



# Full wwPDB X-ray Structure Validation Report i

Jul 25, 2024 – 01:10 pm BST

PDB ID : 9G13  
Title : VHH H3-2 in complex with Tau C-terminal peptide  
Authors : Dupre, E.; Landrieu, I.; Danis, C.; Hanoulle, X.; Mortelecque, J.  
Deposited on : 2024-07-09  
Resolution : 1.80 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 i symbol.

The types of validation reports are described at  
<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.37.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

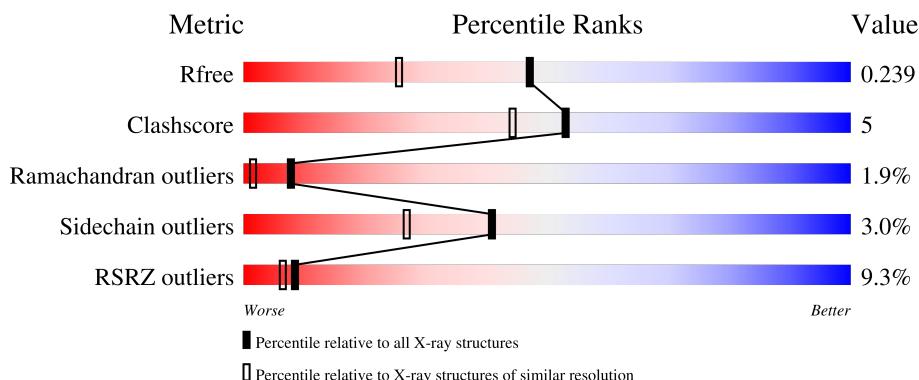
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## X-RAY DIFFRACTION

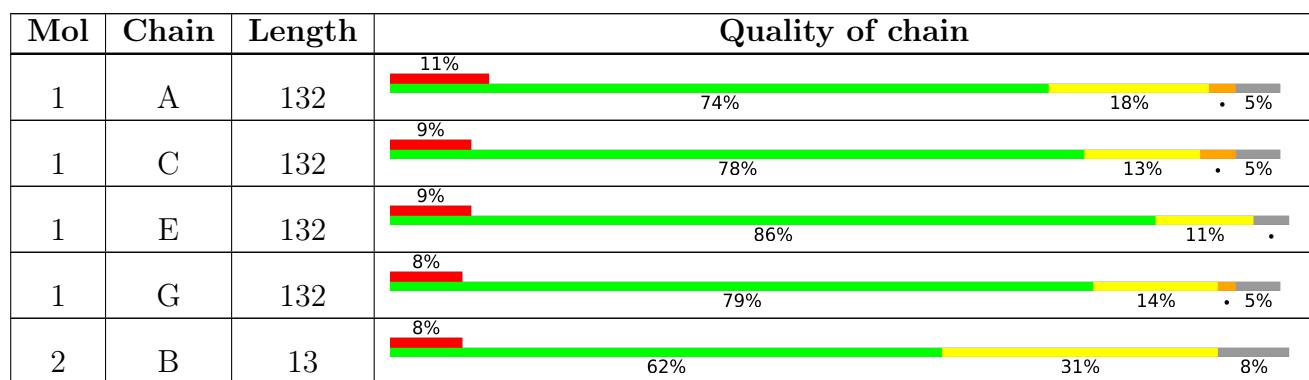
The reported resolution of this entry is 1.80 Å.

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.



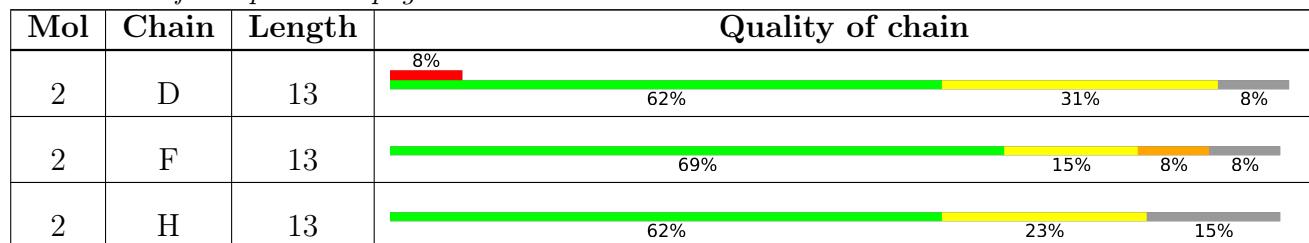
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.



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## 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8787 atoms, of which 4072 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 VHH H3-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	126	Total	C	H	N	O	S	40	0	0
			1840	594	893	162	186	5			
1	E	127	Total	C	H	N	O	S	38	0	0
			1885	609	914	163	194	5			
1	C	125	Total	C	H	N	O	S	39	2	0
			1868	602	908	165	188	5			
1	G	126	Total	C	H	N	O	S	40	0	0
			1844	596	896	162	185	5			

- Molecule 2 is a protein called Isoform Tau-F of Microtubule-associated protein tau.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	12	Total	C	H	N	O	4	0	0
			226	69	119	20	18			
2	F	12	Total	C	H	N	O	4	0	0
			226	69	119	20	18			
2	D	12	Total	C	H	N	O	4	0	0
			226	69	119	20	18			
2	H	11	Total	C	H	N	O	4	0	0
			202	63	104	18	17			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	107	Total	O	0	0
			107	107		
3	B	17	Total	O	0	0
			17	17		
3	E	103	Total	O	0	0
			103	103		
3	F	19	Total	O	0	0
			19	19		

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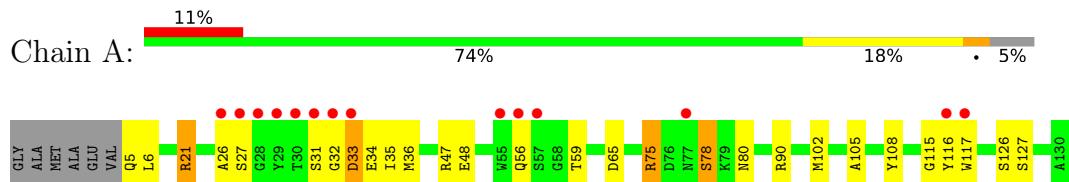
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	105	Total O 105 105	0	0
3	D	16	Total O 16 16	0	0
3	G	86	Total O 86 86	0	0
3	H	17	Total O 17 17	0	0

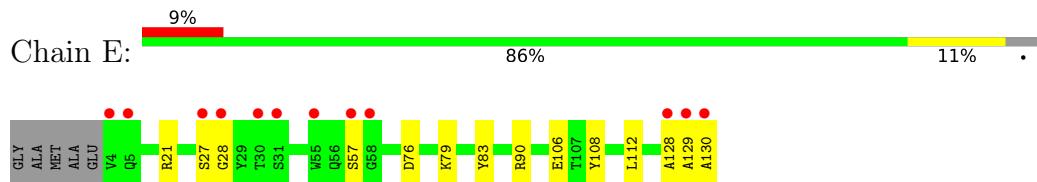
### 3 Residue-property plots

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 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.

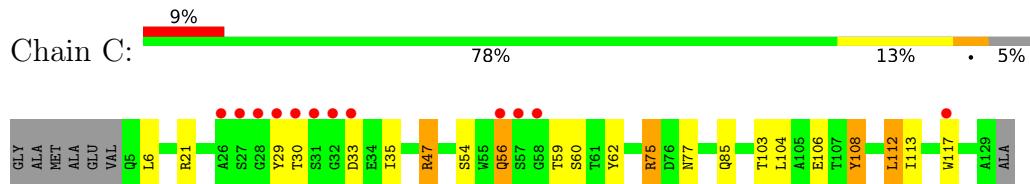
- Molecule 1: VHH H3-2



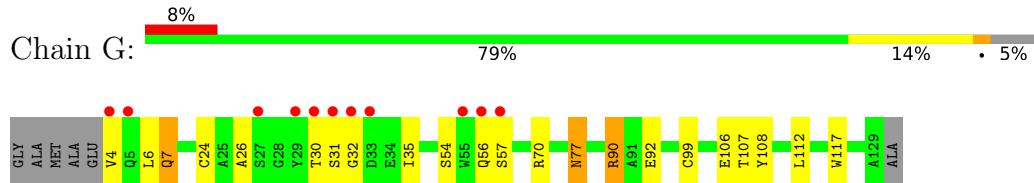
- Molecule 1: VHH H3-2



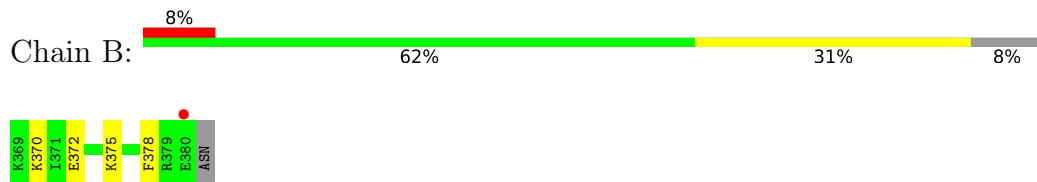
- Molecule 1: VHH H3-2



- Molecule 1: VHH H3-2



- Molecule 2: Isoform Tau-F of Microtubule-associated protein tau



- Molecule 2: Isoform Tau-F of Microtubule-associated protein tau



- Molecule 2: Isoform Tau-F of Microtubule-associated protein tau



- Molecule 2: Isoform Tau-F of Microtubule-associated protein tau



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.39 Å   76.35 Å   95.56 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	45.55 – 1.80 45.51 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.55-1.80) 100.0 (45.51-1.80)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) >$ <sup>1</sup>	1.95 (at 1.79 Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
$R$ , $R_{free}$	0.172 , 0.231 0.182 , 0.239	Depositor DCC
$R_{free}$ test set	2348 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.4	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 48.7	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.49$ , $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8787	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $< |L| >$ ,  $< L^2 >$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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	0.84	1/969 (0.1%)	1.38	7/1315 (0.5%)
1	C	0.79	0/988	1.30	5/1340 (0.4%)
1	E	0.80	1/994 (0.1%)	1.32	8/1349 (0.6%)
1	G	0.78	0/970	1.23	3/1317 (0.2%)
2	B	0.70	0/108	1.53	1/141 (0.7%)
2	D	0.62	0/108	1.38	2/141 (1.4%)
2	F	0.78	0/108	1.29	1/141 (0.7%)
2	H	0.89	0/99	1.58	0/130
All	All	0.80	2/4344 (0.0%)	1.32	27/5874 (0.5%)

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	3
1	C	0	1
1	E	0	2
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	127	SER	CA-CB	-5.82	1.44	1.52
1	E	106	GLU	CG-CD	5.63	1.60	1.51

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	21	ARG	NE-CZ-NH1	17.22	128.91	120.30
1	E	106	GLU	OE1-CD-OE2	-12.23	108.62	123.30
1	A	21	ARG	NE-CZ-NH2	-11.77	114.41	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	47	ARG	NE-CZ-NH1	7.98	124.29	120.30
1	G	112	LEU	CB-CG-CD2	-7.64	98.00	111.00
1	G	70	ARG	NE-CZ-NH1	-7.22	116.69	120.30
1	E	130	ALA	CA-C-O	-6.86	105.70	120.10
1	A	90	ARG	NE-CZ-NH2	-6.85	116.87	120.30
1	C	104	LEU	CB-CG-CD1	6.83	122.61	111.00
1	E	21	ARG	NE-CZ-NH1	6.82	123.71	120.30
1	E	90	ARG	NE-CZ-NH1	-6.77	116.91	120.30
2	D	376	LEU	N-CA-CB	-6.50	97.40	110.40
1	E	90	ARG	NE-CZ-NH2	6.38	123.49	120.30
1	A	59	THR	CA-CB-OG1	-6.31	95.76	109.00
2	F	379	ARG	NE-CZ-NH1	6.29	123.44	120.30
1	G	90	ARG	NE-CZ-NH2	-6.28	117.16	120.30
1	C	47	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	A	56	GLN	N-CA-CB	-6.11	99.61	110.60
1	C	108	TYR	N-CA-CB	5.38	120.29	110.60
1	E	21	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	E	83	TYR	CB-CG-CD2	-5.21	117.87	121.00
2	B	372	GLU	CG-CD-OE1	5.19	128.68	118.30
1	A	108	TYR	CB-CG-CD2	5.13	124.08	121.00
1	A	36	MET	CG-SD-CE	5.11	108.37	100.20
1	E	112	LEU	CB-CG-CD2	-5.08	102.36	111.00
1	C	62	TYR	O-C-N	5.08	130.83	122.70
2	D	376	LEU	CB-CG-CD2	-5.02	102.46	111.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	21	ARG	Sidechain
1	A	47	ARG	Sidechain
1	A	75	ARG	Sidechain
1	C	75	ARG	Sidechain
1	E	128	ALA	Peptide
1	E	57	SER	Peptide

## 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 MolProbit. 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	947	893	881	12	1
1	C	960	908	901	11	0
1	E	971	914	911	3	0
1	G	948	896	882	12	1
2	B	107	119	115	3	0
2	D	107	119	115	3	0
2	F	107	119	115	3	0
2	H	98	104	102	1	0
3	A	107	0	0	8	0
3	B	17	0	0	0	1
3	C	105	0	0	1	0
3	D	16	0	0	1	0
3	E	103	0	0	1	0
3	F	19	0	0	3	0
3	G	86	0	0	1	0
3	H	17	0	0	1	1
All	All	4715	4072	4022	44	2

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 5.

All (44) 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:G:35:ILE:HG12	1:G:54:SER:HB3	1.41	0.99
1:E:79:LYS:O	3:E:201:HOH:O	2.04	0.75
2:F:370:LYS:HD3	3:F:417:HOH:O	1.86	0.74
1:A:6:LEU:HD23	1:A:26:ALA:HA	1.74	0.70
1:A:48:GLU:OE2	3:A:201:HOH:O	2.09	0.69
1:A:48:GLU:OE2	3:A:202:HOH:O	2.11	0.68
1:A:65:ASP:CG	3:A:232:HOH:O	2.32	0.67
1:A:78:SER:HB3	3:A:204:HOH:O	1.94	0.66
1:A:5:GLN:HA	1:A:5:GLN:OE1	1.94	0.65
1:A:78:SER:CB	3:A:204:HOH:O	2.48	0.62
3:A:270:HOH:O	1:C:103:THR:HG23	2.02	0.59
1:C:21[A]:ARG:HH11	1:C:85:GLN:HE21	1.54	0.56
1:G:56:GLN:O	1:G:57:SER:OG	2.21	0.55
1:C:35:ILE:HG12	1:C:54:SER:HB3	1.88	0.55
2:D:369:LYS:HB3	3:D:414:HOH:O	2.06	0.55
1:C:117:TRP:CZ3	2:D:378:PHE:CE2	2.95	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ASP:O	1:A:35:ILE:N	2.38	0.54
2:F:369:LYS:N	3:F:401:HOH:O	2.41	0.53
1:C:6:LEU:HB3	3:C:277:HOH:O	2.08	0.52
2:F:370:LYS:NZ	3:F:402:HOH:O	2.44	0.51
1:A:105:ALA:HB2	1:C:112:LEU:HD22	1.94	0.50
1:A:75:ARG:NH2	1:A:80:ASN:OD1	2.44	0.50
3:A:236:HOH:O	2:B:370:LYS:HG2	2.12	0.49
1:G:4:VAL:HG13	3:G:286:HOH:O	2.12	0.49
1:G:24:CYS:CB	1:G:99:CYS:SG	3.01	0.48
1:G:106:GLU:HG2	1:G:108:TYR:CE1	2.47	0.48
1:G:77:ASN:OD1	1:G:77:ASN:N	2.47	0.47
2:B:378:PHE:CZ	1:C:47:ARG:HD2	2.50	0.47
1:G:106:GLU:HG3	1:G:107:THR:N	2.31	0.46
1:E:76:ASP:OD2	1:E:79:LYS:HG3	2.15	0.46
1:E:27:SER:OG	1:E:28:GLY:N	2.49	0.46
1:G:106:GLU:HG2	1:G:108:TYR:CZ	2.51	0.46
1:G:30:THR:O	1:G:32:GLY:N	2.48	0.46
1:C:54:SER:O	1:C:59:THR:HA	2.16	0.45
1:G:90:ARG:HG3	1:G:92:GLU:HG2	1.97	0.45
1:C:75:ARG:HH22	1:C:77:ASN:ND2	2.15	0.44
1:G:6:LEU:HD23	1:G:26:ALA:HA	2.00	0.43
2:D:379:ARG:HD3	2:D:379:ARG:HA	1.81	0.43
1:A:102:MET:HG2	1:C:113:ILE:HG12	1.99	0.42
1:G:7:GLN:HE21	1:G:7:GLN:HA	1.83	0.42
2:H:375:LYS:HE3	3:H:414:HOH:O	2.19	0.42
1:A:115:GLY:O	1:A:117:TRP:CD1	2.72	0.41
1:C:106:GLU:HG2	1:C:108:TYR:CE1	2.55	0.41
3:A:236:HOH:O	2:B:370:LYS:CG	2.69	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	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:TYR:HH	1:G:117:TRP:H[1_455]	1.23	0.37
3:B:408:HOH:O	3:H:411:HOH:O[3_544]	1.92	0.28

## 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	124/132 (94%)	113 (91%)	7 (6%)	4 (3%)	4 0
1	C	125/132 (95%)	117 (94%)	4 (3%)	4 (3%)	4 0
1	E	125/132 (95%)	119 (95%)	5 (4%)	1 (1%)	19 7
1	G	124/132 (94%)	118 (95%)	5 (4%)	1 (1%)	19 7
2	B	10/13 (77%)	10 (100%)	0	0	100 100
2	D	10/13 (77%)	8 (80%)	2 (20%)	0	100 100
2	F	10/13 (77%)	10 (100%)	0	0	100 100
2	H	9/13 (69%)	9 (100%)	0	0	100 100
All	All	537/580 (93%)	504 (94%)	23 (4%)	10 (2%)	8 1

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	31	SER
1	A	32	GLY
1	A	33	ASP
1	C	29	TYR
1	A	31	SER
1	C	30	THR
1	C	33	ASP
1	A	34	GLU
1	E	129	ALA
1	C	56	GLN

### 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	94/102 (92%)	91 (97%)	3 (3%)	39 25
1	C	97/102 (95%)	94 (97%)	3 (3%)	40 25
1	E	100/102 (98%)	99 (99%)	1 (1%)	76 71
1	G	94/102 (92%)	92 (98%)	2 (2%)	53 42
2	B	12/13 (92%)	11 (92%)	1 (8%)	11 3
2	D	12/13 (92%)	12 (100%)	0	100 100
2	F	12/13 (92%)	11 (92%)	1 (8%)	11 3
2	H	11/13 (85%)	9 (82%)	2 (18%)	1 0
All	All	432/460 (94%)	419 (97%)	13 (3%)	41 27

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	SER
1	A	78	SER
1	A	126	SER
2	B	375	LYS
1	E	108	TYR
2	F	369	LYS
1	C	56	GLN
1	C	60	SER
1	C	112	LEU
1	G	7	GLN
1	G	77	ASN
2	H	370	LYS
2	H	380	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	41	GLN
1	C	77	ASN
1	C	85	GLN
1	G	7	GLN
1	G	15	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 [\(i\)](#)

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 i

### 6.1 Protein, DNA and RNA chains i

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(Å <sup>2</sup> )	Q<0.9
1	A	126/132 (95%)	0.24	14 (11%) 5   4	19, 30, 87, 126	0
1	C	125/132 (94%)	0.30	12 (9%) 8   6	21, 30, 93, 121	0
1	E	127/132 (96%)	0.18	12 (9%) 8   6	21, 32, 81, 94	0
1	G	126/132 (95%)	0.34	11 (8%) 10   8	20, 33, 86, 145	0
2	B	12/13 (92%)	0.28	1 (8%) 11   8	26, 37, 83, 97	0
2	D	12/13 (92%)	0.57	1 (8%) 11   8	26, 43, 89, 105	0
2	F	12/13 (92%)	0.15	0 100   100	24, 36, 63, 69	0
2	H	11/13 (84%)	0.15	0 100   100	23, 32, 73, 77	0
All	All	551/580 (95%)	0.27	51 (9%) 8   6	19, 32, 89, 145	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	32	GLY	8.9
1	A	117	TRP	7.9
1	G	31	SER	7.8
1	C	27	SER	6.1
1	A	33	ASP	5.9
1	C	57	SER	5.9
1	E	31	SER	5.3
1	A	32	GLY	5.2
1	G	57	SER	4.8
1	A	30	THR	4.5
1	C	30	THR	4.5
1	G	30	THR	4.5
1	C	33	ASP	4.5
1	C	56	GLN	4.2
1	C	31	SER	4.2
1	E	5	GLN	4.0

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Mol	Chain	Res	Type	RSRZ
1	G	4	VAL	4.0
1	E	130	ALA	3.9
1	E	129	ALA	3.9
1	A	31	SER	3.9
1	E	30	THR	3.9
1	A	29	TYR	3.9
1	C	29	TYR	3.7
1	G	5	GLN	3.6
1	G	33	ASP	3.5
1	G	29	TYR	3.5
1	E	4	VAL	3.5
1	A	56	GLN	3.4
1	A	28	GLY	3.3
1	E	128	ALA	3.3
1	E	57	SER	3.2
1	G	55	TRP	3.1
1	E	28	GLY	3.1
1	A	116	TYR	2.8
1	A	27	SER	2.8
1	C	117	TRP	2.8
1	G	56	GLN	2.7
1	C	28	GLY	2.7
1	G	27	SER	2.7
1	E	55	TRP	2.6
1	E	27	SER	2.6
1	E	58	GLY	2.6
1	A	57	SER	2.6
1	A	26	ALA	2.4
1	C	32	GLY	2.3
1	C	58	GLY	2.3
2	B	380	GLU	2.3
1	C	26	ALA	2.2
1	A	55	TRP	2.2
2	D	380	GLU	2.1
1	A	77	ASN	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

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

### 6.3 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [\(i\)](#)

There are no ligands in this entry.

### 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.