

Full wwPDB X-ray Structure Validation Report (i)

Oct 30, 2023 – 12:52 PM JST

PDB ID : 8H4F

Title : Blasnase-T13A/P55F with D-asn Authors : Lu, F.; Wang, W.; Chi, H.; Ran, T.

2022-10-10 Deposited on

1.90 Å(reported) Resolution

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 (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

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13

EDS 2.36

20191225.v01 (using entries in the PDB archive December 25th 2019) Percentile statistics

> Refmac 5.8.0158

CCP4 7.0.044 (Gargrove)

Ideal geometry (proteins) Engh & Huber (2001) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

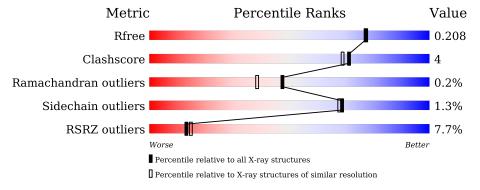
Validation Pipeline (wwPDB-VP) 2.36

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 1.90 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	328	88%	10%	-
1	В	328	91%	6%	



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5468 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.

\mathbf{Mol}	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	319	Total	С	N	О	S	0	0	0
1	Λ	919	2481	1580	422	471	8		U	0
1	B	320	Total	С	N	О	S	0	0	0
1	Ъ	320	2493	1588	423	474	8			

There are 16 discrepancies between the modelled and reference sequences:

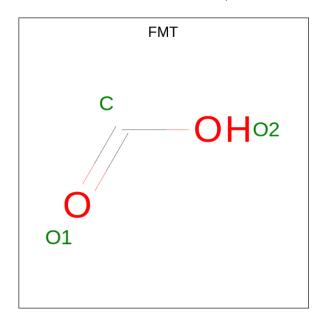
Chain	Residue	Modelled	Actual	Comment	Reference
A	13	ALA	THR	engineered mutation	UNP A0A6I7U6Y2
A	55	PHE	PRO	engineered mutation	UNP A0A6I7U6Y2
A	323	LEU	-	expression tag	UNP A0A6I7U6Y2
A	324	GLU	ı	expression tag	UNP A0A6I7U6Y2
A	325	HIS	-	expression tag	UNP A0A6I7U6Y2
A	326	HIS	-	expression tag	UNP A0A6I7U6Y2
A	327	HIS	-	expression tag	UNP A0A6I7U6Y2
A	328	HIS	-	expression tag	UNP A0A6I7U6Y2
В	13	ALA	THR	engineered mutation	UNP A0A6I7U6Y2
В	55	PHE	PRO	engineered mutation	UNP A0A6I7U6Y2
В	323	LEU	-	expression tag	UNP A0A6I7U6Y2
В	324	GLU	-	expression tag	UNP A0A6I7U6Y2
В	325	HIS	-	expression tag	UNP A0A6I7U6Y2
В	326	HIS	=	expression tag	UNP A0A6I7U6Y2
В	327	HIS	-	expression tag	UNP A0A6I7U6Y2
В	328	HIS	-	expression tag	UNP A0A6I7U6Y2

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mg 2 2	2	0
2	В	2	Total Mg 2 2	2	0



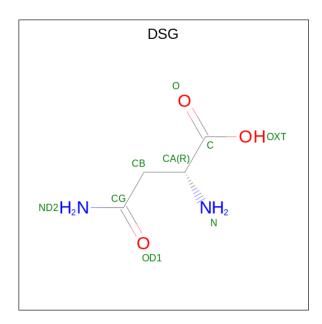
 \bullet Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: $\mathrm{CH_2O_2}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 3 1 2	3	0
3	A	1	Total C O 3 1 2	3	0
3	A	1	Total C O 3 1 2	3	0
3	В	1	Total C O 3 1 2	3	0
3	В	1	Total C O 3 1 2	3	0
3	В	1	Total C O 3 1 2	0	0
3	В	1	Total C O 3 1 2	0	0

 \bullet Molecule 4 is D-ASPARAGINE (three-letter code: DSG) (formula: $\mathrm{C_4H_8N_2O_3}).$





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 9		N 2		9	0
4	В	1	Total 9	C 4	N 2	O 3	9	0

• Molecule 5 is water.

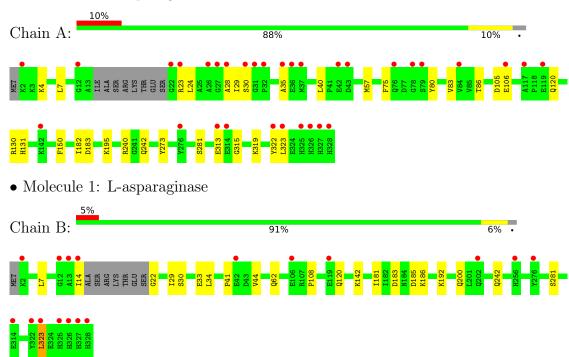
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	215	Total O 215 215	0	0
5	В	236	Total O 236 236	0	0



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





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	92.44Å 92.44Å 231.51Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.82 - 1.90	Depositor
resolution (A)	19.97 - 1.85	EDS
% Data completeness	99.9 (19.82-1.90)	Depositor
(in resolution range)	100.0 (19.97-1.85)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.58 (at 1.85Å)	Xtriage
Refinement program	PHENIX v1.16	Depositor
R, R_{free}	0.191 , 0.211	Depositor
it, it free	0.189 , 0.208	DCC
R_{free} test set	4248 reflections $(4.92%)$	wwPDB-VP
Wilson B-factor (Å ²)	36.0	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 44.6	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5468	wwPDB-VP
Average B, all atoms $(Å^2)$	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: FMT, MG, DSG

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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.47	0/2531	0.62	0/3427	
1	В	0.56	0/2543	0.64	0/3443	
All	All	0.52	0/5074	0.63	0/6870	

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	2481	0	2451	21	0
1	В	2493	0	2466	14	0
2	A	2	0	0	0	0
2	В	2	0	0	0	0
3	A	9	0	3	0	0
3	В	12	0	4	0	0
4	A	9	0	7	0	0
4	В	9	0	7	0	0
5	A	215	0	0	1	0
5	В	236	0	0	3	0
All	All	5468	0	4938	35	0



The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 4.

All (35) 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:A:23:ARG:HG2	1:A:29:ILE:HG13	1.66	0.76
1:A:195:LYS:HE3	1:A:323:LEU:HD23	1.71	0.73
1:A:23:ARG:HG3	1:A:28:ALA:HB3	1.70	0.72
1:B:30:SER:OG	1:B:33:GLU:HG3	1.94	0.68
1:B:22:GLY:N	5:B:506:HOH:O	2.32	0.61
1:B:323:LEU:O	1:B:323:LEU:HD12	2.03	0.58
1:B:242:GLN:HG3	1:B:281:SER:HA	1.87	0.57
1:A:35:ALA:HA	1:A:40:LEU:HD12	1.88	0.56
1:A:242:GLN:HG3	1:A:281:SER:HA	1.89	0.54
1:A:29:ILE:HG22	1:A:30:SER:O	2.08	0.54
1:B:142:LYS:O	1:B:192:LYS:NZ	2.35	0.54
1:A:23:ARG:NH1	1:A:28:ALA:O	2.31	0.53
1:B:108:PRO:HD3	1:B:142:LYS:HG2	1.90	0.52
1:B:181:ILE:C	1:B:181:ILE:HD12	2.31	0.51
1:A:4:LYS:HG2	1:A:80:TYR:CD1	2.47	0.49
1:A:40:LEU:HD23	1:A:130:ARG:HG3	1.95	0.49
1:B:29:ILE:CG1	1:B:33:GLU:HB2	2.43	0.49
1:A:323:LEU:O	1:A:323:LEU:HG	2.14	0.48
1:A:120:GLN:O	5:A:501:HOH:O	2.20	0.47
1:A:24:LEU:HA	1:A:29:ILE:HD12	1.97	0.47
1:B:120:GLN:O	5:B:501:HOH:O	2.20	0.47
1:A:105:ASP:OD1	1:A:106:GLU:N	2.49	0.46
1:A:195:LYS:HE3	1:A:323:LEU:HB3	1.98	0.46
1:B:7:LEU:HD22	1:B:34:LEU:CD1	2.47	0.45
1:B:41:PRO:O	1:B:44:VAL:HG12	2.17	0.45
1:A:131:HIS:CD2	1:A:182:ILE:HG21	2.52	0.45
1:B:14:ILE:C	5:B:502:HOH:O	2.55	0.44
1:A:240:ARG:HD3	1:A:273:TYR:CZ	2.53	0.44
1:A:315:GLY:O	1:A:319:LYS:HG2	2.18	0.44
1:B:185:ASP:C	1:B:186:LYS:HD2	2.39	0.43
1:A:23:ARG:HG2	1:A:29:ILE:CG1	2.42	0.43
1:A:75:PHE:CE1	1:A:83:VAL:HG23	2.53	0.42
1:A:7:LEU:HD11	1:A:86:THR:HG23	2.01	0.42
1:A:57:MET:O	1:A:57:MET:HG3	2.20	0.41
1:B:142:LYS:HB3	1:B:142:LYS:HE2	1.80	0.40

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	Percentile	s
1	A	315/328~(96%)	304 (96%)	10 (3%)	1 (0%)	41 31	
1	В	$316/328 \ (96\%)$	309 (98%)	7 (2%)	0	100 100	
All	All	631/656 (96%)	613 (97%)	17 (3%)	1 (0%)	47 38	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	322	TYR

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	$262/271 \ (97\%)$	259 (99%)	3 (1%)	73 73		
1	В	$264/271 \ (97\%)$	260 (98%)	4 (2%)	65 62		
All	All	526/542 (97%)	519 (99%)	7 (1%)	69 68		

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	150	PHE
1	A	183	ASP
1	A	313	GLU
1	В	62	GLN
1	В	183	ASP

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Mol	Chain	Res	Type
1	В	200	GLN
1	В	323	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	В	104	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 13 ligands modelled in this entry, 4 are monoatomic - leaving 9 for Mogul analysis.

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).

Mal	Mol Type		Dag	Link	B	ond leng	gths	Bond angles		
IVIOI	Type	Chain	Res	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	FMT	В	403	-	2,2,2	0.05	0	1,1,1	0.05	0
4	DSG	A	406	_	6,8,8	1.13	1 (16%)	8,10,10	0.86	0
3	FMT	A	403	2	2,2,2	0.72	0	1,1,1	0.24	0
3	FMT	В	405	-	2,2,2	0.17	0	1,1,1	0.12	0
3	FMT	В	404	-	2,2,2	0.19	0	1,1,1	0.21	0



Mol Type C		Chain	Res	Link	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	DSG	В	407	-	6,8,8	1.02	1 (16%)	8,10,10	1.10	0
3	FMT	В	406	-	2,2,2	0.22	0	1,1,1	0.16	0
3	FMT	A	404	-	2,2,2	0.22	0	1,1,1	0.10	0
3	FMT	A	405	-	2,2,2	0.14	0	1,1,1	0.29	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
4	DSG	В	407	-	-	2/8/8/8	-
4	DSG	A	406	-	-	3/8/8/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
4	A	406	DSG	OXT-C	-2.71	1.21	1.30
4	В	407	DSG	OXT-C	-2.36	1.22	1.30

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	406	DSG	C-CA-CB-CG
4	A	406	DSG	O-C-CA-CB
4	В	407	DSG	O-C-CA-CB
4	A	406	DSG	OXT-C-CA-CB
4	В	407	DSG	OXT-C-CA-CB

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 (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, 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	319/328 (97%)	0.31	32 (10%) 7 8	27, 40, 72, 82	0
1	В	320/328~(97%)	0.14	17 (5%) 26 29	27, 37, 62, 82	0
All	All	639/656 (97%)	0.22	49 (7%) 13 15	27, 38, 66, 82	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	323	LEU	10.2
1	A	323	LEU	7.9
1	A	322	TYR	7.2
1	В	322	TYR	6.5
1	A	23	ARG	6.2
1	В	14	ILE	5.5
1	В	325	HIS	5.4
1	В	328	HIS	5.3
1	В	327	HIS	5.0
1	A	43	ASP	4.8
1	A	28	ALA	4.6
1	В	119	GLU	4.6
1	A	32	PRO	4.5
1	A	36	GLU	4.5
1	В	326	HIS	4.1
1	A	313	GLU	3.9
1	A	119	GLU	3.8
1	A	26	ALA	3.8
1	A	328	HIS	3.6
1	В	42	GLU	3.5
1	A	325	HIS	3.5
1	A	2	LYS	3.4
1	A	42	GLU	3.4
1	В	12	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	12	GLY	3.4
1	A	76	GLN	3.4
1	A	22	GLY	3.3
1	В	314	GLU	3.3
1	В	13	ALA	3.2
1	В	276	TYR	3.2
1	В	256	HIS	2.9
1	В	106	GLU	2.7
1	A	276	TYR	2.6
1	A	327	HIS	2.5
1	A	30	SER	2.5
1	A	35	ALA	2.5
1	A	106	GLU	2.4
1	A	84	VAL	2.4
1	A	27	GLY	2.4
1	A	326	HIS	2.4
1	A	314	GLU	2.3
1	A	31	GLY	2.3
1	В	2	LYS	2.3
1	A	78	GLY	2.3
1	A	142	LYS	2.2
1	A	79	SER	2.2
1	A	37	MET	2.1
1	A	117	ALA	2.1
1	В	202	GLN	2.1

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 monosaccharides in this entry.

6.4 Ligands (i)

LIGAND-RSR INFOmissingINFO



6.5 Other polymers (i)

There are no such residues in this entry.

