Full wwPDB X-ray Structure Validation Report ⓘ

Sep 4, 2022 – 10:13 pm BST

PDB ID	:	7R57
Title	:	Escherichia coli type II Asparaginase N24S mutant in its apo form
Authors	:	Maggi, M.; Scotti, C.
Deposited on	:	2022-02-10
Resolution	:	1.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

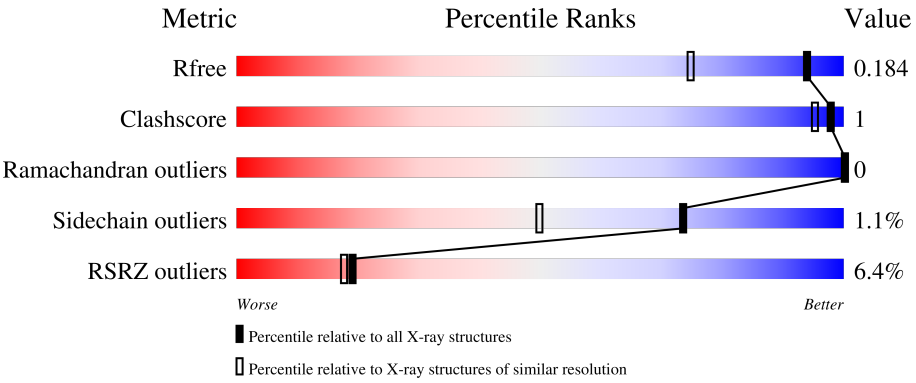
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.30
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.30

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 1.40 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	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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	332	4% 91% · 7%
1	B	332	4% 91% · 6%
1	C	332	9% 91% · 7%
1	D	332	7% 91% · 5%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 19708 atoms, of which 9257 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 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	310	Total	C	H	N	O	S	0	0	0
			4623	1449	2306	395	465	8			
1	B	311	Total	C	H	N	O	S	0	0	0
			4642	1455	2315	396	468	8			
1	C	309	Total	C	H	N	O	S	0	0	0
			4591	1441	2286	393	463	8			
1	D	316	Total	C	H	N	O	S	0	0	0
			4708	1474	2350	402	474	8			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP P00805
A	-4	HIS	-	expression tag	UNP P00805
A	-3	HIS	-	expression tag	UNP P00805
A	-2	HIS	-	expression tag	UNP P00805
A	-1	HIS	-	expression tag	UNP P00805
A	0	HIS	-	expression tag	UNP P00805
A	24	SER	ASN	engineered mutation	UNP P00805
B	-5	HIS	-	expression tag	UNP P00805
B	-4	HIS	-	expression tag	UNP P00805
B	-3	HIS	-	expression tag	UNP P00805
B	-2	HIS	-	expression tag	UNP P00805
B	-1	HIS	-	expression tag	UNP P00805
B	0	HIS	-	expression tag	UNP P00805
B	24	SER	ASN	engineered mutation	UNP P00805
C	-5	HIS	-	expression tag	UNP P00805
C	-4	HIS	-	expression tag	UNP P00805
C	-3	HIS	-	expression tag	UNP P00805
C	-2	HIS	-	expression tag	UNP P00805
C	-1	HIS	-	expression tag	UNP P00805
C	0	HIS	-	expression tag	UNP P00805
C	24	SER	ASN	engineered mutation	UNP P00805

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-5	HIS	-	expression tag	UNP P00805
D	-4	HIS	-	expression tag	UNP P00805
D	-3	HIS	-	expression tag	UNP P00805
D	-2	HIS	-	expression tag	UNP P00805
D	-1	HIS	-	expression tag	UNP P00805
D	0	HIS	-	expression tag	UNP P00805
D	24	SER	ASN	engineered mutation	UNP P00805

- Molecule 2 is water.

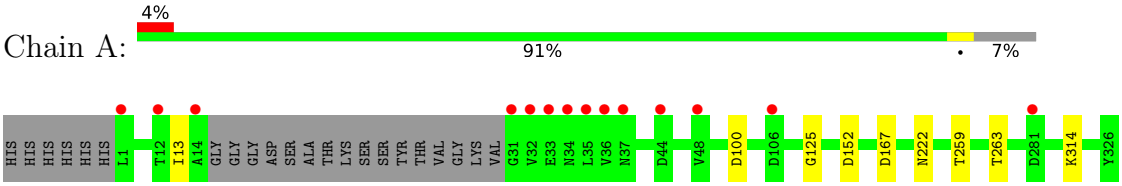
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	329	Total O 329 329	0	0
2	B	311	Total O 311 311	0	0
2	C	226	Total O 226 226	0	0
2	D	278	Total O 278 278	0	0

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.

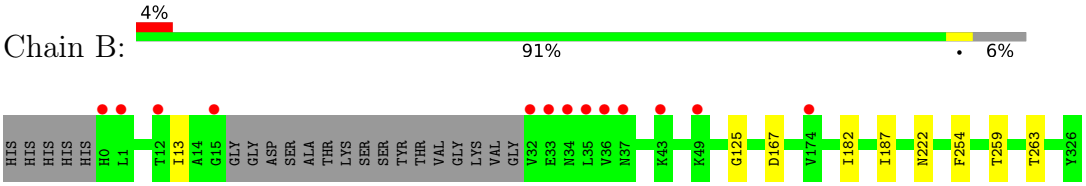
• Molecule 1: L-asparaginase 2

Chain A:



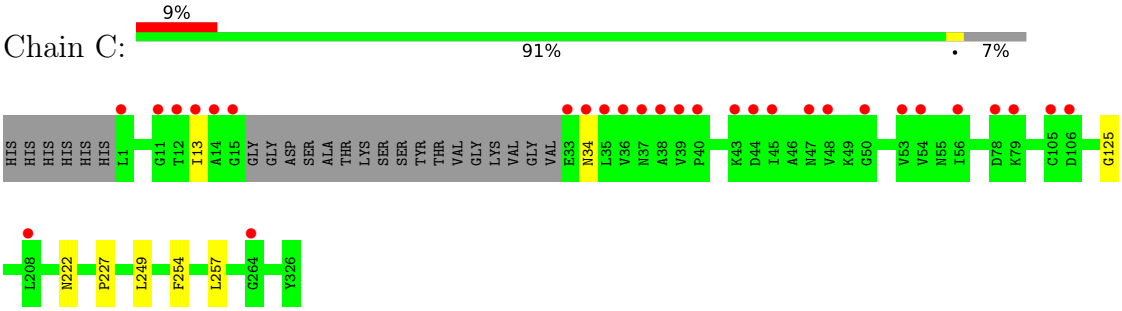
• Molecule 1: L-asparaginase 2

Chain B:



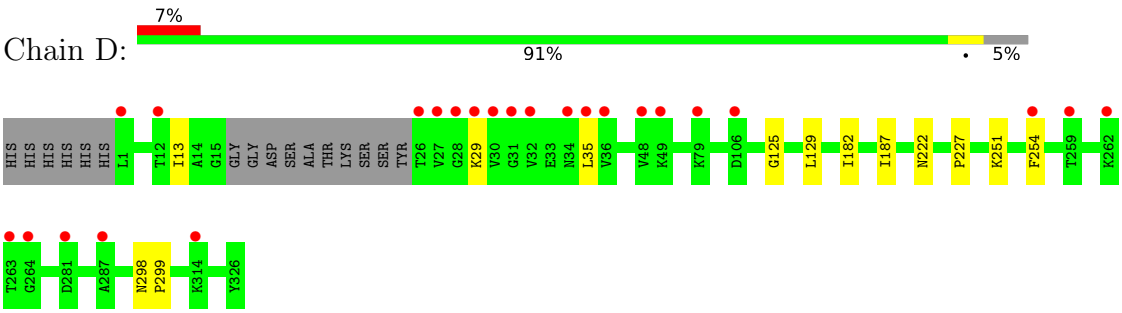
• Molecule 1: L-asparaginase 2

Chain C:



• Molecule 1: L-asparaginase 2

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	152.14Å 62.44Å 143.41Å 90.00° 118.19° 90.00°	Depositor
Resolution (Å)	47.09 – 1.40 47.09 – 1.40	Depositor EDS
% Data completeness (in resolution range)	98.5 (47.09-1.40) 98.4 (47.09-1.40)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.40 (at 1.40Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.165 , 0.184 0.164 , 0.184	Depositor DCC
R_{free} test set	1758 reflections (0.77%)	wwPDB-VP
Wilson B-factor (Å^2)	18.6	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	19708	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.75% 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

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	0.48	0/2352	0.73	3/3205 (0.1%)
1	B	0.46	0/2362	0.72	2/3218 (0.1%)
1	C	0.37	0/2340	0.63	0/3189
1	D	0.38	0/2393	0.65	0/3260
All	All	0.43	0/9447	0.68	5/12872 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	167	ASP	CB-CG-OD1	6.49	124.14	118.30
1	A	167	ASP	CB-CG-OD1	5.67	123.40	118.30
1	A	152	ASP	CB-CG-OD1	5.65	123.38	118.30
1	A	100	ASP	CB-CG-OD2	-5.56	113.29	118.30
1	B	167	ASP	CB-CG-OD2	-5.27	113.56	118.30

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	2317	2306	2306	2	0
1	B	2327	2315	2314	3	0
1	C	2305	2286	2289	3	0
1	D	2358	2350	2352	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	329	0	0	0	0
2	B	311	0	0	0	0
2	C	226	0	0	0	0
2	D	278	0	0	1	1
All	All	10451	9257	9261	13	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 1.

All (13) 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:LEU:HD11	1:D:129:LEU:HD22	1.83	0.60
1:D:35:LEU:HD22	2:D:585:HOH:O	2.04	0.56
1:C:227:PRO:HB3	1:D:227:PRO:HB3	1.97	0.46
1:B:13:ILE:O	1:B:125:GLY:HA3	2.17	0.45
1:A:259:THR:O	1:A:263:THR:HG23	2.17	0.44
1:B:182:ILE:HG12	1:B:187:ILE:HG12	1.98	0.44
1:D:182:ILE:HG12	1:D:187:ILE:HG12	2.00	0.43
1:A:13:ILE:O	1:A:125:GLY:HA3	2.19	0.42
1:D:13:ILE:O	1:D:125:GLY:HA3	2.19	0.42
1:C:249:LEU:HD22	1:C:257:LEU:HD12	2.03	0.41
1:B:259:THR:O	1:B:263:THR:HG23	2.20	0.41
1:D:298:ASN:HB2	1:D:299:PRO:CD	2.51	0.41
1:C:13:ILE:O	1:C:125:GLY:HA3	2.21	0.40

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)
2:D:514:HOH:O	2:D:625:HOH:O[2_555]	2.15	0.05

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	306/332 (92%)	301 (98%)	5 (2%)	0	100	100
1	B	307/332 (92%)	302 (98%)	5 (2%)	0	100	100
1	C	305/332 (92%)	296 (97%)	9 (3%)	0	100	100
1	D	312/332 (94%)	307 (98%)	5 (2%)	0	100	100
All	All	1230/1328 (93%)	1206 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	253/272 (93%)	251 (99%)	2 (1%)	81	62
1	B	254/272 (93%)	252 (99%)	2 (1%)	81	62
1	C	251/272 (92%)	248 (99%)	3 (1%)	71	47
1	D	258/272 (95%)	254 (98%)	4 (2%)	62	33
All	All	1016/1088 (93%)	1005 (99%)	11 (1%)	73	50

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	222	ASN
1	A	314	LYS
1	B	222	ASN
1	B	254	PHE
1	C	34	ASN
1	C	222	ASN
1	C	254	PHE
1	D	29	LYS
1	D	222	ASN
1	D	251	LYS

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Mol	Chain	Res	Type
1	D	254	PHE

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

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)

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

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	A	310/332 (93%)	0.33	14 (4%)	33	33	12, 18, 35, 54	0
1	B	311/332 (93%)	0.33	13 (4%)	36	37	12, 18, 37, 56	0
1	C	309/332 (93%)	0.61	29 (9%)	8	7	17, 27, 45, 78	0
1	D	316/332 (95%)	0.48	24 (7%)	13	13	16, 23, 44, 76	0
All	All	1246/1328 (93%)	0.44	80 (6%)	19	18	12, 21, 42, 78	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	35	LEU	12.4
1	C	36	VAL	11.6
1	D	30	VAL	9.8
1	B	36	VAL	7.7
1	C	34	ASN	7.1
1	C	37	ASN	7.0
1	A	36	VAL	6.6
1	C	1	LEU	6.4
1	C	15	GLY	6.3
1	D	28	GLY	5.9
1	D	27	VAL	5.8
1	D	35	LEU	5.2
1	D	29	LYS	5.1
1	B	15	GLY	4.8
1	D	31	GLY	4.7
1	C	12	THR	4.7
1	D	34	ASN	4.6
1	A	31	GLY	4.6
1	B	34	ASN	4.6
1	C	33	GLU	4.5
1	A	35	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	34	ASN	4.1
1	B	32	VAL	4.0
1	C	38	ALA	4.0
1	B	35	LEU	3.9
1	C	264	GLY	3.9
1	A	37	ASN	3.8
1	D	32	VAL	3.6
1	C	43	LYS	3.6
1	C	48	VAL	3.5
1	C	40	PRO	3.5
1	A	32	VAL	3.4
1	D	106	ASP	3.4
1	B	43	LYS	3.4
1	B	12	THR	3.2
1	C	14	ALA	3.2
1	A	12	THR	3.1
1	D	48	VAL	3.1
1	C	44	ASP	3.1
1	D	263	THR	3.1
1	A	106	ASP	3.1
1	C	13	ILE	3.1
1	A	33	GLU	3.1
1	C	11	GLY	3.1
1	C	79	LYS	3.0
1	C	208	LEU	3.0
1	D	262	LYS	3.0
1	D	264	GLY	2.9
1	B	49	LYS	2.9
1	A	48	VAL	2.9
1	B	33	GLU	2.8
1	D	259	THR	2.8
1	C	47	ASN	2.8
1	C	56	ILE	2.7
1	B	0	HIS	2.7
1	D	26	THR	2.6
1	C	45	ILE	2.6
1	C	105	CYS	2.6
1	A	1	LEU	2.5
1	D	1	LEU	2.5
1	A	44	ASP	2.4
1	C	106	ASP	2.4
1	C	53	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	79	LYS	2.4
1	C	54	VAL	2.3
1	C	78	ASP	2.3
1	D	281	ASP	2.3
1	D	314	LYS	2.2
1	A	281	ASP	2.2
1	B	37	ASN	2.2
1	D	36	VAL	2.2
1	D	254	PHE	2.2
1	B	1	LEU	2.2
1	D	49	LYS	2.1
1	A	14	ALA	2.1
1	D	287	ALA	2.1
1	C	50	GLY	2.0
1	B	174	VAL	2.0
1	C	39	VAL	2.0
1	D	12	THR	2.0

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.