



wwPDB X-ray Structure Validation Summary Report ⓘ

May 3, 2016 – 11:19 AM EDT

PDB ID : 5JME
Title : Crystal structure of acetylcholine binding protein (AChBP) from Aplysia Californica in complex with alpha-conotoxin PeIA
Authors : Bobango, J.; Sankaran, B.; McIntosh, J.M.; Talley, T.T.
Deposited on : 2016-04-28
Resolution : 2.34 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027457
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

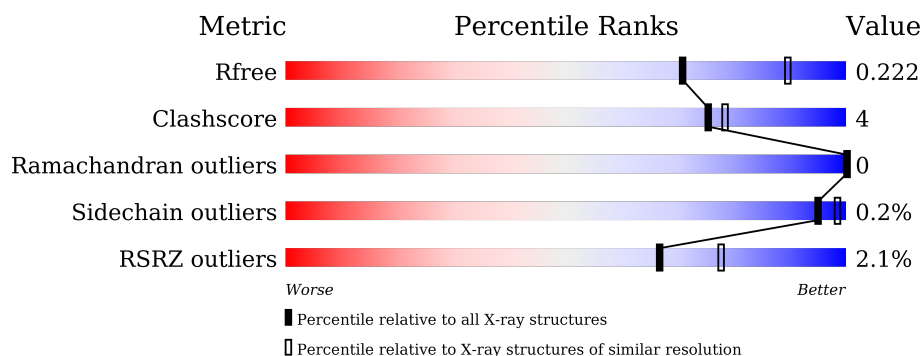
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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.




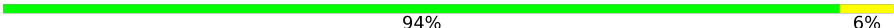

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1406 (2.36-2.32)
Clashscore	102246	1509 (2.36-2.32)
Ramachandran outliers	100387	1490 (2.36-2.32)
Sidechain outliers	100360	1491 (2.36-2.32)
RSRZ outliers	91569	1412 (2.36-2.32)

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 on the lower 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 $\leq 5\%$. 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	230	<div> <div>82%</div> <div>7%</div> <div>11%</div> </div>
1	B	230	<div> <div>3%</div> <div>80%</div> <div>11%</div> <div>9%</div> </div>
1	C	230	<div> <div>%</div> <div>80%</div> <div>9%</div> <div>11%</div> </div>
1	D	230	<div> <div>4%</div> <div>81%</div> <div>8%</div> <div>11%</div> </div>
1	E	230	<div> <div>%</div> <div>84%</div> <div>6%</div> <div>10%</div> </div>
2	F	17	<div> <div>76%</div> <div>24%</div> </div>

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Mol	Chain	Length	Quality of chain
2	G	17	 82%18%
2	H	17	 94%6%
2	I	17	 65%35%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8760 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
1	A	205	Total	C	N	O	S	0	0	0
			1592	1008	256	321	7			
1	B	209	Total	C	N	O	S	0	1	0
			1636	1033	267	328	8			
1	C	205	Total	C	N	O	S	0	1	0
			1594	1012	262	313	7			
1	D	205	Total	C	N	O	S	0	1	0
			1561	989	251	315	6			
1	E	208	Total	C	N	O	S	0	1	0
			1608	1018	263	320	7			

There are 55 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ASP	-	expression tag	UNP Q8WSF8
A	-7	TYR	-	expression tag	UNP Q8WSF8
A	-6	LYS	-	expression tag	UNP Q8WSF8
A	-5	ASP	-	expression tag	UNP Q8WSF8
A	-4	ASP	-	expression tag	UNP Q8WSF8
A	-3	ASP	-	expression tag	UNP Q8WSF8
A	-2	ASP	-	expression tag	UNP Q8WSF8
A	-1	LYS	-	expression tag	UNP Q8WSF8
A	0	LEU	-	expression tag	UNP Q8WSF8
A	220	SER	-	expression tag	UNP Q8WSF8
A	221	ARG	-	expression tag	UNP Q8WSF8
B	-8	ASP	-	expression tag	UNP Q8WSF8
B	-7	TYR	-	expression tag	UNP Q8WSF8
B	-6	LYS	-	expression tag	UNP Q8WSF8
B	-5	ASP	-	expression tag	UNP Q8WSF8
B	-4	ASP	-	expression tag	UNP Q8WSF8
B	-3	ASP	-	expression tag	UNP Q8WSF8
B	-2	ASP	-	expression tag	UNP Q8WSF8
B	-1	LYS	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	0	LEU	-	expression tag	UNP Q8WSF8
B	220	SER	-	expression tag	UNP Q8WSF8
B	221	ARG	-	expression tag	UNP Q8WSF8
C	-8	ASP	-	expression tag	UNP Q8WSF8
C	-7	TYR	-	expression tag	UNP Q8WSF8
C	-6	LYS	-	expression tag	UNP Q8WSF8
C	-5	ASP	-	expression tag	UNP Q8WSF8
C	-4	ASP	-	expression tag	UNP Q8WSF8
C	-3	ASP	-	expression tag	UNP Q8WSF8
C	-2	ASP	-	expression tag	UNP Q8WSF8
C	-1	LYS	-	expression tag	UNP Q8WSF8
C	0	LEU	-	expression tag	UNP Q8WSF8
C	220	SER	-	expression tag	UNP Q8WSF8
C	221	ARG	-	expression tag	UNP Q8WSF8
D	-8	ASP	-	expression tag	UNP Q8WSF8
D	-7	TYR	-	expression tag	UNP Q8WSF8
D	-6	LYS	-	expression tag	UNP Q8WSF8
D	-5	ASP	-	expression tag	UNP Q8WSF8
D	-4	ASP	-	expression tag	UNP Q8WSF8
D	-3	ASP	-	expression tag	UNP Q8WSF8
D	-2	ASP	-	expression tag	UNP Q8WSF8
D	-1	LYS	-	expression tag	UNP Q8WSF8
D	0	LEU	-	expression tag	UNP Q8WSF8
D	220	SER	-	expression tag	UNP Q8WSF8
D	221	ARG	-	expression tag	UNP Q8WSF8
E	-8	ASP	-	expression tag	UNP Q8WSF8
E	-7	TYR	-	expression tag	UNP Q8WSF8
E	-6	LYS	-	expression tag	UNP Q8WSF8
E	-5	ASP	-	expression tag	UNP Q8WSF8
E	-4	ASP	-	expression tag	UNP Q8WSF8
E	-3	ASP	-	expression tag	UNP Q8WSF8
E	-2	ASP	-	expression tag	UNP Q8WSF8
E	-1	LYS	-	expression tag	UNP Q8WSF8
E	0	LEU	-	expression tag	UNP Q8WSF8
E	220	SER	-	expression tag	UNP Q8WSF8
E	221	ARG	-	expression tag	UNP Q8WSF8

- Molecule 2 is a protein called alpha-conotoxin PeIA from *Conus pergrandis*.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	17	Total	C	N	O	S	0	0	1
			112	65	22	21	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	17	Total 112	C 65	N 22	O 21	S 4	0	0	1
2	H	17	Total 105	C 60	N 22	O 19	S 4	0	0	1
2	I	17	Total 108	C 63	N 22	O 19	S 4	0	0	1

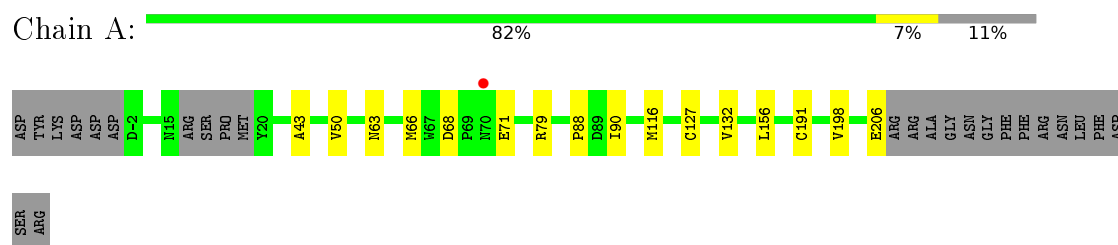
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	75	Total 75	O 75	0	0
3	B	79	Total 79	O 79	0	0
3	C	62	Total 62	O 62	0	0
3	D	48	Total 48	O 48	0	0
3	E	64	Total 64	O 64	0	0
3	F	2	Total 2	O 2	0	0
3	G	2	Total 2	O 2	0	0

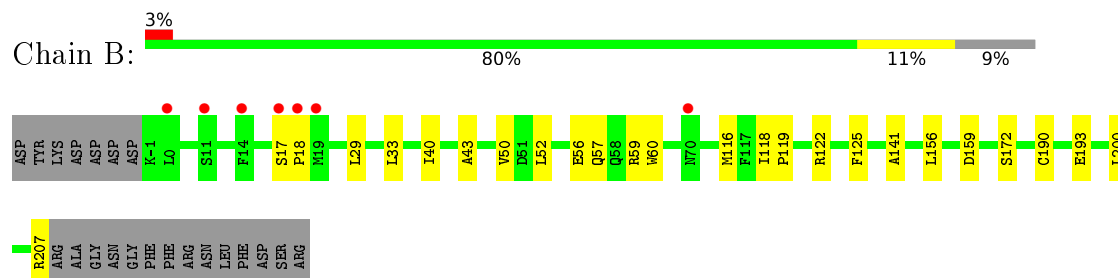
3 Residue-property plots [i](#)

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 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.

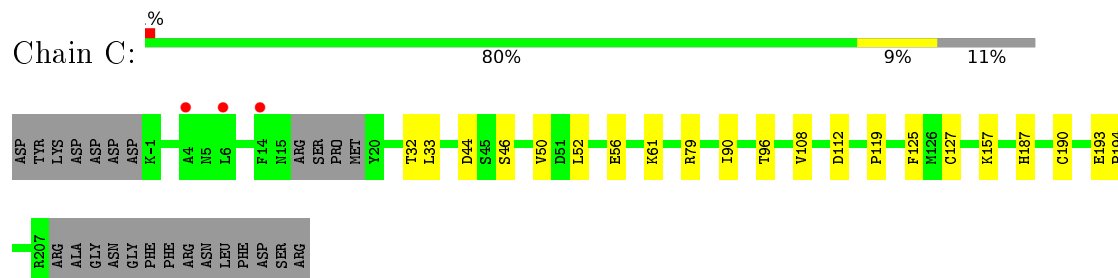
- Molecule 1: Soluble acetylcholine receptor



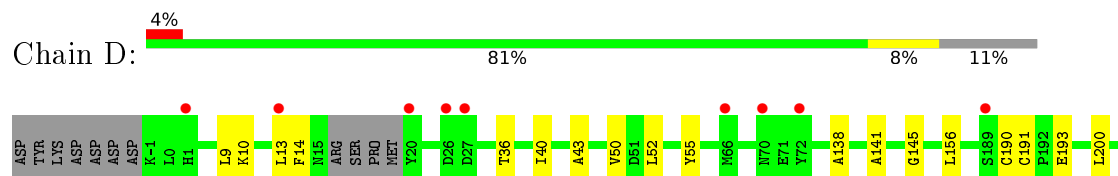
- Molecule 1: Soluble acetylcholine receptor

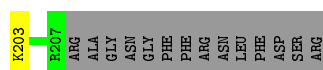


- Molecule 1: Soluble acetylcholine receptor

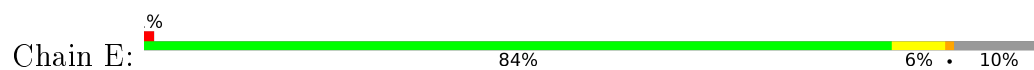


- Molecule 1: Soluble acetylcholine receptor





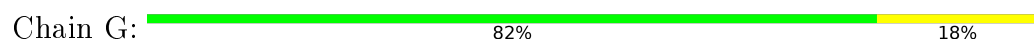
- Molecule 1: Soluble acetylcholine receptor



- Molecule 2: alpha-conotoxin PeIA from Conus pergrandis



- Molecule 2: alpha-conotoxin PeIA from Conus pergrandis



- Molecule 2: alpha-conotoxin PeIA from Conus pergrandis



- Molecule 2: alpha-conotoxin PeIA from Conus pergrandis



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	145.12Å 147.89Å 146.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.82 – 2.34 48.82 – 2.34	Depositor EDS
% Data completeness (in resolution range)	98.9 (48.82-2.34) 92.6 (48.82-2.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 2.34Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.10.1_2155)	Depositor
R, R_{free}	0.196 , 0.229 0.190 , 0.222	Depositor DCC
R_{free} test set	1859 reflections (3.01%)	DCC
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.745	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8760	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	0.41	1/1630 (0.1%)	0.62	0/2230
1	B	0.44	0/1679	0.64	0/2298
1	C	0.38	0/1635	0.58	0/2236
1	D	0.37	0/1601	0.58	0/2198
1	E	0.42	0/1649	0.70	4/2258 (0.2%)
2	F	0.62	0/114	0.65	0/155
2	G	0.43	0/114	0.64	0/155
2	H	0.46	0/107	0.41	0/146
2	I	0.35	0/110	0.58	0/150
All	All	0.41	1/8639 (0.0%)	0.62	4/11826 (0.0%)

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	B	0	1
1	C	0	1
1	D	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	191	CYS	CB-SG	5.48	1.91	1.82

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	190	CYS	C-N-CA	9.06	144.34	121.70
1	E	190	CYS	CA-CB-SG	-8.21	99.23	114.00
1	E	116	MET	CA-CB-CG	5.68	122.96	113.30
1	E	191	CYS	CA-CB-SG	-5.54	104.03	114.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	190	CYS	Peptide
1	C	190	CYS	Peptide
1	D	190	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	1592	0	1484	8	0
1	B	1636	0	1533	18	0
1	C	1594	0	1504	13	0
1	D	1561	0	1431	11	0
1	E	1608	0	1494	9	0
2	F	112	0	96	4	0
2	G	112	0	96	1	0
2	H	105	0	83	1	0
2	I	108	0	92	7	0
3	A	75	0	0	1	0
3	B	79	0	0	0	0
3	C	62	0	0	0	0
3	D	48	0	0	0	0
3	E	64	0	0	0	0
3	F	2	0	0	0	0
3	G	2	0	0	0	0
All	All	8760	0	7813	64	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 4.

The worst 5 of 64 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:B:59:ARG:NH2	1:B:159:ASP:OD2	2.00	0.94
1:E:190:CYS:SG	1:E:191:CYS:N	2.42	0.86
1:A:68:ASP:HB3	1:A:71:GLU:HG3	1.77	0.67
1:C:79:ARG:NH2	2:H:11:ASN:OD1	2.27	0.67
1:E:193:GLU:OE1	1:E:193:GLU:N	2.23	0.63

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	201/230 (87%)	196 (98%)	5 (2%)	0	100	100
1	B	208/230 (90%)	201 (97%)	7 (3%)	0	100	100
1	C	202/230 (88%)	196 (97%)	6 (3%)	0	100	100
1	D	202/230 (88%)	196 (97%)	6 (3%)	0	100	100
1	E	205/230 (89%)	198 (97%)	7 (3%)	0	100	100
2	F	15/17 (88%)	15 (100%)	0	0	100	100
2	G	15/17 (88%)	15 (100%)	0	0	100	100
2	H	15/17 (88%)	15 (100%)	0	0	100	100
2	I	15/17 (88%)	15 (100%)	0	0	100	100
All	All	1078/1218 (88%)	1047 (97%)	31 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	176/208 (85%)	175 (99%)	1 (1%)	90	96
1	B	182/208 (88%)	182 (100%)	0	100	100
1	C	175/208 (84%)	175 (100%)	0	100	100
1	D	168/208 (81%)	168 (100%)	0	100	100
1	E	175/208 (84%)	175 (100%)	0	100	100
2	F	14/14 (100%)	14 (100%)	0	100	100
2	G	14/14 (100%)	13 (93%)	1 (7%)	18	19
2	H	12/14 (86%)	12 (100%)	0	100	100
2	I	13/14 (93%)	13 (100%)	0	100	100
All	All	929/1096 (85%)	927 (100%)	2 (0%)	95	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	CYS
2	G	10	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	57	GLN
1	C	57	GLN
1	D	15	ASN
2	F	5	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 [i](#)

There are no carbohydrates 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](#)

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, 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	205/230 (89%)	-0.06	1 (0%) 91 96	23, 34, 57, 87	0
1	B	209/230 (90%)	0.10	7 (3%) 50 61	25, 34, 60, 75	0
1	C	205/230 (89%)	0.08	3 (1%) 76 84	26, 38, 65, 78	0
1	D	205/230 (89%)	0.15	9 (4%) 38 50	25, 40, 72, 80	0
1	E	208/230 (90%)	-0.00	3 (1%) 78 85	23, 35, 60, 82	0
2	F	16/17 (94%)	0.04	0 100 100	36, 44, 52, 56	0
2	G	16/17 (94%)	-0.03	0 100 100	31, 41, 48, 50	0
2	H	16/17 (94%)	0.27	0 100 100	48, 56, 75, 77	0
2	I	16/17 (94%)	0.21	0 100 100	40, 50, 62, 62	0
All	All	1096/1218 (89%)	0.06	23 (2%) 67 78	23, 37, 66, 87	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	17	SER	4.6
1	D	26	ASP	3.5
1	D	70	ASN	3.4
1	D	13	LEU	3.2
1	D	20	TYR	3.1

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.