Full wwPDB X-ray Structure Validation Report (i)

Mar 6, 2026 – 07:41 PM UTC

PDB ID	:	1BNG / pdb_00001bng
Title	:	BARNASE S85C/H102C DISULFIDE MUTANT
Authors	:	Clarke, J.; Henrick, K.; Fersht, A.R.
Deposited on	:	1995-03-31
Resolution	:	2.10 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 (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 (i)) were used in the production of this report:

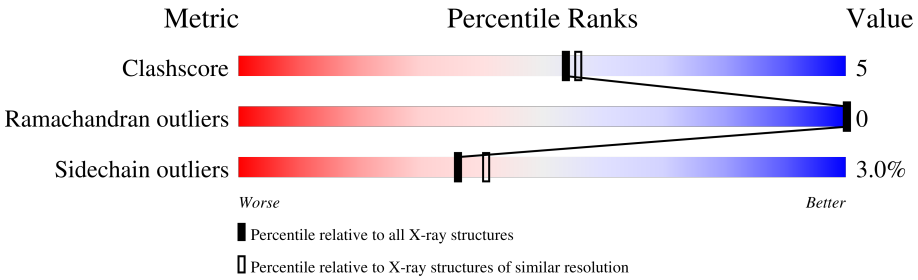
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 2.10 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	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	110	79% 18% • •
1	B	110	83% 13% • •
1	C	110	77% 15% 5% •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2757 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 BARNASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	108	Total	C	N	O	S	2	0	0
			849	538	145	164	2			
1	B	107	Total	C	N	O	S	0	0	0
			839	531	143	163	2			
1	C	107	Total	C	N	O	S	4	0	0
			853	539	147	165	2			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	85	CYS	SER	conflict	UNP P00648
A	102	CYS	HIS	conflict	UNP P00648
B	85	CYS	SER	conflict	UNP P00648
B	102	CYS	HIS	conflict	UNP P00648
C	85	CYS	SER	conflict	UNP P00648
C	102	CYS	HIS	conflict	UNP P00648

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	63	Total	O	0	0
			63	63		
2	B	73	Total	O	0	0
			73	73		
2	C	80	Total	O	0	0
			80	80		

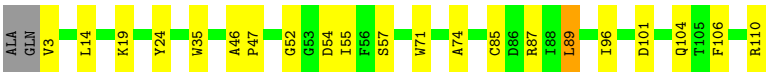
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

- Molecule 1: BARNASE

Chain A:



- Molecule 1: BARNASE

Chain B:

- Molecule 1: BARNASE

Chain C:

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	59.45Å 59.45Å 81.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.10)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.170 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2757	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

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	1.06	4/869 (0.5%)	1.57	6/1176 (0.5%)
1	B	1.01	1/859 (0.1%)	1.46	2/1163 (0.2%)
1	C	1.16	2/873 (0.2%)	1.72	16/1180 (1.4%)
All	All	1.08	7/2601 (0.3%)	1.59	24/3519 (0.7%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	39	LYS	CD-CE	-18.47	0.97	1.52
1	C	59	ARG	CZ-NH2	7.60	1.43	1.33
1	A	19	LYS	CE-NZ	5.63	1.66	1.49
1	A	85	CYS	CA-C	5.52	1.60	1.52
1	A	35	TRP	NE1-CE2	-5.23	1.31	1.37
1	A	71	TRP	NE1-CE2	-5.19	1.31	1.37
1	B	35	TRP	NE1-CE2	-5.12	1.31	1.37

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	39	LYS	CG-CD-CE	13.69	142.79	111.30
1	C	59	ARG	CD-NE-CZ	9.47	137.66	124.40
1	C	57	SER	N-CA-C	7.01	118.61	110.97
1	C	31	GLN	OE1-CD-NE2	-6.18	116.42	122.60
1	C	59	ARG	NE-CZ-NH1	6.12	127.62	121.50
1	C	7	PHE	CA-CB-CG	5.76	119.56	113.80
1	A	55	ILE	O-C-N	5.72	128.50	122.67
1	C	21	PRO	CB-CA-C	5.70	118.47	111.12
1	A	14	LEU	N-CA-C	5.67	117.55	111.36
1	C	29	GLU	CG-CD-OE1	5.49	131.02	118.40
1	A	54	ASP	CA-C-N	5.47	127.91	120.63
1	A	54	ASP	C-N-CA	5.47	127.91	120.63
1	C	59	ARG	NH1-CZ-NH2	-5.47	112.19	119.30
1	A	110	ARG	NE-CZ-NH2	5.40	124.06	119.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	110	ARG	NE-CZ-NH2	5.38	124.04	119.20
1	C	50	SER	O-C-N	5.37	129.85	123.24
1	C	110	ARG	NE-CZ-NH2	5.32	123.98	119.20
1	C	41	ASN	N-CA-C	5.23	118.97	112.59
1	C	59	ARG	CB-CG-CD	5.21	123.28	111.30
1	C	107	THR	CA-CB-OG1	-5.18	101.83	109.60
1	A	87	ARG	NE-CZ-NH2	5.13	123.82	119.20
1	C	29	GLU	CB-CG-CD	5.13	121.32	112.60
1	C	19	LYS	CA-C-O	-5.08	115.52	121.10
1	B	72	ARG	NE-CZ-NH2	5.01	123.71	119.20

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	849	0	813	6	0
1	B	839	0	795	11	0
1	C	853	0	820	7	0
2	A	63	0	0	0	0
2	B	73	0	0	0	0
2	C	80	0	0	0	0
All	All	2757	0	2428	24	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 5.

All (24) 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:C:96:ILE:HB	1:C:110:ARG:HB2	1.77	0.66
1:A:89:LEU:HD13	1:A:106:PHE:HE1	1.65	0.61
1:B:96:ILE:HG13	1:B:110:ARG:HB2	1.82	0.61
1:A:89:LEU:HD13	1:A:106:PHE:CE1	2.42	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:ALA:HB3	1:B:88:ILE:CG2	2.39	0.53
1:B:91:SER:OG	1:B:95:LEU:HB2	2.11	0.51
1:B:63:LEU:HD11	1:B:89:LEU:HD22	1.95	0.49
1:B:74:ALA:HB3	1:B:88:ILE:HG22	1.97	0.47
1:B:96:ILE:HB	1:B:110:ARG:HB2	1.97	0.47
1:A:52:GLY:HA2	1:A:74:ALA:HA	1.97	0.46
1:C:7:PHE:CE1	1:C:98:LYS:HB2	2.51	0.46
1:B:96:ILE:CG1	1:B:110:ARG:HB2	2.45	0.46
1:B:57:SER:O	1:B:58:ASN:HB3	2.17	0.45
1:C:109:ILE:O	1:C:110:ARG:HD3	2.17	0.45
1:B:94:TRP:HA	1:B:94:TRP:CE3	2.52	0.44
1:B:7:PHE:CE1	1:B:98:LYS:HB2	2.52	0.44
1:B:96:ILE:HG13	1:B:110:ARG:CB	2.48	0.43
1:C:74:ALA:HB3	1:C:88:ILE:HG22	1.99	0.43
1:A:24:TYR:CE1	1:A:74:ALA:HB1	2.55	0.42
1:C:63:LEU:HD11	1:C:89:LEU:HD22	2.02	0.41
1:A:101:ASP:CG	1:A:104:GLN:HB2	2.45	0.41
1:A:46:ALA:N	1:A:47:PRO:HD3	2.36	0.41
1:C:101:ASP:O	1:C:104:GLN:HG3	2.20	0.41
1:C:21:PRO:HD2	1:C:24:TYR:CD2	2.56	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	Percentiles	
1	A	106/110 (96%)	102 (96%)	4 (4%)	0	100	100
1	B	105/110 (96%)	101 (96%)	4 (4%)	0	100	100
1	C	105/110 (96%)	102 (97%)	3 (3%)	0	100	100
All	All	316/330 (96%)	305 (96%)	11 (4%)	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	A	89/92 (97%)	85 (96%)	4 (4%)	24	25
1	B	87/92 (95%)	85 (98%)	2 (2%)	44	51
1	C	90/92 (98%)	88 (98%)	2 (2%)	45	53
All	All	266/276 (96%)	258 (97%)	8 (3%)	36	41

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	VAL
1	A	57	SER
1	A	89	LEU
1	A	96	ILE
1	B	92	SER
1	B	96	ILE
1	C	57	SER
1	C	96	ILE

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 (i)

There are no oligosaccharides 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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.