wwPDB X-ray Structure Validation Summary Report (i)

Feb 4, 2024 – 10:09 PM EST

PDB ID	:	1XFU
Title	:	Crystal structure of anthrax edema factor (EF) truncation mutant, EF-delta 64 in complex with calmodulin
Authors	:	Shen, Y.; Zhukovskaya, N.L.; Guo, Q.; Florian, J.; Tang, W.J.
Deposited on	:	2004-09-15
Resolution	:	3.35 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

The following versions of software and data (see references (1)) were used in the production of this report:

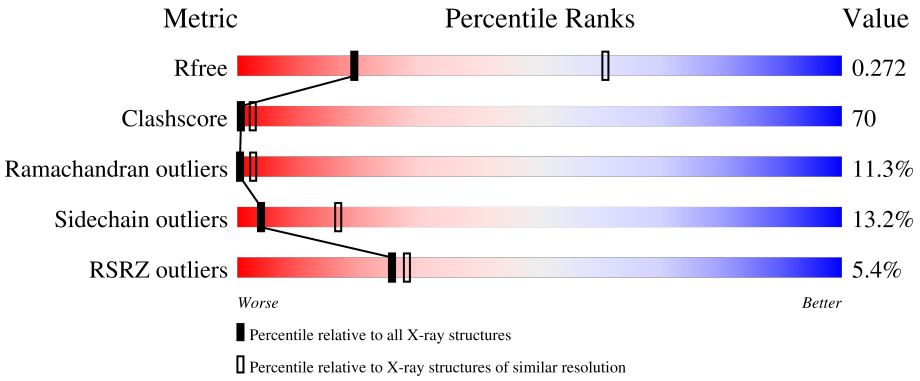
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	747	6% 24% 58% 14%
1	B	747	6% 24% 58% 15%
1	C	747	7% 24% 58% 14%
1	D	747	6% 24% 58% 15%
1	E	747	5% 24% 59% 14%

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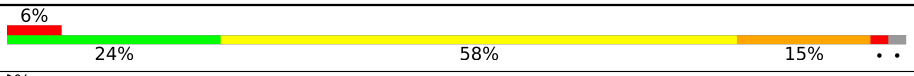
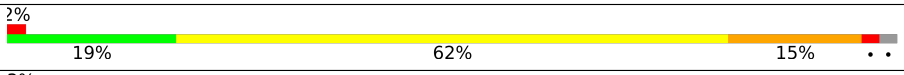
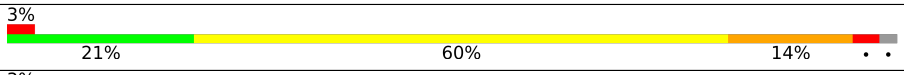
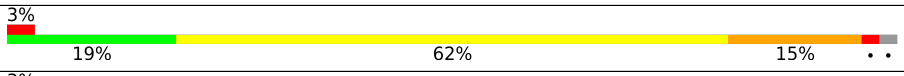
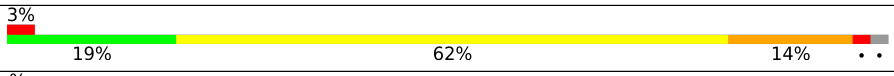
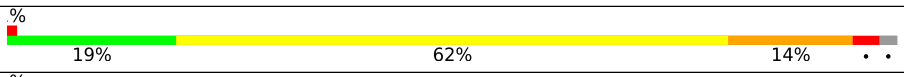
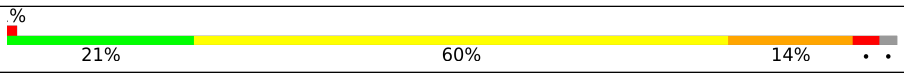
Mol	Chain	Length	Quality of chain
1	F	747	
2	O	149	
2	P	149	
2	Q	149	
2	R	149	
2	S	149	
2	T	149	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 42852 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Calmodulin-sensitive adenylate cyclase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	B	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	C	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	D	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	E	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	F	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	54	MET	-	initiating methionine	UNP P40136
A	55	HIS	-	expression tag	UNP P40136
A	56	HIS	-	expression tag	UNP P40136
A	57	HIS	-	expression tag	UNP P40136
A	58	HIS	-	expression tag	UNP P40136
A	59	HIS	-	expression tag	UNP P40136
A	60	HIS	-	expression tag	UNP P40136
A	61	ALA	-	cloning artifact	UNP P40136
A	62	ALA	-	cloning artifact	UNP P40136
A	63	ALA	-	cloning artifact	UNP P40136
B	54	MET	-	initiating methionine	UNP P40136
B	55	HIS	-	expression tag	UNP P40136
B	56	HIS	-	expression tag	UNP P40136
B	57	HIS	-	expression tag	UNP P40136
B	58	HIS	-	expression tag	UNP P40136
B	59	HIS	-	expression tag	UNP P40136
B	60	HIS	-	expression tag	UNP P40136

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Chain	Residue	Modelled	Actual	Comment	Reference
B	61	ALA	-	cloning artifact	UNP P40136
B	62	ALA	-	cloning artifact	UNP P40136
B	63	ALA	-	cloning artifact	UNP P40136
C	54	MET	-	initiating methionine	UNP P40136
C	55	HIS	-	expression tag	UNP P40136
C	56	HIS	-	expression tag	UNP P40136
C	57	HIS	-	expression tag	UNP P40136
C	58	HIS	-	expression tag	UNP P40136
C	59	HIS	-	expression tag	UNP P40136
C	60	HIS	-	expression tag	UNP P40136
C	61	ALA	-	cloning artifact	UNP P40136
C	62	ALA	-	cloning artifact	UNP P40136
C	63	ALA	-	cloning artifact	UNP P40136
D	54	MET	-	initiating methionine	UNP P40136
D	55	HIS	-	expression tag	UNP P40136
D	56	HIS	-	expression tag	UNP P40136
D	57	HIS	-	expression tag	UNP P40136
D	58	HIS	-	expression tag	UNP P40136
D	59	HIS	-	expression tag	UNP P40136
D	60	HIS	-	expression tag	UNP P40136
D	61	ALA	-	cloning artifact	UNP P40136
D	62	ALA	-	cloning artifact	UNP P40136
D	63	ALA	-	cloning artifact	UNP P40136
E	54	MET	-	initiating methionine	UNP P40136
E	55	HIS	-	expression tag	UNP P40136
E	56	HIS	-	expression tag	UNP P40136
E	57	HIS	-	expression tag	UNP P40136
E	58	HIS	-	expression tag	UNP P40136
E	59	HIS	-	expression tag	UNP P40136
E	60	HIS	-	expression tag	UNP P40136
E	61	ALA	-	cloning artifact	UNP P40136
E	62	ALA	-	cloning artifact	UNP P40136
E	63	ALA	-	cloning artifact	UNP P40136
F	54	MET	-	initiating methionine	UNP P40136
F	55	HIS	-	expression tag	UNP P40136
F	56	HIS	-	expression tag	UNP P40136
F	57	HIS	-	expression tag	UNP P40136
F	58	HIS	-	expression tag	UNP P40136
F	59	HIS	-	expression tag	UNP P40136
F	60	HIS	-	expression tag	UNP P40136
F	61	ALA	-	cloning artifact	UNP P40136
F	62	ALA	-	cloning artifact	UNP P40136

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Chain	Residue	Modelled	Actual	Comment	Reference
F	63	ALA	-	cloning artifact	UNP P40136

- Molecule 2 is a protein called Calmodulin 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	O	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			
2	P	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			
2	Q	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			
2	R	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			
2	S	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			
2	T	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		
3	F	1	Total	Mg	0	0
			1	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	O	3	Total	Ca	0	0
			3	3		
4	P	3	Total	Ca	0	0
			3	3		

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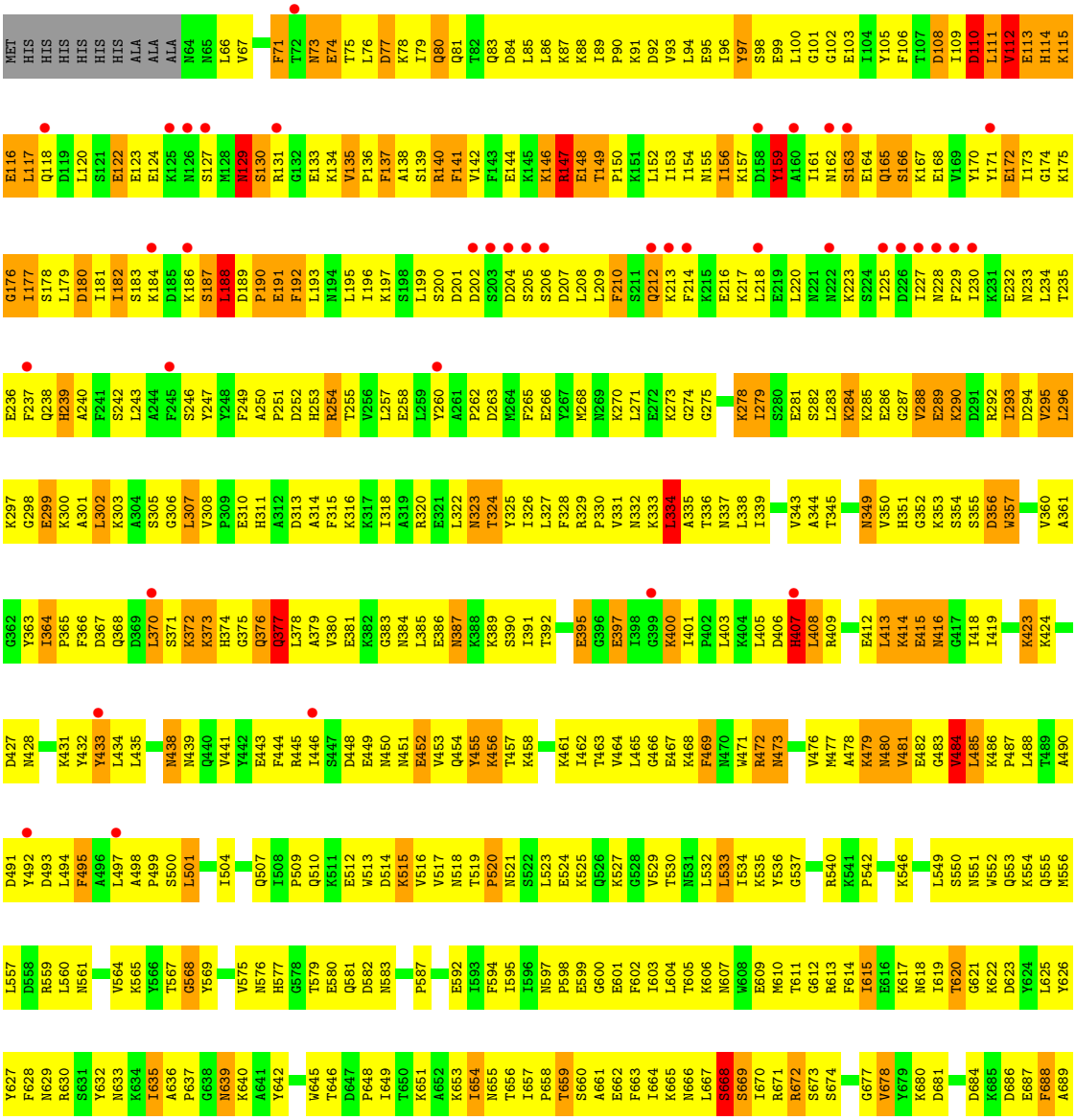
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	Q	3	Total Ca 3 3	0	0
4	R	3	Total Ca 3 3	0	0
4	S	3	Total Ca 3 3	0	0
4	T	3	Total Ca 3 3	0	0

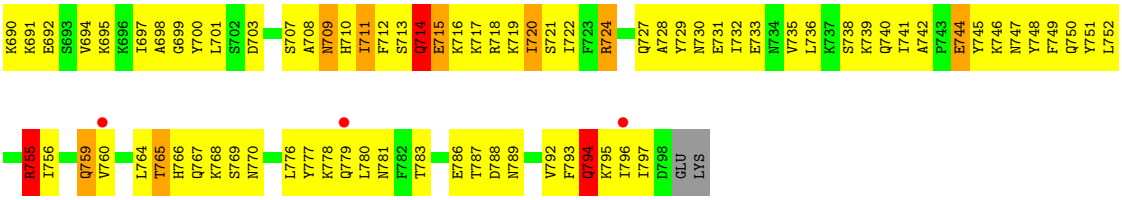
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

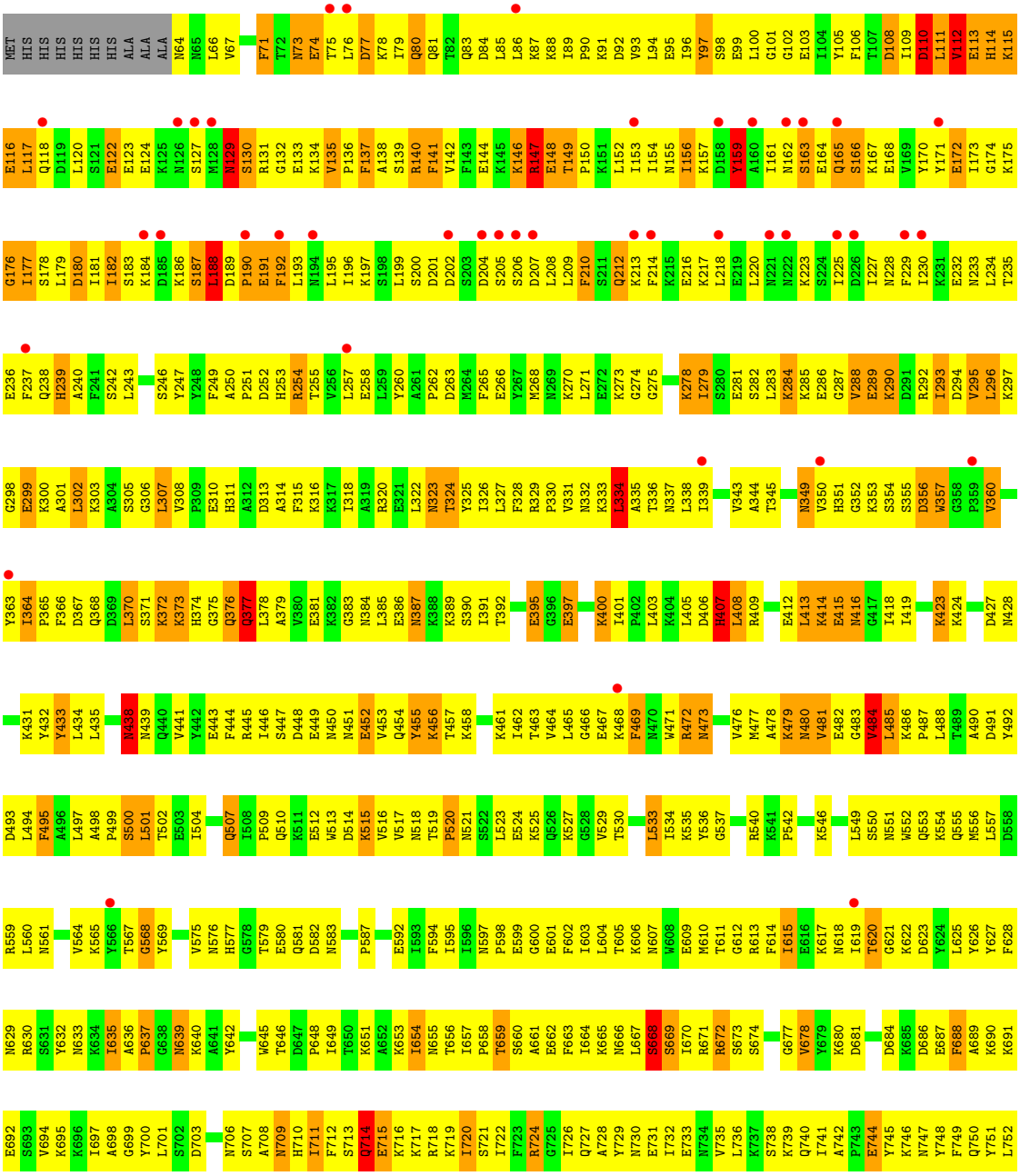
• Molecule 1: Calmodulin-sensitive adenylate cyclase

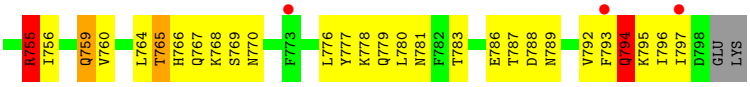
Chain A:





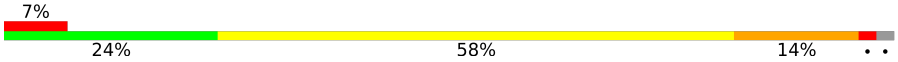
• Molecule 1: Calmodulin-sensitive adenylate cyclase

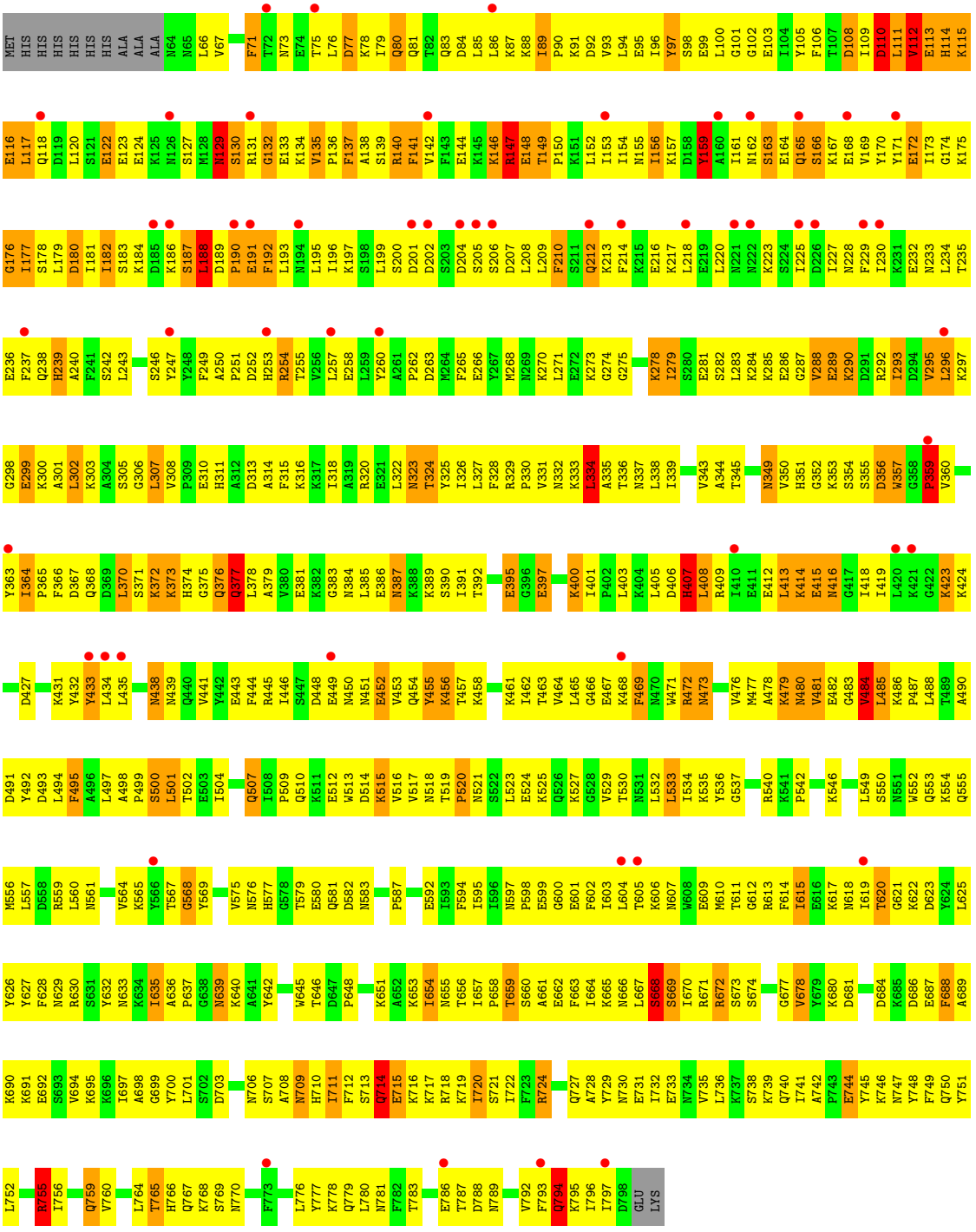




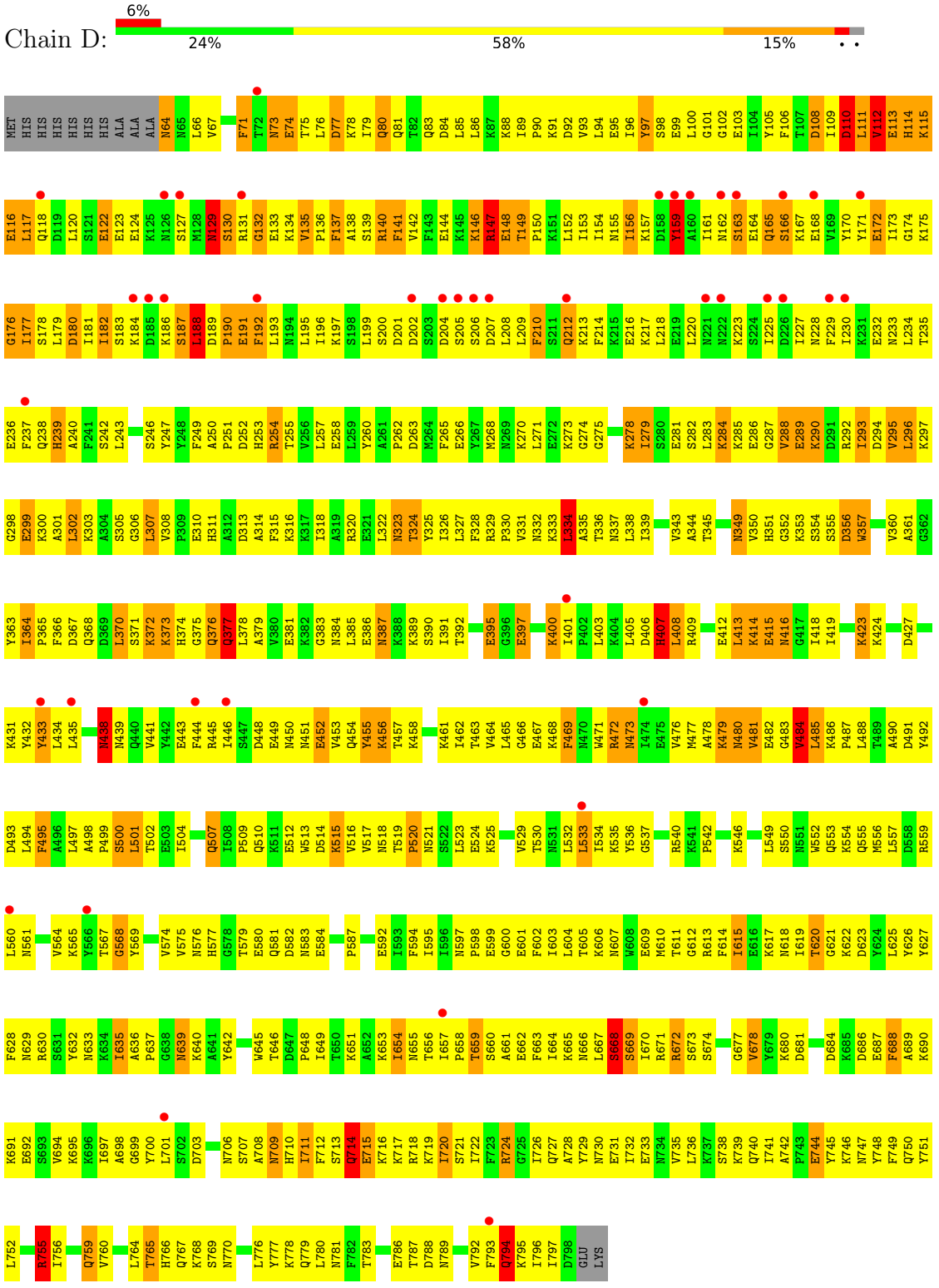
• Molecule 1: Calmodulin-sensitive adenylate cyclase

Chain C:

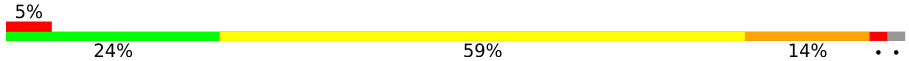


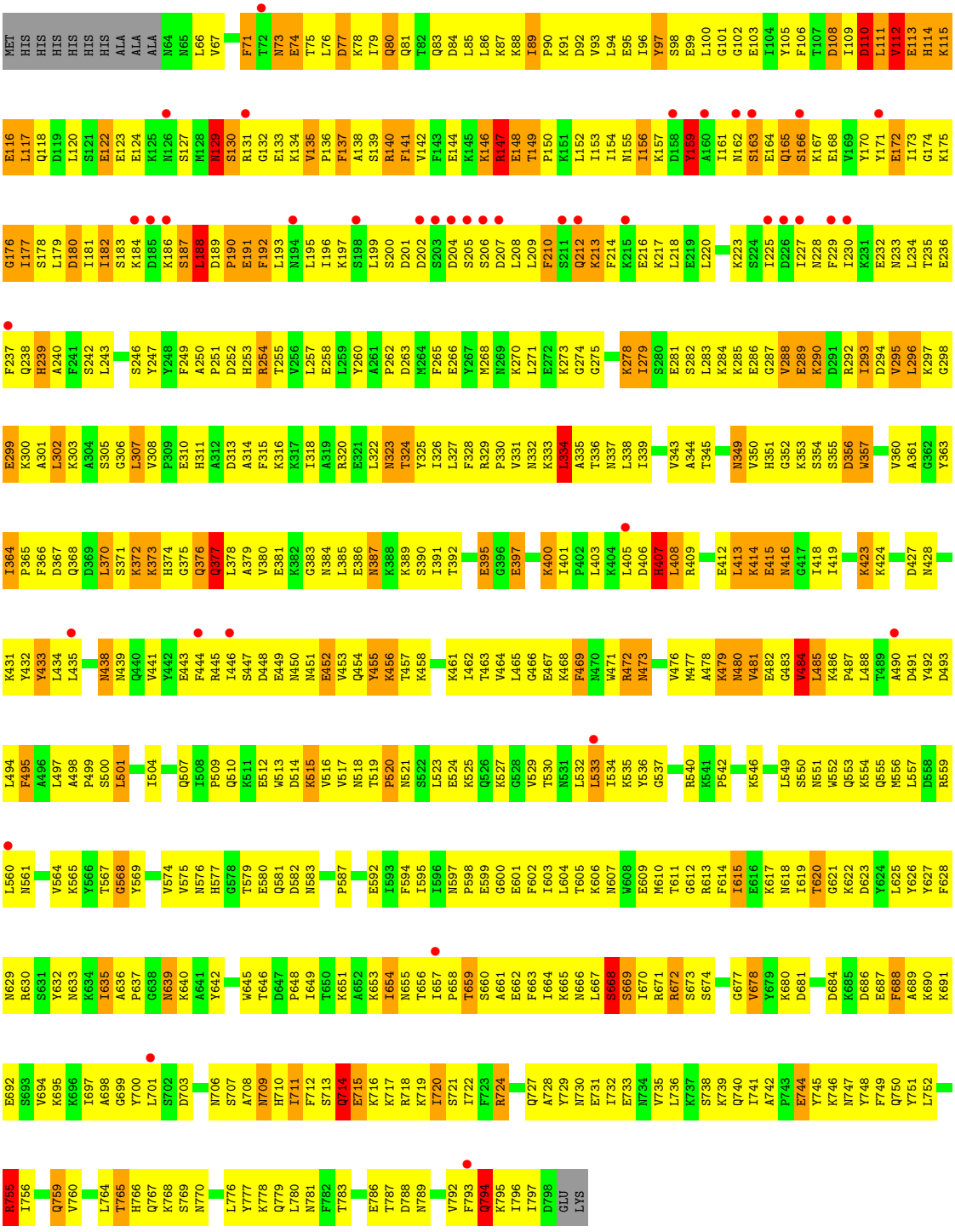


• Molecule 1: Calmodulin-sensitive adenylate cyclase



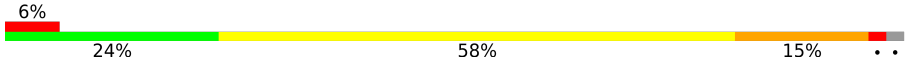
• Molecule 1: Calmodulin-sensitive adenylate cyclase

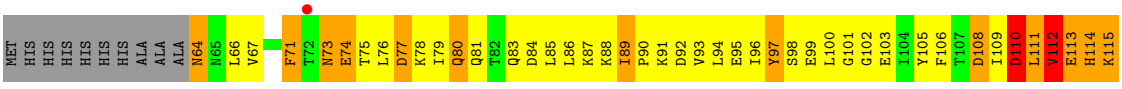


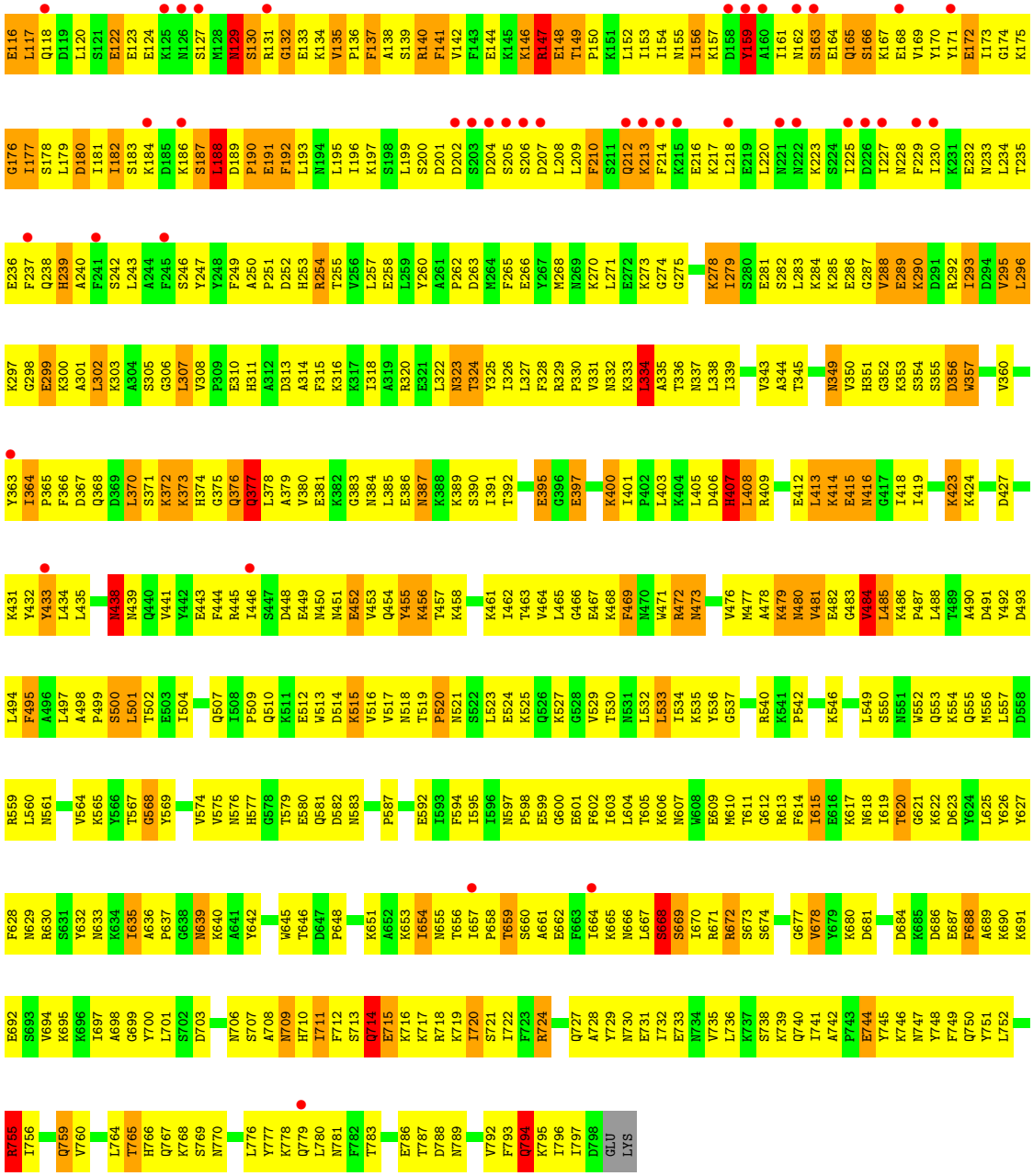


• Molecule 1: Calmodulin-sensitive adenylate cyclase

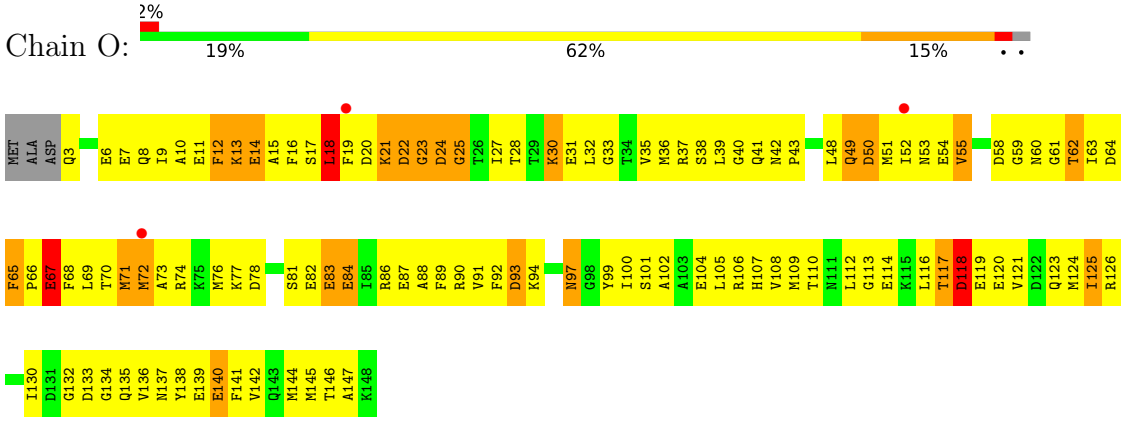
Chain F:





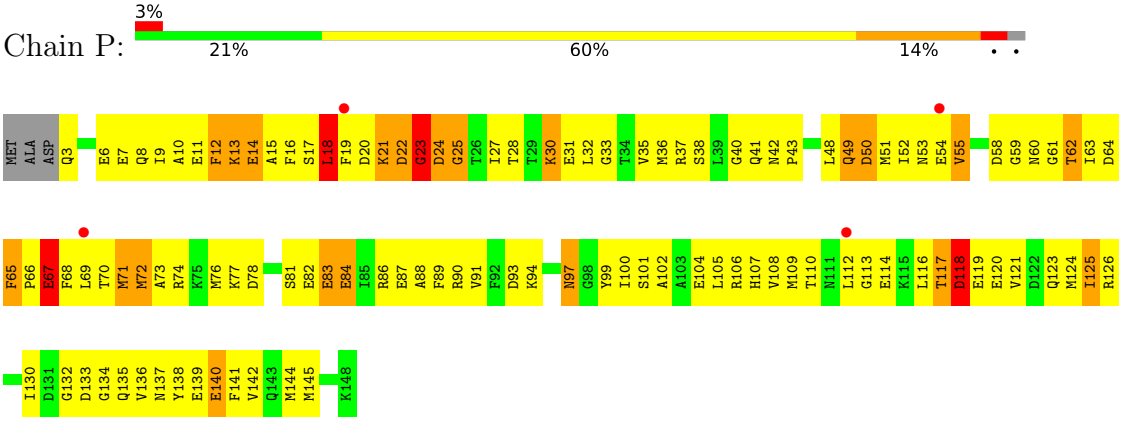


• Molecule 2: Calmodulin 2



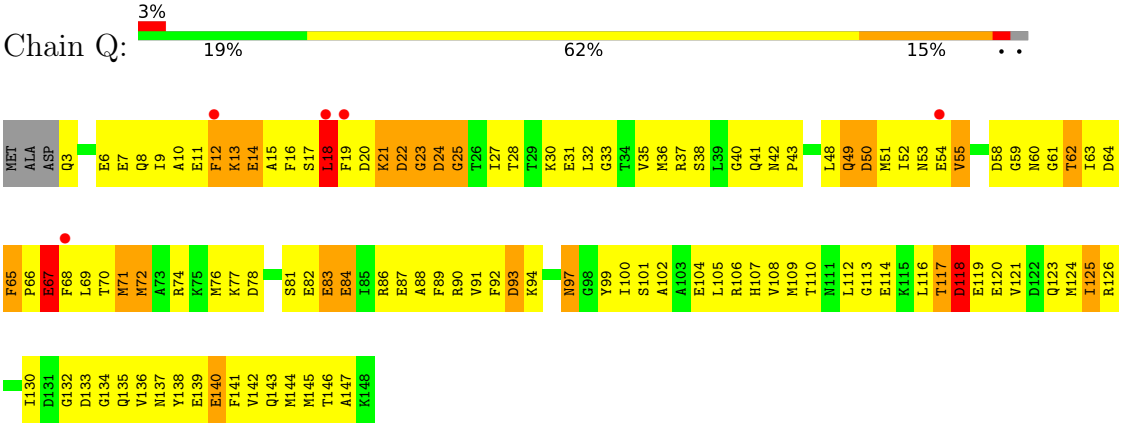
• Molecule 2: Calmodulin 2

Chain P:



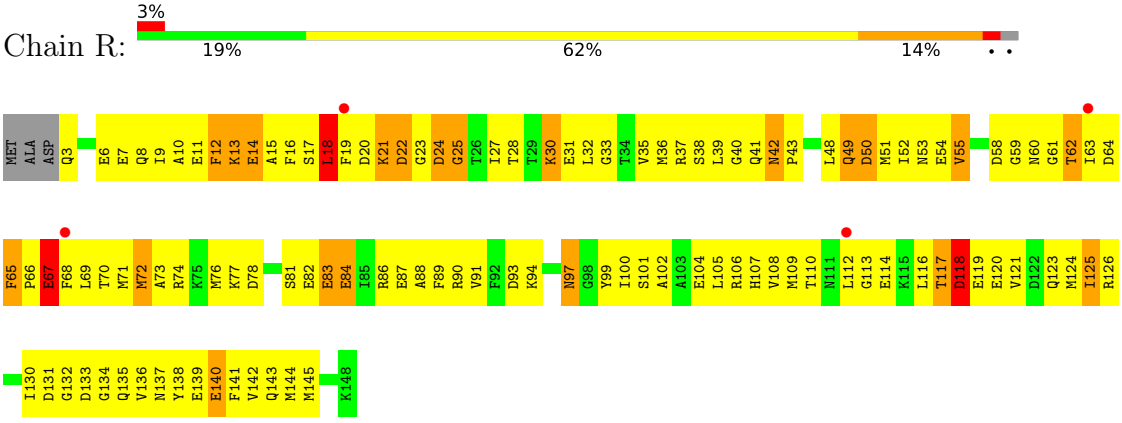
• Molecule 2: Calmodulin 2

Chain Q:



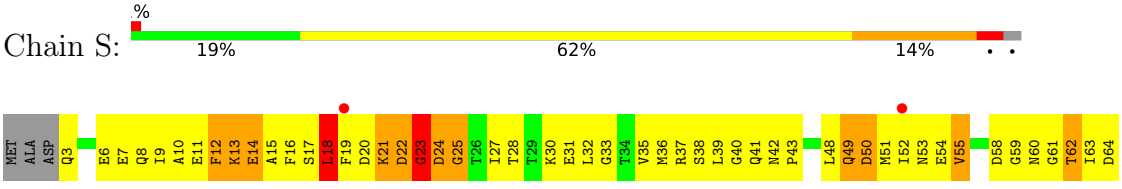
• Molecule 2: Calmodulin 2

Chain R:

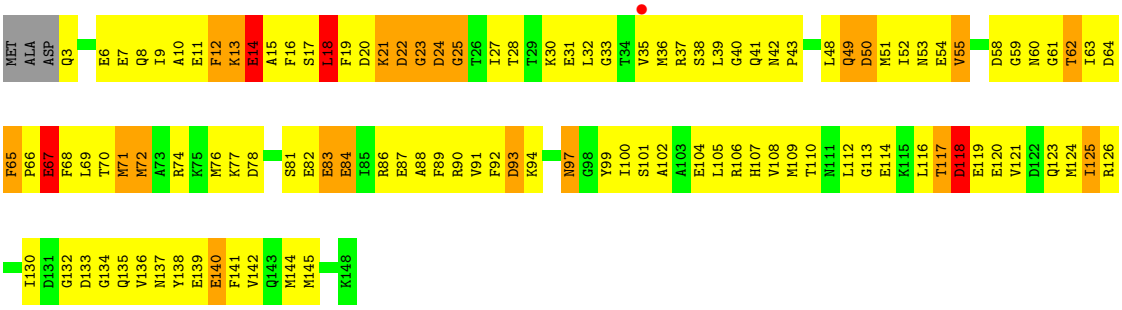


• Molecule 2: Calmodulin 2

Chain S:



• Molecule 2: Calmodulin 2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	317.56Å 183.11Å 141.12Å 90.00° 90.05° 90.00°	Depositor
Resolution (Å)	29.99 – 3.35 40.47 – 3.30	Depositor EDS
% Data completeness (in resolution range)	95.8 (29.99-3.35) 94.8 (40.47-3.30)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.03	Depositor
$< I/\sigma(I) >$ [1]	2.58 (at 3.32Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.283 , 0.300 0.255 , 0.272	Depositor DCC
R_{free} test set	6103 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	100.0	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 42.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.468 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.468 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.468 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.460 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.468 for -h,-k,l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	42852	wwPDB-VP
Average B, all atoms (Å^2)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.52	0/6104	0.79	7/8208 (0.1%)
1	B	0.53	0/6104	0.79	8/8208 (0.1%)
1	C	0.54	1/6104 (0.0%)	0.80	9/8208 (0.1%)
1	D	0.53	1/6104 (0.0%)	0.79	7/8208 (0.1%)
1	E	0.53	0/6104	0.79	7/8208 (0.1%)
1	F	0.54	1/6104 (0.0%)	0.79	7/8208 (0.1%)
2	O	0.56	0/1158	0.75	1/1553 (0.1%)
2	P	0.57	0/1158	0.75	1/1553 (0.1%)
2	Q	0.57	0/1158	0.75	1/1553 (0.1%)
2	R	0.57	0/1158	0.75	0/1553
2	S	0.57	0/1158	0.75	1/1553 (0.1%)
2	T	0.57	0/1158	0.75	1/1553 (0.1%)
All	All	0.54	3/43572 (0.0%)	0.79	50/58566 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	132	GLY	C-N	6.49	1.49	1.34
1	C	132	GLY	C-N	5.91	1.47	1.34
1	D	132	GLY	C-N	5.80	1.47	1.34

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	147	ARG	N-CA-C	6.70	129.09	111.00
1	F	147	ARG	N-CA-C	6.70	129.08	111.00
1	C	147	ARG	N-CA-C	6.69	129.05	111.00
1	A	147	ARG	N-CA-C	6.69	129.05	111.00
1	E	147	ARG	N-CA-C	6.68	129.04	111.00

There are no chirality outliers.

There are no planarity outliers.

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	5992	0	6010	821	0
1	B	5992	0	6010	835	0
1	C	5992	0	6010	821	0
1	D	5992	0	6010	827	0
1	E	5992	0	6010	826	0
1	F	5992	0	6010	836	0
2	O	1146	0	1071	189	0
2	P	1146	0	1071	184	0
2	Q	1146	0	1071	187	0
2	R	1146	0	1071	193	0
2	S	1146	0	1071	193	0
2	T	1146	0	1071	191	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	O	3	0	0	0	0
4	P	3	0	0	0	0
4	Q	3	0	0	0	0
4	R	3	0	0	0	0
4	S	3	0	0	0	0
4	T	3	0	0	0	0
All	All	42852	0	42486	5969	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 70.

The worst 5 of 5969 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:154:ILE:HG13	1:A:171:TYR:HE1	1.02	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:165:GLN:HE21	1:E:251:PRO:HG2	1.07	1.17
1:E:154:ILE:HG13	1:E:171:TYR:HE1	1.01	1.15
1:B:165:GLN:HE21	1:B:251:PRO:HG2	1.06	1.14
1:F:154:ILE:HG13	1:F:171:TYR:HE1	1.03	1.14

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 X-ray entries followed by that with respect to entries of similar resolution.

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	733/747 (98%)	503 (69%)	145 (20%)	85 (12%)	0	2
1	B	733/747 (98%)	507 (69%)	142 (19%)	84 (12%)	0	2
1	C	733/747 (98%)	506 (69%)	145 (20%)	82 (11%)	0	2
1	D	733/747 (98%)	504 (69%)	144 (20%)	85 (12%)	0	2
1	E	733/747 (98%)	502 (68%)	146 (20%)	85 (12%)	0	2
1	F	733/747 (98%)	503 (69%)	146 (20%)	84 (12%)	0	2
2	O	144/149 (97%)	90 (62%)	39 (27%)	15 (10%)	0	3
2	P	144/149 (97%)	91 (63%)	39 (27%)	14 (10%)	0	4
2	Q	144/149 (97%)	90 (62%)	39 (27%)	15 (10%)	0	3
2	R	144/149 (97%)	90 (62%)	39 (27%)	15 (10%)	0	3
2	S	144/149 (97%)	92 (64%)	37 (26%)	15 (10%)	0	3
2	T	144/149 (97%)	92 (64%)	36 (25%)	16 (11%)	0	2
All	All	5262/5376 (98%)	3570 (68%)	1097 (21%)	595 (11%)	0	2

5 of 595 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	ASN

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Mol	Chain	Res	Type
1	A	74	GLU
1	A	80	GLN
1	A	108	ASP
1	A	111	LEU

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 X-ray entries followed by that with respect to entries of similar resolution.

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	664/675 (98%)	581 (88%)	83 (12%)	4	18
1	B	664/675 (98%)	580 (87%)	84 (13%)	4	18
1	C	664/675 (98%)	577 (87%)	87 (13%)	4	17
1	D	664/675 (98%)	578 (87%)	86 (13%)	4	17
1	E	664/675 (98%)	580 (87%)	84 (13%)	4	18
1	F	664/675 (98%)	578 (87%)	86 (13%)	4	17
2	O	123/127 (97%)	104 (85%)	19 (15%)	2	12
2	P	123/127 (97%)	104 (85%)	19 (15%)	2	12
2	Q	123/127 (97%)	105 (85%)	18 (15%)	3	13
2	R	123/127 (97%)	104 (85%)	19 (15%)	2	12
2	S	123/127 (97%)	105 (85%)	18 (15%)	3	13
2	T	123/127 (97%)	105 (85%)	18 (15%)	3	13
All	All	4722/4812 (98%)	4101 (87%)	621 (13%)	4	17

5 of 621 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	397	GLU
2	R	55	VAL
1	F	456	LYS
1	F	395	GLU
2	O	67	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 218 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	767	GLN
1	E	747	ASN
2	R	41	GLN
1	E	83	GLN
1	E	480	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 24 ligands modelled in this entry, 24 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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	735/747 (98%)	0.21	42 (5%)	23	26	24, 80, 134, 147	0
1	B	735/747 (98%)	0.22	45 (6%)	21	23	25, 80, 134, 148	0
1	C	735/747 (98%)	0.25	56 (7%)	13	16	25, 80, 134, 147	0
1	D	735/747 (98%)	0.20	42 (5%)	23	26	26, 80, 134, 147	0
1	E	735/747 (98%)	0.20	39 (5%)	26	28	26, 80, 135, 147	0
1	F	735/747 (98%)	0.21	42 (5%)	23	26	25, 81, 134, 147	0
2	O	146/149 (97%)	-0.05	3 (2%)	63	67	24, 65, 127, 137	0
2	P	146/149 (97%)	0.00	4 (2%)	54	57	24, 65, 126, 137	0
2	Q	146/149 (97%)	0.04	5 (3%)	45	47	23, 65, 126, 137	0
2	R	146/149 (97%)	-0.03	4 (2%)	54	57	24, 65, 126, 137	0
2	S	146/149 (97%)	-0.04	2 (1%)	75	78	24, 66, 126, 137	0
2	T	146/149 (97%)	-0.07	1 (0%)	87	91	23, 65, 126, 137	0
All	All	5286/5376 (98%)	0.18	285 (5%)	25	28	23, 77, 134, 148	0

The worst 5 of 285 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	225	ILE	13.5
1	A	230	ILE	11.2
1	E	226	ASP	10.2
1	F	230	ILE	10.0
1	E	225	ILE	9.1

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	CA	S	709	1/1	0.84	0.16	78,78,78,78	0
4	CA	Q	806	1/1	0.88	0.17	46,46,46,46	0
3	MG	C	902	1/1	0.90	0.13	14,14,14,14	0
4	CA	R	808	1/1	0.92	0.19	41,41,41,41	0
4	CA	R	707	1/1	0.93	0.22	79,79,79,79	0
4	CA	O	802	1/1	0.93	0.18	44,44,44,44	0
3	MG	B	901	1/1	0.93	0.16	13,13,13,13	0
4	CA	T	812	1/1	0.93	0.18	43,43,43,43	0
4	CA	Q	705	1/1	0.94	0.07	79,79,79,79	0
4	CA	P	703	1/1	0.94	0.17	71,71,71,71	0
4	CA	T	711	1/1	0.94	0.14	77,77,77,77	0
4	CA	P	804	1/1	0.94	0.18	43,43,43,43	0
4	CA	S	810	1/1	0.95	0.18	45,45,45,45	0
4	CA	O	801	1/1	0.96	0.15	29,29,29,29	0
4	CA	Q	805	1/1	0.96	0.13	32,32,32,32	0
4	CA	S	809	1/1	0.96	0.12	25,25,25,25	0
3	MG	D	903	1/1	0.97	0.20	19,19,19,19	0
3	MG	E	904	1/1	0.97	0.16	14,14,14,14	0
3	MG	F	905	1/1	0.97	0.23	16,16,16,16	0
4	CA	P	803	1/1	0.97	0.13	33,33,33,33	0
4	CA	T	811	1/1	0.97	0.16	31,31,31,31	0
4	CA	O	701	1/1	0.97	0.12	83,83,83,83	0
4	CA	R	807	1/1	0.98	0.13	33,33,33,33	0
3	MG	A	900	1/1	0.98	0.27	18,18,18,18	0

6.5 Other polymers (i)

There are no such residues in this entry.