Full wwPDB EM Validation Report ⓘ

Oct 26, 2026 – 05:33 PM JST

PDB ID	:	26IT / pdb_000026it
EMDB ID	:	EMD-80688
Title	:	Structure of recombinant RyR2 in the open state (Ca2+ dataset, Local refinement of Core domain)
Authors	:	Otori, Y.; Takeuchi, S.; Ogawa, H.
Deposited on	:	2026-05-01
Resolution	:	2.46 Å(reported)

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

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

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

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

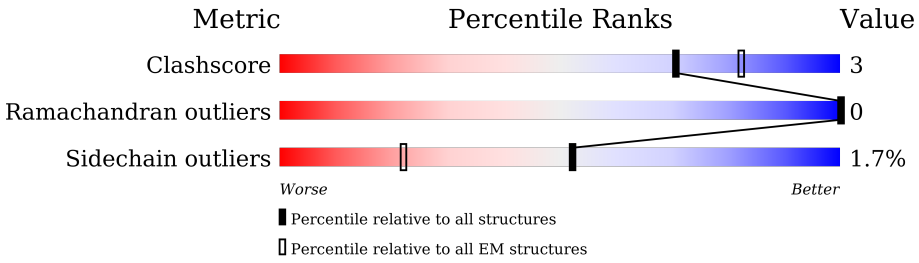
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

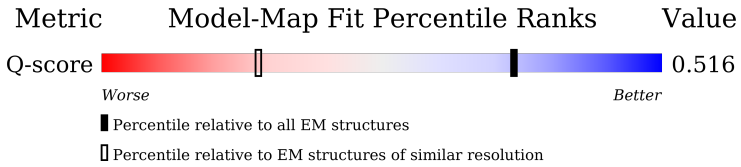
1 Overall quality at a glance

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

The reported resolution of this entry is 2.46 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	6014 (1.96 - 2.96)

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

Mol	Chain	Length	Quality of chain
1	A	4966	7% 19% 79%
1	B	4966	7% 19% 79%
1	C	4966	7% 19% 79%
1	D	4966	7% 19% 79%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 67212 atoms, of which 33196 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 Ryanodine receptor 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1041	Total	C	H	N	O	S	0	0
			16801	5472	8299	1370	1604	56		
1	B	1041	Total	C	H	N	O	S	0	0
			16801	5472	8299	1370	1604	56		
1	C	1041	Total	C	H	N	O	S	0	0
			16801	5472	8299	1370	1604	56		
1	D	1041	Total	C	H	N	O	S	0	0
			16801	5472	8299	1370	1604	56		

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Zn	0
			1	1	
2	B	1	Total	Zn	0
			1	1	
2	C	1	Total	Zn	0
			1	1	
2	D	1	Total	Zn	0
			1	1	

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Ca	0
			1	1	
3	B	1	Total	Ca	0
			1	1	
3	C	1	Total	Ca	0
			1	1	
3	D	1	Total	Ca	0
			1	1	

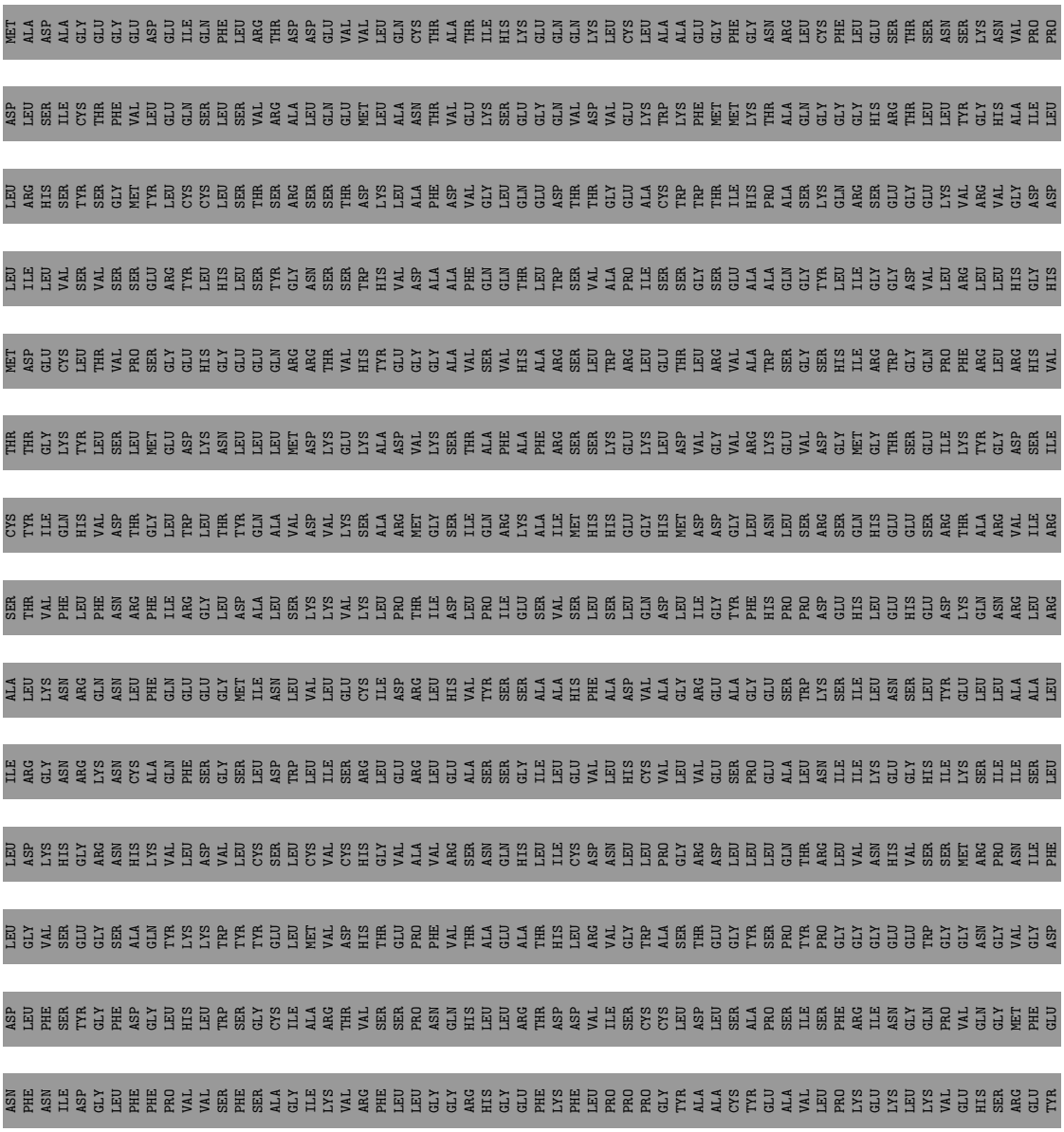
3 Residue-property plots (i)

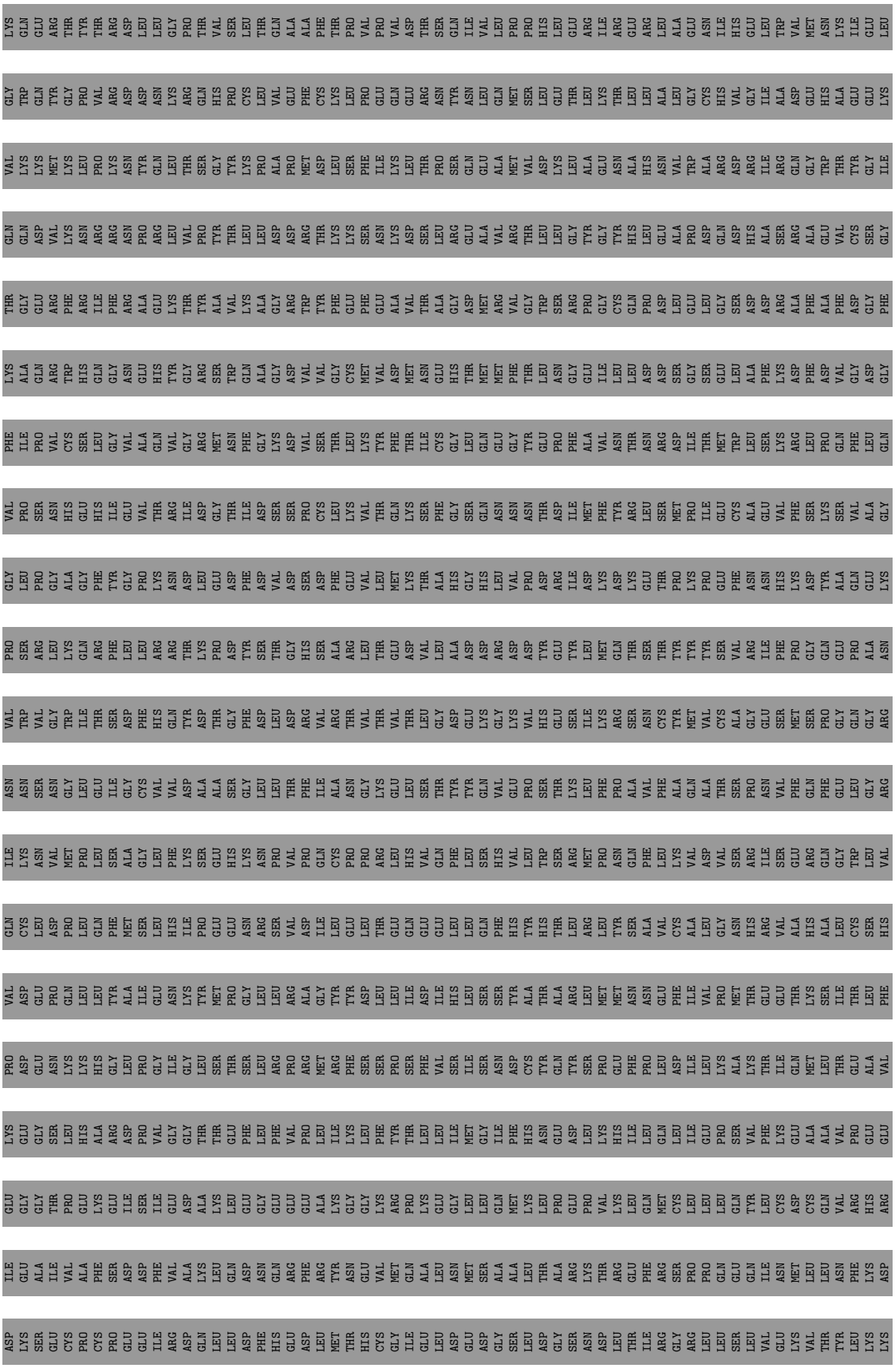
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

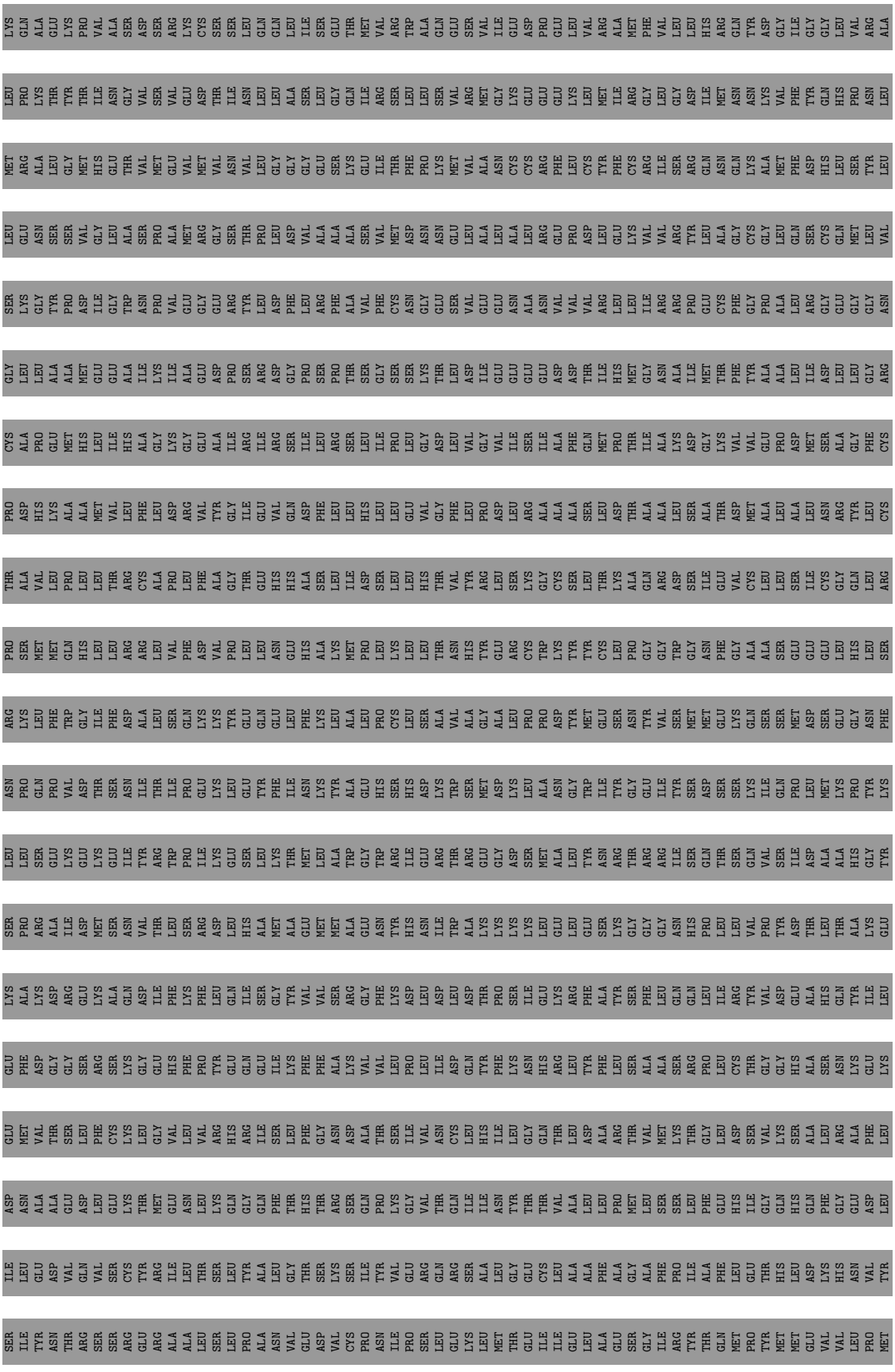
- Molecule 1: Ryanodine receptor 2

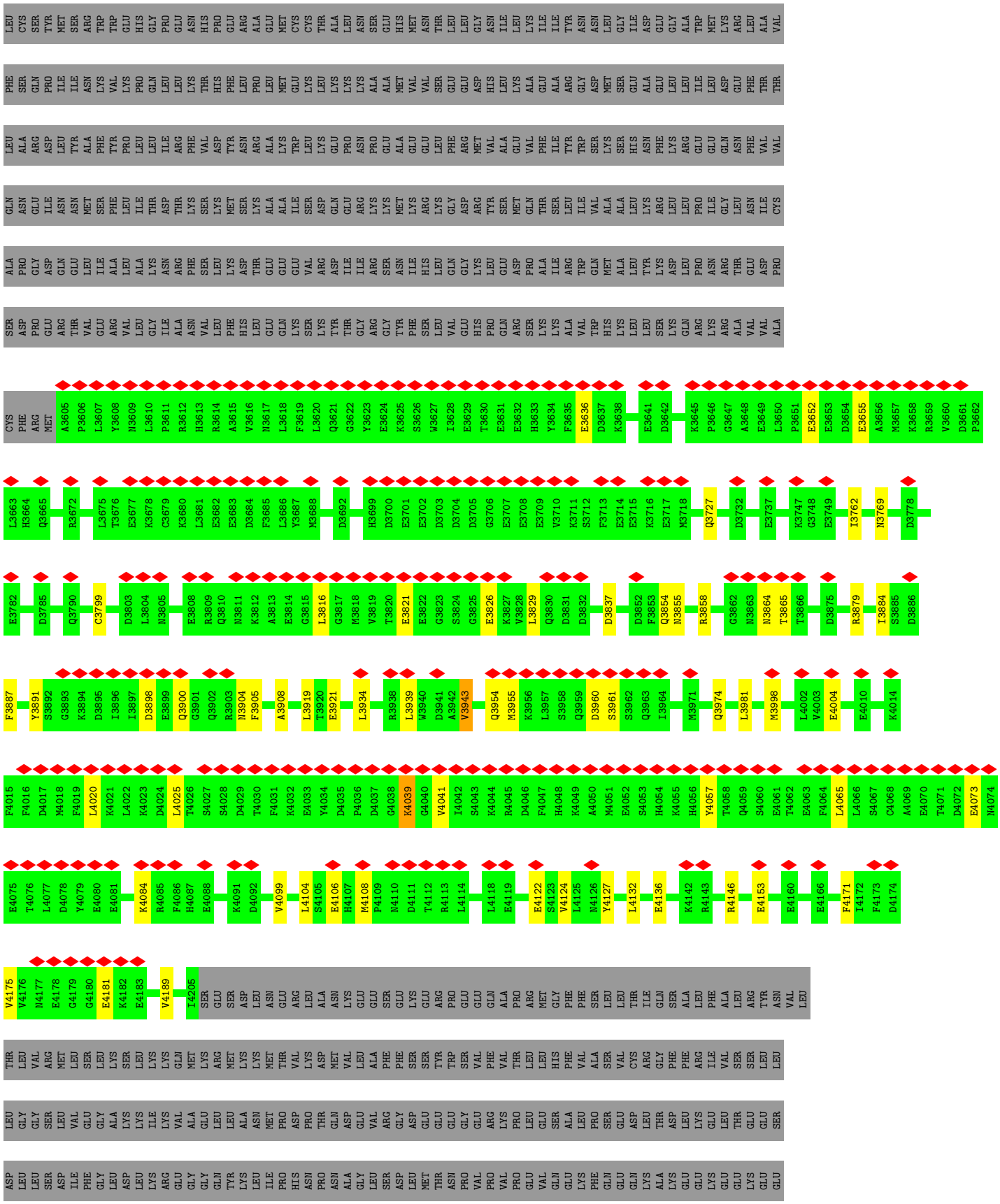
Chain A:

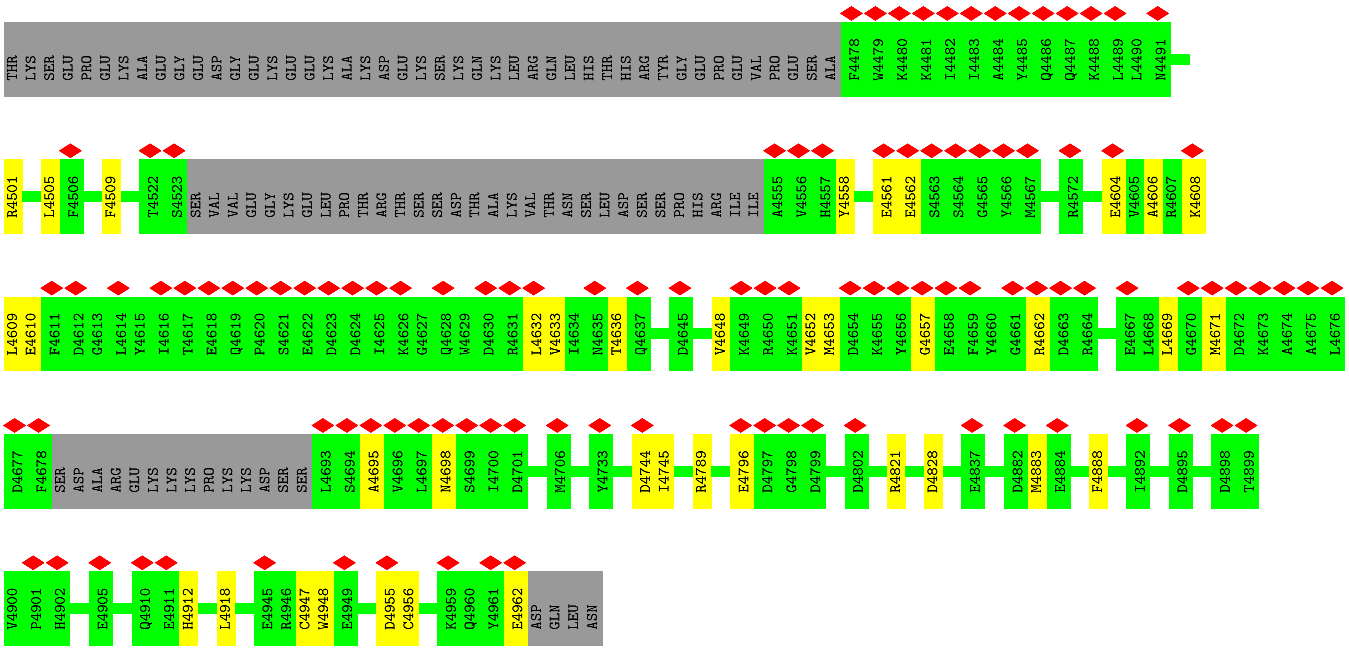




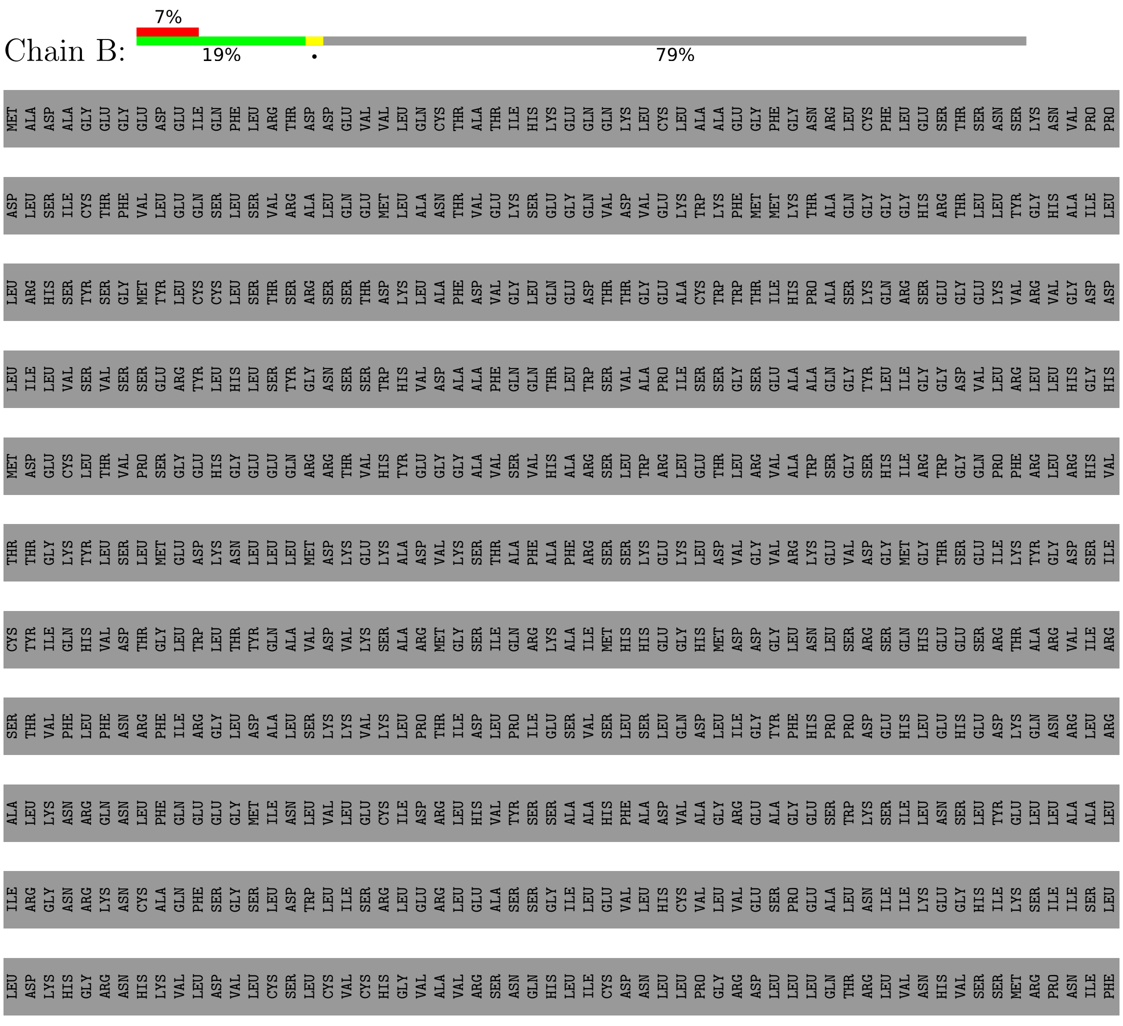

LYS GLN GLU ARG THR TYR THR ARG ASP LEU LEU GLY PRO THR VAL SER LEU THR GLN ALA ALA PHE THR PRO VAL PRO VAL ASP THR SER GLN ILE VAL LEU PRO PRO HIS LEU GLU ARG ILE ARG GLU ARG LEU ALA GLU ASN ILE HIS GLU LEU LEU TRP VAL MET ASN LYS ILE GLU LEU
GLY TRP GLN TYR GLY PRO VAL ARG ASP ASP ASN LYS ARG GLN HIS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

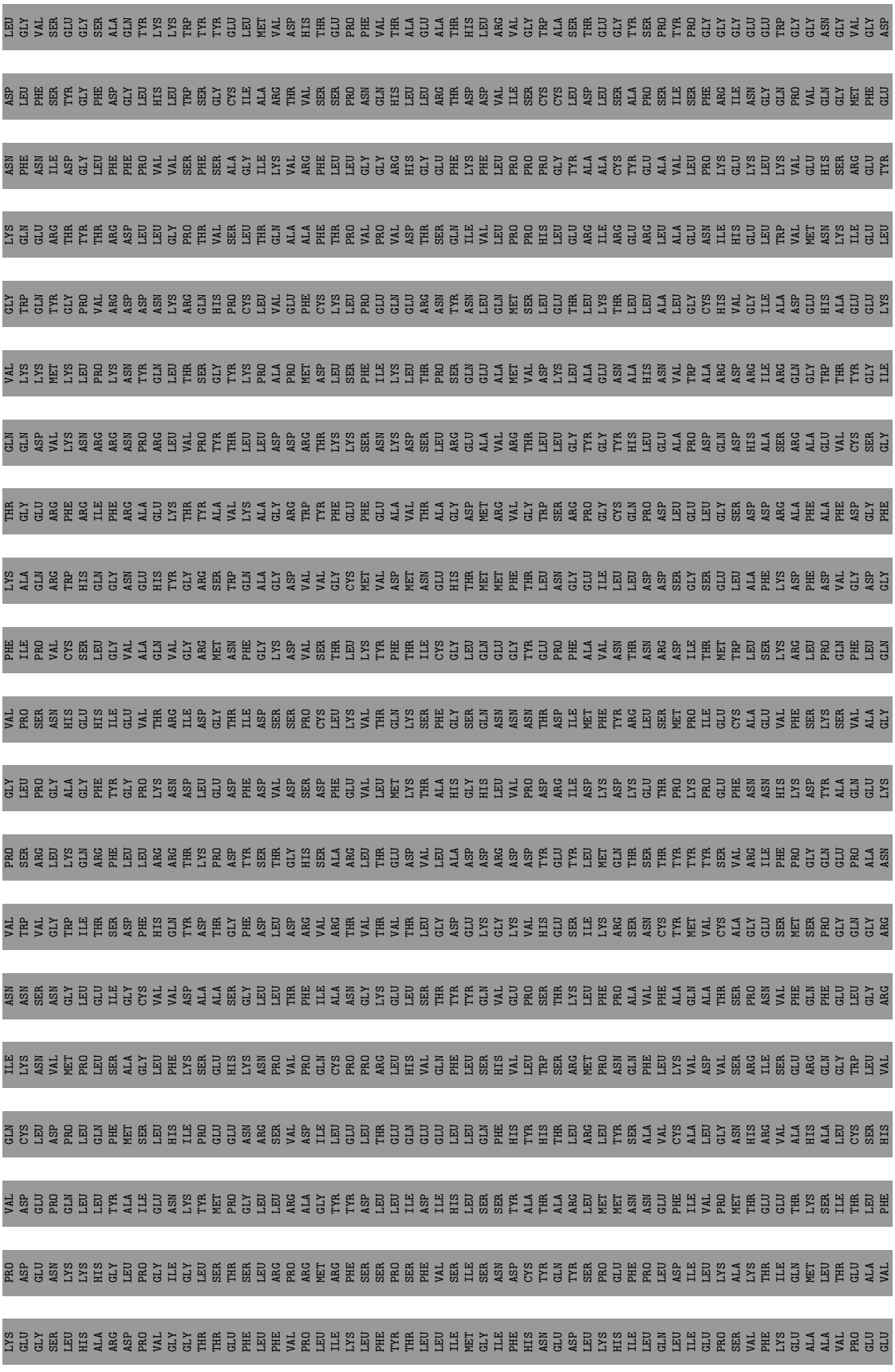

LYS GLN ALA GLU LYS PRO VAL ALA SER ASP SER ARG LYS CYS SER SER LEU GLN GLN LEU ILE SER GLU GLY THR MET VAL ARG TRP ALA GLN GLU SER VAL ILE GLU ASP PRO GLU LEU VAL ARG ALA MET PHE VAL LEU LEU HIS ARG GLN TYR ASP GLY ILE GLY LEU VAL ARG
LEU PRO LYS THR TYR THR ILE ASN GLY VAL SER VAL GLU ASP THR ILE ASN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

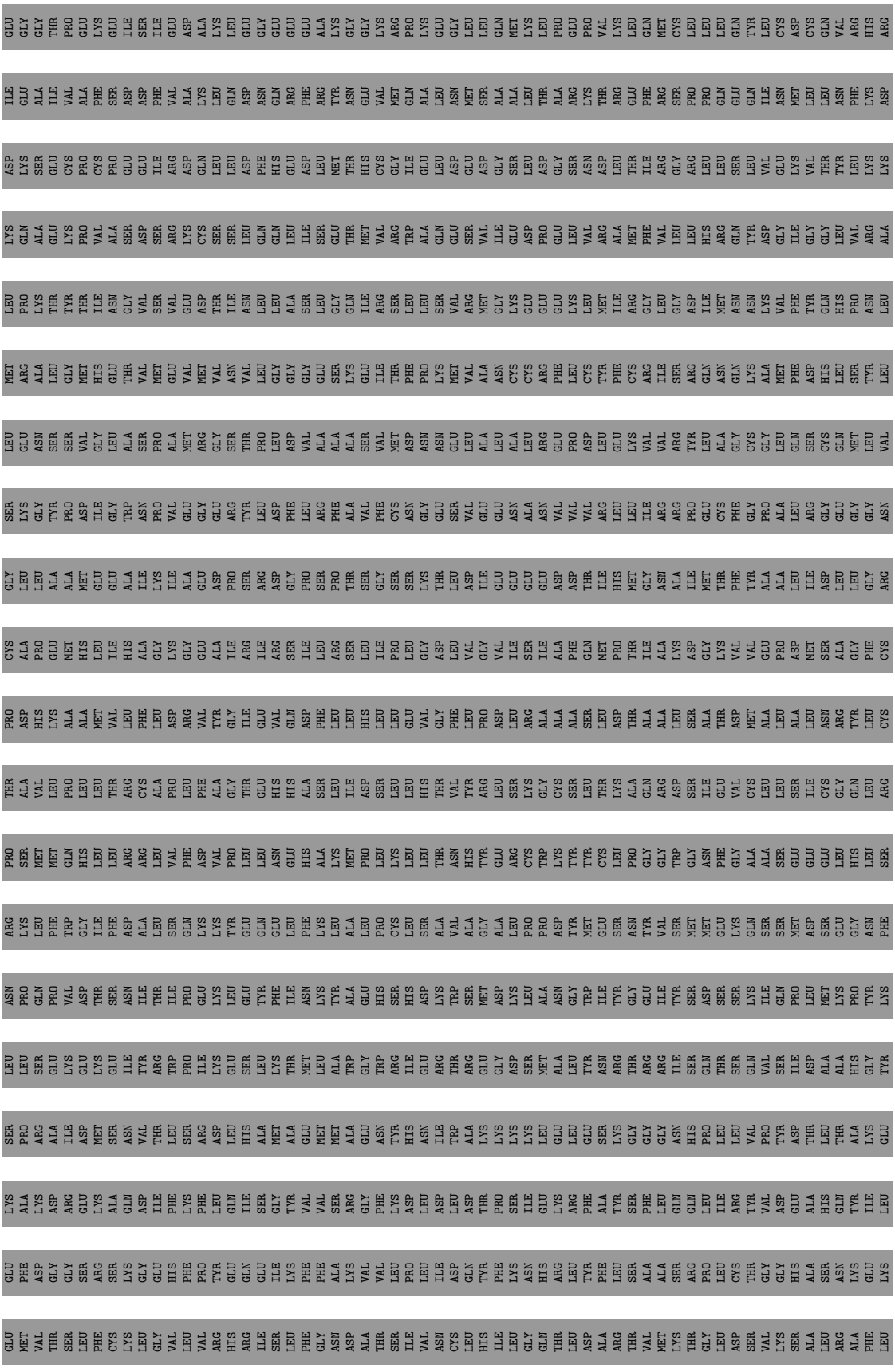


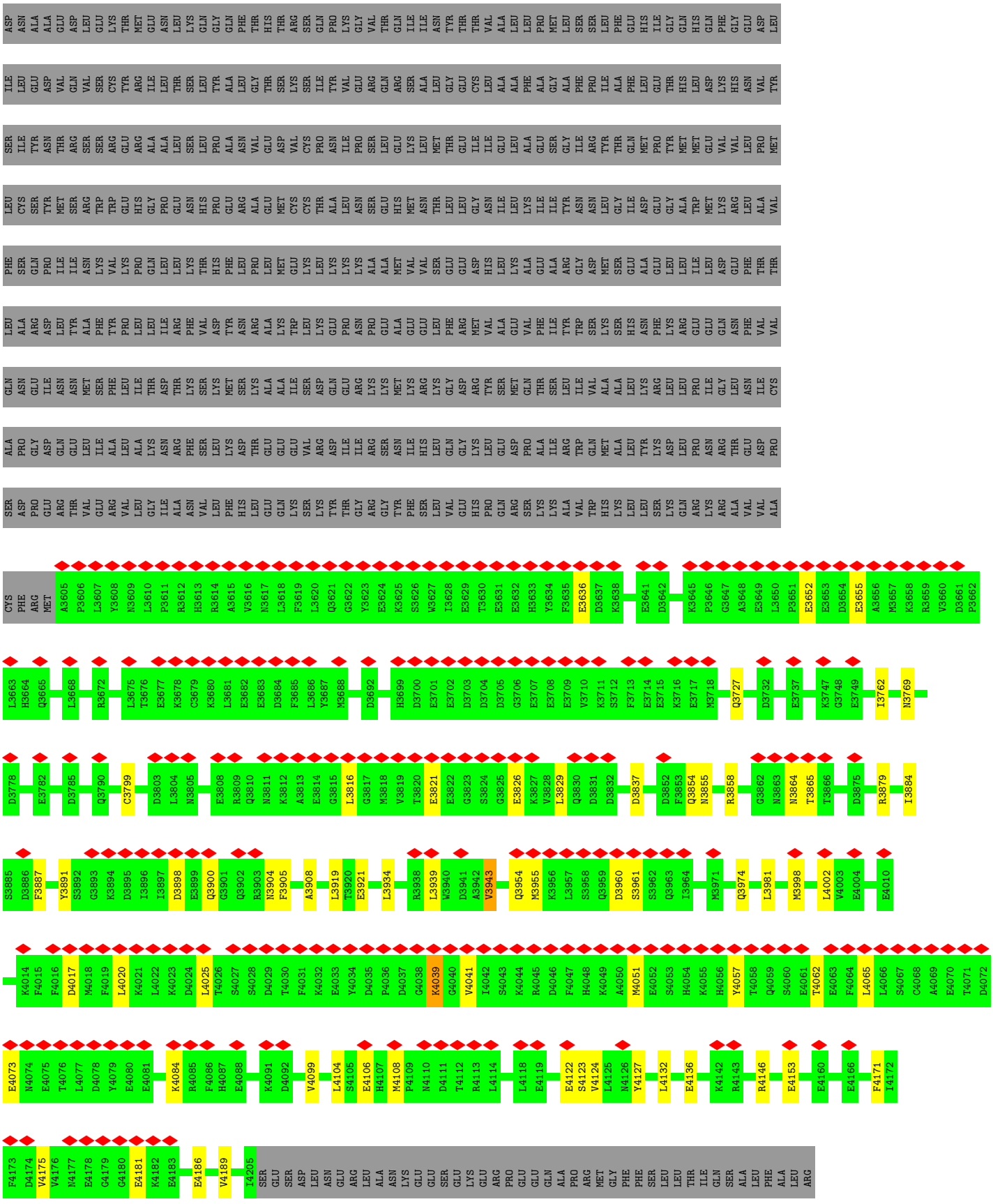


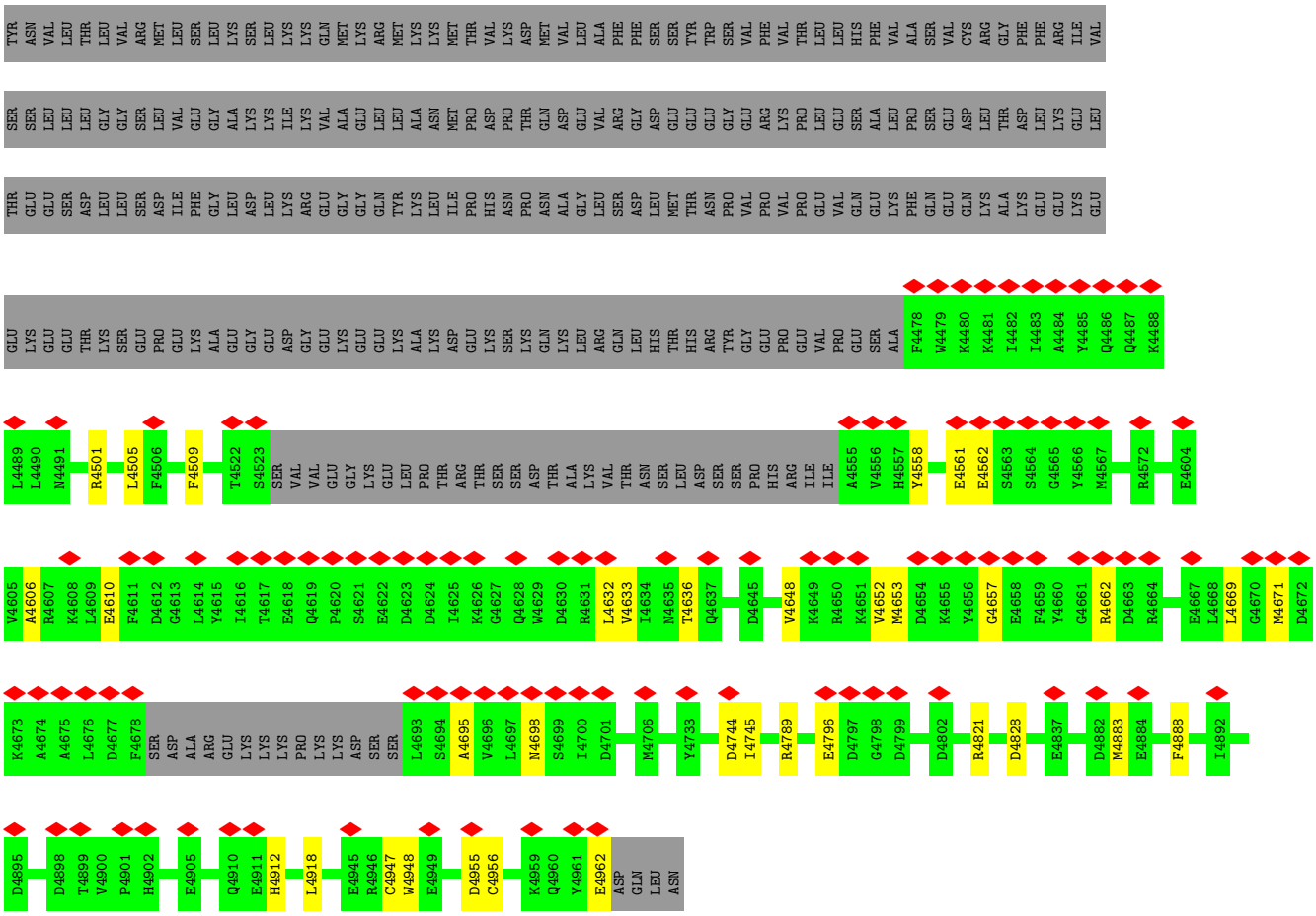
• Molecule 1: Ryanodine receptor 2




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


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

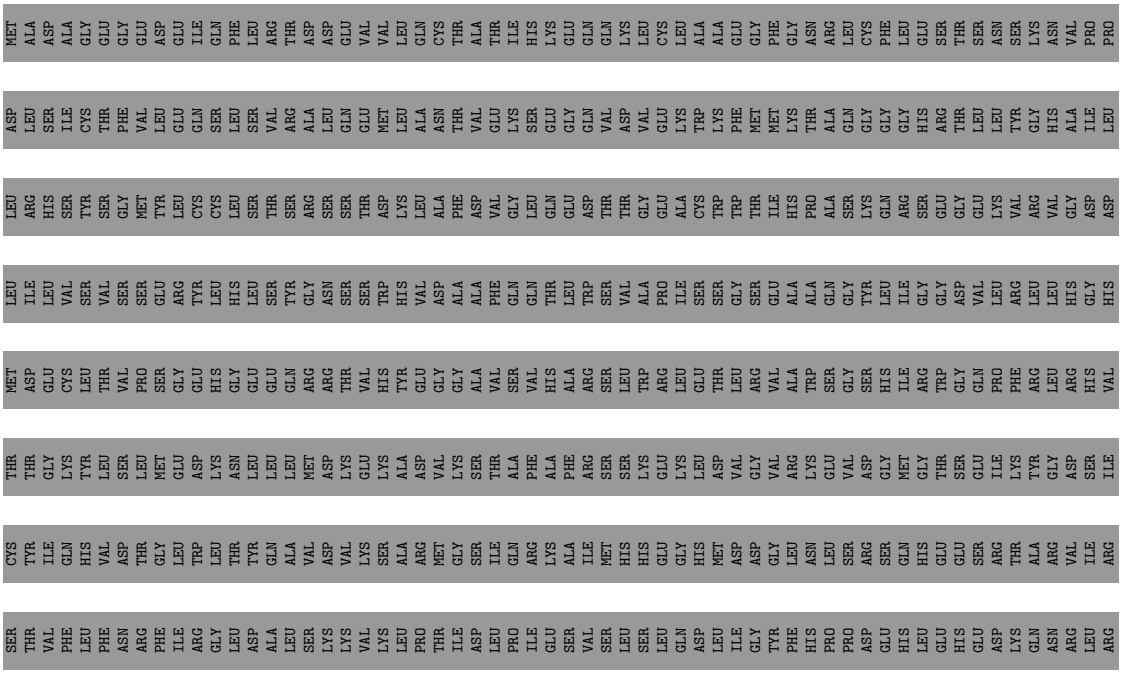

ASP ASN ALA ALA GLU ASP LEU GLU GLU LYS THR MET GLU ASN LEU LYS GLN GLY GLN PHE THR HIS THR ARG SER GLN PRO LYS GLY VAL THR GLN ILE ILE ASN TYR THR VAL ALA LEU LEU PRO MET LEU SER SER LEU PHE GLU HIS ILE GLY GLN HIS GLN PHE GLY GLU ASP LEU
ILE LEU GLU ASP VAL GLN VAL SER CYS TYR ARG ILE LEU THR SER LEU TYR ALA LEU GLY THR SER LYS SER ILE TYR VAL GLU ARG GLN ARG SER ALA LEU GLY GLU CYS LEU ALA ALA PHE ALA GLY ALA PHE PRO ILE ALA PHE LEU GLU THR HIS LEU ASP LYS HIS ASN VAL TYR
SER ILE TYR ASN THR ARG SER SER ARG GLU ARG ALA ALA LEU SER LEU PRO ALA ASN VAL GLU ASP VAL CYS PRO ASN ILE PRO SER SER LEU GLU GLU LYS LEU MET THR GLU ILE ILE GLU LEU ALA PHE GLU ALA GLU SER GLY ILE ARG TYR THR GLN MET PRO TYR MET MET GLU VAL VAL LEU PRO MET
LEU CYS SER TYR MET SER ARG TRP TRP GLU HIS GLY PRO GLU GLU ASN HIS PRO GLU ARG ALA ALA GLU MET CYS CYS THR ALA LEU ASN SER GLU HIS MET ASN THR LEU LEU GLY ASN ILE LEU LYS ILE ILE TYR ASN ASN LEU GLY ILE ASP GLU GLY ALA TRP MET LYS ARG LEU ASP ALA VAL
PHE SER GLN PRO ILE ILE ASN LYS VAL LYS PRO GLN LEU LEU LEU LYS THR HIS PHE LEU PRO PRO LEU MET GLU LYS LEU LYS LYS LYS ALA ALA MET VAL VAL SER GLU GLU GLU ASP HIS LEU LYS ALA GLU ALA ARG GLY ASP GLU PHE THR THR
LEU ALA ARG ASP LEU TYR ALA PHE TYR PRO LEU LEU LEU ILE ARG PHE VAL ASP TYR ASN ARG ALA ALA LYS TRP LEU LYS GLU GLU PRO ASN PRO GLU ALA ALA MET VAL GLU GLU GLU LEU PHE ARG MET VAL ALA GLU VAL PHE ILE TYR TRP SER LYS SER HIS ASN PHE LYS ARG GLU LEU ASP PHE VAL VAL
GLN ASN GLU ILE ASN ASN MET SER PHE LEU ILE THR ASP THR LYS SER LYS MET SER LYS ALA ALA ILE SER ASP GLN GLU ARG LYS LYS MET LYS ARG LYS GLY ASP ARG TYR SER MET GLN THR SER LEU ILE VAL ALA ALA LEU LYS ARG LEU LEU PRO ILE GLY LEU ASN ILE CYS
ALA PRO GLY ASP GLN GLU LEU ILE ALA LEU ASP GLU GLU VAL ARG ASP ILE ILE ARG SER ASN ILE HIS LEU GLN GLY LYS LEU GLU ASP PRO ALA ILE ARG TRP GLN MET ALA LEU TYR LYS ASP LEU PRO LEU ASN ARG THR GLU ASP PRO
SER ASP PRO GLU ARG THR VAL GLU ARG VAL LEU GLY ILE ALA ASN VAL LEU PHE HIS LEU GLU GLN LYS SER LYS TYR THR GLY ARG GLY TYR PHE SER LEU VAL GLU HIS PRO GLN ARG SER LYS LYS ALA VAL TRP HIS LYS LEU LEU SER LYS GLN ARG LYS ARG ALA VAL VAL ALA
CYS PHE ARG MET A3605 P3606 L3607 Y3608 N3609 L3610 P3611 R3612 H3613 R3614 A3615 V3616 N3617 L3618 F3619 L3620 Q3621 G3622 Y3623 E3624 K3625 S3626 W3627 I3628 E3629 T3630 E3631 E3632 H3633 Y3634 F3635 E3636 D3637 K3638 E3641 D3642 K3645 P3646 G3647 A3648 E3649 L3650 P3651 E3652 E3653 D3654 E3655 A3656 M3657 K3658 R3659 V3660 D3661 P3662
L3663 H3664 Q3665 L3668 R3672 L3675 T3676 E3677 K3678 C3679 K3680 L3681 E3682 E3683 D3684 F3685 L3686 Y3687 M3688 D3692 H3699 D3700 E3701 E3702 D3703 D3704 D3705 G3706 E3707 E3708 E3709 V3710 K3711 S3712 F3713 E3714 E3715 K3716 E3717 M3718 Q3727 D3732 E3737 K3747 G3748 E3749 I3762 N3769
D3778 E3782 D3785 Q3790 C3799 D3803 L3804 N3805 E3808 R3809 Q3810 N3811 K3812 A3813 E3814 G3815 L3816 G3817 M3818 V3819 T3820 E3821 E3822 G3823 S3824 G3825 E3826 K3827 V3828 L3829 Q3830 D3831 D3832 D3837 D3852 F3853 Q3854 N3855 R3858 G3862 N3863 N3864 T3865 T3866 D3875 R3879 I3884
S3885 D3886 F3887 Y3891 S3892 G3893 K3894 D3895 I3896 I3897 D3898 E3899 Q3900 G3901 Q3902 R3903 N3904 F3905 A3908 L3919 T3920 E3921 L3934 R3938 L3939 W3940 D3941 A3942 V3943 Q3954 M3955 K3956 L3957 S3958 Q3959 D3960 S3961 S3962 Q3963 I3964 M3971 Q3974 L3981 M3998 L4002 V4003 E4004 E4010
K4014 F4015 F4016 D4017 M4018 F4019 L4020 K4021 L4022 K4023 D4024 L4025 T4026 S4027 S4028 D4029 T4030 F4031 K4032 E4033 Y4034 D4035 P4036 D4037 G4038 K4039 G4040 V4041 I4042 S4043 K4044 R4045 D4046 F4047 H4048 K4049 A4050 M4051 E4052 S4053 H4054 K4055 H4056 Y4057 T4058 Q4059 S4060 E4061 T4062 E4063 F4064 L4065 L4066 S4067 C4068 A4069 E4070 T4071 D4072
E4073 N4074 E4075 T4076 L4077 D4078 Y4079 E4080 E4081 K4084 R4085 F4086 H4087 E4088 K4091 D4092 V4099 L4104 S4105 E4106 H4107 M4108 P4109 N4110 D4111 T4112 R4113 L4114 L4118 E4119 E4122 S4123 V4124 L4125 N4126 Y4127 L4132 E4136 K4142 R4143 R4146 E4153 E4160 E4166 F4171 I4172
F4173 D4174 V4175 V4176 N4177 E4178 G4179 G4180 E4181 K4182 E4183 E4186 V4189 T4205 SER GLU SER ASP LEU ASN GLU ARG LEU ALA ASN LYS GLU GLU SER GLU LYS GLU ARG PRO GLU GLU GLN ALA PRO ARG MET GLY PHE PHE SER LEU LEU THR ILE GLN SER ALA LEU PHE ALA LEU ARG

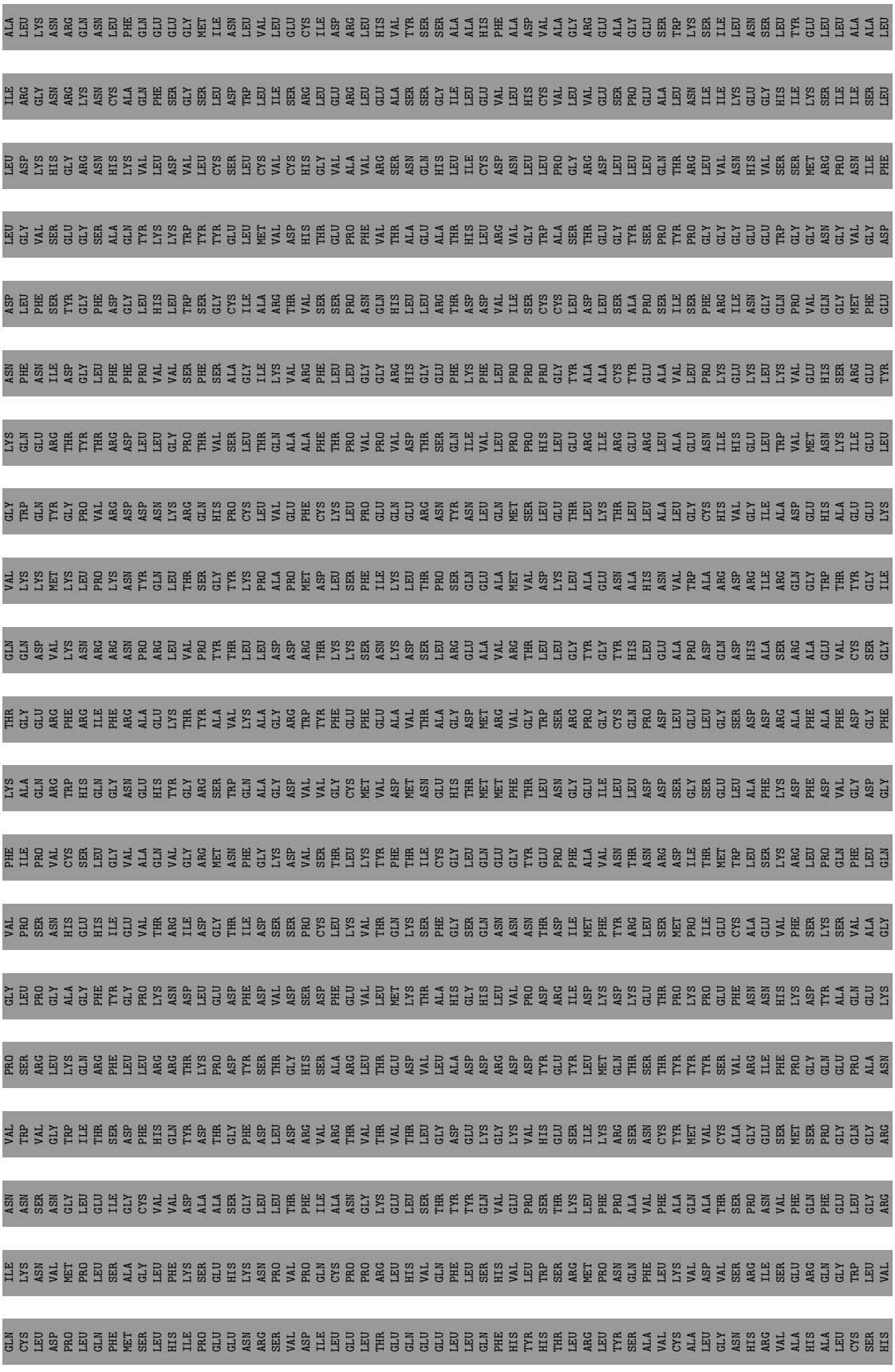


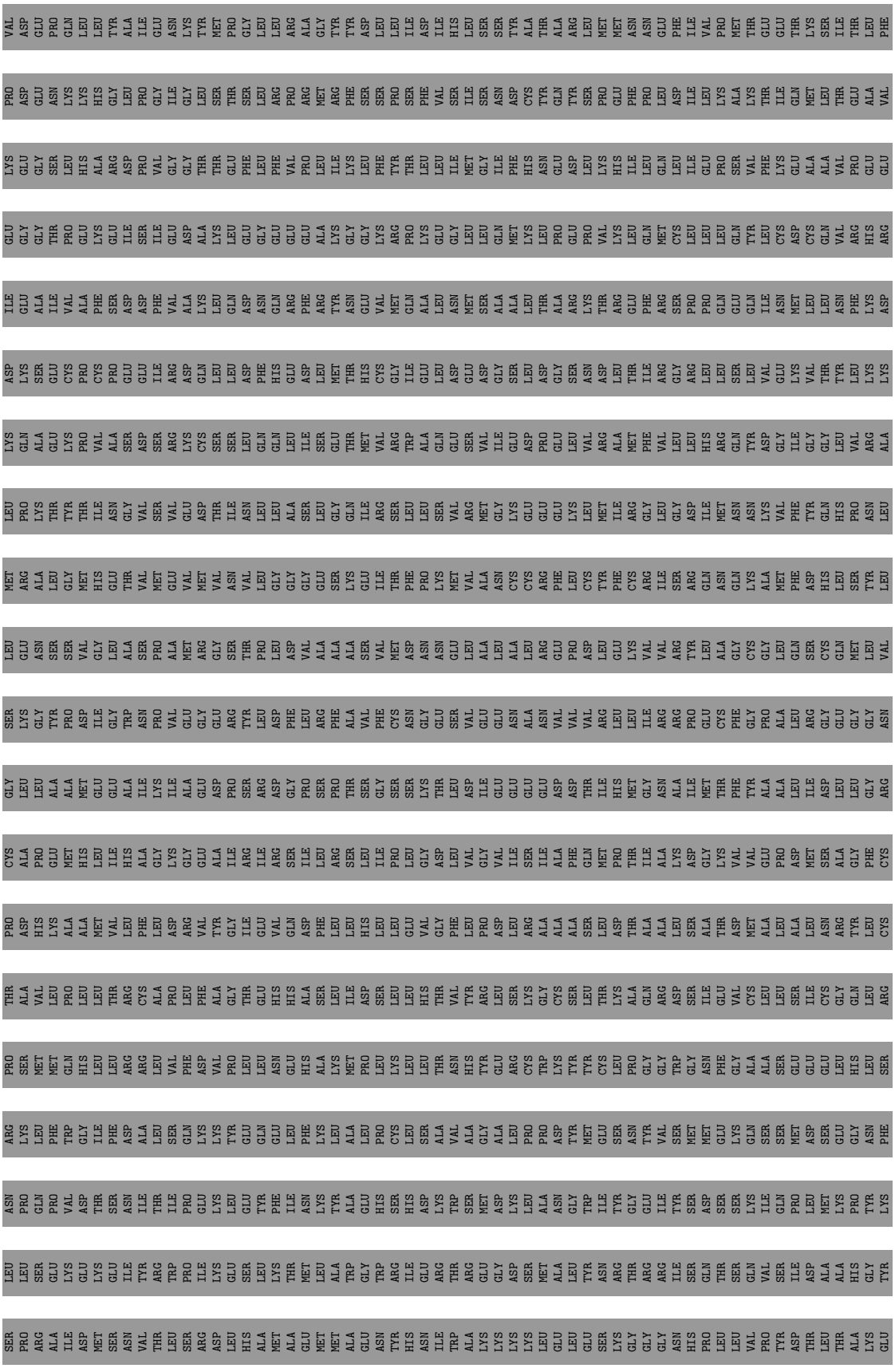
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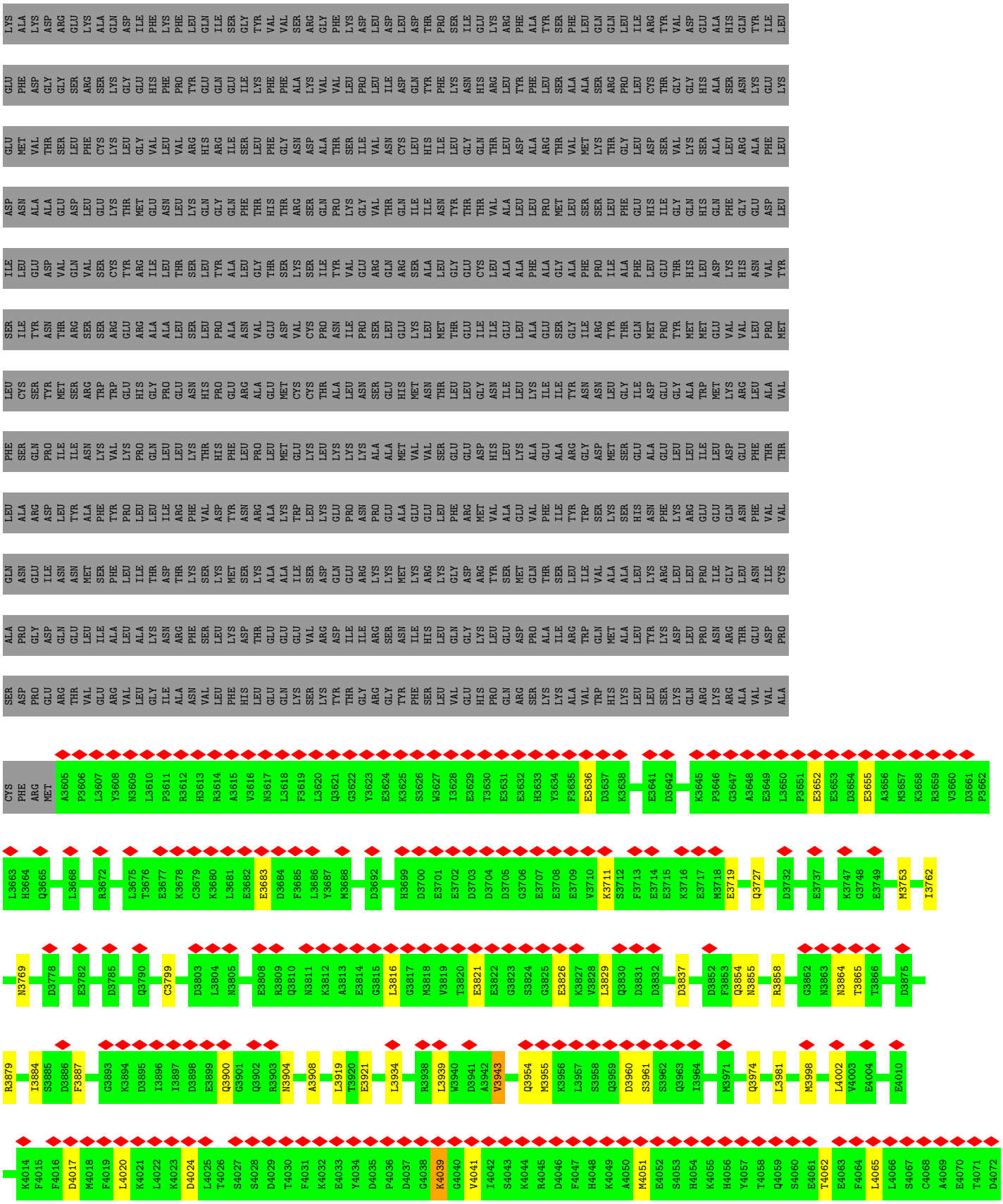
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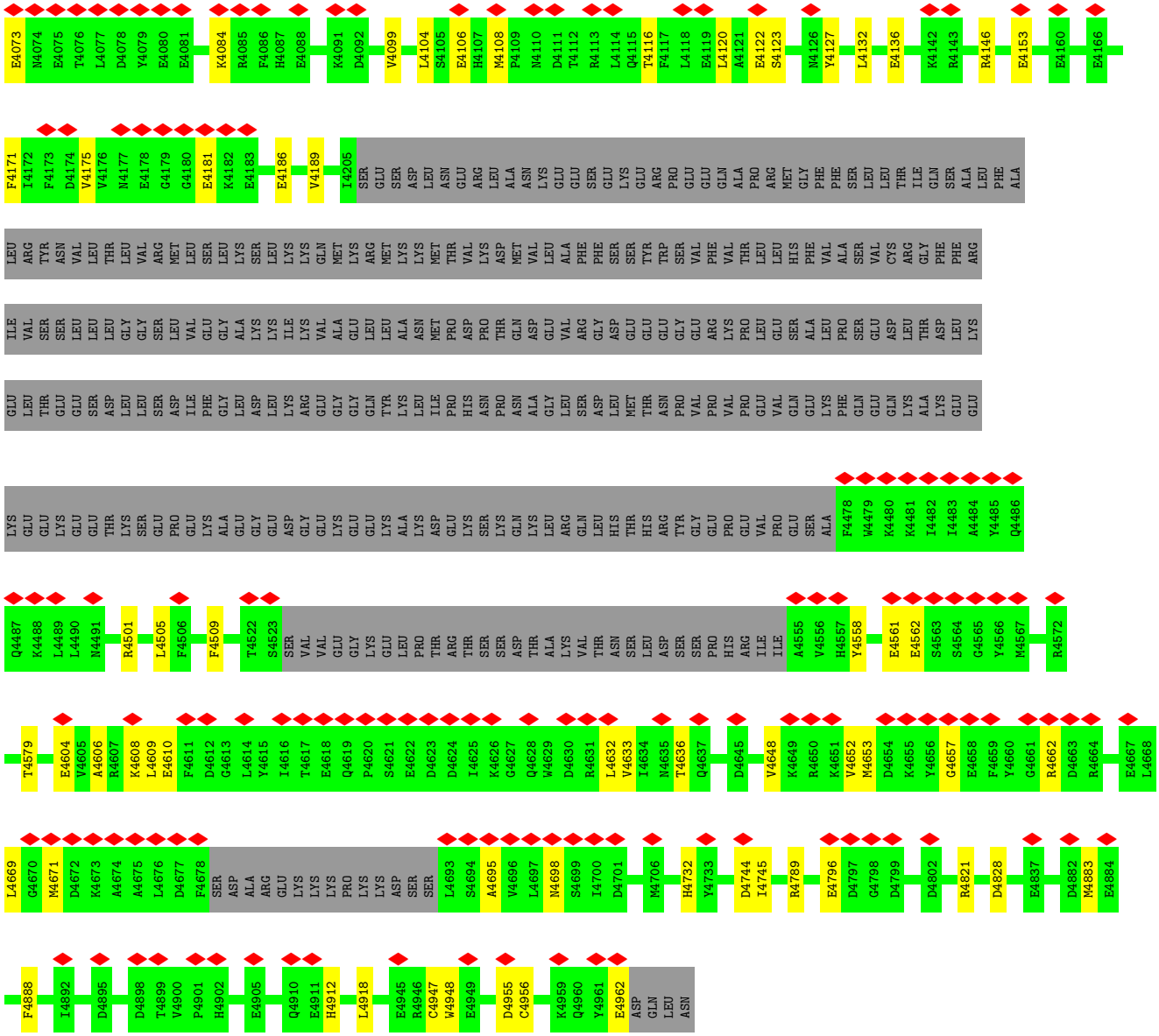






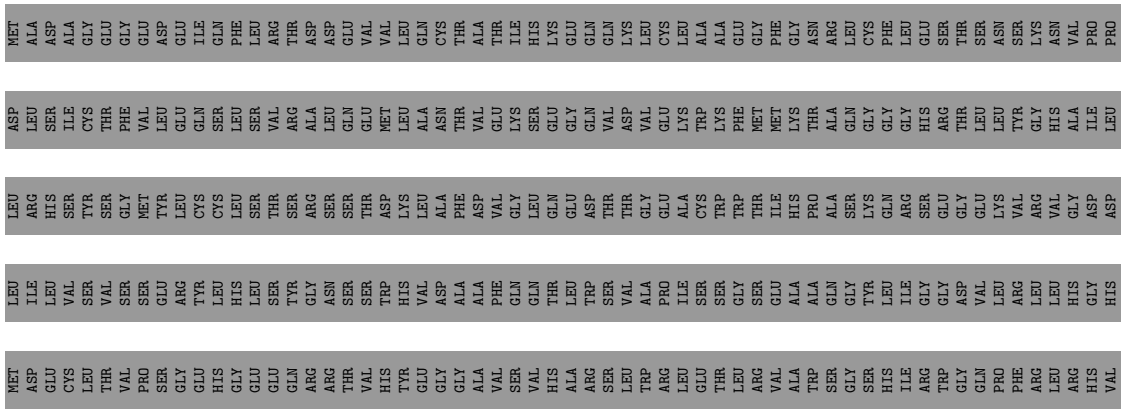


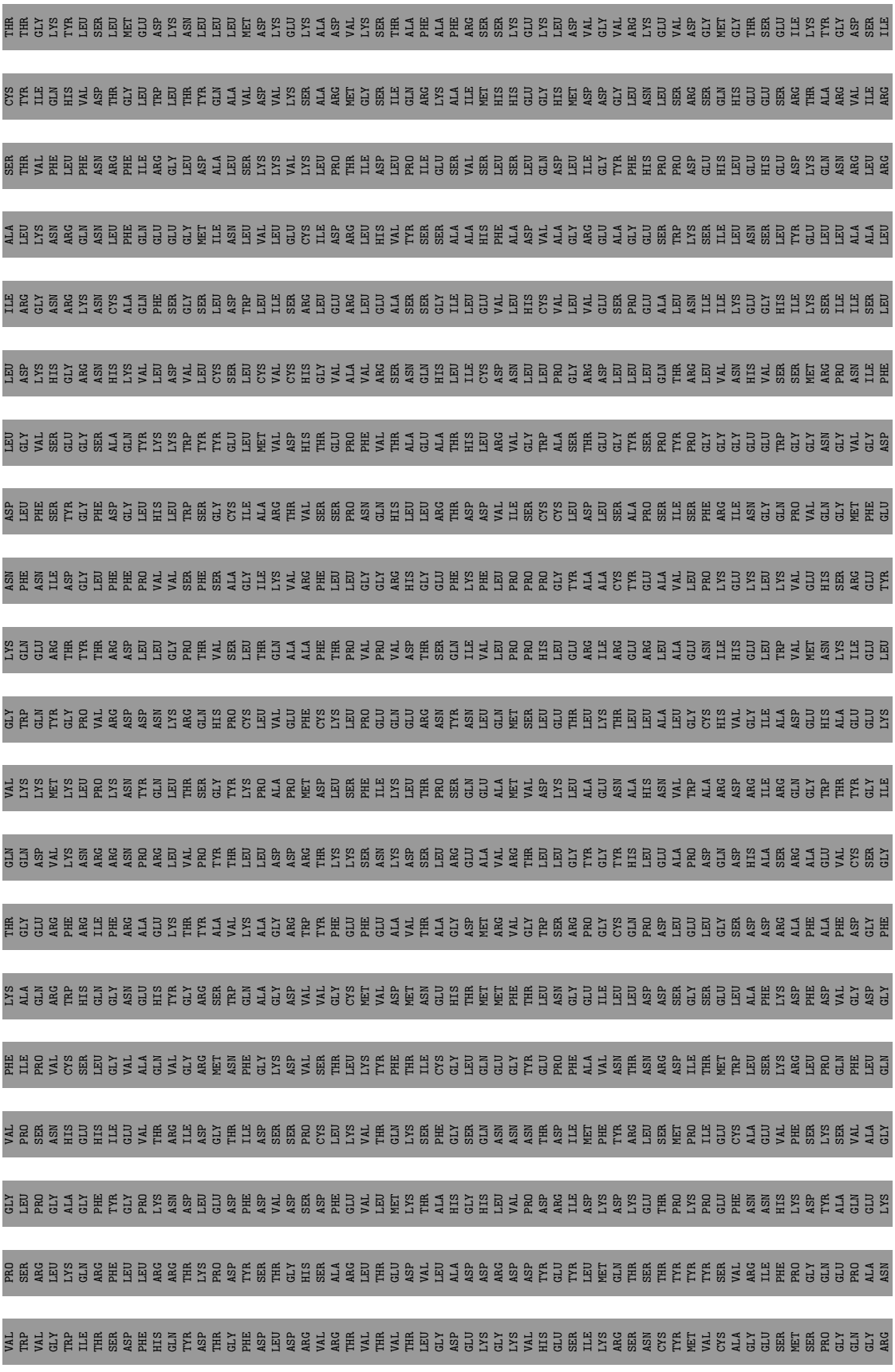

LYS ALA LYS ASP ARG GLU LYS ALA GLN ASP ILE PHE LYS PHE LEU GLN ILE SER GLY TYR VAL VAL SER ARG GLY PHE LYS ASP LEU ASP LEU ASP THR PRO SER ILE GLU LYS ARG PHE ALA TYR SER PHE LEU GLN GLN LEU ILE ARG TYR VAL ASP GLU ALA HIS GLN ILE
GLU PHE ASP GLY GLY SER ARG SER LYS GLY GLU HIS PHE PRO TYR GLU GLN GLU ILE LYS PHE PHE ALA LYS VAL VAL LEU PRO LEU ILE ASP GLN TYR PHE LYS ASN HIS ARG LEU TYR PHE LEU SER ALA ALA SER ARG PRO LEU CYS THR GLY GLY HIS ALA SER ASN LYS GLU LYS
GLU MET VAL THR SER LEU PHE CYS LYS LEU GLY VAL LEU VAL ARG HIS ARG ILE SER LEU PHE GLY ASN ASP ALA THR SER ILE VAL ASN CYS LEU HIS ILE LEU GLY GLN THR LEU ASP ALA ARG THR VAL MET LYS THR GLY LEU ASP SER VAL LYS SER ALA LEU ARG ALA PHE LEU
ASP ASN ALA ALA GLU ASP LEU GLU LYS THR MET GLU ASN LEU LYS GLN GLY GLN PHE THR HIS THR ARG SER GLN PRO LYS GLY VAL THR GLN ILE ILE ASN TYR THR THR VAL ALA LEU LEU PRO MET LEU SER SER LEU PHE GLU HIS ILE GLY GLN HIS GLN PHE GLY GLU ASP LEU
ILE LEU GLU ASP VAL GLN VAL SER CYS TYR ARG ILE LEU THR SER LEU TYR ALA LEU GLY THR SER LYS SER ILE TYR VAL GLU ARG GLN ARG SER ALA LEU GLU ILE ILE LEU GLY GLU CYS LEU ALA ALA LEU LEU PRO MET LEU SER ILE ALA PHE ALA GLY ALA PHE PRO ILE ALA PHE LEU GLU LEU THR HIS LEU ASP LYS HIS ASN VAL TYR
SER ILE TYR ASN THR ARG SER SER ARG GLU ARG ALA ALA LEU SER LEU PRO ALA ASN VAL GLU ASP VAL CYS PRO ASN ILE PRO SER LEU GLU LYS LEU MET THR GLU ILE ILE GLU LEU ALA ALA GLU SER GLY ILE ARG TYR THR GLN MET PRO TYR MET MET GLU VAL VAL LEU PRO MET
LEU CYS SER TYR MET SER ARG TRP TRP GLU HIS GLY PRO GLU ASN HIS PRO GLU ARG ALA GLU MET CYS CYS THR ALA LEU ASN SER GLU HIS MET ASN THR LEU LEU LEU GLY ASN ILE LEU LYS ILE ILE TYR ASN ASN LEU GLY ILE ASP GLU GLY ALA TRP MET LYS ARG LEU ALA VAL
PHE SER GLN PRO ILE ILE ASN LYS VAL LYS PRO GLN LEU LEU LYS THR HIS PHE LEU PRO LEU MET GLU LYS LEU LYS LYS LYS LYS ALA ALA MET VAL VAL SER GLU GLU GLU ASP HIS LEU LYS ALA GLU VAL PHE ILE ALA ARG GLY ASP MET SER GLU ALA ALA ILE LEU ASP PHE THR THR
LEU ALA ARG ASP LEU TYR ALA PHE TYR PRO LEU LEU LEU ILE ARG PHE VAL ASP TYR ASN ARG ALA ALA LYS TRP LEU LYS GLU GLU ALA ILE LEU ARG GLU ASP PRO GLU ALA GLU GLU GLU PHE ARG MET VAL ALA GLU VAL PHE ILE TYR TRP SER LYS SER HIS ASN PHE LYS ARG GLU GLU GLN ASN PHE VAL VAL
GLN ASN GLU ILE ASN ASN MET SER PHE LEU ILE THR ASP THR LYS SER LYS MET SER LYS ALA ALA ILE SER ASP GLN GLU ASP LYS LYS MET LYS ARG LYS GLY ASP ARG TYR SER MET GLN THR SER LEU ILE VAL ALA ALA LEU LYS ARG LEU LEU PRO ILE GLY LEU ASN ILE CYS
ALA PRO GLY ASP GLN GLU LEU ILE ALA LEU ALA LYS ASN ARG PHE SER LEU LYS ASP THR GLU GLU VAL ARG ASP ILE ILE ARG SER ASN ILE HIS LEU GLN LYS LYS LEU GLU VAL ASP PRO ALA ILE ARG TRP GLN MET ALA LEU LEU TYR LYS ASP PRO ILE ASN ARG THR GLU ASP PRO
SER ASP PRO GLU ARG ILE LEU GLU LYS TYR THR GLY ARG GLY TYR PHE SER LEU VAL GLU HIS PRO GLN ARG SER LYS LYS ALA VAL TRP HIS LYS LEU LEU LEU SER LYS GLN ARG LYS ARG ALA VAL VAL ALA
CYS PHE ARG MET A3605 P3606 L3607 Y3608 N3609 L3610 P3611 R3612 H3613 R3614 A3615 V3616 N3617 L3618 F3619 L3620 Q3621 G3622 Y3623 E3624 K3625 S3626 W3627 I3628 E3629 T3630 E3631 E3632 H3633 Y3634 F3635 E3636 D3637 K3638 E3641 D3642 K3645 P3646 G3647 A3648 E3649 L3650 P3651 E3652 E3653 D3654 E3655 A3656 M3657 K3658 R3659 V3660 D3661 P3662
L3663 H3664 Q3665 L3668 R3672 L3675 T3676 E3677 K3678 C3679 K3680 L3681 E3682 E3683 D3684 F3685 L3686 Y3687 M3688 D3692 H3699 D3700 E3701 E3702 D3703 D3704 D3705 G3706 E3707 E3708 E3709 V3710 K3711 S3712 F3713 E3714 E3715 K3716 E3717 M3718 E3719 Q3727 D3732 E3737 K3747 G3748 E3749 M3753 I3762
M3769 D3778 E3782 D3785 Q3790 C3799 D3803 L3804 N3805 E3808 R3809 Q3810 N3811 K3812 A3813 E3814 G3815 L3816 G3817 M3818 V3819 T3820 E3821 E3822 G3823 S3824 G3825 E3826 K3827 V3828 L3829 Q3830 D3831 D3832 D3837 D3852 F3853 Q3854 N3855 R3858 G3862 N3863 N3864 T3865 T3866 D3875
R3879 I3884 S3885 D3886 F3887 G3893 K3894 D3895 I3896 I3897 D3898 E3899 Q3900 G3901 Q3902 R3903 N3904 A3908 L3919 T3920 E3921 L3934 R3938 L3939 W3940 D3941 A3942 V3943 Q3954 M3955 K3956 L3957 S3958 Q3959 D3960 S3961 S3962 Q3963 I3964 M3971 Q3974 L3981 M3998 L4002 Y4003 E4004 E4010
K4014 F4015 F4016 D4017 M4018 F4019 L4020 K4021 L4022 K4023 D4024 L4025 T4026 S4027 S4028 D4029 T4030 F4031 K4032 E4033 Y4034 D4035 P4036 D4037 G4038 K4039 G4040 V4041 I4042 S4043 K4044 R4045 D4046 F4047 H4048 K4049 A4050 M4051 E4052 S4053 H4054 K4055 H4056 Y4057 T4058 Q4059 S4060 E4061 T4062 E4063 F4064 L4065 L4066 S4067 C4068 A4069 E4070 T4071 D4072

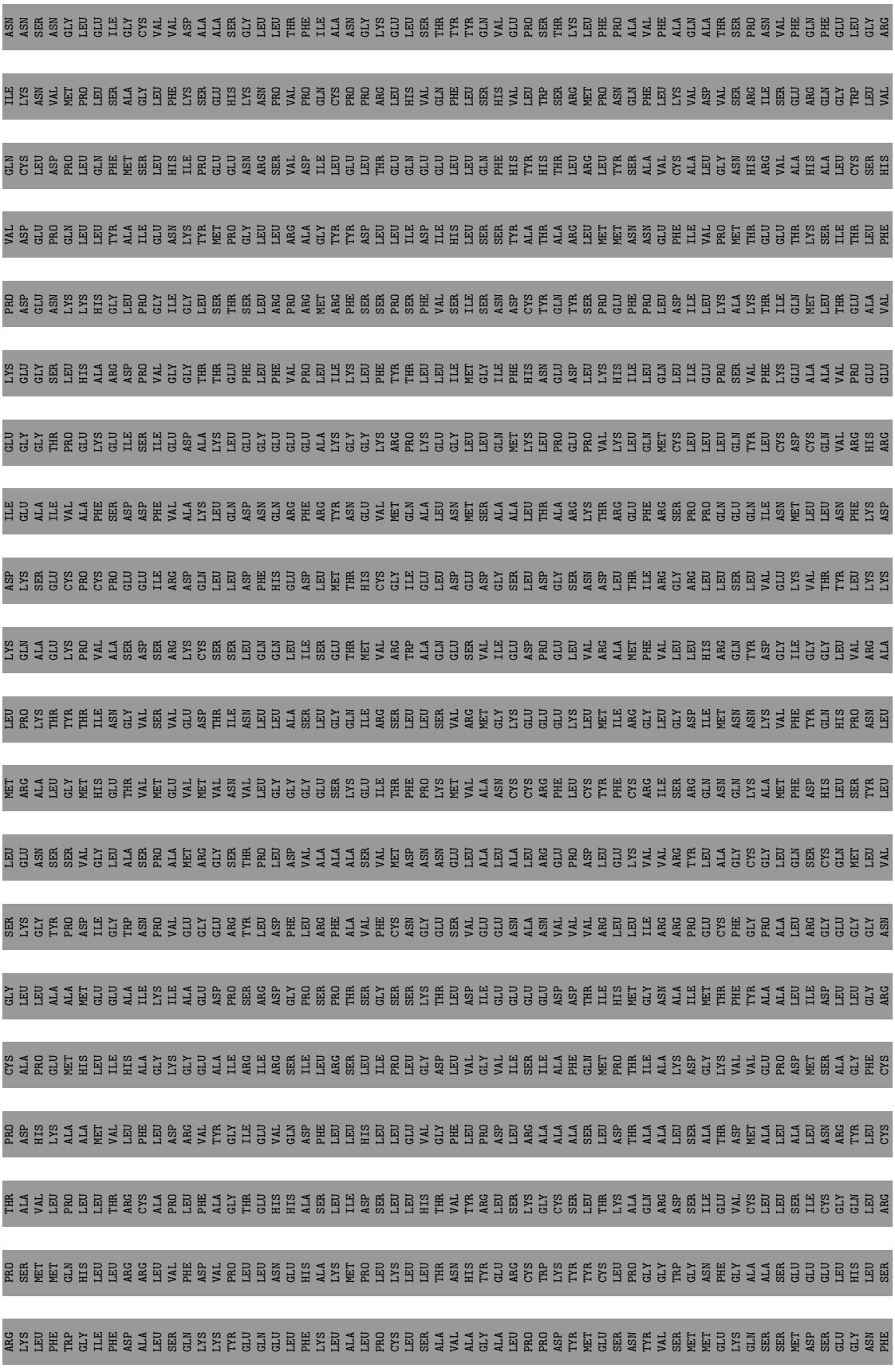


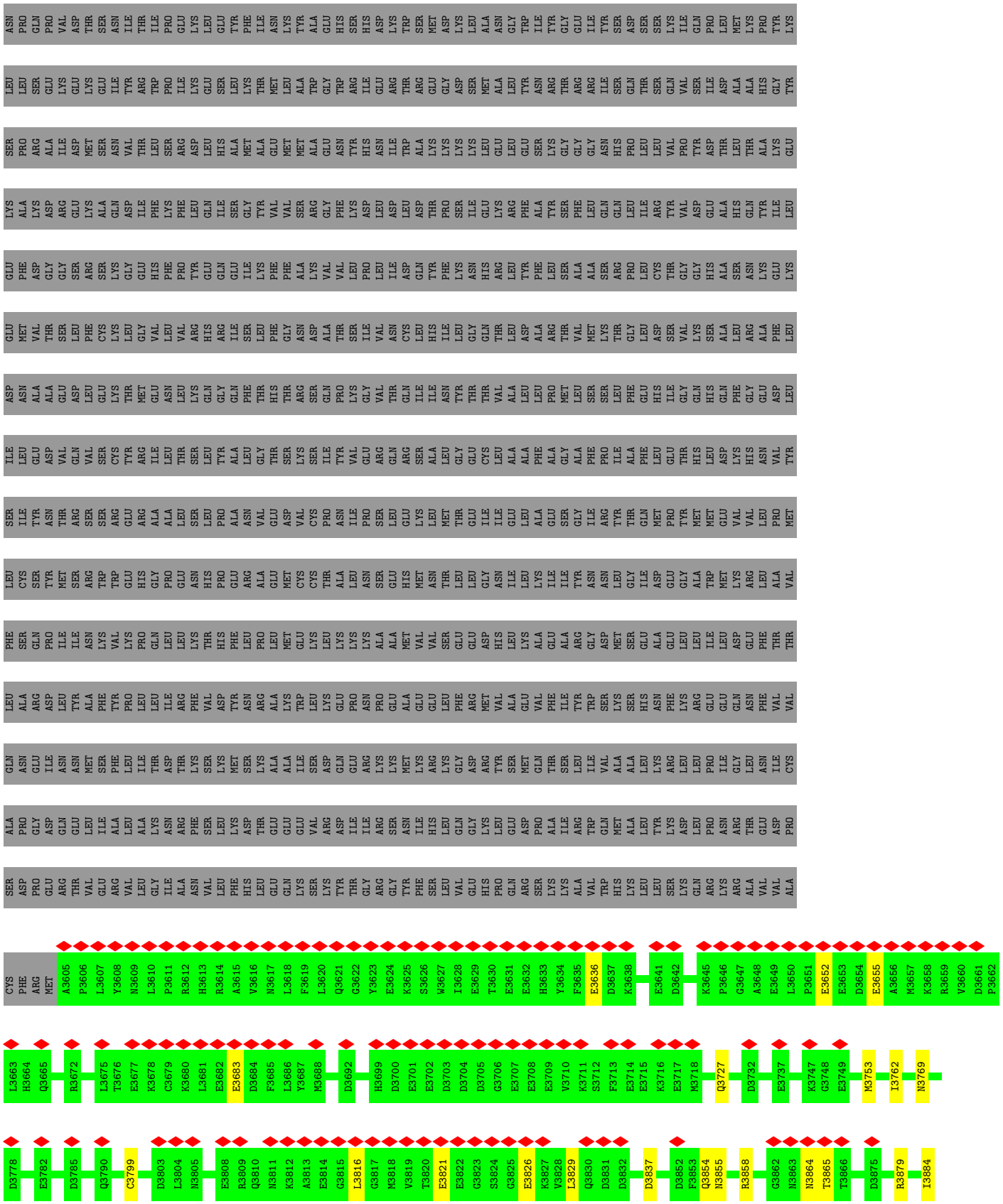
• Molecule 1: Ryanodine receptor 2

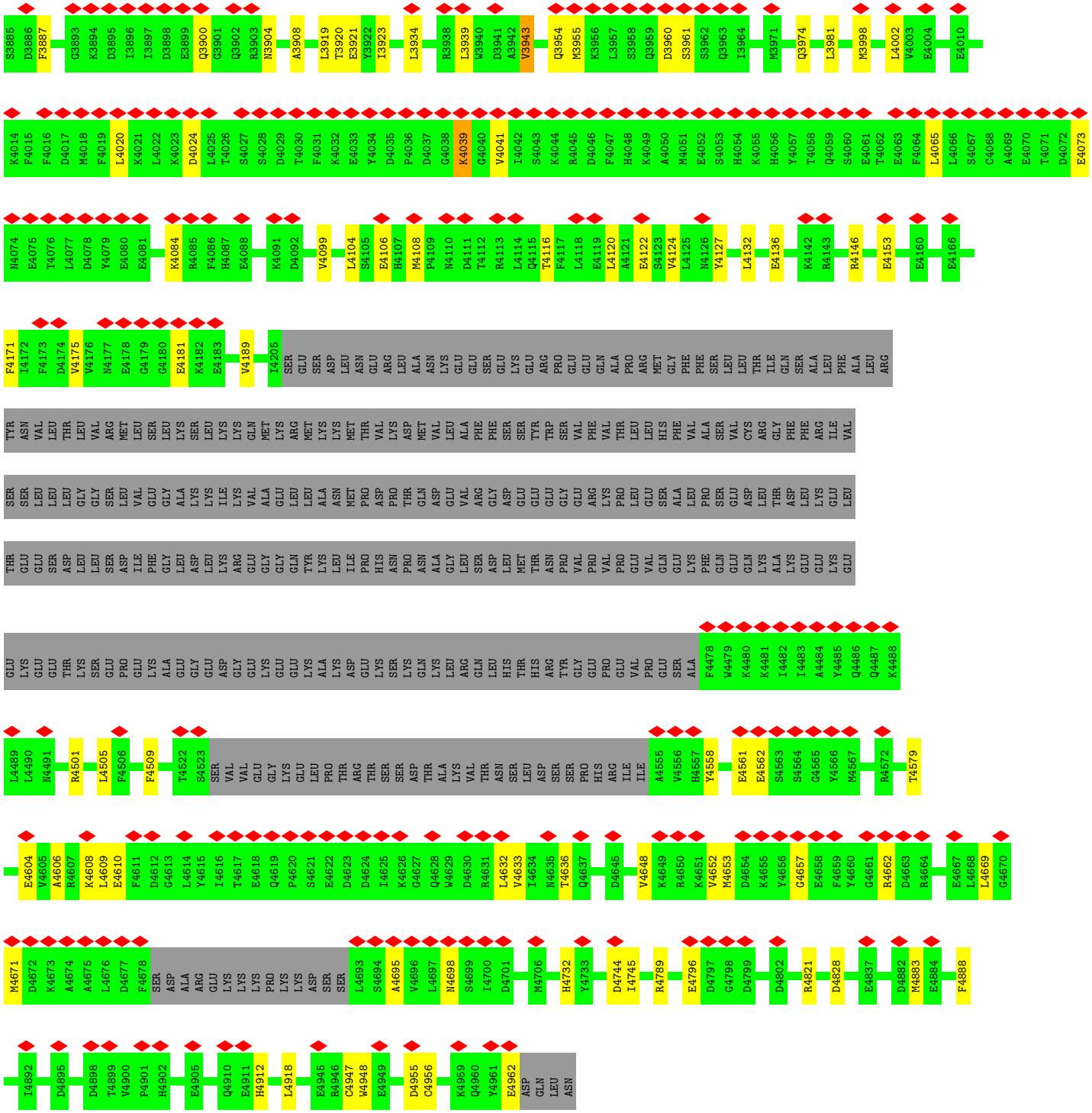







ASN ASN SER ASN GLY LEU GLU ILE GLY CYS VAL VAL ASP ALA ALA SER GLY LEU LEU THR PHE ILE ALA ASN GLY LYS GLU LEU SER THR TYR TYR GLN VAL GLU PRO SER THR LYS LEU PHE PRO ALA VAL PHE ALA GLN ALA THR SER PRO ASN VAL PHE GLN PHE GLU ARG
ILE LYS ASN VAL MET PRO LEU SER ALA GLY LEU PHE LYS SER GLU HIS LYS ASN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


ASN PRO GLN PRO VAL ASP THR SER ASN ILE THR ILE PRO GLU LYS LEU GLU TYR PHE ILE ASN LYS TYR ALA GLU HIS SER HIS ASP LYS TRP SER MET ASP LYS LEU ALA ASN GLY TRP ILE TYR GLY GLU ILE TYR SER ASP SER SER LYS ILE GLN PRO LEU MET LYS PRO TYR LYS
LEU LEU SER GLU LYS GLU LYS GLU ILE TYR ARG TRP PRO ILE LYS GLU SER LEU LYS THR MET LEU ALA TRP GLY TRP ARG ILE GLU ARG THR ARG GLU GLY ASP SER MET ALA LEU TYR ASN ARG THR ARG ARG ILE SER GLN THR SER GLN VAL SER ILE ASP ALA ALA HIS GLY TYR
SER PRO ARG ALA ILE ASP MET SER ASN VAL THR LEU SER ARG ASP LEU HIS ALA MET ALA ALA GLU MET MET ALA GLU ASN TYR HIS ASN ILE TRP ALA LYS LYS LYS LYS LEU GLU GLU LEU GLU SER LYS GLY GLY GLY ASN HIS PRO LEU LEU VAL PRO TYR ASP THR LEU THR ALA LYS GLU
LYS ALA LYS ASP ARG GLU LYS ALA GLN ASP ILE PHE LYS PHE LEU GLN ILE SER GLY TYR VAL VAL SER ARG GLY PHE LYS ASP LEU GLN ILE LEU ASP LEU ASP THR PRO SER ILE GLU LYS ARG PHE ALA TYR SER PHE LEU GLN GLN LEU ILE ARG TYR VAL ASP GLU ALA HIS GLN ILE LEU
GLU PHE ASP GLY GLY SER ARG SER LYS GLY GLU HIS PHE PRO TYR GLU GLN GLU ILE LYS PHE PHE ALA LYS VAL VAL LEU PRO LEU ILE ASP GLN TYR PHE LYS ASN HIS ARG LEU TYR PHE LEU SER SER ALA ALA SER ARG PRO LEU CYS THR GLY GLY GLY HIS ALA SER ASN LYS GLU GLU
GLU MET VAL THR SER LEU PHE CYS LYS LEU GLY VAL LEU ARG ILE SER LEU PHE GLY ASN ASP ALA THR SER ILE LEU VAL ASN CYS LEU HIS ILE LEU GLY GLN THR LEU ASP ALA ARG THR VAL MET LYS THR GLY LEU ASP SER VAL LYS GLN LEU SER ALA LEU ARG ALA PHE LEU
ASP ASN ALA ALA GLU ASP LEU GLU LYS THR MET GLU ASN LEU LYS GLN GLY GLN PHE THR HIS THR ARG SER GLN PRO LYS GLY VAL THR GLN ILE TYR VAL GLU ARG GLN ARG SER ALA ILE ILE ASN TYR THR GLN ILE LEU GLU HIS ILE GLY GLN HIS ILE LEU ASP ALA PHE PRO ILE
ILE LEU GLU ASP VAL GLN VAL SER CYS TYR ARG ILE LEU THR SER LEU TYR ALA LEU GLY THR SER LYS SER ILE TYR VAL GLU ARG GLN ARG SER ALA LEU GLY GLU CYS LEU ALA ALA PHE PRO ILE ALA PHE LEU GLU HIS ILE GLY GLN HIS LEU ASP LYS HIS ASN VAL TYR
SER ILE TYR ASN THR ARG SER SER ARG GLU ARG ALA ALA LEU SER LEU PRO ALA ASN VAL GLU ASP VAL CYS PRO ASN ILE PRO SER LEU GLU LYS LEU MET THR GLU ILE ILE GLU LEU ALA GLU SER GLY ILE ARG TYR THR GLN MET PRO TYR MET MET GLU VAL VAL LEU PRO MET
LEU CYS SER TYR MET SER ARG TRP TRP GLU HIS GLY PRO GLU ASN HIS PRO GLU ARG ALA GLU MET CYS CYS THR ALA LEU ASN SER GLU HIS MET ASN THR LEU LEU GLY ASN ILE LEU LYS ILE ILE TYR ASN ASN LEU GLY ILE ASP GLU GLY ALA TRP MET LYS ARG LEU ALA VAL
PHE SER GLN PRO ILE ILE ASN LYS VAL LYS PRO GLN LEU LEU LYS THR HIS PHE LEU PRO LEU MET GLU GLU LYS LEU LYS LYS LYS ALA ALA MET VAL VAL SER GLU GLU GLU ASP HIS LEU LYS ALA GLU ILE LEU ASP GLU PHE THR THR
LEU ALA ARG ASP LEU ILE ARG PHE VAL ASP TYR ASN ARG ALA ALA LYS TRP LEU LYS GLU GLU PRO ASN PRO GLU ALA GLU LEU ARG PHE TYR TRP SER LYS SER HIS ASN PHE LYS ARG GLU GLU LEU VAL VAL
GLN ASN GLU ILE ASN ASN MET SER PHE LEU ILE THR ASP THR LYS SER LYS MET SER LYS ALA ALA ILE SER ASP GLN GLU ARG LYS ALA LYS MET ILE LYS ARG LYS GLY ASP ARG TYR SER MET GLN THR SER LEU ILE VAL ALA LEU LYS PRO ILE GLY LEU ASN ILE CYS
ALA PRO GLY ASP GLN GLU LEU ILE ALA LEU ALA LYS ALA LYS LEU GLU GLU VAL ARG ASP ILE ILE ARG SER ASN ILE HIS LEU GLN GLY LYS LEU GLU ASP PRO ALA ILE ARG TRP GLN MET ALA LEU TYR LYS ASP LEU PRO LEU ASN ARG ASP PHE ASN ILE ASP ARG ASP ARG ASP ASP
SER ASP PRO GLU ARG LEU PHE LYS ASP THR GLU GLU VAL ARG ASP ILE ARG GLY ARG TYR PHE SER LEU VAL GLU HIS PRO GLN ARG SER LYS LYS ALA VAL TRP HIS LYS LEU LEU SER LYS GLN ARG LYS ARG ALA VAL VAL ALA
CYS PHE ARG MET A3605 P3606 L3607 Y3608 N3609 L3610 P3611 R3612 H3613 R3614 A3615 V3616 N3617 L3618 F3619 L3620 Q3621 G3622 Y3623 E3624 K3625 S3626 W3627 I3628 E3629 T3630 E3631 E3632 H3633 Y3634 F3635 E3636 D3637 K3638 E3641 D3642 K3645 P3646 G3647 A3648 E3649 L3650 P3651 E3652 E3653 D3654 E3655 A3656 M3657 K3658 R3659 V3660 D3661 P3662
L3663 H3664 Q3665 R3672 L3675 T3676 E3677 K3678 C3679 K3680 L3681 E3682 E3683 D3684 F3685 L3686 Y3687 M3688 D3692 H3699 D3700 E3701 E3702 D3703 D3704 D3705 G3706 E3707 E3708 E3709 V3710 K3711 S3712 F3713 E3714 E3715 K3716 E3717 M3718 Q3727 D3732 E3737 K3747 G3748 E3749 M3753 I3762 N3769
D3778 E3782 D3785 Q3790 C3799 D3803 L3804 N3805 E3808 R3809 Q3810 N3811 K3812 A3813 E3814 G3815 L3816 G3817 M3818 V3819 T3820 E3821 E3822 G3823 S3824 G3825 E3826 K3827 V3828 L3829 Q3830 D3831 D3832 D3837 D3852 F3853 Q3854 N3855 R3858 G3862 N3863 N3864 T3865 T3866 D3875 R3879 I3884


S3885 D3886 F3887 G3893 K3894 D3895 I3896 I3897 D3898 E3899 Q3900 G3901 Q3902 R3903 N3904 A3908 L3919 T3920 E3921 Y3922 I3923 L3934 R3938 L3939 W3940 D3941 A3942 V3943 Q3954 M3955 K3956 L3957 S3958 Q3959 D3960 S3961 S3962 Q3963 I3964 M3971 Q3974 L3981 M3998 L4002 V4003 E4004 E4010
K4014 F4015 F4016 D4017 M4018 F4019 L4020 K4021 L4022 K4023 D4024 L4025 T4026 S4027 S4028 D4029 T4030 F4031 K4032 E4033 Y4034 D4035 P4036 D4037 G4038 K4039 G4040 V4041 I4042 S4043 K4044 R4045 D4046 F4047 H4048 K4049 A4050 M4051 E4052 S4053 H4054 K4055 H4056 Y4057 T4058 Q4059 S4060 E4061 T4062 E4063 F4064 L4065 L4066 S4067 C4068 A4069 E4070 T4071 D4072 E4073
N4074 E4075 T4076 L4077 D4078 Y4079 E4080 E4081 K4084 R4085 F4086 H4087 E4088 K4091 D4092 V4099 L4104 S4105 E4106 H4107 M4108 P4109 N4110 D4111 T4112 R4113 L4114 Q4115 T4116 F4117 L4118 E4119 L4120 A4121 E4122 S4123 V4124 L4125 N4126 Y4127 L4132 E4136 K4142 R4143 R4146 E4153 E4160 E4166
F4171 I4172 F4173 D4174 V4175 V4176 N4177 E4178 G4179 G4180 E4181 K4182 E4183 V4189 I4205 SER GLU SER ASP LEU ASN GLU ARG LEU ALA ASN LYS GLU GLU SER GLU LYS GLU ARG PRO GLU GLU GLN ALA PRO ARG MET GLY PHE PHE SER LEU LEU THR ILE GLN SER ALA LEU PHE ALA LEU ARG
TYR ASN VAL LEU THR LEU VAL ARG MET LEU SER LEU LYS SER LEU LYS LYS GLN MET LYS ARG MET LYS LYS MET THR VAL LYS ASP MET VAL LEU ALA PHE PHE SER GLU LYS GLU SER TYR TRP SER VAL PHE VAL THR LEU HIS PHE VAL ALA SER VAL CYS ARG GLY PHE PHE ARG ILE VAL
SER SER LEU LEU LEU GLY GLY SER LEU VAL GLU GLY ALA LYS LYS ILE LYS VAL ALA GLU LEU LEU ALA ASN MET PRO ASP PRO THR GLN ASP GLU VAL ARG GLY ASP GLU GLU GLU GLY GLU ARG LYS PRO LEU GLU SER ALA LEU PRO SER GLU ASP LEU THR ASP LEU LYS GLU LEU
THR GLU GLU SER ASP LEU LEU SER ASP ILE PHE GLY LEU ASP LEU LYS ARG GLU GLY GLN TYR LYS LEU ILE PRO HIS ASN PRO ASN ALA GLY LEU SER ASP LEU MET THR ASN PRO VAL PRO VAL PRO GLU VAL GLN GLU LYS PHE GLN GLU GLN LYS ALA LYS GLU GLU LYS GLU
GLU LYS GLU GLU THR LYS SER GLU PRO GLU LYS ALA GLU GLY GLU ASP GLY GLU LYS GLU GLU LYS ALA LYS ASP GLU LYS SER LYS GLN LYS LEU ARG GLN LEU HIS THR HIS ARG TYR GLY GLU PRO GLU VAL PRO GLU SER ALA F4478 W4479 K4480 K4481 I4482 I4483 A4484 Y4485 Q4486 Q4487 K4488
L4489 L4490 N4491 R4501 L4505 F4506 F4509 T4522 S4523 SER VAL VAL GLU GLU GLY LYS GLU LEU PRO THR ARG THR SER SER ASP THR ALA LYS VAL THR ASN SER LEU ASP SER SER PRO HIS ARG ILE ILE A4555 V4556 H4557 Y4558 E4561 E4562 S4563 S4564 G4565 Y4566 M4567 R4572 T4579
E4604 V4605 A4606 R4607 K4608 L4609 E4610 F4611 D4612 G4613 L4614 Y4615 I4616 T4617 E4618 Q4619 P4620 S4621 E4622 D4623 D4624 I4625 K4626 G4627 Q4628 W4629 D4630 R4631 L4632 V4633 I4634 N4635 T4636 Q4637 D4645 V4648 K4649 R4650 K4651 V4652 M4653 D4654 K4655 Y4656 G4657 E4658 F4659 Y4660 G4661 R4662 D4663 R4664 E4667 L4668 L4669 G4670
M4671 D4672 K4673 A4674 A4675 L4676 D4677 F4678 SER ASP ALA ARG GLU LYS LYS LYS PRO LYS LYS ASP SER SER L4693 S4694 A4695 V4696 L4697 N4698 S4699 I4700 D4701 M4706 H4732 Y4733 D4744 I4745 R4789 E4796 D4797 G4798 D4799 D4802 R4821 D4828 E4837 D4882 M4883 E4884 F4888
I4892 D4895 D4898 T4899 V4900 P4901 H4902 E4905 Q4910 E4911 H4912 L4918 E4945 R4946 C4947 W4948 E4949 D4955 C4956 K4959 Q4960 Y4961 E4962 ASP GLN LEU ASN

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	256984	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	20000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.260	Depositor
Minimum map value	-0.104	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	469.504, 469.504, 469.504	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.917, 0.917, 0.917	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, CA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.16	0/8686	0.30	0/11709
1	B	0.16	0/8686	0.30	0/11709
1	C	0.16	0/8686	0.30	0/11709
1	D	0.16	0/8686	0.30	0/11709
All	All	0.16	0/34744	0.30	0/46836

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8502	8299	8299	57	0
1	B	8502	8299	8299	61	0
1	C	8502	8299	8299	62	0
1	D	8502	8299	8299	60	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	34016	33196	33196	232	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 3.

All (232) 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:C:3934:LEU:HD12	1:C:3939:LEU:HD22	1.44	0.97
1:B:3934:LEU:HD12	1:B:3939:LEU:HD22	1.44	0.96
1:A:3934:LEU:HD12	1:A:3939:LEU:HD22	1.44	0.96
1:D:3934:LEU:HD12	1:D:3939:LEU:HD22	1.44	0.95
1:A:4695:ALA:O	1:A:4698:ASN:ND2	2.28	0.67
1:C:4695:ALA:O	1:C:4698:ASN:ND2	2.27	0.67
1:C:4633:VAL:O	1:C:4636:THR:OG1	2.10	0.67
1:A:4633:VAL:O	1:A:4636:THR:OG1	2.10	0.66
1:D:4695:ALA:O	1:D:4698:ASN:ND2	2.28	0.66
1:B:4695:ALA:O	1:B:4698:ASN:ND2	2.27	0.66
1:C:3954:GLN:NE2	1:C:3974:GLN:OE1	2.29	0.66
1:B:4017:ASP:OD1	1:B:4123:SER:OG	2.11	0.66
1:A:3954:GLN:NE2	1:A:3974:GLN:OE1	2.29	0.65
1:C:4017:ASP:OD1	1:C:4123:SER:OG	2.11	0.65
1:D:3954:GLN:NE2	1:D:3974:GLN:OE1	2.29	0.65
1:B:3954:GLN:NE2	1:B:3974:GLN:OE1	2.29	0.65
1:A:4122:GLU:N	1:A:4122:GLU:OE1	2.31	0.64
1:D:4122:GLU:OE1	1:D:4122:GLU:N	2.31	0.64
1:D:4579:THR:OG1	1:D:4732:HIS:NE2	2.29	0.63
1:A:4558:TYR:OH	1:D:4789:ARG:NH1	2.32	0.63
1:B:4122:GLU:OE1	1:B:4122:GLU:N	2.31	0.63
1:B:3891:TYR:OH	1:B:3898:ASP:OD1	2.11	0.62
1:C:4122:GLU:N	1:C:4122:GLU:OE1	2.31	0.62
1:D:4633:VAL:O	1:D:4636:THR:OG1	2.15	0.61
1:B:4633:VAL:O	1:B:4636:THR:OG1	2.15	0.60
1:B:3799:CYS:O	1:B:3879:ARG:NH2	2.36	0.58
1:C:4604:GLU:OE2	1:C:4608:LYS:NZ	2.36	0.58
1:A:3799:CYS:O	1:A:3879:ARG:NH2	2.36	0.58
1:A:3891:TYR:OH	1:A:3898:ASP:OD1	2.11	0.58
1:D:4604:GLU:OE2	1:D:4608:LYS:NZ	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3799:CYS:O	1:C:3879:ARG:NH2	2.36	0.58
1:C:4962:GLU:N	1:C:4962:GLU:OE1	2.37	0.58
1:A:4604:GLU:OE2	1:A:4608:LYS:NZ	2.36	0.58
1:B:4962:GLU:N	1:B:4962:GLU:OE1	2.37	0.58
1:D:3799:CYS:O	1:D:3879:ARG:NH2	2.37	0.57
1:A:4962:GLU:OE1	1:A:4962:GLU:N	2.37	0.57
1:C:4579:THR:OG1	1:C:4732:HIS:NE2	2.30	0.57
1:D:4962:GLU:OE1	1:D:4962:GLU:N	2.37	0.57
1:C:4106:GLU:OE1	1:C:4146:ARG:NH1	2.38	0.56
1:D:4106:GLU:OE1	1:D:4146:ARG:NH1	2.38	0.56
1:D:4562:GLU:OE1	1:D:4562:GLU:N	2.39	0.56
1:A:4106:GLU:OE1	1:A:4146:ARG:NH1	2.39	0.56
1:A:4562:GLU:OE1	1:A:4562:GLU:N	2.39	0.56
1:C:4562:GLU:N	1:C:4562:GLU:OE1	2.39	0.56
1:B:4106:GLU:OE1	1:B:4146:ARG:NH1	2.38	0.56
1:B:4562:GLU:N	1:B:4562:GLU:OE1	2.39	0.56
1:C:3855:ASN:OD1	1:C:3858:ARG:NH2	2.39	0.55
1:B:3855:ASN:OD1	1:B:3858:ARG:NH2	2.39	0.55
1:B:4653:MET:SD	1:B:4662:ARG:NH1	2.80	0.55
1:D:3855:ASN:OD1	1:D:3858:ARG:NH2	2.39	0.54
1:D:4653:MET:SD	1:D:4662:ARG:NH1	2.81	0.54
1:A:4653:MET:SD	1:A:4662:ARG:NH1	2.81	0.54
1:A:4153:GLU:N	1:A:4153:GLU:OE1	2.42	0.53
1:C:4153:GLU:OE1	1:C:4153:GLU:N	2.42	0.53
1:C:4653:MET:SD	1:C:4662:ARG:NH1	2.81	0.53
1:A:3919:LEU:HD22	1:A:3934:LEU:HD11	1.91	0.53
1:A:4104:LEU:O	1:A:4108:MET:N	2.42	0.53
1:B:4153:GLU:OE1	1:B:4153:GLU:N	2.42	0.52
1:A:3855:ASN:OD1	1:A:3858:ARG:NH2	2.39	0.52
1:C:3919:LEU:HD22	1:C:3934:LEU:HD11	1.91	0.52
1:C:4020:LEU:HD22	1:C:4127:TYR:CE2	2.45	0.52
1:D:4104:LEU:O	1:D:4108:MET:N	2.43	0.52
1:A:4501:ARG:NH2	1:A:4744:ASP:OD1	2.42	0.52
1:C:4181:GLU:N	1:C:4181:GLU:OE1	2.42	0.52
1:B:4104:LEU:O	1:B:4108:MET:N	2.42	0.52
1:B:3919:LEU:HD22	1:B:3934:LEU:HD11	1.92	0.52
1:D:4020:LEU:HD22	1:D:4127:TYR:CE2	2.45	0.52
1:D:4153:GLU:N	1:D:4153:GLU:OE1	2.42	0.52
1:D:4181:GLU:OE1	1:D:4181:GLU:N	2.42	0.52
1:B:4181:GLU:N	1:B:4181:GLU:OE1	2.42	0.52
1:C:4104:LEU:O	1:C:4108:MET:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4606:ALA:HB1	1:C:4648:VAL:HG21	1.91	0.52
1:A:4606:ALA:HB1	1:A:4648:VAL:HG21	1.92	0.51
1:B:3821:GLU:N	1:B:3821:GLU:OE1	2.43	0.51
1:C:3821:GLU:N	1:C:3821:GLU:OE1	2.43	0.51
1:A:3821:GLU:OE1	1:A:3821:GLU:N	2.43	0.51
1:C:4501:ARG:NH2	1:C:4744:ASP:OD1	2.42	0.51
1:D:3981:LEU:HD22	1:D:3998:MET:SD	2.50	0.51
1:A:4181:GLU:OE1	1:A:4181:GLU:N	2.42	0.51
1:D:3919:LEU:HD22	1:D:3934:LEU:HD11	1.90	0.51
1:C:3981:LEU:HD22	1:C:3998:MET:SD	2.51	0.51
1:B:4501:ARG:NH2	1:B:4744:ASP:OD1	2.42	0.51
1:C:4955:ASP:OD1	1:C:4956:CYS:N	2.43	0.51
1:D:4955:ASP:OD1	1:D:4956:CYS:N	2.43	0.51
1:A:3981:LEU:HD22	1:A:3998:MET:SD	2.51	0.51
1:D:4653:MET:O	1:D:4657:GLY:N	2.44	0.51
1:B:4020:LEU:HD22	1:B:4127:TYR:CE2	2.46	0.51
1:D:3821:GLU:OE1	1:D:3821:GLU:N	2.44	0.51
1:B:3981:LEU:HD22	1:B:3998:MET:SD	2.51	0.50
1:D:4606:ALA:HB1	1:D:4648:VAL:HG21	1.91	0.50
1:A:4020:LEU:HD22	1:A:4127:TYR:CE2	2.46	0.50
1:A:3900:GLN:O	1:A:3904:ASN:ND2	2.44	0.50
1:B:4955:ASP:OD1	1:B:4956:CYS:N	2.43	0.50
1:C:3900:GLN:O	1:C:3904:ASN:ND2	2.45	0.50
1:D:4501:ARG:NH2	1:D:4744:ASP:OD1	2.43	0.50
1:B:3900:GLN:O	1:B:3904:ASN:ND2	2.44	0.50
1:D:4505:LEU:HD11	1:D:4745:ILE:CG2	2.42	0.50
1:C:4653:MET:O	1:C:4657:GLY:N	2.44	0.50
1:D:4669:LEU:HD12	1:D:4671:MET:HE2	1.94	0.50
1:B:4669:LEU:HD12	1:B:4671:MET:HE2	1.93	0.49
1:D:3655:GLU:N	1:D:3655:GLU:OE1	2.45	0.49
1:D:3900:GLN:O	1:D:3904:ASN:ND2	2.45	0.49
1:C:3655:GLU:N	1:C:3655:GLU:OE1	2.45	0.49
1:A:3762:ILE:HD11	1:A:3837:ASP:O	2.13	0.49
1:A:4669:LEU:HD12	1:A:4671:MET:HE2	1.94	0.49
1:A:4821:ARG:NH1	1:D:4828:ASP:OD1	2.46	0.49
1:B:3727:GLN:OE1	1:B:3769:ASN:ND2	2.45	0.49
1:D:3864:ASN:OD1	1:D:3865:THR:N	2.46	0.49
1:A:4653:MET:O	1:A:4657:GLY:N	2.45	0.49
1:A:4955:ASP:OD1	1:A:4956:CYS:N	2.43	0.48
1:B:3655:GLU:OE1	1:B:3655:GLU:N	2.45	0.48
1:C:3864:ASN:OD1	1:C:3865:THR:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3727:GLN:OE1	1:C:3769:ASN:ND2	2.45	0.48
1:B:3762:ILE:HD11	1:B:3837:ASP:O	2.13	0.48
1:A:3655:GLU:N	1:A:3655:GLU:OE1	2.45	0.48
1:B:4606:ALA:HB1	1:B:4648:VAL:HG21	1.94	0.48
1:C:3762:ILE:HD11	1:C:3837:ASP:O	2.13	0.48
1:C:4669:LEU:HD12	1:C:4671:MET:HE2	1.96	0.48
1:C:4828:ASP:OD1	1:D:4821:ARG:NH1	2.46	0.48
1:D:3762:ILE:HD11	1:D:3837:ASP:O	2.13	0.48
1:B:3864:ASN:OD1	1:B:3865:THR:N	2.46	0.48
1:B:4020:LEU:HD22	1:B:4127:TYR:CD2	2.48	0.48
1:A:3652:GLU:N	1:A:3652:GLU:OE1	2.47	0.48
1:B:4653:MET:O	1:B:4657:GLY:N	2.46	0.48
1:A:3864:ASN:OD1	1:A:3865:THR:N	2.46	0.48
1:B:4883:MET:HE1	1:B:4888:PHE:HD1	1.79	0.48
1:B:3652:GLU:N	1:B:3652:GLU:OE1	2.47	0.48
1:C:3652:GLU:OE1	1:C:3652:GLU:N	2.47	0.48
1:C:4020:LEU:HD22	1:C:4127:TYR:CD2	2.49	0.47
1:D:3652:GLU:N	1:D:3652:GLU:OE1	2.47	0.47
1:A:4828:ASP:OD1	1:B:4821:ARG:NH1	2.46	0.47
1:D:4883:MET:HE1	1:D:4888:PHE:HD1	1.79	0.47
1:B:4505:LEU:HD11	1:B:4745:ILE:CG2	2.44	0.47
1:D:4020:LEU:HD22	1:D:4127:TYR:CD2	2.49	0.47
1:A:4020:LEU:HD22	1:A:4127:TYR:CD2	2.48	0.47
1:A:3727:GLN:OE1	1:A:3769:ASN:ND2	2.45	0.47
1:A:3826:GLU:OE1	1:A:3826:GLU:N	2.47	0.47
1:A:4883:MET:HE1	1:A:4888:PHE:HD1	1.80	0.47
1:C:4136:GLU:OE1	1:C:4912:HIS:NE2	2.47	0.47
1:D:3727:GLN:OE1	1:D:3769:ASN:ND2	2.45	0.47
1:B:4136:GLU:OE1	1:B:4912:HIS:NE2	2.47	0.46
1:B:4171:PHE:CE1	1:B:4175:VAL:HG11	2.51	0.46
1:B:3854:GLN:NE2	1:B:3921:GLU:O	2.49	0.46
1:B:4073:GLU:OE1	1:B:4073:GLU:N	2.46	0.46
1:B:4828:ASP:OD1	1:C:4821:ARG:NH1	2.46	0.46
1:C:4883:MET:HE1	1:C:4888:PHE:HD1	1.80	0.46
1:B:4610:GLU:HA	1:B:4652:VAL:HG12	1.98	0.46
1:D:4171:PHE:CE1	1:D:4175:VAL:HG11	2.51	0.46
1:A:4610:GLU:HA	1:A:4652:VAL:HG12	1.98	0.46
1:A:4171:PHE:CE1	1:A:4175:VAL:HG11	2.51	0.46
1:B:3826:GLU:OE1	1:B:3826:GLU:N	2.49	0.46
1:C:4171:PHE:CE1	1:C:4175:VAL:HG11	2.51	0.46
1:A:4073:GLU:OE1	1:A:4073:GLU:N	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4505:LEU:HD11	1:C:4745:ILE:CG2	2.47	0.45
1:B:4099:VAL:HG22	1:B:4132:LEU:HD23	1.99	0.45
1:D:4610:GLU:HA	1:D:4652:VAL:HG12	1.98	0.45
1:A:4099:VAL:HG22	1:A:4132:LEU:HD23	1.99	0.45
1:C:4610:GLU:HA	1:C:4652:VAL:HG12	1.98	0.45
1:D:4099:VAL:HG22	1:D:4132:LEU:HD23	1.99	0.45
1:A:3636:GLU:OE1	1:A:3636:GLU:N	2.48	0.45
1:A:4505:LEU:HD11	1:A:4745:ILE:CG2	2.46	0.45
1:C:4073:GLU:OE1	1:C:4073:GLU:N	2.46	0.45
1:C:4099:VAL:HG22	1:C:4132:LEU:HD23	1.99	0.45
1:D:4136:GLU:OE1	1:D:4912:HIS:NE2	2.47	0.45
1:A:4789:ARG:NH1	1:B:4558:TYR:OH	2.51	0.44
1:D:4073:GLU:OE1	1:D:4073:GLU:N	2.46	0.44
1:C:3884:ILE:HD11	1:C:3908:ALA:CB	2.48	0.44
1:A:4136:GLU:OE1	1:A:4912:HIS:NE2	2.47	0.44
1:C:3884:ILE:HD11	1:C:3908:ALA:HB1	2.00	0.44
1:D:3636:GLU:OE1	1:D:3636:GLU:N	2.48	0.44
1:D:3884:ILE:HD11	1:D:3908:ALA:CB	2.48	0.44
1:D:4039:LYS:HG2	1:D:4041:VAL:HG12	2.00	0.44
1:A:4039:LYS:HG2	1:A:4041:VAL:HG12	2.00	0.43
1:B:3884:ILE:HD11	1:B:3908:ALA:CB	2.48	0.43
1:C:3826:GLU:OE1	1:C:3826:GLU:N	2.49	0.43
1:A:3884:ILE:HD11	1:A:3908:ALA:HB1	1.99	0.43
1:D:3826:GLU:OE1	1:D:3826:GLU:N	2.48	0.43
1:B:3884:ILE:HD11	1:B:3908:ALA:HB1	2.00	0.43
1:A:3943:VAL:HG21	1:A:3981:LEU:HD21	2.00	0.43
1:B:4039:LYS:HG2	1:B:4041:VAL:HG12	2.00	0.43
1:C:3854:GLN:NE2	1:C:3921:GLU:O	2.49	0.43
1:B:4020:LEU:HD12	1:B:4124:VAL:HG22	2.01	0.43
1:C:4039:LYS:HG2	1:C:4041:VAL:HG12	2.00	0.43
1:C:4789:ARG:NH1	1:D:4558:TYR:OH	2.51	0.43
1:D:3884:ILE:HD11	1:D:3908:ALA:HB1	2.00	0.43
1:B:4789:ARG:NH1	1:C:4558:TYR:OH	2.51	0.43
1:A:3854:GLN:NE2	1:A:3921:GLU:O	2.49	0.42
1:A:3884:ILE:HD11	1:A:3908:ALA:CB	2.48	0.42
1:B:4186:GLU:OE1	1:B:4948:TRP:NE1	2.51	0.42
1:D:3943:VAL:HG21	1:D:3981:LEU:HD21	2.00	0.42
1:B:3943:VAL:HG21	1:B:3981:LEU:HD21	2.00	0.42
1:B:3960:ASP:OD1	1:B:3961:SER:N	2.52	0.42
1:D:4505:LEU:HD11	1:D:4745:ILE:HG23	2.00	0.42
1:C:3711:LYS:NZ	1:C:3719:GLU:OE2	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3960:ASP:OD1	1:A:3961:SER:N	2.52	0.42
1:C:3960:ASP:OD1	1:C:3961:SER:N	2.53	0.42
1:A:4020:LEU:HD12	1:A:4124:VAL:HG22	2.01	0.42
1:A:4189:VAL:HG11	1:A:4948:TRP:CH2	2.55	0.41
1:C:3943:VAL:HG21	1:C:3981:LEU:HD21	2.01	0.41
1:D:3960:ASP:OD1	1:D:3961:SER:N	2.53	0.41
1:A:4883:MET:HE2	1:A:4883:MET:HA	2.02	0.41
1:B:4189:VAL:HG11	1:B:4948:TRP:CH2	2.55	0.41
1:D:4189:VAL:HG11	1:D:4948:TRP:CH2	2.55	0.41
1:C:4883:MET:HA	1:C:4883:MET:HE2	2.03	0.41
1:C:3636:GLU:OE1	1:C:3636:GLU:N	2.48	0.41
1:C:4189:VAL:HG11	1:C:4948:TRP:CH2	2.55	0.41
1:D:4796:GLU:OE1	1:D:4796:GLU:N	2.54	0.41
1:C:4051:MET:HE1	1:C:4062:THR:HA	2.03	0.41
1:D:4116:THR:O	1:D:4120:LEU:HD23	2.21	0.41
1:A:4025:LEU:HD22	1:A:4057:TYR:CE2	2.56	0.41
1:A:4099:VAL:HG22	1:A:4132:LEU:CD2	2.51	0.41
1:A:4796:GLU:N	1:A:4796:GLU:OE1	2.54	0.41
1:B:4796:GLU:N	1:B:4796:GLU:OE1	2.54	0.41
1:C:3998:MET:O	1:C:4002:LEU:HD23	2.21	0.41
1:D:4883:MET:HA	1:D:4883:MET:HE2	2.03	0.41
1:B:3636:GLU:OE1	1:B:3636:GLU:N	2.48	0.41
1:B:4883:MET:HA	1:B:4883:MET:HE2	2.03	0.41
1:C:4116:THR:O	1:C:4120:LEU:HD23	2.21	0.41
1:C:4796:GLU:N	1:C:4796:GLU:OE1	2.54	0.41
1:B:4025:LEU:HD22	1:B:4057:TYR:CE2	2.57	0.40
1:B:4099:VAL:HG22	1:B:4132:LEU:CD2	2.51	0.40
1:B:4653:MET:HB2	1:B:4671:MET:HE1	2.03	0.40
1:D:3854:GLN:NE2	1:D:3921:GLU:O	2.51	0.40
1:D:3998:MET:O	1:D:4002:LEU:HD23	2.21	0.40
1:D:4099:VAL:HG22	1:D:4132:LEU:CD2	2.51	0.40
1:D:3683:GLU:HA	1:D:3753:MET:HE3	2.03	0.40
1:D:4020:LEU:HD12	1:D:4124:VAL:HG22	2.03	0.40
1:B:3998:MET:O	1:B:4002:LEU:HD23	2.21	0.40
1:B:4051:MET:HE1	1:B:4062:THR:HA	2.04	0.40
1:C:3683:GLU:HA	1:C:3753:MET:HE3	2.03	0.40
1:C:4099:VAL:HG22	1:C:4132:LEU:CD2	2.51	0.40
1:C:4186:GLU:OE1	1:C:4948:TRP:NE1	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1033/4966 (21%)	1008 (98%)	25 (2%)	0	100	100
1	B	1033/4966 (21%)	1008 (98%)	25 (2%)	0	100	100
1	C	1033/4966 (21%)	1008 (98%)	25 (2%)	0	100	100
1	D	1033/4966 (21%)	1008 (98%)	25 (2%)	0	100	100
All	All	4132/19864 (21%)	4032 (98%)	100 (2%)	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	A	928/4355 (21%)	912 (98%)	16 (2%)	53	67
1	B	928/4355 (21%)	914 (98%)	14 (2%)	57	70
1	C	928/4355 (21%)	913 (98%)	15 (2%)	55	69
1	D	928/4355 (21%)	911 (98%)	17 (2%)	51	65
All	All	3712/17420 (21%)	3650 (98%)	62 (2%)	52	67

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3816	LEU
1	A	3829	LEU

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Mol	Chain	Res	Type
1	A	3887	PHE
1	A	3905	PHE
1	A	3943	VAL
1	A	3955	MET
1	A	4004	GLU
1	A	4039	LYS
1	A	4065	LEU
1	A	4084	LYS
1	A	4509	PHE
1	A	4561	GLU
1	A	4609	LEU
1	A	4632	LEU
1	A	4918	LEU
1	A	4947	CYS
1	B	3816	LEU
1	B	3829	LEU
1	B	3887	PHE
1	B	3905	PHE
1	B	3943	VAL
1	B	3955	MET
1	B	4039	LYS
1	B	4065	LEU
1	B	4084	LYS
1	B	4509	PHE
1	B	4561	GLU
1	B	4632	LEU
1	B	4918	LEU
1	B	4947	CYS
1	C	3816	LEU
1	C	3829	LEU
1	C	3887	PHE
1	C	3943	VAL
1	C	3955	MET
1	C	4024	ASP
1	C	4039	LYS
1	C	4065	LEU
1	C	4084	LYS
1	C	4509	PHE
1	C	4561	GLU
1	C	4609	LEU
1	C	4632	LEU
1	C	4918	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	4947	CYS
1	D	3816	LEU
1	D	3829	LEU
1	D	3887	PHE
1	D	3920	THR
1	D	3923	ILE
1	D	3943	VAL
1	D	3955	MET
1	D	4024	ASP
1	D	4039	LYS
1	D	4065	LEU
1	D	4084	LYS
1	D	4509	PHE
1	D	4561	GLU
1	D	4609	LEU
1	D	4632	LEU
1	D	4918	LEU
1	D	4947	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4557	HIS
1	A	4698	ASN
1	A	4765	GLN
1	B	4698	ASN
1	B	4765	GLN
1	C	4557	HIS
1	C	4698	ASN
1	C	4765	GLN
1	D	4557	HIS
1	D	4698	ASN
1	D	4765	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

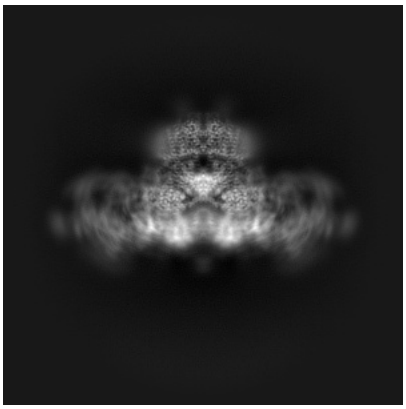
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-80688. These allow visual inspection of the internal detail of the map and identification of artifacts.

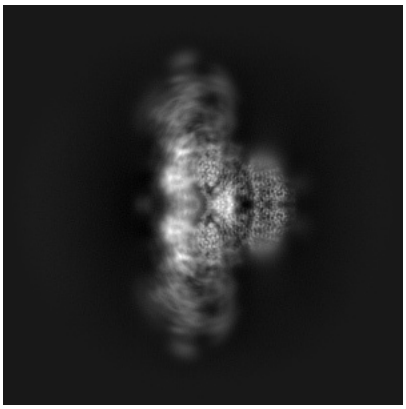
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

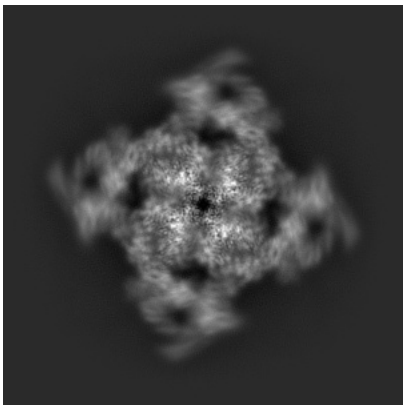
6.1.1 Primary map



X

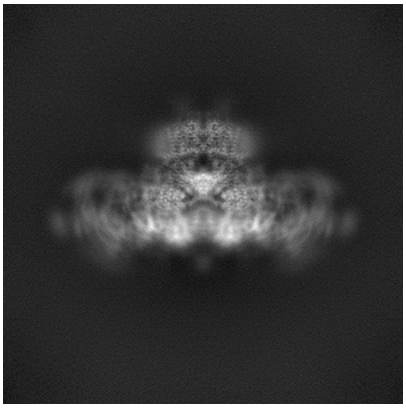


Y

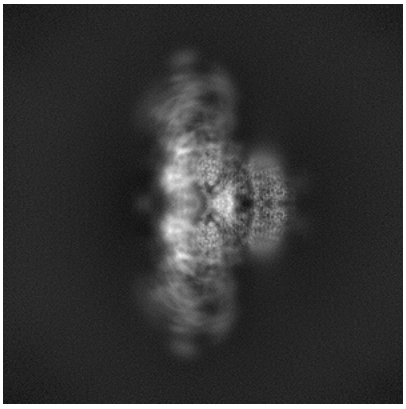


Z

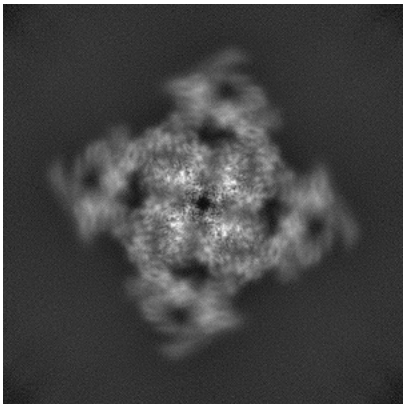
6.1.2 Raw map



X



Y

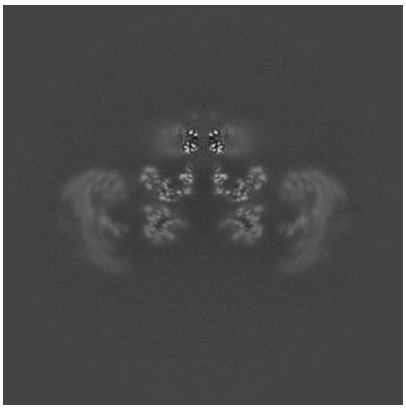


Z

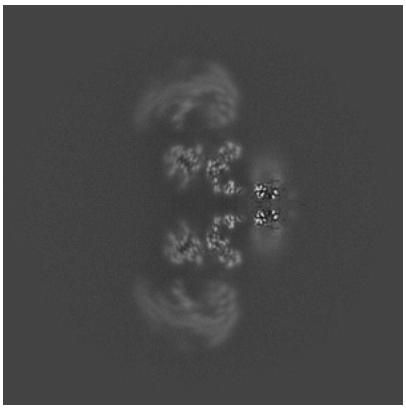
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

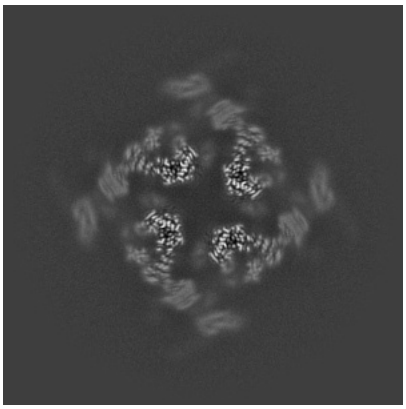
6.2.1 Primary map



X Index: 256

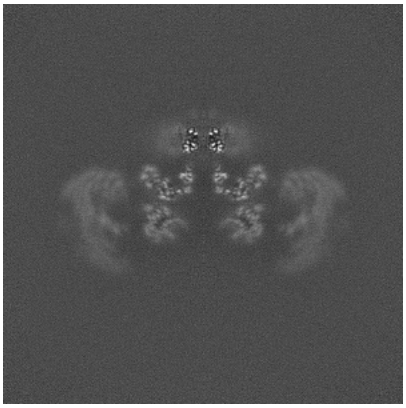


Y Index: 256

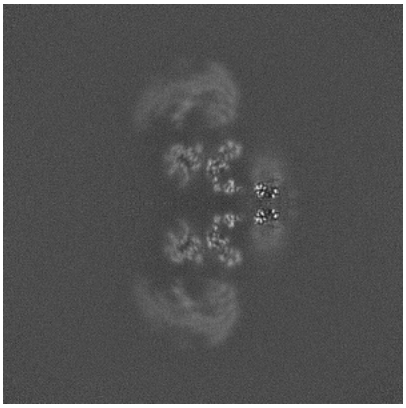


Z Index: 256

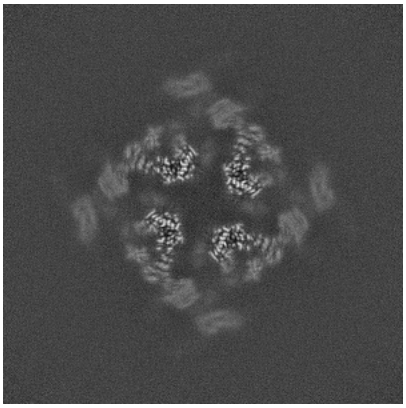
6.2.2 Raw map



X Index: 256



Y Index: 256

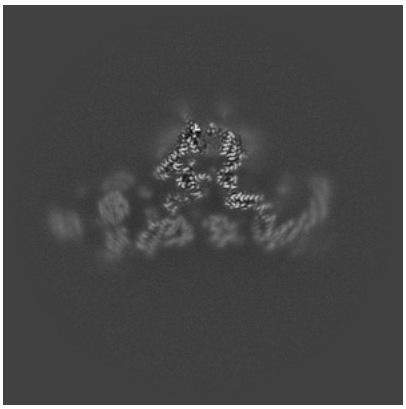


Z Index: 256

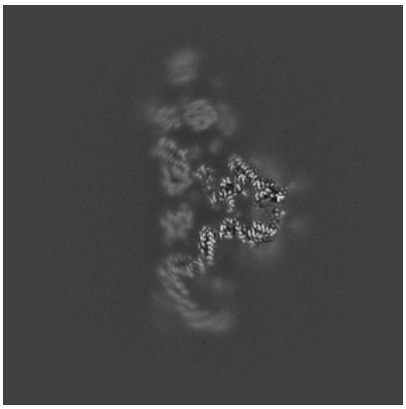
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

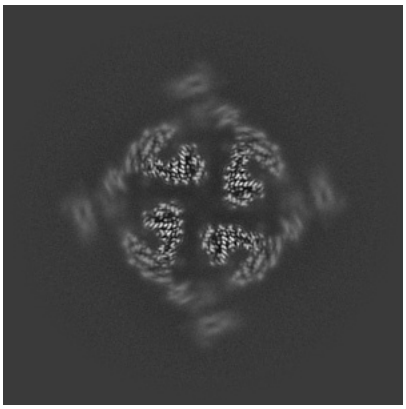
6.3.1 Primary map



X Index: 229

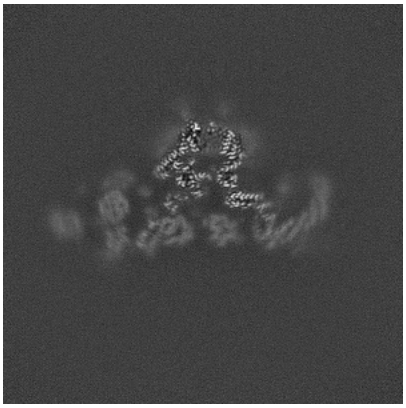


Y Index: 229

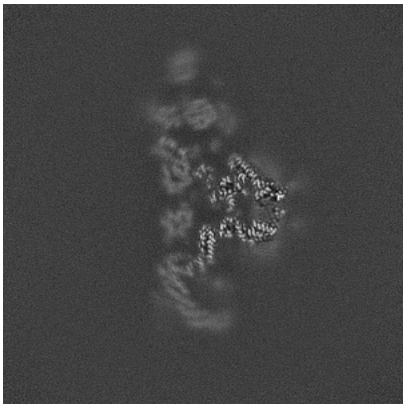


Z Index: 264

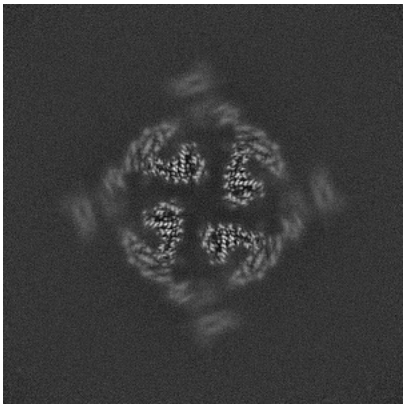
6.3.2 Raw map



X Index: 229



Y Index: 229

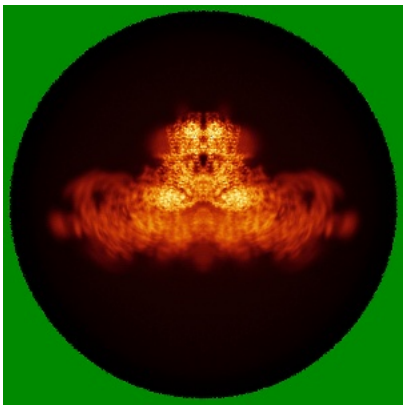


Z Index: 264

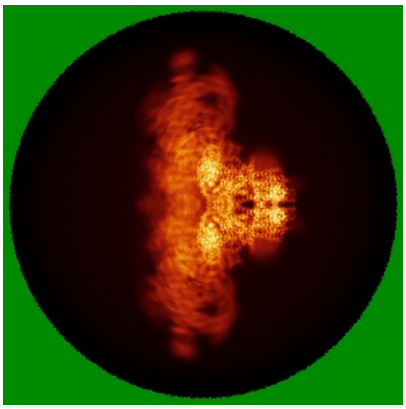
The images above show the largest variance slices of the map in three orthogonal directions.

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

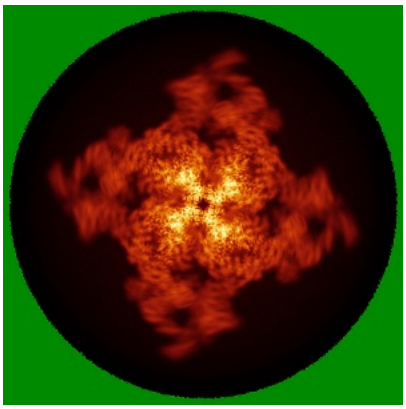
6.4.1 Primary map



X

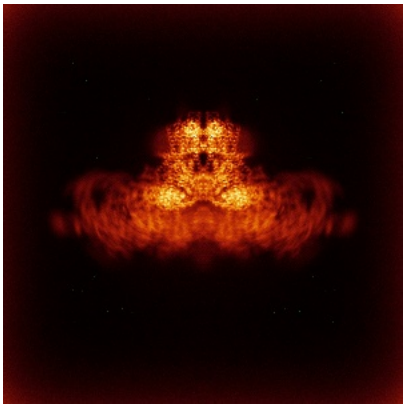


Y

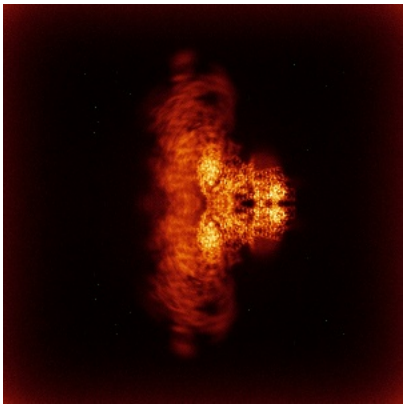


Z

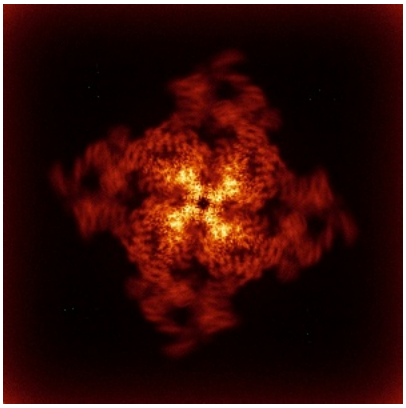
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

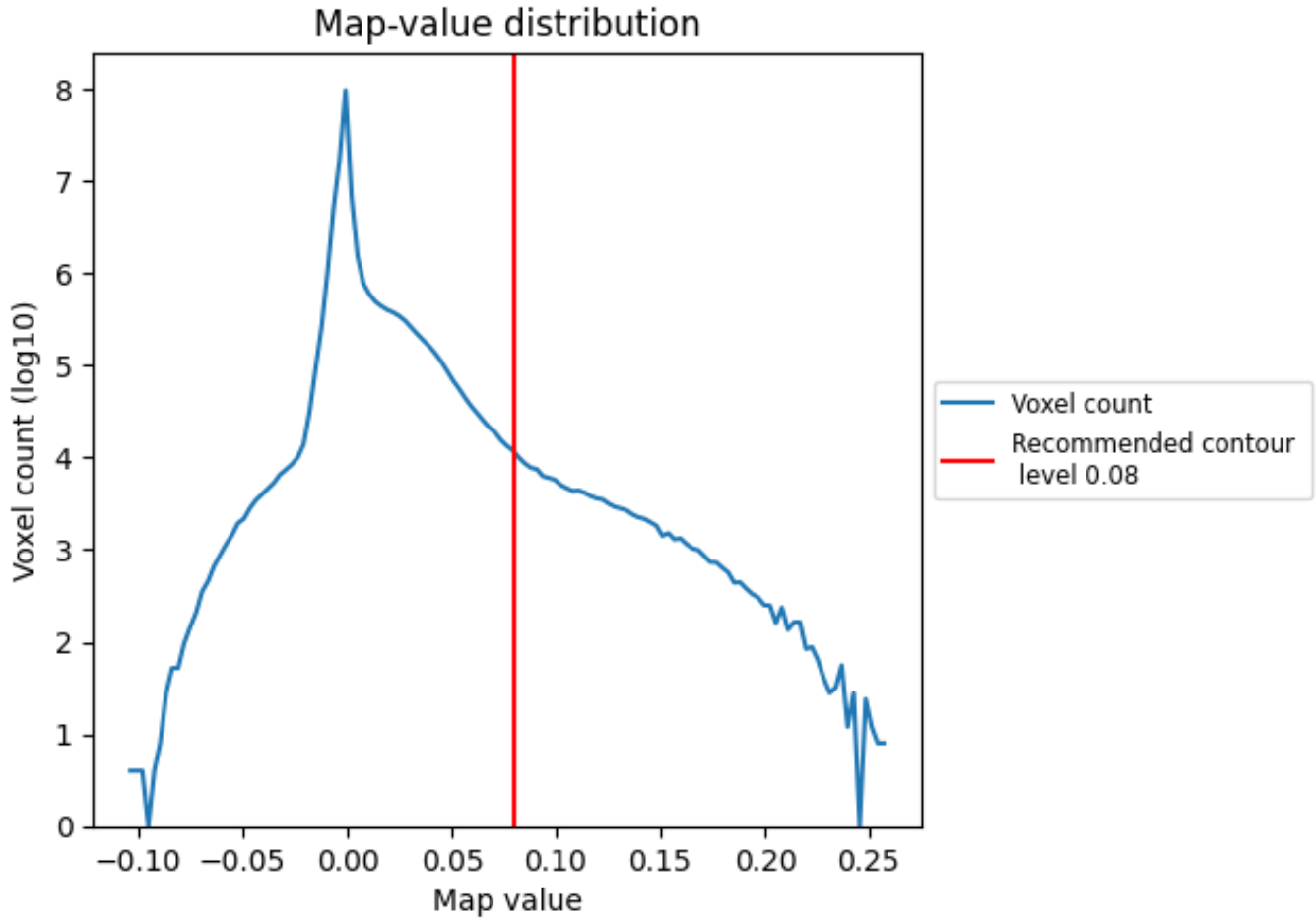
6.6 Mask visualisation (i)

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

7 Map analysis

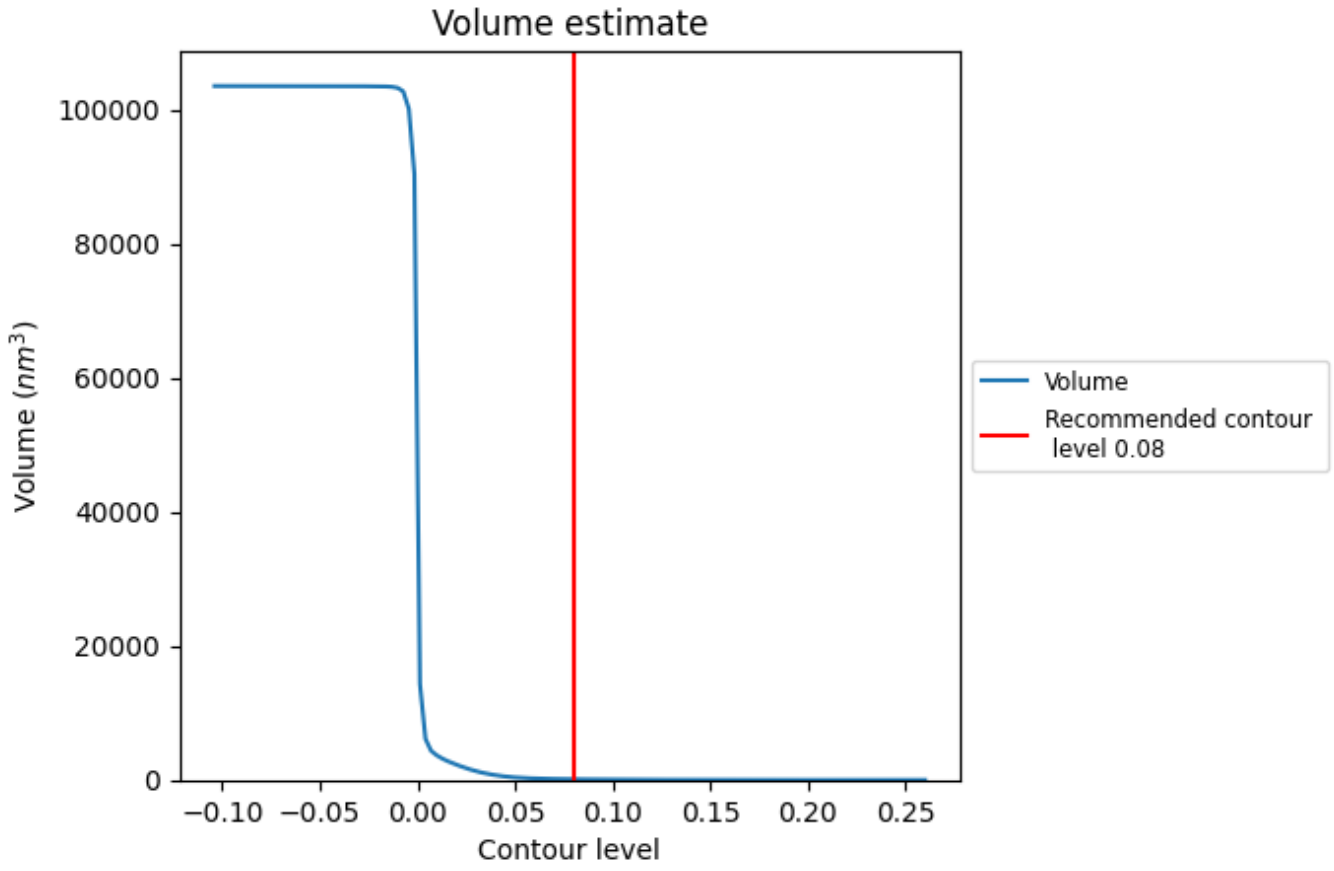
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

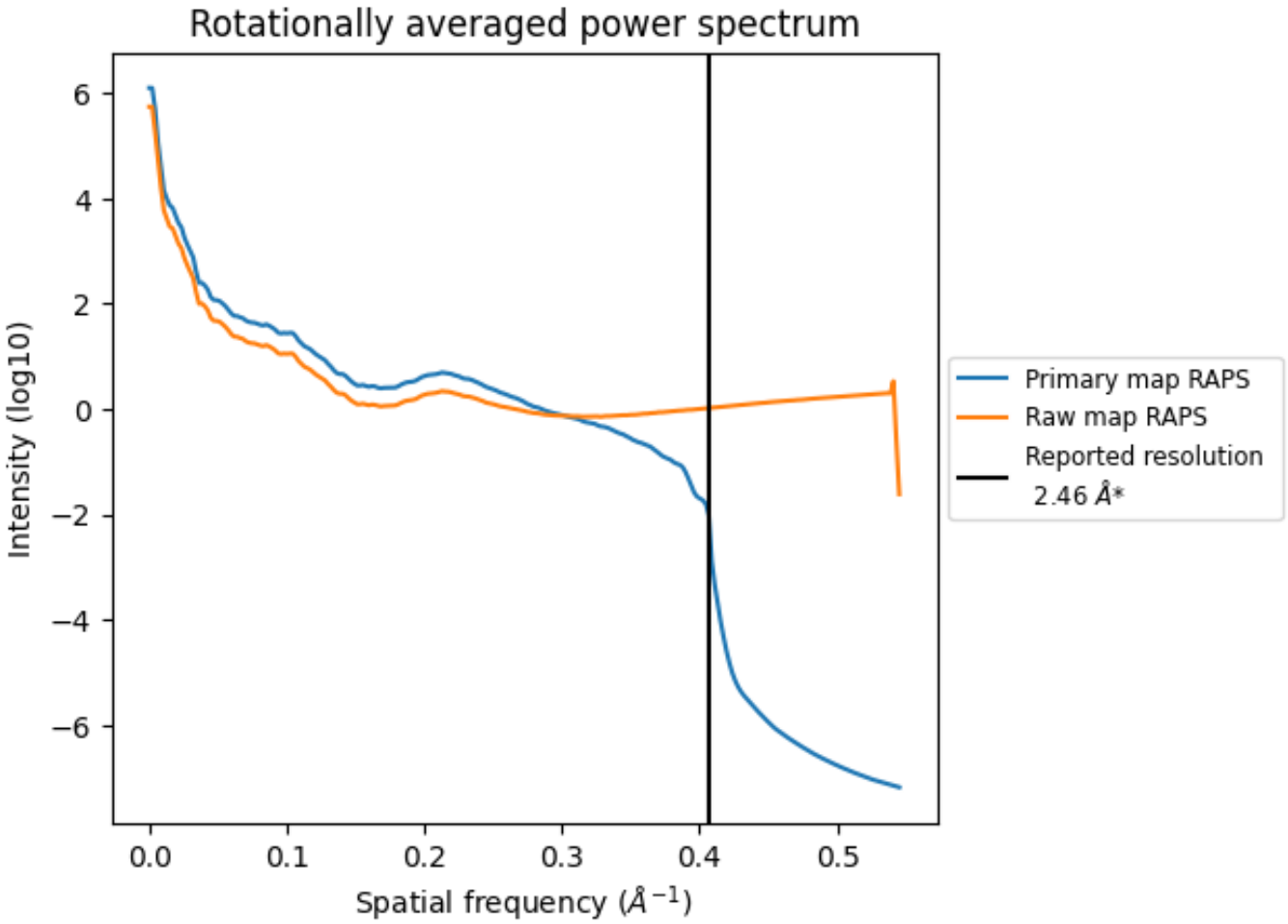
7.2 Volume estimate



The volume at the recommended contour level is 103 nm^3; this corresponds to an approximate mass of 93 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)

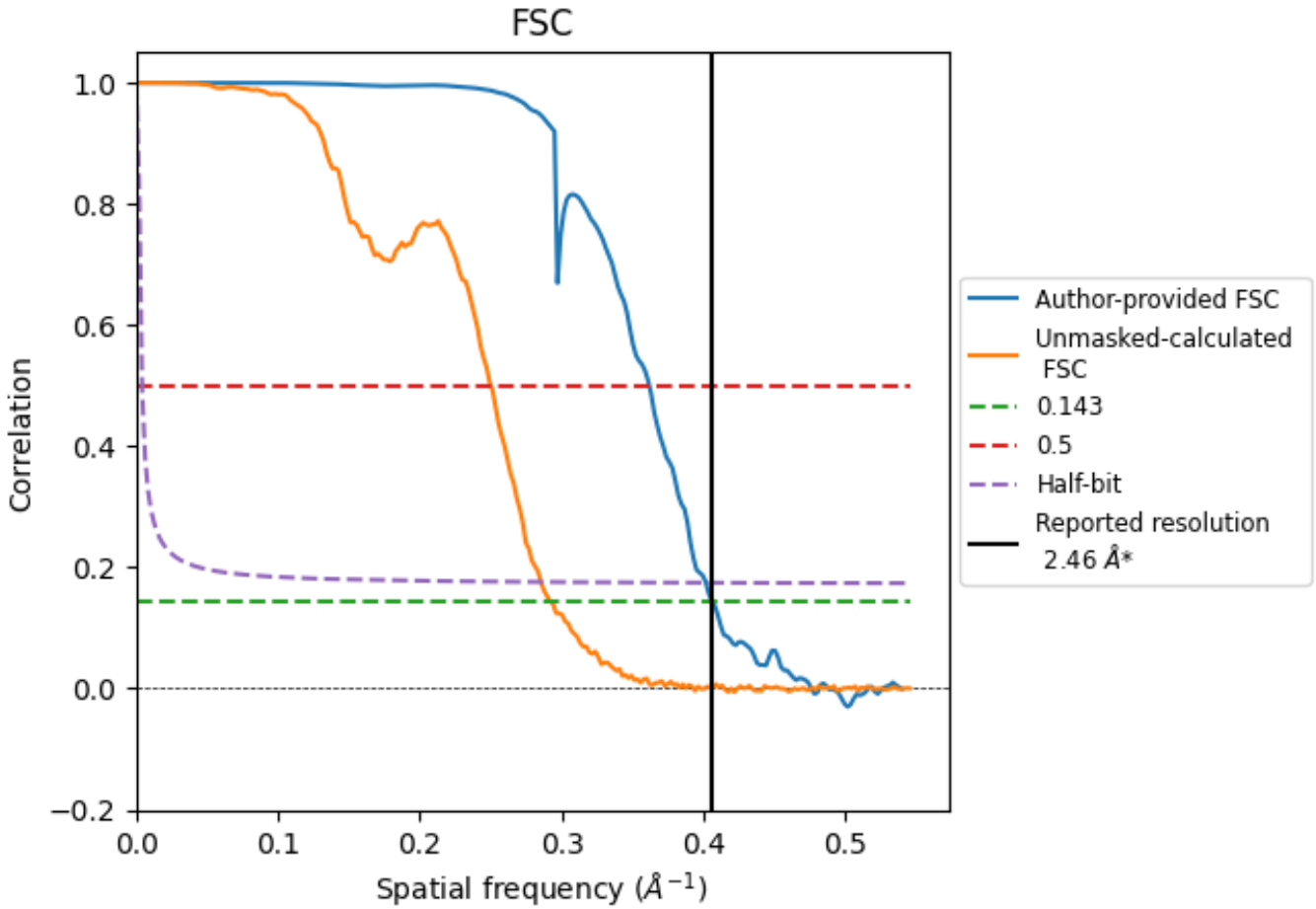


*Reported resolution corresponds to spatial frequency of 0.407 Å^{-1}

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.407 Å^{-1}

8.2 Resolution estimates (i)

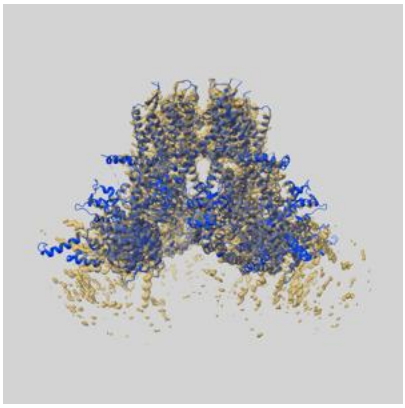
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.46	-	-
Author-provided FSC curve	2.46	2.76	2.49
Unmasked-calculated*	3.42	4.00	3.50

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.42 differs from the reported value 2.46 by more than 10 %

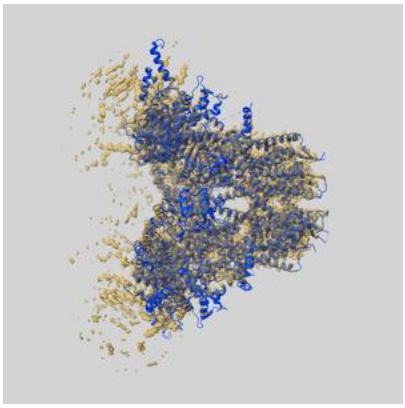
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-80688 and PDB model 26IT. Per-residue inclusion information can be found in section 3 on page 4.

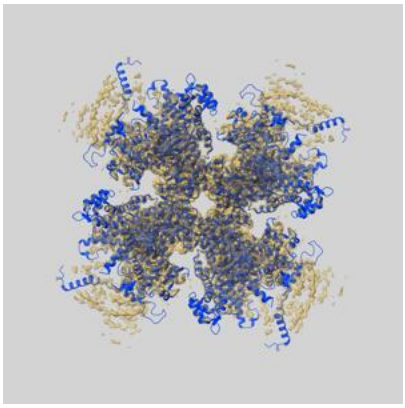
9.1 Map-model overlay



X



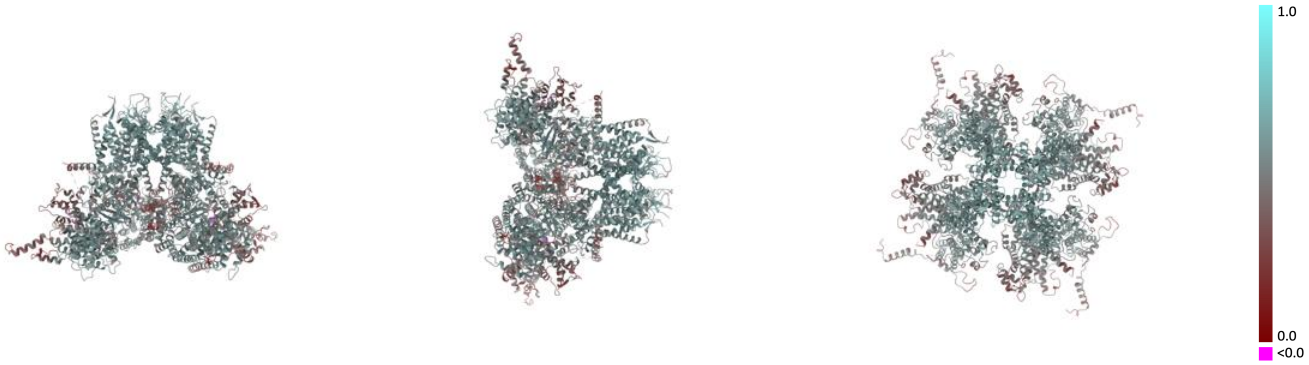
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

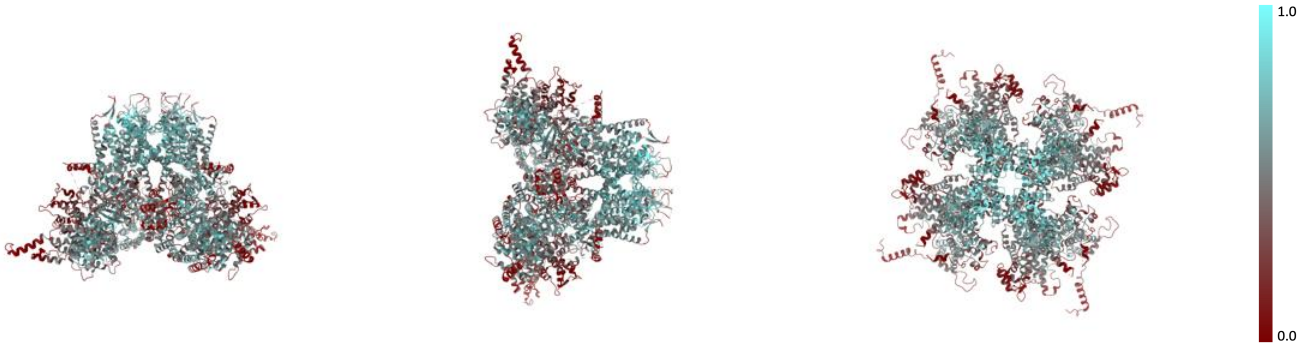
9.2 Q-score mapped to coordinate model



X Y Z

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

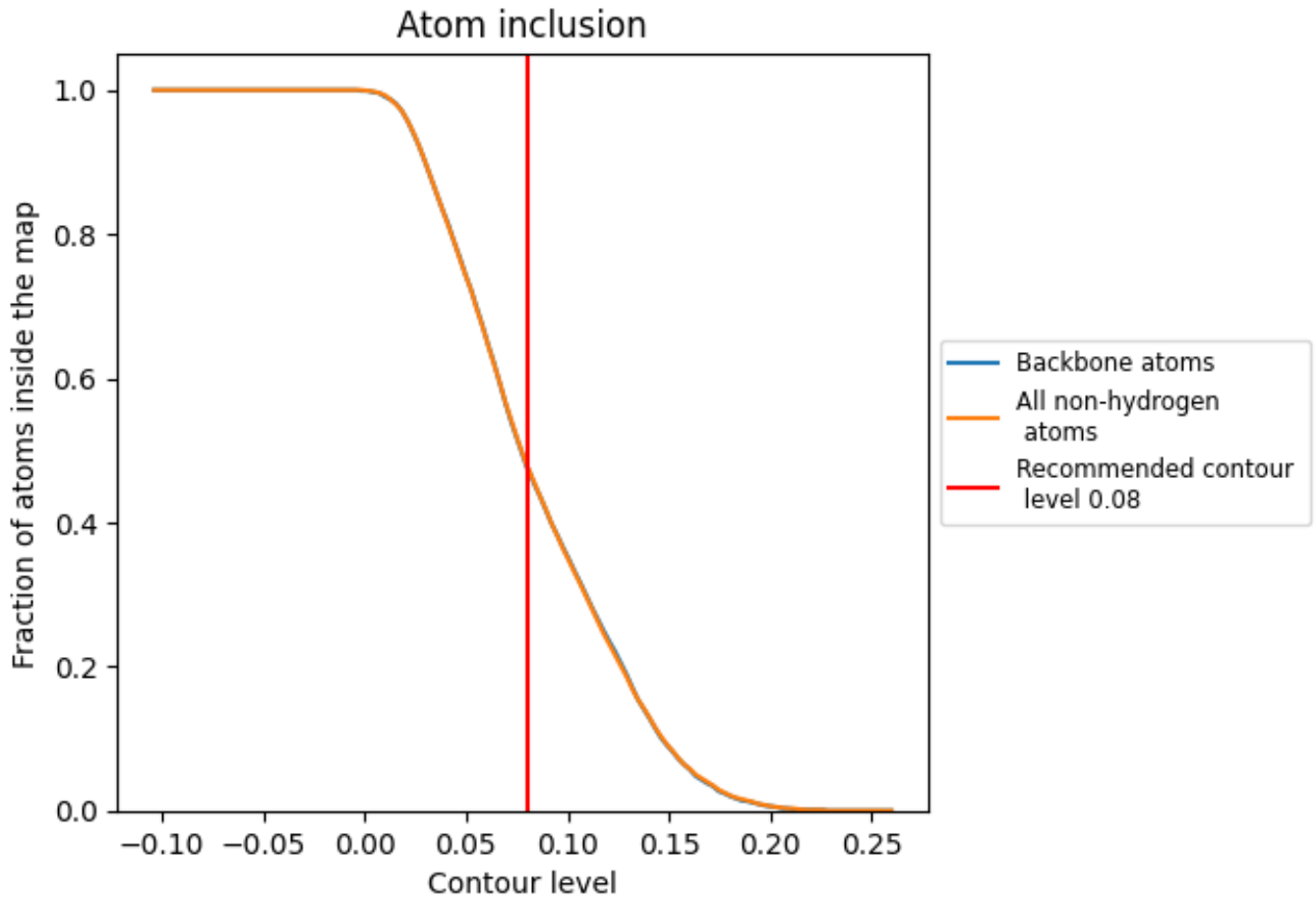
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.08).

9.4 Atom inclusion (i)



At the recommended contour level, 48% of all backbone atoms, 48% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.08) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.4780	0.5160
A	0.4890	0.5170
B	0.4890	0.5160
C	0.4890	0.5160
D	0.4890	0.5170