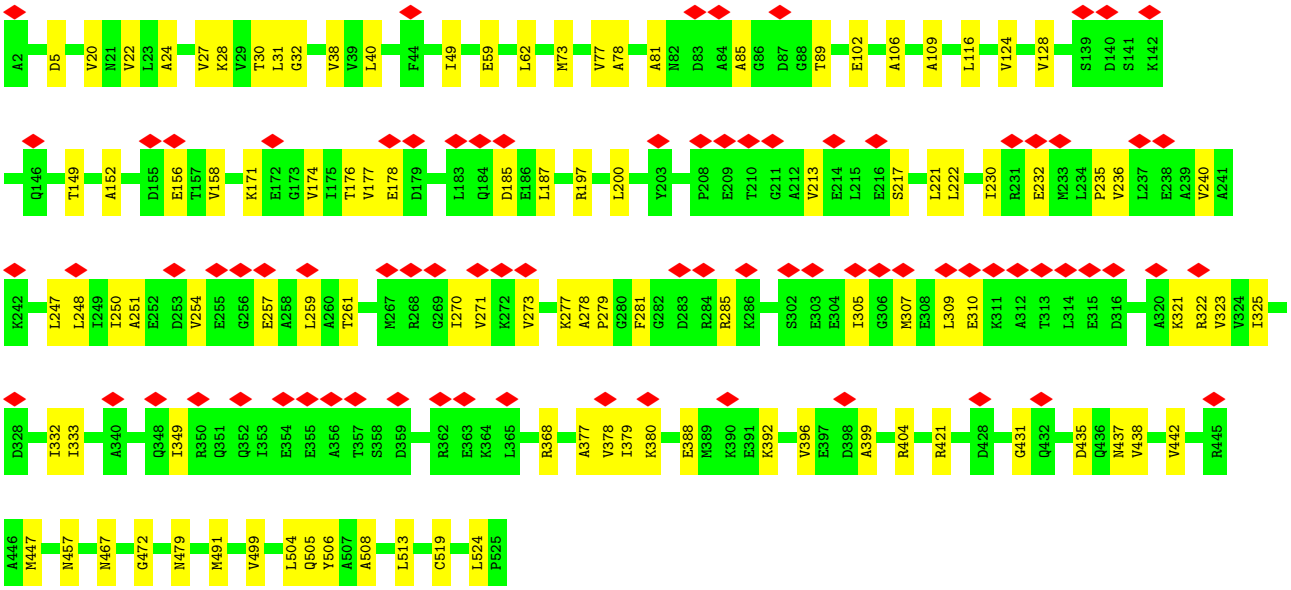
- Molecule 1: 60 kDa chaperonin

Chain 1-C:



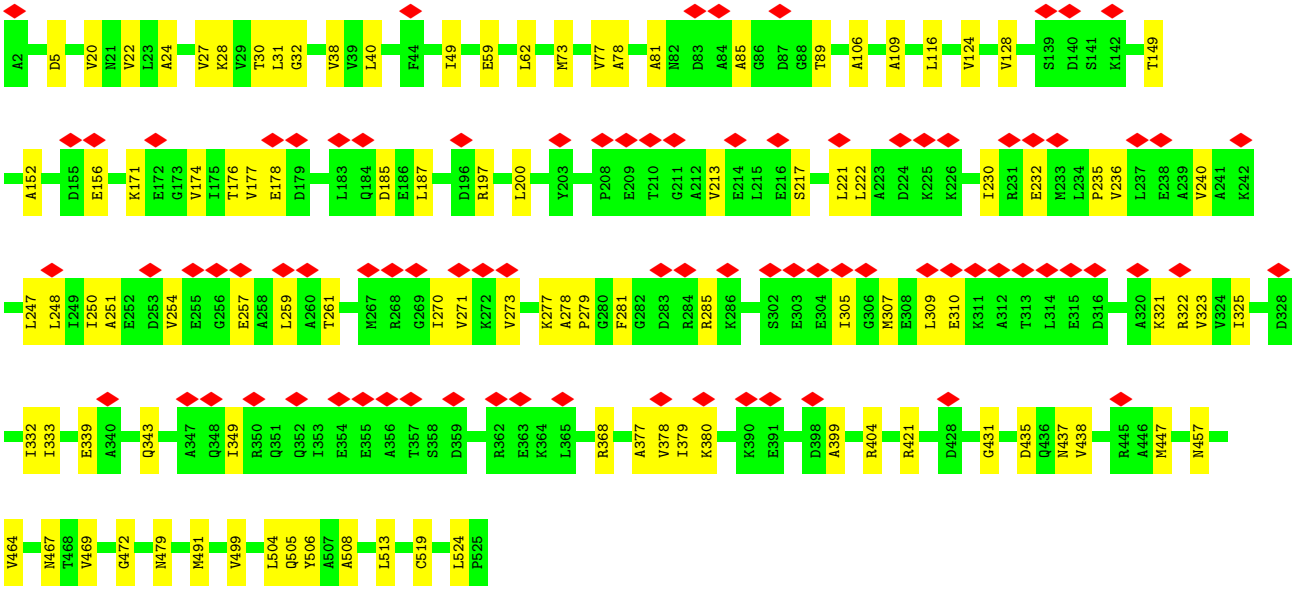
- Molecule 1: 60 kDa chaperonin

Chain 1-D:



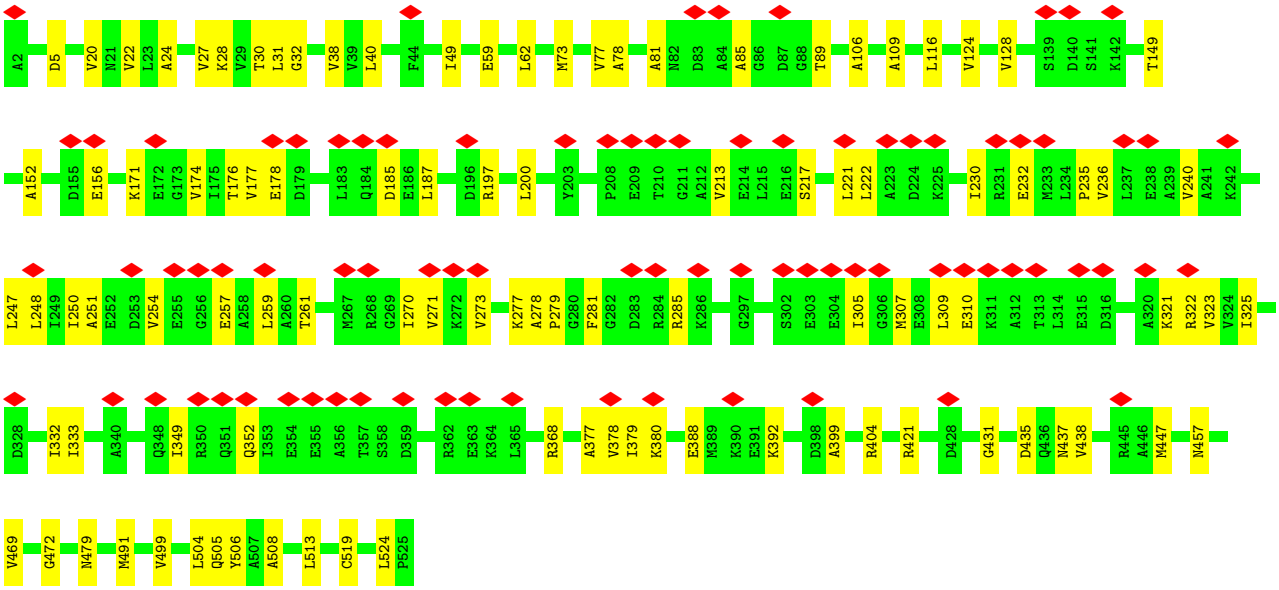
- Molecule 1: 60 kDa chaperonin

Chain 1-E:



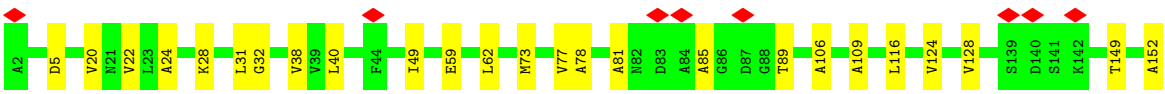
- Molecule 1: 60 kDa chaperonin

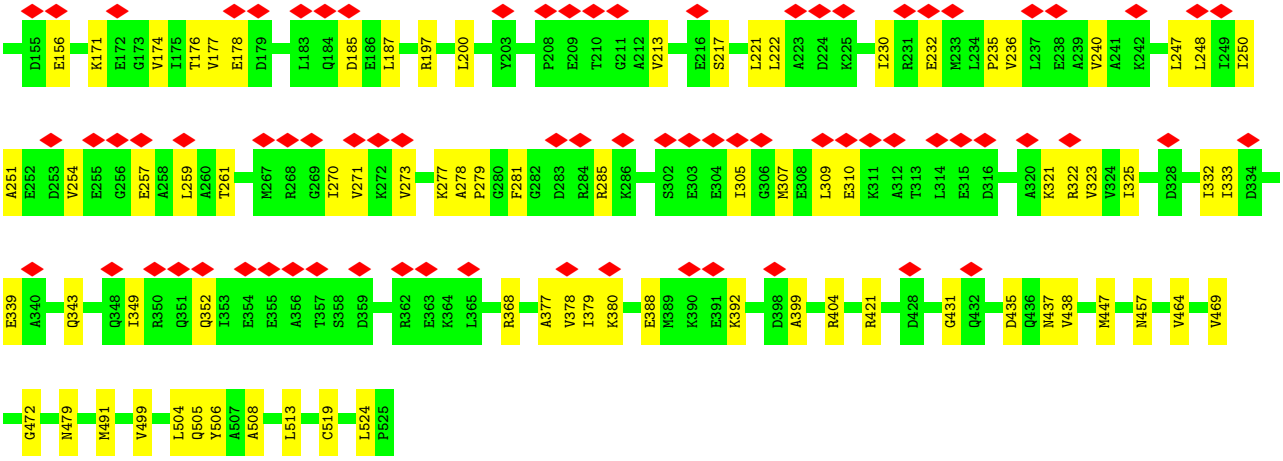
Chain 1-F:



- Molecule 1: 60 kDa chaperonin

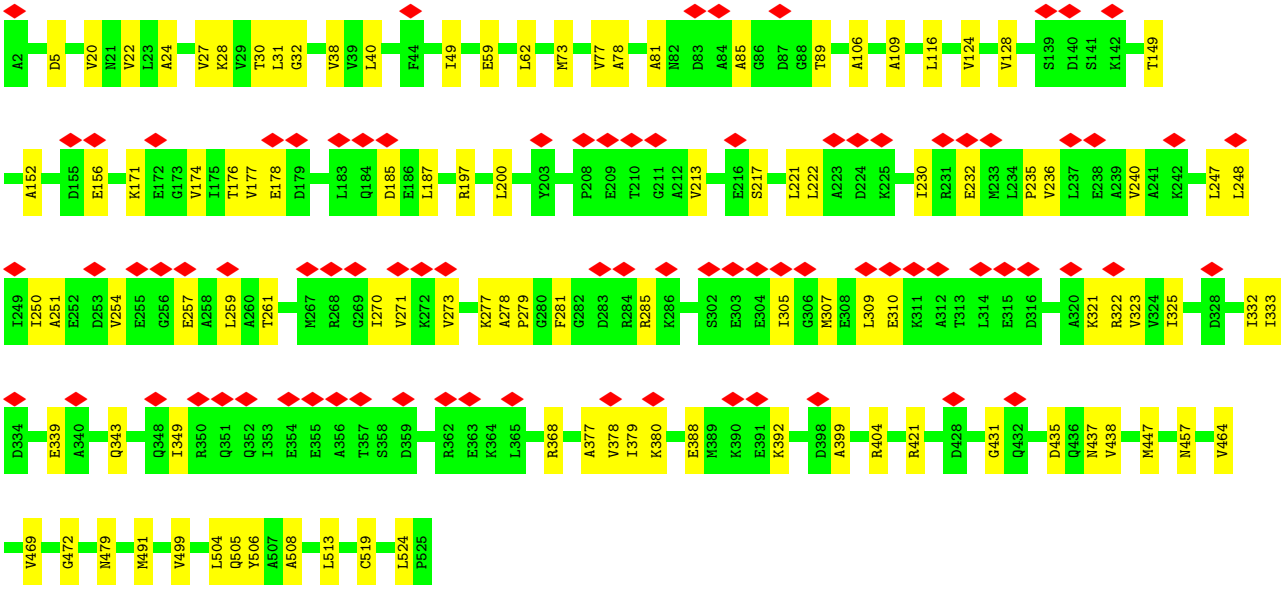
Chain 1-G:





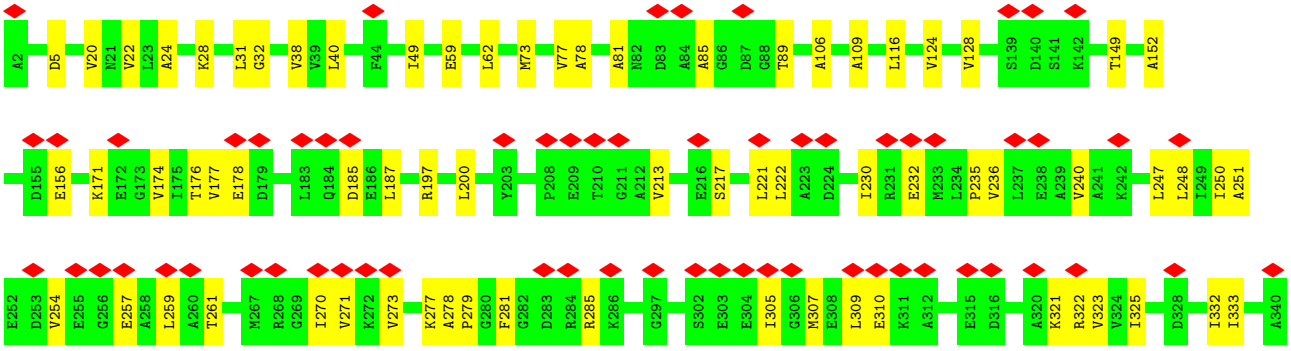
- Molecule 1: 60 kDa chaperonin

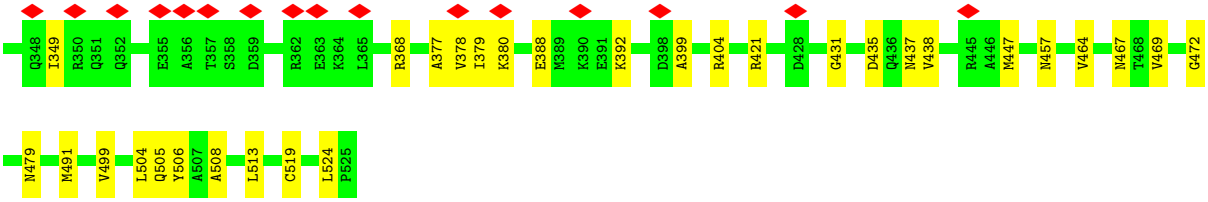
Chain 1-H:



- Molecule 1: 60 kDa chaperonin

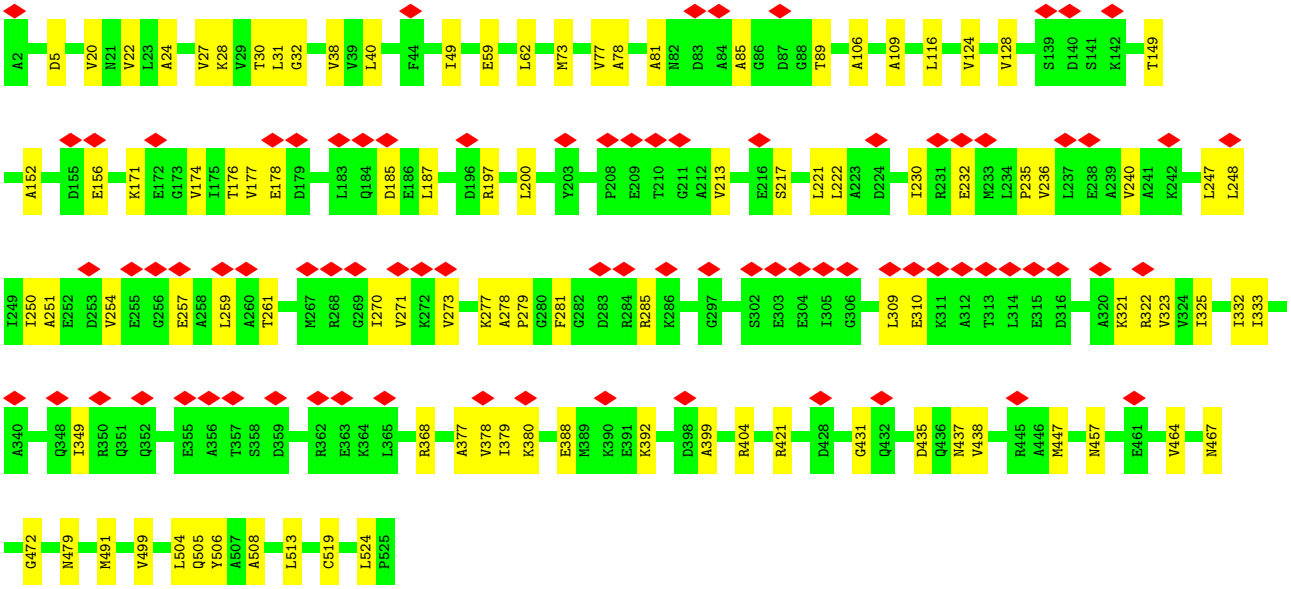
Chain 1-I:





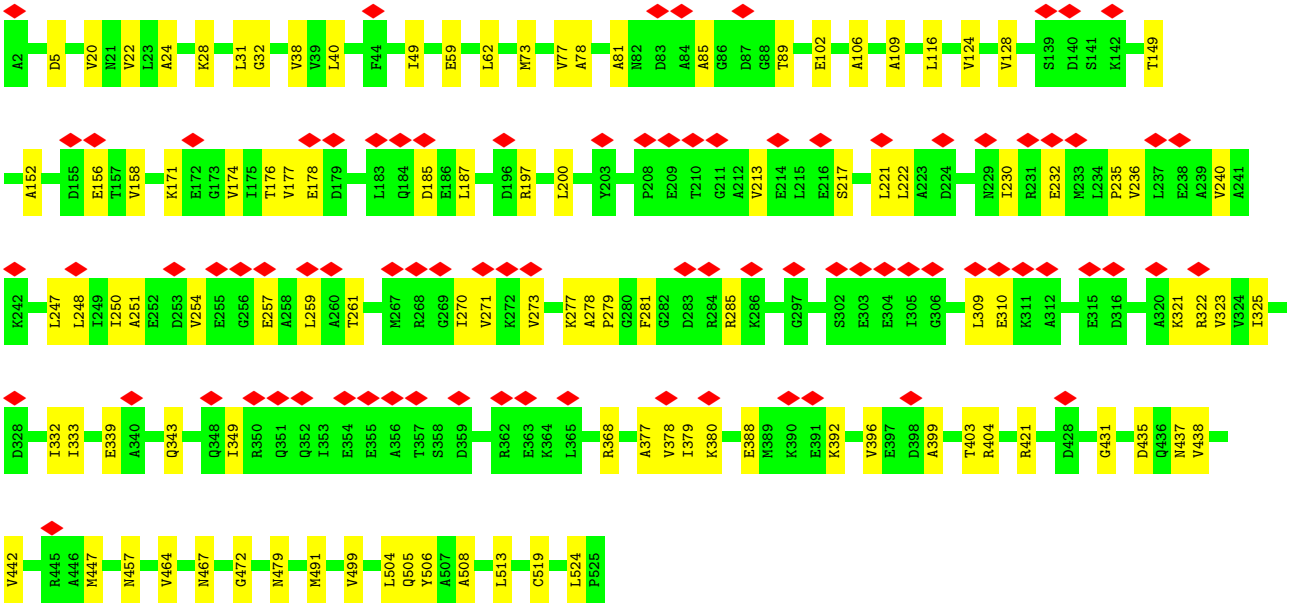
• Molecule 1: 60 kDa chaperonin

Chain 1-J:



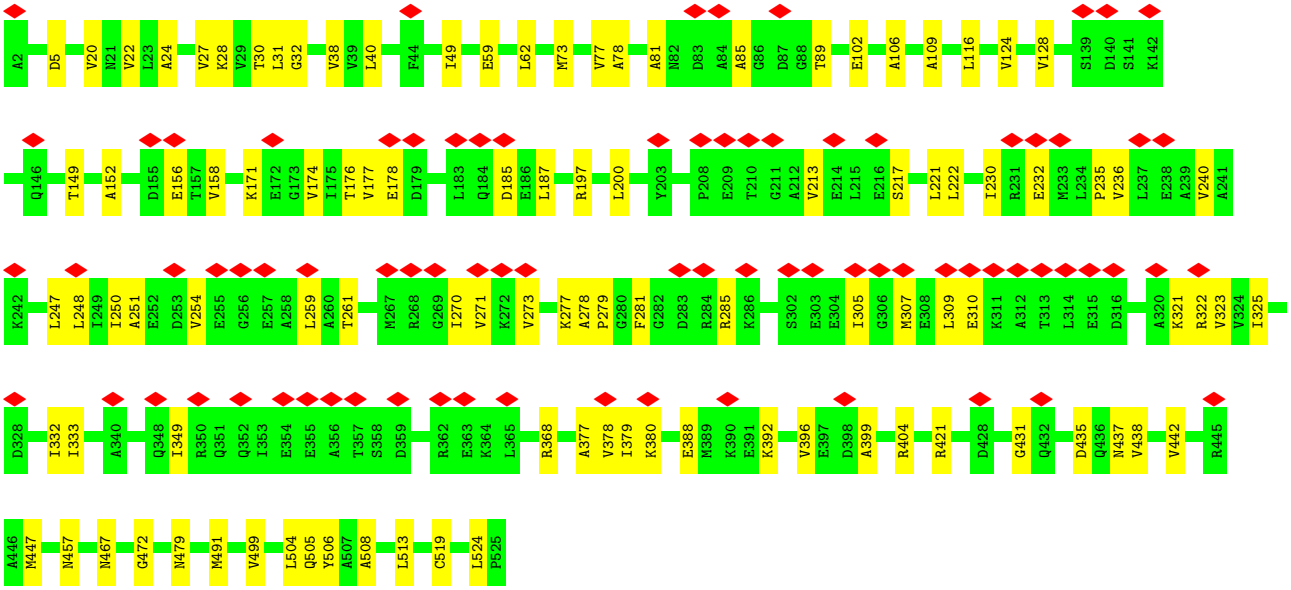
• Molecule 1: 60 kDa chaperonin

Chain 1-K:



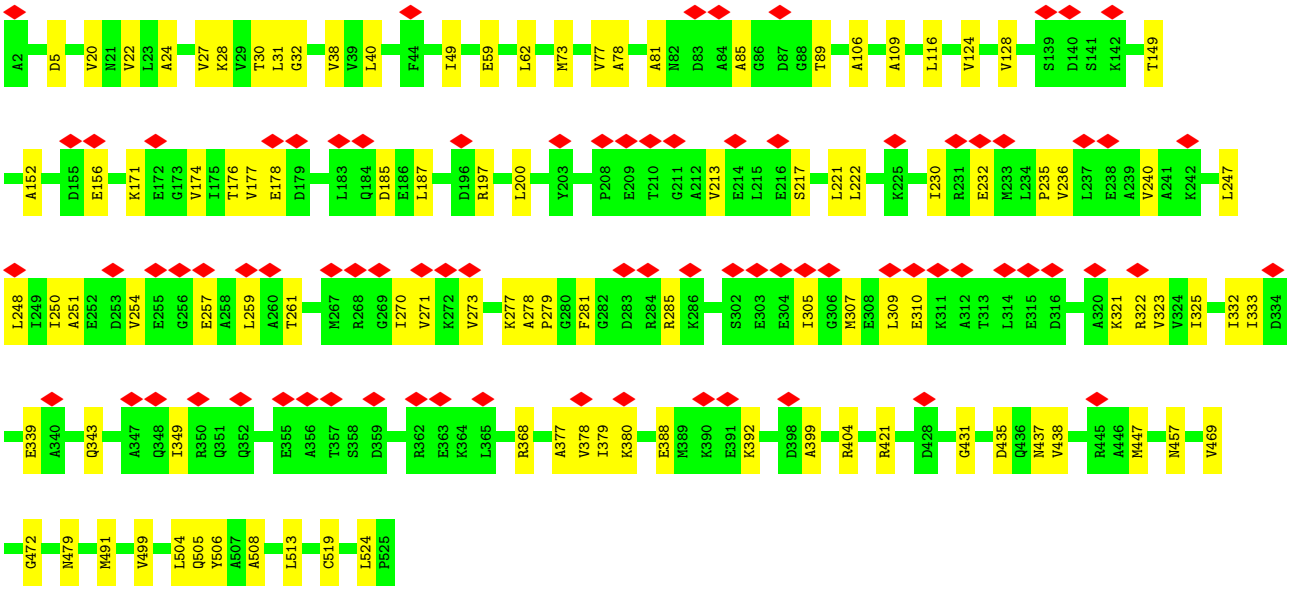
• Molecule 1: 60 kDa chaperonin

Chain 1-L:



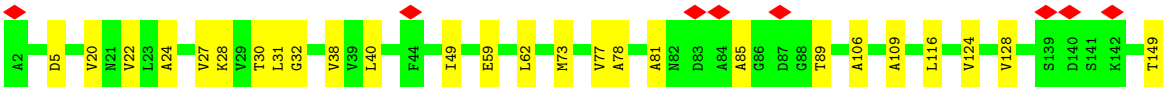
• Molecule 1: 60 kDa chaperonin

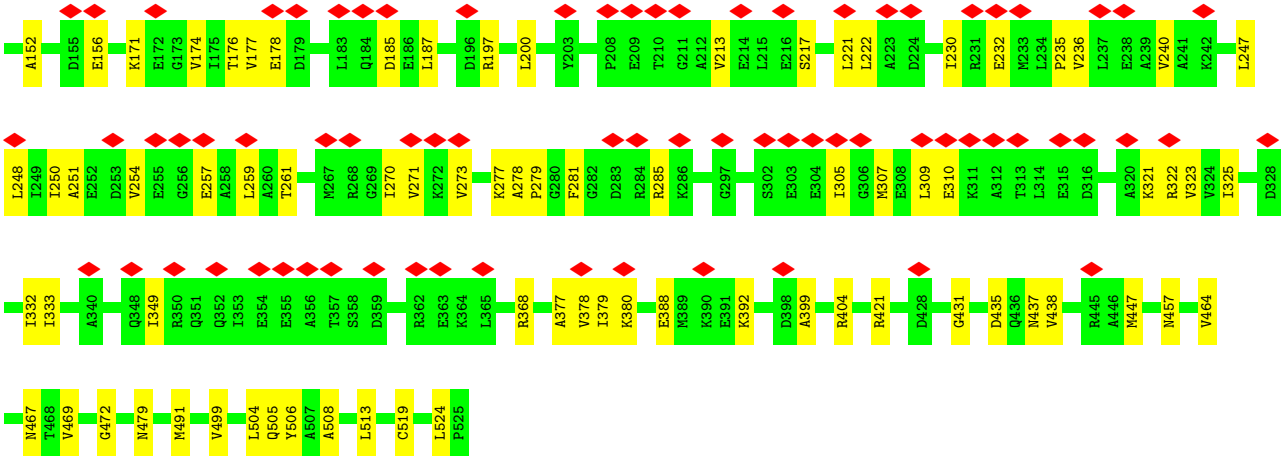
Chain 1-M:



• Molecule 1: 60 kDa chaperonin

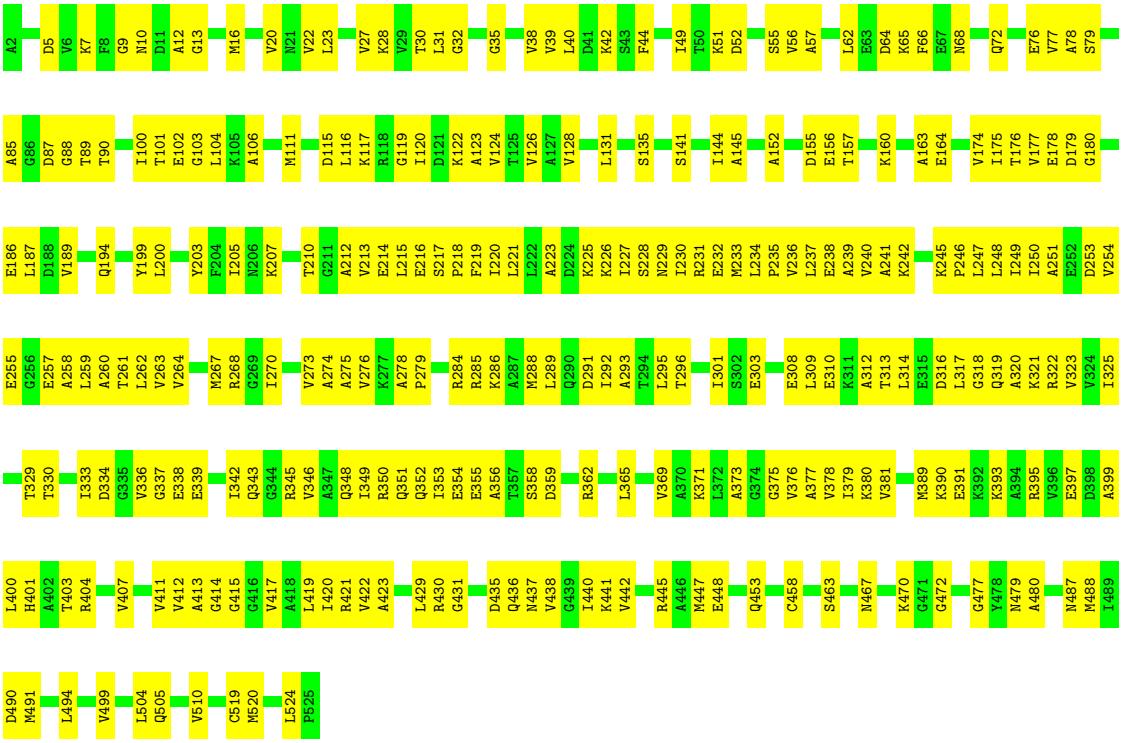
Chain 1-N:





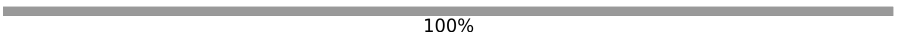
- Molecule 1: 60 kDa chaperonin

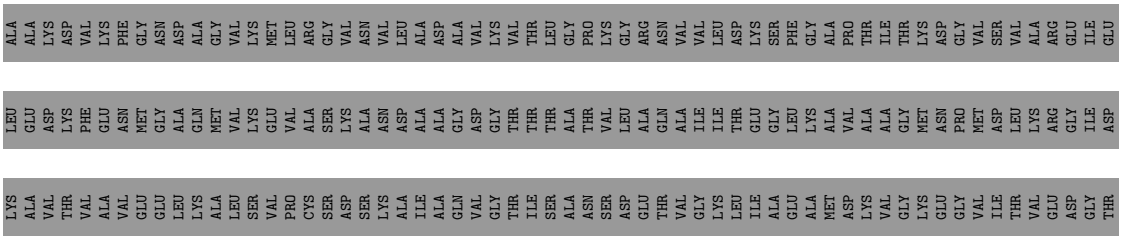
Chain 2-A:



- Molecule 1: 60 kDa chaperonin

Chain 2-B:





GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA LYS LEU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL ALA GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 2-C: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA LYS LEU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL ALA GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 2-D: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA GLU VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA PRO GLY ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY GLY VAL ALA GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 2-E: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA GLU VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA PRO GLY ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY GLY VAL ALA GLY VAL ALA LEU ILE ARG

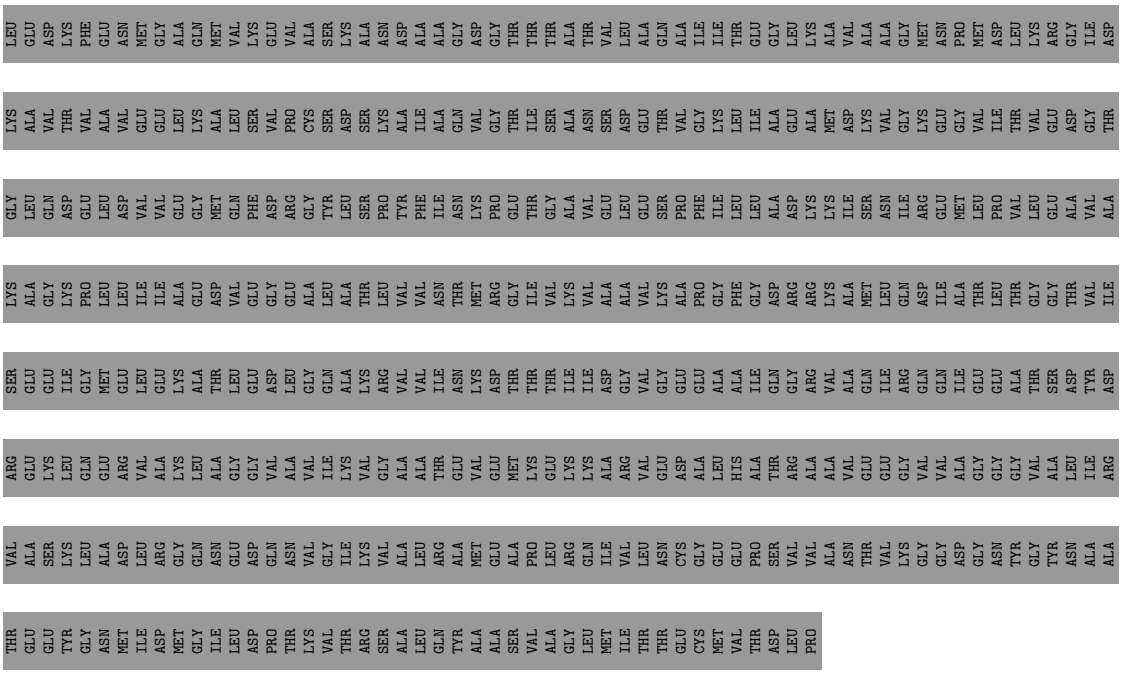
VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

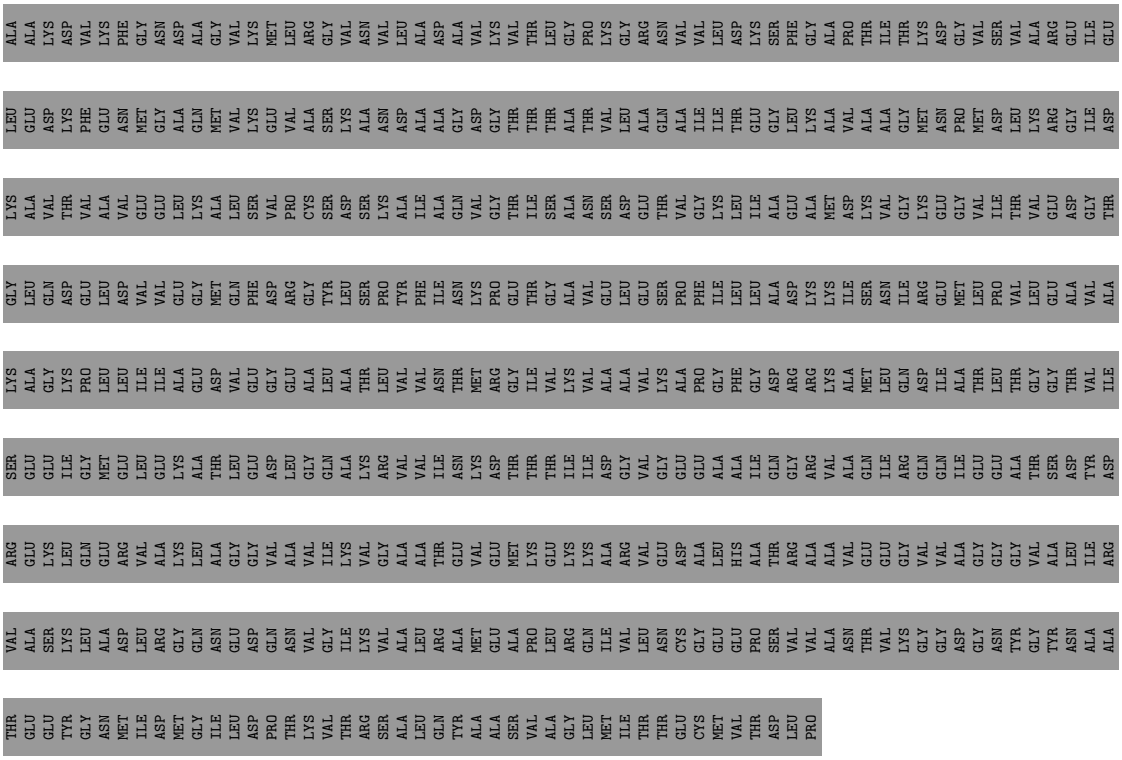
Chain 2-F: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU



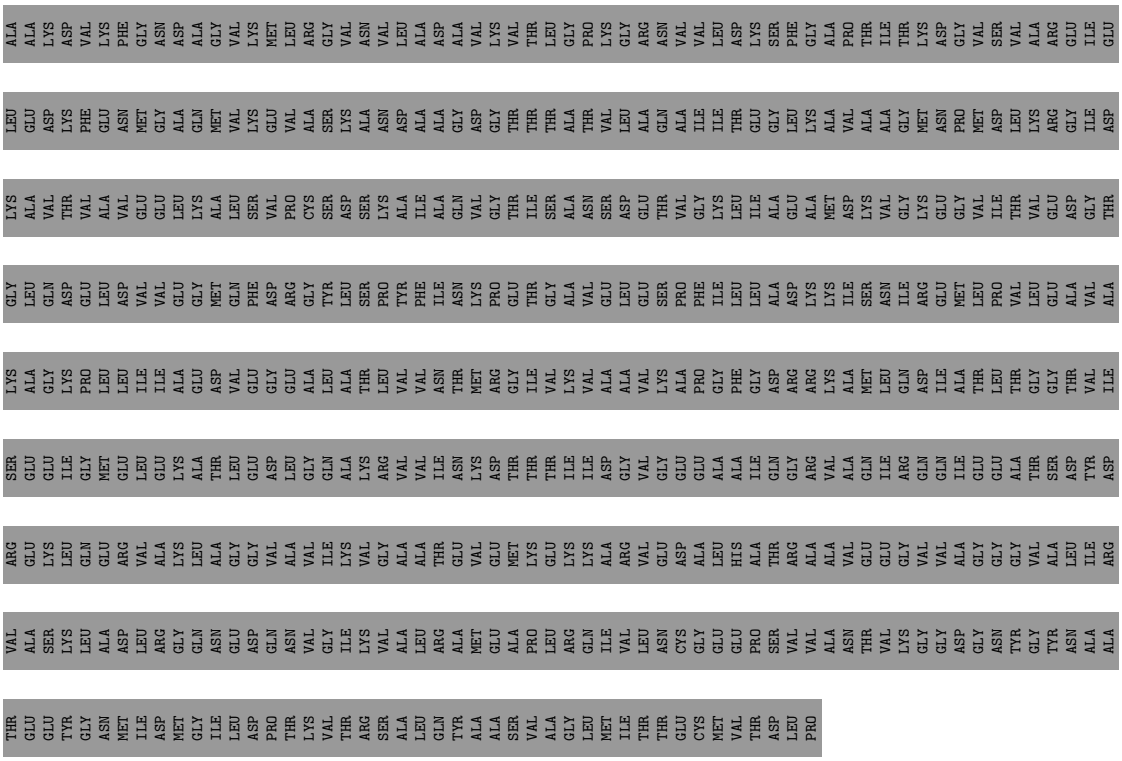
- Molecule 1: 60 kDa chaperonin

Chain 2-G: 100%



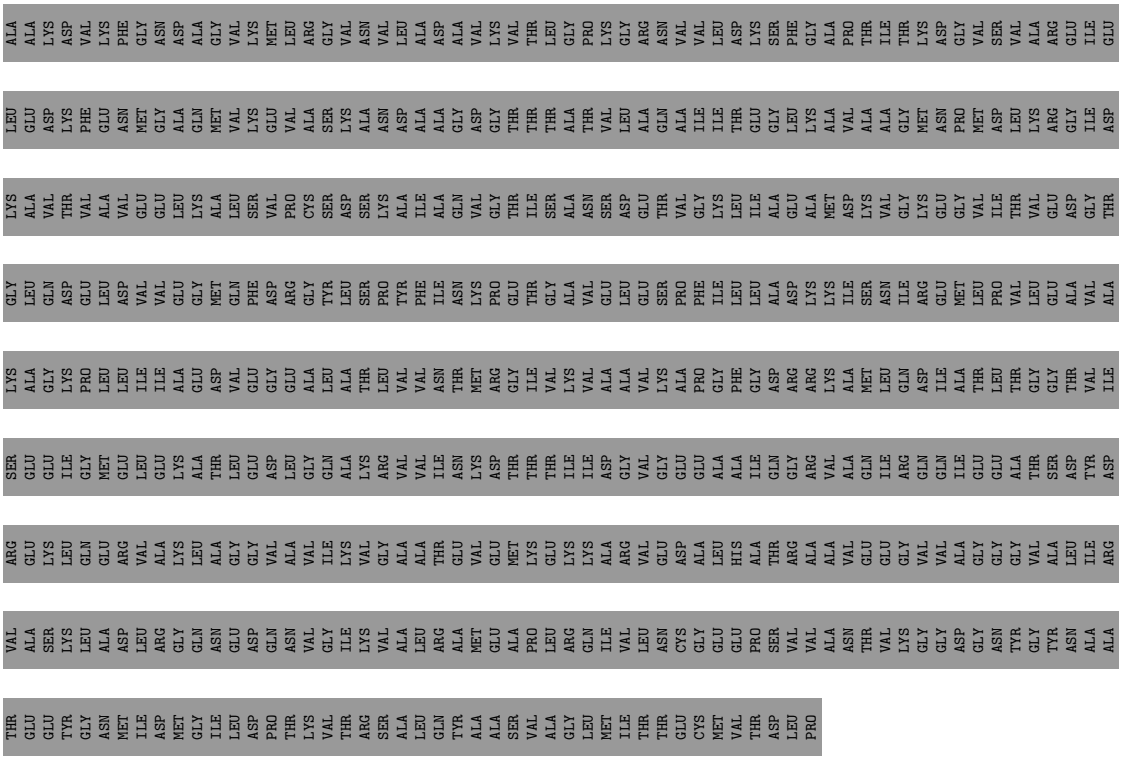
- Molecule 1: 60 kDa chaperonin

Chain 2-H: 100%



- Molecule 1: 60 kDa chaperonin

Chain 2-I: 100%



- Molecule 1: 60 kDa chaperonin

Chain 2-J: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS VAL GLU ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLU GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLY VAL GLY GLY GLY VAL ALA LEU VAL ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 2-K: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS VAL GLU ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLU GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLY VAL GLY GLY GLY VAL ALA LEU VAL ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

• Molecule 1: 60 kDa chaperonin

Chain 2-L: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ASP ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLU GLY LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU GLN GLY ARG VAL ALA ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

• Molecule 1: 60 kDa chaperonin

Chain 2-M: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ASP ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

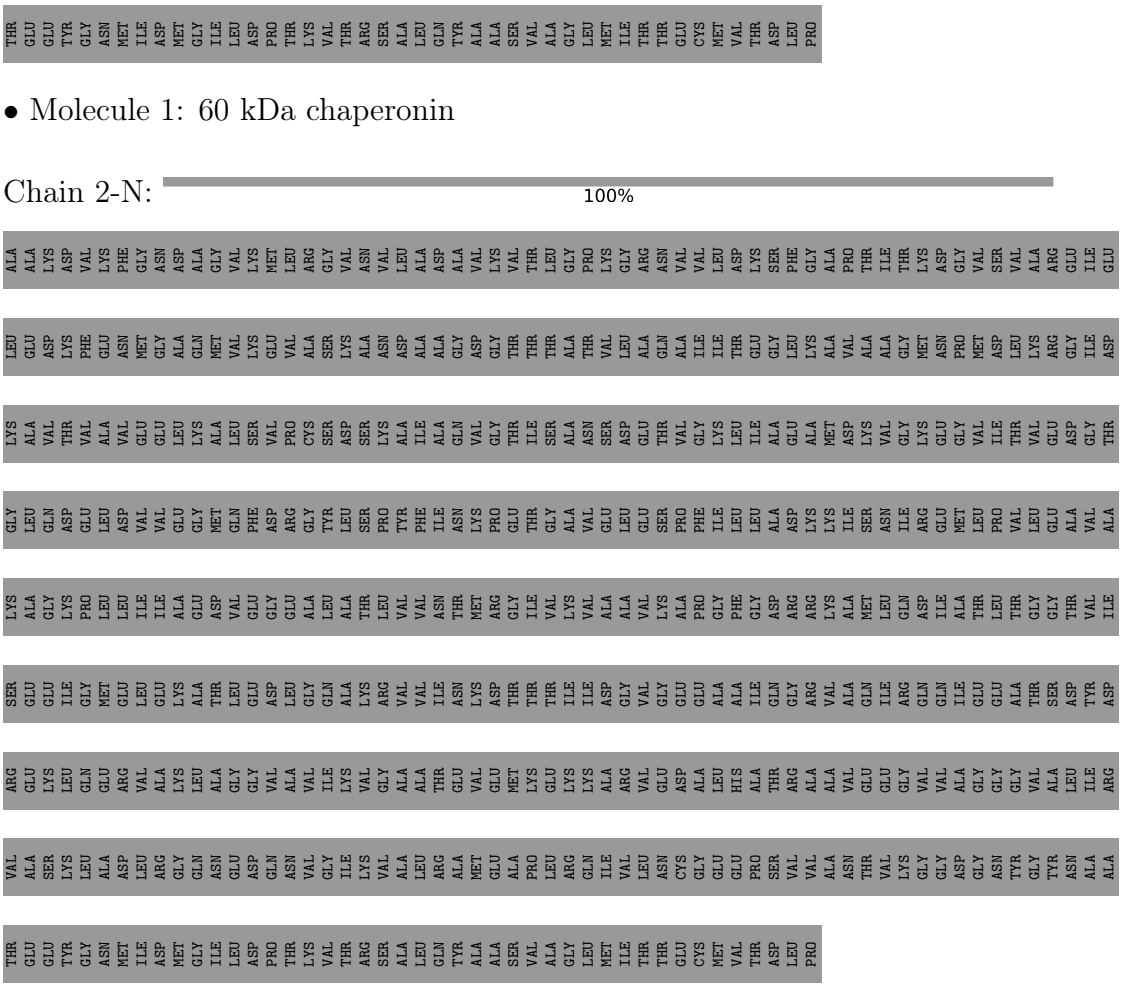
GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLU GLY LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU GLN GLY ARG VAL ALA ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

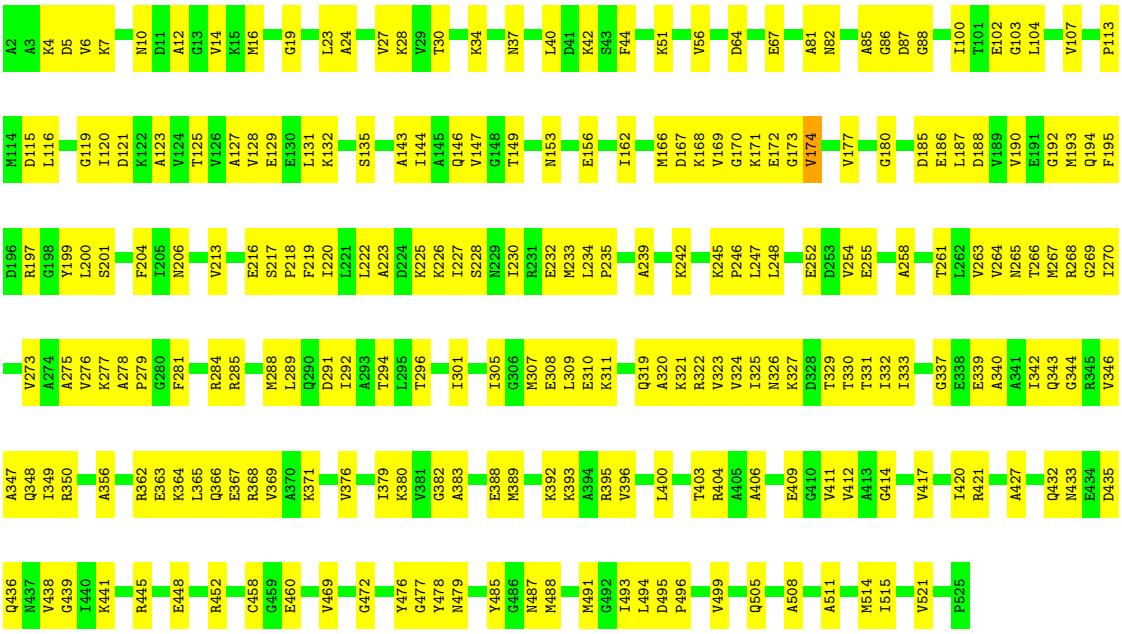


- Molecule 1: 60 kDa chaperonin

Chain 2-N: 100%

- Molecule 1: 60 kDa chaperonin

Chain 3-A: 56% 44%



• Molecule 1: 60 kDa chaperonin

Chain 3-B: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS LEU GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU ALA GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU VAL ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

• Molecule 1: 60 kDa chaperonin

Chain 3-C: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

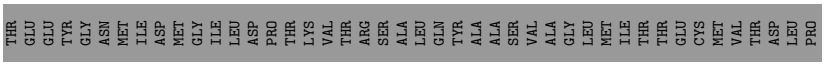
LYS LEU GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU ALA GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU VAL ILE ARG

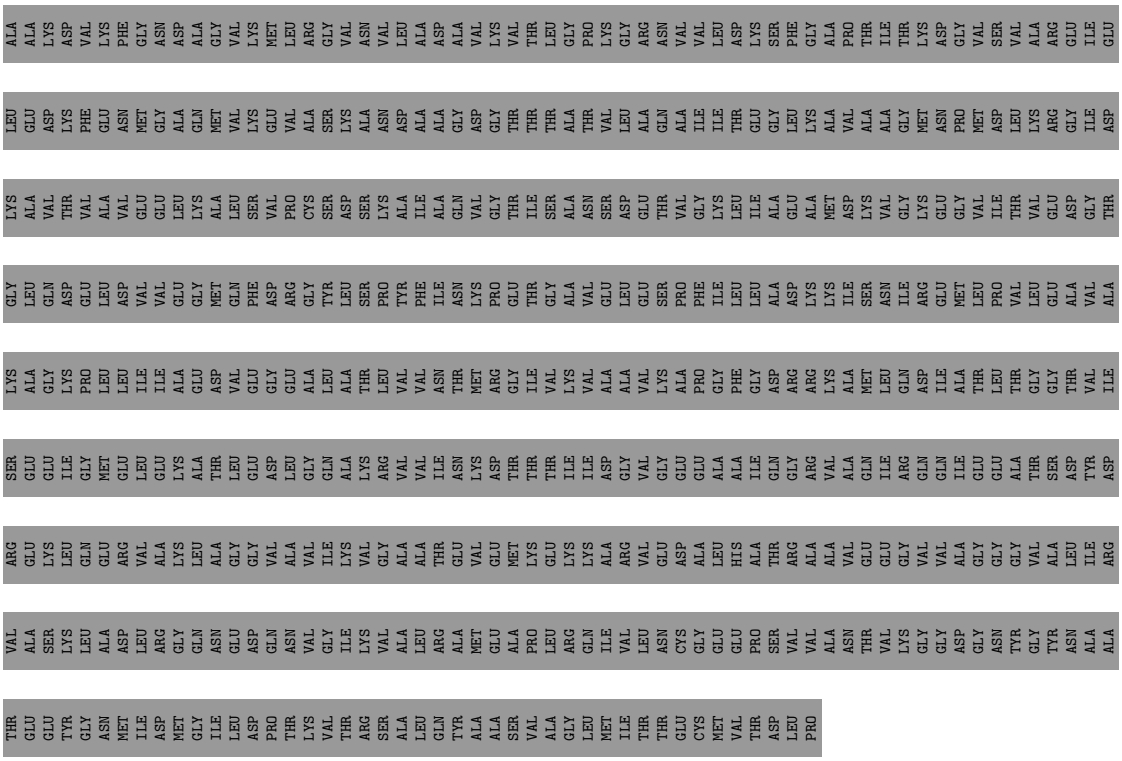
VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO



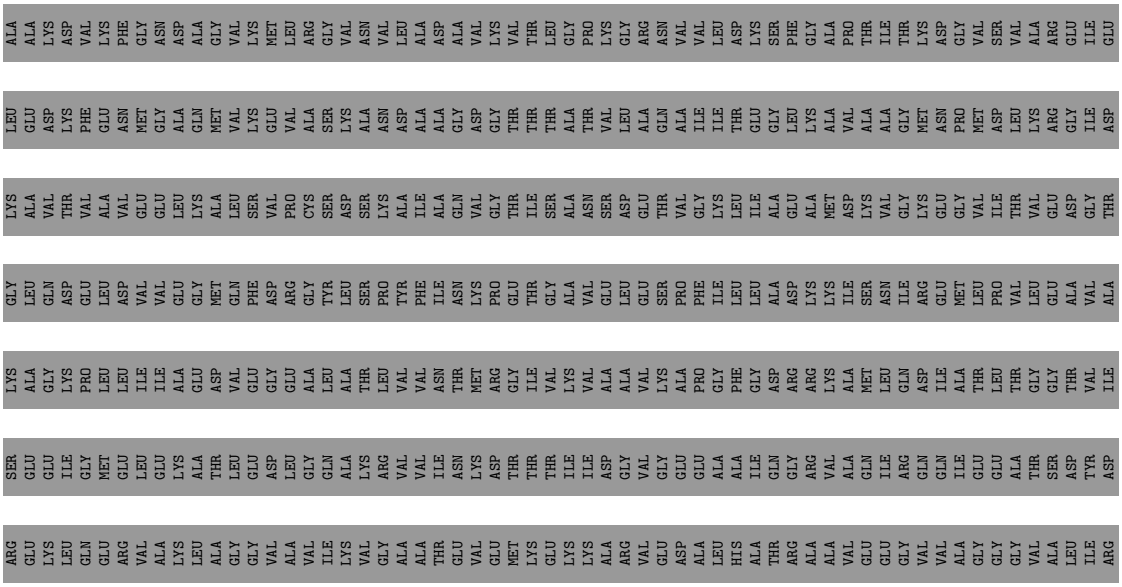
- Molecule 1: 60 kDa chaperonin

Chain 3-D:



- Molecule 1: 60 kDa chaperonin

Chain 3-E:



VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 3-F: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU VAL ILE THR VAL GLU ASP ILE GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA ASN SER ASP GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS VAL GLY GLU ALA ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA LYS GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 3-G: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU VAL ILE THR VAL GLU ASP ILE GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA ASN SER ASP GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS VAL GLY LYS GLU VAL ILE THR VAL GLU ASP ILE GLY THR

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA LYS GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 3-H: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA VAL GLY VAL GLY ILE THR VAL GLU ASP GLY

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU LEU ALA ASP LYS LYS ILE LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ILE ARG GLN GLN ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU ALA ILE ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 3-I: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA VAL GLY VAL GLY ILE THR VAL GLU ASP GLY

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU LEU ALA ASP LYS LYS ILE LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ILE ARG GLN GLN ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 3-J: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

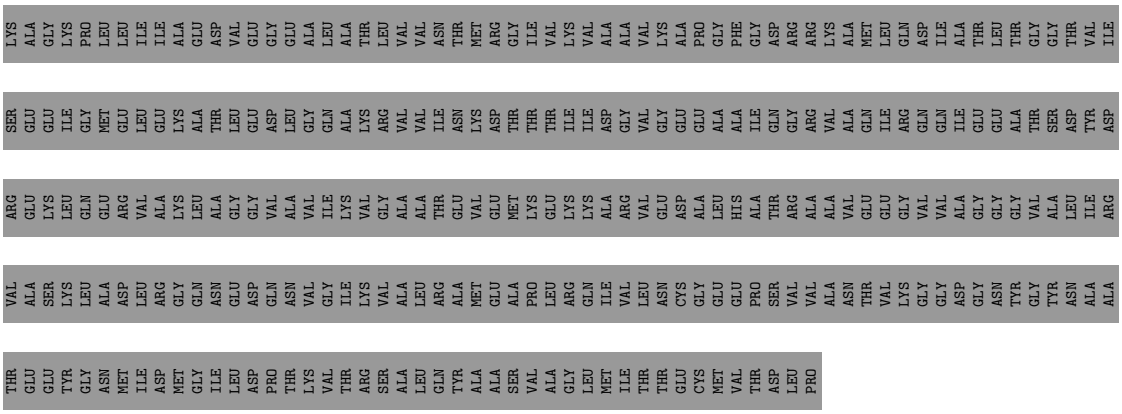
Chain 3-K: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

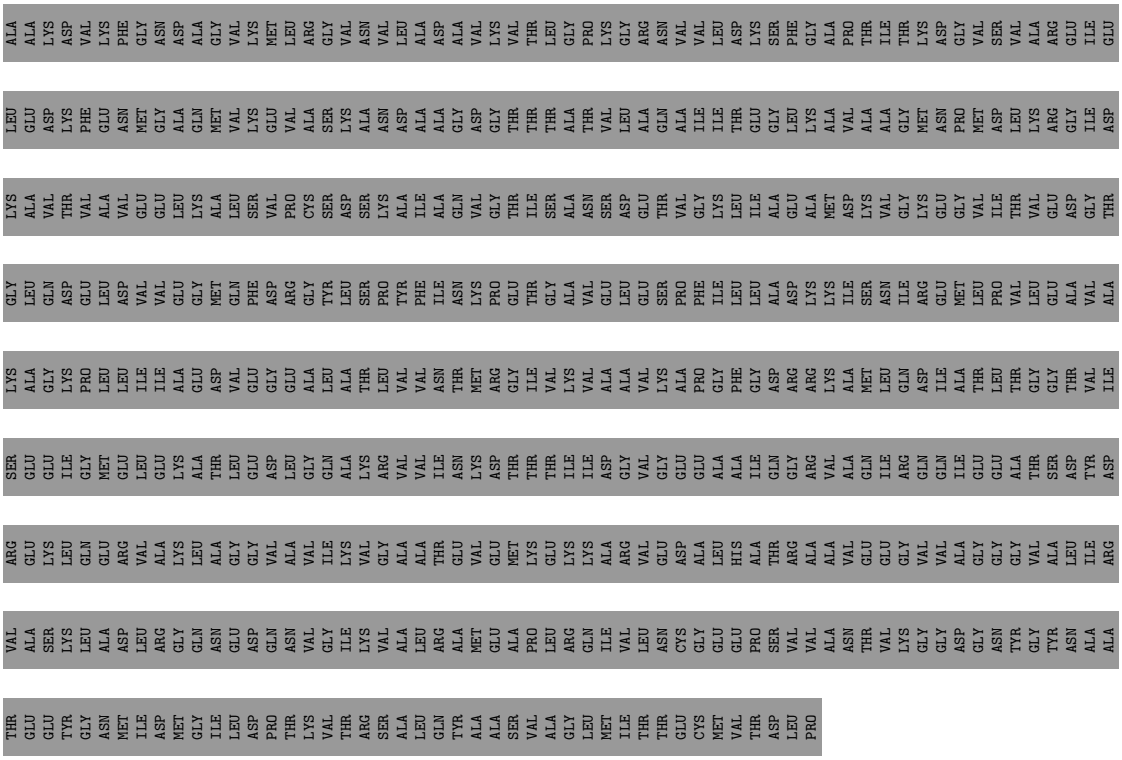
LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA



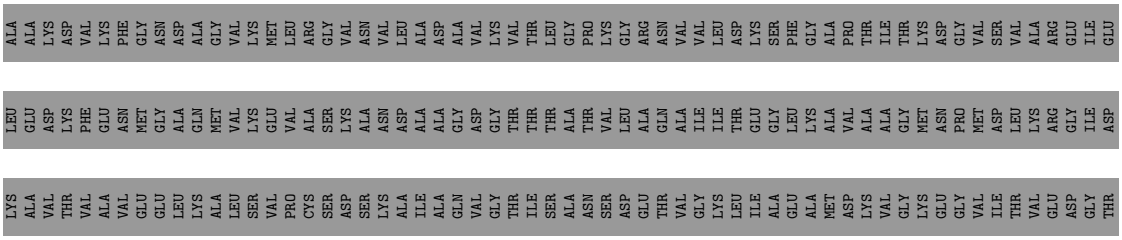
- Molecule 1: 60 kDa chaperonin

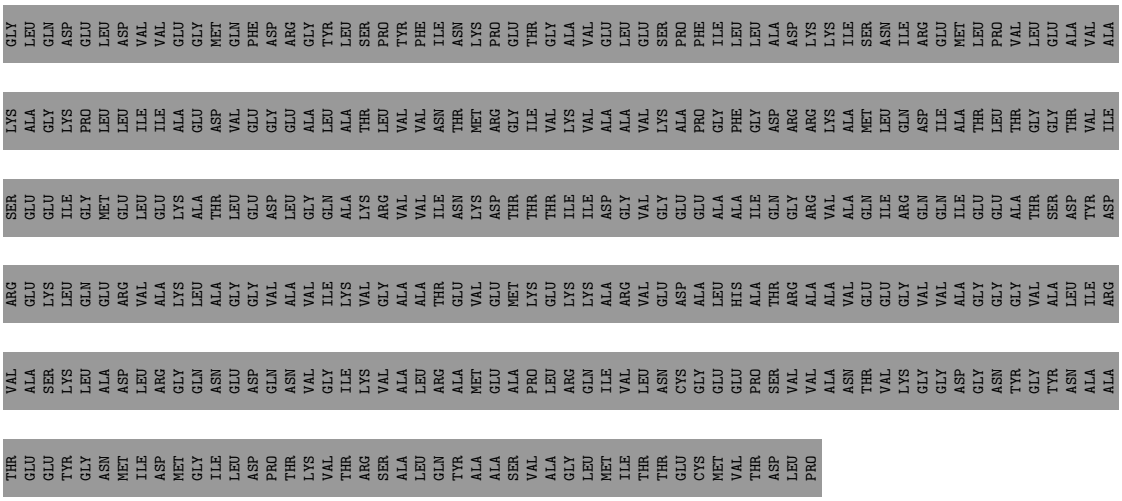
Chain 3-L: 100%



- Molecule 1: 60 kDa chaperonin

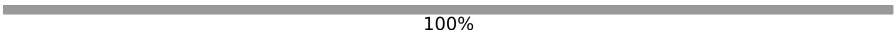
Chain 3-M: 100%

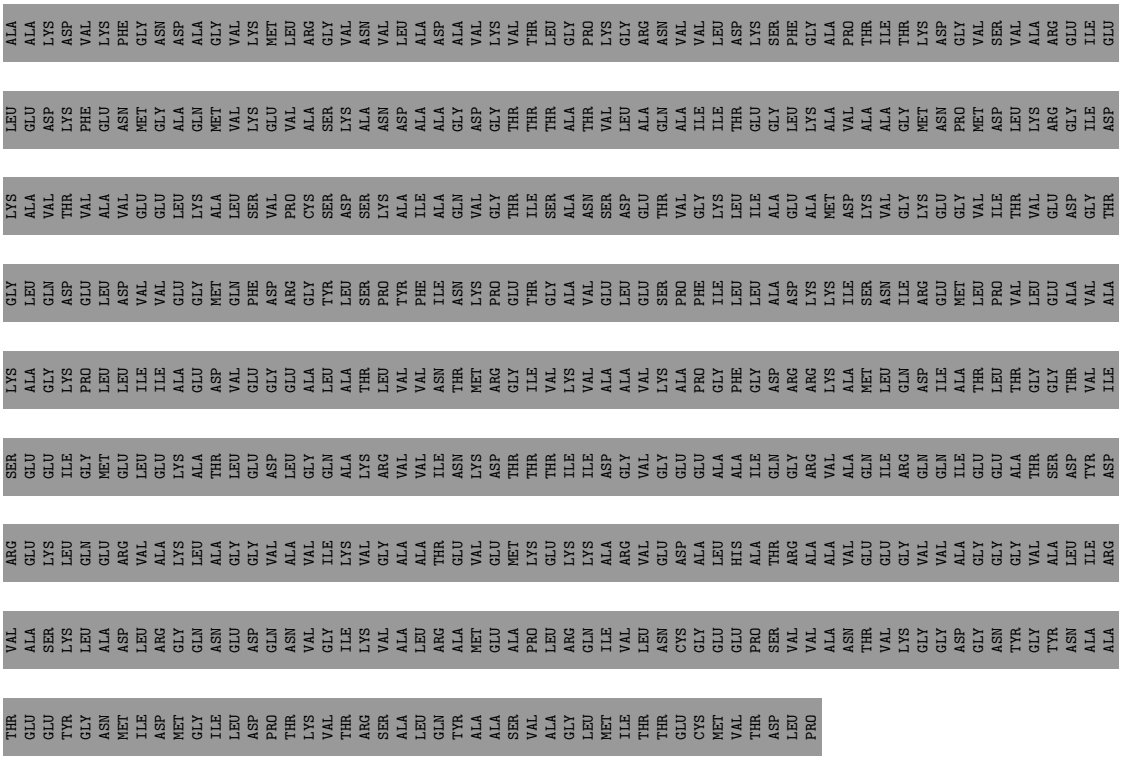




- Molecule 1: 60 kDa chaperonin

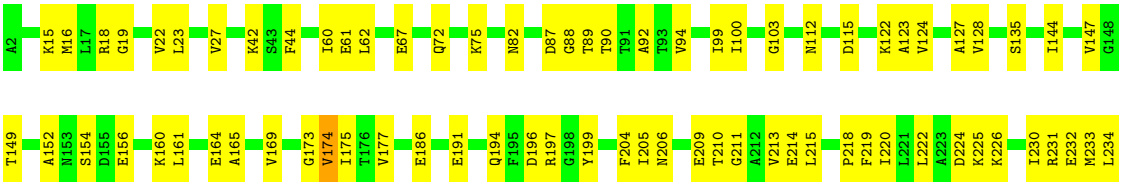
Chain 3-N:

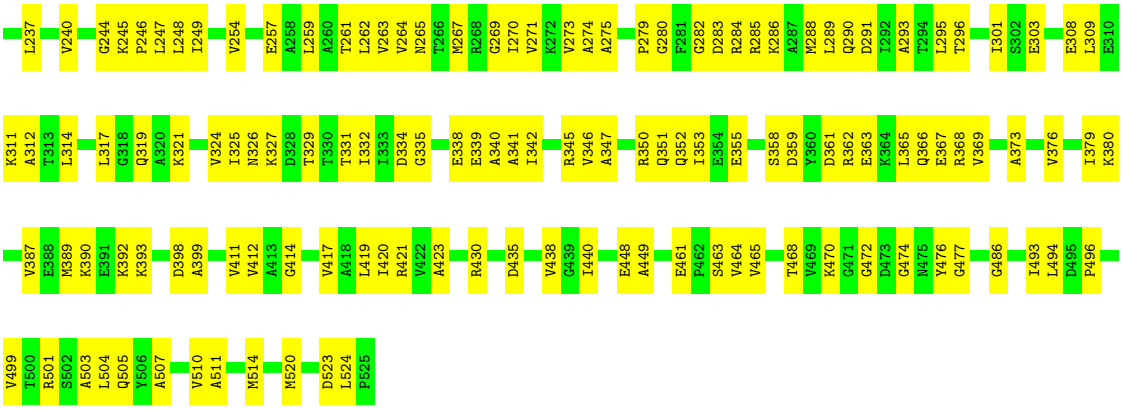




- Molecule 1: 60 kDa chaperonin

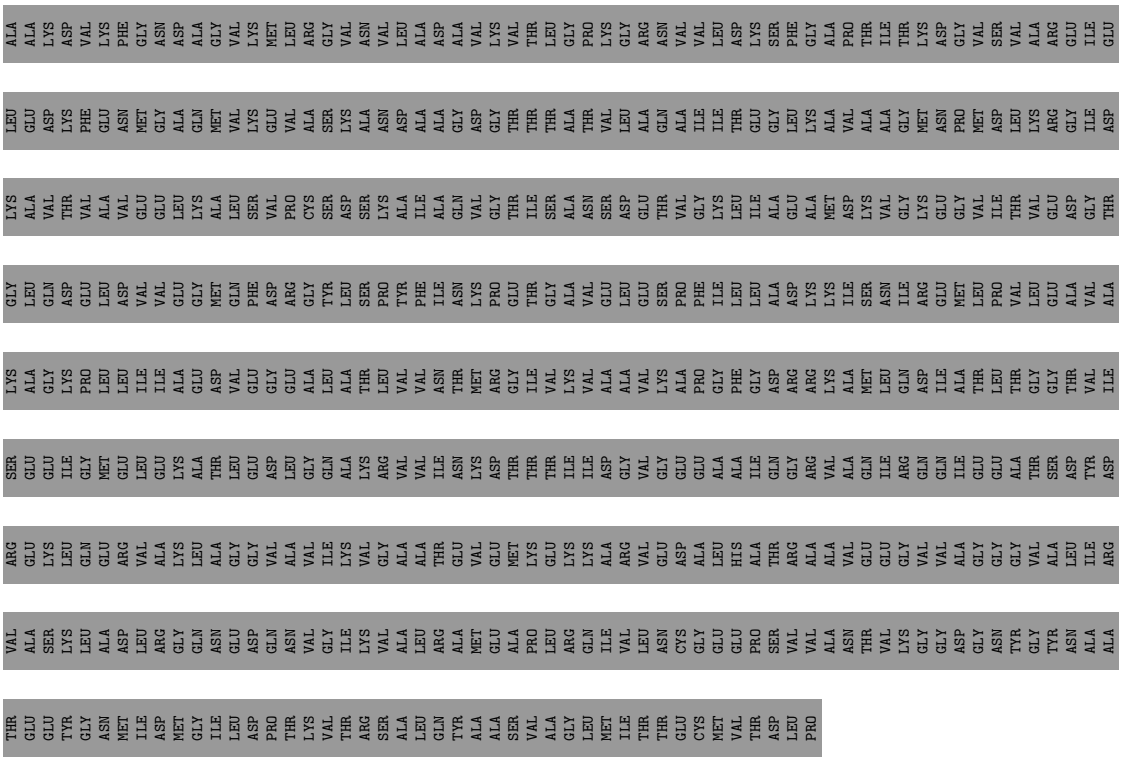
Chain 4-A:





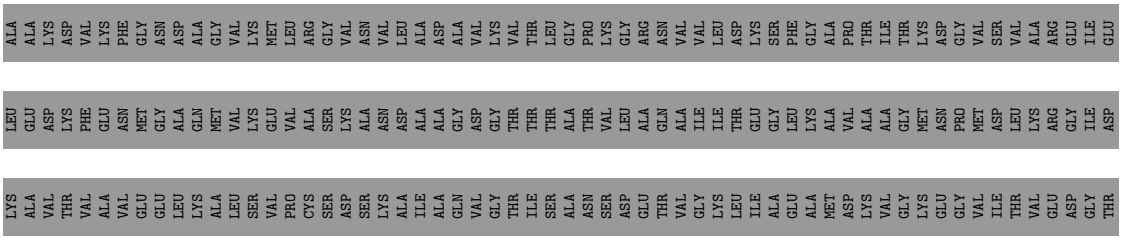
- Molecule 1: 60 kDa chaperonin

Chain 4-B: 100%



- Molecule 1: 60 kDa chaperonin

Chain 4-C: 100%



GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA LYS LEU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL GLY GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ASN CYS GLY GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 4-D: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA LYS LEU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL GLY GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ASN CYS GLY GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 4-E: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA GLU VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA GLY GLN ILE ILE ILE GLU ALA THR GLU GLU ILE ARG GLN GLN ILE GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY GLY VAL VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 4-F: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA GLU VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA GLY GLN ILE ILE ILE GLU ALA THR GLU GLU ILE ARG GLN GLN ILE GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY GLY VAL VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 4-G: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

• Molecule 1: 60 kDa chaperonin

Chain 4-H: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

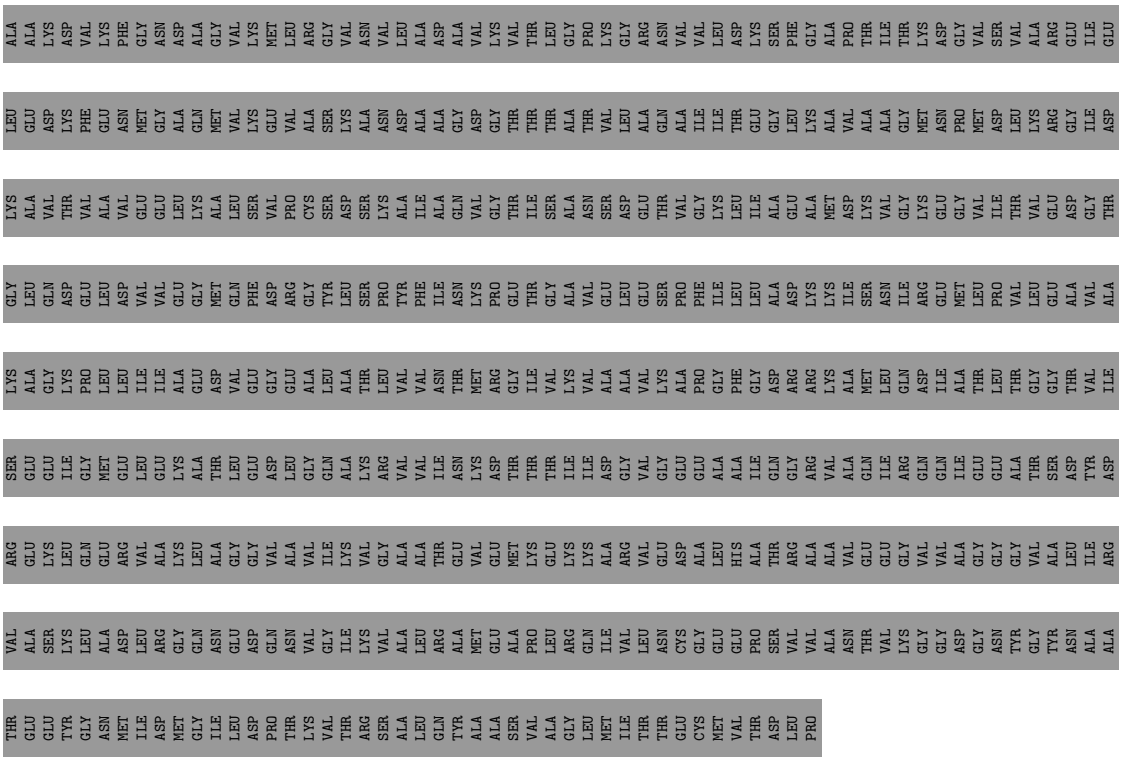
ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

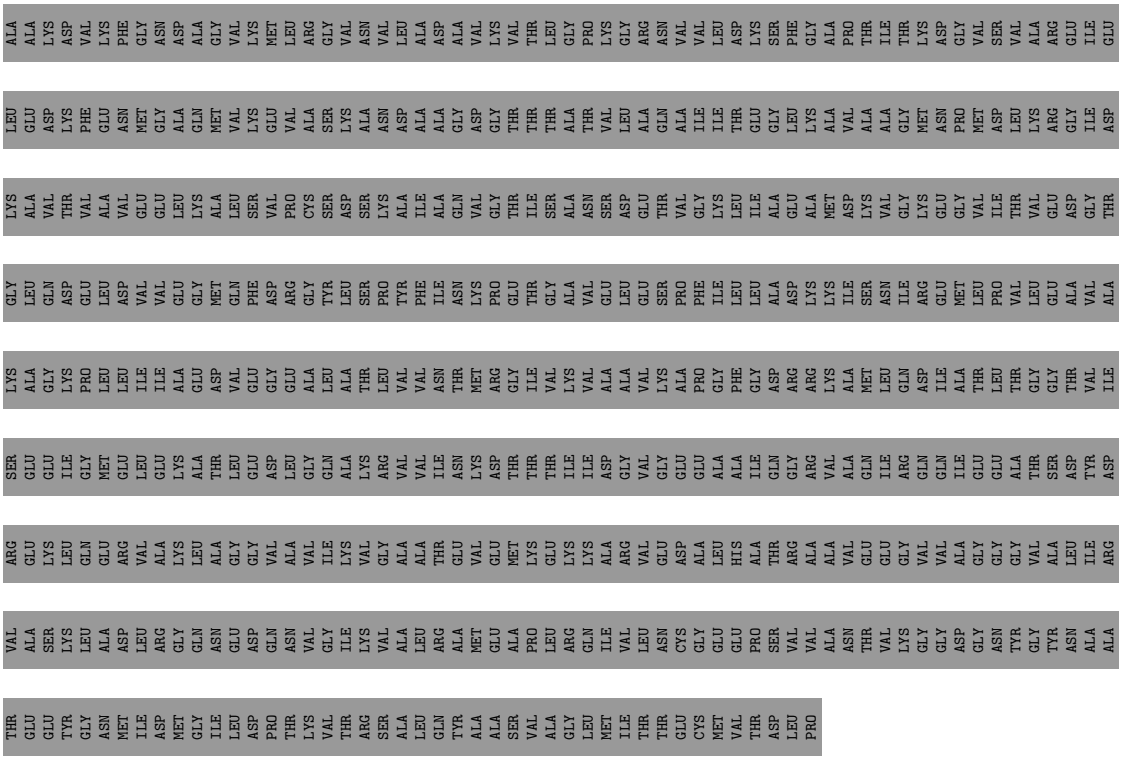
• Molecule 1: 60 kDa chaperonin

Chain 4-I: 100%



• Molecule 1: 60 kDa chaperonin

Chain 4-J: 100%



• Molecule 1: 60 kDa chaperonin

Chain 4-K: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS VAL GLU ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA ALA LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLY VAL GLY GLY VAL ALA LEU ILE

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 4-L: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS VAL GLU ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA ALA LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY VAL ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLY VAL GLY GLY VAL ALA LEU ILE

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 4-M: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

- Molecule 1: 60 kDa chaperonin

Chain 4-N: 100%

ALA ALA LYS ASP VAL LYS PHE GLY ASN ASP ALA GLY VAL LYS MET LEU ARG GLY VAL ASN VAL LEU ALA ASP ALA VAL LYS VAL THR LEU GLY PRO LYS GLY ARG ASN VAL VAL LEU ASP LYS SER PHE GLY ALA PRO THR ILE THR LYS ASP GLY VAL SER VAL ALA ARG GLU ILE GLU

LEU GLU ASP LYS PHE GLU ASN MET GLY ALA GLN MET VAL LYS GLU VAL ALA SER LYS ALA ASN ASP ALA ALA GLY ASP GLY THR THR THR ALA THR VAL LEU ALA GLN ALA ILE ILE THR GLU GLY LEU LYS ALA VAL ALA ALA GLY MET ASN PRO MET ASP LEU LYS ARG GLY ILE ASP

LYS ALA VAL THR VAL ALA VAL GLU GLU LEU LYS ALA LEU SER VAL PRO CYS SER ASP SER LYS ALA ILE ALA GLN VAL GLY THR ILE SER ALA ASN SER ASP GLU THR VAL GLY LYS LEU ILE ALA GLU ALA MET ASP LYS VAL GLY LYS GLU GLY VAL ILE THR VAL GLU ASP GLY THR

GLY LEU GLN ASP GLU LEU ASP VAL VAL GLU GLY MET GLN PHE ASP ARG GLY TYR LEU SER PRO TYR PHE ILE ASN LYS PRO GLU THR GLY ALA VAL GLU LEU GLU SER PRO PHE ILE LEU LEU ALA ASP LYS LYS ILE SER ASN ILE ARG GLU MET LEU PRO VAL LEU GLU ALA VAL ALA

LYS ALA GLY LYS PRO LEU LEU ILE ILE ALA GLU ASP VAL GLU GLY GLU ALA LEU ALA THR LEU VAL VAL ASN THR MET ARG GLY ILE VAL LYS VAL ALA ALA VAL LYS ALA PRO GLY PHE GLY ASP ARG ARG LYS ALA MET LEU GLN ASP ILE ALA THR LEU THR GLY GLY THR VAL ILE

SER GLU GLU ILE GLY MET GLU LEU GLU LYS ALA THR LEU GLU ASP LEU GLY GLN ALA LYS ARG VAL VAL ILE ASN LYS ASP THR THR THR ILE ILE ASP GLY VAL GLY GLU GLU ALA ALA ILE GLN GLY ARG VAL ALA GLN ILE ARG GLN GLN ILE GLU GLU ALA THR SER ASP TYR ASP

ARG GLU LYS LEU GLN GLU ARG VAL ALA LYS LEU ALA GLY GLY VAL ALA VAL ILE LYS VAL GLY ALA ALA THR GLU VAL GLU MET LYS GLU LYS LYS ALA ARG VAL GLU ASP ALA LEU HIS ALA THR ARG ALA ALA VAL GLU GLU GLY VAL VAL ALA GLY GLY GLY VAL ALA LEU ILE ARG

VAL ALA SER LYS LEU ALA ASP LEU ARG GLY GLN ASN GLU ASP GLN ASN VAL GLY ILE LYS VAL ALA LEU ARG ALA MET GLU ALA PRO LEU ARG GLN ILE VAL LEU ASN CYS GLY GLU GLU PRO SER VAL VAL ALA ASN THR VAL LYS GLY GLY ASP GLY ASN TYR GLY TYR ASN ALA ALA

THR GLU GLU TYR GLY ASN MET ILE ASP MET GLY ILE LEU ASP PRO THR LYS VAL THR ARG SER ALA LEU GLN TYR ALA ALA SER VAL ALA GLY LEU MET ILE THR THR GLU CYS MET VAL THR ASP LEU PRO

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D7	Depositor
Number of particles used	37367	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.204	Depositor
Minimum map value	-0.111	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	295.2, 295.2, 295.2	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.23, 1.23, 1.23	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	1-A	0.21	0/3879	0.24	0/5237
1	1-B	0.35	0/3879	0.62	0/5237
1	1-C	0.35	0/3879	0.62	0/5237
1	1-D	0.35	0/3879	0.62	0/5237
1	1-E	0.35	0/3879	0.62	0/5237
1	1-F	0.35	0/3879	0.62	0/5237
1	1-G	0.35	0/3879	0.62	0/5237
1	1-H	0.35	0/3879	0.62	0/5237
1	1-I	0.35	0/3879	0.62	0/5237
1	1-J	0.35	0/3879	0.62	0/5237
1	1-K	0.35	0/3879	0.62	0/5237
1	1-L	0.35	0/3879	0.62	0/5237
1	1-M	0.35	0/3879	0.62	0/5237
1	1-N	0.35	0/3879	0.62	0/5237
1	2-A	0.21	0/3879	0.24	0/5237
1	3-A	0.21	0/3879	0.24	0/5237
1	4-A	0.21	0/3879	0.24	0/5237
All	All	0.32	0/65943	0.55	0/89029

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	1-A	0	1
1	1-B	0	1
1	1-C	0	1
1	1-D	0	1
1	1-E	0	1
1	1-F	0	1
1	1-G	0	1
1	1-H	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	1-I	0	1
1	1-J	0	1
1	1-K	0	1
1	1-L	0	1
1	1-M	0	1
1	1-N	0	1
All	All	0	14

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-A	32	GLY	Peptide
1	1-B	32	GLY	Peptide
1	1-C	32	GLY	Peptide
1	1-D	32	GLY	Peptide
1	1-E	32	GLY	Peptide
1	1-F	32	GLY	Peptide
1	1-G	32	GLY	Peptide
1	1-H	32	GLY	Peptide
1	1-I	32	GLY	Peptide
1	1-J	32	GLY	Peptide
1	1-K	32	GLY	Peptide
1	1-L	32	GLY	Peptide
1	1-M	32	GLY	Peptide
1	1-N	32	GLY	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-A	3851	0	3970	63	0
1	1-B	3851	0	3970	61	0
1	1-C	3851	0	3970	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-D	3851	0	3970	63	0
1	1-E	3851	0	3970	63	0
1	1-F	3851	0	3970	62	0
1	1-G	3851	0	3970	63	0
1	1-H	3851	0	3970	63	0
1	1-I	3851	0	3970	62	0
1	1-J	3851	0	3970	61	0
1	1-K	3851	0	3970	64	0
1	1-L	3851	0	3970	62	0
1	1-M	3851	0	3970	62	0
1	1-N	3851	0	3970	63	0
1	2-A	3851	0	3970	250	0
1	3-A	3851	0	3970	198	0
1	4-A	3851	0	3970	151	0
2	1-A	19	0	0	1	0
2	1-B	12	0	0	0	0
2	1-C	14	0	0	0	0
2	1-D	14	0	0	0	0
2	1-E	10	0	0	0	0
2	1-F	6	0	0	0	0
2	1-G	13	0	0	0	0
2	1-H	1	0	0	0	0
2	1-I	3	0	0	0	0
2	1-J	5	0	0	0	0
2	1-K	1	0	0	0	0
2	1-L	2	0	0	0	0
2	1-M	5	0	0	0	0
2	1-N	2	0	0	0	0
All	All	65574	0	67490	1416	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 21.

All (1416) 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:A:176:THR:O	1:A:377:ALA:HB3	1.56	1.04
1:A:221:LEU:O	1:A:248:LEU:CB	2.14	0.95
1:A:264:VAL:HA	1:A:267:MET:HG2	1.51	0.92
1:A:197:ARG:HE	1:A:279:PRO:HA	1.35	0.92
1:A:237:LEU:O	1:A:241:ALA:HB2	1.70	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:187:LEU:HA	1:F:378:VAL:O	1.72	0.90
1:N:187:LEU:HA	1:N:378:VAL:O	1.72	0.90
1:M:187:LEU:HA	1:M:378:VAL:O	1.72	0.90
1:E:187:LEU:HA	1:E:378:VAL:O	1.72	0.90
1:G:187:LEU:HA	1:G:378:VAL:O	1.72	0.90
1:H:187:LEU:HA	1:H:378:VAL:O	1.72	0.90
1:A:220:ILE:HB	1:A:318:GLY:O	1.72	0.90
1:I:187:LEU:HA	1:I:378:VAL:O	1.72	0.89
1:A:187:LEU:HA	1:A:378:VAL:O	1.72	0.89
1:D:187:LEU:HA	1:D:378:VAL:O	1.72	0.89
1:J:187:LEU:HA	1:J:378:VAL:O	1.72	0.89
1:A:282:GLY:H	1:A:285:ARG:HH21	1.19	0.89
1:B:187:LEU:HA	1:B:378:VAL:O	1.72	0.89
1:L:187:LEU:HA	1:L:378:VAL:O	1.72	0.89
1:C:187:LEU:HA	1:C:378:VAL:O	1.72	0.88
1:K:187:LEU:HA	1:K:378:VAL:O	1.72	0.88
1:A:220:ILE:HG22	1:A:248:LEU:HB3	1.56	0.88
1:L:185:ASP:HA	1:L:380:LYS:O	1.78	0.83
1:D:185:ASP:HA	1:D:380:LYS:O	1.78	0.83
1:E:185:ASP:HA	1:E:380:LYS:O	1.78	0.83
1:A:427:ALA:O	1:A:441:LYS:NZ	2.11	0.83
1:M:185:ASP:HA	1:M:380:LYS:O	1.78	0.83
1:G:185:ASP:HA	1:G:380:LYS:O	1.78	0.83
1:H:185:ASP:HA	1:H:380:LYS:O	1.78	0.83
1:F:185:ASP:HA	1:F:380:LYS:O	1.78	0.83
1:A:185:ASP:HA	1:A:380:LYS:O	1.78	0.82
1:K:185:ASP:HA	1:K:380:LYS:O	1.78	0.82
1:N:185:ASP:HA	1:N:380:LYS:O	1.78	0.82
1:C:185:ASP:HA	1:C:380:LYS:O	1.78	0.82
1:I:185:ASP:HA	1:I:380:LYS:O	1.78	0.82
1:J:185:ASP:HA	1:J:380:LYS:O	1.78	0.82
1:B:185:ASP:HA	1:B:380:LYS:O	1.78	0.82
1:A:377:ALA:HB1	1:A:379:ILE:HG13	1.62	0.81
1:A:205:ILE:HA	1:A:213:VAL:HG22	1.60	0.81
1:A:284:ARG:NH1	1:A:288:MET:SD	2.53	0.81
1:A:128:VAL:HG21	1:A:505:GLN:HE21	1.46	0.81
1:A:180:GLY:HA2	1:A:380:LYS:HB3	1.61	0.80
1:A:325:ILE:HG22	1:A:330:THR:HG23	1.63	0.80
1:A:186:GLU:HB2	1:A:380:LYS:HG3	1.64	0.80
1:A:103:GLY:O	1:A:106:ALA:N	2.13	0.80
1:A:221:LEU:O	1:A:248:LEU:HB3	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:VAL:O	1:A:267:MET:N	2.16	0.79
1:A:249:ILE:HB	1:A:275:ALA:HA	1.65	0.79
1:A:285:ARG:O	1:A:288:MET:N	2.15	0.79
1:A:172:GLU:HA	1:A:404:ARG:HH12	1.48	0.78
1:A:421:ARG:NH1	1:A:469:VAL:O	2.17	0.77
1:A:214:GLU:OE2	1:A:322:ARG:NH2	2.17	0.77
1:A:448:GLU:OE2	1:A:470:LYS:NZ	2.16	0.77
1:A:220:ILE:HD11	1:A:296:THR:HG21	1.66	0.76
1:A:218:PRO:HB3	1:A:246:PRO:HG2	1.68	0.76
1:A:221:LEU:HD13	1:A:247:LEU:HD11	1.66	0.75
1:A:225:LYS:NZ	1:A:301:ILE:O	2.20	0.75
1:A:81:ALA:O	1:A:85:ALA:HB3	1.87	0.74
1:I:81:ALA:O	1:I:85:ALA:HB3	1.87	0.74
1:G:81:ALA:O	1:G:85:ALA:HB3	1.87	0.74
1:H:81:ALA:O	1:H:85:ALA:HB3	1.87	0.74
1:L:81:ALA:O	1:L:85:ALA:HB3	1.87	0.74
1:D:81:ALA:O	1:D:85:ALA:HB3	1.87	0.74
1:M:81:ALA:O	1:M:85:ALA:HB3	1.87	0.74
1:B:81:ALA:O	1:B:85:ALA:HB3	1.87	0.73
1:E:81:ALA:O	1:E:85:ALA:HB3	1.87	0.73
1:J:81:ALA:O	1:J:85:ALA:HB3	1.87	0.73
1:A:30:THR:OG1	1:A:51:LYS:O	2.06	0.73
1:F:81:ALA:O	1:F:85:ALA:HB3	1.87	0.73
1:N:81:ALA:O	1:N:85:ALA:HB3	1.87	0.73
1:K:81:ALA:O	1:K:85:ALA:HB3	1.87	0.73
1:C:81:ALA:O	1:C:85:ALA:HB3	1.87	0.72
1:A:215:LEU:HD23	1:A:246:PRO:HB2	1.70	0.72
1:A:16:MET:HE2	1:A:514:MET:HE2	1.72	0.72
1:A:226:LYS:HG2	1:A:253:ASP:HB3	1.70	0.72
1:A:291:ASP:OD1	1:A:345:ARG:NH2	2.23	0.72
1:A:356:ALA:O	1:A:362:ARG:NH2	2.23	0.72
1:A:82:ASN:O	1:A:86:GLY:N	2.22	0.71
1:A:281:PHE:HA	1:A:285:ARG:HH21	1.54	0.71
1:A:112:ASN:HB3	1:A:115:ASP:HB2	1.71	0.71
1:A:321:LYS:HG2	1:A:334:ASP:HB2	1.73	0.71
1:A:308:GLU:OE1	1:A:310:GLU:N	2.23	0.71
1:A:291:ASP:OD1	1:A:345:ARG:NH1	2.24	0.71
1:A:194:GLN:O	1:A:371:LYS:NZ	2.21	0.71
1:A:362:ARG:O	1:A:366:GLN:N	2.23	0.71
1:A:349:ILE:HD11	1:A:365:LEU:HD22	1.71	0.70
1:A:85:ALA:HB1	1:A:499:VAL:HG22	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:LEU:O	1:A:248:LEU:HB2	1.90	0.70
1:A:261:THR:HA	1:A:264:VAL:HG12	1.73	0.70
1:A:189:VAL:HG13	1:A:375:GLY:HA3	1.74	0.70
1:A:322:ARG:O	1:A:333:ILE:HB	1.92	0.70
1:A:193:MET:HE2	1:A:195:PHE:CE1	2.27	0.70
1:A:448:GLU:OE2	1:A:452:ARG:NH1	2.17	0.69
1:A:153:ASN:OD1	1:A:395:ARG:NH1	2.25	0.69
1:A:339:GLU:O	1:A:343:GLN:HB2	1.92	0.69
1:A:383:ALA:HB3	1:A:389:MET:HG3	1.72	0.69
1:A:288:MET:HE3	1:A:368:ARG:HH12	1.57	0.69
1:A:9:GLY:O	1:A:13:GLY:N	2.22	0.69
1:A:219:PHE:HB2	1:A:245:LYS:HZ3	1.57	0.69
1:A:152:ALA:HB2	1:A:399:ALA:HB2	1.75	0.69
1:A:369:VAL:O	1:A:373:ALA:N	2.25	0.69
1:A:128:VAL:HG23	1:A:501:ARG:HG3	1.74	0.69
1:A:432:GLN:N	1:A:436:GLN:OE1	2.20	0.68
1:A:219:PHE:HB2	1:A:245:LYS:HE2	1.75	0.68
1:A:221:LEU:HA	1:A:317:LEU:HD22	1.73	0.68
1:A:411:VAL:HG21	1:A:494:LEU:HD13	1.76	0.68
1:A:232:GLU:HG3	1:A:309:LEU:HB2	1.75	0.68
1:A:232:GLU:HB3	1:A:309:LEU:HD12	1.76	0.68
1:A:460:GLU:N	1:A:460:GLU:OE1	2.27	0.67
1:A:100:ILE:HD11	1:A:511:ALA:HA	1.74	0.67
1:A:179:ASP:O	1:A:380:LYS:HD2	1.94	0.67
1:B:176:THR:O	1:B:377:ALA:HB3	1.95	0.67
1:J:176:THR:O	1:J:377:ALA:HB3	1.95	0.67
1:A:219:PHE:H	1:A:245:LYS:HD3	1.60	0.67
1:A:192:GLY:HA3	1:A:376:VAL:HG23	1.76	0.67
1:A:176:THR:O	1:A:377:ALA:HB3	1.95	0.66
1:K:176:THR:O	1:K:377:ALA:HB3	1.95	0.66
1:A:323:VAL:HG12	1:A:332:ILE:HA	1.76	0.66
1:C:176:THR:O	1:C:377:ALA:HB3	1.95	0.66
1:F:176:THR:O	1:F:377:ALA:HB3	1.95	0.66
1:A:218:PRO:HB3	1:A:246:PRO:HG2	1.76	0.66
1:I:176:THR:O	1:I:377:ALA:HB3	1.95	0.66
1:A:378:VAL:HG22	1:A:380:LYS:HD3	1.76	0.66
1:L:176:THR:O	1:L:377:ALA:HB3	1.95	0.66
1:N:176:THR:O	1:N:377:ALA:HB3	1.95	0.66
1:D:176:THR:O	1:D:377:ALA:HB3	1.95	0.66
1:G:176:THR:O	1:G:377:ALA:HB3	1.95	0.66
1:E:176:THR:O	1:E:377:ALA:HB3	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:176:THR:O	1:M:377:ALA:HB3	1.95	0.66
1:H:176:THR:O	1:H:377:ALA:HB3	1.95	0.66
1:A:229:ASN:ND2	1:A:232:GLU:OE1	2.30	0.65
1:A:220:ILE:HD11	1:A:296:THR:HG21	1.78	0.65
1:B:247:LEU:HB3	1:B:273:VAL:HG22	1.79	0.64
1:A:262:LEU:HD22	1:A:273:VAL:HG11	1.79	0.64
1:F:247:LEU:HB3	1:F:273:VAL:HG22	1.79	0.64
1:G:247:LEU:HB3	1:G:273:VAL:HG22	1.79	0.64
1:J:247:LEU:HB3	1:J:273:VAL:HG22	1.79	0.64
1:A:247:LEU:HB3	1:A:273:VAL:HG22	1.79	0.64
1:H:247:LEU:HB3	1:H:273:VAL:HG22	1.79	0.64
1:I:247:LEU:HB3	1:I:273:VAL:HG22	1.79	0.64
1:M:247:LEU:HB3	1:M:273:VAL:HG22	1.79	0.64
1:N:247:LEU:HB3	1:N:273:VAL:HG22	1.79	0.64
1:C:247:LEU:HB3	1:C:273:VAL:HG22	1.79	0.64
1:E:247:LEU:HB3	1:E:273:VAL:HG22	1.79	0.64
1:A:230:ILE:HA	1:A:233:MET:HB3	1.80	0.64
1:K:247:LEU:HB3	1:K:273:VAL:HG22	1.79	0.64
1:L:247:LEU:HB3	1:L:273:VAL:HG22	1.79	0.64
1:A:365:LEU:O	1:A:369:VAL:N	2.26	0.64
1:D:247:LEU:HB3	1:D:273:VAL:HG22	1.79	0.64
1:A:247:LEU:O	1:A:273:VAL:HA	1.98	0.64
1:A:87:ASP:OD1	1:A:88:GLY:N	2.28	0.63
1:A:119:GLY:HA3	1:A:439:GLY:HA3	1.80	0.63
1:A:280:GLY:HA3	1:A:284:ARG:HH12	1.62	0.63
1:A:479:ASN:OD1	1:A:480:ALA:N	2.31	0.63
1:A:228:SER:HA	1:A:258:ALA:HB2	1.81	0.63
1:A:232:GLU:OE2	1:A:310:GLU:N	2.32	0.63
1:A:61:GLU:OE1	1:A:72:GLN:NE2	2.32	0.62
1:A:197:ARG:HD2	1:A:277:LYS:HB3	1.81	0.62
1:A:76:GLU:O	1:A:79:SER:OG	2.11	0.62
1:D:152:ALA:HB2	1:D:399:ALA:HB2	1.82	0.62
1:L:152:ALA:HB2	1:L:399:ALA:HB2	1.82	0.62
1:A:339:GLU:HA	1:A:342:ILE:HG22	1.81	0.62
1:A:186:GLU:HB3	1:A:380:LYS:HB2	1.82	0.62
1:A:152:ALA:HB2	1:A:399:ALA:HB2	1.82	0.62
1:C:152:ALA:HB2	1:C:399:ALA:HB2	1.82	0.62
1:K:152:ALA:HB2	1:K:399:ALA:HB2	1.82	0.62
1:A:389:MET:O	1:A:393:LYS:N	2.27	0.62
1:B:152:ALA:HB2	1:B:399:ALA:HB2	1.82	0.62
1:E:152:ALA:HB2	1:E:399:ALA:HB2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:152:ALA:HB2	1:G:399:ALA:HB2	1.82	0.62
1:I:152:ALA:HB2	1:I:399:ALA:HB2	1.82	0.62
1:M:152:ALA:HB2	1:M:399:ALA:HB2	1.82	0.62
1:A:321:LYS:HB3	1:A:334:ASP:HB2	1.81	0.62
1:C:479:ASN:HD22	1:C:491:MET:HE2	1.65	0.62
1:F:152:ALA:HB2	1:F:399:ALA:HB2	1.82	0.62
1:H:152:ALA:HB2	1:H:399:ALA:HB2	1.82	0.62
1:J:152:ALA:HB2	1:J:399:ALA:HB2	1.82	0.62
1:N:479:ASN:HD22	1:N:491:MET:HE2	1.65	0.62
1:A:237:LEU:O	1:A:241:ALA:CB	2.46	0.62
1:A:479:ASN:HD22	1:A:491:MET:HE2	1.65	0.62
1:F:479:ASN:HD22	1:F:491:MET:HE2	1.65	0.62
1:I:479:ASN:HD22	1:I:491:MET:HE2	1.65	0.62
1:K:479:ASN:HD22	1:K:491:MET:HE2	1.65	0.62
1:N:152:ALA:HB2	1:N:399:ALA:HB2	1.82	0.61
1:A:124:VAL:HG22	1:A:504:LEU:HD21	1.80	0.61
1:A:186:GLU:HB2	1:A:380:LYS:CG	2.28	0.61
1:L:479:ASN:HD22	1:L:491:MET:HE2	1.65	0.61
1:A:104:LEU:HA	1:A:107:VAL:HG12	1.80	0.61
1:D:479:ASN:HD22	1:D:491:MET:HE2	1.65	0.61
1:A:116:LEU:O	1:A:120:ILE:N	2.25	0.61
1:E:479:ASN:HD22	1:E:491:MET:HE2	1.65	0.61
1:A:100:ILE:O	1:A:103:GLY:N	2.34	0.61
1:A:177:VAL:HG22	1:A:379:ILE:HD12	1.81	0.61
1:A:82:ASN:OD1	1:A:89:THR:OG1	2.18	0.61
1:M:479:ASN:HD22	1:M:491:MET:HE2	1.65	0.61
1:A:326:ASN:OD1	1:A:327:LYS:N	2.34	0.61
1:A:376:VAL:HG12	1:A:377:ALA:H	1.66	0.61
1:A:417:VAL:O	1:A:420:ILE:HG22	2.01	0.60
1:A:37:ASN:OD1	1:A:51:LYS:NZ	2.29	0.60
1:A:178:GLU:HB2	1:A:378:VAL:HG23	1.83	0.60
1:A:219:PHE:HB2	1:A:245:LYS:CE	2.31	0.60
1:A:230:ILE:HG23	1:A:257:GLU:HG3	1.82	0.60
1:K:232:GLU:HB3	1:K:309:LEU:HB2	1.84	0.60
1:A:42:LYS:HZ3	1:A:44:PHE:HE1	1.49	0.60
1:C:230:ILE:HD12	1:C:261:THR:HG21	1.84	0.60
1:K:230:ILE:HD12	1:K:261:THR:HG21	1.84	0.60
1:A:199:TYR:HB3	1:A:325:ILE:HD13	1.83	0.60
1:A:5:ASP:OD1	1:A:6:VAL:N	2.33	0.60
1:A:478:TYR:HB2	1:A:485:TYR:HE1	1.66	0.60
1:C:232:GLU:HB3	1:C:309:LEU:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:232:GLU:HB3	1:N:309:LEU:HB2	1.84	0.60
1:E:232:GLU:HB3	1:E:309:LEU:HB2	1.84	0.60
1:F:232:GLU:HB3	1:F:309:LEU:HB2	1.84	0.60
1:L:232:GLU:HB3	1:L:309:LEU:HB2	1.84	0.60
1:D:232:GLU:HB3	1:D:309:LEU:HB2	1.84	0.60
1:F:230:ILE:HD12	1:F:261:THR:HG21	1.84	0.60
1:G:479:ASN:HD22	1:G:491:MET:HE2	1.65	0.60
1:M:232:GLU:HB3	1:M:309:LEU:HB2	1.84	0.60
1:J:479:ASN:HD22	1:J:491:MET:HE2	1.65	0.60
1:N:230:ILE:HD12	1:N:261:THR:HG21	1.84	0.60
1:B:230:ILE:HD12	1:B:261:THR:HG21	1.84	0.60
1:B:232:GLU:HB3	1:B:309:LEU:HB2	1.84	0.60
1:B:479:ASN:HD22	1:B:491:MET:HE2	1.65	0.60
1:H:479:ASN:HD22	1:H:491:MET:HE2	1.65	0.60
1:J:230:ILE:HD12	1:J:261:THR:HG21	1.84	0.60
1:A:347:ALA:HA	1:A:350:ARG:HB2	1.83	0.60
1:J:232:GLU:HB3	1:J:309:LEU:HB2	1.84	0.60
1:A:143:ALA:HA	1:A:146:GLN:HG2	1.84	0.60
1:A:145:ALA:HB2	1:A:163:ALA:HB2	1.84	0.59
1:G:232:GLU:HB3	1:G:309:LEU:HB2	1.84	0.59
1:H:177:VAL:HG22	1:H:379:ILE:HD12	1.83	0.59
1:H:232:GLU:HB3	1:H:309:LEU:HB2	1.84	0.59
1:K:177:VAL:HG22	1:K:379:ILE:HD12	1.83	0.59
1:M:230:ILE:HD12	1:M:261:THR:HG21	1.84	0.59
1:A:404:ARG:O	1:A:407:VAL:HG22	2.02	0.59
1:G:177:VAL:HG22	1:G:379:ILE:HD12	1.83	0.59
1:I:230:ILE:HD12	1:I:261:THR:HG21	1.84	0.59
1:A:123:ALA:O	1:A:127:ALA:N	2.26	0.59
1:A:100:ILE:HD11	1:A:511:ALA:HA	1.84	0.59
1:D:230:ILE:HD12	1:D:261:THR:HG21	1.84	0.59
1:E:230:ILE:HD12	1:E:261:THR:HG21	1.84	0.59
1:I:232:GLU:HB3	1:I:309:LEU:HB2	1.84	0.59
1:A:232:GLU:HB3	1:A:309:LEU:HB2	1.84	0.59
1:L:177:VAL:HG22	1:L:379:ILE:HD12	1.83	0.59
1:A:411:VAL:HG21	1:A:494:LEU:HD13	1.85	0.59
1:A:230:ILE:HD12	1:A:261:THR:HG21	1.84	0.59
1:C:177:VAL:HG22	1:C:379:ILE:HD12	1.83	0.59
1:A:296:THR:OG1	1:A:319:GLN:N	2.36	0.59
1:A:177:VAL:HG22	1:A:379:ILE:HD12	1.83	0.59
1:D:177:VAL:HG22	1:D:379:ILE:HD12	1.83	0.59
1:F:177:VAL:HG22	1:F:379:ILE:HD12	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:230:ILE:HD12	1:L:261:THR:HG21	1.84	0.59
1:I:177:VAL:HG22	1:I:379:ILE:HD12	1.83	0.59
1:N:177:VAL:HG22	1:N:379:ILE:HD12	1.83	0.59
1:J:177:VAL:HG22	1:J:379:ILE:HD12	1.83	0.59
1:A:413:ALA:HB1	1:A:488:MET:HB2	1.83	0.59
1:B:177:VAL:HG22	1:B:379:ILE:HD12	1.83	0.59
1:G:230:ILE:HD12	1:G:261:THR:HG21	1.84	0.59
1:M:177:VAL:HG22	1:M:379:ILE:HD12	1.83	0.58
1:A:120:ILE:O	1:A:123:ALA:N	2.36	0.58
1:H:230:ILE:HD12	1:H:261:THR:HG21	1.84	0.58
1:A:31:LEU:O	1:A:457:ASN:ND2	2.37	0.58
1:E:177:VAL:HG22	1:E:379:ILE:HD12	1.83	0.58
1:I:31:LEU:O	1:I:457:ASN:ND2	2.37	0.58
1:A:131:LEU:O	1:A:135:SER:N	2.35	0.58
1:A:149:THR:HB	1:A:154:SER:HA	1.86	0.58
1:N:31:LEU:O	1:N:457:ASN:ND2	2.37	0.58
1:A:177:VAL:HG13	1:A:379:ILE:HB	1.86	0.58
1:A:166:MET:HE1	1:A:171:LYS:HG2	1.85	0.58
1:A:230:ILE:HD11	1:A:258:ALA:HA	1.84	0.58
1:F:31:LEU:O	1:F:457:ASN:ND2	2.37	0.58
1:A:203:TYR:OH	1:A:267:MET:HA	2.03	0.58
1:A:255:GLU:HA	1:A:259:LEU:HD13	1.85	0.58
1:A:220:ILE:HG23	1:A:248:LEU:HG	1.85	0.58
1:A:282:GLY:O	1:A:285:ARG:NE	2.36	0.58
1:A:463:SER:O	1:A:467:ASN:HB2	2.04	0.58
1:A:523:ASP:OD1	1:A:524:LEU:N	2.37	0.58
1:G:31:LEU:O	1:G:457:ASN:ND2	2.37	0.57
1:A:218:PRO:HB3	1:A:246:PRO:HG2	1.85	0.57
1:A:128:VAL:HG21	1:A:505:GLN:HE21	1.70	0.57
1:E:31:LEU:O	1:E:457:ASN:ND2	2.37	0.57
1:H:31:LEU:O	1:H:457:ASN:ND2	2.37	0.57
1:J:85:ALA:HB1	1:J:499:VAL:HG12	1.86	0.57
1:A:284:ARG:HG3	1:A:285:ARG:HH22	1.68	0.57
1:A:85:ALA:HB1	1:A:499:VAL:HG12	1.86	0.57
1:B:85:ALA:HB1	1:B:499:VAL:HG12	1.86	0.57
1:I:85:ALA:HB1	1:I:499:VAL:HG12	1.86	0.57
1:I:128:VAL:HG21	1:I:505:GLN:HE21	1.70	0.57
1:A:199:TYR:HB3	1:A:325:ILE:HG12	1.85	0.57
1:G:128:VAL:HG21	1:G:505:GLN:HE21	1.70	0.57
1:H:128:VAL:HG21	1:H:505:GLN:HE21	1.70	0.57
1:M:31:LEU:O	1:M:457:ASN:ND2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:PHE:HE2	1:A:245:LYS:HB3	1.69	0.57
1:L:31:LEU:O	1:L:457:ASN:ND2	2.37	0.57
1:A:353:ILE:HG22	1:A:365:LEU:HB3	1.86	0.57
1:D:31:LEU:O	1:D:457:ASN:ND2	2.37	0.57
1:H:85:ALA:HB1	1:H:499:VAL:HG12	1.86	0.57
1:L:73:MET:HE3	1:M:49:ILE:HD11	1.87	0.57
1:A:346:VAL:O	1:A:350:ARG:N	2.29	0.57
1:K:31:LEU:O	1:K:457:ASN:ND2	2.37	0.57
1:A:414:GLY:H	1:A:494:LEU:HA	1.69	0.57
1:A:206:ASN:OD1	1:A:213:VAL:HA	2.04	0.57
1:A:477:GLY:C	1:A:488:MET:HE2	2.30	0.57
1:A:511:ALA:O	1:A:515:ILE:N	2.32	0.57
1:B:31:LEU:O	1:B:457:ASN:ND2	2.37	0.57
1:C:31:LEU:O	1:C:457:ASN:ND2	2.37	0.57
1:C:124:VAL:HG21	1:C:508:ALA:HB2	1.87	0.57
1:G:85:ALA:HB1	1:G:499:VAL:HG12	1.86	0.57
1:J:128:VAL:HG21	1:J:505:GLN:HE21	1.70	0.57
1:A:219:PHE:O	1:A:245:LYS:NZ	2.37	0.57
1:B:128:VAL:HG21	1:B:505:GLN:HE21	1.70	0.57
1:K:124:VAL:HG21	1:K:508:ALA:HB2	1.87	0.57
1:A:326:ASN:N	1:A:329:THR:O	2.38	0.57
1:D:124:VAL:HG21	1:D:508:ALA:HB2	1.87	0.56
1:J:124:VAL:HG21	1:J:508:ALA:HB2	1.87	0.56
1:L:124:VAL:HG21	1:L:508:ALA:HB2	1.87	0.56
1:M:124:VAL:HG21	1:M:508:ALA:HB2	1.87	0.56
1:A:421:ARG:NH1	1:A:472:GLY:O	2.38	0.56
1:B:124:VAL:HG21	1:B:508:ALA:HB2	1.87	0.56
1:C:85:ALA:HB1	1:C:499:VAL:HG12	1.86	0.56
1:E:124:VAL:HG21	1:E:508:ALA:HB2	1.87	0.56
1:J:31:LEU:O	1:J:457:ASN:ND2	2.37	0.56
1:K:85:ALA:HB1	1:K:499:VAL:HG12	1.86	0.56
1:A:126:VAL:HG11	1:A:429:LEU:HD22	1.87	0.56
1:A:102:GLU:OE1	1:A:445:ARG:NH2	2.38	0.56
1:A:206:ASN:H	1:A:213:VAL:HG23	1.69	0.56
1:D:128:VAL:HG21	1:D:505:GLN:HE21	1.70	0.56
1:F:85:ALA:HB1	1:F:499:VAL:HG12	1.86	0.56
1:L:128:VAL:HG21	1:L:505:GLN:HE21	1.70	0.56
1:N:85:ALA:HB1	1:N:499:VAL:HG12	1.86	0.56
1:A:178:GLU:HB2	1:A:378:VAL:HA	1.88	0.56
1:A:305:ILE:HG23	1:A:307:MET:HG2	1.87	0.56
1:E:85:ALA:HB1	1:E:499:VAL:HG12	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:128:VAL:HG21	1:E:505:GLN:HE21	1.70	0.56
1:I:124:VAL:HG21	1:I:508:ALA:HB2	1.87	0.56
1:A:124:VAL:HG21	1:A:508:ALA:HB2	1.87	0.56
1:M:85:ALA:HB1	1:M:499:VAL:HG12	1.86	0.56
1:A:219:PHE:HB2	1:A:245:LYS:NZ	2.21	0.56
1:A:353:ILE:HA	1:A:356:ALA:HB2	1.88	0.56
1:A:398:ASP:OD1	1:A:399:ALA:N	2.39	0.56
1:A:414:GLY:HA3	1:A:493:ILE:HG22	1.88	0.56
1:M:128:VAL:HG21	1:M:505:GLN:HE21	1.70	0.56
1:N:128:VAL:HG21	1:N:505:GLN:HE21	1.70	0.56
1:A:230:ILE:CD1	1:A:258:ALA:HA	2.35	0.56
1:G:124:VAL:HG21	1:G:508:ALA:HB2	1.87	0.56
1:A:178:GLU:OE2	1:A:333:ILE:HG21	2.05	0.56
1:A:216:GLU:O	1:A:245:LYS:HE2	2.06	0.56
1:A:160:LYS:O	1:A:164:GLU:HG2	2.06	0.56
1:D:85:ALA:HB1	1:D:499:VAL:HG12	1.86	0.56
1:F:124:VAL:HG21	1:F:508:ALA:HB2	1.87	0.56
1:F:128:VAL:HG21	1:F:505:GLN:HE21	1.70	0.56
1:H:124:VAL:HG21	1:H:508:ALA:HB2	1.87	0.56
1:N:124:VAL:HG21	1:N:508:ALA:HB2	1.87	0.56
1:K:128:VAL:HG21	1:K:505:GLN:HE21	1.70	0.56
1:L:85:ALA:HB1	1:L:499:VAL:HG12	1.86	0.56
1:A:199:TYR:CE1	1:A:327:LYS:HA	2.41	0.56
1:A:199:TYR:HA	1:A:276:VAL:HG12	1.88	0.55
1:A:420:ILE:HD11	1:A:448:GLU:HA	1.88	0.55
1:C:128:VAL:HG21	1:C:505:GLN:HE21	1.70	0.55
1:A:279:PRO:O	1:A:285:ARG:NE	2.39	0.55
1:A:199:TYR:CZ	1:A:205:ILE:HD11	2.42	0.55
1:A:116:LEU:O	1:A:119:GLY:N	2.39	0.55
1:A:194:GLN:HA	1:A:330:THR:O	2.06	0.55
1:A:479:ASN:HD22	1:A:491:MET:HE2	1.72	0.55
1:A:219:PHE:CE2	1:A:245:LYS:HB3	2.42	0.55
1:A:122:LYS:NZ	1:A:430:ARG:O	2.34	0.55
1:A:115:ASP:OD2	1:A:436:GLN:N	2.40	0.55
1:A:313:THR:H	1:A:316:ASP:HB2	1.72	0.55
1:B:177:VAL:HG13	1:B:379:ILE:HB	1.89	0.55
1:J:177:VAL:HG13	1:J:379:ILE:HB	1.89	0.55
1:A:175:ILE:HB	1:A:377:ALA:HB2	1.89	0.55
1:A:227:ILE:HD11	1:A:233:MET:HE3	1.89	0.55
1:F:177:VAL:HG13	1:F:379:ILE:HB	1.89	0.55
1:N:177:VAL:HG13	1:N:379:ILE:HB	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:ASP:OD1	1:A:88:GLY:N	2.36	0.55
1:A:32:GLY:O	1:A:35:GLY:N	2.40	0.54
1:A:128:VAL:HG21	1:A:505:GLN:HE21	1.73	0.54
1:E:177:VAL:HG13	1:E:379:ILE:HB	1.90	0.54
1:M:177:VAL:HG13	1:M:379:ILE:HB	1.90	0.54
1:A:87:ASP:OD1	1:A:88:GLY:N	2.37	0.54
1:A:240:VAL:HG23	1:A:245:LYS:HE3	1.90	0.54
1:A:284:ARG:HG3	1:A:285:ARG:NH2	2.22	0.54
1:A:40:LEU:HD11	1:A:56:VAL:HG22	1.89	0.54
1:A:177:VAL:HG13	1:A:379:ILE:HB	1.90	0.54
1:C:177:VAL:HG13	1:C:379:ILE:HB	1.89	0.54
1:I:177:VAL:HG13	1:I:379:ILE:HB	1.90	0.54
1:A:319:GLN:O	1:A:336:VAL:HG23	2.07	0.54
1:H:177:VAL:HG13	1:H:379:ILE:HB	1.89	0.54
1:K:177:VAL:HG13	1:K:379:ILE:HB	1.90	0.54
1:A:135:SER:HA	1:A:412:VAL:HG12	1.89	0.54
1:A:131:LEU:HG	1:A:422:VAL:HG11	1.89	0.54
1:A:431:GLY:H	1:A:437:ASN:ND2	2.06	0.54
1:A:281:PHE:O	1:A:284:ARG:NH1	2.40	0.54
1:A:353:ILE:HD13	1:A:365:LEU:HG	1.90	0.54
1:D:177:VAL:HG13	1:D:379:ILE:HB	1.90	0.54
1:A:27:VAL:HA	1:A:30:THR:HG22	1.90	0.54
1:A:294:THR:O	1:A:337:GLY:HA3	2.08	0.54
1:G:177:VAL:HG13	1:G:379:ILE:HB	1.90	0.54
1:L:177:VAL:HG13	1:L:379:ILE:HB	1.90	0.54
1:A:19:GLY:HA2	1:A:67:GLU:OE2	2.08	0.54
1:A:7:LYS:CB	1:A:12:ALA:HB2	2.38	0.53
1:A:16:MET:HE2	1:A:520:MET:HE3	1.90	0.53
1:A:195:PHE:CZ	1:A:330:THR:HB	2.43	0.53
1:A:220:ILE:CB	1:A:318:GLY:O	2.52	0.53
1:A:435:ASP:HA	1:A:438:VAL:HG22	1.91	0.53
1:A:123:ALA:HB2	1:A:440:ILE:HG23	1.88	0.53
1:A:293:ALA:O	1:A:296:THR:OG1	2.26	0.53
1:H:49:ILE:HD11	1:N:73:MET:HE3	1.91	0.53
1:A:7:LYS:HB3	1:A:12:ALA:HB2	1.90	0.53
1:A:176:THR:O	1:A:377:ALA:CB	2.45	0.53
1:M:323:VAL:HG12	1:M:332:ILE:HA	1.91	0.53
1:A:348:GLN:O	1:A:351:GLN:HB3	2.09	0.53
1:F:73:MET:HE3	1:G:49:ILE:HD11	1.91	0.53
1:A:16:MET:HE3	1:A:520:MET:SD	2.48	0.53
1:E:323:VAL:HG12	1:E:332:ILE:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:73:MET:HE3	1:I:49:ILE:HD11	1.91	0.53
1:M:73:MET:HE3	1:N:49:ILE:HD11	1.91	0.53
1:A:401:HIS:O	1:A:404:ARG:HB3	2.09	0.53
1:A:247:LEU:O	1:A:274:ALA:N	2.39	0.53
1:D:73:MET:HE3	1:E:49:ILE:HD11	1.91	0.53
1:A:107:VAL:HG21	1:A:113:PRO:HG3	1.90	0.53
1:A:301:ILE:HG12	1:A:307:MET:HE3	1.91	0.53
1:A:49:ILE:HD11	1:G:73:MET:HE3	1.91	0.53
1:J:323:VAL:HG12	1:J:332:ILE:HA	1.91	0.53
1:N:323:VAL:HG12	1:N:332:ILE:HA	1.91	0.53
1:A:201:SER:H	1:A:204:PHE:HE2	1.54	0.53
1:A:417:VAL:HG21	1:A:477:GLY:HA3	1.91	0.53
1:L:323:VAL:HG12	1:L:332:ILE:HA	1.91	0.52
1:A:186:GLU:H	1:A:380:LYS:HB2	1.74	0.52
1:D:323:VAL:HG12	1:D:332:ILE:HA	1.91	0.52
1:F:323:VAL:HG12	1:F:332:ILE:HA	1.91	0.52
1:I:323:VAL:HG12	1:I:332:ILE:HA	1.91	0.52
1:A:219:PHE:CE2	1:A:245:LYS:HB2	2.45	0.52
1:B:323:VAL:HG12	1:B:332:ILE:HA	1.91	0.52
1:C:323:VAL:HG12	1:C:332:ILE:HA	1.91	0.52
1:J:73:MET:HE3	1:K:49:ILE:HD11	1.91	0.52
1:K:323:VAL:HG12	1:K:332:ILE:HA	1.91	0.52
1:A:250:ILE:HA	1:A:276:VAL:O	2.09	0.52
1:A:64:ASP:HB3	1:A:67:GLU:HB3	1.91	0.52
1:H:323:VAL:HG12	1:H:332:ILE:HA	1.91	0.52
1:A:230:ILE:HD12	1:A:231:ARG:N	2.23	0.52
1:A:461:GLU:OE1	1:A:464:VAL:N	2.39	0.52
1:A:323:VAL:HG12	1:A:332:ILE:HA	1.91	0.52
1:E:24:ALA:O	1:E:28:LYS:HB3	2.10	0.52
1:G:323:VAL:HG12	1:G:332:ILE:HA	1.91	0.52
1:M:24:ALA:O	1:M:28:LYS:HB3	2.10	0.52
1:A:219:PHE:CD2	1:A:245:LYS:HE2	2.45	0.52
1:A:113:PRO:C	1:A:115:ASP:H	2.16	0.52
1:A:135:SER:HA	1:A:412:VAL:HG12	1.92	0.52
1:A:421:ARG:NH1	1:A:472:GLY:O	2.42	0.52
1:A:122:LYS:NZ	1:A:430:ARG:O	2.33	0.52
1:A:73:MET:HE3	1:B:49:ILE:HD11	1.92	0.52
1:F:349:ILE:HG12	1:F:368:ARG:HH21	1.75	0.52
1:N:349:ILE:HG12	1:N:368:ARG:HH21	1.75	0.52
1:A:77:VAL:HG21	1:A:510:VAL:CG1	2.40	0.52
1:A:126:VAL:HG11	1:A:429:LEU:CD2	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:24:ALA:O	1:F:28:LYS:HB3	2.10	0.52
1:N:24:ALA:O	1:N:28:LYS:HB3	2.10	0.52
1:A:230:ILE:HD12	1:A:231:ARG:N	2.24	0.52
1:A:417:VAL:HA	1:A:420:ILE:HG22	1.90	0.52
1:B:73:MET:HE3	1:C:49:ILE:HD11	1.91	0.52
1:D:24:ALA:O	1:D:28:LYS:HB3	2.10	0.52
1:D:187:LEU:HD13	1:D:379:ILE:HG12	1.92	0.52
1:A:296:THR:HB	1:A:318:GLY:HA3	1.91	0.52
1:A:363:GLU:HA	1:A:366:GLN:HE21	1.75	0.52
1:E:349:ILE:HG12	1:E:368:ARG:HH21	1.75	0.52
1:H:349:ILE:HG12	1:H:368:ARG:HH21	1.75	0.52
1:L:24:ALA:O	1:L:28:LYS:HB3	2.10	0.52
1:L:187:LEU:HD13	1:L:379:ILE:HG12	1.92	0.52
1:M:349:ILE:HG12	1:M:368:ARG:HH21	1.75	0.52
1:A:27:VAL:HG12	1:A:90:THR:HG23	1.92	0.52
1:A:179:ASP:HB3	1:A:389:MET:HE1	1.91	0.52
1:A:303:GLU:OE1	1:A:303:GLU:N	2.37	0.52
1:I:73:MET:HE3	1:J:49:ILE:HD11	1.92	0.52
1:A:240:VAL:CG2	1:A:245:LYS:HE3	2.40	0.52
1:D:349:ILE:HG12	1:D:368:ARG:HH21	1.75	0.51
1:E:73:MET:HE3	1:F:49:ILE:HD11	1.92	0.51
1:G:349:ILE:HG12	1:G:368:ARG:HH21	1.75	0.51
1:M:187:LEU:HD13	1:M:379:ILE:HG12	1.92	0.51
1:A:162:ILE:HD12	1:A:162:ILE:H	1.75	0.51
1:A:217:SER:O	1:A:245:LYS:NZ	2.38	0.51
1:A:156:GLU:O	1:A:160:LYS:HD3	2.09	0.51
1:A:421:ARG:NH1	1:A:472:GLY:O	2.43	0.51
1:C:187:LEU:HD13	1:C:379:ILE:HG12	1.92	0.51
1:E:187:LEU:HD13	1:E:379:ILE:HG12	1.92	0.51
1:J:187:LEU:HD13	1:J:379:ILE:HG12	1.92	0.51
1:B:24:ALA:O	1:B:28:LYS:HB3	2.10	0.51
1:B:187:LEU:HD13	1:B:379:ILE:HG12	1.92	0.51
1:C:24:ALA:O	1:C:28:LYS:HB3	2.10	0.51
1:G:24:ALA:O	1:G:28:LYS:HB3	2.10	0.51
1:G:171:LYS:O	1:G:404:ARG:NH1	2.44	0.51
1:H:24:ALA:O	1:H:28:LYS:HB3	2.10	0.51
1:H:171:LYS:O	1:H:404:ARG:NH1	2.44	0.51
1:K:24:ALA:O	1:K:28:LYS:HB3	2.10	0.51
1:L:349:ILE:HG12	1:L:368:ARG:HH21	1.75	0.51
1:A:228:SER:C	1:A:257:GLU:HB3	2.35	0.51
1:A:340:ALA:O	1:A:343:GLN:HG3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:LEU:HD13	1:A:237:LEU:HD11	1.92	0.51
1:F:171:LYS:O	1:F:404:ARG:NH1	2.44	0.51
1:I:171:LYS:O	1:I:404:ARG:NH1	2.44	0.51
1:I:349:ILE:HG12	1:I:368:ARG:HH21	1.75	0.51
1:J:24:ALA:O	1:J:28:LYS:HB3	2.10	0.51
1:K:187:LEU:HD13	1:K:379:ILE:HG12	1.92	0.51
1:A:31:LEU:HB2	1:A:90:THR:HG21	1.92	0.51
1:A:171:LYS:O	1:A:404:ARG:NH1	2.44	0.51
1:E:171:LYS:O	1:E:404:ARG:NH1	2.44	0.51
1:M:171:LYS:O	1:M:404:ARG:NH1	2.44	0.51
1:N:171:LYS:O	1:N:404:ARG:NH1	2.44	0.51
1:A:219:PHE:HD2	1:A:245:LYS:HE2	1.75	0.51
1:A:254:VAL:HG12	1:A:259:LEU:HD12	1.93	0.51
1:A:213:VAL:O	1:A:324:VAL:HA	2.11	0.51
1:A:504:LEU:O	1:A:507:ALA:N	2.44	0.51
1:C:73:MET:HE3	1:D:49:ILE:HD11	1.92	0.51
1:J:349:ILE:HG12	1:J:368:ARG:HH21	1.75	0.51
1:A:288:MET:HG2	1:A:368:ARG:NH1	2.26	0.51
1:A:349:ILE:HG12	1:A:368:ARG:HH21	1.75	0.51
1:A:187:LEU:HD13	1:A:379:ILE:HG12	1.93	0.51
1:A:234:LEU:HD23	1:A:235:PRO:HD3	1.93	0.51
1:D:257:GLU:O	1:D:261:THR:OG1	2.26	0.51
1:I:24:ALA:O	1:I:28:LYS:HB3	2.10	0.51
1:I:187:LEU:HD13	1:I:379:ILE:HG12	1.92	0.51
1:K:349:ILE:HG12	1:K:368:ARG:HH21	1.75	0.51
1:A:223:ALA:O	1:A:250:ILE:C	2.53	0.51
1:A:165:ALA:HB1	1:A:175:ILE:HD12	1.92	0.51
1:A:24:ALA:O	1:A:28:LYS:HB3	2.10	0.51
1:A:187:LEU:HD13	1:A:379:ILE:HG12	1.92	0.51
1:A:281:PHE:HA	1:A:285:ARG:HE	1.76	0.51
1:B:349:ILE:HG12	1:B:368:ARG:HH21	1.75	0.51
1:I:281:PHE:HA	1:I:285:ARG:HE	1.76	0.51
1:A:122:LYS:HD3	1:A:440:ILE:HD11	1.92	0.51
1:A:223:ALA:HB3	1:A:249:ILE:HG23	1.91	0.51
1:F:187:LEU:HD13	1:F:379:ILE:HG12	1.92	0.51
1:F:281:PHE:HA	1:F:285:ARG:HE	1.76	0.51
1:N:187:LEU:HD13	1:N:379:ILE:HG12	1.92	0.51
1:A:213:VAL:HG22	1:A:325:ILE:HB	1.92	0.51
1:A:224:ASP:O	1:A:225:LYS:HD2	2.11	0.51
1:A:254:VAL:HG23	1:A:259:LEU:HB3	1.92	0.51
1:D:171:LYS:O	1:D:404:ARG:NH1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:171:LYS:O	1:L:404:ARG:NH1	2.44	0.50
1:N:281:PHE:HA	1:N:285:ARG:HE	1.76	0.50
1:A:390:LYS:O	1:A:393:LYS:HB3	2.11	0.50
1:A:388:GLU:O	1:A:392:LYS:N	2.37	0.50
1:A:505:GLN:O	1:A:508:ALA:N	2.44	0.50
1:C:200:LEU:HD21	1:C:277:LYS:HG3	1.93	0.50
1:C:349:ILE:HG12	1:C:368:ARG:HH21	1.75	0.50
1:D:421:ARG:NH1	1:D:472:GLY:O	2.45	0.50
1:H:187:LEU:HD13	1:H:379:ILE:HG12	1.92	0.50
1:K:73:MET:HE3	1:L:49:ILE:HD11	1.93	0.50
1:K:200:LEU:HD21	1:K:277:LYS:HG3	1.93	0.50
1:G:187:LEU:HD13	1:G:379:ILE:HG12	1.92	0.50
1:J:171:LYS:O	1:J:404:ARG:NH1	2.44	0.50
1:K:281:PHE:HA	1:K:285:ARG:HE	1.76	0.50
1:L:421:ARG:NH1	1:L:472:GLY:O	2.45	0.50
1:A:34:LYS:HG3	1:A:458:CYS:SG	2.50	0.50
1:B:171:LYS:O	1:B:404:ARG:NH1	2.44	0.50
1:C:171:LYS:O	1:C:404:ARG:NH1	2.44	0.50
1:C:281:PHE:HA	1:C:285:ARG:HE	1.76	0.50
1:D:281:PHE:HA	1:D:285:ARG:HE	1.76	0.50
1:E:421:ARG:NH1	1:E:472:GLY:O	2.45	0.50
1:K:171:LYS:O	1:K:404:ARG:NH1	2.44	0.50
1:L:281:PHE:HA	1:L:285:ARG:HE	1.76	0.50
1:M:421:ARG:NH1	1:M:472:GLY:O	2.45	0.50
1:A:389:MET:O	1:A:392:LYS:N	2.43	0.50
1:A:249:ILE:N	1:A:274:ALA:O	2.31	0.50
1:A:421:ARG:NH1	1:A:472:GLY:O	2.45	0.50
1:F:200:LEU:HD21	1:F:277:LYS:HG3	1.93	0.50
1:H:421:ARG:NH1	1:H:472:GLY:O	2.45	0.50
1:I:421:ARG:NH1	1:I:472:GLY:O	2.45	0.50
1:J:200:LEU:HD21	1:J:277:LYS:HG3	1.93	0.50
1:N:200:LEU:HD21	1:N:277:LYS:HG3	1.93	0.50
1:A:288:MET:HA	1:A:291:ASP:OD2	2.12	0.50
1:A:109:ALA:HB2	1:J:109:ALA:HB2	1.94	0.50
1:B:200:LEU:HD21	1:B:277:LYS:HG3	1.93	0.50
1:G:200:LEU:HD21	1:G:277:LYS:HG3	1.93	0.50
1:G:421:ARG:NH1	1:G:472:GLY:O	2.45	0.50
1:K:421:ARG:NH1	1:K:472:GLY:O	2.45	0.50
1:A:141:SER:O	1:A:144:ILE:HG22	2.12	0.50
1:A:257:GLU:O	1:A:261:THR:HB	2.11	0.50
1:A:295:LEU:O	1:A:337:GLY:N	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:ILE:O	1:A:346:VAL:HG23	2.12	0.50
1:C:421:ARG:NH1	1:C:472:GLY:O	2.45	0.50
1:D:200:LEU:HD21	1:D:277:LYS:HG3	1.93	0.50
1:G:281:PHE:HA	1:G:285:ARG:HE	1.76	0.50
1:L:200:LEU:HD21	1:L:277:LYS:HG3	1.93	0.50
1:E:200:LEU:HD21	1:E:277:LYS:HG3	1.93	0.50
1:F:109:ALA:HB2	1:L:109:ALA:HB2	1.93	0.50
1:H:281:PHE:HA	1:H:285:ARG:HE	1.76	0.50
1:M:200:LEU:HD21	1:M:277:LYS:HG3	1.93	0.50
1:A:10:ASN:O	1:A:14:VAL:HG22	2.12	0.50
1:A:23:LEU:HD13	1:A:60:ILE:HD11	1.93	0.50
1:B:109:ALA:HB2	1:I:109:ALA:HB2	1.94	0.50
1:H:200:LEU:HD21	1:H:277:LYS:HG3	1.93	0.50
1:A:115:ASP:OD2	1:A:433:ASN:ND2	2.32	0.50
1:A:213:VAL:HG22	1:A:325:ILE:CG2	2.42	0.50
1:A:254:VAL:HG21	1:A:275:ALA:HB1	1.93	0.50
1:F:421:ARG:NH1	1:F:472:GLY:O	2.45	0.49
1:G:109:ALA:HB2	1:K:109:ALA:HB2	1.93	0.49
1:A:155:ASP:OD1	1:A:156:GLU:N	2.40	0.49
1:A:24:ALA:O	1:A:28:LYS:HG2	2.11	0.49
1:A:435:ASP:O	1:A:438:VAL:HG12	2.12	0.49
1:N:247:LEU:O	1:N:273:VAL:HA	2.13	0.49
1:N:421:ARG:NH1	1:N:472:GLY:O	2.45	0.49
1:A:223:ALA:HB3	1:A:227:ILE:HD11	1.93	0.49
1:A:94:VAL:HG12	1:A:449:ALA:HB1	1.95	0.49
1:B:421:ARG:NH1	1:B:472:GLY:O	2.45	0.49
1:D:22:VAL:HG11	1:D:62:LEU:HD21	1.95	0.49
1:E:22:VAL:HG11	1:E:62:LEU:HD21	1.95	0.49
1:E:281:PHE:HA	1:E:285:ARG:HE	1.76	0.49
1:F:247:LEU:O	1:F:273:VAL:HA	2.13	0.49
1:G:247:LEU:O	1:G:273:VAL:HA	2.13	0.49
1:H:247:LEU:O	1:H:273:VAL:HA	2.13	0.49
1:J:281:PHE:HA	1:J:285:ARG:HE	1.76	0.49
1:J:421:ARG:NH1	1:J:472:GLY:O	2.45	0.49
1:L:22:VAL:HG11	1:L:62:LEU:HD21	1.95	0.49
1:M:22:VAL:HG11	1:M:62:LEU:HD21	1.95	0.49
1:A:116:LEU:HD21	1:A:438:VAL:HG23	1.94	0.49
1:A:365:LEU:HA	1:A:368:ARG:HB2	1.93	0.49
1:A:247:LEU:O	1:A:273:VAL:HA	2.13	0.49
1:C:22:VAL:HG11	1:C:62:LEU:HD21	1.94	0.49
1:C:257:GLU:O	1:C:261:THR:OG1	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:247:LEU:O	1:E:273:VAL:HA	2.13	0.49
1:K:257:GLU:O	1:K:261:THR:OG1	2.26	0.49
1:M:281:PHE:HA	1:M:285:ARG:HE	1.76	0.49
1:A:196:ASP:HA	1:A:329:THR:HG23	1.94	0.49
1:B:281:PHE:HA	1:B:285:ARG:HE	1.77	0.49
1:C:109:ALA:HB2	1:H:109:ALA:HB2	1.94	0.49
1:I:247:LEU:O	1:I:273:VAL:HA	2.13	0.49
1:M:247:LEU:O	1:M:273:VAL:HA	2.13	0.49
1:A:39:VAL:HG22	1:A:49:ILE:HG12	1.95	0.49
1:A:350:ARG:O	1:A:353:ILE:HG12	2.12	0.49
1:A:479:ASN:HD22	1:A:491:MET:HE2	1.78	0.49
1:A:326:ASN:HB3	1:A:329:THR:H	1.77	0.49
1:F:22:VAL:HG11	1:F:62:LEU:HD21	1.95	0.49
1:I:200:LEU:HD21	1:I:277:LYS:HG3	1.93	0.49
1:N:22:VAL:HG11	1:N:62:LEU:HD21	1.95	0.49
1:A:257:GLU:O	1:A:261:THR:CB	2.61	0.49
1:A:314:LEU:HD22	1:A:317:LEU:HD11	1.95	0.49
1:K:22:VAL:HG11	1:K:62:LEU:HD21	1.95	0.49
1:A:235:PRO:HG3	1:A:310:GLU:HA	1.95	0.49
1:A:441:LYS:O	1:A:445:ARG:HG3	2.13	0.49
1:A:368:ARG:O	1:A:371:LYS:HB3	2.13	0.49
1:A:496:PRO:HD2	1:A:499:VAL:HG11	1.94	0.49
1:A:387:VAL:HG23	1:A:390:LYS:HZ1	1.78	0.49
1:A:200:LEU:HD21	1:A:277:LYS:HG3	1.93	0.49
1:B:247:LEU:O	1:B:273:VAL:HA	2.13	0.49
1:A:199:TYR:HA	1:A:276:VAL:HG12	1.93	0.49
1:D:247:LEU:O	1:D:273:VAL:HA	2.13	0.49
1:J:247:LEU:O	1:J:273:VAL:HA	2.13	0.49
1:L:247:LEU:O	1:L:273:VAL:HA	2.13	0.49
1:A:102:GLU:HB2	1:A:442:VAL:HG13	1.95	0.49
1:A:420:ILE:CD1	1:A:448:GLU:HA	2.42	0.49
1:D:109:ALA:HB2	1:N:109:ALA:HB2	1.94	0.49
1:A:222:LEU:O	1:A:301:ILE:HG22	2.13	0.49
1:C:247:LEU:O	1:C:273:VAL:HA	2.13	0.48
1:A:219:PHE:CD1	1:A:319:GLN:HB2	2.48	0.48
1:A:213:VAL:H	1:A:325:ILE:HG22	1.78	0.48
1:J:248:LEU:HD22	1:J:323:VAL:HG21	1.95	0.48
1:K:247:LEU:O	1:K:273:VAL:HA	2.13	0.48
1:A:205:ILE:HG23	1:A:212:ALA:O	2.13	0.48
1:A:338:GLU:O	1:A:342:ILE:N	2.33	0.48
1:A:270:ILE:HG22	1:A:271:VAL:HG23	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:LEU:HD22	1:B:323:VAL:HG21	1.95	0.48
1:C:40:LEU:HD13	1:C:59:GLU:HG3	1.96	0.48
1:D:40:LEU:HD13	1:D:59:GLU:HG3	1.96	0.48
1:E:248:LEU:HD22	1:E:323:VAL:HG21	1.95	0.48
1:A:10:ASN:O	1:A:13:GLY:N	2.46	0.48
1:A:463:SER:O	1:A:467:ASN:CB	2.62	0.48
1:A:135:SER:HA	1:A:412:VAL:HG12	1.95	0.48
1:A:219:PHE:HB3	1:A:317:LEU:HD13	1.94	0.48
1:A:289:LEU:HD12	1:A:290:GLN:N	2.27	0.48
1:A:248:LEU:HD22	1:A:323:VAL:HG21	1.95	0.48
1:F:519:CYS:HB3	1:G:38:VAL:HG22	1.96	0.48
1:H:38:VAL:HG22	1:N:519:CYS:HB3	1.95	0.48
1:K:40:LEU:HD13	1:K:59:GLU:HG3	1.96	0.48
1:L:40:LEU:HD13	1:L:59:GLU:HG3	1.96	0.48
1:M:40:LEU:HD13	1:M:59:GLU:HG3	1.96	0.48
1:M:519:CYS:HB3	1:N:38:VAL:HG22	1.95	0.48
1:A:157:THR:O	1:A:160:LYS:HB3	2.13	0.48
1:A:519:CYS:SG	1:A:520:MET:N	2.86	0.48
1:A:339:GLU:HA	1:A:342:ILE:HG22	1.95	0.48
1:A:487:ASN:O	1:A:491:MET:HG3	2.12	0.48
1:A:169:VAL:HG12	1:A:173:GLY:HA3	1.96	0.48
1:A:421:ARG:NE	1:A:474:GLY:O	2.46	0.48
1:A:472:GLY:HA3	1:A:476:TYR:CD2	2.48	0.48
1:A:458:CYS:SG	2:A:602:HOH:O	2.60	0.48
1:B:22:VAL:HG11	1:B:62:LEU:HD21	1.95	0.48
1:E:40:LEU:HD13	1:E:59:GLU:HG3	1.96	0.48
1:F:40:LEU:HD13	1:F:59:GLU:HG3	1.96	0.48
1:G:22:VAL:HG11	1:G:62:LEU:HD21	1.95	0.48
1:G:40:LEU:HD13	1:G:59:GLU:HG3	1.96	0.48
1:H:40:LEU:HD13	1:H:59:GLU:HG3	1.96	0.48
1:M:248:LEU:HD22	1:M:323:VAL:HG21	1.95	0.48
1:A:178:GLU:CD	1:A:322:ARG:HD3	2.39	0.48
1:A:253:ASP:OD1	1:A:254:VAL:N	2.45	0.48
1:A:166:MET:O	1:A:170:GLY:N	2.47	0.48
1:A:247:LEU:HD13	1:A:248:LEU:N	2.28	0.48
1:A:194:GLN:HG3	1:A:331:THR:HG22	1.95	0.48
1:A:308:GLU:OE2	1:A:311:LYS:NZ	2.38	0.48
1:H:22:VAL:HG11	1:H:62:LEU:HD21	1.95	0.48
1:I:248:LEU:HD22	1:I:323:VAL:HG21	1.95	0.48
1:J:22:VAL:HG11	1:J:62:LEU:HD21	1.95	0.48
1:N:40:LEU:HD13	1:N:59:GLU:HG3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:THR:O	1:A:264:VAL:HB	2.12	0.48
1:A:289:LEU:HA	1:A:292:ILE:HG22	1.95	0.48
1:A:16:MET:O	1:A:19:GLY:N	2.45	0.48
1:F:248:LEU:HD22	1:F:323:VAL:HG21	1.95	0.48
1:H:519:CYS:HB3	1:I:38:VAL:HG22	1.96	0.48
1:N:248:LEU:HD22	1:N:323:VAL:HG21	1.95	0.48
1:A:220:ILE:H	1:A:319:GLN:HA	1.78	0.48
1:A:260:ALA:O	1:A:264:VAL:HG23	2.14	0.48
1:A:358:SER:O	1:A:362:ARG:HG3	2.14	0.48
1:A:232:GLU:OE2	1:A:308:GLU:HG3	2.13	0.48
1:B:257:GLU:O	1:B:261:THR:OG1	2.26	0.48
1:F:257:GLU:O	1:F:261:THR:OG1	2.26	0.48
1:I:40:LEU:HD13	1:I:59:GLU:HG3	1.96	0.48
1:L:519:CYS:HB3	1:M:38:VAL:HG22	1.94	0.48
1:A:308:GLU:CD	1:A:309:LEU:N	2.72	0.48
1:A:362:ARG:O	1:A:366:GLN:NE2	2.47	0.48
1:C:248:LEU:HD22	1:C:323:VAL:HG21	1.95	0.48
1:H:77:VAL:HG12	1:H:506:TYR:HB3	1.96	0.48
1:K:248:LEU:HD22	1:K:323:VAL:HG21	1.95	0.48
1:A:221:LEU:O	1:A:248:LEU:O	2.32	0.48
1:A:121:ASP:O	1:A:125:THR:HG22	2.14	0.48
1:A:240:VAL:O	1:A:244:GLY:N	2.45	0.48
1:A:38:VAL:HG22	1:G:519:CYS:HB3	1.96	0.48
1:A:40:LEU:HD13	1:A:59:GLU:HG3	1.96	0.48
1:A:77:VAL:HG12	1:A:506:TYR:HB3	1.96	0.48
1:B:447:MET:HE2	1:B:504:LEU:HD11	1.96	0.48
1:C:447:MET:HE2	1:C:504:LEU:HD11	1.96	0.48
1:J:40:LEU:HD13	1:J:59:GLU:HG3	1.96	0.48
1:J:217:SER:N	1:J:321:LYS:O	2.46	0.48
1:J:270:ILE:HG22	1:J:271:VAL:HG23	1.96	0.48
1:J:447:MET:HE2	1:J:504:LEU:HD11	1.96	0.48
1:A:167:ASP:OD1	1:A:168:LYS:N	2.46	0.48
1:B:40:LEU:HD13	1:B:59:GLU:HG3	1.96	0.47
1:B:217:SER:N	1:B:321:LYS:O	2.46	0.47
1:D:270:ILE:HG22	1:D:271:VAL:HG23	1.96	0.47
1:G:77:VAL:HG12	1:G:506:TYR:HB3	1.96	0.47
1:G:447:MET:HE2	1:G:504:LEU:HD11	1.96	0.47
1:H:447:MET:HE2	1:H:504:LEU:HD11	1.96	0.47
1:I:77:VAL:HG12	1:I:506:TYR:HB3	1.96	0.47
1:J:257:GLU:O	1:J:261:THR:OG1	2.26	0.47
1:L:270:ILE:HG22	1:L:271:VAL:HG23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:217:SER:N	1:M:321:LYS:O	2.46	0.47
1:M:270:ILE:HG22	1:M:271:VAL:HG23	1.96	0.47
1:A:219:PHE:HA	1:A:319:GLN:HA	1.95	0.47
1:A:230:ILE:HG23	1:A:257:GLU:CG	2.43	0.47
1:A:303:GLU:OE1	1:A:303:GLU:N	2.44	0.47
1:A:177:VAL:HG12	1:A:393:LYS:NZ	2.29	0.47
1:A:200:LEU:HG	1:A:276:VAL:HA	1.96	0.47
1:A:221:LEU:HD22	1:A:236:VAL:HG11	1.97	0.47
1:B:270:ILE:HG22	1:B:271:VAL:HG23	1.96	0.47
1:E:270:ILE:HG22	1:E:271:VAL:HG23	1.96	0.47
1:F:77:VAL:HG12	1:F:506:TYR:HB3	1.96	0.47
1:I:447:MET:HE2	1:I:504:LEU:HD11	1.96	0.47
1:K:447:MET:HE2	1:K:504:LEU:HD11	1.96	0.47
1:N:77:VAL:HG12	1:N:506:TYR:HB3	1.96	0.47
1:N:257:GLU:O	1:N:261:THR:OG1	2.26	0.47
1:A:288:MET:O	1:A:291:ASP:N	2.48	0.47
1:C:270:ILE:HG22	1:C:271:VAL:HG23	1.96	0.47
1:D:221:LEU:HD22	1:D:236:VAL:HG11	1.97	0.47
1:D:248:LEU:HD22	1:D:323:VAL:HG21	1.95	0.47
1:E:217:SER:N	1:E:321:LYS:O	2.46	0.47
1:F:447:MET:HE2	1:F:504:LEU:HD11	1.96	0.47
1:I:221:LEU:HD22	1:I:236:VAL:HG11	1.97	0.47
1:K:270:ILE:HG22	1:K:271:VAL:HG23	1.96	0.47
1:A:115:ASP:OD2	1:A:436:GLN:HG3	2.14	0.47
1:A:194:GLN:HE21	1:A:329:THR:HG21	1.79	0.47
1:A:237:LEU:HD21	1:A:247:LEU:HG	1.96	0.47
1:A:213:VAL:N	1:A:325:ILE:HG22	2.29	0.47
1:A:225:LYS:HE3	1:A:227:ILE:HG12	1.96	0.47
1:A:22:VAL:HG11	1:A:62:LEU:HD21	1.95	0.47
1:A:447:MET:HE2	1:A:504:LEU:HD11	1.96	0.47
1:B:77:VAL:HG12	1:B:506:TYR:HB3	1.96	0.47
1:B:221:LEU:HD22	1:B:236:VAL:HG11	1.97	0.47
1:C:221:LEU:HD22	1:C:236:VAL:HG11	1.97	0.47
1:D:447:MET:HE2	1:D:504:LEU:HD11	1.96	0.47
1:I:270:ILE:HG22	1:I:271:VAL:HG23	1.96	0.47
1:J:77:VAL:HG12	1:J:506:TYR:HB3	1.96	0.47
1:K:221:LEU:HD22	1:K:236:VAL:HG11	1.97	0.47
1:L:221:LEU:HD22	1:L:236:VAL:HG11	1.97	0.47
1:L:248:LEU:HD22	1:L:323:VAL:HG21	1.95	0.47
1:N:447:MET:HE2	1:N:504:LEU:HD11	1.96	0.47
1:A:270:ILE:HG22	1:A:271:VAL:HG23	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:22:VAL:HG11	1:I:62:LEU:HD21	1.95	0.47
1:J:221:LEU:HD22	1:J:236:VAL:HG11	1.97	0.47
1:K:254:VAL:HG12	1:K:259:LEU:HB2	1.97	0.47
1:L:447:MET:HE2	1:L:504:LEU:HD11	1.96	0.47
1:A:77:VAL:HG21	1:A:510:VAL:HG13	1.97	0.47
1:A:155:ASP:HB2	1:A:395:ARG:HH12	1.79	0.47
1:A:296:THR:O	1:A:336:VAL:HB	2.15	0.47
1:A:352:GLN:HA	1:A:355:GLU:OE2	2.15	0.47
1:A:519:CYS:HB3	1:B:38:VAL:HG22	1.96	0.47
1:C:254:VAL:HG12	1:C:259:LEU:HB2	1.97	0.47
1:G:221:LEU:HD22	1:G:236:VAL:HG11	1.97	0.47
1:L:254:VAL:HG12	1:L:259:LEU:HB2	1.97	0.47
1:M:221:LEU:HD22	1:M:236:VAL:HG11	1.97	0.47
1:A:339:GLU:O	1:A:343:GLN:CB	2.60	0.47
1:A:197:ARG:NE	1:A:278:ALA:O	2.48	0.47
1:A:403:THR:HA	1:A:406:ALA:HB3	1.96	0.47
1:A:478:TYR:HB2	1:A:485:TYR:CE1	2.49	0.47
1:B:254:VAL:HG12	1:B:259:LEU:HB2	1.97	0.47
1:D:254:VAL:HG12	1:D:259:LEU:HB2	1.97	0.47
1:E:109:ALA:HB2	1:M:109:ALA:HB2	1.96	0.47
1:E:221:LEU:HD22	1:E:236:VAL:HG11	1.97	0.47
1:E:447:MET:HE2	1:E:504:LEU:HD11	1.96	0.47
1:F:270:ILE:HG22	1:F:271:VAL:HG23	1.96	0.47
1:G:248:LEU:HD22	1:G:323:VAL:HG21	1.95	0.47
1:H:221:LEU:HD22	1:H:236:VAL:HG11	1.97	0.47
1:I:519:CYS:HB3	1:J:38:VAL:HG22	1.96	0.47
1:J:254:VAL:HG12	1:J:259:LEU:HB2	1.97	0.47
1:J:519:CYS:HB3	1:K:38:VAL:HG22	1.95	0.47
1:M:447:MET:HE2	1:M:504:LEU:HD11	1.96	0.47
1:N:270:ILE:HG22	1:N:271:VAL:HG23	1.96	0.47
1:A:391:GLU:OE2	1:A:395:ARG:NE	2.27	0.47
1:A:419:LEU:HD22	1:A:504:LEU:HD12	1.95	0.47
1:A:461:GLU:OE1	1:A:463:SER:N	2.48	0.47
1:G:270:ILE:HG22	1:G:271:VAL:HG23	1.96	0.47
1:H:248:LEU:HD22	1:H:323:VAL:HG21	1.95	0.47
1:H:270:ILE:HG22	1:H:271:VAL:HG23	1.96	0.47
1:M:254:VAL:HG12	1:M:259:LEU:HB2	1.97	0.47
1:N:221:LEU:HD22	1:N:236:VAL:HG11	1.97	0.47
1:A:356:ALA:O	1:A:362:ARG:NH2	2.48	0.47
1:A:174:VAL:HG21	1:A:194:GLN:CD	2.39	0.47
1:A:361:ASP:O	1:A:365:LEU:HD23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:254:VAL:HG12	1:E:259:LEU:HB2	1.97	0.47
1:F:221:LEU:HD22	1:F:236:VAL:HG11	1.97	0.47
1:M:513:LEU:HB3	1:N:49:ILE:HD13	1.97	0.47
1:A:389:MET:O	1:A:392:LYS:N	2.48	0.47
1:D:77:VAL:HG12	1:D:506:TYR:HB3	1.96	0.47
1:E:77:VAL:HG12	1:E:506:TYR:HB3	1.96	0.47
1:E:435:ASP:HA	1:E:438:VAL:HG22	1.97	0.47
1:E:519:CYS:HB3	1:F:38:VAL:HG22	1.96	0.47
1:H:217:SER:N	1:H:321:LYS:O	2.46	0.47
1:K:77:VAL:HG12	1:K:506:TYR:HB3	1.96	0.47
1:A:193:MET:HE3	1:A:292:ILE:HG21	1.97	0.47
1:B:519:CYS:HB3	1:C:38:VAL:HG22	1.96	0.46
1:C:77:VAL:HG12	1:C:506:TYR:HB3	1.96	0.46
1:F:254:VAL:HG12	1:F:259:LEU:HB2	1.97	0.46
1:M:435:ASP:HA	1:M:438:VAL:HG22	1.97	0.46
1:N:254:VAL:HG12	1:N:259:LEU:HB2	1.97	0.46
1:A:7:LYS:HB3	1:A:12:ALA:HB2	1.95	0.46
1:A:245:LYS:HD2	1:A:245:LYS:C	2.40	0.46
1:A:115:ASP:OD2	1:A:435:ASP:HB2	2.15	0.46
1:A:129:GLU:O	1:A:132:LYS:N	2.48	0.46
1:A:149:THR:HG21	1:A:156:GLU:HA	1.97	0.46
1:A:193:MET:SD	1:A:332:ILE:HD13	2.55	0.46
1:A:230:ILE:O	1:A:234:LEU:N	2.42	0.46
1:A:364:LYS:O	1:A:367:GLU:HB2	2.15	0.46
1:D:519:CYS:HB3	1:E:38:VAL:HG22	1.96	0.46
1:G:217:SER:N	1:G:321:LYS:O	2.46	0.46
1:L:77:VAL:HG12	1:L:506:TYR:HB3	1.96	0.46
1:M:27:VAL:O	1:M:30:THR:OG1	2.33	0.46
1:M:77:VAL:HG12	1:M:506:TYR:HB3	1.96	0.46
1:A:28:LYS:HD3	1:A:453:GLN:NE2	2.30	0.46
1:A:226:LYS:HD3	1:A:255:GLU:OE2	2.15	0.46
1:A:194:GLN:HE21	1:A:329:THR:HG21	1.79	0.46
1:A:496:PRO:O	1:A:499:VAL:HG12	2.15	0.46
1:D:435:ASP:HA	1:D:438:VAL:HG22	1.97	0.46
1:F:435:ASP:HA	1:F:438:VAL:HG22	1.97	0.46
1:L:435:ASP:HA	1:L:438:VAL:HG22	1.97	0.46
1:N:435:ASP:HA	1:N:438:VAL:HG22	1.97	0.46
1:A:236:VAL:HG22	1:A:312:ALA:O	2.15	0.46
1:A:124:VAL:O	1:A:127:ALA:N	2.48	0.46
1:G:254:VAL:HG12	1:G:259:LEU:HB2	1.97	0.46
1:H:254:VAL:HG12	1:H:259:LEU:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:ASP:CG	1:A:88:GLY:H	2.23	0.46
1:A:265:ASN:O	1:A:269:GLY:N	2.48	0.46
1:A:254:VAL:HG12	1:A:259:LEU:HB2	1.97	0.46
1:A:251:ALA:O	1:A:278:ALA:N	2.30	0.46
1:A:219:PHE:HB2	1:A:247:LEU:HD23	1.98	0.46
1:B:27:VAL:O	1:B:30:THR:OG1	2.33	0.46
1:G:435:ASP:HA	1:G:438:VAL:HG22	1.97	0.46
1:I:254:VAL:HG12	1:I:259:LEU:HB2	1.97	0.46
1:A:203:TYR:CD2	1:A:263:VAL:HG13	2.51	0.46
1:A:369:VAL:O	1:A:373:ALA:N	2.40	0.46
1:A:16:MET:SD	1:A:514:MET:HG3	2.56	0.46
1:A:199:TYR:CE1	1:A:327:LYS:HA	2.50	0.46
1:J:27:VAL:O	1:J:30:THR:OG1	2.33	0.46
1:A:230:ILE:O	1:A:234:LEU:HG	2.16	0.46
1:A:257:GLU:O	1:A:261:THR:OG1	2.26	0.46
1:A:200:LEU:H	1:A:200:LEU:HD23	1.81	0.46
1:A:417:VAL:HG21	1:A:477:GLY:HA3	1.97	0.46
1:A:78:ALA:HB1	1:A:89:THR:HG23	1.97	0.46
1:A:197:ARG:HE	1:A:279:PRO:HA	1.81	0.46
1:H:435:ASP:HA	1:H:438:VAL:HG22	1.97	0.46
1:L:78:ALA:HB1	1:L:89:THR:HG23	1.97	0.46
1:L:217:SER:N	1:L:321:LYS:O	2.46	0.46
1:A:20:VAL:O	1:A:23:LEU:N	2.49	0.46
1:A:144:ILE:HA	1:A:147:VAL:HG12	1.97	0.46
1:A:259:LEU:O	1:A:263:VAL:HG23	2.16	0.46
1:G:78:ALA:HB1	1:G:89:THR:HG23	1.97	0.46
1:I:197:ARG:HE	1:I:279:PRO:HA	1.81	0.46
1:K:78:ALA:HB1	1:K:89:THR:HG23	1.97	0.46
1:A:180:GLY:H	1:A:389:MET:CE	2.29	0.46
1:A:185:ASP:CA	1:A:382:GLY:H	2.29	0.46
1:A:510:VAL:O	1:A:514:MET:N	2.44	0.46
1:C:519:CYS:HB3	1:D:38:VAL:HG22	1.96	0.45
1:D:78:ALA:HB1	1:D:89:THR:HG23	1.97	0.45
1:D:213:VAL:HB	1:D:325:ILE:HB	1.99	0.45
1:H:197:ARG:HE	1:H:279:PRO:HA	1.81	0.45
1:I:78:ALA:HB1	1:I:89:THR:HG23	1.97	0.45
1:I:257:GLU:O	1:I:261:THR:OG1	2.26	0.45
1:K:197:ARG:HE	1:K:279:PRO:HA	1.81	0.45
1:L:213:VAL:HB	1:L:325:ILE:HB	1.99	0.45
1:A:232:GLU:O	1:A:233:MET:HE2	2.16	0.45
1:A:458:CYS:SG	1:A:480:ALA:HB1	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:GLU:O	1:A:261:THR:N	2.49	0.45
1:A:359:ASP:HA	1:A:362:ARG:HE	1.80	0.45
1:B:197:ARG:HE	1:B:279:PRO:HA	1.81	0.45
1:C:78:ALA:HB1	1:C:89:THR:HG23	1.97	0.45
1:C:197:ARG:HE	1:C:279:PRO:HA	1.81	0.45
1:D:217:SER:N	1:D:321:LYS:O	2.46	0.45
1:G:197:ARG:HE	1:G:279:PRO:HA	1.81	0.45
1:H:78:ALA:HB1	1:H:89:THR:HG23	1.97	0.45
1:A:239:ALA:O	1:A:242:LYS:HG3	2.16	0.45
1:A:85:ALA:HB1	1:A:499:VAL:HG23	1.99	0.45
1:A:197:ARG:O	1:A:330:THR:OG1	2.24	0.45
1:A:19:GLY:HA2	1:A:67:GLU:OE2	2.17	0.45
1:A:363:GLU:O	1:A:367:GLU:HG3	2.17	0.45
1:B:78:ALA:HB1	1:B:89:THR:HG23	1.97	0.45
1:C:213:VAL:HB	1:C:325:ILE:HB	1.99	0.45
1:G:235:PRO:HG3	1:G:310:GLU:HA	1.99	0.45
1:J:197:ARG:HE	1:J:279:PRO:HA	1.81	0.45
1:J:213:VAL:HB	1:J:325:ILE:HB	1.99	0.45
1:K:213:VAL:HB	1:K:325:ILE:HB	1.99	0.45
1:K:519:CYS:HB3	1:L:38:VAL:HG22	1.97	0.45
1:A:487:ASN:HB3	1:A:490:ASP:HB2	1.97	0.45
1:A:100:ILE:O	1:A:103:GLY:N	2.45	0.45
1:A:343:GLN:O	1:A:347:ALA:N	2.32	0.45
1:A:213:VAL:HB	1:A:325:ILE:HB	1.99	0.45
1:A:435:ASP:HA	1:A:438:VAL:HG22	1.97	0.45
1:B:213:VAL:HB	1:B:325:ILE:HB	1.99	0.45
1:B:435:ASP:HA	1:B:438:VAL:HG22	1.97	0.45
1:I:213:VAL:HB	1:I:325:ILE:HB	1.99	0.45
1:I:217:SER:N	1:I:321:LYS:O	2.46	0.45
1:J:78:ALA:HB1	1:J:89:THR:HG23	1.97	0.45
1:J:435:ASP:HA	1:J:438:VAL:HG22	1.97	0.45
1:L:235:PRO:HG3	1:L:310:GLU:HA	1.99	0.45
1:A:194:GLN:HG2	1:A:331:THR:HB	1.98	0.45
1:D:235:PRO:HG3	1:D:310:GLU:HA	1.99	0.45
1:E:213:VAL:HB	1:E:325:ILE:HB	1.99	0.45
1:H:235:PRO:HG3	1:H:310:GLU:HA	1.99	0.45
1:K:435:ASP:HA	1:K:438:VAL:HG22	1.97	0.45
1:M:213:VAL:HB	1:M:325:ILE:HB	1.99	0.45
1:N:197:ARG:HE	1:N:279:PRO:HA	1.81	0.45
1:A:193:MET:HB3	1:A:332:ILE:HB	1.97	0.45
1:A:232:GLU:OE2	1:A:310:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:LEU:O	1:A:164:GLU:HB2	2.16	0.45
1:A:235:PRO:HG3	1:A:310:GLU:HA	1.99	0.45
1:C:435:ASP:HA	1:C:438:VAL:HG22	1.97	0.45
1:I:435:ASP:HA	1:I:438:VAL:HG22	1.97	0.45
1:A:221:LEU:O	1:A:248:LEU:C	2.60	0.45
1:A:320:ALA:HA	1:A:334:ASP:O	2.17	0.45
1:A:414:GLY:N	1:A:494:LEU:HA	2.31	0.45
1:A:217:SER:N	1:A:321:LYS:O	2.46	0.45
1:E:78:ALA:HB1	1:E:89:THR:HG23	1.97	0.45
1:F:197:ARG:HE	1:F:279:PRO:HA	1.81	0.45
1:F:235:PRO:HG3	1:F:310:GLU:HA	1.99	0.45
1:H:27:VAL:O	1:H:30:THR:OG1	2.33	0.45
1:I:235:PRO:HG3	1:I:310:GLU:HA	1.99	0.45
1:M:78:ALA:HB1	1:M:89:THR:HG23	1.97	0.45
1:M:235:PRO:HG3	1:M:310:GLU:HA	1.99	0.45
1:N:235:PRO:HG3	1:N:310:GLU:HA	1.99	0.45
1:A:176:THR:H	1:A:376:VAL:HG12	1.81	0.45
1:A:397:GLU:O	1:A:400:LEU:HB3	2.17	0.45
1:A:191:GLU:OE1	1:A:335:GLY:N	2.47	0.45
1:A:293:ALA:HA	1:A:296:THR:HG22	1.98	0.45
1:A:353:ILE:HA	1:A:365:LEU:HD11	1.97	0.45
1:D:197:ARG:HE	1:D:279:PRO:HA	1.81	0.45
1:E:235:PRO:HG3	1:E:310:GLU:HA	1.99	0.45
1:F:78:ALA:HB1	1:F:89:THR:HG23	1.97	0.45
1:L:197:ARG:HE	1:L:279:PRO:HA	1.81	0.45
1:A:5:ASP:HB2	1:A:524:LEU:HD22	1.97	0.45
1:A:215:LEU:HB2	1:A:323:VAL:CG2	2.47	0.45
1:A:346:VAL:O	1:A:350:ARG:HG2	2.17	0.45
1:A:311:LYS:N	1:A:311:LYS:HD2	2.31	0.45
1:A:42:LYS:HZ3	1:A:44:PHE:HB3	1.82	0.45
1:A:265:ASN:OD1	1:A:270:ILE:HB	2.17	0.45
1:C:235:PRO:HG3	1:C:310:GLU:HA	1.99	0.45
1:F:513:LEU:HB3	1:G:49:ILE:HD13	1.99	0.45
1:G:213:VAL:HB	1:G:325:ILE:HB	1.99	0.45
1:H:49:ILE:HD13	1:N:513:LEU:HB3	1.99	0.45
1:H:213:VAL:HB	1:H:325:ILE:HB	1.99	0.45
1:K:235:PRO:HG3	1:K:310:GLU:HA	1.99	0.45
1:N:78:ALA:HB1	1:N:89:THR:HG23	1.97	0.45
1:A:214:GLU:C	1:A:215:LEU:HD22	2.41	0.45
1:A:217:SER:HA	1:A:321:LYS:HA	1.99	0.45
1:A:186:GLU:OE1	1:A:187:LEU:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:228:SER:OG	1:A:255:GLU:O	2.29	0.45
1:A:346:VAL:HA	1:A:349:ILE:HG22	1.98	0.45
1:A:128:VAL:HG21	1:A:505:GLN:NE2	2.31	0.45
1:M:197:ARG:HE	1:M:279:PRO:HA	1.81	0.44
1:A:252:GLU:HB2	1:A:285:ARG:NH1	2.32	0.44
1:A:417:VAL:HG21	1:A:477:GLY:HA3	1.98	0.44
1:A:233:MET:O	1:A:237:LEU:HD12	2.18	0.44
1:A:346:VAL:O	1:A:349:ILE:HG22	2.18	0.44
1:A:264:VAL:HA	1:A:267:MET:HB3	1.98	0.44
1:B:235:PRO:HG3	1:B:310:GLU:HA	1.99	0.44
1:D:222:LEU:HD23	1:D:250:ILE:HB	1.99	0.44
1:E:197:ARG:HE	1:E:279:PRO:HA	1.81	0.44
1:F:213:VAL:HB	1:F:325:ILE:HB	1.99	0.44
1:K:222:LEU:HD23	1:K:250:ILE:HB	1.99	0.44
1:L:222:LEU:HD23	1:L:250:ILE:HB	1.99	0.44
1:M:149:THR:HG22	1:M:156:GLU:HA	1.99	0.44
1:D:149:THR:HG22	1:D:156:GLU:HA	1.99	0.44
1:J:235:PRO:HG3	1:J:310:GLU:HA	1.99	0.44
1:L:149:THR:HG22	1:L:156:GLU:HA	1.99	0.44
1:N:106:ALA:HB3	1:N:116:LEU:HD21	1.99	0.44
1:N:213:VAL:HB	1:N:325:ILE:HB	1.99	0.44
1:A:245:LYS:HD2	1:A:246:PRO:O	2.17	0.44
1:A:359:ASP:OD1	1:A:362:ARG:NH1	2.50	0.44
1:A:107:VAL:CG2	1:A:113:PRO:HG3	2.47	0.44
1:A:406:ALA:HA	1:A:496:PRO:HB3	1.98	0.44
1:C:222:LEU:HD23	1:C:250:ILE:HB	2.00	0.44
1:F:106:ALA:HB3	1:F:116:LEU:HD21	1.99	0.44
1:A:233:MET:SD	1:A:237:LEU:HD23	2.57	0.44
1:A:419:LEU:O	1:A:423:ALA:N	2.41	0.44
1:D:27:VAL:O	1:D:30:THR:OG1	2.33	0.44
1:E:106:ALA:HB3	1:E:116:LEU:HD21	1.99	0.44
1:J:513:LEU:HB3	1:K:49:ILE:HD13	1.99	0.44
1:M:106:ALA:HB3	1:M:116:LEU:HD21	1.99	0.44
1:N:149:THR:HG22	1:N:156:GLU:HA	1.99	0.44
1:A:30:THR:HB	1:A:51:LYS:O	2.17	0.44
1:A:106:ALA:HB3	1:A:116:LEU:HD21	1.99	0.44
1:A:111:MET:SD	1:A:438:VAL:HG21	2.58	0.44
1:A:228:SER:HA	1:A:258:ALA:CB	2.46	0.44
1:A:174:VAL:HG11	1:A:376:VAL:HG22	2.00	0.44
1:A:205:ILE:HG12	1:A:211:GLY:O	2.18	0.44
1:A:295:LEU:HD12	1:A:296:THR:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:GLU:HA	1:A:366:GLN:HB3	2.00	0.44
1:A:513:LEU:HB3	1:B:49:ILE:HD13	1.99	0.44
1:E:149:THR:HG22	1:E:156:GLU:HA	1.99	0.44
1:G:222:LEU:HD23	1:G:250:ILE:HB	1.99	0.44
1:H:222:LEU:HD23	1:H:250:ILE:HB	1.99	0.44
1:I:513:LEU:HB3	1:J:49:ILE:HD13	1.99	0.44
1:A:268:ARG:NH1	1:A:270:ILE:HG21	2.33	0.44
1:A:396:VAL:O	1:A:400:LEU:N	2.50	0.44
1:B:513:LEU:HB3	1:C:49:ILE:HD13	1.99	0.44
1:C:149:THR:HG22	1:C:156:GLU:HA	1.99	0.44
1:F:149:THR:HG22	1:F:156:GLU:HA	1.99	0.44
1:K:149:THR:HG22	1:K:156:GLU:HA	1.99	0.44
1:A:245:LYS:NZ	1:A:246:PRO:O	2.39	0.44
1:A:286:LYS:HD3	1:A:286:LYS:H	1.83	0.44
1:A:294:THR:HG21	1:A:342:ILE:HA	1.99	0.44
1:A:344:GLY:O	1:A:348:GLN:N	2.35	0.44
1:A:213:VAL:HG12	1:A:325:ILE:HB	1.99	0.44
1:A:301:ILE:HD13	1:A:309:LEU:HA	2.00	0.44
1:A:339:GLU:HA	1:A:342:ILE:HB	1.99	0.44
1:A:411:VAL:HG21	1:A:494:LEU:HB3	2.00	0.44
1:H:513:LEU:HB3	1:I:49:ILE:HD13	1.99	0.44
1:L:106:ALA:HB3	1:L:116:LEU:HD21	1.99	0.44
1:A:149:THR:CG2	1:A:156:GLU:HA	2.48	0.44
1:A:222:LEU:HD22	1:A:289:LEU:HD12	2.00	0.44
1:A:197:ARG:HH21	1:A:280:GLY:N	2.16	0.44
1:D:106:ALA:HB3	1:D:116:LEU:HD21	1.99	0.43
1:G:106:ALA:HB3	1:G:116:LEU:HD21	1.99	0.43
1:H:106:ALA:HB3	1:H:116:LEU:HD21	1.99	0.43
1:H:149:THR:HG22	1:H:156:GLU:HA	1.99	0.43
1:L:27:VAL:O	1:L:30:THR:OG1	2.33	0.43
1:L:513:LEU:HB3	1:M:49:ILE:HD13	1.99	0.43
1:A:38:VAL:HG11	1:A:56:VAL:HG11	2.00	0.43
1:A:365:LEU:O	1:A:369:VAL:HG12	2.17	0.43
1:A:209:GLU:OE1	1:A:209:GLU:N	2.37	0.43
1:A:226:LYS:HD3	1:A:226:LYS:H	1.83	0.43
1:D:513:LEU:HB3	1:E:49:ILE:HD13	1.99	0.43
1:E:222:LEU:HD23	1:E:250:ILE:HB	1.99	0.43
1:G:149:THR:HG22	1:G:156:GLU:HA	1.99	0.43
1:M:222:LEU:HD23	1:M:250:ILE:HB	1.99	0.43
1:A:268:ARG:HB2	1:A:270:ILE:HG13	2.00	0.43
1:A:378:VAL:CG2	1:A:380:LYS:HD3	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:VAL:HG11	1:A:393:LYS:N	2.34	0.43
1:A:49:ILE:HD13	1:G:513:LEU:HB3	1.99	0.43
1:B:222:LEU:HD23	1:B:250:ILE:HB	2.00	0.43
1:J:222:LEU:HD23	1:J:250:ILE:HB	2.00	0.43
1:K:513:LEU:HB3	1:L:49:ILE:HD13	1.99	0.43
1:A:221:LEU:HD12	1:A:236:VAL:HG11	1.99	0.43
1:A:225:LYS:O	1:A:251:ALA:HB1	2.17	0.43
1:A:190:VAL:HG11	1:A:333:ILE:HG23	2.01	0.43
1:A:230:ILE:O	1:A:233:MET:N	2.50	0.43
1:A:285:ARG:O	1:A:288:MET:N	2.51	0.43
1:I:149:THR:HG22	1:I:156:GLU:HA	1.99	0.43
1:A:222:LEU:O	1:A:301:ILE:N	2.51	0.43
1:A:245:LYS:HG3	1:A:246:PRO:HD2	1.99	0.43
1:B:106:ALA:HB3	1:B:116:LEU:HD21	1.99	0.43
1:E:513:LEU:HB3	1:F:49:ILE:HD13	2.01	0.43
1:J:106:ALA:HB3	1:J:116:LEU:HD21	1.99	0.43
1:A:10:ASN:C	1:A:12:ALA:N	2.77	0.43
1:A:389:MET:O	1:A:393:LYS:HG2	2.18	0.43
1:B:149:THR:HG22	1:B:156:GLU:HA	1.99	0.43
1:J:149:THR:HG22	1:J:156:GLU:HA	2.00	0.43
1:A:40:LEU:HA	1:A:40:LEU:HD23	1.75	0.43
1:A:216:GLU:OE2	1:A:322:ARG:NE	2.25	0.43
1:A:403:THR:O	1:A:407:VAL:HG13	2.18	0.43
1:A:177:VAL:HG12	1:A:393:LYS:HE2	2.00	0.43
1:A:149:THR:HG22	1:A:156:GLU:HA	1.99	0.43
1:C:431:GLY:H	1:C:437:ASN:ND2	2.17	0.43
1:D:20:VAL:O	1:D:24:ALA:HB3	2.18	0.43
1:I:322:ARG:O	1:I:333:ILE:HB	2.19	0.43
1:J:20:VAL:O	1:J:24:ALA:HB3	2.18	0.43
1:K:106:ALA:HB3	1:K:116:LEU:HD21	1.99	0.43
1:L:20:VAL:O	1:L:24:ALA:HB3	2.19	0.43
1:A:100:ILE:O	1:A:101:THR:C	2.61	0.43
1:A:262:LEU:HD23	1:A:262:LEU:HA	1.79	0.43
1:A:255:GLU:N	1:A:255:GLU:OE1	2.51	0.43
1:A:283:ASP:O	1:A:286:LYS:HG2	2.19	0.43
1:A:322:ARG:O	1:A:333:ILE:HB	2.19	0.43
1:B:20:VAL:O	1:B:24:ALA:HB3	2.18	0.43
1:B:431:GLY:H	1:B:437:ASN:ND2	2.17	0.43
1:C:106:ALA:HB3	1:C:116:LEU:HD21	1.99	0.43
1:J:322:ARG:O	1:J:333:ILE:HB	2.19	0.43
1:J:431:GLY:H	1:J:437:ASN:ND2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:431:GLY:H	1:K:437:ASN:ND2	2.17	0.43
1:A:31:LEU:HD12	1:A:32:GLY:H	1.83	0.43
1:A:144:ILE:HG13	1:A:403:THR:HG23	2.01	0.43
1:A:265:ASN:O	1:A:270:ILE:HG13	2.19	0.43
1:A:278:ALA:HB1	1:A:289:LEU:HD21	2.00	0.43
1:A:431:GLY:H	1:A:437:ASN:ND2	2.17	0.43
1:C:513:LEU:HB3	1:D:49:ILE:HD13	2.00	0.43
1:F:431:GLY:H	1:F:437:ASN:ND2	2.17	0.43
1:G:322:ARG:O	1:G:333:ILE:HB	2.19	0.43
1:H:322:ARG:O	1:H:333:ILE:HB	2.19	0.43
1:I:431:GLY:H	1:I:437:ASN:ND2	2.17	0.43
1:A:68:ASN:O	1:A:72:GLN:HG2	2.19	0.43
1:A:237:LEU:HA	1:A:240:VAL:CG1	2.49	0.43
1:A:448:GLU:OE2	1:A:470:LYS:NZ	2.25	0.43
1:A:363:GLU:O	1:A:367:GLU:HG3	2.19	0.43
1:A:124:VAL:O	1:A:128:VAL:HG12	2.18	0.43
1:A:106:ALA:HB3	1:A:116:LEU:HD21	1.99	0.43
1:B:322:ARG:O	1:B:333:ILE:HB	2.19	0.43
1:I:20:VAL:O	1:I:24:ALA:HB3	2.18	0.43
1:I:106:ALA:HB3	1:I:116:LEU:HD21	1.99	0.43
1:K:20:VAL:O	1:K:24:ALA:HB3	2.19	0.43
1:L:431:GLY:H	1:L:437:ASN:ND2	2.17	0.43
1:M:20:VAL:O	1:M:24:ALA:HB3	2.18	0.43
1:N:431:GLY:H	1:N:437:ASN:ND2	2.17	0.43
1:A:87:ASP:HB3	1:A:499:VAL:HG21	2.01	0.43
1:A:421:ARG:NH2	1:A:476:TYR:O	2.52	0.43
1:A:161:LEU:HD11	1:A:379:ILE:HG23	2.00	0.43
1:A:249:ILE:O	1:A:275:ALA:HA	2.19	0.43
1:C:20:VAL:O	1:C:24:ALA:HB3	2.19	0.42
1:D:431:GLY:H	1:D:437:ASN:ND2	2.17	0.42
1:E:20:VAL:O	1:E:24:ALA:HB3	2.18	0.42
1:F:322:ARG:O	1:F:333:ILE:HB	2.19	0.42
1:N:322:ARG:O	1:N:333:ILE:HB	2.19	0.42
1:A:144:ILE:HA	1:A:147:VAL:HG12	2.01	0.42
1:A:22:VAL:HG11	1:A:62:LEU:HD21	2.00	0.42
1:A:215:LEU:HB3	1:A:218:PRO:HB3	2.00	0.42
1:K:178:GLU:HG2	1:K:322:ARG:HH11	1.85	0.42
1:M:431:GLY:H	1:M:437:ASN:ND2	2.17	0.42
1:A:20:VAL:O	1:A:24:ALA:HB3	2.19	0.42
1:A:222:LEU:HD23	1:A:250:ILE:HB	1.99	0.42
1:C:178:GLU:HG2	1:C:322:ARG:HH11	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:240:VAL:HG21	1:E:247:LEU:HD22	2.02	0.42
1:F:27:VAL:O	1:F:30:THR:OG1	2.33	0.42
1:M:240:VAL:HG21	1:M:247:LEU:HD22	2.02	0.42
1:A:247:LEU:HD13	1:A:248:LEU:N	2.34	0.42
1:B:178:GLU:HG2	1:B:322:ARG:HH11	1.85	0.42
1:D:240:VAL:HG21	1:D:247:LEU:HD22	2.02	0.42
1:E:431:GLY:H	1:E:437:ASN:ND2	2.17	0.42
1:F:20:VAL:O	1:F:24:ALA:HB3	2.18	0.42
1:F:222:LEU:HD23	1:F:250:ILE:HB	1.99	0.42
1:G:20:VAL:O	1:G:24:ALA:HB3	2.18	0.42
1:J:178:GLU:HG2	1:J:322:ARG:HH11	1.85	0.42
1:A:359:ASP:O	1:A:362:ARG:HB2	2.19	0.42
1:A:81:ALA:O	1:A:85:ALA:N	2.52	0.42
1:A:219:PHE:CD1	1:A:319:GLN:HG3	2.54	0.42
1:D:178:GLU:HG2	1:D:322:ARG:HH11	1.84	0.42
1:F:240:VAL:HG21	1:F:247:LEU:HD22	2.02	0.42
1:H:431:GLY:H	1:H:437:ASN:ND2	2.17	0.42
1:I:222:LEU:HD23	1:I:250:ILE:HB	1.99	0.42
1:L:178:GLU:HG2	1:L:322:ARG:HH11	1.85	0.42
1:L:240:VAL:HG21	1:L:247:LEU:HD22	2.02	0.42
1:N:20:VAL:O	1:N:24:ALA:HB3	2.18	0.42
1:N:222:LEU:HD23	1:N:250:ILE:HB	2.00	0.42
1:A:104:LEU:HD23	1:A:104:LEU:HA	1.69	0.42
1:A:4:LYS:HD2	1:A:521:VAL:HG12	2.01	0.42
1:A:177:VAL:HG11	1:A:393:LYS:HG3	2.00	0.42
1:A:204:PHE:CE2	1:A:213:VAL:HG21	2.54	0.42
1:A:262:LEU:HD12	1:A:273:VAL:O	2.19	0.42
1:A:358:SER:HB3	1:A:361:ASP:OD2	2.20	0.42
1:G:431:GLY:H	1:G:437:ASN:ND2	2.17	0.42
1:H:5:ASP:HB2	1:H:524:LEU:HD23	2.02	0.42
1:H:20:VAL:O	1:H:24:ALA:HB3	2.18	0.42
1:K:217:SER:N	1:K:321:LYS:O	2.46	0.42
1:K:322:ARG:O	1:K:333:ILE:HB	2.19	0.42
1:N:5:ASP:HB2	1:N:524:LEU:HD23	2.02	0.42
1:N:217:SER:N	1:N:321:LYS:O	2.46	0.42
1:N:240:VAL:HG21	1:N:247:LEU:HD22	2.02	0.42
1:A:193:MET:HE2	1:A:195:PHE:CD1	2.53	0.42
1:A:205:ILE:HA	1:A:213:VAL:HB	2.01	0.42
1:A:178:GLU:HG2	1:A:322:ARG:HH11	1.85	0.42
1:B:251:ALA:O	1:B:278:ALA:N	2.53	0.42
1:C:322:ARG:O	1:C:333:ILE:HB	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:5:ASP:HB2	1:F:524:LEU:HD23	2.02	0.42
1:F:251:ALA:O	1:F:278:ALA:N	2.53	0.42
1:N:27:VAL:O	1:N:30:THR:OG1	2.33	0.42
1:N:178:GLU:HG2	1:N:322:ARG:HH11	1.85	0.42
1:N:251:ALA:O	1:N:278:ALA:N	2.53	0.42
1:A:235:PRO:O	1:A:238:GLU:HB2	2.20	0.42
1:A:419:LEU:HA	1:A:419:LEU:HD23	1.82	0.42
1:A:19:GLY:HA2	1:A:67:GLU:CD	2.44	0.42
1:A:383:ALA:HB1	1:A:388:GLU:CG	2.50	0.42
1:A:61:GLU:OE2	1:A:75:LYS:NZ	2.53	0.42
1:A:359:ASP:HA	1:A:362:ARG:NE	2.35	0.42
1:A:251:ALA:O	1:A:278:ALA:N	2.53	0.42
1:D:251:ALA:O	1:D:278:ALA:N	2.53	0.42
1:E:251:ALA:O	1:E:278:ALA:N	2.53	0.42
1:E:322:ARG:O	1:E:333:ILE:HB	2.19	0.42
1:G:5:ASP:HB2	1:G:524:LEU:HD23	2.02	0.42
1:H:178:GLU:HG2	1:H:322:ARG:HH11	1.85	0.42
1:H:257:GLU:O	1:H:261:THR:OG1	2.26	0.42
1:I:178:GLU:HG2	1:I:322:ARG:HH11	1.85	0.42
1:J:251:ALA:O	1:J:278:ALA:N	2.53	0.42
1:K:399:ALA:O	1:K:403:THR:OG1	2.31	0.42
1:L:251:ALA:O	1:L:278:ALA:N	2.53	0.42
1:M:178:GLU:HG2	1:M:322:ARG:HH11	1.85	0.42
1:M:251:ALA:O	1:M:278:ALA:N	2.53	0.42
1:A:175:ILE:HD12	1:A:175:ILE:O	2.19	0.42
1:A:350:ARG:O	1:A:354:GLU:HG2	2.20	0.42
1:A:209:GLU:HG2	1:A:210:THR:N	2.34	0.42
1:E:178:GLU:HG2	1:E:322:ARG:HH11	1.85	0.42
1:F:217:SER:N	1:F:321:LYS:O	2.46	0.42
1:G:20:VAL:O	1:G:24:ALA:CB	2.68	0.42
1:G:178:GLU:HG2	1:G:322:ARG:HH11	1.85	0.42
1:G:251:ALA:O	1:G:278:ALA:N	2.53	0.42
1:G:257:GLU:O	1:G:261:THR:OG1	2.26	0.42
1:G:421:ARG:NH2	1:G:469:VAL:O	2.53	0.42
1:H:20:VAL:O	1:H:24:ALA:CB	2.68	0.42
1:H:240:VAL:HG21	1:H:247:LEU:HD22	2.02	0.42
1:M:322:ARG:O	1:M:333:ILE:HB	2.19	0.42
1:A:52:ASP:HB3	1:A:55:SER:HB2	2.02	0.42
1:A:365:LEU:HD13	1:A:365:LEU:HA	1.75	0.42
1:A:132:LYS:HE2	1:A:409:GLU:OE1	2.20	0.42
1:A:252:GLU:O	1:A:277:LYS:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:VAL:HG13	1:A:90:THR:HG22	2.01	0.42
1:A:152:ALA:HB2	1:A:399:ALA:HB2	2.00	0.42
1:C:217:SER:N	1:C:321:LYS:O	2.46	0.42
1:C:240:VAL:HG21	1:C:247:LEU:HD22	2.02	0.42
1:E:464:VAL:HG11	1:N:467:ASN:HD22	1.85	0.42
1:F:20:VAL:O	1:F:24:ALA:CB	2.68	0.42
1:F:178:GLU:HG2	1:F:322:ARG:HH11	1.85	0.42
1:G:240:VAL:HG21	1:G:247:LEU:HD22	2.02	0.42
1:H:251:ALA:O	1:H:278:ALA:N	2.53	0.42
1:H:421:ARG:NH2	1:H:469:VAL:O	2.53	0.42
1:I:5:ASP:HB2	1:I:524:LEU:HD23	2.02	0.42
1:I:251:ALA:O	1:I:278:ALA:N	2.53	0.42
1:K:240:VAL:HG21	1:K:247:LEU:HD22	2.02	0.42
1:N:20:VAL:O	1:N:24:ALA:CB	2.68	0.42
1:A:27:VAL:HG21	1:A:57:ALA:HB2	2.02	0.42
1:A:390:LYS:HD3	1:A:393:LYS:HD3	2.01	0.42
1:A:64:ASP:HB3	1:A:67:GLU:CB	2.50	0.42
1:A:214:GLU:C	1:A:215:LEU:HD12	2.45	0.42
1:A:247:LEU:HD13	1:A:248:LEU:N	2.35	0.42
1:A:341:ALA:O	1:A:345:ARG:N	2.51	0.42
1:E:5:ASP:HB2	1:E:524:LEU:HD23	2.02	0.41
1:M:5:ASP:HB2	1:M:524:LEU:HD23	2.02	0.41
1:A:285:ARG:NE	1:A:285:ARG:HA	2.34	0.41
1:A:195:PHE:HB2	1:A:279:PRO:HB3	2.02	0.41
1:A:213:VAL:HG22	1:A:325:ILE:CB	2.50	0.41
1:A:233:MET:C	1:A:235:PRO:HD2	2.45	0.41
1:A:239:ALA:HA	1:A:242:LYS:HE3	2.01	0.41
1:A:350:ARG:HE	1:A:369:VAL:HG21	1.84	0.41
1:A:87:ASP:CG	1:A:88:GLY:H	2.26	0.41
1:A:226:LYS:HG2	1:A:226:LYS:O	2.20	0.41
1:A:338:GLU:HG3	1:A:340:ALA:H	1.84	0.41
1:A:5:ASP:HB2	1:A:524:LEU:HD23	2.02	0.41
1:D:322:ARG:O	1:D:333:ILE:HB	2.19	0.41
1:A:116:LEU:O	1:A:117:LYS:C	2.61	0.41
1:A:247:LEU:O	1:A:274:ALA:HB3	2.20	0.41
1:A:23:LEU:HD12	1:A:23:LEU:HA	1.83	0.41
1:A:301:ILE:HG23	1:A:307:MET:HG3	2.02	0.41
1:A:325:ILE:HG13	1:A:326:ASN:O	2.19	0.41
1:A:15:LYS:O	1:A:67:GLU:HA	2.20	0.41
1:A:295:LEU:HD13	1:A:332:ILE:HD13	2.02	0.41
1:A:465:VAL:O	1:A:468:THR:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:VAL:O	1:A:24:ALA:CB	2.68	0.41
1:E:421:ARG:NH2	1:E:469:VAL:O	2.53	0.41
1:I:20:VAL:O	1:I:24:ALA:CB	2.68	0.41
1:L:322:ARG:O	1:L:333:ILE:HB	2.19	0.41
1:M:421:ARG:NH2	1:M:469:VAL:O	2.53	0.41
1:A:66:PHE:HD1	1:A:520:MET:HE2	1.85	0.41
1:A:178:GLU:HG2	1:A:322:ARG:HH11	1.85	0.41
1:A:221:LEU:O	1:A:248:LEU:CA	2.67	0.41
1:A:242:LYS:NZ	1:A:314:LEU:HD11	2.35	0.41
1:A:162:ILE:HD11	1:A:396:VAL:HG23	2.03	0.41
1:A:240:VAL:HG21	1:A:247:LEU:HD22	2.02	0.41
1:A:464:VAL:HG11	1:K:467:ASN:HD22	1.86	0.41
1:A:22:VAL:HG11	1:A:62:LEU:HD21	2.03	0.41
1:A:64:ASP:O	1:A:65:LYS:C	2.62	0.41
1:A:265:ASN:OD1	1:A:270:ILE:HD11	2.20	0.41
1:A:346:VAL:O	1:A:350:ARG:HG2	2.20	0.41
1:A:99:ILE:O	1:A:103:GLY:N	2.54	0.41
1:A:262:LEU:HD11	1:A:275:ALA:HB2	2.02	0.41
1:A:352:GLN:OE1	1:A:365:LEU:HD13	2.20	0.41
1:B:240:VAL:HG21	1:B:247:LEU:HD22	2.02	0.41
1:C:251:ALA:O	1:C:278:ALA:N	2.53	0.41
1:C:467:ASN:HD22	1:I:464:VAL:HG11	1.86	0.41
1:E:20:VAL:O	1:E:24:ALA:CB	2.68	0.41
1:A:247:LEU:C	1:A:248:LEU:HD22	2.46	0.41
1:A:116:LEU:HD23	1:A:439:GLY:HA2	2.03	0.41
1:A:177:VAL:HG22	1:A:379:ILE:CG2	2.50	0.41
1:A:169:VAL:CG1	1:A:173:GLY:HA3	2.50	0.41
1:A:476:TYR:HA	1:A:486:GLY:O	2.20	0.41
1:A:467:ASN:HD22	1:K:464:VAL:HG11	1.86	0.41
1:J:240:VAL:HG21	1:J:247:LEU:HD22	2.02	0.41
1:K:251:ALA:O	1:K:278:ALA:N	2.53	0.41
1:M:20:VAL:O	1:M:24:ALA:CB	2.68	0.41
1:A:113:PRO:C	1:A:115:ASP:N	2.79	0.41
1:A:92:ALA:HB2	1:A:503:ALA:HA	2.01	0.41
1:G:388:GLU:O	1:G:392:LYS:CB	2.69	0.41
1:H:388:GLU:O	1:H:392:LYS:CB	2.69	0.41
1:I:240:VAL:HG21	1:I:247:LEU:HD22	2.02	0.41
1:A:169:VAL:HG22	1:A:173:GLY:HA3	2.03	0.41
1:A:266:THR:C	1:A:269:GLY:H	2.28	0.41
1:A:352:GLN:HA	1:A:355:GLU:OE2	2.20	0.41
1:B:5:ASP:HB2	1:B:524:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:388:GLU:O	1:C:392:LYS:CB	2.69	0.41
1:C:464:VAL:HG11	1:I:467:ASN:HD22	1.86	0.41
1:J:5:ASP:HB2	1:J:524:LEU:HD23	2.02	0.41
1:K:20:VAL:O	1:K:24:ALA:CB	2.68	0.41
1:K:388:GLU:O	1:K:392:LYS:CB	2.69	0.41
1:L:5:ASP:HB2	1:L:524:LEU:HD23	2.02	0.41
1:N:388:GLU:O	1:N:392:LYS:CB	2.69	0.41
1:A:175:ILE:HB	1:A:377:ALA:CB	2.50	0.41
1:A:213:VAL:HB	1:A:325:ILE:HG13	2.03	0.41
1:A:415:GLY:C	1:A:417:VAL:H	2.29	0.41
1:A:205:ILE:H	1:A:205:ILE:HD12	1.85	0.41
1:A:309:LEU:O	1:A:312:ALA:N	2.45	0.41
1:A:421:ARG:NH2	1:A:469:VAL:O	2.53	0.41
1:B:20:VAL:O	1:B:24:ALA:CB	2.68	0.41
1:B:464:VAL:HG11	1:J:467:ASN:HD22	1.86	0.41
1:C:5:ASP:HB2	1:C:524:LEU:HD23	2.02	0.41
1:C:20:VAL:O	1:C:24:ALA:CB	2.68	0.41
1:D:5:ASP:HB2	1:D:524:LEU:HD23	2.02	0.41
1:D:20:VAL:O	1:D:24:ALA:CB	2.68	0.41
1:E:27:VAL:O	1:E:30:THR:OG1	2.33	0.41
1:E:257:GLU:O	1:E:261:THR:OG1	2.26	0.41
1:E:305:ILE:HG21	1:E:307:MET:HE2	2.03	0.41
1:E:467:ASN:HD22	1:N:464:VAL:HG11	1.86	0.41
1:F:305:ILE:HG21	1:F:307:MET:HE2	2.03	0.41
1:F:388:GLU:O	1:F:392:LYS:CB	2.69	0.41
1:J:20:VAL:O	1:J:24:ALA:CB	2.68	0.41
1:K:5:ASP:HB2	1:K:524:LEU:HD23	2.02	0.41
1:L:20:VAL:O	1:L:24:ALA:CB	2.68	0.41
1:A:22:VAL:CG1	1:A:62:LEU:HD11	2.51	0.41
1:A:248:LEU:HD13	1:A:248:LEU:HA	1.87	0.41
1:A:376:VAL:HG12	1:A:377:ALA:N	2.33	0.41
1:A:423:ALA:HB2	1:A:447:MET:HB2	2.03	0.41
1:A:40:LEU:HD21	1:A:56:VAL:HA	2.02	0.41
1:A:321:LYS:HG2	1:A:322:ARG:HH11	1.86	0.41
1:A:411:VAL:HG23	1:A:495:ASP:O	2.21	0.41
1:A:488:MET:SD	1:A:493:ILE:HD11	2.61	0.41
1:A:283:ASP:O	1:A:285:ARG:N	2.54	0.41
1:A:388:GLU:O	1:A:392:LYS:CB	2.69	0.41
1:B:467:ASN:HD22	1:J:464:VAL:HG11	1.86	0.41
1:F:352:GLN:OE1	1:F:368:ARG:NH2	2.53	0.41
1:I:421:ARG:NH2	1:I:469:VAL:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:257:GLU:O	1:M:261:THR:OG1	2.26	0.41
1:M:305:ILE:HG21	1:M:307:MET:HE2	2.03	0.41
1:N:305:ILE:HG21	1:N:307:MET:HE2	2.03	0.41
1:D:388:GLU:O	1:D:392:LYS:CB	2.69	0.40
1:G:305:ILE:HG21	1:G:307:MET:HE2	2.03	0.40
1:H:305:ILE:HG21	1:H:307:MET:HE2	2.03	0.40
1:I:388:GLU:O	1:I:392:LYS:CB	2.69	0.40
1:K:339:GLU:O	1:K:343:GLN:CB	2.70	0.40
1:A:42:LYS:NZ	1:A:44:PHE:HB3	2.36	0.40
1:A:207:LYS:HE3	1:A:210:THR:OG1	2.20	0.40
1:A:263:VAL:O	1:A:267:MET:HB3	2.22	0.40
1:A:188:ASP:OD1	1:A:188:ASP:N	2.50	0.40
1:A:224:ASP:C	1:A:225:LYS:HD2	2.46	0.40
1:A:347:ALA:O	1:A:351:GLN:HG2	2.21	0.40
1:B:388:GLU:O	1:B:392:LYS:CB	2.69	0.40
1:C:27:VAL:O	1:C:30:THR:OG1	2.33	0.40
1:C:339:GLU:O	1:C:343:GLN:CB	2.70	0.40
1:J:388:GLU:O	1:J:392:LYS:CB	2.69	0.40
1:L:388:GLU:O	1:L:392:LYS:CB	2.69	0.40
1:A:301:ILE:HD13	1:A:301:ILE:HA	1.96	0.40
1:A:193:MET:HG3	1:A:371:LYS:NZ	2.36	0.40
1:A:252:GLU:HB2	1:A:285:ARG:HH11	1.86	0.40
1:A:232:GLU:O	1:A:309:LEU:HD12	2.20	0.40
1:A:305:ILE:HG21	1:A:307:MET:HE2	2.03	0.40
1:C:102:GLU:HB2	1:C:442:VAL:HG13	2.04	0.40
1:D:467:ASN:HD22	1:H:464:VAL:HG11	1.86	0.40
1:G:464:VAL:HG11	1:L:467:ASN:HD22	1.86	0.40
1:H:339:GLU:O	1:H:343:GLN:CB	2.70	0.40
1:K:102:GLU:HB2	1:K:442:VAL:HG13	2.04	0.40
1:A:349:ILE:O	1:A:353:ILE:HG23	2.20	0.40
1:A:64:ASP:O	1:A:67:GLU:HB3	2.21	0.40
1:A:320:ALA:HB1	1:A:333:ILE:O	2.21	0.40
1:A:18:ARG:HG3	1:A:67:GLU:HG2	2.03	0.40
1:A:324:VAL:HG22	1:A:331:THR:OG1	2.21	0.40
1:D:305:ILE:HG21	1:D:307:MET:HE2	2.03	0.40
1:F:421:ARG:NH2	1:F:469:VAL:O	2.53	0.40
1:G:339:GLU:O	1:G:343:GLN:CB	2.70	0.40
1:G:352:GLN:OE1	1:G:368:ARG:NH2	2.53	0.40
1:I:305:ILE:HG21	1:I:307:MET:HE2	2.03	0.40
1:K:158:VAL:HG13	1:K:396:VAL:HG22	2.04	0.40
1:L:102:GLU:HB2	1:L:442:VAL:HG13	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:158:VAL:HG13	1:L:396:VAL:HG22	2.04	0.40
1:L:305:ILE:HG21	1:L:307:MET:HE2	2.03	0.40
1:M:339:GLU:O	1:M:343:GLN:CB	2.70	0.40
1:M:388:GLU:O	1:M:392:LYS:CB	2.69	0.40
1:A:254:VAL:HG13	1:A:258:ALA:CB	2.52	0.40
1:A:447:MET:HE2	1:A:504:LEU:HD11	2.04	0.40
1:C:158:VAL:HG13	1:C:396:VAL:HG22	2.04	0.40
1:D:102:GLU:HB2	1:D:442:VAL:HG13	2.04	0.40
1:D:158:VAL:HG13	1:D:396:VAL:HG22	2.04	0.40
1:E:339:GLU:O	1:E:343:GLN:CB	2.70	0.40
1:N:421:ARG:NH2	1:N:469:VAL:O	2.53	0.40
1:A:78:ALA:HB1	1:A:89:THR:HG23	2.03	0.40
1:A:309:LEU:HD23	1:A:309:LEU:HA	1.77	0.40
1:A:333:ILE:HG22	1:A:334:ASP:CG	2.46	0.40
1:A:131:LEU:HA	1:A:131:LEU:HD23	1.79	0.40
1:A:220:ILE:HG22	1:A:248:LEU:HG	2.03	0.40
1:A:228:SER:OG	1:A:255:GLU:O	2.38	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-A	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-B	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-C	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-D	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-E	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-F	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-G	522/524 (100%)	506 (97%)	16 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-H	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-I	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-J	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-K	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-L	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-M	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	1-N	522/524 (100%)	506 (97%)	16 (3%)	0	100	100
1	2-A	522/524 (100%)	445 (85%)	77 (15%)	0	100	100
1	3-A	522/524 (100%)	452 (87%)	70 (13%)	0	100	100
1	4-A	522/524 (100%)	468 (90%)	54 (10%)	0	100	100
All	All	8874/8908 (100%)	8449 (95%)	425 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1-A	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-B	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-C	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-D	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-E	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-F	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-G	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-H	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-I	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-J	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-K	404/404 (100%)	403 (100%)	1 (0%)	87	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1-L	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-M	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	1-N	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	2-A	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	3-A	404/404 (100%)	403 (100%)	1 (0%)	87	85
1	4-A	404/404 (100%)	403 (100%)	1 (0%)	87	85
All	All	6868/6868 (100%)	6851 (100%)	17 (0%)	85	85

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1-A	174	VAL
1	1-B	174	VAL
1	1-C	174	VAL
1	1-D	174	VAL
1	1-E	174	VAL
1	1-F	174	VAL
1	1-G	174	VAL
1	1-H	174	VAL
1	1-I	174	VAL
1	1-J	174	VAL
1	1-K	174	VAL
1	1-L	174	VAL
1	1-M	174	VAL
1	1-N	174	VAL
1	2-A	174	VAL
1	3-A	174	VAL
1	4-A	174	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
1	1-A	37	ASN
1	1-A	479	ASN
1	1-A	505	GLN
1	1-B	37	ASN
1	1-B	479	ASN
1	1-B	505	GLN
1	1-C	37	ASN

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Mol	Chain	Res	Type
1	1-C	479	ASN
1	1-C	505	GLN
1	1-D	37	ASN
1	1-D	467	ASN
1	1-D	479	ASN
1	1-D	505	GLN
1	1-E	37	ASN
1	1-E	467	ASN
1	1-E	479	ASN
1	1-E	505	GLN
1	1-F	37	ASN
1	1-F	479	ASN
1	1-F	505	GLN
1	1-G	37	ASN
1	1-G	479	ASN
1	1-G	505	GLN
1	1-H	37	ASN
1	1-H	479	ASN
1	1-H	505	GLN
1	1-I	37	ASN
1	1-I	479	ASN
1	1-I	505	GLN
1	1-J	37	ASN
1	1-J	479	ASN
1	1-J	505	GLN
1	1-K	37	ASN
1	1-K	479	ASN
1	1-K	505	GLN
1	1-L	37	ASN
1	1-L	290	GLN
1	1-L	467	ASN
1	1-L	479	ASN
1	1-L	505	GLN
1	1-M	37	ASN
1	1-M	467	ASN
1	1-M	479	ASN
1	1-M	505	GLN
1	1-N	37	ASN
1	1-N	479	ASN
1	1-N	505	GLN
1	2-A	82	ASN
1	2-A	146	GLN

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Mol	Chain	Res	Type
1	2-A	290	GLN
1	2-A	453	GLN
1	2-A	505	GLN
1	3-A	453	GLN
1	3-A	467	ASN
1	3-A	479	ASN
1	3-A	505	GLN
1	4-A	37	ASN
1	4-A	72	GLN
1	4-A	453	GLN
1	4-A	505	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no 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.

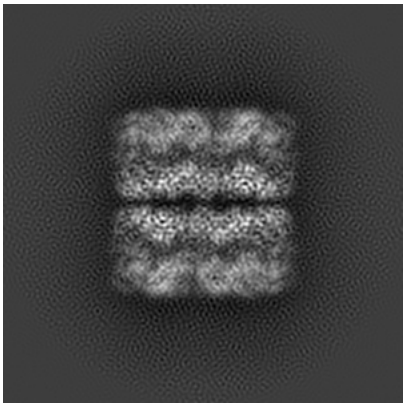
6 Map visualisation (i)

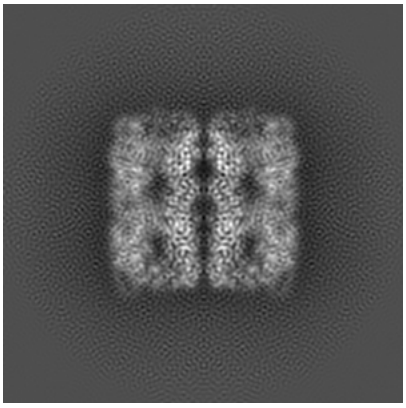
This section contains visualisations of the EMDB entry EMD-8750. These allow visual inspection of the internal detail of the map and identification of artifacts.

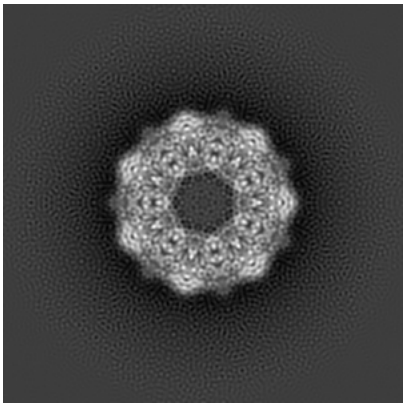
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map


X


Y

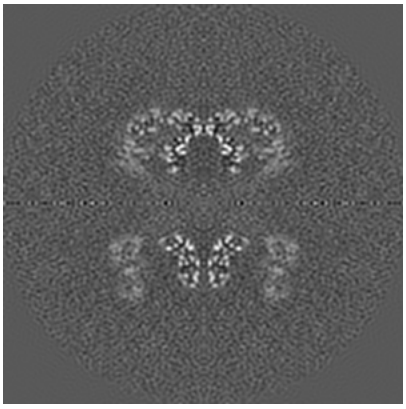

Z

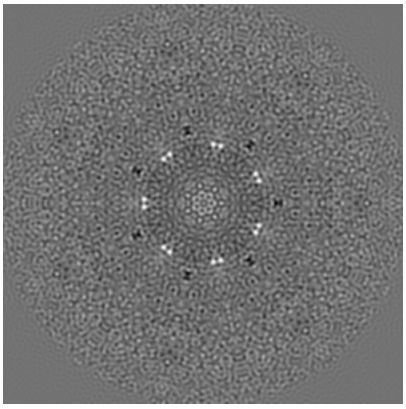
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map

X Index: 120

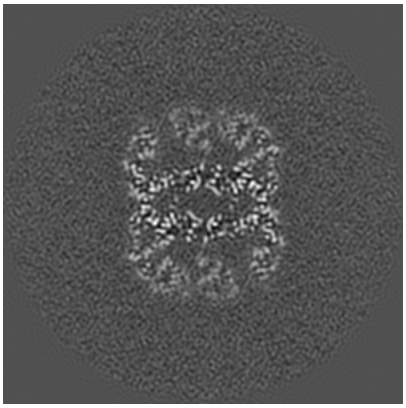

Y Index: 120

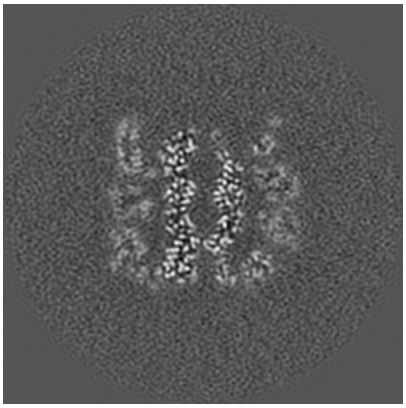

Z Index: 120

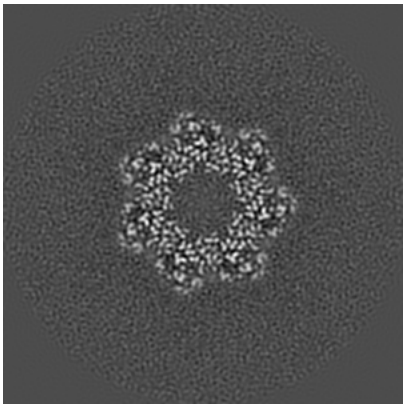
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map


X Index: 148

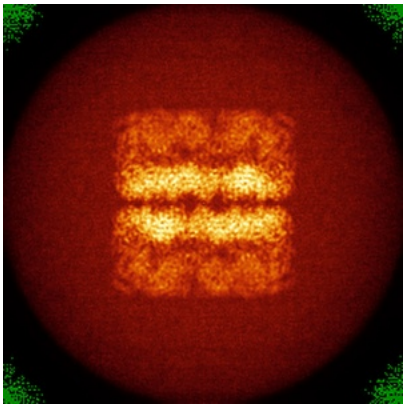

Y Index: 94

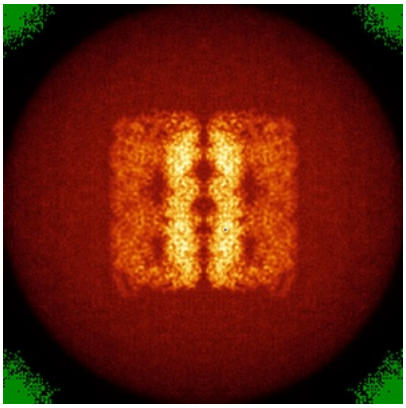

Z Index: 133

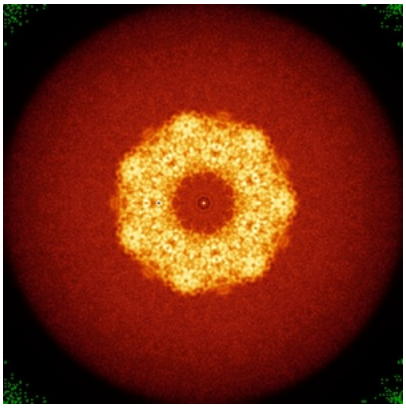
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map


X

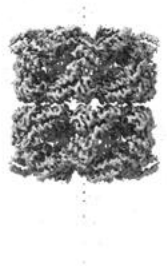

Y


Z

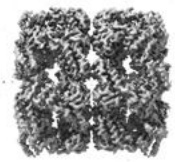
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

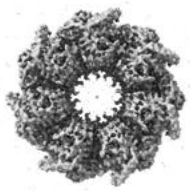
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

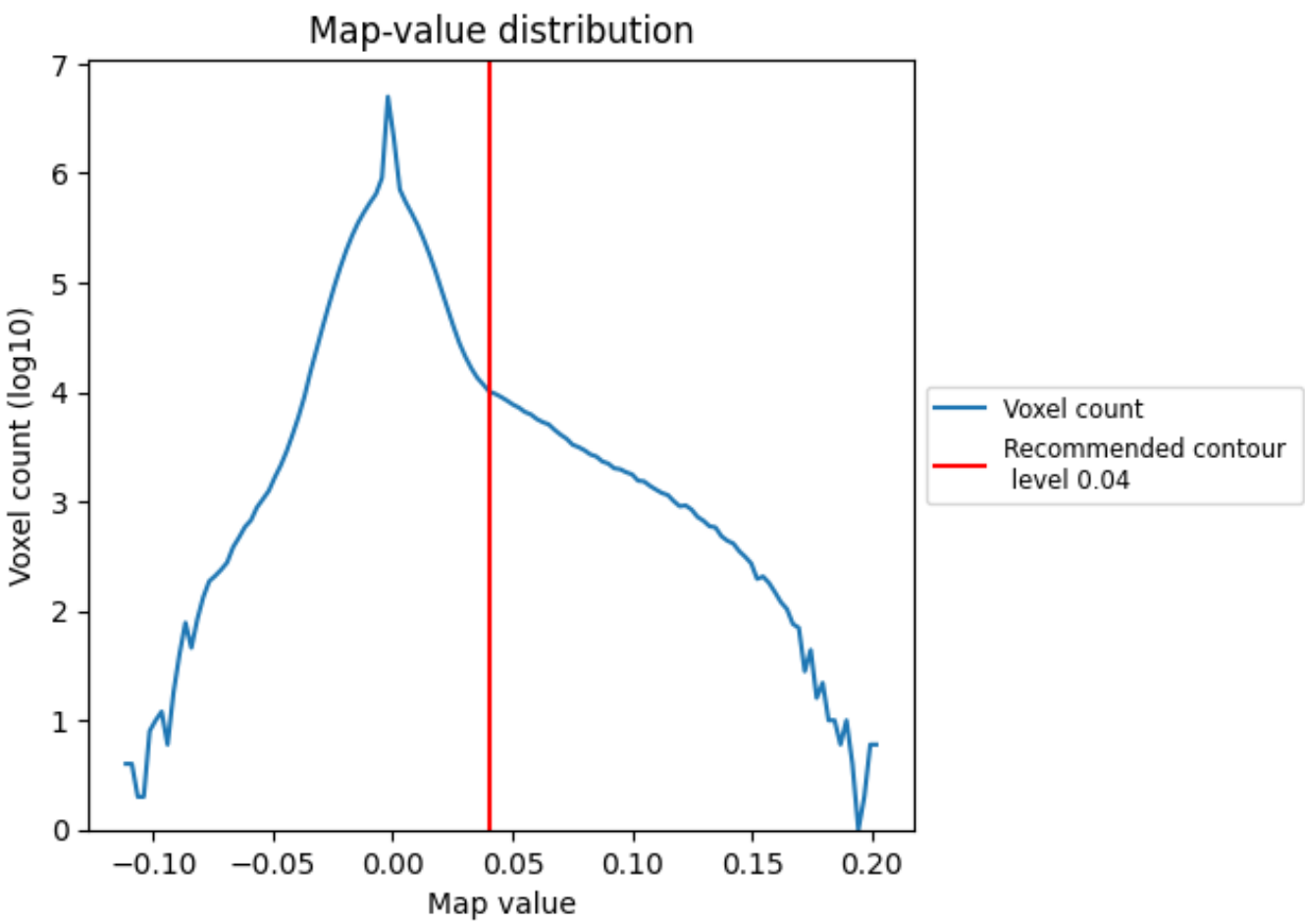
6.6 Mask visualisation (i)

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

7 Map analysis (i)

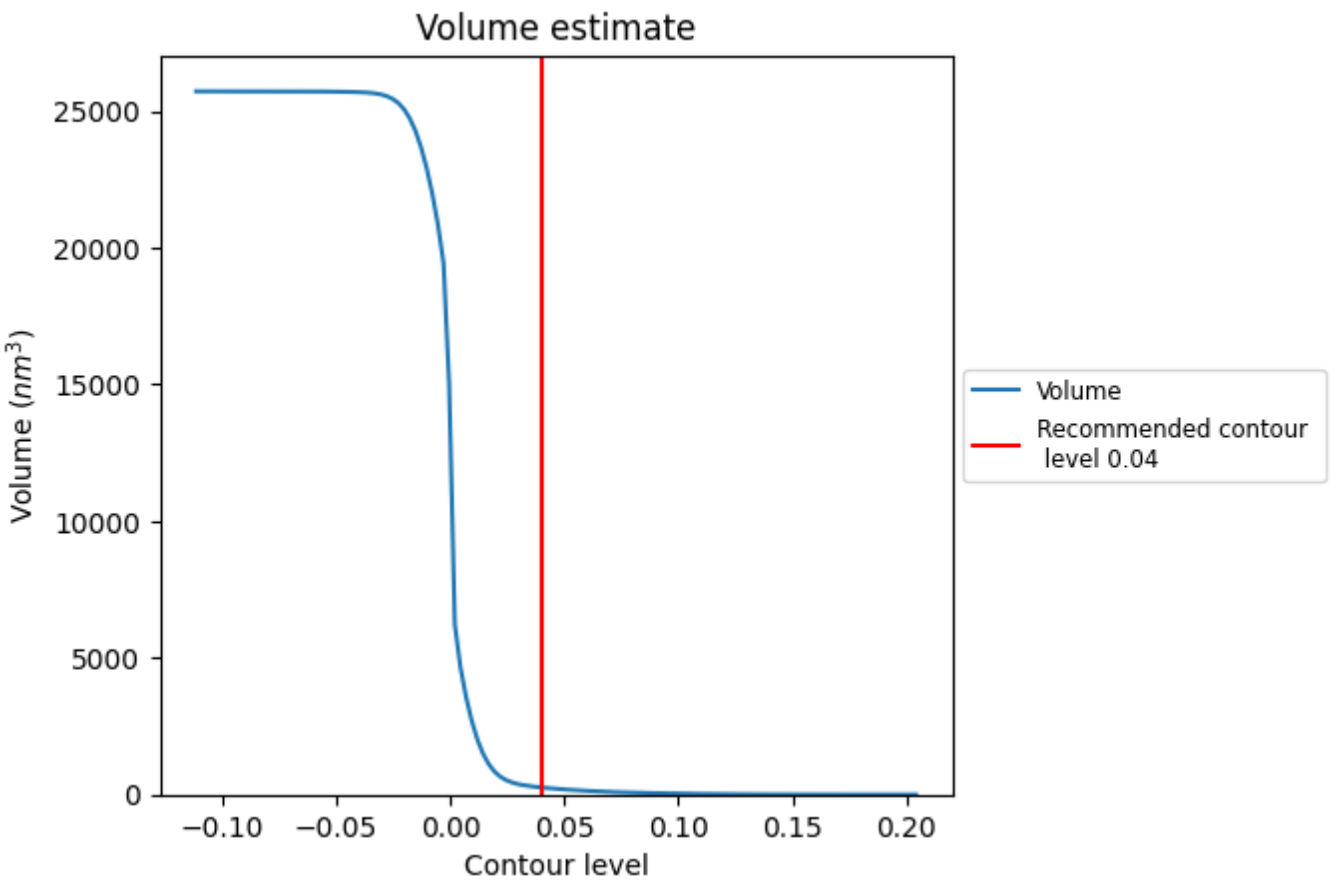
This section contains the results of statistical analysis of the map.

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.

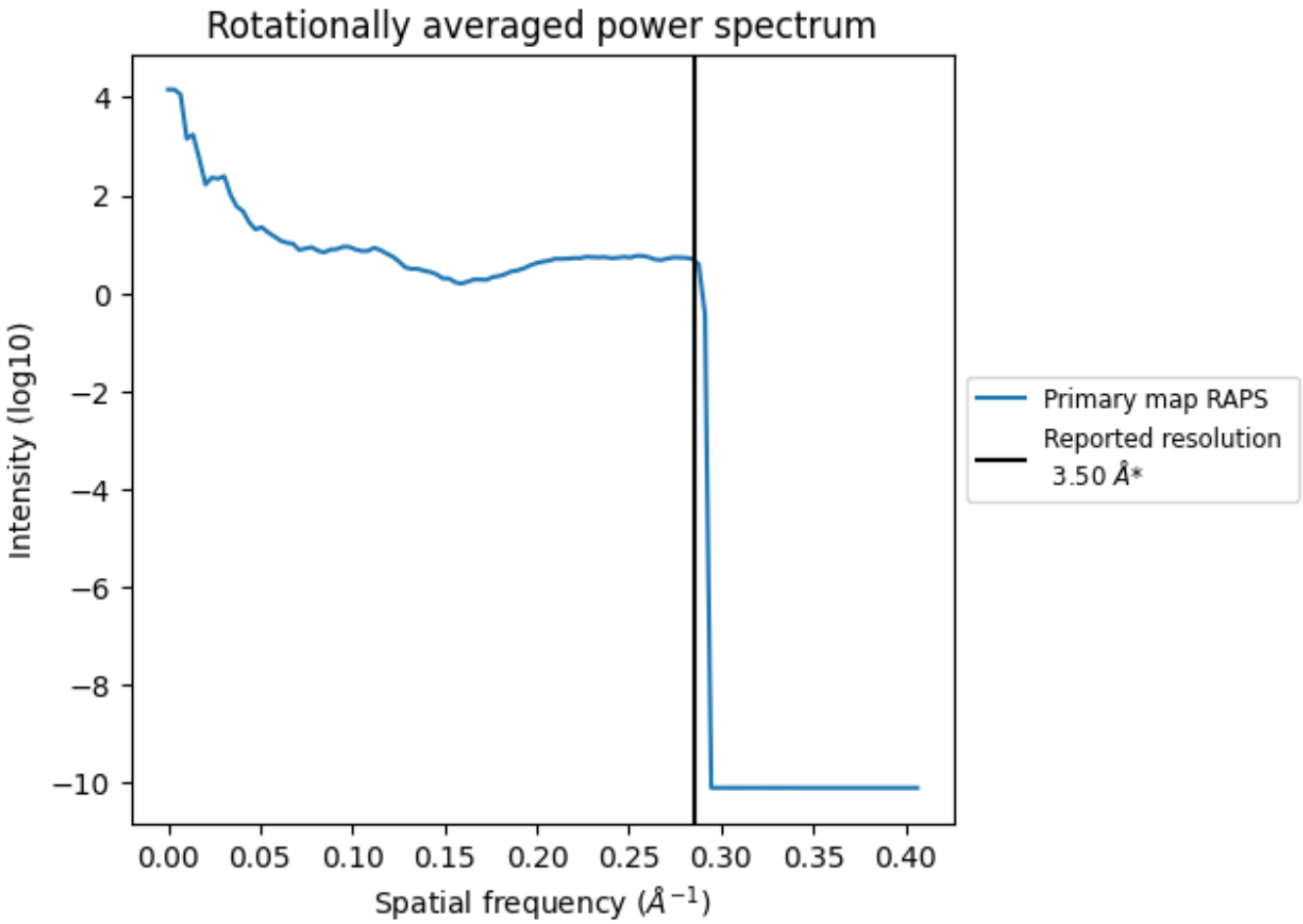
7.2 Volume estimate (i)



The volume at the recommended contour level is 259 nm^3; this corresponds to an approximate mass of 234 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)

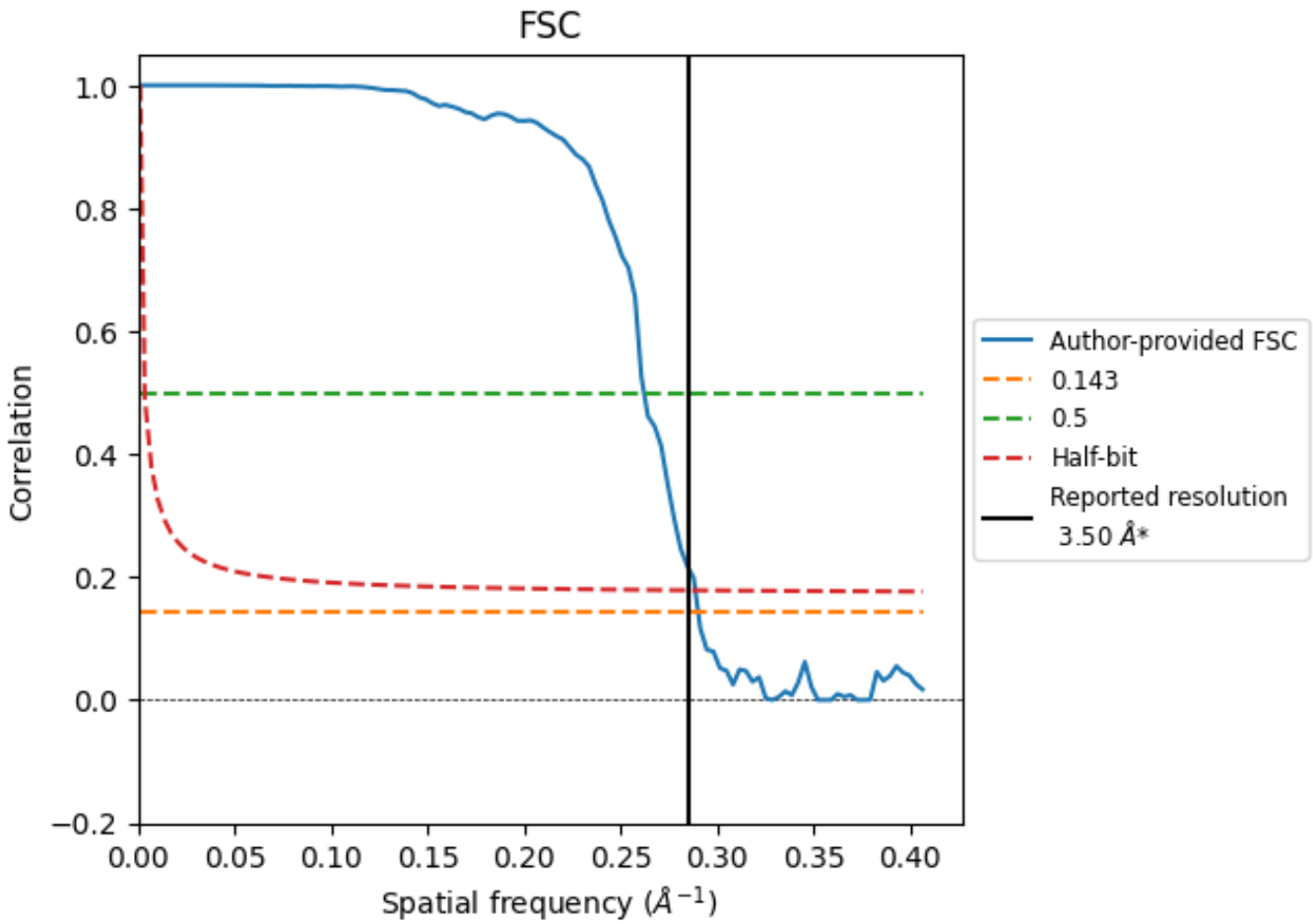


*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.286 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.45	3.81	3.46
Unmasked-calculated*	-	-	-

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

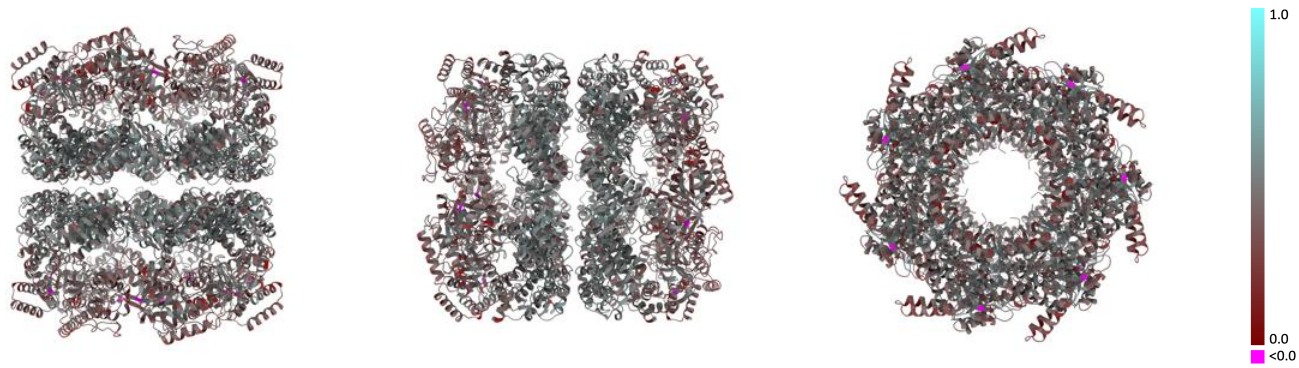
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8750 and PDB model 5W0S. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay (i)

This section was not generated.

9.2 Q-score mapped to coordinate model (i)



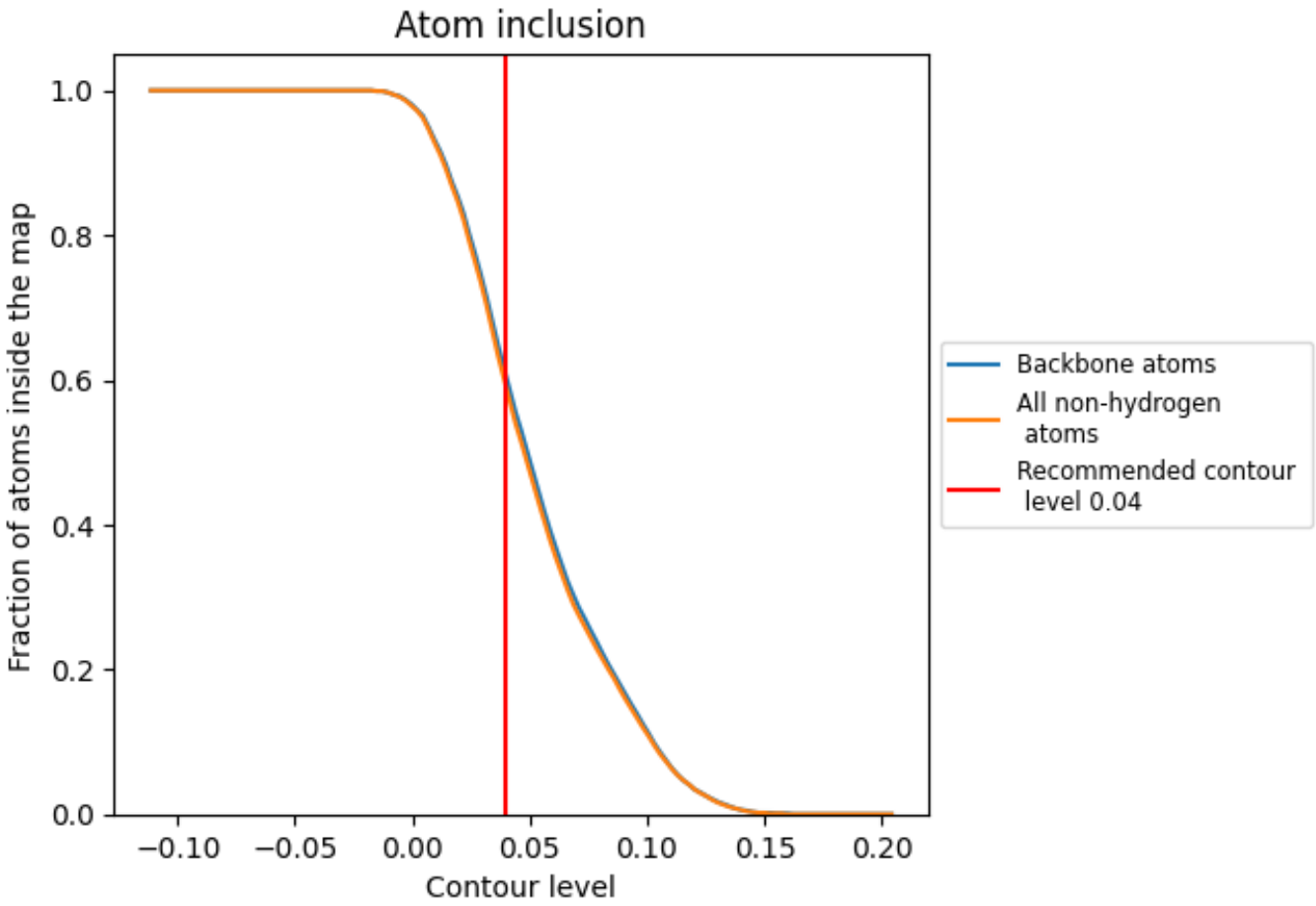
X Y Z

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)

This section was not generated.

9.4 Atom inclusion (i)



At the recommended contour level, 60% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5900	0.4240
A	0.5960	0.4250
B	0.5970	0.4240
C	0.5960	0.4230
D	0.5960	0.4230
E	0.5950	0.4240
F	0.5940	0.4250
G	0.5960	0.4240
H	0.5960	0.4250
I	0.5960	0.4260
J	0.5960	0.4230
K	0.5960	0.4230
L	0.5960	0.4230
M	0.5930	0.4230
N	0.5950	0.4260