



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2018 – 07:14 am GMT

PDB ID : 1HFW
Title : X-ray structure of the complex between *Erwinia chrysanthemi* L-asparaginase and L-Glutamate
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Deposited on : 2000-12-08
Resolution : 1.80 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 ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix)	:	1.13
EDS	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

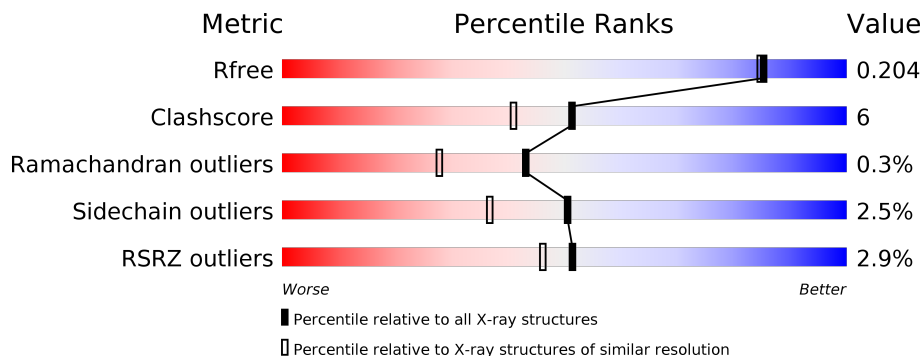
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	111664	5253 (1.80-1.80)
Clashscore	122126	6077 (1.80-1.80)
Ramachandran outliers	120053	6011 (1.80-1.80)
Sidechain outliers	120020	6010 (1.80-1.80)
RSRZ outliers	108989	5157 (1.80-1.80)

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	327	<div> <div>4%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>• 6%</div> </div> </div>
1	B	327	<div> <div>2%</div> <div> <div></div> <div>80%</div> <div>14%</div> <div>6%</div> </div> </div>
1	C	327	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>• 6%</div> </div> </div>
1	D	327	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>12%</div> <div>• 6%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10354 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 L-ASPARAGINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2340	1472	412	447	9			
1	B	309	Total	C	N	O	S	0	0	0
			2348	1477	413	449	9			
1	C	307	Total	C	N	O	S	0	0	0
			2335	1468	411	447	9			
1	D	306	Total	C	N	O	S	0	0	0
			2330	1465	410	446	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	156	ILE	LEU	variant	UNP P06608
A	178	ARG	LYS	variant	UNP P06608
A	267	LEU	MET	variant	UNP P06608
A	274	MET	ILE	variant	UNP P06608
B	156	ILE	LEU	variant	UNP P06608
B	178	ARG	LYS	variant	UNP P06608
B	267	LEU	MET	variant	UNP P06608
B	274	MET	ILE	variant	UNP P06608
C	156	ILE	LEU	variant	UNP P06608
C	178	ARG	LYS	variant	UNP P06608
C	267	LEU	MET	variant	UNP P06608
C	274	MET	ILE	variant	UNP P06608
D	156	ILE	LEU	variant	UNP P06608
D	178	ARG	LYS	variant	UNP P06608
D	267	LEU	MET	variant	UNP P06608
D	274	MET	ILE	variant	UNP P06608

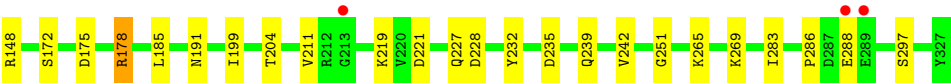
- Molecule 2 is GLUTAMIC ACID (three-letter code: GLU) (formula: C₅H₉NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	5	1	4		
2	B	1	Total	C	N	O	0	0
			10	5	1	4		
2	C	1	Total	C	N	O	0	0
			10	5	1	4		
2	D	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	216	Total	O	0	0
			216	216		
3	B	251	Total	O	0	0
			251	251		
3	C	235	Total	O	0	0
			235	235		
3	D	259	Total	O	0	0
			259	259		



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	108.47Å 91.70Å 130.62Å 90.00° 91.94° 90.00°	Depositor
Resolution (Å)	10.00 – 1.80 23.34 – 1.80	Depositor EDS
% Data completeness (in resolution range)	76.2 (10.00-1.80) 86.9 (23.34-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 1.80Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.168 , 0.188 0.185 , 0.204	Depositor DCC
R_{free} test set	2184 reflections (1.99%)	wwPDB-VP
Wilson B-factor (Å ²)	14.5	Xtriage
Anisotropy	0.305	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 64.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10354	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.31	0/2374	0.62	0/3217
1	B	0.32	0/2382	0.63	0/3229
1	C	0.32	0/2369	0.62	0/3211
1	D	0.33	0/2364	0.63	0/3204
All	All	0.32	0/9489	0.62	0/12861

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 [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	2340	0	2388	38	0
1	B	2348	0	2394	30	0
1	C	2335	0	2378	24	0
1	D	2330	0	2373	26	0
2	A	10	0	5	2	0
2	B	10	0	5	0	0
2	C	10	0	5	0	0
2	D	10	0	5	0	0
3	A	216	0	0	7	0
3	B	251	0	0	5	0
3	C	235	0	0	7	0
3	D	259	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	10354	0	9553	115	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 6.

The worst 5 of 115 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:145:LYS:HD3	1:B:145:LYS:H	1.19	1.03
1:B:239:GLN:HG2	3:B:2182:HOH:O	1.78	0.81
1:D:43:VAL:HG11	1:D:135:LEU:HD23	1.60	0.81
1:B:145:LYS:N	1:B:145:LYS:HD3	1.96	0.81
1:D:68:ASP:O	1:D:72:LYS:HD3	1.82	0.80

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	303/327 (93%)	294 (97%)	8 (3%)	1 (0%)	43	28
1	B	305/327 (93%)	298 (98%)	6 (2%)	1 (0%)	43	28
1	C	303/327 (93%)	296 (98%)	6 (2%)	1 (0%)	43	28
1	D	302/327 (92%)	295 (98%)	6 (2%)	1 (0%)	43	28
All	All	1213/1308 (93%)	1183 (98%)	26 (2%)	4 (0%)	43	28

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	204	THR

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Mol	Chain	Res	Type
1	D	204	THR
1	A	204	THR
1	B	204	THR

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	254/264 (96%)	246 (97%)	8 (3%)	43	28
1	B	254/264 (96%)	249 (98%)	5 (2%)	58	47
1	C	253/264 (96%)	246 (97%)	7 (3%)	47	33
1	D	253/264 (96%)	248 (98%)	5 (2%)	58	47
All	All	1014/1056 (96%)	989 (98%)	25 (2%)	50	37

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	80	LEU
1	C	53	LYS
1	D	172	SER
1	B	145	LYS
1	C	112	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	227	GLN
1	D	227	GLN
1	D	146	GLN
1	A	227	GLN
1	D	191	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GLU	A	350	-	1,9,9	0.11	0	1,11,11	0.33	0
2	GLU	B	350	-	1,9,9	0.03	0	1,11,11	0.21	0
2	GLU	C	350	-	1,9,9	0.07	0	1,11,11	0.41	0
2	GLU	D	350	-	1,9,9	0.12	0	1,11,11	0.27	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLU	A	350	-	-	0/3/9/9	0/0/0/0
2	GLU	B	350	-	-	0/3/9/9	0/0/0/0
2	GLU	C	350	-	-	0/3/9/9	0/0/0/0
2	GLU	D	350	-	-	0/3/9/9	0/0/0/0

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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	350	GLU	2	0

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	307/327 (93%)	-0.02	14 (4%) 32 27	9, 18, 39, 46	0
1	B	309/327 (94%)	-0.21	8 (2%) 56 51	7, 14, 30, 50	0
1	C	307/327 (93%)	-0.19	7 (2%) 60 56	8, 16, 33, 45	0
1	D	306/327 (93%)	-0.29	7 (2%) 60 56	7, 13, 33, 40	0
All	All	1229/1308 (93%)	-0.18	36 (2%) 51 46	7, 15, 34, 50	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	33	ALA	15.8
1	B	34	LEU	9.3
1	A	17	ALA	6.5
1	A	3	LYS	5.8
1	A	37	ASP	4.3

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 carbohydrates 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(\AA^2)	Q<0.9
2	GLU	A	350	10/10	0.94	0.10	16,18,23,24	0
2	GLU	D	350	10/10	0.96	0.07	11,12,15,15	0
2	GLU	C	350	10/10	0.96	0.08	15,16,18,19	0
2	GLU	B	350	10/10	0.97	0.06	10,13,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.