wwPDB EM Map/Model Validation Report (i)

Sep 14, 2016 – 11:13 AM EDT

PDB ID	:	5GL1
EMDB ID:	:	EMD-9521
Title	:	Structure of RyR1 in an open state
Authors	:	Bai, X.C.; Yan, Z.; Wu, J.P.; Yan, N.
Deposited on	:	2016-07-07
Resolution	:	5.70 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

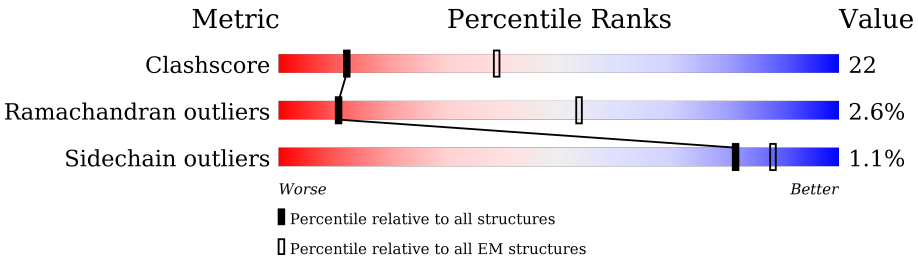
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027939

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 5.70 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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%

Mol	Chain	Length	Quality of chain
1	A	5037	41% 28% • 28%
1	C	5037	41% 28% • 28%
1	E	5037	41% 28% • 28%
1	G	5037	41% 29% • 28%
2	B	108	53% 44% • •
2	D	108	56% 40% • •
2	F	108	56% 40% • •
2	H	108	52% 45% • •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 110704 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3645	Total	C	N	O	S	0	0
			26843	17063	4667	4956	157		
1	C	3645	Total	C	N	O	S	0	0
			26843	17063	4667	4956	157		
1	E	3645	Total	C	N	O	S	0	0
			26843	17063	4667	4956	157		
1	G	3645	Total	C	N	O	S	0	0
			26843	17063	4667	4956	157		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	D	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	F	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	H	107	Total	C	N	O	S	0	0
			832	527	146	155	4		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

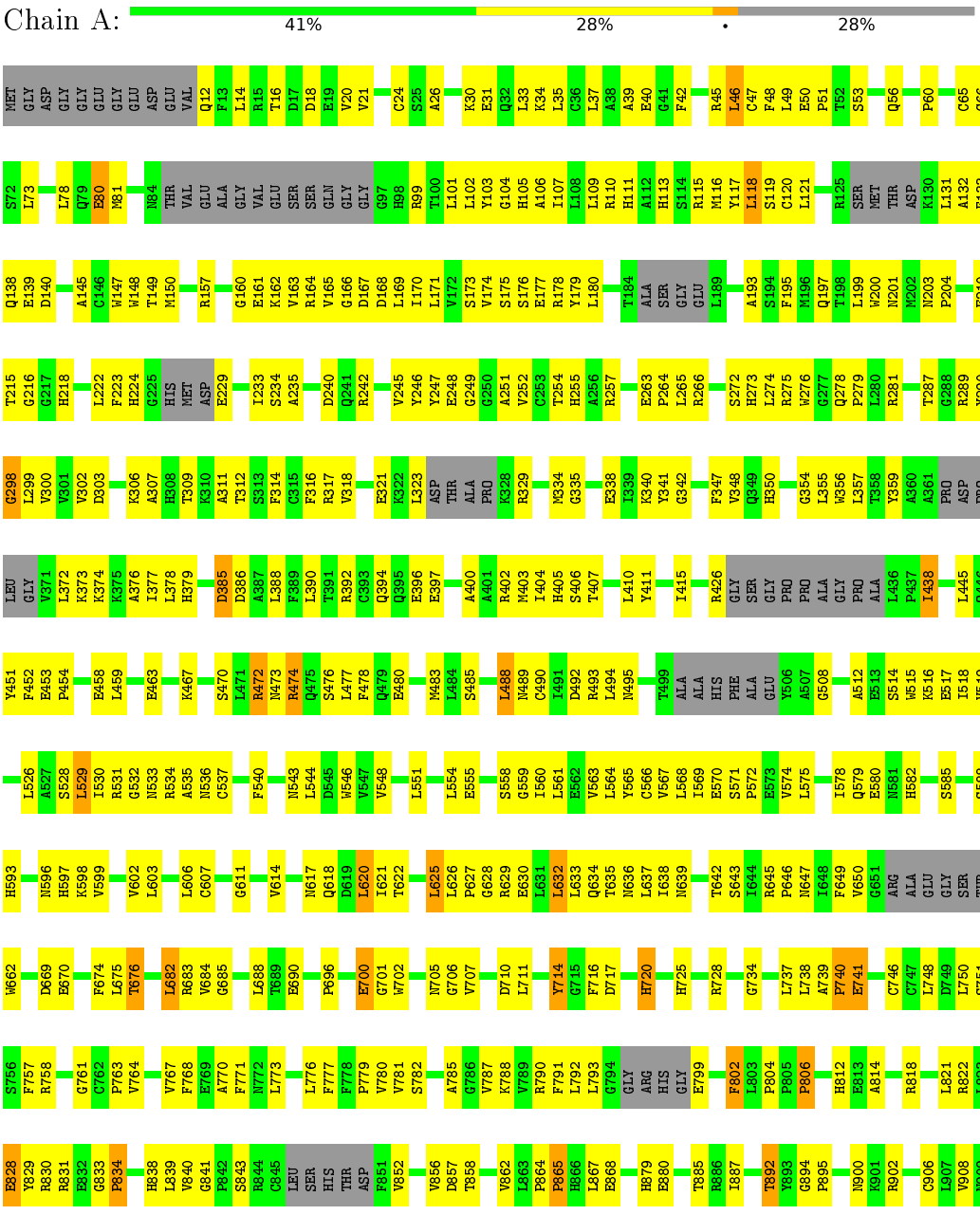
Mol	Chain	Residues	Atoms		AltConf
3	G	1	Total	Zn	0
			1	1	
3	A	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	

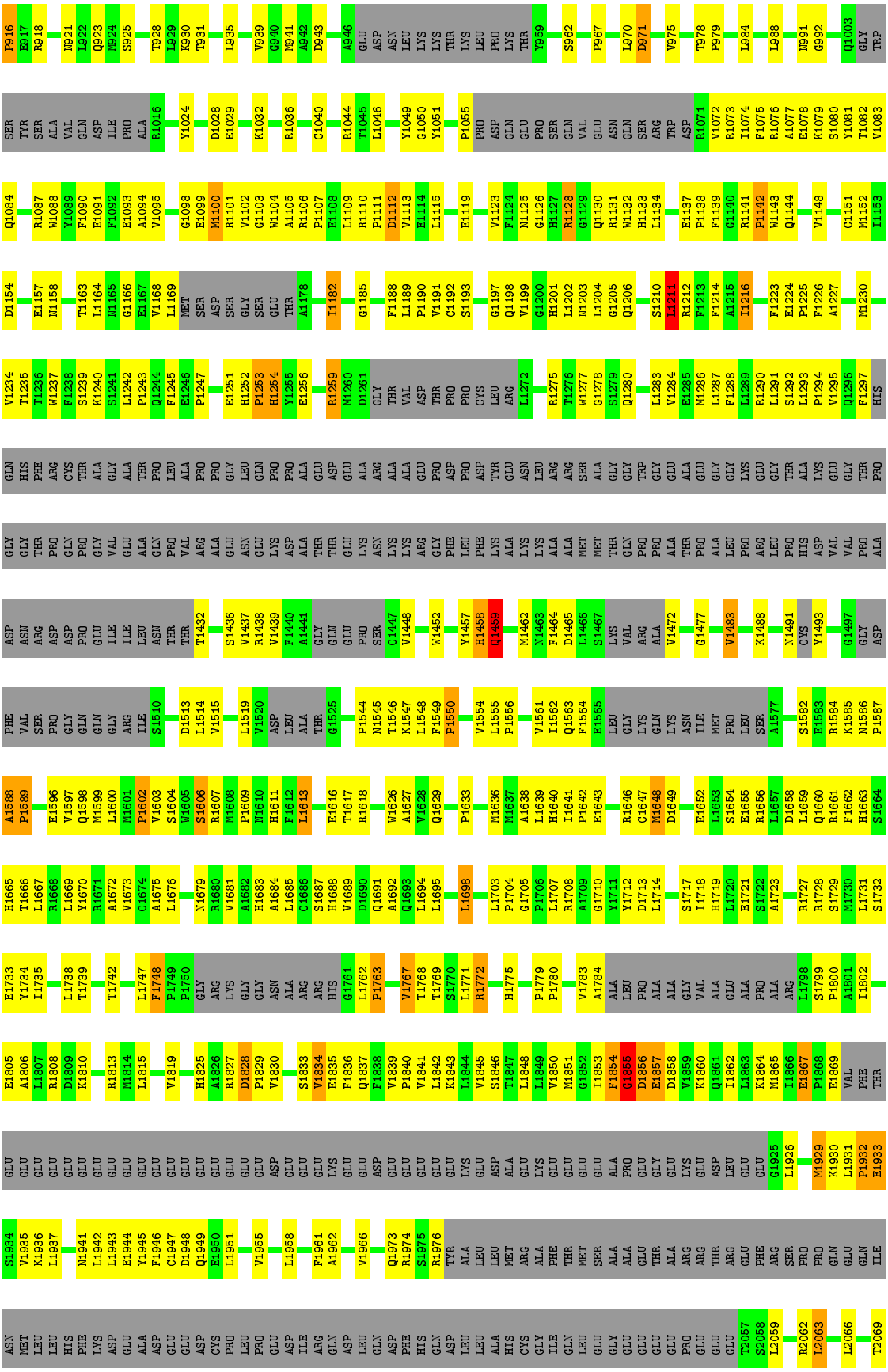
3 Residue-property plots (i)

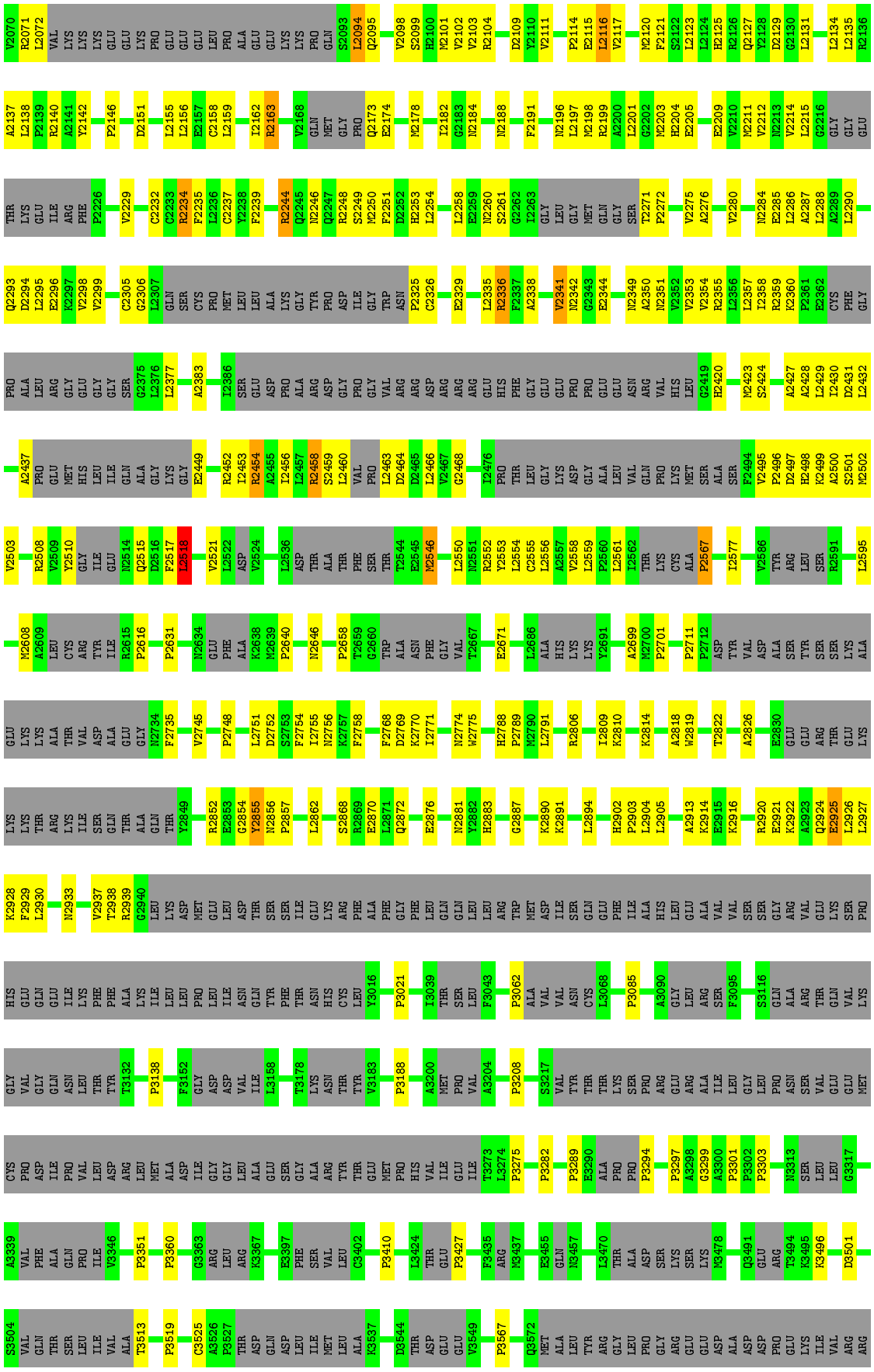
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. 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.

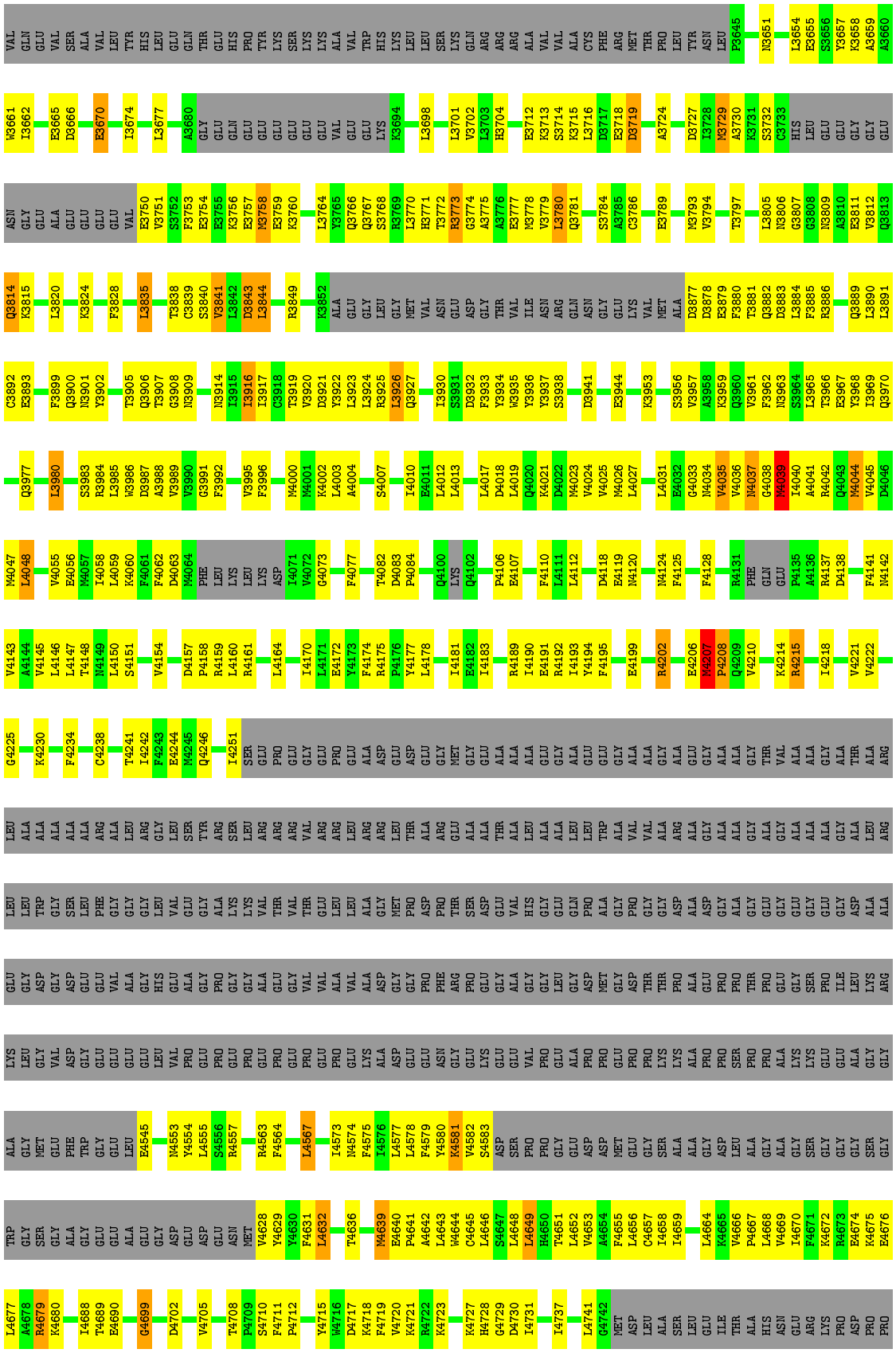
- Molecule 1: Ryanodine receptor 1

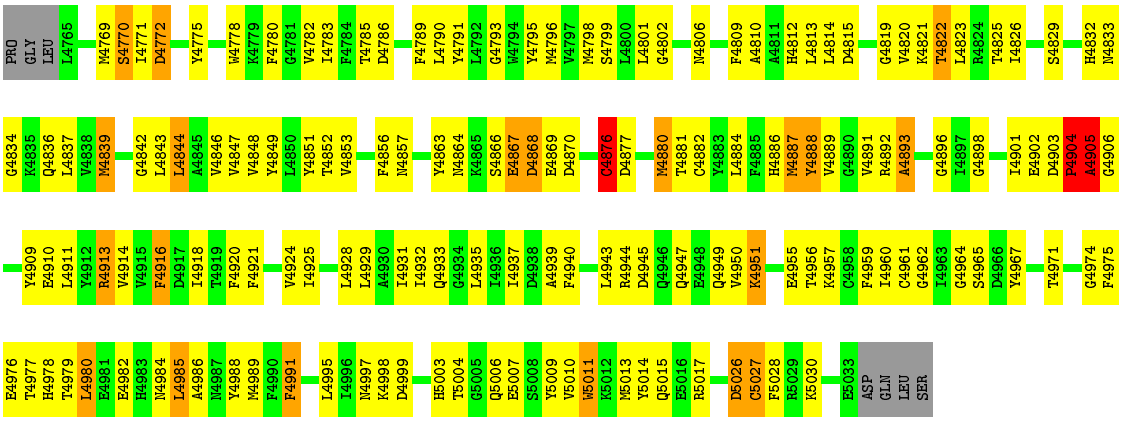
Chain A:





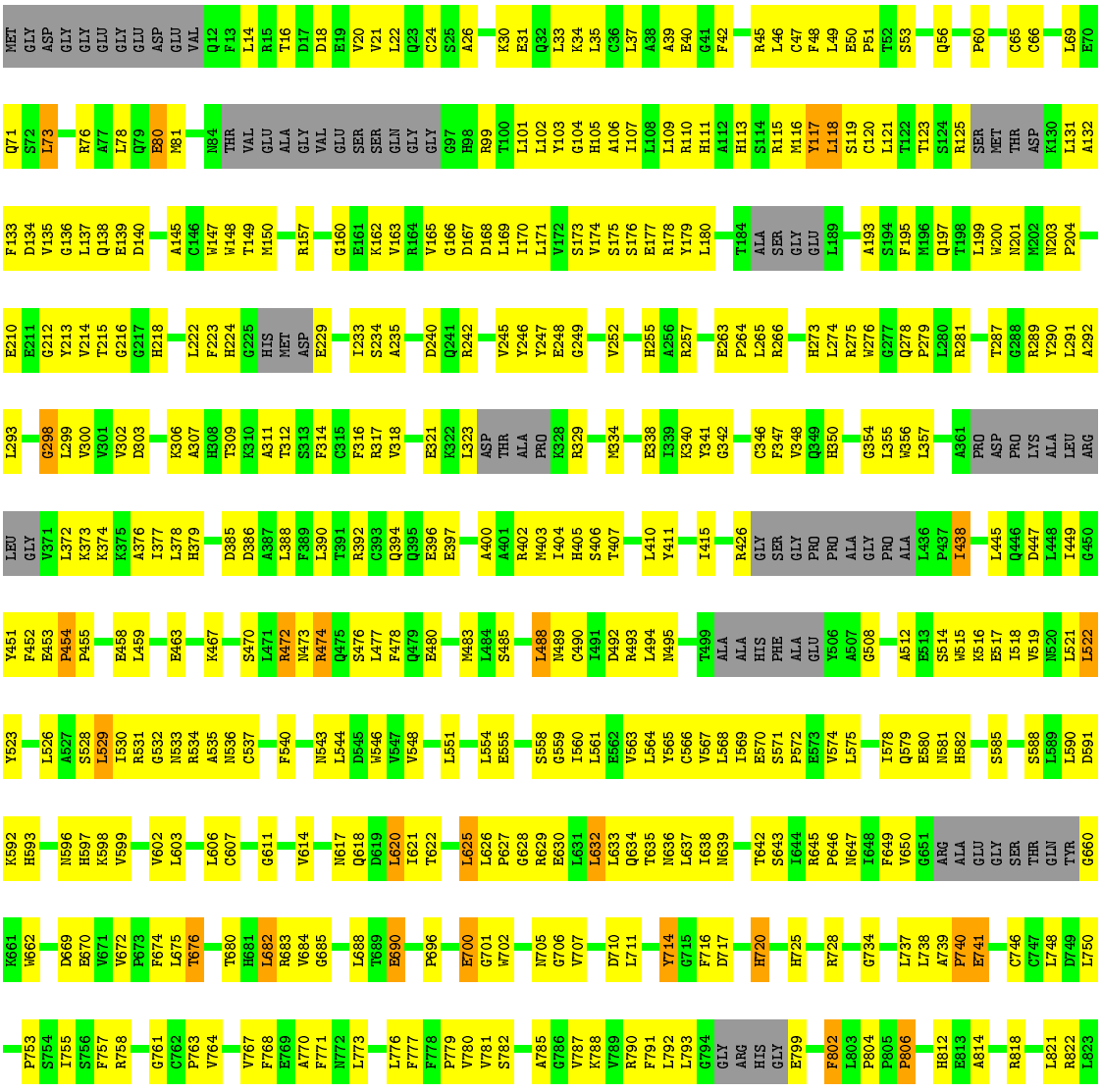


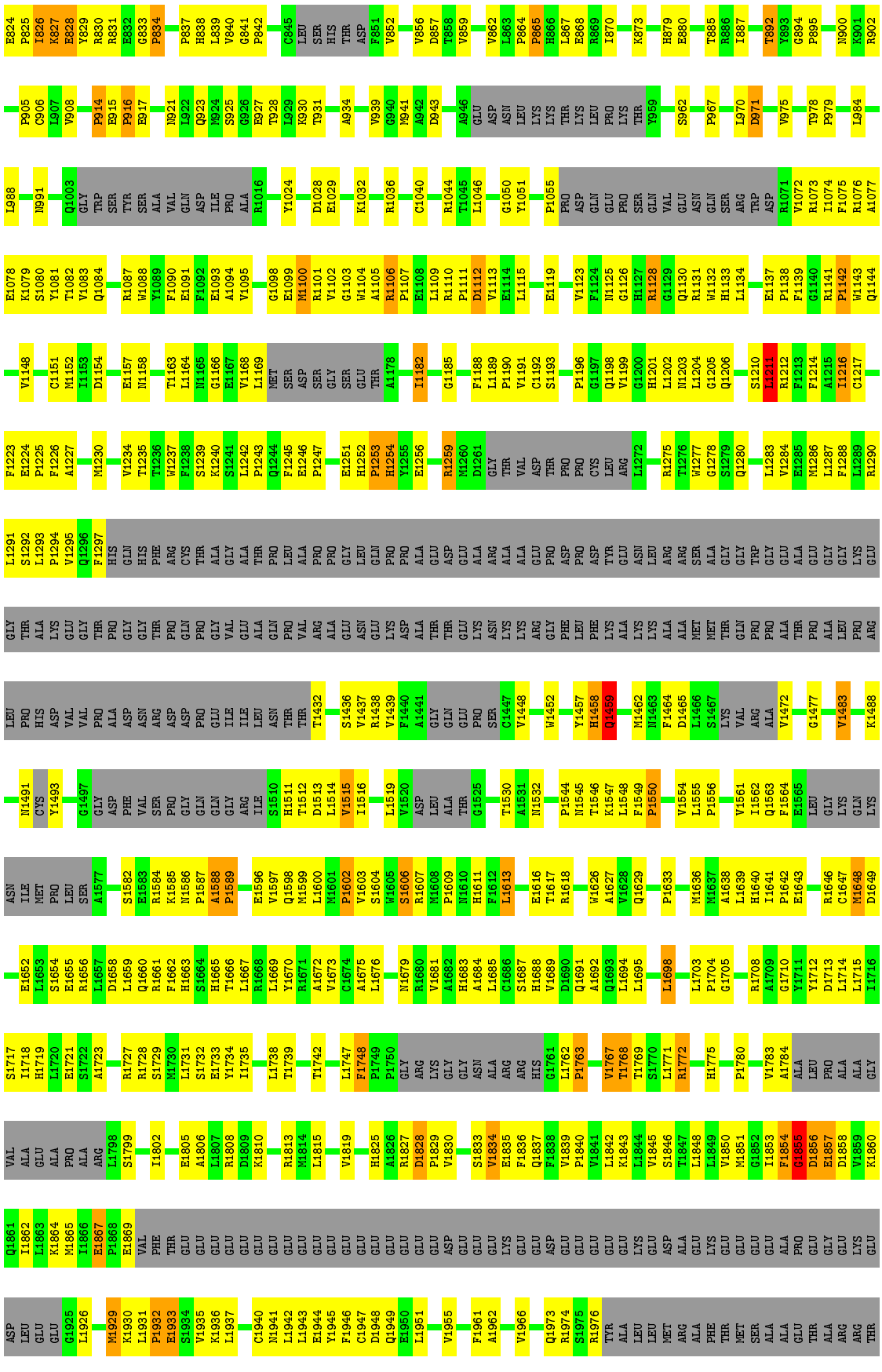


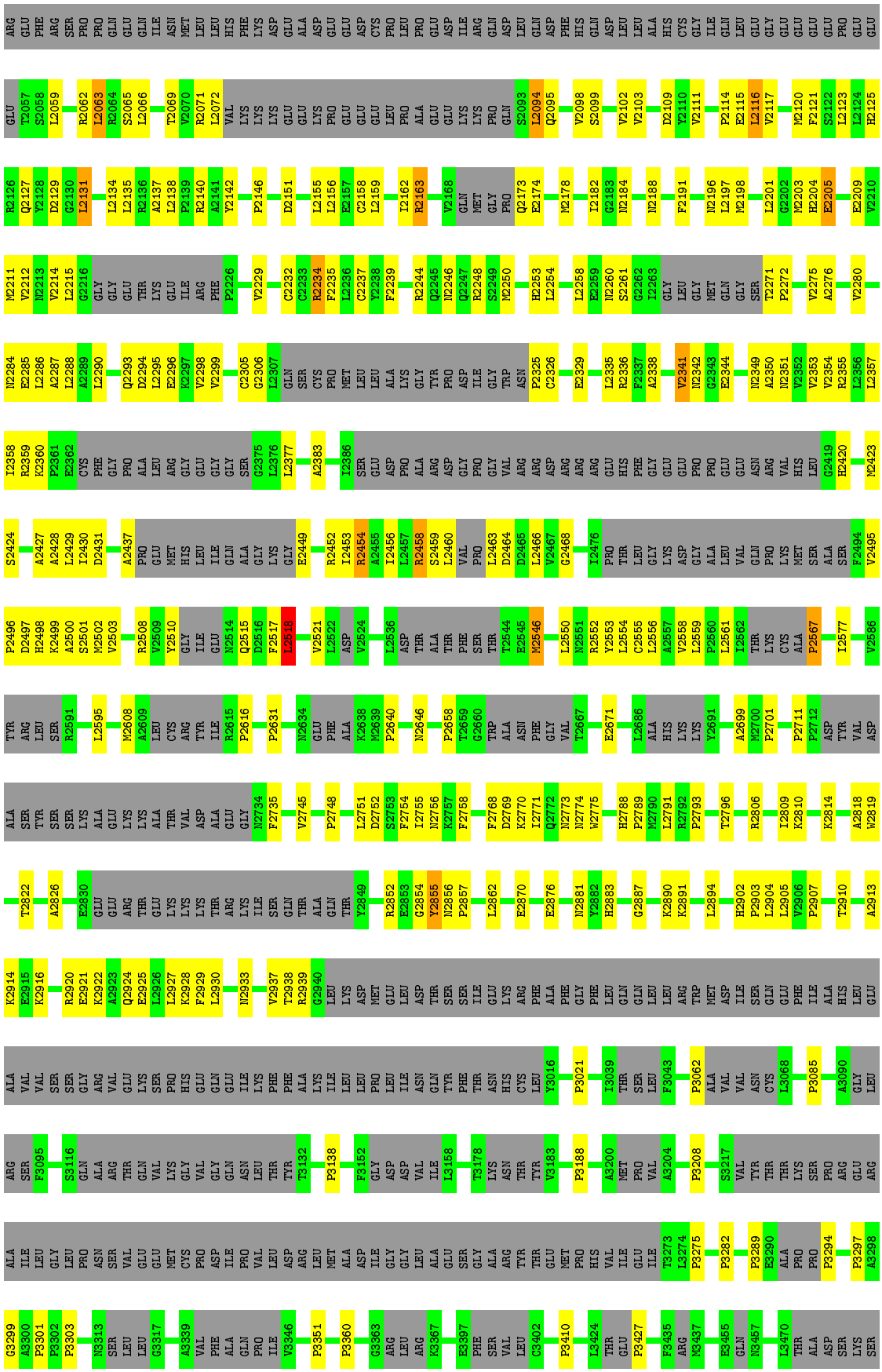


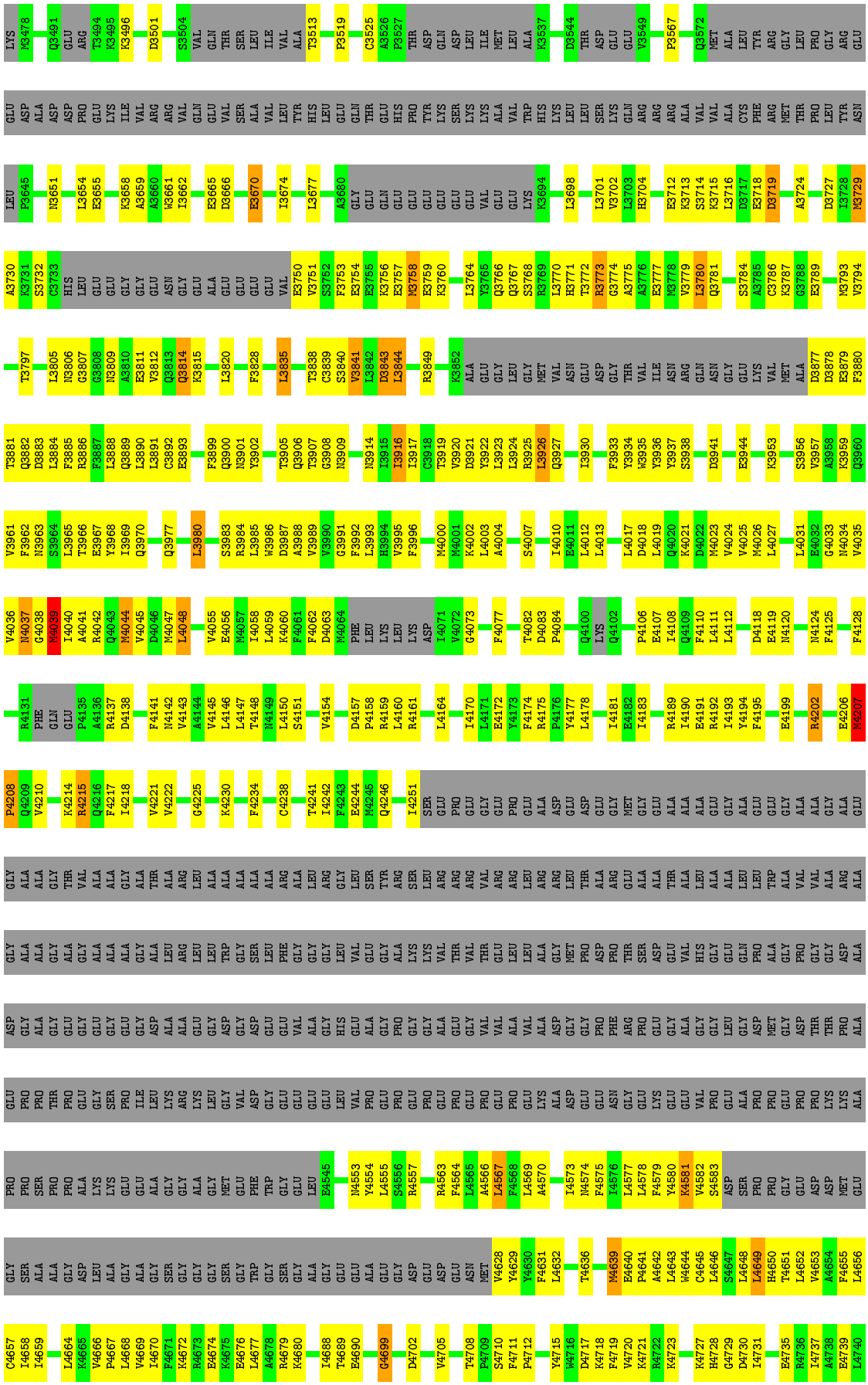
• Molecule 1: Ryanodine receptor 1

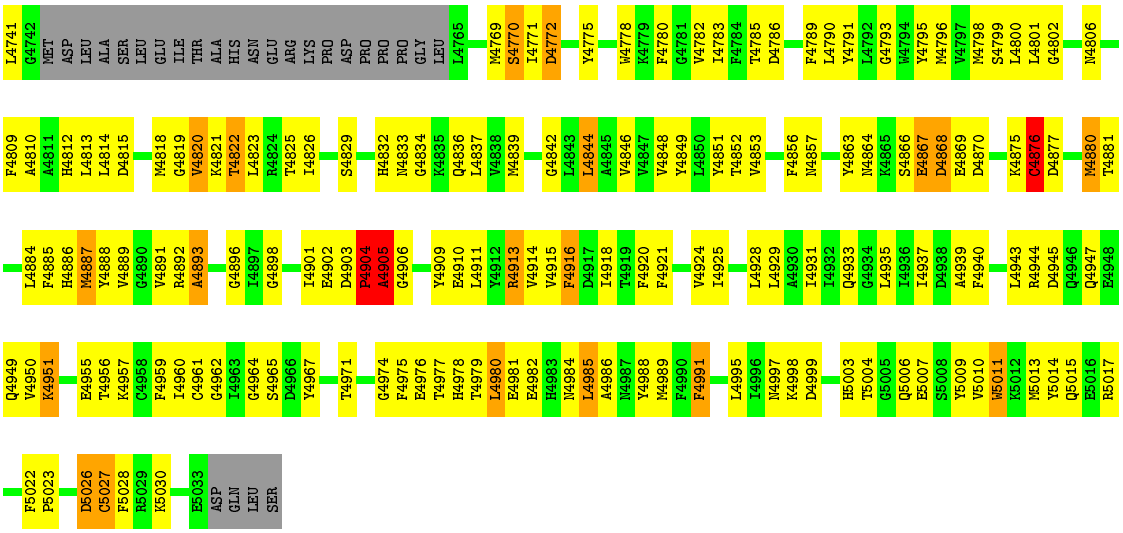
Chain C:





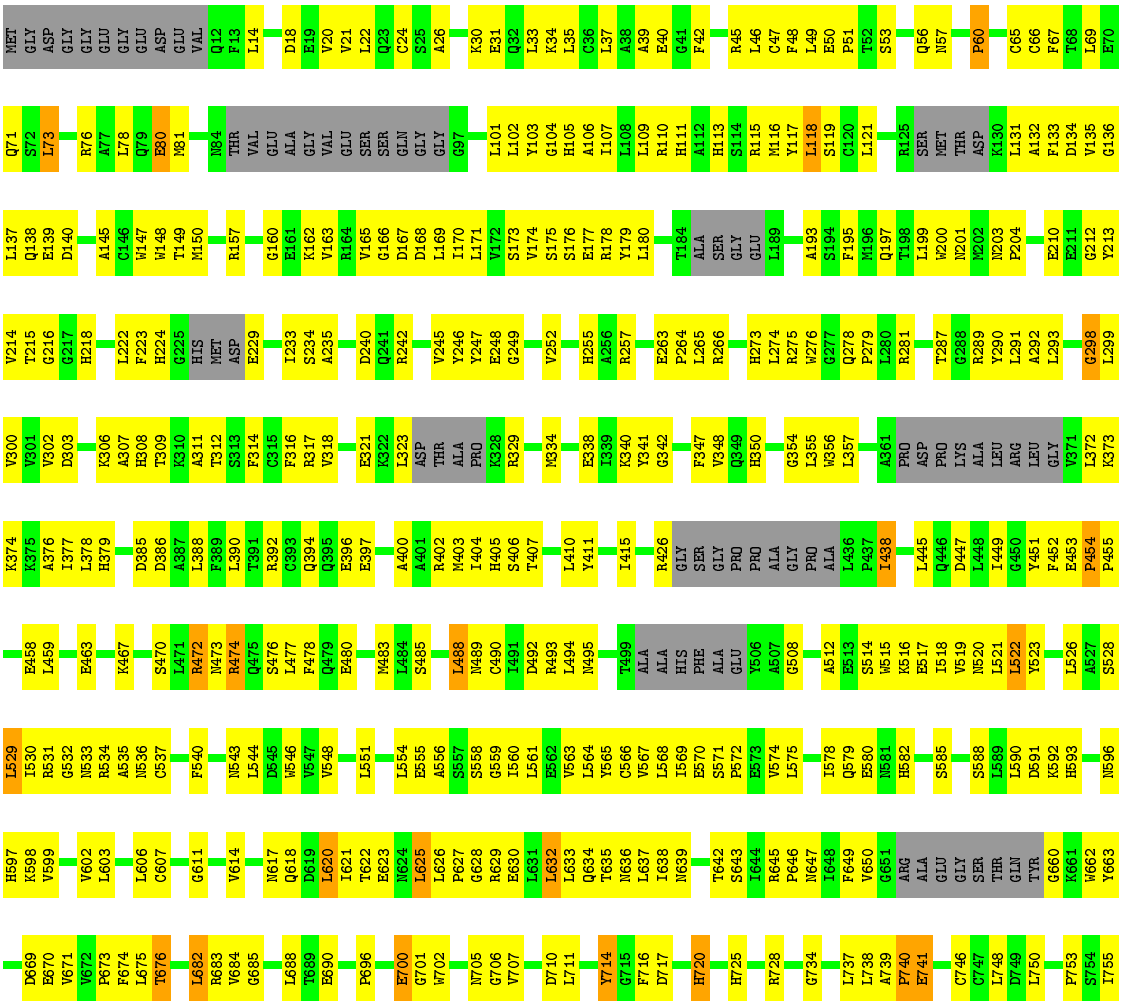


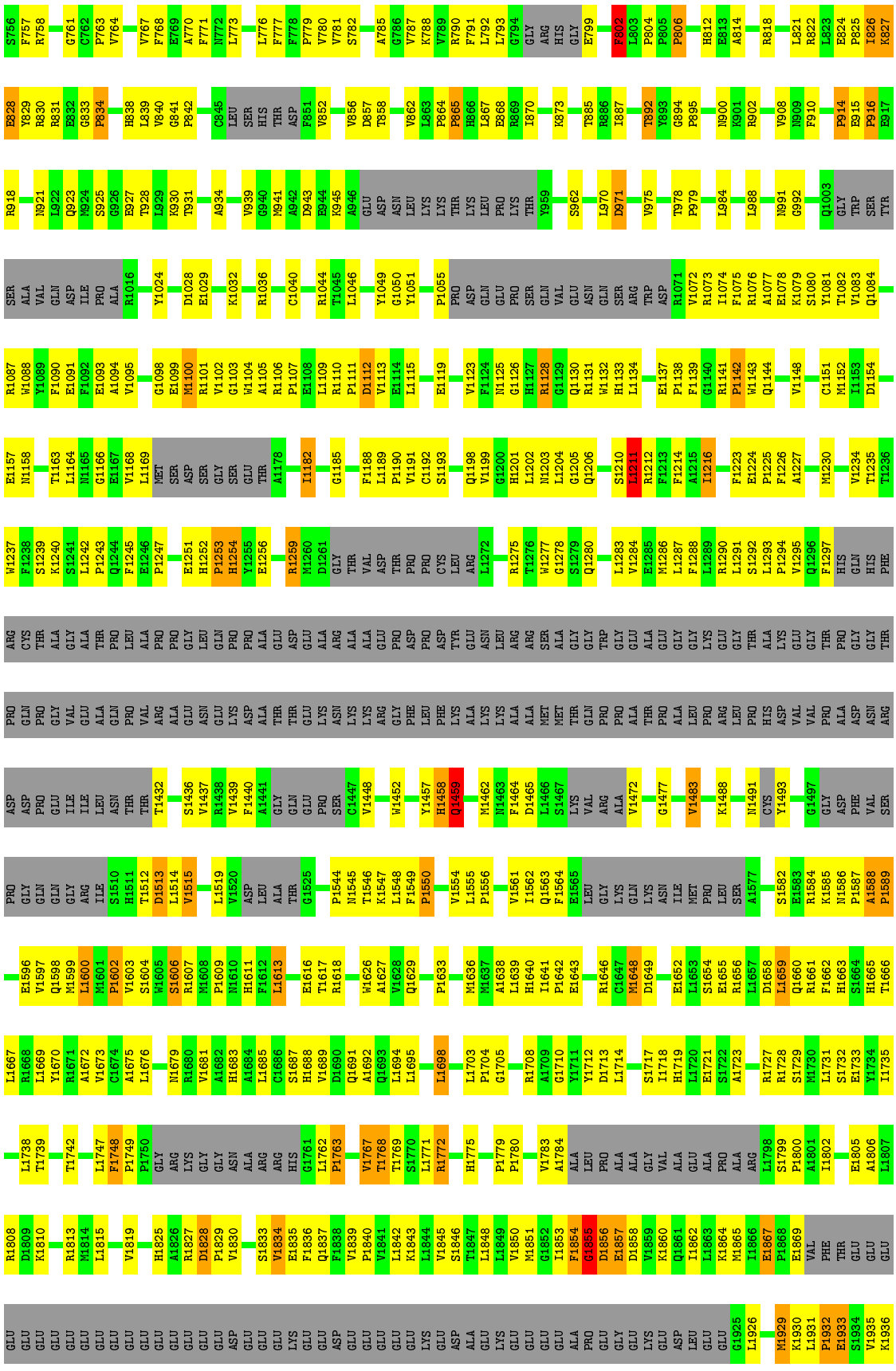


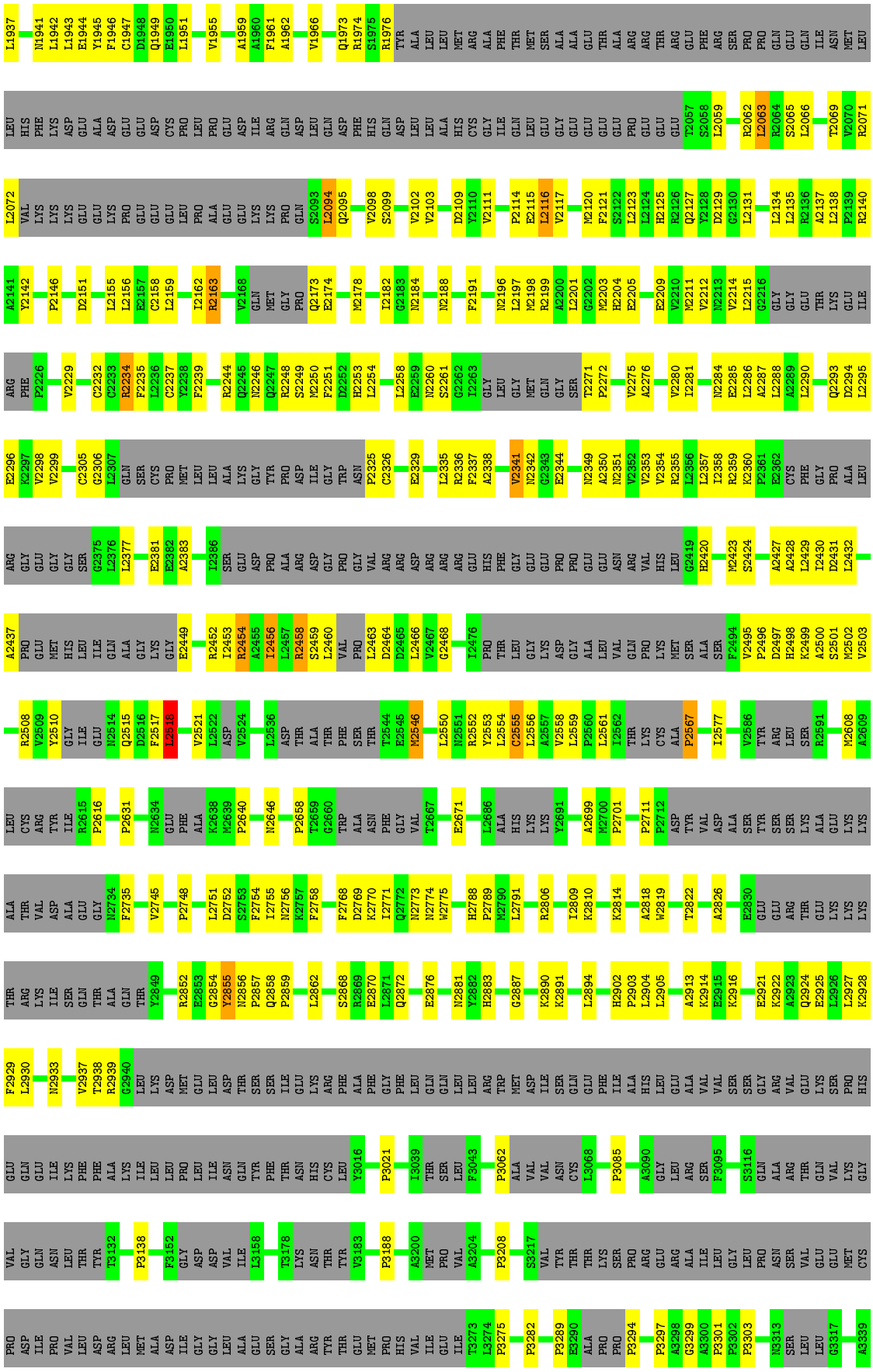


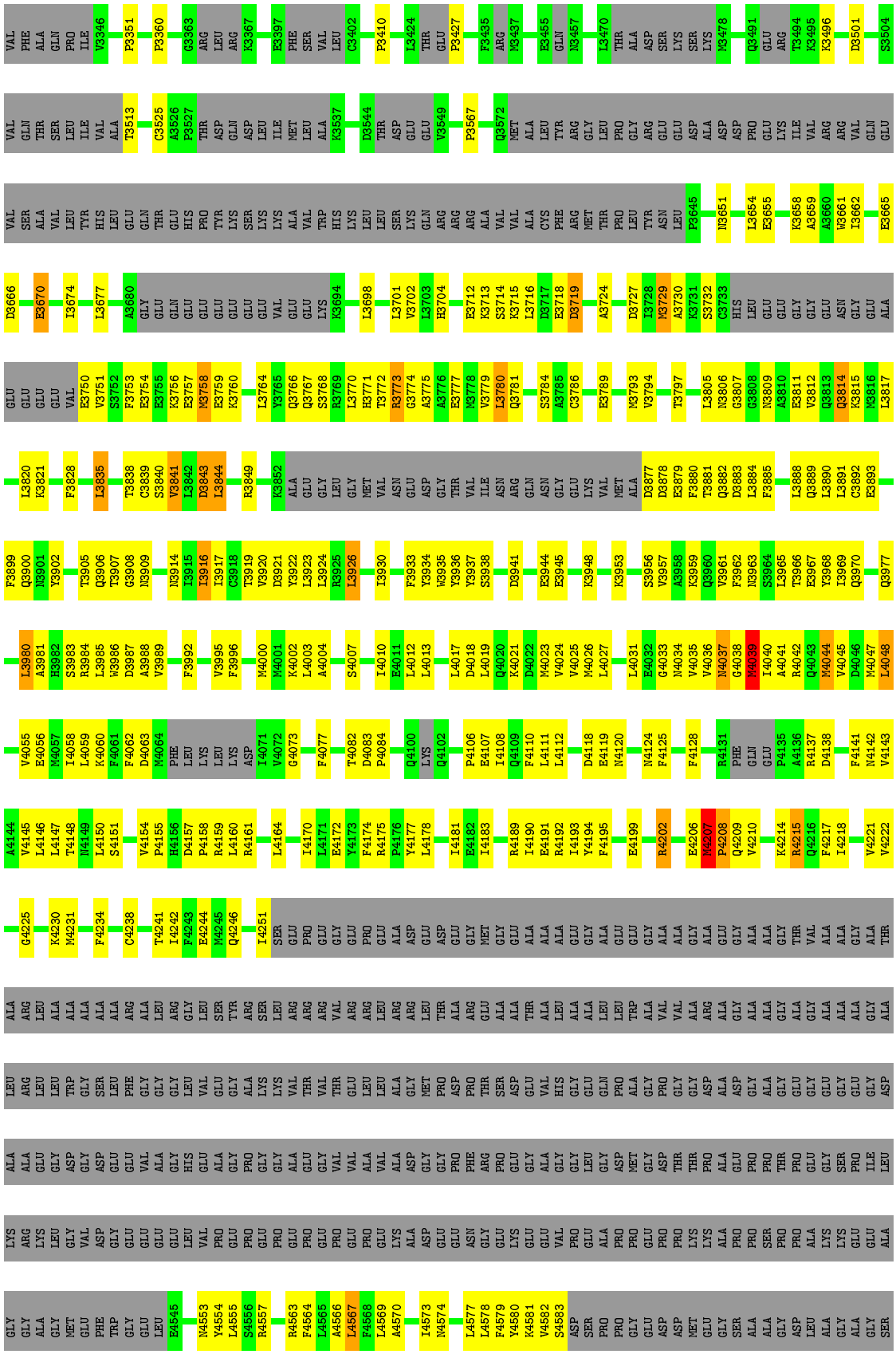
- Molecule 1: Ryanodine receptor 1

Chain E:








VAL PHE ALA GLN PRO ILE V3346 P3351 P3360 G3363 ARG LEU ARG K3367 E3397 PHE SER VAL LEU C3402 P3410 L3424 THR GLU P3427 F3435 ARG M3437 E3455 GLN N3457 L3470 THR ALA ASP SER LYS SER LYS M3478 Q3491 GLU ARG T3494 K3495 K3496 D3501 S3504
VAL GLN THR SER LEU ILE VAL ALA T3513 C3525 A3526 P3527 THR ASP GLN ASP LEU ILE MET LEU ALA K3537 D3544 THR ASP GLU GLU V3549 P3567 Q3572 MET ALA LEU TYR ARG GLY LEU PRO GLY ARG GLU GLU ASP ALA ASP PRO GLU LYS ILE VAL ARG ARG VAL GLN GLU
VAL SER ALA VAL LEU TYR HIS LEU GLU GLN THR GLU HIS PRO TYR LYS SER LYS LYS ALA VAL TRP HIS LYS LEU LEU SER LYS GLN ARG ARG ALA VAL VAL ALA CYS PHE ARG MET THR PRO LEU TYR ASN LEU P3645 N3651 L3654 E3655 K3658 A3659 A3660 W3661 I3662 E3665
D3666 E3670 I3674 L3677 A3680 GLY GLU GLN GLU GLU GLU GLU GLU VAL GLU GLU LYS K3694 L3698 L3701 V3702 L3703 H3704 E3712 K3713 S3714 K3715 L3716 D3717 E3718 D3719 A3724 D3727 I3728 M3729 A3730 K3731 S3732 C3733 HIS LEU GLU GLU GLY GLY GLU ASN GLY GLU ALA
GLU GLU GLU VAL E3750 V3751 S3752 F3753 E3754 E3755 K3756 E3757 M3758 E3759 K3760 L3764 Y3765 Q3766 Q3767 S3768 R3769 L3770 H3771 T3772 R3773 G3774 A3775 A3776 E3777 M3778 V3779 L3780 Q3781 S3784 A3785 C3786 E3789 M3793 V3794 T3797 L3805 N3806 G3807 G3808 N3809 A3810 E3811 V3812 Q3813 Q3814 K3815 M3816 L3817
L3820 K3821 F3828 L3835 T3838 C3839 S3840 V3841 L3842 D3843 L3844 R3849 K3852 ALA GLU GLY LEU GLY MET VAL ASN GLU ASP GLY THR VAL ILE ASN ARG GLN ASN GLY GLU LYS VAL MET ALA D3877 D3878 E3879 F3880 T3881 Q3882 D3883 L3884 F3885 L3888 Q3889 L3890 L3891 C3892 E3893
F3899 Q3900 N3901 Y3902 T3905 Q3906 T3907 G3908 N3909 N3914 I3915 I3916 I3917 C3918 T3919 V3920 D3921 Y3922 L3923 L3924 R3925 L3926 I3930 F3933 Y3934 W3935 Y3936 Y3937 S3938 D3941 E3944 E3945 K3948 K3953 S3956 V3957 A3958 K3959 Q3960 V3961 F3962 N3963 S3964 L3965 T3966 E3967 Y3968 I3969 Q3970 Q3977
L3980 A3981 H3982 S3983 R3984 L3985 W3986 D3987 A3988 V3989 F3992 V3995 F3996 M4000 M4001 K4002 L4003 A4004 S4007 I4010 E4011 L4012 L4013 L4017 D4018 L4019 Q4020 K4021 D4022 M4023 V4024 V4025 M4026 L4027 L4031 E4032 G4033 N4034 V4035 V4036 N4037 G4038 M4039 I4040 A4041 R4042 Q4043 M4044 V4045 D4046 M4047 L4048
V4055 E4056 M4057 I4058 L4059 K4060 F4061 F4062 D4063 M4064 PHE LEU LYS LEU LYS ASP I4071 V4072 G4073 F4077 T4082 D4083 P4084 Q4100 LYS Q4102 P4106 E4107 I4108 Q4109 F4110 L4111 L4112 D4118 E4119 N4120 N4124 F4125 F4128 R4131 PHE GLN GLU P4135 A4136 R4137 D4138 F4141 N4142 V4143
A4144 V4145 L4146 L4147 T4148 N4149 L4150 S4151 V4154 P4155 H4156 D4157 P4158 R4159 L4160 R4161 L4164 I4170 L4171 E4172 Y4173 F4174 R4175 P4176 Y4177 L4178 I4181 E4182 I4183 R4189 I4190 E4191 R4192 I4193 Y4194 F4195 E4199 R4202 E4206 M4207 P4208 Q4209 V4210 K4214 R4215 Q4216 F4217 I4218 V4221 V4222
G4225 K4230 M4231 F4234 C4238 T4241 I4242 F4243 E4244 M4245 Q4246 I4251 SER GLU PRO GLU GLY GLU PRO GLU ALA ASP GLU GLY ASP GLU GLY MET GLY GLU GLY ALA ALA GLY GLU GLY ALA ALA GLU GLY GLY ALA ALA GLY ALA GLU GLY GLU GLY ALA ALA GLY THR VAL ALA ALA ALA GLY
ALA ARG LEU ALA ALA ALA LEU ARG GLY LEU SER TYR ARG SER LEU ARG ARG ARG VAL ARG ARG LEU ARG ARG GLU THR ALA ARG ALA ALA ALA THR ALA ARG ALA ALA ALA

GLY GLY GLY SER GLY TRP GLY SER GLY ALA GLY GLU GLU ALA GLU GLY ASP GLU ASP GLU ASN MET V4628 F4631 L4632 T4636 M4639 E4640 P4641 A4642 L4643 W4644 C4645 L4646 S4647 L4648 L4649 H4650 T4651 L4652 F4655 L4656 C4657 I4658 I4659 L4664 K4665 V4666 P4667 L4668 V4669 I4670 F4671 K4672 R4673

E4674 K4675 E4676 L4677 A4678 R4679 K4680 I4688 T4689 E4690 Q4691 P4692 G4699 D4702 V4705 T4708 P4709 S4710 F4711 P4712 Y4715 W4716 D4717 K4718 F4719 V4720 K4721 R4722 K4723 K4727 H4728 G4729 D4730 I4731 F4732 G4733 R4734 E4735 R4736 I4737 A4738 E4739 L4740 L4741 G4742 MET ASP LEU ALA SER LEU GLU ILE

THR ALA HIS ASN GLU ARG LYS PRO ASP PRO PRO GLY LEU L4765 M4769 S4770 I4771 D4772 Y4775 W4778 K4779 F4780 G4781 V4782 I4783 F4784 T4785 D4786 F4789 L4790 Y4791 L4792 G4793 W4794 Y4795 M4796 V4797 M4798 S4799 L4800 L4801 G4802 N4806 F4809 A4810 A4811 H4812 L4813 L4814 D4815 G4819 V4820

K4821 T4822 L4823 R4824 T4825 I4826 S4829 H4832 N4833 G4834 K4835 Q4836 L4837 V4838 M4839 G4842 L4843 L4844 A4845 V4846 V4847 V4848 Y4849 L4850 Y4851 T4852 V4853 F4856 N4857 Y4863 N4864 K4865 S4866 E4867 D4868 E4869 D4870 K4875 C4876 D4877 M4880 T4881 L4884 F4885 H4886 M4887 Y4888 V4889 G4890 V4891 R4892 A4893

G4896 I4897 G4898 I4901 E4902 D4903 P4904 A4905 G4906 Y4909 E4910 L4911 Y4912 R4913 V4914 V4915 F4916 D4917 I4918 T4919 F4920 F4921 V4924 L4928 L4929 A4930 I4931 I4932 Q4933 G4934 L4935 I4936 I4937 D4938 A4939 F4940 G4941 E4942 L4943 R4944 D4945 Q4946 Q4947 E4948 Q4949 V4950 K4951 E4955 T4956 K4957 C4958 F4959 I4960 C4961

G4962 I4963 G4964 S4965 D4966 Y4967 T4971 G4974 F4975 E4976 T4977 H4978 T4979 L4980 E4981 E4982 H4983 N4984 L4985 A4986 N4987 Y4988 M4989 F4990 F4991 L4995 I4996 N4997 K4998 D4999 H5003 T5004 G5005 Q5006 E5007 S5008 Y5009 V5010 W5011 K5012 M5013 Y5014 Q5015 E5016 R5017 F5022 D5026 C5027 F5028 R5029 K5030 E5033 ASP

GLN LEU SER

- Molecule 1: Ryanodine receptor 1

Chain G: 41% 29% • 28%

MET GLY ASP GLY GLY GLU GLY GLU ASP GLU VAL Q12 F13 L14 R15 T16 D17 D18 E19 V20 V21 L22 Q23 C24 S25 A26 K30 E31 Q32 L33 K34 L35 C36 L37 A38 A39 E40 G41 F42 R45 L46 C47 F48 L49 E50 P51 T52 S53 Q56 P60 C65 C66 F67 T68 L69

E70 Q71 S72 L73 R76 A77 L78 Q79 E80 M81 N84 THR VAL GLU ALA GLY VAL GLU SER SER GLN GLY GLY G97 H98 R99 T100 L101 L102 Y103 G104 H105 A106 I107 L108 L109 R110 H111 A112 H113 S114 R115 M116 Y117 L118 S119 C120 L121 T122 T123 S124 R125 SER MET THR ASP K130 L131

A132 F133 D134 V135 G136 L137 Q138 E139 D140 A145 C146 W147 W148 T149 M150 R157 G160 E161 K162 V163 R164 V165 G166 D167 D168 L169 I170 L171 V172 S173 V174 S175 S176 E177 R178 Y179 L180 T184 ALA SER GLY GLU L189 A193 S194 F195 M196 Q197 T198 L199 W200 N201 M202 N203 P204

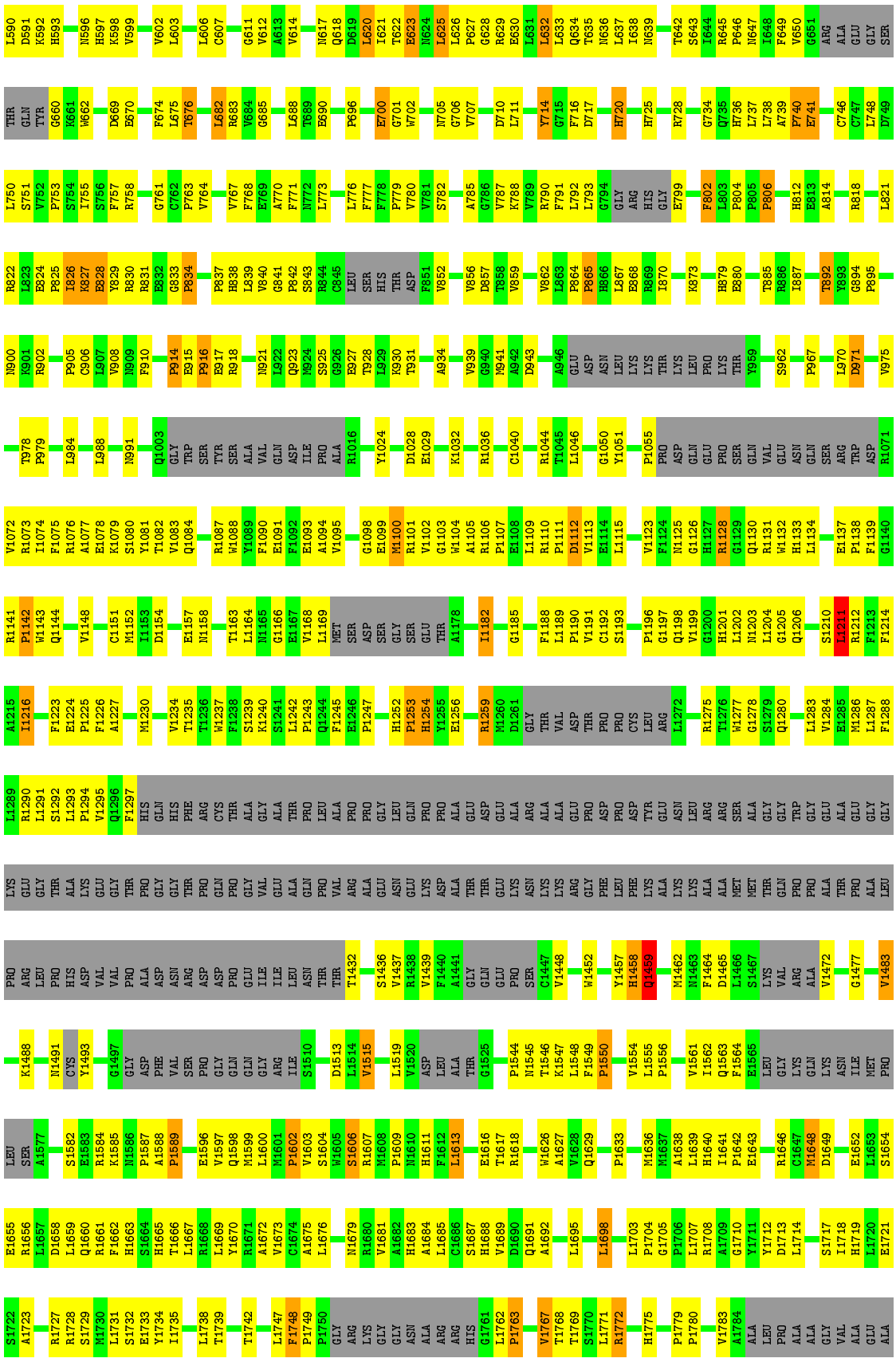
E210 E211 G212 Y213 V214 T215 G216 G217 H218 L222 F223 H224 G225 HIS MET ASP E229 I233 S234 A235 D240 Q241 R242 V245 Y246 Y247 E248 G249 V252 H255 A256 R257 E263 P264 L265 R266 H273 L274 R275 W276 G277 Q278 P279 L280 R281 T287 G288 R289 Y290 L291

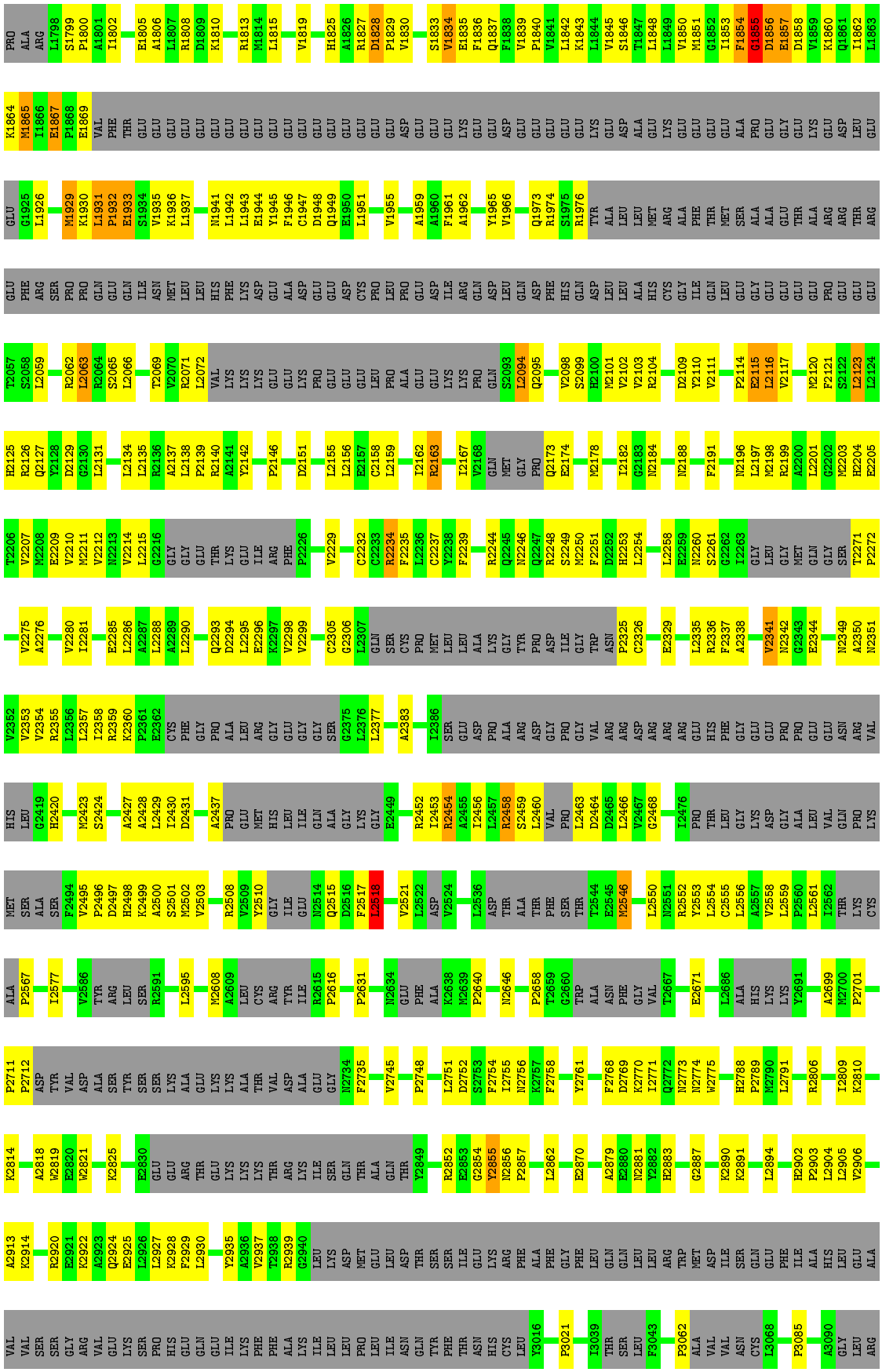
A292 L293 G298 L299 V300 V301 V302 D303 K306 A307 H308 T309 K310 A311 T312 S313 F314 C315 F316 R317 V318 E321 K322 L323 ASP THR ALA PRO K328 R329 M334 E338 I339 K340 Y341 G342 F347 V348 Q349 H350 G354 L355 W356 L357 A361 PRO ASP PRO LYS ALA LEU ARG

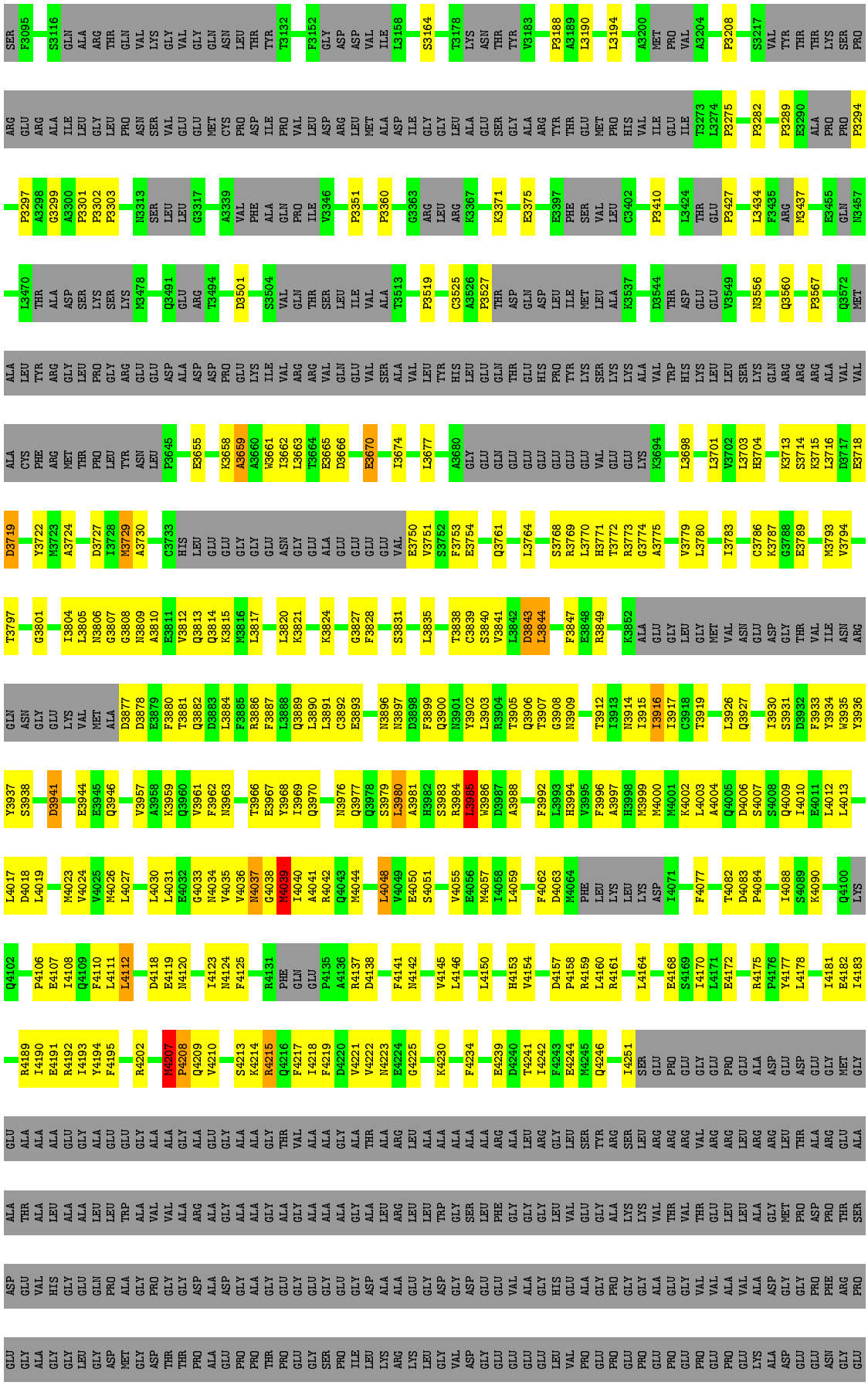
LEU GLY V371 L372 K373 K374 K375 A376 I377 L378 H379 D385 D386 A387 L388 F389 L390 T391 R392 C393 Q394 Q395 E396 E397 A400 A401 R402 M403 I404 H405 S406 T407 L410 Y411 I415 R426 GLY SER GLY PRO PRO ALA GLY PRO ALA L436 P437 I438 L445 Q446 D447 L448 I449 G450

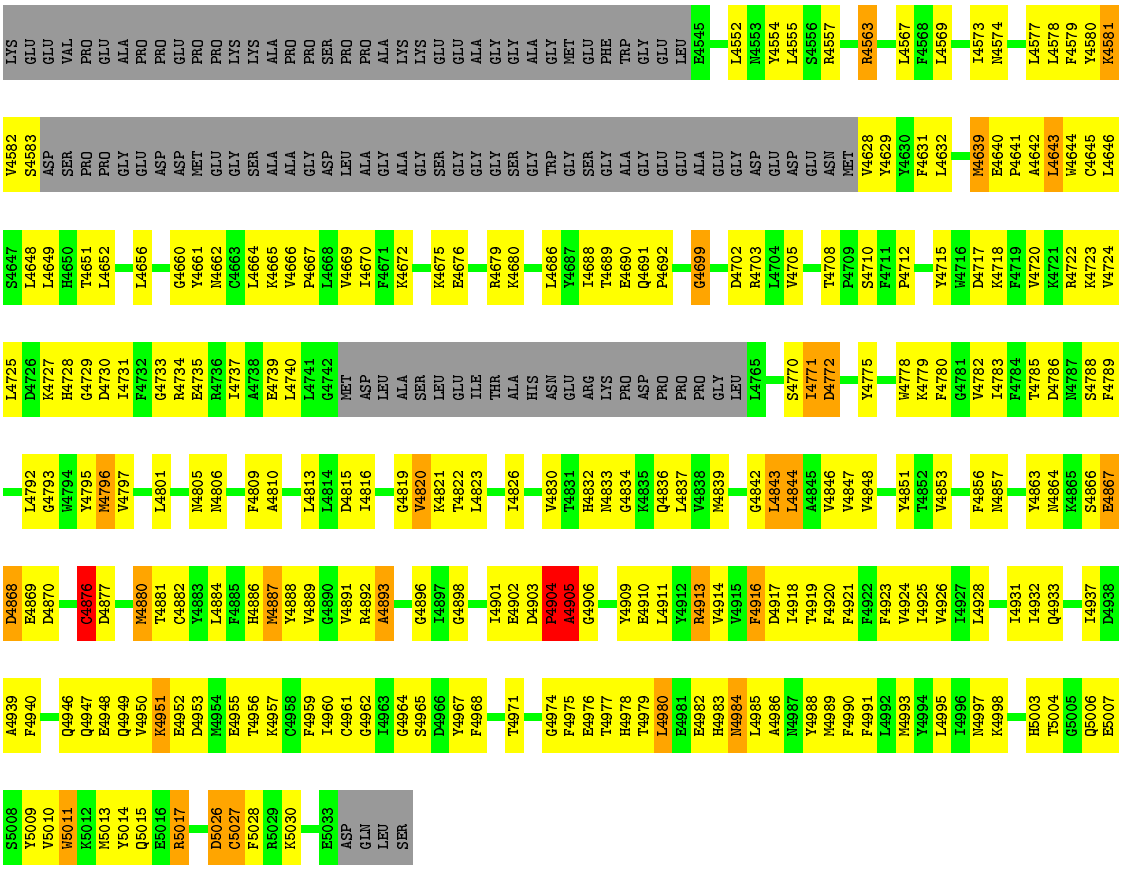
Y451 F452 E453 P454 P455 E458 L459 E463 K467 S470 L471 R472 N473 R474 Q475 S476 L477 F478 Q479 E480 M483 L484 S485 L488 N489 C490 I491 D492 R493 L494 N495 V496 Y497 T498 T499 ALA ALA HIS PHE ALA GLU Y506 A507 G508 A512 E513 S514 W515 K516 E517 I518 V519 N520

L521 L522 Y523 L526 A527 S528 L529 I530 R531 G532 N533 R534 A535 N536 C537 F540 N543 L544 D545 W546 V547 V548 L551 L554 E555 S558 G559 I560 L561 E562 V563 L564 Y565 C566 V567 L568 I569 E570 S571 P572 E573 V574 L575 I578 Q579 E580 N581 H582 S585 S588 L589



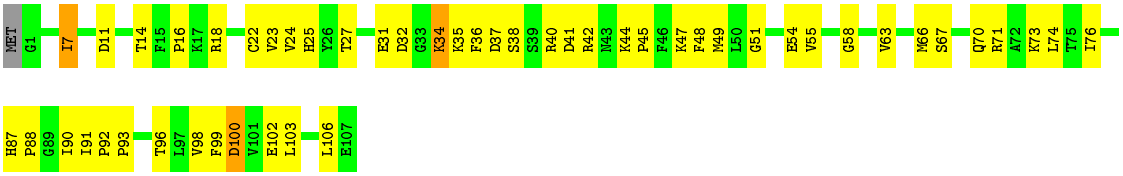






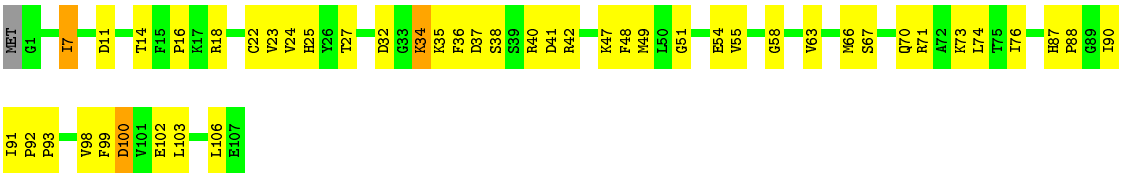
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain B:



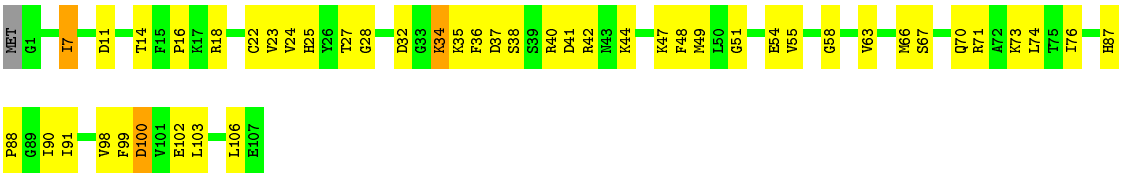
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain D:



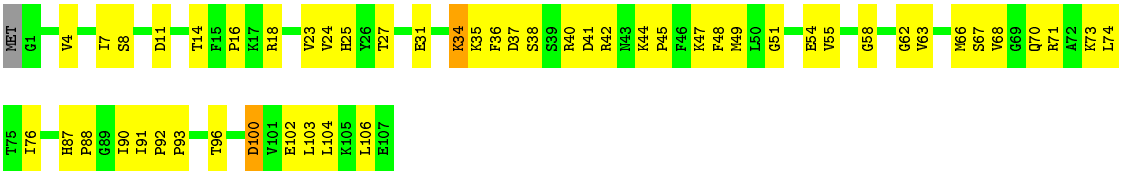
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain F:



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain H:



4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	30000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	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

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	#$\|Z\|>2$	RMSZ	#$\|Z\|>2$
1	A	1.21	41/27312 (0.2%)	1.12	151/37004 (0.4%)
1	C	1.20	39/27312 (0.1%)	1.12	154/37004 (0.4%)
1	E	1.21	35/27312 (0.1%)	1.12	158/37004 (0.4%)
1	G	1.21	38/27312 (0.1%)	1.11	145/37004 (0.4%)
2	B	0.91	1/851 (0.1%)	0.93	2/1146 (0.2%)
2	D	0.91	1/851 (0.1%)	0.92	2/1146 (0.2%)
2	F	0.91	1/851 (0.1%)	0.92	2/1146 (0.2%)
2	H	0.93	1/851 (0.1%)	0.90	0/1146
All	All	1.20	157/112652 (0.1%)	1.11	614/152600 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	36
1	C	0	35
1	E	0	36
1	G	0	34
All	All	0	141

The worst 5 of 157 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	80	GLU	CG-CD	11.12	1.68	1.51
1	G	3661	TRP	CB-CG	10.06	1.68	1.50
1	A	3661	TRP	CB-CG	9.81	1.68	1.50
1	G	1976	ARG	NE-CZ	9.78	1.45	1.33
1	A	741	GLU	CG-CD	9.74	1.66	1.51

The worst 5 of 614 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	80	GLU	OE1-CD-OE2	-10.92	110.20	123.30
1	A	1212	ARG	NE-CZ-NH1	10.39	125.49	120.30
1	G	4796	MET	CG-SD-CE	10.33	116.73	100.20
1	G	1976	ARG	CD-NE-CZ	10.23	137.93	123.60
1	C	1212	ARG	NE-CZ-NH1	10.17	125.39	120.30

There are no chirality outliers.

5 of 141 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	31	GLU	Mainchain,Peptide
1	A	329	ARG	Mainchain,Peptide
1	A	734	GLY	Peptide
1	A	841	GLY	Mainchain,Peptide
1	A	894	GLY	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	26843	0	24428	1190	0
1	C	26843	0	24428	1200	0
1	E	26843	0	24428	1194	0
1	G	26843	0	24427	1209	0
2	B	832	0	831	58	0
2	D	832	0	831	54	0
2	F	832	0	831	58	0
2	H	832	0	831	58	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
All	All	110704	0	101035	4733	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 22.

The worst 5 of 4733 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:4880:MET:HA	1:G:4578:LEU:HD11	1.26	1.17
1:A:4578:LEU:HD11	1:C:4880:MET:HA	1.18	1.17
1:E:4578:LEU:HD11	1:G:4880:MET:HA	1.25	1.16
1:C:4578:LEU:HD11	1:E:4880:MET:HA	1.17	1.10
1:A:4822:THR:HG22	1:C:4839:MET:SD	1.93	1.08

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	3483/5037 (69%)	3132 (90%)	258 (7%)	93 (3%)	6	44
1	C	3483/5037 (69%)	3133 (90%)	254 (7%)	96 (3%)	6	44
1	E	3483/5037 (69%)	3134 (90%)	255 (7%)	94 (3%)	6	44
1	G	3483/5037 (69%)	3137 (90%)	252 (7%)	94 (3%)	6	44
2	B	105/108 (97%)	95 (90%)	9 (9%)	1 (1%)	19	65
2	D	105/108 (97%)	95 (90%)	9 (9%)	1 (1%)	19	65
2	F	105/108 (97%)	96 (91%)	8 (8%)	1 (1%)	19	65
2	H	105/108 (97%)	97 (92%)	8 (8%)	0	100	100
All	All	14352/20580 (70%)	12919 (90%)	1053 (7%)	380 (3%)	11	45

5 of 380 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	806	PRO
1	A	900	ASN
1	A	914	PRO

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Mol	Chain	Res	Type
1	A	916	PRO
1	A	971	ASP

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	2502/4276 (58%)	2472 (99%)	30 (1%)	78	90
1	C	2504/4276 (59%)	2476 (99%)	28 (1%)	80	91
1	E	2501/4276 (58%)	2472 (99%)	29 (1%)	78	90
1	G	2501/4276 (58%)	2474 (99%)	27 (1%)	80	91
2	B	89/90 (99%)	88 (99%)	1 (1%)	80	91
2	D	89/90 (99%)	88 (99%)	1 (1%)	80	91
2	F	89/90 (99%)	88 (99%)	1 (1%)	80	91
2	H	89/90 (99%)	88 (99%)	1 (1%)	80	91
All	All	10364/17464 (59%)	10246 (99%)	118 (1%)	81	91

5 of 118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3987	ASP
1	E	928	THR
1	G	2518	LEU
1	C	4039	MET
2	D	34	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 155 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	3896	ASN
1	E	543	ASN
1	G	3809	ASN

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Mol	Chain	Res	Type
1	C	3906	GLN
1	E	113	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 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.