wwPDB X-ray Structure Validation Summary Report (i)

Nov 13, 2023 – 09:53 PM JST

PDB ID	:	5Y9N
Title	:	Crystal structure of Pyrococcus furiosus PbaA (monoclinic form), an archaeal homolog of proteasome-assembly chaperone
Authors	:	Yagi-Utsumi, M.; Sikdar, A.; Kozai, T.; Inoue, R.; Sugiyama, M.; Uchihashi, T.; Satoh, T.; Kato, K.
Deposited on	:	2017-08-26
Resolution	:	2.55 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:

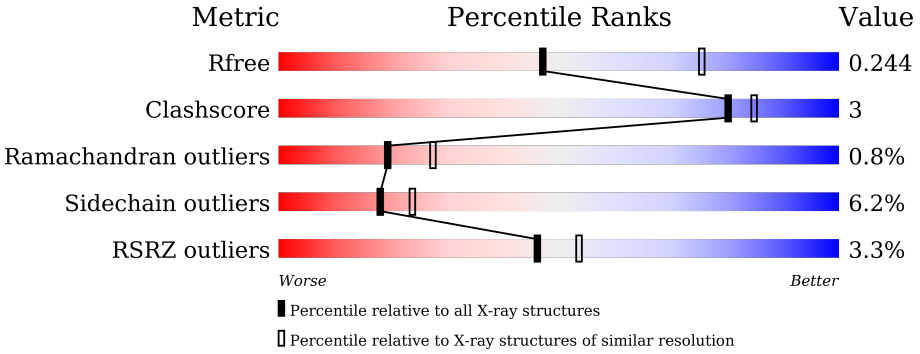
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	245	2%, 89%, 7% • •
1	B	245	%, 90%, 5% • •
1	C	245	3%, 88%, 7% • •
1	D	245	3%, 88%, 8% • •
1	E	245	2%, 86%, 9% • •
1	F	245	6%, 88%, 8% • •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	245	% 88% 8%
1	H	245	4% 87% 8%
1	I	245	4% 87% 9%
1	J	245	5% 87% 8%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 18821 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 PbaA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	238	1867	1206	305	346	10	0	0	0
1	B	238	1867	1206	305	346	10	0	0	0
1	C	238	1867	1206	305	346	10	0	0	0
1	D	238	1867	1206	305	346	10	0	0	0
1	E	238	1867	1206	305	346	10	0	0	0
1	F	238	1867	1206	305	346	10	0	0	0
1	G	238	1867	1206	305	346	10	0	0	0
1	H	238	1867	1206	305	346	10	0	0	0
1	I	238	1867	1206	305	346	10	0	0	0
1	J	238	1867	1206	305	346	10	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q8U4Q9
A	-1	SER	-	expression tag	UNP Q8U4Q9
A	0	HIS	-	expression tag	UNP Q8U4Q9
B	-2	GLY	-	expression tag	UNP Q8U4Q9
B	-1	SER	-	expression tag	UNP Q8U4Q9
B	0	HIS	-	expression tag	UNP Q8U4Q9
C	-2	GLY	-	expression tag	UNP Q8U4Q9
C	-1	SER	-	expression tag	UNP Q8U4Q9
C	0	HIS	-	expression tag	UNP Q8U4Q9

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	GLY	-	expression tag	UNP Q8U4Q9
D	-1	SER	-	expression tag	UNP Q8U4Q9
D	0	HIS	-	expression tag	UNP Q8U4Q9
E	-2	GLY	-	expression tag	UNP Q8U4Q9
E	-1	SER	-	expression tag	UNP Q8U4Q9
E	0	HIS	-	expression tag	UNP Q8U4Q9
F	-2	GLY	-	expression tag	UNP Q8U4Q9
F	-1	SER	-	expression tag	UNP Q8U4Q9
F	0	HIS	-	expression tag	UNP Q8U4Q9
G	-2	GLY	-	expression tag	UNP Q8U4Q9
G	-1	SER	-	expression tag	UNP Q8U4Q9
G	0	HIS	-	expression tag	UNP Q8U4Q9
H	-2	GLY	-	expression tag	UNP Q8U4Q9
H	-1	SER	-	expression tag	UNP Q8U4Q9
H	0	HIS	-	expression tag	UNP Q8U4Q9
I	-2	GLY	-	expression tag	UNP Q8U4Q9
I	-1	SER	-	expression tag	UNP Q8U4Q9
I	0	HIS	-	expression tag	UNP Q8U4Q9
J	-2	GLY	-	expression tag	UNP Q8U4Q9
J	-1	SER	-	expression tag	UNP Q8U4Q9
J	0	HIS	-	expression tag	UNP Q8U4Q9

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
2	A	1	1	1	0	0
2	B	1	1	1	0	0
2	C	2	2	2	0	0
2	D	2	2	2	0	0
2	E	2	2	2	0	0
2	G	1	1	1	0	0
2	H	1	1	1	0	0

- Molecule 3 is water.

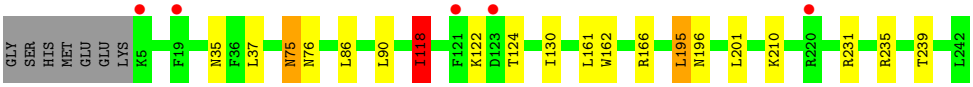
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	11	11	11	0	0
			Total	O		
3	B	16	16	16	0	0
			Total	O		
3	C	19	19	19	0	0
			Total	O		
3	D	12	12	12	0	0
			Total	O		
3	E	10	10	10	0	0
			Total	O		
3	F	10	10	10	0	0
			Total	O		
3	G	20	20	20	0	0
			Total	O		
3	H	16	16	16	0	0
			Total	O		
3	I	15	15	15	0	0
			Total	O		
3	J	12	12	12	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.

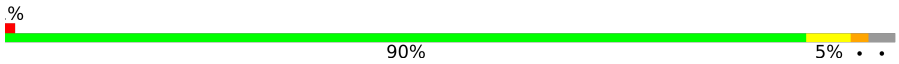
- Molecule 1: PbaA

Chain A:



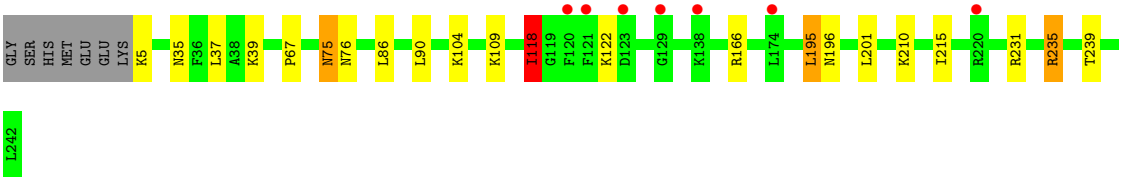
- Molecule 1: PbaA

Chain B:



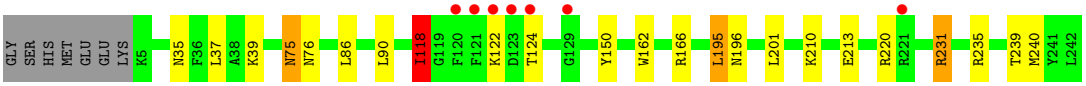
- Molecule 1: PbaA

Chain C:



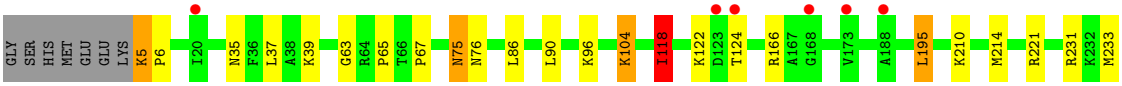
- Molecule 1: PbaA

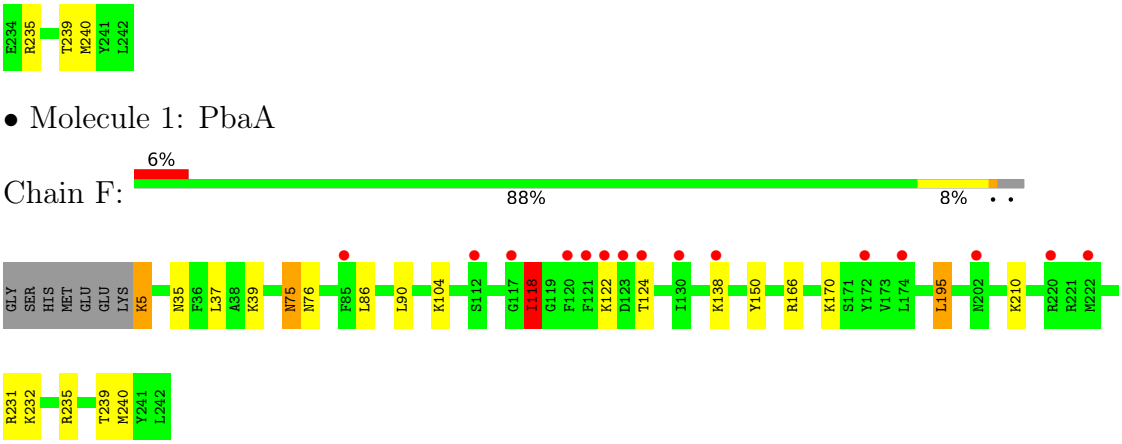
Chain D:

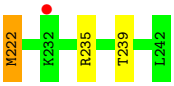


- Molecule 1: PbaA

Chain E:




E234 R235 T239 M240 Y241 L242
• Molecule 1: PbaA
Chain F:
6%
88%
8%
GLY SER HIS MET GLU GLU LYS K5 N35 F36 L37 A38 K39 N75 N76 F85 L86 L90 K104 S112 G117 I118 G119 F120 F121 K122 D123 T124 I130 K138 Y150 R166 K170 S171 Y172 V173 L174 L195 N202 K210 R220 R221 M222
R231 K232 R235 T239 M240 Y241 L242
• Molecule 1: PbaA
Chain G:
%
88%
8%
GLY SER HIS MET GLU GLU LYS K5 E15 N35 F36 L37 I60 N75 N76 L86 L90 K104 I118 G119 F120 F121 K122 D123 T124 I130 R166 L195 N196 L201 K210 R221 E228 R231 K232 M233 E234 R235 T239 L242
• Molecule 1: PbaA
Chain H:
4%
87%
8%
GLY SER HIS MET GLU GLU LYS K5 N8 E15 N16 I20 N35 F36 L37 A38 K39 N75 N76 L86 L90 N106 I118 G119 F120 F121 K122 D123 T124 I130 E135 G144 R166 L195 N202 K210 R220 R221 R230 R231 R235
T239 L242
• Molecule 1: PbaA
Chain I:
4%
87%
9%
GLY SER HIS MET GLU GLU LYS K5 N8 A34 N35 F36 L37 A38 K39 I60 N75 N76 A80 L86 L90 K104 I118 G119 F120 F121 K122 D123 T124 R166 L195 N196 L201 K210 M214 I215 L219 R220 E224 R231 R235
T239 L242
• Molecule 1: PbaA
Chain J:
5%
87%
8%
GLY SER HIS MET GLU GLU LYS K5 I20 N35 F36 L37 A38 K39 N75 N76 L86 L90 I98 V99 K104 I118 G119 F120 F121 K122 D123 T124 G129 I130 E163 R166 V173 L174 L195 N196 L201 K210 M214 I215 L219 R220 R221


M222
K232
R235
T239
L242

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	92.69Å 200.94Å 92.76Å 90.00° 110.96° 90.00°	Depositor
Resolution (Å)	20.00 – 2.55 19.99 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.0 (20.00-2.55) 99.2 (19.99-2.55)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.64 (at 2.56Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.208 , 0.240 0.214 , 0.244	Depositor DCC
R_{free} test set	5085 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	76.3	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 55.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	18821	wwPDB-VP
Average B, all atoms (Å^2)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% 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 (i)

5.1 Standard geometry (i)

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

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	0.58	0/1902	0.76	0/2567
1	B	0.63	0/1902	0.79	3/2567 (0.1%)
1	C	0.64	0/1902	0.77	0/2567
1	D	0.59	0/1902	0.77	2/2567 (0.1%)
1	E	0.57	0/1902	0.77	2/2567 (0.1%)
1	F	0.60	0/1902	0.79	2/2567 (0.1%)
1	G	0.60	0/1902	0.78	2/2567 (0.1%)
1	H	0.61	0/1902	0.80	4/2567 (0.2%)
1	I	0.59	0/1902	0.76	1/2567 (0.0%)
1	J	0.58	0/1902	0.77	2/2567 (0.1%)
All	All	0.60	0/19020	0.78	18/25670 (0.1%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	230	ARG	NE-CZ-NH1	-8.15	116.22	120.30
1	H	5	LYS	CA-CB-CG	7.72	130.38	113.40
1	I	5	LYS	CA-CB-CG	7.55	130.02	113.40
1	H	230	ARG	NE-CZ-NH2	6.98	123.79	120.30
1	F	138	LYS	CD-CE-NZ	6.91	127.58	111.70

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	1867	0	1916	13	0
1	B	1867	0	1916	7	0
1	C	1867	0	1916	13	0
1	D	1867	0	1916	15	0
1	E	1867	0	1916	15	0
1	F	1867	0	1916	13	0
1	G	1867	0	1916	11	0
1	H	1867	0	1916	13	0
1	I	1867	0	1916	13	0
1	J	1867	0	1916	11	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	11	0	0	0	0
3	B	16	0	0	0	0
3	C	19	0	0	1	0
3	D	12	0	0	0	0
3	E	10	0	0	0	0
3	F	10	0	0	1	0
3	G	20	0	0	1	0
3	H	16	0	0	3	0
3	I	15	0	0	0	0
3	J	12	0	0	1	0
All	All	18821	0	19160	103	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 3.

The worst 5 of 103 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:E:5:LYS:HB3	1:E:6:PRO:HD2	1.75	0.67
1:J:86:LEU:HD22	1:J:90:LEU:HD23	1.80	0.63
1:I:5:LYS:HD3	1:I:8:ASN:OD1	1.99	0.63
1:H:86:LEU:HD22	1:H:90:LEU:HD23	1.82	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:118:ILE:HD12	1:F:231:ARG:HD3	1.82	0.62

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	236/245 (96%)	229 (97%)	5 (2%)	2 (1%)	19	27
1	B	236/245 (96%)	229 (97%)	5 (2%)	2 (1%)	19	27
1	C	236/245 (96%)	229 (97%)	5 (2%)	2 (1%)	19	27
1	D	236/245 (96%)	229 (97%)	5 (2%)	2 (1%)	19	27
1	E	236/245 (96%)	229 (97%)	5 (2%)	2 (1%)	19	27
1	F	236/245 (96%)	228 (97%)	6 (2%)	2 (1%)	19	27
1	G	236/245 (96%)	229 (97%)	5 (2%)	2 (1%)	19	27
1	H	236/245 (96%)	229 (97%)	5 (2%)	2 (1%)	19	27
1	I	236/245 (96%)	229 (97%)	5 (2%)	2 (1%)	19	27
1	J	236/245 (96%)	229 (97%)	5 (2%)	2 (1%)	19	27
All	All	2360/2450 (96%)	2289 (97%)	51 (2%)	20 (1%)	19	27

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	75	ASN
1	B	75	ASN
1	C	75	ASN
1	D	75	ASN
1	E	75	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	201/207 (97%)	192 (96%)	9 (4%)	27	37
1	B	201/207 (97%)	189 (94%)	12 (6%)	19	25
1	C	201/207 (97%)	189 (94%)	12 (6%)	19	25
1	D	201/207 (97%)	190 (94%)	11 (6%)	21	29
1	E	201/207 (97%)	186 (92%)	15 (8%)	13	17
1	F	201/207 (97%)	188 (94%)	13 (6%)	17	23
1	G	201/207 (97%)	190 (94%)	11 (6%)	21	29
1	H	201/207 (97%)	188 (94%)	13 (6%)	17	23
1	I	201/207 (97%)	187 (93%)	14 (7%)	15	19
1	J	201/207 (97%)	186 (92%)	15 (8%)	13	17
All	All	2010/2070 (97%)	1885 (94%)	125 (6%)	18	24

5 of 125 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	214	MET
1	J	35	ASN
1	F	232	LYS
1	I	224	GLU
1	J	163	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	236	GLN
1	H	76	ASN
1	J	236	GLN
1	G	35	ASN
1	G	236	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)

Of 10 ligands modelled in this entry, 10 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 (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	238/245 (97%)	0.08	5 (2%)	63	70	58, 82, 114, 154	0
1	B	238/245 (97%)	0.05	3 (1%)	77	82	49, 72, 109, 130	0
1	C	238/245 (97%)	0.02	7 (2%)	51	59	49, 67, 106, 132	0
1	D	238/245 (97%)	0.22	7 (2%)	51	59	52, 83, 120, 160	0
1	E	238/245 (97%)	0.19	6 (2%)	57	63	61, 86, 113, 137	0
1	F	238/245 (97%)	0.35	15 (6%)	20	23	58, 86, 121, 172	0
1	G	238/245 (97%)	0.04	3 (1%)	77	82	53, 73, 104, 136	0
1	H	238/245 (97%)	0.09	9 (3%)	40	47	54, 73, 113, 126	0
1	I	238/245 (97%)	0.23	10 (4%)	36	42	60, 83, 117, 146	0
1	J	238/245 (97%)	0.20	13 (5%)	25	30	59, 87, 116, 154	0
All	All	2380/2450 (97%)	0.15	78 (3%)	46	53	49, 80, 115, 172	0

The worst 5 of 78 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	123	ASP	5.5
1	J	123	ASP	4.7
1	I	123	ASP	4.1
1	F	120	PHE	3.9
1	G	123	ASP	3.8

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)

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
2	CL	C	302	1/1	0.91	0.16	89,89,89,89	0
2	CL	E	302	1/1	0.94	0.16	93,93,93,93	0
2	CL	H	301	1/1	0.94	0.22	91,91,91,91	0
2	CL	D	302	1/1	0.95	0.15	94,94,94,94	0
2	CL	B	301	1/1	0.95	0.23	83,83,83,83	0
2	CL	A	301	1/1	0.95	0.23	86,86,86,86	0
2	CL	C	301	1/1	0.96	0.28	84,84,84,84	0
2	CL	D	301	1/1	0.97	0.23	97,97,97,97	0
2	CL	G	301	1/1	0.97	0.25	78,78,78,78	0
2	CL	E	301	1/1	0.97	0.21	87,87,87,87	0

6.5 Other polymers (i)

There are no such residues in this entry.