



# Full wwPDB X-ray Structure Validation Report

Aug 31, 2020 – 08:45 AM BST

PDB ID : 1B98  
Title : NEUROTROPHIN 4 (HOMODIMER)  
Authors : Robinson, R.C.; Radziejewski, C.; Stuart, D.I.; Jones, E.Y.; Choe, S.  
Deposited on : 1999-02-22  
Resolution : 2.75 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](mailto: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.

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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  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13

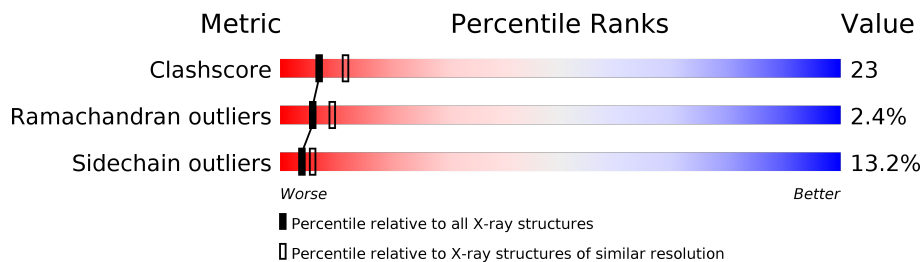
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)

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 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	130	
1	M	130	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1671 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 PROTEIN (NEUROTROPHIN-4).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	103	779	480	148	145	6	0	0	0
1	M	113	842	517	164	155	6	0	0	0

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		

- Molecule 3 is water.

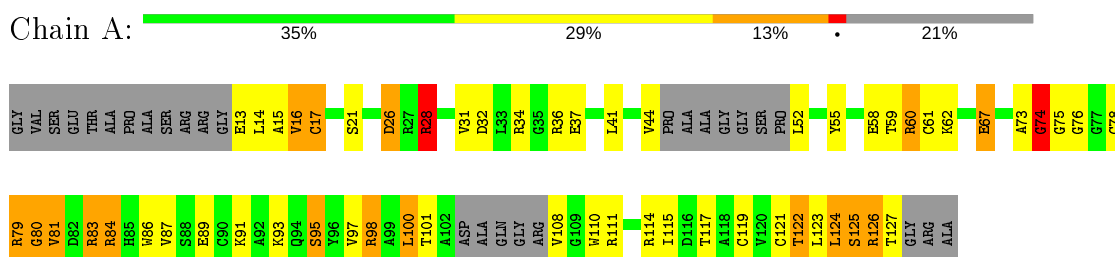
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	21	Total	O	0	0
			21	21		
3	M	28	Total	O	0	0
			28	28		

### 3 Residue-property plots [i](#)

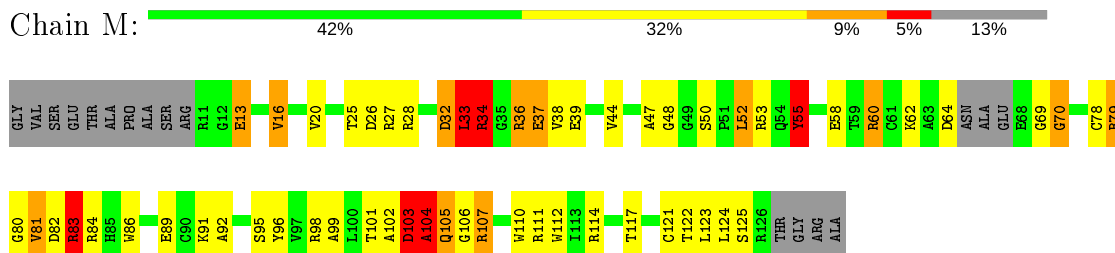
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: PROTEIN (NEUROTROPHIN-4)



- Molecule 1: PROTEIN (NEUROTROPHIN-4)



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	43.80 Å 50.80 Å 53.00 Å 90.00° 109.40° 90.00°	Depositor
Resolution (Å)	20.00 – 2.75	Depositor
% Data completeness (in resolution range)	93.0 (20.00-2.75)	Depositor
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.235 , 0.336	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	1671	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

## 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:  
CL

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	0.78	0/790	2.23	37/1066 (3.5%)
1	M	0.81	0/856	2.57	47/1155 (4.1%)
All	All	0.79	0/1646	2.41	84/2221 (3.8%)

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	2
1	M	0	5
All	All	0	7

There are no bond length outliers.

All (84) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	114	ARG	CD-NE-CZ	37.25	175.75	123.60
1	A	98	ARG	CD-NE-CZ	15.65	145.51	123.60
1	M	103	ASP	C-N-CA	15.52	160.51	121.70
1	A	60	ARG	NE-CZ-NH2	-15.29	112.65	120.30
1	M	28	ARG	NE-CZ-NH2	14.12	127.36	120.30
1	M	36	ARG	CD-NE-CZ	12.98	141.77	123.60
1	M	114	ARG	NE-CZ-NH2	-12.71	113.94	120.30
1	A	83	ARG	CD-NE-CZ	12.71	141.39	123.60
1	M	98	ARG	NE-CZ-NH1	12.61	126.60	120.30
1	A	79	ARG	NE-CZ-NH1	12.13	126.37	120.30
1	M	103	ASP	O-C-N	-12.02	103.47	122.70
1	A	60	ARG	CD-NE-CZ	11.97	140.35	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	98	ARG	CD-NE-CZ	11.25	139.35	123.60
1	A	79	ARG	CD-NE-CZ	10.45	138.24	123.60
1	M	103	ASP	CA-C-O	10.40	141.93	120.10
1	M	26	ASP	CB-CG-OD1	10.32	127.59	118.30
1	A	28	ARG	NE-CZ-NH2	-9.97	115.32	120.30
1	M	37	GLU	OE1-CD-OE2	9.72	134.97	123.30
1	M	32	ASP	CB-CG-OD1	9.72	127.05	118.30
1	A	55	TYR	CA-CB-CG	9.29	131.06	113.40
1	M	83	ARG	NE-CZ-NH1	9.26	124.93	120.30
1	M	103	ASP	CA-CB-CG	-9.13	93.32	113.40
1	A	125	SER	N-CA-CB	-8.91	97.13	110.50
1	M	103	ASP	N-CA-C	8.77	134.68	111.00
1	M	98	ARG	NH1-CZ-NH2	-8.43	110.13	119.40
1	A	83	ARG	NE-CZ-NH1	8.31	124.45	120.30
1	M	27	ARG	NE-CZ-NH2	8.28	124.44	120.30
1	A	55	TYR	CB-CG-CD1	7.89	125.73	121.00
1	M	36	ARG	CG-CD-NE	7.88	128.35	111.80
1	A	28	ARG	NE-CZ-NH1	7.68	124.14	120.30
1	A	125	SER	N-CA-C	7.64	131.64	111.00
1	A	60	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	A	79	ARG	NE-CZ-NH2	-7.62	116.49	120.30
1	M	79	ARG	NE-CZ-NH1	-7.46	116.57	120.30
1	M	33	LEU	CB-CG-CD1	7.26	123.34	111.00
1	M	114	ARG	NE-CZ-NH1	7.05	123.82	120.30
1	A	26	ASP	CB-CG-OD2	-6.88	112.10	118.30
1	A	84	ARG	CD-NE-CZ	6.85	133.19	123.60
1	M	79	ARG	CG-CD-NE	6.71	125.89	111.80
1	M	125	SER	C-N-CA	6.60	138.20	121.70
1	A	125	SER	CB-CA-C	-6.57	97.62	110.10
1	A	52	LEU	C-N-CA	6.55	138.08	121.70
1	A	67	GLU	N-CA-CB	6.53	122.36	110.60
1	A	16	VAL	N-CA-CB	-6.52	97.16	111.50
1	M	32	ASP	CB-CG-OD2	-6.51	112.44	118.30
1	M	37	GLU	O-C-N	-6.51	112.29	122.70
1	A	55	TYR	CB-CG-CD2	-6.50	117.10	121.00
1	M	36	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	M	91	LYS	CB-CA-C	-6.40	97.60	110.40
1	A	111	ARG	NE-CZ-NH1	-6.29	117.16	120.30
1	A	16	VAL	CG1-CB-CG2	6.25	120.90	110.90
1	A	80	GLY	CA-C-O	-6.19	109.46	120.60
1	M	105	GLN	N-CA-CB	6.16	121.68	110.60
1	A	100	LEU	N-CA-CB	6.13	122.66	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	79	ARG	NE-CZ-NH2	6.06	123.33	120.30
1	A	114	ARG	NE-CZ-NH1	-6.01	117.30	120.30
1	M	70	GLY	N-CA-C	5.98	128.04	113.10
1	M	82	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	A	95	SER	N-CA-CB	5.87	119.31	110.50
1	M	34	ARG	CG-CD-NE	5.83	124.05	111.80
1	M	98	ARG	NE-CZ-NH2	5.79	123.19	120.30
1	M	106	GLY	C-N-CA	5.67	135.88	121.70
1	A	32	ASP	CB-CG-OD1	5.65	123.38	118.30
1	A	74	GLY	CA-C-O	-5.63	110.47	120.60
1	M	37	GLU	CB-CA-C	5.52	121.44	110.40
1	M	104	ALA	CA-C-N	5.49	129.28	117.20
1	A	122	THR	N-CA-CB	5.41	120.58	110.30
1	A	73	ALA	C-N-CA	5.39	133.62	122.30
1	M	64	ASP	CB-CG-OD1	5.38	123.14	118.30
1	M	28	ARG	NH1-CZ-NH2	-5.37	113.50	119.40
1	M	28	ARG	CD-NE-CZ	5.34	131.08	123.60
1	M	83	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	74	GLY	CA-C-N	5.25	126.70	116.20
1	M	64	ASP	CA-CB-CG	5.23	124.90	113.40
1	M	81	VAL	N-CA-CB	5.19	122.92	111.50
1	A	62	LYS	CA-CB-CG	5.18	124.81	113.40
1	M	55	TYR	O-C-N	-5.17	114.42	122.70
1	M	104	ALA	CA-C-O	-5.14	109.31	120.10
1	A	80	GLY	CA-C-N	5.14	128.50	117.20
1	A	34	ARG	NE-CZ-NH1	-5.12	117.74	120.30
1	M	92	ALA	N-CA-CB	5.11	117.26	110.10
1	M	37	GLU	N-CA-CB	-5.03	101.54	110.60
1	M	34	ARG	CA-C-N	5.03	126.26	116.20
1	A	75	GLY	C-N-CA	5.02	132.83	122.30

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	CYS	Mainchain
1	A	21	SER	Mainchain
1	M	103	ASP	Mainchain
1	M	104	ALA	Mainchain
1	M	37	GLU	Mainchain
1	M	55	TYR	Mainchain
1	M	99	ALA	Mainchain



## 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	779	0	740	41	0
1	M	842	0	812	44	0
2	A	1	0	0	0	0
3	A	21	0	0	1	0
3	M	28	0	0	6	0
All	All	1671	0	1552	71	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 23.

All (71) 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:41:LEU:HD22	1:A:100:LEU:HD23	1.41	1.02
1:A:14:LEU:HD22	1:M:123:LEU:HB2	1.55	0.88
1:A:13:GLU:OE1	1:M:122:THR:HG21	1.90	0.71
1:A:124:LEU:HA	1:M:13:GLU:HG3	1.74	0.67
1:A:91:LYS:HB2	3:A:211:HOH:O	1.94	0.66
1:M:33:LEU:HD22	1:M:96:TYR:CD1	2.31	0.65
1:A:84:ARG:HD3	1:M:84:ARG:HH12	1.62	0.65
1:M:103:ASP:HA	3:M:154:HOH:O	2.01	0.61
1:A:110:TRP:HE1	1:M:48:GLY:CA	2.12	0.61
1:A:87:VAL:CG1	1:A:124:LEU:HD12	2.31	0.61
1:M:34:ARG:HG3	1:M:34:ARG:HH11	1.69	0.58
1:A:126:ARG:O	1:A:127:THR:C	2.41	0.57
1:M:58:GLU:OE1	1:M:60:ARG:NH2	2.38	0.56
1:A:86:TRP:HE3	1:A:125:SER:HG	1.54	0.55
1:M:44:VAL:HG11	1:M:47:ALA:HB3	1.88	0.55
1:A:98:ARG:NH1	1:M:53:ARG:O	2.40	0.54
1:M:16:VAL:HA	1:M:79:ARG:HB3	1.88	0.54
1:M:104:ALA:N	3:M:154:HOH:O	2.40	0.54
1:M:32:ASP:OD2	1:M:34:ARG:HD3	2.09	0.53
1:M:89:GLU:OE1	1:M:124:LEU:HD11	2.08	0.53
1:M:81:VAL:O	1:M:83:ARG:HD3	2.08	0.53
1:M:32:ASP:OD1	1:M:34:ARG:HG2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:THR:HG21	1:M:13:GLU:HG2	1.92	0.52
1:A:58:GLU:OE1	1:A:60:ARG:NH2	2.43	0.52
1:A:97:VAL:HG11	1:A:115:ILE:HD11	1.92	0.52
1:A:28:ARG:HH11	1:A:28:ARG:HG3	1.75	0.52
1:A:16:VAL:HG22	1:A:79:ARG:O	2.10	0.51
1:A:87:VAL:HB	1:A:125:SER:CB	2.40	0.51
1:A:87:VAL:HG12	1:A:125:SER:HB3	1.93	0.51
1:A:61:CYS:HB3	1:A:74:GLY:HA2	1.93	0.50
1:A:14:LEU:HD22	1:M:123:LEU:CB	2.36	0.49
1:A:59:THR:HB	1:A:117:THR:C	2.31	0.49
1:A:110:TRP:HE1	1:M:48:GLY:HA3	1.78	0.49
1:M:16:VAL:HG22	1:M:79:ARG:O	2.13	0.48
1:A:61:CYS:CB	1:A:74:GLY:HA2	2.44	0.48
1:A:101:THR:O	1:A:108:VAL:HA	2.13	0.48
1:A:41:LEU:HD22	1:A:100:LEU:CD2	2.29	0.48
1:M:95:SER:OG	1:M:117:THR:HG21	2.14	0.47
1:M:62:LYS:HE2	3:M:147:HOH:O	2.14	0.47
1:M:79:ARG:HD2	1:M:79:ARG:HH11	1.53	0.47
1:M:47:ALA:HB2	1:M:110:TRP:HZ2	1.79	0.47
1:M:105:GLN:HB3	3:M:151:HOH:O	2.13	0.47
1:A:67:GLU:HG2	1:A:67:GLU:O	2.14	0.47
1:A:86:TRP:CE3	1:A:123:LEU:HB3	2.50	0.46
1:A:16:VAL:CG1	1:A:121:CYS:HB2	2.46	0.46
1:A:16:VAL:HG13	1:A:78:CYS:HB3	1.98	0.45
1:A:87:VAL:HG13	1:A:124:LEU:HD12	1.98	0.45
1:M:33:LEU:HD23	1:M:112:TRP:HB3	1.98	0.45
1:M:62:LYS:HE3	3:M:152:HOH:O	2.17	0.45
1:M:38:VAL:HG11	1:M:111:ARG:HE	1.82	0.44
1:A:17:CYS:HB3	1:A:119:CYS:SG	2.57	0.44
1:A:14:LEU:HD23	1:A:15:ALA:N	2.33	0.44
1:A:84:ARG:NH1	1:M:84:ARG:HH11	2.15	0.43
1:A:28:ARG:NH1	1:A:28:ARG:HG3	2.34	0.43
1:A:76:GLY:O	1:A:89:GLU:HA	2.19	0.43
1:M:44:VAL:HB	1:M:52:LEU:HD23	2.00	0.43
1:M:25:THR:HG22	1:M:55:TYR:HB3	2.00	0.43
1:M:32:ASP:OD1	1:M:34:ARG:HD3	2.18	0.42
1:M:102:ALA:O	1:M:103:ASP:HB2	2.20	0.42
1:A:28:ARG:H	1:A:28:ARG:HG3	1.57	0.41
1:M:32:ASP:CG	1:M:34:ARG:HD3	2.41	0.41
1:A:80:GLY:HA2	1:M:86:TRP:NE1	2.36	0.41
1:M:39:GLU:O	1:M:101:THR:HB	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:ARG:NH1	1:M:84:ARG:NH1	2.68	0.41
1:M:78:CYS:CB	1:M:121:CYS:SG	3.09	0.41
1:M:107:ARG:HB2	3:M:154:HOH:O	2.20	0.41
1:A:14:LEU:CD2	1:M:123:LEU:HD12	2.51	0.41
1:M:78:CYS:SG	1:M:121:CYS:CB	3.08	0.40
1:M:34:ARG:HG3	1:M:34:ARG:NH1	2.36	0.40
1:A:31:VAL:HA	1:A:36:ARG:O	2.20	0.40
1:A:81:VAL:HB	1:M:80:GLY:O	2.20	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	97/130 (75%)	90 (93%)	5 (5%)	2 (2%)	7	12
1	M	109/130 (84%)	100 (92%)	6 (6%)	3 (3%)	5	7
All	All	206/260 (79%)	190 (92%)	11 (5%)	5 (2%)	6	9

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	GLY
1	M	104	ALA
1	M	69	GLY
1	M	70	GLY
1	A	126	ARG

### 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	77/96 (80%)	68 (88%)	9 (12%)	5	8
1	M	82/96 (85%)	70 (85%)	12 (15%)	3	4
All	All	159/192 (83%)	138 (87%)	21 (13%)	4	6

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	ASP
1	A	28	ARG
1	A	37	GLU
1	A	44	VAL
1	A	81	VAL
1	A	83	ARG
1	A	93	LYS
1	A	95	SER
1	A	124	LEU
1	M	13	GLU
1	M	16	VAL
1	M	20	VAL
1	M	33	LEU
1	M	34	ARG
1	M	36	ARG
1	M	50	SER
1	M	52	LEU
1	M	60	ARG
1	M	83	ARG
1	M	103	ASP
1	M	107	ARG

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

Mol	Chain	Res	Type
1	M	94	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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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.

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

### 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.