



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:33 PM GMT

PDB ID : 1PH4  
Title : CRYSTAL STRUCTURE OF THE OXYTRICHA NOVA TELOMERE  
END-BINDING PROTEIN COMPLEXED WITH NONCOGNATE SSDNA  
GGGGTTTTGGCG  
Authors : Theobald, D.L.; Schultz, S.C.  
Deposited on : 2003-05-29  
Resolution : 2.30 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

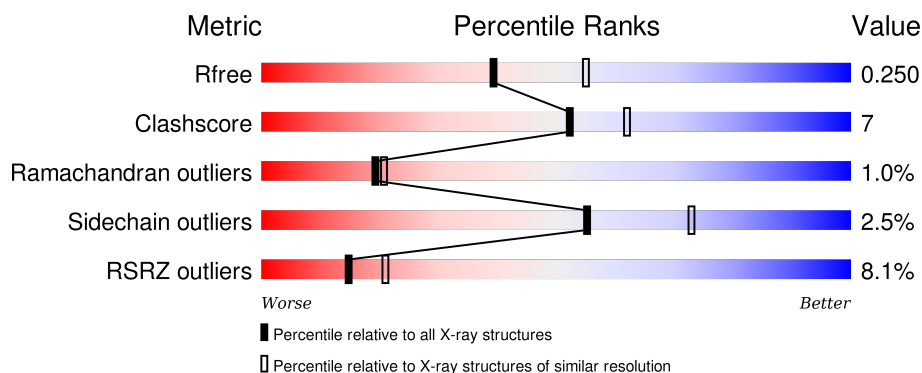
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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. 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.

Mol	Chain	Length	Quality of chain
1	G	13	<div> <div>8%</div> <div> <div></div> <div>62%</div> <div>31%</div> <div>8%</div> </div> </div>
1	H	13	<div> <div>8%</div> <div> <div></div> <div>62%</div> <div>31%</div> <div>8%</div> </div> </div>
2	D	12	<div> <div>8%</div> <div> <div></div> <div>58%</div> <div>42%</div> </div> </div>
3	A	460	<div> <div>7%</div> <div> <div></div> <div>86%</div> <div>13%</div> <div>•</div> </div> </div>
4	B	216	<div> <div>12%</div> <div> <div></div> <div>77%</div> <div>22%</div> <div>•</div> </div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6703 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 DNA chain called 5'-D(\*GP\*GP\*GP\*GP\*TP\*TP\*TP\*TP\*GP\*GP\*GP\*GP\*T)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	12	Total	C	N	O	P	0	0	0
			253	120	48	74	11			
1	H	12	Total	C	N	O	P	0	0	0
			253	120	48	74	11			

- Molecule 2 is a DNA chain called 5'-D(\*GP\*GP\*GP\*GP\*TP\*TP\*TP\*TP\*GP\*GP\*CP\*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	12	Total	C	N	O	P	0	0	0
			250	119	46	74	11			

- Molecule 3 is a protein called Telomere-binding protein alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	460	Total	C	N	O	S	0	0	0
			3706	2355	637	712	2			

- Molecule 4 is a protein called Telomere-binding protein beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	216	Total	C	N	O	S	0	0	0
			1733	1112	294	326	1			

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	3	Total	Na	0	0
			3	3		
5	G	1	Total	Na	0	0
			1	1		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	327	Total O 327 327	0	0
7	B	73	Total O 73 73	0	0
7	D	34	Total O 34 34	0	0
7	G	32	Total O 32 32	0	0
7	H	37	Total O 37 37	0	0

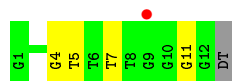
### 3 Residue-property plots [i](#)

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.

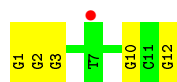
- Molecule 1: 5'-D(\*GP\*GP\*GP\*GP\*TP\*TP\*TP\*TP\*GP\*GP\*GP\*GP\*T)-3'



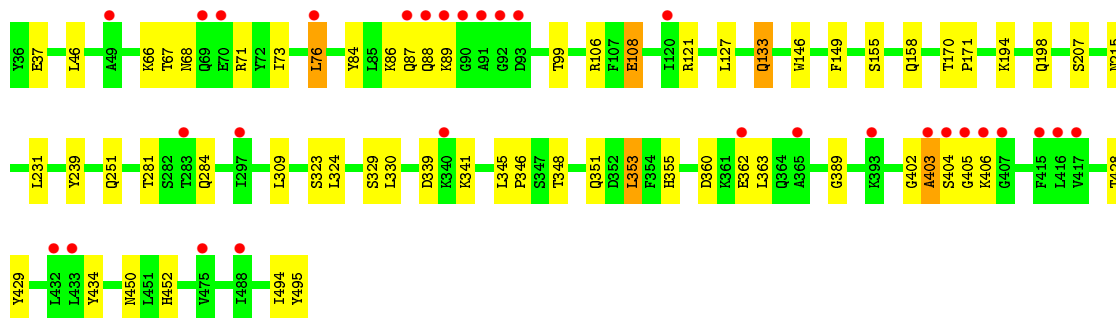
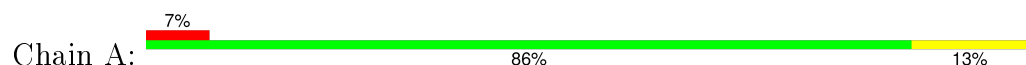
- Molecule 1: 5'-D(\*GP\*GP\*GP\*GP\*TP\*TP\*TP\*TP\*GP\*GP\*GP\*GP\*T)-3'



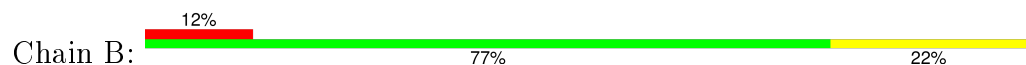
- Molecule 2: 5'-D(\*GP\*GP\*GP\*GP\*TP\*TP\*TP\*TP\*GP\*GP\*CP\*G)-3'

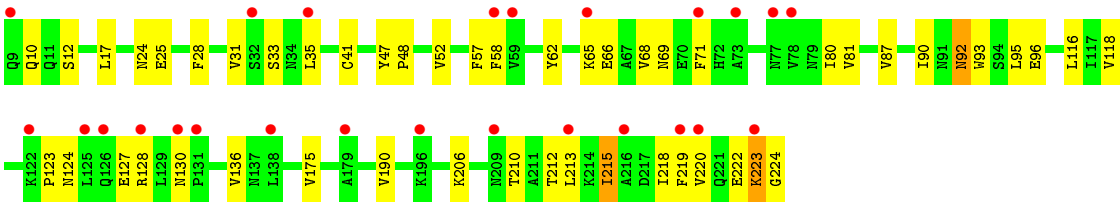


- Molecule 3: Telomere-binding protein alpha subunit



- Molecule 4: Telomere-binding protein beta subunit





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.45Å 93.45Å 422.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.12 – 2.30 28.12 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.7 (28.12-2.30) 99.6 (28.12-2.25)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.97 (at 2.26Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.214 , 0.251 0.213 , 0.250	Depositor DCC
$R_{free}$ test set	4949 reflections (9.94%)	DCC
Wilson B-factor (Å <sup>2</sup> )	38.3	Xtriage
Anisotropy	0.280	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 47.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 52811 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6703	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% 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  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 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: NA, 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	G	0.35	0/284	0.61	0/440
1	H	0.37	0/284	0.64	0/440
2	D	0.42	0/280	0.75	0/433
3	A	0.38	0/3777	0.63	0/5104
4	B	0.35	0/1771	0.50	0/2391
All	All	0.37	0/6396	0.60	0/8808

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	G	253	0	138	3	0
1	H	253	0	138	3	0
2	D	250	0	138	5	0
3	A	3706	0	3699	34	0
4	B	1733	0	1718	39	1
5	G	1	0	0	0	0
5	H	3	0	0	0	0
6	A	1	0	0	0	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	327	0	0	3	0
7	B	73	0	0	0	0
7	D	34	0	0	0	0
7	G	32	0	0	0	0
7	H	37	0	0	0	0
All	All	6703	0	5831	80	1

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 7.

All (80) 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)
4:B:10:GLN:HE21	4:B:12:SER:H	1.09	0.91
4:B:80:ILE:HD12	4:B:218:ILE:HD11	1.54	0.89
3:A:99:THR:HG23	3:A:133:GLN:HE22	1.37	0.86
3:A:345:LEU:HD12	3:A:346:PRO:HD2	1.66	0.76
4:B:28:PHE:O	4:B:31:VAL:HG12	1.92	0.68
3:A:99:THR:HG23	3:A:133:GLN:NE2	2.08	0.67
4:B:81:VAL:HG11	4:B:219:PHE:HD1	1.61	0.65
4:B:90:ILE:HG23	4:B:118:VAL:HG13	1.79	0.64
4:B:17:LEU:HD21	4:B:35:LEU:HB3	1.81	0.62
3:A:108:GLU:CD	3:A:108:GLU:H	2.02	0.61
4:B:10:GLN:NE2	4:B:12:SER:H	1.91	0.60
3:A:281:THR:HB	4:B:10:GLN:HE22	1.67	0.59
3:A:284:GLN:HG3	3:A:330:LEU:HD12	1.84	0.59
3:A:194:LYS:O	3:A:198:GLN:HG3	2.02	0.59
4:B:219:PHE:CE1	4:B:223:LYS:HD2	2.38	0.58
4:B:96:GLU:OE2	4:B:210:THR:HG22	2.03	0.58
3:A:339:ASP:OD1	3:A:341:LYS:HG2	2.04	0.57
4:B:71:PHE:HE1	4:B:123:PRO:HD3	1.69	0.57
3:A:155:SER:H	3:A:158:GLN:NE2	2.03	0.56
4:B:71:PHE:CE1	4:B:123:PRO:HD3	2.40	0.56
3:A:99:THR:CG2	3:A:133:GLN:HE22	2.16	0.56
4:B:65:LYS:HA	4:B:213:LEU:HD11	1.87	0.56
3:A:215:ASN:HA	3:A:251:GLN:HG3	1.89	0.55
4:B:81:VAL:HG11	4:B:219:PHE:CD1	2.41	0.55
3:A:76:LEU:N	3:A:76:LEU:HD23	2.22	0.55
4:B:10:GLN:HE21	4:B:12:SER:N	1.91	0.54
3:A:323:SER:HB2	3:A:329:SER:OG	2.08	0.53
1:H:4:DG:H1'	1:H:5:DT:H5'	1.89	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:215:ILE:O	4:B:218:ILE:HG22	2.08	0.53
4:B:48:PRO:O	4:B:215:ILE:HG21	2.09	0.53
4:B:81:VAL:O	4:B:81:VAL:HG12	2.09	0.53
4:B:92:ASN:C	4:B:92:ASN:HD22	2.13	0.52
4:B:81:VAL:HG23	4:B:222:GLU:OE1	2.09	0.52
3:A:46:LEU:HD23	3:A:127:LEU:HG	1.91	0.52
2:D:12:DG:H2'	2:D:12:DG:N3	2.26	0.51
3:A:389:GLY:HA3	3:A:406:LYS:HB2	1.92	0.51
3:A:106:ARG:HB3	3:A:108:GLU:OE2	2.11	0.51
4:B:87:VAL:HG11	4:B:127:GLU:HB3	1.94	0.50
3:A:402:GLY:O	3:A:403:ALA:HB3	2.12	0.49
3:A:324:LEU:HD23	7:A:1208:HOH:O	2.13	0.49
3:A:67:THR:HG21	3:A:73:ILE:HD12	1.94	0.49
4:B:57:PHE:CD2	4:B:136:VAL:HG23	2.49	0.48
3:A:76:LEU:HA	7:A:1232:HOH:O	2.14	0.48
4:B:206:LYS:O	4:B:206:LYS:HG3	2.14	0.48
4:B:62:TYR:HB3	4:B:212:THR:OG1	2.15	0.47
4:B:17:LEU:CD2	4:B:35:LEU:HB3	2.44	0.47
3:A:155:SER:H	3:A:158:GLN:HE21	1.61	0.47
3:A:450:ASN:OD1	3:A:452:HIS:HB2	2.15	0.47
3:A:434:TYR:CD2	4:B:175:VAL:HG21	2.50	0.46
4:B:92:ASN:HD22	4:B:93:TRP:N	2.12	0.46
2:D:1:DG:H3'	2:D:2:DG:H5''	1.96	0.46
4:B:95:LEU:HD23	4:B:116:LEU:HA	1.98	0.46
3:A:86:LYS:O	3:A:88:GLN:N	2.50	0.45
4:B:220:VAL:HG13	4:B:224:GLY:HA2	1.99	0.44
4:B:47:TYR:HB2	4:B:81:VAL:HG13	2.00	0.44
1:G:4:DG:H1'	1:G:5:DT:H5'	2.00	0.44
4:B:52:VAL:O	4:B:58:PHE:HA	2.18	0.44
2:D:1:DG:H3'	2:D:2:DG:C5'	2.48	0.43
3:A:429:TYR:CD1	3:A:429:TYR:N	2.86	0.43
3:A:348:THR:CG2	3:A:353:LEU:HD13	2.49	0.43
3:A:428:THR:CG2	4:B:190:VAL:HB	2.48	0.43
3:A:121:ARG:O	3:A:146:TRP:HA	2.19	0.43
3:A:66:LYS:HE2	3:A:68:ASN:O	2.19	0.43
4:B:219:PHE:O	4:B:223:LYS:HG2	2.19	0.42
4:B:68:VAL:HG23	4:B:69:ASN:N	2.34	0.42
4:B:24:ASN:C	4:B:25:GLU:HG2	2.40	0.42
2:D:3:DG:H2'	2:D:3:DG:N3	2.35	0.42
4:B:128:ARG:HA	4:B:128:ARG:HD2	1.75	0.42
3:A:351:GLN:O	3:A:355:HIS:HB2	2.21	0.41

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:10:DG:H2'	2:D:10:DG:N3	2.35	0.41
4:B:87:VAL:HG13	4:B:124:ASN:HB2	2.03	0.41
3:A:170:THR:HA	3:A:171:PRO:HD3	1.96	0.41
1:G:7:DT:H73	7:A:1146:HOH:O	2.20	0.41
3:A:149:PHE:CZ	3:A:171:PRO:HG3	2.56	0.41
1:G:1:DG:C2	1:H:7:DT:H1'	2.55	0.41
1:H:11:DG:H5'	1:H:11:DG:N3	2.36	0.41
4:B:81:VAL:HG21	4:B:219:PHE:HA	2.02	0.41
3:A:494:ILE:HG13	3:A:495:TYR:CD1	2.56	0.40
4:B:33:SER:C	4:B:35:LEU:H	2.25	0.40
3:A:360:ASP:OD2	3:A:363:LEU:HG	2.21	0.40

All (1) 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)
4:B:130:ASN:ND2	4:B:130:ASN:ND2[12_555]	2.17	0.03

## 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	
3	A	458/460 (100%)	437 (95%)	15 (3%)	6 (1%)	15	15
4	B	214/216 (99%)	201 (94%)	12 (6%)	1 (0%)	34	41
All	All	672/676 (99%)	638 (95%)	27 (4%)	7 (1%)	19	21

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	87	GLN
3	A	404	SER

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type
3	A	89	LYS
3	A	403	ALA
4	B	223	LYS
3	A	84	TYR
3	A	405	GLY

### 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	
3	A	408/408 (100%)	397 (97%)	11 (3%)	52	70
4	B	189/189 (100%)	185 (98%)	4 (2%)	61	78
All	All	597/597 (100%)	582 (98%)	15 (2%)	55	73

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	37	GLU
3	A	71	ARG
3	A	76	LEU
3	A	108	GLU
3	A	133	GLN
3	A	207	SER
3	A	231	LEU
3	A	239	TYR
3	A	309	LEU
3	A	353	LEU
3	A	362	GLU
4	B	41	CYS
4	B	66	GLU
4	B	92	ASN
4	B	215	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	87	GLN
3	A	158	GLN
3	A	327	ASN
3	A	372	GLN
3	A	426	ASN
4	B	10	GLN
4	B	79	ASN
4	B	92	ASN
4	B	149	GLN
4	B	221	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 are 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 ⓘ

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(Å <sup>2</sup> )	Q<0.9
1	G	12/13 (92%)	0.44	1 (8%) 14 20	45, 52, 60, 63	0
1	H	12/13 (92%)	0.79	1 (8%) 14 20	52, 55, 61, 65	0
2	D	12/12 (100%)	-0.32	1 (8%) 14 20	28, 37, 58, 71	0
3	A	460/460 (100%)	0.23	30 (6%) 22 30	22, 34, 61, 92	0
4	B	216/216 (100%)	0.63	25 (11%) 6 10	27, 55, 83, 92	0
All	All	712/714 (99%)	0.36	58 (8%) 15 21	22, 40, 78, 92	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	88	GLN	10.8
3	A	405	GLY	10.1
3	A	403	ALA	9.4
3	A	91	ALA	8.1
3	A	404	SER	8.1
3	A	92	GLY	7.8
3	A	90	GLY	7.6
4	B	126	GLN	6.7
3	A	89	LYS	6.6
3	A	69	GLN	5.5
3	A	406	LYS	5.2
4	B	77	ASN	5.1
4	B	131	PRO	4.8
3	A	93	ASP	4.4
4	B	130	ASN	4.4
4	B	9	GLN	4.3
4	B	216	ALA	4.0
3	A	70	GLU	3.9
4	B	219	PHE	3.9
4	B	196	LYS	3.8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
3	A	87	GLN	3.8
4	B	65	LYS	3.7
3	A	415	PHE	3.3
3	A	407	GLY	3.3
4	B	73	ALA	3.3
4	B	125	LEU	3.3
4	B	209	ASN	3.1
3	A	297	ILE	3.1
4	B	59	VAL	3.0
3	A	488	ILE	3.0
4	B	35	LEU	2.9
3	A	49	ALA	2.9
4	B	122	LYS	2.8
4	B	128	ARG	2.7
4	B	223	LYS	2.7
2	D	7	DT	2.7
4	B	179	ALA	2.6
3	A	76	LEU	2.6
4	B	78	VAL	2.5
4	B	138	LEU	2.5
3	A	362	GLU	2.5
3	A	393	LYS	2.4
1	G	11	DG	2.4
3	A	283	THR	2.4
3	A	433	LEU	2.4
4	B	213	LEU	2.4
3	A	475	VAL	2.3
3	A	417	VAL	2.3
3	A	432	LEU	2.2
3	A	340	LYS	2.2
4	B	32	SER	2.2
4	B	58	PHE	2.2
3	A	120	ILE	2.1
4	B	71	PHE	2.1
3	A	365	ALA	2.1
1	H	9	DG	2.1
4	B	220	VAL	2.0
3	A	416	LEU	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 [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
6	CL	A	1005	1/1	0.97	0.10	-0.55	56,56,56,56	0
5	NA	H	1004	1/1	0.93	0.13	-1.89	61,61,61,61	0
5	NA	G	1001	1/1	0.96	0.06	-1.97	48,48,48,48	0
5	NA	H	1002	1/1	0.97	0.05	-2.66	47,47,47,47	0
5	NA	H	1003	1/1	0.96	0.07	-2.91	56,56,56,56	0

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

There are no such residues in this entry.