



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:19 AM UTC

PDB ID : 1BSB / pdb_00001bsb
Title : CRYSTAL STRUCTURAL ANALYSIS OF MUTATIONS IN THE HYDROPHOBIC CORES OF BARNASE
Authors : Buckle, A.M.; Henrick, K.; Fersht, A.R.
Deposited on : 1993-07-19
Resolution : 2.00 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	:	4-5-2 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

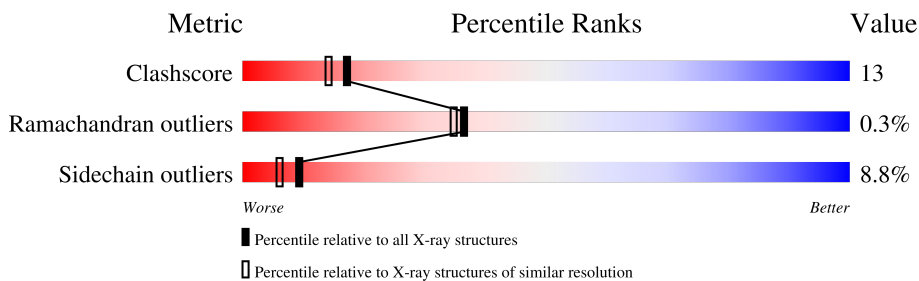
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	110	
1	B	110	
1	C	110	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2794 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	0	0	0
			846	536	147	163			
1	B	108	Total	C	N	O	0	0	0
			840	533	144	163			
1	C	108	Total	C	N	O	0	0	0
			850	538	146	166			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	76	VAL	ILE	conflict	UNP P00648
B	76	VAL	ILE	conflict	UNP P00648
C	76	VAL	ILE	conflict	UNP P00648

- Molecule 2 is water.

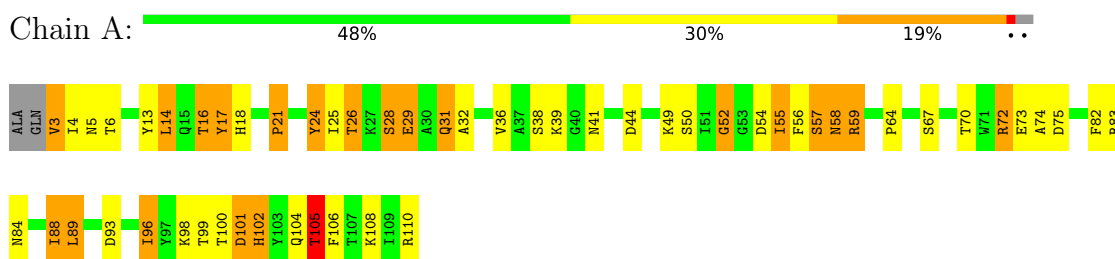
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	77	Total	O	0	0
			77	77		
2	B	85	Total	O	0	0
			85	85		
2	C	96	Total	O	0	0
			96	96		

3 Residue-property plots

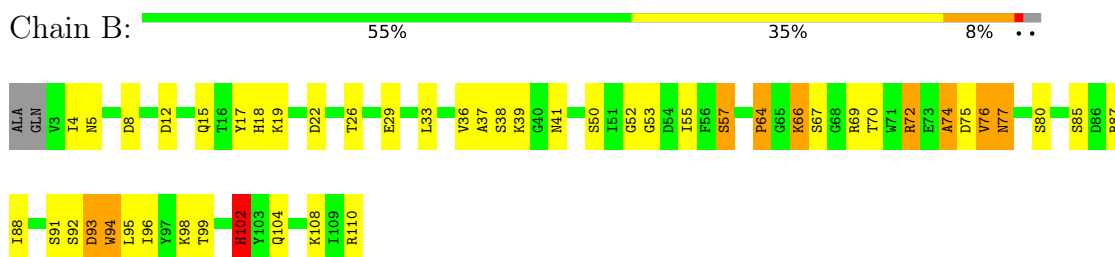
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

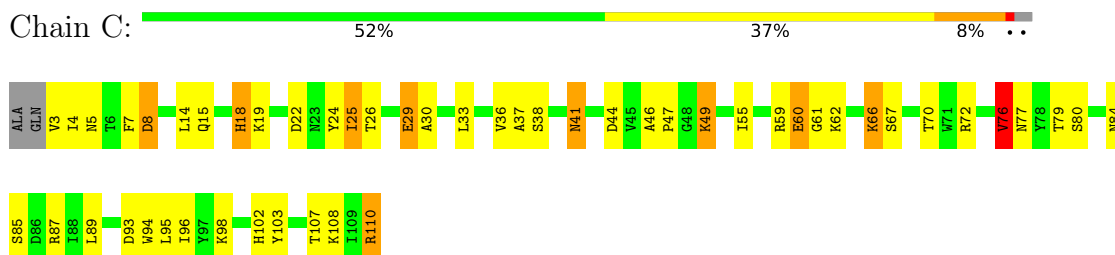
• Molecule 1: BARNASE



• Molecule 1: BARNASE



• Molecule 1: BARNASE



4 Data and refinement statistics

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	58.65Å 58.65Å 81.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.166 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2794	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	1.27	0/867	2.51	59/1178 (5.0%)
1	B	1.22	0/861	2.46	53/1171 (4.5%)
1	C	1.21	0/871	2.85	61/1182 (5.2%)
All	All	1.23	0/2599	2.61	173/3531 (4.9%)

There are no bond length outliers.

All (173) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	60	GLU	OE1-CD-OE2	-28.11	55.42	122.90
1	C	60	GLU	CA-CB-CG	24.68	163.46	114.10
1	C	60	GLU	CG-CD-OE1	24.61	175.01	118.40
1	C	60	GLU	CB-CG-CD	17.27	141.96	112.60
1	A	102	HIS	CA-C-N	13.24	141.55	122.08
1	A	102	HIS	C-N-CA	13.24	141.55	122.08
1	A	41	ASN	OD1-CG-ND2	-12.15	110.45	122.60
1	C	60	GLU	N-CA-C	-11.92	98.11	112.89
1	C	22	ASP	CA-CB-CG	-11.80	100.80	112.60
1	C	61	GLY	CA-C-O	11.64	133.88	119.80
1	C	110	ARG	NE-CZ-NH2	11.46	129.51	119.20
1	A	17	TYR	CA-C-O	-10.45	106.53	119.38
1	C	60	GLU	CA-C-N	9.87	137.94	120.77
1	C	60	GLU	C-N-CA	9.87	137.94	120.77
1	C	60	GLU	CA-C-O	9.77	131.43	119.31
1	C	41	ASN	N-CA-C	9.61	123.68	112.72
1	C	24	TYR	CA-C-O	-9.46	110.12	121.28
1	C	61	GLY	O-C-N	-9.26	113.33	122.41
1	C	89	LEU	CA-C-O	-9.22	110.33	120.38
1	C	59	ARG	CA-C-N	8.64	136.26	121.14
1	C	59	ARG	C-N-CA	8.64	136.26	121.14
1	B	50	SER	CA-C-O	-8.54	111.11	121.11
1	A	101	ASP	CA-C-O	-8.15	111.86	121.32
1	B	12	ASP	CA-CB-CG	-8.09	104.51	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	5	ASN	OD1-CG-ND2	-8.01	114.59	122.60
1	C	18	HIS	CA-CB-CG	-7.95	105.85	113.80
1	B	4	ILE	CA-C-O	-7.92	111.39	120.65
1	B	102	HIS	CA-CB-CG	-7.76	106.03	113.80
1	B	33	LEU	CA-C-O	-7.74	109.92	119.28
1	C	72	ARG	NE-CZ-NH1	7.69	129.19	121.50
1	C	94	TRP	N-CA-C	7.66	122.08	111.74
1	C	107	THR	CA-C-O	-7.64	111.88	120.66
1	C	60	GLU	O-C-N	-7.61	111.96	122.46
1	B	77	ASN	OD1-CG-ND2	7.56	130.16	122.60
1	B	52	GLY	CA-C-O	-7.37	114.41	121.49
1	B	93	ASP	CA-C-O	-7.33	111.69	120.55
1	B	110	ARG	CA-C-O	-7.31	108.37	120.80
1	A	105	THR	CA-CB-CG2	7.30	122.91	110.50
1	A	105	THR	N-CA-CB	-7.20	97.97	111.00
1	B	26	THR	CA-CB-OG1	-7.17	98.84	109.60
1	A	84	ASN	OD1-CG-ND2	-7.16	115.44	122.60
1	C	36	VAL	CA-C-O	7.16	128.03	120.51
1	B	80	SER	CA-C-N	7.13	131.63	120.65
1	B	80	SER	C-N-CA	7.13	131.63	120.65
1	B	12	ASP	O-C-N	7.09	130.23	122.15
1	C	29	GLU	CA-C-O	7.08	128.00	120.70
1	B	102	HIS	CA-C-O	7.00	130.78	122.03
1	B	19	LYS	CA-CB-CG	-6.96	100.18	114.10
1	B	72	ARG	NE-CZ-NH2	-6.96	112.94	119.20
1	A	93	ASP	CA-CB-CG	6.95	119.55	112.60
1	B	75	ASP	CA-C-O	-6.93	113.40	121.16
1	B	99	THR	N-CA-CB	6.86	123.40	111.13
1	A	88	ILE	CB-CA-C	6.84	121.21	110.81
1	C	110	ARG	NE-CZ-NH1	-6.68	114.82	121.50
1	B	93	ASP	O-C-N	6.65	130.71	122.20
1	C	60	GLU	CB-CA-C	6.64	123.86	109.99
1	A	29	GLU	CG-CD-OE1	6.63	133.66	118.40
1	A	104	GLN	CA-C-O	6.63	127.60	120.24
1	A	102	HIS	CA-CB-CG	-6.61	107.19	113.80
1	B	57	SER	N-CA-C	6.59	118.46	111.28
1	A	16	THR	CA-CB-OG1	-6.53	99.80	109.60
1	A	52	GLY	CA-C-O	-6.50	114.59	121.29
1	A	105	THR	CA-CB-OG1	-6.49	99.86	109.60
1	C	8	ASP	O-C-N	6.49	129.00	122.12
1	B	4	ILE	N-CA-C	-6.49	98.31	108.23
1	A	57	SER	CA-C-O	-6.46	113.57	120.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	77	ASN	CA-C-O	-6.41	112.75	120.12
1	A	55	ILE	CB-CA-C	-6.37	102.29	111.34
1	C	95	LEU	N-CA-C	-6.36	100.16	110.20
1	A	16	THR	OG1-CB-CG2	6.35	122.00	109.30
1	C	103	TYR	CA-C-O	-6.31	112.88	120.32
1	A	72	ARG	NE-CZ-NH2	-6.29	113.53	119.20
1	C	8	ASP	CA-CB-CG	-6.29	106.31	112.60
1	B	64	PRO	CA-C-N	6.25	128.52	120.64
1	B	64	PRO	C-N-CA	6.25	128.52	120.64
1	A	100	THR	N-CA-C	-6.17	104.23	112.94
1	C	37	ALA	O-C-N	6.17	128.68	122.08
1	B	37	ALA	CA-C-O	-6.09	114.38	120.90
1	A	28	SER	CA-C-O	-6.04	114.01	120.42
1	B	94	TRP	CA-CB-CG	-6.02	102.16	113.60
1	B	53	GLY	O-C-N	5.99	128.92	122.22
1	B	94	TRP	N-CA-C	5.98	119.90	112.24
1	C	93	ASP	CA-C-N	5.98	130.62	122.19
1	C	93	ASP	C-N-CA	5.98	130.62	122.19
1	A	59	ARG	O-C-N	5.96	129.20	122.22
1	C	87	ARG	NH1-CZ-NH2	-5.94	111.58	119.30
1	B	98	LYS	N-CA-CB	5.90	122.10	111.37
1	B	93	ASP	CB-CA-C	-5.87	101.67	111.13
1	A	101	ASP	O-C-N	5.85	129.73	121.83
1	A	36	VAL	O-C-N	5.84	129.79	122.66
1	A	24	TYR	O-C-N	-5.84	116.38	123.10
1	B	57	SER	O-C-N	5.82	128.29	122.12
1	A	5	ASN	OD1-CG-ND2	-5.81	116.79	122.60
1	B	74	ALA	O-C-N	-5.78	116.33	123.33
1	A	32	ALA	N-CA-C	-5.76	105.00	111.28
1	B	8	ASP	CA-CB-CG	-5.74	106.86	112.60
1	A	4	ILE	CA-C-O	-5.74	114.14	120.97
1	A	38	SER	O-C-N	5.71	130.34	122.46
1	B	95	LEU	N-CA-C	-5.70	101.19	110.20
1	A	106	PHE	CA-C-O	-5.66	114.48	121.11
1	C	72	ARG	CD-NE-CZ	5.66	132.33	124.40
1	C	47	PRO	CA-C-O	5.66	127.48	121.32
1	C	4	ILE	N-CA-CB	-5.62	103.65	111.41
1	B	33	LEU	CA-C-N	-5.62	113.29	122.40
1	B	33	LEU	C-N-CA	-5.62	113.29	122.40
1	B	52	GLY	N-CA-C	5.60	118.67	110.38
1	A	82	PHE	CA-C-N	5.60	129.21	120.75
1	A	82	PHE	C-N-CA	5.60	129.21	120.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	THR	N-CA-CB	5.58	121.12	111.13
1	C	15	GLN	N-CA-CB	5.58	118.92	110.28
1	B	22	ASP	N-CA-C	5.57	119.56	112.87
1	C	29	GLU	CA-CB-CG	5.57	125.23	114.10
1	C	76	VAL	CB-CA-C	5.56	119.59	110.69
1	B	102	HIS	CB-CG-CD2	-5.51	124.03	131.20
1	A	44	ASP	CA-CB-CG	5.50	118.10	112.60
1	C	59	ARG	N-CA-CB	-5.50	101.82	110.46
1	A	56	PHE	CB-CA-C	5.48	119.17	110.19
1	A	59	ARG	N-CA-CB	5.48	118.65	110.22
1	A	6	THR	CA-C-O	-5.47	114.98	121.66
1	A	70	THR	CA-CB-OG1	-5.47	101.40	109.60
1	A	83	ARG	NE-CZ-NH1	-5.46	116.03	121.50
1	B	17	TYR	CA-C-O	-5.46	112.96	119.35
1	B	26	THR	CA-C-N	5.44	127.88	120.54
1	B	26	THR	C-N-CA	5.44	127.88	120.54
1	C	5	ASN	CA-C-O	-5.43	113.38	119.08
1	A	13	TYR	O-C-N	-5.41	116.50	122.07
1	A	54	ASP	CB-CG-OD2	5.41	130.84	118.40
1	C	33	LEU	CA-C-N	5.40	129.49	122.26
1	C	33	LEU	C-N-CA	5.40	129.49	122.26
1	B	110	ARG	N-CA-CB	5.39	119.67	110.50
1	B	41	ASN	N-CA-C	5.39	119.17	112.59
1	C	87	ARG	NE-CZ-NH2	5.38	124.05	119.20
1	A	28	SER	O-C-N	5.37	128.27	122.15
1	A	14	LEU	CA-C-O	-5.37	114.86	120.55
1	A	21	PRO	CA-C-N	5.35	129.25	120.63
1	A	21	PRO	C-N-CA	5.35	129.25	120.63
1	B	41	ASN	N-CA-CB	-5.35	102.36	110.92
1	C	26	THR	CA-CB-OG1	-5.33	101.60	109.60
1	C	37	ALA	CA-C-O	-5.31	115.23	121.07
1	A	39	LYS	CA-C-N	5.31	128.12	120.11
1	A	39	LYS	C-N-CA	5.31	128.12	120.11
1	B	72	ARG	O-C-N	5.31	130.05	123.15
1	A	64	PRO	CA-C-N	5.31	128.36	122.15
1	A	64	PRO	C-N-CA	5.31	128.36	122.15
1	A	31	GLN	CB-CG-CD	-5.30	103.60	112.60
1	C	108	LYS	O-C-N	-5.30	116.84	123.04
1	C	15	GLN	O-C-N	5.29	128.78	122.27
1	C	80	SER	CA-CB-OG	-5.29	100.53	111.10
1	C	60	GLU	N-CA-CB	5.28	119.00	110.40
1	C	79	THR	CB-CA-C	5.26	120.90	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	95	LEU	CA-CB-CG	5.23	134.60	116.30
1	C	61	GLY	CA-C-N	5.20	129.40	120.72
1	C	61	GLY	C-N-CA	5.20	129.40	120.72
1	A	58	ASN	N-CA-C	-5.17	104.99	111.92
1	C	14	LEU	N-CA-C	5.17	116.92	111.28
1	B	75	ASP	CA-C-N	-5.16	114.49	122.69
1	B	75	ASP	C-N-CA	-5.16	114.49	122.69
1	A	70	THR	CA-C-N	-5.15	114.57	122.87
1	A	70	THR	C-N-CA	-5.15	114.57	122.87
1	C	59	ARG	CA-C-O	-5.13	113.07	119.18
1	B	108	LYS	CA-C-O	5.13	126.71	120.81
1	A	31	GLN	CA-C-N	5.11	127.12	120.28
1	A	31	GLN	C-N-CA	5.11	127.12	120.28
1	A	26	THR	CA-C-O	-5.08	116.19	121.99
1	B	29	GLU	N-CA-C	-5.08	105.75	111.28
1	C	38	SER	O-C-N	5.07	128.98	122.39
1	C	72	ARG	CA-C-N	-5.06	114.65	122.59
1	C	72	ARG	C-N-CA	-5.06	114.65	122.59
1	A	72	ARG	NE-CZ-NH1	5.04	126.54	121.50
1	C	84	ASN	CA-C-N	-5.04	114.74	122.60
1	C	84	ASN	C-N-CA	-5.04	114.74	122.60
1	B	17	TYR	CA-CB-CG	-5.04	104.84	113.90
1	A	75	ASP	O-C-N	-5.02	117.09	123.01

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	846	0	799	26	0
1	B	840	0	788	14	0
1	C	850	0	802	22	1
2	A	77	0	0	7	0
2	B	85	0	0	3	0
2	C	96	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2794	0	2389	62	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 13.

All (62) 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:3:VAL:HG22	2:A:166:HOH:O	1.48	1.09
1:C:25:ILE:HD12	1:C:30:ALA:HB2	1.57	0.86
1:A:26:THR:OG1	1:A:29:GLU:HG3	1.78	0.82
1:C:25:ILE:CD1	1:C:30:ALA:HB2	2.17	0.75
1:C:60:GLU:OE1	1:C:62:LYS:NZ	2.14	0.74
1:A:55:ILE:HD11	1:A:72:ARG:NH2	2.02	0.73
1:B:18:HIS:HB3	1:B:94:TRP:CZ2	2.24	0.72
1:C:60:GLU:CD	1:C:62:LYS:HZ1	1.97	0.72
1:A:3:VAL:HG13	2:A:166:HOH:O	1.95	0.66
1:A:16:THR:HG22	1:A:17:TYR:N	2.12	0.65
1:C:55:ILE:CD1	1:C:70:THR:CG2	2.75	0.65
1:C:41:ASN:O	1:C:44:ASP:HB2	1.99	0.62
1:A:55:ILE:CD1	1:A:72:ARG:CZ	2.78	0.61
1:B:87:ARG:NH2	1:B:102:HIS:NE2	2.49	0.61
1:B:85:SER:HA	1:B:102:HIS:CD2	2.36	0.61
1:A:3:VAL:CG2	2:A:166:HOH:O	2.24	0.60
1:A:55:ILE:HD11	1:A:72:ARG:CZ	2.32	0.59
1:C:3:VAL:CB	2:C:203:HOH:O	2.49	0.59
1:C:55:ILE:HD12	1:C:70:THR:CG2	2.32	0.59
1:A:101:ASP:OD2	1:A:105:THR:HB	2.04	0.57
1:A:3:VAL:CB	2:A:166:HOH:O	2.50	0.57
1:A:96:ILE:HG13	1:A:110:ARG:HB2	1.87	0.56
1:A:57:SER:O	1:A:58:ASN:HB3	2.07	0.55
1:A:21:PRO:HD2	1:A:24:TYR:CD2	2.42	0.54
1:A:3:VAL:CG1	2:A:166:HOH:O	2.55	0.52
1:B:104:GLN:CB	2:B:143:HOH:O	2.58	0.52
1:B:66:LYS:O	1:B:69:ARG:HB3	2.10	0.51
1:C:3:VAL:C	2:C:203:HOH:O	2.55	0.49
1:A:96:ILE:CG1	1:A:110:ARG:HB2	2.42	0.49
1:C:46:ALA:O	1:C:49:LYS:HB2	2.13	0.48
1:B:36:VAL:HB	1:B:39:LYS:HD3	1.96	0.48
1:C:76:VAL:O	1:C:77:ASN:HB2	2.13	0.48
1:B:76:VAL:O	1:B:77:ASN:HB2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:SER:HA	1:A:31:GLN:HE21	1.80	0.46
1:C:66:LYS:HG2	1:C:67:SER:N	2.28	0.46
1:A:108:LYS:NZ	2:A:159:HOH:O	2.36	0.46
1:A:28:SER:HA	1:A:31:GLN:NE2	2.31	0.45
1:B:64:PRO:O	1:B:69:ARG:NH1	2.42	0.45
1:C:60:GLU:CD	1:C:62:LYS:NZ	2.69	0.44
1:B:66:LYS:O	1:B:67:SER:C	2.61	0.44
1:C:55:ILE:CD1	1:C:70:THR:HG22	2.46	0.44
1:C:60:GLU:CD	1:C:62:LYS:HE3	2.42	0.44
1:A:55:ILE:HD13	1:A:72:ARG:CZ	2.48	0.44
1:C:85:SER:HB2	1:C:102:HIS:CD2	2.53	0.43
1:A:25:ILE:HG23	1:A:49:LYS:HD2	2.00	0.43
1:A:72:ARG:O	1:A:89:LEU:HA	2.19	0.43
1:A:73:GLU:HA	1:A:88:ILE:O	2.19	0.43
1:B:74:ALA:HB3	1:B:88:ILE:HG22	2.00	0.43
1:B:64:PRO:HD3	2:B:173:HOH:O	2.18	0.42
1:C:7:PHE:CE1	1:C:98:LYS:HB2	2.52	0.42
1:C:55:ILE:CD1	1:C:70:THR:HG21	2.50	0.42
1:A:52:GLY:HA2	1:A:74:ALA:HA	2.00	0.42
1:C:60:GLU:CD	1:C:62:LYS:CE	2.92	0.42
1:C:8:ASP:OD1	1:C:110:ARG:NH2	2.45	0.41
1:C:85:SER:HB3	1:C:102:HIS:NE2	2.35	0.41
1:A:3:VAL:HG21	2:A:141:HOH:O	2.19	0.41
1:B:55:ILE:HG13	1:B:72:ARG:NH1	2.34	0.41
1:B:15:GLN:HA	2:B:126:HOH:O	2.19	0.41
1:A:14:LEU:O	1:A:18:HIS:HA	2.20	0.41
1:B:69:ARG:HG3	1:B:91:SER:HB2	2.03	0.41
1:C:66:LYS:CG	1:C:67:SER:N	2.84	0.41
1:A:24:TYR:HA	1:A:50:SER:O	2.21	0.41

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)
1:C:18:HIS:ND1	1:C:60:GLU:OE1[3_675]	2.18	0.02

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	106/110 (96%)	102 (96%)	4 (4%)	0	100	100
1	B	106/110 (96%)	100 (94%)	5 (5%)	1 (1%)	14	9
1	C	106/110 (96%)	101 (95%)	5 (5%)	0	100	100
All	All	318/330 (96%)	303 (95%)	14 (4%)	1 (0%)	36	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	66	LYS

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	87/92 (95%)	79 (91%)	8 (9%)	8	5
1	B	86/92 (94%)	78 (91%)	8 (9%)	8	5
1	C	88/92 (96%)	81 (92%)	7 (8%)	11	8
All	All	261/276 (95%)	238 (91%)	23 (9%)	9	6

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	VAL
1	A	59	ARG

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Mol	Chain	Res	Type
1	A	67	SER
1	A	89	LEU
1	A	96	ILE
1	A	98	LYS
1	A	102	HIS
1	A	105	THR
1	B	38	SER
1	B	57	SER
1	B	70	THR
1	B	76	VAL
1	B	92	SER
1	B	93	ASP
1	B	96	ILE
1	B	102	HIS
1	C	19	LYS
1	C	25	ILE
1	C	29	GLU
1	C	49	LYS
1	C	66	LYS
1	C	76	VAL
1	C	96	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	31	GLN
1	B	31	GLN
1	C	77	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 [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.