



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 11:25 PM GMT

PDB ID : 1JJA
Title : CRYSTAL STRUCTURE OF ORTHORHOMBIC FORM OF D90E MUTANT OF ESCHERICHIA COLI L-ASPARAGINASE II
Authors : Borek, D.; Kozak, M.; Jaskolski, M.
Deposited on : 2001-07-04
Resolution : 2.30 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

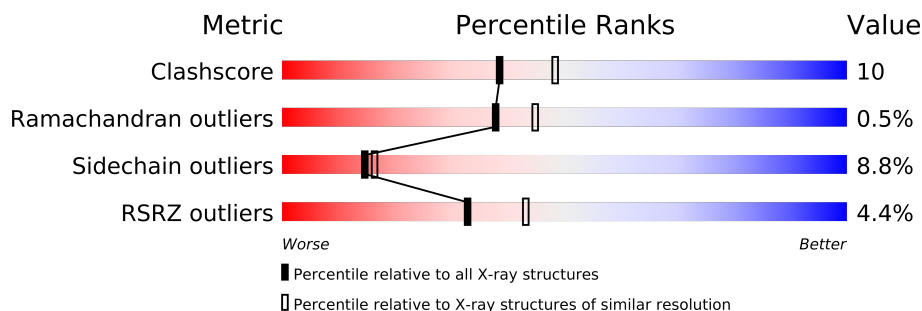
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.30 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))
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	326	
1	B	326	
1	C	326	
1	D	326	
1	E	326	
1	F	326	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14499 atoms, of which 0 are hydrogen and 0 are deuterium.

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 L-ASPARAGINASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	1	0
			2319	1450	397	464	8			
1	B	304	Total	C	N	O	S	0	2	0
			2284	1428	390	458	8			
1	C	326	Total	C	N	O	S	0	1	0
			2438	1522	417	491	8			
1	D	307	Total	C	N	O	S	0	1	0
			2307	1444	394	461	8			
1	E	307	Total	C	N	O	S	0	2	0
			2307	1443	394	462	8			
1	F	320	Total	C	N	O	S	0	1	0
			2400	1499	411	482	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	90	GLU	ASP	ENGINEERED	UNP P00805
B	90	GLU	ASP	ENGINEERED	UNP P00805
C	90	GLU	ASP	ENGINEERED	UNP P00805
D	90	GLU	ASP	ENGINEERED	UNP P00805
E	90	GLU	ASP	ENGINEERED	UNP P00805
F	90	GLU	ASP	ENGINEERED	UNP P00805

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	57	Total	O	0	0
			57	57		
2	B	63	Total	O	0	0
			63	63		
2	C	89	Total	O	0	0
			89	89		

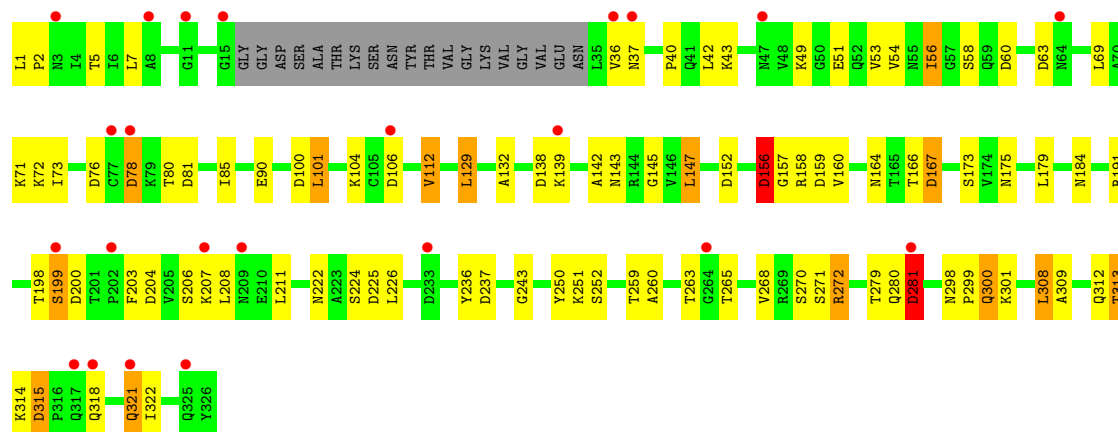
Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	53	Total 53	O 53	0	0
2	E	65	Total 65	O 65	0	0
2	F	117	Total 117	O 117	0	0

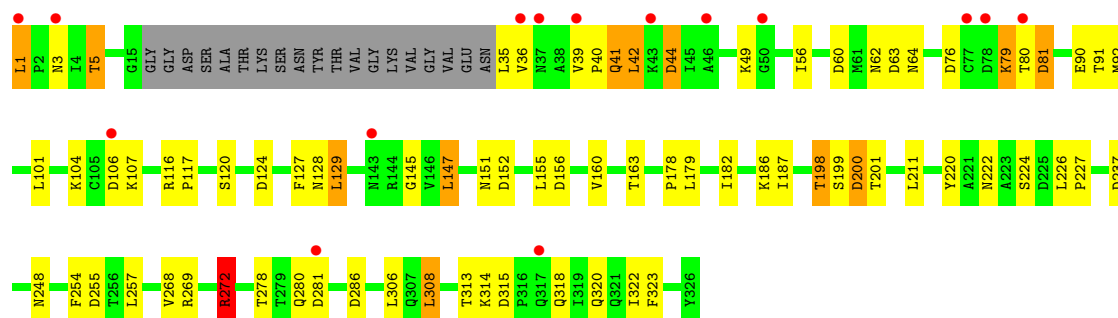
- Molecule 1: L-ASPARAGINASE II

Chain D:



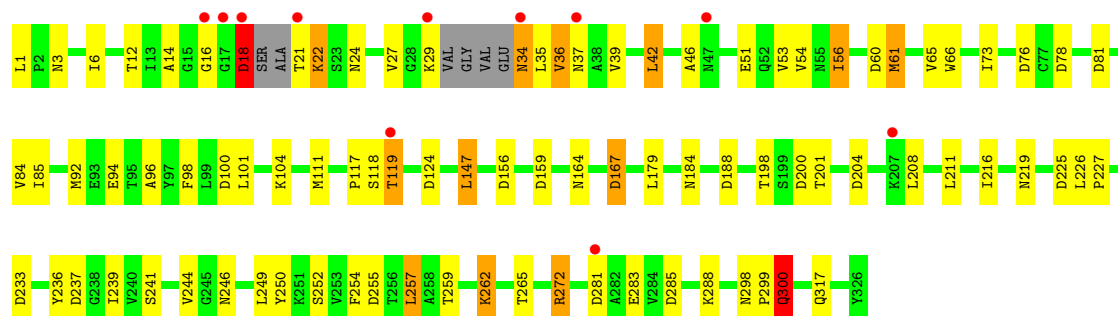
- Molecule 1: L-ASPARAGINASE II

Chain E:



- Molecule 1: L-ASPARAGINASE II

Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	225.42Å 128.05Å 62.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.30 10.00 – 2.33	Depositor EDS
% Data completeness (in resolution range)	96.9 (10.00-2.30) 96.9 (10.00-2.33)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.33Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.186 , 0.204 0.186 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	35.4	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 74882 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14499	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 9.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.62	0/2359	0.95	14/3212 (0.4%)
1	B	0.61	0/2330	0.97	14/3172 (0.4%)
1	C	0.65	0/2480	0.99	12/3377 (0.4%)
1	D	0.60	0/2347	0.92	10/3196 (0.3%)
1	E	0.76	0/2353	1.04	14/3204 (0.4%)
1	F	0.74	0/2440	1.07	19/3319 (0.6%)
All	All	0.67	0/14309	0.99	83/19480 (0.4%)

There are no bond length outliers.

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	272	ARG	NE-CZ-NH2	-9.25	115.67	120.30
1	E	272	ARG	NE-CZ-NH1	9.22	124.91	120.30
1	C	269	ARG	NE-CZ-NH2	-8.74	115.93	120.30
1	E	156	ASP	CB-CG-OD2	8.52	125.97	118.30
1	C	272	ARG	NE-CZ-NH1	8.07	124.33	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2319	0	2312	65	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2284	0	2278	46	0
1	C	2438	0	2429	40	0
1	D	2307	0	2303	60	0
1	E	2307	0	2304	41	0
1	F	2400	0	2390	45	0
2	A	57	0	0	1	0
2	B	63	0	0	0	0
2	C	89	0	0	4	0
2	D	53	0	0	1	0
2	E	65	0	0	0	0
2	F	117	0	0	1	0
All	All	14499	0	14016	274	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

The worst 5 of 274 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:112:VAL:HG11	1:D:132:ALA:HB2	1.23	1.09
1:F:21:THR:O	1:F:22:LYS:HB2	1.62	0.98
1:D:156:ASP:O	1:D:160:VAL:HG12	1.66	0.96
1:E:79:LYS:NZ	1:E:79:LYS:HB3	1.84	0.92
1:A:205:VAL:HA	1:A:208:LEU:HD13	1.52	0.90

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	306/326 (94%)	288 (94%)	17 (6%)	1 (0%)	50	60
1	B	302/326 (93%)	290 (96%)	12 (4%)	0	100	100
1	C	325/326 (100%)	318 (98%)	6 (2%)	1 (0%)	50	60
1	D	304/326 (93%)	290 (95%)	12 (4%)	2 (1%)	30	34

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	305/326 (94%)	289 (95%)	14 (5%)	2 (1%)	30	34
1	F	315/326 (97%)	302 (96%)	10 (3%)	3 (1%)	22	23
All	All	1857/1956 (95%)	1777 (96%)	71 (4%)	9 (0%)	38	45

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	22	LYS
1	A	35	LEU
1	D	281	ASP
1	E	199	SER
1	D	199	SER

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	A	254/266 (96%)	232 (91%)	22 (9%)	15	17
1	B	251/266 (94%)	228 (91%)	23 (9%)	13	15
1	C	267/266 (100%)	253 (95%)	14 (5%)	32	42
1	D	253/266 (95%)	226 (89%)	27 (11%)	10	10
1	E	254/266 (96%)	229 (90%)	25 (10%)	12	13
1	F	263/266 (99%)	239 (91%)	24 (9%)	14	15
All	All	1542/1596 (97%)	1407 (91%)	135 (9%)	14	16

5 of 135 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	51	GLU
1	D	211	LEU
1	F	208	LEU
1	D	56	ILE
1	D	139	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such

sidechains are listed below:

Mol	Chain	Res	Type
1	D	128	ASN
1	D	209	ASN
1	F	300	GLN
1	D	184	ASN
1	D	312	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	309/326 (94%)	0.02	17 (5%) 24 33	22, 43, 69, 86	0
1	B	304/326 (93%)	-0.12	10 (3%) 44 54	24, 43, 59, 67	0
1	C	326/326 (100%)	-0.35	6 (1%) 65 74	21, 33, 52, 74	0
1	D	307/326 (94%)	0.13	23 (7%) 14 21	25, 46, 63, 73	0
1	E	307/326 (94%)	-0.07	15 (4%) 28 39	17, 34, 57, 71	0
1	F	320/326 (98%)	-0.26	11 (3%) 43 53	15, 29, 59, 75	0
All	All	1873/1956 (95%)	-0.11	82 (4%) 33 43	15, 38, 61, 86	0

The worst 5 of 82 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	19	SER	6.0
1	A	16	GLY	5.7
1	A	37	ASN	5.2
1	F	47	ASN	5.1
1	F	17	GLY	4.5

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.