



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 10, 2023 – 09:19 pm GMT

PDB ID : 2C9T  
Title : Crystal Structure Of Acetylcholine Binding Protein (AChBP) From Aplysia Californica In Complex With alpha-Conotoxin ImI  
Authors : Ulens, C.; Hogg, R.C.; Celie, P.H.; Bertrand, D.; Tsetlin, V.; Smit, A.B.; Sixma, T.K.  
Deposited on : 2005-12-14  
Resolution : 2.25 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) 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

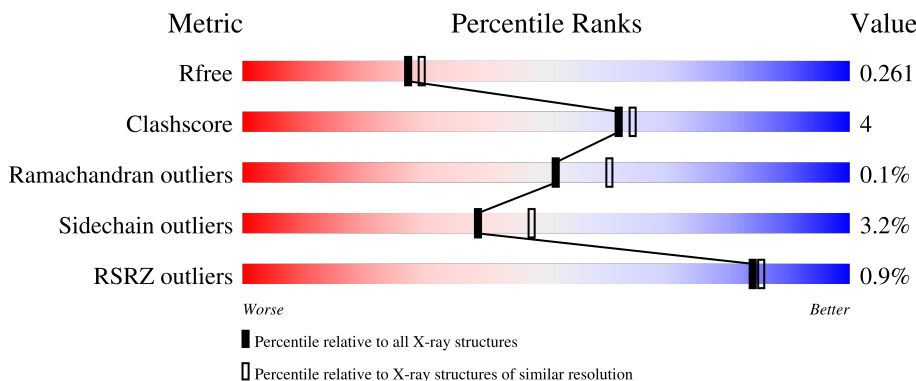
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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  $\geq 3$ , 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	217	 79% 11% 5% 6%
1	B	217	 81% 11% • 6%
1	C	217	 2% 85% 7% • 6%
1	D	217	 % 85% 8% • 6%
1	E	217	 % 83% 10% • 6%

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Mol	Chain	Length	Quality of chain
1	F	217	<p>2% 82% 12% • 6%</p>
1	G	217	<p>% 82% 11% • 6%</p>
1	H	217	<p>88% 6% • 6%</p>
1	I	217	<p>86% 8% • 6%</p>
1	J	217	<p>87% 7% 6%</p>
2	K	13	<p>77% 23%</p>
2	M	13	<p>8% 100%</p>
2	O	13	<p>85% 15%</p>
2	P	13	<p>100%</p>
2	Q	13	<p>8% 77% 23%</p>
2	R	13	<p>69% 23% 8%</p>
2	S	13	<p>77% 23%</p>
2	T	13	<p>92% 8%</p>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18606 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 SOLUBLE ACETYLCHOLINE RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	205	1636	1036	266	325	9	0	0	0
1	B	205	1636	1036	266	325	9	0	0	0
1	C	205	1636	1036	266	325	9	0	0	0
1	D	205	1636	1036	266	325	9	0	0	0
1	E	205	1636	1036	266	325	9	0	0	0
1	F	205	1640	1040	266	325	9	0	1	0
1	G	205	1636	1036	266	325	9	0	0	0
1	H	205	1636	1036	266	325	9	0	0	0
1	I	205	1636	1036	266	325	9	0	0	0
1	J	205	1636	1036	266	325	9	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	VAL	ALA	conflict	UNP Q8WSF8
A	136	VAL	ALA	conflict	UNP Q8WSF8
B	41	VAL	ALA	conflict	UNP Q8WSF8
B	136	VAL	ALA	conflict	UNP Q8WSF8
C	41	VAL	ALA	conflict	UNP Q8WSF8
C	136	VAL	ALA	conflict	UNP Q8WSF8
D	41	VAL	ALA	conflict	UNP Q8WSF8
D	136	VAL	ALA	conflict	UNP Q8WSF8
E	41	VAL	ALA	conflict	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
E	136	VAL	ALA	conflict	UNP Q8WSF8
F	41	VAL	ALA	conflict	UNP Q8WSF8
F	136	VAL	ALA	conflict	UNP Q8WSF8
G	41	VAL	ALA	conflict	UNP Q8WSF8
G	136	VAL	ALA	conflict	UNP Q8WSF8
H	41	VAL	ALA	conflict	UNP Q8WSF8
H	136	VAL	ALA	conflict	UNP Q8WSF8
I	41	VAL	ALA	conflict	UNP Q8WSF8
I	136	VAL	ALA	conflict	UNP Q8WSF8
G	41	VAL	ALA	conflict	UNP Q8WSF8
G	136	VAL	ALA	conflict	UNP Q8WSF8

- Molecule 2 is a protein called ALPHA-CONOTOXIN IMI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	K	13	91	52	20	15	4	0	0	1
2	M	13	91	52	20	15	4	0	0	1
2	O	13	91	52	20	15	4	0	0	1
2	P	13	91	52	20	15	4	0	0	1
2	Q	13	91	52	20	15	4	0	0	1
2	R	13	91	52	20	15	4	0	0	1
2	S	13	91	52	20	15	4	0	0	1
2	T	13	91	52	20	15	4	0	0	1

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	139	Total 139	O 139	0	0
3	B	165	Total 165	O 165	0	0
3	C	173	Total 173	O 173	0	0
3	D	155	Total 155	O 155	0	0

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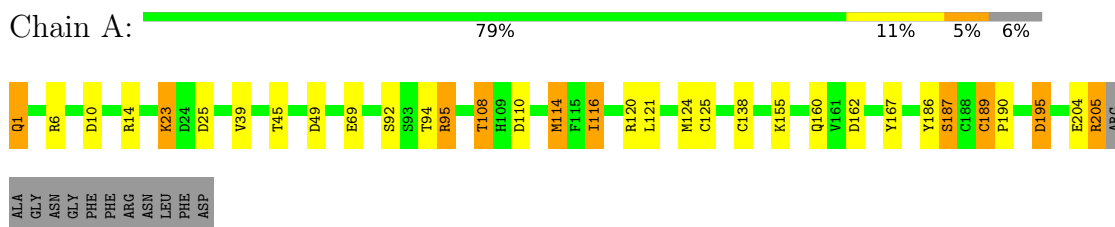
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	136	Total 136	O 136	0	0
3	F	136	Total 136	O 136	0	0
3	G	126	Total 126	O 126	0	0
3	H	128	Total 128	O 128	0	0
3	I	161	Total 161	O 161	0	0
3	J	157	Total 157	O 157	0	0
3	K	5	Total 5	O 5	0	0
3	M	4	Total 4	O 4	0	0
3	O	6	Total 6	O 6	0	0
3	P	2	Total 2	O 2	0	0
3	Q	3	Total 3	O 3	0	0
3	R	11	Total 11	O 11	0	0
3	S	2	Total 2	O 2	0	0
3	T	5	Total 5	O 5	0	0

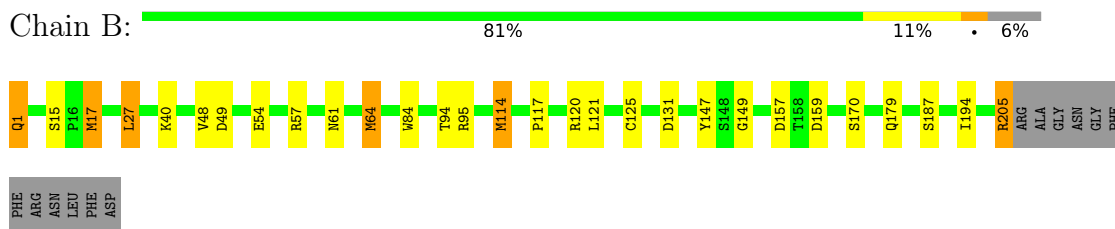
### 3 Residue-property plots [i](#)

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.

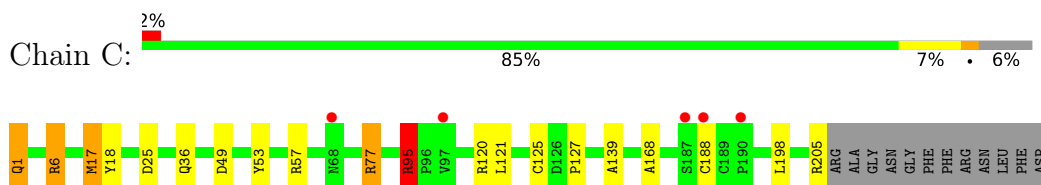
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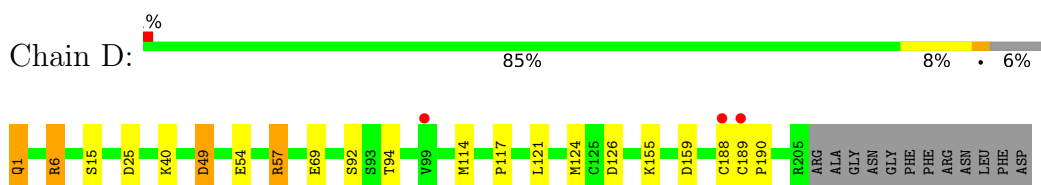
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



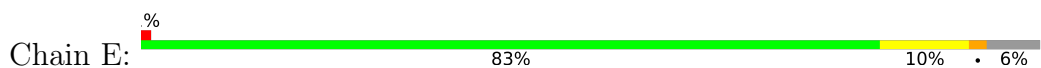
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

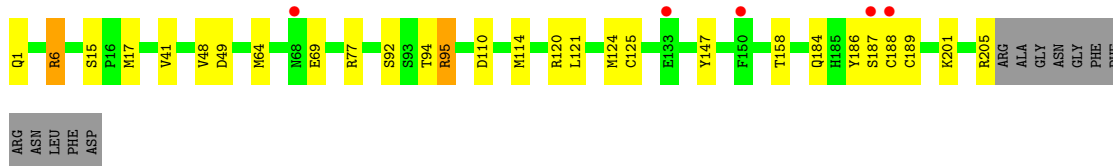
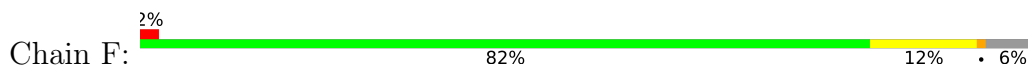


- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR

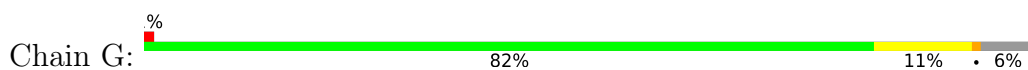




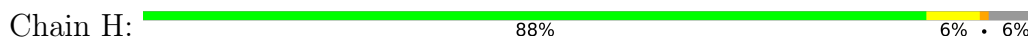
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



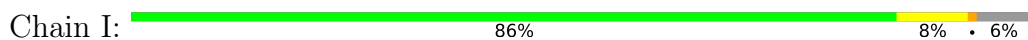
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



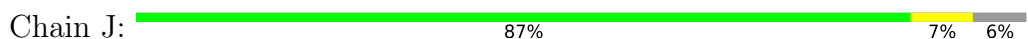
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



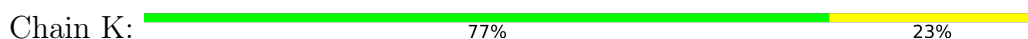
- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



- Molecule 1: SOLUBLE ACETYLCHOLINE RECEPTOR



- Molecule 2: ALPHA-CONOTOXIN IMI

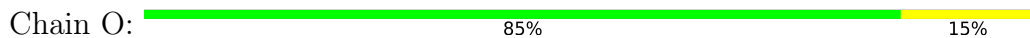


- Molecule 2: ALPHA-CONOTOXIN IMI





- Molecule 2: ALPHA-CONOTOXIN IMI

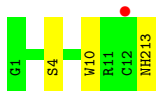
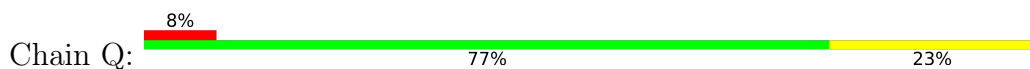


- Molecule 2: ALPHA-CONOTOXIN IMI

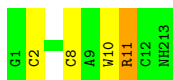


There are no outlier residues recorded for this chain.

- Molecule 2: ALPHA-CONOTOXIN IMI



- Molecule 2: ALPHA-CONOTOXIN IMI



- Molecule 2: ALPHA-CONOTOXIN IMI



- Molecule 2: ALPHA-CONOTOXIN IMI



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.21Å 123.13Å 118.75Å 90.00° 117.47° 90.00°	Depositor
Resolution (Å)	105.41 – 2.25 54.05 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.1 (105.41-2.25) 96.8 (54.05-2.25)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.39 (at 2.25Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.168 , 0.227 0.208 , 0.261	Depositor DCC
$R_{free}$ test set	6659 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.4	Xtrriage
Anisotropy	0.184	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 38.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	18606	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: NH2

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	0.89	4/1676 (0.2%)	0.91	7/2287 (0.3%)
1	B	0.84	0/1676	0.87	2/2287 (0.1%)
1	C	0.86	0/1676	0.85	2/2287 (0.1%)
1	D	0.83	0/1676	0.88	4/2287 (0.2%)
1	E	0.84	0/1676	0.84	1/2287 (0.0%)
1	F	0.86	4/1683 (0.2%)	0.89	3/2297 (0.1%)
1	G	0.83	1/1676 (0.1%)	0.88	2/2287 (0.1%)
1	H	0.81	0/1676	0.85	2/2287 (0.1%)
1	I	0.89	0/1676	0.93	2/2287 (0.1%)
1	J	0.88	0/1676	0.87	2/2287 (0.1%)
2	K	0.75	0/92	0.95	0/123
2	M	0.86	0/92	0.78	0/123
2	O	0.75	0/92	0.96	0/123
2	P	0.81	0/92	0.73	0/123
2	Q	0.76	0/92	0.71	0/123
2	R	0.83	0/92	0.79	0/123
2	S	0.90	0/92	0.83	0/123
2	T	0.94	0/92	1.03	0/123
All	All	0.85	9/17503 (0.1%)	0.88	27/23864 (0.1%)

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	C	0	1
1	D	0	1
1	E	0	1
1	H	0	1
1	J	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	5

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	186	TYR	C-N	-10.29	1.10	1.34
1	A	187	SER	C-N	-9.33	1.12	1.34
1	F	189	CYS	C-N	-9.24	1.16	1.34
1	A	190	PRO	C-N	-7.19	1.17	1.34
1	A	189	CYS	CB-SG	-6.36	1.71	1.82

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	6	ARG	NE-CZ-NH2	-9.83	115.39	120.30
1	G	6	ARG	NE-CZ-NH2	-8.19	116.21	120.30
1	F	6	ARG	NE-CZ-NH2	-7.85	116.38	120.30
1	H	6	ARG	NE-CZ-NH2	-7.75	116.43	120.30
1	J	6	ARG	NE-CZ-NH1	7.33	123.97	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	188	CYS	Peptide
1	D	188	CYS	Peptide
1	E	188	CYS	Peptide
1	H	188	CYS	Peptide
1	J	188	CYS	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1636	0	1572	22	0
1	B	1636	0	1572	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1636	0	1572	14	0
1	D	1636	0	1572	11	0
1	E	1636	0	1572	22	0
1	F	1640	0	1580	16	0
1	G	1636	0	1572	14	0
1	H	1636	0	1572	7	0
1	I	1636	0	1572	17	0
1	J	1636	0	1572	14	0
2	K	91	0	78	1	0
2	M	91	0	78	0	0
2	O	91	0	78	1	0
2	P	91	0	78	0	0
2	Q	91	0	78	2	0
2	R	91	0	78	4	0
2	S	91	0	78	1	0
2	T	91	0	78	0	0
3	A	139	0	0	3	0
3	B	165	0	0	1	1
3	C	173	0	0	5	0
3	D	155	0	0	4	0
3	E	136	0	0	4	0
3	F	136	0	0	3	0
3	G	126	0	0	2	0
3	H	128	0	0	0	0
3	I	161	0	0	5	0
3	J	157	0	0	1	1
3	K	5	0	0	0	0
3	M	4	0	0	0	0
3	O	6	0	0	0	0
3	P	2	0	0	0	0
3	Q	3	0	0	1	0
3	R	11	0	0	1	0
3	S	2	0	0	0	0
3	T	5	0	0	0	0
All	All	18606	0	16352	145	1

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 4.

The worst 5 of 145 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:1:GLN:N	1:C:1:GLN:OE1	1.90	1.05
1:E:91:TYR:CE1	3:E:2075:HOH:O	2.14	1.01
1:B:1:GLN:N	1:B:1:GLN:OE1	1.91	1.01
1:D:1:GLN:HA	1:D:1:GLN:OE1	1.57	0.99
1:F:95:ARG:HD2	3:F:2044:HOH:O	1.64	0.98

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:2129:HOH:O	3:J:2057:HOH:O[1_655]	2.17	0.03

## 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	203/217 (94%)	202 (100%)	1 (0%)	0	100	100
1	B	203/217 (94%)	196 (97%)	7 (3%)	0	100	100
1	C	203/217 (94%)	199 (98%)	4 (2%)	0	100	100
1	D	203/217 (94%)	201 (99%)	2 (1%)	0	100	100
1	E	203/217 (94%)	198 (98%)	4 (2%)	1 (0%)	29	29
1	F	204/217 (94%)	200 (98%)	3 (2%)	1 (0%)	29	29
1	G	203/217 (94%)	197 (97%)	6 (3%)	0	100	100
1	H	203/217 (94%)	200 (98%)	3 (2%)	0	100	100
1	I	203/217 (94%)	201 (99%)	2 (1%)	0	100	100
1	J	203/217 (94%)	200 (98%)	3 (2%)	0	100	100
2	K	11/13 (85%)	11 (100%)	0	0	100	100
2	M	11/13 (85%)	11 (100%)	0	0	100	100
2	O	11/13 (85%)	10 (91%)	1 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	P	11/13 (85%)	11 (100%)	0	0	100	100
2	Q	11/13 (85%)	10 (91%)	1 (9%)	0	100	100
2	R	11/13 (85%)	10 (91%)	1 (9%)	0	100	100
2	S	11/13 (85%)	10 (91%)	1 (9%)	0	100	100
2	T	11/13 (85%)	11 (100%)	0	0	100	100
All	All	2119/2274 (93%)	2078 (98%)	39 (2%)	2 (0%)	51	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	187	SER
1	E	72	ASN

### 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	188/197 (95%)	177 (94%)	11 (6%)	19	19
1	B	188/197 (95%)	180 (96%)	8 (4%)	29	33
1	C	188/197 (95%)	184 (98%)	4 (2%)	53	62
1	D	188/197 (95%)	184 (98%)	4 (2%)	53	62
1	E	188/197 (95%)	182 (97%)	6 (3%)	39	47
1	F	189/197 (96%)	184 (97%)	5 (3%)	46	55
1	G	188/197 (95%)	180 (96%)	8 (4%)	29	33
1	H	188/197 (95%)	184 (98%)	4 (2%)	53	62
1	I	188/197 (95%)	185 (98%)	3 (2%)	62	73
1	J	188/197 (95%)	185 (98%)	3 (2%)	62	73
2	K	10/10 (100%)	9 (90%)	1 (10%)	7	5
2	M	10/10 (100%)	10 (100%)	0	100	100
2	O	10/10 (100%)	9 (90%)	1 (10%)	7	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	10/10 (100%)	10 (100%)	0	100	100
2	Q	10/10 (100%)	9 (90%)	1 (10%)	7	5
2	R	10/10 (100%)	9 (90%)	1 (10%)	7	5
2	S	10/10 (100%)	9 (90%)	1 (10%)	7	5
2	T	10/10 (100%)	9 (90%)	1 (10%)	7	5
All	All	1961/2050 (96%)	1899 (97%)	62 (3%)	39	47

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	23	LYS
1	J	187	SER
1	F	114	MET
1	J	68	ASN
2	R	11	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	182	GLN
1	C	55	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2
1	F	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	190:PRO	C	191:GLU	N	1.17
1	F	189:CYS	C	190:PRO	N	1.16
1	A	187:SER	C	188:CYS	N	1.12
1	F	186:TYR	C	187:SER	N	1.10

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	205/217 (94%)	-0.21	0 <a href="#">100</a> <a href="#">100</a>	39, 45, 52, 60	0
1	B	205/217 (94%)	-0.14	0 <a href="#">100</a> <a href="#">100</a>	39, 46, 56, 62	0
1	C	205/217 (94%)	0.10	5 (2%) <a href="#">59</a> <a href="#">62</a>	37, 45, 53, 60	0
1	D	205/217 (94%)	0.13	3 (1%) <a href="#">73</a> <a href="#">75</a>	39, 45, 55, 63	0
1	E	205/217 (94%)	-0.09	2 (0%) <a href="#">82</a> <a href="#">84</a>	39, 45, 54, 60	0
1	F	205/217 (94%)	-0.09	5 (2%) <a href="#">59</a> <a href="#">62</a>	38, 45, 53, 60	0
1	G	205/217 (94%)	-0.12	2 (0%) <a href="#">82</a> <a href="#">84</a>	38, 45, 54, 58	0
1	H	205/217 (94%)	-0.09	1 (0%) <a href="#">91</a> <a href="#">91</a>	39, 45, 52, 61	0
1	I	205/217 (94%)	0.15	0 <a href="#">100</a> <a href="#">100</a>	40, 46, 53, 59	0
1	J	205/217 (94%)	-0.10	0 <a href="#">100</a> <a href="#">100</a>	40, 45, 53, 62	0
2	K	12/13 (92%)	-0.62	0 <a href="#">100</a> <a href="#">100</a>	33, 39, 47, 50	0
2	M	12/13 (92%)	0.42	1 (8%) <a href="#">11</a> <a href="#">12</a>	38, 43, 53, 54	0
2	O	12/13 (92%)	0.46	0 <a href="#">100</a> <a href="#">100</a>	39, 43, 53, 55	0
2	P	12/13 (92%)	0.38	0 <a href="#">100</a> <a href="#">100</a>	40, 47, 54, 55	0
2	Q	12/13 (92%)	0.24	1 (8%) <a href="#">11</a> <a href="#">12</a>	37, 48, 54, 55	0
2	R	12/13 (92%)	-0.35	0 <a href="#">100</a> <a href="#">100</a>	30, 37, 46, 47	0
2	S	12/13 (92%)	-0.37	0 <a href="#">100</a> <a href="#">100</a>	30, 38, 46, 49	0
2	T	12/13 (92%)	0.42	0 <a href="#">100</a> <a href="#">100</a>	35, 39, 48, 51	0
All	All	2146/2274 (94%)	-0.04	20 (0%) <a href="#">84</a> <a href="#">85</a>	30, 45, 54, 63	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	187	SER	3.5
1	E	188	CYS	3.0
2	M	12	CYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	F	188	CYS	2.6
1	C	188	CYS	2.5

## 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 [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.