wwPDB X-ray Structure Validation Summary Report (i)

Apr 27, 2023 – 07:34 pm BST

PDB ID	:	8BP9
Title	:	Structure of E. coli Class 2 L-asparaginase EcAIII, mutant M200W (crystal M200W#2)
Authors	:	Sciuk, A.; Jaskolski, M.; Loch, J.I.
Deposited on	:	2022-11-16
Resolution	:	1.70 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:

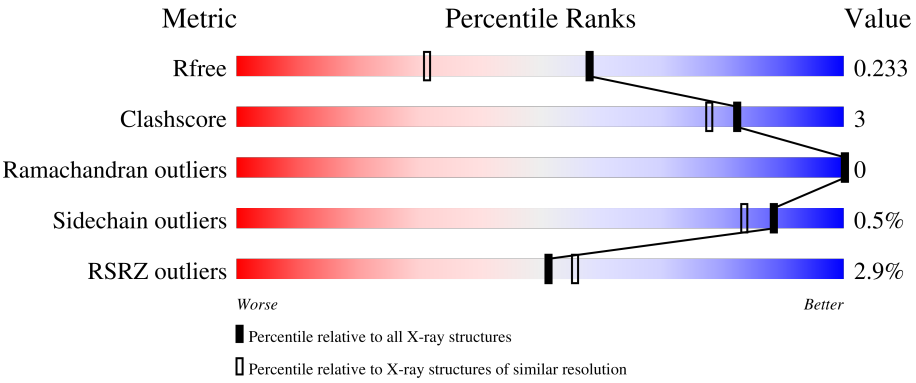
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.32.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.32.2

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 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	AAA	178	4% 83% · 13%
1	CCC	178	2% 86% · 11%
2	BBB	143	2% 85% 9% 6%
2	DDD	143	2% 89% 5% 6%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4629 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 Isoaspartyl peptidase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	155	Total	C	N	O	S	0	4	0
			1194	742	211	232	9			
1	CCC	159	Total	C	N	O	S	0	2	0
			1203	747	215	232	9			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	1	MET	-	initiating methionine	UNP P37595
CCC	1	MET	-	initiating methionine	UNP P37595

- Molecule 2 is a protein called Isoaspartyl peptidase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	BBB	135	Total	C	N	O	S	0	5	0
			990	616	167	201	6			
2	DDD	134	Total	C	N	O	S	0	3	0
			969	607	163	193	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BBB	200	TRP	MET	engineered mutation	UNP P37595
DDD	200	TRP	MET	engineered mutation	UNP P37595

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	2	Total	Na	0	0
			2	2		
3	CCC	1	Total	Na	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	1	Total Cl 1 1	0	0
4	BBB	2	Total Cl 2 2	0	0

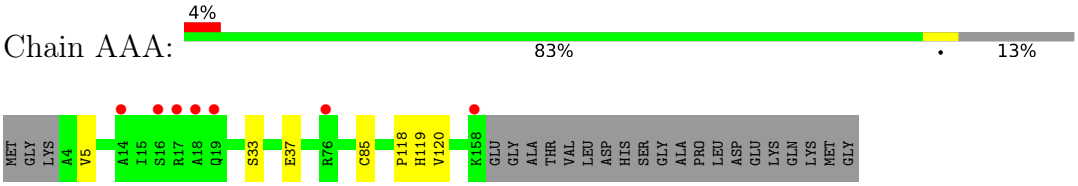
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	AAA	86	Total O 86 86	0	0
5	BBB	63	Total O 63 63	0	0
5	CCC	78	Total O 79 79	0	1
5	DDD	39	Total O 39 39	0	0

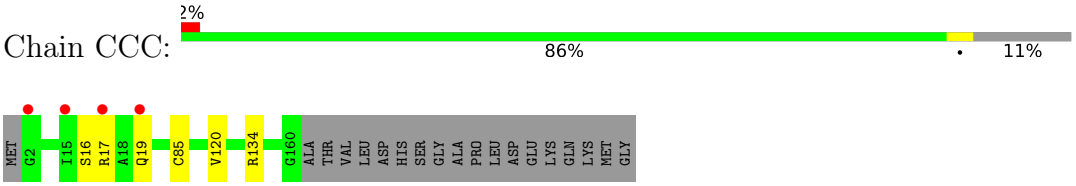
3 Residue-property plots (i)

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.

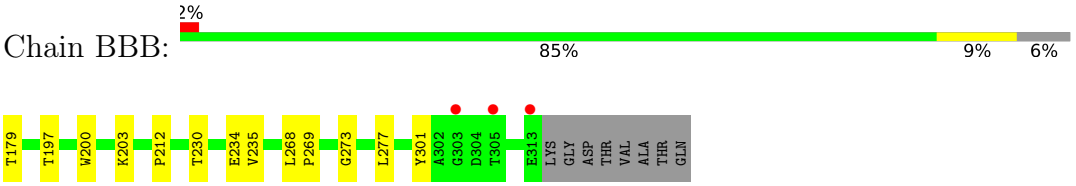
• Molecule 1: Isoaspartyl peptidase subunit alpha



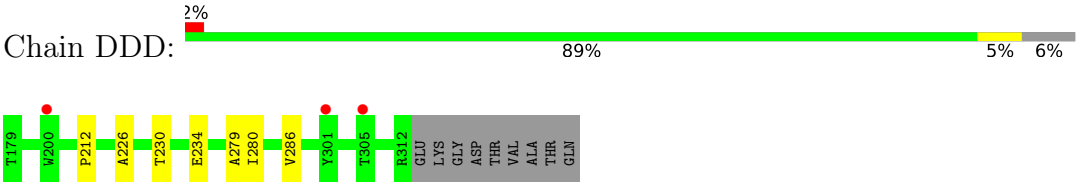
• Molecule 1: Isoaspartyl peptidase subunit alpha



• Molecule 2: Isoaspartyl peptidase subunit beta



• Molecule 2: Isoaspartyl peptidase subunit beta



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	50.97Å 74.47Å 146.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.40 – 1.70 20.15 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (73.40-1.70) 98.9 (20.15-1.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.38 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.193 , 0.228 0.202 , 0.233	Depositor DCC
R_{free} test set	1056 reflections (1.71%)	wwPDB-VP
Wilson B-factor (Å^2)	10.7	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 43.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.41$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4629	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.93% 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

5.1 Standard geometry

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

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	AAA	0.76	0/1209	0.86	0/1631
1	CCC	0.76	0/1217	0.88	0/1640
2	BBB	0.75	0/1007	0.86	0/1374
2	DDD	0.74	0/989	0.85	0/1350
All	All	0.75	0/4422	0.86	0/5995

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	AAA	1194	0	1190	8	0
1	CCC	1203	0	1203	5	0
2	BBB	990	0	950	9	0
2	DDD	969	0	943	9	0
3	AAA	2	0	0	0	0
3	CCC	1	0	0	0	0
4	AAA	1	0	0	0	0
4	BBB	2	0	0	0	0
5	AAA	86	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	BBB	63	0	0	0	0
5	CCC	79	0	0	1	0
5	DDD	39	0	0	0	0
All	All	4629	0	4286	22	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 22 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:AAA:118:PRO:O	2:DDD:234[B]:GLU:HG2	1.72	0.89
1:AAA:120:VAL:HG23	2:DDD:234[A]:GLU:HG2	1.69	0.74
1:CCC:17:ARG:NH2	5:CCC:301:HOH:O	2.23	0.70
2:BBB:235:VAL:HG11	2:BBB:273[A]:GLY:HA3	1.83	0.59
1:CCC:16:SER:HB3	1:CCC:19:GLN:NE2	2.19	0.58

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	AAA	158/178 (89%)	156 (99%)	2 (1%)	0	100	100
1	CCC	159/178 (89%)	158 (99%)	1 (1%)	0	100	100
2	BBB	137/143 (96%)	131 (96%)	6 (4%)	0	100	100
2	DDD	135/143 (94%)	129 (96%)	6 (4%)	0	100	100
All	All	589/642 (92%)	574 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	AAA	124/136 (91%)	124 (100%)	0	100	100
1	CCC	123/136 (90%)	123 (100%)	0	100	100
2	BBB	97/99 (98%)	96 (99%)	1 (1%)	76	67
2	DDD	95/99 (96%)	94 (99%)	1 (1%)	73	63
All	All	439/470 (93%)	437 (100%)	2 (0%)	88	83

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

Mol	Chain	Res	Type
2	BBB	230	THR
2	DDD	230	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 6 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

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, 95^{th} 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	AAA	155/178 (87%)	0.15	7 (4%)	33	37	4, 10, 27, 50	0
1	CCC	159/178 (89%)	0.11	4 (2%)	57	61	5, 11, 25, 39	0
2	BBB	135/143 (94%)	0.00	3 (2%)	62	66	4, 9, 22, 44	0
2	DDD	134/143 (93%)	0.05	3 (2%)	62	66	4, 10, 20, 28	0
All	All	583/642 (90%)	0.08	17 (2%)	51	56	4, 10, 24, 50	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	18	ALA	9.3
2	BBB	313	GLU	5.2
2	DDD	200	TRP	3.9
2	BBB	303	GLY	3.8
2	DDD	305[A]	THR	3.6

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 monosaccharides 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, 95^{th} 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	NA	AAA	202	1/1	0.94	0.10	11,11,11,11	0
4	CL	BBB	401	1/1	0.96	0.05	21,21,21,21	0
4	CL	AAA	203	1/1	0.98	0.04	13,13,13,13	0
3	NA	CCC	201	1/1	0.99	0.05	6,6,6,6	0
4	CL	BBB	402	1/1	0.99	0.03	15,15,15,15	0
3	NA	AAA	201	1/1	1.00	0.03	7,7,7,7	0

6.5 Other polymers (i)

There are no such residues in this entry.