



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 01:46 AM UTC

PDB ID : 1XFU / pdb_00001xfu
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 ⓘ 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:

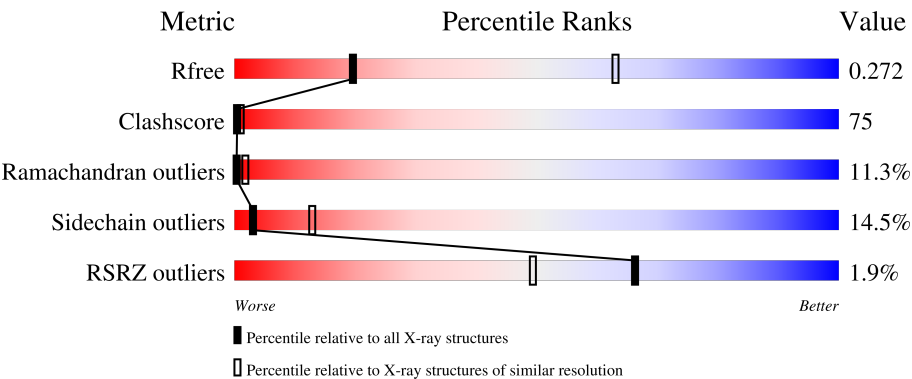
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
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}	180053	1099 (3.40-3.32)
Clashscore	190562	1116 (3.40-3.32)
Ramachandran outliers	187476	1101 (3.40-3.32)
Sidechain outliers	187428	1101 (3.40-3.32)
RSRZ outliers	180081	1099 (3.40-3.32)

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 $\leq 5\%$. 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	3% 21% 54% 20%
1	B	747	2% 20% 55% 20%
1	C	747	2% 21% 55% 19%
1	D	747	2% 20% 54% 20%
1	E	747	2% 20% 55% 20%

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Mol	Chain	Length	Quality of chain			
1	F	747	2% 21% 55% 19%			
2	O	149	17% 59% 19%			
2	P	149	18% 60% 17%			
2	Q	149	% 17% 60% 18%			
2	R	149	17% 60% 18%			
2	S	149	18% 58% 18%			
2	T	149	% 18% 59% 17%			

2 Entry composition

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 (CCD ID: 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 (CCD ID: 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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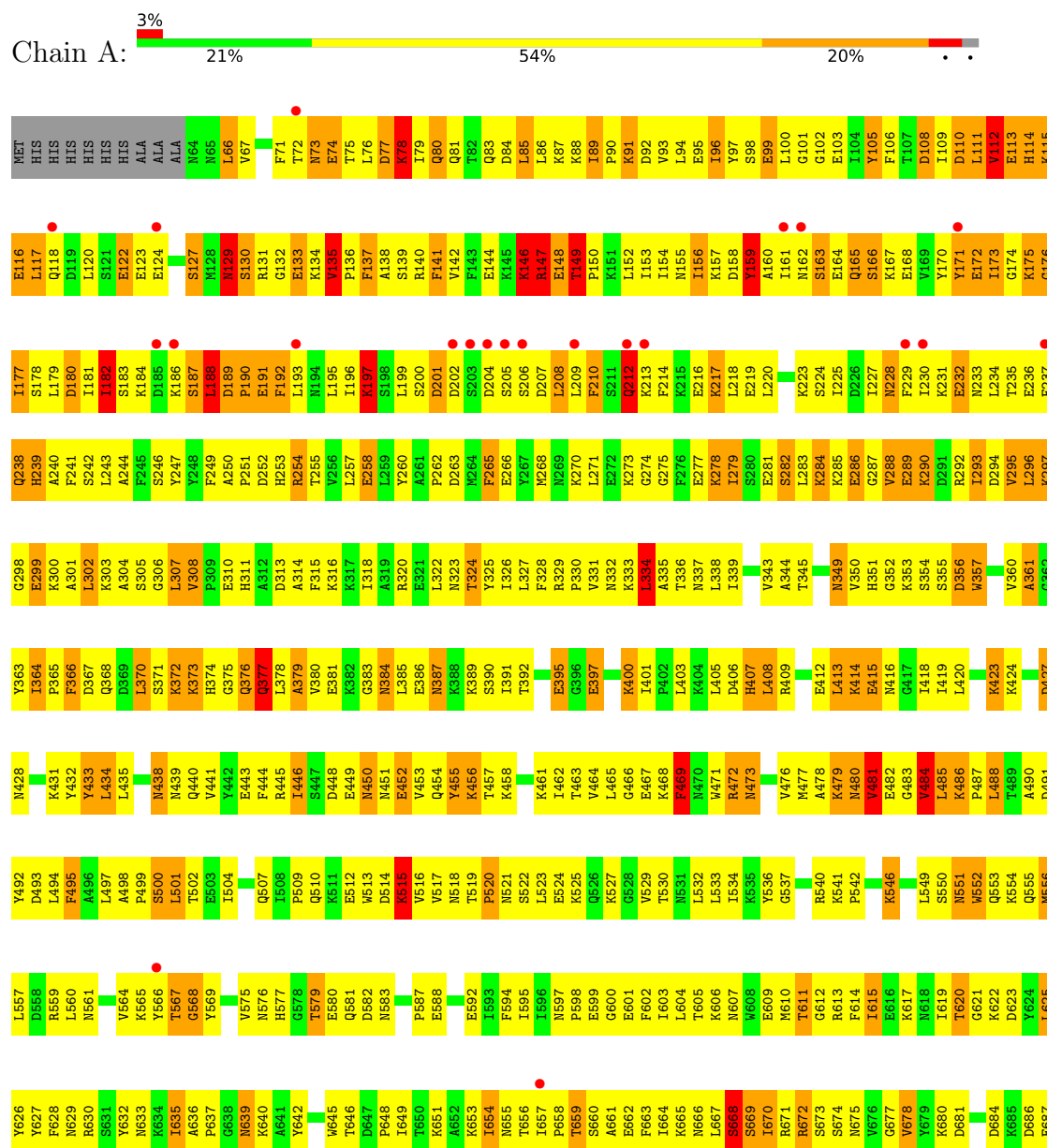
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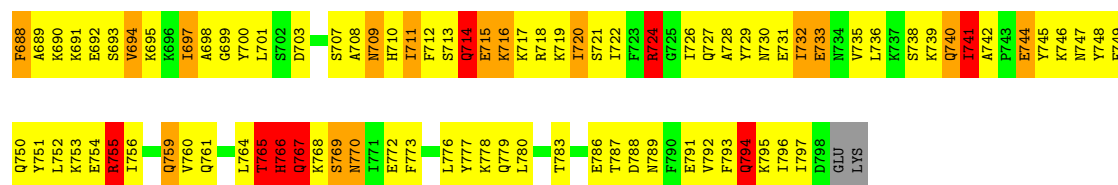
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	Q	3	Total 3	Ca 3	0	0
4	R	3	Total 3	Ca 3	0	0
4	S	3	Total 3	Ca 3	0	0
4	T	3	Total 3	Ca 3	0	0

3 Residue-property plots

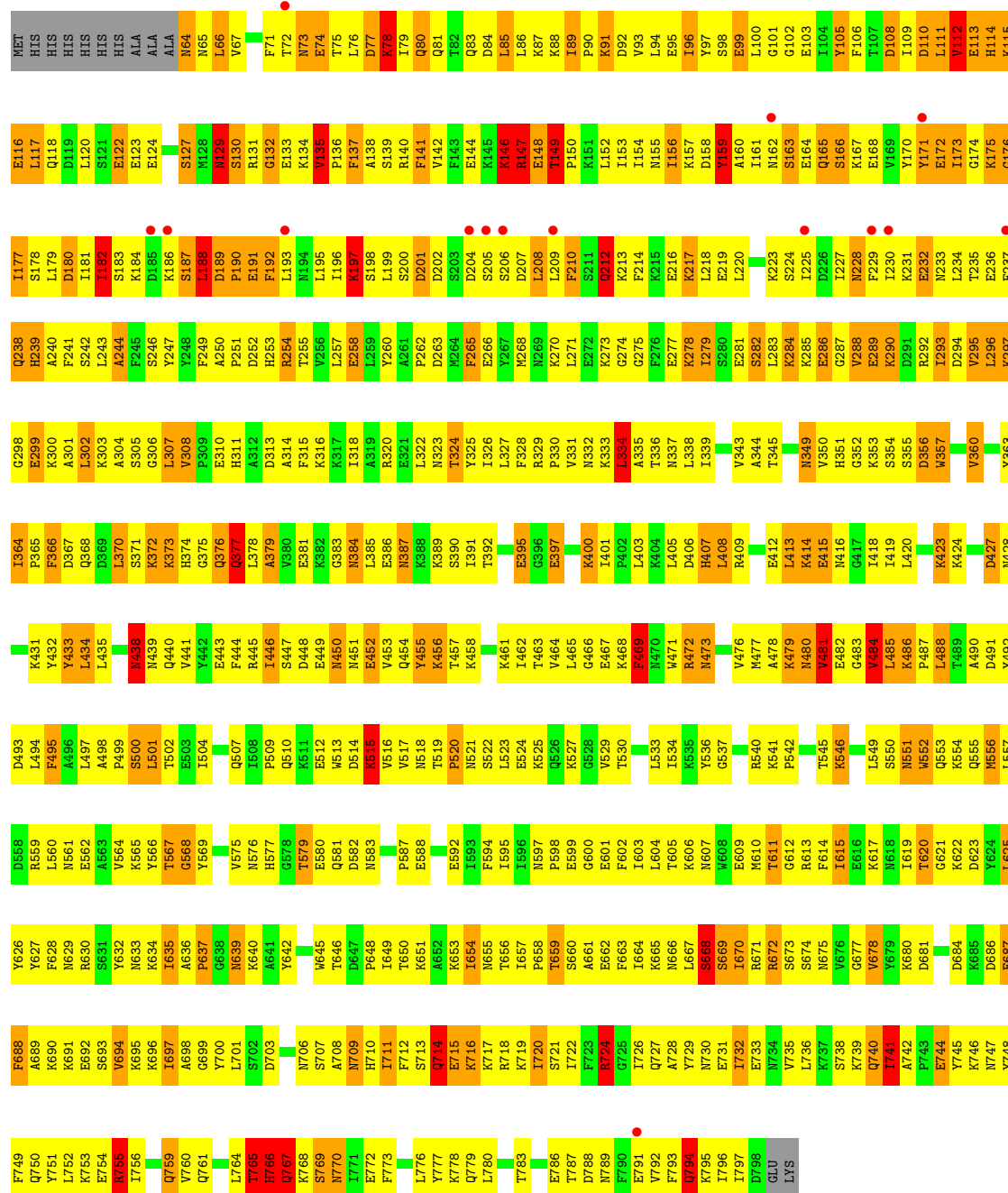
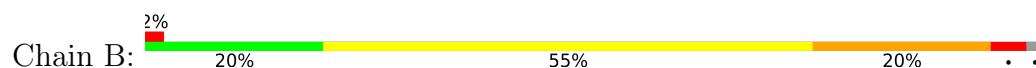
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

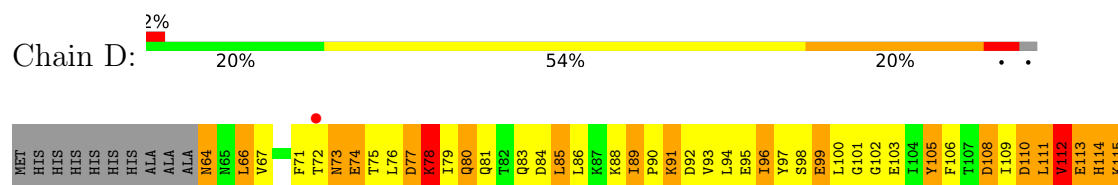
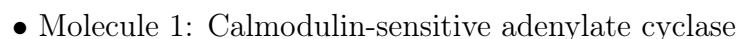


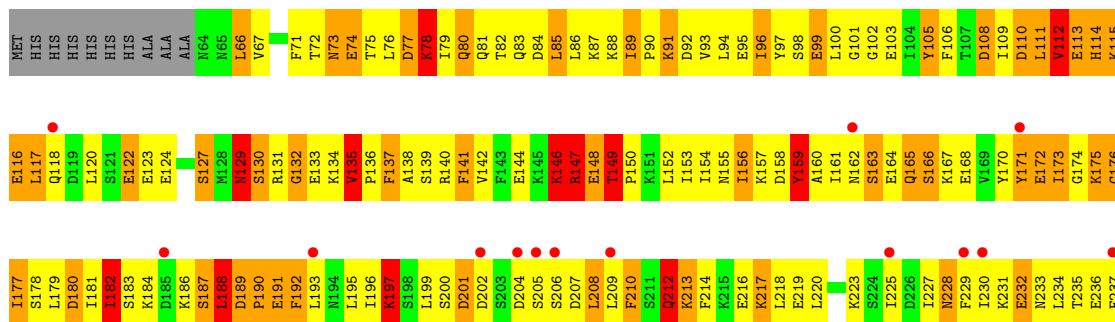


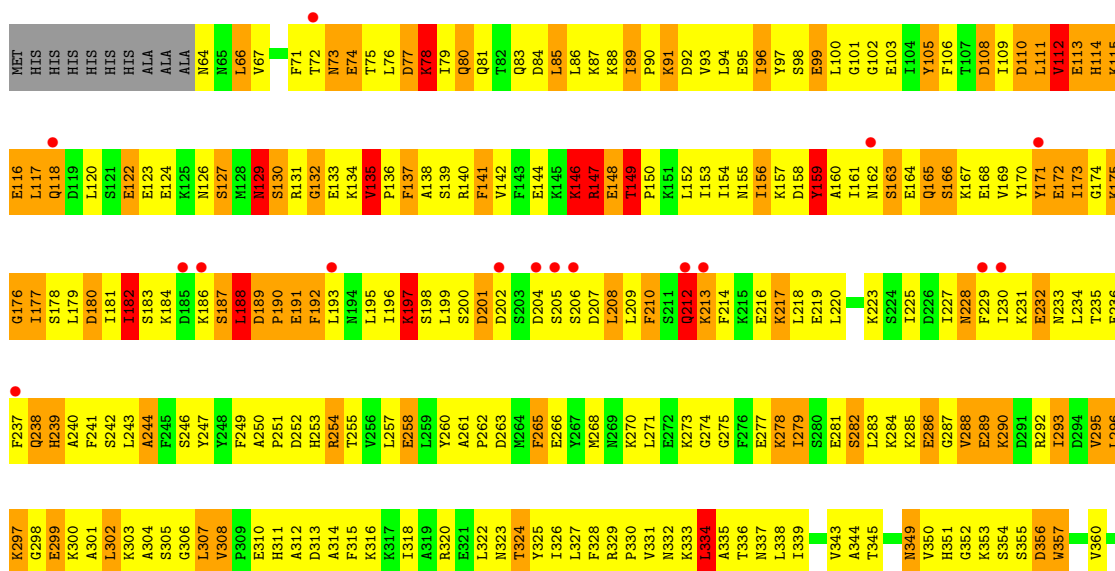
• Molecule 1: Calmodulin-sensitive adenylate cyclase

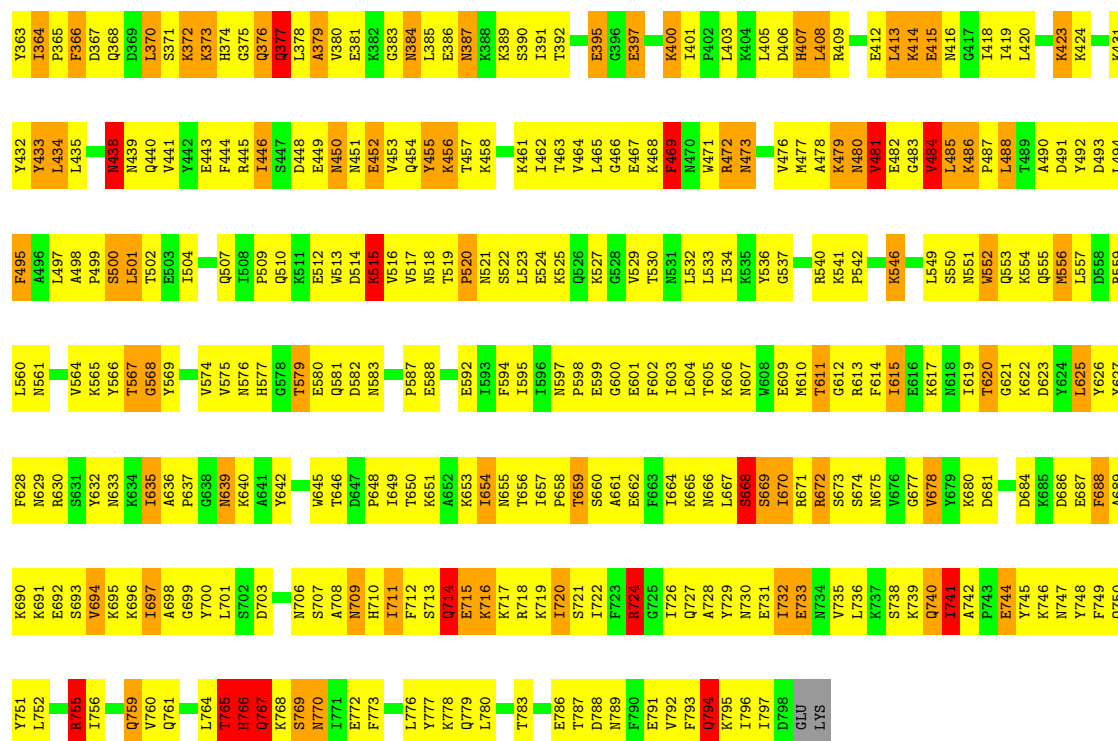


• Molecule 1: Calmodulin-sensitive adenylate cyclase

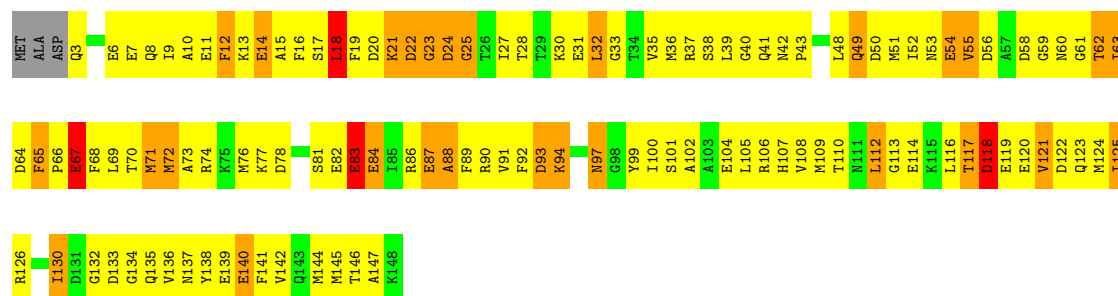




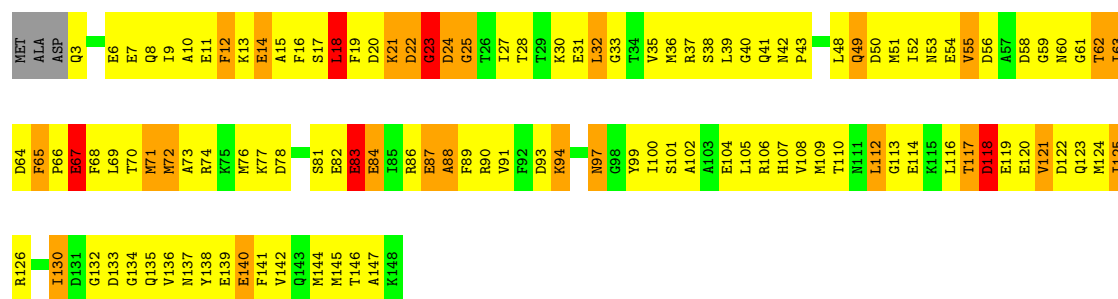
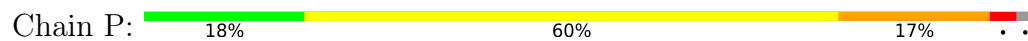




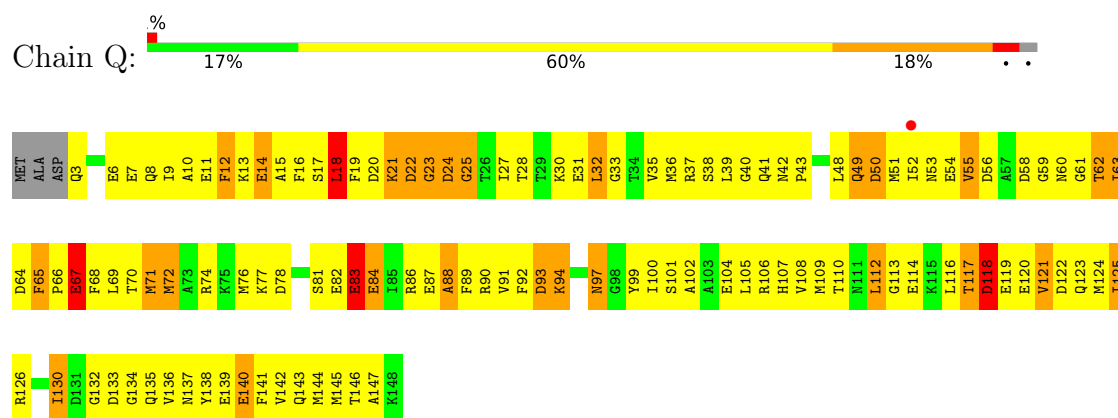
• Molecule 2: Calmodulin 2



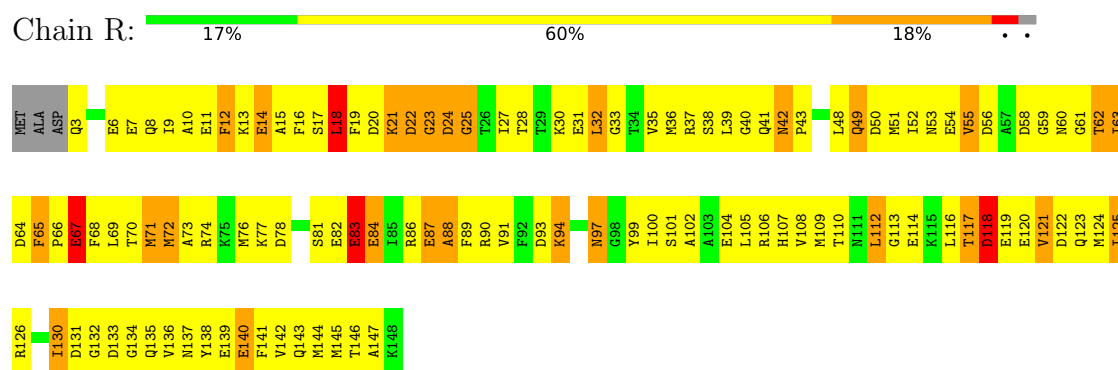
• Molecule 2: Calmodulin 2



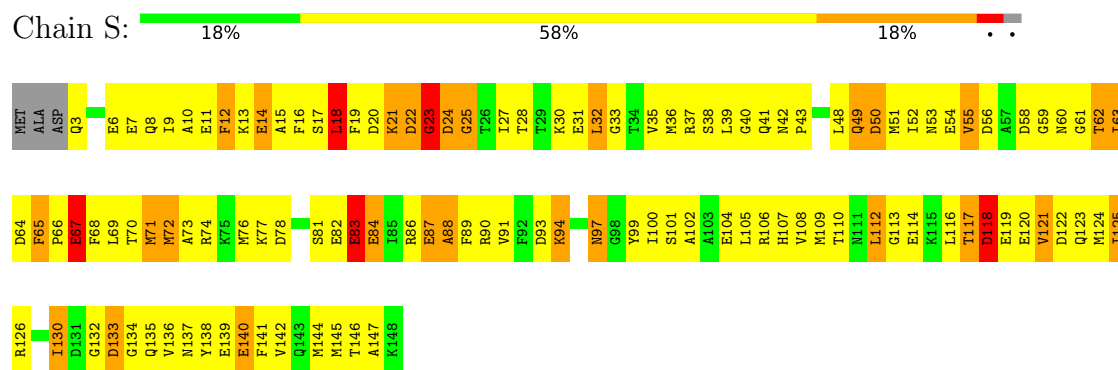
• Molecule 2: Calmodulin 2



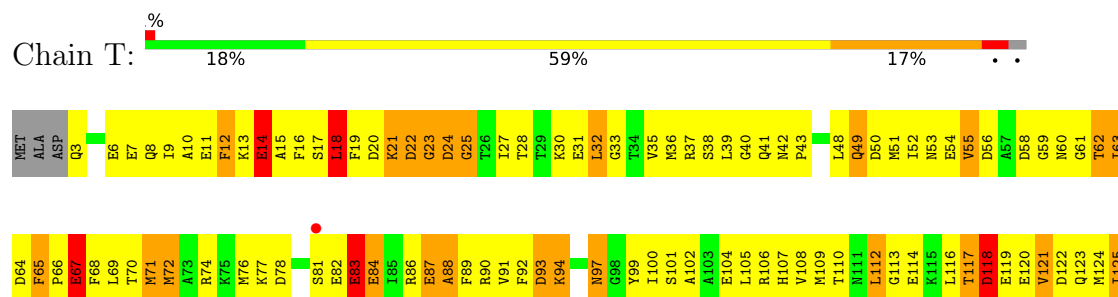
• Molecule 2: Calmodulin 2



• Molecule 2: Calmodulin 2



• Molecule 2: Calmodulin 2



R126	
I130	
D131	
G132	
D133	
G134	
Q135	
V136	
N137	
Y138	
E139	
E140	
F141	
V142	
Q143	
M144	
M145	
T146	
A147	
R148	

4 Data and refinement statistics

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 29.99 – 3.35	Depositor EDS
% Data completeness (in resolution range)	95.8 (29.99-3.35) 95.7 (29.99-3.35)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.03	Depositor
$\langle I/\sigma(I) \rangle$ 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 , 67.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: CA, MG

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	0.65	1/6104 (0.0%)	1.22	79/8208 (1.0%)
1	B	0.66	2/6104 (0.0%)	1.22	80/8208 (1.0%)
1	C	0.68	4/6104 (0.1%)	1.24	83/8208 (1.0%)
1	D	0.67	2/6104 (0.0%)	1.22	81/8208 (1.0%)
1	E	0.67	2/6104 (0.0%)	1.22	80/8208 (1.0%)
1	F	0.68	4/6104 (0.1%)	1.22	79/8208 (1.0%)
2	O	0.68	0/1158	1.17	10/1553 (0.6%)
2	P	0.70	0/1158	1.18	10/1553 (0.6%)
2	Q	0.70	0/1158	1.16	9/1553 (0.6%)
2	R	0.71	0/1158	1.17	10/1553 (0.6%)
2	S	0.72	0/1158	1.17	10/1553 (0.6%)
2	T	0.70	0/1158	1.16	10/1553 (0.6%)
All	All	0.68	15/43572 (0.0%)	1.22	541/58566 (0.9%)

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	132	GLY	C-N	10.92	1.49	1.33
1	C	132	GLY	C-N	9.96	1.47	1.33
1	D	132	GLY	C-N	9.79	1.47	1.33
1	E	132	GLY	C-N	7.90	1.44	1.33
1	B	132	GLY	C-N	7.42	1.44	1.33

The worst 5 of 541 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	159	TYR	N-CA-C	14.45	126.72	110.97
1	C	159	TYR	N-CA-C	14.42	126.69	110.97
1	A	159	TYR	N-CA-C	14.40	126.67	110.97
1	F	159	TYR	N-CA-C	14.40	126.67	110.97
1	D	159	TYR	N-CA-C	14.36	126.62	110.97

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	5992	0	6010	878	0
1	B	5992	0	6010	883	0
1	C	5992	0	6010	880	0
1	D	5992	0	6010	888	0
1	E	5992	0	6010	881	0
1	F	5992	0	6010	892	0
2	O	1146	0	1071	210	0
2	P	1146	0	1071	203	0
2	Q	1146	0	1071	212	0
2	R	1146	0	1071	210	0
2	S	1146	0	1071	214	0
2	T	1146	0	1071	212	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	6413	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 75.

The worst 5 of 6413 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
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

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	1
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	1
1	E	733/747 (98%)	502 (68%)	146 (20%)	85 (12%)	0	1
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	2
2	P	144/149 (97%)	91 (63%)	39 (27%)	14 (10%)	0	3
2	Q	144/149 (97%)	90 (62%)	39 (27%)	15 (10%)	0	2
2	R	144/149 (97%)	90 (62%)	39 (27%)	15 (10%)	0	2
2	S	144/149 (97%)	92 (64%)	37 (26%)	15 (10%)	0	2
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 ⓘ

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%)	569 (86%)	95 (14%)	3	13
1	B	664/675 (98%)	566 (85%)	98 (15%)	3	12
1	C	664/675 (98%)	568 (86%)	96 (14%)	3	13
1	D	664/675 (98%)	567 (85%)	97 (15%)	3	12
1	E	664/675 (98%)	569 (86%)	95 (14%)	3	13
1	F	664/675 (98%)	568 (86%)	96 (14%)	3	13
2	O	123/127 (97%)	105 (85%)	18 (15%)	3	12
2	P	123/127 (97%)	105 (85%)	18 (15%)	3	12
2	Q	123/127 (97%)	105 (85%)	18 (15%)	3	12
2	R	123/127 (97%)	105 (85%)	18 (15%)	3	12
2	S	123/127 (97%)	105 (85%)	18 (15%)	3	12
2	T	123/127 (97%)	105 (85%)	18 (15%)	3	12
All	All	4722/4812 (98%)	4037 (86%)	685 (14%)	3	13

5 of 685 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	672	ARG
1	F	766	HIS
1	E	759	GLN
1	E	670	ILE
1	F	395	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 258 such sidechains are listed below:

Mol	Chain	Res	Type
2	Q	49	GLN
2	R	49	GLN
1	C	618	ASN
1	C	577	HIS
2	R	143	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 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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%)	-0.22	22 (2%)	52	38	24, 80, 134, 147	0
1	B	735/747 (98%)	-0.21	15 (2%)	65	48	25, 80, 134, 148	0
1	C	735/747 (98%)	-0.22	18 (2%)	59	44	25, 80, 134, 147	0
1	D	735/747 (98%)	-0.22	15 (2%)	65	48	26, 80, 134, 147	0
1	E	735/747 (98%)	-0.23	14 (1%)	66	49	26, 80, 135, 147	0
1	F	735/747 (98%)	-0.22	16 (2%)	62	46	25, 81, 134, 147	0
2	O	146/149 (97%)	-0.31	0	100	100	24, 65, 127, 137	0
2	P	146/149 (97%)	-0.33	0	100	100	24, 65, 126, 137	0
2	Q	146/149 (97%)	-0.33	1 (0%)	84	73	23, 65, 126, 137	0
2	R	146/149 (97%)	-0.30	0	100	100	24, 65, 126, 137	0
2	S	146/149 (97%)	-0.34	0	100	100	24, 66, 126, 137	0
2	T	146/149 (97%)	-0.31	1 (0%)	84	73	23, 65, 126, 137	0
All	All	5286/5376 (98%)	-0.24	102 (1%)	66	49	23, 77, 134, 148	0

The worst 5 of 102 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	171	TYR	6.0
1	F	171	TYR	5.5
1	D	171	TYR	5.3
1	A	171	TYR	5.0
1	B	171	TYR	4.9

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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, 95th 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
3	MG	B	901	1/1	0.96	0.05	13,13,13,13	0
3	MG	A	900	1/1	0.97	0.09	18,18,18,18	0
3	MG	D	903	1/1	0.97	0.08	19,19,19,19	0
3	MG	E	904	1/1	0.97	0.06	14,14,14,14	0
4	CA	R	707	1/1	0.97	0.04	79,79,79,79	0
4	CA	S	709	1/1	0.97	0.03	78,78,78,78	0
4	CA	S	810	1/1	0.97	0.04	45,45,45,45	0
4	CA	T	711	1/1	0.97	0.04	77,77,77,77	0
4	CA	P	703	1/1	0.98	0.03	71,71,71,71	0
4	CA	P	804	1/1	0.98	0.05	43,43,43,43	0
4	CA	Q	705	1/1	0.98	0.02	79,79,79,79	0
4	CA	Q	806	1/1	0.98	0.04	46,46,46,46	0
3	MG	C	902	1/1	0.98	0.07	14,14,14,14	0
4	CA	R	808	1/1	0.98	0.04	41,41,41,41	0
3	MG	F	905	1/1	0.98	0.08	16,16,16,16	0
4	CA	O	701	1/1	0.98	0.03	83,83,83,83	0
4	CA	O	802	1/1	0.98	0.04	44,44,44,44	0
4	CA	T	812	1/1	0.98	0.04	43,43,43,43	0
4	CA	O	801	1/1	0.99	0.05	29,29,29,29	0
4	CA	S	809	1/1	0.99	0.04	25,25,25,25	0
4	CA	P	803	1/1	0.99	0.03	33,33,33,33	0
4	CA	R	807	1/1	0.99	0.04	33,33,33,33	0
4	CA	T	811	1/1	0.99	0.04	31,31,31,31	0
4	CA	Q	805	1/1	0.99	0.04	32,32,32,32	0

6.5 Other polymers ⓘ

There are no such residues in this entry.