wwPDB X-ray Structure Validation Summary Report (i)

Jan 31, 2016 – 11:58 PM GMT

PDB ID : 1Z8W
Title : Structure of Mutant Pyrrolidone Carboxyl Peptidase (E192I) from a Hyperthermophile, Pyrococcus furiosus
Authors : Kaushik, J.K.; Yamagata, Y.; Ogasahara, K.; Yutani, K.
Deposited on : 2005-03-31
Resolution : 2.00 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 (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:
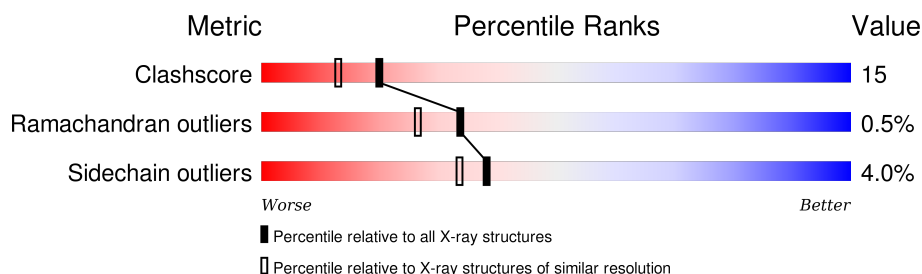
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.00 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	Percentile Ranks	Value
Clashscore		15
Ramachandran outliers		0.5%
Sidechain outliers		4.0%

Worse *Better*

▮ Percentile relative to all X-ray structures

◻ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)

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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	208	73% 25% •
1	B	208	73% 25% •
1	C	208	74% 24% •
1	D	208	71% 26% •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7287 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 Pyrrolidone-carboxylate peptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1604	1041	263	294	6			
1	B	208	Total	C	N	O	S	0	0	0
			1604	1041	263	294	6			
1	C	208	Total	C	N	O	S	0	0	0
			1604	1041	263	294	6			
1	D	208	Total	C	N	O	S	0	0	0
			1604	1041	263	294	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	142	SER	CYS	ENGINEERED	UNP O73944
A	188	SER	CYS	ENGINEERED	UNP O73944
A	192	ILE	GLU	ENGINEERED	UNP O73944
B	142	SER	CYS	ENGINEERED	UNP O73944
B	188	SER	CYS	ENGINEERED	UNP O73944
B	192	ILE	GLU	ENGINEERED	UNP O73944
C	142	SER	CYS	ENGINEERED	UNP O73944
C	188	SER	CYS	ENGINEERED	UNP O73944
C	192	ILE	GLU	ENGINEERED	UNP O73944
D	142	SER	CYS	ENGINEERED	UNP O73944
D	188	SER	CYS	ENGINEERED	UNP O73944
D	192	ILE	GLU	ENGINEERED	UNP O73944

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	206	Total	O	0	0
			206	206		
2	B	239	Total	O	0	0
			239	239		

Continued on next page...

Continued from previous page...

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	225	Total 225	O 225	0	0
2	D	201	Total 201	O 201	0	0

3 Residue-property plots ⓘ

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.
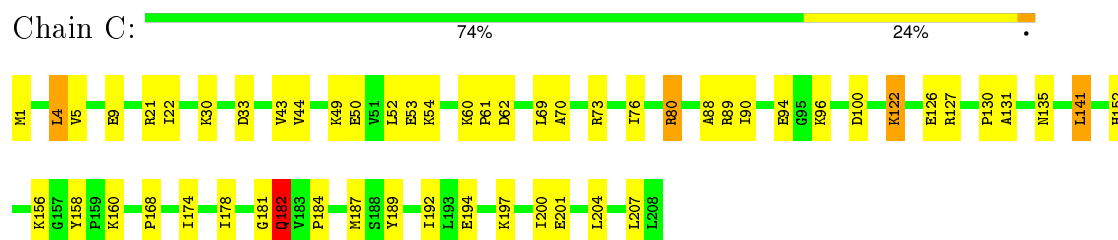
Note EDS was not executed.
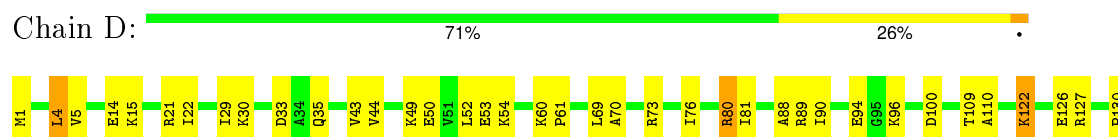
- Molecule 1: Pyrrolidone-carboxylate peptidase
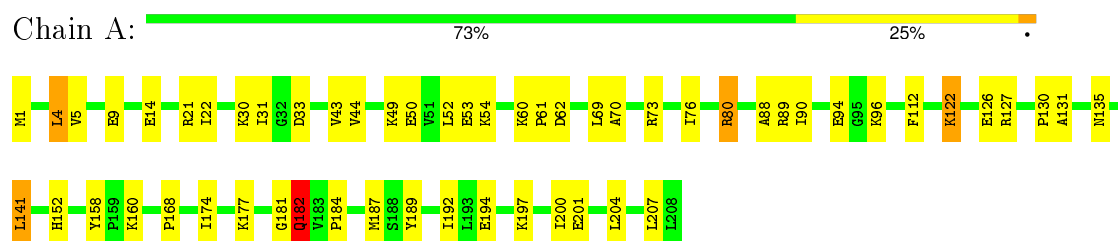
- Molecule 1: Pyrrolidone-carboxylate peptidase
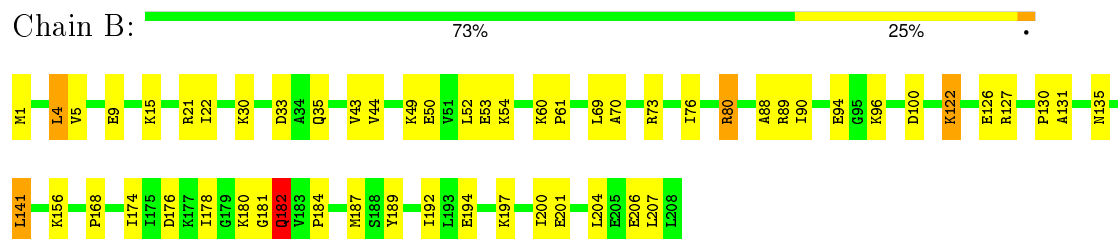
- Molecule 1: Pyrrolidone-carboxylate peptidase

- Molecule 1: Pyrrolidone-carboxylate peptidase

A131 N135 L141 H152 Y158 I174 I175 D176 K177 I178 G179 K180 G181 Q182 V183 P184 M187 S188 Y189 I192 L193 E194 K197 I200 E201 L204 L207 L208

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	47.41Å 103.92Å 186.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00	Depositor
% Data completeness (in resolution range)	95.2 (40.00-2.00)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.242	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7287	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.30	0/1638	0.61	0/2215
1	B	0.30	0/1638	0.61	0/2215
1	C	0.31	0/1638	0.62	0/2215
1	D	0.29	0/1638	0.61	0/2215
All	All	0.30	0/6552	0.61	0/8860

There are no bond length outliers.

There are no bond angle outliers.

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	1604	0	1676	52	0
1	B	1604	0	1676	49	1
1	C	1604	0	1676	53	0
1	D	1604	0	1676	57	1
2	A	206	0	0	8	0
2	B	239	0	0	7	0
2	C	225	0	0	7	0
2	D	201	0	0	11	0
All	All	7287	0	6704	194	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 15.

The worst 5 of 194 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:D:35:GLN:HA	2:D:296:HOH:O	1.59	1.02
1:D:96:LYS:HG3	2:D:216:HOH:O	1.76	0.84
1:D:30:LYS:HG2	2:D:296:HOH:O	1.79	0.81
1:A:181:GLY:HA3	1:B:89:ARG:HD2	1.64	0.80
1:C:181:GLY:HA3	1:D:89:ARG:HD2	1.66	0.77

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)
1:B:206:GLU:O	1:D:33:ASP:OD2[4_456]	2.13	0.07

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	206/208 (99%)	198 (96%)	7 (3%)	1 (0%)	34	26
1	B	206/208 (99%)	198 (96%)	7 (3%)	1 (0%)	34	26
1	C	206/208 (99%)	198 (96%)	7 (3%)	1 (0%)	34	26
1	D	206/208 (99%)	198 (96%)	7 (3%)	1 (0%)	34	26
All	All	824/832 (99%)	792 (96%)	28 (3%)	4 (0%)	34	26

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	182	GLN
1	B	182	GLN
1	C	182	GLN
1	D	182	GLN

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	174/174 (100%)	167 (96%)	7 (4%)	38	33
1	B	174/174 (100%)	167 (96%)	7 (4%)	38	33
1	C	174/174 (100%)	167 (96%)	7 (4%)	38	33
1	D	174/174 (100%)	167 (96%)	7 (4%)	38	33
All	All	696/696 (100%)	668 (96%)	28 (4%)	38	33

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	141	LEU
1	C	52	LEU
1	D	122	LYS
1	B	182	GLN
1	C	4	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	152	HIS
1	C	93	ASN
1	D	93	ASN
1	B	135	ASN
1	D	35	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 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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates (i)

EDS was not executed - this section will therefore be empty.

6.4 Ligands (i)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers (i)

EDS was not executed - this section will therefore be empty.