



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:47 AM UTC

PDB ID : 1BGS / pdb_00001bgs
Title : RECOGNITION BETWEEN A BACTERIAL RIBONUCLEASE, BAR-
NASE, AND ITS NATURAL INHIBITOR, BARSTAR
Authors : Guillet, V.; Laphorn, A.; Mauguen, Y.
Deposited on : 1993-11-02
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

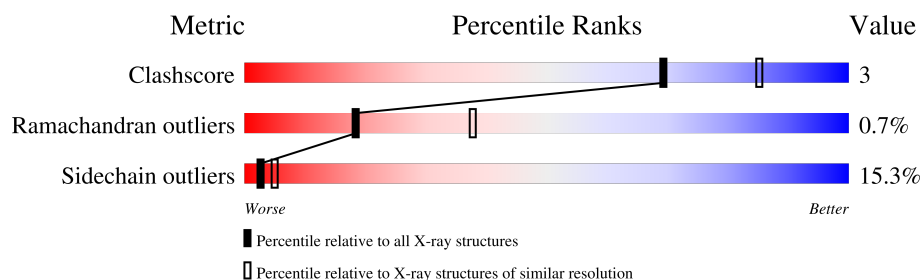
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

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	69% 26% . .
1	B	110	79% 15% 5% .
1	C	110	70% 24% 5% .
2	E	89	62% 25% 13%
2	F	89	67% 29% . .
2	G	89	65% 29% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4987 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	110	Total	C	N	O	0	0	0
			878	555	153	170			
1	B	110	Total	C	N	O	0	0	0
			878	555	153	170			
1	C	110	Total	C	N	O	0	0	0
			878	555	153	170			

- Molecule 2 is a protein called BARSTAR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	89	Total	C	N	O	0	0	0
			718	459	118	141			
2	F	89	Total	C	N	O	0	0	0
			718	459	118	141			
2	G	89	Total	C	N	O	0	0	0
			718	459	118	141			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	40	ALA	CYS	conflict	UNP P11540
E	82	ALA	CYS	conflict	UNP P11540
F	40	ALA	CYS	conflict	UNP P11540
F	82	ALA	CYS	conflict	UNP P11540
G	40	ALA	CYS	conflict	UNP P11540
G	82	ALA	CYS	conflict	UNP P11540

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	51	Total	O	0	0
			51	51		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	43	Total 43	O 43	0	0
3	C	42	Total 42	O 42	0	0
3	E	21	Total 21	O 21	0	0
3	F	24	Total 24	O 24	0	0
3	G	18	Total 18	O 18	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. 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: 



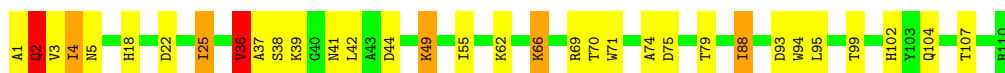
- Molecule 1: BARNASE

Chain B: 



- Molecule 1: BARNASE

Chain C: 



- Molecule 2: BARSTAR

Chain E: 



- Molecule 2: BARSTAR

Chain F: 



- Molecule 2: BARSTAR

Chain G: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	205.36Å 44.44Å 84.25Å 90.00° 110.52° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.60	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.170 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4987	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

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	1.14	5/899 (0.6%)	1.95	26/1216 (2.1%)
1	B	1.21	6/899 (0.7%)	1.86	17/1216 (1.4%)
1	C	1.08	6/899 (0.7%)	2.00	26/1216 (2.1%)
2	E	1.13	2/731 (0.3%)	2.10	21/989 (2.1%)
2	F	1.05	0/731	1.87	13/989 (1.3%)
2	G	1.12	2/731 (0.3%)	2.00	24/989 (2.4%)
All	All	1.13	21/4890 (0.4%)	1.96	127/6615 (1.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	10	VAL	CA-CB	9.34	1.67	1.54
1	A	102	HIS	CD2-NE2	-7.42	1.29	1.37
1	A	36	VAL	CA-CB	6.72	1.62	1.53
1	C	36	VAL	CA-CB	6.33	1.63	1.54
1	B	36	VAL	CA-CB	6.12	1.61	1.53
2	E	50	VAL	CA-CB	6.10	1.62	1.54
1	B	88	ILE	CA-CB	6.09	1.62	1.54
1	C	102	HIS	CD2-NE2	-6.06	1.31	1.37
2	G	10	ILE	CA-CB	5.70	1.60	1.53
1	C	18	HIS	CD2-NE2	-5.61	1.31	1.37
1	C	88	ILE	CA-CB	5.50	1.61	1.54
1	A	102	HIS	CG-ND1	-5.49	1.32	1.38
1	A	18	HIS	CG-ND1	-5.49	1.32	1.38
2	G	70	VAL	CA-CB	5.39	1.61	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	18	HIS	CD2-NE2	-5.36	1.31	1.37
1	A	18	HIS	CD2-NE2	-5.33	1.31	1.37
1	B	18	HIS	CG-ND1	-5.33	1.32	1.38
1	C	99	THR	CA-CB	5.28	1.62	1.53
2	E	10	ILE	CA-CB	5.24	1.59	1.53
1	B	102	HIS	CD2-NE2	-5.21	1.32	1.37
1	C	102	HIS	CG-ND1	-5.06	1.32	1.38

All (127) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2	LYS	N-CA-C	10.39	126.11	108.23
1	A	37	ALA	N-CA-C	9.97	123.39	111.33
2	E	9	GLN	OE1-CD-NE2	-9.56	113.03	122.60
1	C	94	TRP	N-CA-C	9.56	124.54	111.54
2	G	65	ASN	OD1-CG-ND2	-9.47	113.13	122.60
2	E	61	GLN	OE1-CD-NE2	-9.36	113.24	122.60
1	C	5	ASN	OD1-CG-ND2	-9.09	113.51	122.60
2	F	72	GLN	OE1-CD-NE2	-8.88	113.72	122.60
2	E	65	ASN	OD1-CG-ND2	-8.68	113.92	122.60
1	B	101	ASP	CA-CB-CG	8.54	121.14	112.60
1	C	18	HIS	ND1-CG-CD2	8.42	114.52	106.10
1	A	41	ASN	OD1-CG-ND2	-8.25	114.35	122.60
1	C	102	HIS	ND1-CG-CD2	7.93	114.03	106.10
1	C	75	ASP	CA-CB-CG	7.89	120.49	112.60
2	G	72	GLN	OE1-CD-NE2	-7.51	115.09	122.60
1	B	94	TRP	N-CA-C	7.42	121.75	111.74
1	C	5	ASN	CB-CG-ND2	7.41	127.51	116.40
2	G	63	THR	N-CA-CB	-7.39	99.09	110.92
2	G	29	TYR	N-CA-C	7.28	121.99	113.18
2	G	78	LYS	CA-CB-CG	7.22	128.53	114.10
1	A	102	HIS	ND1-CG-CD2	7.19	113.29	106.10
1	A	31	GLN	N-CA-C	-7.12	103.60	111.36
2	E	61	GLN	CG-CD-NE2	6.97	126.86	116.40
2	E	8	GLU	CB-CG-CD	6.86	124.25	112.60
2	F	17	HIS	ND1-CG-CD2	6.77	112.87	106.10
2	E	15	ASP	CA-CB-CG	6.75	119.35	112.60
1	A	104	GLN	OE1-CD-NE2	-6.63	115.97	122.60
1	C	18	HIS	CG-CD2-NE2	-6.62	100.58	107.20
1	C	3	VAL	N-CA-C	6.59	118.30	108.54
2	E	10	ILE	N-CA-CB	-6.59	105.67	112.06
2	F	61	GLN	OE1-CD-NE2	-6.55	116.05	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	TRP	N-CA-C	6.52	120.54	111.74
2	G	17	HIS	ND1-CG-CD2	6.49	112.59	106.10
1	B	62	LYS	CB-CG-CD	-6.43	96.51	111.30
2	G	78	LYS	N-CA-C	-6.38	104.41	111.36
1	B	77	ASN	OD1-CG-ND2	-6.37	116.23	122.60
2	E	55	GLN	OE1-CD-NE2	-6.35	116.25	122.60
1	A	71	TRP	CG-CD2-CE3	6.33	140.23	133.90
1	C	2	GLN	OE1-CD-NE2	-6.26	116.34	122.60
1	C	4	ILE	CB-CA-C	6.26	117.54	110.41
1	B	94	TRP	CG-CD2-CE3	6.23	140.13	133.90
2	F	72	GLN	CG-CD-NE2	6.23	125.75	116.40
1	A	2	GLN	CG-CD-NE2	6.21	125.72	116.40
1	A	93	ASP	CA-CB-CG	6.21	118.81	112.60
2	G	6	ASN	OD1-CG-ND2	-6.21	116.39	122.60
1	B	69	ARG	NE-CZ-NH2	-6.20	113.62	119.20
1	C	44	ASP	CA-CB-CG	6.20	118.80	112.60
1	C	41	ASN	N-CA-C	6.17	119.54	112.57
2	F	61	GLN	CA-CB-CG	6.15	126.40	114.10
1	A	87	ARG	NH1-CZ-NH2	-6.12	111.34	119.30
2	E	45	VAL	N-CA-CB	-6.12	101.88	110.26
2	E	1	LYS	CA-C-O	-6.11	110.41	120.80
1	C	93	ASP	CA-CB-CG	6.11	118.70	112.60
2	G	65	ASN	CA-CB-CG	6.05	118.65	112.60
2	E	17	HIS	CA-CB-CG	-6.04	107.76	113.80
2	G	65	ASN	CB-CG-ND2	6.04	125.46	116.40
2	G	58	GLN	CA-C-N	6.04	128.65	120.44
2	G	58	GLN	C-N-CA	6.04	128.65	120.44
1	A	77	ASN	OD1-CG-ND2	-6.04	116.56	122.60
1	A	32	ALA	N-CA-C	6.01	118.62	111.71
1	C	104	GLN	OE1-CD-NE2	-5.95	116.65	122.60
1	B	72	ARG	NE-CZ-NH2	-5.91	113.88	119.20
1	C	93	ASP	CA-C-N	5.90	130.51	122.07
1	C	93	ASP	C-N-CA	5.90	130.51	122.07
1	B	28	SER	CA-C-N	5.88	128.15	120.28
1	B	28	SER	C-N-CA	5.88	128.15	120.28
1	A	15	GLN	CB-CA-C	-5.86	101.06	110.79
2	F	38	TRP	CG-CD2-CE3	5.83	139.73	133.90
2	F	38	TRP	CE2-CD2-CG	-5.80	100.24	107.20
2	E	9	GLN	CG-CD-NE2	5.79	125.08	116.40
2	G	61	GLN	CA-CB-CG	5.77	125.63	114.10
1	A	18	HIS	ND1-CG-CD2	5.76	111.86	106.10
2	F	64	GLU	CB-CG-CD	5.71	122.31	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	47	TYR	CA-CB-CG	-5.67	103.70	113.90
1	B	94	TRP	CE2-CD2-CG	-5.60	100.48	107.20
2	G	14	SER	N-CA-C	-5.58	105.28	111.36
2	F	17	HIS	CG-CD2-NE2	-5.56	101.64	107.20
1	A	94	TRP	CE2-CD2-CG	-5.56	100.53	107.20
1	C	102	HIS	CG-CD2-NE2	-5.55	101.65	107.20
2	G	73	VAL	N-CA-C	-5.54	105.10	110.42
2	E	56	PHE	N-CA-C	5.53	117.30	111.28
2	G	83	ASP	CA-CB-CG	5.52	118.12	112.60
2	E	4	VAL	N-CA-C	5.48	115.48	107.37
2	E	66	GLY	O-C-N	-5.48	115.81	122.71
1	A	15	GLN	CA-CB-CG	5.47	125.04	114.10
2	G	47	TYR	O-C-N	-5.43	117.13	121.80
2	G	61	GLN	OE1-CD-NE2	-5.42	117.18	122.60
2	G	17	HIS	CB-CG-CD2	-5.41	124.17	131.20
1	A	15	GLN	CB-CG-CD	-5.36	103.50	112.60
1	B	102	HIS	ND1-CG-CD2	5.35	111.45	106.10
1	A	103	TYR	N-CA-C	5.34	119.37	112.86
1	B	18	HIS	ND1-CG-CD2	5.32	111.42	106.10
2	G	72	GLN	CB-CG-CD	5.32	121.65	112.60
1	B	76	ILE	O-C-N	5.31	128.78	123.10
1	C	22	ASP	N-CA-C	5.31	122.11	110.80
1	C	94	TRP	CE2-CD2-CG	-5.30	100.84	107.20
2	F	53	TRP	CD2-CE2-CZ2	-5.29	117.11	122.40
1	C	1	ALA	CA-C-N	5.29	131.64	121.54
1	C	1	ALA	C-N-CA	5.29	131.64	121.54
2	E	86	ILE	N-CA-CB	-5.27	104.67	110.99
1	A	62	LYS	CA-CB-CG	-5.26	103.57	114.10
1	C	36	VAL	N-CA-C	-5.26	98.40	109.34
1	A	84	ASN	OD1-CG-ND2	-5.25	117.35	122.60
2	G	21	LYS	CA-C-O	-5.24	115.50	121.00
1	B	25	ILE	CB-CG1-CD1	-5.24	102.81	113.80
1	A	102	HIS	CG-CD2-NE2	-5.18	102.02	107.20
1	A	36	VAL	N-CA-C	-5.18	99.05	107.28
2	E	45	VAL	N-CA-C	5.17	116.24	109.21
2	F	18	GLN	CB-CA-C	-5.17	102.73	110.90
2	G	63	THR	CA-CB-OG1	-5.16	101.86	109.60
1	A	2	GLN	OE1-CD-NE2	-5.16	117.44	122.60
1	A	71	TRP	CE2-CD2-CG	-5.13	101.04	107.20
1	B	15	GLN	OE1-CD-NE2	-5.12	117.48	122.60
2	G	38	TRP	CE2-CD2-CG	-5.11	101.06	107.20
1	C	71	TRP	CG-CD2-CE3	5.11	139.01	133.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	ASN	CA-CB-CG	5.10	117.70	112.60
1	B	108	LYS	CA-C-N	-5.09	115.75	122.16
1	B	108	LYS	C-N-CA	-5.09	115.75	122.16
2	E	66	GLY	N-CA-C	-5.09	108.35	114.66
1	C	79	THR	N-CA-C	-5.08	105.31	112.12
2	E	61	GLN	CA-CB-CG	5.06	124.21	114.10
2	G	82	ALA	O-C-N	-5.05	117.13	123.04
2	F	26	LEU	N-CA-CB	-5.02	102.85	109.78
1	C	36	VAL	CA-C-O	5.02	127.05	120.78
1	C	104	GLN	N-CA-C	-5.01	105.28	111.40
2	E	38	TRP	CE2-CD2-CG	-5.01	101.19	107.20
1	A	43	ALA	N-CA-C	5.01	117.47	111.71

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	87	ARG	Sidechain

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	878	0	849	5	0
1	B	878	0	849	7	0
1	C	878	0	849	7	0
2	E	718	0	714	5	0
2	F	718	0	714	7	0
2	G	718	0	714	2	0
3	A	51	0	0	1	0
3	B	43	0	0	0	0
3	C	42	0	0	1	0
3	E	21	0	0	1	0
3	F	24	0	0	2	0
3	G	18	0	0	1	0
All	All	4987	0	4689	33	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 3.

All (33) 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)
2:E:24:LEU:HB2	2:E:26:LEU:HD13	1.64	0.77
1:B:10:VAL:HG22	1:B:88:ILE:HD13	1.74	0.68
1:B:36:VAL:HG22	1:B:39:LYS:HB2	1.83	0.60
2:E:11:ARG:HH11	2:E:11:ARG:HG3	1.66	0.60
1:A:36:VAL:H	1:A:41:ASN:HD21	1.50	0.58
2:E:21:LYS:HA	2:E:26:LEU:HB2	1.85	0.57
2:F:8:GLU:HG3	2:F:55:GLN:HG3	1.86	0.56
1:B:101:ASP:O	1:B:104:GLN:HG3	2.07	0.54
1:C:25:ILE:HG13	1:C:49:LYS:HG2	1.93	0.49
1:C:66:LYS:HG3	1:C:69:ARG:HB2	1.95	0.49
1:A:59:ARG:HD2	3:E:105:HOH:O	2.12	0.48
1:C:74:ALA:HB3	1:C:88:ILE:HG22	1.96	0.48
2:F:1:LYS:N	3:F:103:HOH:O	2.47	0.48
1:B:6:THR:O	1:B:10:VAL:HG13	2.14	0.48
2:F:27:PRO:HD3	2:F:44:TRP:CE2	2.51	0.46
1:B:62:LYS:HD3	1:B:106:PHE:HE1	1.81	0.46
2:G:24:LEU:HB3	2:G:26:LEU:HD13	2.00	0.44
2:F:21:LYS:HA	2:F:26:LEU:HB2	1.98	0.44
2:E:27:PRO:HD3	2:E:44:TRP:CD1	2.54	0.43
1:B:36:VAL:HG22	1:B:39:LYS:H	1.83	0.43
1:C:62:LYS:HB2	3:C:157:HOH:O	2.19	0.42
2:E:27:PRO:O	2:E:30:TYR:HB2	2.19	0.42
2:G:1:LYS:HA	3:G:103:HOH:O	2.20	0.42
1:A:55:ILE:HA	1:A:72:ARG:HG2	2.02	0.41
1:C:36:VAL:HG22	1:C:39:LYS:HG2	2.02	0.41
1:A:54:ASP:HB2	3:A:140:HOH:O	2.20	0.41
1:B:25:ILE:HG21	1:B:25:ILE:HD13	1.86	0.41
2:F:1:LYS:HD2	2:F:48:PRO:O	2.20	0.41
1:C:55:ILE:HD12	1:C:55:ILE:HG23	1.80	0.41
2:F:58:GLN:HG2	3:F:113:HOH:O	2.21	0.41
1:A:52:GLY:HA2	1:A:74:ALA:HA	2.03	0.40
1:C:36:VAL:HG22	1:C:39:LYS:CG	2.51	0.40
2:F:30:TYR:CE2	2:F:32:GLU:HA	2.56	0.40

There are no symmetry-related clashes.

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	108/110 (98%)	105 (97%)	2 (2%)	1 (1%)	14	30
1	B	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
1	C	108/110 (98%)	102 (94%)	4 (4%)	2 (2%)	6	13
2	E	87/89 (98%)	84 (97%)	3 (3%)	0	100	100
2	F	87/89 (98%)	84 (97%)	3 (3%)	0	100	100
2	G	87/89 (98%)	82 (94%)	4 (5%)	1 (1%)	11	25
All	All	585/597 (98%)	562 (96%)	19 (3%)	4 (1%)	18	38

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	65	ASN
1	C	2	GLN
1	C	37	ALA
1	A	64	PRO

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	92/92 (100%)	81 (88%)	11 (12%)	5	10
1	B	92/92 (100%)	86 (94%)	6 (6%)	15	35
1	C	92/92 (100%)	81 (88%)	11 (12%)	5	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	76/76 (100%)	54 (71%)	22 (29%)	0	1
2	F	76/76 (100%)	63 (83%)	13 (17%)	2	3
2	G	76/76 (100%)	62 (82%)	14 (18%)	1	3
All	All	504/504 (100%)	427 (85%)	77 (15%)	3	5

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	SER
1	A	31	GLN
1	A	36	VAL
1	A	41	ASN
1	A	42	LEU
1	A	55	ILE
1	A	67	SER
1	A	70	THR
1	A	80	SER
1	A	89	LEU
1	A	95	LEU
1	B	10	VAL
1	B	28	SER
1	B	36	VAL
1	B	42	LEU
1	B	70	THR
1	B	92	SER
1	C	2	GLN
1	C	4	ILE
1	C	25	ILE
1	C	36	VAL
1	C	38	SER
1	C	42	LEU
1	C	49	LYS
1	C	66	LYS
1	C	70	THR
1	C	95	LEU
1	C	107	THR
2	E	1	LYS
2	E	2	LYS
2	E	8	GLU
2	E	10	ILE
2	E	11	ARG

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Mol	Chain	Res	Type
2	E	15	ASP
2	E	16	LEU
2	E	18	GLN
2	E	20	LEU
2	E	24	LEU
2	E	26	LEU
2	E	41	LEU
2	E	45	VAL
2	E	49	LEU
2	E	50	VAL
2	E	55	GLN
2	E	60	LYS
2	E	61	GLN
2	E	62	LEU
2	E	69	SER
2	E	70	VAL
2	E	88	LEU
2	F	8	GLU
2	F	16	LEU
2	F	20	LEU
2	F	22	LYS
2	F	26	LEU
2	F	28	GLU
2	F	34	LEU
2	F	41	LEU
2	F	45	VAL
2	F	57	GLU
2	F	62	LEU
2	F	70	VAL
2	F	72	GLN
2	G	2	LYS
2	G	13	ILE
2	G	16	LEU
2	G	18	GLN
2	G	20	LEU
2	G	26	LEU
2	G	41	LEU
2	G	50	VAL
2	G	59	SER
2	G	64	GLU
2	G	70	VAL
2	G	72	GLN

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Mol	Chain	Res	Type
2	G	78	LYS
2	G	80	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	41	ASN
1	C	2	GLN
2	E	6	ASN
2	E	55	GLN
2	F	55	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 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.