



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 09:54 AM GMT

PDB ID : 1RNB  
Title : CRYSTAL STRUCTURE OF A BARNASE-D(\*GP\*C) COMPLEX AT 1.9  
ANGSTROMS RESOLUTION  
Authors : Janin, J.; Baudet, S.  
Deposited on : 1991-03-19  
Resolution : 1.90 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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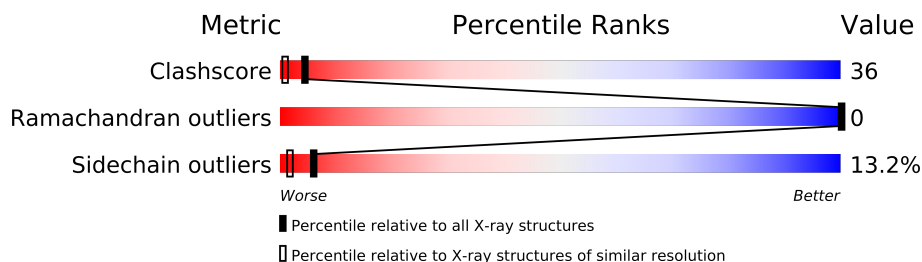
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	C	2	
2	A	110	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 1008 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA chain called DNA (5'-D(\*GP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	2	Total	C	N	O	P	0	0	0
			38	19	8	10	1			

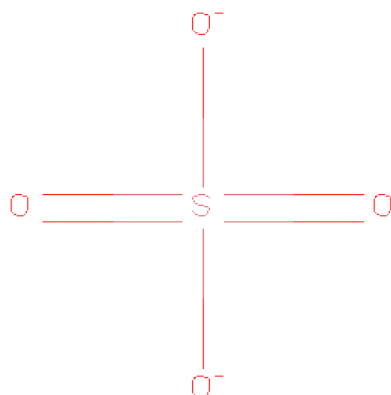
- Molecule 2 is a protein called BARNASE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	A	109	Total	C	N	O			
			869	550	151	168	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	ASN	ASP	CONFLICT	UNP P00648
A	23	ASP	ASN	CONFLICT	UNP P00648

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	88	Total	O	0	0
			88	88		
4	C	8	Total	O	0	0
			8	8		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

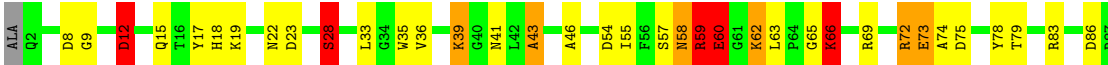
- Molecule 1: DNA (5'-D(\*GP\*C)-3')

Chain C: 

  
G111  
C112

- Molecule 2: BARNASE

Chain A: 

  
ALA  
G2  
D8  
G9  
D12  
Q15  
T16  
Y17  
H18  
K19  
N22  
D23  
S28  
L33  
G34  
W35  
V36  
K39  
G40  
N41  
L42  
A43  
A46  
D54  
I55  
F56  
S57  
N58  
R59  
E60  
G61  
K62  
L63  
F64  
G65  
K66  
R69  
R72  
E73  
A74  
D75  
Y78  
T79  
R83  
D86  
R87  
I88  
S91  
D93  
W94  
L95  
I96  
Y97  
K98  
Y103  
Q104  
T105  
F106  
T107  
K108  
I109  
R110

## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.97Å 57.97Å 85.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.90)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.214 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1008	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	C	3.15	5/42 (11.9%)	3.91	12/63 (19.0%)
2	A	1.11	0/890	2.41	43/1204 (3.6%)
All	All	1.27	5/932 (0.5%)	2.50	55/1267 (4.3%)

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
2	A	1	0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	112	DC	P-O5'	8.66	1.68	1.59
1	C	111	DG	C5-C4	-6.39	1.33	1.38
1	C	112	DC	N1-C2	-5.88	1.34	1.40
1	C	111	DG	N7-C5	-5.44	1.35	1.39
1	C	112	DC	C4'-O4'	-5.00	1.40	1.45

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	86	ASP	CB-CG-OD1	15.60	132.34	118.30
2	A	72	ARG	NE-CZ-NH2	-14.71	112.94	120.30
2	A	69	ARG	NE-CZ-NH1	12.48	126.54	120.30
2	A	12	ASP	CB-CG-OD1	-11.48	107.96	118.30
2	A	104	GLN	CB-CG-CD	11.00	140.20	111.60
2	A	12	ASP	CA-CB-CG	-10.16	91.04	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	111	DG	O4'-C4'-C3'	-10.13	99.92	106.00
1	C	112	DC	C2-N3-C4	-10.02	114.89	119.90
2	A	59	ARG	CB-CA-C	9.52	129.44	110.40
2	A	109	ILE	CA-CB-CG1	9.13	128.35	111.00
1	C	112	DC	C5-C6-N1	-8.68	116.66	121.00
1	C	111	DG	OP2-P-O3'	8.48	123.85	105.20
2	A	93	ASP	CB-CG-OD1	8.42	125.88	118.30
1	C	112	DC	N1-C2-N3	8.38	125.06	119.20
2	A	28	SER	N-CA-CB	-7.86	98.71	110.50
1	C	112	DC	N1-C2-O2	-7.83	114.20	118.90
2	A	75	ASP	CB-CG-OD1	-7.64	111.42	118.30
2	A	103	TYR	CB-CG-CD1	7.62	125.57	121.00
2	A	78	TYR	CB-CG-CD1	-7.57	116.46	121.00
2	A	73	GLU	OE1-CD-OE2	-7.48	114.32	123.30
2	A	86	ASP	CB-CG-OD2	-7.30	111.73	118.30
2	A	107	THR	CA-CB-CG2	7.29	122.61	112.40
2	A	110	ARG	NE-CZ-NH1	-7.23	116.69	120.30
2	A	95	LEU	CB-CG-CD2	-7.13	98.88	111.00
2	A	110	ARG	CD-NE-CZ	-7.05	113.73	123.60
2	A	59	ARG	NE-CZ-NH1	-6.77	116.92	120.30
2	A	83	ARG	NE-CZ-NH1	-6.70	116.95	120.30
1	C	111	DG	C2-N3-C4	6.41	115.11	111.90
2	A	54	ASP	CB-CG-OD2	-6.34	112.60	118.30
2	A	46	ALA	CB-CA-C	6.29	119.53	110.10
2	A	91	SER	C-N-CA	6.12	137.00	121.70
2	A	73	GLU	CG-CD-OE2	6.07	130.44	118.30
2	A	17	TYR	CB-CG-CD1	-6.01	117.39	121.00
2	A	66	LYS	N-CA-CB	5.85	121.14	110.60
1	C	112	DC	C5'-C4'-O4'	5.84	120.39	109.30
1	C	111	DG	C1'-O4'-C4'	5.82	115.92	110.10
2	A	94	TRP	N-CA-C	5.82	126.70	111.00
2	A	69	ARG	NE-CZ-NH2	-5.79	117.40	120.30
2	A	23	ASP	CB-CG-OD2	5.79	123.52	118.30
1	C	111	DG	O4'-C1'-C2'	-5.77	101.28	105.90
2	A	43	ALA	CA-C-O	-5.74	108.04	120.10
2	A	97	TYR	CB-CG-CD2	5.73	124.44	121.00
2	A	106	PHE	CB-CG-CD1	-5.67	116.83	120.80
2	A	12	ASP	OD1-CG-OD2	5.61	133.97	123.30
1	C	111	DG	N1-C2-N3	-5.57	120.56	123.90
1	C	111	DG	C5-C6-N1	5.53	114.27	111.50
2	A	60	GLU	OE1-CD-OE2	5.42	129.81	123.30
2	A	12	ASP	CA-C-O	5.29	131.21	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	41	ASN	N-CA-CB	-5.25	101.14	110.60
2	A	79	THR	CA-CB-OG1	-5.25	97.98	109.00
2	A	63	LEU	CD1-CG-CD2	5.11	125.81	110.50
2	A	58	ASN	C-N-CA	-5.06	109.04	121.70
2	A	92	SER	N-CA-CB	-5.06	102.90	110.50
2	A	95	LEU	CA-CB-CG	5.03	126.86	115.30
2	A	35	TRP	CH2-CZ2-CE2	-5.02	112.38	117.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	109	ILE	CB

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	38	0	24	1	0
2	A	869	0	835	61	0
3	C	5	0	0	1	1
4	A	88	0	0	17	2
4	C	8	0	0	2	1
All	All	1008	0	859	63	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 36.

All (63) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:15:GLN:NE2	2:A:110:ARG:HG3	1.83	0.92
2:A:15:GLN:HG3	2:A:110:ARG:NH2	1.86	0.91
2:A:15:GLN:HE22	2:A:110:ARG:HG3	1.36	0.90
2:A:36:VAL:HB	2:A:39:LYS:HG2	1.53	0.90

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:108:LYS:HE3	2:A:110:ARG:OXT	1.72	0.89
2:A:62:LYS:HB3	4:A:313:HOH:O	1.73	0.88
2:A:92:SER:HB3	4:A:315:HOH:O	1.74	0.87
2:A:62:LYS:CB	4:A:313:HOH:O	2.23	0.87
2:A:15:GLN:HA	2:A:110:ARG:HH21	1.41	0.84
2:A:57:SER:O	2:A:59:ARG:NH2	2.13	0.82
2:A:36:VAL:HB	2:A:39:LYS:CG	2.12	0.79
2:A:8:ASP:OD1	4:A:329:HOH:O	2.01	0.77
2:A:36:VAL:HG11	2:A:39:LYS:HD3	1.68	0.74
2:A:15:GLN:NE2	2:A:110:ARG:CG	2.51	0.73
2:A:15:GLN:HE22	2:A:110:ARG:CG	2.02	0.73
2:A:15:GLN:HA	2:A:110:ARG:NH2	2.03	0.72
2:A:18:HIS:HE1	4:A:260:HOH:O	1.73	0.71
2:A:96:ILE:N	2:A:110:ARG:O	2.18	0.70
2:A:15:GLN:CG	2:A:110:ARG:NH2	2.54	0.70
2:A:36:VAL:CG1	2:A:39:LYS:HD3	2.22	0.69
2:A:96:ILE:HD12	2:A:110:ARG:HE	1.59	0.68
1:C:111:DG:N3	1:C:111:DG:H2'	2.09	0.68
3:C:150:SO4:O4	4:C:257:HOH:O	2.14	0.65
2:A:65:GLY:O	2:A:66:LYS:HD3	1.97	0.65
2:A:15:GLN:NE2	2:A:110:ARG:NE	2.44	0.65
2:A:60:GLU:HB2	2:A:62:LYS:HD2	1.80	0.64
2:A:15:GLN:HG3	2:A:110:ARG:CZ	2.27	0.63
2:A:55:ILE:O	4:A:305:HOH:O	2.15	0.63
2:A:9:GLY:O	2:A:12:ASP:HB3	2.00	0.62
2:A:15:GLN:CA	2:A:110:ARG:HH21	2.11	0.61
2:A:28:SER:HB2	4:A:208:HOH:O	2.01	0.60
2:A:8:ASP:O	2:A:12:ASP:HB2	2.03	0.59
2:A:12:ASP:HB3	4:A:211:HOH:O	2.02	0.59
2:A:15:GLN:CG	2:A:110:ARG:CZ	2.80	0.58
2:A:15:GLN:NE2	2:A:110:ARG:CD	2.67	0.58
2:A:57:SER:O	2:A:58:ASN:CB	2.50	0.56
2:A:98:LYS:O	2:A:106:PHE:HA	2.06	0.55
2:A:15:GLN:CB	2:A:110:ARG:NH2	2.70	0.55
2:A:57:SER:O	2:A:58:ASN:HB3	2.07	0.54
2:A:43:ALA:HA	4:A:328:HOH:O	2.06	0.54
2:A:109:ILE:HG22	2:A:110:ARG:HB2	1.90	0.53
2:A:9:GLY:O	2:A:12:ASP:CB	2.56	0.53
2:A:72:ARG:NE	4:A:212:HOH:O	2.12	0.53
2:A:55:ILE:HD11	2:A:72:ARG:NH2	2.25	0.52
2:A:15:GLN:CA	2:A:110:ARG:NH2	2.71	0.50
2:A:55:ILE:HD12	4:A:212:HOH:O	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:22:ASN:HB2	4:A:230:HOH:O	2.12	0.49
2:A:36:VAL:O	2:A:39:LYS:HG2	2.13	0.48
2:A:73:GLU:HA	2:A:88:ILE:O	2.14	0.48
2:A:18:HIS:CE1	4:A:260:HOH:O	2.58	0.48
2:A:15:GLN:CD	2:A:110:ARG:CZ	2.84	0.47
2:A:15:GLN:CB	2:A:110:ARG:HH21	2.29	0.46
4:C:257:HOH:O	2:A:104:GLN:NE2	2.46	0.45
2:A:108:LYS:NZ	4:A:250:HOH:O	2.50	0.45
2:A:59:ARG:HA	2:A:59:ARG:HD3	1.80	0.45
2:A:55:ILE:CD1	4:A:212:HOH:O	2.64	0.45
2:A:62:LYS:HB2	4:A:313:HOH:O	2.04	0.44
2:A:62:LYS:HG2	2:A:62:LYS:H	1.36	0.43
2:A:55:ILE:HD11	2:A:72:ARG:CZ	2.49	0.42
2:A:62:LYS:HB2	2:A:106:PHE:CE2	2.56	0.41
2:A:92:SER:CB	4:A:315:HOH:O	2.48	0.41
2:A:74:ALA:HB3	2:A:88:ILE:HG22	2.03	0.40
2:A:58:ASN:OD1	2:A:62:LYS:HG2	2.20	0.40

All (2) 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	Distance(Å)	Clash(Å)
4:C:240:HOH:O	4:A:263:HOH:O[5_666]	2.07	0.13
3:C:150:SO4:O4	4:A:273:HOH:O[5_666]	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
2	A	107/110 (97%)	103 (96%)	4 (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
2	A	91/92 (99%)	79 (87%)	12 (13%)	6 2

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	12	ASP
2	A	19	LYS
2	A	28	SER
2	A	33	LEU
2	A	39	LYS
2	A	59	ARG
2	A	60	GLU
2	A	62	LYS
2	A	66	LYS
2	A	92	SER
2	A	104	GLN
2	A	110	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	15	GLN
2	A	18	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

1 ligand is modelled in this entry.

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	SO4	C	150	-	4,4,4	1.06	0	6,6,6	0.50	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
3	SO4	C	150	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.