



# Full wwPDB X-ray Structure Validation Report

Aug 4, 2014 – 06:49 PM EDT

PDB ID : 4EDX  
Title : Nerve Growth Factor in Complex with Fab from mouse mAb 911  
Authors : Eigenbrot, C.; Ultsch, M.  
Deposited on : 2012-03-27  
Resolution : 2.50 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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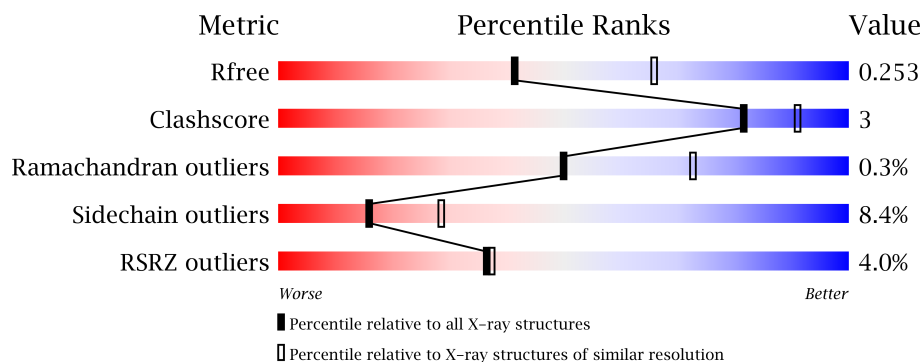
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable23489  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable23489

# 1 Overall quality at a glance

The reported resolution of this entry is 2.50 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))
$R_{free}$	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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.

Mol	Chain	Length	Quality of chain
1	V	120	
1	W	120	
2	A	214	
2	L	214	
3	B	221	
3	H	221	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8298 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 protein called Beta-nerve growth factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	W	102	Total	C	N	O	S	0	0	0
			799	502	139	150	8			
1	V	101	Total	C	N	O	S	0	0	0
			793	499	138	148	8			

- Molecule 2 is a protein called light chain of FAB of murine anti-NGF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	214	Total	C	N	O	S	0	0	0
			1669	1035	283	344	7			
2	L	214	Total	C	N	O	S	0	0	0
			1669	1035	283	344	7			

- Molecule 3 is a protein called heavy chain of Fab of murine anti-NGF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	216	Total	C	N	O	S	0	0	0
			1635	1037	265	326	7			
3	H	216	Total	C	N	O	S	3	0	0
			1635	1037	265	326	7			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	W	9	Total	O	0	0
			9	9		
4	A	14	Total	O	0	0
			14	14		
4	B	23	Total	O	0	0
			23	23		
4	V	13	Total	O	0	0
			13	13		

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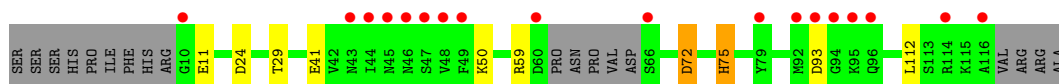
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	22	Total 22	O 22	0	0
4	H	17	Total 17	O 17	0	0

### 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.

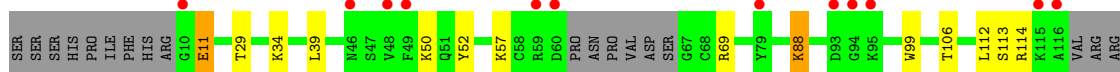
- Molecule 1: Beta-nerve growth factor

Chain W: 



- Molecule 1: Beta-nerve growth factor

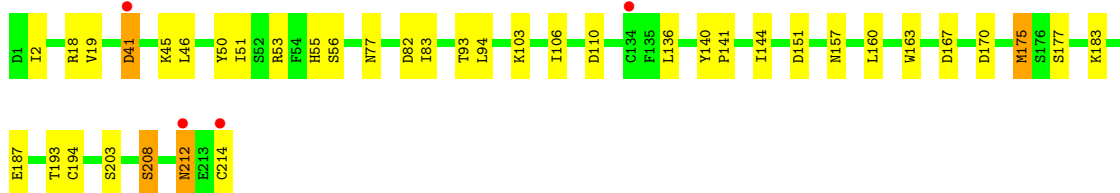
Chain V: 



ALA

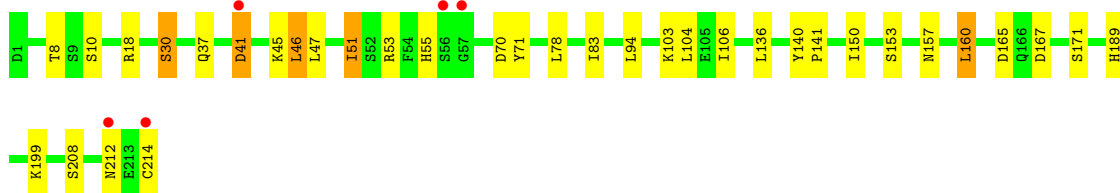
- Molecule 2: light chain of FAB of murine anti-NGF

Chain A: 



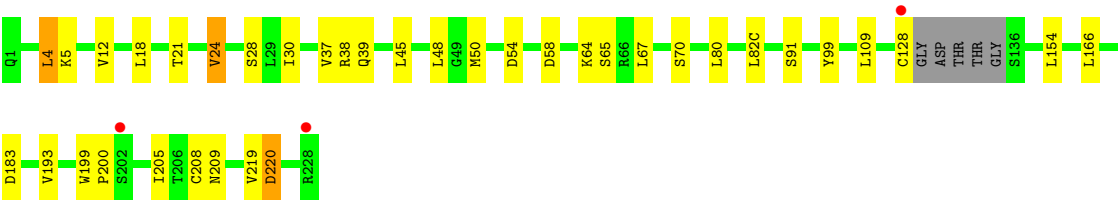
- Molecule 2: light chain of FAB of murine anti-NGF

Chain L: 



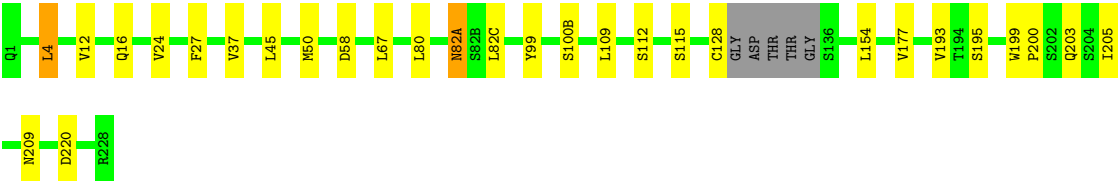
- Molecule 3: heavy chain of Fab of murine anti-NGF

Chain B: 



● Molecule 3: heavy chain of Fab of murine anti-NGF

Chain H:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.75Å 69.93Å 83.74Å 104.34° 94.13° 110.42°	Depositor
Resolution (Å)	30.49 – 2.50 29.95 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.49-2.50) 96.0 (29.95-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.16 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.208 , 0.258 0.211 , 0.253	Depositor DCC
$R_{free}$ test set	1015 reflections (2.68%)	DCC
Wilson B-factor (Å <sup>2</sup> )	44.8	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 26.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 38881 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	8298	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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	V	0.42	0/807	0.73	0/1086
1	W	0.44	0/813	0.74	2/1094 (0.2%)
2	A	0.39	0/1704	0.74	6/2311 (0.3%)
2	L	0.42	0/1704	0.74	4/2311 (0.2%)
3	B	0.42	0/1678	0.71	4/2294 (0.2%)
3	H	0.40	0/1678	0.69	2/2294 (0.1%)
All	All	0.41	0/8384	0.72	18/11390 (0.2%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	70	ASP	CB-CG-OD2	6.32	123.99	118.30
2	A	41	ASP	CB-CG-OD2	5.71	123.44	118.30
3	B	220	ASP	CB-CG-OD2	5.69	123.42	118.30
2	A	151	ASP	CB-CG-OD2	5.57	123.31	118.30
3	H	58	ASP	CB-CG-OD2	5.56	123.31	118.30
2	A	82	ASP	CB-CG-OD2	5.54	123.29	118.30
2	A	170	ASP	CB-CG-OD2	5.39	123.15	118.30
2	L	41	ASP	CB-CG-OD2	5.36	123.12	118.30
2	A	110	ASP	CB-CG-OD2	5.32	123.09	118.30
1	W	93	ASP	CB-CG-OD2	5.26	123.03	118.30
3	H	220	ASP	CB-CG-OD2	5.24	123.02	118.30
2	L	165	ASP	CB-CG-OD2	5.24	123.02	118.30
2	L	167	ASP	CB-CG-OD2	5.18	122.96	118.30
3	B	58	ASP	CB-CG-OD2	5.18	122.96	118.30
3	B	54	ASP	CB-CG-OD2	5.12	122.90	118.30
3	B	183	ASP	CB-CG-OD2	5.08	122.87	118.30
1	W	24	ASP	CB-CG-OD2	5.06	122.85	118.30
2	A	167	ASP	CB-CG-OD2	5.05	122.85	118.30

There are no chirality outliers.



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	V	793	0	773	2	0
1	W	799	0	778	2	0
2	A	1669	0	1596	14	0
2	L	1669	0	1596	11	0
3	B	1635	0	1593	15	0
3	H	1635	0	1593	13	0
4	A	14	0	0	0	0
4	B	23	0	0	0	0
4	H	17	0	0	0	0
4	L	22	0	0	0	0
4	V	13	0	0	0	0
4	W	9	0	0	0	0
All	All	8298	0	7929	52	0

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 3.

All (52) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:166:LEU:HD21	3:B:193:VAL:HG11	1.69	0.74
3:H:4:LEU:HD23	3:H:24:VAL:HG22	1.76	0.68
2:L:94:LEU:HD11	3:H:50:MET:CE	2.25	0.66
3:H:67:LEU:HD11	3:H:80:LEU:HD11	1.81	0.62
2:A:50:TYR:O	2:A:51:ILE:HG22	2.03	0.59
2:L:160:LEU:HG	3:H:177:VAL:HG11	1.85	0.57
3:B:37:VAL:CG1	3:B:45:LEU:HD22	2.35	0.57
3:B:67:LEU:HD11	3:B:80:LEU:HD11	1.90	0.54
3:B:39:GLN:HB2	3:B:45:LEU:HD23	1.90	0.53
3:B:199:TRP:CG	3:B:200:PRO:HA	2.43	0.53
2:L:30:SER:O	2:L:71:TYR:OH	2.21	0.53
3:H:24:VAL:HG13	3:H:27:PHE:CE1	2.45	0.52
1:W:72:ASP:OD2	1:W:75:HIS:ND1	2.42	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:38:ARG:HB2	3:B:48:LEU:HD11	1.90	0.52
2:L:46:LEU:HD13	2:L:55:HIS:HB2	1.92	0.52
2:A:83:ILE:HG13	2:A:106:ILE:HD12	1.92	0.51
2:L:136:LEU:N	2:L:136:LEU:HD12	2.26	0.50
3:H:37:VAL:CG1	3:H:45:LEU:HD22	2.41	0.49
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.94	0.49
2:A:144:ILE:HG22	2:A:163:TRP:CZ3	2.48	0.49
2:L:83:ILE:HG13	2:L:106:ILE:HD12	1.94	0.49
2:A:212:ASN:C	2:A:212:ASN:HD22	2.16	0.48
3:B:193:VAL:HG21	3:B:205:ILE:CD1	2.43	0.48
2:A:163:TRP:N	2:A:163:TRP:CD1	2.82	0.48
2:L:150:ILE:HG22	2:L:189:HIS:CD2	2.50	0.47
2:A:50:TYR:O	2:A:51:ILE:CG2	2.63	0.47
3:H:82(A):ASN:HD22	3:H:82(A):ASN:C	2.18	0.47
2:A:94:LEU:HD11	3:B:50:MET:CE	2.45	0.46
3:B:67:LEU:CD1	3:B:80:LEU:HD11	2.46	0.46
3:H:193:VAL:HG21	3:H:205:ILE:CD1	2.46	0.46
3:B:193:VAL:HG21	3:B:205:ILE:HD11	1.97	0.45
2:A:136:LEU:HD12	2:A:136:LEU:N	2.30	0.45
3:B:12:VAL:HG12	3:B:109:LEU:HD11	1.97	0.45
2:L:78:LEU:HD11	2:L:104:LEU:HD21	1.98	0.45
2:A:193:THR:HG1	2:A:208:SER:HG	1.63	0.44
3:H:12:VAL:HG12	3:H:109:LEU:HD11	2.00	0.44
1:V:11:GLU:HB3	2:L:53:ARG:HD3	2.00	0.44
2:A:140:TYR:CG	2:A:141:PRO:HA	2.53	0.43
3:H:195:SER:O	3:H:199:TRP:O	2.37	0.43
3:B:208:CYS:O	3:B:220:ASP:HA	2.20	0.42
2:A:2:ILE:HD12	2:A:93:THR:HG22	2.01	0.42
3:B:28:SER:OG	3:B:30:ILE:HG22	2.20	0.42
2:L:140:TYR:CG	2:L:141:PRO:HA	2.55	0.42
1:W:11:GLU:HB3	2:A:53:ARG:HD3	2.01	0.42
3:H:199:TRP:CG	3:H:200:PRO:HA	2.55	0.42
1:V:88:LYS:HG2	1:V:99:TRP:CD1	2.55	0.42
2:A:175:MET:HE2	2:A:177:SER:HB2	2.02	0.41
3:H:67:LEU:CD1	3:H:80:LEU:HD11	2.48	0.41
2:A:55:HIS:ND1	2:A:56:SER:N	2.68	0.41
3:B:199:TRP:HB2	3:B:205:ILE:HD12	2.02	0.41
3:B:4:LEU:HD23	3:B:24:VAL:HG22	2.02	0.41
3:H:4:LEU:CD2	3:H:24:VAL:HG22	2.48	0.41

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	V	97/120 (81%)	92 (95%)	5 (5%)	0	100	100
1	W	98/120 (82%)	93 (95%)	5 (5%)	0	100	100
2	A	212/214 (99%)	205 (97%)	7 (3%)	0	100	100
2	L	212/214 (99%)	205 (97%)	6 (3%)	1 (0%)	38	60
3	B	212/221 (96%)	206 (97%)	5 (2%)	1 (0%)	38	60
3	H	212/221 (96%)	207 (98%)	4 (2%)	1 (0%)	38	60
All	All	1043/1110 (94%)	1008 (97%)	32 (3%)	3 (0%)	50	73

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	99	TYR
3	H	99	TYR
2	L	51	ILE

### 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	V	88/106 (83%)	75 (85%)	13 (15%)	4	8
1	W	89/106 (84%)	82 (92%)	7 (8%)	18	31
2	A	193/193 (100%)	176 (91%)	17 (9%)	14	26
2	L	193/193 (100%)	176 (91%)	17 (9%)	14	26
3	B	189/192 (98%)	175 (93%)	14 (7%)	20	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	H	189/192 (98%)	178 (94%)	11 (6%)	28	49
All	All	941/982 (96%)	862 (92%)	79 (8%)	16	28

All (79) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	W	29	THR
1	W	41	GLU
1	W	50	LYS
1	W	59	ARG
1	W	72	ASP
1	W	75	HIS
1	W	112	LEU
2	A	18	ARG
2	A	19	VAL
2	A	41	ASP
2	A	45	LYS
2	A	46	LEU
2	A	77	ASN
2	A	103	LYS
2	A	157	ASN
2	A	160	LEU
2	A	175	MET
2	A	183	LYS
2	A	187	GLU
2	A	194	CYS
2	A	203	SER
2	A	208	SER
2	A	212	ASN
2	A	214	CYS
3	B	4	LEU
3	B	5	LYS
3	B	18	LEU
3	B	21	THR
3	B	24	VAL
3	B	64	LYS
3	B	65	SER
3	B	70	SER
3	B	82(C)	LEU
3	B	91	SER
3	B	128	CYS
3	B	154	LEU

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Mol	Chain	Res	Type
3	B	209	ASN
3	B	219	VAL
1	V	11	GLU
1	V	29	THR
1	V	34	LYS
1	V	39	LEU
1	V	50	LYS
1	V	52	TYR
1	V	57	LYS
1	V	69	ARG
1	V	88	LYS
1	V	106	THR
1	V	112	LEU
1	V	113	SER
1	V	114	ARG
2	L	8	THR
2	L	10	SER
2	L	18	ARG
2	L	30	SER
2	L	41	ASP
2	L	45	LYS
2	L	46	LEU
2	L	51	ILE
2	L	103	LYS
2	L	153	SER
2	L	157	ASN
2	L	160	LEU
2	L	171	SER
2	L	199	LYS
2	L	208	SER
2	L	212	ASN
2	L	214	CYS
3	H	4	LEU
3	H	16	GLN
3	H	82(A)	ASN
3	H	82(C)	LEU
3	H	100(B)	SER
3	H	112	SER
3	H	115	SER
3	H	128	CYS
3	H	154	LEU
3	H	203	GLN

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Mol	Chain	Res	Type
3	H	209	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	W	45	ASN
2	A	27	GLN
2	A	77	ASN
2	A	212	ASN
1	V	45	ASN
2	L	137	ASN
2	L	212	ASN
3	H	82(A)	ASN
3	H	203	GLN

### 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 ⓘ

There are no ligands in this entry.

## 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 ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å²)	Q<0.9	
1	V	101/120 (84%)	0.42	12 (11%)	5	5	29, 56, 112, 130	1 (0%)
1	W	102/120 (85%)	0.59	18 (17%)	2	2	29, 55, 109, 133	0
2	A	214/214 (100%)	-0.03	4 (1%)	64	66	23, 49, 84, 121	0
2	L	214/214 (100%)	-0.12	5 (2%)	57	60	25, 43, 73, 112	1 (0%)
3	B	216/221 (97%)	-0.09	3 (1%)	72	74	25, 45, 86, 114	1 (0%)
3	H	216/221 (97%)	-0.09	0	100	100	27, 50, 86, 112	1 (0%)
All	All	1063/1110 (95%)	0.03	42 (3%)	36	37	23, 48, 90, 133	4 (0%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	214	CYS	9.4
1	V	116	ALA	6.8
2	A	214	CYS	5.8
1	W	116	ALA	5.4
1	W	44	ILE	5.2
3	B	128	CYS	4.9
1	W	46	ASN	4.8
1	V	48	VAL	4.6
1	W	48	VAL	4.4
1	V	46	ASN	4.3
1	W	93	ASP	4.2
1	W	45	ASN	4.1
1	W	47	SER	3.5
3	B	202	SER	3.2
3	B	228	ARG	3.2
1	V	94	GLY	3.1
2	A	212	ASN	3.1
2	A	41	ASP	3.0
1	W	49	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	W	43	ASN	2.8
2	L	57	GLY	2.8
1	W	95	LYS	2.8
1	W	10	GLY	2.7
1	W	66	SER	2.7
2	L	212	ASN	2.6
1	W	60	ASP	2.5
1	V	93	ASP	2.5
1	W	114	ARG	2.5
1	V	49	PHE	2.5
1	V	79	TYR	2.5
1	V	60	ASP	2.5
2	L	41	ASP	2.4
1	V	115	LYS	2.4
1	V	95	LYS	2.3
2	L	56	SER	2.2
2	A	134	CYS	2.2
1	V	59	ARG	2.2
1	W	94	GLY	2.1
1	W	79	TYR	2.1
1	W	96	GLN	2.1
1	W	92	MET	2.0
1	V	10	GLY	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.